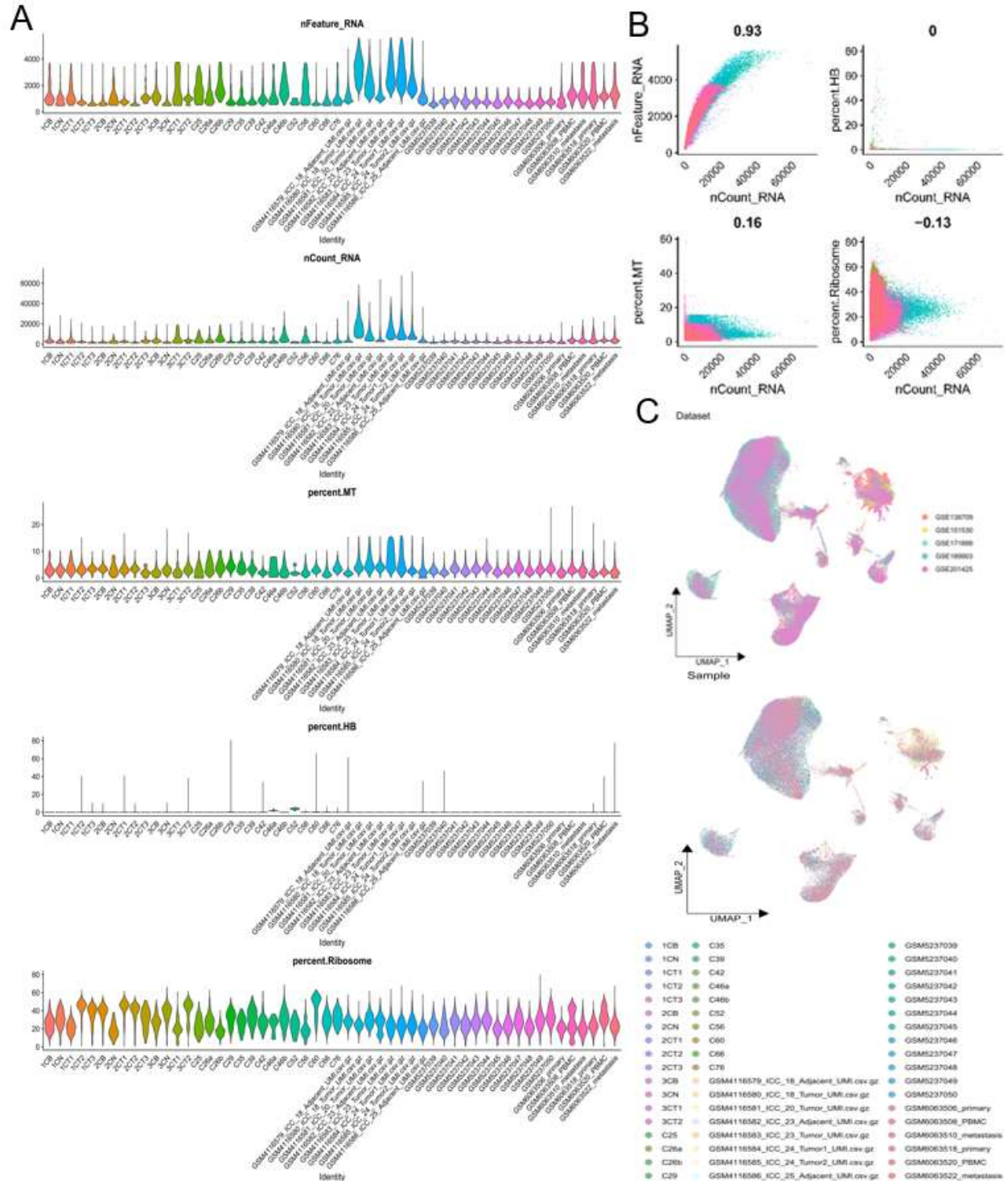
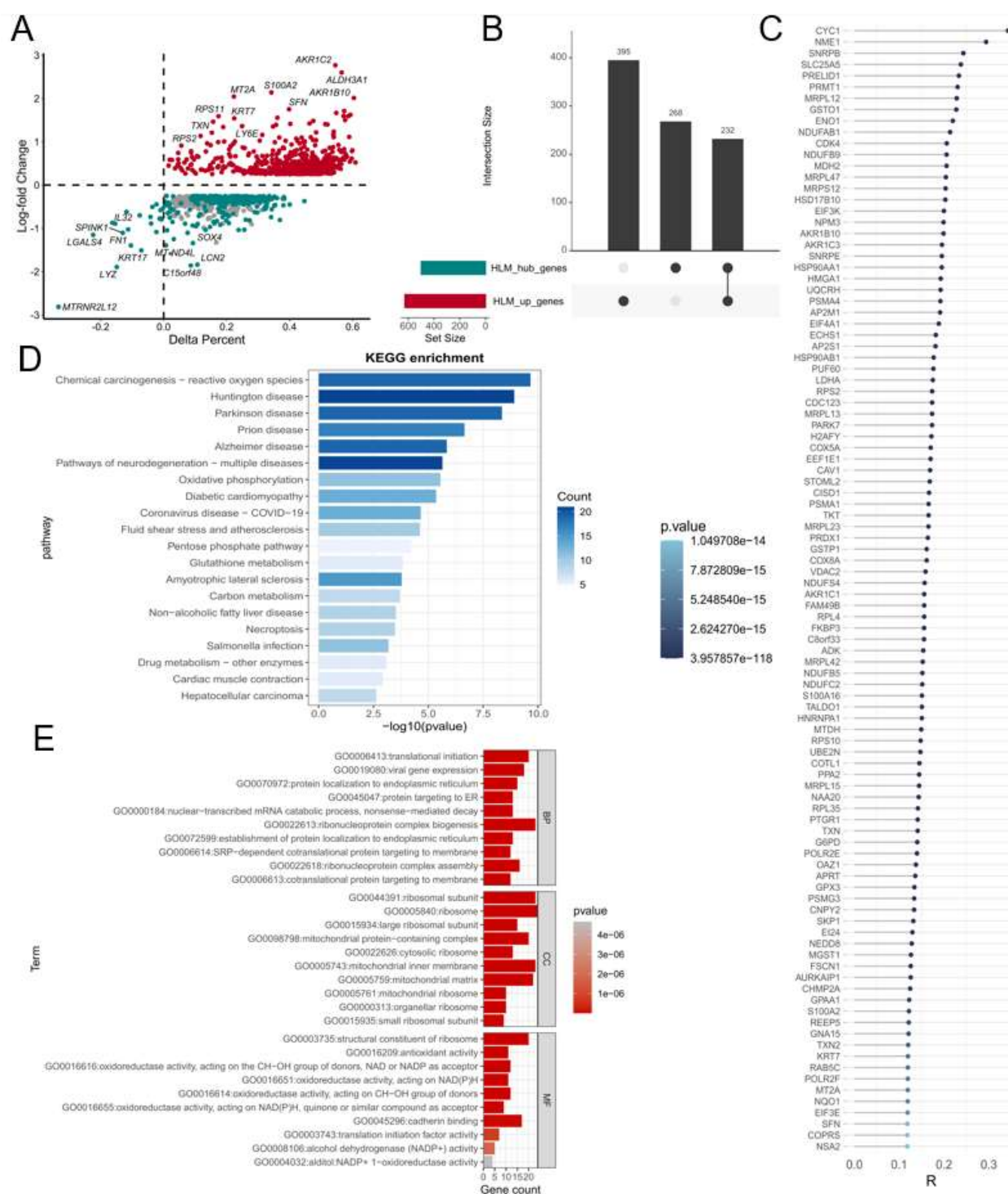


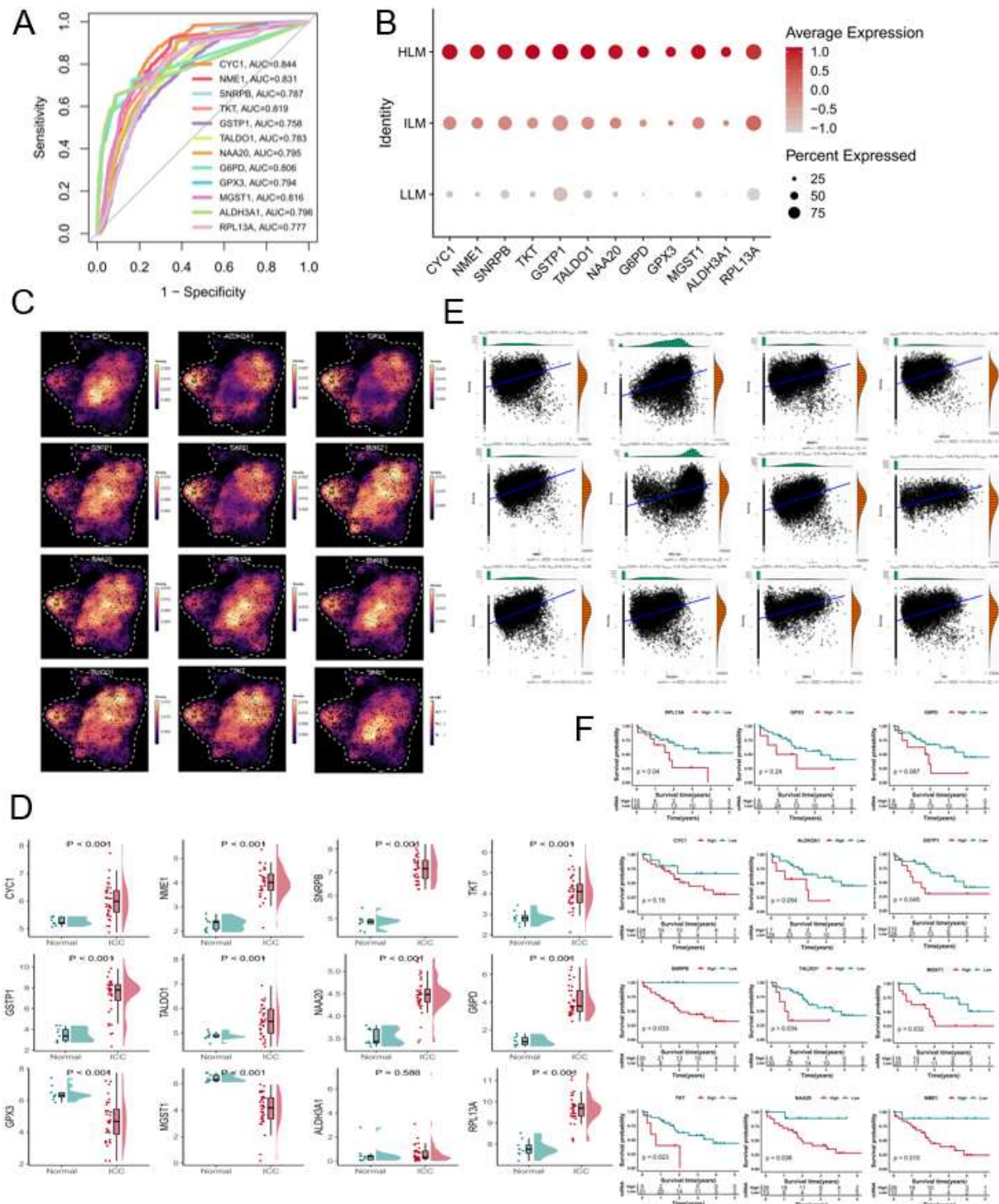


Supplementary Figure 1 Quality control and dataset integration of ICC single-cell data. A: Violin plots showing distributions of key quality control metrics across all samples; B: Correlation analysis among QC parameters; C: UMAP visualization of the integrated dataset after batch correction.



Supplementary Figure 2 Functional characterization of HLM signature genes. A: Volcano plot showing DEGs in in HLM malignant cells; **B:** UpSet plot identifying 232 intersecting genes between DEGs and hdWGCNA hub genes; **C:** Correlation analysis of

LM-associated genes; top 100 genes ranked by Pearson R; D: KEGG pathway enrichment analysis; E: GO enrichment analysis of biological processes, cellular components, and molecular functions for LM-associated genes.



Supplementary Figure 3 Expression and prognostic validation of LM-related feature genes. A: ROC curves showing predictive performance of feature genes; B: Dot-plot of average expression in ICC malignant cells; C: The distribution density of feature genes;

D: Expression analysis of feature genes in ICC vs. normal tissues; E: Correlation between LM activity scores and gene expression; F: Kaplan-Meier survival analysis of feature genes in the TCGA cohort.

Supplementary Table 1 The detailed information of all enrolled datasets

Accession number	Disease type	Number of Samples	Survival information	Data Type	Dataset URL
TCGA-CHOL	Cholangiocarcinoma	36 ICC and normal samples	Yes (n = 936)	Bulk-RNA	https://portal.gdc.cancer.gov/
GSE138709	Intrahepatic Cholangiocarcinoma	5 ICC and 3 normal samples	No	scRNA	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE138709
GSE151530	Intrahepatic Cholangiocarcinoma	14 ICC samples	No	scRNA	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE151530
GSE171899	Intrahepatic Cholangiocarcinoma	6 ICC and 6 normal samples	No	scRNA	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE171899
GSE189903	Intrahepatic Cholangiocarcinoma	11 ICC and 3 normal samples	No	scRNA	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE189903
GSE201425	Intrahepatic Cholangiocarcinoma	6 ICC samples	No	scRNA	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE201425

Supplementary Table 2 A total of 262 lactate metabolism-related genes

Gene name
EMB

SLC16A1
SLC16A3
SLC16A7
SLC16A8
SLC5A12
SLC5A8
LDHA
LDHAL6A
LDHAL6B
LDHB
LDHC
LDHD
C12orf65
COG8
DNM1L
HPDL
HSD17B10
MT-CO1
MT-CO2
MT-CO3
MT-ND1
MT-ND4
MT-ND5
MT-ND6
MT-TF
MT-TH
MT-TL1
MT-TQ

MT-TS2
MT-TW
NDUFAF3
NDUFB8
NDUFS2
SCO2
SUCLG1
SURF1
ACAD9
ACADM
B3GALNT2
B4GAT1
CALR
CD46
CFH
CFI
CHEK2
COL4A1
CRPPA
DAG1
FKRP
FKTN
FLI1
GAA
GATA1
HBB
HELLPAR
INPP5K

IRAK1

JAK2

KCNN4

LARGE1

LYST

MPL

MVK

MYC

PIEZO1

PLA2G6

PLEC

PNPLA2

POMGNT1

POMGNT2

POMK

POMT1

POMT2

RB1

RHAG

RPS14

RXYLT1

SIL1

SLC25A13

SLC4A1

SLC7A7

SPP1

STAT4

TET2

TP53
USB1
VPS13A
AIFM1
COA8
COQ8A
COX10
COX14
COX15
COX20
COX4I1
COX6B1
COX8A
DARS2
ECHS1
FOXRED1
GFM1
GFM2
HTRA2
LIPT1
LONP1
LRPPRC
MDH2
MECP2
MPV17
MRPS34
MT-ATP6
MT-ND2

MT-ND3
MT-TK
MT-TN
MT-TV
MTFMT
NARS2
NAXE
NDUFA1
NDUFA10
NDUFA11
NDUFA12
NDUFA13
NDUFA2
NDUFA4
NDUFA6
NDUFA9
NDUFAF1
NDUFAF2
NDUFAF4
NDUFAF5
NDUFAF6
NDUFAF8
NDUFB10
NDUFB11
NDUFB3
NDUFB9
NDUFS1
NDUFS3

NDUFS4
NDUFS6
NDUFS7
NDUFS8
NDUFV1
NDUFV2
NUBPL
PDHA1
PDHX
PET100
PET117
PNPT1
RARS2
RMND1
SDHA
SLC13A3
SLC19A3
SLC25A19
SLC39A8
TACO1
TIMMDC1
TMEM126B
TRAPPC12
TRMT10C
TXN2
AARS2
ACAT1
ACAT2

ADAMTS13

AGK

ATAD3A

ATPAF2

BCS1L

C1QBP

CA5A

CARS2

CHCHD10

CLPB

COQ2

COQ4

COQ9

COX5A

COX6A2

CYC1

DGUOK

DLD

DNAJC19

EARS2

FARS2

FASTKD2

FBXL4

FDX2

GOT2

GTPBP3

GYS2

HIBCH

HMGCL
HS6ST2
ISCA1
ISCU
LIAS
LIPT2
LYRM7
MICOS13
MIEP
MPC1
MRPL12
MRPL3
MRPL44
MRPS14
MRPS16
MRPS22
MRPS28
MT-TI
MT-TL2
MT-TP
MTO1
NGLY1
OCRL
OGDH
PC
PDP1
PDSS1
PDSS2

PMPCB
PNPLA8
PNPO
POLG
POLG2
PUS1
PYGL
RARS1
RNASEH1
RRM2B
SCO1
SERAC1
SFXN4
SLC25A10
SLC25A26
SLC25A3
SLC25A4
SLC25A42
SOD1
SYNJ1
TANGO2
TARS2
TIMM22
TIMM50
TK2
TMEM70
TRMT5
TRMU

TSFM
TUFM
TWNK
UQCC3
UQCRB
UQCRC2
UQCRQ
WARS2
YARS2

Supplementary Table 3 Oligonucleotides used in research

Oligonucleotides	Nucleotide sequence (5'-3')
siRNA	
Scramble control	GCUUCGCGCCGUAGUCUUA
Si-CYC1-1	CCCATCTACACAGATGTCTTA
Si-CYC1-2	GCACAAGTGGTCAGTCCTGAA
Primer	
GAPDH	GACAGTCAGCCGCATCTTCT (forward)
	GCGCCCAATACGACCAAATC (reverse)
CYC1	GAGGTGGAGGTTCAAGACGG (forward)
	TAGCTCGCACGATGTAGCTG (reverse)

Supplementary Table 4 A total of 500 hub genes from hdWGCNA

Gene name	module	kME
GSTP1	brown	0.523743152
SLC25A5	brown	0.525431966
RHOD	brown	0.526385318
HEBP2	brown	0.530241707

MCL1	brown	0.530559371
TSPO	brown	0.530678382
LMNA	brown	0.531820409
GTF3C5	brown	0.531844162
PIM3	brown	0.532626942
HSBP1	brown	0.533310273
SERPINB1	brown	0.535197162
COTL1	brown	0.535714803
PTGR1	brown	0.537326521
AP2S1	brown	0.53829078
S100A16	brown	0.538654301
PSMG3	brown	0.540957755
CAPN2	brown	0.542496082
APRT	brown	0.542697312
NCOA7	brown	0.545189207
KRT16	brown	0.546617266
UBE2H	brown	0.54668486
CSTA	brown	0.54856522
SERPINB5	brown	0.54947781
FHL2	brown	0.552452956
CLEC2B	brown	0.552540322
GNA15	brown	0.553713149
DHRS9	brown	0.554231652
NAMPT	brown	0.554367815
CTSD	brown	0.555811374
TPM4	brown	0.557615778
MALL	brown	0.558283693
AKR1C3	brown	0.558787117

ASPH	brown	0.559628646
RND3	brown	0.559812821
SQSTM1	brown	0.561092221
CSNK1A1	brown	0.561687726
TINAGL1	brown	0.565544982
SRCAP	brown	0.566728881
NAA20	brown	0.56720564
EGR1	brown	0.56788992
GLUL	brown	0.569946794
FOSL1	brown	0.570833782
TRIB1	brown	0.574462925
ARPC1B	brown	0.579979244
ATF3	brown	0.580232324
DUSP5	brown	0.58109943
CES1	brown	0.586573204
AKR1C1	brown	0.586968483
CAV1	brown	0.587455406
CLDN4	brown	0.588058131
MUC4	brown	0.589457698
AGR3	brown	0.591565898
FXYP3	brown	0.593238132
ST3GAL4	brown	0.593779937
UGDH	brown	0.594337483
AP2M1	brown	0.595391668
ANXA2	brown	0.597240605
FABP5	brown	0.599283478
PGD	brown	0.599684784
TSPAN1	brown	0.600023607

ZBTB43	brown	0.601225646
HMGA1	brown	0.603982588
ADIRF	brown	0.606421504
OAZ1	brown	0.607800123
PHLDA2	brown	0.608012567
PSCA	brown	0.60896467
FSCN1	brown	0.611248281
GADD45A	brown	0.611267681
NQO1	brown	0.615754348
TXNRD1	brown	0.6184227
HBEGF	brown	0.619655305
PLAUR	brown	0.621984676
TKT	brown	0.628897826
TALDO1	brown	0.632911869
EREG	brown	0.633328867
S100A9	brown	0.633684538
KLF4	brown	0.633814035
PLK3	brown	0.636692948
MGST1	brown	0.640769435
MT2A	brown	0.640874163
S100P	brown	0.642447829
RPS11	brown	0.648201146
TXN	brown	0.663324571
KRT19	brown	0.663802134
ANXA1	brown	0.664039927
LY6E	brown	0.665249498
AKR1B10	brown	0.667737487
SYT8	brown	0.676673799

S100A2	brown	0.678640975
KRT7	brown	0.682810199
SNCG	brown	0.687196527
EFHD2	brown	0.695427651
TACSTD2	brown	0.713306553
ALDH3A1	brown	0.718466546
GPX3	brown	0.71919254
G6PD	brown	0.719542938
FAM83A	brown	0.732043287
EMP1	brown	0.733175871
AKR1C2	brown	0.752829026
SFN	brown	0.772021571
DBI	black	0.279190124
POLR3K	black	0.282326619
TIMM17A	black	0.286907344
SUMO3	black	0.289613962
CALM1	black	0.289703633
MMADHC	black	0.292516744
NDUFB2	black	0.295660938
CLNS1A	black	0.296585669
RAB25	black	0.296806249
FBXO2	black	0.29820774
NUDCD2	black	0.298281936
CACYBP	black	0.299124106
PRSS21	black	0.305288141
FAM162A	black	0.305407483
S100A6	black	0.306441892
YWHAZ	black	0.307259946

CDK2AP2	black	0.309586123
WDR34	black	0.309893488
FIBP	black	0.311297761
SDF2L1	black	0.315558338
PITHD1	black	0.317888708
DNAJC15	black	0.321374403
AP3S1	black	0.322113655
BIK	black	0.322298895
MALSU1	black	0.326360724
PFDN2	black	0.32931918
RALA	black	0.330217265
IFI27	black	0.330322923
C7orf50	black	0.332069047
MAD2L2	black	0.332637403
GTF3A	black	0.332816275
HERPUD1	black	0.332943143
METTL9	black	0.333051232
PHF5A	black	0.333881081
RPL22	black	0.342758819
PDCD6	black	0.343009649
SRI	black	0.346010884
SMS	black	0.347667522
MT1X	black	0.350145355
TAGLN2	black	0.353531881
RAC1	black	0.35550737
SLC25A39	black	0.35681291
SERP1	black	0.358647542
CCNI	black	0.359562781

ADIPOR1	black	0.362135651
TMEM219	black	0.367140724
TOMM20	black	0.367436293
ACP1	black	0.369180952
RNF7	black	0.372225809
COX14	black	0.372574174
ARF1	black	0.375489032
AGTRAP	black	0.376777094
RPS19BP1	black	0.381218159
COX5B	black	0.385174575
NDUFB10	black	0.38538827
SSR3	black	0.388027593
B2M	black	0.38841954
UPP1	black	0.392382068
EIF4EBP1	black	0.394305496
HPCAL1	black	0.397742195
HTATIP2	black	0.398573837
SDHB	black	0.403742095
ARF5	black	0.405890159
GPX4	black	0.407772599
POLR2E	black	0.411345781
NDUFB5	black	0.41309649
SMDT1	black	0.423171811
PDCD5	black	0.430303641
GPX2	black	0.433866331
VDAC2	black	0.439178498
ATP6V1F	black	0.440621264
RPL11	black	0.453950812

NMB	black	0.456279653
RHEB	black	0.463246356
NDUFA6	black	0.463751749
LGALS3	black	0.474394249
CIB1	black	0.474649781
UQCRH	black	0.47959079
CHCHD2	black	0.480569489
MDH2	black	0.482400701
MRPS12	black	0.483854749
TOMM7	black	0.48454284
COX8A	black	0.484810449
LDHA	black	0.48776518
NDUFAB1	black	0.488711304
SOD1	black	0.491127921
EIF3K	black	0.497657012
PSMD8	black	0.510525765
FTH1	black	0.515591003
COX5A	black	0.516135136
GUK1	black	0.519122049
PRELID1	black	0.526539105
PRDX1	black	0.536029671
BLVRB	black	0.539549274
FTL	black	0.545901331
AURKAIP1	black	0.546874509
PARK7	black	0.559002106
GAPDH	black	0.568675545
ENO1	black	0.612678226
ALDOA	black	0.632790633

PNRC2	green	0.271226193
DAZAP2	green	0.271762041
EIF4EBP3	green	0.272609651
OSTC	green	0.273448809
GRB7	green	0.274552736
URM1	green	0.275088598
MTRNR2L12	green	0.275126782
PSMB1	green	0.276283028
MT1G	green	0.277728608
SLC50A1	green	0.277957841
UFM1	green	0.280152987
LGALS7B	green	0.280218389
FABP3	green	0.280430072
AKR1A1	green	0.280577136
SAP18	green	0.281959702
ANXA3	green	0.287398218
NPDC1	green	0.287966167
RPS7	green	0.288439735
SH3YL1	green	0.288568363
PSMB3	green	0.288633814
DPM2	green	0.288963933
DCXR	green	0.289663977
FAM3B	green	0.290425196
LCN2	green	0.291892075
PRDX3	green	0.292092949
FAM96A	green	0.292516587
PSMB8	green	0.293094773
IFT172	green	0.294551251

ESD	green	0.295379711
COQ4	green	0.295456109
COMMD6	green	0.295710817
TM4SF5	green	0.296257882
NDUFA5	green	0.29724384
C12orf75	green	0.297382529
BRK1	green	0.29791909
TIMM50	green	0.298331487
SUMO2	green	0.299627847
VAPA	green	0.299834176
PYCR1	green	0.300450598
NGRN	green	0.301168673
ANAPC16	green	0.30263175
MTCH1	green	0.304156312
RNF181	green	0.30544583
PPDPF	green	0.305664004
SWI5	green	0.305730349
PSMC4	green	0.306335024
GABARAPL2	green	0.306561009
FXVD5	green	0.307078428
SSU72	green	0.308202165
SPINT2	green	0.308909964
FOLR1	green	0.309561341
MIA2	green	0.309999668
LGALS2	green	0.311749274
RPL41	green	0.313123764
MIF	green	0.313196839
ASS1	green	0.31407118

POP4	green	0.31725736
RPS13	green	0.317414722
ALKBH7	green	0.317818489
RPL29	green	0.318537654
ANXA4	green	0.319512332
ACTG1	green	0.320304285
RNASET2	green	0.320397686
PLD3	green	0.322030923
MRPL18	green	0.322526226
MYL12B	green	0.32343174
RPL30	green	0.323852348
SSR2	green	0.324644857
ANAPC11	green	0.32502304
MGST3	green	0.327571684
GSTM3	green	0.329272651
SPCS1	green	0.33110987
TMEM141	green	0.336516692
TSPAN8	green	0.34007147
NME2	green	0.341001719
MIEN1	green	0.346356368
CNBP	green	0.347448635
RPL19	green	0.349958883
GPI	green	0.350359558
TSPAN3	green	0.353251115
PDZK1IP1	green	0.355706398
CLDN7	green	0.367191237
CYSTM1	green	0.367924787
SRP9	green	0.368079477

C1orf43	green	0.369230831
PSMD3	green	0.374217583
ATP6V0C	green	0.376050573
PRR13	green	0.379674245
TPI1	green	0.388221282
CISD3	green	0.388551837
FKBP4	green	0.389075092
COX7A2L	green	0.391750383
ARF4	green	0.394266874
UQCRFS1	green	0.403974378
LGALS4	green	0.405666998
CLIC1	green	0.417436731
GABARAP	green	0.418665719
RHOA	green	0.418981895
PGK1	green	0.422557408
CMPK1	green	0.443873615
CD63	blue	0.400543127
IL18	blue	0.40098638
PAH	blue	0.401097277
METTL7B	blue	0.401502531
TXN2	blue	0.40310536
CHMP4C	blue	0.403230731
GGH	blue	0.404289619
LYPD6B	blue	0.404352867
ATP6AP2	blue	0.404936858
LGALS1	blue	0.408691945
PABPC1	blue	0.409539601
CDC42EP1	blue	0.410288519

DHRS7B	blue	0.410712587
AZGP1	blue	0.41104193
APCS	blue	0.412842519
SNAP25	blue	0.413638763
KDEL3	blue	0.414106874
HHEX	blue	0.414402951
LACTB2	blue	0.416646818
VTCN1	blue	0.41671761
UBE2W	blue	0.417346998
TMEM59	blue	0.419055366
NDUFB9	blue	0.41925661
ATP6V1H	blue	0.419370017
DHRS7	blue	0.423010099
LAMP2	blue	0.425658083
KIF12	blue	0.425873995
POLR2F	blue	0.426690887
UBD	blue	0.42802275
EMC2	blue	0.428747338
UQCRB	blue	0.429271609
SERPINA4	blue	0.431296549
MRPL13	blue	0.432904052
GPAA1	blue	0.432979301
BCO2	blue	0.433678118
LDHB	blue	0.434085294
SPAG16	blue	0.435204434
COPS5	blue	0.437073862
MEG3	blue	0.437637605
PEBP1	blue	0.43998626

VPS28	blue	0.440386549
TSPAN6	blue	0.440747228
MRPL15	blue	0.441411767
PMVK	blue	0.444043941
CSPP1	blue	0.445177207
EPCAM	blue	0.446281947
RARRES2	blue	0.447673464
H1FO	blue	0.449032657
AGT	blue	0.450703504
CDH6	blue	0.451215147
CXCL6	blue	0.453106979
ITGB1	blue	0.454654896
IMPDH2	blue	0.455139213
PUF60	blue	0.457473096
CAPS	blue	0.458923739
GSDMD	blue	0.463087132
LYPLA1	blue	0.468619693
ATP1A1	blue	0.470301531
LAPTM4B	blue	0.471591509
SYNGR1	blue	0.471880869
C8orf59	blue	0.472258806
TST	blue	0.47328906
SLC12A2	blue	0.473732245
PRDX2	blue	0.476931343
MPC2	blue	0.478237568
SERPINA1	blue	0.481122705
GJB1	blue	0.481342889
EIF3E	blue	0.481640711

ASGR2	blue	0.484100867
SERPING1	blue	0.487701967
TMEM205	blue	0.488113341
MRPS28	blue	0.489506969
TM4SF4	blue	0.489984293
LAPTM4A	blue	0.490096532
SERPINE2	blue	0.493039499
CTSC	blue	0.496219769
CLDN10	blue	0.497818831
BST2	blue	0.500200363
RPL17	blue	0.502556984
CTHRC1	blue	0.508070146
DECR1	blue	0.509602647
THOP1	blue	0.511060698
RAB2A	blue	0.511067953
TMEM176B	blue	0.513716273
FXVD2	blue	0.515960374
RPL3	blue	0.516524622
TPD52	blue	0.525606041
ID2	blue	0.52594692
GMNN	blue	0.531444759
ANXA13	blue	0.534447231
GC	blue	0.542695168
ITIH2	blue	0.549267598
BICC1	blue	0.549460311
TRAM1	blue	0.55263966
EIF3D	blue	0.560042643
EIF3L	blue	0.560182048

DCDC2	blue	0.566650861
MPST	blue	0.575120729
VTN	blue	0.579318707
ITIH5	blue	0.593067674
KRT8	red	0.332129028
THEM6	red	0.332485078
HNRNPC	red	0.332503841
LRP10	red	0.334985421
PPA2	red	0.335262776
SPTSSA	red	0.336899704
C8orf33	red	0.338958232
LEPROT	red	0.340567123
HSP90B1	red	0.341347898
ANXA11	red	0.341420112
ATP6V1D	red	0.341824353
PRPF31	red	0.342312713
CDK4	red	0.342890088
MRPL42	red	0.345819828
NME4	red	0.34984698
ATP6V0B	red	0.350887831
ARL2	red	0.350920286
CAP1	red	0.352387233
HSP90AA1	red	0.353447108
MRPL47	red	0.353697714
PFDN6	red	0.354122291
COPRS	red	0.357052096
VASP	red	0.357425925
MCTS1	red	0.359828063

PSMD9	red	0.360546598
TGFB1	red	0.3620068
MRPL28	red	0.362235196
SUB1	red	0.362703908
CDC123	red	0.363391611
RPL35	red	0.364448937
SMIM7	red	0.368678102
ADK	red	0.368871269
PMF1	red	0.368930528
PKP3	red	0.373246994
ALCAM	red	0.37487002
UBE2N	red	0.374969849
PPP2R1A	red	0.377544057
HSF1	red	0.379479712
HSP90AB1	red	0.38134322
NSA2	red	0.385356134
METAP2	red	0.392306628
STOML2	red	0.398444609
RHOC	red	0.398455887
CISD1	red	0.39857407
BLOC1S1	red	0.399194671
RPL23A	red	0.399655103
COMMD7	red	0.4014385
CHMP4A	red	0.401588719
PRMT1	red	0.407095797
FKBP3	red	0.407274399
SKP1	red	0.413568798
PSME1	red	0.414662542

ECHS1	red	0.415897624
RDX	red	0.417097872
EI24	red	0.417303647
ECH1	red	0.418174971
NDUFS4	red	0.423355879
CHMP2A	red	0.426169318
FAM49B	red	0.432095933
H2AFY	red	0.439481684
HSD17B10	red	0.439544726
BTG1	red	0.441369417
RAB5C	red	0.44240885
EEF1E1	red	0.443594566
TBCA	red	0.443906839
NPM3	red	0.445039348
GSTO1	red	0.447738841
EIF3F	red	0.450381623
CNPY2	red	0.451604933
SNRPE	red	0.45206736
LMAN2	red	0.45255001
REEP5	red	0.457527438
TNFRSF12A	red	0.458955188
TAX1BP3	red	0.459850062
HNRNPA0	red	0.460171162
MRPL12	red	0.464992861
HIST1H2BK	red	0.478228715
RPS9	red	0.479076942
RPL13A	red	0.486046046
MAF1	red	0.498947696

MTDH	red	0.506411099
PSMA4	red	0.507504349
NEDD8	red	0.515129505
RPL4	red	0.51945314
NDUFC2	red	0.522389847
HNRNPA1	red	0.529655233
SNRPB	red	0.552790549
MRPL23	red	0.554900474
RTN4	red	0.556214045
CD59	red	0.557896766
RPS20	red	0.560061123
SLC25A6	red	0.57544951
PSMA1	red	0.575692662
RPL10A	red	0.580236132
RPL7	red	0.584048105
NME1	red	0.591273174
CYC1	red	0.612303667
RPS2	red	0.634005949
EIF4A1	red	0.658187157
RPS10	red	0.700027953

Supplementary Table 5 A total of 627 up-regulated DEGs in malignant cells

Gene name	avg_log2F	pct.1	pct.2	p_val_ad	difference	
	C			j		
PARK7	0	0.51530276	0.983	0.624	0	0.359
PGD	0	0.69815353	0.796	0.27	0	0.526
EFHD2	0	0.80686515	0.765	0.343	0	0.422
MRT04	0	0.30298085	0.563	0.119	0	0.444

MINOS1	0	0.67557789	0.961	0.553	0	0.408
PSMB2	0	0.65490001	0.952	0.472	0	0.48
MRPS15	0	0.61166991	0.869	0.323	0	0.546
YBX1	0	0.95262712	0.997	0.776	0	0.221
EBNA1BP2	0	0.43556117	0.756	0.21	0	0.546
PRDX1	0	0.71502626	0.996	0.788	0	0.208
UQCRH	0	0.63497936	0.997	0.813	0	0.184
HSPB11	0	0.59124254	0.85	0.324	0	0.526
MRPL37	0	0.40103377	0.718	0.193	0	0.525
GCLM	0	0.50373766	0.603	0.121	0	0.482
PSMA5	0	0.39366128	0.869	0.315	0	0.554
HIST2H2AA	0	0.46007614	0.599	0.152	0	0.447
3						
S100A9	0	0.62717806	0.76	0.245	0	0.515
S100A2	0	2.13956839	0.75	0.408	0	0.342
S100A16	0	0.77600572	0.985	0.699	0	0.286
CKS1B	0	0.67448709	0.923	0.407	0	0.516
ADAM15	0	0.29995823	0.662	0.175	0	0.487
MTX1	0	0.30085862	0.711	0.198	0	0.513
PMF1	0	0.34455933	0.648	0.17	0	0.478
PRDX6	0	0.77322878	0.974	0.558	0	0.416
SNRPE	0	0.53289462	0.976	0.59	0	0.386
EPHX1	0	0.65545689	0.78	0.263	0	0.517
PPM1G	0	0.4790752	0.835	0.339	0	0.496
RTN4	0	0.71104217	0.967	0.608	0	0.359
RPS27A	0	0.5798106	1	0.974	0	0.026
CCT7	0	0.37002768	0.834	0.298	0	0.536
POLE4	0	0.57950041	0.844	0.285	0	0.559

SUCLG1	0	0.26633865	0.738	0.215	0	0.523
MZT2B	0	0.85251939	0.975	0.595	0	0.38
MZT2A	0	0.58705226	0.96	0.568	0	0.392
KYNU	0	0.59704355	0.55	0.068	0	0.482
DHRS9	0	0.72785337	0.497	0.058	0	0.439
DTYMK	0	0.37190022	0.619	0.156	0	0.463
TKT	0	1.23330332	0.919	0.379	0	0.54
CSTA	0	0.98417228	0.65	0.203	0	0.447
RUVBL1	0	0.26683626	0.565	0.122	0	0.443
PFN2	0	0.35547946	0.701	0.213	0	0.488
NDUFB5	0	0.46119373	0.889	0.351	0	0.538
PARL	0	0.48542783	0.649	0.139	0	0.51
AP2M1	0	0.91979146	0.921	0.44	0	0.481
TCTEX1D2	0	0.38857814	0.577	0.112	0	0.465
RPL9	0	0.7524979	1	0.913	0	0.087
UGDH	0	0.59630455	0.744	0.264	0	0.48
SPP1	0	1.66579256	0.828	0.28	0	0.548
PPA2	0	0.35267124	0.707	0.195	0	0.512
SLC7A11	0	0.41762229	0.453	0.061	0	0.392
RPS3A	0	0.59366781	1	0.954	0	0.046
NDUFS6	0	0.54302395	0.971	0.555	0	0.416
CMBL	0	0.47704065	0.699	0.202	0	0.497
NDUFS4	0	0.44820057	0.838	0.302	0	0.536
NDUFAF2	0	0.39565929	0.67	0.149	0	0.521
TAF9	0	0.54000722	0.842	0.304	0	0.538
BTF3	0	1.00601815	0.998	0.806	0	0.192
RPS23	0	0.49972085	1	0.953	0	0.047
REEP5	0	0.5446031	0.93	0.44	0	0.49

HINT1	0	1.00583178	0.997	0.771	0	0.226
HBEGF	0	1.00896989	0.617	0.169	0	0.448
SRA1	0	0.39407169	0.736	0.208	0	0.528
RPS14	0	0.91124528	1	0.944	0	0.056
GPX3	0	1.70918125	0.653	0.08	0	0.573
MRPL22	0	0.48663087	0.781	0.217	0	0.564
PTTG1	0	1.03687495	0.6	0.116	0	0.484
NPM1	0	0.89891824	0.998	0.785	0	0.213
RPL26L1	0	0.72507859	0.852	0.275	0	0.577
ATP6V0E1	0	0.67801352	0.982	0.654	0	0.328
BOD1	0	0.38446648	0.641	0.163	0	0.478
NOP16	0	0.33512226	0.612	0.134	0	0.478
HIGD2A	0	0.5405114	0.959	0.55	0	0.409
CLTB	0	0.62663739	0.937	0.497	0	0.44
PRELID1	0	0.69637064	0.961	0.511	0	0.45
LMAN2	0	0.49500043	0.948	0.481	0	0.467
NHP2	0	0.59887002	0.952	0.433	0	0.519
HNRNPAB	0	0.58493713	0.787	0.276	0	0.511
SERPINB1	0	0.77123047	0.858	0.353	0	0.505
NQO2	0	0.4429449	0.554	0.097	0	0.457
ECI2	0	0.3372626	0.547	0.1	0	0.447
EEF1E1	0	0.49864467	0.688	0.152	0	0.536
TMEM14C	0	0.53968561	0.939	0.462	0	0.477
HIST1H2BK	0	0.86115671	0.872	0.345	0	0.527
PFDN6	0	0.41099031	0.788	0.267	0	0.521
HMGA1	0	1.01633509	0.922	0.497	0	0.425
RPS10	0	1.35243402	0.962	0.615	0	0.347
RPL10A	0	0.77570848	0.999	0.865	0	0.134

FKBP5	0	0.43008744	0.463	0.056	0	0.407
MRPS10	0	0.34502554	0.689	0.198	0	0.491
BAG2	0	0.29986342	0.389	0.037	0	0.352
TPD52L1	0	0.56460581	0.701	0.175	0	0.526
PSMG3	0	0.63481604	0.825	0.286	0	0.539
NUDT1	0	0.40104923	0.593	0.128	0	0.465
RPA3	0	0.62445647	0.88	0.365	0	0.515
NDUFA4	0	0.62380265	0.999	0.828	0	0.171
CYCS	0	0.69172024	0.96	0.561	0	0.399
GGCT	0	0.53620763	0.846	0.285	0	0.561
LSM5	0	0.54589583	0.94	0.486	0	0.454
BLVRA	0	0.32653925	0.649	0.172	0	0.477
POLD2	0	0.34375899	0.729	0.212	0	0.517
ARPC1B	0	0.45802396	0.92	0.517	0	0.403
CAV1	0	1.42242555	0.74	0.277	0	0.463
AKR1B1	0	0.78488949	0.748	0.15	0	0.598
SSBP1	0	0.51028509	0.962	0.507	0	0.455
SLC25A6	0	0.85418203	0.989	0.732	0	0.257
PNPLA4	0	0.36876502	0.652	0.151	0	0.501
PIR	0	0.29603711	0.452	0.066	0	0.386
MAOA	0	0.36125274	0.538	0.112	0	0.426
EBP	0	0.36072499	0.706	0.185	0	0.521
HSD17B10	0	0.52169856	0.834	0.225	0	0.609
SLC25A5	0	0.98920305	0.99	0.637	0	0.353
MCTS1	0	0.37764638	0.821	0.282	0	0.539
NAA10	0	0.61940381	0.817	0.279	0	0.538
G6PD	0	1.49979332	0.732	0.156	0	0.576
RPS20	0	0.86688428	0.985	0.734	0	0.251

ASPH	0	1.10287421	0.915	0.448	0	0.467
RPL7	0	0.92178192	0.997	0.848	0	0.149
FABP5	0	1.59726525	0.919	0.348	0	0.571
MTDH	0	0.74104766	0.971	0.607	0	0.364
LAPTM4B	0	0.56034264	0.859	0.327	0	0.532
EIF3E	0	0.79597498	0.971	0.624	0	0.347
MAL2	0	0.78267802	0.927	0.508	0	0.419
MRPL13	0	0.59093728	0.903	0.329	0	0.574
NDUFB9	0	0.52233954	0.994	0.666	0	0.328
THEM6	0	0.36945904	0.637	0.137	0	0.5
LY6E	0	1.36008496	0.952	0.703	0	0.249
EEF1D	0	0.65144144	0.999	0.889	0	0.11
TSTA3	0	0.76384417	0.912	0.348	0	0.564
PUF60	0	0.45356992	0.873	0.364	0	0.509
EXOSC4	0	0.39767323	0.724	0.213	0	0.511
GPAA1	0	0.52395928	0.881	0.369	0	0.512
CYC1	0	1.10715755	0.98	0.44	0	0.54
MAF1	0	0.51931973	0.881	0.361	0	0.52
AQP3	0	0.69147989	0.682	0.209	0	0.473
STOML2	0	0.37403991	0.838	0.311	0	0.527
CTSL	0	0.45374548	0.743	0.222	0	0.521
NANS	0	0.47655476	0.714	0.185	0	0.529
TXN	0	1.46253312	1	0.843	0	0.157
PTGR1	0	0.65583098	0.794	0.212	0	0.582
STOM	0	0.59122862	0.773	0.208	0	0.565
NDUFA8	0	0.45214443	0.806	0.251	0	0.555
PSMB7	0	0.76833612	0.913	0.377	0	0.536
ARPC5L	0	0.62511288	0.873	0.325	0	0.548

ZBTB43	0	0.59965142	0.648	0.195	0	0.453
AK1	0	0.55111938	0.651	0.124	0	0.527
GTF3C5	0	0.63099188	0.635	0.153	0	0.482
AKR1C1	0	1.62175726	0.754	0.161	0	0.593
AKR1C2	0	2.7673953	0.664	0.119	0	0.545
AKR1C3	0	1.59140257	0.885	0.299	0	0.586
NUDT5	0	0.44004833	0.793	0.253	0	0.54
CISD1	0	0.4940648	0.847	0.286	0	0.561
TSPAN15	0	0.4173612	0.763	0.252	0	0.511
ADK	0	0.37107581	0.704	0.193	0	0.511
FAM213A	0	0.51829842	0.8	0.241	0	0.559
SNCG	0	1.55458994	0.796	0.435	0	0.361
PGAM1	0	0.48163246	0.938	0.467	0	0.471
AVPI1	0	0.57491451	0.627	0.157	0	0.47
NPM3	0	0.56524751	0.767	0.205	0	0.562
GSTO1	0	0.51439242	0.892	0.357	0	0.535
DUSP5	0	0.61676194	0.626	0.15	0	0.476
GLRX3	0	0.57958201	0.831	0.288	0	0.543
ECHS1	0	0.42305008	0.902	0.347	0	0.555
TALDO1	0	0.93583453	0.942	0.536	0	0.406
MRPL23	0	0.87609608	0.917	0.379	0	0.538
PSMA1	0	0.68709293	0.913	0.392	0	0.521
CD59	0	0.79794995	0.953	0.586	0	0.367
PTPMT1	0	0.41402225	0.752	0.222	0	0.53
TIMM10	0	0.3902613	0.817	0.296	0	0.521
POLR2G	0	0.34048744	0.781	0.245	0	0.536
DRAP1	0	0.6033858	0.928	0.486	0	0.442
MRPL11	0	0.44520469	0.836	0.293	0	0.543

RHOD	0	0.60095152	0.849	0.362	0	0.487
GSTP1	0	0.78182295	0.999	0.912	0	0.087
NDUFV1	0	0.26503436	0.788	0.255	0	0.533
NDUFS8	0	0.63050184	0.964	0.437	0	0.527
MYEOV	0	0.33453104	0.535	0.109	0	0.426
NDUFC2	0	0.69181403	0.935	0.481	0	0.454
TMEM126A	0	0.25839946	0.645	0.167	0	0.478
ST3GAL4	0	0.6489079	0.607	0.127	0	0.48
CLEC2B	0	0.68591964	0.565	0.091	0	0.474
MGST1	0	1.48118033	0.916	0.441	0	0.475
TUBA1B	0	1.07196186	0.936	0.515	0	0.421
KRT7	0	1.54155583	0.968	0.744	0	0.224
KRT18	0	0.66904584	0.997	0.891	0	0.106
HNRNPA1	0	0.66666047	0.995	0.767	0	0.228
BLOC1S1	0	0.47647922	0.89	0.368	0	0.522
PA2G4	0	0.81138164	0.927	0.369	0	0.558
CNPY2	0	0.49088041	0.893	0.359	0	0.534
MRPL42	0	0.31454969	0.706	0.197	0	0.509
SNRPF	0	0.81802049	0.961	0.505	0	0.456
SLC25A3	0	0.86729693	0.986	0.607	0	0.379
TXNRD1	0	0.74922613	0.678	0.206	0	0.472
VPS29	0	0.43154693	0.903	0.371	0	0.532
SRSF9	0	0.60776638	0.937	0.427	0	0.51
PSMD9	0	0.29228288	0.716	0.198	0	0.518
RAN	0	1.09805452	0.99	0.623	0	0.367
PSMB5	0	0.79127773	0.937	0.424	0	0.513
DHRS4L2	0	0.26839319	0.503	0.091	0	0.412
PSME2	0	0.51324567	0.943	0.48	0	0.463

NEDD8	0	0.60784191	0.969	0.611	0	0.358
FKBP3	0	0.41616414	0.804	0.283	0	0.521
COX5A	0	0.49931254	0.992	0.668	0	0.324
PSMA4	0	0.64784615	0.952	0.482	0	0.47
FAH	0	0.44168281	0.63	0.131	0	0.499
MRPS34	0	0.40456766	0.926	0.436	0	0.49
MSRB1	0	0.33484651	0.609	0.152	0	0.457
RPS2	0	1.13413976	0.997	0.88	0	0.117
UQCRC2	0	0.29340588	0.818	0.277	0	0.541
NDUFAB1	0	0.41595799	0.95	0.472	0	0.478
NUPR1	0	0.49152575	0.765	0.239	0	0.526
TUFM	0	0.49066157	0.933	0.398	0	0.535
SRCAP	0	0.83063889	0.787	0.214	0	0.573
CES1	0	1.16834996	0.595	0.056	0	0.539
MT2A	0	2.0447247	0.834	0.611	0	0.223
NQO1	0	1.06270025	0.83	0.408	0	0.422
GCSH	0	0.80243748	0.78	0.181	0	0.599
APRT	0	0.7577233	0.953	0.55	0	0.403
DEF8	0	0.28770477	0.512	0.097	0	0.415
TAX1BP3	0	0.46203087	0.828	0.292	0	0.536
C1QBP	0	0.37500381	0.885	0.323	0	0.562
EIF4A1	0	1.0053109	0.943	0.499	0	0.444
COPRS	0	0.38468475	0.655	0.157	0	0.498
RPL27	0	0.58957427	1	0.904	0	0.096
PHB	0	0.43436099	0.931	0.396	0	0.535
NME1	0	1.11066879	0.927	0.338	0	0.589
MRPL12	0	0.61290736	0.79	0.193	0	0.597
SLC16A3	0	0.62590894	0.841	0.316	0	0.525

TUBB6	0	0.36036062	0.55	0.114	0	0.436
SNRPB	0	0.77991766	0.971	0.555	0	0.416
NAA20	0	0.9257168	0.908	0.353	0	0.555
COMMD7	0	0.39145391	0.686	0.195	0	0.491
AHCY	0	0.27966868	0.741	0.227	0	0.514
PSMA7	0	0.68875783	0.989	0.72	0	0.269
POLR2E	0	0.38638471	0.912	0.414	0	0.498
C19orf24	0	0.53656199	0.895	0.364	0	0.531
NDUFS7	0	0.6286341	0.932	0.362	0	0.57
PLEKHJ1	0	0.5878953	0.841	0.286	0	0.555
OAZ1	0	1.2093508	1	0.847	0	0.153
LSM7	0	0.6515797	0.979	0.592	0	0.387
TIMM13	0	1.21549812	0.977	0.493	0	0.484
GNA15	0	0.50305171	0.525	0.1	0	0.425
NFIC	0	0.53028531	0.742	0.239	0	0.503
FXVD3	0	1.33964893	0.975	0.786	0	0.189
TMEM147	0	0.49251101	0.96	0.519	0	0.441
CAPNS1	0	0.53299946	0.882	0.402	0	0.48
MRPS12	0	0.52413269	0.9	0.365	0	0.535
RPS16	0	0.74174898	1	0.954	0	0.046
TOMM40	0	0.60867194	0.758	0.22	0	0.538
ERCC1	0	0.41426574	0.721	0.218	0	0.503
AP2S1	0	0.70617914	0.946	0.513	0	0.433
RUVBL2	0	0.30902097	0.683	0.191	0	0.492
PIH1D1	0	0.42487283	0.76	0.228	0	0.532
RPL13A	0	0.99252095	0.989	0.816	0	0.173
RPS11	0	1.58964621	0.995	0.821	0	0.174
C19orf48	0	0.43079199	0.644	0.161	0	0.483

ETFB	0	1.39933836	0.945	0.425	0	0.52
RPS9	0	0.59090116	0.999	0.926	0	0.073
RANBP1	0	0.70616088	0.923	0.505	0	0.418
CHCHD10	0	0.96116514	0.94	0.508	0	0.432
TXN2	0	0.48102913	0.904	0.372	0	0.532
TOMM22	0	0.47037808	0.928	0.423	0	0.505
CBR1	0	0.54156575	0.807	0.216	0	0.591
SFN	0	1.75133573	0.854	0.456	0	0.398
MUC4	0	0.57481472	0.556	0.08	0	0.476
AGR3	0	1.03767899	0.631	0.156	0	0.475
AKR1B10	0	2.01122464	0.709	0.105	0	0.604
NR0B1	0	0.33371726	0.333	0.015	0	0.318
FAM83A	0	1.40552852	0.658	0.145	0	0.513
LY6K	0	0.47559224	0.493	0.046	0	0.447
LYNX1	0	0.89126344	0.536	0.09	0	0.446
SYT8	0	1.39157579	0.774	0.417	0	0.357
ALDH3A1	0	2.59969988	0.648	0.083	0	0.565
KRT16	0	1.09627359	0.624	0.186	0	0.438
H2AFZ	6.1534E-308	0.84866387	0.969	0.587	9.1E-304	0.382
MDH2	6.8081E-308	0.35669689	0.939	0.465	1E-303	0.474
PRPF31	2.1715E-307	0.34782062	0.696	0.207	3.2E-303	0.489
BAK1	1.3963E-306	0.26422357	0.487	0.085	2.1E-302	0.402
NUDT8	2.2231E-305	0.25932941	0.516	0.099	3.3E-301	0.417
H2AFY	3.7678E-305	0.4726915	0.883	0.398	5.6E-	0.485

					301	
RPL35	5.4242E-305	0.51874509	1	0.934	8E-301	0.066
ANP32B	9.8919E-305	0.50477773	0.91	0.464	1.5E-	0.446
					300	
UBE2S	1.1459E-304	0.8366863	0.63	0.194	1.7E-	0.436
					300	
TACSTD2	1.6851E-304	1.0251769	0.949	0.644	2.5E-	0.305
					300	
RPL7A	2.3592E-304	0.4599723	1	0.954	3.5E-	0.046
					300	
MSRB2	3.9127E-304	0.32798538	0.725	0.219	5.8E-	0.506
					300	
UBE2N	3.3377E-303	0.34721375	0.809	0.284	4.9E-	0.525
					299	
MRPS11	4.4347E-303	0.31309395	0.669	0.189	6.6E-	0.48
					299	
SMIM7	1.3162E-302	0.38329738	0.797	0.286	1.9E-	0.511
					298	
MRPS16	2.8353E-302	0.34581188	0.863	0.337	4.2E-	0.526
					298	
TP53I3	3.078E-302	0.43466862	0.633	0.18	4.6E-	0.453
					298	
EIF3I	2.1922E-301	0.42587294	0.893	0.407	3.2E-	0.486
					297	
RNF126	2.3611E-301	0.36361796	0.72	0.234	3.5E-	0.486
					297	
LSM4	1.4831E-300	0.39907824	0.927	0.426	2.2E-	0.501
					296	

POLD4	7.9736E-300	0.57714807	0.908	0.453	1.2E-295	0.455
PRR7	1.5975E-299	0.2807719	0.555	0.124	2.4E-295	0.431
MRPS33	1.692E-299	0.34421896	0.811	0.293	2.5E-295	0.518
BZW2	2.287E-299	0.25819056	0.682	0.195	3.4E-295	0.487
PPA1	2.6952E-299	0.52223913	0.981	0.61	4E-295	0.371
AKT1S1	5.1981E-299	0.30560632	0.61	0.157	7.7E-295	0.453
GADD45A	6.2302E-298	0.72988984	0.738	0.292	9.2E-294	0.446
ALCAM	2.5354E-297	0.37531685	0.623	0.164	3.7E-293	0.459
EIF6	8.9372E-297	0.4674316	0.944	0.495	1.3E-292	0.449
CDK4	2.4281E-295	0.29029794	0.683	0.201	3.6E-291	0.482
UBE2L3	1.2651E-294	0.52458022	0.896	0.436	1.9E-290	0.46
MYC	1.9788E-294	0.4755291	0.678	0.217	2.9E-290	0.461
C16orf74	1.0795E-293	0.52193322	0.575	0.161	1.6E-289	0.414
COMT	2.1815E-293	0.49744276	0.927	0.478	3.2E-289	0.449
PITX1	3.2391E-293	0.34835487	0.542	0.122	4.8E-	0.42

					289	
DESI1	5.6104E-293	0.30580212	0.611	0.163	8.3E-	0.448
					289	
HRASLS2	5.9434E-293	0.3877129	0.412	0.057	8.8E-	0.355
					289	
SQLE	1.5708E-292	0.41025566	0.696	0.224	2.3E-	0.472
					288	
SRP72	1.675E-292	0.34362921	0.737	0.248	2.5E-	0.489
					288	
RPL4	2.626E-292	0.61043555	0.996	0.831	3.9E-	0.165
					288	
CDC123	6.7765E-292	0.26764019	0.695	0.212	1E-287	0.483
COA4	3.3478E-291	0.31261883	0.846	0.328	5E-287	0.518
CRELD2	7.4315E-291	0.33493066	0.644	0.189	1.1E-	0.455
					286	
UBE2C	5.1491E-290	0.49727137	0.443	0.075	7.6E-	0.368
					286	
MRPL9	6.3404E-290	0.26098402	0.686	0.206	9.4E-	0.48
					286	
DNPH1	1.1334E-289	0.28895178	0.886	0.351	1.7E-	0.535
					285	
CHMP2A	5.5749E-289	0.49890521	0.937	0.478	8.2E-	0.459
					285	
BIN1	1.3273E-288	0.28775907	0.529	0.119	2E-284	0.41
MRPL15	1.1324E-286	0.37364652	0.738	0.243	1.7E-	0.495
					282	
RAB8A	1.3351E-286	0.2686	0.635	0.178	2E-282	0.457
LYAR	2.422E-286	0.30950097	0.456	0.081	3.6E-	0.375

					282	
ECH1	2.5834E-286	0.4457856	0.896	0.406	3.8E-	0.49
					282	
ANXA2	4.2241E-286	0.65116203	0.999	0.909	6.2E-	0.09
					282	
CAV2	5.0515E-286	0.53000428	0.841	0.374	7.5E-	0.467
					282	
PRDX5	5.4095E-286	0.65706612	0.992	0.78	8E-282	0.212
CMSS1	1.0303E-285	0.31735122	0.596	0.158	1.5E-	0.438
					281	
EI24	7.4229E-284	0.38420226	0.853	0.36	1.1E-	0.493
					279	
IMPA2	1.1507E-283	0.25468528	0.437	0.069	1.7E-	0.368
					279	
COMTD1	1.9467E-283	0.32700275	0.754	0.257	2.9E-	0.497
					279	
FAM49B	2.6002E-282	0.47271927	0.857	0.361	3.8E-	0.496
					278	
TIMM9	3.6821E-282	0.25832898	0.689	0.209	5.4E-	0.48
					278	
HSBP1	4.9069E-282	0.58142041	0.951	0.607	7.3E-	0.344
					278	
MAPK13	1.1561E-281	0.26595673	0.579	0.145	1.7E-	0.434
					277	
SHARPIN	3.8818E-281	0.32854628	0.842	0.326	5.7E-	0.516
					277	
SRPK1	6.1977E-280	0.27827669	0.648	0.186	9.2E-	0.462
					276	

COA6	2.0762E-279	0.27395138	0.756	0.259	3.1E-275	0.497
LYRM4	3.4675E-279	0.25622024	0.597	0.155	5.1E-275	0.442
TK1	8.0726E-279	0.34452574	0.42	0.068	1.2E-274	0.352
RDX	1.7932E-278	0.40366943	0.767	0.286	2.7E-274	0.481
TPM4	2.1007E-278	0.62564428	0.917	0.518	3.1E-274	0.399
MRPL14	2.6782E-278	0.38512923	0.94	0.481	4E-274	0.459
PPP1CA	6.1613E-278	0.37786982	0.927	0.45	9.1E-274	0.477
TSEN34	1.523E-277	0.29523144	0.772	0.275	2.3E-273	0.497
NDUFA2	1.7091E-277	0.40396724	0.964	0.517	2.5E-273	0.447
KARS	3.1754E-277	0.25185624	0.663	0.195	4.7E-273	0.468
EREG	5.9812E-277	0.7768696	0.642	0.227	8.8E-273	0.415
FAM84B	4.2325E-276	0.28187049	0.572	0.144	6.3E-272	0.428
DERL1	8.808E-276	0.29336915	0.756	0.255	1.3E-271	0.501
FOSL1	5.6468E-275	0.47278529	0.576	0.167	8.4E-271	0.409
SNF8	6.0558E-275	0.38465731	0.811	0.325	9E-271	0.486

MANF	7.317E-275	0.29276379	0.791	0.277	1.1E-270	0.514
PSMA3	9.4705E-275	0.38118755	0.911	0.423	1.4E-270	0.488
RRAS	1.6798E-274	0.46072854	0.617	0.191	2.5E-270	0.426
NOP10	9.4809E-274	0.50453741	0.988	0.678	1.4E-269	0.31
VDAC2	1.22E-272	0.41977538	0.957	0.564	1.8E-268	0.393
ERH	5.3155E-272	0.44453482	0.983	0.63	7.9E-268	0.353
FSCN1	6.8271E-272	0.67394022	0.723	0.318	1E-267	0.405
EIF3K	1.0577E-271	0.47316289	0.989	0.677	1.6E-267	0.312
UQCRQ	1.2245E-271	0.49178382	1	0.785	1.8E-267	0.215
GLTP	1.673E-271	0.31580306	0.572	0.152	2.5E-267	0.42
MRPL40	8.1248E-270	0.30615494	0.756	0.27	1.2E-265	0.486
CHMP4A	2.3148E-269	0.33548366	0.749	0.257	3.4E-265	0.492
MRFAP1	2.4636E-269	0.37634034	0.903	0.425	3.6E-265	0.478
JOSD2	6.9238E-269	0.26796582	0.729	0.243	1E-264	0.486
TGFBI	1.3259E-268	0.34852735	0.638	0.197	2E-264	0.441
MRPL47	1.7007E-268	0.30814761	0.781	0.282	2.5E-	0.499

					264	
UCHL3	4.3178E-268	0.28310038	0.709	0.233	6.4E-	0.476
					264	
SSRP1	6.1492E-268	0.31545482	0.699	0.236	9.1E-	0.463
					264	
SERPINB5	9.6895E-268	0.46422229	0.616	0.2	1.4E-	0.416
					263	
ZDHHC12	1.5295E-267	0.31959015	0.742	0.26	2.3E-	0.482
					263	
GJB3	3.3139E-267	0.30635572	0.556	0.147	4.9E-	0.409
					263	
MRPL21	6.6176E-267	0.31901558	0.829	0.324	9.8E-	0.505
					263	
ATP1B3	2.937E-266	0.33188354	0.801	0.301	4.3E-	0.5
					262	
HTATIP2	1.8565E-265	0.30557764	0.847	0.349	2.7E-	0.498
					261	
RPL8	1.8686E-265	0.58442192	1	0.981	2.8E-	0.019
					261	
SERBP1	4.8096E-264	0.51704846	0.948	0.557	7.1E-	0.391
					260	
MT1E	5.7706E-264	1.02182823	0.769	0.382	8.5E-	0.387
					260	
RCN1	6.1855E-264	0.30931681	0.798	0.297	9.1E-	0.501
					260	
NDUFA10	1.1793E-263	0.26439647	0.801	0.299	1.7E-	0.502
					259	
DNAJC19	2.0013E-263	0.30778171	0.875	0.371	3E-259	0.504

SPTSSA	3.9417E-263	0.28265978	0.809	0.308	5.8E-259	0.501
TBCA	3.9684E-263	0.51050041	0.981	0.655	5.9E-259	0.326
SERPINB6	4.3296E-263	0.25998058	0.77	0.277	6.4E-259	0.493
SLC52A2	6.7295E-263	0.27757093	0.75	0.258	1E-258	0.492
PLK3	1.1478E-262	0.54575319	0.714	0.285	1.7E-258	0.429
ZNF593	3.9739E-262	0.33462896	0.835	0.341	5.9E-258	0.494
MRPL28	4.6469E-262	0.29079947	0.756	0.264	6.9E-258	0.492
BOLA3	1.9583E-260	0.26719803	0.784	0.295	2.9E-256	0.489
LMTK3	1.9641E-260	0.26893394	0.568	0.147	2.9E-256	0.421
PSMD7	1.8414E-259	0.31404743	0.756	0.293	2.7E-255	0.463
IFI16	5.2608E-259	0.36789873	0.603	0.184	7.8E-255	0.419
PSCA	6.5511E-259	1.41302648	0.7	0.298	9.7E-255	0.402
PRMT1	1.2452E-258	0.34068695	0.867	0.379	1.8E-254	0.488
TRAPPC2L	5.236E-258	0.2885195	0.798	0.299	7.7E-254	0.499
DNAJB12	1.061E-257	0.32244819	0.638	0.199	1.6E-	0.439

					253	
PSMC3	1.1699E-257	0.26000155	0.808	0.317	1.7E-	0.491
					253	
ZDHHC4	1.3312E-257	0.26441672	0.718	0.241	2E-253	0.477
GPATCH4	3.2804E-257	0.25811678	0.542	0.137	4.9E-	0.405
					253	
MGST2	2.3339E-256	0.33389876	0.88	0.373	3.5E-	0.507
					252	
GLRX	2.601E-256	0.33919629	0.596	0.174	3.8E-	0.422
					252	
YWHAQ	9.4874E-256	0.4121206	0.946	0.54	1.4E-	0.406
					251	
LSM6	3.7713E-255	0.25479798	0.763	0.272	5.6E-	0.491
					251	
TTC1	8.3644E-255	0.25893273	0.702	0.232	1.2E-	0.47
					250	
PSMG4	1.226E-254	0.2904599	0.619	0.186	1.8E-	0.433
					250	
RAD23B	6.7642E-254	0.3750938	0.774	0.299	1E-249	0.475
COTL1	3.5966E-253	0.42465707	0.754	0.338	5.3E-	0.416
					249	
GRHPR	2.5315E-252	0.2681129	0.605	0.174	3.7E-	0.431
					248	
SRD5A3	5.324E-252	0.3057733	0.651	0.206	7.9E-	0.445
					248	
C8orf33	5.7199E-251	0.28050209	0.68	0.223	8.5E-	0.457
					247	
METTL5	8.317E-251	0.29571856	0.838	0.351	1.2E-	0.487

					246	
MRPL41	9.5826E-251	0.4614275	0.913	0.509	1.4E-	0.404
					246	
CENPU	1.2985E-250	0.30954042	0.325	0.034	1.9E-	0.291
					246	
GHITM	4.3647E-250	0.26974059	0.929	0.456	6.5E-	0.473
					246	
RAMP1	1.2081E-249	0.44077917	0.641	0.226	1.8E-	0.415
					245	
NME4	4.5987E-249	0.35072225	0.829	0.348	6.8E-	0.481
					245	
MALL	9.5583E-248	0.4467765	0.676	0.254	1.4E-	0.422
					243	
PSMD2	2.4412E-246	0.2734498	0.762	0.295	3.6E-	0.467
					242	
EIF3H	6.3209E-246	0.47423784	0.987	0.694	9.3E-	0.293
					242	
LETM2	3.2301E-245	0.26575711	0.36	0.051	4.8E-	0.309
					241	
KRT19	4.0914E-245	0.96271835	0.978	0.84	6.1E-	0.138
					241	
CKS2	4.631E-245	0.3944389	0.758	0.308	6.8E-	0.45
					241	
HMGB3	8.5522E-245	0.2511917	0.55	0.149	1.3E-	0.401
					240	
TINAGL1	1.2229E-244	0.53041571	0.736	0.322	1.8E-	0.414
					240	
NSA2	7.492E-244	0.3612566	0.844	0.356	1.1E-	0.488

					239	
EMC2	1.9176E-243	0.25807772	0.666	0.219	2.8E-	0.447
					239	
PKP3	2.7214E-243	0.27890841	0.781	0.303	4E-239	0.478
NAMPT	4.4843E-243	0.44980967	0.761	0.333	6.6E-	0.428
					239	
CYBA	4.7694E-243	0.52163216	0.977	0.68	7.1E-	0.297
					239	
HSPE1	1.1965E-242	0.46293289	0.997	0.781	1.8E-	0.216
					238	
COX7C	2.809E-242	0.46197876	0.999	0.851	4.2E-	0.148
					238	
RAB5C	5.99E-241	0.32383836	0.804	0.324	8.9E-	0.48
					237	
BAX	7.4933E-241	0.31331935	0.82	0.329	1.1E-	0.491
					236	
EHD1	8.6984E-241	0.26279208	0.581	0.172	1.3E-	0.409
					236	
ARPC3	4.931E-240	0.40141829	0.991	0.715	7.3E-	0.276
					236	
ZWINT	5.6458E-240	0.27946997	0.319	0.034	8.3E-	0.285
					236	
EIF3M	5.624E-239	0.27064513	0.878	0.398	8.3E-	0.48
					235	
DECR1	1.8455E-238	0.40920869	0.728	0.268	2.7E-	0.46
					234	
FDX1	2.9018E-237	0.3138852	0.794	0.311	4.3E-	0.483
					233	

NEK6	1.3004E-236	0.25788033	0.526	0.14	1.9E-232	0.386
PHLDA2	1.9788E-236	0.65789246	0.964	0.669	2.9E-232	0.295
DENND2C	6.82E-236	0.28740454	0.385	0.068	1E-231	0.317
OCIAD2	1.0335E-235	0.57902053	0.965	0.665	1.5E-231	0.3
SLIRP	1.2361E-235	0.44201814	0.971	0.569	1.8E-231	0.402
SNRPG	2.2811E-235	0.46368631	0.99	0.694	3.4E-231	0.296
CYB5A	8.1908E-235	0.25678229	0.896	0.4	1.2E-230	0.496
RPL23A	9.1061E-235	0.47761189	1	0.912	1.3E-230	0.088
NINJ1	1.1623E-234	0.26979881	0.67	0.229	1.7E-230	0.441
XIST	1.5373E-234	0.2587156	0.748	0.275	2.3E-230	0.473
GSPT1	2.8175E-234	0.33509163	0.75	0.29	4.2E-230	0.46
VPS28	2.9091E-234	0.38939768	0.966	0.549	4.3E-230	0.417
MGMT	7.1118E-234	0.27574322	0.802	0.314	1.1E-229	0.488
BTG1	3.3117E-233	0.55935676	0.937	0.568	4.9E-229	0.369
NUDC	9.1041E-233	0.27163597	0.843	0.36	1.3E-	0.483

					228	
MKKS	2.5742E-232	0.28985111	0.783	0.305	3.8E-	0.478
					228	
ENO1	2.6301E-232	0.45640289	0.987	0.766	3.9E-	0.221
					228	
COX8A	1.6481E-231	0.39977351	0.995	0.762	2.4E-	0.233
					227	
RRP7A	2.5168E-231	0.27345108	0.682	0.24	3.7E-	0.442
					227	
PPP2CA	5.7386E-231	0.25939186	0.718	0.259	8.5E-	0.459
					227	
GSDMD	3.8859E-230	0.28279939	0.716	0.262	5.7E-	0.454
					226	
EMP3	2.219E-229	0.34347399	0.61	0.205	3.3E-	0.405
					225	
HSPD1	2.5481E-229	0.3506397	0.973	0.608	3.8E-	0.365
					225	
TMED9	3.8001E-229	0.28282719	0.93	0.476	5.6E-	0.454
					225	
PDLIM7	7.9446E-229	0.2561081	0.636	0.215	1.2E-	0.421
					224	
HMGB2	1.2635E-228	0.60553273	0.621	0.225	1.9E-	0.396
					224	
OCIAD1	2.7376E-228	0.30754563	0.9	0.415	4E-224	0.485
TSPAN4	5.3133E-228	0.25363522	0.493	0.127	7.9E-	0.366
					224	
NDUFA13	9.1616E-228	0.46472204	0.948	0.5	1.4E-	0.448
					223	

KCNN4	2.5674E-227	0.31172273	0.602	0.202	3.8E-223	0.4
GCLC	1.1885E-226	0.25192891	0.403	0.08	1.8E-222	0.323
MRPS28	4.1988E-226	0.32466287	0.624	0.206	6.2E-222	0.418
DUSP23	1.8061E-225	0.28270252	0.892	0.421	2.7E-221	0.471
DUT	6.4075E-225	0.46996773	0.849	0.395	9.5E-221	0.454
THOP1	7.4351E-225	0.37133538	0.519	0.145	1.1E-220	0.374
TJP2	1.0228E-224	0.30225367	0.63	0.211	1.5E-220	0.419
CCT4	2.8134E-223	0.25454161	0.873	0.403	4.2E-219	0.47
RPL35A	5.8024E-223	0.38545016	1	0.964	8.6E-219	0.036
ALDOA	2.3854E-222	0.55038445	0.991	0.806	3.5E-218	0.185
POLR2F	9.1391E-222	0.39217299	0.936	0.484	1.4E-217	0.452
CAPN1	1.8005E-221	0.33873368	0.83	0.384	2.7E-217	0.446
EMG1	2.4099E-221	0.26417787	0.613	0.198	3.6E-217	0.415
RPL5	4.5486E-221	0.46452562	0.999	0.913	6.7E-217	0.086

PLAC8	2.1041E-220	0.38407467	0.461	0.119	3.1E-216	0.342
CDKN3	1.3389E-219	0.30052027	0.303	0.036	2E-215	0.267
CSNK1A1	2.2121E-219	0.46318878	0.859	0.448	3.3E-215	0.411
EMC4	9.1615E-219	0.27677549	0.895	0.411	1.4E-214	0.484
MMP28	4.0861E-218	0.27239874	0.436	0.102	6E-214	0.334
METAP2	1.9595E-217	0.28656486	0.832	0.351	2.9E-213	0.481
PCBD1	1.9702E-217	0.3225744	0.963	0.538	2.9E-213	0.425
RPL27A	5.0151E-217	0.52706262	0.996	0.839	7.4E-213	0.157
TMEM40	1.5869E-216	0.32291907	0.464	0.123	2.3E-212	0.341
SYTL1	5.7603E-216	0.26907886	0.595	0.197	8.5E-212	0.398
S100P	7.423E-216	1.1587362	0.762	0.449	1.1E-211	0.313
PCNA	9.1875E-216	0.39048763	0.523	0.16	1.4E-211	0.363
EIF3F	1.8017E-214	0.3808243	0.945	0.533	2.7E-210	0.412
DUSP1	1.7002E-213	0.69188711	0.924	0.58	2.5E-209	0.344
CCNB1	1.5632E-212	0.27242994	0.33	0.052	2.3E-208	0.278

SOD1	3.2301E-212	0.34128208	0.977	0.669	4.8E-208	0.308
CTSD	6.4659E-212	0.58062318	0.94	0.618	9.6E-208	0.322
LAMTOR1	2.9679E-211	0.27346043	0.911	0.45	4.4E-207	0.461
NDUFA12	3.9659E-210	0.28325142	0.911	0.441	5.9E-206	0.47
ENY2	1.1939E-209	0.40486222	0.982	0.646	1.8E-205	0.336
ARHGDIB	6.3895E-209	0.35208497	0.66	0.258	9.4E-205	0.402
SET	7.5182E-209	0.47853893	0.951	0.566	1.1E-204	0.385
ENSA	9.16E-209	0.28027374	0.915	0.469	1.4E-204	0.446
IGFBP6	1.7959E-208	0.42427059	0.561	0.195	2.7E-204	0.366
TMED3	2.1701E-208	0.25977061	0.89	0.417	3.2E-204	0.473
SGMS2	2.1979E-208	0.25441351	0.569	0.187	3.3E-204	0.382
ARL5B	2.5834E-208	0.36072463	0.64	0.239	3.8E-204	0.401
TRIB1	1.4972E-207	0.47235753	0.756	0.341	2.2E-203	0.415
TUBA1C	4.1577E-207	0.25612521	0.801	0.365	6.1E-203	0.436

EMP2	5.4129E-207	0.40017865	0.858	0.421	8E-203	0.437
TSPO	7.4919E-207	0.50885486	0.975	0.763	1.1E-202	0.212
U2AF1	7.3278E-205	0.32871553	0.806	0.324	1.1E-200	0.482
ARL6IP4	1.4969E-204	0.28089811	0.952	0.538	2.2E-200	0.414
GMNN	6.388E-204	0.383173	0.576	0.192	9.4E-200	0.384
GCHFR	1.1344E-202	0.25339484	0.707	0.277	1.7E-198	0.43
CD63	1.7745E-202	0.48071896	0.995	0.787	2.6E-198	0.208
RPL18	3.5594E-201	0.39186046	1	0.946	5.3E-197	0.054
TIMM8B	1.0665E-200	0.30440642	0.908	0.451	1.6E-196	0.457
EMP1	1.2601E-200	0.67126575	0.735	0.422	1.9E-196	0.313
DKK1	2.286E-200	0.26501027	0.478	0.137	3.4E-196	0.341
TMEM14B	5.8474E-200	0.26938134	0.882	0.431	8.6E-196	0.451
ANKRD36C	1.6731E-199	0.69635428	0.545	0.201	2.5E-195	0.344
MRPL20	2.3524E-199	0.28702074	0.912	0.509	3.5E-195	0.403
COX16	1.1725E-198	0.26092973	0.909	0.444	1.7E-	0.465

					194	
KDELR2	2.3587E-198	0.32445413	0.958	0.59	3.5E-	0.368
					194	
PSME1	3.227E-198	0.30271207	0.965	0.569	4.8E-	0.396
					194	
CAPN2	4.6045E-198	0.36455255	0.84	0.438	6.8E-	0.402
					194	
TOMM7	9.6864E-198	0.44279459	0.996	0.822	1.4E-	0.174
					193	
GADD45GIP	1.8823E-197	0.27549167	0.934	0.475	2.8E-	0.459
1					193	
HNRNPA0	3.3933E-196	0.33944409	0.883	0.429	5E-192	0.454
PSENEN	4.3784E-196	0.26524812	0.906	0.442	6.5E-	0.464
					192	
ATP6V0B	3.7744E-195	0.30041709	0.958	0.559	5.6E-	0.399
					191	
DEK	3.5901E-194	0.49330757	0.864	0.469	5.3E-	0.395
					190	
NDUFA11	8.3689E-194	0.35356946	0.954	0.528	1.2E-	0.426
					189	
ATRAID	1.6889E-193	0.25868088	0.923	0.473	2.5E-	0.45
					189	
BCL10	8.2071E-193	0.25601305	0.601	0.22	1.2E-	0.381
					188	
ADIRF	8.6887E-191	0.73010356	0.786	0.515	1.3E-	0.271
					186	
PLP2	4.6373E-190	0.33186892	0.936	0.551	6.9E-	0.385
					186	

H2AFV	1.1711E-188	0.35659504	0.899	0.493	1.7E-184	0.406
SKP1	2.495E-188	0.36801358	0.994	0.751	3.7E-184	0.243
TNFRSF12A	3.1395E-188	0.42951306	0.955	0.602	4.6E-184	0.353
SUB1	8.9621E-188	0.34696948	0.994	0.722	1.3E-183	0.272
AURKAIP1	1.3389E-187	0.30127052	0.935	0.566	2E-183	0.369
EIF3L	2.6759E-186	0.64842765	0.91	0.515	4E-182	0.395
COX4I1	2.0413E-185	0.41143178	0.996	0.825	3E-181	0.171
COX7B	4.5185E-184	0.33374546	0.995	0.739	6.7E-180	0.256
BAG3	1.7726E-183	0.31048528	0.662	0.265	2.6E-179	0.397
PTGES	1.7597E-182	0.28633541	0.566	0.206	2.6E-178	0.36
NACA	9.4973E-182	0.29652022	1	0.902	1.4E-177	0.098
EIF3D	1.1718E-181	0.47296173	0.894	0.46	1.7E-177	0.434
RHOC	1.3412E-181	0.3257858	0.928	0.541	2E-177	0.387
EIF1AX	5.1687E-181	0.29337023	0.905	0.482	7.6E-177	0.423
PKM	9.2147E-181	0.43076178	0.989	0.799	1.4E-176	0.19
HEBP2	1.823E-179	0.32957487	0.792	0.372	2.7E-175	0.42

GTF2A2	5.8946E-179	0.25870097	0.867	0.44	8.7E-175	0.427
NAP1L1	1.5281E-177	0.40145367	0.942	0.555	2.3E-173	0.387
TSPAN1	2.25E-177	0.53166301	0.785	0.476	3.3E-173	0.309
DAAM1	8.8204E-177	0.43759955	0.689	0.306	1.3E-172	0.383
HSP90AB1	1.029E-176	0.39060809	0.996	0.851	1.5E-172	0.145
ANXA1	3.8258E-176	0.82691167	0.772	0.564	5.7E-172	0.208
CLDN10	8.8719E-176	0.4509318	0.56	0.208	1.3E-171	0.352
HSP90AA1	2.405E-175	0.40602157	0.995	0.823	3.6E-171	0.172
UBA52	7.4269E-175	0.34949541	0.999	0.857	1.1E-170	0.142
SMC4	4.8983E-174	0.32347352	0.548	2.02E-01	7.2E-170	0.346
RPSA	1.2079E-173	0.37582175	0.996	8.42E-01	1.8E-169	0.154
HMGN2	1.6692E-173	0.51120909	0.93	5.85E-01	2.5E-169	0.345
LEPROT	8.0911E-173	0.25808868	0.83	3.88E-01	1.2E-168	0.442
RPL23	9.0494E-172	0.35576259	0.999	8.77E-01	1.3E-167	0.122

SERPINE1	1.0836E-167	0.27771209	0.41	1.21E-01	1.6E-163	0.289
EGR1	3.432E-166	0.31375746	0.773	3.76E-01	5.1E-162	0.397
UBE2I	2.6885E-164	0.28245128	0.912	5.13E-01	4E-160	0.399
MCL1	6.3649E-164	0.36866547	0.874	4.89E-01	9.4E-160	0.385
CP	8.8822E-163	0.27571524	0.415	0.126	1.3E-158	0.289
PLAUR	9.1E-163	0.31499813	0.691	0.326	1.3E-158	0.365
GLUL	8.2597E-161	0.50839106	0.836	0.463	1.2E-156	0.373
LDHA	2.42E-160	0.26042559	0.995	0.74	3.6E-156	0.255
PCBP1	5.9577E-160	0.26850791	0.943	0.584	8.8E-156	0.359
IFI27	6.3931E-160	0.30006881	0.951	0.598	9.5E-156	0.353
TGM2	4.6647E-159	0.33769928	0.777	0.394	6.9E-155	0.383
DDT	7.0506E-156	0.26082466	0.893	0.537	1E-151	0.356
CAST	1.0945E-155	0.35733123	0.885	0.51	1.6E-151	0.375
SLPI	1.6079E-152	0.33728596	0.983	0.742	2.4E-148	0.241
VAMP8	3.3841E-152	0.2853754	0.989	0.695	5E-148	0.294
COX6C	7.2838E-151	0.26751225	1	0.898	1.1E-	0.102

					146	
RPL6	1.5039E-150	0.38387563	1	0.923	2.2E-	0.077
					146	
FHL2	1.2752E-147	0.29339583	0.707	0.371	1.9E-	0.336
					143	
PIM3	1.7455E-147	0.26190474	0.745	0.372	2.6E-	0.373
					143	
KRT10	3.4426E-147	0.32850404	0.952	0.608	5.1E-	0.344
					143	
CTSC	6.1632E-143	0.44733995	0.793	0.389	9.1E-	0.404
					139	
CNN2	2.3356E-142	0.26327681	0.788	0.396	3.5E-	0.392
					138	
SERPINE2	1.9164E-141	0.38460884	0.437	0.154	2.8E-	0.283
					137	
POLR2L	5.2971E-141	0.34439605	0.987	0.745	7.8E-	0.242
					137	
RBX1	3.0076E-139	0.30510076	0.955	0.612	4.4E-	0.343
					135	
KLF4	9.7312E-137	0.28735918	0.696	0.359	1.4E-	0.337
					132	
ARPC2	1.7464E-135	0.36349714	0.972	0.673	2.6E-	0.299
					131	
RPL37A	2.464E-134	0.34856857	0.998	0.907	3.6E-	0.091
					130	
SEC61B	5.0591E-134	0.27013456	0.985	0.687	7.5E-	0.298
					130	
IFITM3	5.7496E-134	0.34419371	0.981	0.752	8.5E-	0.229

					130	
TRMT112	1.5689E-133	0.30511431	0.994	0.743	2.3E-	0.251
					129	
DYNLL1	4.0216E-133	0.3154135	0.993	0.772	5.9E-	0.221
					129	
HSP90B1	1.011E-131	0.26879766	0.975	0.682	1.5E-	0.293
					127	
EEF1B2	2.2288E-131	0.25414177	0.997	0.843	3.3E-	0.154
					127	
ARL6IP1	2.2351E-131	0.35006287	0.895	0.504	3.3E-	0.391
					127	
NBEAL1	2.4414E-129	0.30019935	0.924	0.518	3.6E-	0.406
					125	
KLF6	3.736E-129	0.27062145	0.921	0.603	5.5E-	0.318
					125	
IL18	6.826E-128	0.25681513	0.774	0.387	1E-123	0.387
SQSTM1	9.2183E-127	0.33897433	0.94	0.654	1.4E-	0.286
					122	
APLP2	5.4155E-123	0.2516694	0.937	0.579	8E-119	0.358
RPS5	1.2354E-121	0.33763854	1	0.941	1.8E-	0.059
					117	
KRT8	2.6771E-121	0.35619156	0.996	0.878	4E-117	0.118
NPC2	3.4119E-119	0.43885454	0.916	0.625	5E-115	0.291
PHLDA1	1.4632E-116	0.32546905	0.652	0.327	2.2E-	0.325
					112	
NUCKS1	2.6374E-115	0.27549419	0.936	0.575	3.9E-	0.361
					111	
C19orf33	1.1403E-110	0.37939299	0.94	0.752	1.7E-	0.188

					106	
SRP14	5.7611E-108	0.29761305	0.998	0.814	8.5E-	0.184
					104	
MT-CO3	8.59692E-98	0.26672651	0.999	0.93	1.27E-	0.069
					93	
UBC	5.36328E-95	0.33153678	0.994	0.862	7.93E-	0.132
					91	
RPL3	2.24138E-93	0.45311634	1	0.956	3.31E-	0.044
					89	
FTL	1.65305E-89	0.44851119	1	0.984	2.44E-	0.016
					85	
HSD17B11	9.47557E-70	0.38449598	0.622	0.338	1.4E-65	0.284
CAPS	2.08054E-64	0.29395867	0.616	0.355	3.08E-	0.261
					60	
HIST1H4C	7.55097E-64	0.30200998	0.638	0.353	1.12E-	0.285
					59	
CTGF	1.31066E-61	0.41621384	0.415	0.219	1.94E-	0.196
					57	

Supplementary Table 6 A total of 232 intersecting genes

Gene name

GSTP1

SLC25A5

RHOD

HEBP2

MCL1

TSPO

GTF3C5

PIM3
HSBP1
SERPINB1
COTL1
PTGR1
AP2S1
S100A16
PSMG3
CAPN2
APRT
KRT16
CSTA
SERPINB5
FHL2
CLEC2B
GNA15
DHRS9
NAMPT
CTSD
TPM4
MALL
AKR1C3
ASPH
SQSTM1
CSNK1A1
TINAGL1
SRCAP
NAA20

EGR1
GLUL
FOSL1
TRIB1
ARPC1B
DUSP5
CES1
AKR1C1
CAV1
MUC4
AGR3
FXVD3
ST3GAL4
UGDH
AP2M1
ANXA2
FABP5
PGD
TSPAN1
ZBTB43
HMGA1
ADIRF
OAZ1
PHLDA2
PSCA
FSCN1
GADD45A
NQO1

TXNRD1
HBEGF
PLAUR
TKT
TALDO1
EREG
S100A9
KLF4
PLK3
MGST1
MT2A
S100P
RPS11
TXN
KRT19
ANXA1
LY6E
AKR1B10
SYT8
S100A2
KRT7
SNCG
EFHD2
TACSTD2
ALDH3A1
GPX3
G6PD
FAM83A

EMP1
AKR1C2
SFN
IFI27
HTATIP2
POLR2E
NDUFB5
VDAC2
UQCRH
MDH2
MRPS12
TOMM7
COX8A
LDHA
NDUFAB1
SOD1
EIF3K
COX5A
PRELID1
PRDX1
FTL
AURKAIP1
PARK7
ENO1
ALDOA
CD63
IL18
TXN2

NDUFB9

POLR2F

EMC2

MRPL13

GPAA1

VPS28

MRPL15

PUF60

CAPS

GSDMD

LAPTM4B

EIF3E

MRPS28

SERPINE2

CTSC

CLDN10

DECR1

THOP1

RPL3

GMNN

EIF3D

EIF3L

KRT8

THEM6

PPA2

SPTSSA

C8orf33

LEPROT

HSP90B1
PRPF31
CDK4
MRPL42
NME4
ATP6V0B
HSP90AA1
MRPL47
PFDN6
COPRS
MCTS1
PSMD9
TGFB1
MRPL28
SUB1
CDC123
RPL35
SMIM7
ADK
PMF1
PKP3
ALCAM
UBE2N
HSP90AB1
NSA2
METAP2
STOML2
RHOC

CISD1
BLOC1S1
RPL23A
COMMD7
CHMP4A
PRMT1
FKBP3
SKP1
PSME1
ECHS1
RDX
EI24
ECH1
NDUFS4
CHMP2A
FAM49B
H2AFY
HSD17B10
BTG1
RAB5C
EEF1E1
TBCA
NPM3
GSTO1
EIF3F
CNPY2
SNRPE
LMAN2

REEP5
TNFRSF12A
TAX1BP3
HNRNPA0
MRPL12
HIST1H2BK
RPS9
RPL13A
MAF1
MTDH
PSMA4
NEDD8
RPL4
NDUFC2
HNRNPA1
SNRPB
MRPL23
RTN4
CD59
RPS20
SLC25A6
PSMA1
RPL10A
RPL7
NME1
CYC1
RPS2
EIF4A1

Supplementary Table 7 A total of 190 positive genes identified by Pearson correlation analysis

	gene	cor	p.value	label	p
cor5933	CYC1	0.342933	3.9579E-118	CYC1	232
cor10403	NME1	0.293993	6.89889E-86	NME1	231
cor10842	SNRPB	0.243194	1.57899E-58	SNRPB	230
cor5424	SLC25A5	0.237606	7.0987E-56	SLC25A5	229
cor3838	PRELID1	0.233223	7.65229E-54	PRELID1	228
cor11911	PRMT1	0.230409	1.46924E-52	PRMT1	227
cor10615	MRPL12	0.228413	1.16561E-51	MRPL12	226
cor6820	GSTO1	0.227456	3.12539E-51	GSTO1	225
cor82	ENO1	0.21981	7.0161E-48	ENO1	224
cor9503	NDUFAB1	0.213691	2.73986E-45	NDUFAB1	223
cor7992	CDK4	0.20618	3.23919E-42	CDK4	222
cor5875	NDUFB9	0.205787	4.65907E-42	NDUFB9	221
cor4787	MDH2	0.205708	5.00925E-42	MDH2	220
cor2789	MRPL47	0.204277	1.863E-41	MRPL47	219
cor11696	MRPS12	0.203464	3.91223E-41	MRPS12	218
cor5280	HSD17B10	0.202946	6.26787E-41	HSD17B10	217
cor11686	EIF3K	0.199869	1.00238E-39	EIF3K	216
cor6793	NPM3	0.19894	2.294E-39	NPM3	215
cor13114	AKR1B10	0.198939	2.29644E-39	AKR1B10	214
cor6463	AKR1C3	0.195451	4.95734E-38	AKR1C3	213
cor1121	SNRPE	0.195087	6.80629E-38	SNRPE	212
cor8886	HSP90AA1	0.19491	7.93971E-38	HSP90AA1	211
cor4150	HMGA1	0.192668	5.51569E-37	HMGA1	210

cor437	UQCRH	0.192429	6.77061E-37	UQCRH	209
cor9211	PSMA4	0.191953	1.01817E-36	PSMA4	208
cor2808	AP2M1	0.191308	1.76666E-36	AP2M1	207
cor10007	EIF4A1	0.188405	2.05819E-35	EIF4A1	206
cor6904	ECHS1	0.181711	5.08528E-33	ECHS1	205
cor11847	AP2S1	0.181097	8.34216E-33	AP2S1	204
cor4244	HSP90AB1	0.176765	2.60634E-31	HSP90AB1	203
cor5924	PUF60	0.176219	3.99657E-31	PUF60	202
cor7043	LDHA	0.175085	9.67355E-31	LDHA	201
cor9347	RPS2	0.17356	3.14456E-30	RPS2	200
cor6487	CDC123	0.173556	3.15272E-30	CDC123	199
cor5857	MRPL13	0.17351	3.26758E-30	MRPL13	198
cor78	PARK7	0.173335	3.73703E-30	PARK7	197
cor3668	H2AFY	0.171863	1.15253E-29	H2AFY	196
cor9182	COX5A	0.170251	3.90825E-29	COX5A	195
cor3918	EEF1E1	0.169968	4.83944E-29	EEF1E1	194
cor4963	CAV1	0.168943	1.04408E-28	CAV1	193
cor6049	STOML2	0.168217	1.7953E-28	STOML2	192
cor6590	CISD1	0.166613	5.89403E-28	CISD1	191
cor7028	PSMA1	0.165665	1.18266E-27	PSMA1	190
cor2457	TKT	0.165595	1.24538E-27	TKT	189
cor6947	MRPL23	0.16532	1.52298E-27	MRPL23	188
cor425	PRDX1	0.163994	4.00025E-27	PRDX1	187
cor7339	GSTP1	0.161309	2.75826E-26	GSTP1	186
cor7221	COX8A	0.161307	2.76215E-26	COX8A	185
cor6669	VDAC2	0.158753	1.68073E-25	VDAC2	184
cor3429	NDUFS4	0.156826	6.43805E-25	NDUFS4	183
cor6461	AKR1C1	0.155886	1.23173E-24	AKR1C1	182

cor5885	FAM49B	0.15586	1.25392E-24	FAM49B	181
cor9135	RPL4	0.155801	1.30584E-24	RPL4	180
cor8641	FKBP3	0.15554	1.56238E-24	FKBP3	179
cor5963	C8orf33	0.155466	1.64454E-24	C8orf33	178
cor6666	ADK	0.153648	5.68291E-24	ADK	177
cor8072	MRPL42	0.152613	1.14342E-23	MRPL42	176
cor2790	NDUFB5	0.15175	2.04131E-23	NDUFB5	175
cor7417	NDUFC2	0.151477	2.44926E-23	NDUFC2	174
cor812	S100A16	0.150805	3.83337E-23	S100A16	173
cor6929	TALDO1	0.150787	3.88054E-23	TALDO1	172
cor7917	HNRNPA1	0.150583	4.44488E-23	HNRNPA1	171
cor5804	MTDH	0.149174	1.12779E-22	MTDH	170
cor4152	RPS10	0.147784	2.80104E-22	RPS10	169
cor8071	UBE2N	0.147291	3.86071E-22	UBE2N	168
cor9826	COTL1	0.145132	1.55177E-21	COTL1	167
cor3183	PPA2	0.14449	2.33733E-21	PPA2	166
cor5706	MRPL15	0.144362	2.53484E-21	MRPL15	165
cor10906	NAA20	0.143505	4.36461E-21	NAA20	164
cor6287	RPL35	0.141701	1.3559E-20	RPL35	163
cor6224	PTGR1	0.141268	1.77537E-20	PTGR1	162
cor6222	TXN	0.141228	1.82005E-20	TXN	161
cor5530	G6PD	0.140329	3.17908E-20	G6PD	160
cor11168	POLR2E	0.139711	4.6511E-20	POLR2E	159
cor11203	OAZ1	0.137335	1.98079E-19	OAZ1	158
cor9859	APRT	0.135947	4.5653E-19	APRT	157
cor3758	GPX3	0.133812	1.62101E-18	GPX3	156
cor4564	PSMG3	0.13341	2.05343E-18	PSMG3	155
cor7955	CNPY2	0.133192	2.33328E-18	CNPY2	154

cor3653	SKP1	0.13157	6.00247E-18	SKP1	153
cor7594	EI24	0.129463	2.01213E-17	EI24	152
cor8586	NEDD8	0.127983	4.65288E-17	NEDD8	151
cor7761	MGST1	0.126247	1.22781E-16	MGST1	150
cor4586	FSCN1	0.125733	1.63285E-16	FSCN1	149
cor20	AURKAIP1	0.12563	1.72807E-16	AURKAIP1	148
cor12111	CHMP2A	0.124463	3.28281E-16	CHMP2A	147
cor5932	GPAA1	0.122319	1.05109E-15	GPAA1	146
cor811	S100A2	0.12173	1.44197E-15	S100A2	145
cor3596	REEP5	0.121299	1.815E-15	REEP5	144
cor11219	GNA15	0.120977	2.15456E-15	GNA15	143
cor12256	TXN2	0.119989	3.63655E-15	TXN2	142
cor7891	KRT7	0.119509	4.68293E-15	KRT7	141
cor10276	RAB5C	0.119427	4.88886E-15	RAB5C	140
cor12284	POLR2F	0.119279	5.28328E-15	POLR2F	139
cor9648	MT2A	0.119178	5.57107E-15	MT2A	138
cor9751	NQO1	0.119015	6.06802E-15	NQO1	137
cor5836	EIF3E	0.118808	6.76113E-15	EIF3E	136
cor12574	SFN	0.118121	9.67258E-15	SFN	135
cor10168	COPRS	0.117998	1.03105E-14	COPRS	134
cor3500	NSA2	0.117963	1.04971E-14	NSA2	133
cor7321	RHOD	0.117927	1.0694E-14	NA	132
cor10135	RPL23A	0.116692	2.02285E-14	NA	131
cor6462	AKR1C2	0.116234	2.55702E-14	NA	130
cor4137	PFDN6	0.115544	3.63509E-14	NA	129
cor9301	MRPL28	0.114208	7.13959E-14	NA	128
cor12432	SOD1	0.113473	1.03154E-13	NA	127
cor5805	LAPTM4B	0.112762	1.46975E-13	NA	126

cor8245	PSMD9	0.111313	3.00201E-13	NA	125
cor405	ATP6V0B	0.109127	8.6668E-13	NA	124
cor879	PMF1	0.108932	9.51382E-13	NA	123
cor5439	MCTS1	0.107117	2.25497E-12	NA	122
cor9095	ANXA2	0.106145	3.55874E-12	NA	121
cor280	TINAGL1	0.105582	4.62538E-12	NA	120
cor3381	SUB1	0.104656	7.10006E-12	NA	119
cor12258	EIF3D	0.104504	7.61709E-12	NA	118
cor11901	RPS11	0.103406	1.25907E-11	NA	117
cor8584	CHMP4A	0.102676	1.75328E-11	NA	116
cor128	EFHD2	0.100886	3.9131E-11	NA	115
cor11994	PRPF31	0.099978	5.84696E-11	NA	114
cor9303	NME4	0.099861	6.15669E-11	NA	113
cor98	PGD	0.09954	7.08861E-11	NA	112
cor3515	TBCA	0.099097	8.60489E-11	NA	111
cor9556	ALDOA	0.098525	1.10392E-10	NA	110
cor8576	PSME1	0.095475	4.07098E-10	NA	109
cor6377	GTF3C5	0.093581	8.96999E-10	NA	108
cor5711	RPS20	0.090973	2.59697E-09	NA	107
cor5916	GSDMD	0.090685	2.91471E-09	NA	106
cor4163	RPL10A	0.090514	3.12174E-09	NA	105
cor5747	RPL7	0.089362	4.93334E-09	NA	104
cor13653	KRT16	0.0885	6.92534E-09	NA	103
cor11212	THOP1	0.087867	8.86325E-09	NA	102
cor3889	SERPINB1	0.087646	9.66065E-09	NA	101
cor13710	SERPINB5	0.087555	1.00064E-08	NA	100
cor5124	SLC25A6	0.087305	1.10237E-08	NA	99
cor10939	COMMD7	0.08606	1.77684E-08	NA	98

cor11690	ECH1	0.085979	1.83252E-08	NA	97
cor13643	ALDH3A1	0.085804	1.95846E-08	NA	96
cor8081	METAP2	0.085001	2.65349E-08	NA	95
cor3742	CSNK1A1	0.084334	3.40859E-08	NA	94
cor3674	HNRNPA0	0.084159	3.63864E-08	NA	93
cor3700	HBEGF	0.083219	5.15637E-08	NA	92
cor5722	ASPH	0.083029	5.53133E-08	NA	91
cor6990	EIF3F	0.083006	5.57715E-08	NA	90
cor3964	GMNN	0.081423	9.93686E-08	NA	89
cor1721	FHL2	0.080837	1.2269E-07	NA	88
cor9382	TNFRSF12A	0.080024	1.6404E-07	NA	87
cor5935	MAF1	0.079494	1.97908E-07	NA	86
cor7492	RDX	0.079441	2.01709E-07	NA	85
cor7052	HTATIP2	0.078767	2.55601E-07	NA	84
cor11900	RPL13A	0.07871	2.60784E-07	NA	83
cor9921	TAX1BP3	0.076187	6.22031E-07	NA	82
cor5759	MRPS28	0.076004	6.61744E-07	NA	81
cor8115	HSP90B1	0.075134	8.87095E-07	NA	80
cor3671	TGFBI	0.073983	1.30055E-06	NA	79
cor13202	FAM83A	0.073975	1.30397E-06	NA	78
cor7506	IL18	0.073278	1.63988E-06	NA	77
cor12282	EIF3L	0.071564	2.85522E-06	NA	76
cor5764	FABP5	0.067918	8.915E-06	NA	75
cor11476	SMIM7	0.067638	9.70709E-06	NA	74
cor3007	UGDH	0.06646	1.38388E-05	NA	73
cor11605	FXYP3	0.065499	1.84051E-05	NA	72
cor9818	HSBP1	0.064718	2.3138E-05	NA	71
cor5781	DECR1	0.061256	6.19178E-05	NA	70

cor7290	FOSL1	0.061126	6.4192E-05	NA	69
cor4852	ARPC1B	0.060887	6.8575E-05	NA	68
cor12310	RPL3	0.059733	9.39942E-05	NA	67
cor11886	FTL	0.059576	9.8072E-05	NA	66
cor7074	CD59	0.059163	0.00010962	NA	65
cor13332	SYT8	0.058715	0.000123568	NA	64
cor4628	TOMM7	0.058335	0.000136708	NA	63
cor5837	EMC2	0.058168	0.00014291	NA	62
cor13330	PKP3	0.055709	0.000270466	NA	61
cor521	GADD45A	0.053275	0.000496365	NA	60
cor11466	TPM4	0.052276	0.000632371	NA	59
cor5906	THEM6	0.051793	0.000710031	NA	58
cor8121	TXNRD1	0.050499	0.000963374	NA	57
cor10263	KRT19	0.049962	0.001091334	NA	56
cor1506	RTN4	0.048893	0.001393927	NA	55
cor5944	VPS28	0.048892	0.001394266	NA	54
cor12000	RPS9	0.047937	0.00172829	NA	53
cor3839	LMAN2	0.04548	0.00295311	NA	52
cor5908	LY6E	0.043838	0.00416786	NA	51
cor7928	BLOC1S1	0.041893	0.006183191	NA	50
cor6959	PHLDA2	0.040768	0.007714683	NA	49
cor9641	CES1	0.040646	0.007899704	NA	48
cor1203	CAPN2	0.040056	0.008850772	NA	47
cor674	RHOC	0.0372	0.015057204	NA	46
cor805	S100A9	0.033558	0.028319607	NA	45
cor8618	SPTSSA	0.030509	0.046208821	NA	44
cor12386	PIM3	0.030055	0.049551324	NA	43

Supplementary Table 8 Result of KEGG enrichment

I	Des	G	B	pv	p.	qv	geneID
D	cript	en	g	al	ad	al	
	ion	eR	R	ue	ju	ue	
		ati	at		st		
		o	io				
hs	Che	19	22	2.1	4.2	3.5	CYC1/SLC25A5/GSTO1/NDUFAB1/NDUFB9/A
a0	mica	/1	7	9E	1E	77	KR1C3/UQCRH/COX5A/COX8A/VDAC2/NDU
52	l	29	/	-10	-08	09	FS4/AKR1C1/NDUFB5/NDUFC2/MGST1/NQO1
08	carci		93			E-	/AKR1C2/SOD1/SLC25A6
	noge		96			08	
	nesi						
	s	-					
	react						
	ive						
	oxyg						
	en						
	spec						
	ies						
hs	Hun	21	31	1.2	1.1	9.8	CYC1/SLC25A5/NDUFAB1/NDUFB9/UQCRH/P
a0	tingt	/1	1	1E	6E	98	SMA4/AP2M1/AP2S1/COX5A/PSMA1/COX8A/
50	on	29	/	-09	-07	86	VDAC2/NDUFS4/NDUFB5/NDUFC2/POLR2E/
16	dise		93			E-	GPX3/POLR2F/SOD1/PSMD9/SLC25A6
	ase		96			08	
hs	Park	19	27	4.3	2.8	2.3	CYC1/SLC25A5/NDUFAB1/NDUFB9/UQCRH/P
a0	inso	/1	1	8E	0E	80	SMA4/PARK7/COX5A/PSMA1/COX8A/VDAC2
50	n	29	/	-09	-07	43	/NDUFS4/NDUFB5/NDUFC2/TXN/TXN2/SOD
12	dise		93			E-	1/PSMD9/SLC25A6
	ase		96			07	
hs	Prio	17	27	2.2	1.0	9.1	CYC1/SLC25A5/NDUFAB1/NDUFB9/UQCRH/P

a0	n	/1	8	5E	8E	82	SMA4/COX5A/CAV1/PSMA1/COX8A/VDAC2/
50	dise	29	/	-07	-05	7E	NDUFS4/NDUFB5/NDUFC2/SOD1/PSMD9/SLC
20	ase		93			-06	25A6
			96				
hs	Alzh	19	39	1.4	5.5	4.6	CYC1/SLC25A5/NDUFAB1/NDUFB9/HSD17B10
a0	eime	/1	1	4E	1E	85	/UQCRH/PSMA4/COX5A/PSMA1/COX8A/VD
50	r	29	/	-06	-05	01	AC2/NDUFS4/NDUFB5/NDUFC2/PSMD9/SLC2
10	dise		93			E-	5A6/CSNK1A1/RTN4/CAPN2
	ase		96			05	
hs	Path	21	48	2.2	7.3	6.2	CYC1/SLC25A5/NDUFAB1/NDUFB9/HSD17B10
a0	way	/1	3	8E	0E	00	/UQCRH/PSMA4/PARK7/COX5A/PSMA1/COX
50	s of	29	/	-06	-05	14	8A/VDAC2/NDUFS4/NDUFB5/NDUFC2/GPX3
22	neur		93			E-	/SOD1/PSMD9/SLC25A6/CSNK1A1/CAPN2
	ode		96			05	
	gene						
	ratio						
	n -						
	mult						
	iple						
	dise						
	ases						
hs	Oxi	11	13	2.7	7.6	6.5	CYC1/NDUFAB1/NDUFB9/UQCRH/COX5A/C
a0	dati	/1	8	9E	7E	13	OX8A/NDUFS4/NDUFB5/NDUFC2/PPA2/ATP6
01	ve	29	/	-06	-05	82	V0B
90	phos		93			E-	
	phor		96			05	
	ylati						
	on						

hs	Diab	13	20	4.4	1.0	9.0	CYC1/SLC25A5/NDUFAB1/NDUFB9/UQCRH/
a0	etic	/1	5	2E	6E	15	COX5A/COX8A/VDAC2/NDUFS4/NDUFB5/ND
54	card	29	/	-06	-04	6E	UFC2/G6PD/SLC25A6
15	iom		93			-05	
	yop		96				
	athy						
hs	Cor	13	23	2.2	4.6	0.0	RPS2/RPL4/RPS10/RPL35/RPL23A/RPS11/RPS2
a0	ona	/1	8	15	2E	00	0/RPL10A/RPL7/HBEGF/RPL13A/RPL3/RPS9
51	viru	29	/	85	-04	39	
71	s		93	E-		25	
	dise		96	05		62	
	ase -						
	CO						
	VID-						
	19						
hs	Flui	10	14	2.4	4.6	0.0	GSTO1/HSP90AA1/HSP90AB1/CAV1/GSTP1/TX
a0	d	/1	2	06	2E	00	N/MGST1/TXN2/NQO1/HSP90B1
54	shea	29	/	03	-04	39	
18	r		93	E-		25	
	stres		96	05		62	
	s						
	and						
	athe						
	roscl						
	erosi						
	s						
hs	Pent	5/	31	5.7	0.0	0.0	TKT/TALDO1/G6PD/PGD/ALDOA
a0	ose	12	/	58	01	00	

00	phos	9	93	16	00	85	
30	phat		96	E-	50	40	
	e			05	61	81	
	path						
	way						
hs	Glut	6/	59	0.0	0.0	0.0	GSTO1/GSTP1/G6PD/GPX3/MGST1/PGD
a0	athi	12	/	00	02	02	
04	one	9	93	14	36	01	
80	met		96	79	79	22	
	abol			98	73	58	
	ism						
hs	Am	15	37	0.0	0.0	0.0	CYC1/NDUFAB1/NDUFB9/UQCRH/PSMA4/C
a0	yotr	/1	1	00	02	02	OX5A/PSMA1/COX8A/NDUFS4/NDUFB5/NDU
50	ophi	29	/	16	42	06	FC2/HNRNPA1/GPX3/SOD1/PSMD9
14	c		93	42	55	12	
	later		96	32	82	13	
	al						
	scler						
	osis						
hs	Carb	8/	11	0.0	0.0	0.0	ENO1/MDH2/ECHS1/TKT/TALDO1/G6PD/PG
a0	on	12	7	00	02	02	D/ALDOA
12	met	9	/	19	71	30	
00	abol		93	78	38	61	
	ism		96	85	51	78	
hs	Non	9/	15	0.0	0.0	0.0	CYC1/NDUFAB1/NDUFB9/UQCRH/COX5A/C
a0	-	12	7	00	03	03	OX8A/NDUFS4/NDUFB5/NDUFC2
49	alco	9	/	29	83	25	
32	holic		93	95	46	85	

	fatty		96	8	24	89	
	liver						
	dise						
	ase						
hs	Necr	9/	15	0.0	0.0	0.0	SLC25A5/HSP90AA1/HSP90AB1/VDAC2/CHMP
a0	opto	12	9	00	03	03	2A/CHMP4A/SLC25A6/FTL/CAPN2
42	sis	9	/	32	94	35	
17			93	90	89	57	
			96	79	51	42	
hs	Sal	11	25	0.0	0.0	0.0	HSP90AA1/HSP90AB1/TXN/SKP1/TXN2/RAB5
a0	mon	/1	1	00	07	06	C/ANXA2/GSDMD/HSP90B1/IL18/ARPC1B
51	ella	29	/	65	39	28	
32	infec		93	50	82	69	
	tion		96	57	86	21	
hs	Dru	6/	81	0.0	0.0	0.0	NME1/GSTO1/GSTP1/MGST1/NME4/CES1
a0	g	12	/	00	08	07	
09	met	9	93	83	89	55	
83	abol		96	36	26	67	
	ism			85	44	97	
	-						
	othe						
	r						
	enzy						
	mes						
hs	Car	6/	87	0.0	0.0	0.0	CYC1/UQCRH/COX5A/COX8A/ASPH/TPM4
a0	diac	12	/	01	12	10	
42	mus	9	93	21	26	41	
60	cle		96	33	08	90	

	cont			09	11	01	
	racti						
	on						
hs	Hep	8/	17	0.0	0.0	0.0	GSTO1/CDK4/GSTP1/MGST1/NQO1/CSNK1A1
a0	atoc	12	0	02	22	18	/GADD45A/TXNRD1
52	ellul	9	/	32	27	93	
25	ar		93	04	63	00	
	carci		96	56	79	37	
	nom						
	a						
hs	Prot	4/	46	0.0	0.0	0.0	PSMA4/PSMA1/PSMD9/PSME1
a0	easo	12	/	03	31	26	
30	me	9	93	54	55	81	
50			96	34	34	35	
				09	96	52	
hs	p53	5/	75	0.0	0.0	0.0	CDK4/EI24/SFN/SERPINB5/GADD45A
a0	sign	12	/	03	31	26	
41	alin	9	93	61	55	81	
15	g		96	55	34	35	
	path			05	96	52	
	way						
hs	Met	5/	79	0.0	0.0	0.0	GSTO1/GSTP1/AKR1C1/MGST1/ALDH3A1
a0	abol	12	/	04	37	32	
09	ism	9	93	52	73	06	
80	of		96	04	62	75	
	xeno			87	42	3	
	bioti						
	cs						

	by						
	cyto						
	chro						
	me						
	P450						
hs	Ther	9/	23	0.0	0.0	0.0	CYC1/NDUFAB1/NDUFB9/UQCRH/COX5A/C
a0	mog	12	5	04	39	33	OX8A/NDUFS4/NDUFB5/NDUFC2
47	enes	9	/	99	97	96	
14	is		93	64	13	68	
			96	19	55	86	
hs	IL-	5/	95	0.0	0.0	0.0	HSP90AA1/HSP90AB1/HSP90B1/FOSL1/S100A9
a0	17	12	/	09	75	63	
46	sign	9	93	77	05	78	
57	alin		96	31	77	26	
	g			46	63	39	
	path						
	way						
hs	Estr	6/	13	0.0	0.0	0.0	HSP90AA1/HSP90AB1/KRT16/HBEGF/HSP90B1
a0	ogen	12	9	12	89	76	/KRT19
49	sign	9	/	12	57	11	
15	alin		93	94	14	60	
	g		96	66	39	81	
	path						
	way						
hs	Glyc	4/	67	0.0	0.0	0.0	ENO1/LDHA/ALDOA/ALDH3A1
a0	olysi	12	/	13	94	80	
00	s /	9	93	35	96	69	
10	Gluc		96	42	32	79	

	oneo			06	44	32	
	gene						
	sis						
hs	Spin	6/	14	0.0	0.0	0.0	SLC25A5/PSMA4/PSMA1/VDAC2/PSMD9/SLC2
a0	ocer	12	4	14	97	83	5A6
50	ebell	9	/	24	68	01	
17	ar		93	64	98	49	
	ataxi		96	38	57	55	
	a						
hs	NO	7/	18	0.0	0.1	0.0	HSP90AA1/HSP90AB1/VDAC2/TXN/TXN2/GS
a0	D-	12	9	15	00	85	DMD/IL18
46	like	9	/	21	76	62	
21	rece		93	91	12	50	
	ptor		96	54	95	04	
	sign						
	alin						
	g						
	path						
	way						
hs	Che	4/	71	0.0	0.1	0.0	GSTO1/GSTP1/MGST1/AKR1C2
a0	mica	12	/	16	03	88	
52	l	9	93	23	91	30	
04	carci		96	70	71	67	
	noge			55	55	93	
	nesi						
	s -						
	DN						
	A						

	add						
	ucts						
hs	Dru	4/	73	0.0	0.1	0.0	GSTO1/GSTP1/MGST1/ALDH3A1
a0	g	12	/	17	10	93	
09	met	9	93	81	33	75	
82	abol		96	39	16	76	
	ism			62	33	93	
	-						
	cyto						
	chro						
	me						
	P450						
hs	Bios	4/	75	0.0	0.1	0.0	ENO1/TKT/TALDO1/ALDOA
a0	ynth	12	/	19	16	99	
12	esis	9	93	48	89	33	
30	of		96	32	94	89	
	ami			48	88	29	
	no						
	acid						
	s						
hs	Cell	6/	15	0.0	0.1	0.1	SLC25A5/CDK4/VDAC2/SLC25A6/GADD45A/C
a0	ular	12	7	20	21	03	APN2
42	sene	9	/	93	78	48	
18	scen		93	09	00	63	
	ce		96	47	57	43	
hs	End	8/	25	0.0	0.1	0.1	AP2M1/AP2S1/CAV1/CHMP2A/RAB5C/CHMP
a0	ocyt	12	2	22	27	08	4A/ARPC1B/VPS28
41	osis	9	/	60	62	45	

44			93	06	74	53	
			96	93	41	36	
hs	Cyto	4/	83	0.0	0.1	0.1	POLR2E/POLR2F/GSDMD/IL18
a0	solic	12	/	27	48	26	
46	DN	9	93	10	71	37	
23	A-		96	95	50	51	
	sens			11	3	62	
	ing						
	path						
	way						
hs	Nucl	4/	85	0.0	0.1	0.1	NME1/ADK/APRT/NME4
a0	eoti	12	/	29	56	32	
12	de	9	93	25	04	60	
32	met		96	84	52	42	
	abol			78	18	15	
	ism						
hs	Prot	6/	17	0.0	0.1	0.1	HSP90AA1/HSP90AB1/SKP1/HSP90B1/LMAN2/
a0	ein	12	1	30	56	33	CAPN2
41	proc	9	/	22	82	27	
41	essi		93	23	96	08	
	ng		96	81	5	1	
	in						
	end						
	opla						
	smic						
	retic						
	ulu						
	m						

Supplementary Table 9 Result of GO enrichment

O	I	Des	G	B	p	p.	q	geneID	C
n	D	crip	e	g	v	a	v		o
t		tion	n	R	al	dj	al		u
o			e	at	u	u	u		nt
l			R	io	e	st	e		
o			at						
g			io						
y									
B	G	tran	20	1	3.	1.	8.	EIF3K/EIF4A1/RPS2/CDC123/RPL4/RPS10/	20
P	O:	slati	/	9	7	0	7	RPL35/EIF3E/RPL23A/MCTS1/EIF3D/RPS1	
	00	onal	18	3	9	6	0	1/RPS20/RPL10A/RPL7/EIF3F/RPL13A/EIF	
	06	initi	4	/	E-	E-	E-	3L/RPL3/RPS9	
	41	atio		1	1	1	1		
	3	n		8	5	1	2		
				8					
				6					
				2					
B	G	vira	18	1	9.	1.	1.	RPS2/RPL4/RPS10/RPL35/POLR2E/POLR2F	18
P	O:	l	/	9	2	3	0	/RPL23A/MCTS1/EIF3D/RPS11/RPS20/RPL	
	00	gen	18	8	8	0	6	10A/RPL7/EIF3F/RPL13A/EIF3L/RPL3/RPS	
	19	e	4	/	E-	E-	E-	9	
	08	exp		1	1	0	0		
	0	ress		8	3	9	9		
		ion		8					
				6					
				2					
B	G	prot	15	1	2.	2.	1.	RPS2/RPL4/RPS10/RPL35/GPAA1/RPL23A	15
P	O:	ein	/	5	4	2	8	/RPS11/CHMP4A/RPS20/RPL10A/RPL7/RP	

	00	loca	18	2	2	6	5	L13A/RPL3/RTN4/RPS9	
	70	lizat	4	/	E-	E-	E-		
	97	ion		1	1	0	0		
	2	to		8	1	8	8		
		end		8					
		opla		6					
		smi		2					
		c							
		retic							
		ulu							
		m							
B	G	nucl	13	1	1.	9.	7.	RPS2/RPL4/RPS10/RPL35/EIF3E/RPL23A/R	13
P	O:	ear-	/	2	6	3	6	PS11/RPS20/RPL10A/RPL7/RPL13A/RPL3/	
	00	tran	18	0	7	2	6	RPS9	
	00	scri	4	/	E-	E-	E-		
	18	bed		1	1	0	0		
	4	mR		8	0	8	8		
		NA		8					
		cata		6					
		boli		2					
		c							
		pro							
		cess							
		,							
		non							
		sens							
		e-							
		me							

		diat								
		ed								
		dec								
		ay								
B	G	prot	13	1	1.	9.	7.	RPS2/RPL4/RPS10/RPL35/RPL23A/RPS11/	13	
P	O:	ein	/	2	6	3	6	CHMP4A/RPS20/RPL10A/RPL7/RPL13A/R		
	00	targ	18	0	7	2	6	PL3/RPS9		
	45	etin	4	/	E-	E-	E-			
	04	g to		1	1	0	0			
	7	ER		8	0	8	8			
				8						
				6						
				2						
B	G	ribo	23	4	2.	1.	8.	SNRPB/EIF3K/NPM3/SNRPE/HSP90AA1/	23	
P	O:	nucl	/	7	4	0	2	HSP90AB1/PUF60/RPS2/RPS10/RPL35/EIF3		
	00	eop	18	3	5	1	8	E/NSA2/RPL23A/MCTS1/EIF3D/PRPF31/R		
	22	rote	4	/	E-	E-	E-	PL10A/RPL7/EIF3F/RPL13A/EIF3L/RPL3/R		
	61	in		1	1	0	0	PS9		
	3	com		8	0	7	8			
		plex		8						
		biog		6						
		enes		2						
		is								
B	G	esta	13	1	2.	1.	8.	RPS2/RPL4/RPS10/RPL35/RPL23A/RPS11/	13	
P	O:	blis	/	2	5	0	2	CHMP4A/RPS20/RPL10A/RPL7/RPL13A/R		
	00	hme	18	4	3	1	8	PL3/RPS9		
	72	nt	4	/	E-	E-	E-			
	59	of		1	1	0	0			

	9	prot		8	0	7	8		
		ein		8					
		loca		6					
		lizat		2					
		ion							
		to							
		end							
		opla							
		smi							
		c							
		retic							
		ulu							
		m							
B	G	SRP	12	1	4.	1.	1.	RPS2/RPL4/RPS10/RPL35/RPL23A/RPS11/	12
P	O:	-	/	0	5	6	3	RPS20/RPL10A/RPL7/RPL13A/RPL3/RPS9	
	00	dep	18	5	9	0	2		
	06	end	4	/	E-	E-	E-		
	61	ent		1	1	0	0		
	4	cotr		8	0	7	7		
		ansl		8					
		atio		6					
		nal		2					
		prot							
		ein							
		targ							
		etin							
		g to							
		me							

		mbr								
		ane								
B	G	ribo	16	2	6.	2.	1.	SNRPB/EIF3K/SNRPE/HSP90AA1/HSP90A	16	
P	O:	nucl	/	2	6	0	6	B1/PUF60/RPS10/EIF3E/RPL23A/MCTS1/E		
	00	eop	18	4	3	6	9	IF3D/PRPF31/EIF3F/RPL13A/EIF3L/RPL3		
	22	rote	4	/	E-	E-	E-			
	61	in		1	1	0	0			
	8	com		8	0	7	7			
		plex		8						
		asse		6						
		mbl		2						
		y								
B	G	cotr	12	1	7.	2.	1.	RPS2/RPL4/RPS10/RPL35/RPL23A/RPS11/	12	
P	O:	ansl	/	1	9	2	8	RPS20/RPL10A/RPL7/RPL13A/RPL3/RPS9		
	00	atio	18	0	3	1	2			
	06	nal	4	/	E-	E-	E-			
	61	prot		1	1	0	0			
	3	ein		8	0	7	7			
		targ		8						
		etin		6						
		g to		2						
		me								
		mbr								
		ane								
B	G	deto	13	1	9.	2.	1.	GSTO1/AKR1B10/PARK7/PRDX1/GSTP1/T	13	
P	O:	xific	/	3	6	2	8	XN/GPX3/MGST1/MT2A/NQO1/SOD1/TX		
	00	atio	18	8	6	3	3	NRD1/S100A9		
	98	n	4	/	E-	E-	E-			

			75		1	1	0	0		
			4		8	0	7	7		
					8					
					6					
					2					
B	G	cyto	8	3	1.	2.	1.	EIF3K/EIF4A1/EIF3E/MCTS1/EIF3D/EIF3F/	8	
P	O:	plas	/	4	0	2	8	RPL13A/EIF3L		
		00 mic	18	/	3	3	3			
		02 tran	4	1	E-	E-	E-			
		18 slati		8	0	0	0			
		3 onal		8	9	7	7			
		initi		6						
		atio		2						
		n								
B	G	ribo	16	2	1.	2.	1.	SNRPB/EIF3K/SNRPE/HSP90AA1/HSP90A	16	
P	O:	nucl	/	3	0	2	8	B1/PUF60/RPS10/EIF3E/RPL23A/MCTS1/E		
		00 eop	18	1	4	3	3	IF3D/PRPF31/EIF3F/RPL13A/EIF3L/RPL3		
		71 rote	4	/	E-	E-	E-			
		82 in		1	0	0	0			
		6 com		8	9	7	7			
		plex		8						
		sub		6						
		unit		2						
		org								
		aniz								
		atio								
		n								
B	G	cell	12	1	1.	2.	2.	GSTO1/AKR1B10/PARK7/PRDX1/GSTP1/T	12	

P	O:	ular	/	1	3	6	1	XN/GPX3/MGST1/NQO1/SOD1/TXNRD1/	
	19	deto	18	5	3	6	8	S100A9	
	90	xific	4	/	E-	E-	E-		
	74	atio		1	0	0	0		
	8	n		8	9	7	7		
				8					
				6					
				2					
B	G	cell	12	1	2.	4.	3.	GSTO1/AKR1B10/PARK7/PRDX1/GSTP1/T	12
P	O:	ular	/	2	6	6	8	XN/GPX3/MGST1/NQO1/SOD1/TXNRD1/	
	00	resp	18	2	5	9	5	S100A9	
	97	ons	4	/	E-	E-	E-		
	23	e to		1	0	0	0		
	7	toxi		8	9	7	7		
		c		8					
		sub		6					
		stan		2					
		ce							
B	G	vira	14	1	2.	4.	3.	RPS2/RPL4/RPS10/RPL35/POLR2E/POLR2F	14
P	O:	l	/	8	6	6	8	/RPL23A/RPS11/RPS20/RPL10A/RPL7/RPL	
	00	tran	18	0	9	9	5	13A/RPL3/RPS9	
	19	scri	4	/	E-	E-	E-		
	08	ptio		1	0	0	0		
	3	n		8	9	7	7		
				8					
				6					
				2					
B	G	cell	14	1	4.	7.	5.	CYC1/PRELID1/NDUFAB1/NDUFB9/MDH	14

P	O:	ular	/	8	4	2	9	2/UQCRH/PARK7/COX5A/CISD1/COX8A/	
	00	resp	18	7	1	1	2	NDUFS4/NDUFB5/NDUFC2/BLOC1S1	
	45	irati	4	/	E-	E-	E-		
	33	on		1	0	0	0		
	3			8	9	7	7		
				8					
				6					
				2					
B	G	cell	11	1	4.	7.	5.	GSTO1/PARK7/PRDX1/GSTP1/TXN/GPX3/	11
P	O:	ular	/	0	6	2	9	MGST1/NQO1/SOD1/TXNRD1/S100A9	
	00	oxid	18	2	5	1	2		
	98	ant	4	/	E-	E-	E-		
	86	deto		1	0	0	0		
	9	xific		8	9	7	7		
		atio		8					
		n		6					
				2					
B	G	mR	19	3	5.	7.	6.	PSMA4/RPS2/PSMA1/RPL4/RPS10/RPL35/	19
P	O:	NA	/	7	0	4	1	EIF3E/RPL23A/PSMD9/RPS11/PSME1/RPS2	
	00	cata	18	5	6	3	0	0/RPL10A/RPL7/HNRNPA0/RPL13A/RPL3	
	06	boli	4	/	E-	E-	E-	/PKP3/RPS9	
	40	c		1	0	0	0		
	2	pro		8	9	7	7		
		cess		8					
				6					
				2					
B	G	resp	15	2	1.	1.	1.	GSTO1/CDK4/AKR1B10/PARK7/PRDX1/G	15
P	O:	ons	/	3	3	8	5	STP1/TXN/GPX3/MGST1/MT2A/NQO1/SO	

	00	e to	18	9	4	8	4	D1/TXNRD1/CES1/S100A9	
	09	toxi	4	/	E-	E-	E-		
	63	c		1	0	0	0		
	6	sub		8	8	6	6		
		stan		8					
		ce		6					
				2					
B	G	mit	10	8	1.	1.	1.	MRPL12/MRPL47/MRPS12/MRPL13/MRPL	10
P	O:	och	/	8	4	9	5	23/MRPL42/MRPL15/AURKAIP1/MRPL28/	
	00	ond	18	/	3	0	6	MRPS28	
	70	rial	4	1	E-	E-	E-		
	12	tran		8	0	0	0		
	5	slati		8	8	6	6		
		onal		6					
		elon		2					
		gati							
		on							
B	G	mit	10	8	1.	2.	1.	MRPL12/MRPL47/MRPS12/MRPL13/MRPL	10
P	O:	och	/	9	5	0	6	23/MRPL42/MRPL15/AURKAIP1/MRPL28/	
	00	ond	18	/	9	2	6	MRPS28	
	70	rial	4	1	E-	E-	E-		
	12	tran		8	0	0	0		
	6	slati		8	8	6	6		
		onal		6					
		ter		2					
		min							
		atio							
		n							

B	G	RN	19	4	2.	3.	2.	PSMA4/RPS2/PSMA1/RPL4/RPS10/RPL35/	19
P	O:	A	/	1	4	0	4	EIF3E/RPL23A/PSMD9/RPS11/PSME1/RPS2	
		00	cata	18	4	9	2	8	0/RPL10A/RPL7/HNRNPA0/RPL13A/RPL3
		06	boli	4	/	E-	E-	E-	/PKP3/RPS9
		40	c		1	0	0	0	
		1	pro		8	8	6	6	
			cess		8				
					6				
					2				
B	G	cell	15	2	3.	3.	2.	HSD17B10/AKR1B10/AKR1C3/PSMA4/PAR	15
P	O:	ular	/	5	0	5	8	K7/CAV1/PSMA1/AKR1C1/OAZ1/NQO1/	
		00	keto	18	4	3	2	9	AKR1C2/PSMD9/PSME1/FABP5/CES1
		42	ne	4	/	E-	E-	E-	
		18	met		1	0	0	0	
		0	abol		8	8	6	6	
			ic		8				
			pro		6				
			cess		2				
B	G	mit	10	9	4.	5.	4.	CYC1/NDUFAB1/NDUFB9/UQCRH/PARK7	10
P	O:	och	/	9	4	0	1	/COX5A/COX8A/NDUFS4/NDUFB5/NDUF	
		00	ond	18	/	9	2	2	C2
		42	rial	4	1	E-	E-	E-	
		77	AT		8	0	0	0	
		5	P		8	8	6	6	
			synt		6				
			hesi		2				
			s						
			cou						

			ple							
			d							
			elec							
			tron							
			tran							
			spor							
			t							
B	G	AT	10	1	4.	5.	4.	CYC1/NDUFAB1/NDUFB9/UQCRH/PARK7	10	
P	O:	P	/	0	9	3	3	/COX5A/COX8A/NDUFS4/NDUFB5/NDUF		
	00	synt	18	0	5	1	6	C2		
	42	hesi	4	/	E-	E-	E-			
	77	s		1	0	0	0			
	3	cou		8	8	6	6			
		ple		8						
		d		6						
		elec		2						
		tron								
		tran								
		spor								
		t								
B	G	tran	10	1	7.	8.	6.	MRPL12/MRPL47/MRPS12/MRPL13/MRPL	10	
P	O:	slati	/	0	9	1	7	23/MRPL42/MRPL15/AURKAIP1/MRPL28/		
	00	onal	18	5	1	8	2	MRPS28		
	06	ter	4	/	E-	E-	E-			
	41	min		1	0	0	0			
	5	atio		8	8	6	6			
		n		8						
				6						

				2						
B	G	ener	15	2	9.	9.	8.	CYC1/PRELID1/NDUFAB1/NDUFB9/MDH	15	
P	O:	gy	/	7	9	9	1	2/UQCRH/PARK7/COX5A/CISD1/COX8A/		
	00	deri	18	8	4	1	4	NDUFS4/NDUFB5/NDUFC2/BLOC1S1/PHL		
	15	vati	4	/	E-	E-	E-	DA2		
	98	on		1	0	0	0			
	0	by		8	8	6	6			
		oxid		8						
		atio		6						
		n of		2						
		org								
		anic								
		com								
		pou								
		nds								
B	G	nucl	13	2	1.	1.	1.	RPS2/RPL4/RPS10/RPL35/EIF3E/RPL23A/R	13	
P	O:	ear-	/	0	3	3	0	PS11/RPS20/RPL10A/RPL7/RPL13A/RPL3/		
	00	tran	18	8	5	0	7	RPS9		
	00	scri	4	/	E-	E-	E-			
	95	bed		1	0	0	0			
	6	mR		8	7	5	5			
		NA		8						
		cata		6						
		boli		2						
		c								
		pro								
		cess								
B	G	prot	13	2	1.	1.	1.	RPS2/RPL4/RPS10/RPL35/RPL23A/RPS11/	13	

P	O:	ein	/	1	6	4	2	CHMP4A/RPS20/RPL10A/RPL7/RPL13A/R	
	00	targ	18	1	0	9	2	PL3/RPS9	
	06	etin	4	/	E-	E-	E-		
	61	g to		1	0	0	0		
	2	me		8	7	5	5		
		mbr		8					
		ane		6					
				2					
B	G	resp	10	1	2.	1.	1.	CYC1/NDUFAB1/NDUFB9/UQCRH/PARK7	10
P	O:	irat	/	1	2	9	6	/COX5A/COX8A/NDUFS4/NDUFB5/NDUF	
	00	ory	18	7	1	7	2	C2	
	22	elec	4	/	E-	E-	E-		
	90	tron		1	0	0	0		
	4	tran		8	7	5	5		
		spor		8					
		t		6					
		chai		2					
		n							
B	G	oxid	11	1	2.	1.	1.	CYC1/NDUFAB1/NDUFB9/UQCRH/PARK7	11
P	O:	ativ	/	4	2	9	6	/COX5A/STOML2/COX8A/NDUFS4/NDUF	
	00	e	18	8	6	7	2	B5/NDUFC2	
	06	pho	4	/	E-	E-	E-		
	11	sph		1	0	0	0		
	9	oryl		8	7	5	5		
		atio		8					
		n		6					
				2					
B	G	for	5	1	3.	2.	2.	EIF3K/EIF3E/EIF3D/EIF3F/EIF3L	5

P	O:	mat	/	6	3	8	3	
	00	ion	18	/	5	3	3	
	01	of	4	1	E-	E-	E-	
	73	cyto		8	0	0	0	
	2	plas		8	7	5	5	
		mic		6				
		tran		2				
		slati						
		on						
		initi						
		atio						
		n						
		com						
		plex						
B	G	esta	16	3	4.	3.	2.	HSP90AA1/RPS2/RPL4/RPS10/RPL35/SFN/ 16
P	O:	blis	/	5	1	3	7	RPL23A/RPS11/CHMP4A/RPS20/RPL10A/
	00	hme	18	4	0	6	6	RPL7/RPL13A/RPL3/EMC2/RPS9
	90	nt	4	/	E-	E-	E-	
	15	of		1	0	0	0	
	0	prot		8	7	5	5	
		ein		8				
		loca		6				
		lizat		2				
		ion						
		to						
		me						
		mbr						
		ane						

B	G	mit	11	1	6.	5.	4.	MRPL12/MRPL47/MRPS12/HSD17B10/MRP	11
P	O:	och	/	6	7	3	4	L13/MRPL23/MRPL42/MRPL15/AURKAIP1	
	01	ond	18	5	5	6	0	/MRPL28/MRPS28	
	40	rial	4	/	E-	E-	E-		
	05	gen		1	0	0	0		
	3	e		8	7	5	5		
		exp		8					
		ress		6					
		ion		2					
B	G	cyto	9	1	6.	5.	4.	EIF3K/EIF4A1/EIF3E/MCTS1/EIF3D/RPL10	9
P	O:	plas	/	0	9	3	4	A/EIF3F/RPL13A/EIF3L	
	00	mic	18	2	1	6	0		
	02	tran	4	/	E-	E-	E-		
	18	slati		1	0	0	0		
	1	on		8	7	5	5		
				8					
				6					
				2					
B	G	tran	10	1	7.	5.	4.	MRPL12/MRPL47/MRPS12/MRPL13/MRPL	10
P	O:	slati	/	3	8	7	7	23/MRPL42/MRPL15/AURKAIP1/MRPL28/	
	00	onal	18	4	4	6	3	MRPS28	
	06	elon	4	/	E-	E-	E-		
	41	gati		1	0	0	0		
	4	on		8	7	5	5		
				8					
				6					
				2					
B	G	mit	10	1	7.	5.	4.	MRPL12/MRPL47/MRPS12/MRPL13/MRPL	10

P	O:	och	/	3	8	7	7	23/MRPL42/MRPL15/AURKAIP1/MRPL28/	
	00	ond	18	4	4	6	3	MRPS28	
	32	rial	4	/	E-	E-	E-		
	54	tran		1	0	0	0		
	3	slati		8	7	5	5		
		on		8					
				6					
				2					
B	G	prot	15	3	8.	5.	4.	MRPL12/MRPL47/MRPS12/HMGA1/MRPL	15
P	O:	ein-	/	2	2	9	8	13/CAV1/MRPL23/MRPL42/MRPL15/AUR	
	00	cont	18	8	6	1	5	KAIP1/CHMP2A/MRPL28/CSNK1A1/RDX/	
	32	aini	4	/	E-	E-	E-	MRPS28	
	98	ng		1	0	0	0		
	4	com		8	7	5	5		
		plex		8					
		disa		6					
		sse		2					
		mbl							
		y							
B	G	elec	11	1	1.	9.	8.	CYC1/NDUFAB1/NDUFB9/UQCRH/PARK7	11
P	O:	tron	/	7	4	9	1	/COX5A/COX8A/NDUFS4/NDUFB5/NDUF	
	00	tran	18	8	3	7	9	C2/ASPH	
	22	spor	4	/	E-	E-	E-		
	90	t		1	0	0	0		
	0	chai		8	6	5	5		
		n		8					
				6					
				2					

B	G	prot	17	4	1.	1.	8.	HSP90AA1/RPS2/RPL4/RPS10/RPL35/RPL2	17
P	O:	ein	/	4	6	0	9	3A/RPS11/CHMP4A/RPS20/RPL10A/RPL7/	
	00	targ	18	1	0	9	3	SLC25A6/ECH1/RPL13A/RPL3/TOMM7/RP	
	06	etin	4	/	E-	E-	E-	S9	
	60	g		1	0	0	0		
	5			8	6	4	5		
				8					
				6					
				2					
B	G	ami	4	1	1.	1.	9.	AKR1B10/AKR1C3/AKR1C1/AKR1C2	4
P	O:	nog	/	0	7	1	6		
	00	lyco	18	/	6	7	0		
	30	side	4	1	E-	E-	E-		
	64	anti		8	0	0	0		
	7	biot		8	6	4	5		
		ic		6					
		met		2					
		abol							
		ic							
		pro							
		cess							
B	G	reg	11	1	2.	1.	1.	AKR1C3/PSMA4/PARK7/CAV1/PSMA1/O	11
P	O:	ulat	/	8	0	3	1	AZ1/NQO1/PSMD9/PSME1/FABP5/CES1	
	00	ion	18	5	8	5	1		
	10	of	4	/	E-	E-	E-		
	56	cell		1	0	0	0		
	5	ular		8	6	4	4		
		keto		8					

		ne		6							
		met		2							
		abol									
		ic									
		pro									
		cess									
B	G	reg	7	6	2.	1.	1.	PSMA4/PARK7/PSMA1/OAZ1/NQO1/PSM	7		
P	O:	ulat	/	2	3	4	2	D9/PSME1			
	00	ion	18	/	5	9	2				
	06	of	4	1	E-	E-	E-				
	52	cell		8	0	0	0				
	1	ular		8	6	4	4				
		ami		6							
		no		2							
		acid									
		met									
		abol									
		ic									
		pro									
		cess									
B	G	AT	14	3	2.	1.	1.	CYC1/ENO1/NDUFAB1/NDUFB9/UQCRH	14		
P	O:	P	/	1	5	5	2	/LDHA/PARK7/COX5A/STOML2/COX8A/			
	00	met	18	3	2	6	8	NDUFS4/NDUFB5/NDUFC2/ALDOA			
	46	abol	4	/	E-	E-	E-				
	03	ic		1	0	0	0				
	4	pro		8	6	4	4				
		cess		8							
				6							

				2						
B	G	reac	13	2	4.	2.	2.	AKR1C3/HSP90AA1/HSP90AB1/PARK7/CA	13	
P	O:	tive	/	8	0	4	0	V1/PRDX1/GSTP1/NDUFS4/G6PD/GPX3/		
	00	oxy	18	1	3	4	1	NQO1/SOD1/GADD45A		
	72	gen	4	/	E-	E-	E-			
	59	spec		1	0	0	0			
	3	ies		8	6	4	4			
		met		8						
		abol		6						
		ic		2						
		pro								
		cess								
B	G	pros	6	4	6.	4.	3.	AKR1C3/GSTP1/AKR1C1/PTGR1/AKR1C2/	6	
P	O:	tano	/	8	9	0	3	FABP5		
	00	id	18	/	4	3	1			
	06	met	4	1	E-	E-	E-			
	69	abol		8	0	0	0			
	2	ic		8	6	4	4			
		pro		6						
		cess		2						
B	G	pros	6	4	6.	4.	3.	AKR1C3/GSTP1/AKR1C1/PTGR1/AKR1C2/	6	
P	O:	tagl	/	8	9	0	3	FABP5		
	00	and	18	/	4	3	1			
	06	in	4	1	E-	E-	E-			
	69	met		8	0	0	0			
	3	abol		8	6	4	4			
		ic		6						
		pro		2						

		cess								
B	G	neu	17	5	8.	4.	3.	HSP90AA1/HSP90AB1/GSTP1/NDUFC2/CO	17	
P	O:	trop	/	0	5	8	9	TL1/APRT/MGST1/RAB5C/ANXA2/ALDO		
	00	hil	18	0	0	4	8	A/GSDMD/SERPINB1/IL18/FABP5/FTL/C		
	42	acti	4	/	E-	E-	E-	D59/S100A9		
	11	vati		1	0	0	0			
	9	on		8	6	4	4			
				8						
				6						
				2						
B	G	posi	10	1	8.	4.	3.	AKR1C3/HSP90AA1/HSP90AB1/PARK7/M	10	
P	O:	tive	/	7	7	8	9	TDH/TXN/AKR1C2/HBEGF/IL18/RTN4		
	00	reg	18	5	0	6	9			
	51	ulat	4	/	E-	E-	E-			
	89	ion		1	0	0	0			
	7	of		8	6	4	4			
		prot		8						
		ein		6						
		kina		2						
		se B								
		sign								
		alin								
		g								
B	G	reg	7	7	1.	5.	4.	PSMA4/PARK7/PSMA1/OAZ1/NQO1/PSM	7	
P	O:	ulat	/	7	0	5	5	D9/PSME1		
	00	ion	18	/	1	5	6			
	33	of	4	1	E-	E-	E-			
	23	cell		8	0	0	0			

	8	ular		8	5	4	4		
		ami		6					
		ne		2					
		met							
		abol							
		ic							
		pro							
		cess							
B	G	pen	4	1	1.	5.	4.	TKT/TALDO1/G6PD/PGD	4
P	O:	tose	/	5	1	9	8		
	00	met	18	/	0	0	5		
	19	abol	4	1	E-	E-	E-		
	32	ic		8	0	0	0		
	1	pro		8	5	4	4		
		cess		6					
				2					
B	G	cell	11	2	1.	6.	4.	MRPL12/MRPL47/MRPS12/MRPL13/MRPL	11
P	O:	ular	/	2	1	0	9	23/MRPL42/MRPL15/AURKAIP1/MRPL28/	
	00	prot	18	1	4	3	5	RDX/MRPS28	
	43	ein	4	/	E-	E-	E-		
	62	com		1	0	0	0		
	4	plex		8	5	4	4		
		disa		8					
		sse		6					
		mbl		2					
		y							
B	G	pen	4	1	1.	7.	6.	TKT/TALDO1/G6PD/PGD	4
P	O:	tose	/	6	4	3	0		

		00	-	18	/	6	9	7		
		06	pho	4	1	E-	E-	E-		
		09	sph		8	0	0	0		
		8	ate		8	5	4	4		
			shu		6					
			nt		2					
B	G	vira	4	1	1.	7.	6.	MCTS1/EIF3D/EIF3F/EIF3L	4	
P	O:	l	/	6	4	3	0			
		00	tran	18	/	6	9	7		
		19	slati	4	1	E-	E-	E-		
		08	on		8	0	0	0		
		1			8	5	4	4		
					6					
					2					
B	G	mit	6	5	1.	7.	6.	NDUFAB1/NDUFB9/PARK7/NDUFS4/NDU	6	
P	O:	och	/	5	5	7	3	FB5/NDUFC2		
		00	ond	18	/	5	2	4		
		06	rial	4	1	E-	E-	E-		
		12	elec		8	0	0	0		
		0	tron		8	5	4	4		
			tran		6					
			spor		2					
			t,							
			NA							
			DH							
			to							
			ubi							
			qui							

		non								
		e								
B	G	NA	5	3	2.	1.	8.	TKT/TALDO1/G6PD/NQO1/PGD		5
P	O:	DP	/	5	1	0	6			
		00 met	18	/	4	5	1			
		06 abol	4	1	E-	E-	E-			
		73 ic		8	0	0	0			
		9 pro		8	5	3	4			
		cess		6						
				2						
B	G	neu	16	4	2.	1.	9.	HSP90AA1/HSP90AB1/GSTP1/NDUFC2/CO	16	
P	O:	trop	/	8	2	1	0	TL1/APRT/MGST1/RAB5C/ANXA2/ALDO		
		00 hil	18	5	9	0	4	A/GSDMD/SERPINB1/FABP5/FTL/CD59/S		
		43 deg	4	/	E-	E-	E-	100A9		
		31 ran		1	0	0	0			
		2 ulat		8	5	3	4			
		ion		8						
				6						
				2						
B	G	xen	8	1	2.	1.	9.	GSTO1/HSP90AB1/GSTP1/AKR1C1/MGST1	8	
P	O:	obio	/	2	3	1	0	/NQO1/ALDH3A1/CES1		
		00 tic	18	0	3	0	7			
		06 met	4	/	E-	E-	E-			
		80 abol		1	0	0	0			
		5 ic		8	5	3	4			
		pro		8						
		cess		6						
				2						

B	G	NA	4	1	2.	1.	9.	TKT/TALDO1/G6PD/PGD	4
P	O:	DP	/	8	4	1	2		
	00	H	18	/	1	2	1		
	06	rege	4	1	E-	E-	E-		
	74	nera		8	0	0	0		
	0	tion		8	5	3	4		
				6					
				2					
B	G	neu	16	4	2.	1.	9.	HSP90AA1/HSP90AB1/GSTP1/NDUFC2/CO	16
P	O:	trop	/	8	4	1	2	TL1/APRT/MGST1/RAB5C/ANXA2/ALDO	
	00	hil	18	8	6	3	6	A/GSDMD/SERPINB1/FABP5/FTL/CD59/S	
	02	acti	4	/	E-	E-	E-	100A9	
	28	vati		1	0	0	0		
	3	on		8	5	3	4		
		inv		8					
		olve		6					
		d in		2					
		im							
		mu							
		ne							
		resp							
		ons							
		e							
B	G	cell	8	1	3.	0.	1.	GSTO1/HSP90AB1/GSTP1/AKR1C1/MGST1	8
P	O:	ular	/	2	1	0	1	/NQO1/ALDH3A1/CES1	
	00	resp	18	5	3	0	4		
	71	ons	4	/	E-	1	E-		
	46	e to		1	0	3	0		

	6	xen		8	5	8	3		
		obio		8		8			
		tic		6		6			
		stim		2		9			
		ulus							
B	G	resp	15	4	3.	0.	1.	AKR1C3/LDHA/PARK7/PRDX1/GSTP1/TX	15
P	O:	ons	/	4	1	0	1	N/G6PD/GPX3/MGST1/TXN2/NQO1/SOD	
	00	e to	18	4	6	0	4	1/FOSL1/TXNRD1/CAPN2	
	06	oxid	4	/	E-	1	E-		
	97	ativ		1	0	3	0		
	9	e		8	5	8	3		
		stre		8		8			
		ss		6		6			
				2		9			
B	G	neu	16	4	3.	0.	1.	HSP90AA1/HSP90AB1/GSTP1/NDUFC2/CO	16
P	O:	trop	/	9	2	0	1	TL1/APRT/MGST1/RAB5C/ANXA2/ALDO	
	00	hil	18	9	2	0	4	A/GSDMD/SERPINB1/FABP5/FTL/CD59/S	
	02	me	4	/	E-	1	E-	100A9	
	44	diat		1	0	3	0		
	6	ed		8	5	8	3		
		im		8		8			
		mu		6		6			
		nity		2		9			
B	G	cell	5	3	3.	0.	1.	NME1/CDK4/AKR1C3/AKR1C1/AKR1C2	5
P	O:	ular	/	8	2	0	1		
	00	resp	18	/	3	0	4		
	71	ons	4	1	E-	1	E-		
	39	e to		8	0	3	0		

	8	fatt		8	5	8	3		
		y		6		8			
		acid		2		6			
						9			
B	G	cell	6	6	3.	0.	1.	AKR1C3/PARK7/TKT/AKR1C1/TALDO1/A	6
P	O:	ular	/	3	4	0	1	LDH3A1	
	00	alde	18	/	0	0	8		
	06	hyd	4	1	E-	1	E-		
	08	e		8	0	4	0		
	1	met		8	5	3	3		
		abol		6		8			
		ic		2		6			
		pro				5			
		cess							
B	G	terti	4	2	3.	0.	1.	AKR1B10/AKR1C3/AKR1C1/AKR1C2	4
P	O:	ary	/	0	7	0	2		
	19	alco	18	/	6	0	9		
	02	hol	4	1	E-	1	E-		
	64	met		8	0	5	0		
	4	abol		8	5	6	3		
		ic		6		5			
		pro		2		4			
		cess				3			
B	G	glyc	8	1	3.	0.	0.	NME1/AKR1B10/AKR1C3/AKR1C1/ADK/	8
P	O:	osyl	/	2	9	0	0	APRT/AKR1C2/NME4	
	19	com	18	9	3	0	0		
	01	pou	4	/	E-	1	1		
	65	nd		1	0	6	3		

	7	met		8	5	1	2		
		abol		8		2	4		
		ic		6		8	8		
		pro		2		8	8		
		cess							
B	G	resp	8	1	4.	0.	0.	NME1/LDHA/NDUFS4/AKR1C1/SOD1/AL	8
P	O:	ons	/	3	1	0	0	DH3A1/HSP90B1/FOSL1	
	00	e to	18	0	5	0	0		
	46	org	4	/	E-	1	1		
	68	ano		1	0	6	3		
	3	pho		8	5	7	7		
		sph		8		9	9		
		oru		6		7	8		
		s		2		9	5		
B	G	resp	8	1	4.	0.	0.	GSTO1/HSP90AB1/GSTP1/AKR1C1/MGST1	8
P	O:	ons	/	3	3	0	0	/NQO1/ALDH3A1/CES1	
	00	e to	18	1	9	0	0		
	09	xen	4	/	E-	1	1		
	41	obio		1	0	7	4		
	0	tic		8	5	4	3		
		stim		8		8	6		
		ulus		6		9	6		
				2		8	8		
B	G	posi	9	1	4.	0.	0.	NME1/HSP90AB1/PARK7/CAV1/TXN/EIF3	9
P	O:	tive	/	7	5	0	0	E/ANXA2/EIF3D/GMNN	
	00	reg	18	0	1	0	0		
	51	ulat	4	/	E-	1	1		
	09	ion		1	0	7	4		

	9	of		8	5	6	4		
		bin		8		1	6		
		din		6		3	8		
		g		2		3	2		
B	G	mo	7	9	4.	0.	0.	ENO1/MDH2/TKT/TALDO1/G6PD/PGD/	7
P	O:	nos	/	7	6	0	0	ALDOA	
	00	acc	18	/	0	0	0		
	46	hari	4	1	E-	1	1		
	36	de		8	0	7	4		
	4	bios		8	5	6	4		
		ynt		6		1	6		
		heti		2		3	8		
		c				3	2		
		pro							
		cess							
B	G	glyc	4	2	4.	0.	0.	AKR1B10/AKR1C3/AKR1C1/AKR1C2	4
P	O:	osid	/	1	6	0	0		
	00	e	18	/	1	0	0		
	16	met	4	1	E-	1	1		
	13	abol		8	0	7	4		
	7	ic		8	5	6	4		
		pro		6		1	6		
		cess		2		3	8		
						3	2		
B	G	puri	6	6	5.	0.	0.	NME1/ENO1/STOML2/ADK/NME4/ALDO	6
P	O:	ne	/	8	2	0	0	A	
	00	nucl	18	/	6	0	0		
	09	eosi	4	1	E-	1	1		

	14	de		8	0	9	6		
	5	trip		8	5	8	3		
		hos		6		5	0		
		pha		2		3	8		
		te				3	2		
		bios							
		ynt							
		heti							
		c							
		pro							
		cess							
B	G	puri	4	2	5.	0.	0.	NME1/ADK/APRT/NME4	4
P	O:	ne	/	2	5	0	0		
	00	nucl	18	/	9	0	0		
	42	eosi	4	1	E-	1	1		
	45	de		8	0	9	6		
	1	bios		8	5	9	4		
		ynt		6		9	2		
		heti		2		4	4		
		c				3	1		
		pro							
		cess							
B	G	ribo	4	2	5.	0.	0.	NME1/ADK/APRT/NME4	4
P	O:	nucl	/	2	5	0	0		
	00	eosi	18	/	9	0	0		
	42	de	4	1	E-	1	1		
	45	bios		8	0	9	6		
	5	ynt		8	5	9	4		

		heti		6		9	2		
		c		2		4	4		
		pro				3	1		
		cess							
B	G	puri	4	2	5.	0.	0.	NME1/ADK/APRT/NME4	4
P	O:	ne	/	2	5	0	0		
	00	ribo	18	/	9	0	0		
	46	nucl	4	1	E-	1	1		
	12	eosi		8	0	9	6		
	9	de		8	5	9	4		
		bios		6		9	2		
		ynt		2		4	4		
		heti				3	1		
		c							
		pro							
		cess							
B	G	cha	4	2	5.	0.	0.	HSP90AA1/HSP90AB1/PSMG3/PFDN6	4
P	O:	per	/	2	5	0	0		
	00	one-	18	/	9	0	0		
	51	me	4	1	E-	1	1		
	13	diat		8	0	9	6		
	1	ed		8	5	9	4		
		prot		6		9	2		
		ein		2		4	4		
		com				3	1		
		plex							
		asse							
		mbl							

		y								
B	G	posi	7	1	5.	0.	0.	AKR1C3/HSP90AA1/HSP90AB1/PARK7/GS	7	
P	O:	tive	/	0	9	0	0	TP1/SOD1/GADD45A		
	20	reg	18	1	6	0	0			
	00	ulat	4	/	E-	2	1			
	37	ion		1	0	0	7			
	9	of		8	5	8	0			
		reac		8		0	8			
		tive		6		1	6			
		oxy		2		2	9			
		gen								
		spec								
		ies								
		met								
		abol								
		ic								
		pro								
		cess								
B	G	cell	5	4	5.	0.	0.	PRDX1/TXN/TXN2/NQO1/TXNRD1	5	
P	O:	red	/	3	9	0	0			
	00	ox	18	/	6	0	0			
	45	ho	4	1	E-	2	1			
	45	meo		8	0	0	7			
	4	stasi		8	5	8	0			
		s		6		0	8			
				2		1	6			
						2	9			
B	G	resp	10	2	7.	0.	0.	AKR1C3/LDHA/PARK7/PRDX1/GSTP1/TX	10	

P	O:	ons	/	2	2	0	0	N/NQO1/SOD1/FOSL1/CAPN2	
	00	e to	18	4	2	0	0		
	00	reac	4	/	E-	2	2		
	30	tive		1	0	4	0		
	2	oxy		8	5	7	3		
		gen		8		6	4		
		spec		6		3	1		
		ies		2		7	9		
B	G	ribo	6	7	7.	0.	0.	RPL35/NSA2/RPL23A/RPL10A/RPL7/RPL3	6
P	O:	som	/	2	2	0	0		
	00	al	18	/	8	0	0		
	42	larg	4	1	E-	2	2		
	27	e		8	0	4	0		
	3	sub		8	5	7	3		
		unit		6		6	4		
		biog		2		3	1		
		enes				7	9		
		is							
B	G	gluc	4	2	9.	0.	0.	TKT/TALDO1/G6PD/PGD	4
P	O:	ose	/	5	4	0	0		
	00	6-	18	/	4	0	0		
	51	pho	4	1	E-	3	2		
	15	sph		8	0	1	6		
	6	ate		8	5	7	0		
		met		6		5	8		
		abol		2		8	8		
		ic				9			
		pro							

		cess								
B	G	reg	14	4	1.	0.	0.	ENO1/AKR1C3/PSMA4/PARK7/CAV1/PS	14	
P	O:	ulat	/	3	0	0	0	MA1/OAZ1/NQO1/SOD1/PSMD9/PSME1/		
	00	ion	18	7	3	0	0	FABP5/PHLDA2/CES1		
	62	of	4	/	E-	3	2			
	01	sma		1	0	4	8			
	2	ll		8	4	1	0			
		mol		8		0	1			
		ecul		6		5	5			
		e		2		7	7			
		met								
		abol								
		ic								
		pro								
		cess								
B	G	reg	9	1	1.	0.	0.	AKR1C3/HSP90AA1/HSP90AB1/PARK7/CA	9	
P	O:	ulat	/	9	1	0	0	V1/GSTP1/G6PD/SOD1/GADD45A		
	20	ion	18	2	5	0	0			
	00	of	4	/	E-	3	3			
	37	reac		1	0	7	1			
	7	tive		8	4	7	0			
		oxy		8		7	3			
		gen		6		6	1			
		spec		2		6	1			
		ies								
		met								
		abol								
		ic								

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		l	6	1	6				
		tran	2	7	1				
		slati		7	4				
		onal							
		initi							
		atio							
		n							
B	G	mat	4	2	1.	0.	0.	RPL35/NSA2/RPL10A/RPL7	4
P	O:	urat	/	8	4	0	0		
		00 ion	18	/	9	0	0		
		00 of	4	1	E-	4	3		
		47 LSU		8	0	6	8		
		0 -		8	4	8	4		
		rRN		6		5	8		
		A		2		5	9		
						7			
B	G	cell	12	3	1.	0.	0.	AKR1C3/PARK7/CAV1/PRDX1/GSTP1/TX	12
P	O:	ular	/	4	6	0	0	N/G6PD/GPX3/MGST1/NQO1/SOD1/TXN	
		00 resp	18	7	0	0	0	RD1	
		62 ons	4	/	E-	4	4		
		19 e to		1	0	9	0		
		7 che		8	4	5	6		
		mic		8		2	8		
		al		6		7	4		
		stre		2		8			
		ss							
B	G	reg	10	2	1.	0.	0.	AKR1C3/HSP90AA1/HSP90AB1/PARK7/M	10
P	O:	ulat	/	4	6	0	0	TDH/TXN/AKR1C2/HBEGF/IL18/RTN4	

		00	ion	18	7	1	0	0		
		51	of	4	/	E-	4	4		
		89	prot		1	0	9	0		
		6	ein		8	4	5	6		
			kina		8		2	8		
			se B		6		7	4		
			sign		2		8			
			alin							
			g							
B	G	nucl	6	8	1.	0.	0.		NME1/ENO1/STOML2/ADK/NME4/ALDO	6
P	O:	eosi	/	4	7	0	0		A	
		00	de	18	/	2	0	0		
		09	trip	4	1	E-	5	4		
		14	hos		8	0	2	2		
		2	pha		8	4	1	8		
			te		6		3	2		
			bios		2		8	8		
			ynt				9	9		
			heti							
			c							
			pro							
			cess							
B	G	cell	11	2	1.	0.	0.		AKR1C3/PARK7/PRDX1/GSTP1/TXN/G6P	11
P	O:	ular	/	9	7	0	0		D/GPX3/MGST1/NQO1/SOD1/TXNRD1	
		00	resp	18	9	7	0	0		
		34	ons	4	/	E-	5	4		
		59	e to		1	0	3	3		
		9	oxid		8	4	0	5		

		ativ	8	0	3				
		e	6	1	7				
		stre	2	7	6				
		ss							
B	G	puri	6	8	1.	0.	0.	NME1/ENO1/STOML2/ADK/NME4/ALDO	6
P	O:	ne	/	6	9	0	0	A	
	00	nucl	18	/	6	0	0		
	09	eosi	4	1	E-	5	4		
	14	de		8	0	8	7		
	4	trip		8	4	0	7		
		hos		6		8	1		
		pha		2		1	0		
		te				9	7		
		met							
		abol							
		ic							
		pro							
		cess							
B	G	mai	9	2	2.	0.	0.	GSTO1/PARK7/CAV1/TXN/SKP1/GPAA1/	9
P	O:	nte	/	0	1	0	0	HSP90B1/FTL/S100A9	
	00	nan	18	9	8	0	0		
	51	ce	4	/	E-	6	5		
	65	of		1	0	3	2		
	1	loca		8	4	7	3		
		tion		8		0	2		
		in		6		0	6		
		cell		2		7	1		
B	G	neg	12	3	2.	0.	0.	PRMT1/CDK4/PSMA4/HSP90AB1/PSMA1/	12

P	O:	ativ	/	5	1	0	0	SKP1/AURKAIP1/CHMP2A/SFN/PSMD9/P	
	00	e	18	9	9	0	0	SME1/GADD45A	
	10	reg	4	/	E-	6	5		
	94	ulat		1	0	3	2		
	8	ion		8	4	7	3		
		of		8		0	2		
		cell		6		0	6		
		cycl		2		7	1		
		e							
		pro							
		cess							
B	G	end	4	3	2.	0.	0.	CHMP2A/LAPTM4B/CHMP4A/VPS28	4
P	O:	oso	/	1	2	0	0		
	00	me	18	/	4	0	0		
	32	tran	4	1	E-	6	5		
	50	spor		8	0	4	3		
	9	t via		8	4	5	0		
		mul		6		7	4		
		tive		2		5	4		
		sicu				7	9		
		lar							
		bod							
		y							
		sort							
		ing							
		pat							
		hwa							
		y							

B	G	low	3	1	3.	0.	0.	AP2M1/ AP2S1/ ANXA2	3
P	O:	-	/	4	0	0	0		
	00	den	18	/	7	0	0		
	32	sity	4	1	E-	8	7		
	79	lipo		8	0	6	1		
	9	prot		8	4	5	1		
		ein		6		8	2		
		rece		2		3	3		
		ptor				9	3		
		part							
		icle							
		met							
		abol							
		ic							
		pro							
		cess							
B	G	low	3	1	3.	0.	0.	AP2M1/ AP2S1/ ANXA2	3
P	O:	-	/	4	0	0	0		
	00	den	18	/	7	0	0		
	32	sity	4	1	E-	8	7		
	80	lipo		8	0	6	1		
	2	prot		8	4	5	1		
		ein		6		8	2		
		part		2		3	3		
		icle				9	3		
		rece							
		ptor							
		cata							

		boli								
		c								
		pro								
		cess								
B	G	resp	5	6	3.	0.	0.	NME1/CDK4/AKR1C3/AKR1C1/AKR1C2	5	
P	O:	ons	/	1	2	0	0			
	00	e to	18	/	0	0	0			
	70	fatt	4	1	E-	8	7			
	54	y		8	0	9	3			
	2	acid		8	4	2	3			
				6		6	2			
				2		0	2			
						8	1			
B	G	qui	4	3	3.	0.	0.	AKR1B10/AKR1C3/AKR1C1/AKR1C2	4	
P	O:	non	/	4	2	0	0			
	19	e	18	/	3	0	0			
	01	met	4	1	E-	8	7			
	66	abol		8	0	9	3			
	1	ic		8	4	3	3			
		pro		6		4	9			
		cess		2		6	2			
						5	6			
B	G	mo	10	2	3.	0.	0.	GSTO1/ENO1/MDH2/TKT/TALDO1/G6PD	10	
P	O:	nos	/	7	5	0	0	/PGD/ALDOA/FABP5/PHLDA2		
	00	acc	18	2	0	0	0			
	05	hari	4	/	E-	9	7			
	99	de		1	0	5	8			
	6	met		8	4	6	5			

		abol	8	7	9			
		ic	6	5	1			
		pro	2					
		cess						
B	G	prot	10	2	3.	0.	0.	AKR1C3/HSP90AA1/HSP90AB1/PARK7/M 10
P	O:	ein	/	7	6	0	0	TDH/TXN/AKR1C2/HBEGF/IL18/RTN4
	00	kina	18	3	0	0	0	
	43	se B	4	/	E-	9	8	
	49	sign		1	0	7	0	
	1	alin		8	4	5	1	
		g		8		3	1	
				6		1	5	
				2		3	9	
B	G	resp	7	1	3.	0.	0.	LDHA/PARK7/TXN/NQO1/SOD1/FOSL1/ 7
P	O:	ons	/	3	6	0	0	CAPN2
	00	e to	18	5	3	0	0	
	42	hyd	4	/	E-	9	8	
	54	rog		1	0	7	0	
	2	en		8	4	5	1	
		per		8		3	1	
		oxid		6		1	6	
		e		2		5		
B	G	pro	3	1	3.	0.	0.	AKR1C3/AKR1C1/AKR1C2 3
P	O:	gest	/	5	8	0	0	
	00	ero	18	/	1	1	0	
	42	ne	4	1	E-	0	8	
	44	met		8	0	1	3	
	8	abol		8	4	3	2	

		ic	6	1	2			
		pro	2	4	3			
		cess		4	4			
B	G	glut	5	6	4.	0.	0.	GSTO1/PARK7/GSTP1/G6PD/SOD1
P	O:	athi	/	4	0	0	0	5
	00	one	18	/	0	1	0	
	06	met	4	1	E-	0	8	
	74	abol		8	0	4	5	
	9	ic		8	4	4	7	
		pro		6		2	7	
		cess		2		4	8	
						4	1	
B	G	mai	5	6	4.	0.	0.	PARK7/CAV1/TXN/SKP1/GPAA1
P	O:	nte	/	4	0	0	0	5
	00	nan	18	/	0	1	0	
	32	ce	4	1	E-	0	8	
	50	of		8	0	4	5	
	7	prot		8	4	4	7	
		ein		6		2	7	
		loca		2		4	8	
		tion				4	1	
		in						
		cell						
B	G	resp	12	3	4.	0.	0.	ENO1/CDK4/PSMA4/LDHA/CAV1/PSMA1
P	O:	ons	/	8	1	0	0	12
	00	e to	18	5	3	1	0	/TXN2/PSMD9/PSME1/ALDH3A1/HSP90B
	70	oxy	4	/	E-	0	8	1/CAPN2
	48	gen		1	0	6	7	

	2	leve		8	4	6	5	
		ls		8		3	9	
				6		3	2	
				2		6	8	
B	G	NA	5	6	4.	0.	0.	NDUFAB1/NDUFB9/NDUFS4/NDUFB5/ND 5
P	O:	DH	/	5	3	0	0	UFC2
	00	deh	18	/	0	1	0	
	10	ydr	4	1	E-	0	8	
	25	oge		8	0	9	9	
	7	nas		8	4	1	6	
		e		6		8	8	
		com		2		0	5	
		plex				7	1	
		asse						
		mbl						
		y						
B	G	mit	5	6	4.	0.	0.	NDUFAB1/NDUFB9/NDUFS4/NDUFB5/ND 5
P	O:	och	/	5	3	0	0	UFC2
	00	ond	18	/	0	1	0	
	32	rial	4	1	E-	0	8	
	98	resp		8	0	9	9	
	1	irat		8	4	1	6	
		ory		6		8	8	
		chai		2		0	5	
		n				7	1	
		com						
		plex						
		I						

		asse								
		mbl								
		y								
B	G	mul	4	3	4.	0.	0.	CHMP2A/LAPTM4B/CHMP4A/VPS28	4	
P	O:	tive	/	7	5	0	0			
	00	sicu	18	/	0	1	0			
	71	lar	4	1	E-	1	9			
	98	bod		8	0	3	2			
	5	y		8	4	1	9			
		sort		6		6	6			
		ing		2		8	0			
		pat				2	6			
		hwa								
		y								
B	G	resp	9	2	4.	0.	0.	CDK4/AKR1C3/GSTP1/G6PD/NQO1/AKR1	9	
P	O:	ons	/	3	8	0	0	C2/SOD1/FOSL1/CES1		
	00	e to	18	3	3	1	0			
	97	alco	4	/	E-	2	9			
	30	hol		1	0	0	8			
	5			8	4	4	9			
				8		5	4			
				6		3	4			
				2		3	9			
B	G	puri	5	6	4.	0.	0.	NME1/ENO1/STOML2/NME4/ALDOA	5	
P	O:	ne	/	7	9	0	0			
	00	ribo	18	/	5	1	1			
	09	nucl	4	1	E-	2	0			
	20	eosi		8	0	2	0			

	6	de		8	4	2	3		
		trip		6		2	9		
		hos		2		2	7		
		pha				1	8		
		te							
		bios							
		ynt							
		heti							
		c							
		pro							
		cess							
B	G	nucl	4	3	4.	0.	0.	NME1/ADK/APRT/NME4	4
P	O:	eosi	/	8	9	0	0		
	00	de	18	/	9	1	1		
	09	bios	4	1	E-	2	0		
	16	ynt		8	0	2	0		
	3	heti		8	4	2	3		
		c		6		2	9		
		pro		2		2	7		
		cess				1	8		
B	G	inte	6	1	5.	0.	0.	PSMA4/PSMA1/UBE2N/SKP1/PSMD9/PSM	6
P	O:	rleu	/	0	1	0	0	E1	
	00	kin-	18	3	9	1	1		
	70	1-	4	/	E-	2	0		
	49	me		1	0	5	3		
	8	diat		8	4	9	4		
		ed		8		6	7		
		sign		6		8	5		

		alin	2	6	3				
		g							
		pat							
		hwa							
		y							
B	G	resp	7	1	5.	0.	0.	NME1/LDHA/NDUFS4/SOD1/ALDH3A1/	7
P	O:	ons	/	4	3	0	0	HSP90B1/FOSL1	
	00	e to	18	4	6	1	1		
	14	puri	4	/	E-	2	0		
	07	ne-		1	0	8	5		
	4	cont		8	4	9	9		
		aini		8		6	3		
		ng		6		3	5		
		com		2		5	4		
		pou							
		nd							
B	G	C21	4	4	6.	0.	0.	HSD17B10/AKR1C3/AKR1C1/AKR1C2	4
P	O:	-	/	0	0	0	0		
	00	ster	18	/	9	1	1		
	08	oid	4	1	E-	4	1		
	20	hor		8	0	5	9		
	7	mo		8	4	2	2		
		ne		6		2	9		
		met		2		1	0		
		abol				5	4		
		ic							
		pro							
		cess							

B	G	resp	8	1	6.	0.	0.	NME1/CDK4/AKR1C3/PARK7/CAV1/NQO	8
P	O:	ons	/	9	2	0	0	1/AKR1C2/FOSL1	
	19	e to	18	3	7	1	1		
	01	keto	4	/	E-	4	2		
	65	ne		1	0	8	1		
	4			8	4	3	8		
				8		1	3		
				6		4	1		
				2		5	1		
B	G	resp	11	3	6.	0.	0.	ENO1/PSMA4/LDHA/CAV1/PSMA1/TXN2	11
P	O:	ons	/	4	3	0	0	/PSMD9/PSME1/ALDH3A1/HSP90B1/CAP	
	00	e to	18	8	8	1	1	N2	
	01	hyp	4	/	E-	4	2		
	66	oxia		1	0	9	2		
	6			8	4	7	9		
				8		3	9		
				6		5	8		
				2		5	3		
B	G	reg	5	7	6.	0.	0.	PRELID1/PARK7/STOML2/PPA2/SOD1	5
P	O:	ulat	/	1	4	0	0		
	00	ion	18	/	7	1	1		
	51	of	4	1	E-	5	2		
	88	mit		8	0	0	3		
	1	och		8	4	5	6		
		ond		6		0	3		
		rial		2		4	0		
		me				8	3		
		mbr							

		ane								
		pote								
		ntia								
		l								
B	G	Wnt	6	1	6.	0.	0.	PSMA4/AP2M1/AP2S1/PSMA1/PSMD9/PS	6	
P	O:	sign	/	0	6	0	0	ME1		
	00	alin	18	8	7	1	1			
	60	g	4	/	E-	5	2			
	07	pat		1	0	3	5			
	1	hwa		8	4	1	8			
		y,		8		5	1			
		pla		6		9	1			
		nar		2		8	1			
		cell								
		pola								
		rity								
		pat								
		hwa								
		y								
B	G	low	4	4	6.	0.	0.	AP2M1/AP2S1/CNPY2/ANXA2	4	
P	O:	-	/	1	6	0	0			
	00	den	18	/	9	1	1			
	34	sity	4	1	E-	5	2			
	38	lipo		8	0	3	5			
	3	prot		8	4	1	8			
		ein		6		5	1			
		part		2		9	1			
		icle				8	1			

		le								
B	G	glyc	4	4	7.	0.	0.	NME1/ADK/APRT/NME4		4
P	O:	osyl	/	2	3	0	0			
	19	com	18	/	4	1	1			
	01	pou	4	1	E-	6	3			
	65	nd		8	0	2	3			
	9	bios		8	4	7	7			
		ynt		6		8	2			
		heti		2		8	0			
		c				9	9			
		pro								
		cess								
B	G	ribo	5	7	7.	0.	0.	NME1/ENO1/STOML2/NME4/ALDOA		5
P	O:	nucl	/	3	3	0	0			
	00	eosi	18	/	5	1	1			
	09	de	4	1	E-	6	3			
	20	trip		8	0	2	3			
	1	hos		8	4	7	7			
		pha		6		8	2			
		te		2		8	0			
		bios				9	9			
		ynt								
		heti								
		c								
		pro								
		cess								
B	G	reg	11	3	7.	0.	0.	NME1/HSP90AB1/PARK7/CAV1/TXN/EIF3		11
P	O:	ulat	/	5	8	0	0	E/ANXA2/EIF3D/CSNK1A1/GMNN/PHLD		

		00	ion	18	7	7	1	1	A2	
		51	of	4	/	E-	7	4		
		09	bin		1	0	3	2		
		8	din		8	4	0	1		
			g		8		1	2		
					6		6	2		
					2		8	5		
B	G	neg	9	2	8.	0.	0.		PRMT1/CDK4/PSMA4/PSMA1/SKP1/SFN/	9
P	O:	ativ	/	5	0	0	0		PSMD9/PSME1/GADD45A	
		19	e	18	0	0	1	1		
		01	reg	4	/	E-	7	4		
		99	ulat		1	0	3	2		
		1	ion		8	4	4	5		
			of		8		8	0		
			mit		6		3	5		
			otic		2		2	5		
			cell							
			cycl							
			e							
			pha							
			se							
			tran							
			sitio							
			n							
B	G	NA	4	4	8.	0.	0.		ENO1/MDH2/NQO1/ALDOA	4
P	O:	DH	/	3	0	0	0			
		00	met	18	/	4	1	1		
		06	abol	4	1	E-	7	4		

	73	ic		8	0	3	2		
	4	pro		8	4	4	5		
		cess		6		8	0		
				2		3	5		
						2	5		
B	G	reg	6	1	8.	0.	0.	PSMA4/ AP2M1/ AP2S1/ PSMA1/ PSMD9/ PS	6
P	O:	ulat	/	1	0	0	0	ME1	
	00	ion	18	2	8	1	1		
	90	of	4	/	E-	7	4		
	17	esta		1	0	3	2		
	5	blis		8	4	4	5		
		hme		8		8	0		
		nt		6		3	5		
		of		2		2	5		
		pla							
		nar							
		pola							
		rity							
B	G	reg	9	2	8.	0.	0.	HSP90AA1/ HSP90AB1/ PARK7/ CAV1/ LAPT	9
P	O:	ulat	/	5	2	0	0	M4B/ ANXA2/ PSME1/ CSNK1A1/ RDX	
	19	ion	18	1	3	1	1		
	03	of	4	/	E-	7	4		
	36	cell		1	0	5	4		
	2	ular		8	4	3	0		
		prot		8		0	0		
		ein		6		3	0		
		cata		2		1	5		
		boli							

		c								
		pro								
		cess								
B	G	resp	11	3	8.	0.	0.	ENO1/PSMA4/LDHA/CAV1/PSMA1/TXN2	11	
P	O:	ons	/	6	4	0	0	/PSMD9/PSME1/ALDH3A1/HSP90B1/CAP		
	00	e to	18	0	3	1	1	N2		
	36	decr	4	/	E-	7	4			
	29	ease		1	0	8	6			
	3	d		8	4	2	3			
		oxy		8		2	9			
		gen		6		1	7			
		leve		2			4			
		ls								
B	G	ribo	10	3	8.	0.	0.	NPM3/RPS2/RPS10/RPL35/NSA2/RPL23A/	10	
P	O:	som	/	0	9	0	0	RPL10A/RPL7/RPL3/RPS9		
	00	e	18	7	3	1	1			
	42	biog	4	/	E-	8	5			
	25	enes		1	0	7	3			
	4	is		8	4	4	9			
				8		5	8			
				6		3	0			
				2			9			
B	G	end	13	4	9.	0.	0.	CAV1/CHMP2A/REEP5/SOD1/LAPTM4B/	13	
P	O:	ome	/	8	2	0	0	CHMP4A/CSNK1A1/EMC2/RTN4/VPS28/L		
	00	mbr	18	2	5	1	1	MAN2/BLOC1S1/S100A9		
	10	ane	4	/	E-	8	5			
	25	syst		1	0	9	5			
	6	em		8	4	1	4			

		org	8	8	0				
		aniz	6	7	5				
		atio	2	3	5				
		n							
B	G	uns	6	1	0.	0.	0.	AKR1C3/GSTP1/AKR1C1/PTGR1/AKR1C2/	6
P	O:	atur	/	1	0	0	0	FABP5	
	00	ated	18	5	0	1	1		
	33	fatt	4	/	0	8	5		
	55	y		1	9	9	5		
	9	acid		8	2	1	4		
		met		8	7	8	0		
		abol		6	8	7	5		
		ic		2	2	3	5		
		pro							
		cess							
B	G	cell	7	1	0.	0.	0.	PSMA4/PARK7/PSMA1/OAZ1/NQO1/PSM	7
P	O:	ular	/	5	0	0	0	D9/PSME1	
	00	ami	18	8	0	1	1		
	44	ne	4	/	0	8	5		
	10	met		1	9	9	5		
	6	abol		8	2	1	4		
		ic		8	8	8	0		
		pro		6	0	7	5		
		cess		2	8	3	5		
B	G	reg	8	2	0.	0.	0.	HSP90AA1/HSP90AB1/RPS2/PARK7/CAV1	8
P	O:	ulat	/	0	0	0	0	/UBE2N/SKP1/VPS28	
	00	ion	18	5	0	1	1		
	31	of	4	/	0	8	5		

		39	prot	1	9	9	5		
		6	ein	8	2	1	4		
			ubi	8	8	8	0		
			quit	6	6	7	5		
			inat	2	5	3	5		
			ion						
B	G	cell	6	1	0.	0.	0.	SKP1/NEDD8/MT2A/SOD1/FTL/S100A9	6
P	O:	ular	/	1	0	0	0		
		00	tran	18	8	0	2	1	
		46	sitio	4	/	1	1	7	
		91	n	1	0	4	6		
		6	met	8	6	2	0		
			al	8	0	8	1		
			ion	6	8	1	8		
			ho	2		1	5		
			meo						
			stasi						
			s						
B	G	vira	3	2	0.	0.	0.	CHMP2A/CHMP4A/VPS28	3
P	O:	l	/	1	0	0	0		
		00	bud	18	/	0	2	1	
		39	din	4	1	1	1	7	
		70	g	8	0	4	6		
		2	via	8	6	2	0		
			host	6	7	8	1		
			ESC	2	1	1	8		
			RT		8	1	5		
			com						

			plex							
B	G	ami	7	1	0.	0.	0.	PSMA4/PARK7/PSMA1/OAZ1/NQO1/PSM	7	
P	O:	ne	/	6	0	0	0	D9/PSME1		
	00	met	18	3	0	2	1			
	09	abol	4	/	1	2	8			
	30	ic		1	1	0	1			
	8	pro		8	1	4	0			
		cess		8	2	0	5			
				6	9	8	1			
				2	9	1	4			
B	G	puri	5	8	0.	0.	0.	NME1/ENO1/STOML2/NME4/ALDOA	5	
P	O:	ne	/	0	0	0	0			
	00	ribo	18	/	0	2	1			
	09	nucl	4	1	1	2	8			
	20	eosi		8	1	0	1			
	5	de		8	1	4	0			
		trip		6	3	0	5			
		hos		2	4	8	1			
		pha			9	1	4			
		te								
		met								
		abol								
		ic								
		pro								
		cess								
B	G	inte	4	4	0.	0.	0.	GSTO1/TALDO1/SOD1/ANXA2	4	
P	O:	rleu	/	7	0	0	0			
	00	kin-	18	/	0	2	1			

	35	12-	4	1	1	2	8		
	72	me		8	1	1	1		
	2	diat		8	2	4	9		
		ed		6	6	6	1		
		sign		2	7	2	7		
		alin			5		1		
		g							
		pat							
		hwa							
		y							
B	G	mai	10	3	0.	0.	0.	GSTO1/PARK7/CAV1/TXN/SKP1/GPAA1/	10
P	O:	nte	/	1	0	0	0	HSP90B1/FTL/CES1/S100A9	
	00	nan	18	9	0	2	1		
	51	ce	4	/	1	3	9		
	23	of		1	1	2	1		
	5	loca		8	9	8	2		
		tion		8	2	0	3		
				6	7	1	2		
				2	9	8	1		
B	G	reg	4	4	0.	0.	0.	ENO1/LAPTM4B/ANXA2/CHMP4A	4
P	O:	ulat	/	8	0	0	0		
	00	ion	18	/	0	2	1		
	44	of	4	1	1	3	9		
	08	vac		8	2	4	2		
	8	uole		8	1	5	6		
		org		6	9	3	5		
		aniz		2	9	2	3		
		atio			1	4	7		

		n								
B	G	glut	3	2	0.	0.	0.	GSTO1/GSTP1/MGST1		3
P	O:	athi	/	2	0	0	0			
	19	one	18	/	0	2	1			
	01	deri	4	1	1	3	9			
	68	vati		8	2	4	2			
	5	ve		8	2	5	6			
		met		6	6	3	5			
		abol		2	8	2	3			
		ic			6	4	7			
		pro								
		cess								
B	G	glut	3	2	0.	0.	0.	GSTO1/GSTP1/MGST1		3
P	O:	athi	/	2	0	0	0			
	19	one	18	/	0	2	1			
	01	deri	4	1	1	3	9			
	68	vati		8	2	4	2			
	7	ve		8	2	5	6			
		bios		6	6	3	5			
		ynt		2	8	2	3			
		heti			6	4	7			
		c								
		pro								
		cess								
B	G	neg	10	3	0.	0.	0.	PRMT1/CDK4/PSMA4/PSMA1/SKP1/AUR		10
P	O:	ativ	/	2	0	0	0	KAIP1/SFN/PSMD9/PSME1/GADD45A		
	00	e	18	1	0	2	1			
	45	reg	4	/	1	3	9			

		93	ulat	1	2	7	4		
		0	ion	8	4	3	9		
			of	8	9	0	3		
			mit	6	8	6	2		
			otic	2	8	5	4		
			cell						
			cycl						
			e						
B	G	neg	9	2	0.	0.	0.	PRMT1/CDK4/PSMA4/PSMA1/SKP1/SFN/	9
P	O:	ativ	/	6	0	0	0	PSMD9/PSME1/GADD45A	
		19	e	18	8	0	2	1	
		01	reg	4	/	1	4	9	
		98	ulat	1	3	0	7		
		8	ion	8	0	4	5		
			of	8	1	8	4		
			cell	6	3	8	6		
			cycl	2	8	5	3		
			e						
			pha						
			se						
			tran						
			sitio						
			n						
B	G	esta	6	1	0.	0.	0.	PSMA4/ AP2M1/ AP2S1/PSMA1/PSMD9/PS	6
P	O:	blis	/	2	0	0	0	ME1	
		00	hme	18	3	0	2	1	
		01	nt	4	/	1	4	9	
		73	of	1	3	0	7		

	6	pla		8	1	4	5	
		nar		8	4	8	4	
		pola		6	4	8	6	
		urity		2	1	5	3	
B	G	icos	6	1	0.	0.	0.	AKR1C3/GSTP1/AKR1C1/PTGR1/AKR1C2/ 6
P	O:	anoi	/	2	0	0	0	FABP5
	00	d	18	3	0	2	1	
	06	met	4	/	1	4	9	
	69	abol		1	3	0	7	
	0	ic		8	1	4	5	
		pro		8	4	8	4	
		cess		6	4	8	6	
				2	1	5	3	
B	G	esta	6	1	0.	0.	0.	PSMA4/AP2M1/AP2S1/PSMA1/PSMD9/PS 6
P	O:	blis	/	2	0	0	0	ME1
	00	hme	18	3	0	2	1	
	07	nt	4	/	1	4	9	
	16	of		1	3	0	7	
	4	tiss		8	1	4	5	
		ue		8	4	8	4	
		pola		6	4	8	6	
		urity		2	1	5	3	
B	G	reac	6	1	0.	0.	0.	HSP90AA1/HSP90AB1/PARK7/CAV1/NQO 6
P	O:	tive	/	2	0	0	0	1/SOD1
	19	oxy	18	3	0	2	1	
	03	gen	4	/	1	4	9	
	40	spec		1	3	0	7	
	9	ies		8	1	4	5	

		bios	8	4	8	4			
		ynt	6	4	8	6			
		heti	2	1	5	3			
		c							
		pro							
		cess							
B	G	cell	4	4	0.	0.	0.	GSTO1/TALDO1/SOD1/ANXA2	4
P	O:	ular	/	9	0	0	0		
	00	resp	18	/	0	2	1		
	71	ons	4	1	1	4	9		
	34	e to		8	3	0	7		
	9	inte		8	1	4	5		
		rleu		6	8	8	4		
		kin-		2	3	8	6		
		12			4	5	3		
B	G	reg	11	3	0.	0.	0.	HSP90AA1/HSP90AB1/PARK7/CAV1/OAZ	11
P	O:	ulat	/	8	0	0	0	1/LAPTM4B/ANXA2/PSME1/CSNK1A1/RD	
	00	ion	18	3	0	2	2	X/VPS28	
	42	of	4	/	1	5	0		
	17	prot		1	3	0	5		
	6	ein		8	8	6	8		
		cata		8	7	2	6		
		boli		6	2	1	9		
		c		2		6	9		
		pro							
		cess							
B	G	rem	3	2	0.	0.	0.	PRDX1/NQO1/SOD1	3
P	O:	oval	/	3	0	0	0		

	00	of	18	/	0	2	2		
	19	sup	4	1	1	5	0		
	43	erox		8	4	0	5		
	0	ide		8	0	6	8		
		radi		6	0	2	6		
		cals		2	8	1	9		
					2	6	9		
B	G	mai	3	2	0.	0.	0.	PARK7/TXN/SKP1	3
P	O:	nte	/	3	0	0	0		
	00	nan	18	/	0	2	2		
	51	ce	4	1	1	5	0		
	45	of		8	4	0	5		
	7	prot		8	0	6	8		
		ein		6	0	2	6		
		loca		2	8	1	9		
		tion			2	6	9		
		in							
		nucl							
		eus							
B	G	resp	4	5	0.	0.	0.	GSTO1/TALDO1/SOD1/ANXA2	4
P	O:	ons	/	0	0	0	0		
	00	e to	18	/	0	2	2		
	70	inte	4	1	1	5	0		
	67	rleu		8	4	2	7		
	1	kin-		8	2	8	6		
		12		6	2	2	7		
				2	1	0	6		
					7	9	5		

B	G	NA	4	5	0.	0.	0.	ENO1/LDHA/NQO1/ALDOA	4
P	O:	D	/	1	0	0	0		
	00	met	18	/	0	2	2		
	19	abol	4	1	1	7	2		
	67	ic		8	5	0	1		
	4	pro		8	3	1	9		
		cess		6	1	7	3		
				2	5	6	3		
					8	5	1		
B	G	aero	5	8	0.	0.	0.	MDH2/UQCRH/COX5A/COX8A/BLOC1S1	5
P	O:	bic	/	6	0	0	0		
	00	resp	18	/	0	2	2		
	09	irati	4	1	1	7	2		
	06	on		8	5	0	1		
	0			8	3	1	9		
				6	9	7	3		
				2	1	6	3		
					6	5	1		
B	G	cell	10	3	0.	0.	0.	HSD17B10/PSMA4/PARK7/EEF1E1/PSMA1	10
P	O:	ular	/	3	0	0	0	/PPA2/OAZ1/NQO1/PSMD9/PSME1	
	00	ami	18	1	0	2	2		
	06	no	4	/	1	7	2		
	52	acid		1	5	3	4		
	0	met		8	6	8	9		
		abol		8	9	3	3		
		ic		6	8	2	5		
		pro		2			8		
		cess							

B	G	ribo	5	8	0.	0.	0.	NME1/ENO1/STOML2/NME4/ALDOA	5
P	O:	nucl	/	7	0	0	0		
	00	eosi	18	/	0	2	2		
	09	de	4	1	1	7	2		
	19	trip		8	6	9	9		
	9	hos		8	2	3	4		
		pha		6	0	5	7		
		te		2	3	4	2		
		met			1	2			
		abol							
		ic							
		pro							
		cess							
B	G	tum	7	1	0.	0.	0.	PSMA4/PSMA1/GSTP1/PSMD9/PSME1/CO	7
P	O:	or	/	7	0	0	0	MMD7/TNFRSF12A	
	00	necr	18	4	0	2	2		
	33	osis	4	/	1	7	2		
	20	fact		1	6	9	9		
	9	or-		8	2	3	4		
		me		8	1	5	7		
		diat		6	4	4	2		
		ed		2	8	2			
		sign							
		alin							
		g							
		pat							
		hwa							
		y							

B	G	puri	7	1	0.	0.	0.	NME1/ENO1/STOML2/ADK/APRT/NME4	7
P	O:	ne	/	7	0	0	0	/ALDOA	
		00	ribo	18	5	0	2	2	
		09	nucl	4	/	1	8	3	
		15	eoti		1	6	6	5	
		2	de		8	7	8	6	
			bios		8	5	7	4	
			ynt		6	4	4	9	
			heti		2		4	4	
			c						
			pro						
			cess						
B	G	reg	4	5	0.	0.	0.	RPS2/PARK7/UBE2N/SKP1	4
P	O:	ulat	/	3	0	0	0		
		00	ion	18	/	0	2	2	
		51	of	4	1	1	9	4	
		43	ubi		8	7	9	6	
		8	quit		8	6	7	2	
			in-		6	7	2	0	
			prot		2	7	2	3	
			ein			3	3	1	
			tran						
			sfer						
			ase						
			acti						
			vity						
B	G	late	3	2	0.	0.	0.	CHMP2A/CHMP4A/VPS28	3
P	O:	end	/	5	0	0	0		

		00	oso	18	/	0	2	2		
		45	me	4	1	1	9	4		
		32	to		8	7	9	6		
		4	vac		8	9	7	2		
			uole		6	3	2	0		
			tran		2	3	2	3		
			spor			9	3	1		
			t							
B	G	cell	3	2	0.	0.	0.		PRDX1/NQO1/SOD1	3
P	O:	ular	/	5	0	0	0			
		00	resp	18	/	0	2	2		
		71	ons	4	1	1	9	4		
		45	e to		8	7	9	6		
		0	oxy		8	9	7	2		
			gen		6	3	2	0		
			radi		2	3	2	3		
			cal			9	3	1		
B	G	cell	3	2	0.	0.	0.		PRDX1/NQO1/SOD1	3
P	O:	ular	/	5	0	0	0			
		00	resp	18	/	0	2	2		
		71	ons	4	1	1	9	4		
		45	e to		8	7	9	6		
		1	sup		8	9	7	2		
			erox		6	3	2	0		
			ide		2	3	2	3		
						9	3	1		
B	G	vira	3	2	0.	0.	0.		CHMP2A/CHMP4A/VPS28	3
P	O:	l	/	6	0	0	0			

		00	bud	18	/	0	3	2		
		46	din	4	1	2	3	7		
		75	g		8	0	4	4		
		5			8	1	3	6		
					6	2	9	8		
					2	8	9	8		
					7	4	2			
B	G	mai	5	9	0.	0.	0.		PARK7/CAV1/TXN/SKP1/GPAA1	5
P	O:	nte	/	2	0	0	0			
		00	nan	18	/	0	3	2		
		45	ce	4	1	2	4	8		
		18	of		8	0	2	1		
		5	prot		8	7	5	3		
			ein		6	3	0	4		
			loca		2	9	4	6		
			tion		3	7	1			
B	G	seco	4	5	0.	0.	0.		AKR1B10/ AKR1C3/ AKR1C1/ AKR1C2	4
P	O:	nda	/	6	0	0	0			
		00	ry	18	/	0	3	2		
		19	met	4	1	2	5	8		
		74	abol		8	1	0	8		
		8	ic		8	6	8	1		
			pro		6	7	4	9		
			cess		2	5	7	9		
					9	8	5			
B	G	hyd	4	5	0.	0.	0.		PARK7/PRDX1/GPX3/SOD1	4
P	O:	rog	/	6	0	0	0			
		00	en	18	/	0	3	2		

		42	per	4	1	2	5	8		
		74	oxid		8	1	0	8		
		3	e		8	6	8	1		
			met		6	7	4	9		
			abol		2	5	7	9		
			ic			9	8	5		
			pro							
			cess							
B	G	SCF	5	9	0.	0.	0.	PSMA4/PSMA1/SKP1/PSMD9/PSME1	5	
P	O:	-	/	3	0	0	0			
	00	dep	18	/	0	3	2			
	31	end	4	1	2	5	8			
	14	ent		8	1	0	8			
	6	prot		8	7	8	1			
		easo		6	4	4	9			
		mal		2	7	7	9			
		ubi			3	8	5			
		quit								
		in-								
		dep								
		end								
		ent								
		prot								
		ein								
		cata								
		boli								
		c								
		pro								

		cess								
B	G	resp	5	9	0.	0.	0.	NME1/LDHA/NDUFS4/ALDH3A1/FOSL1	5	
P	O:	ons	/	3	0	0	0			
	00	e to	18	/	0	3	2			
	51	cA	4	1	2	5	8			
	59	MP		8	1	0	8			
	1			8	7	8	1			
				6	4	4	9			
				2	7	7	9			
				3	8	5				
B	G	nucl	3	2	0.	0.	0.	NME1/NME4/TXNRD1	3	
P	O:	eob	/	7	0	0	0			
	00	ase-	18	/	0	3	2			
	15	cont	4	1	2	5	9			
	94	aini		8	2	8	4			
	9	ng		8	4	5	5			
		sma		6	8	7	4			
		ll		2	3	8	9			
		mol		4	7	9				
		ecul								
		e								
		inte								
		rco								
		nve								
		rsio								
		n								
B	G	pep	3	2	0.	0.	0.	PRMT1/PARK7/COPRS	3	
P	O:	tidy	/	7	0	0	0			

	00	l-	18	/	0	3	2		
	18	argi	4	1	2	5	9		
	19	nine		8	2	8	4		
	5	mo		8	4	5	5		
		difi		6	8	7	4		
		cati		2	3	8	9		
		on			4	7	9		
B	G	reg	10	3	0.	0.	0.	SLC25A5/PRELID1/ENO1/PARK7/CAV1/G	10
P	O:	ulat	/	4	0	0	0	STP1/VDAC2/SOD1/TNFRSF12A/S100A9	
	20	ion	18	8	0	3	2		
	01	of	4	/	2	5	9		
	23	apo		1	2	9	4		
	3	ptot		8	6	0	9		
		ic		8	4	6	5		
		sign		6	2	9	2		
		alin		2	9	3	9		
		g							
		pat							
		hwa							
		y							
B	G	pri	5	9	0.	0.	0.	AKR1B10/AKR1C3/PARK7/AKR1C1/AKR1	5
P	O:	mar	/	4	0	0	0	C2	
	00	y	18	/	0	3	2		
	34	alco	4	1	2	5	9		
	30	hol		8	2	9	5		
	8	met		8	7	3	1		
		abol		6	9	6	9		
		ic		2	0	9	9		

		pro		6	9	8			
		cess							
B	G	reg	8	2	0.	0.	0.	HSP90AA1/HSP90AB1/RPS2/PARK7/CAV1	8
P	O:	ulat	/	3	0	0	0	/UBE2N/SKP1/VPS28	
	19	ion	18	7	0	3	2		
	03	of	4	/	2	6	9		
	32	prot		1	3	4	9		
	0	ein		8	2	2	2		
		mo		8	3	7	3		
		difi		6	2	7	1		
		cati		2	3	4	1		
		on							
		by							
		sma							
		ll							
		prot							
		ein							
		conj							
		uga							
		tion							
		or							
		rem							
		oval							
B	G	tran	6	1	0.	0.	0.	SKP1/NEDD8/MT2A/SOD1/FTL/S100A9	6
P	O:	sitio	/	3	0	0	0		
	00	n	18	9	0	3	3		
	55	met	4	/	2	7	1		
	07	al		1	4	8	0		

	6	ion		8	4	2	6		
		ho		8	4	1	8		
		meo		6	6	8	2		
		stasi		2	6	7	9		
		s							
B	G	Fc	8	2	0.	0.	0.	HSP90AA1/PSMA4/HSP90AB1/PSMA1/SKP	8
P	O:	rece	/	3	0	0	0	1/PSMD9/PSME1/ARPC1B	
	00	ptor	18	9	0	3	3		
	38	sign	4	/	2	7	1		
	09	alin		1	4	8	0		
	3	g		8	4	2	6		
		pat		8	6	1	8		
		hwa		6	9	8	2		
		y		2	2	7	9		
B	G	resp	10	3	0.	0.	0.	CDK4/AKR1C3/PARK7/CAV1/S100A16/G6	10
P	O:	ons	/	5	0	0	0	PD/MT2A/NQO1/SOD1/SYT8	
	00	e to	18	2	0	3	3		
	10	met	4	/	2	7	1		
	03	al		1	4	8	0		
	8	ion		8	5	2	6		
				8	9	1	8		
				6	1	8	2		
				2	6	7	9		
B	G	puri	4	5	0.	0.	0.	NME1/ADK/APRT/NME4	4
P	O:	ne	/	8	0	0	0		
	00	ribo	18	/	0	3	3		
	46	nucl	4	1	2	7	1		
	12	eosi		8	4	8	0		

	8	de		8	6	2	6		
		met		6	6	1	8		
		abol		2	3	8	2		
		ic			5	7	9		
		pro							
		cess							
B	G	resp	3	2	0.	0.	0.	PRDX1/NQO1/SOD1	3
P	O:	ons	/	8	0	0	0		
	00	e to	18	/	0	3	3		
	00	sup	4	1	2	8	1		
	30	erox		8	5	0	2		
	3	ide		8	0	9	9		
				6	0	6	3		
				2	2	0	5		
				2	6	3			
B	G	ribo	7	1	0.	0.	0.	NME1/ENO1/STOML2/ADK/APRT/NME4	7
P	O:	nucl	/	8	0	0	0	/ALDOA	
	00	eoti	18	8	0	3	3		
	09	de	4	/	2	8	1		
	26	bios		1	5	0	2		
	0	ynt		8	1	9	9		
		heti		8	1	6	3		
		c		6	5	0	5		
		pro		2	3	6	3		
		cess							
B	G	resp	3	2	0.	0.	0.	PRDX1/NQO1/SOD1	3
P	O:	ons	/	9	0	0	0		
	00	e to	18	/	0	4	3		

		00	oxy	4	1	2	1	4		
		30	gen		8	7	7	3		
		5	radi		8	6	7	1		
			cal		6	8	2	3		
					2	8	2	3		
						5	9	2		
B	G	posi	4	6	0.	0.	0.	PARK7/CAV1/SOD1/S100A9	4	
P	O:	tive	/	0	0	0	0			
		20	reg	18	/	0	4	3		
		01	ulat	4	1	2	1	4		
		24	ion		8	7	8	4		
		4	of		8	9	9	1		
			intri		6	2	8	7		
			nsic		2	2	8	3		
			apo			6	9	2		
			ptot							
			ic							
			sign							
			alin							
			g							
			pat							
			hwa							
			y							
B	G	reg	6	1	0.	0.	0.	HSP90AA1/HSP90AB1/PARK7/CAV1/TXN	6	
P	O:	ulat	/	4	0	0	0	/GADD45A		
		00	ion	18	3	0	4	3		
		33	of	4	/	2	2	4		
		13	pep		1	8	0	5		

	5	tidy	8	1	3	2			
		l-	8	6	1	6			
		seri	6	1	2	0			
		ne	2	4	9	7			
		pho							
		sph							
		oryl							
		atio							
		n							
B	G	mor	6	1	0.	0.	0.	PSMA4/ AP2M1/ AP2S1/ PSMA1/ PSMD9/ PS	6
P	O:	pho	/	4	0	0	0	ME1	
	00	gen	18	4	0	4	3		
	01	esis	4	/	2	3	5		
	73	of a		1	9	2	5		
	8	pola		8	1	7	5		
		rize		8	5	9	1		
		d		6	2	4	3		
		epit		2	8	8	8		
		heli							
		um							
B	G	puri	4	6	0.	0.	0.	NME1/ ADK/ APRT/ NME4	4
P	O:	ne	/	1	0	0	0		
	00	nucl	18	/	0	4	3		
	42	eosi	4	1	2	3	5		
	27	de		8	9	7	9		
	8	met		8	6	9	7		
		abol		6	5	6	5		
		ic		2	7	0	6		

		pro		6	1	8			
		cess							
B	G	neg	5	1	0.	0.	0.	PSMA4/PSMA1/SKP1/PSMD9/PSME1	5
P	O:	ativ	/	0	0	0	0		
	00	e	18	0	0	4	3		
	10	reg	4	/	2	3	5		
	97	ulat		1	9	8	9		
	2	ion		8	8	2	9		
		of		8	3		5		
		G2/		6	0		3		
		M		2	9		8		
		tran							
		sitio							
		n of							
		mit							
		otic							
		cell							
		cycl							
		e							
B	G	mul	3	3	0.	0.	0.	CHMP2A/CHMP4A/VPS28	3
P	O:	tive	/	0	0	0	0		
	00	sicu	18	/	0	4	3		
	36	lar	4	1	3	4	6		
	25	bod		8	0	6	6		
	8	y		8	5	3	6		
		asse		6	4	5	5		
		mbl		2	6	8	5		
		y			2	4	4		

B	G	mit	5	1	0.	0.	0.	NDUFAB1/NDUFB9/NDUFS4/NDUFB5/ND	5
P	O:	och	/	0	0	0	0	UFC2	
		00	ond	18	1	0	4	3	
		33	rial	4	/	3	5	7	
		10	resp		1	1	2	1	
		8	irat		8	1	6	8	
			ory		8	4	8	4	
			chai		6	1	1	9	
			n		2	1	2	2	
			com						
			plex						
			asse						
			mbl						
			y						
B	G	puri	7	1	0.	0.	0.	NME1/ENO1/STOML2/ADK/APRT/NME4	7
P	O:	ne	/	9	0	0	0	/ALDOA	
		00	nucl	18	7	0	4	3	
		06	eoti	4	/	3	7	8	
		16	de		1	2	0	6	
		4	bios		8	5	9	8	
			ynt		8	6	4	4	
			heti		6	5	0	7	
			c		2	9	2	8	
			pro						
			cess						
B	G	acti	6	1	0.	0.	0.	HSP90AA1/PSMA4/PSMA1/SKP1/PSMD9/	6
P	O:	vati	/	4	0	0	0	PSME1	
		00	on	18	8	0	4	3	

		02	of	4	/	3	7	9		
		21	inna			1	3	5	0	
		8	te			8	3	7	7	
			im			8	8	2	7	
			mu			6	1	4	7	
			ne			2	4	5	9	
			resp							
			ons							
			e							
B	G	posi	3	3	0.	0.	0.	CAV1/ANXA2/CES1		3
P	O:	tive	/	1	0	0	0			
	00	reg	18	/	0	4	3			
	32	ulat	4	1	3	7	9			
	37	ion		8	3	5	0			
	3	of		8	5	7	7			
		ster		6	7	2	7			
		ol		2	8	4	7			
		tran			6	5	9			
		spor								
		t								
B	G	posi	3	3	0.	0.	0.	CAV1/ANXA2/CES1		3
P	O:	tive	/	1	0	0	0			
	00	reg	18	/	0	4	3			
	32	ulat	4	1	3	7	9			
	37	ion		8	3	5	0			
	6	of		8	5	7	7			
		chol		6	7	2	7			
		este		2	8	4	7			

		rol		6	5	9			
		tran							
		spor							
		t							
B	G	mul	3	3	0.	0.	0.	CHMP2A/CHMP4A/VPS28	3
P	O:	tive	/	1	0	0	0		
	00	sicu	18	/	0	4	3		
	36	lar	4	1	3	7	9		
	25	bod		8	3	5	0		
	7	y		8	5	7	7		
		org		6	7	2	7		
		aniz		2	8	4	7		
		atio			6	5	9		
		n							
B	G	sma	11	4	0.	0.	0.	ENO1/HSD17B10/AKR1B10/AKR1C3/ECHS	11
P	O:	ll	/	3	0	0	0	1/PARK7/TXN2/PGD/ALDOA/ECH1/DEC	
	00	mol	18	1	0	4	4	R1	
	44	ecul	4	/	3	8	0		
	28	e		1	4	7	0		
	2	cata		8	6	8	7		
		boli		8	1	7	6		
		c		6	1	9	2		
		pro		2	3	8	7		
		cess							
B	G	reg	3	3	0.	0.	0.	PARK7/TXN/SFN	3
P	O:	ulat	/	2	0	0	0		
	00	ion	18	/	0	5	4		
	46	of	4	1	3	1	2		

		82	prot	8	6	3	1		
		5	ein	8	7	3	7		
			exp	6	8	8	1		
			ort	2	8	8	6		
			fro		9	7	6		
			m						
			nucl						
			eus						
B	G	cell	3	3	0.	0.	0.	CDK4/HSP90AB1/RPL3	3
P	O:	ular	/	2	0	0	0		
		00	resp	18	/	0	5	4	
		71	ons	4	1	3	1	2	
		35	e to		8	6	3	1	
		3	inte		8	7	3	7	
			rleu		6	8	8	1	
			kin-		2	8	8	6	
			4			9	7	6	
B	G	plas	4	6	0.	0.	0.	AP2M1/ AP2S1/ CNPY2/ ANXA2	4
P	O:	ma	/	5	0	0	0		
		00	lipo	18	/	0	5	4	
		34	prot	4	1	3	1	2	
		38	ein		8	7	8	5	
		1	part		8	3	4	8	
			icle		6	3	1	4	
			clea		2	4	6	6	
			ranc			9	3	5	
			e						
B	G	reg	7	2	0.	0.	0.	CDK4/HSP90AA1/PSMA4/PSMA1/SKP1/PS	7

P	O:	ulat	/	0	0	0	0	MD9/PSME1	
	00	ion	18	3	0	5	4		
	10	of	4	/	3	3	3		
	38	G2/		1	8	0	5		
	9	M		8	3	5	8		
		tran		8	9	5	2		
		sitio		6	9	8	0		
		n of		2	4	3	4		
		mit							
		otic							
		cell							
		cycl							
		e							
B	G	non	6	1	0.	0.	0.	PSMA4/ AP2M1/ AP2S1/ PSMA1/ PSMD9/ PS	6
P	O:	-	/	5	0	0	0	ME1	
	00	can	18	3	0	5	4		
	35	onic	4	/	3	3	3		
	56	al		1	9	5	9		
	7	Wnt		8	2	1	5		
		sign		8	9	1	5		
		alin		6	0	0	9		
		g		2	6	1	4		
		pat							
		hwa							
		y							
B	G	T	7	2	0.	0.	0.	PSMA4/STOML2/PSMA1/UBE2N/SKP1/PS	7
P	O:	cell	/	0	0	0	0	MD9/PSME1	
	00	rece	18	4	0	5	4		

	50	ptor	4	/	3	3	3		
	85	sign		1	9	5	9		
	2	alin		8	4	1	5		
		g		8	4	1	5		
		pat		6	4	0	9		
		hwa		2	1	1	4		
		y							
B	G	reg	11	4	0.	0.	0.	PRMT1/CDK4/HSP90AA1/PSMA4/PSMA1/	11
P	O:	ulat	/	3	0	0	0	SKP1/SFN/PSMD9/PSME1/RDX/GADD45A	
	19	ion	18	9	0	5	4		
	01	of	4	/	3	3	3		
	99	mit		1	9	5	9		
	0	otic		8	7	1	5		
		cell		8	3	1	5		
		cycl		6	2	0	9		
		e		2		1	4		
		pha							
		se							
		tran							
		sitio							
		n							
B	G	posi	5	1	0.	0.	0.	HSP90AA1/HSP90AB1/PARK7/CAV1/TXN	5
P	O:	tive	/	0	0	0	0		
	00	reg	18	7	0	5	4		
	33	ulat	4	/	3	3	3		
	13	ion		1	9	5	9		
	8	of		8	8	1	5		
		pep		8	8	1	5		

		tidy	6	8	0	9		
		l-	2	8	1	4		
		seri						
		ne						
		pho						
		sph						
		oryl						
		atio						
		n						
B	G	UT	2	1	0.	0.	NME1/NME4	2
P	O:	P	/	0	0	0	0	
	00	bios	18	/	0	5	4	
	06	ynt	4	1	4	3	3	
	22	heti		8	0	5	9	
	8	c		8	4	1	5	
		pro		6	5	1	5	
		cess		2	4	0	9	
					4	1	4	
B	G	isop	2	1	0.	0.	AKR1B10/AKR1C3	2
P	O:	ren	/	0	0	0	0	
	00	oid	18	/	0	5	4	
	08	cata	4	1	4	3	3	
	30	boli		8	0	5	9	
	0	c		8	4	1	5	
		pro		6	5	1	5	
		cess		2	4	0	9	
					4	1	4	
B	G	gas	2	1	0.	0.	CAV1/GSTP1	2

P	O:	ho	/	0	0	0	0		
	00	meo	18	/	0	5	4		
	33	stasi	4	1	4	3	3		
	48	s		8	0	5	9		
	3			8	4	1	5		
				6	5	1	5		
				2	4	0	9		
				4	1	4			
B	G	posi	2	1	0.	0.	0.	CDK4/HSP90AB1	2
P	O:	tive	/	0	0	0	0		
	00	reg	18	/	0	5	4		
	45	ulat	4	1	4	3	3		
	79	ion		8	0	5	9		
	3	of		8	4	1	5		
		cell		6	5	1	5		
		size		2	4	0	9		
				4	1	4			
B	G	com	2	1	0.	0.	0.	HSP90AB1/CD59	2
P	O:	ple	/	0	0	0	0		
	00	men	18	/	0	5	4		
	97	t-	4	1	4	3	3		
	27	dep		8	0	5	9		
	8	end		8	4	1	5		
		ent		6	5	1	5		
		cyto		2	4	0	9		
		toxi			4	1	4		
		city							
B	G	posi	3	3	0.	0.	0.	RPS2/UBE2N/SKP1	3

P	O:	tive	/	4	0	0	0	
	00	reg	18	/	0	5	4	
	51	ulat	4	1	4	7	7	
	44	ion		8	3	4	1	
	3	of		8	7	4	8	
		ubi		6	5	5	7	
		quit		2	5	2	6	
		in-			8	5	8	
		prot						
		ein						
		tran						
		sfer						
		ase						
		acti						
		vity						
B	G	puri	7	2	0.	0.	0.	NME1/ENO1/STOML2/ADK/APRT/NME4 7
P	O:	ne-	/	0	0	0	0	/ALDOA
	00	cont	18	8	0	5	4	
	72	aini	4	/	4	7	7	
	52	ng		1	3	4	1	
	2	com		8	8	4	8	
		pou		8	4	5	7	
		nd		6	0	2	6	
		bios		2	3	5	8	
		ynt						
		heti						
		c						
		pro						

	B	G	carb	7	2	0.	0.	0.	ENO1/MDH2/TKT/TALDO1/G6PD/PGD/	7
P	O:	ohy	/	0	0	0	0	0	ALDOA	
	00	drat	18	9	0	5	4			
	16	e	4	/	4	8	8			
	05	bios		1	4	6	2			
	1	ynt		8	9	8	0			
		heti		8	9	2	4			
		c		6	5	8	3			
		pro		2	1	7				
		cess								
B	G	neg	5	1	0.	0.	0.	PSMA4/PSMA1/SKP1/PSMD9/PSME1		5
P	O:	ativ	/	1	0	0	0			
	19	e	18	1	0	6	4			
	02	reg	4	/	4	0	9			
	75	ulat		1	6	4	6			
	0	ion		8	6	0	1			
		of		8	1	3	7			
		cell		6	7	8	9			
		cycl		2	4	1	4			
		e								
		G2/								
		M								
		pha								
		se								
		tran								
		sitio								
		n								

B	G	cell	6	1	0.	0.	0.	AKR1C3/PARK7/PRDX1/TXN/NQO1/SOD	6
P	O:	ular	/	5	0	0	0	1	
	00	resp	18	9	0	6	4		
	34	ons	4	/	4	0	9		
	61	e to		1	7	4	6		
	4	reac		8	3	0	1		
		tive		8	6	3	7		
		oxy		6	5	8	9		
		gen		2	9	1	4		
		spec							
		ies							
B	G	acti	3	3	0.	0.	0.	PARK7/TXN/IL18	3
P	O:	vati	/	5	0	0	0		
	00	on	18	/	0	6	4		
	32	of	4	1	4	0	9		
	14	prot		8	7	4	6		
	8	ein		8	5	0	1		
		kina		6	1	3	7		
		se B		2	8	8	9		
		acti			3	1	4		
		vity							
B	G	resp	3	3	0.	0.	0.	CDK4/HSP90AB1/RPL3	3
P	O:	ons	/	5	0	0	0		
	00	e to	18	/	0	6	4		
	70	inte	4	1	4	0	9		
	67	rleu		8	7	4	6		
	0	kin-		8	5	0	1		
	4			6	1	3	7		

				2	8	8	9		
					3	1	4		
B	G	neg	7	2	0.	0.	0.	PSMA4/CAV1/PSMA1/PSMD9/PSME1/CS	7
P	O:	ativ	/	1	0	0	0	NK1A1/TAX1BP3	
	00	e	18	2	0	6	4		
	30	reg	4	/	4	0	9		
	17	ulat		1	8	4	6		
	8	ion		8	5	0	1		
		of		8	9	3	7		
		Wnt		6	7	8	9		
		sign		2	6	1	4		
		alin							
		g							
		pat							
		hwa							
		y							
B	G	sup	4	7	0.	0.	0.	PRDX1/GSTP1/NQO1/SOD1	4
P	O:	erox	/	0	0	0	0		
	00	ide	18	/	0	6	4		
	06	met	4	1	4	0	9		
	80	abol		8	8	4	6		
	1	ic		8	6	0	1		
		pro		6	9	3	7		
		cess		2	5	8	9		
					2	1	4		
B	G	cell	4	7	0.	0.	0.	SKP1/NEDD8/SOD1/FTL	4
P	O:	ular	/	0	0	0	0		
	00	iron	18	/	0	6	4		

	06	ion	4	1	4	0	9		
	87	ho		8	8	4	6		
	9	meo		8	6	0	1		
		stasi		6	9	3	7		
		s		2	5	8	9		
					2	1	4		
B	G	reg	6	1	0.	0.	0.	ENO1/PARK7/CAV1/VDAC2/SOD1/S100A	6
P	O:	ulat	/	6	0	0	0	9	
	20	ion	18	0	0	6	4		
	01	of	4	/	4	0	9		
	24	intri		1	8	4	6		
	2	nsic		8	8	0	1		
		apo		8	2	3	7		
		ptot		6	2	8	9		
		ic		2	2	1	4		
		sign							
		alin							
		g							
		pat							
		hwa							
		y							
B	G	for	2	1	0.	0.	0.	MCTS1/RPL13A	2
P	O:	mat	/	1	0	0	0		
	00	ion	18	/	0	6	4		
	01	of	4	1	4	0	9		
	73	tran		8	9	4	6		
	1	slati		8	1	0	1		
		on		6	2	3	7		

		prei	2	8	8	9			
		niti		1	1	4			
		atio							
		n							
		com							
		plex							
B	G	me	2	1	0.	0.	0.	CAV1/ANXA2	2
P	O:	mbr	/	1	0	0	0		
	00	ane	18	/	0	6	4		
	01	raft	4	1	4	0	9		
	76	asse		8	9	4	6		
	5	mbl		8	1	0	1		
		y		6	2	3	7		
				2	8	8	9		
				1	1	4			
B	G	GT	2	1	0.	0.	0.	NME1/NME4	2
P	O:	P	/	1	0	0	0		
	00	bios	18	/	0	6	4		
	06	ynt	4	1	4	0	9		
	18	heti		8	9	4	6		
	3	c		8	1	0	1		
		pro		6	2	3	7		
		cess		2	8	8	9		
				1	1	4			
B	G	hist	2	1	0.	0.	0.	PRMT1/COPRS	2
P	O:	one	/	1	0	0	0		
	00	argi	18	/	0	6	4		
	34	nine	4	1	4	0	9		

	96	met		8	9	4	6		
	9	hyla		8	1	0	1		
		tion		6	2	3	7		
				2	8	8	9		
					1	1	4		
B	G	reg	2	1	0.	0.	0.	EIF3E/EIF3D	2
P	O:	ulat	/	1	0	0	0		
	19	ion	18	/	0	6	4		
	05	of	4	1	4	0	9		
	21	RN		8	9	4	6		
	4	A		8	1	0	1		
		bin		6	2	3	7		
		din		2	8	8	9		
		g			1	1	4		
B	G	resp	4	7	0.	0.	0.	LDHA/CAV1/ARPC1B/KRT19	4
P	O:	ons	/	1	0	0	0		
	00	e to	18	/	0	6	5		
	43	estr	4	1	5	2	1		
	62	oge		8	1	6	4		
	7	n		8	2	9	9		
				6	1	4	9		
				2	6	7	7		
						3	9		
B	G	rece	3	3	0.	0.	0.	AP2M1/AP2S1/ANXA2	3
P	O:	ptor	/	6	0	0	0		
	00	cata	18	/	0	6	5		
	32	boli	4	1	5	2	1		
	80	c		8	1	7	5		

	1	pro		8	4	3	2			
		cess		6	7	0	9			
				2	0	9	5			
					4	7	6			
B	G	stim	5	1	0.	0.	0.	PSMA4/PSMA1/SKP1/PSMD9/PSME1	5	
P	O:	ulat	/	1	0	0	0			
	00	ory	18	4	0	6	5			
	02	C-	4	/	5	3	1			
	22	type		1	2	3	9			
	3	lecti		8	1	0	9			
		n		8	6	3	9			
		rece		6	7	6	9			
		ptor		2	1	2	5			
		sign								
		alin								
		g								
		pat								
		hwa								
		y								
B	G	ribo	4	7	0.	0.	0.	NME1/ADK/APRT/NME4	4	
P	O:	nucl	/	2	0	0	0			
	00	eosi	18	/	0	6	5			
	09	de	4	1	5	5	3			
	11	met		8	3	0	4			
	9	abol		8	8	3	1			
		ic		6	2	0	8			
		pro		2	2	1	2			
		cess			9	7	1			

B	G	nitri	4	7	0.	0.	0.	HSP90AA1/HSP90AB1/CAV1/NQO1	4
P	O:	c	/	3	0	0	0		
	00	oxid	18	/	0	6	5		
	06	e	4	1	5	7	5		
	80	bios		8	6	9	8		
	9	ynt		8	5	9	5		
		heti		6	1	0	0		
		c		2	7	9	3		
		pro				6	1		
		cess							
B	G	reg	7	2	0.	0.	0.	CDK4/HSP90AA1/PSMA4/PSMA1/SKP1/PS	7
P	O:	ulat	/	1	0	0	0	MD9/PSME1	
	19	ion	18	9	0	6	5		
	02	of	4	/	5	9	6		
	74	cell		1	7	2	9		
	9	cycl		8	8	7	0		
		e		8	4	4	5		
		G2/		6	6	9			
		M		2	3	2			
		pha							
		se							
		tran							
		sitio							
		n							
B	G	reg	2	1	0.	0.	0.	PARK7/UBE2N	2
P	O:	ulat	/	2	0	0	0		
	00	ion	18	/	0	6	5		
	33	of	4	1	5	9	6		

	18	hist		8	8	2	9		
	2	one		8	5	7	0		
		ubi		6	7	4	5		
		quit		2	7	9			
		inat			1	2			
		ion							
B	G	UT	2	1	0.	0.	0.	NME1/NME4	2
P	O:	P	/	2	0	0	0		
	00	met	18	/	0	6	5		
	46	abol	4	1	5	9	6		
	05	ic		8	8	2	9		
	1	pro		8	5	7	0		
		cess		6	7	4	5		
				2	7	9			
					1	2			
B	G	cell	2	1	0.	0.	0.	AKR1B10/PARK7	2
P	O:	ular	/	2	0	0	0		
	01	resp	18	/	0	6	5		
	10	ons	4	1	5	9	6		
	09	e to		8	8	2	9		
	6	alde		8	5	7	0		
		hyd		6	7	4	5		
		e		2	7	9			
					1	2			
B	G	reg	4	7	0.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1	4
P	O:	ulat	/	4	0	0	0		
	19	ion	18	/	0	6	5		
	02	of	4	1	5	9	7		

	03	hem		8	9	8	3		
	6	ato		8	2	3	6		
		poie		6	9	3	3		
		tic		2	9	5	8		
		ste			7	3	7		
		m							
		cell							
		diff							
		eren							
		tiati							
		on							
B	G	cell	3	3	0.	0.	0.	AKR1C3/MT2A/SOD1	3
P	O:	ular	/	8	0	0	0		
	00	resp	18	/	0	7	5		
	71	ons	4	1	5	0	7		
	27	e to		8	9	3	7		
	6	cad		8	9	0	5		
		miu		6	5	7	3		
		m		2	3	2			
		ion			9	5			
B	G	inna	5	1	0.	0.	0.	PSMA4/PSMA1/SKP1/PSMD9/PSME1	5
P	O:	te	/	1	0	0	0		
	00	im	18	8	0	7	5		
	02	mu	4	/	6	0	7		
	22	ne		1	0	3	8		
	0	resp		8	2	8	1		
		ons		8	7	6	8		
		e		6	3	5	1		

	9	and	8	1	2	2		
		pres	6	7	0	1		
		enta	2	2	5	0		
		tion		2	5	8		
		of						
		exo						
		gen						
		ous						
		pep						
		tide						
		anti						
		gen						
		via						
		MH						
		C						
		clas						
		s I,						
		TA						
		P-						
		dep						
		end						
		ent						
B	G	DN	4	7	0.	0.	0.	SNRPB/SNRPE/POLR2E/POLR2F
P	O:	A-	/	5	0	0	0	4
	00	tem	18	/	0	7	5	
	06	plat	4	1	6	1	8	
	35	ed		8	2	1	4	
	3	tran		8	1	2	2	

		scri	6	7	0	1			
		ptio	2	2	5	0			
		n,		2	5	8			
		ter							
		min							
		atio							
		n							
B	G	fatt	4	7	0.	0.	0.	HSD17B10/ECHS1/ECH1/DECR1	4
P	O:	y	/	5	0	0	0		
	00	acid	18	/	0	7	5		
	06	beta	4	1	6	1	8		
	63	-		8	2	1	4		
	5	oxid		8	1	2	2		
		atio		6	7	0	1		
		n		2	2	5	0		
				2	5	8			
B	G	reg	10	4	0.	0.	0.	CDK4/AKR1C3/CAV1/STOML2/SOD1/FHL	10
P	O:	ulat	/	0	0	0	0	2/FABP5/TXNRD1/CES1/CAPN2	
	00	ion	18	2	0	7	5		
	19	of	4	/	6	1	8		
	21	lipi		1	2	1	4		
	6	d		8	3	2	2		
		met		8	1	0	1		
		abol		6	9	5	0		
		ic		2	8	5	8		
		pro							
		cess							
B	G	inna	5	1	0.	0.	0.	PSMA4/PSMA1/SKP1/PSMD9/PSME1	5

P	O:	te	/	1	0	0	0	
	00	im	18	9	0	7	5	
	02	mu	4	/	6	1	8	
	75	ne		1	2	1	4	
	8	resp		8	4	2	2	
		ons		8	3	0	1	
		e-		6	1	5	0	
		acti		2	2	5	8	
		vati						
		ng						
		sign						
		al						
		tran						
		sdu						
		ctio						
		n						
B	G	lipi	9	3	0.	0.	0.	CDK4/HSD17B10/AKR1B10/AKR1C3/ECHS 9
P	O:	d	/	4	0	0	0	1/ECH1/FABP5/DECR1/CES1
	00	cata	18	0	0	7	5	
	16	boli	4	/	6	1	8	
	04	c		1	2	4	7	
	2	pro		8	9	7	1	
		cess		8	9	3	1	
				6	7	6	1	
				2	2	5	2	
B	G	mo	7	2	0.	0.	0.	NDUFAB1/HSD17B10/AKR1C3/PARK7/GS 7
P	O:	noc	/	2	0	0	0	TP1/FABP5/CES1
	00	arb	18	4	0	7	6	

		72	oxyl	4	/	6	3	0		
		33	ic		1	5	6	5		
		0	acid		8	2	9	3		
			bios		8	1	3	4		
			ynt		6	7	3	4		
			heti		2	7	2	4		
			c							
			pro							
			cess							
B	G	nucl	9	3	0.	0.	0.	SNRPB/SNRPE/HMGA1/HSP90AB1/PARK7	9	
P	O:	ear	/	4	0	0	0	/HNRNPA1/TXN/SFN/HTATIP2		
		00	tran	18	3	0	7	6		
		51	spor	4	/	6	4	1		
		16	t		1	6	9	5		
		9			8	5	3	5		
					8	8	2	2		
					6	2	5	3		
					2	8	1	6		
B	G	nitri	4	7	0.	0.	0.	HSP90AA1/HSP90AB1/CAV1/NQO1	4	
P	O:	c	/	7	0	0	0			
		00	oxid	18	/	0	7	6		
		46	e	4	1	6	5	1		
		20	met		8	8	2	8		
		9	abol		8	1	8	4		
			ic		6	9	6	3		
			pro		2	1	5	1		
			cess			4	3	7		
B	G	reg	4	7	0.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1	4	

P	O:	ulat	/	7	0	0	0		
	00	ion	18	/	0	7	6		
	61	of	4	1	6	5	1		
	41	tran		8	8	2	8		
	8	scri		8	1	8	4		
		ptio		6	9	6	3		
		n		2	1	5	1		
		fro			4	3	7		
		m							
		RN							
		A							
		pol							
		yme							
		rase							
		II							
		pro							
		mot							
		er							
		in							
		resp							
		ons							
		e to							
		hyp							
		oxia							
B	G	neg	4	7	0.	0.	0.	HSP90AB1/PARK7/LAPTM4B/ANXA2	4
P	O:	ativ	/	7	0	0	0		
	19	e	18	/	0	7	6		
	03	reg	4	1	6	5	1		

		36	ulat		8	8	2	8		
		3	ion		8	1	8	4		
			of		6	9	6	3		
			cell		2	1	5	1		
			ular			4	3	7		
			prot							
			ein							
			cata							
			boli							
			c							
			pro							
			cess							
B	G	pep	2	1	0.	0.	0.	NAA20/METAP2		2
P	O:	tidy	/	3	0	0	0			
	00	l-	18	/	0	7	6			
	18	met	4	1	6	5	1			
	20	hio		8	8	2	8			
	6	nine		8	7	8	4			
		mo		6	8	6	3			
		difi		2	5	5	1			
		cati			6	3	7			
		on								
B	G	neg	2	1	0.	0.	0.	HSP90AB1/LAPTM4B		2
P	O:	ativ	/	3	0	0	0			
	00	e	18	/	0	7	6			
	71	reg	4	1	6	5	1			
	63	ulat		8	8	2	8			
	5	ion		8	7	8	4			

		of	6	8	6	3			
		tran	2	5	5	1			
		sfor		6	3	7			
		min							
		g							
		gro							
		wth							
		fact							
		or							
		beta							
		pro							
		duc							
		tion							
B	G	gua	2	1	0.	0.	0.	NME1/NME4	2
P	O:	nosi	/	3	0	0	0		
	19	ne-	18	/	0	7	6		
	01	cont	4	1	6	5	1		
	07	aini		8	8	2	8		
	0	ng		8	7	8	4		
		com		6	8	6	3		
		pou		2	5	5	1		
		nd			6	3	7		
		bios							
		ynt							
		heti							
		c							
		pro							
		cess							

B	G	reg	2	1	0.	0.	0.	HSP90AA1/HSP90AB1	2
P	O:	ulat	/	3	0	0	0		
	19	ion	18	/	0	7	6		
	02	of	4	1	6	5	1		
	94	tau-		8	8	2	8		
	7	prot		8	7	8	4		
		ein		6	8	6	3		
		kina		2	5	5	1		
		se			6	3	7		
		acti							
		vity							
B	G	viri	3	4	0.	0.	0.	CHMP2A/CHMP4A/VPS28	3
P	O:	on	/	0	0	0	0		
	00	asse	18	/	0	7	6		
	19	mbl	4	1	6	5	1		
	06	y		8	9	4	9		
	8			8	2	7	9		
				6	2	1	5		
				2	5	7	3		
					3	8	4		
B	G	reac	4	7	0.	0.	0.	HSP90AA1/HSP90AB1/CAV1/NQO1	4
P	O:	tive	/	8	0	0	0		
	20	nitr	18	/	0	7	6		
	01	oge	4	1	7	7	3		
	05	n		8	1	4	6		
	7	spec		8	3	5	2		
		ies		6	4	7	6		
		met		2	0	2	2		

		abol		5	4	7			
		ic							
		pro							
		cess							
B	G	rRN	7	2	0.	0.	0.	NPM3/RPS2/RPL35/NSA2/RPL10A/RPL7/	7
P	O:	A	/	2	0	0	0	RPS9	
	00	pro	18	8	0	7	6		
	06	cess	4	/	7	7	3		
	36	ing		1	1	4	6		
	4			8	6	5	2		
				8	0	7	6		
				6	1	2	2		
				2	5	4	7		
B	G	reg	6	1	0.	0.	0.	PRMT1/CDK4/SFN/PSME1/RDX/GADD45	6
P	O:	ulat	/	7	0	0	0	A	
	20	ion	18	4	0	7	6		
	00	of	4	/	7	8	4		
	04	G1/		1	2	4	4		
	5	S		8	8	8	7		
		tran		8	3	6	1		
		sitio		6	3	2	5		
		n of		2	9	9	7		
		mit							
		otic							
		cell							
		cycl							
		e							
B	G	prot	7	2	0.	0.	0.	PRMT1/HSD17B10/STOML2/CHMP2A/AL	7

P	O:	ein	/	2	0	0	0	DOA/GSDMD/UGDH	
		00	com	18	9	0	7	6	
		51	plex	4	/	7	8	4	
		25	olig		1	3	6	6	
		9	ome		8	2	4	0	
			riza		8	6	9	5	
			tion		6	7	7	8	
					2	4	4	4	
B	G	reg	11	4	0.	0.	0.	PRMT1/CDK4/HSP90AA1/PSMA4/PSMA1/	11
P	O:	ulat	/	7	0	0	0	SKP1/SFN/PSMD9/PSME1/RDX/GADD45A	
		19	ion	18	8	0	7	6	
		01	of	4	/	7	9	4	
		98	cell		1	4	0	8	
		7	cycl		8	0	0	9	
			e		8	0	2	5	
			pha		6	2	2	3	
			se		2	4	3	8	
			tran						
			sitio						
			n						
B	G	resp	3	4	0.	0.	0.	NME1/CDK4/NQO1	3
P	O:	ons	/	1	0	0	0		
		00	e to	18	/	0	7	6	
		33	test	4	1	7	9	4	
		57	oste		8	4	0	8	
		4	ron		8	1	0	9	
			e		6	6	2	5	
					2	1	2	3	

					9	3	8		
B	G	cell	7	2	0.	0.	0.	HSD17B10/AKR1B10/AKR1C3/ECHS1/ECH	7
P	O:	ular	/	3	0	0	0	1/FABP5/DECR1	
		00 lipi	18	0	0	7	6		
		44 d	4	/	7	9	5		
		24 cata		1	4	5	3		
		2 boli		8	9	5	4		
		c		8	6	0	6		
		pro		6	1	8	0		
		cess		2	9	5	3		
B	G	reg	9	3	0.	0.	0.	HSP90AB1/PARK7/TXN/OAZ1/REEP5/SFN	9
P	O:	ulat	/	5	0	0	0	/ANXA2/RDX/TOMM7	
		00 ion	18	0	0	7	6		
		32 of	4	/	7	9	5		
		38 intr		1	5	8	6		
		6 acel		8	5	8	1		
		lula		8	5	1	7		
		r		6	9	0	3		
		tran		2	3	8			
		spor							
		t							
B	G	reg	6	1	0.	0.	0.	PSMA4/AP2M1/AP2S1/PSMA1/PSMD9/PS	6
P	O:	ulat	/	7	0	0	0	ME1	
		20 ion	18	6	0	8	6		
		00 of	4	/	7	0	6		
		02 ani		1	6	6	2		
		7 mal		8	8	3	3		
		org		8	5	3	5		

		an	6	5	6	4			
		mor	2		2	7			
		pho							
		gen							
		esis							
B	G	reg	4	8	0.	0.	0.	EIF3K/CDC123/EIF3E/RPL13A	4
P	O:	ulat	/	0	0	0	0		
	00	ion	18	/	0	8	6		
	06	of	4	1	7	0	6		
	44	tran		8	7	6	2		
	6	slati		8	9	3	3		
		onal		6	2	3	5		
		initi		2	3	6	4		
		atio			6	2	7		
		n							
B	G	end	4	8	0.	0.	0.	CHMP2A/LAPTM4B/CHMP4A/VPS28	4
P	O:	oso	/	0	0	0	0		
	00	me	18	/	0	8	6		
	07	org	4	1	7	0	6		
	03	aniz		8	7	6	2		
	2	atio		8	9	3	3		
		n		6	2	3	5		
				2	3	6	4		
					6	2	7		
B	G	anti	4	8	0.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1	4
P	O:	gen	/	0	0	0	0		
	00	pro	18	/	0	8	6		
	42	cess	4	1	7	0	6		

	59	ing	8	7	6	2	
	0	and	8	9	3	3	
		pres	6	2	3	5	
		enta	2	3	6	4	
		tion		6	2	7	
		of					
		exo					
		gen					
		ous					
		pep					
		tide					
		anti					
		gen					
		via					
		MH					
		C					
		clas					
		s I					
B	G	anti	6	1	0.	0.	PSMA4/ AP2M1/ AP2S1/ PSMA1/ PSMD9/ PS
P	O:	gen	/	7	0	0	ME1
	00	pro	18	7	0	8	6
	02	cess	4	/	7	0	6
	47	ing		1	8	6	2
	8	and		8	9	3	3
		pres		8	2	3	5
		enta		6	4	6	4
		tion		2	5	2	7
		of					

		exo								
		gen								
		ous								
		pep								
		tide								
		anti								
		gen								
B	G	posi	5	1	0.	0.	0.	PARK7/CAV1/SOD1/TNFRSF12A/S100A9	5	
P	O:	tive	/	2	0	0	0			
	20	reg	18	6	0	8	6			
	01	ulat	4	/	7	0	6			
	23	ion		1	9	6	2			
	5	of		8	0	3	3			
		apo		8	7	3	5			
		ptot		6	5	6	4			
		ic		2	8	2	7			
		sign								
		alin								
		g								
		pat								
		hwa								
		y								
B	G	resp	3	4	0.	0.	0.	NME1/NQO1/SOD1	3	
P	O:	ons	/	2	0	0	0			
	00	e to	18	/	0	8	6			
	14	ami	4	1	7	0	6			
	07	ne		8	9	6	2			
	5			8	3	3	3			

				6	0	3	5		
				2	1	6	4		
				7	2	7			
B	G	resp	3	4	0.	0.	0.	PARK7/MT2A/SOD1	3
P	O:	ons	/	2	0	0	0		
	00	e to	18	/	0	8	6		
	46	cop	4	1	7	0	6		
	68	per		8	9	6	2		
	8	ion		8	3	3	3		
				6	0	3	5		
				2	1	6	4		
				7	2	7			
B	G	mit	2	1	0.	0.	0.	CYC1/UQCRH	2
P	O:	och	/	4	0	0	0		
	00	ond	18	/	0	8	6		
	06	rial	4	1	7	0	6		
	12	elec		8	9	6	2		
	2	tron		8	7	3	3		
		tran		6	3	3	5		
		spor		2	8	6	4		
		t,				2	7		
		ubi							
		qui							
		nol							
		to							
		cyto							
		chr							
		ome							

		c								
B	G	CTP	2	1	0.	0.	0.	NME1/NME4		2
P	O:	bios	/	4	0	0	0			
	00	ynt	18	/	0	8	6			
	06	heti	4	1	7	0	6			
	24	c		8	9	6	2			
	1	pro		8	7	3	3			
		cess		6	3	3	5			
				2	8	6	4			
						2	7			
B	G	nucl	2	1	0.	0.	0.	ADK/APRT		2
P	O:	eoti	/	4	0	0	0			
	00	de	18	/	0	8	6			
	43	salv	4	1	7	0	6			
	17	age		8	9	6	2			
	3			8	7	3	3			
				6	3	3	5			
				2	8	6	4			
						2	7			
B	G	posi	2	1	0.	0.	0.	STOML2/CAPN2		2
P	O:	tive	/	4	0	0	0			
	19	reg	18	/	0	8	6			
	03	ulat	4	1	7	0	6			
	72	ion		8	9	6	2			
	7	of		8	7	3	3			
		pho		6	3	3	5			
		sph		2	8	6	4			
		olip				2	7			

		id								
		met								
		abol								
		ic								
		pro								
		cess								
B	G	neg	6	1	0.	0.	0.	PSMA4/CAV1/PSMA1/PSMD9/PSME1/CS	6	
P	O:	ativ	/	7	0	0	0	NK1A1		
	00	e	18	9	0	8	6			
	90	reg	4	/	8	3	8			
	09	ulat		1	3	8	8			
	0	ion		8	1	1	4			
		of		8	8	4	8			
		can		6	3	1	0			
		onic		2	5	1	4			
		al								
		Wnt								
		sign								
		alin								
		g								
		pat								
		hwa								
		y								
B	G	cell	6	1	0.	0.	0.	PSMA4/PSMA1/UBE2N/SKP1/PSMD9/PSM	6	
P	O:	ular	/	8	0	0	0	E1		
	00	resp	18	0	0	8	7			
	71	ons	4	/	8	5	0			
	34	e to		1	5	7	4			

		7	inte		8	3	1	0		
			rleu		8	7	1	6		
			kin-		6	3	6	7		
			1		2	8	5	5		
B	G	ana	4	8	0.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1		4
P	O:	pha	/	3	0	0	0			
	00	se-	18	/	0	8	7			
	31	pro	4	1	8	8	2			
	14	mot		8	8	0	3			
	5	ing		8	5	6	3			
		com		6	2	1	7			
		plex		2	7	6	1			
		-			5	4	1			
		dep								
		end								
		ent								
		cata								
		boli								
		c								
		pro								
		cess								
B	G	rRN	7	2	0.	0.	0.	NPM3/RPS2/RPL35/NSA2/RPL10A/RPL7/		7
P	O:	A	/	3	0	0	0	RPS9		
	00	met	18	8	0	8	7			
	16	abol	4	/	8	8	2			
	07	ic		1	9	0	3			
	2	pro		8	5	6	3			
		cess		8	8	1	7			

				6	1	6	1		
				2	1	4	1		
B	G	prot	10	4	0.	0.	0.	PSMA4/HSP90AB1/PARK7/CAV1/PSMA1/	10
P	O:	easo	/	2	0	0	0	SKP1/PSMD9/PSME1/CSNK1A1/HSP90B1	
	00	me-	18	5	0	8	7		
	43	me	4	/	9	8	2		
	16	diat		1	0	0	3		
	1	ed		8	4	6	3		
		ubi		8	3	1	7		
		quit		6	6	6	1		
		in-		2	6	4	1		
		dep							
		end							
		ent							
		prot							
		ein							
		cata							
		boli							
		c							
		pro							
		cess							
B	G	mat	2	1	0.	0.	0.	RPL35/RPL7	2
P	O:	urat	/	5	0	0	0		
	00	ion	18	/	0	8	7		
	00	of	4	1	9	8	2		
	46	LSU		8	1	0	3		
	3	-		8	4	6	3		
		rRN		6	1	1	7		

		A	2	9	6	1		
		fro			4	1		
		m						
		trici						
		stro						
		nic						
		rRN						
		A						
		tran						
		scri						
		pt						
		(SS						
		U-						
		rRN						
		A,						
		5.8S						
		rRN						
		A,						
		LSU						
		-						
		rRN						
		A)						
B	G	lact	2	1	0.	0.	0.	LDHA/PARK7
P	O:	ate	/	5	0	0	0	
	00	met	18	/	0	8	7	
	06	abol	4	1	9	8	2	
	08	ic		8	1	0	3	
	9	pro		8	4	6	3	

		cess	6	1	1	7		
			2	9	6	1		
					4	1		
B	G	pyri	2	1	0.	0.	0.	NME1/NME4
P	O:	mid	/	5	0	0	0	2
	00	ine	18	/	0	8	7	
	09	ribo	4	1	9	8	2	
	20	nucl		8	1	0	3	
	9	eosi		8	4	6	3	
		de		6	1	1	7	
		trip		2	9	6	1	
		hos				4	1	
		pha						
		te						
		bios						
		ynt						
		heti						
		c						
		pro						
		cess						
B	G	deto	2	1	0.	0.	0.	PARK7/MT2A
P	O:	xific	/	5	0	0	0	2
	00	atio	18	/	0	8	7	
	10	n of	4	1	9	8	2	
	27	cop		8	1	0	3	
	3	per		8	4	6	3	
		ion		6	1	1	7	
				2	9	6	1	

					4	1			
B	G	pep	2	1	0.	0.	0.	PRMT1/COPRS	2
P	O:	tidy	/	5	0	0	0		
	00	l-	18	/	0	8	7		
	18	argi	4	1	9	8	2		
	21	nine		8	1	0	3		
	6	met		8	4	6	3		
		hyla		6	1	1	7		
		tion		2	9	6	1		
					4	1			
B	G	reti	2	1	0.	0.	0.	AKR1C3/AKR1C1	2
P	O:	nal	/	5	0	0	0		
	00	met	18	/	0	8	7		
	42	abol	4	1	9	8	2		
	57	ic		8	1	0	3		
	4	pro		8	4	6	3		
		cess		6	1	1	7		
				2	9	6	1		
					4	1			
B	G	puri	2	1	0.	0.	0.	ADK/APRT	2
P	O:	ne-	/	5	0	0	0		
	00	cont	18	/	0	8	7		
	43	aini	4	1	9	8	2		
	10	ng		8	1	0	3		
	1	com		8	4	6	3		
		pou		6	1	1	7		
		nd		2	9	6	1		
		salv			4	1			

		age							
B	G	stre	2	1	0.	0.	0.	PARK7/MT2A	2
P	O:	ss	/	5	0	0	0		
	19	resp	18	/	0	8	7		
	90	ons	4	1	9	8	2		
	16	e to		8	1	0	3		
	9	cop		8	4	6	3		
		per		6	1	1	7		
		ion		2	9	6	1		
					4	1			
B	G	posi	9	3	0.	0.	0.	HSP90AA1/PSMA4/PARK7/PSMA1/SKP1/	9
P	O:	tive	/	6	0	0	0	PSMD9/PSME1/IL18/S100A9	
	00	reg	18	1	0	8	7		
	31	ulat	4	/	9	8	2		
	34	ion		1	1	0	3		
	9	of		8	5	6	3		
		defe		8	0	1	7		
		nse		6	0	6	1		
		resp		2	8	4	1		
		ons							
		e							
B	G	mo	5	1	0.	0.	0.	HSD17B10/ECHS1/PGD/ECH1/DECR1	5
P	O:	noc	/	3	0	0	0		
	00	arb	18	1	0	8	7		
	72	oxyl	4	/	9	8	3		
	32	ic		1	2	9	0		
	9	acid		8	7	1	3		
		cata		8	0	2	5		

		boli		6	3	1	7		
		c		2	1	5	6		
		pro							
		cess							
B	G	nucl	5	1	0.	0.	0.	NME1/ENO1/LDHA/NME4/ALDOA	5
P	O:	eosi	/	3	0	0	0		
	00	de	18	2	0	9	7		
	06	dip	4	/	9	1	5		
	16	hos		1	5	3	0		
	5	pha		8	6	8	6		
		te		8	1	6	8		
		pho		6	0	8	6		
		sph		2	8	9	1		
		oryl							
		atio							
		n							
B	G	posi	4	8	0.	0.	0.	PRELID1/CAV1/ANXA2/CES1	4
P	O:	tive	/	5	0	0	0		
	00	reg	18	/	0	9	7		
	32	ulat	4	1	9	1	5		
	37	ion		8	6	5	1		
	0	of		8	0	3	9		
		lipi		6	9	6	1		
		d		2	5	7	6		
		tran			5	3	8		
		spor							
		t							
B	G	anti	6	1	0.	0.	0.	PSMA4/AP2M1/AP2S1/PSMA1/PSMD9/PS	6

P	O:	gen	/	8	0	0	0	ME1	
	00	pro	18	5	0	9	7		
	19	cess	4	/	9	1	5		
	88	ing		1	6	7	3		
	4	and		8	9	2	4		
		pres		8	5	5	6		
		enta		6	0	0	4		
		tion		2	6	9	1		
		of							
		exo							
		gen							
		ous							
		anti							
		gen							
B	G	NIK	6	1	0.	0.	0.	PSMA4/PSMA1/SKP1/PSMD9/PSME1/IL18	6
P	O:	/N	/	8	0	0	0		
	00	F-	18	5	0	9	7		
	38	kap	4	/	9	1	5		
	06	paB		1	6	7	3		
	1	sign		8	9	2	4		
		alin		8	5	5	6		
		g		6	0	0	4		
				2	6	9	1		
B	G	posi	5	1	0.	0.	0.	CDK4/CDC123/EIF3E/EIF3D/RPS9	5
P	O:	tive	/	3	0	0	0		
	00	reg	18	3	0	9	7		
	45	ulat	4	/	9	2	6		
	72	ion		1	8	6	0		

	7	of		8	5	3	9		
		tran		8	8	9	7		
		slati		6	0	3	3		
		on		2	7		8		
B	G	nucl	5	1	0.	0.	0.	NME1/ENO1/LDHA/NME4/ALDOA	5
P	O:	eoti	/	3	0	0	0		
	00	de	18	3	0	9	7		
	46	pho	4	/	9	2	6		
	93	sph		1	8	6	0		
	9	oryl		8	5	3	9		
		atio		8	8	9	7		
		n		6	0	3	3		
				2	7		8		
B	G	end	4	8	0.	0.	0.	REEP5/EMC2/RTN4/LMAN2	4
P	O:	opla	/	6	0	0	0		
	00	smi	18	/	1	9	7		
	07	c	4	1	0	3	6		
	02	retic		8	0	3	7		
	9	ulu		8	0	7	0		
		m		6	3	4	1		
		org		2	2	6	4		
		aniz			3	3	1		
		atio							
		n							
B	G	iron	4	8	0.	0.	0.	SKP1/NEDD8/SOD1/FTL	4
P	O:	ion	/	6	0	0	0		
	00	ho	18	/	1	9	7		
	55	meo	4	1	0	3	6		

	07	stasi		8	0	3	7		
	2	s		8	0	7	0		
				6	3	4	1		
				2	2	6	4		
				3	3	1			
B	G	lact	3	4	0.	0.	0.	NME1/CAV1/APRT	3
P	O:	atio	/	6	0	0	0		
	00	n	18	/	1	9	7		
	07		4	1	0	3	7		
	59			8	1	7	0		
	5			8	9	6	2		
				6	2	8	4		
				2	8	1	6		
				8	2	3			
B	G	prot	2	1	0.	0.	0.	TXN/S100A9	2
P	O:	ein	/	6	0	0	0		
	00	nitr	18	/	1	9	7		
	17	osyl	4	1	0	3	7		
	01	atio		8	3	7	0		
	4	n		8	8	6	2		
				6	1	8	4		
				2	3	1	6		
				5	2	3			
B	G	pep	2	1	0.	0.	0.	TXN/S100A9	2
P	O:	tidy	/	6	0	0	0		
	00	l-	18	/	1	9	7		
	18	cyst	4	1	0	3	7		
	11	eine		8	3	7	0		

	9	S-		8	8	6	2		
		nitr		6	1	8	4		
		osyl		2	3	1	6		
		atio			5	2	3		
		n							
B	G	pri	2	1	0.	0.	0.	AKR1B10/ AKR1C3	2
P	O:	mar	/	6	0	0	0		
	00	y	18	/	1	9	7		
	34	alco	4	1	0	3	7		
	31	hol		8	3	7	0		
	0	cata		8	8	6	2		
		boli		6	1	8	4		
		c		2	3	1	6		
		pro			5	2	3		
		cess							
B	G	nucl	2	1	0.	0.	0.	ADK/ APRT	2
P	O:	eosi	/	6	0	0	0		
	00	de	18	/	1	9	7		
	43	salv	4	1	0	3	7		
	17	age		8	3	7	0		
	4			8	8	6	2		
				6	1	8	4		
				2	3	1	6		
					5	2	3		
B	G	AM	2	1	0.	0.	0.	ADK/ APRT	2
P	O:	P	/	6	0	0	0		
	00	met	18	/	1	9	7		
	46	abol	4	1	0	3	7		

		03	ic		8	3	7	0		
		3	pro		8	8	6	2		
			cess		6	1	8	4		
					2	3	1	6		
						5	2	3		
B	G	CTP	2	1	0.	0.	0.		NME1/NME4	2
P	O:	met	/	6	0	0	0			
		00	abol	18	/	1	9	7		
		46	ic	4	1	0	3	7		
		03	pro		8	3	7	0		
		6	cess		8	8	6	2		
					6	1	8	4		
					2	3	1	6		
						5	2	3		
B	G	seq	2	1	0.	0.	0.		FTL/S100A9	2
P	O:	uest	/	6	0	0	0			
		00	erin	18	/	1	9	7		
		51	g of	4	1	0	3	7		
		23	met		8	3	7	0		
		8	al		8	8	6	2		
			ion		6	1	8	4		
					2	3	1	6		
						5	2	3		
B	G	nucl	2	1	0.	0.	0.		SLC25A5/SLC25A6	2
P	O:	eoti	/	6	0	0	0			
		19	de	18	/	1	9	7		
		01	tran	4	1	0	3	7		
		67	sme		8	3	7	0		

	9	mbr		8	8	6	2		
		ane		6	1	8	4		
		tran		2	3	1	6		
		spor			5	2	3		
		t							
B	G	posi	2	1	0.	0.	0.	PARK7/SOD1	2
P	O:	tive	/	6	0	0	0		
	19	reg	18	/	1	9	7		
	03	ulat	4	1	0	3	7		
	20	ion		8	3	7	0		
	9	of		8	8	6	2		
		oxid		6	1	8	4		
		ativ		2	3	1	6		
		e			5	2	3		
		stre							
		ss-							
		ind							
		uce							
		d							
		cell							
		deat							
		h							
B	G	plac	5	1	0.	0.	0.	HSP90AB1/SOD1/FOSL1/KRT19/PHLDA2	5
P	O:	enta	/	3	0	0	0		
	00	dev	18	5	1	9	7		
	01	elop	4	/	0	4	7		
	89	men		1	4	2	4		
	0	t		8	7	7	3		

				8	0	2	8		
				6	9	4	8		
				2	6	1	8		
B	G	ribo	10	4	0.	0.	0.	NME1/ENO1/LDHA/STOML2/TKT/ADK/	10
P	O:	se	/	3	0	0	0	G6PD/APRT/NME4/ALDOA	
	00	pho	18	5	1	9	7		
	19	sph	4	/	0	4	7		
	69	ate		1	5	5	6		
	3	met		8	3	2	4		
		abol		8	3	8	9		
		ic		6	2	3	0		
		pro		2	5	3	9		
		cess							
B	G	cell	5	1	0.	0.	0.	HSD17B10/AKR1B10/AKR1C3/AKR1C1/AK	5
P	O:	ular	/	3	0	0	0	R1C2	
	00	hor	18	6	1	9	7		
	34	mo	4	/	0	6	9		
	75	ne		1	7	1	0		
	4	met		8	8	8	1		
		abol		8	6	8	2		
		ic		6	9	5	8		
		pro		2	8	2	4		
		cess							
B	G	hist	3	4	0.	0.	0.	PARK7/UBE2N/SKP1	3
P	O:	one	/	7	0	0	0		
	00	ubi	18	/	1	9	7		
	16	quit	4	1	0	6	9		
	57	inat		8	8	1	0		

	4	ion		8	1	8	1		
				6	1	8	2		
				2	0	5	8		
					2	2	4		
B	G	hem	4	8	0.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1	4
P	O:	ato	/	8	0	0	0		
	00	poie	18	/	1	9	7		
	60	tic	4	1	0	6	9		
	21	ste		8	8	1	0		
	8	m		8	2	8	1		
		cell		6	1	8	2		
		diff		2	6	5	8		
		eren			4	2	4		
		tiati							
		on							
B	G	cell	4	8	0.	0.	0.	CDK4/AKR1C3/AKR1C2/CES1	4
P	O:	ular	/	9	0	0	0		
	00	resp	18	/	1	9	8		
	97	ons	4	1	1	9	1		
	30	e to		8	2	3	5		
	6	alco		8	4	3	9		
		hol		6	6	2	5		
				2	5	8	6		
					7		7		
B	G	reg	4	8	0.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1	4
P	O:	ulat	/	9	0	0	0		
	19	ion	18	/	1	9	8		
	01	of	4	1	1	9	1		

		53	hem	8	2	3	5		
		2	ato	8	4	3	9		
			poie	6	6	2	5		
			tic	2	5	8	6		
			pro		7		7		
			geni						
			tor						
			cell						
			diff						
			eren						
			tiati						
			on						
B	G	pep	3	4	0.	0.	0.	PARK7/TXN/S100A9	3
P	O:	tidy	/	8	0	1	0		
	00	l-	18	/	1	0	8		
	18	cyst	4	1	1	0	2		
	19	eine		8	4	3	4		
	8	mo		8	5	9	6		
		difi		6	0	5	8		
		cati		2	4	8	8		
		on			3	1	7		
B	G	reg	4	9	0.	0.	0.	SLC25A5/VDAC2/SFN/LAPTM4B	4
P	O:	ulat	/	0	0	1	0		
	00	ion	18	/	1	0	8		
	90	of	4	1	1	0	2		
	55	me		8	6	3	4		
	9	mbr		8	8	9	6		
		ane		6	2	5	8		

		per	2	1	8	8			
		mea			1	7			
		bilit							
		y							
B	G	AT	2	1	0.	0.	0.	SLC25A5/SLC25A6	2
P	O:	P	/	7	0	1	0		
	00	tran	18	/	1	0	8		
	15	spor	4	1	1	0	2		
	86	t		8	6	3	4		
	7			8	9	9	6		
				6	0	5	8		
				2	6	8	8		
					6	1	7		
B	G	late	2	1	0.	0.	0.	CHMP4A/VPS28	2
P	O:	end	/	7	0	1	0		
	00	oso	18	/	1	0	8		
	32	me	4	1	1	0	2		
	51	to		8	6	3	4		
	1	vac		8	9	9	6		
		uole		6	0	5	8		
		tran		2	6	8	8		
		spor			6	1	7		
		t via							
		mul							
		tive							
		sicu							
		lar							
		bod							

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	61	absc	4	1	1	0	2		
	95	issi		8	6	3	4		
	2	on		8	9	9	6		
				6	0	5	8		
				2	6	8	8		
					6	1	7		
B	G	cell	2	1	0.	0.	0.	SOD1/HSP90B1	2
P	O:	ular	/	7	0	1	0		
	00	resp	18	/	1	0	8		
	71	ons	4	1	1	0	2		
	31	e to		8	6	3	4		
	8	AT		8	9	9	6		
		P		6	0	5	8		
				2	6	8	8		
					6	1	7		
B	G	puri	2	1	0.	0.	0.	SLC25A5/SLC25A6	2
P	O:	ne-	/	7	0	1	0		
	00	cont	18	/	1	0	8		
	72	aini	4	1	1	0	2		
	53	ng		8	6	3	4		
	0	com		8	9	9	6		
		pou		6	0	5	8		
		nd		2	6	8	8		
		tran			6	1	7		
		sme							
		mbr							
		ane							
		tran							

sitio									
n									
B	G	cell	4	9	0.	0.	0.	CDK4/AKR1C3/PARK7/AKR1C2	4
P	O:	ular	/	2	0	1	0		
	19	resp	18	/	1	0	8		
	01	ons	4	1	2	7	7		
	65	e to		8	5	0	9		
	5	keto		8	8	9	6		
		ne		6	5	0	8		
				2	3	5	1		
					5	6	9		
B	G	neg	7	2	0.	0.	0.	HSP90AB1/PARK7/LAPTM4B/ANXA2/CH	7
P	O:	ativ	/	5	0	1	0	MP4A/HNRNPA0/PKP3	
	00	e	18	5	1	0	8		
	31	reg	4	/	2	7	8		
	33	ulat		1	7	8	6		
	0	ion		8	4	7	1		
		of		8	4	5	2		
		cell		6	6	0	6		
		ular		2	5	7	1		
		cata							
		boli							
		c							
		pro							
		cess							
B	G	bile	3	5	0.	0.	0.	HSD17B10/AKR1C1/CES1	3
P	O:	acid	/	0	0	1	0		
	00	met	18	/	1	0	8		

		08	abol	4	1	2	7	8		
		20	ic		8	7	8	6		
		6	pro		8	9	7	1		
			cess		6	3	5	2		
					2	5	0	6		
							7	1		
B	G	inte	3	5	0.	0.	0.	SOD1/KRT16/CSNK1A1		3
P	O:	rme	/	0	0	1	0			
		00	diat	18	/	1	0	8		
		45	e	4	1	2	7	8		
		10	fila		8	7	8	6		
		4	men		8	9	7	1		
			t		6	3	5	2		
			cyto		2	5	0	6		
			skel				7	1		
			eton							
			org							
			aniz							
			atio							
			n							
B	G	pyri	2	1	0.	0.	0.	NME1/NME4		2
P	O:	mid	/	8	0	1	0			
		00	ine	18	/	1	0	8		
		09	ribo	4	1	3	8	9		
		20	nucl		8	0	5	1		
		8	eosi		8	6	5	6		
			de		6	8	3	9		
			trip		2	3	0	5		

		hos		7	4	2			
		pha							
		te							
		met							
		abol							
		ic							
		pro							
		cess							
B	G	posi	2	1	0.	0.	0.	GSTP1/SOD1	2
P	O:	tive	/	8	0	1	0		
	00	reg	18	/	1	0	8		
	32	ulat	4	1	3	8	9		
	93	ion		8	0	5	1		
	0	of		8	6	5	6		
		sup		6	8	3	9		
		erox		2	3	0	5		
		ide			7	4	2		
		anio							
		n							
		gen							
		erat							
		ion							
B	G	kera	2	1	0.	0.	0.	KRT16/HBEGF	2
P	O:	tino	/	8	0	1	0		
	00	cyte	18	/	1	0	8		
	51	mig	4	1	3	8	9		
	54	rati		8	0	5	1		
	6	on		8	6	5	6		

				6	8	3	9		
				2	3	0	5		
					7	4	2		
B	G	cell	2	1	0.	0.	0.	GSTO1/HNRNPA1	2
P	O:	ular	/	8	0	1	0		
	00	resp	18	/	1	0	8		
	71	ons	4	1	3	8	9		
	24	e to		8	0	5	1		
	3	arse		8	6	5	6		
		nic-		6	8	3	9		
		cont		2	3	0	5		
		aini			7	4	2		
		ng							
		sub							
		stan							
		ce							
B	G	stre	2	1	0.	0.	0.	PARK7/MT2A	2
P	O:	ss	/	8	0	1	0		
	00	resp	18	/	1	0	8		
	97	ons	4	1	3	8	9		
	50	e to		8	0	5	1		
	1	met		8	6	5	6		
		al		6	8	3	9		
		ion		2	3	0	5		
					7	4	2		
B	G	neg	8	3	0.	0.	0.	GSTO1/PARK7/CAV1/TXN/OAZ1/PSMD9	8
P	O:	ativ	/	1	0	1	0	/FABP5/PIM3	
	00	e	18	9	1	0	9		

		43	reg	4	/	3	9	0		
		27	ulat			1	2	6	0	
		1	ion			8	3	2	4	
			of			8	6	1	7	
			ion			6	2	5	2	
			tran			2	8	5	3	
			spor							
			t							
B	G		inte	3	5	0.	0.	0.	SOD1/KRT16/CSNK1A1	3
P	O:		rme	/	1	0	1	0		
		00	diat	18	/	1	1	9		
		45	e	4	1	3	1	1		
		10	fila		8	4	0	2		
		3	men		8	9	8	4		
			t-		6	7	2	7		
			base		2	3	5	3		
			d			7	6	6		
			pro							
			cess							
B	G		G2/	7	2	0.	0.	0.	CDK4/HSP90AA1/PSMA4/PSMA1/SKP1/PS	7
P	O:		M	/	5	0	1	0	MD9/PSME1	
		00	tran	18	8	1	1	9		
		00	sitio	4	/	3	1	1		
		08	n of		1	5	0	2		
		6	mit		8	1	8	4		
			otic		8	6	2	7		
			cell		6	7	5	3		
			cycl		2		6	6		

		e								
B	G	chol	4	9	0.	0.	0.	CAV1/AKR1C1/IL18/CES1		4
P	O:	este	/	4	0	1	0			
	00	rol	18	/	1	1	9			
	42	ho	4	1	3	1	1			
	63	meo		8	5	0	2			
	2	stasi		8	3	8	4			
		s		6	2	2	7			
				2	0	5	3			
					9	6	6			
B	G	ster	4	9	0.	0.	0.	CAV1/AKR1C1/IL18/CES1		4
P	O:	ol	/	5	0	1	0			
	00	ho	18	/	1	1	9			
	55	meo	4	1	4	4	4			
	09	stasi		8	0	7	2			
	2	s		8	2	6	7			
				6	1	6	3			
				2	9	4	4			
					9	8	7			
B	G	reg	10	4	0.	0.	0.	PRELID1/PARK7/CAV1/SFN/ANXA2/PSM	10	
P	O:	ulat	/	5	0	1	0	E1/SERPINB1/SERPINB5/ASPH/S100A9		
	00	ion	18	5	1	1	9			
	52	of	4	/	4	4	4			
	54	pep		1	0	7	2			
	7	tida		8	6	8	9			
		se		8	5	7	0			
		acti		6	7	6	8			
		vity		2	1	9	9			

B	G	spli	3	5	0.	0.	0.	SNRPB/SNRPE/PRPF31	3
P	O:	ceos	/	2	0	1	0		
	00	oma	18	/	1	1	9		
	00	l	4	1	4	5	5		
	38	snR		8	2	7	0		
	7	NP		8	2	3	6		
		asse		6	2	2	6		
		mbl		2	9	2	7		
		y			2	4	8		
B	G	pyri	2	1	0.	0.	0.	NME1/NME4	2
P	O:	mid	/	9	0	1	0		
	00	ine	18	/	1	1	9		
	09	nucl	4	1	4	7	6		
	14	eosi		8	5	0	1		
	8	de		8	1	6	6		
		trip		6	3	9	4		
		hos		2	0		8		
		pha			3		4		
		te							
		bios							
		ynt							
		heti							
		c							
		pro							
		cess							
B	G	reg	2	1	0.	0.	0.	CNPY2/ANXA2	2
P	O:	ulat	/	9	0	1	0		
	00	ion	18	/	1	1	9		

		10	of	4	1	4	7	6		
		98	low		8	5	0	1		
		8	-		8	1	6	6		
			den		6	3	9	4		
			sity		2	0		8		
			lipo			3		4		
			prot							
			ein							
			part							
			icle							
			clea							
			ranc							
			e							
B	G	neg	2	1	0.	0.	0.	EIF3E/RPL13A		2
P	O:	ativ	/	9	0	1	0			
		00	e	18	/	1	1	9		
		45	reg	4	1	4	7	6		
		94	ulat		8	5	0	1		
		7	ion		8	1	6	6		
			of		6	3	9	4		
			tran		2	0		8		
			slati			3		4		
			onal							
			initi							
			atio							
			n							
B	G	cell-	5	1	0.	0.	0.	CAV1/MTDH/FSCN1/PKP3/RHOC		5
P	O:	cell	/	4	0	1	0			

		00	junc	18	7	1	1	9		
		07	tion	4	/	4	7	6		
		04	asse		1	7	9	8		
		3	mbl		8	0	1	6		
			y		8	2	6	0		
					6	5	1	7		
					2	5	7	5		
B	G	posi	5	1	0.	0.	0.	PSMA4/CAV1/PSMA1/PSMD9/PSME1	5	
P	O:	tive	/	4	0	1	0			
		00	reg	18	7	1	1	9		
		90	ulat	4	/	4	7	6		
		26	ion		1	7	9	8		
		3	of		8	0	1	6		
			can		8	2	6	0		
			onic		6	5	1	7		
			al		2	5	7	5		
			Wnt							
			sign							
			alin							
			g							
			pat							
			hwa							
			y							
B	G	reg	6	2	0.	0.	0.	CDK4/AKR1C3/SOD1/FABP5/CES1/CAPN	6	
P	O:	ulat	/	0	0	1	0	2		
		00	ion	18	3	1	1	9		
		46	of	4	/	4	8	7		
		89	lipi		1	7	2	1		

	0	d	8	9	8	6		
		bios	8	1	9	7		
		ynt	6	4	0	0		
		heti	2	3	5	4		
		c						
		pro						
		cess						
B	G	resp	8	3	0.	0.	0.	CDK4/GSTP1/MTDH/MGST1/HNRNPA0/I 8
P	O:	ons	/	2	0	1	0	L18/CAPN2/S100A9
	00	e to	18	6	1	1	9	
	32	lipo	4	/	4	8	7	
	49	pol		1	9	8	6	
	6	ysac		8	0	6	4	
		char		8	6	9	3	
		ide		6	6	6	9	
				2	2	4	6	
B	G	posi	4	9	0.	0.	0.	CAV1/IL18/FABP5/DECR1 4
P	O:	tive	/	7	0	1	0	
	01	reg	18	/	1	1	9	
	20	ulat	4	1	5	9	8	
	16	ion		8	0	5	2	
	2	of		8	3	5	0	
		cold		6	5	3	5	
		-		2	2	6	7	
		ind			2		9	
		uce						
		d						
		ther						

		mo								
		gen								
		esis								
B	G	carb	8	3	0.	0.	0.	NDUFAB1/HSD17B10/AKR1C3/PARK7/GS	8	
P	O:	oxyl	/	2	0	1	0	TP1/FABP5/UGDH/CES1		
	00	ic	18	7	1	1	9			
	46	acid	4	/	5	9	8			
	39	bios		1	1	8	4			
	4	ynt		8	5	6	6			
		heti		8	7	8	4			
		c		6	2	1	1			
		pro		2		7	9			
		cess								
B	G	nucl	7	2	0.	0.	0.	NME1/ENO1/STOML2/ADK/APRT/NME4	7	
P	O:	eoti	/	6	0	1	0	/ALDOA		
	00	de	18	4	1	1	9			
	09	bios	4	/	5	9	8			
	16	ynt		1	1	8	4			
	5	heti		8	6	6	6			
		c		8	0	8	4			
		pro		6	6	1	1			
		cess		2	8	7	9			
B	G	posi	7	2	0.	0.	0.	PARK7/CAV1/MTDH/UBE2N/IL18/FOSL1	7	
P	O:	tive	/	6	0	1	1	/S100A9		
	00	reg	18	6	1	2	0			
	51	ulat	4	/	5	3	1			
	09	ion		1	7	0	0			
	1	of		8	3	6	8			

		DN	8	9	0	6		
		A-	6	0	6	6		
		bin	2	4	8	4		
		din						
		g						
		tran						
		scri						
		ptio						
		n						
		fact						
		or						
		acti						
		vity						
B	G	resp	6	2	0.	0.	0.	PSMA4/PSMA1/UBE2N/SKP1/PSMD9/PSM 6
P	O:	ons	/	0	0	1	1	E1
	00	e to	18	6	1	2	0	
	70	inte	4	/	5	3	1	
	55	rleu		1	7	0	0	
	5	kin-		8	9	6	8	
		1		8	2	0	6	
				6	6	6	6	
				2	9	8	4	
B	G	reg	2	2	0.	0.	0.	GSTP1/SOD1 2
P	O:	ulat	/	0	0	1	1	
	00	ion	18	/	1	2	0	
	32	of	4	1	6	3	1	
	92	sup		8	0	0	0	
	8	erox		8	2	6	8	

		ide	6	3	0	6			
		anio	2	2	6	6			
		n		2	8	4			
		gen							
		erat							
		ion							
B	G	mus	2	2	0.	0.	0.	SOD1/ALDOA	2
P	O:	cle	/	0	0	1	1		
	00	cell	18	/	1	2	0		
	46	cell	4	1	6	3	1		
	71	ular		8	0	0	0		
	6	ho		8	2	6	8		
		meo		6	3	0	6		
		stasi		2	2	6	6		
		s			2	8	4		
B	G	neg	2	2	0.	0.	0.	PARK7/TXN	2
P	O:	ativ	/	0	0	1	1		
	00	e	18	/	1	2	0		
	46	reg	4	1	6	3	1		
	82	ulat		8	0	0	0		
	3	ion		8	2	6	8		
		of		6	3	0	6		
		nucl		2	2	6	6		
		eoc			2	8	4		
		yto							
		plas							
		mic							
		tran							

		spor							
		t							
B	G	por	2	2	0.	0.	0.	GSDMD/RTN4	2
P	O:	e	/	0	0	1	1		
	00	com	18	/	1	2	0		
	46	plex	4	1	6	3	1		
	93	asse		8	0	0	0		
	1	mbl		8	2	6	8		
		y		6	3	0	6		
				2	2	6	6		
					2	8	4		
B	G	cell	2	2	0.	0.	0.	AKR1C3/AKR1C2	2
P	O:	ular	/	0	0	1	1		
	00	resp	18	/	1	2	0		
	71	ons	4	1	6	3	1		
	37	e to		8	0	0	0		
	9	pros		8	2	6	8		
		tagl		6	3	0	6		
		and		2	2	6	6		
		in			2	8	4		
		stim							
		ulus							
B	G	neg	2	2	0.	0.	0.	PARK7/TXN	2
P	O:	ativ	/	0	0	1	1		
	19	e	18	/	1	2	0		
	03	reg	4	1	6	3	1		
	20	ulat		8	0	0	0		
	6	ion		8	2	6	8		

		of	6	3	0	6			
		hyd	2	2	6	6			
		rog		2	8	4			
		en							
		per							
		oxid							
		e-							
		ind							
		uce							
		d							
		cell							
		deat							
		h							
B	G	posi	2	2	0.	0.	0.	HMGA1/EEF1E1	2
P	O:	tive	/	0	0	1	1		
	20	reg	18	/	1	2	0		
	00	ulat	4	1	6	3	1		
	77	ion		8	0	0	0		
	4	of		8	2	6	8		
		cell		6	3	0	6		
		ular		2	2	6	6		
		sene			2	8	4		
		scen							
		ce							
B	G	nucl	7	2	0.	0.	0.	NME1/ENO1/STOML2/ADK/APRT/NME4	7
P	O:	eosi	/	6	0	1	1	/ALDOA	
	19	de	18	7	1	2	0		
	01	pho	4	/	6	3	1		

		29	sph	1	0	0	0		
		3	ate	8	3	6	8		
			bios	8	4	0	6		
			ynt	6	0	6	6		
			heti	2	3	8	4		
			c						
			pro						
			cess						
B	G	anti	4	9	0.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1	4
P	O:	gen	/	9	0	1	1		
	00	pro	18	/	1	2	0		
	02	cess	4	1	6	3	1		
	47	ing		8	0	0	0		
	4	and		8	9	6	8		
		pres		6	3	0	6		
		enta		2	5	6	6		
		tion			7	8	4		
		of							
		pep							
		tide							
		anti							
		gen							
		via							
		MH							
		C							
		clas							
		s I							
B	G	reg	4	9	0.	0.	0.	HSP90AA1/HSP90AB1/PARK7/CAV1	4

P	O:	ulat	/	9	0	1	1		
	19	ion	18	/	1	2	0		
	03	of	4	1	6	3	1		
	42	reac		8	0	0	0		
	6	tive		8	9	6	8		
		oxy		6	3	0	6		
		gen		2	5	6	6		
		spec			7	8	4		
		ies							
		bios							
		ynt							
		heti							
		c							
		pro							
		cess							
B	G	mit	3	5	0.	0.	0.	SLC25A5/VDAC2/SFN	3
P	O:	och	/	5	0	1	1		
	00	ond	18	/	1	2	0		
	97	rial	4	1	6	5	3		
	34	oute		8	5	7	2		
	5	r		8	3	1	6		
		me		6	0	2	4		
		mbr		2	4	2	6		
		ane			1		9		
		per							
		mea							
		biliz							
		atio							

n									
B	G	posi	3	5	0.	0.	0.	HSP90AA1/HSP90AB1/PARK7	3
P	O:	tive	/	5	0	1	1		
	19	reg	18	/	1	2	0		
	03	ulat	4	1	6	5	3		
	42	ion		8	5	7	2		
	8	of		8	3	1	6		
		reac		6	0	2	4		
		tive		2	4	2	6		
		oxy			1		9		
		gen							
		spec							
		ies							
		bios							
		ynt							
		heti							
		c							
		pro							
		cess							
B	G	cell-	6	2	0.	0.	0.	CAV1/MTDH/FSCN1/RDX/PKP3/RHOC	6
P	O:	cell	/	0	0	1	1		
	00	junc	18	9	1	2	0		
	45	tion	4	/	6	7	4		
	21	org		1	8	7	9		
	6	aniz		8	3	1	1		
		atio		8	9	8	2		
		n		6	9	4	7		
				2	9	8	2		

B	G	reg	8	3	0.	0.	0.	PSMA4/PUF60/PSMA1/HNRNPA1/PSMD9	8
P	O:	ulat	/	3	0	1	1	/PSME1/HNRNPA0/PKP3	
	19	ion	18	4	1	2	0		
	03	of	4	/	6	8	5		
	31	mR		1	9	5	5		
	1	NA		8	9	1	6		
		met		8	7	4	6		
		abol		6	7	0	2		
		ic		2	6	6	5		
		pro							
		cess							
B	G	reg	4	1	0.	0.	0.	AP2M1/AP2S1/CNPY2/ANXA2	4
P	O:	ulat	/	0	0	1	1		
	00	ion	18	1	1	2	0		
	97	of	4	/	7	8	5		
	00	plas		1	1	5	5		
	6	ma		8	9	1	6		
		lipo		8	7	4	6		
		prot		6	6	0	2		
		ein		2		6	5		
		part							
		icle							
		leve							
		ls							
B	G	gluc	6	2	0.	0.	0.	ENO1/MDH2/G6PD/ALDOA/FABP5/PHL	6
P	O:	ose	/	1	0	1	1	DA2	
	00	met	18	0	1	2	0		
	06	abol	4	/	7	8	5		

		00	ic		1	1	5	5		
		6	pro		8	9	1	6		
			cess		8	9	4	6		
					6	4	0	2		
					2	8	6	5		
B	G	reg	6	2	0.	0.	0.		PSMA4/PSMA1/PSMD9/PSME1/HNRNPA0	6
P	O:	ulat	/	1	0	1	1		/PKP3	
		00	ion	18	0	1	2	0		
		61	of	4	/	7	8	5		
		01	mR		1	1	5	5		
		3	NA		8	9	1	6		
			cata		8	9	4	6		
			boli		6	4	0	2		
			c		2	8	6	5		
			pro							
			cess							
B	G	org	8	3	0.	0.	0.		NDUFAB1/HSD17B10/AKR1C3/PARK7/GS	8
P	O:	anic	/	3	0	1	1		TP1/FABP5/UGDH/CES1	
		00	acid	18	5	1	2	0		
		16	bios	4	/	7	8	5		
		05	ynt		1	2	5	5		
		3	heti		8	7	1	6		
			c		8	3	4	6		
			pro		6	2	0	2		
			cess		2	9	6	5		
B	G	AT	3	5	0.	0.	0.		ENO1/STOML2/ALDOA	3
P	O:	P	/	6	0	1	1			
		00	bios	18	/	1	2	0		

	06	ynt	4	1	7	8	5		
	75	heti		8	3	5	5		
	4	c		8	4	1	6		
		pro		6	3	4	6		
		cess		2	4	0	2		
						6	5		
B	G	DN	3	5	0.	0.	0.	PRMT1/SFN/GADD45A	3
P	O:	A	/	6	0	1	1		
	00	da	18	/	1	2	0		
	06	mag	4	1	7	8	5		
	97	e		8	3	5	5		
	7	resp		8	4	1	6		
		ons		6	3	4	6		
		e,		2	4	0	2		
		sign				6	5		
		al							
		tran							
		sdu							
		ctio							
		n by							
		p53							
		clas							
		s							
		me							
		diat							
		or							
		resu							
		ltin							

		g in								
		cell								
		cycl								
		e								
		arre								
		st								
B	G	posi	3	5	0.	0.	0.	NME1/PARK7/TXN		3
P	O:	tive	/	6	0	1	1			
	00	reg	18	/	1	2	0			
	43	ulat	4	1	7	8	5			
	38	ion		8	3	5	5			
	8	of		8	4	1	6			
		DN		6	3	4	6			
		A		2	4	0	2			
		bin				6	5			
		din								
		g								
B	G	mit	2	2	0.	0.	0.	COX5A/COX8A		2
P	O:	och	/	1	0	1	1			
	00	ond	18	/	1	2	0			
	06	rial	4	1	7	8	5			
	12	elec		8	5	5	5			
	3	tron		8	9	1	6			
		tran		6	7	4	6			
		spor		2	5	0	2			
		t,			4	6	5			
		cyto								
		chr								

		pro								
		cess								
B	G	posi	2	2	0.	0.	0.	CAV1/CES1		2
P	O:	tive	/	1	0	1	1			
	00	reg	18	/	1	2	0			
	10	ulat	4	1	7	8	5			
	87	ion		8	5	5	5			
	5	of		8	9	1	6			
		chol		6	7	4	6			
		este		2	5	0	2			
		rol			4	6	5			
		effl								
		ux								
B	G	aero	2	2	0.	0.	0.	COX5A/COX8A		2
P	O:	bic	/	1	0	1	1			
	00	elec	18	/	1	2	0			
	19	tron	4	1	7	8	5			
	64	tran		8	5	5	5			
	6	spor		8	9	1	6			
		t		6	7	4	6			
		chai		2	5	0	2			
		n			4	6	5			
B	G	beta	2	2	0.	0.	0.	CAV1/CSNK1A1		2
P	O:	-	/	1	0	1	1			
	19	cate	18	/	1	2	0			
	04	nin	4	1	7	8	5			
	88	dest		8	5	5	5			
	6	ruct		8	9	1	6			

		ion	6	7	4	6		
		com	2	5	0	2		
		plex		4	6	5		
		disa						
		sse						
		mbl						
		y						
B	G	acti	5	1	0.	0.	0.	FSCN1/RHOD/RDX/HSP90B1/RHOC
P	O:	n	/	5	0	1	1	5
	00	fila	18	4	1	2	0	
	51	men	4	/	7	8	5	
	01	t		1	6	5	5	
	7	bun		8	3	1	6	
		dle		8	5	4	6	
		asse		6	5	0	2	
		mbl		2	7	6	5	
		y						
B	G	mit	7	2	0.	0.	0.	SLC25A5/HSP90AA1/STOML2/VDAC2/SFN
P	O:	och	/	7	0	1	1	7
	00	ond	18	4	1	3	0	/SLC25A6/TOMM7
	06	rial	4	/	8	2	8	
	83	tran		1	2	3	7	
	9	spor		8	0	5	1	
		t		8	9	3	9	
				6	8	3	9	
				2	5	6	9	
B	G	reg	4	1	0.	0.	0.	HSP90AB1/PARK7/TXN/SFN
P	O:	ulat	/	0	0	1	1	4

	00	ion	18	3	1	3	0		
	46	of	4	/	8	3	9		
	82	nucl		1	3	0	2		
	2	eoc		8	4	1	5		
		yto		8	7	0	9		
		plas		6	8	1	4		
		mic		2	7	2	8		
		tran							
		spor							
		t							
B	G	G1/	7	2	0.	0.	0.	PRMT1/CDK4/SFN/PSME1/GMNN/RDX/	7
P	O:	S	/	7	0	1	1	GADD45A	
	00	tran	18	5	1	3	0		
	00	sitio	4	/	8	3	9		
	08	n of		1	5	7	8		
	2	mit		8	3	0	3		
		otic		8	6	6	1		
		cell		6	8	1	2		
		cycl		2	2	4	2		
		e							
B	G	nucl	5	1	0.	0.	0.	NME1/ENO1/LDHA/NME4/ALDOA	5
P	O:	eosi	/	5	0	1	1		
	00	de	18	6	1	3	0		
	09	dip	4	/	8	3	9		
	13	hos		1	5	7	8		
	2	pha		8	3	0	3		
		te		8	9	6	1		
		met		6	6	1	2		

		abol	2	9	4	2		
		ic						
		pro						
		cess						
B	G	nucl	8	3	0.	0.	0.	SNRPB/SNRPE/HSP90AB1/PARK7/HNRNP 8
P	O:	eoc	/	4	0	1	1	A1/TXN/SFN/HTATIP2
	00	yto	18	0	1	3	1	
	06	plas	4	/	8	4	0	
	91	mic		1	6	5	4	
	3	tran		8	9	1	9	
		spor		8	9	0	2	
		t		6	4	6	0	
				2	4	5	7	
B	G	cell	7	2	0.	0.	0.	CDK4/HSP90AA1/PSMA4/PSMA1/SKP1/PS 7
P	O:	cycl	/	7	0	1	1	MD9/PSME1
	00	e	18	6	1	3	1	
	44	G2/	4	/	8	4	0	
	83	M		1	8	5	5	
	9	pha		8	6	4	2	
		se		8	7	5	1	
		tran		6	9	8		
		sitio		2	1	7		
		n						
B	G	resp	10	4	0.	0.	0.	AKR1C3/LDHA/GSTP1/HNRNPA1/G6PD/ 10
P	O:	ons	/	7	0	1	1	TXN2/NQO1/SOD1/ALDH3A1/FOSL1
	00	e to	18	7	1	3	1	
	09	extr	4	/	8	4	0	
	99	acel		1	9	5	5	

	1	lula		8	0	4	2		
		r		8	5	5	1		
		stim		6	8	8			
		ulus		2	4	7			
B	G	nucl	4	1	0.	0.	0.	NME1/ADK/APRT/NME4	4
P	O:	eosi	/	0	0	1	1		
	00	de	18	4	1	3	1		
	09	met	4	/	8	4	0		
	11	abol		1	9	5	5		
	6	ic		8	4	4	2		
		pro		8	0	5	1		
		cess		6	5	8			
				2		7			
B	G	prot	5	1	0.	0.	0.	PARK7/COX5A/STOML2/COX8A/ATP6V0B	5
P	O:	on	/	5	0	1	1		
	19	tran	18	7	1	3	1		
	02	sme	4	/	9	4	0		
	60	mbr		1	0	5	5		
	0	ane		8	0	4	2		
		tran		8	3	5	1		
		spor		6		8			
		t		2		7			
B	G	posi	3	5	0.	0.	0.	HMGA1/POLR2E/POLR2F	3
P	O:	tive	/	8	0	1	1		
	00	reg	18	/	1	3	1		
	45	ulat	4	1	9	4	0		
	81	ion		8	0	5	5		
	5	of		8	3	4	2		

		gen	6	5	5	1			
		e	2	4	8				
		exp		1	7				
		ress							
		ion,							
		epig							
		enet							
		ic							
B	G	posi	10	4	0.	0.	0.	PRELID1/HSP90AB1/CAV1/OAZ1/SFN/PS	10
P	O:	tive	/	7	0	1	1	MD9/ANXA2/TOMM7/VPS28/CES1	
	19	reg	18	8	1	3	1		
	03	ulat	4	/	9	4	0		
	79	ion		1	1	5	5		
	3	of		8	5	4	2		
		anio		8	1	5	1		
		n		6	6	8			
		tran		2	8	7			
		spor							
		t							
B	G	pyri	2	2	0.	0.	0.	NME1/NME4	2
P	O:	mid	/	2	0	1	1		
	00	ine	18	/	1	3	1		
	09	ribo	4	1	9	4	0		
	22	nucl		8	2	5	5		
	0	eoti		8	3	4	2		
		de		6	4	5	1		
		bios		2	6	8			
		ynt			1	7			

		heti								
		c								
		pro								
		cess								
B	G	prot	2	2	0.	0.	0.	PSMA4/PSMA1		2
P	O:	easo	/	2	0	1	1			
	00	mal	18	/	1	3	1			
	10	ubi	4	1	9	4	0			
	49	quit		8	2	5	5			
	9	in-		8	3	4	2			
		inde		6	4	5	1			
		pen		2	6	8				
		den			1	7				
		t								
		prot								
		ein								
		cata								
		boli								
		c								
		pro								
		cess								
B	G	reg	2	2	0.	0.	0.	PRELID1/CISD1		2
P	O:	ulat	/	2	0	1	1			
	00	ion	18	/	1	3	1			
	43	of	4	1	9	4	0			
	45	cell		8	2	5	5			
	7	ular		8	3	4	2			
		resp		6	4	5	1			

		irati	2	6	8				
		on		1	7				
B	G	resp	2	2	0.	0.	0.	CDK4/CAV1	2
P	O:	ons	/	2	0	1	1		
	00	e to	18	/	1	3	1		
	55	hyp	4	1	9	4	0		
	09	erox		8	2	5	5		
	3	ia		8	3	4	2		
				6	4	5	1		
				2	6	8			
				1	7				
B	G	neg	2	2	0.	0.	0.	PARK7/TXN	2
P	O:	ativ	/	2	0	1	1		
	19	e	18	/	1	3	1		
	01	reg	4	1	9	4	0		
	03	ulat		8	2	5	5		
	2	ion		8	3	4	2		
		of		6	4	5	1		
		resp		2	6	8			
		ons			1	7			
		e to							
		reac							
		tive							
		oxy							
		gen							
		spec							
		ies							
B	G	acti	5	1	0.	0.	0.	FSCN1/RHOD/RDX/HSP90B1/RHOC	5

P	O:	n	/	5	0	1	1		
	00	fila	18	8	1	3	1		
	61	men	4	/	9	5	1		
	57	t		1	4	6	4		
	2	bun		8	7	9	6		
		dle		8	3	5	5		
		org		6	8	9	6		
		aniz		2	8	1	8		
		atio							
		n							
B	G	fatt	4	1	0.	0.	0.	HSD17B10/ECHS1/ECH1/DECR1	4
P	O:	y	/	0	0	1	1		
	00	acid	18	5	1	3	1		
	19	oxid	4	/	9	5	1		
	39	atio		1	5	6	4		
	5	n		8	4	9	6		
				8	4	5	5		
				6	8	9	6		
				2	8	1	8		
B	G	reg	4	1	0.	0.	0.	CDK4/HSP90AB1/SFN/GADD45A	4
P	O:	ulat	/	0	0	1	1		
	19	ion	18	5	1	3	1		
	04	of	4	/	9	5	1		
	02	cycl		1	5	6	4		
	9	in-		8	4	9	6		
		dep		8	4	5	5		
		end		6	8	9	6		
		ent		2	8	1	8		

		surf								
		ace								
		rece								
		ptor								
		sign								
		alin								
		g								
		pat								
		hwa								
		y								
B	G	im	10	4	0.	0.	0.	HSP90AA1/PSMA4/HSP90AB1/STOML2/PS	10	
P	O:	mu	/	8	0	1	1	MA1/UBE2N/SKP1/PSMD9/PSME1/ARPC1		
		00	ne	18	1	1	3	1	B	
		02	resp	4	/	9	6	2		
		75	ons		1	9	8	3		
		7	e-		8	0	2	9		
			acti		8	3	3	1		
			vati		6	3	2	6		
			ng		2	5	1	9		
		sign								
		al								
		tran								
		sdu								
		ctio								
		n								
B	G	reg	3	5	0.	0.	0.	HSP90AA1/HSP90AB1/CAV1		3
P	O:	ulat	/	9	0	1	1			
		00	ion	18	/	1	3	1		

		45	of	4	1	9	6	2		
		42	nitri		8	9	8	3		
		8	c		8	1	2	9		
			oxid		6	4	3	1		
			e		2	4	2	6		
			bios			9	1	9		
			ynt							
			heti							
			c							
			pro							
			cess							
B	G	posi	5	1	0.	0.	0.	CAV1/MTDH/UBE2N/IL18/S100A9	5	
P	O:	tive	/	5	0	1	1			
	00	reg	18	9	1	3	1			
	51	ulat	4	/	9	6	2			
	09	ion		1	9	8	3			
	2	of		8	5	2	9			
		NF-		8	2	3	1			
		kap		6	3	2	6			
		paB		2	6	1	9			
		tran								
		scri								
		ptio								
		n								
		fact								
		or								
		acti								
		vity								

B	G	fatt	4	1	0.	0.	0.	HSD17B10/ECHS1/ECH1/DECR1	4
P	O:	y	/	0	0	1	1		
	00	acid	18	6	2	3	1		
	09	cata	4	/	0	7	3		
	06	boli		1	1	5	0		
	2	c		8	6	7	1		
		pro		8	1	8	1		
		cess		6	0	3	9		
				2	6		5		
B	G	DN	4	1	0.	0.	0.	PRMT1/EEF1E1/SFN/GADD45A	4
P	O:	A	/	0	0	1	1		
	00	da	18	6	2	3	1		
	30	mag	4	/	0	7	3		
	33	e		1	1	5	0		
	0	resp		8	6	7	1		
		ons		8	1	8	1		
		e,		6	0	3	9		
		sign		2	6		5		
		al							
		tran							
		sdu							
		ctio							
		n by							
		p53							
		clas							
		s							
		me							
		diat							

		or							
B	G	hor	6	2	0.	0.	0.	HSD17B10/AKR1B10/AKR1C3/AKR1C1/AK	6
P	O:	mo	/	1	0	1	1	R1C2/CES1	
	00	ne	18	8	2	3	1		
	42	met	4	/	0	7	3		
	44	abol		1	2	9	3		
	5	ic		8	6	6	3		
		pro		8	7	6	0		
		cess		6	3	2	6		
				2	4	2			
B	G	prot	10	4	0.	0.	0.	PSMA4/HSP90AB1/PARK7/CAV1/PSMA1/	10
P	O:	easo	/	8	0	1	1	SKP1/PSMD9/PSME1/CSNK1A1/HSP90B1	
	00	mal	18	3	2	3	1		
	10	prot	4	/	0	8	3		
	49	ein		1	4	6	8		
	8	cata		8	1	4	8		
		boli		8	6	2	6		
		c		6	3	4	0		
		pro		2	5	3	7		
		cess							
B	G	resp	8	3	0.	0.	0.	CDK4/GSTP1/MTDH/MGST1/HNRNPA0/I	8
P	O:	ons	/	4	0	1	1	L18/CAPN2/S100A9	
	00	e to	18	6	2	3	1		
	02	mol	4	/	0	9	4		
	23	ecul		1	5	0	1		
	7	e of		8	1	0	8		
		bact		8	9	8	6		
		erial		6	9	0	3		

		orig	2	9	1	7			
		in							
B	G	posi	6	2	0.	0.	0.	HSP90AB1/OAZ1/SFN/ANXA2/RDX/TOM	6
P	O:	tive	/	1	0	1	1	M7	
	00	reg	18	9	2	3	1		
	32	ulat	4	/	0	9	4		
	38	ion		1	6	4	5		
	8	of		8	7	3	3		
		intr		8	5	7	8		
		acel		6	3	2	9		
		lula		2		1	3		
		r							
		tran							
		spor							
		t							
B	G	posi	3	6	0.	0.	0.	SLC25A5/VDAC2/SFN	3
P	O:	tive	/	0	0	1	1		
	19	reg	18	/	2	3	1		
	02	ulat	4	1	0	9	4		
	11	ion		8	8	4	5		
	0	of		8	1	3	3		
		mit		6	5	7	8		
		och		2	6	2	9		
		ond			6	1	3		
		rial							
		me							
		mbr							
		ane							

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B	G	puri	2	2	0.	0.	0.	ADK/APRT
P	O:	ne	/	3	0	1	1	
	00	nucl	18	/	2	3	1	
	09	eosi	4	1	0	9	4	
	12	de		8	9	4	5	
	7	mo		8	3	3	3	
		nop		6	3	7	8	
		hos		2	0	2	9	
		pha			7	1	3	
		te						
		bios						
		ynt						
		heti						
		c						
		pro						
		cess						

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B	G	puri	2	2	0.	0.	0.	SLC25A5/SLC25A6	2
P	O:	ne	/	3	0	1	1		
	00	ribo	18	/	2	3	1		
	15	nucl	4	1	0	9	4		
	86	eoti		8	9	4	5		
	8	de		8	3	3	3		
		tran		6	3	7	8		
		spor		2	0	2	9		
		t			7	1	3		
B	G	ade	2	2	0.	0.	0.	SLC25A5/SLC25A6	2
P	O:	nine	/	3	0	1	1		
	00	nucl	18	/	2	3	1		
	51	eoti	4	1	0	9	4		
	50	de		8	9	4	5		
	3	tran		8	3	3	3		
		spor		6	3	7	8		
		t		2	0	2	9		
					7	1	3		
B	G	posi	2	2	0.	0.	0.	HMGA1/EEF1E1	2
P	O:	tive	/	3	0	1	1		
	00	reg	18	/	2	3	1		
	90	ulat	4	1	0	9	4		
	34	ion		8	9	4	5		
	3	of		8	3	3	3		
		cell		6	3	7	8		
		agin		2	0	2	9		
		g			7	1	3		
B	G	mit	2	2	0.	0.	0.	CHMP2A/CHMP4A	2

P	O:	otic	/	3	0	1	1	
	19	cyto	18	/	2	3	1	
	02	kine	4	1	0	9	4	
	41	tic		8	9	4	5	
	0	pro		8	3	3	3	
		cess		6	3	7	8	
				2	0	2	9	
					7	1	3	
B	G	prot	7	2	0.	0.	0.	PSMA4/PARK7/PSMA1/NEDD8/PSMD9/P
P	O:	ein	/	8	0	1	1	SME1/EIF3F
	00	deu	18	3	2	4	1	
	16	biq	4	/	1	1	6	
	57	uiti		1	3	2	0	
	9	nati		8	0	2	0	
		on		8	2	4	7	
				6	5	5	1	
				2	9	5	2	
B	G	intri	7	2	0.	0.	0.	ENO1/PARK7/CAV1/VDAC2/SFN/SOD1/S
P	O:	nsic	/	8	0	1	1	100A9
	00	apo	18	3	2	4	1	
	97	ptot	4	/	1	1	6	
	19	ic		1	3	2	0	
	3	sign		8	0	2	0	
		alin		8	2	4	7	
		g		6	5	5	1	
		pat		2	9	5	2	
		hwa						
		y						

B	G	lipi	5	1	0.	0.	0.	CAV1/AKR1C1/IL18/RTN4/CES1	5
P	O:	d	/	6	0	1	1		
	00	ho	18	2	2	4	1		
	55	meo	4	/	1	1	6		
	08	stasi		1	4	7	4		
	8	s		8	3	5	4		
				8	3	8	5		
				6	8	2	5		
				2	8	3			
B	G	resp	6	2	0.	0.	0.	NME1/LDHA/GSTP1/TXN2/NQO1/PIM3	6
P	O:	ons	/	2	0	1	1		
	00	e to	18	1	2	4	1		
	09	carb	4	/	1	1	6		
	74	ohy		1	5	9	5		
	3	drat		8	0	1	7		
		e		8	7	1	1		
				6	9	4	3		
				2		6	7		
B	G	resp	3	6	0.	0.	0.	AKR1C3/MT2A/SOD1	3
P	O:	ons	/	1	0	1	1		
	00	e to	18	/	2	4	1		
	46	cad	4	1	1	2	7		
	68	miu		8	7	6	1		
	6	m		8	3	5	8		
		ion		6	8	7	4		
				2	9	5	2		
					3	6	4		
B	G	reg	3	6	0.	0.	0.	HSP90AA1/HSP90AB1/CAV1	3

P	O:	ulat	/	1	0	1	1		
	00	ion	18	/	2	4	1		
	80	of	4	1	1	2	7		
	16	nitri		8	7	6	1		
	4	c		8	3	5	8		
		oxid		6	8	7	4		
		e		2	9	5	2		
		met			3	6	4		
		abol							
		ic							
		pro							
		cess							
B	G	posi	5	1	0.	0.	0.	CDK4/CDC123/EIF3E/EIF3D/RPS9	5
P	O:	tive	/	6	0	1	1		
	00	reg	18	3	2	4	1		
	34	ulat	4	/	1	2	7		
	25	ion		1	9	6	1		
	0	of		8	4	5	8		
		cell		8	3	7	4		
		ular		6	2	5	2		
		ami		2	2	6	4		
		de							
		met							
		abol							
		ic							
		pro							
		cess							
B	G	imp	5	1	0.	0.	0.	SNRPB/SNRPE/HSP90AB1/HNRNPA1/HT	5

P	O:	ort	/	6	0	1	1	ATIP2	
	00	into	18	3	2	4	1		
	51	nucl	4	/	1	2	7		
	17	eus		1	9	6	1		
	0			8	4	5	8		
				8	3	7	4		
				6	2	5	2		
				2	2	6	4		
B	G	vesi	4	1	0.	0.	0.	AP2M1/ANXA2/CHMP4A/CD59	4
P	O:	cle	/	0	0	1	1		
	00	bud	18	9	2	4	1		
	06	din	4	/	2	2	7		
	90	g		1	0	6	1		
	0	fro		8	8	5	8		
		m		8	1	7	4		
		me		6		5	2		
		mbr		2		6	4		
		ane							
B	G	chol	4	1	0.	0.	0.	CAV1/AKR1C1/ANXA2/CES1	4
P	O:	este	/	0	0	1	1		
	00	rol	18	9	2	4	1		
	30	tran	4	/	2	2	7		
	30	spor		1	0	6	1		
	1	t		8	8	5	8		
				8	1	7	4		
				6		5	2		
				2		6	4		
B	G	reg	4	1	0.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1	4

P	O:	ulat	/	0	0	1	1		
	00	ion	18	9	2	4	1		
	43	of	4	/	2	2	7		
	61	tran		1	0	6	1		
	8	scri		8	8	5	8		
		ptio		8	1	7	4		
		n		6		5	2		
		fro		2		6	4		
		m							
		RN							
		A							
		pol							
		yme							
		rase							
		II							
		pro							
		mot							
		er							
		in							
		resp							
		ons							
		e to							
		stre							
		ss							
B	G	ncR	4	1	0.	0.	0.	NPM3/POLR2E/POLR2F/GTF3C5	4
P	O:	NA	/	0	0	1	1		
	00	tran	18	9	2	4	1		
	98	scri	4	/	2	2	7		

	78	ptio		1	0	6	1		
	1	n		8	8	5	8		
				8	1	7	4		
				6		5	2		
				2		6	4		
B	G	mit	4	1	0.	0.	0.	SLC25A5/STOML2/SLC25A6/TOMM7	4
P	O:	och	/	0	0	1	1		
	19	ond	18	9	2	4	1		
	90	rial	4	/	2	2	7		
	54	tran		1	0	6	1		
	2	sme		8	8	5	8		
		mbr		8	1	7	4		
		ane		6		5	2		
		tran		2		6	4		
		spor							
		t							
B	G	posi	6	2	0.	0.	0.	HSP90AA1/PSMA4/PSMA1/SKP1/PSMD9/	6
P	O:	tive	/	2	0	1	1	PSME1	
	00	reg	18	3	2	4	1		
	45	ulat	4	/	2	4	8		
	08	ion		1	3	1	4		
	9	of		8	6	4	0		
		inna		8	2	5	6		
		te		6	9	3	3		
		im		2	2		3		
		mu							
		ne							
		resp							

			ons								
			e								
B	G	mus	8	3	0.	0.	0.	GSTO1/ENO1/CAV1/SOD1/ALDOA/ASPH	8		
P	O:	cle	/	5	0	1	1	/HSBP1/TPM4			
		00	cont	18	2	2	4	1			
		06	racti	4	/	2	4	8			
		93	on		1	4	2	4			
		6			8	6	5	9			
					8	3	6	7			
					6	4	7	9			
					2	4	8				
B	G	mit	3	6	0.	0.	0.	PRMT1/SFN/GADD45A		3	
P	O:	otic	/	2	0	1	1				
		00	G1	18	/	2	4	1			
		31	DN	4	1	2	4	8			
		57	A		8	6	2	4			
		1	da		8	8	5	9			
			mag		6	4	6	7			
			e		2	3	7	9			
			chec			1	8				
			kpo								
			int								
			sign								
			alin								
			g								
B	G	mit	3	6	0.	0.	0.	SLC25A5/VDAC2/SFN		3	
P	O:	och	/	2	0	1	1				
		19	ond	18	/	2	4	1			

	02	rial	4	1	2	4	8	
	68	oute		8	6	2	4	
	6	r		8	8	5	9	
		me		6	4	6	7	
		mbr		2	3	7	9	
		ane			1	8		
		per						
		mea						
		biliz						
		atio						
		n						
		inv						
		olve						
		d in						
		pro						
		gra						
		mm						
		ed						
		cell						
		deat						
		h						
B	G	hist	2	2	0.	0.	0.	SNRPB/SNRPE
P	O:	one	/	4	0	1	1	
	00	mR	18	/	2	4	1	
	08	NA	4	1	2	4	8	
	33	met		8	6	2	4	
	4	abol		8	9	5	9	
		ic		6	1	6	7	

		pro	2	5	7	9		
		cess		7	8			
B	G	GT	2	2	0.	0.	0.	NME1/NME4
P	O:	P	/	4	0	1	1	
	00	met	18	/	2	4	1	
	46	abol	4	1	2	4	8	
	03	ic		8	6	2	4	
	9	pro		8	9	5	9	
		cess		6	1	6	7	
				2	5	7	9	
				7	8			
B	G	esta	2	2	0.	0.	0.	SFN/KRT16
P	O:	blis	/	4	0	1	1	
	00	hme	18	/	2	4	1	
	61	nt	4	1	2	4	8	
	43	of		8	6	2	4	
	6	skin		8	9	5	9	
		barr		6	1	6	7	
		ier		2	5	7	9	
				7	8			
B	G	lipi	4	1	0.	0.	0.	HSD17B10/ECHS1/ECH1/DECR1
P	O:	d	/	1	0	1	1	
	00	oxid	18	0	2	4	1	
	34	atio	4	/	2	4	8	
	44	n		1	7	2	4	
	0			8	4	5	9	
				8	4	6	7	
				6	9	7	9	

				2	4	8			
B	G	neg	6	2	0.	0.	0.	SLC25A5/PRELID1/ENO1/PARK7/GSTP1/	6
P	O:	ativ	/	2	0	1	1	VDAC2	
		20	e	18	4	2	4	1	
		01	reg	4	/	2	4	8	
		23	ulat		1	7	2	4	
		4	ion		8	9	5	9	
			of		8	8	6	7	
			apo		6	9	7	9	
			ptot		2	2	8		
			ic						
			sign						
			alin						
			g						
			pat						
			hwa						
			y						
B	G	ncR	10	4	0.	0.	0.	HSD17B10/NPM3/RPS2/EEF1E1/PPA2/RPL	10
P	O:	NA	/	9	0	1	1	35/NSA2/RPL10A/RPL7/RPS9	
		00	met	18	2	2	4	1	
		34	abol	4	/	2	4	8	
		66	ic		1	8	2	4	
		0	pro		8	4	5	9	
			cess		8	5	6	7	
					6	3	7	9	
					2	9	8		
B	G	resp	5	1	0.	0.	0.	AKR1C3/LDHA/GSTP1/NQO1/ALDH3A1	5
P	O:	ons	/	6	0	1	1		

		00	e to	18	5	2	4	1	
		07	nutr	4	/	2	4	8	
		58	ient		1	9	8	9	
		4			8	8	1	5	
					8	5	3	4	
					6	3	0	8	
					2	8	6	6	
B	G	posi	6	2	0.	0.	0.	HSP90AA1/CAV1/OAZ1/CSNK1A1/RDX/V	6
P	O:	tive	/	2	0	1	1	PS28	
		00	reg	18	5	2	4	2	
		45	ulat	4	/	3	6	0	
		73	ion		1	2	0	0	
		2	of		8	4	9	0	
			prot		8	0	1	4	
			ein		6	6	2	8	
			cata		2	1	9	4	
			boli						
			c						
			pro						
			cess						
B	G	posi	4	1	0.	0.	0.	PRELID1/CAV1/ANXA2/CES1	4
P	O:	tive	/	1	0	1	1		
		19	reg	18	1	2	4	2	
		05	ulat	4	/	3	6	0	
		95	ion		1	4	8	6	
		4	of		8	2	9	6	
			lipi		8	0	4	4	
			d		6	9	0	2	

		loca	2	5	9	9			
		lizat							
		ion							
B	G	mit	3	6	0.	0.	0.	PRMT1/SFN/GADD45A	3
P	O:	otic	/	3	0	1	1		
	00	G1/	18	/	2	4	2		
	44	S	4	1	3	7	1		
	81	tran		8	6	6	3		
	9	sitio		8	5	7	0		
		n		6	1	8	8		
		chec		2	8	2	4		
		kpo				1			
		int							
		sign							
		alin							
		g							
B	G	neg	3	6	0.	0.	0.	PARK7/CAV1/G6PD	3
P	O:	ativ	/	3	0	1	1		
	20	e	18	/	2	4	2		
	00	reg	4	1	3	7	1		
	37	ulat		8	6	6	3		
	8	ion		8	5	7	0		
		of		6	1	8	8		
		reac		2	8	2	4		
		tive				1			
		oxy							
		gen							
		spec							

		ies								
		met								
		abol								
		ic								
		pro								
		cess								
B	G	neg	4	1	0.	0.	0.	AP2M1/PARK7/TXN/TAX1BP3		4
P	O:	ativ	/	1	0	1	1			
	19	e	18	2	2	4	2			
	03	reg	4	/	4	9	3			
	82	ulat		1	1	8	1			
	8	ion		8	0	6	0			
		of		8	9	2	2			
		cell		6	0	8	9			
		ular		2	7	1				
		prot								
		ein								
		loca								
		lizat								
		ion								
B	G	reg	4	1	0.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1		4
P	O:	ulat	/	1	0	1	1			
	20	ion	18	2	2	4	2			
	00	of	4	/	4	9	3			
	73	ste		1	1	8	1			
	6	m		8	0	6	0			
		cell		8	9	2	2			
		diff		6	0	8	9			

		eren	2	7	1			
		tiati						
		on						
B	G	reg	9	4	0.	0.	0.	PRELID1/PARK7/SFN/ANXA2/PSME1/SER 9
P	O:	ulat	/	2	0	1	1	PINB1/SERPINB5/ ASPH/S100A9
	00	ion	18	6	2	5	2	
	52	of	4	/	4	0	3	
	54	end		1	2	3	4	
	8	ope		8	3	3	9	
		ptid		8	9	9	4	
		ase		6	6	5	5	
		acti		2	2	3		
		vity						
B	G	pyri	2	2	0.	0.	0.	NME1/NME4 2
P	O:	mid	/	5	0	1	1	
	00	ine	18	/	2	5	2	
	09	nucl	4	1	4	0	3	
	14	eosi		8	5	6	7	
	7	de		8	0	6	6	
		trip		6	8	9	5	
		hos		2	8	7	7	
		pha				7	7	
		te						
		met						
		abol						
		ic						
		pro						
		cess						

B	G	puri	2	2	0.	0.	0.	SLC25A5/SLC25A6	2
P	O:	ne	/	5	0	1	1		
	00	nucl	18	/	2	5	2		
	15	eoti	4	1	4	0	3		
	86	de		8	5	6	7		
	5	tran		8	0	6	6		
		spor		6	8	9	5		
		t		2	8	7	7		
						7	7		
B	G	me	2	2	0.	0.	0.	CAV1/ANXA2	2
P	O:	mbr	/	5	0	1	1		
	00	ane	18	/	2	5	2		
	31	raft	4	1	4	0	3		
	57	org		8	5	6	7		
	9	aniz		8	0	6	6		
		atio		6	8	9	5		
		n		2	8	7	7		
						7	7		
B	G	reg	2	2	0.	0.	0.	ANXA2/PHLDA2	2
P	O:	ulat	/	5	0	1	1		
	19	ion	18	/	2	5	2		
	00	of	4	1	4	0	3		
	12	rece		8	5	6	7		
	0	ptor		8	0	6	6		
		bin		6	8	9	5		
		din		2	8	7	7		
		g				7	7		
B	G	posi	3	6	0.	0.	0.	SLC25A5/VDAC2/SFN	3

P	O:	tive	/	4	0	1	1		
	00	reg	18	/	2	5	2		
	35	ulat	4	1	4	0	3		
	79	ion		8	6	8	8		
	4	of		8	4	2	8		
		mit		6	1	0	9		
		och		2	3	3	5		
		ond			8	9			
		rial							
		me							
		mbr							
		ane							
		per							
		mea							
		bilit							
		y							
B	G	ribo	3	6	0.	0.	0.	RPS10/RPL23A/RPL3	3
P	O:	som	/	4	0	1	1		
	00	e	18	/	2	5	2		
	42	asse	4	1	4	0	3		
	25	mbl		8	6	8	8		
	5	y		8	4	2	8		
				6	1	0	9		
				2	3	3	5		
					8	9			
B	G	cor	4	1	0.	0.	0.	KRT7/KRT16/PKP3/KRT19	4
P	O:	nific	/	1	0	1	1		
	00	atio	18	3	2	5	2		

	70	n	4	/	4	1	4		
	26				1	8	5	4	
	8				8	0	1	6	
					8	9	6	0	
					6	3	0	9	
					2	3	7	6	
B	G	prot	7	2	0.	0.	0.	ENO1/NDUFAB1/STOML2/NAA20/METAP	7
P	O:	ein	/	9	0	1	1	2/ASPH/CES1	
	00	mat	18	3	2	5	2		
	51	urat	4	/	5	3	5		
	60	ion		1	1	0	6		
	4			8	4	1	9		
				8	8	6	3		
				6	0	6	6		
				2	8	8	2		
B	G	Fc-	5	1	0.	0.	0.	PSMA4/PSMA1/SKP1/PSMD9/PSME1	5
P	O:	epsi	/	6	0	1	1		
	00	lon	18	9	2	5	2		
	38	rece	4	/	5	3	5		
	09	ptor		1	1	0	6		
	5	sign		8	6	1	9		
		alin		8	4	6	3		
		g		6	6	6	6		
		pat		2	9	8	2		
		hwa							
		y							
B	G	prot	7	2	0.	0.	0.	HSP90AA1/VDAC2/COTL1/CHMP2A/CH	7
P	O:	ein	/	9	0	1	1	MP4A/RDX/ARPC1B	

	00	pol	18	4	2	5	2		
	51	yme	4	/	5	4	7		
	25	riza		1	5	9	3		
	8	tion		8	5	7	0		
				8	7	3	0		
				6	1	3	8		
				2	3	2	7		
B	G	reg	3	6	0.	0.	0.	HSP90AA1/PARK7/CAV1	3
P	O:	ulat	/	5	0	1	1		
	00	ion	18	/	2	5	2		
	32	of	4	1	5	4	7		
	76	mo		8	6	9	3		
	8	noo		8	5	7	0		
		xyg		6	3	3	0		
		ena		2	0	3	8		
		se			5	2	7		
		acti							
		vity							
B	G	posi	3	6	0.	0.	0.	HSP90AA1/HSP90AB1/HNRNPA1	3
P	O:	tive	/	5	0	1	1		
	20	reg	18	/	2	5	2		
	00	ulat	4	1	5	4	7		
	57	ion		8	6	9	3		
	3	of		8	5	7	0		
		DN		6	3	3	0		
		A		2	0	3	8		
		bios			5	2	7		
		ynt							

		heti								
		c								
		pro								
		cess								
B	G	posi	7	2	0.	0.	0.	HSP90AB1/PARK7/SFN/RDX/TOMM7/RT	7	
P	O:	tive	/	9	0	1	1	N4/VPS28		
	19	reg	18	5	2	5	2			
	03	ulat	4	/	5	6	8			
	82	ion		1	9	0	1			
	9	of		8	7	4	7			
		cell		8	0	1	7			
		ular		6	7	1	9			
		prot		2	3		8			
		ein								
		loca								
		lizat								
		ion								
B	G	cell	6	2	0.	0.	0.	ENO1/PSMA4/CAV1/PSMA1/PSMD9/PSM	6	
P	O:	ular	/	3	0	1	1	E1		
	00	resp	18	1	2	5	2			
	71	ons	4	/	6	6	8			
	45	e to		1	0	0	1			
	3	oxy		8	1	4	7			
		gen		8	1	1	7			
		leve		6	9	1	9			
		ls		2	3		8			
B	G	plas	4	1	0.	0.	0.	CAV1/SOD1/CHMP4A/S100A9	4	
P	O:	ma	/	1	0	1	1			

		00	me	18	5	2	5	2		
		07	mbr	4	/	6	6	8		
		00	ane		1	2	0	1		
		9	org		8	4	4	7		
			aniz		8	6	1	7		
			atio		6	4	1	9		
			n		2	8		8		
B	G	nucl	4	1	0.	0.	0.	NME1/ADK/APRT/NME4		4
P	O:	eob	/	1	0	1	1			
		00	ase-	18	5	2	5	2		
		34	cont	4	/	6	6	8		
		40	aini		1	2	0	1		
		4	ng		8	4	4	7		
			sma		8	6	1	7		
			ll		6	4	1	9		
			mol		2	8		8		
			ecul							
			e							
			bios							
			ynt							
			heti							
			c							
			pro							
			cess							
B	G	reg	4	1	0.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1		4
P	O:	ulat	/	1	0	1	1			
		00	ion	18	5	2	5	2		
		43	of	4	/	6	6	8		

	62	DN		1	2	0	1		
	0	A-		8	4	4	7		
		tem		8	6	1	7		
		plat		6	4	1	9		
		ed		2	8		8		
		tran							
		scri							
		ptio							
		n in							
		resp							
		ons							
		e to							
		stre							
		ss							
B	G	ethe	2	2	0.	0.	0.	TXN/TXN2	2
P	O:	r	/	6	0	1	1		
	00	met	18	/	2	5	2		
	18	abol	4	1	6	6	8		
	90	ic		8	3	0	1		
	4	pro		8	8	4	7		
		cess		6	3	1	7		
				2	4	1	9		
				7			8		
B	G	reg	2	2	0.	0.	0.	SFN/KRT16	2
P	O:	ulat	/	6	0	1	1		
	00	ion	18	/	2	5	2		
	33	of	4	1	6	6	8		
	56	wat		8	3	0	1		

	1	er		8	8	4	7		
		loss		6	3	1	7		
		via		2	4	1	9		
		skin			7		8		
B	G	posi	2	2	0.	0.	0.	POLR2E/POLR2F	2
P	O:	tive	/	6	0	1	1		
	00	reg	18	/	2	5	2		
	50	ulat	4	1	6	6	8		
	43	ion		8	3	0	1		
	4	of		8	8	4	7		
		vira		6	3	1	7		
		l		2	4	1	9		
		tran			7		8		
		scri							
		ptio							
		n							
B	G	reg	2	2	0.	0.	0.	PARK7/TXN	2
P	O:	ulat	/	6	0	1	1		
	19	ion	18	/	2	5	2		
	03	of	4	1	6	6	8		
	20	hyd		8	3	0	1		
	5	rog		8	8	4	7		
		en		6	3	1	7		
		per		2	4	1	9		
		oxid			7		8		
		e-							
		ind							
		uce							

		bilit							
		y							
		inv							
		olve							
		d in							
		apo							
		ptot							
		ic							
		pro							
		cess							
B	G	cell	7	2	0.	0.	0.	PRMT1/CDK4/SFN/PSME1/GMNN/RDX/	7
P	O:	cycl	/	9	0	1	1	GADD45A	
	00	e	18	8	2	6	3		
	44	G1/	4	/	7	0	1		
	84	S		1	2	0	4		
	3	pha		8	3	5	7		
		se		8	8	2	2		
		tran		6	9	1	7		
		sitio		2	8		7		
		n							
B	G	acti	9	4	0.	0.	0.	COTL1/FSCN1/RHOD/ALDOA/RDX/HSP9	9
P	O:	n	/	3	0	1	1	0B1/ARPC1B/TPM4/RHOC	
	00	fila	18	5	2	6	3		
	07	men	4	/	7	0	1		
	01	t		1	2	0	4		
	5	org		8	3	5	7		
		aniz		8	9	2	2		
		atio		6	2	1	7		

		n	2	5	7				
B	G	anti	6	2	0.	0.	0.	PSMA4/AP2M1/AP2S1/PSMA1/PSMD9/PS	6
P	O:	gen	/	3	0	1	1	ME1	
	00	pro	18	4	2	6	3		
	19	cess	4	/	7	1	2		
	88	ing		1	4	1	3		
	2	and		8	7	0	4		
		pres		8	6	8	0		
		enta		6	7	2	3		
		tion		2	2	5	3		
B	G	posi	8	3	0.	0.	0.	PRELID1/ENO1/CAV1/AURKAIP1/PSME1/	8
P	O:	tive	/	6	0	1	1	CSNK1A1/ASPH/S100A9	
	00	reg	18	7	2	6	3		
	45	ulat	4	/	7	2	3		
	86	ion		1	8	9	8		
	2	of		8	8	3	4		
		prot		8	4	8	3		
		eoly		6	8	4	7		
		sis		2	3	4	2		
B	G	prot	7	3	0.	0.	0.	PSMA4/PARK7/PSMA1/NEDD8/PSMD9/P	7
P	O:	ein	/	0	0	1	1	SME1/EIF3F	
	00	mo	18	0	2	6	3		
	70	difi	4	/	8	2	3		
	64	cati		1	1	9	8		
	6	on		8	0	3	4		
		by		8	7	8	3		
		sma		6	5	4	7		
		ll		2	6	4	2		

		prot								
		ein								
		rem								
		oval								
B	G	NA	2	2	0.	0.	0.	ENO1/ALDOA		2
P	O:	DH	/	7	0	1	1			
	00	rege	18	/	2	6	3			
	06	nera	4	1	8	2	3			
	73	tion		8	3	9	8			
	5			8	1	3	4			
				6	4	8	3			
				2	2	4	7			
				8	4	2				
B	G	intr	2	2	0.	0.	0.	ANXA2/CES1		2
P	O:	acel	/	7	0	1	1			
	00	lula	18	/	2	6	3			
	32	r	4	1	8	2	3			
	36	ster		8	3	9	8			
	6	ol		8	1	3	4			
		tran		6	4	8	3			
		spor		2	2	4	7			
		t		8	4	2				
B	G	intr	2	2	0.	0.	0.	ANXA2/CES1		2
P	O:	acel	/	7	0	1	1			
	00	lula	18	/	2	6	3			
	32	r	4	1	8	2	3			
	36	chol		8	3	9	8			
	7	este		8	1	3	4			

		rol	6	4	8	3		
		tran	2	2	4	7		
		spor		8	4	2		
		t						
B	G	posi	2	2	0.	0.	0.	CAV1/RTN4
P	O:	tive	/	7	0	1	1	2
	00	reg	18	/	2	6	3	
	34	ulat	4	1	8	2	3	
	12	ion		8	3	9	8	
	3	of		8	1	3	4	
		toll-		6	4	8	3	
		like		2	2	4	7	
		rece			8	4	2	
		ptor						
		sign						
		alin						
		g						
		pat						
		hwa						
		y						
B	G	can	2	2	0.	0.	0.	ENO1/ALDOA
P	O:	onic	/	7	0	1	1	2
	00	al	18	/	2	6	3	
	61	glyc	4	1	8	2	3	
	62	olys		8	3	9	8	
	1	is		8	1	3	4	
				6	4	8	3	
				2	2	4	7	

					8	4	2		
B	G	gluc	2	2	0.	0.	0.	ENO1/ALDOA	2
P	O:	ose	/	7	0	1	1		
	00	cata	18	/	2	6	3		
	61	boli	4	1	8	2	3		
	71	c		8	3	9	8		
	8	pro		8	1	3	4		
		cess		6	4	8	3		
		to		2	2	4	7		
		pyr			8	4	2		
		uva							
		te							
B	G	neg	2	2	0.	0.	0.	PARK7/TXN	2
P	O:	ativ	/	7	0	1	1		
	19	e	18	/	2	6	3		
	02	reg	4	1	8	2	3		
	88	ulat		8	3	9	8		
	3	ion		8	1	3	4		
		of		6	4	8	3		
		resp		2	2	4	7		
		ons			8	4	2		
		e to							
		oxid							
		ativ							
		e							
		stre							
		ss							
B	G	apo	4	1	0.	0.	0.	SLC25A5/PRELID1/VDAC2/SFN	4

P	O:	ptot	/	1	0	1	1		
	00	ic	18	8	2	6	3		
	08	mit	4	/	8	3	4		
	63	och		1	4	3	1		
	7	ond		8	9	0	4		
		rial		8	4	0	1		
		cha		6	2	9	4		
		nge		2	8	2	7		
		s							
B	G	posi	4	1	0.	0.	0.	RPS2/CAV1/UBE2N/SKP1	4
P	O:	tive	/	1	0	1	1		
	00	reg	18	8	2	6	3		
	31	ulat	4	/	8	3	4		
	39	ion		1	4	3	1		
	8	of		8	9	0	4		
		prot		8	4	0	1		
		ein		6	2	9	4		
		ubi		2	8	2	7		
		quit							
		inat							
		ion							
B	G	tran	3	6	0.	0.	0.	POLR2E/POLR2F/MAF1	3
P	O:	scri	/	8	0	1	1		
	00	ptio	18	/	2	6	3		
	06	n by	4	1	8	4	4		
	36	RN		8	8	1	8		
	0	A		8	2	5	4		
		pol		6	0	8	5		

		yme	2	3	3	8		
		rase		5	6	1		
		I						
B	G	telo	3	6	0.	0.	0.	HSP90AA1/HSP90AB1/HNRNPA1
P	O:	mer	/	8	0	1	1	3
	00	e	18	/	2	6	3	
	07	mai	4	1	8	4	4	
	00	nte		8	8	1	8	
	4	nan		8	2	5	4	
		ce		6	0	8	5	
		via		2	3	3	8	
		telo			5	6	1	
		mer						
		ase						
B	G	reg	3	6	0.	0.	0.	PARK7/TXN/SOD1
P	O:	ulat	/	8	0	1	1	3
	19	ion	18	/	2	6	3	
	03	of	4	1	8	4	4	
	20	oxid		8	8	1	8	
	1	ativ		8	2	5	4	
		e		6	0	8	5	
		stre		2	3	3	8	
		ss-			5	6	1	
		ind						
		uce						
		d						
		cell						
		deat						

			h							
B	G	reg	7	3	0.	0.	0.	HSP90AB1/PARK7/G6PD/NQO1/SOD1/CH	7	
P	O:	ulat	/	0	0	1	1	MP4A/CAPN2		
	19	ion	18	2	2	6	3			
	01	of	4	/	8	4	5			
	21	neu		1	9	8	3			
	4	ron		8	9	1	8			
		deat		8	4	5	5			
		h		6	7	5	6			
				2	9	7	6			
B	G	neg	4	1	2.	1.	1.	GSTO1/CAV1/OAZ1/FABP5	4	
P	O:	ativ	/	1	9	6	3			
	00	e	18	9	3	5	6			
	34	reg	4	/	E-	E-	E-			
	76	ulat		1	0	0	0			
	6	ion		8	2	1	1			
		of		8						
		ion		6						
		tran		2						
		sme								
		mbr								
		ane								
		tran								
		spor								
		t								
B	G	olefi	4	1	2.	1.	1.	AKR1C3/GSTP1/AKR1C1/AKR1C2	4	
P	O:	nic	/	1	9	6	3			
	01	com	18	9	3	5	6			

		20	pou	4	/	E-	E-	E-		
		25	nd		1	0	0	0		
		4	met		8	2	1	1		
			abol		8					
			ic		6					
			pro		2					
			cess							
B	G	neg	4	1	2.	1.	1.	PRMT1/CDK4/SFN/GADD45A		4
P	O:	ativ	/	1	9	6	3			
		20	e	18	9	3	5	6		
		00	reg	4	/	E-	E-	E-		
		13	ulat		1	0	0	0		
		4	ion		8	2	1	1		
			of		8					
			G1/		6					
			S		2					
			tran							
			sitio							
			n of							
			mit							
			otic							
			cell							
			cycl							
			e							
B	G	prot	5	1	2.	1.	1.	PRMT1/HSD17B10/CHMP2A/ALDOA/GSD		5
P	O:	ein	/	7	9	6	3	MD		
		00	ho	18	7	9	8	8		
		51	mo	4	/	E-	E-	E-		

	26	olig		1	0	0	0		
	0	ome		8	2	1	1		
		riza		8					
		tion		6					
				2					
B	G	posi	3	6	2.	1.	1.	SLC25A5/VDAC2/SFN	3
P	O:	tive	/	9	9	6	3		
	19	reg	18	/	9	8	8		
	05	ulat	4	1	E-	E-	E-		
	71	ion		8	0	0	0		
	0	of		8	2	1	1		
		me		6					
		mbr		2					
		ane							
		per							
		mea							
		bilit							
		y							
B	G	neg	4	1	3.	1.	1.	GSTO1/CAV1/OAZ1/FABP5	4
P	O:	ativ	/	2	0	6	3		
	00	e	18	0	1	9	9		
	34	reg	4	/	E-	E-	E-		
	76	ulat		1	0	0	0		
	3	ion		8	2	1	1		
		of		8					
		tran		6					
		sme		2					
		mbr							

		ane								
		tran								
		spor								
		t								
B	G	alco	8	3	3.	1.	1.	AKR1B10/AKR1C3/PARK7/AKR1C1/G6PD	8	
P	O:	hol	/	7	0	6	3	/AKR1C2/SOD1/CES1		
	00	met	18	3	3	9	9			
	06	abol	4	/	E-	E-	E-			
	06	ic		1	0	0	0			
	6	pro		8	2	1	1			
		cess		8						
				6						
				2						
B	G	ribo	2	2	3.	1.	1.	RPL23A/RPL3	2	
P	O:	som	/	8	0	6	3			
	00	al	18	/	3	9	9			
	00	larg	4	1	E-	E-	E-			
	02	e		8	0	0	0			
	7	sub		8	2	1	1			
		unit		6						
		asse		2						
		mbl								
		y								
B	G	glyc	2	2	3.	1.	1.	ENO1/ALDOA	2	
P	O:	olyt	/	8	0	6	3			
	00	ic	18	/	3	9	9			
	61	pro	4	1	E-	E-	E-			
	62	cess		8	0	0	0			

		0	thro	8	2	1	1		
			ugh	6					
			gluc	2					
			ose-						
			6-						
			pho						
			sph						
			ate						
B	G	reg	2	2	3.	1.	1.	PARK7/SOD1	2
P	O:	ulat	/	8	0	6	3		
	19	ion	18	/	3	9	9		
	02	of	4	1	E-	E-	E-		
	17	oxid		8	0	0	0		
	5	ativ		8	2	1	1		
		e		6					
		stre		2					
		ss-							
		ind							
		uce							
		d							
		intri							
		nsic							
		apo							
		ptot							
		ic							
		sign							
		alin							
		g							

		pat								
		hwa								
		y								
B	G	neg	4	1	3.	1.	1.	HSP90AB1/PARK7/LAPTM4B/ANXA2		4
P	O:	ativ	/	2	0	7	4			
	00	e	18	1	9	2	1			
	42	reg	4	/	E-	E-	E-			
	17	ulat		1	0	0	0			
	7	ion		8	2	1	1			
		of		8						
		prot		6						
		ein		2						
		cata								
		boli								
		c								
		pro								
		cess								
B	G	mit	3	7	3.	1.	1.	CHMP2A/CHMP4A/RHOC		3
P	O:	otic	/	0	1	7	4			
	00	cyto	18	/	0	2	1			
	00	kine	4	1	E-	E-	E-			
	28	sis		8	0	0	0			
	1			8	2	1	1			
				6						
				2						
B	G	reg	3	7	3.	1.	1.	CAV1/ANXA2/CES1		3
P	O:	ulat	/	0	1	7	4			
	00	ion	18	/	0	2	1			

		32	of	4	1	E-	E-	E-		
		37	ster		8	0	0	0		
		1	ol		8	2	1	1		
			tran		6					
			spor		2					
			t							
B	G	reg	3	7	3.	1.	1.	CAV1/ANXA2/CES1		3
P	O:	ulat	/	0	1	7	4			
		00	ion	18	/	0	2	1		
		32	of	4	1	E-	E-	E-		
		37	chol		8	0	0	0		
		4	este		8	2	1	1		
			rol		6					
			tran		2					
			spor							
			t							
B	G	posi	5	1	3.	1.	1.	PSMA4/CAV1/PSMA1/PSMD9/PSME1		5
P	O:	tive	/	7	1	7	4			
		00	reg	18	9	2	2	1		
		30	ulat	4	/	E-	E-	E-		
		17	ion		1	0	0	0		
		7	of		8	2	1	1		
			Wnt		8					
			sign		6					
			alin		2					
			g							
			pat							
			hwa							

		y							
B	G	reg	9	4	3.	1.	1.	HSP90AA1/PARK7/VDAC2/COTL1/FSCN1	9
P	O:	ulat	/	4	1	7	4	/RDX/RPL13A/ARPC1B/RHOC	
	00	ion	18	6	3	2	1		
	43	of	4	/	E-	E-	E-		
	25	prot		1	0	0	0		
	4	ein-		8	2	1	1		
		cont		8					
		aini		6					
		ng		2					
		com							
		plex							
		asse							
		mbl							
		y							
B	G	end	6	2	3.	1.	1.	CHMP2A/LAPTM4B/TINAGL1/CHMP4A/	6
P	O:	oso	/	4	1	7	4	VPS28/BLOC1S1	
	00	mal	18	2	6	4	3		
	16	tran	4	/	E-	E-	E-		
	19	spor		1	0	0	0		
	7	t		8	2	1	1		
				8					
				6					
				2					
B	G	ster	4	1	3.	1.	1.	CAV1/AKR1C1/ANXA2/CES1	4
P	O:	ol	/	2	1	7	4		
	00	tran	18	2	7	4	3		
	15	spor	4	/	E-	E-	E-		

	91	t		1	0	0	0		
	8			8	2	1	1		
				8					
				6					
				2					
B	G	pyri	2	2	3.	1.	1.	NME1/NME4	2
P	O:	mid	/	9	2	7	4		
	00	ine	18	/	3	5	4		
	09	ribo	4	1	E-	E-	E-		
	21	nucl		8	0	0	0		
	8	eoti		8	2	1	1		
		de		6					
		met		2					
		abol							
		ic							
		pro							
		cess							
B	G	N-	2	2	3.	1.	1.	NAA20/METAP2	2
P	O:	ter	/	9	2	7	4		
	00	min	18	/	3	5	4		
	31	al	4	1	E-	E-	E-		
	36	prot		8	0	0	0		
	5	ein		8	2	1	1		
		ami		6					
		no		2					
		acid							
		mo							
		difi							

		cati							
		on							
B	G	resp	2	2	3.	1.	1.	CDK4/CAV1	2
P	O:	ons	/	9	2	7	4		
	00	e to	18	/	3	5	4		
	36	incr	4	1	E-	E-	E-		
	29	ease		8	0	0	0		
	6	d		8	2	1	1		
		oxy		6					
		gen		2					
		leve							
		ls							
B	G	reg	2	2	3.	1.	1.	AP2M1/AP2S1	2
P	O:	ulat	/	9	2	7	4		
	00	ion	18	/	3	5	4		
	50	of	4	1	E-	E-	E-		
	69	defe		8	0	0	0		
	0	nse		8	2	1	1		
		resp		6					
		ons		2					
		e to							
		viru							
		s by							
		viru							
		s							
B	G	glyc	2	2	3.	1.	1.	ENO1/ALDOA	2
P	O:	olyt	/	9	2	7	4		
	00	ic	18	/	3	5	4		

	61	pro	4	1	E-	E-	E-		
	61	cess		8	0	0	0		
	5	thro		8	2	1	1		
		ugh		6					
		fruc		2					
		tose							
		-6-							
		pho							
		sph							
		ate							
B	G	reg	2	2	3.	1.	1.	CAV1/RDX	2
P	O:	ulat	/	9	2	7	4		
	19	ion	18	/	3	5	4		
	00	of	4	1	E-	E-	E-		
	02	ruffl		8	0	0	0		
	7	e		8	2	1	1		
		asse		6					
		mbl		2					
		y							
B	G	posi	2	2	3.	1.	1.	PRMT1/GADD45A	2
P	O:	tive	/	9	2	7	4		
	19	reg	18	/	3	5	4		
	00	ulat	4	1	E-	E-	E-		
	74	ion		8	0	0	0		
	5	of		8	2	1	1		
		p38		6					
		MA		2					
		PK							

		casc								
		ade								
B	G	sulf	8	3	3.	1.	1.	GSTO1/PARK7/GSTP1/G6PD/MGST1/TXN	8	
P	O:	ur	/	7	2	7	4	2/SOD1/UGDH		
	00	com	18	8	4	5	4			
	06	pou	4	/	E-	E-	E-			
	79	nd		1	0	0	0			
	0	met		8	2	1	1			
		abol		8						
		ic		6						
		pro		2						
		cess								
B	G	neg	4	1	3.	1.	1.	PARK7/TXN/PSMD9/PIM3	4	
P	O:	ativ	/	2	2	7	4			
	00	e	18	3	5	5	4			
	51	reg	4	/	E-	E-	E-			
	22	ulat		1	0	0	0			
	4	ion		8	2	1	1			
		of		8						
		prot		6						
		ein		2						
		tran								
		spor								
		t								
B	G	pep	7	3	3.	1.	1.	HSP90AA1/HSP90AB1/PARK7/CAV1/TXN	7	
P	O:	tidy	/	1	2	7	4	/CSNK1A1/GADD45A		
	00	l-	18	0	7	6	5			
	18	seri	4	/	E-	E-	E-			

	10	ne		1	0	0	0		
	5	pho		8	2	1	1		
		sph		8					
		oryl		6					
		atio		2					
		n							
B	G	reg	5	1	3.	1.	1.	HSP90AB1/PARK7/CAV1/PSME1/CSNK1A	5
P	O:	ulat	/	8	3	7	4	1	
	00	ion	18	2	1	8	6		
	61	of	4	/	E-	E-	E-		
	13	prot		1	0	0	0		
	6	easo		8	2	1	1		
		mal		8					
		prot		6					
		ein		2					
		cata							
		boli							
		c							
		pro							
		cess							
B	G	resp	9	4	3.	1.	1.	AKR1C3/LDHA/GSTP1/HNRNPA1/G6PD/	9
P	O:	ons	/	5	3	7	4	TXN2/NQO1/SOD1/ALDH3A1	
	00	e to	18	1	2	8	6		
	31	nutr	4	/	E-	E-	E-		
	66	ient		1	0	0	0		
	7	leve		8	2	1	1		
		ls		8					
				6					

				2							
B	G	neg	4	1	3.	1.	1.	PRMT1/CDK4/SFN/GADD45A			4
P	O:	ativ	/	2	3	7	4				
	19	e	18	4	3	8	6				
	02	reg	4	/	E-	E-	E-				
	80	ulat		1	0	0	0				
	7	ion		8	2	1	1				
		of		8							
		cell		6							
		cycl		2							
		e									
		G1/									
		S									
		pha									
		se									
		tran									
		sitio									
		n									
B	G	chol	3	7	3.	1.	1.	G6PD/SOD1/CES1			3
P	O:	este	/	2	3	7	4				
	00	rol	18	/	4	8	6				
	06	bios	4	1	E-	E-	E-				
	69	ynt		8	0	0	0				
	5	heti		8	2	1	1				
		c		6							
		pro		2							
		cess									
B	G	seco	3	7	3.	1.	1.	G6PD/SOD1/CES1			3

P	O:	nda	/	2	3	7	4		
	19	ry	18	/	4	8	6		
	02	alco	4	1	E-	E-	E-		
	65	hol		8	0	0	0		
	3	bios		8	2	1	1		
		ynt		6					
		heti		2					
		c							
		pro							
		cess							
B	G	neg	7	3	3.	1.	1.	HSP90AB1/PARK7/LAPTM4B/ANXA2/CH	7
P	O:	ativ	/	1	3	7	4	MP4A/HNRNPA0/PKP3	
	00	e	18	2	7	9	7		
	09	reg	4	/	E-	E-	E-		
	89	ulat		1	0	0	0		
	5	ion		8	2	1	1		
		of		8					
		cata		6					
		boli		2					
		c							
		pro							
		cess							
B	G	mus	9	4	3.	1.	1.	GSTO1/ENO1/CAV1/G6PD/SOD1/ALDOA	9
P	O:	cle	/	5	4	8	4	/ASPH/HSBP1/TPM4	
	00	syst	18	3	0	0	8		
	03	em	4	/	E-	E-	E-		
	01	pro		1	0	0	0		
	2	cess		8	2	1	1		

		rase									
		I									
		pro									
		mot									
		er									
B	G	neg	2	3	3.	1.	1.	CAV1/GADD45A			2
P	O:	ativ	/	0	4	8	4				
	00	e	18	/	4	1	8				
	33	reg	4	1	E-	E-	E-				
	13	ulat		8	0	0	0				
	7	ion		8	2	1	1				
		of		6							
		pep		2							
		tidy									
		l-									
		seri									
		ne									
		pho									
		sph									
		oryl									
		atio									
		n									
B	G	resp	2	3	3.	1.	1.	AKR1C3/AKR1C2			2
P	O:	ons	/	0	4	8	4				
	00	e to	18	/	4	1	8				
	34	pros	4	1	E-	E-	E-				
	69	tagl		8	0	0	0				
	4	and		8	2	1	1				

		in		6						
				2						
B	G	cell	2	3	3.	1.	1.	PARK7/TXN		2
P	O:	deat	/	0	4	8	4			
	00	h in	18	/	4	1	8			
	36	resp	4	1	E-	E-	E-			
	47	ons		8	0	0	0			
	4	e to		8	2	1	1			
		hyd		6						
		rog		2						
		en								
		per								
		oxid								
		e								
B	G	resp	2	3	3.	1.	1.	GSTO1/HNRNPA1		2
P	O:	ons	/	0	4	8	4			
	00	e to	18	/	4	1	8			
	46	arse	4	1	E-	E-	E-			
	68	nic-		8	0	0	0			
	5	cont		8	2	1	1			
		aini		6						
		ng		2						
		sub								
		stan								
		ce								
B	G	RN	8	3	3.	1.	1.	SNRPB/SNRPE/PUF60/HNRNPA1/POLR2E	8	
P	O:	A	/	8	4	8	4	/POLR2F/PRPF31/HNRNPA0		
	00	spli	18	3	6	1	9			

	00	cing	4	/	E-	E-	E-	
	37	, via		1	0	0	0	
	7	tran		8	2	1	1	
		sest		8				
		erifi		6				
		cati		2				
		on						
		reac						
		tion						
		s						
		wit						
		h						
		bul						
		ged						
		ade						
		nosi						
		ne						
		as						
		nucl						
		eop						
		hile						
B	G	mR	8	3	3.	1.	1.	SNRPB/SNRPE/PUF60/HNRNPA1/POLR2E 8
P	O:	NA	/	8	4	8	4	/POLR2F/PRPF31/HNRNPA0
	00	spli	18	3	6	1	9	
	00	cing	4	/	E-	E-	E-	
	39	, via		1	0	0	0	
	8	spli		8	2	1	1	
		ceos		8				

		ome	6							
			2							
B	G	reg	6	2	3.	1.	1.	HSP90AB1/PARK7/TXN/OAZ1/SFN/TOM	6	
P	O:	ulat	/	4	5	8	5	M7		
		00 ion	18	8	0	2	0			
		33 of	4	/	E-	E-	E-			
		15 intr		1	0	0	0			
		7 acel		8	2	1	1			
		lula		8						
		r		6						
		prot		2						
		ein								
		tran								
		spor								
		t								
B	G	resp	4	1	3.	1.	1.	GSTP1/G6PD/NQO1/SOD1	4	
P	O:	ons	/	2	5	8	5			
		00 e to	18	6	0	2	0			
		45 etha	4	/	E-	E-	E-			
		47 nol		1	0	0	0			
		1		8	2	1	1			
				8						
				6						
				2						
B	G	reg	7	3	3.	1.	1.	HSP90AA1/PSMA4/HSP90AB1/PSMA1/SKP	7	
P	O:	ulat	/	1	5	8	5	1/PSMD9/PSME1		
		00 ion	18	5	2	3	0			
		45 of	4	/	E-	E-	E-			

		08	inna	1	0	0	0		
		8	te	8	2	1	1		
			im	8					
			mu	6					
			ne	2					
			resp						
			ons						
			e						
B	G	DN	6	2	3.	1.	1.	CDK4/POLR2E/POLR2F/SUB1/GTF3C5/FO	6
P	O:	A-	/	4	5	8	5	SL1	
		00	tem	18	9	6	5	2	
		06	plat	4	/	E-	E-	E-	
		35	ed		1	0	0	0	
		2	tran		8	2	1	1	
			scri		8				
			ptio		6				
			n,		2				
			initi						
			atio						
			n						
B	G	neg	4	1	3.	1.	1.	PARK7/TXN/PSMD9/PIM3	4
P	O:	ativ	/	2	5	8	5		
		19	e	18	7	9	6	3	
		04	reg	4	/	E-	E-	E-	
		95	ulat		1	0	0	0	
		0	ion		8	2	1	1	
			of		8				
			esta		6				

		cess	2	3	3.	1.	1.	AKR1C3/FABP5	2
			6						
			2						
B	G	pros	2	3	3.	1.	1.	AKR1C3/FABP5	2
P	O:	tagl	/	1	6	8	5		
	00	and	18	/	6	7	3		
	01	in	4	1	E-	E-	E-		
	51	bios		8	0	0	0		
	6	ynt		8	2	1	1		
		heti		6					
		c		2					
		pro							
		cess							
B	G	ter	2	3	3.	1.	1.	POLR2E/POLR2F	2
P	O:	min	/	1	6	8	5		
	00	atio	18	/	6	7	3		
	06	n of	4	1	E-	E-	E-		
	36	RN		8	0	0	0		
	3	A		8	2	1	1		
		pol		6					
		yme		2					
		rase							
		I							
		tran							
		scri							
		ptio							
		n							
B	G	reg	2	3	3.	1.	1.	CNPY2/ANXA2	2

P	O:	ulat	/	1	6	8	5		
	00	ion	18	/	6	7	3		
	10	of	4	1	E-	E-	E-		
	98	lipo		8	0	0	0		
	4	prot		8	2	1	1		
		ein		6					
		part		2					
		icle							
		clea							
		ranc							
		e							
B	G	resp	2	3	3.	1.	1.	SOD1/HSP90B1	2
P	O:	ons	/	1	6	8	5		
	00	e to	18	/	6	7	3		
	33	AT	4	1	E-	E-	E-		
	19	P		8	0	0	0		
	8			8	2	1	1		
				6					
				2					
B	G	hyd	2	3	3.	1.	1.	PRDX1/GPX3	2
P	O:	rog	/	1	6	8	5		
	00	en	18	/	6	7	3		
	42	per	4	1	E-	E-	E-		
	74	oxid		8	0	0	0		
	4	e		8	2	1	1		
		cata		6					
		boli		2					
		c							

		pro							
		cess							
B	G	pros	2	3	3.	1.	1.	AKR1C3/FABP5	2
P	O:	tano	/	1	6	8	5		
	00	id	18	/	6	7	3		
	46	bios	4	1	E-	E-	E-		
	45	ynt		8	0	0	0		
	7	heti		8	2	1	1		
		c		6					
		pro		2					
		cess							
B	G	org	6	2	3.	1.	1.	HSD17B10/AKR1C3/PARK7/G6PD/SOD1/C	6
P	O:	anic	/	5	6	8	5	ES1	
	19	hyd	18	1	8	7	4		
	01	rox	4	/	E-	E-	E-		
	61	y		1	0	0	0		
	7	com		8	2	1	1		
		pou		8					
		nd		6					
		bios		2					
		ynt							
		heti							
		c							
		pro							
		cess							
B	G	RN	3	7	3.	1.	1.	HSP90AA1/HSP90AB1/HNRNPA1	3
P	O:	A-	/	5	7	8	5		
	00	dep	18	/	0	8	4		

	06	end	4	1	E-	E-	E-		
	27	ent		8	0	0	0		
	8	DN		8	2	1	1		
		A		6					
		bios		2					
		ynt							
		heti							
		c							
		pro							
		cess							
B	G	reg	3	7	3.	0.	1.	SLC25A5/VDAC2/SFN	3
P	O:	ulat	/	5	7	1	5		
	00	ion	18	/	0	8	4		
	46	of	4	1	E-	7	E-		
	90	mit		8	0	6	0		
	2	och		8	2	4	1		
		ond		6		1			
		rial		2		0			
		me				4			
		mbr							
		ane							
		per							
		mea							
		bilit							
		y							
B	G	reg	5	1	3.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1/HNRNPA0	5
P	O:	ulat	/	8	7	1	1		
	00	ion	18	8	3	8	5		

		43	of	4	/	E-	8	5		
		48	mR		1	0	9	2		
		8	NA		8	2	6	2		
			stab		8		4	2		
			ility		6		6	6		
					2		3			
B	G	resp	7	3	3.	0.	0.		PSMA4/PSMA1/GSTP1/PSMD9/PSME1/CO	7
P	O:	ons	/	2	7	1	1		MMD7/TNFRSF12A	
		00	e to	18	0	8	9	5		
		34	tum	4	/	E-	1	7		
		61	or		1	0	3	1		
		2	necr		8	2	4	7		
			osis		8		0	4		
			fact		6		5	2		
			or		2		6	7		
B	G	cell	5	1	3.	0.	0.		AKR1C3/MT2A/NQO1/SOD1/SYT8	5
P	O:	ular	/	8	8	1	1			
		00	resp	18	9	0	9	5		
		71	ons	4	/	E-	1	7		
		24	e to		1	0	9	6		
		8	met		8	2	3	5		
			al		8		0	8		
			ion		6		2	6		
					2		7	9		
B	G	ster	5	1	0.	0.	0.		HSD17B10/ AKR1C3/G6PD/SOD1/CES1	5
P	O:	oid	/	9	0	1	1			
		00	bios	18	0	3	9	5		
		06	ynt	4	/	8	3	9		

	69	heti		1	7	9	2		
	4	c		8	6	0	8		
		pro		8	0	4	0		
		cess		6	0	8	6		
				2	3	3	7		
B	G	reg	2	3	0.	0.	0.	PARK7/PSMA1	2
P	O:	ulat	/	2	0	1	1		
	00	ion	18	/	3	9	5		
	02	of	4	1	8	3	9		
	86	infl		8	7	9	2		
	1	am		8	6	0	8		
		mat		6	7	4	0		
		ory		2	0	8	6		
		resp			7	3	7		
		ons							
		e to							
		anti							
		geni							
		c							
		stim							
		ulus							
B	G	nucl	2	3	0.	0.	0.	SLC25A5/SLC25A6	2
P	O:	eoti	/	2	0	1	1		
	00	de	18	/	3	9	5		
	06	tran	4	1	8	3	9		
	86	spor		8	7	9	2		
	2	t		8	6	0	8		
				6	7	4	0		

				2	0	8	6		
					7	3	7		
B	G	ERB	2	3	0.	0.	0.	HSP90AA1/HBEGF	2
P	O:	B2	/	2	0	1	1		
	00	sign	18	/	3	9	5		
	38	alin	4	1	8	3	9		
	12	g		8	7	9	2		
	8	pat		8	6	0	8		
		hwa		6	7	4	0		
		y		2	0	8	6		
					7	3	7		
B	G	reg	2	3	0.	0.	0.	GSTP1/SOD1	2
P	O:	ulat	/	2	0	1	1		
	00	ion	18	/	3	9	5		
	90	of	4	1	8	3	9		
	32	sup		8	7	9	2		
	2	erox		8	6	0	8		
		ide		6	7	4	0		
		met		2	0	8	6		
		abol			7	3	7		
		ic							
		pro							
		cess							
B	G	anti	7	3	0.	0.	0.	PSMA4/STOML2/PSMA1/UBE2N/SKP1/PS	7
P	O:	gen	/	2	0	1	1	MD9/PSME1	
	00	rece	18	3	3	9	6		
	50	ptor	4	/	9	6	1		
	85	-		1	4	3	2		

		1	me		8	7	0	5		
			diat		8	2	4	1		
			ed		6	8	1	5		
			sign		2	7	9	9		
			alin							
			g							
			pat							
			hwa							
			y							
B	G	posi	3	7	0.	0.	0.	HSP90AA1/POLR2E/POLR2F		3
P	O:	tive	/	7	0	1	1			
	00	reg	18	/	3	9	6			
	32	ulat	4	1	9	6	1			
	48	ion		8	5	3	2			
	1	of		8	0	0	5			
		type		6	2	4	1			
		I		2	2	1	5			
		inte				9	9			
		rfer								
		on								
		pro								
		duc								
		tion								
B	G	prot	3	7	0.	0.	0.	HSP90AA1/SFN/EMC2		3
P	O:	ein	/	7	0	1	1			
	00	inse	18	/	3	9	6			
	51	rtio	4	1	9	6	1			
	20	n		8	5	3	2			

	5	into		8	0	0	5		
		me		6	2	4	1		
		mbr		2	2	1	5		
		ane				9	9		
B	G	sign	4	1	0.	0.	0.	PRMT1/EEF1E1/SFN/GADD45A	4
P	O:	al	/	3	0	1	1		
	00	tran	18	1	3	9	6		
	42	sdu	4	/	9	6	1		
	77	ctio		1	5	3	2		
	0	n in		8	2	0	5		
		resp		8	8	4	1		
		ons		6	1	1	5		
		e to		2	1	9	9		
		DN							
		A							
		da							
		mag							
		e							
B	G	ma	4	1	0.	0.	0.	NME1/CAV1/APRT/RTN4	4
P	O:	mm	/	3	0	2	1		
	00	ary	18	2	4	0	6		
	30	glan	4	/	0	0	4		
	87	d		1	4	2	4		
	9	dev		8	6	4	8		
		elop		8	4	2	6		
		men		6	5	2	4		
		t		2	8	7	8		
B	G	reg	4	1	0.	0.	0.	HSP90AB1/PARK7/CAV1/CSNK1A1	4

P	O:	ulat	/	3	0	2	1		
	00	ion	18	2	4	0	6		
	32	of	4	/	0	0	4		
	43	prot		1	4	2	4		
	4	easo		8	6	4	8		
		mal		8	4	2	6		
		ubi		6	5	2	4		
		quit		2	8	7	8		
		in-							
		dep							
		end							
		ent							
		prot							
		ein							
		cata							
		boli							
		c							
		pro							
		cess							
B	G	ster	3	7	0.	0.	0.	G6PD/SOD1/CES1	3
P	O:	ol	/	8	0	2	1		
	00	bios	18	/	4	0	6		
	16	ynt	4	1	0	1	5		
	12	heti		8	7	5	5		
	6	c		8	9	0	2		
		pro		6	6	6	5		
		cess		2	9	9	3		
					3	8	6		

B	G	7-	2	3	0.	0.	0.	POLR2E/POLR2F	2
P	O:	met	/	3	0	2	1		
	00	hyl	18	/	4	0	6		
	06	gua	4	1	1	1	5		
	37	nosi		8	0	5	5		
	0	ne		8	0	0	2		
		mR		6	8	6	5		
		NA		2	9	9	3		
		cap			5	8	6		
		pin							
		g							
B	G	rRN	2	3	0.	0.	0.	NPM3/GTF3C5	2
P	O:	A	/	3	0	2	1		
	00	tran	18	/	4	0	6		
	09	scri	4	1	1	1	5		
	30	ptio		8	0	5	5		
	3	n		8	0	0	2		
				6	8	6	5		
				2	9	9	3		
					5	8	6		
B	G	posi	2	3	0.	0.	0.	HSP90AA1/HSP90AB1	2
P	O:	tive	/	3	0	2	1		
	00	reg	18	/	4	0	6		
	51	ulat	4	1	1	1	5		
	97	ion		8	0	5	5		
	3	of		8	0	0	2		
		telo		6	8	6	5		
		mer		2	9	9	3		

		ase		5	8	6			
		acti							
		vity							
B	G	posi	6	2	0.	0.	0.	HSP90AA1/PSMA4/PSMA1/SKP1/PSMD9/	6
P	O:	tive	/	5	0	2	1	PSME1	
	00	reg	18	8	4	0	6		
	02	ulat	4	/	1	1	5		
	83	ion		1	1	6	6		
	3	of		8	7	2	2		
		resp		8	8	8	5		
		ons		6	2	7	3		
		e to		2		1	5		
		biot							
		ic							
		stim							
		ulus							
B	G	org	6	2	0.	0.	0.	HSD17B10/ECHS1/TXN2/PGD/ECH1/DEC	6
P	O:	anic	/	5	0	2	1	R1	
	00	acid	18	8	4	0	6		
	16	cata	4	/	1	1	5		
	05	boli		1	1	6	6		
	4	c		8	7	2	2		
		pro		8	8	8	5		
		cess		6	2	7	3		
				2		1	5		
B	G	cell	9	4	0.	0.	0.	ENO1/HSP90AA1/HSP90AB1/G6PD/EI24/S	9
P	O:	gro	/	7	0	2	1	FN/HBEGF/RTN4/S100A9	
	00	wth	18	0	4	0	6		

			16	4	/	1	2	6		
			04			1	3	3	2	
			9			8	9	4	1	
						8	7	7	5	
						6	4	4	7	
						2	9	4	4	
B	G	neg	3	7	0.	0.	0.	PARK7/CAV1/VPS28		3
P	O:	ativ	/	9	0	2	1			
	00	e	18	/	4	0	6			
	31	reg	4	1	2	4	8			
	39	ulat		8	1	7	2			
	7	ion		8	1	6	0			
		of		6	2	8	4			
		prot		2	9	5	5			
		ein			2	7	4			
		ubi								
		quit								
		inat								
		ion								
B	G	reg	3	7	0.	0.	0.	CDK4/GSTP1/NDUFS4		3
P	O:	ulat	/	9	0	2	1			
	00	ion	18	/	4	0	6			
	48	of	4	1	2	4	8			
	14	fibr		8	1	7	2			
	5	obla		8	1	6	0			
		st		6	2	8	4			
		prol		2	9	5	5			
		ifer			2	7	4			

		atio							
		n							
B	G	reg	3	7	0.	0.	0.	HSP90AA1/HSP90AB1/HSBP1	3
P	O:	ulat	/	9	0	2	1		
	19	ion	18	/	4	0	6		
	00	of	4	1	2	4	8		
	03	cell		8	1	7	2		
	4	ular		8	1	6	0		
		resp		6	2	8	4		
		ons		2	9	5	5		
		e to			2	7	4		
		heat							
B	G	ncR	8	4	0.	0.	0.	HSD17B10/NPM3/RPS2/RPL35/NSA2/RPL1	8
P	O:	NA	/	0	0	2	1	0A/RPL7/RPS9	
	00	pro	18	0	4	0	6		
	34	cess	4	/	2	6	9		
	47	ing		1	8	9	9		
	0			8	6	4	9		
				8	7	4	1		
				6	0		5		
				2	7		3		
B	G	ster	7	3	0.	0.	0.	HSD17B10/AKR1C3/AKR1C1/G6PD/AKR1C	7
P	O:	oid	/	2	0	2	1	2/SOD1/CES1	
	00	met	18	9	4	0	6		
	08	abol	4	/	2	6	9		
	20	ic		1	8	9	9		
	2	pro		8	6	4	9		
		cess		8	9	4	1		

				6	0		5		
				2	2		3		
B	G	ribo	2	3	0.	0.	0.	ADK/APRT	2
P	O:	nucl	/	4	0	2	1		
	00	eosi	18	/	4	0	6		
	09	de	4	1	3	6	9		
	15	mo		8	2	9	9		
	6	nop		8	9	4	9		
		hos		6	8	4	1		
		pha		2	5		5		
		te			3		3		
		bios							
		ynt							
		heti							
		c							
		pro							
		cess							
B	G	7-	2	3	0.	0.	0.	POLR2E/POLR2F	2
P	O:	met	/	4	0	2	1		
	00	hyl	18	/	4	0	6		
	09	gua	4	1	3	6	9		
	45	nosi		8	2	9	9		
	2	ne		8	9	4	9		
		RN		6	8	4	1		
		A		2	5		5		
		cap			3		3		
		pin							
		g							

B	G	RN	2	3	0.	0.	0.	POLR2E/POLR2F	2
P	O:	A	/	4	0	2	1		
	00	cap	18	/	4	0	6		
	36	pin	4	1	3	6	9		
	26	g		8	2	9	9		
	0			8	9	4	9		
				6	8	4	1		
				2	5		5		
				3			3		
B	G	cell	2	3	0.	0.	0.	ADK/APRT	2
P	O:	ular	/	4	0	2	1		
	00	met	18	/	4	0	6		
	43	abol	4	1	3	6	9		
	09	ic		8	2	9	9		
	4	com		8	9	4	9		
		pou		6	8	4	1		
		nd		2	5		5		
		salv			3		3		
		age							
B	G	wo	2	3	0.	0.	0.	HBEGF/RHOC	2
P	O:	und	/	4	0	2	1		
	00	heal	18	/	4	0	6		
	44	ing,	4	1	3	6	9		
	31	spre		8	2	9	9		
	9	adi		8	9	4	9		
		ng		6	8	4	1		
		of		2	5		5		
		cells			3		3		

B	G	epib	2	3	0.	0.	0.	HBEGF/RHOC	2
P	O:	oly	/	4	0	2	1		
	00	inv	18	/	4	0	6		
	90	olve	4	1	3	6	9		
	50	d in		8	2	9	9		
	5	wo		8	9	4	9		
		und		6	8	4	1		
		heal		2	5		5		
		ing			3		3		
B	G	resp	5	1	0.	0.	0.	NME1/LDHA/GSTP1/TXN2/PIM3	5
P	O:	ons	/	9	0	2	1		
	00	e to	18	6	4	0	6		
	34	mo	4	/	3	6	9		
	28	nos		1	3	9	9		
	4	acc		8	2	4	9		
		hari		8	9	4	1		
		de		6	8		5		
				2	6		3		
B	G	reg	5	1	0.	0.	0.	HSP90AB1/PARK7/CAV1/ANXA2/PHLDA2	5
P	O:	ulat	/	9	0	2	1		
	00	ion	18	6	4	0	6		
	43	of	4	/	3	6	9		
	39	prot		1	3	9	9		
	3	ein		8	2	4	9		
		bin		8	9	4	1		
		din		6	8		5		
		g		2	6		3		
B	G	telo	3	8	0.	0.	0.	HSP90AA1/HSP90AB1/HNRNPA1	3

P	O:	mer	/	0	0	2	1		
	00	e	18	/	4	0	6		
	10	mai	4	1	3	6	9		
	83	nte		8	4	9	9		
	3	nan		8	5	4	9		
		ce		6	0	4	1		
		via		2	0		5		
		telo			8		3		
		mer							
		e							
		leng							
		the							
		nin							
		g							
B	G	fibr	3	8	0.	0.	0.	CDK4/GSTP1/NDUFS4	3
P	O:	obla	/	0	0	2	1		
	00	st	18	/	4	0	6		
	48	prol	4	1	3	6	9		
	14	ifer		8	4	9	9		
	4	atio		8	5	4	9		
		n		6	0	4	1		
				2	0		5		
					8		3		
B	G	reg	5	1	0.	0.	0.	HSP90AB1/PARK7/G6PD/NQO1/SOD1	5
P	O:	ulat	/	9	0	2	1		
	00	ion	18	7	4	0	7		
	43	of	4	/	4	9	1		
	52	neu		1	1	0	7		

	3	ron		8	2	7	3		
		apo		8	1	2	9		
		ptot		6	7	4	9		
		ic		2	1	6	2		
		pro							
		cess							
B	G	reg	5	1	0.	0.	0.	CAV1/POLR2E/CHMP2A/POLR2F/LY6E	5
P	O:	ulat	/	9	0	2	1		
	00	ion	18	7	4	0	7		
	43	of	4	/	4	9	1		
	90	biol		1	1	0	7		
	3	ogic		8	2	7	3		
		al		8	1	2	9		
		pro		6	7	4	9		
		cess		2	1	6	2		
		inv							
		olve							
		d in							
		sym							
		biot							
		ic							
		inte							
		racti							
		on							
B	G	cell	5	1	0.	0.	0.	CDK4/GSTP1/MTDH/IL18/CAPN2	5
P	O:	ular	/	9	0	2	1		
	00	resp	18	7	4	0	7		
	71	ons	4	/	4	9	1		

	22	e to		1	1	0	7		
	2	lipo		8	2	7	3		
		pol		8	1	2	9		
		ysac		6	7	4	9		
		char		2	1	6	2		
		ide							
B	G	cell	5	1	0.	0.	0.	GSTO1/PARK7/GSTP1/G6PD/SOD1	5
P	O:	ular	/	9	0	2	1		
	00	mo	18	8	4	1	7		
	06	difi	4	/	4	1	4		
	57	ed		1	9	9	0		
	5	ami		8	2	2	8		
		no		8	2	4	2		
		acid		6	2	1	4		
		met		2	1	8	3		
		abol							
		ic							
		pro							
		cess							
B	G	reg	5	1	0.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1/HNRNPA0	5
P	O:	ulat	/	9	0	2	1		
	00	ion	18	8	4	1	7		
	43	of	4	/	4	1	4		
	48	RN		1	9	9	0		
	7	A		8	2	2	8		
		stab		8	2	4	2		
		ility		6	2	1	4		
				2	1	8	3		

B	G	pep	7	3	0.	0.	0.	HSP90AA1/HSP90AB1/PARK7/CAV1/TXN	7
P	O:	tidy	/	3	0	2	1	/CSNK1A1/GADD45A	
	00	l-	18	3	4	1	7		
	18	seri	4	/	5	1	4		
	20	ne		1	2	9	0		
	9	mo		8	3	2	8		
		difi		8	5	4	2		
		cati		6	3	1	4		
		on		2	7	8	3		
B	G	posi	4	1	0.	0.	0.	RPS2/CAV1/UBE2N/SKP1	4
P	O:	tive	/	3	0	2	1		
	19	reg	18	7	4	1	7		
	03	ulat	4	/	5	1	4		
	32	ion		1	3	9	0		
	2	of		8	3	2	8		
		prot		8	5	4	2		
		ein		6	4	1	4		
		mo		2	4	8	3		
		difi							
		cati							
		on							
		by							
		sma							
		ll							
		prot							
		ein							
		conj							
		uga							

		tion								
		or								
		rem								
		oval								
B	G	repr	8	4	4.	2.	1.	AKR1C3/HSP90AB1/MGST1/SOD1/SERPIN	8	
P	O:	odu	/	0	5	1	7	B5/FOSL1/KRT19/PHLDA2		
	00	ctiv	18	5	5	2	4			
	48	e	4	/	E-	E-	E-			
	60	stru		1	0	0	0			
	8	ctur		8	2	1	1			
		e		8						
		dev		6						
		elop		2						
		men								
		t								
B	G	ter	2	3	4.	2.	1.	SNRPB/SNRPE	2	
P	O:	min	/	5	5	1	7			
	00	atio	18	/	6	2	4			
	06	n of	4	1	E-	E-	E-			
	36	RN		8	0	0	0			
	9	A		8	2	1	1			
		pol		6						
		yme		2						
		rase								
		II								
		tran								
		scri								
		ptio								

		n								
B	G	cent	2	3	4.	2.	1.	HSP90AA1/HSP90AB1		2
P	O:	ral	/	5	5	1	7			
	00	ner	18	/	6	2	4			
	21	vou	4	1	E-	E-	E-			
	95	s		8	0	0	0			
	5	syst		8	2	1	1			
		em		6						
		neu		2						
		ron								
		axo								
		nog								
		enes								
		is								
B	G	sup	2	3	4.	2.	1.	GSTP1/SOD1		2
P	O:	erox	/	5	5	1	7			
	00	ide	18	/	6	2	4			
	42	anio	4	1	E-	E-	E-			
	55	n		8	0	0	0			
	4	gen		8	2	1	1			
		erat		6						
		ion		2						
B	G	neg	2	3	4.	2.	1.	PSMD9/PIM3		2
P	O:	ativ	/	5	5	1	7			
	00	e	18	/	6	2	4			
	46	reg	4	1	E-	E-	E-			
	67	ulat		8	0	0	0			
	6	ion		8	2	1	1			

		ynt							
		heti							
		c							
		pro							
		cess							
B	G	neg	2	3	4.	2.	1.	OAZ1/FABP5	2
P	O:	ativ	/	5	5	1	7		
	19	e	18	/	6	2	4		
	03	reg	4	1	E-	E-	E-		
	96	ulat		8	0	0	0		
	0	ion		8	2	1	1		
		of		6					
		anio		2					
		n							
		tran							
		sme							
		mbr							
		ane							
		tran							
		spor							
		t							
B	G	posi	5	2	4.	2.	1.	PRELID1/CAV1/PSME1/ASPH/S100A9	5
P	O:	tive	/	0	6	1	7		
	00	reg	18	0	5	6	7		
	10	ulat	4	/	E-	E-	E-		
	95	ion		1	0	0	0		
	2	of		8	2	1	1		
		pep		8					

		tida	6							
		se	2							
		acti								
		vity								
B	G	puri	8	4	4.	2.	1.	NME1/ENO1/LDHA/STOML2/ADK/APRT	8	
P	O:	ne	/	0	7	1	7	/NME4/ALDOA		
	00	ribo	18	8	2	8	9			
	09	nucl	4	/	E-	E-	E-			
	15	eoti		1	0	0	0			
	0	de		8	2	1	1			
		met		8						
		abol		6						
		ic		2						
		pro								
		cess								
B	G	repr	8	4	4.	2.	1.	AKR1C3/HSP90AB1/MGST1/SOD1/SERPIN	8	
P	O:	odu	/	0	7	1	7	B5/FOSL1/KRT19/PHLDA2		
	00	ctiv	18	8	2	8	9			
	61	e	4	/	E-	E-	E-			
	45	syst		1	0	0	0			
	8	em		8	2	1	1			
		dev		8						
		elop		6						
		men		2						
		t								
B	G	neg	4	1	4.	2.	1.	PARK7/VDAC2/RDX/RPL13A		4
P	O:	ativ	/	3	7	1	8			
	00	e	18	9	4	9	0			

		31	reg	4	/	E-	E-	E-		
		33	ulat		1	0	0	0		
		3	ion		8	2	1	1		
			of		8					
			prot		6					
			ein-		2					
			cont							
			aini							
			ng							
			com							
			plex							
			asse							
			mbl							
			y							
B	G	posi	3	8	4.	2.	1.	HSP90AB1/CAV1/ANXA2		3
P	O:	tive	/	3	7	1	8			
	00	reg	18	/	6	9	0			
	32	ulat	4	1	E-	E-	E-			
	09	ion		8	0	0	0			
	2	of		8	2	1	1			
		prot		6						
		ein		2						
		bin								
		din								
		g								
B	G	prot	7	3	4.	2.	1.	PSMA4/PSMA1/UBE2N/SKP1/PSMD9/PSM	7	
P	O:	ein	/	3	7	1	8	E1/THOP1		
	00	pol	18	7	7	9	0			

	00	yub	4	/	E-	E-	E-		
	20	iqui		1	0	0	0		
	9	tina		8	2	1	1		
		tion		8					
				6					
				2					
B	G	gluc	2	3	4.	2.	1.	ENO1/ALDOA	2
P	O:	ose	/	6	8	1	8		
	00	cata	18	/	0	9	0		
	06	boli	4	1	E-	E-	E-		
	00	c		8	0	0	0		
	7	pro		8	2	1	1		
		cess		6					
				2					
B	G	neg	2	3	4.	2.	1.	HSP90AB1/PARK7	2
P	O:	ativ	/	6	8	1	8		
	00	e	18	/	0	9	0		
	32	reg	4	1	E-	E-	E-		
	43	ulat		8	0	0	0		
	5	ion		8	2	1	1		
		of		6					
		prot		2					
		easo							
		mal							
		ubi							
		quit							
		in-							
		dep							

P	O:	ulat	/	6	8	1	8
19	ion	18	/	0	9	0	
03	of	4	1	E-	E-	E-	
72	pho		8	0	0	0	
5	sph		8	2	1	1	
	olip		6				
	id		2				
	met						
	abol						
	ic						

			pro							
			cess							
B	G	posi	2	3	4.	2.	1.	SUB1/FOSL1		2
P	O:	tive	/	6	8	1	8			
	20	reg	18	/	0	9	0			
	00	ulat	4	1	E-	E-	E-			
	14	ion		8	0	0	0			
	4	of		8	2	1	1			
		DN		6						
		A-		2						
		tem								
		plat								
		ed								
		tran								
		scri								
		ptio								
		n,								
		initi								
		atio								
		n								
B	G	reg	3	8	4.	0.	0.	PARK7/TXN/SOD1		3
P	O:	ulat	/	4	9	2	1			
	19	ion	18	/	0	2	8			
	00	of	4	1	E-	3	3			
	40	cell		8	0	1	2			
	7	ular		8	2	3	9			
		resp		6		5	2			
		ons		2		9	2			

		e to			7	1			
		oxid							
		ativ							
		e							
		stre							
		ss							
C	G	ribo	23	1	4.	1.	9.	MRPL12/NDUFAB1/MRPL47/MRPS12/RPS2	23
C	O:	som	/	8	1	3	9	/MRPL13/MRPL23/RPL4/MRPL42/RPS10/	
	00	al	18	7	1	9	3	MRPL15/RPL35/RPL23A/MRPL28/MCTS1/	
	44	sub	7	/	E-	5	9	RPS11/RPS20/RPL10A/RPL7/RPL13A/MRP	
	39	unit		1	1	9	8	S28/RPL3/RPS9	
	1			9	9	E-	E-		
				5		1	1		
				2		6	7		
				0					
C	G	ribo	24	2	1.	2.	1.	MRPL12/NDUFAB1/MRPL47/MRPS12/RPS2	24
C	O:	som	/	4	1	0	4	/MRPL13/MRPL23/RPL4/MRPL42/RPS10/	
	00	e	18	3	8	0	2	MRPL15/RPL35/AURKAIP1/RPL23A/MRPL	
	05		7	/	E-	4	7	28/MCTS1/RPS11/RPS20/RPL10A/RPL7/RP	
	84			1	1	4	3	L13A/MRPS28/RPL3/RPS9	
	0			9	7	E-	E-		
				5		1	1		
				2		5	5		
				0					
C	G	larg	15	1	3.	3.	2.	MRPL12/NDUFAB1/MRPL47/MRPL13/MRP	15
C	O:	e	/	1	1	5	5	L23/RPL4/MRPL42/MRPL15/RPL35/RPL23	
	00	ribo	18	5	0	1	0	A/MRPL28/RPL10A/RPL7/RPL13A/RPL3	
	15	som	7	/	E-	2	0		

	93	al		1	1	E-	8		
	4	sub		9	3	1	E-		
		unit		5		1	1		
				2			1		
				0					
C	G	mit	20	2	1.	9.	6.	CYC1/MRPL12/NDUFAB1/NDUFB9/MRPL	20
C	O:	och	/	6	1	7	9	47/MRPS12/HSD17B10/UQCRH/MRPL13/C	
	00	ond	18	5	5	3	3	OX5A/MRPL23/NDUFS4/MRPL42/NDUFB5	
	98	rial	7	/	E-	6	3	/NDUFC2/MRPL15/MRPL28/SLC25A6/MR	
	79	prot		1	1	5	1	PS28/TOMM7	
	8	ein-		9	2	E-	E-		
		cont		5		1	1		
		aini		2		1	1		
		ng		0					
		com							
		plex							
C	G	cyto	13	1	3.	2.	1.	RPS2/RPL4/RPS10/RPL35/RPL23A/MCTS1/	13
C	O:	sol	/	0	1	1	5	RPS11/RPS20/RPL10A/RPL7/RPL13A/RPL3	
	00	c	18	7	1	1	0	/RPS9	
	22	ribo	7	/	E-	3	5		
	62	som		1	1	7	1		
	6	e		9	1	E-	E-		
				5		0	0		
				2		9	9		
				0					
C	G	mit	23	4	3.	2.	1.	CYC1/SLC25A5/MRPL12/NDUFAB1/NDUF	23
C	O:	och	/	9	9	2	5	B9/MRPL47/MRPS12/UQCRH/MRPL13/CO	
	00	ond	18	3	4	3	9	X5A/STOML2/MRPL23/COX8A/NDUFS4/	

		05	rial	7	/	E-	4	0	MRPL42/NDUFB5/NDUFC2/MRPL15/AUR	
		74	inne		1	1	E-	8	KAIP1/MRPL28/NME4/SLC25A6/MRPS28	
		3	r		9	0	0	E-		
			me		5		8	0		
			mbr		2			8		
			ane		0					
C	G	mit	22	4	1.	5.	4.		SLC25A5/MRPL12/NDUFAB1/MDH2/MRP	22
C	O:	och	/	7	1	6	0		L47/MRPS12/HSD17B10/ECHS1/MRPL13/P	
		00	ond	18	6	6	4	1	ARK7/MRPL23/VDAC2/MRPL42/PPA2/MR	
		05	rial	7	/	E-	4	9	PL15/TXN2/MRPL28/SOD1/NME4/MRPS28	
		75	mat		1	0	1	E-	/DECRI/BLOC1S1	
		9	rix		9	9	E-	0		
					5		0	8		
					2		8			
					0					
C	G	org	10	8	1.	4.	2.		MRPL12/NDUFAB1/MRPL47/MRPS12/MRP	10
C	O:	anel	/	7	0	0	9		L13/MRPL23/MRPL42/MRPL15/MRPL28/M	
		00	lar	18	/	8	8	0	RPS28	
		00	ribo	7	1	E-	3	7		
		31	som		9	0	1	5		
		3	e		5	8	E-	E-		
					2		0	0		
					0		7	7		
C	G	mit	10	8	1.	4.	2.		MRPL12/NDUFAB1/MRPL47/MRPS12/MRP	10
C	O:	och	/	7	0	0	9		L13/MRPL23/MRPL42/MRPL15/MRPL28/M	
		00	ond	18	/	8	8	0	RPS28	
		05	rial	7	1	E-	3	7		
		76	ribo		9	0	1	5		

	1	som		5	8	E-	E-		
		e		2		0	0		
				0		7	7		
C	G	sma	9	7	3.	1.	8.	MRPS12/RPS2/MRPL42/RPS10/MCTS1/RPS	9
C	O:	ll	/	4	6	2	7	11/RPS20/MRPS28/RPS9	
	00	ribo	18	/	2	3	7		
	15	som	7	1	3	2	3		
	93	al		9	8	1	5		
	5	sub		5	E-	E-	E-		
		unit		2	0	0	0		
				0	8	6	7		
C	G	org	8	5	6.	1.	1.	MRPL12/NDUFAB1/MRPL47/MRPL13/MRP	8
C	O:	anel	/	7	7	9	3	L23/MRPL42/MRPL15/MRPL28	
	00	lar	18	/	5	1	6		
	00	larg	7	1	6	4	3		
	31	e		9	6	4	2		
	5	ribo		5	E-	E-	E-		
		som		2	0	0	0		
		al		0	8	6	6		
		sub							
		unit							
C	G	mit	8	5	6.	1.	1.	MRPL12/NDUFAB1/MRPL47/MRPL13/MRP	8
C	O:	och	/	7	7	9	3	L23/MRPL42/MRPL15/MRPL28	
	00	ond	18	/	5	1	6		
	05	rial	7	1	6	4	3		
	76	larg		9	6	4	2		
	2	e		5	E-	E-	E-		
		ribo		2	0	0	0		

		som	0	8	6	6			
		al							
		sub							
		unit							
C	G	foca	18	4	1.	2.	2.	HMGA1/RPS2/CAV1/RPL4/RPS10/RPS11/	18
C	O:	l	/	1	1	9	0	RPL10A/RPL7/FHL2/RDX/RPL13A/HSP90B	
	00	adh	18	6	0	0	6	1/ARPC1B/RPL3/CD59/TPM4/RPS9/CAPN	
	05	esio	7	/	8	0	5	2	
	92	n		1	9	2	2		
	5			9	E-	E-	E-		
				5	0	0	0		
				2	7	6	6		
				0					
C	G	cell-	18	4	1.	3.	2.	HMGA1/RPS2/CAV1/RPL4/RPS10/RPS11/	18
C	O:	sub	/	2	4	4	4	RPL10A/RPL7/FHL2/RDX/RPL13A/HSP90B	
	00	stra	18	3	2	2	3	1/ARPC1B/RPL3/CD59/TPM4/RPS9/CAPN	
	30	te	7	/	1	5	9	2	
	05	junc		1	6	6	3		
	5	tion		9	E-	E-	E-		
				5	0	0	0		
				2	7	6	6		
				0					
C	G	resp	9	8	1.	3.	2.	CYC1/NDUFAB1/NDUFB9/UQCRH/COX5	9
C	O:	irat	/	7	5	4	4	A/COX8A/NDUFS4/NDUFB5/NDUFC2	
	00	ory	18	/	1	2	3		
	98	chai	7	1	1	5	9		
	80	n		9	3	6	3		
	3	com		5	E-	E-	E-		

		plex	2	0	0	0			
			0	7	6	6			
C	G	euk	5	1	2.	4.	3.	EIF3K/EIF3E/EIF3D/EIF3F/EIF3L	5
C	O:	ary	/	5	1	5	2		
	00	otic	18	/	2	1	1		
	33	48S	7	1	4	5	5		
	29	prei		9	8	2	2		
	0	niti		5	E-	E-	E-		
		atio		2	0	0	0		
		n		0	7	6	6		
		com							
		plex							
C	G	euk	5	1	4.	8.	5.	EIF3K/EIF3E/EIF3D/EIF3F/EIF3L	5
C	O:	ary	/	7	3	1	7		
	00	otic	18	/	1	4	9		
	05	tran	7	1	0	2	8		
	85	slati		9	7	4	E-		
	2	on		5	E-	E-	0		
		initi		2	0	0	6		
		atio		0	7	6			
		n							
		fact							
		or 3							
		com							
		plex							
C	G	euk	5	1	4.	8.	5.	EIF3K/EIF3E/EIF3D/EIF3F/EIF3L	5
C	O:	ary	/	7	3	1	7		
	00	otic	18	/	1	4	9		

	16	43S	7	1	0	2	8		
	28	prei		9	7	4	E-		
	2	niti		5	E-	E-	0		
		atio		2	0	0	6		
		n		0	7	6			
		com							
		plex							
C	G	tran	5	1	5.	1.	7.	EIF3K/EIF3E/EIF3D/EIF3F/EIF3L	5
C	O:	slati	/	8	9	0	5		
	00	on	18	/	2	5	4		
	70	prei	7	1	2	9	6		
	99	niti		9	4	8	5		
	3	atio		5	E-	E-	E-		
		n		2	0	0	0		
		com		0	7	5	6		
		plex							
C	G	resp	9	1	6.	1.	7.	CYC1/NDUFAB1/NDUFB9/UQCRH/COX5	9
C	O:	iras	/	0	4	1	8	A/COX8A/NDUFS4/NDUFB5/NDUFC2	
	00	ome	18	3	8	0	4		
	70		7	/	4	2	9		
	46			1	E-	3	E-		
	9			9	0	E-	0		
				5	7	0	6		
				2		5			
				0					
C	G	cyto	7	5	1.	1.	1.	RPL4/RPL35/RPL23A/RPL10A/RPL7/RPL13	7
C	O:	solli	/	7	1	8	3	A/RPL3	
	00	c	18	/	6	9	4		

	22	larg	7	1	7	0	6		
	62	e		9	6	4	1		
	5	ribo		5	E-	E-	E-		
		som		2	0	0	0		
		al		0	6	5	5		
		sub							
		unit							
C	G	mit	8	8	1.	2.	1.	PRELID1/PARK7/STOML2/SOD1/NME4/T	8
C	O:	och	/	3	3	0	4	HOP1/BLOC1S1/CAPN2	
	00	ond	18	/	0	1	3		
	05	rial	7	1	4	6	5		
	75	inte		9	6	2	7		
	8	rme		5	E-	E-	E-		
		mbr		2	0	0	0		
		ane		0	6	5	5		
		spa							
		ce							
C	G	mit	8	8	2.	3.	2.	CYC1/NDUFAB1/NDUFB9/UQCRH/COX5	8
C	O:	och	/	9	2	2	3	A/NDUFS4/NDUFB5/NDUFC2	
	00	ond	18	/	2	8	4		
	05	rial	7	1	4	8	1		
	74	resp		9	5	4	6		
	6	iras		5	E-	E-	E-		
		ome		2	0	0	0		
				0	6	5	5		
C	G	org	8	9	3.	4.	3.	PRELID1/PARK7/STOML2/SOD1/NME4/T	8
C	O:	anel	/	3	1	3	1	HOP1/BLOC1S1/CAPN2	
	00	le	18	/	0	9	3		

	31	env	7	1	4	8	2		
	97	elop		9	9	6	1		
	0	e		5	E-	E-	E-		
		lum		2	0	0	0		
		en		0	6	5	5		
C	G	cyto	6	4	4.	6.	4.	RPS2/RPS10/MCTS1/RPS11/RPS20/RPS9	6
C	O:	sol	/	6	8	6	7		
	00	c	18	/	5	0	0		
	22	sma	7	1	9	8	6		
	62	ll		9	5	9	E-		
	7	ribo		5	E-	E-	0		
		som		2	0	0	5		
		al		0	6	5			
		sub							
		unit							
C	G	inne	9	1	9.	0.	8.	CYC1/NDUFAB1/NDUFB9/UQCRH/COX5	9
C	O:	r	/	4	3	0	7	A/NDUFS4/NDUFB5/NDUFC2/SLC25A6	
	00	mit	18	2	7	0	2		
	98	och	7	/	E-	0	5		
	80	ond		1	0	1	1		
	0	rial		9	6	2	E-		
		me		5		2	0		
		mbr		2		5	5		
		ane		0		3			
		prot							
		ein							
		com							
		plex							

C	G	secre	12	3	6.	0.	0.	HSP90AA1/HSP90AB1/GSTP1/COTL1/APR	12
C	O:	etor	/	2	7	0	0	T/ANXA2/ALDOA/GSDMD/SERPINB1/FA	
	00	y	18	2	1	0	0	BP5/FTL/S100A9	
	34	gra	7	/	7	0	0		
	77	nule		1	7	8	6		
	4	lum		9	E-	4	0		
		en		5	0	5	2		
				2	5	9	3		
				0		4	7		
C	G	cyto	12	3	7.	0.	0.	HSP90AA1/HSP90AB1/GSTP1/COTL1/APR	12
C	O:	plas	/	2	5	0	0	T/ANXA2/ALDOA/GSDMD/SERPINB1/FA	
	00	mic	18	6	5	0	0	BP5/FTL/S100A9	
	60	vesi	7	/	6	0	0		
	20	cle		1	1	9	6		
	5	lum		9	E-	1	5		
		en		5	0	7	3		
				2	5	5	3		
				0		3	5		
C	G	vesi	12	3	8.	0.	0.	HSP90AA1/HSP90AB1/GSTP1/COTL1/APR	12
C	O:	cle	/	2	0	0	0	T/ANXA2/ALDOA/GSDMD/SERPINB1/FA	
	00	lum	18	8	0	0	0	BP5/FTL/S100A9	
	31	en	7	/	8	0	0		
	98			1	1	9	6		
	3			9	E-	3	6		
				5	0	8	8		
				2	5	8	5		
				0		8	5		
C	G	oxid	7	1	9.	0.	0.	CYC1/NDUFAB1/NDUFB9/UQCRH/NDUF	7

C	O:	ore	/	1	7	0	0	S4/NDUFB5/NDUFC2
	19	duc	18	1	1	0	0	
	90	tase	7	/	2	1	0	
	20	com		1	9	1	7	
	4	plex		9	E-	0	8	
				5	0	0	3	
				2	5	7	8	
				0		9	5	
C	G	mit	5	5	0.	0.	0.	NDUFAB1/NDUFB9/NDUFS4/NDUFB5/ND 5
C	O:	och	/	0	0	0	0	UFC2
	00	ond	18	/	0	0	0	
	05	rial	7	1	0	1	0	
	74	resp		9	1	1	8	
	7	irat		5	1	7	3	
		ory		2	4	7	8	
		chai		0	2	0	1	
		n			5	9	8	
		com						
		plex						
		I						
C	G	NA	5	5	0.	0.	0.	NDUFAB1/NDUFB9/NDUFS4/NDUFB5/ND 5
C	O:	DH	/	0	0	0	0	UFC2
	00	deh	18	/	0	0	0	
	30	ydr	7	1	0	1	0	
	96	oge		9	1	1	8	
	4	nas		5	1	7	3	
		e		2	4	7	8	
		com		0	2	0	1	

		plex		5	9	8		
C	G	resp	5	5	0.	0.	0.	NDUFAB1/NDUFB9/NDUFS4/NDUFB5/ND 5
C	O:	irat	/	0	0	0	0	UFC2
	00	ory	18	/	0	0	0	
	45	chai	7	1	0	1	0	
	27	n		9	1	1	8	
	1	com		5	1	7	3	
		plex		2	4	7	8	
		I		0	2	0	1	
				5	9	8		
C	G	met	3	1	0.	0.	0.	SNRPB/PRMT1/SNRPE 3
C	O:	hyl	/	2	0	0	0	
	00	oso	18	/	0	0	0	
	34	me	7	1	0	1	1	
	70			9	1	7	2	
	9			5	7	8	7	
				2	8	6	1	
				0	6	0	7	
					3	9		
C	G	U4	3	1	0.	0.	0.	SNRPB/SNRPE/PRPF31 3
C	O:	snR	/	3	0	0	0	
	00	NP	18	/	0	0	0	
	05		7	1	0	2	1	
	68			9	2	2	5	
	7			5	3	3	9	
				2	0	9	4	
				0	5	6	7	
				5	2	8		

C	G	cyto	4	3	0.	0.	0.	CYC1/UQCRH/COX5A/COX8A	4
C	O:	chr	/	6	0	0	0		
	00	ome	18	/	0	0	0		
	70	com	7	1	0	3	2		
	06	plex		9	3	5	5		
	9			5	7	7	4		
				2	8	0	2		
				0	0	2	2		
				2	2	6			
C	G	end	5	6	0.	0.	0.	PSMA4/PSMA1/GPAA1/PSMD9/PSME1	5
C	O:	ope	/	8	0	0	0		
	19	ptid	18	/	0	0	0		
	05	ase	7	1	0	4	3		
	36	com		9	4	4	2		
	9	plex		5	8	9	0		
				2	9	4	0		
				0	1	8	6		
				4	4	6			
C	G	mel	6	1	0.	0.	0.	HSP90AA1/HSP90AB1/PRDX1/RAB5C/AN	6
C	O:	ano	/	0	0	0	0	XA2/HSP90B1	
	00	som	18	6	0	0	0		
	42	e	7	/	0	4	3		
	47			1	5	8	4		
	0			9	5	0	1		
				5	0	0	8		
				2	6	6	4		
				0	7	8	4		
C	G	pig	6	1	0.	0.	0.	HSP90AA1/HSP90AB1/PRDX1/RAB5C/AN	6

C	O:	men	/	0	0	0	0	XA2/HSP90B1	
	00	t	18	6	0	0	0		
	48	gra	7	/	0	4	3		
	77	nule		1	5	8	4		
	0			9	5	0	1		
				5	0	0	8		
				2	6	6	4		
				0	7	8	4		
C	G	cell	10	3	0.	0.	0.	ENO1/CAV1/COTL1/FSCN1/RHOD/ASPH	10
C	O:	cort	/	0	0	0	0	/RDX/KRT19/CAPN2/RHOC	
	00	ex	18	1	0	0	0		
	05		7	/	0	5	4		
	93			1	6	7	0		
	8			9	7	0	6		
				5	1	5	2		
				2	2	6	8		
				0	6	7	6		
C	G	ficol	6	1	0.	0.	0.	HSP90AA1/HSP90AB1/GSTP1/COTL1/ALD	6
C	O:	in-	/	2	0	0	0	OA/GSDMD	
	19	1-	18	4	0	1	0		
	04	rich	7	/	1	0	7		
	81	gra		1	2	3	3		
	3	nule		9	5	7	8		
		lum		5	1	6	8		
		en		2	2	2	6		
				0	5		3		
C	G	end	3	2	0.	0.	0.	REEP5/ASPH/RTN4	3
C	O:	opla	/	3	0	0	0		

	00	smi	18	/	0	1	0		
	71	c	7	1	1	0	7		
	78	retic		9	3	7	6		
	2	ulu		5	3	7	6		
		m		2	0	0	9		
		tub		0	4	2	2		
		ular			4	5	2		
		net							
		wor							
		k							
C	G	M	3	2	0.	0.	0.	ENO1/ALDOA/FHL2	3
C	O:	ban	/	4	0	0	0		
	00	d	18	/	0	1	0		
	31		7	1	1	1	8		
	43			9	5	9	5		
	0			5	0	3	0		
				2	9	8	0		
				0	8	3	9		
					5	4	9		
C	G	pep	5	9	0.	0.	0.	PSMA4/PSMA1/GPAA1/PSMD9/PSME1	5
C	O:	tida	/	2	0	0	0		
	19	se	18	/	0	1	1		
	05	com	7	1	1	4	0		
	36	plex		9	9	8	5		
	8			5	1	2	5		
				2	8	6	7		
				0	7	9	8		
					8	6	9		

C	G	ESC	3	2	0.	0.	0.	CHMP2A/CHMP4A/VPS28	3
C	O:	RT	/	7	0	0	0		
	00	com	18	/	0	1	1		
	36	plex	7	1	2	6	1		
	45			9	1	1	4		
	2			5	3	4	9		
				2	6	2	4		
				0	4	1	3		
					6	2	9		
C	G	fibri	6	1	0.	0.	0.	MRPL23/MTDH/UBE2N/POLR2F/TAX1BP3	6
C	O:	llar	/	3	0	0	0	/TXNRD1	
	00	cent	18	9	0	1	1		
	01	er	7	/	2	6	1		
	65			1	2	5	7		
	0			9	3	3	7		
				5	6	3	3		
				2	9	9	4		
				0	5	8	2		
C	G	org	3	2	0.	0.	0.	MRPS12/MRPL42/MRPS28	3
C	O:	anel	/	8	0	0	0		
	00	lar	18	/	0	1	1		
	00	sma	7	1	2	6	1		
	31	ll		9	3	8	9		
	4	ribo		5	7	3	8		
		som		2	6	0	4		
		al		0	0	6	6		
		sub			9	6	8		
		unit							

C	G	mit	3	2	0.	0.	0.	MRPS12/MRPL42/MRPS28	3
C	O:	och	/	8	0	0	0		
	00	ond	18	/	0	1	1		
	05	rial	7	1	2	6	1		
	76	sma		9	3	8	9		
	3	ll		5	7	3	8		
		ribo		2	6	0	4		
		som		0	0	6	6		
		al			9	6	8		
		sub							
		unit							
C	G	prot	4	6	0.	0.	0.	PSMA4/PSMA1/PSMD9/PSME1	4
C	O:	easo	/	2	0	0	0		
	00	me	18	/	0	2	1		
	00	com	7	1	2	0	4		
	50	plex		9	9	4	5		
	2			5	5	7	7		
				2	0	4	9		
				0	8	9	6		
						2	6		
C	G	pri	6	1	0.	0.	0.	NDUFC2/MGST1/RAB5C/ANXA2/FABP5/F	6
C	O:	mar	/	5	0	0	0	TL	
	00	y	18	5	0	2	1		
	05	lyso	7	/	3	5	8		
	76	som		1	8	5	1		
	6	e		9	3	3	8		
				5	8	5	2		
				2	6	2	9		

				0	4	4	9		
C	G	azu	6	1	0.	0.	0.	NDUFC2/MGST1/RAB5C/ANXA2/FABP5/F	6
C	O:	rop	/	5	0	0	0	TL	
		00	hil	18	5	0	2	1	
		42	gra	7	/	3	5	8	
		58	nule		1	8	5	1	
		2			9	3	3	8	
					5	8	5	2	
					2	6	2	9	
					0	4	4	9	
C	G	AP-	2	1	0.	0.	0.	AP2M1/AP2S1	2
C	O:	2	/	0	0	0	0		
		00	ada	18	/	0	2	1	
		30	ptor	7	1	3	5	8	
		12	com		9	9	5	1	
		2	plex		5	0	3	8	
					2	5	5	2	
					0	3	2	9	
					9	4	9		
C	G	ESC	2	1	0.	0.	0.	CHMP2A/CHMP4A	2
C	O:	RT	/	1	0	0	0		
		00	III	18	/	0	2	2	
		00	com	7	1	4	9	1	
		81	plex		9	7	8	2	
		5			5	4	6	6	
					2	3	5	6	
					0	2	0	1	
					8	7	5		

C	G	clat	2	1	0.	0.	0.	AP2M1/AP2S1	2
C	O:	hrin	/	1	0	0	0		
	00	coat	18	/	0	2	2		
	30	of	7	1	4	9	1		
	12	end		9	7	8	2		
	8	ocyt		5	4	6	6		
		ic		2	3	5	6		
		vesi		0	2	0	1		
		cle			8	7	5		
C	G	A	3	3	0.	0.	0.	ENO1/ALDOA/FHL2	3
C	O:	ban	/	7	0	0	0		
	00	d	18	/	0	3	2		
	31		7	1	5	2	3		
	67			9	2	7	2		
	2			5	9	1	9		
				2	1	0	2		
				0	3	0			
				3	6				
C	G	clat	3	3	0.	0.	0.	AP2M1/AP2S1/HBEGF	3
C	O:	hrin	/	9	0	0	0		
	00	-	18	/	0	3	2		
	30	coat	7	1	6	7	6		
	66	ed		9	1	2	5		
	9	end		5	3	6	3		
		ocyt		2	7	1	3		
		ic		0	2	9	3		
		vesi			7	8			
		cle							

		me								
		mbr								
		ane								
C	G	RN	2	1	0.	0.	0.	POLR2E/POLR2F		2
C	O:	A	/	3	0	0	0			
	00	pol	18	/	0	3	2			
	05	yme	7	1	6	8	7			
	73	rase		9	6	6	5			
	6	I		5	4	3	1			
		com		2	2	5	1			
		plex		0	6	0	0			
					9	5	3			
C	G	den	2	1	0.	0.	0.	HSP90AA1/HSP90AB1		2
C	O:	drit	/	3	0	0	0			
	00	e	18	/	0	3	2			
	44	ter	7	1	6	8	7			
	29	min		9	6	6	5			
	2	us		5	4	3	1			
				2	2	5	1			
				0	6	0	0			
					9	5	3			
C	G	cort	4	7	0.	0.	0.	COTL1/RDX/KRT19/CAPN2		4
C	O:	ical	/	8	0	0	0			
	00	acti	18	/	0	3	2			
	30	n	7	1	6	8	7			
	86	cyto		9	7	6	5			
	4	skel		5	0	3	1			
		eton		2	4	5	1			

				0	3	0	0		
					2	5	3		
C	G	U4/	3	4	0.	0.	0.	SNRPB/SNRPE/PRPF31	3
C	O:	U6	/	1	0	0	0		
	00	x	18	/	0	4	2		
	46	U5	7	1	7	0	8		
	54	tri-		9	0	0	4		
	0	snR		5	5	0	8		
		NP		2	9	3	5		
		com		0	4	6	5		
		plex			6	1	4		
C	G	spli	3	4	0.	0.	0.	SNRPB/SNRPE/PRPF31	3
C	O:	ceos	/	2	0	0	0		
	00	oma	18	/	0	4	2		
	97	l tri-	7	1	7	1	9		
	52	snR		9	5	5	5		
	6	NP		5	4	6	9		
		com		2	9	2	5		
		plex		0	6	3	4		
					6		5		
C	G	mit	2	1	0.	0.	0.	CYC1/UQCRH	2
C	O:	och	/	4	0	0	0		
	00	ond	18	/	0	4	2		
	05	rial	7	1	7	1	9		
	75	resp		9	7	5	5		
	0	irat		5	0	6	9		
		ory		2	1	2	5		
		chai		0	2	3	4		

		n		5	5				
		com							
		plex							
		III							
C	G	resp	2	1	0.	0.	0.	CYC1/UQCRH	2
C	O:	irat	/	4	0	0	0		
	00	ory	18	/	0	4	2		
	45	chai	7	1	7	1	9		
	27	n		9	7	5	5		
	5	com		5	0	6	9		
		plex		2	1	2	5		
		III		0	2	3	4		
				5		5			
C	G	nucl	3	4	0.	0.	0.	SLC25A5/HSD17B10/VDAC2	3
C	O:	eoid	/	4	0	0	0		
	00		18	/	0	4	3		
	09		7	1	8	4	1		
	29			9	5	6	7		
	5			5	8	3	8		
				2	9	4	3		
				0	1	8	3		
				7	1				
C	G	mit	3	4	0.	0.	0.	SLC25A5/HSD17B10/VDAC2	3
C	O:	och	/	4	0	0	0		
	00	ond	18	/	0	4	3		
	42	rial	7	1	8	4	1		
	64	nucl		9	5	6	7		
	5	eoid		5	8	3	8		

				2	9	4	3			
				0	1	8	3			
					7	1				
C	G	vac	10	4	0.	0.	0.	AP2M1/AP2S1/HSP90AB1/NDUFC2/MGST	10	
C	O:	uola	/	3	0	0	0	1/RAB5C/LAPTM4B/ATP6V0B/ANXA2/BL		
	00	r	18	1	0	4	3	OC1S1		
	05	me	7	/	8	4	1			
	77	mbr		1	8	6	7			
	4	ane		9	2	3	8			
				5	1	4	3			
				2	1	8	3			
				0	5	1				
C	G	RN	2	1	0.	0.	0.	POLR2E/POLR2F	2	
C	O:	A	/	5	0	0	0			
	00	pol	18	/	0	4	3			
	05	yme	7	1	8	4	1			
	66	rase		9	8	6	7			
	5	II,		5	3	3	8			
		core		2	0	4	3			
		com		0	4	8	3			
		plex			2	1				
C	G	ficol	6	1	0.	0.	0.	HSP90AA1/HSP90AB1/GSTP1/COTL1/ALD	6	
C	O:	in-	/	8	0	0	0	OA/GSDMD		
	01	1-	18	5	0	4	3			
	01	rich	7	/	8	4	1			
	00	gra		1	9	6	7			
	2	nule		9	2	3	8			
				5	6	4	3			

				2	9	8	3		
				0	6	1			
C	G	end	8	3	0.	0.	0.	HSP90AA1/AP2M1/AP2S1/CAV1/RAB5C/	8
C	O:	ocyt	/	0	0	0	0	ATP6V0B/HBEGF/HSP90B1	
	00	ic	18	7	0	4	3		
	30	vesi	7	/	9	7	3		
	13	cle		1	6	3	7		
	9			9	7	5	2		
				5	8	8	2		
				2	7	0	4		
				0	6	9	8		
C	G	clat	2	1	0.	0.	0.	AP2M1/AP2S1	2
C	O:	hrin	/	6	0	0	0		
	00	coat	18	/	1	4	3		
	30	of	7	1	0	7	3		
	13	coat		9	0	3	7		
	2	ed		5	2	5	2		
		pit		2	8	8	2		
				0	7	0	4		
				7	9	8			
C	G	end	2	1	0.	0.	0.	AP2M1/AP2S1	2
C	O:	olys	/	6	0	0	0		
	00	oso	18	/	1	4	3		
	36	me	7	1	0	7	3		
	02	me		9	0	3	7		
	0	mbr		5	2	5	2		
		ane		2	8	8	2		
				0	7	0	4		

				7	9	8			
C	G	sper	2	1	0.	0.	0.	HSP90AB1/ALDOA	2
C	O:	m	/	6	0	0	0		
	00	hea	18	/	1	4	3		
	61	d	7	1	0	7	3		
	82			9	0	3	7		
	7			5	2	5	2		
				2	8	8	2		
				0	7	0	4		
				7	9	8			
C	G	lyso	9	3	0.	0.	0.	AP2M1/AP2S1/HSP90AB1/NDUFC2/MGST	9
C	O:	som	/	7	0	0	0	1/RAB5C/LAPTM4B/ANXA2/BLOC1S1	
	00	al	18	8	1	4	3		
	05	me	7	/	0	9	5		
	76	mbr		1	8	9	5		
	5	ane		9	6	3	5		
				5	7	1	5		
				2	4	6	0		
				0	7	1	1		
C	G	lytic	9	3	0.	0.	0.	AP2M1/AP2S1/HSP90AB1/NDUFC2/MGST	9
C	O:	vac	/	7	0	0	0	1/RAB5C/LAPTM4B/ANXA2/BLOC1S1	
	00	uole	18	8	1	4	3		
	98	me	7	/	0	9	5		
	85	mbr		1	8	9	5		
	2	ane		9	6	3	5		
				5	7	1	5		
				2	4	6	0		
				0	7	1	1		

C	G	late	5	1	0.	0.	0.	CHMP2A/LAPTM4B/ANXA2/CHMP4A/VP	5
C	O:	end	/	4	0	0	0	S28	
	00	oso	18	0	1	5	3		
	31	me	7	/	1	1	6		
	90	me		1	2	1	4		
	2	mbr		9	8	4	1		
		ane		5	2	5	9		
				2		0	0		
				0		5	8		
C	G	me	4	9	0.	0.	0.	AP2M1/AP2S1/CHMP2A/CHMP4A	4
C	O:	mbr	/	2	0	0	0		
	00	ane	18	/	1	5	3		
	30	coat	7	1	1	2	7		
	11			9	8	3	2		
	7			5	4	1	5		
				2	8	8	4		
				0	6	6	7		
				4	6	7			
C	G	coat	4	9	0.	0.	0.	AP2M1/AP2S1/CHMP2A/CHMP4A	4
C	O:	ed	/	2	0	0	0		
	00	me	18	/	1	5	3		
	48	mbr	7	1	1	2	7		
	47	ane		9	8	3	2		
	5			5	4	1	5		
				2	8	8	4		
				0	6	6	7		
				4	6	7			
C	G	U2-	3	5	0.	0.	0.	SNRPB/SNRPE/PRPF31	3

C	O:	type	/	0	0	0	0		
	00	prec	18	/	1	5	3		
	71	atal	7	1	2	3	7		
	00	ytic		9	1	1	8		
	5	spli		5	9	4	4		
		ceos		2	1	3	1		
		ome		0	6	1	8		
					5		3		
C	G	RN	2	1	0.	0.	0.	POLR2E/POLR2F	2
C	O:	A	/	8	0	0	0		
	00	pol	18	/	1	5	3		
	05	yme	7	1	2	4	8		
	66	rase		9	6	3	6		
	6	III		5	2	4	9		
		com		2	7	5	8		
		plex		0	3	6	1		
					8	8	6		
C	G	lipi	4	9	0.	0.	0.	CAV1/RAB5C/ANXA2/CES1	4
C	O:	d	/	5	0	0	0		
	00	dro	18	/	1	5	3		
	05	plet	7	1	3	6	9		
	81			9	2	1	9		
	1			5	0	2	6		
				2	6	6	6		
				0	2	6	3		
					6	2	3		
C	G	met	4	9	0.	0.	0.	SNRPB/PRMT1/SNRPE/PRPF31	4
C	O:	hylv	/	6	0	0	0		

	00	rans	18	/	1	5	4		
	34	fera	7	1	3	7	0		
	70	se		9	6	4	8		
	8	com		5	7	2	8		
		plex		2	9	1	8		
				0	8	7	5		
					9	5	5		
C	G	SM	2	1	0.	0.	0.	SNRPB/SNRPE	2
C	O:	N-	/	9	0	0	0		
	00	Sm	18	/	1	5	4		
	34	prot	7	1	4	8	1		
	71	ein		9	0	1	4		
	9	com		5	2	5	0		
		plex		2	4	1	8		
				0	8	8	4		
					7	8	6		
C	G	prec	3	5	0.	0.	0.	SNRPB/SNRPE/PRPF31	3
C	O:	atal	/	3	0	0	0		
	00	ytic	18	/	1	5	4		
	71	spli	7	1	4	8	1		
	01	ceos		9	2	4	6		
	1	ome		5	7	6	2		
				2	1	0	8		
				0	2	4	2		
					4	8	1		
C	G	prot	2	2	0.	0.	0.	PSMA4/PSMA1	2
C	O:	easo	/	0	0	0	0		
	00	me	18	/	1	6	4		

	05	core	7	1	5	1	4		
	83	com		9	4	9	1		
	9	plex		5	8	4	0		
				2	6	3	8		
				0		9	7		
						8	2		
C	G	end	2	2	0.	0.	0.	HSP90AA1/HSP90B1	2
C	O:	ocyt	/	0	0	0	0		
	00	ic	18	/	1	6	4		
	71	vesi	7	1	5	1	4		
	68	cle		9	4	9	1		
	2	lum		5	8	4	0		
		en		2	6	3	8		
				0		9	7		
						8	2		
C	G	clat	3	5	0.	0.	0.	AP2M1/AP2S1/HBEGF	3
C	O:	hrin	/	7	0	0	0		
	00	-	18	/	1	6	4		
	45	coat	7	1	7	8	8		
	33	ed		9	3	5	8		
	4	end		5	3	4	0		
		ocyt		2	8	5	9		
		ic		0	0	8	7		
		vesi			8	9	7		
		cle							
C	G	cort	4	1	0.	0.	0.	COTL1/RDX/KRT19/CAPN2	4
C	O:	ical	/	0	0	0	0		
	00	cyto	18	4	1	6	4		

		30	skel	7	/	7	9	9		
		86	eton			1	8	7	6	
		3				9	5	9	9	
						5	9	4	8	
						2	1	4	8	
						0	6	3	2	
C	G	azu	3	5	0.	0.	0.	NDUFC2/MGST1/RAB5C		3
C	O:	rop	/	8	0	0	0			
		00	hil	18	/	1	7	4		
		35	gra	7	1	8	0	9		
		57	nule		9	1	1	9		
		7	me		5	5	5	5		
			mbr		2	7	4	5		
			ane		0	7	7	3		
							4	9		
C	G	telo	2	2	0.	0.	0.	SNRPB/SNRPE		2
C	O:	mer	/	2	0	0	0			
		00	ase	18	/	1	7	5		
		05	holo	7	1	8	0	0		
		69	enz		9	5	2	0		
		7	yme		5	9	4	1		
			com		2	3	3	8		
			plex		0	8	5	6		
						7	2			
C	G	resp	2	2	0.	0.	0.	COX5A/COX8A		2
C	O:	irat	/	2	0	0	0			
		00	ory	18	/	1	7	5		
		45	chai	7	1	8	0	0		

	27	n		9	5	2	0		
	7	com		5	9	4	1		
		plex		2	3	3	8		
		IV		0	8	5	6		
					7	2			
C	G	U5	2	2	0.	0.	0.	SNRPB/SNRPE	2
C	O:	snR	/	3	0	0	0		
	00	NP	18	/	2	7	5		
	05		7	1	0	5	3		
	68			9	2	6	8		
	2			5	3	1	4		
				2	8	4	3		
				0	0	5	1		
					1	4	7		
C	G	end	5	1	0.	0.	0.	AP2M1/ AP2S1/CAV1/ATP6V0B/HBEGF	5
C	O:	ocyt	/	6	0	0	0		
	00	ic	18	3	2	7	5		
	30	vesi	7	/	0	5	3		
	66	cle		1	4	7	9		
	6	me		9	9	3	3		
		mbr		5	3	8	1		
		ane		2	9	4	4		
				0	4	9	3		
C	G	mul	3	6	0.	0.	0.	CHMP2A/LAPTM4B/CHMP4A	3
C	O:	tive	/	2	0	0	0		
	00	sicu	18	/	2	7	5		
	05	lar	7	1	1	7	5		
	77	bod		9	6	7	3		

	1	y		5	4	0	3		
				2	8	6	2		
				0	8	1	5		
					8	8	7		
C	G	prot	2	2	0.	0.	0.	PSMD9/PSME1	2
C	O:	easo	/	4	0	0	0		
	00	me	18	/	2	7	5		
	22	acce	7	1	1	7	5		
	62	ssor		9	9	7	3		
	4	y		5	4	0	3		
		com		2	0	6	2		
		plex		0	5	1	5		
					7	8	7		
C	G	clat	2	2	0.	0.	0.	AP2M1/AP2S1	2
C	O:	hrin	/	4	0	0	0		
	00	ada	18	/	2	7	5		
	30	ptor	7	1	1	7	5		
	13	com		9	9	7	3		
	1	plex		5	4	0	3		
				2	0	6	2		
				0	5	1	5		
					7	8	7		
C	G	end	2	2	0.	0.	0.	AP2M1/AP2S1	2
C	O:	olys	/	4	0	0	0		
	00	oso	18	/	2	7	5		
	36	me	7	1	1	7	5		
	01			9	9	7	3		
	9			5	4	0	3		

				2	0	6	2		
				0	5	1	5		
				7	8	7			
C	G	U2	2	2	0.	0.	0.	SNRPB/SNRPE	2
C	O:	snR	/	5	0	0	0		
	00	NP	18	/	2	8	5		
	05		7	1	3	3	9		
	68			9	7	0	1		
	6			5	0	7	5		
				2	0	3	4		
				0	2	2	2		
				9			9		
C	G	clat	2	2	0.	0.	0.	AP2M1/AP2S1	2
C	O:	hrin	/	8	0	0	0		
	00	vesi	18	/	2	9	7		
	30	cle	7	1	9	9	0		
	12	coat		9	3	6	9		
	5			5	1	5	6		
				2	0	4	1		
				0	1	5	4		
				7	8	6			
C	G	den	2	2	0.	0.	0.	SOD1/SYT8	2
C	O:	se	/	8	0	0	0		
	00	core	18	/	2	9	7		
	31	gra	7	1	9	9	0		
	04	nule		9	3	6	9		
	5			5	1	5	6		
				2	0	4	1		

				0	1	5	4		
					7	8	6		
C	G	axo	2	2	0.	0.	0.	HSP90AA1/HSP90AB1	2
C	O:	nal	/	8	0	0	0		
	00	gro	18	/	2	9	7		
	44	wth	7	1	9	9	0		
	29	con		9	3	6	9		
	5	e		5	1	5	6		
				2	0	4	1		
				0	1	5	4		
					7	8	6		
C	G	U12	2	2	0.	0.	0.	SNRPB/SNRPE	2
C	O:	-	/	9	0	1	0		
	00	type	18	/	3	0	7		
	05	spli	7	1	1	5	4		
	68	ceos		9	2	3	9		
	9	oma		5	8	2	9		
		l		2	6	0	5		
		com		0	3	3	9		
		plex			5	9	4		
C	G	U2-	2	3	0.	0.	0.	SNRPB/SNRPE	2
C	O:	type	/	0	0	1	0		
	00	cata	18	/	3	1	7		
	71	lytic	7	1	3	1	9		
	00	step		9	3	0	0		
	7	2		5	1	4	7		
		spli		2	3	5	2		
		ceos		0	6	6	7		

		ome			8	1	2		
C	G	me	7	3	0.	0.	0.	SLC25A5/PARK7/CAV1/STOML2/ANXA2/	7
C	O:	mbr	/	2	0	1	0	EFHD2/CAPN2	
		00	ane	18	3	3	1	8	
		45	raft	7	/	6	8	4	
		12			1	3	9	7	
		1			9	9	9	3	
					5	8	4	3	
					2	4	8	1	
					0	2	2	5	
C	G	me	7	3	0.	0.	0.	SLC25A5/PARK7/CAV1/STOML2/ANXA2/	7
C	O:	mbr	/	2	0	1	0	EFHD2/CAPN2	
		00	ane	18	3	3	1	8	
		98	mic	7	/	6	8	4	
		85	rod		1	3	9	7	
		7	oma		9	9	9	3	
			in		5	8	4	3	
					2	4	8	1	
					0	2	2	5	
C	G	U1	2	3	0.	0.	0.	SNRPB/SNRPE	2
C	O:	snR	/	3	0	1	0		
		00	NP	18	/	3	2	9	
		05		7	1	9	7	1	
		68			9	6	9	1	
		5			5	9	8	3	
					2	1	3	4	
					0	1	8		
					7	3			

C	G	mit	5	1	0.	0.	0.	NME1/CISD1/VDAC2/MGST1/TOMM7	5
C	O:	och	/	9	0	1	0		
	00	ond	18	5	3	2	9		
	05	rial	7	/	9	7	1		
	74	oute		1	9	9	1		
	1	r		9	0	8	3		
		me		5	0	3	4		
		mbr		2	8	8			
		ane		0	4	3			
C	G	per	4	1	0.	0.	0.	TKT/MGST1/SOD1/ECH1	4
C	O:	oxis	/	3	0	1	0		
	00	ome	18	6	4	3	9		
	05		7	/	1	2	4		
	77			1	9	1	0		
	7			9	7	3	9		
				5	3	8	2		
				2	4	7	6		
				0	8	4			
C	G	mic	4	1	0.	0.	0.	TKT/MGST1/SOD1/ECH1	4
C	O:	rob	/	3	0	1	0		
	00	ody	18	6	4	3	9		
	42		7	/	1	2	4		
	57			1	9	1	0		
	9			9	7	3	9		
				5	3	8	2		
				2	4	7	6		
				0	8	4			
C	G	sarc	5	2	0.	0.	0.	ENO1/ALDOA/FHL2/TPM4/KRT19	5

C	O:	ome	/	0	0	1	1		
	00	re	18	3	4	4	0		
	30		7	/	6	3	2		
	01			1	0	6	2		
	7			9	5	4	8		
				5	1	6	6		
				2	2		6		
				0	2		2		
C	G	CO	2	3	0.	0.	0.	HSP90AB1/STOML2	2
C	O:	P9	/	6	0	1	1		
	00	sign	18	/	4	4	0		
	08	alos	7	1	6	3	2		
	18	ome		9	4	6	3		
	0			5	8	9	1		
				2	8	2	9		
				0	6	1	4		
					3	2	7		
M	G	stru	20	1	1.	7.	6.	MRPL12/MRPL47/MRPS12/RPS2/MRPL13/	20
F	O:	ctur	/	8	8	4	0	MRPL23/RPL4/MRPL42/RPS10/MRPL15/R	
	00	al	18	0	2	2	0	PL35/RPL23A/MRPL28/RPS11/RPS20/RPL1	
	03	con	5	/	7	1	3	0A/RPL7/RPL13A/RPL3/RPS9	
	73	stit		1	9	4	3		
	5	uen		8	E-	E-	E-		
		t of		3	1	1	1		
		ribo		3	5	3	3		
		som		7					
		e							
M	G	anti	11	8	1.	2.	1.	GSTO1/PARK7/PRDX1/GSTP1/TXN/GPX3/	11

F	O:	oxid	/	6	0	1	7	MGST1/NQO1/SOD1/TXNRD1/S100A9	
	00	ant	18	/	3	0	0		
	16	acti	5	1	7	5	3		
	20	vity		8	3	7	3		
	9			3	E-	E-	E-		
				3	0	0	0		
				7	9	7	7		
M	G	oxid	12	1	3.	4.	3.	MDH2/HSD17B10/AKR1B10/AKR1C3/LDH	12
F	O:	ore	/	2	1	2	4	A/AKR1C1/PTGR1/G6PD/AKR1C2/PGD/A	
	00	duc	18	0	7	9	7	LDH3A1/UGDH	
	16	tase	5	/	6	8	7		
	61	acti		1	5	9	4		
	6	vity		8	E-	E-	E-		
		,		3	0	0	0		
		acti		3	9	7	7		
		ng		7					
		on							
		the							
		CH-							
		OH							
		gro							
		up							
		of							
		don							
		ors,							
		NA							
		D or							
		NA							

as

		acce							
		ptor							
M	G	cad	17	3	4.	2.	2.	ENO1/HSP90AB1/PUF60/LDHA/RPS2/PAR	17
F	O:	heri	/	3	7	7	2	K7/PRDX1/FSCN1/EIF3E/SFN/RPL23A/A	
		00 n	18	2	0	2	0	NXA2/EFHD2/ALDOA/RDX/PKP3/RTN4	
		45 bin	5	/	6	9	7		
		29 din		1	E-	5	9		
		6 g		8	0	E-	E-		
				3	8	0	0		
				3		6	6		
				7					
M	G	tran	7	5	7.	3.	3.	EIF3K/EIF4A1/EIF3E/MCTS1/EIF3D/EIF3F/	7
F	O:	slati	/	1	5	8	1	EIF3L	
		00 on	18	/	5	3	0		
		03 initi	5	1	7	5	2		
		74 atio		8	7	5	6		
		3 n		3	E-	E-	E-		
		fact		3	0	0	0		
		or		7	7	5	5		
		acti							
		vity							
M	G	alco	5	2	1.	7.	6.	AKR1B10/ AKR1C3/ AKR1C1/ AKR1C2/ALD	5
F	O:	hol	/	1	7	9	4	H3A1	
		00 deh	18	/	6	7	4		
		08 ydr	5	1	7	2	9		
		10 oge		8	3	7	2		
		6 nas		3	E-	E-	E-		
		e		3	0	0	0		

		(NA	7	6	5	5			
		DP							
		+)							
		acti							
		vity							
M	G	aldi	4	1	4.	0.	0.	AKR1B10/ AKR1C3/ AKR1C1/ AKR1C2	4
F	O:	tol:	/	2	6	0	0		
	00	NA	18	/	6	0	0		
	04	DP	5	1	0	0	0		
	03	+ 1-		8	4	1	1		
	2	oxid		3	E-	8	5		
		ore		3	0	9	3		
		duc		7	6	2	0		
		tase				1	6		
		acti							
		vity							
M	G	oxid	5	2	5.	0.	0.	AKR1C3/ AKR1C1/ PTGR1/ AKR1C2/ DECR1	5
F	O:	ore	/	6	4	0	0		
	00	duc	18	/	8	0	0		
	16	tase	5	1	3	0	0		
	62	acti		8	9	2	1		
	8	vity		3	E-	0	6		
		,		3	0	2	3		
		acti		7	6	4	7		
		ng				1	3		
		on							
		the							
		CH-							

		3	acid	3	E-	2	8	
			bin	3	0	8	5	
			din	7	6	7	0	
			g			8	7	
M	G	NA	6	4	8.	0.	0.	NDUFAB1/NDUFB9/NDUFS4/NDUFB5/ND 6
F	O:	D(P	/	8	3	0	0	UFC2/NQO1
		00)H	18	/	9	0	0	
		03 deh	5	1	1	0	0	
		95 ydr		8	7	2	1	
		5 oge		3	E-	4	9	
		nas		3	0	3	6	
		e		7	6	3	8	
		(qui				6	6	
		non						
		e)						
		acti						
		vity						
M	G	elec	9	1	1.	0.	0.	NDUFAB1/NDUFB9/UQCRH/COX5A/COX 9
F	O:	tron	/	3	1	0	0	8A/NDUFS4/NDUFB5/NDUFC2/ ASPH
		00 tran	18	8	1	0	0	
		09 sfer	5	/	7	0	0	
		05 acti		1	3	3	2	
		5 vity		8	E-	0	4	
				3	0	2	4	
				3	5	4	6	
				7		1	2	
M	G	tran	7	8	2.	0.	0.	EIF3K/EIF4A1/EIF3E/MCTS1/EIF3D/EIF3F/ 7
F	O:	slati	/	4	2	0	0	EIF3L

		00	on	18	/	3	0	0		
		08	fact	5	1	4	0	0		
		13	or		8	7	5	4		
		5	acti		3	E-	6	5		
			vity		3	0	7	8		
			,		7	5	0	6		
			RN				5	9		
			A							
			bin							
			din							
			g							
M	G	estr	4	1	2.	0.	0.		HSD17B10/AKR1C3/AKR1C1/AKR1C2	4
F	O:	adio	/	8	7	0	0			
		00 l 17-	18	/	4	0	0			
		04 beta	5	1	7	0	0			
		30 -		8	5	6	5			
		3 deh		3	E-	5	3			
		ydr		3	0	6	0			
		oge		7	5	1	7			
		nas				7	9			
		e								
		acti								
		vity								
M	G	tran	8	1	8.	0.	0.		EIF3K/EIF4A1/EIF3E/MCTS1/EIF3D/EIF3F/	8
F	O:	slati	/	3	0	0	0		EIF3L/RPS9	
		00 on	18	8	1	0	0			
		45 reg	5	/	5	1	1			
		18 ulat		1	3	6	3			

	2	or		8	E-	8	6	
		acti		3	0	6	3	
		vity		3	5	1	9	
				7		4	5	
M	G	NA	5	4	8.	0.	0.	NDUFAB1/NDUFB9/NDUFS4/NDUFB5/ND 5
F	O:	DH	/	5	7	0	0	UFC2
	00	deh	18	/	2	0	0	
	03	ydr	5	1	1	1	1	
	95	oge		8	4	6	3	
	4	nas		3	E-	8	6	
		e		3	0	6	3	
		acti		7	5	1	9	
		vity				4	5	
M	G	NA	5	4	8.	0.	0.	NDUFAB1/NDUFB9/NDUFS4/NDUFB5/ND 5
F	O:	DH	/	5	7	0	0	UFC2
	00	deh	18	/	2	0	0	
	08	ydr	5	1	1	1	1	
	13	oge		8	4	6	3	
	7	nas		3	E-	8	6	
		e		3	0	6	3	
		(ubi		7	5	1	9	
		qui				4	5	
		non						
		e)						
		acti						
		vity						
M	G	NA	5	4	8.	0.	0.	NDUFAB1/NDUFB9/NDUFS4/NDUFB5/ND 5
F	O:	DH	/	5	7	0	0	UFC2

		00	deh	18	/	2	0	0	
		50	ydr	5	1	1	1	1	
		13	oge		8	4	6	3	
		6	nas		3	E-	8	6	
			e		3	0	6	3	
			(qui		7	5	1	9	
			non				4	5	
			e)						
			acti						
			vity						
M	G	tran	7	1	0.	0.	0.	EIF3K/EIF4A1/EIF3E/MCTS1/EIF3D/EIF3F/	7
F	O:	slati	/	0	0	0	0	EIF3L	
		00	on	18	8	0	0	0	
		90	reg	5	/	0	2	1	
		07	ulat		1	1	0	6	
		9	or		8	1	3	4	
			acti		3	2	1	3	
			vity		3	2	5	3	
			,		7	9	1	3	
			nucl						
			eic						
			acid						
			bin						
			din						
			g						
M	G	test	3	1	0.	0.	0.	HSD17B10/AKR1C3/AKR1C1	3
F	O:	oste	/	0	0	0	0		
		00	ron	18	/	0	0	0	

		30	e	5	1	0	2	1		
		28	deh		8	1	0	6		
		3	ydr		3	1	3	4		
			oge		3	5	1	3		
			nas		7	0	5	3		
			e			9	1	3		
			[NA							
			D(P							
			)]							
			acti							
			vity							
M	G	bile	3	1	0.	0.	0.	AKR1C3/AKR1C1/AKR1C2		3
F	O:	acid	/	1	0	0	0			
	00	bin	18	/	0	0	0			
	32	din	5	1	0	2	2			
	05	g		8	1	5	0			
	2			3	5	5	6			
				3	7	0	3			
				7	0	7	3			
				7	9	8				
M	G	card	3	1	0.	0.	0.	STOML2/NME4/GSDMD		3
F	O:	ioli	/	1	0	0	0			
	19	pin	18	/	0	0	0			
	01	bin	5	1	0	2	2			
	61	din		8	1	5	0			
	2	g		3	5	5	6			
				3	7	0	3			
				7	0	7	3			

			7	9	8				
M	G	ster	4	3	0.	0.	0.	HSD17B10/AKR1C3/AKR1C1/AKR1C2	4
F	O:	oid	/	0	0	0	0		
	00	deh	18	/	0	0	0		
	33	ydr	5	1	0	3	2		
	76	oge		8	2	4	8		
	4	nas		3	2	9	2		
		e		3	3	5	7		
		acti		7	8	5	5		
		vity			5	2	9		
		,							
		acti							
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		on							
		the							
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		don							
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		NA							
		D or							
		NA							
		DP							
		as							
		acce							

			ptor							
M	G	oxid	5	5	0.	0.	0.	PARK7/PRDX1/GSTP1/GPX3/MGST1		5
F	O:	ore	/	7	0	0	0			
	00	duc	18	/	0	0	0			
	16	tase	5	1	0	4	3			
	68	acti		8	2	0	2			
	4	vity		3	7	7	9			
		,		3	1	6	7			
		acti		7	0	1	2			
		ng			7	5	7			
		on								
		per								
		oxid								
		e as								
		acce								
		ptor								
M	G	oxid	5	5	0.	0.	0.	AKR1C3/AKR1C1/PTGR1/AKR1C2/DECR1		5
F	O:	ore	/	9	0	0	0			
	00	duc	18	/	0	0	0			
	16	tase	5	1	0	4	3			
	62	acti		8	3	6	7			
	7	vity		3	1	2	4			
		,		3	8	3	0			
		acti		7	8	8	3			
		ng			9	6	3			
		on								
		the								
		CH-								

		CH								
		gro								
		up								
		of								
		don								
		ors								
M	G	ster	4	3	0.	0.	0.	HSD17B10/AKR1C3/AKR1C1/AKR1C2		4
F	O:	oid	/	4	0	0	0			
	00	deh	18	/	0	0	0			
	16	ydr	5	1	0	5	4			
	22	oge		8	3	1	1			
	9	nas		3	6	3	5			
		e		3	7	9	7			
		acti		7	0	1	1			
		vity			8	1	2			
M	G	pho	3	1	0.	0.	0.	STOML2/NME4/GSDMD		3
F	O:	sph	/	5	0	0	0			
	19	atid	18	/	0	0	0			
	01	ylgl	5	1	0	5	4			
	61	ycer		8	4	6	6			
	1	ol		3	2	8	0			
		bin		3	0	9	2			
		din		7	4	7	5			
		g			3	9	7			
M	G	fatt	4	3	0.	0.	0.	NDUFAB1/GSTP1/FABP5/S100A9		4
F	O:	y	/	7	0	0	0			
	00	acid	18	/	0	0	0			
	05	bin	5	1	0	6	5			

		50	din		8	5	6	4			
		4	g		3	1	8	0			
					3	0	7	9			
					7	5	0	2			
						9	4	8			
M	G	disu	4	4	0.	0.	0.		GSTO1/TXN/TXN2/TXNRD1		4
F	O:	lfid	/	0	0	0	0				
	00	e	18	/	0	0	0				
	15	oxid	5	1	0	8	7				
	03	ore		8	6	7	0				
	6	duc		3	9	5	8				
		tase		3	0	5	2				
		acti		7	0	4	4				
		vity			8	4	4				
M	G	prot	3	2	0.	0.	0.		TXN/TXN2/TXNRD1		3
F	O:	ein-	/	1	0	0	0				
	00	disu	18	/	0	1	1				
	15	lfid	5	1	1	4	1				
	03	e		8	1	4	6				
	5	red		3	7	6	9				
		ucta		3	5	1	7				
		se		7	4	1	8				
		acti			1	1	6				
		vity									
M	G	glut	3	2	0.	0.	0.		GSTP1/GPX3/MGST1		3
F	O:	athi	/	2	0	0	0				
	00	one	18	/	0	1	1				
	04	per	5	1	1	6	3				

		60	oxid	8	3	1	0		
		2	ase	3	5	3	4		
			acti	3	0	1	9		
			vity	7	9	9	4		
					5	7	6		
M	G	calc	5	8	0.	0.	0.	S100A16/S100A2/ANXA2/SYT8/S100A9	5
F	O:	ium	/	4	0	0	0		
		00	-	18	/	0	1	1	
		48	dep	5	1	1	8	5	
		30	end		8	6	6	0	
		6	ent		3	0	2	6	
			prot		3	5	6	7	
			ein		7	7	7	5	
			bin			5	5	3	
			din						
			g						
M	G	per	4	5	0.	0.	0.	PRDX1/GSTP1/GPX3/MGST1	4
F	O:	oxid	/	3	0	0	0		
		00	ase	18	/	0	2	1	
		04	acti	5	1	1	2	8	
		60	vity		8	9	5	2	
		1			3	9	2	1	
					3	7	3	9	
					7	1	2	4	
						4	5	8	
M	G	glut	3	2	0.	0.	0.	GSTO1/GSTP1/MGST1	3
F	O:	athi	/	6	0	0	0		
		00	one	18	/	0	2	1	

		04	tran	5	1	2	4	9		
		36	sfer		8	2	2	6		
		4	ase		3	1	9	5		
			acti		3	4	7	4		
			vity		7	2	3	6		
						9	9	2		
M	G	mo		5	9	0.	0.	0.	GSTP1/MGST1/ANXA2/GSDMD/SYT8	5
F	O:	difi	/	3	0	0	0	0		
		00	ed	18	/	0	2	2		
		72	ami	5	1	2	6	1		
		34	no		8	5	8	7		
		1	acid		3	1	5	2		
			bin		3	3	7	5		
			din		7	7	3	4		
			g			4	3			
M	G	carb		7	1	0.	0.	0.	NDUFAB1/AKR1C3/GSTP1/AKR1C1/AKR1	7
F	O:	oxyl	/	8	0	0	0	0	C2/FABP5/S100A9	
		00	ic	18	4	0	2	2		
		31	acid	5	/	2	7	2		
		40	bin		1	6	9	5		
		6	din		8	8	3	9		
			g		3	2	0	3		
					3	9	2	3		
					7	6	9	4		
M	G	oxid		4	5	0.	0.	0.	GSTO1/TXN/TXN2/TXNRD1	4
F	O:	ore	/	8	0	0	0	0		
		00	duc	18	/	0	2	2		
		16	tase	5	1	2	8	2		

		66	acti		8	7	2	8		
		7	vity		3	8	4	4		
			,		3	2	5	8		
			acti		7	8	9	6		
			ng			5	1	5		
			on a							
			sulf							
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			up							
			of							
			don							
			ors							
M	G	rRN	4	6	0.	0.	0.		RPL23A/RPS11/RPL3/RPS9	4
F	O:	A	/	4	0	0	0			
		00	bin	18	/	0	3	3		
		19	din	5	1	3	9	1		
		84	g		8	9	3	8		
		3			3	7	8	5		
					3	7	3	8		
					7	1	4	0		
						5	8	4		
M	G	mo	4	6	0.	0.	0.		TALDO1/G6PD/ALDOA/LMAN2	4
F	O:	nos	/	7	0	0	0			
		00	acc	18	/	0	4	3		
		48	hari	5	1	4	5	6		
		02	de		8	6	3	6		
		9	bin		3	8	0	5		

		din	3	7	8	0			
		g	7	1	6	9			
					1	9			
M	G	AT	2	1	0.	0.	0.	SLC25A5/SLC25A6	2
F	O:	P	/	1	0	0	0		
	00	tran	18	/	0	4	4		
	05	sme	5	1	5	9	0		
	34	mbr		8	2	5	0		
	7	ane		3	4	1	5		
		tran		3	4	8	6		
		spor		7	5	3	3		
		ter			5	1			
		acti							
		vity							
M	G	oxid	3	3	0.	0.	0.	AKR1B10/AKR1C3/ALDH3A1	3
F	O:	ore	/	6	0	0	0		
	00	duc	18	/	0	5	4		
	16	tase	5	1	5	2	2		
	62	acti		8	6	1	1		
	0	vity		3	4	1	6		
		,		3	8	9	0		
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M	G	glut	2	1	0.	0.	0.	GSTP1/MGST1		2
F	O:	athi	/	2	0	0	0			
	00	one	18	/	0	5	4			
	43	bin	5	1	6	4	3			
	29	din		8	2	0	6			
	5	g		3	5	0	8			
				3	1	5	6			
				7	8	6	1			
					9	5	9			
M	G	NA	2	1	0.	0.	0.	AKR1B10/AKR1C3		2
F	O:	DP-	/	2	0	0	0			
	00	reti	18	/	0	5	4			
	52	nol	5	1	6	4	3			
	65	deh		8	2	0	6			
	0	ydr		3	5	0	8			
		oge		3	1	5	6			
		nas		7	8	6	1			
		e			9	5	9			
		acti								
		vity								
M	G	olig	2	1	0.	0.	0.	GSTP1/MGST1		2

F	O:	ope	/	3	0	0	0		
	19	ptid	18	/	0	6	5		
	00	e	5	1	7	2	0		
	75	bin		8	3	0	2		
	0	din		3	3	8	1		
		g		3	9	2	9		
				7	8	6	8		
					2	8	5		
M	G	stru	3	4	0.	0.	0.	ASPH/TPM4/KRT19	3
F	O:	ctur	/	2	0	0	0		
	00	al	18	/	0	7	5		
	08	con	5	1	8	0	7		
	30	stit		8	6	5	0		
	7	uen		3	9	6	8		
		t of		3	0	3	0		
		mus		7	0	5	1		
		cle			9	2	6		
M	G	nucl	3	4	0.	0.	0.	NME1/ADK/NME4	3
F	O:	eob	/	2	0	0	0		
	00	ase-	18	/	0	7	5		
	19	cont	5	1	8	0	7		
	20	aini		8	6	5	0		
	5	ng		3	9	6	8		
		com		3	0	3	0		
		pou		7	0	5	1		
		nd			9	2	6		
		kina							
		se							

		acti							
		vity							
M	G	oxid	3	4	0.	0.	0.	AKR1B10/ AKR1C3/ ALDH3A1	3
F	O:	ore	/	4	0	0	0		
	00	duc	18	/	0	7	6		
	16	tase	5	1	9	8	3		
	90	acti		8	8	6	6		
	3	vity		3	7	4	1		
		,		3	9	8	9		
		acti		7	4	1	9		
		ng			5	5	7		
		on							
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		oxo							
		gro							
		up							
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		don							
		ors							
M	G	ade	2	1	0.	0.	0.	SLC25A5/SLC25A6	2
F	O:	nine	/	6	0	0	0		
	00	nucl	18	/	1	8	6		
	00	eoti	5	1	1	3	7		
	29	de		8	0	2	3		
	5	tran		3	7	3	2		

		sme	3	0	2	7		
		mbr	7	2	0	9		
		ane		7	2	5		
		tran						
		spor						
		ter						
		acti						
		vity						
M	G	puri	2	1	0.	0.	0.	SLC25A5/SLC25A6
								2
F	O:	ne	/	6	0	0	0	
		00	ribo	18	/	1	8	6
		05	nucl	5	1	1	3	7
		34	eoti		8	0	2	3
		6	de		3	7	3	2
			tran		3	0	2	7
			sme		7	2	0	9
			mbr			7	2	5
			ane					
			tran					
			spor					
			ter					
			acti					
			vity					
M	G	clat	2	1	0.	0.	0.	AP2M1/AP2S1
								2
F	O:	hrin	/	6	0	0	0	
		00	ada	18	/	1	8	6
		35	ptor	5	1	1	3	7
		61	acti		8	0	2	3

	5	vity		3	7	3	2		
				3	0	2	7		
				7	2	0	9		
				7	2	5			
M	G	MH	2	1	0.	0.	0.	HSP90AA1/HSP90AB1	2
F	O:	C	/	7	0	0	0		
	00	clas	18	/	1	8	7		
	23	s II	5	1	2	9	2		
	02	prot		8	4	2	1		
	6	ein		3	6	4	9		
		com		3	3	6	3		
		plex		7	7	6	3		
		bin			6	6			
		din							
		g							
M	G	carg	2	1	0.	0.	0.	AP2M1/AP2S1	2
F	O:	o	/	7	0	0	0		
	01	ada	18	/	1	8	7		
	40	ptor	5	1	2	9	2		
	31	acti		8	4	2	1		
	2	vity		3	6	4	9		
				3	3	6	3		
				7	7	6	3		
				6	6				
M	G	oxid	3	4	0.	0.	0.	AKR1C3/AKR1C1/AKR1C2	3
F	O:	ore	/	8	0	0	0		
	00	duc	18	/	1	8	7		
	16	tase	5	1	2	9	2		

70	acti	8	5	2	1
9	vity	3	2	4	9
	,	3	9	6	3
	acti	7	7	6	3
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M	G	nucl	2	1	0.	0.	0.	NME1/NME4		2
F	O:	eosi	/	8	0	0	0			
	00	de	18	/	1	9	7			
	04	dip	5	1	3	5	7			
	55	hos		8	9	8	5			
	0	pha		3	2	5	3			
		te		3	9	4	8			
		kina		7	5	2	3			
		se			6	6	2			
		acti								
		vity								
M	G	cad	2	1	0.	0.	0.	ANXA2/PKP3		2
F	O:	heri	/	8	0	0	0			

		00	n	18	/	1	9	7		
		98	bin	5	1	3	5	7		
		64	din		8	9	8	5		
		1	g		3	2	5	3		
			inv		3	9	4	8		
			olve		7	5	2	3		
			d in			6	6	2		
			cell-							
			cell							
			adh							
			esio							
			n							
M	G	RN	2	1	0.	0.	0.	EIF4A1/EIF3D		2
F	O:	A	/	9	0	1	0			
		00	cap	18	/	1	0	8		
		00	bin	5	1	5	1	1		
		33	din		8	4	2	9		
		9	g		3	6	7	2		
					3	6	7	5		
					7	0	8	5		
						8	6	7		
M	G	puri	2	1	0.	0.	0.	SLC25A5/SLC25A6		2
F	O:	ne	/	9	0	1	0			
		00	nucl	18	/	1	0	8		
		15	eoti	5	1	5	1	1		
		21	de		8	4	2	9		
		6	tran		3	6	7	2		
			sme		3	6	7	5		

		mbr	7	0	8	5		
		ane		8	6	7		
		tran						
		spor						
		ter						
		acti						
		vity						
M	G	cera	2	1	0.	0.	0.	VDAC2/LAPTM4B
F	O:	mid	/	9	0	1	0	
	00	e	18	/	1	0	8	
	97	bin	5	1	5	1	1	
	00	din		8	4	2	9	
	1	g		3	6	7	2	
				3	6	7	5	
				7	0	8	5	
				8	6	7		
M	G	tran	7	2	0.	0.	0.	HMGA1/PARK7/MTDH/PSMD9/PMF1/SU
F	O:	scri	/	5	0	1	0	B1/HTATIP2
	00	ptio	18	8	1	0	8	
	03	n	5	/	5	2	3	
	71	coac		1	9	6	0	
	3	tiva		8	6	7	5	
		tor		3	9	5	6	
		acti		3	8	9	5	
		vity		7	3	5	1	
M	G	NA	3	5	0.	0.	0.	G6PD/PGD/DECR1
F	O:	DP	/	3	0	1	0	
	00	bin	18	/	1	0	8	

		50	din	5	1	6	2	3		
		66	g		8	3	6	0		
		1			3	6	7	5		
					3	1	5	6		
					7	8	9	5		
						3	5	1		
M	G	pho	10	4	0.	0.	0.		STOML2/VDAC2/CHMP2A/GPAA1/LAPT	10
F	O:	sph	/	5	0	1	0		M4B/ANXA2/NME4/GSDMD/SYT8/PHLD	
		00	olip	18	1	1	0	8	A2	
		05	id	5	/	6	2	3		
		54	bin		1	4	6	0		
		3	din		8	3	7	5		
			g		3	8	5	6		
					3	2	9	5		
					7	7	5	1		
M	G	DN	2	2	0.	0.	0.		HSP90AA1/HSP90AB1	2
F	O:	A	/	0	0	1	0			
		00	pol	18	/	1	0	8		
		70	yme	5	1	7	5	4		
		18	rase		8	0	0	9		
		2	bin		3	7	1	5		
			din		3	1	7	0		
			g		7	7	1	3		
						5	5	5		
M	G	ami	9	3	0.	0.	0.		AP2M1/HSP90AB1/GSTP1/VDAC2/FKBP3/	9
F	O:	de	/	9	0	1	0		MGST1/PFDN6/LAPTM4B/THOP1	
		00	bin	18	1	1	0	8		
		33	din	5	/	7	9	8		

	21	g		1	9	0	2		
	8			8	9	6	2		
				3	8	6	5		
				3	6	5	9		
				7	7	4	8		
M	G	tran	3	5	0.	0.	0.	GSTO1/GSTP1/MGST1	3
F	O:	sfer	/	7	0	1	0		
	00	ase	18	/	1	1	9		
	16	acti	5	1	9	8	5		
	76	vity		8	8	5	8		
	5	,		3	4	1	6		
		tran		3	9	2	7		
		sfer		7	4	8	2		
		ring			4	4	7		
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		hyl)							
		gro							
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M	G	low	2	2	0.	0.	0.	AP2M1/HSP90B1	2
F	O:	-	/	3	0	1	1		
	00	den	18	/	2	3	0		

		50	sity	5	1	2	1	6		
		75	lipo		8	2	1	0		
		0	prot		3	8	4	8		
			ein		3	8	6	7		
			part		7	4	7	1		
			icle			9	9	1		
			rece							
			ptor							
			bin							
			din							
			g							
M	G		pho	3	6	0.	0.	0.	ANXA2/GSDMD/SYT8	3
F	O:		sph	/	0	0	1	1		
		00	atid	18	/	2	3	0		
		01	ylse	5	1	2	1	6		
		78	rine		8	7	7	5		
		6	bin		3	1	3	6		
			din		3	3	6	3		
			g		7	1	0	7		
							1	4		
M	G		tran	10	4	0.	0.	0.	HMGA1/PARK7/MTDH/PSMD9/PMF1/SU	10
F	O:		scri	/	8	0	1	1	B1/GMNN/FHL2/HTATIP2/HSBP1	
		00	ptio	18	0	2	3	1		
		03	n	5	/	4	7	1		
		71	core		1	1	8	4		
		2	gula		8	0	2	8		
			tor		3	2	3	8		
			acti		3	2	8	2		

		vity		7		3	9		
M	G	nucl	2	2	0.	0.	0.	SLC25A5/SLC25A6	2
F	O:	eoti	/	5	0	1	1		
	00	de	18	/	2	4	1		
	15	tran	5	1	6	7	8		
	21	sme		8	0	0	9		
	5	mbr		3	8	8	8		
		ane		3	4	8	2		
		tran		7	5	0	2		
		spor			8	4	9		
		ter							
		acti							
		vity							
M	G	hyd	3	6	0.	0.	0.	ENO1/ECHS1/PARK7	3
F	O:	ro-	/	4	0	1	1		
	00	lyas	18	/	2	4	2		
	16	e	5	1	6	9	0		
	83	acti		8	8	3	8		
	6	vity		3	6	9	5		
				3	2	8	1		
				7	3	8	5		
					5	5	5		
M	G	MH	2	2	0.	0.	0.	HSP90AA1/HSP90AB1	2
F	O:	C	/	6	0	1	1		
	00	prot	18	/	2	5	2		
	23	ein	5	1	8	1	2		
	02	com		8	0	9	9		
	3	plex		3	7	7	3		

		bin		3	3	2	3		
		din		7	7	6	5		
		g			7	7	6		
M	G	bH	2	2	0.	0.	0.	PSMD9/FHL2	2
F	O:	LH	/	6	0	1	1		
	00	tran	18	/	2	5	2		
	43	scri	5	1	8	1	2		
	42	ptio		8	0	9	9		
	5	n		3	7	7	3		
		fact		3	3	2	3		
		or		7	7	6	5		
		bin			7	7	6		
		din							
		g							
M	G	ubi	7	2	0.	0.	0.	SLC25A5/HSP90AA1/HSP90AB1/UBE2N/N	7
F	O:	quit	/	9	0	1	1	EDD8/LAPTM4B/RTN4	
	00	in	18	3	2	5	2		
	31	prot	5	/	9	7	7		
	62	ein		1	4	2	2		
	5	liga		8	3	7	1		
		se		3	9	0	9		
		bin		3	8	6	2		
		din		7	3	8	2		
		g							
M	G	mol	3	6	0.	0.	0.	NDUFAB1/PARK7/EMC2	3
F	O:	ecul	/	7	0	1	1		
	01	ar	18	/	3	5	2		
	40	carr	5	1	0	9	8		

	10	ier		8	2	3	9		
	4	acti		3	2	5	0		
		vity		3	1	1	2		
				7	8	7	6		
					8	3	1		
M	G	clat	3	6	0.	0.	0.	AP2M1/AP2S1/SYT8	3
F	O:	hrin	/	8	0	1	1		
	00	bin	18	/	3	5	2		
	30	din	5	1	1	9	9		
	27	g		8	3	5	0		
	6			3	8	6	7		
				3	8	5	5		
				7	6	1	2		
					7	8	9		
M	G	cyto	2	2	0.	0.	0.	COX5A/COX8A	2
F	O:	chr	/	8	0	1	1		
	00	ome	18	/	3	5	2		
	04	-c	5	1	2	9	9		
	12	oxid		8	2	5	0		
	9	ase		3	2	6	7		
		acti		3	7	5	5		
		vity		7	4	1	2		
					5	8	9		
M	G	oxid	2	2	0.	0.	0.	COX5A/COX8A	2
F	O:	ore	/	8	0	1	1		
	00	duc	18	/	3	5	2		
	16	tase	5	1	2	9	9		
	67	acti		8	2	5	0		

	5	vity		3	2	6	7		
		,		3	7	5	5		
		acti		7	4	1	2		
		ng			5	8	9		
		on a							
		hem							
		e							
		gro							
		up							
		of							
		don							
		ors							
M	G	sphi	2	2	0.	0.	0.	VDAC2/LAPTM4B	2
F	O:	ngo	/	8	0	1	1		
	00	lipi	18	/	3	5	2		
	46	d	5	1	2	9	9		
	62	bin		8	2	5	0		
	5	din		3	2	6	7		
		g		3	7	5	5		
				7	4	1	2		
					5	8	9		
M	G	lipo	2	2	0.	0.	0.	AP2M1/HSP90B1	2
F	O:	prot	/	8	0	1	1		
	00	ein	18	/	3	5	2		
	70	part	5	1	2	9	9		
	32	icle		8	2	5	0		
	5	rece		3	2	6	7		
		ptor		3	7	5	5		

		bin	7	4	1	2			
		din		5	8	9			
		g							
M	G	unf	4	1	0.	0.	0.	HSP90AA1/HSP90AB1/PFDN6/HSP90B1	4
F	O:	olde	/	2	0	1	1		
	00	d	18	0	3	6	3		
	51	prot	5	/	3	3	2		
	08	ein		1	3	3	1		
	2	bin		8	9	3	2		
		din		3	0	2	2		
		g		3	5	2	5		
				7	9	8	6		
M	G	NF-	2	2	0.	0.	0.	MTDH/COMMD7	2
F	O:	kap	/	9	0	1	1		
	00	paB	18	/	3	6	3		
	51	bin	5	1	4	6	4		
	05	din		8	3	2	4		
	9	g		3	8	1	5		
				3	9	4	4		
				7	2	5	0		
					1	1	5		
M	G	org	2	3	0.	0.	0.	SLC25A5/SLC25A6	2
F	O:	ano	/	0	0	1	1		
	00	pho	18	/	3	7	4		
	15	sph	5	1	6	4	1		
	60	ate		8	6	8	4		
	5	este		3	0	4	3		
		r		3	5	6	6		

		tran	7	7	5	6			
		sme		9		3			
		mbr							
		ane							
		tran							
		spor							
		ter							
		acti							
		vity							
M	G	anio	2	3	0.	0.	0.	SLC25A5/SLC25A6	2
F	O:	n:an	/	1	0	1	1		
	00	ion	18	/	3	7	4		
	15	anti	5	1	8	7	3		
	30	port		8	8	1	3		
	1	er		3	7	7	2		
		acti		3	5	6	1		
		vity		7	8	2	2		
				9	4				
M	G	pho	2	3	0.	0.	0.	VDAC2/CHMP2A	2
F	O:	sph	/	1	0	1	1		
	00	atid	18	/	3	7	4		
	31	ylch	5	1	8	7	3		
	21	olin		8	8	1	3		
	0	e		3	7	7	2		
		bin		3	5	6	1		
		din		7	8	2	2		
		g			9	4			
M	G	qua	2	3	0.	0.	0.	VDAC2/CHMP2A	2

F	O:	tern	/	1	0	1	1		
	00	ary	18	/	3	7	4		
	50	am	5	1	8	7	3		
	99	mo		8	8	1	3		
	7	niu		3	7	7	2		
		m		3	5	6	1		
		gro		7	8	2	2		
		up			9	4			
		bin							
		din							
		g							
M	G	solu	2	3	0.	0.	0.	SLC25A5/SLC25A6	2
F	O:	te:a	/	1	0	1	1		
	01	nio	18	/	3	7	4		
	40	n	5	1	8	7	3		
	32	anti		8	8	1	3		
	3	port		3	7	7	2		
		er		3	5	6	1		
		acti		7	8	2	2		
		vity			9	4			
M	G	ubi	7	3	0.	0.	0.	SLC25A5/HSP90AA1/HSP90AB1/UBE2N/N	7
F	O:	quit	/	1	0	1	1	EDD8/LAPTM4B/RTN4	
	00	in-	18	2	3	7	4		
	44	like	5	/	9	7	3		
	38	prot		1	2	1	3		
	9	ein		8	7	7	2		
		liga		3	5	6	1		
		se		3	5	2	2		

		bin		7	2	4			
		din							
		g							
M	G	dou	3	7	0.	0.	0.	EIF4A1/HSP90AB1/MTDH	3
F	O:	ble-	/	6	0	1	1		
	00	stra	18	/	4	8	4		
	03	nde	5	1	1	5	9		
	72	d		8	5	4	9		
	5	RN		3	5	1	8		
		A		3	8	4	5		
		bin		7	4	7	4		
		din			7		5		
		g							
M	G	carb	3	7	0.	0.	0.	ENO1/ECHS1/PARK7	3
F	O:	on-	/	9	0	2	1		
	00	oxy	18	/	4	0	6		
	16	gen	5	1	5	0	2		
	83	lyas		8	7	7	4		
	5	e		3	4	9	2		
		acti		3	9	2	5		
		vity		7	2	8	1		
					4	9	6		
M	G	diso	2	3	0.	0.	0.	HSP90AA1/HSP90AB1	2
F	O:	rder	/	4	0	2	1		
	00	ed	18	/	4	0	6		
	97	do	5	1	5	0	2		
	71	mai		8	9	7	4		
	8	n		3	9	9	2		

		spec	3	4	2	5		
		ific	7	4	8	1		
		bin		3	9	6		
		din						
		g						
M	G	ribo	4	1	0.	0.	0.	NME1/SNRPB/EIF3K/PRPF31
F	O:	nucl	/	3	0	2	1	
	00	eop	18	4	4	0	6	
	43	rote	5	/	6	2	3	
	02	in		1	9	6	9	
	1	com		8	1	5	2	
		plex		3	9	2	9	
		bin		3	6	9	7	
		din		7	5	4	8	
		g						

Supplementary Table 10 Features selection for Random Forest algorithm

Gene	importance
CYC1	6.898585076
NME1	6.869623572
SNRPB	6.820322191
MRPL13	6.5528371
MRPL12	6.520280868
AKR1C3	6.490940228
GSTP1	6.304718637
PTGR1	6.288611857
NAA20	6.168785048
GPX3	6.137763523

TKT	5.975878063
TALDO1	5.921704522
RPL13A	5.863158059
AKR1B10	5.854664565
MGST1	5.750495583
ALDH3A1	5.680416943
RPS2	5.460204567
G6PD	5.375939691
SLC25A5	5.340885415
CISD1	5.335474679

Supplementary Table 11 Features selection for GBM algorithm

Gene	Importance
RPL13A	6.658211483
CYC1	6.537403077
NME1	6.435004845
SNRPB	6.313784074
MRPL13	6.031503676
TALDO1	5.914978135
GSTP1	5.792808594
TKT	5.589721896
SLC25A5	4.857301012
G6PD	4.833534528
GPX3	4.649124477
MGST1	4.528749064
FABP5	4.236020106
ALDH3A1	4.194378009
COX5A	4.15835295

MDH2	4.088489
NAA20	3.935055017
GSTO1	3.800979767
MRPS12	3.687379093
COX8A	3.392370927

Supplementary Table 12 features selection for LASSO algorithm

Gene	Coef
COX5A	0.927795
MRPL12	0.859888
HSD17B10	0.709911
GPX3	0.696423
ECHS1	0.662434
MDH2	0.604046
CYC1	0.588597
NDUFB9	0.577374
AURKAIP1	0.56056
SOD1	0.552567
NME1	0.518754
MTDH	0.517894
MRPS28	0.50957
SYT8	0.489973
NPM3	0.452779
SLC25A5	0.443515
PTGR1	0.414078
GSTP1	0.39921
LAPTM4B	0.393381
COX8A	0.381853

HTATIP2	0.380326
PPA2	0.358556
NDUFS4	0.346176
PIM3	0.342285
FSCN1	0.335053
EIF3K	0.333677
MCTS1	0.331854
PARK7	0.315706
MGST1	0.30076
CISD1	0.298841
POLR2E	0.294807
RPL10A	0.293238
BLOC1S1	0.291984
MRPS12	0.28455
RPL23A	0.28355
STOML2	0.279121
SLC25A6	0.261614
PMF1	0.240061
AP2S1	0.222992
NDUFB5	0.215446
ECH1	0.212974
NDUFAB1	0.210493
UQCRH	0.198593
RHOD	0.198392
PFDN6	0.195904
TBCA	0.190791
HBEGF	0.184304
CES1	0.184286

NME4	0.180563
ALDH3A1	0.174159
LMAN2	0.168778
RPS2	0.166466
COTL1	0.161502
EIF3F	0.161036
APRT	0.152122
UBE2N	0.148387
EIF4A1	0.146699
EMC2	0.141286
PRELID1	0.141057
FKBP3	0.139463
ARPC1B	0.139001
AKR1C1	0.109859
TXN	0.107269
PSMA4	0.106454
PRPF31	0.106291
ATP6V0B	0.103574
LDHA	0.10129
EFHD2	0.099988
TALDO1	0.098851
TINAGL1	0.098433
RPL4	0.092354
MRPL15	0.091153
NDUFC2	0.089012
SNRPB	0.085893
PSMG3	0.079554
SUB1	0.07733

FXYD3	0.076068
THOP1	0.073546
MRPL28	0.072166
RPS10	0.069964
TKT	0.066278
MRPL13	0.065342
CSNK1A1	0.05744
H2AFY	0.056974
EI24	0.05138
TPM4	0.051337
SERPINB5	0.045162
HSP90AA1	0.04505
MRPL47	0.04446
MRPL23	0.044323
NAA20	0.038586
ENO1	0.035965
G6PD	0.035139
S100A2	0.034528
HSP90B1	0.027714
CHMP2A	0.024206
FHL2	0.020928
RPL13A	0.018553
ADK	0.013021
GMNN	0.010221
NQO1	0.008647
COPRS	0.008367
CDC123	0.002053
PGD	0.001188

Supplementary Table 13 Features selection for Decision Tree algorithm

Gene	Overall
CYC1	10.83039
NME1	10.59546
ALDH3A1	10.48443
MGST1	10.13902
MRPL15	8.862203
GSTP1	8.840791
TKT	8.783742
MRPS28	8.398797
G6PD	7.936802
GPX3	7.762907
TALDO1	7.189118
RPL13A	7.113778
PRELID1	7.062859
NAA20	6.951628
SNRPB	6.86315
NDUFB9	6.862525
MDH2	6.829519
GSTO1	6.505056
NDUFB5	6.407333
PARK7	6.194189

Supplementary Table 14 Features selection for ABESS algorithm

support.vars
CYC1
NME1
SNRPB

SLC25A5
PRELID1
MRPL12
GSTO1
TKT
NDUFAB1
NDUFB9
RPL13A
MRPS12
HSD17B10
EIF3K
GPX3
PSMA4
ECHS1
AP2S1
MRPL13
PARK7
COX5A
STOML2
CISD1
GSTP1
COX8A
NDUFS4
FKBP3
NDUFB5
TALDO1
MTDH
RPS10

UBE2N
ALDH3A1
NAA20
PTGR1
G6PD
POLR2E
PSMG3
CNPY2
MGST1
AURKAIP1
REEP5
TXN2
SOD1
LAPTM4B
MCTS1
EFHD2
PGD
ECH1
EIF3F
HTATIP2
MRPS28
FABP5
SYT8
LMAN2
LY6E
BLOC1S1
CES1
S100A9

Supplementary Table 15 Result of Benchmark

learner_id	classif.auc	classif.sensiti vity	classif.specifi city	classif.fnr	classif.fpr
classif.log_reg	0.944585513	0.858614869	0.876738204	0.14138513 1	0.12326179 6
classif.xgboost	0.950825952	0.903516355	0.869084397	0.09648364 5	0.13091560 3
classif.lda	0.943833128	0.854600931	0.884938928	0.14539906 9	0.11506107 2
classif.svm	0.968641439	0.902945833	0.911711021	0.09705416 7	0.08828897 9
classif.naive_b ayes	0.93227374	0.715291116	0.935009971	0.28470888 4	0.06499002 9
classif.kknn	0.951313902	0.923487	0.857786337	0.076513	0.14221366 3
classif.rpart	0.900039407	0.864202618	0.893484302	0.13579738 2	0.10651569 8
classif.ranger	0.972342717	0.907930791	0.917915959	0.09206920 9	0.08208404 1