

Supplementary Table 1 The markers of 25 immune cells as the signature matrix

	Ma st Cel ls	Neutr ophil Cells	Eosin ophil Cells	B Cells Mem ory	B Cell s Naiv e	Plas ma Cell s	T Cells CD8 Active	T Cells CD8 Naive	T Cells CD8 Memor y	M0 Macr opha ge	M1 Macr opha ge	M2 Macr opha ge	Tre g Cel ls	T Cells CD4 Memor y	T Cells CD4 Naive	T Cells CD4 Follicul ar	Th 1 Cel ls	Th1 7 Cel ls	Th 2 Cel ls	Mo noc yte	Gamm aDelta T Cells	NK Res ting	NK. Acti ved	DC Acti ved	DC Imm ature
Ngp	39.2 379 95	18916. 353	5776.0 376	65.81 7689	65.30 0643	70.8 7438 6	38.6719 84	53.645 295	57.4739 55	45.929 185	36.595 365	41.062 042	56. 508 448	44.3978 94	46.492 421	39.04533 8	38. 751 675	47.7 250 53	60. 898 532	207 .99 263	54.4393 8	83.1 821 26	46.1 6378 4	181 2.85 02	3399. 456
Cam p	41.1 047 77	16257. 716	320.91 29	61.61 5683	55.47 1245	52.8 5008	40.9035 99	48.871 369	51.3270 29	48.057 799	82.888 799	57.483 197	68. 801 949	47.5146 67	50.181 858	44.95094 3	61. 547 567	56.8 600 97	61. 685 258	179 .59 7	47.9601 21	88.3 197 51	62.7 7502 3	650. 577 76	884.4 5451
Mmp 8	69.2 756 18	12196. 486	572.64 5	39.40 6753	30.70 6337	43.6 3392 5	18.7687 78	27.028 379	23.8245 69	569.88 804	90.962 175	359.04 725	23. 694 175	20.1707 22	22.517 954	25.44667 4	29. 536 598	25.5 868 33	29. 879 662	565 .20 523	26.4497 92	27.2 701 53	24.2 5089 9	204 1.14 55	4568. 4981
Cd17 7	16.2 304 55	11646. 908	86.680 879	12.65 6065	10.91 5883	12.4 7852 9	15.1775 91	11.882 783	14.2902 57	17.297 947	18.235 666	16.773 951	16. 518 901	15.8577 98	19.818 145	13.54382 8	16. 455 292	15.4 353 5	14. 908 228	817 .05 758	15.7680 15	15.0 971 55	13.5 2214 6	38.1 409 16	96.70 0474
Mmp 9	34.2 733 11	10154. 764	435.80 185	51.43 5896	48.78 5544	47.8 8114 7	30.7982 06	33.860 734	35.0698 23	47.705 776	50.150 327	45.261 745	44. 427 528	76.0931 53	47.993 814	44.35418 1	27. 539 216	51.7 275 72	39. 673 08	29. 961 727	30.5989 23	44.5 885 1	38.0 8909 9	261. 149 63	451.6 5973
Fpr2	30.5 686 97	10047. 499	171.66 383	38.44 7115	39.06 1446	46.6 7533 1	46.2295 75	54.265 532	53.6184 88	381.75 709	8546.6 881	132.59 873	30. 171 638	28.6615 57	30.353 911	30.86052 4	25. 449 121	47.8 248 84	31. 818 039	217 0.3 682	35.8121 17	38.2 561 56	26.1 2390 2	562 9.91 78	3522. 2995
Ifitm 6	28.6 662 67	9701.3 888	480.50 936	34.02 728	26.36 7868	33.6 0071 7	23.4007 53	26.982 195	28.1584 81	91.360 752	213.89 047	41.267 729	27. 287 262	24.5358 53	22.529 284	21.31090 1	24. 503 077	33.9 835 19	64. 446 855	760 5.0 134	26.0193 06	29.7 715 8	29.7 4365 8	392. 481 66	1050. 4318

Chi3l3	23.002509	9514.7457	1180.3729	9.803574	11.064887	10.194896	9.2345527	10.70494	12.661735	30.069775	13.233189	580.30734	14.47466	15.138114	11.163053	10.938448	11.569	12.5155	67.771	8353.6	10.914518	17.5484	10.59802	6416.36	7930.9618
1810033B17Rik	34.885184	6147.6096	205.21207	38.110192	50.11635	55.872308	40.17371	44.04201	41.348328	70.954993	80.54052	39.76608	38.309347	37.208432	32.760482	27.29804	46.594631	40.7912	37.254	4014.7	46.594601	60.5631	47.12454	1399.72	1955.28
Itgb2l	69.70812	5640.2119	119.13667	58.763829	70.738974	67.389873	69.640598	65.03461	52.215391	50.39229	74.507476	59.461237	52.308985	92.581184	54.058599	52.050204	65.61008	54.8073	51.105	86.746	51.850732	57.3960	49.27929	121.210	143.44108
Trem3	38.705685	5347.6617	212.36656	66.850024	65.529408	56.469599	33.853373	44.567839	44.729217	43.116913	106.52832	39.0051	39.568146	52.076271	41.745197	40.533871	32.556	33.7206	37.916	1834.9	64.040203	47.0400	54.89161	207.451	131.18992
Nfe2f8	1117.1068	4863.7522	3243.6584	38.990463	24.299407	27.466803	17.492339	18.533241	19.314732	22.071821	18.640828	37.160965	27.218474	30.13309	22.464485	36.350673	24.896	23.929	23.853	2075.6	20.155738	95.2283	30.82734	80.2310	432.57587
Csf3r	65.745118	4749.0389	210.72883	81.116348	79.09996	88.191012	50.523585	64.147705	59.435961	504.92492	889.8911	890.5702	63.813686	77.538646	67.693406	64.512798	74.650	64.0362	55.173	1562.9	72.259597	60.4810	42.81841	564.001	471.13461
Fpr1	25.914103	4740.2185	152.71822	34.441989	24.778562	57.464195	23.542073	32.116908	32.244738	102.76484	3854.3902	36.575308	28.392699	46.259036	31.068722	27.145217	27.092	26.2988	27.562	161.22	34.453717	30.366	22.32	2026.42	1168.0391
Pram1	75.719986	4583.1184	127.83449	223.24237	138.31076	205.21593	55.213744	81.666971	67.468471	77.286689	80.453227	59.78019	61.897732	124.62627	86.323966	66.180862	74.925	63.5666	55.789	895.58	62.424861	100.757	77.14180	118.133	278.41819
Clec4d	107.28704	4548.0662	1933.7903	36.305598	31.552557	38.38593	22.856705	25.314663	27.23787	6536.0128	4872.5623	3721.6785	27.604016	24.578403	28.355036	24.259128	26.167	49.0672	30.537	312.18	26.750083	27.4285	35.78118	4440.50	3910.6572

Sell	30.2	4200.9	911.99	1458.	3370.	113.	727.765	4363.1	4631.33	25.414	780.44	28.783	142	644.359	4251.5	424.7087	248	40.3	34.	985	29.8407	322	1182	309.	186.9
	432	023	679	5427	7549	1930	72	915	64	413	458	473	5.6	66	804	8	.46	014	620	.61	72	2.94	.014	012	9212
	79					2							226				281	78	637	059		24	3	65	
Cd30	341	4157.0	4422.6	30.69	20.79	22.1	14.1507	17.857	16.5920	3181.5	646.50	5987.5	18.	24.7985	18.982		19.	15.9	18.	340	62.5158	25.3	34.7	107.	1239.
	1.12	107	442	175	3463	7625	71	03	78	394	091	497	938	15	875	18.52522	020	709	932	9.6	59	925	2546	657	2696
	69												241				371	94	586	441		64	5	45	
Cxcr2	51.0	3964.6	338.51	160.3	75.28	140.	43.0299	55.971	51.6327	50.988	43.155	58.849	65.	80.9316	68.990	69.00874	132	95.0	84.	81.	95.7103	117.	97.9	91.8	113.1
	806	525	076	9862	9362	3401	41	669	72	616	83	11	512	43	982	2	.26	471	159	435	12	831	7125	008	4741
	33					9							145				891	9	456	295		45	5	35	
Hck	54.6	3913.8	2538.5	905.6	1071.	39.3	16.4894	36.567	49.6935	1912.5	4046.7	998.14	32.	82.3351	24.526		32.	28.5	25.	653	30.8224	85.2	31.6	406	1867.
	120	639	514	887	0889	9746	77	314	69	843	234	46	131	59	435	22.29528	294	427	484	3.5	08	131	9446	6.80	7806
	19					3							38				577	26	742	497		57	5	96	
Slfn1	16.1	3815.9	15.561	15.50	15.65	13.2	40.4693	294.88	466.333	22.405	614.50	14.976	386	826.664	613.37	225.0489	124	147	726	848	22.0833	14.5	14.5	175	287.4
	969	773	872	51	5165	8837	5	494	79	061	58	19	.34	71	747	3	.38	8.65	.89	.78	5	078	7692	3.60	3902
	54					8							054				537	29	266	008		26	7	68	
Hk3	38.0	3491.9	692.65	78.82	58.10	66.4	32.7713	56.729	64.8463	1024.5	3749.7	1041.4	39.	63.8575	52.263	39.99125	32.	36.3	37.	555	46.8111	134.	86.2	159	555.5
	741	172	645	8262	7954	4145	62	147	62	488	422	041	791	43	421	8	883	961	189	.43	57	697	3542	8.63	7651
	59					4							89				366	03	012	034		37	9	68	
Ltb	103.	3266.9	2065.8	2850.	3250.	53.0	1486.15	9130.6	7694.76	79.976	171.09	69.386	707	5781.13	9094.0	7354.916	212		159	229	2039.59	124	463.	128.	331.2
	941	971	693	893	9567	8903	51	52	26	629	259	585	2.7	72	866	1	.93	846	6.8	.07	45	1.51	5311	281	1113
	82					8							624				637	2.52	474	672		73	6	56	
Adpg	96.0	3093.9	249.80	107.9	103.5	131.	135.523	156.72	211.869	74.282	59.163	84.448	233	140.570	175.47	99.88485	251	129.	131	127	65.3868	74.8		76.9	136.7
	460	759	01	9849	6888	6812	62	989	23	14	903	425	.10	48	342	4	.03	810	.01	.71	67	287	110.	918	5254
	63					8							522				936	26	838	288		83	5345	54	
Slfn4	21.0	2987.3	18.773	28.15	29.85	28.5	22.2933	20.806	22.7851	41.980	4949.4	30.510	29.	21.7463	26.987	29.74240	18.	25.4	23.	714	25.8717	20.8	21.6	306	94.35
	140	237	426	7357	6239	3085	67	015	45	996	861	133	323	09	822	8	703	261	419	.78	05	168	0391	7.17	6184
	16					9							615				745	04	971	326		55	9	65	

Pilra	181.50772	2969.8468	285.01271	20.623695	23.543896	25.747185	19.025479	35.014491	41.888105	102.03983	799.78041	59.498174	27.01057	21.031157	25.001869	23.20193	25.649	26.9718	23.568	1093.5	27.433576	29.3951	22.67769	1778.06	2080.9361	
	Pirb	928.34535	2942.4774	1631.0077	405.14419	424.23962	50.53453	49.452117	45.750094	45.634194	1658.0614	2177.0909	961.91875	28.498294	119.72916	42.37727	38.048499	38.079	31.5649	28.927	3072.0	31.748731	40.7857	39.45244	1727.34	1422.8486
		Itgam	18.303194	2898.0718	1151.984	23.238978	25.284353	23.883718	17.723138	15.663508	17.014726	1580.9734	1691.5118	1550.0283	20.150646	21.633446	23.484266	20.311813	19.994	24.7106	17.042	1075.6	23.894268	232.947	58.26258	986.263
Padi4			19.905692	2745.4415	2177.2048	20.857381	21.213457	36.531351	20.239722	22.768403	21.848718	25.532452	20.661789	22.163799	23.286427	20.983715	27.154279	185.6391	18.700	19.7797	24.567	116.59	21.350197	44.1295	32.33455	135.390
	Igsf6		21.936402	2575.0838	869.40148	24.503946	26.591415	24.181832	17.548584	27.517958	23.65995	1674.9338	1665.4789	1078.5281	19.417699	41.464903	20.364493	17.248762	23.947	24.2801	17.891	4112.8	16.747589	29.7572	21.79895	1423.31
		Alox5	4358.1707	2567.4058	2195.9078	87.435548	75.784732	75.142111	65.700027	86.555189	70.082783	78.016028	84.185556	73.010275	72.790275	103.53075	74.272678	69.681319	64.952	66.1741	218.34	346.64	124.51837	119.402	103.6509	255.782
Rgs18			3099.479	2456.5739	1666.1215	38.054397	180.93694	11.298621	12.37993	12.329894	12.158404	656.47099	23.891415	315.06065	12.295927	11.161034	11.467266	11.930043	11.069	10.9609	16.585	761.40	11.248155	65.5139	84.56981	36.4879
	Il1b		251.78101	2374.4032	866.38607	51.650652	49.982995	65.69261	53.212365	66.707149	53.747714	89.040168	2652.3119	93.367785	49.446687	67.956242	45.466453	45.710527	53.697	140.358	45.820	628.75	44.832711	105.239	62.57413	7568.59
		Fgr	47.476545	2292.1724	550.36669	215.94295	186.70609	111.10821	66.535496	65.388797	89.127131	133.28598	197.4511	190.39084	72.955179	88.890102	53.731235	63.086392	88.943	51.9089	52.863	2024.8	367.42952	184.361	133.4873	428.102
																			522	06	369	842		82	2	33

Fcgr4	37.8	2160.0	291.52	34.16	30.96	32.2	29.3435	47.685	64.8321	1061.2	5424.9	866.10	29.	30.7896	27.364	27.24673	30.	28.2	27.	759	37.2247	31.4	28.2	115	182.9
	289	276	733	6497	4342	1280	89	175	13	897	765	978	327	24	803	5	717	347	141	.29	35	849	4017	1.71	9389
	78					7							652				693	49	753	995		27	1	54	
Clec5a	12.4	2056.5	150.38	14.37	13.29	14.5	14.4959	13.700		264.50	131.76	275.09	15.	17.0062	14.205	14.10981	16.	16.9	14.	134	17.0038	14.8	17.0	470.	453.7
	344	614	402	3825	6056	2569	29	276	13.9497	369	665	928	555	26	698	5	676	205	703	.71	13	666	9494	208	8775
	42					3							075				7	34	146	205		73	6	42	
4930438A08Rik	26.4	1999.6	38.351	23.83	26.59	31.0	27.0955	26.938	28.2947	27.471	26.507	25.753	28.	29.2014	28.011		29.	28.6	30.	45.	38.0957	23.1	31.8	36.6	37.98
	126	513	096	2163	283	0061	07	482	92	197	706	265	804	61	82	27.04303	241	955	216	165	35	195	1768	325	4967
	57					1							115				332	94	514	098		33	9	56	
Bmx	17.9	1989.9	18.617	22.23	17.32	16.0	14.2900	14.482	14.9645	14.513	15.312	13.890	13.	14.2723	15.045	13.57516	14.	15.1	14.	365	13.5346	18.5	17.5	14.4	22.69
	483	56	661	6678	8026	278	92	28	59	612	471	815	862	95	017	4	876	476	913	.36	87	509	6214	503	547
	25												261				554	16	168	403		06	7	94	
Tlr13	27.1	1898.4	443.61	26.32	41.26	32.4	32.7482	30.948	30.9017	1980.2	1177.0	726.73	31.	23.3957	28.134		24.	30.9	25.	237	23.6406	25.6	25.2	396.	414.8
	644	284	182	5992	3112	3814	59	571	63	941	463	998	695	66	606	25.55324	292	991	821	4.1	27	166	1895	366	0995
	36					2							825				647	65	112	113		08	9	03	
Slc15a3	20.6	1751.6	866.48	130.6	136.0	75.3	108.139	30.704	39.6374	1715.7	4617.3	2459.5	189	46.7561	22.233	66.97891	307	319.	35.	704	20.2063	40.1	23.7	476	2092.
	465	387	648	0914	2281	5527	07	408	04	185	166	54	.94	07	219	7	.13	891	891	.93	85	847	9651	0.07	7989
	69					1							55				923	15	409	04		59	2	02	
Ccr1	158.	1746.0	793.05	61.90	21.43	13.0	15.3965	14.655	13.7817	71.039	139.45	76.594	16.	13.7847	13.547		16.	61.0	146	83.	14.0297	12.4	13.4	446.	817.0
	493	219	146	647	5376	4486	75	349	14	593	381	65	549	64	221	14.56232	895	946	.47	339	65	529	1024	755	9829
	76					7							168				693	94	417	383		48	1	8	
Gpr97	196	1637.5	673.36	55.31	30.44	25.3	32.2284	133.88	100.597	33.529	30.874	35.469	39.	29.2151	97.299	36.74689	25.	115.	258	51.	40.1030	73.0	132.	67.9	85.48
	8.81	813	406	3243	3182	4780	58	532	63	775	301	085	468	61	177	5	556	001	.31	212	13	094	4006	861	7757
	04					2							843				284	02	942	016		83	7	66	
Lin28a	11.7	1614.4	157.19	14.81	13.32	15.2	13.5092	14.191	13.7068	11.807	12.769	16.151	13.	12.1023	12.617	12.57870	10.	12.6	12.	15.	12.9847	11.6	12.9	13.8	14.92
	387	72	447	472	5646	7151	63	551	73	968	011	798	845	6	134	1	882	038	809	250	81	583	0498	607	618
	9					2							246				088	58	361	909		49	4	86	

Cd30	30.9	1557.2	185.31	36.25	28.61	31.8	23.5590	33.589	26.4486	1564.1	664.97	2465.2	29.	29.3696	28.063	29.99721	36.	31.3	31.	861	34.9021	34.5	32.4	89.7	248.4
Old	448	294	505	5254	1507	6705	77	778	3	882	183	683	590	31	986	9	762	81	918	058	92	96	8	46	5194
Tbc1	445.	1520.2	875.78	986.2	856.2	193.	616.509	3260.9	4452.14	29.107	30.120	28.731	189	3556.43	2636.5	2528.765	807	310	208	133	3479.56	170	1225	35.6	91.02
d10c	088	545	674	4823	2453	9347	5	314	34	932	872	411	2.7	78	533	1	.99	2.30	3.7	.54	18	3.69	.498	476	8288
Cyp4	21.1	1436.2	3036.0	889.4	827.5	159.	17.9762	18.709	18.6989	144.12	65.682	86.394	20.	32.7104	20.559	21.46129	21.	17.9	19.	220	16.8795	37.2	20.9	286.	550.1
f18	176	938	562	7059	6842	1383	83	912	73	498	515	781	700	72	821	8	759	620	346	6.5	3	354	3602	405	2165
Nfam	58.5	1402.9	190.95	33.43	35.68	27.0	24.8810	30.805	26.2101	221.91	103.78	218.80	27.	27.0242	29.409	25.71249	29.	28.6	31.	670	24.0765	25.3	24.6	168.	417.5
1	351	456	636	2157	9863	8388	46	708		432	714	912	231	09	015	9	482	969	396	.81	5	993	0593	615	3871
Fcnb	28.8	1367.5	48.772	27.69	49.72	35.2	33.3951	42.094	37.2281	31.302	36.039	30.800	33.	30.2759	39.291	30.07277	25.	32.9	29.	80.	30.1760	29.2	26.8	65.8	71.39
	441	632	403	2526	0488	4017	87	559	77	442	556	214	601	36	805	5	648	104	741	721	05	840	8772	116	4775
Il18ra	528.	1334.2	455.72	65.09	69.06	52.4	400.123	116.82	772.570	39.700	42.376	41.455	100	298.664	89.053	131.2470	245	306.	249	54.	46.9041	276	1445	83.9	123.6
p	082	643	107	4261	1814	2154	4	445	52	933	523	147	.52	76	599	5	.87	083	.16	780	72	7.67	.099	532	9153
Klra1	28.0	1289.1	89.584	30.81	21.41	23.6	17.4304	17.526	17.6640	49.048	21.769	26.515	17.	17.8400	18.748	14.68403	18.	16.8	15.	28.	20.0847	24.7	24.1	81.8	74.22
7	513	441	794	0482	3149	6778	63	763	15	635	455	873	466	94	717	5	286	511	025	499	93	127	9029	859	7383
Btg1	158.	1277.5	65.643	769.2	1004.	42.2	194.916	3077.6	1435.12	107.52	200.30	112.93	385	766.322	2197.4	1555.879	99.	127	897	549	1025.66	477	689.	162.	271.4
	629	362	229	2233	5421	7164	73	338	36	862	385	254	.35	81	968	7	704	5.98	.73	.96	22	4.58	0839	965	5615
Il1f9	39.5	1261.9	85.247	29.35	38.00	39.2	25.0019	33.182	27.3704	29.160	438.08	30.058	28.	29.1492	28.563	27.62475	35.	28.4	28.	34.	28.8341	34.0	30.1	120	134.7
	426	899	93	8014	1215	9853	47	42	56	039	642	656	647	88	305	9	843	515	029	926		379	2501	2.03	6536
	4					4							144				621	96	311	968		67	8	75	

Ear2	16.0	1164.3	15625.	12.62	16.76	10.8	12.1993	15.622	18.3078	22.591	26.294	29.520	14.	46.8143	15.917	15.54759	14.	11.4	14.	395	15.9944	15.8	13.3	844.	1751.
	288	748	721	1767	6036	4597	93	547	41	125	498	286	958	37	769	9	776	27	136	086	15	35	7	49	259
	5												97												
Hvcn	216.	1140.0	1689.7	4781.	5750.	660.	208.129	871.75	1066.17	834.05	395.53	1085.0	323	652.949	760.20	517.0581	353	636.	144	84.	1750.71	641.	363.	107	1117.
	393	052	532	0439	293	0941	11	524	23	796	804	519	.28	24	276	7	.72	434	.96	078	49	769	4525	3.40	7585
	1					3							672				534	01	638	45		98	2	99	
Cd3d	28.3	1075.7	54.656	25.98	47.07	32.1	4612.61	9589.6	10288.9	36.281	43.177	36.881	709	3084.90	9276.1		502	948	900	64.	9316.51	129.	67.2	30.5	29.73
	186	204	22	1135	037	4787	56	063	88	671	1	303	9.6	24	147	9411.197	5.9	0.28	1.4	647	7	219	9269	066	5185
	89					9							845				004	3	611	022		16	9	26	
Clec4	16.9	1042.9	590.69	13.95	15.14	14.1	11.8786	13.009	12.7738	128.24	1801.7	37.196	14.	13.5553	13.374	14.15105	13.	24.6	12.	240	13.8753	20.9	19.3	368	515.4
	177	569	799	0562	6014	4112	46	826	62	274	16	362	382	05	377	7	688	720	155	.05	76	849	6575	5.74	8048
	7					6							663				763	31	974	843		4	6	96	
C5ar1	54.3	966.59	121.91	20.64	20.23	20.2	19.8757	21.074	21.3344	132.07	92.501	46.405	21.	27.1509	21.722	22.40184	22.	22.4	24.	75.	21.1779	24.7	23.0	226.	495.6
	267	448	858	415	9967	6098	2	766	02	064	932	383	788	93	32	5	486	745	361	314	71	086	9213	428	0745
	06					1							54				152	14	652	352		74	8	98	
Nlrp	18.2	953.60	243.13	22.77	18.94	22.3	16.2026	17.722	18.2302	18.643	20.129	19.087	17.	21.7718	18.180	19.41691	21.	18.5	17.	19.	15.2590	21.7	21.7	17.1	18.70
	603	184	188	7406	8084	3839	27	183	61	226	243	854	425	89	248	3	498	878	706	336	62	619	4750	725	3649
	35					3							834				083	62	372	762		25	1	12	
Trem	27.7	933.34	92.953	36.73	31.18	25.1	30.8804	33.153		31.637	39.900	26.756	28.	30.5693	30.969	28.82023	27.	25.7	26.	107	33.7373	24.7	25.1	155.	117.3
	223	1	309	3703	3487	5432	24	65	26.4348	02	276	241	110	92	26	5	602	788	443	.87	04	999	0958	482	2046
	61					6							113				604	52	535	006		76	8	44	
Cnr2	110.	876.62	510.65	860.5	1386.	13.6	24.4752	243.51	189.010	202.73	31.603	288.92	55.	29.5366	113.69	51.64347	18.	73.5	37.	273	15.3525	45.0	22.2	19.1	171.0
	978	497	557	7637	783	5184	31	067	38	047	154	598	328	98	131	2	201	803	547	.06	72	878	9852	851	5497
	34					8							759				627	94	854	322		48	2	74	
Il1rn	31.0	866.13	543.40	37.65	36.47	33.2	30.1874	29.223	27.3041	166.65	4441.3	171.35	65.	30.7924	26.302	54.52734	31.	38.5	28.	58.	30.9618	31.7	32.7	731	1274.
	684	417	414	864	2326	1856	07	928	43	408	287	924	817	88	853	2	008	199	624	104		593	3141	0.64	4527
	71					3							851				359	79	695	024		58	8	53	

Naps a	743. 402 42	845.55 956	3075.9 444	2035. 6021	1445. 4975	445. 614	51.9100 75	48.205 761	41.9064 51	798.23 564	363.24 088	709.20 615	45. 527 074	57.6599 62	40.521 556	52.62934 6	147 .84	110. 026	117 .98	477 4.9	763.575 88	316. 541	237. 3578	186 9.94	3164. 9557
	14.6 214 22	815.01 827	53.917 85	12.98 6166	16.42 3536	12.2 5434 3	13.4106 51	13.526 173	12.8868 75	13.701 033	14.433 863	15.615 249	20. 105 59	22.1437 37	12.848 835	251.4398 7	15. 200	17.0 626	14. 745	13. 002	15.0207 56	13.2 698	15.4 6824	63.7 593	134.5 7193
	120 0.12 58	804.66 65	1448.0 829	1926. 6066	1895. 6448	632. 3663	34.1303 68	36.562 535	31.9194 06	312.86 851	141.62 309	205.07 407	92. 020 997	91.2421 53	47.011 689	58.57532 9	52. 128	71.7 601	41. 235	175 3.7	329.103 13	97.9 868	52.2 3516	91.7 174	310.2 989
Ccno	66.0 023 58	794.56 688	46.229 817	33.81 3769	32.19 3857	39.8 9164 1	53.3396 71	50.795 234	46.6474 25	43.176 19	51.980 836	42.271 368	46. 995 442	40.5551 83	43.609 68	35.89937 7	46. 652	35.8 592	42. 709	38. 036	62.9389 47	31.0 178	41.4 4399	39.6 806	45.93 4025
	147. 265 54	775.26 708	149.55 559	169.4 4374	181.4 3981	151. 0557 8	174.561 85	227.35 857	152.925 12	132.31 933	170.71 831	139.49 271	416 .57 227	251.222 6	385.47 293	250.5625 5	926 .70	108 8.43	748 .77	508 .19	269.448 23	298. 485	212. 6954	248. 029	184.7 9241
AF25 1705	657. 729 17	745.43 829	567.00 596	113.7 5146	101.7 2788	135. 9442 7	78.1431 27	106.40 584	99.6059 55	3370.7 846	1119.8 56	3639.7 464	76. 336 519	168.281 8	93.794 411	77.64185 3	101 .33	81.2 711	72. 273	195 5.1	104.841 32	96.3 160	88.4 3428	761. 083	1557. 6499
	60.9 019 3	713.31 213	71.566 507	2869. 5042	1244. 322	801. 3676 5	31.7828 2	51.892 7	52.2680 61	2971.3 742	649.07 003	2568.7 652	61. 124 398	48.2135 16	67.710 794	50.31936 9	32. 513	53.8 202	53. 634	199 .90	5684.39 02	103. 072	80.6 1058	67.1 166	99.02 2685
Tspa n32	164. 158 46	688.03 676	927.23 175	126.8 5229	70.53 0069	16.3 8715 6	81.4099 31	589.56 147	250.099 23	44.785 006	17.065 166	25.754 542	119 6.9 815	1729.29 64	2442.3 248	2282.314 1	97. 742	132 3.96	130 7.9	128 .56	13.5827 44	451. 483	48.3 0621	79.4 972	441.1 1343
	17.8 585 a2	662.22 489	413.17 77	13.28 201	13.33 297	18.9 7666 6	15.0492 78	15.466 433	17.8771 08	216.96 769	87.629 653	135.56 873	16. 077 996	17.4147 48	15.610 385	16.07926 2	16. 574	16.2 254	16. 138	69. 205	14.3096 93	18.6 009	17.0 4515	39.9 754	141.3 9381
	4																957	61	519	421	27	7			



Chst1 3	43.2	635.22	1328.9	59.23	35.21	41.9	43.9552	51.164	48.1935	37.902	28.354	35.654	42.	32.2712	46.323	38.81484	40.	39.6	42.	59.	44.9112	42.6	43.3	55.8	60.90
	843	462	633	1675	244	1871	7	06	78	253	557	413	420	35	395	5	883	888	313	016	17	531	6292	933	8875
	62					2							616				942	55	37	89		55	8	22	
AI83 9979	37.9	602.49	39.022	33.28	50.64	24.5	23.4524	28.063	20.9162	116.45	33.731	50.781	29.	24.3691	23.499	25.71593	25.	24.4	25.	119	26.0620	30.5	27.5	32.1	131.9
	752	171	521	5334	0117	2447	14	725	22	822	219	108	629	64	384	4	129	710	595	1.4	15	608	9709	155	742
	81					1							061				407	2	719	143		32	5	82	
Rab4 4	244	600.26	805.31	33.59	25.08	32.4	34.2064	28.367	30.6970	31.069	38.313	43.318	28.	31.6154	32.323		34.	28.5	28.	129	26.0176	29.2	25.0	53.4	79.95
	4.12	694	522	2505	3112	9736	79	518	41	707	702	521	997	9	372	31.2459	026	162	314	.08	56	185	4350	396	3814
	66					5							975				845	05	389	255		59	5	72	
Igj	20.1	548.12	16.978	175.3	18.75	1314	16.9141	67.826	54.4989	17.777	15.921	16.058	101	477.203	31.096	112.7881	24.	16.0	19.	34.	23.5102	40.0	16.5	36.0	39.86
	203	27	829	3242	2073	3.33	96	78	98	957	393	413	.81	09	666	8	830	281	298	683	21	649	3744	150	8232
	37					2							83				761	32	315	656		68	6	41	
23100 05G1 3Rik	11.8	504.56	11.778	10.16	13.33	11.0	10.3470	11.680	10.3464	10.555	14.117	11.136	11.	10.6019	10.865	12.05469	12.	9.99	11.	10.	10.5824	11.2	11.8	10.4	10.65
	643	924	159	4698	2443	3923	42	373	58	949	44	498	707	6	494	5	428	607	623	327	49	934	3564	555	4402
	31					2							364				267	39	181	313		82	48		
Csf2r b2	869	489.50	5685.6	90.34	26.80	37.8	17.0998	19.509	21.2583	2686.0	1891.1	3754.4	18.	20.5022	22.117	19.78875	19.	20.1	48.	408	25.7126	21.2	16.4	329	4160.
	2.48	575	33	538	1349	2573	42	591	9	203	88	477	149	85	719	9	414	647	420	.34	69	663	6750	7.34	2504
	52					5							11				255	92	948	849		72	4	23	
Myb	101	474.56	1562.8	26.89	47.36	42.9	739.278	235.02	396.849	13.849	14.533	13.663	718	95.3733	235.39	531.0320	435	312.	96.	28.	21.9565	250.	164.	25.3	29.26
	5.17	969	261	7119	9321	3195	54	13	76	615	773	376	.17	79	372	3	.69	267	506	155	65	597	1257	603	8684
	23					4							458				041	39	052	547		37	6	4	
Aqp9	210.	464.50	486.16	36.97	31.23	38.7	66.7072	36.677	95.7607	25.840	28.063	31.887	43.	39.7539	40.652	27.02820	35.	174.	881	41.	32.3019	50.4	53.9	253.	168.9
	367	789	133	2677	2986	8056	34	257	88	466	347	075	037	08	396	7	970	271	.96	591	91	533	6729	143	1068
						7							477				73	51	895	453		51	6	82	
Lime 1	95.0	455.38	90.922	149.1	75.59	121.	648.487	1332.0	1953.71	69.700	86.000	68.529	664	1048.97	1449.2	2085.121	584	196	101	100	960.934	424.	352.	101.	86.15
	583	381	187	9204	7755	5496	86	196	46	294	99	35	.60	51	389	3	.44	0.76	6.2	.32	88	691	0847	674	7188
	66					3							666				978	63	075	592		23	6	06	

Olr1	15.1	446.00	1331.1	12.24	13.68	12.5	16.9972	10.470	10.0290	10.909	13.882	33.914	11.	10.3622	10.470	16.14657	19.	13.1	11.	60.	10.6305	10.6	10.3	122	341.8
	982	012	674	4655	7529	9203	22	204	15	206	712	156	762	31	675	1	532	070	668	384	81	025	9359	5.95	2814
	23					5							79				5	49	991	298		61	7	69	
Ifi204	10.1	412.56	57.806	10.82	12.59	22.1	11.9698	9.8282	16.0781	511.53	1385.9	266.26	9.1	12.6194	10.271	43.85388	9.3	9.90	10.	135	8.65162	17.5	11.8	259	350.6
	117	79	915	9249	7734	6035	69	99	72	106	287	157	140	03	614	9	332	895	049	3.1	64	572	4937	0.56	4076
	03					3							786				671	65	437	537		76	9	89	
Cd5l	36.9	405.25	318.93	34.96	29.79	88.8	24.4001	87.552	140.088	7157.3	1415.8	5680.2	57.	79.4496	29.291	28.42256	107	24.6	32.	37.	37.2043	60.2	31.5	53.7	48.28
	592	06	79	8744	7522	8267	28	529	1	889	822	521	316	15	666	8	.21	099	880	370	18	64	8225	400	6309
	55					3							878				461	46	684	062		64	7	41	
Bank 1	50.3	401.23	189.32	10279	9441.	901.	31.0759	147.98	92.2847	87.485	42.194	32.971	87.	99.0788	69.100	50.08504	30.	31.8	21.	143	23.0972	330.	60.6	36.2	61.40
	944	828	319	.768	6079	0419	47	137	07	027	631	207	855	61	092	3	974	413	336	.85	77	476	1212	428	7729
	94					3							017				805	9	886	223		14	5	52	
Il18b p	82.0	398.70	124.76	78.07	79.59	104.	67.1732	82.073	82.1929	370.49	2546.8	486.80	97.	131.025	77.983	61.94317	98.	78.6	79.	98.	96.8746	83.6	75.7	152	362.7
	644	587	652	9988	0269	2708	98	052	29	546	453	664	578	28	59	3	013	485	618	003	18	884	0133	0.50	4444
	78					1							998				582	01	714	669		47	1	67	
Cd30 0a	593.	349.27	421.87	37.21	37.10	40.2	29.8589	35.247	39.7580	633.87	131.22	509.77	29.	41.6610	31.946	28.30497	33.	28.4	29.	849	31.4068	42.0	35.4	57.5	190.9
	885	534	914	6909	8222	0734	62	465	44	467	784	237	870	69	115	7	634	030	218	.34	14	468	3396	283	3258
	49					2							186				909	05	001	72		97	6	47	
C130 050O 18Rik	32.4	349.20	186.74	29.71	47.24	33.3	23.4310	24.312	22.4334	78.069	76.276	61.639	29.	40.5387	24.468	22.93271	33.	29.6	27.	651	25.2812	27.4	22.8	67.1	164.7
	758	392	93	6212	4468	4287	75	232	12	266	369	94	268	46	02	5	578	505	530	.07	33	254	4945	619	8501
	61					3							348				448	55	1	714		49	2	79	
Trem l4	13.9	325.91	118.84	12.12	13.41	18.6	15.8257	32.719	40.5329	52.246	104.90	28.997	15.	23.9037	16.600	15.70531	13.	13.2	14.	178	17.2736	29.4	13.4	75.2	39.16
	799	563	143	914	1546	8601	91	702	49	381	099	518	587	61	072	1	959	455	929	6.8	65	835	8986	404	4935
	58					4							966				695	65	532	37		99	4	95	
Clec4 a3	14.5	318.41	201.98	13.14	22.13	18.1	11.5232	18.488	38.3088	2081.3	719.54	2025.8	13.	20.8674	13.855	13.25385	12.	13.8	14.	849	13.7572	20.0	12.9	657.	1149.
	032	395	776	8125	6252	2839	32	737	68	04	752	304	627	03	716	8	839	246	531	4.3	54	503	5609	239	9007
	28					8							357				702	07	629	309		81	2	41	

Lct	18.0	300.04	26.382	26.24	37.84	32.0	24.9408	21.863	23.7493	19.182	19.569	17.971	19.	15.5098	19.353	21.57217	18.	17.6	18.	17.	402.186	23.5	28.0	18.5	19.76
	281	028	733	6853	305	7751	9	016	91	266	854	177	657	94	643	6	366	509	368	448	14	042	6199	402	6923
	52					3							974				102	57	698	185		59	1	72	
Tbxas	983.	277.98	569.45	35.84	52.41	75.3	85.2919	69.872	71.4024	762.66	636.65	1590.6	54.	106.866	68.035	55.35234	73.	58.5	51.	212	75.1405	44.8	53.4	486.	1164.
	583	76	319	6595	5767	2355	63	328	24	071	13	889	964	48	3	1	082	583	702	.89	48	327	9475	800	2254
	19					1							088				458	21	848	941		73	6	01	
Irg1	25.4	250.36	713.95	23.67	20.10	29.4	19.8599	26.510	23.2380	487.87	10547.	393.49	22.	23.9391	25.018	40.10207	26.	28.8	22.	25.	31.5130	21.4	20.7	114	1796.
	132	129	012	8999	293	4688	59	54	29	864	216	299	786	95	264	7	998	167	735	882	81	699	8707	65.5	4199
	6					5							512				911	17	554	072		21	3	82	
Tlr8	23.9	248.30	34.599	35.11	34.48	35.6	23.5498	25.869	21.5866	371.11	228.32	552.33	26.	31.2027	27.454	28.73641	27.	26.1	26.	301	30.3907	43.8	28.0	126.	114.8
	095	723	185	4873	2314	5854	21	686	5	253	545	289	951	02	602	7	010	971	075	.66	18	440	3909	176	9404
	15												446				875	32	452	043		51	8	69	
Ddx6	14.8	246.36	30.629	22.61	54.11	16.8	20.2606	151.43	155.390	275.32	1789.9	79.367	34.	47.7175	121.23	81.27537	15.	25.9	16.	27.	31.2241	43.3	22.3	618.	31.99
	804	65	11	0012	9888	8998	02	149	37	753	376	294	721	01	105	4	158	762	577	142	31	971	1308	277	1196
	36					5							432				283	53	483	045		68	8	03	
Itgax	40.5	246.26	267.52	34.26	47.36	38.9	60.3053	41.938	144.760	523.07	193.69	703.00	31.	72.1465	30.626		39.	53.4	41.	290	44.6468	133	579.	176	2403.
	123	599	756	9843	3603	5925	7	144	47	814	288	088	906	11	581	35.16005	870	060	481	.34	64	1.79	6009	8.24	9017
	82					4							704				6	87	325	55		78	5	89	
Prss1	32.9	231.18	45.955	177.6	52.50	415.	72.6854	50.987	51.4806	51.002	51.094	47.656	49.	60.5742	64.473	55.32963	70.	181.	56.	45.	37.6226	68.2	63.7	36.7	45.69
	411	603	569	2476	5807	6126	07	287	79	762	546	234	540	09	897	9	034	052	877	243	66	805	2972	249	6182
	57					7							88				301	57	632	048		84	1	02	
Tlr7	22.0	227.67	72.684	182.7	210.0	71.8	31.8324	68.379	69.7542	906.96	677.30	769.25	117	47.2172	59.979	33.27506	26.	25.9	22.	120	26.6059	43.7	35.9	453.	192.2
	839	579	383	0829	0049	8609	97	061	91	354	95	781	.02	18	851	3	036	461	653	3.3	66	212	5168	733	9991
	1					2							778				112	89	148	662		14	2	48	
Cxcl2	15.7	224.10	600.09	17.95	18.13	22.1	14.7162	16.967	13.8939	149.91	510.21	89.194	41.	23.3876	14.668	68.72753	20.	53.3	74.	38.	15.3147	20.5	15.4	742	920.0
	767	44	956	6416	5083	2959	27	449	46	904	361	58	071	02	15	1	796	310	640	417	07	112	9230	1.58	1655
	92					6							132				032	11	703	531		08	4	97	



Jak3	133.16582	183.36369	83.874811	58.067668	64.119371	67.775373	139.49906	156.38248	287.21234	53.242403	93.955526	60.154481	615.91479	444.57532	188.92205	255.5014	946.57	123.049	134.13	127.83	723.50142	179.570	155.2952	206.293	158.58502
	327.15609	172.31875	4185.935	49.671569	23.323417	26.995949	26.871222	24.35194	25.29711	19.236961	23.415008	24.027586	23.617176	34.73182	24.994551	25.816537	25.056	21.2992	30.506	39.207	34.265678	27.6224	26.08516	42.1633	45.321939
	618.2858	171.79662	192.37295	105.57539	165.69625	103.22976	1962.4283	487.645	702.37141	34.461992	33.821028	35.641031	285.887	549.11648	939.27512	2755.5957	244.62	185.337	520.95	36.792	782.20285	754.799	1023.148	142.527	152.69111
P2rx1	487.49644	171.17926	1255.1104	33.736065	30.154908	36.901057	36.206934	37.262536	33.848286	28.391854	31.873434	29.911744	32.119258	26.502366	33.575286	30.280506	35.114	30.1650	31.587	51.604	29.477403	35.2312	31.51059	33.9742	33.744849
	31.258548	169.38893	23.021845	11.615434	13.050315	10.405482	9.9955017	9.8921939	9.7197017	10.607443	25.46814	9.8336387	10.396648	12.253995	10.790727	9.9243095	11.408	11.3075	11.085	330.70	10.285535	10.8536	10.57023	23.7857	19.248777
Zbtbd6	17.24301	169.33599	68.793834	28.068682	32.113197	227.52359	58.709253	12.207506	13.547781	20.127576	15.192734	19.546159	29.019075	15.825632	16.187046	26.525332	26.029	21.029	27.84	24.707	18.597608	17.4505	43.49594	15.0427	19.08999
	99.645565	168.46425	577.71737	18.413859	19.207452	31.957909	17.087053	31.69177	34.740853	501.02789	525.01389	301.83613	16.772462	28.138556	18.087389	17.525807	16.756	61.1049	20.892	115.79	16.395743	23.3428	17.21157	698.102	8908.4961
Hal	24.609596	162.12581	22.414881	18.379227	19.088013	23.261654	26.570124	24.13186	26.639295	835.2099	71.616234	307.82889	25.599405	26.950846	26.410776	24.779781	22.034	34.6119	32.972	67.288	31.487861	40.9199	29.36291	31.3216	37.491653
	20.084	156.36831	22.775943	33.335078	23.006288	5183.1779	23.795673	34.653452	26.669323	24.284853	23.299007	26.373364	38.579441	42.961032	29.373566	26.367347	21.318	22.2670	22.558	34.151	23.566663	21.1042	18.96557	47.4787	46.971283
Ighg2b	84	831	943	5078	6288	9	73	452	23	853	007	364	441	32	566	7	387	65	108	557	63	1	3	33	

Pld4	35.0	155.76	318.32	983.1	700.0	922.	26.9439	37.944	69.0442	1360.4	1054.6	1188.0	53.	103.004	35.613	37.28598	45.	37.7	38.	529	38.2168	89.4	37.2	794.	1809.
	727	968	243	9021	6797	6936	66	168	49	968	386	04	659	25	82	1	133	261	712	0.5	56	366	3092	396	6281
	5					8							852				429	26	81	328		47	47		
Mzb1	80.1	153.26	47.753	2692.	1831.	1290	61.6740	69.275	63.4854	58.651	65.742	59.033	88.	91.2658	75.093	63.63442	68.	62.0	74.	96.	81.1330	159.	57.4	123.	84.99
	217	436	563	2272	5533	4.11	3	009	94	26	775	129	089	89	512	8	307	057	020	670	35	166	3523	573	8937
	68					5							94				37	29	637	958		07	5	82	
Spns	731.	148.44	1472.9	160.3	177.3	82.2	56.2019	70.008	58.6982	61.444	81.875	63.538	59.	153.260	68.412	64.49026	70.	63.5	95.	111	96.9656	77.9	71.6	101.	89.88
	965	962	915	29	2815	8767	21	036	17	703	423	814	301	67	053	3	842	241	739	.29	47	795	7143	967	4733
	3					1							282				673	76	327	355		85	3	89	
Lfng	41.8	146.61	65.228	36.80	31.07	28.8	61.2718	78.004	72.2729	49.903	39.443	49.674	152	60.2449	129.39	67.57386	197	190.	288	62.	64.2839	60.3	63.5	51.9	85.31
	972	212	016	4747	2265	5639	06	318	37	446	448	642	.72	08	223	9	.15	440	.37	344	48	235	9319	496	594
	32					4							591				881	16	763	798		3	8	36	
Fcr11	22.1	146.01	20.928	3533.	3298.	320.	27.0414	20.861	23.1265	111.32	42.150	28.883	88.	104.435	27.611	193.2813	119	29.3	27.	76.	28.9540	56.4	23.0	20.7	19.98
	742	742	311	1442	0155	3125	37	586	42	18	647	514	472	9	173	2	.79	436	551	942	53	290	4835	368	3883
	58					1							313				291	83	659	942		31	6	36	
Ccl4	119	143.83	522.92	107.6	69.19	108.	4231.13	128.73	498.499	420.54	2351.2	453.38	226	91.1511	84.180	97.27051	695	84.4	68.	140	1162.08	622.	812.	507	426.6
	5.20	894	164	3019	7066	8136	85	364	75	86	724	052	.83	47	471	6	6.0	618	752	.99	46	971	4624	1.92	3931
	13					2							924				866	02	264	445		91	3	96	
Clec1	12.4	141.25	487.74	14.51	18.31	18.6	12.5161	17.417	22.3690	31.437	24.528	24.015	14.	20.5086	15.108	14.09236	12.	15.0	16.	207	14.4113	20.5	16.2	25.6	56.47
	177	924	929	2654	3252	2178	89	681	86	478	426	73	181	82	275	2	585	536	062	.33	53	249	9170	128	5094
	32					4							021				676	33	082	226		86	3	36	
Gm9	39.6	139.16	39.499	24.17	20.43	37.4	60.6810	71.589	83.8219	76.152	2013.6	48.296	63.			92.895	33.	38.8	45.	44.	47.4431	55.0	51.0	232	41.99
	279	317	505	0752	4833	7287	18	337	28	99	661	674	821	41.3212		142	180	849	089	000	65	016	6365	2.12	0359
	706					2							733				683	46	452	959		34	4	91	
Rnas	366.	138.94	973.36	1889.	1867.	881.	10.4866	17.392	17.6909	20.179	195.57	19.166	12.	16.6532	12.987	11.44107	11.	11.5	9.8	339	9.84883	78.2	13.0	38.0	298.8
	320	584	164	3615	7578	3018	89	184	08	381	681	38	481	61	001	8	181	763	971	4.0	02	739	0179	669	4937
	e6					7							549				203	66	158	358		03	1		

Hem gn	13.5	138.17	40.460	27.59	71.25	15.3	395.969	12.232	15.0137	12.716	12.026	12.180	23.	13.0535	13.532	15.24710	20.	110.	73.	17.	14.3985	86.7	903.	14.2	14.68
	582	338	894	6706	1116	1176	02	701	91	934	205	026	879	49	245	4	450	819	210	274	09	686	3535	631	0775
	74					6							082				875	7	386	161		62	2	5	
Rcbtb 2	126.	138.16	169.53	83.80	107.9	418.	44.6347	137.31	181.825	896.12	92.018	484.04	91.	165.748	148.95	134.4501	36.	113.	268	154	174.494	130.	212.	122.	746.7
	971	525	712	0982	111	5044	16	353	15	502	459	306	707	96	846	3	296	519	.49	.87	55	783	0386	364	2065
	63					6							529				657	76	592	353		37	1	36	
Cd20 Or1	434.	129.96	121.63	14.05	12.36	13.5	15.7817	19.927	19.6846	435.98	68.145	362.01	28.	24.0872	66.966	84.07828	15.	49.9	470	16.	951.032	16.7	16.7	215.	623.7
	448	63	662	3062	8902	3366	05	206	95	458	994	551	748	7	361	9	862	898	.12	726	58	606	9770	234	0935
	2					3							024				016	74	715	264		86	5	83	
Itga2 b	598	123.41	2290.7	87.39	71.63	91.2	49.4747	61.101	65.9347	65.830	61.475	60.290	67.	55.8262	84.908	63.11441	52.	54.0	72.	145	72.8330	67.9	56.9	121.	109.3
	2.25	753	431	2712	3289	1796	59	842	91	079	835	439	597	91	088	5	864	384	282	.60	67	765	8123	731	8001
	21					7							275				636	93	823	328		95	72		
Ubas h3a	29.1	123.39	41.902	29.93	25.39	31.4	264.849	267.87	310.002	29.028	23.408	26.790	537		359.09	408.4577	227	474.	563	31.	27.7030	107.	123.	24.5	25.58
	615	82	206	1411	7151	8061	52	434	38	798	448	544	.12	439.039	945	1	.18	372	.11	941	74	434	8404	500	6872
	34					6							807				29	85	612	311		23	7	93	
Emr4	15.2	119.64	960.79	21.57	24.06	30.6	16.1191	36.293	35.2704	143.95	16.923	74.909	18.	22.7318	17.700	16.93415	14.	15.9	14.	314	17.4987	37.4	15.5	479.	1228.
	289	645	727	636	9324	8818	23	263	15	261	651	524	852	19	035	3	933	403	100	9.4	85	526	0509	922	6916
	28												743				448	62	37	025		12	13		
Gima p3	118.	118.30	58.274	551.5	386.9	152.	263.116	1402.4	1869.51	61.381	62.809	65.518	238	3987.09	1732.7	1358.630	106	346	195	118	2807.97	121	1144	209.	124.6
	381	017	69	4196	7646	3986	3	204	93	855	749	329	2.9	97	282	5	3.4	3.22	8.3	.03	93	3.12	.897	615	6295
	64					8							67				52	32	199	639		08	2	12	
Prg2	14.4	113.59	25141.	17.89	13.93	37.8	15.8742	17.009	16.3522	22.147	21.349	17.657	27.	18.8114	15.162	15.09857	19.	13.4	14.	19.	15.1910	14.3	17.6	142	1522.
	365	637	756	6456	7675	3663	38	046	95	539	915	891	346	53	015	2	332	482	333	635	52	205	0819	1.59	9992
	73					3							744				466	67	399	768		59	93		
Tal1	317	109.67	425.65	33.97	25.25	35.9	23.9716	29.157	27.3257	92.956	76.232	83.352	26.	24.0079	24.131	21.78130	23.	24.6	23.	30.	24.3163	27.8	29.7	145.	169.9
	8.73	224	673	8317	0381	5294	89	162	22	467	356	454	616	75	775	3	637	180	043	349	77	787	6823	364	0896
	39												819				143	22	801	339		99	7	42	

Cd3e	57.6	109.04	44.371	48.23	49.89	67.4	475.823	1133.7	2931.72	54.305	58.174	46.461	198	1523.73	1651.9	1504.663	153	222	157	79.	3367.03	63.8	64.8	77.4	53.00
	296	975	626	7288	843	6624	55	062	97	602	921	028	0.6	13	211	1	2.0	1.58	1.7	850	3	893	0137	407	9893
	68					6							108				134	31	761	248		78	3	04	
Cd72	134.	107.17	206.39	1368.	2533.	59.3	191.837	893.06	637.068	829.33	3569.6	877.70	390	229.516	315.74	161.2168	56.	266.	54.	62.	58.8126	143	623.	329.	134.0
	687	741	74	5504	5147	6615	44	785	09	282	622	966	.01	29	395	8	359	590	489	961	59	1.93	2250	638	3729
	67					9							754				373	7	867	057		94	4	15	
Trem 2	90.2	106.74	593.50	120.9	87.96	111.	89.6306	110.23	85.1366	5166.8	555.55	4707.2	68.	111.737	92.692	76.55482	94.	81.3	84.	262	74.9351	160.	111.	809.	1836.
	731	796	168	8097	0821	2563	11	974	66	341	443	27	037	57	237	8	028	201	461	.03	76	531	6863	208	5843
	79					8							231				465	56	429	818		59	8	71	
Pyhi n1	14.7	105.62	33.338	2913.	4536.	1170	203.142	2596.8	1821.80	433.28	4017.0	222.51	239	2128.51	2142.8	1233.441	22.	712.	344	243	459.923	860.	338.	485	320.2
	121	503	941	772	8409	.057	31	629	95	962	04	228	.96	85	729	1	375	877	.64	9.6	14	215	3120	9.74	275
	81					7							081				656	04	372	871		6	2	75	
Gpr3 5	35.0	105.19	101.59	23.77	24.51	19.9	22.4367	23.678	22.2097	30.172	104.46	25.700	20.	28.1616	21.357	48.92242	22.	21.6	20.	140	22.4270	24.6		204.	189.8
	872	887	847	3933	262	9939	85	003	95	21	542	653	689	27	098	5	822	351	306	2.0	77	487	5325	754	2683
	16					6							549				788	02	816	146		7		08	
Cd24 4	524.	103.26	156.47	31.89	25.47	14.5	24.4895	18.779	26.9450	20.064	23.766	27.794	16.	18.0551	16.658		16.	16.7	25.	571	4046.83	176	1982	36.5	72.24
	323	668	103	0589	2866	7613	5	333	42	165	55	506	178	28	072	14.38101	798	763	448	.30	98	4.96	.465	260	7921
	23					8							557				369	99	237	611		3	9	76	
Fam7 1b	21.9	102.47	16.100	18.35	16.51	25.8	389.459	167.24	89.3588	18.604	16.847	21.058	45.	21.2985	35.716	53.89902	301	86.6	194	18.	68.3728	18.3	24.7	21.8	19.62
	568	457	565	4783	2786	9303	19	966	68	732	998	128	332	11	016	6	.18	963	.17	770	11	409	9382	563	5923
	49					8							488				458	47	854	315		06	3	88	
Cd6	51.6	101.83	48.649	56.90	78.92	73.6	750.385	867.81	1120.86	50.095	60.324	53.494	175	2081.90	1310.4		282	122	291	58.	69.2856	53.2	51.2	76.0	79.18
	504	346	054	4436	0586	2366	88	591	38	972	868	305	5.2	39	898	1805.366	4.0	1.86	.34	544	33	466	1708	349	5217
	58					5							016				576	01	633	155		31	4	91	
Ms4a 1	20.0	97.241	15.224	12133	1009	1315	22.2906	44.011	23.0375	19.455	16.492	19.020	25.	73.1468	18.236	18.39731	18.	16.0	17.	46.	22.4158	280.	17.6	23.9	23.55
	182	462	71	.27	5.428	.009	52	111	21	057	116	818	714	85	053	7	691	334	074	634	39	571	4852	027	5446
	93					8							867				613	2	969	861		5	8	62	



H2-DMb2	45.698303	93.61397	45.441347	109.26895	112.91309	37.898648	41.32863	43.400414	40.529727	64.24631	70.98336	65.242879	58.900389	45.268883	39.835718	64.776305	46.716	68.216	41.993	93.771	49.297888	51.008	35.005	986.61	1171.7879
Klrk1	34.432601	93.111343	58.290144	61.458485	56.051768	53.81068	1568.6413	97.889159	1605.4902	52.930481	1217.2064	52.0846	60.645936	67.896932	68.746677	44.883216	164.66	44.3745	41.436	205.38	78.251561	253.616	1932.561	516.272	233.97506
Fcgr1	40.269661	92.232551	103.9517	36.936469	30.795746	37.75456	29.234258	38.23995	41.503553	719.11014	2943.2185	314.72609	40.265526	38.09353	45.313212	37.713949	31.270	36.9723	42.104	509.50	35.114851	36.7502	34.05661	146.1.64	570.47531
Ly6i	50.170688	92.008554	50.889892	46.873498	46.585165	45.22043	49.868994	44.604126	46.299167	75.59244	494.91919	67.022139	46.623101	42.794301	55.034818	47.297769	56.683	53.4202	50.570	389.11	57.765554	44.7770	44.18058	290.2.35	1161.9723
Ms4a4c	12.324781	91.466492	50.213371	260.14481	1890.3584	14.301506	880.75074	1533.5991	3266.1523	238.96738	5316.1747	112.04243	105.00473	292.31116	327.37051	180.57761	48.806	21.7411	15.573	436.6.7	13.344581	391.030	107.2280	283.9.35	44.910762
Ly9	23.647499	90.790967	408.33635	124.4661	121.91892	137.88492	648.62031	1092.6499	1377.0734	1379.0585	1358.4673	1066.7697	638.10159	338.84766	1168.3264	1058.0491	292.98	573.035	476.69	131.88	46.897182	313.152	208.5696	654.944	250.45228
Klrb1a	12.802383	90.605198	15.538566	10.225756	14.37628	10.853641	15.302688	14.909582	14.560539	31.911565	12.738775	21.510477	11.126744	14.780977	11.481536	38.2195	12.713	11.9202	11.950	13.258	64.123204	743.501	440.3493	15.4798	57.415549
Ctsw	72.878222	88.778485	56.554554	50.658436	33.023534	74.039914	805.21902	3664.1039	7643.5447	39.986307	46.89243	47.070605	238.57224	1406.2051	818.40515	363.42845	392.53	149.6.69	206.19	69.665	7840.4198	548.3.39	5367.170	64.4270	56.773676
Hist1h1e	13.925979	88.494261	20.451208	144.96518	160.85274	142.77503	51.247952	30.591439	26.737926	13.088684	11.960325	12.127758	32.430653	17.066008	52.584685	44.853093	18.534	86.8690	73.910	21.936	21.716456	38.4120	15.32794	12.7081	12.484501

Spib	23.8	88.316	101.11	2404.	2032.	24.8	27.2107	26.940	25.0716	22.536	21.815	22.179	38.	48.9096	22.730	28.27818	43.	25.0	19.	44.	31.3496	87.4	20.4	152.	318.5
	445	418	836	2402	6966	6286	19	417	02	216	904	304	129	18	471	5	000	270	008	380	93	929	5278	443	8286
	78					4							873				023	72	204	848		77	9	62	
Ighg1	28.4	87.888	25.349	1667.	26.89	1964	25.5297	25.596	29.1127	29.564	30.128	29.201	41.	34.1791	27.127	30.26841	36.	26.8	27.	40.	25.2468	21.7	23.6	23.0	24.28
	330	601	791	0567	5162	9.66	91	634	8	633	545	135	307	66	031	6	563	506	648	776	53	813	2010	567	7002
	41												364				9	43	85	136		56	1	18	
Herc 6	53.6	87.463	24.490	56.23	61.21	45.7	88.8004	131.08	107.998	158.82	1734.3	106.02	73.	64.3084	112.00	99.33163	78.	121.	112	95.	69.0138	75.2	98.6	866.	64.32
	285	738	045	7696	157	3835	62	37	59	212	048	318	908	05	998	3	755	112	.71	051	77	882	0879	795	8752
	81					3							651				65	23	31	756		99	9	31	
Gm2 0199	37.4	83.363	39.577	803.6	535.8	306.	46.7363	80.386	65.2718	38.527	35.284	43.966	33.	56.2052	89.746	71.45960	38.	46.6	43.	87.	64.2083	603.	258.	44.2	41.61
	644	705	683	7863	8252	4548	44	334	74	753	527	681	275	8	906	1	653	771	811	154	44	182	5979	799	5773
	72					1							05				387	95	399	59		15	7	73	
Cxcr3	36.4	83.311	60.180	530.3	38.56	709.	408.347	417.27	4701.22	205.72	44.646	144.24	348	4029.27	157.10	2944.703	410	50.5	45.	68.	373.077	263		51.4	47.62
	439	76	673	9606	5803	1549	7	649	93	791	509	341	.87	34	241	7	.32	898	616	568	06	1.80	1640	052	0647
	21					7							365				834	99	878	64		92	.975	65	
A430 035B 10Rik	40.4	82.753	39.428	26.59	91.51	193.	15.4761	23.504	23.6314	26.804	19.250	26.412	21.	15.2488	27.063	25.23813	14.	18.0	16.	16.	27.6722	25.1	24.5	16.6	21.10
	842	741	071	2372	2922	6735	19	049	69	377	9	169	647	42	806	2	307	639	577	973	23	081	8607	190	7512
	29					1							847				263	47	981	53		42	2	83	
H2- Eb2	61.2	81.395	47.617	1425.	1211.	452.	94.4986	103.06	98.6002	57.702	104.20	73.520	69.	83.1339	86.677	70.77548	62.	58.2	61.	73.	113.165	89.5	59.4	223.	158.5
	358	827	283	456	3827	1896	95	172	6	042	86	933	165	08	834	9	088	590	051	093	61	883	8259	400	0428
	96					9							84				283	14	796	953		85	4	18	
Nmr k1	150.	79.781	124.54	143.2	30.78	78.4	543.482	118.05	151.633	113.33	46.191	79.213	35.	19.4057	64.931	35.97775	186	133.	41.	14.	137.169	31.3	38.0	33.1	35.33
	145	932	013	9921	4068	906	53	127	32	084	106	807	608	71	699	7	.62	319	931	579	36	042	5422	859	4414
	02												296				984	51	119	754		22	6	38	
Gpr1 14	48.2	78.599	54.771	152.5	72.95	112.	193.616	1460.9	1650.02	53.761	62.325	61.569	68.	159.826	76.304	60.29118	105	318.	61.	88.	1507.94	299.	399.	64.3	79.18
	527	306	317	961	5453	3477	8	49	66	265	194	49	438	83	476	9	.08	324	632	536	39	321	1050	841	5096
	78					4							784				064	69	91	914		49	6	22	

Cpa3	167	77.981	9487.6	61.69	26.28	25.0	32.2048	30.847	25.1524	24.616	25.698	27.307	27.	23.5684	24.388	24.45335	44.	22.1	46.	31.	41.5352	27.8	23.5	64.1	77.09
	71.7	778	164	7515	4943	8447	11	573	67	733	46	923	168	04	405	6	629	727	348	512	59	704	1	54	1914
	22					9							089				069	96	098	117					
Faim3	20.3	76.919	21.739	5201.	1055	92.3	106.728	29.518	22.3999	20.794	22.405	20.574	234	205.095	22.768		82.	82.3	322	52.	22.4888	231.	31.8	46.4	29.43
	162	12	138	174	7.316	4785	96	798	5	572	87	367	.38	92	944	92.49716	607	215	.76	240	49	856	9461	319	7353
	97					3							728				308	96	629	673		1	1	69	
Ccl3	216	75.963	3646.8	46.89	17.41	16.2	9339.51	29.810	119.584	564.97	2656.3	282.37	94.	29.9085	17.397	31.32126	950	79.9	17.	102	1054.37	136	828.	654	394.7
	9.24	334	236	2373	6375	8199	07	558	21	746	31	507	767	7	787	6	7.2	713	535	.85	3	6.88	1102	8.09	937
	25					9							325				875	66	804	065		32	8	41	
Cd4	63.1	75.691	55.147	68.09	81.91	79.9	51.9040	56.896	50.6781	58.673	68.682	60.516	368	321.183	260.74	351.3329	616	226	109	75.	59.9370	79.5	70.1	75.8	60.98
	055	094	123	9177	2518	3815	19	451	86	309	313	074	.92	64	565	7	.44	7.12	5.6	273	96	705	5183	420	1227
	49					9							241				689	39	742	295		45	5	95	
Lck	62.0	75.302	48.238	125.4	171.5	62.2	1731.51	4529.9	5056.18	61.535	84.521	54.105	454	5041.14	5373.3	5737.224	291	438	223	89.	5017.48	350		126.	66.60
	616	736	997	24	1929	1681	32	098	71	074	889	658	9.1	94	661	8	0.8	0.11	1.2	679	68	0.72	3360	276	4693
	54					8							229				538	15	927	732		97	.93	75	
Ccr2	19.6	75.249	157.97	15.77	15.23	17.1	103.439	25.120	201.834	49.283	30.352	27.044	43.	55.3081	26.727	43.90991	60.	483.	391	295	15.7667	652.	986.	184.	1826.
	570	401	77	3326	2478	8409	86	381	76	845	761	02	232	6	194	8	998	564	2.7	5.4	23	695	1645	318	1122
	91					1							593				305	87	03	26		09	7	35	
Cd7	69.1	74.357	94.360	48.74	34.05	50.3	78.6026	448.82	819.530	42.886	48.367	46.590	141	181.938	230.75	87.68620	50.	66.9	54.	86.	14460.2	888.	364.	69.5	59.44
	754	711	7	5175	5306	5681	02	446	09	239	583	321	.08	8	752	5	555	706	307	273	73	404	0271	624	795
	32					4							085				65	24	883	555		01	6	17	
H2-Ea-ps	67.2	73.667	52.348	66.04	100.0	87.4	61.0419	68.889	58.8726	1147.2	812.60	1141.0	57.	61.7062	61.977	52.14403	80.	52.1	57.	76.	68.0423	66.4	62.4	82.9	69.18
	789	588	734	4547	3771	9942	71	174	95	512	185	577	212	25	89	6	658	787	556	661	03	353	6793	942	3992
	62												161				204	3	558	353		9	2	8	
Gpr18	22.7	71.695	604.52	3795.	3439.	521.	481.301	1706.6	1718.73	58.884	925.80	38.852	645	903.236	1110.1	302.5290	105	127	41.	846	4346.25	890.	357.	67.8	61.38
	929	601	501	776	3764	3391	64	15	17	3	131	813	.55	35	791	1	2.4	7.14	973	.82	38	229	6935	498	9444
	02					7							639				172	29	831	488		38	3	27	

Nkg7	48.0	71.629	135.10	25.60	21.33	22.0	3249.30	2983.4	7888.42	22.193	23.515	18.906	499	671.460	161.24	267.1448	352	44.5	87.	72.	8616.70	774	6636	29.2	25.94
	958	065	343	0475	1962	2741	53	225	88	711	888	141	.74	66	2	2	2.8	259	337	594	02	9.91	.129	211	0735
	89					7							35				173	03	316	587		89	1	6	
Lair1	78.8	71.308	351.67	27.72	19.90	19.9	28.4846	82.956	185.771	503.37	434.80	902.03	40.	23.6052	79.413	36.86546	18.	40.4	26.	272	17.6461	79.6	66.8	76.1	120.9
	890	571	63	5788	6101	5786	06	119	89	986	544	779	884	12	101	3	364	819	273	.95	7	644	8721	426	4664
	15					8							354				171	18	066	853		93	1	29	
Cd19	40.6	69.898	40.479	624.7	429.6	104.	39.8511	45.141	44.3322	42.218	39.264	41.344	50.	126.262	56.591	43.43026	61.	45.2	47.	79.	56.3399	112.	49.9	86.1	64.93
	031	4	136	0873	5398	1264	5	832	18	79	826	736	771	85	429	1	576	150	753	027	6	109	2868	891	0252
	6					9							526				71	81	456	316		17	2	87	
Gm1	18.0	69.654	18.608	1501.	1661.	122.	19.5192	2421.1	1622.63	18.120	16.122	14.842	88.	927.724	2477.9	294.4564	19.	139.	28.	15.	17.8624	455.	115.	12.1	12.81
	932	077	192	7625	571	7934	12	214	33	245	595	103	652	63	391	8	934	344	499	583	06	091	7645	171	4157
	1346	04				7							927				878	95	562	46		45	9	41	
Klrg1	107.	67.724	202.72	51.41	27.72	47.8	60.4386	82.888	160.059	41.971	60.895	43.695	232	982.802	109.65	169.7043	76.	48.7	63.	63.	123.813	393	646.	55.1	43.02
	452	958	795	1673	6746	9689	14	32	24	735	353	021	.19	57	378	8	622	102	219	109	06	5.18	8019	768	6297
	49					3							817				084	34	112	283		97	5	22	
Ccl5	62.1	66.552	108.65	33.32	39.29	53.5	1739.28	2062.7	13808.7	653.80	15297.	504.89	195	3547.27	1188.9	825.8505	332	97.3	70.	121	19189.0	126	3533	134	5119.
	703	983	517	2797	7683	5484	13	615	34	924	824	976	.40	91	214	7	8.5	604	128	.21	26	86.6	.516	32.5	6788
	84					2							391				36	71	894	642		06	3	89	
BC02	47.7	66.038	38.123	59.82	40.38	64.3	115.608	349.09	537.887	32.292	46.320	38.845	638	623.889	539.34	802.4825	215		753	70.	63.1475	65.1	53.2	72.1	52.95
	893	155	718	6795	1209	6128	22	109	57	681	625	995	.04	97	104	6	.14	445.	.69	616	95	664	8981	118	3812
	1614	41				7							714				513	555	91	755		23	2	66	
Hc	25.4	65.632	20.946	15.79	27.26	25.4	20.5584	18.066	17.0217	16.992	18.447	16.303	22.	24.3080	22.014	36.63882	27.	23.3	422	21.	20.4528	20.3	18.7	24.4	20.91
	229	509	368	7287	2292	1342	34	313	08	759	678	594	222	13	747	7	273	392	.32	571	61	019	7668	707	1944
	62					9							01				654	09	022	328		72	7	83	
Gzma	29.1	63.532	23.476	41.02	54.45	61.5	54.2567	105.46	132.397	26.078	23.018	25.681	40.	136.175	117.43	66.93238	510	127.	706	119	16768.1	173	1435	30.4	30.69
	229	495	09	3599	9271	3945	7	892	77	342	051	032	693	57	741	4	9.0	186	8.9	.82	7	93.4	7.77	460	1975
	75					1							038				737	67	173	196		71	2	87	

Btla	20.5	63.466	91.439	10106	1125	282.	420.117	1282.4	1529.26	18.764	27.030	18.290	118	3716.21	1483.5	3252.411	206	179	163	115	23.7503	242.	23.6	550.	86.33
	547	798	583	.228	9.768	8210	78	378	83	625	516	423	2.6	46	267	4	6.0	9.82	.90	6.1	6	586	0164	497	0354
	38					8							416				216	86	177	343		77	1	5	
Gm1	26.0	62.636	32.547	38.49	19.22	21.0	20.3022	42.349	43.0758	30.021	34.269	26.979	84.	70.6604	285.59	35.35732	20.	29.0	93.	35.	21.9460	26.2	21.8	26.5	26.74
	277	288	793	7083	0058	8476	45	479	33	812	465	967	359	76	809	7	662	784	958	706	14	600	6689	900	9664
	5708	77				7							439				608	7	078	115		47	3	9	
Ear1	10.5	62.586	22212.	11.65	11.13	10.3	9.79679	8.6108	9.60130	11.355	10.224	10.208	16.	11.4400	11.033	9.486972	15.	10.8	9.1	13.	9.76667	12.9	11.8	530.	486.2
	093	668	359	9713	5856	5000	2	303	41	136	535	381	065	14	01	8	638	978	476	272	06	358	9028	123	065
	35					3							847				484	66	502	999		61	4	6	
Il1r1	776	62.547	396.43	43.17	33.77	37.3	85.6011	39.728	31.8331	40.918	44.883	55.078	49.	74.5894	40.174	40.89062	64.	36.9	588	31.	36.3792	42.9	49.5	65.9	71.04
	6.60	811	809	191	6512	7517	09	006	52	567	085	48	815	14	578	5	741	392	.02	671	79	092	6302	669	0641
	97					9							653				735	45	198	453		01	5	86	
Batf3	51.9	61.806	135.69	58.49	52.32	66.9	1180.36	73.477	61.5734	149.28	244.25	896.06	98.	51.7550	56.676		173	471.	55.	275	72.5036	95.8	74.5	567.	654.8
	509	276	807	42	3329	2552	49	712	42	695	062	177	618	45	003	52.94736	7.5	647	164	.53	2	666	8831	331	4089
	14												957				425	62	793	234		01	1	72	
Gata1	957.	60.506	1637.7	41.72	39.75	42.8	32.7537	49.759	34.3905	31.543	33.902	36.062	197	47.8561	99.370	42.05937	29.	43.7	65.	28.	29.1638	38.1	38.2	43.8	47.27
	556	669	137	3934	9221	3904	8	536	49	596	774	329	.95	16	418	2	459	436	570	822	88	008	0668	413	082
	96					8							894				518	65	906	666		3	4	32	
Pou2	11.2	60.460	9.6323	2923.	3013.	4846	35.9904	166.70	145.432	9.9890	9.8763	10.115	65.	295.229	112.14	1171.367	348	66.0	11.	18.	11.9529	76.8	12.1	12.0	11.60
	575	335	694	7881	7573	.151	1	16	61	57	029	545	075	75	925	5	.08	512	500	911	66	769	8934	834	3911
	3					6							752				162	99	371	617		97	1	25	
Gngt	154.	60.389	61.599	48.29	49.42	25.5	32.2603	56.167	61.9973	391.67	407.29	211.18	42.	35.2907	45.195	35.22927	36.	80.9	44.	104	51.3608	28.3	33.8	392.	210.5
	981	44	818	2444	4739	0701	63	621	85	274	738	533	741	89	333	4	886	045	768	2.9	47	341	4227	452	6883
	2	63				5							759				719	86	079	6		84	9	71	
58304	60.5	60.030	42.034	57.42	59.66	61.3	45.9008	57.502	243.640	43.029	54.187	47.115	62.	88.0621	53.956	58.68110	55.	223.	54.	61.	74.6747	54.9		91.4	81.14
	11N0	661	223	892	2728	8958	41	722	56	098	647	15	431	71	84	8	713	138	127	317	91	338	0044	132	9997
	6Rik	17				4							143				377	69	133	197		14		17	

Nrp	125.38523	59.574126	56.786299	192.33171	193.25129	199.00745	167.11425	233.88779	172.68206	78.117927	53.492677	88.562223	224.79079	92.843563	246.34792	173.01969	297.62056	444.80180	494.369236	85.72191	98.6518191	178.191	184.9800	76.3555	123.31355
	19.855852	58.935885	52.113839	23.816256	26.696223	21.396853	16.360145	18.218418	21.829827	19.748545	17.5215	17.351704	17.996434	18.417334	18.586829	16.913585	22.47898	19.040835	18.994995	726.67463	20.62452	21.8637	18.23118	26.6246	58.338851
	39.4088P1	58.371786	23.825322	52.027669	70.892611	27.786488	44.068725	140.52898	176.74847	32.515806	30.83392	32.914178	41.747652	35.55412	86.07969	66.023368	30.793	141.298	72.545	23.686	38.248894	35.7371	44.46689	18.2570	20.854708
Folr4	47.780178	56.443238	35.896213	51.467112	105.14789	38.674442	82.620422	118.08385	78.19315	41.708059	42.843235	43.238023	269.03527	1807.1438	382.10242	2040.818	325.16	138.418	953.83	49.205	60.303308	63.5990	48.07680	43.6273	40.120784
	18.364646	56.399817	28.746433	10.547551	14.511391	14.229814	15.24485	14.780264	15.769755	63.608397	66.480896	122.74228	15.542057	15.304087	14.027047	12.305584	12.911	13.5958	13.041	12.990	12.589937	13.0878	14.30877	26.5880	22.537745
Trac	46.951663	56.301551	51.042463	45.943123	48.937969	59.215129	3087.5153	7317.5934	7627.4307	43.352974	56.873913	47.227985	573.04659	4205.1333	9046.2985	10724.954	333.01	881.280	604.80	88.059	5071.6805	155.098	125.5910	52.2090	50.932507
	52.608077	56.224458	39.040298	59.331066	52.222911	51.119734	49.37586	54.012321	160.18722	45.840702	42.676899	43.913042	51.528138	112.46205	59.088475	106.37438	48.075	43.5628	44.232	68.366	52.217905	602.237	4087.147	61.1692	54.005782
Blk	45.740106	55.740571	36.183987	1032.2335	913.85261	133.07839	40.761487	50.302696	49.461342	38.730849	40.178847	33.897764	58.865947	73.602381	49.239988	52.749342	47.484	57.2548	40.222	71.708	79.144751	80.5163	36.55067	102.128	75.979665
	34.30853	54.166298	9426.9276	37.193914	27.318858	40.994104	33.920072	36.212901	34.938592	27.897897	33.819763	27.575483	30.723171	27.115832	34.642752	32.210809	35.386	28.5145	31.657	40.545	39.386804	35.6041	34.99141	111.692	97.438987
Prg3																	935	81	4	418		22	5	67	

E230	17.9					19.4							22.				24.	17.6	24.	293		18.2	14.6	43.1	
029C	269	53.676	17.894	25.40	17.00	1277	32.1656	21.065	17.2937	23.370	25.590	29.187	571	18.2287	17.551	21.22869	476	476	884	.49	21.2440	102	3330	646	76.61
05Rik	99	084	837	4117	0563	5	51	949	84	96	055	701	387	72	931	7	937	2	062	15	75	88	3	24	9557
Flt3l	404.					14.9							300				116	482.	108	36.		58.2	108.	30.1	
	702	53.588	111.23	13.35	16.20	0032	60.0828	278.00	317.487	58.939	106.88	43.911	.15	54.0452	654.57	242.8939	.04	376	4.4	503	256.350	341	3532	507	36.05
	76	986	09	4002	498	2	97	905	25	787	854	774	709	11	022	4	184	65	532	809	9	99	7	97	5357
Bach	218.												972				115	147	214	75.		791.	281.	17.1	
2	750	52.744	32.703	1264.	1459.	18.6	592.638	1776.7	927.417	38.596	19.007	41.277	.38	603.777	1936.5	186.9868	4.0	0.47	.85	528	24.4031	031	7917	518	24.86
	66	766	63	2279	6676	2189	47	731	33	061	697	62	936	92	596	5	241	51	982	356	32	95	1	69	4609
	537												493				172	156	370	55.		134	1033	445.	
Cst7	0.82	52.160	1177.2	26.78	17.52	31.7	783.926	984.66	2932.68	39.644	2388.4	71.548	.07	1220.95	189.34	1606.831	8.9	4.89	7.0	425	4212.19	8.39	.292	694	62.57
	37	807	401	6622	0747	4581	01	291	81	137	547	826	741	57	646	7	104	94	592	904	3	88	2	12	4433
	224					41.9							32.				46.	40.5	42.	64.		953.	177.	48.8	
Cma1	07.8	51.253	54.248	39.80	36.85	8944	32.7780	33.459	30.0592	28.725	29.766	29.703	202	45.4093	37.454	34.15756	574	602	696	966	45.8912	420	1104	369	37.56
	1	026	02	7942	9064	4	58	272	15	678	286	923	6	52	182	3	941	9	76	461	43	46	9	94	9159
	539					20.8							33.				128	34.8	146	351		156.	329.	420.	
Lat2	6.00	50.807	650.20	23.29	16.53	4399	34.3366	24.408	30.9384	1563.3	857.08	1301.0	933	21.7738	27.218	39.70378	.65	646	.13	.04	1507.55	987	6926	107	561.0
	46	696	288	0682	8354	6	76	138	64	397	566	78	85	98	803	7	909	38	857	725	05	87	9	6	3958
	578					49.9							43.				55.	46.6	45.	47.		49.2	55.6	60.6	
Tpsb	5.29	50.745	44.362	46.91	47.00	3501	47.2258	52.861	44.6789	38.065	40.400	41.043	949	57.1238	48.651	46.86096	306	011	511	305	62.2265	951	2027	090	53.22
2	77	15	505	975	6601	6	51	458	2	102	627	994	199	93	564	5	624	74	153	154	44	12	7	53	6848
	43.6					1517							41.				40.	49.7	38.	45.		41.4	38.4	56.2	
Endo	748	50.401	35.031	125.9	228.1	.602	43.2776	46.271	36.7364	42.044	49.214	43.620	668	39.6748	47.540	44.93327	297	572	866	013	47.6692	229	6095	277	45.57
u	71	307	902	7562	7238	2	1	017	17	358	669	621	096	85	537	5	048	13	157	354	08	88	9	31	0854
	12.7												222				27.	87.5	22.	752		720.	704.	161	
Fam2	200	50.337	17.600	378.5	907.0	187.	106.431	840.46	998.889	472.06	5471.7	149.71	.52	579.676	660.45	332.3986	926	089	396	.27	245.900	550	9028	9.78	38.84
6f	06	315	061	4789	2681	3029	78	503	53	903	608	597	548	67	783	4	496	57	326	631	69	79	7	39	1132

Tifab	18.2	50.126	48.939	17.77	18.95	23.8	20.2495	22.216	21.1454	105.31	133.87	184.44	19.	21.8276	18.239	18.85757	20.	26.0	20.	132	20.7525	22.6	18.2	160.	597.4
	095	829	406	2045	9974	5862	01	505	34	668	355	322	632	89	187	3	668	301	748	6.4	12	420	2843	652	5792
	89					6							329				862	56	689	721		66	5	86	
Ccr3	17.5	50.049	872.68	20.43	15.53	17.0	14.9179	19.250	23.5510	45.647	20.042	28.203	23.	12.6908	13.569	15.60402	15.	19.1	25.	15.	17.9271	15.1	13.2	23.1	22.31
	741	285	24	8667	0627	3879	38	796	81	68	44	327	100	98	33	4	434	025	422	930	59	587	1296	857	9608
	53					5							78				621	66	607	707		14	4	6	
Trbj2	34.7	49.870	71.933	44.20	68.13	106.	693.766	1770.0	1475.70	76.041	46.895	59.895	115	1115.81	2931.9	3064.502	860	269	147	79.	1140.42	168.	145.	30.4	30.74
	981	504	322	3853	9207	6781	91	513	45	233	551	992	1.7	08	459	9	.51	0.60	3.8	802	87	862	5929	888	6368
	-1	4				3							504				608	56	5	366		66	3	17	
Fam1	22.5	49.691	44.191	257.1	266.1	158.	266.278	545.76	611.249	19.685	22.643	21.653	530	545.630	542.02	394.3960	182	351.	61.	24.	44.1593	26.0	24.7	27.5	29.73
	332	033	645	0807	3269	7024	18	436	16	864	886	706	.27	97	858	2	.69	336	711	444	65	424	0599	244	728
	69b	69				7							507				828	15	309	658		73	2	26	
Tlr1	12.5	49.660	133.50	2518.	1526.	12.8	114.202	1777.4	758.409	583.19	1267.4	475.68	476	1206.87	929.54	717.8328	31.	384.	605	456	12.7093	40.3	15.1	667.	104.8
	364	039	316	186	0873	5942	59	194	04	819	325	535	.82	18	414	5	128	827	.34	.34	15	026	0920	639	1782
	52					8							603				653	5	861	853		66	2	07	
Gzm	44.5	48.924	38.241	39.08	41.25	49.9	66.0606	91.660	2454.34	38.415	38.972	42.062	51.	77.8171	62.881	52.05445	40.	40.0	44.	46.	54.3881	99.6	67.0	42.6	44.78
	386	719	341	8324	5676	9737	38	858	81	273	284	793	502	15	643	4	477	541	634	719	26	530	7151	354	6985
	m	75				1							983				818	35	135	45		25	8	58	
Tnfrs	34.4	48.412	37.934	4870.	4698.	1883	54.2527	72.295	63.5082	37.340	41.818	38.548	57.	39.1653	33.952	50.22465	55.	33.8	33.	40.	56.5457	161.	62.3	39.3	31.69
	465	156	799	919	4885	.154	45	96	79	481	378	649	444	41	462	2	682	967	280	630	46	275	7597	651	261
	f13c	22				5							018				513	37	019	852		47	6	18	
Cd22	30.4	48.214	41.358	732.5	644.7	34.7	28.6757	33.174	148.122	171.81	105.69	160.01	42.	60.8559	32.552	177.0769	29.	32.5	35.	84.	33.2444	102.	35.2	55.9	65.83
	279	668	474	6637	9865	2540	37	057	09	609	091	005	102	88	625	1	640	313	318	802	42	794	7695	657	2148
	18					2							632				613	05	211	576		81	8	63	
Slc18	598	48.203	1819.1	16.49	18.05	11.6	16.9874	14.745	12.9710	16.748	14.104	12.993	14.	14.7038	14.567	18.81266	17.	15.3	15.	22.	16.1481	60.7	33.1	17.0	18.99
	9.39	824	451	8237	799	7080	49	037	09	079	474	848	200	11	288	7	266	333	022	956	74	909	8730	010	0959
	a2	6				5							776				027	97	113	402		52	2	82	



Ccl1	176.7797	47.891753	32.943447	27.372822	26.261258	39.5606707	316.93307	36.631684	33.71938	28.563126	39.870536	34.530923	83.47649	67.654403	36.359393	44.82882	100.25	35.5265	44.487	44.225	31.815046	48.6844	61.12658	41.8972	29.679048
	26.008656	47.680652	150.1111	62.063037	32.865351	19.396102	23.175198	32.055322	80.510157	16.330965	17.333815	17.101483	35.643609	53.85665	36.350007	59.962766	21.038	116.691	20.051	122.24	49.402741	886.813	632.5768	39.0295	58.379211
	37.355607	47.462526	139.62993	80.611795	74.297519	44.956165	45.602188	45.80626	43.671761	445.36247	187.03029	380.75594	46.201582	52.81321	41.621392	40.46578	44.156	45.4194	42.484	92.872	55.819888	44.3311	39.29733	175.055	312.98383
Bcl2	448.05484	47.326394	76.282525	346.79423	271.09907	45.467278	356.63217	871.15212	1543.2519	49.522546	44.425527	61.21393	427.38345	513.41785	974.25819	286.90191	307.59	130.698	150.85	129.27	1344.5426	798.498	1724.654	41.2356	46.383345
	37.180057	47.268629	92.40802	43.774528	44.993377	44.144381	39.247545	40.185059	38.346556	897.0833	1799.4265	611.92706	40.012214	30.551515	38.943313	33.457698	33.540	36.5572	34.040	375.58	35.432638	32.9943	35.50265	876.346	625.43205
Slfn5	23.578978	47.221192	27.613872	25.560237	26.461246	19.192301	20.873532	36.119326	30.964718	283.84726	761.86616	113.54973	27.762664	25.151405	68.073791	54.636494	24.557	28.9499	26.325	82.409	23.043155	23.7946	18.84761	162.308	36.053009
	48.218372	47.063823	44.372203	32.298458	33.001467	230.91146	89.905408	33.298036	30.56012	35.420978	35.965436	37.341336	68.566212	39.235372	35.944237	53.690695	86.155	63.2387	85.632	38.980	37.569177	34.1259	68.53290	32.4016	36.565107
Il13	217.68318	46.390598	214.2618	48.394606	47.96939	49.927818	57.113921	45.100626	35.748662	36.449871	40.756265	38.238815	35.743608	37.200025	35.944898	39.519783	86.545	43.9336	965.36	33.370	29.295444	35.0362	32.90230	29.8225	26.536241
	A430093F15Rik	22.562133	45.968258	20.496515	24.331191	26.968168	28.964204	398.02878	168.55572	335.32041	24.085979	22.257742	23.27294	937.00297	484.47777	264.52964	1094.8657	903.19	551.209	243.11	32.734	23.048195	26.3097	21.22240	38.0892

Mcpt-ps1	224	45.910	28.933	42.26	39.80	36.2	29.5089	29.757	30.0568	29.549	32.353	29.436	35.	36.0687	31.749	30.1986	37.	36.3	30.	34.	39.6331	39.0	39.8	46.7	39.09																		
	7.15					4584							559													535	143	791	071	740	0681	074	6341										
	68					296							238													6788	6983	8	3	666	1	763	314	662	138	69	957	731	13	206	927	64	57
Kel	35.6	45.363	29.681	34.67	39.95	45.6	31.5237	33.404	31.8930	34.347	36.473	36.664	38.	25.0448	36.205	32.42599	31.	31.1	305	34.	36.1601	36.3	33.9	36.9	35.00																		
	436					4958							87													904	67	379	54	683	130	17	768	6	892	729	.59	665	16	935	9869	226	2441
	58					931							982													2774	5729	4958	87	904	67	379	54	683	493	17	768	6	165	79	732	038	16
Slc9a9	38.1	45.356	45.259	19.40	22.29	21.7	33.6101	94.887	132.235	340.70	27.931	322.09	48.	94.8491	102.64	314.6739	24.	112.	71.	86.	49.3155	95.7	109.	19.9	28.47																		
	918					0775							334													740	378	699	423	36	826	1511	195	9007									
	7					115							002													7535	2448	4	63	193	62	424	542	251	6	83	088	377	64	536	298	36	02
Ccr6	37.5	45.267	34.643	2518.	1103.	97.2	59.7792	53.715	51.3096	34.876	37.550	37.473	714	548.011	71.172	299.9325	110	293.	37.	55.	66.7730	111.	64.0	70.1	63.73																		
	952					8152							.10													.95	450	242	408	34	123	6278	608	394									
	82					78							506													8879	7198	6	31	722	91	529	136	514	514	5	13	2	702	75	872	938	34
Saa3	122.	45.264	314.51	30.54	33.06	32.6	40.9610	48.211	37.0501	684.73	12239.	505.73	43.	68.4983	46.330	44.97021	52.	65.0	40.	62.	36.9746	39.5	34.4	130	3503.																		
	938					6653							784													412	774	210	463	41	224	8288	36.5	6954									
	72					857							636													9079	3017	3	44	042	08	906	237	985	317	26	517	9	072	41	544	651	41
Tg	136.	45.076	21.408	29.19	21.10	384.	531.574	23.366	28.5912	22.518	21.453	23.009	65.	30.8900	26.988	69.44596	332	234.	166	24.	25.3410	28.2	25.9	29.3	24.61																		
	232					4507							825													.80	138	.25	407	25	904	2342	863	689									
	84					672							285													0309	3381	4507	21	856	16	723	695	965	363	44	402	9	675	32	358	692	25
2310007L24Rik	30.2	44.305	33.564	32.32	40.52	46.9	26.4165	29.175	30.8049	28.169	30.733	30.877	45.	49.4075	34.755	30.64811	39.	111.	33.	35.	32.7396	31.5	42.1	34.0	32.57																		
	967					4416							212													268	934	876	950	41	966	7212	261	4967									
	94					803							5													4117	5259	6	73	917	47	178	164	878	917	4	518	6	134	76	366	565	41
Zbtb32	30.4	44.287	34.589	77.03	30.53	33.7	1049.27	49.508	62.4366	31.403	57.324	35.071	189	64.8014	46.370	139.4867	117	104.	70.	44.	32.5357	33.8	148.	31.9	32.65																		
	813					8676							.84													1.4	657	271	059	03	155	5575	185	6481									
	24					077							497													5134	6285	5	91	376	61	488	993	158	878	19	87	3	158	04	043	8	03
Lacc1	64.2	43.472	79.465	55.99	48.02	31.4	30.7257	27.987	31.7626	169.73	1335.3	189.73	40.	31.4379	27.567	39.06029	65.	39.2	34.	138	46.1818	29.2	29.0	137	518.4																		
	191					8597							919													756	239	887	.63	24	187	9096	8.87	9002									
	77					721							998													9695	6191	7	38	14		115	613	254	031	96	543	5	27	85	491	25	24

Ighg3	44.1					1572							79.				48.	40.0	34.	44.		38.7	36.4	32.8	
	244	43.282	30.682	820.2	57.39	6.31	42.2319	44.811	44.0963	31.558	30.212	28.608	965	69.0628	43.027	58.51977	252	057	792	831	33.4285	367	3229	402	36.07
	98	12	472	2565	9671	1	62	833	79	411	016	417	454	49	649	7	559	66	004	888	32	38	9	09	191
Zap7	37.3					31.1							153				100	169	176	32.		135	948.	59.0	
	176	43.145	30.847	33.41	46.48	9960	830.752	1264.0	1609.42	41.497	45.294	41.064	6.3	2088.12	1436.1	3164.782	2.3	6.97	7.6	141	2372.84	3.94	3608	329	49.32
	0	449	656	5301	7707	7	65	793	47	061	317	252	745	78	385	8	317	31	848	304	54	7	4	98	3053
Cycl1	49.5					27.7							52.				64.	41.0	28.	146		37.8	26.7	112	
	253	43.058	106.14	36.42	35.83	4222	82.5695	42.518	113.444	137.82	9587.3	56.132	082	95.6120	32.656	599.9119	405	758	342	.80	28.6692	305	1058	74.9	142.9
	0	601	592	4657	9914	8	32	346	91	124	688	16	794	72	711	1	765	23	482	58	05	17	8	91	7902
Kmo	29.0					236.							28.				28.	27.1	24.	142		53.7	25.1	83.8	
	191	42.844	105.01	766.4	1641.	8286	33.0260	29.543	27.2394	39.749	43.436	39.232	076	40.4429	28.609	26.10416	626	561	055	.10	23.3302	129	0787	504	159.7
	63	078	296	6944	5449	3	36	713	94	312	062	881	055	57	897	9	002	96	296	307	37	99	9	63	3524
Spic	11.9					13.0							13.				14.	12.3	13.	47.		11.4	11.9	50.7	
	254	42.572	44.270	29.53	21.72	3446	12.1054	18.979	35.7083	115.21	292.25	40.319	237	19.7283	11.960	12.18059	155	761	418	063	12.0744	405	4032	577	14.36
	2	139	206	2935	3779	3	77	825	43	323	907	929	962	37	344	3	123	23	581	077	92	43	8	35	8562
Apoa	26.6					30.9							31.				34.	32.0	34.	33.		34.1	32.9	29.7	
	541	42.431	27.352	23.81	25.21	1615	28.0251	31.210	27.3528	31.599	32.334	30.548	043	36.8775	38.829	35.54515	358	025	628	587	2801.49	725	6007	689	27.06
	1	931	251	9708	5482	4	45	607	35	081	061	534	493	65	564	3	66	91	661	312	83	11	3	77	2889
Fam1	37.7					41.7							89.				26.	46.6	53.	34.		62.2	29.2	53.1	
	232	42.049	28.263	1282.	1768.	2614	44.0021	112.94	115.690	34.042	31.800	36.959	053	48.7152	85.735	74.45727	537	438	576	368	100.928	229	0501	075	48.57
	29c	633	903	7418	4525	6	16	94	84	052	606	24	394	54	48	1	21	24	559	526	41	34	8	82	0658
Alox	31.0					43.2							37.				29.	30.4	33.	37.		31.0	32.4	86.8	
	707	41.971	6918.4	50.88	28.31	9185	26.9177	36.743	31.3542	31.728	34.643	31.599	228	30.3679	36.217	31.68803	712	635	803	722	33.8783	832	9622	650	87.84
	15	117	949	1562	8187	9	2	342	83	078	783	281	476	26	597	9	722	34	048	118	56	31	9	32	5546
Clec4	14.3					13.4							14.				14.	13.9	14.	126		15.3	15.0	90.3	
	480	41.954	19.194	13.18	12.31	7694	15.4775	15.281	21.4567	112.50	14.325	33.004	382	15.6424	13.525	14.26734	151	980	513	.98	12.8059	174	7171	613	617.7
	b1	337	593	1619	123	7	28	305	09	649	294	805	517	3	27	1	862	46	772	844	44	6	8	24	2777

Ch25	35.7	41.764	64.025	29.23	37.05	35.2	28.8566	26.453	31.1735	32.632	1588.1	69.041	32.	24.6869	33.505	33.76586	27.	31.5	30.	28.	37.8121	28.6	25.4	201	70.76
h	935	203	565	9277	4628	6987	52	137	06	509	722	92	797	37	306	6	897	837	892	666	79	463	2499	5.07	4469
18100	521.	41.729	49.566	25.49	25.71	17.4	23.7499	27.724	26.2502	152.88	49.915	302.74	41.	44.7035	31.281	27.23238	21.	25.8	254	40.	117.235	23.7	23.6	29.1	79.04
11H1	613	718	58	4977	4275	3150	86	834	68	489	903	838	966	56	182	2	756	502	.25	984	83	035	9829	627	9568
1Rik	63					4							906				812	4	112	567		59	7	99	
Dcsta	34.8	41.030	53.882	47.78	46.50	50.9	37.1574	36.647	37.9702	163.57	95.921	127.47	41.	39.1665	44.943	43.32889	37.	35.4	40.	46.	51.8576	48.8	42.5	115	1087.
mp	052	646	465	619	6835	9144	07	249	16	977	485	989	353	46	226	9	816	606	676	204	53	482	8855	3.89	4398
	53					9							671				362	89	164	771		87	6	64	
Bamb	22.1	40.904	50.334	19.93	17.42	17.5	35.8025	251.56	65.6828	90.265	826.55	45.347	75.	47.6276	540.54	186.2260	24.	161.	33.	26.	33.3332	20.2	19.7	288.	24.12
i-ps1	913	68	102	0764	7513	7971	83	563	97	569	539	48	534	97	377	9	768	985	795	753	11	438	1539	214	7216
	57					6							806				476	26	807	973		02	4	83	
	755.	40.726	34.473	51.90	54.45	38.1	707.606	2127.9	2665.11	41.137	42.555	38.715	143	654.804	1295.5	760.1009	390	112	251	55.	1297.50	137.	123.	42.1	41.76
Klk8	298	937	265	2929	2905	1758	06	116	26	727	389	058	0.7	81	124	8	.18	3.29	0.4	637	8	719	6987	478	271
	72					8							764				069	26	63	569		75	2	55	
	25.6	40.707	23.048	52.89	29.07	320.	26.3964	26.634	24.8703	23.050	227.06	25.084	23.	23.1410	24.885	24.16535	28.	26.8	24.	29.	52.2206	29.2	24.2	35.1	31.55
Ido1	783	239	962	7577	5891	0557	12	879	97	493	793	774	980	29	503	2	399	077	942	167	98	921	8857	129	922
	7					5							788				341	06	042	581		94	9	53	
BC05	29.9	40.650	23.495	452.7	82.22	73.8	25.9588	32.416	34.7029	27.568	39.604	32.089	28.	70.7135	30.363	34.62177	36.	28.7	28.	38.	25.3212	50.8	39.3	30.0	24.67
1142	406	443	635	954	3323	4090	83	511	17	73	741	802	557	34	853	6	962	089	229	681	84	130	9523	873	4333
	31					9							422				322	85	37	776		37	6	07	
Cryb	46.9	40.413	21.555	19.70	18.83	155.	23.6430	21.657	22.7210	33.972	36.088	26.800	20.	28.8733	22.889	20.92571	21.	22.8	22.	53.	19.9160	22.3	21.1	19.5	19.82
a4	941	215	417	5145	3595	0449	96	426	94	374	315	386	859	35	84	7	243	585	208	128	84	608	0221	030	7605
	21					2							754				433	47	35	474		45	4	08	
	17.4	40.225	173.46	17.69	18.34	15.9	16.2843	19.186	27.6900	545.28	129.71	1731.9	15.	25.8091	16.745	14.69384	17.	16.9	14.	155	15.3907	17.1	15.8	721.	1073.
Tfec	924	598	587	7182	5899	8213	84	213	56	858	866	441	754	27	53	7	373	508	361	.18	62	010	4854	564	6016
	13					5							466				861	19	354	641		19	5	93	

Ccl17	44.9	39.745	127.34	38.06	38.90	37.9	34.0902	39.593	34.8193	35.972	42.432	37.805	43.	47.7417	39.556	37.34716	55.	38.8	40.	37.	49.0149	37.1	34.9	707	5904.
	829	95	176	0987	0127	6524	51	544	92	019	462	282	391	99	218	7	192	264	665	201	18	385	2997	3.21	9165
	66					7							713				005	68	939	284		11	9	61	
Lpxn	327	39.046	653.58	662.6	626.7	146.	1088.88	1228.8	1642.76	1933.1	1643.1	4185.7	176	1886.62	497.77	2216.024	125	255	171	528	2596.34	559.	947.	823.	863.9
	1.74	692	119	7419	4992	9762	91	982	09	888	598	768	8.3	29	07	5	8.4	3.01	8.6	.75	98	512	7276	500	833
	07					4							358				922	8	877	834		71	9	53	
Msc	49.9	38.994	45.357	42.41	49.44	103.	45.6767	43.667	38.2788	40.116	32.915	44.226	43.	54.3426	42.650	39.51039	228	186.	45.	61.	57.5614	41.3	44.3	50.6	43.65
	640	348	697	1309	565	0527	65	639	64	319	792	37	159	02	488	1	.59	924	122	085	56	414	9609	072	0331
	08												423				082	43	138	406		85	9	92	
49304	303.	38.976	44.481	37.48	60.45	43.7	128.726	130.30	261.373	59.534	117.93	47.069	102	88.0160	99.963		57.	331.	102	42.	84.3260	456.	385.	31.2	26.85
	86L2	454				4257	26	51	43	523	268	094	.29	55	951	57.66071	502	676	1.5	353	62	619	2136	370	2358
	4Rik	96	312	021	5952	8422							493				827	52	341	376		33	3	94	
Il12rb	51.7	38.750	48.565	64.94	56.02	53.7	293.023	75.339	156.560	31.452	365.52	30.306	314	240.488	55.307	196.2786	472	258.	633	29.	228.218	204.	531.	81.1	36.64
	337	208	667	0706	5737	2200	22	243	53	128	882	334	.47	13	46	4	.64	723	.20	516	03	360	5638	283	7427
	36					5							72				475	46	944	197		99	5	11	
Prf1	37.5	38.339	45.502	93.32	51.89	66.9	1588.62	485.50	705.178	57.404	76.200	59.553	62.	82.2945	301.20	64.00352	245	46.9	89.	38.	260.252	657	5559	41.8	37.83
	870	884	189	7921	0994	0818	23	568	81	328	763	792	844	11	815	2	1.5	507	495	448	15	8.76	.918	437	7943
	12					2							371				251	99	481	74		9	6	5	
Ms4a	11.9	38.325	33.313	17.75	24.17	11.3	8090.26	12666.	13146.0	35.698	70.101	18.217	207	13489.0	10860.	9573.599	103	291	481	580	11.5002	937	6853	59.1	18.45
	137	53	42	4674	1564	2540	47	17	83	781	345	912	0.4	55	367	2	8.3	8.96	.58	.82	67	1.23	.649	659	5155
	61					4							018				093	24	734	048		7	3	43	
Irf4	27.5	38.165	48.919	304.8	340.2	1641	422.855	41.413	36.2877	25.393	29.518	94.045	508		39.272	157.9558	155	317.	250	152	29.8825	48.2	38.0	448.	272.3
	329	699	75	4225	3816	.414	89	126	43	655	976	859	.75	133.829	206	9	4.5	429	.39	.64	88	600	7868	292	369
	9					1							915				127	92	977	793		91	7	09	
Gp1b	149	37.843	265.60	22.43	16.79	22.2	21.8287	19.898	20.1766	26.152	34.950	32.524	19.	32.1850	22.149	23.01008	24.	20.8	27.	31.	25.7390	27.4	25.2	24.9	22.86
	1.84	972	486	6781	9088	3785	36	886	05	642	12	394	676	23	302	9	628	485	903	740	25	571	5558	512	611
	15					1							843				78	41	051	329		94	3	45	

Il17a	44.0					67.5							46.				57.	231	56.	46.				
	364	37.594	38.358	48.38	53.21	8804	75.8483	53.426	54.6423	49.380	51.623	48.614	189	31.9133	42.841	43.50098	955	6.78	151	838	40.6142	31.1	33.7	68.8
	08	282	915	5045	8328	5	88	046	95	618	175	7	802	01	951	7	364	36	813	548	98	86	5	6
Cyp4a12a	100					49.9							28.				19.	24.6	26.	56.				
	2.28	37.041	46.372	36.49	50.29	7307	30.0326	31.729	30.0126	30.430	32.146	41.770	816	19.2712	27.338	21.91794	582	925	663	074	47.8515	18.0	26.9	66.1
	31	403	766	2522	7079	3	87	942	83	81	632	46	933	44	308	8	945	2	746	992	89	460	3766	991
Tpsg1	531					27.5							34.				38.	31.3	35.	28.				
	8.13	36.530	35.233	23.55	35.64	5853	35.3483	26.399		25.819	29.410	25.053	319	25.1225	30.877	30.55487	396	468	432	637	29.9264	32.3	44.7	30.0
	63	19	414	6832	6695	7	67	642	26.4804	705	297	286	449	07	521	5	891	04	999	359	32	209	7401	431
Gzmb	159					35.9							290				174	301.	143	36.				
	38.3	36.355	124.86	30.06	23.13	4291	18487.9	71.286	198.243	24.652	30.466	24.784	.00	167.111	44.262	121.4916	95.	431	81.	919	18288.1	367	1709	35.1
	84	713	04	7535	4206	16	301	07	13	544	189		419	48	716	4	268	09	396	458	37	9.03	2.61	700
Tcrg-C4	33.9					33.5							81.				153	94.8	111	45.				
	051	36.130	33.591	50.25	36.75	5499	155.278	77.552	248.131	24.612	23.048	25.330	562	123.230	47.971	31.13925	7.1	583	.36	471	9307.52	272.	280.	36.6
	58	737	366	3506	751	51	585	83	754	363	822		142	62	871	4	566	57	826	879	37	670	5551	922
Cyslt2	39.5					47.8							39.				33.	260.	81.	26.				
	103	36.026	29.204	29.52	33.85	7866	43.9803	52.324	71.5825	40.927	263.41	50.153	354	56.3867	41.147	69.16358	154	989	757	501	201.234	105.	124.	50.3
	94	896	551	2014	2477	7	5	908	42	384	385	278	191	56	693	6	43	07	194	668	9	111	2721	381
Ccl7	178					26.0							28.				28.	23.6	24.	26.				
	2.10	35.972	300.98	26.36	20.73	6625	21.8187	24.852	25.9628	62.850	2529.6	212.87	738	19.5201	31.224	25.21641	438	685	709	740	30.5292	24.4	23.6	850.
	84	317	459	8492	934	4	48	008	86	484	074	222	89	43	556	6	165	93	125	064	23	896	4461	310
Cep97	55.9					37.8							119				77.	274.	94.	37.				
	723	35.907	51.260	55.89	52.24	8706	75.1588	222.22	90.6011	41.243	41.802	42.667	.86	130.093	282.27	139.7942	115	272	698	131	53.8291	93.8	92.4	25.1
	54	782	738	4778	9471	3	8	707	15	348	246	385	832	65	889	9	804	59	095	127	65	976	8793	866
Il2rb	29.8					36.1							139				218	565.	500	28.				
	216	35.823	31.295	32.42	24.21	9675	914.261	272.11	2249.93	28.579	32.492	30.467	3.7	539.354	108.36	639.5549	3.2	518	.17	370	2747.97	809.	1229	28.4
	97	128	677	5248	3778	4	26	855	56	472	931	516	407	19	256	5	62	43	642	176	19	339	.870	956

Tcf7	37.2												858				280	400	61.	56.		227.	165.	58.7	
	214	35.694	48.792	59.75	44.79	50.7	351.552	2327.1	2514.84	34.821	35.079	35.742	.83	1490.57	3738.5	2629.367	.13	4.76	002	117	268.654	060	9236	206	64.98
	63	695	324	7551	1686	8945	78	167	94	497	579	876	677	72	792	6	121	53	106	182	03	48	9	9	1141
Gpr1	24.5					29.4							53.				262	208.	103	42.		28.4	26.3	65.6	
	858	35.691	30.201	24.84	32.40	1430	34.3125	44.734	45.6160	25.284	33.215	24.784	883	35.2343	70.382	45.68753	.42	028	.21	712	36.8854	571	2805	663	64.92
	32	791	763	4783	9567	3	72	448	63	051	472	017	231	99	043	2	614	73	149	94	18	93	2	31	6996
Lag3	142.					31.4							152				319	115.	53.	33.		46.9		43.1	
	594	35.529	53.082	33.07	36.05	6629	128.865	36.932	52.5798	38.176	38.387	35.259	.20	100.769	37.173		.42	398	012	093	1220.56	766	46.9	028	36.63
	02	19	999	4184	9238	5	57	943	13	57	898	231	557	41	702	546.2132	207	15	932	3	78	74	1948	16	3894
Fosb	565.					71.1							40.				54.	25.2	79.	64.		145.	28.1	35.4	
	696	35.528	32.121	57.21	33.63	6525	32.6823	51.229	124.390	23.028	24.714	20.963	008	25.2432	43.249		512	277	576	237	43.8341	265	0603	451	29.53
	5	77	342	744	5585	6	98	994	39	585	414	259	984	87	729	79.0002	374	45	367	54	86	94	8	71	0046
Alpk	59.6					267.							46.				185	120.	43.	26.		31.7	30.7	319.	
	857	35.452	26.759	123.8	68.07	0097	68.5136	38.379	44.7092	31.079	37.637	32.144	931	31.8446	31.543	36.14263	.41	056	303	301	38.4682	651	0827	023	78.97
	2	155	365	3241	8295	1	99	13	41	469	694	048	289	68	416	6	287	26	657	014	01	28	6	2	4997
Itgae	63.0					64.7							262				39.	59.6	36.	36.		101.	51.9	40.9	
	639	35.373	88.611	180.9	74.60	8681	37.7269	1468.6	152.009	32.951	41.062	29.678	.45	303.818	47.204	188.1894	088	102	144	549	10246.8	811	4770	746	51.55
	71	901	76	8604	3232	9	46	865	1	321	115	59	18	69	118	6	157	79	716	977	33	6	2	12	2888
Cd40	35.9					57.3							99.				62.	53.2	43.	271		55.6	37.4	303	
	921	35.289	82.818	1621.	1394.	8476	38.3267	42.618	38.8708	120.87	3162.6	421.13	826	61.4997	43.354	40.92191	119	176	473	.57	31.3713	389	2803	8.00	110.9
	55	612	95	4673	4195	4	74	896	73	193	115	012	23	08	335	8	116	4	33	179	13	35	5	04	9526
Timd	17.1					25.7							19.				17.	17.1	19.	20.		18.4	19.8	20.5	
	071	34.227	16.066	20.51	26.67	4301	22.1295	22.313	25.7850	27.900	459.62	22.185	091	18.3569	17.953	16.31072	462	108	894	066	21.3116	455	2152	619	19.19
	4	547	945	1557	2455	5	32	302	95	083	131	031	955	18	416	4	736	81	459	958	98	89	6	07	3386
Piwil	27.6					89.3							31.				36.	163.	261	25.		26.5	35.4	46.7	
	013	33.925	42.315	39.74	24.49	5403	30.4510	19.121	20.5617	28.163	29.248	23.974	413	25.7199	25.127	24.70953	713	899	.44	527	28.6544	685	9911	321	42.96
	2	71	327	3067	1751	8	78	275	17	087	41	791	174	38	289	7	288	72	725	282	19	67	2	75	4772

94300	27.7					192.							32.				31.	29.9	32.	30.					
69I07	018	33.724	26.194	27.21	25.23	7204	26.2436	29.918	31.5997	24.805	24.866	23.689	555	31.2291	31.091	32.66063	149	458	710	666	27.7413	32.0	33.3	27.9	25.95
Rik	48	052	521	8721	1697	4	77	757	55	357	318	959	206	84	618	9	235	74	14	372	46	65	7	08	6319
Ms4a	62.2					15.3							31.				23.	29.1	23.	154					
6d	507	33.426	564.29	16.87	11.82	1053	163.440	182.68	372.059	2950.8	6755.8	4457.3	854	90.1417	101.47	291.4828	053	508	960	4.1	13.7097	23.1	14.9	395	869.5
	46	907	079	503	657	9	35	309	34	617	423	716	248	88	283	3	16	02	855	296	95	55	5	6	194
Zfp94	30.8					67.0							63.				36.	60.2	45.	25.					
	546	33.412	30.851	373.3	327.5	5401	51.4905	67.428	72.3162	43.826	32.124	41.861	908	48.4947	65.699	56.72500	128	430	241	494	30.2343	30.4	39.4	24.0	31.10
	55	872	429	7474	6231	7	82	812	85	22	941	45	95	4	822	5	675	2	743	139	73	09	5765	54	3676
Slamf	33.1					350.							236				114	125.	32.	44.					
6	732	33.405	28.913	331.7	244.6	6038	48.7396	400.85	287.576	50.189	224.55	90.798	.40	1060.98	463.72	1300.857	.12	162	604	583	66.2184	90.3	44.5	155.	68.27
	7	257	526	5599	2057	4	5	37	22	305	85	228	592	46	144	9	837	7	602	337	7	06	2	18	0823
Slamf	18.9					17.9							21.				16.	24.4	19.	649					
8	906	33.379	88.617	15.25	19.61	0435	19.0550	26.639	25.5397	34.393	474.82	46.224	136	18.0776	24.734	24.15203	608	193	537	.15	22.1510	23.0	19.7	943.	433.1
	73	519	104	8688	0057	3	72	124	04	821	709	139	569	71	223	6	589	54	752	069	33	58	4	46	8235
Cd16	35.7					32.7							43.				42.	141.	37.	31.					
3l1	087	32.990	31.661	31.07	32.96	1704	43.0761	49.327	692.534	34.613	34.260	36.461	396	65.7909	34.535	52.54448	460	724	133	780	36.8017	78.6	77.7	29.4	28.25
	19	868	73	2094	5979	8	22	9	91	374	414	044	443	81	04	4	737	28	205	294	87	16	2	85	5838
Tnfrs	25.3					21.4							502				137	527.	91.	22.					
f25	578	32.856	40.704	44.89	19.61	3739	40.1279	200.74	211.518	25.147	31.403	27.935	.05	1142.86	644.70	409.828	.89	439	103	225	24.3926	95.7	50.3	26.6	26.53
	96	382	859	6936	7833	5	83	424	88	007	423	325	112	23	316		051	79	428	061	15	78	8	71	7983
Mcol	39.8					494.							35.				52.	60.5	62.	23.					
n2	246	32.806	125.82	279.6	298.7	4315	158.394	244.05	355.587	690.87	861.76	1052.4	397	56.7133	55.076	72.63097	917	235	825	303	278.871	218.	241.	871.	269.1
	8	082	863	4458	1829	1	73	762	83	269	608	713	912	23	817	8	972	15	023	257	86	89	5	45	5304
Ear11	10.8					10.5							10.				12.	10.8	11.	19.					
	901	32.314	15.203	10.88	9.859	7467	13.1111	12.226	11.8570	12.244	13.877	106.45	923	12.6715	10.286	11.44434	543	937	190	025	11.1708	11.9	12.1	984.	913.0
	12	238	495	1238	6676	1	2	764	88	847	79	359	881	73	272	7	884	91	21	235		99	3	14	0264



Fcrla	28.7					539.							24.				22.	21.5	20.	24.					
	138	32.238	51.603	1105.	1236.	1395	24.6754	24.264	21.5700	23.609	21.954	22.519	242	25.6068	20.678	18.59713	762	133	831	633	22.0816	54.2	22.2	20.4	20.57
	95	603	501	3112	5092	5	22	371	14	252	197	868	342	92	146	5	024	78	134	237	69	16	4	86	1551
Gm4	20.4												66.				39.	20.6	21.	21.					
	117	32.159	19.774	20.14	28.39	21.0	24.9392	48.096	38.0999	118.57	3474.1	291.41	429	63.5705	40.556	45.90488	965	671	641	762	18.4374	26.8	26.8	170	69.94
	951	42	022	9051	4646	1622	64	465	77	602	424	21	783	76	831	2	902	93	288	261	06	95	2	96	1009
Pax5	27.4					29.1							26.				28.	26.2	28.						
	395	32.134	28.786	400.5	223.9	7857	34.2572	33.116	30.4025	25.967	35.040	28.928	844	30.9564	33.694	33.57975	154	385	631	31.	32.6643	30.3	26.7	35.8	30.72
	06	733	019	0964	8407	2	12	728	48	326	68	182	083	82	962	4	271	24	332	608	57	42	8	22	7696
Il27ra	159.					23.0							650				288	991.	430	41.					
	100	32.104	34.591	475.7	603.0	2711	183.513	1016.8	874.525	43.247	35.232	55.367	.91	1133.82	1041.4	1191.574	.19	824	.36	945	428.995	458.	355.	33.3	41.92
	86	693	029	8763	77	8	16	818	09	58	66	384	976	58	009	8	046	79	433	019		07	7	67	698
Il4	593.					36.8							34.				26.	28.6	102	30.					
	641	31.921	1117.0	29.70	29.91	7934	29.1848	23.269	22.8661	24.784	34.305	26.269	078	42.3968	29.718	419.7640	836	660	9.3	522	31.9467	25.4	26.0	30.7	31.68
	29	261	259	7653	9823	5	97	731	81	854	328	691	639	8	07	2	532	8	278	174	1	07	5	91	0246
Slc16a5	27.9					178.							40.				34.	31.5	29.	32.					
	145	31.877	28.344	34.05	23.08	0039	50.0718	346.93	200.946	32.558	32.021	31.898	573	135.606	543.90	146.2670	605	673	749	265	37.9867	40.4	34.3	28.8	29.14
	62	767	767	6233	6521	5	86	038	44	372	791	975	697	46	992	1	037	38	389	51	62	16	4	75	2064
Ccr7	20.2					25.8							166				157	222	39.	34.					
	811	31.812	35.209	404.4	494.3	7504	1981.39	2893.9	1603.20	20.718	74.140	24.000	7.6	704.183	3662.5	402.4578	1.8	7.26	149	681	20.0237	48.7	40.2	399	3159.
	89	484	686	2847	129	2	73	575	54	3	585	32	198	53	783	7	895	67	576	285	82	18	8	49	7838
Cd96	106					38.6							117				248	156	233	35.					
	8.00	31.438	28.668	34.96	38.37	3242	350.418	1490.1	1167.50	28.984	31.071	29.455	7.2	2179.61	1235.2	730.9092	.44	0.54	.77	984	5827.01	107	972.	32.7	31.84
	44	221	972	5467	4143	6	14	981	52	961	583	474	705	31	036		26	21	475	209	96	04	5	09	5614
Ceacam15	52.8					42.2							58.				45.	43.2	42.	41.					
	105	31.296	37.030	53.84	64.83	7895	70.7136	55.961	49.8529	36.391	45.211	38.781	064	41.6603	44.948	42.69079	795	699	419	331	44.3906	33.7	39.7	421.	609.1
	86	299	485	3446	7166	7	3	018	02	021	864	395	013	27	793	2	568	37	769	241	41	18	9	9	1148

Gima p1	551. 203 74	31.275 9	138.15 993	724.5 6708	661.6 2052	363. 0974 6	777.727 11	1797.9 343	1360.08 36	21.067 355	20.098 478	21.735 942	994 .20 258	1675.14 01	2562.9 481	2614.341 7	544 .07	160 9.39	127 7.2	19. 887	1872.61 93	168 4.77	1038 .075	26.3 726	38.91 4057
	Cxcl9	21.1 319	31.183 315	20.264 952	27.62 7758	31.36 3818	26.2 9658 6	27.1437 86	32.553 475	35.4148 61	29.134 309	4137.4 28	26.959 496	23. 028 12	24.9678 66	23.658 421	25.46588 3	25. 170	26.7 927	24. 089	38. 511	23.8593 06	31.6 026	31.4 2274	101 8.03
B3gnt 5	17.4 555 19	30.736 296	23.939 901	799.5 3373	1172. 1485	19.1 8320 6	55.9455 5	110.53 259	174.097 52	22.461 678	17.606 827	19.740 474	43. 538 8	44.7887 7	47.873 271	71.46160 4	25. 334	45.0 150	17. 121	24. 835	22.5531 74	259. 690	75.5 6148	62.7 373	30.89 8116
	Epx	13.4 529 43	30.550 137	19073. 743	25.01 5143	18.46 6223	17.2 3228 2	16.2800 11	17.481 777	24.3534 03	18.627 882	16.979 266	20.938 451	20. 574 661	25.4764 26	18.613 199	15.72486 6	19. 121	17.0 333	16. 405	17. 654	19.5383 14	28.3 207	20.4 0851	225. 845
F7	27.9 582 02	30.528 859	154.60 301	28.19 1871	40.44 5831	25.2 9358 8	30.7613 58	34.616 073	30.0076 2	315.80 648	325.48 982	547.49 986	29. 016 338	22.1437 43	31.317 653	26.21273	28. 539	24.3 762	27. 774	47. 484	35.6925 56	24.0 286	24.2 6703	211 8.87	2224. 9222
	Prss3 0	30.3 244 44	30.402 417	29.819 884	28.37 1093	28.34 8669	37.3 3553 4	55.3865 95	57.430 385	59.6757 95	29.631 094	27.128 008	30.829 573	28. 152 162	36.2783 11	26.281 573	31.90498 1	40. 213	81.5 909	31. 500	32. 497	38.8345 95	31.9 432	38.7 5704	34.7 846
Ninj2	24.3 173 77	30.220 407	29.335 15	37.92 5311	41.19 0308	37.3 8461 4	52.0202 58	67.578 424	54.3171 9	27.658 306	27.356 363	27.700 839	57. 665 468	37.4393 44	48.706 345	48.64908 2	65. 268	91.9 824	47. 362	28. 213	33.1127 94	22.7 477	31.8 9992	34.1 325	31.55 0515
	Ell3	30.9 295 54	30.190 351	28.543 571	848.5 2522	691.4 3744	29.6 3270 9	28.5879 3	30.389 405	29.7229 77	28.863 262	35.326 319	28.388 467	29. 846 17	31.7298 54	30.144 345	30.68157 2	33. 622	31.8 599	28. 517	30. 883	35.3485 54	38.1 241	31.6 7785	39.6 181
Il7r	57.4 977	30.184 374	363.00 057	29.96 3286	28.27 911	20.4 365	601.793 47	4855.1 972	4923.62 22	1902.5 186	747.84 73	1294.2 314	268 .88 31	3168.61 66	3361.5 81	440.1090 2	363 .19	479 1.52	185 3.2	25. 534	27.6687 35	786. 577	144. 8920	174 0.98	941.5 7035
																	601	19	332	549		18	1	86	

Alpi	25.1	30.105	26.306	35.47	32.14	30.2	29.3044	32.683	32.1937	28.186	35.210	27.155	30.	21.8094	36.676	34.18239	32.	30.4	29.	34.	631.106	24.6	24.0	42.0	37.62
	729	451	992	6235	1972	0055	3	779	71	099	023	202	435	22	987	9	719	135	486	588	19	353	9615	980	7644
	58					1							444				312	978	789			66	3	81	
Pbx4	72.9	30.095	38.676	22.19	20.55	25.2	34.5462	31.577	39.0680	36.914	41.028	32.710	37.	52.7562	38.886	45.83753	28.	66.1	39.	37.	29.6489	23.8	24.8	20.7	21.04
	284	603	173	8129	256	7237	53	924	1	611	02	519	179	85	586	1	079	291	142	674	32	794	0945	286	3023
	63					9							704				949	52	723	102		08	3	3	
Lef1	28.1	30.031	25.707	28.59	52.30	42.2	366.284	2184.8	1151.03	27.891	26.777	33.150	788	271.889	2453.4	474.5020	448	257	538	33.	44.0533	238.	188.	29.2	28.74
	855	74	502	8645	0196	5845	5	482	45	718	985	652	.29	49	16	2	.28	1.21	.50	140	75	722	1821	192	499
	34					2							965				778	66	258	778		09	1	04	
F10	22.9	29.962	484.97	18.90	19.46	19.1	19.6920	21.690	20.3781	117.14	379.53	346.96	18.	28.3674	22.162	20.28432	22.	24.1	23.	327	19.0683	20.4	22.5	207	1071.
	216	857	267	8199	2324	3002	33	445	6	615	183	234	961	86	891	8	324	103	219	.91	3	733	6082	3.96	245
	25					7							84				868	78	93	678		67	7	03	
Spo1	27.3	29.598	19.824	21.19	22.97	52.1	30.2135	83.337	118.038	19.673	22.120	20.246	27.	71.4227	70.012	108.2409	21.	184.	24.	21.	33.1742	155.	52.2	24.3	29.28
	000	498	274	2899	8392	4498	63	892	98	314	209	525	635	29	913	1	850	266	388	126	79	051	6458	962	5479
	69					1							526				42	23	41	647		25	3	07	
Icos	29.4	29.598	26.565	30.22	29.41	28.9	326.545	254.86	256.834	27.915	30.088	29.480	111	2218.28	349.43	4084.023	990	121	202	30.	38.4060	151.	211.	53.7	45.75
	205	09	456	4308	1014	7758	32	185	63	741	567	12	8.1	6	501	9	.44	5.27	2.5	214	45	745	3534	557	1298
	88					9							485				671	45	308	805		45	4	22	
Il1a	34.3	29.303	220.15	20.96	27.13	22.1	36.8532	20.926	23.3725	50.587	1079.5	36.742	48.	18.6032	18.227	20.80761	358	47.2	21.	21.	22.6548	24.1	23.7	718	421.7
	916	418	522	8056	7158	0395	83	173	68	37	628	894	474	88	436	6	.24	054	448	877	19	400	9325	6.40	0652
	51					5							399				978	22	94	443		7	5	32	
Cd8a	24.9	29.256	23.304	27.01	25.41	26.9	736.245	2734.0	1980.68	24.888	24.262	24.941	30.	30.0847	25.591	24.35117	42.	22.9	24.	27.	8032.28	24.6	24.3	26.0	29.44
	925	738	158	8525	72	6446	45	778	49	733	855	782	425	36	983	7	938	273	563	800	97	684	5809	142	7343
	62					9							555				522	96	798	285		09	1	36	
Ccl22	38.7	29.184	40.619	27.76	22.67	35.3	35.3791	32.492	36.6408	33.774	47.064	36.659	37.	30.5135	34.550	32.53511	42.	54.8	39.	26.	29.9758	27.2	32.2	626	3645.
	744	716	542	971	9023	8610	11	095	01	347	549	874	982	28	164	9	755	172	130	279	19	825	7562	8.36	4374
	31					7							219				828	64	761	455		99	6	28	

Grap	21.3	29.177	45.109	107.2	133.7	51.1	314.431	432.13	344.745	55.537	80.806	60.157	514	503.548	770.34	616.4998	434	683.	619	23.	86.4384	211.	122.	22.6	22.76
	754	518	554	5483	394	2875	53	31	71	099	457	169	.86	61	182	2	.39	888	.94	304	99	993	9210	946	1544
	86					7							163				705	86	159	101		89	9	49	
C3ar1	196.	29.071	1532.2	31.59	28.61	24.5	20.5432	25.394	24.1177	4230.8	4123.1	4553.5	21.	21.4222	25.784	23.75033	23.	22.9	21.	30.	25.7418	25.1	21.6	984.	752.8
	373	986	306	2515	5608	6864	36	982	7	868	2	388	601	65	628	4	552	291	929	449	73	478	2370	057	7031
	43					8							892				738	21	229	58		22	9	49	
Lif	99.8	29.037	30.441	32.16	37.47	27.0	82.4797	29.407	30.1651	33.311	38.580	32.714	64.	37.2678	31.600	42.52228	104	91.4	169	31.	30.0756	33.0	36.8	40.4	29.33
	444	68	056	4217	7599	5883	5	411	13	651	125	202	720	71	62	9	.40	838	.85	260	08	430	6786	965	6504
	4					7							875				727	27	872	092		97	3	24	
Tnfrs	376.	28.951	65.670	29.21	25.38	22.5	1273.46	42.148	48.9012	28.871	30.209	27.919	851	119.918	48.282		209	353.	147	19.	544.850	166.	1059	234	1192.
	027	102	352	0714	3256	6960	13	703	5	695	13	357	.12	99	83	373.576	9.4	271	6.6	640	7	471	.104	6.01	1399
	53					1							843				278	32	191	627		35	7	33	
Klrd1	14.6	28.861	178.80	13.27	14.09	16.5	1747.05	5353.6	8238.10	12.375	12.396	12.021	77.	132.645	480.36	26.27270	907	127	51.	62.	8832.13	102	7656	22.5	70.88
	247	884	043	6156	0244	9919	17	5	88	75	275	192	025	91	923	1	.98	2.59	361	030	06	89.7	.363	176	4781
	23					9							3				064	77	835	306		2	7	81	
Csf2	33.1	28.622	41.511	31.28	28.81	34.2	2551.09	25.901	115.648	26.820	32.072	29.963	58.	28.1660	32.153	26.72187	456	70.0	113	33.	87.6153	88.3	89.2	31.3	27.30
	930	78	926	1341	5093	7379	48	126	29	277	319	432	540	58	252	1	.53	246	.73	161	02	413	6572	025	1633
	9												678				647	12	126	03		52	5	68	
Scn11	27.9	28.585	29.495	38.39	40.97	214.	31.4558	32.801	33.6031	26.600	31.355	27.072	41.	34.1990	35.731		29.	45.6	34.	37.	44.4108	30.5	33.0	48.5	37.31
	256	943	893	3998	4294	3949	72	864	74	497	018	948	002	82	07	39.24784	994	864	809	830	45	808	2457	166	9216
	57					8							436				086	56	577	018		56	5	17	
Fcer1	163	28.321	1912.3	25.21	15.24	16.4	15.0661	15.629	14.3729	15.288	13.286	14.557	14.	17.3102	13.944		17.	17.9	15.	16.	15.8911	15.5		18.1	20.19
	67.8	534	825	678	0566	5301	54	642	71	575	269	766	354	99	878	15.96639	851	600	894	767	75	550	15.8	047	0701
	9					5							739				757	95	521	052		7	8977	7	
Hpgd	273.	28.191	57.645	28.58	43.90	26.1	23.5019	31.670	40.2980	1468.3	469.37	500.35	28.	23.7957	33.344	36.39749	26.	28.9	96.	24.	49.1399	23.2	23.1	30.2	36.98
	870	88	223	8888	4578	0609	31	023	94	34	892	364	099	21	088	1	249	951	180	623	84	116	7207	799	7851
	44					4							252				857	16	673	535		89	7	05	

Art2b	31.4	28.073	25.744	29.46	26.16	26.8	38.1272	580.44	198.356	30.417	30.381	33.984	167	230.336	368.37	635.9620	24.	66.3	34.	34.	289.446	28.1	31.8	24.6	25.51
	831	467	993	4465	6843	7634	44	606	67	224	943	113	.94	27	546	3	786	022	897	410	06	765	0744	975	5417
	74					9							37				066	58	64	161		2	8	27	
Cd160	22.5	27.490	21.437	27.18	26.23	25.3	163.353	102.15	338.419	23.678	24.208	24.506	49.	56.1828	45.276		41.	29.1	29.	23.	1660.17	303.	172.	20.2	21.95
	708	658	551	9264	103	7416	11	158	34	223	109	404	318	72	313	104.1035	720	978	396	444	56	293	0901	142	6241
	06					9							226				971	53	192	345		17		17	
Tnfrs f8	23.4	27.270	27.281	30.25	31.85	27.7	34.8000	28.260	25.4780	32.184	29.373	29.060	32.	23.2949	27.236	27.84765	303	87.5	70.	31.	28.9159	27.3	26.9	29.9	27.89
	541	843	637	7747	1794	2708	05	808	59	482	87	09	077	01	078	7	.41	707	873	908	74	979	6299	211	057
	96					4							774				144	61	417	649		57	2	71	
Il24	26.4	27.109	22.276	32.87	26.41	48.1	40.9932	33.399	26.9596	29.602	22.044	27.563	41.	34.1158	28.554	26.58383	121	84.4	341	30.	35.1281	23.5	23.2	38.4	36.45
	701	142	132	5795	9081	8157	41	012	21	978	225	428	284	31	287	7	.77	210	.01	864	57	158	9217	639	1354
	12												51				889	27	76	957		9	9	26	
Spink 2	845.	27.100	31.507	21.65	19.98	33.2	39.2685	29.896	30.8697	28.460	40.702	31.301	37.	26.0994	32.717	36.20884	49.	46.2	44.	55.	25.7455	20.7	25.6	363.	417.3
	73	949	322	0859	7538	5608	71	135	74	643	341	209	770	31	078	1	832	519	044	300	08	635	2938	564	5424
						4							263				028	12	344	021		01	9	92	
Ms4a 8a	17.3	26.992	21.855	15.05	20.97	20.1	25.0332	19.668	21.0557	23.385	32.805	28.821	20.	20.7326	19.648	19.89688	22.	20.4	18.	531	85.2234	26.0	19.1	52.8	53.18
	041	762	308	3765	7653	9741	14	219	84	26	623	594	570	79	854	6	524	587	815	.96	88	980	8282	284	3156
	63					5							9				019	38	975	414		69	7	24	
Pdcd 1lg2	138.	26.958	103.90	217.7	39.22	25.0	233.866	27.144	55.6942	23.527	132.95	519.78	354	69.5207	37.719	308.5886	716	64.3	198	34.	92.6709	47.2	59.8	769.	478.2
	015	978	326	6163	2966	0660	51	891	51	346	517	462	.24	62	928	9	.38	002	.97	462	42	828	0915	992	3508
	68					2							089				929	77	658	151		75	2	08	
Xcl1	41.4	26.900	30.490	22.57	33.86	23.5	6588.56	121.27	1565.23	25.042	23.625	24.215	156	56.7775	53.731		334	31.3	29.	19.	2550.48	565.	954.	18.4	20.54
	990	705	246	1899	5414	9275	07	776	75	788	832	992	.54	48	954	80.99388	5.7	696	674	870	3	651	2873	942	1234
	99					4							763				081	59	902	095		24	4	45	
Zg16	28.8	26.865	27.065	22.76	21.19	21.2	28.2802	29.360	26.3232	30.536	34.655	32.021	25.	40.0333	27.772	27.39502	29.	29.6	28.	29.	1830.36	28.6	29.7	27.6	24.81
	959	873	042	8014	3094	8690	98	324	06	754	36	911	942	7	368	2	924	984	530	054	25	988	2173	476	8766
	49					1							548				214	73	406	38		22	6	95	

Capn3	75.848584	26.81255	25.551293	24.952929	21.113069	29.390137	32.007954	41.448825	46.690281	24.365542	23.522293	23.121486	369.68849	118.54514	65.57381	127.54813	34.218	132.479	30.953	34.979	2221.5513	50.4738	54.37258	26.8710	27.514284
Slamf7	21.938071	26.415304	66.532286	216.91739	355.87952	2722.4047	228.06461	45.558011	169.18919	365.28689	2208.0145	255.14663	35.137525	77.371834	35.729189	49.904593	101.24	38.1138	32.096	68.600	279.14227	216.518	150.0477	1439.65	177.42756
Aicda	26.452685	26.353638	26.250793	645.07588	23.127177	28.943996	22.491158	23.61925	26.745604	22.724917	30.192432	24.540743	26.874355	34.767453	29.065175	31.62419	39.887	26.3728	26.161	30.049	25.738368	27.3290	27.63906	26.0047	23.501405
Marc0	24.091666	26.276635	27.458041	20.853706	22.933586	26.713694	25.538567	28.464993	30.111174	88.323374	4192.3262	72.380629	26.508742	44.932027	26.335015	23.982261	30.538	23.9451	23.789	22.356	22.982977	32.6405	28.50941	1144.93	172.5871
Al607873	11.210707	26.124418	61.783991	12.026012	14.200302	13.46211	9.5138831	11.066858	13.266567	275.10677	681.32048	87.253082	9.9846263	11.771068	10.270073	9.8060366	9.8972	11.3264	10.966	1425.3	9.3972945	10.7449	11.26594	1787.92	341.39714
Poln	629.04957	26.109109	92.015667	59.708019	42.353864	45.504537	36.614511	39.683807	43.892808	26.110781	22.878818	20.268173	39.975282	20.493322	28.004609	25.404254	22.998	26.7346	27.338	22.244	27.964421	30.8458	25.30775	24.6199	23.199421
Zfp566	28.700988	26.04118	29.749622	604.33342	609.71779	275.98964	156.27127	225.46794	187.92936	50.332306	21.44011	39.983738	88.33984	166.57486	170.93508	83.044364	70.997	63.5590	59.173	35.681	71.312785	113.438	71.96849	16.1971	24.344588
Eif2ak4	100.58548	25.907621	101.01765	658.92175	805.63468	234.94325	173.34109	113.18949	112.00176	128.62055	70.976192	126.4658	84.213883	157.64017	105.17592	117.85553	99.205	103.522	97.261	170.04	105.64151	66.7840	53.09302	37.9309	60.107105
Ccdc62	30.378456	25.464254	17.609843	295.57101	80.463123	28.108602	16.740023	47.244336	58.123669	23.521183	16.693375	17.861834	33.022288	32.598176	48.22685	34.792743	15.247	24.9134	27.532	20.440	21.96938	22.1935	22.14225	15.3353	17.057057

Xkrx	21.6	25.131	43.737	455.1	468.4	28.2	20.7121	137.55	30.3297	29.128	35.727	27.818	36.	41.7992	130.95	37.32019	24.	24.5	24.	19.	21.6917	40.7	31.3	25.1	22.85
	112	9	837	4893	1129	6971	11	881	12	341	183	709	796	41	388	5	441	047	039	804	65	546	7124	210	7579
	32					5							889				007	34	1	12		99	4	88	
Rgs1	732	25.130	189.54	42.50	24.24	21.3	1259.28	157.02	610.178	495.30	1074.1	241.46	266	651.757	162.16		345	107	455	40.	9419.49	522.	230.	251	418.1
	1.01	15	628	1206	8562	4953	81	74	67	073	136	125	1.9	05	911	1170.104	2.4	9.94	7.8	058	81	821	6073	0.58	4746
	25					3							272				677	1	674	664		48	2	02	
Sit1	23.1	25.076	20.314	73.91	92.35	27.9	137.024	390.13	398.085	26.025	22.788	23.764	409	794.099	916.60	521.9278	72.	509.	328	22.	25.2135	26.4	23.0	21.4	22.31
	128	047	307	4574	1077	5542	06	767	05	867	984	473	.34	11	544	2	638	703	.78	240	37	904	7894	098	0411
	3					2							175				508	75	876	91		14	7	85	
Cd20 Or4	272	24.978	970.16	12.68	15.98	11.6	46.5571	224.95	286.656	490.53	759.85	519.09	18.	42.5397	82.589	41.28794	11.	20.6		13.	11.9003	664.	197.	617.	964.2
	9.39	007	196	8572	6773	1233	1	348	96	169	626	379	098	84	792	5	664	416	162	464	4	030	2629	387	1698
	19					7							042				799	88	.09	551		18	9	07	
Pga5	556.	24.709	309.72	39.15	31.59	26.6	33.7587	28.704	29.5175	27.073	24.393	32.287	35.	35.7540	26.838	24.51475	35.	33.8	26.	34.	34.2072	32.3		25.7	30.68
	807	014	587	5099	1472	1388	02	406	88	022	802	794	347	86	348	6	388	496	124	595	92	865	38.4	362	1452
	22					2							887				297	01	775	841		62	3686	18	
Gzm k	29.6	24.602	20.373	18.44	34.77	25.0	38.6665	90.051	492.074	18.872	18.286	20.399	22.	123.620	38.500	276.9552	21.	17.4	18.	22.	21.2045	51.0	95.1	18.6	18.62
	546	086	103	5134	6794	4159	86	655	55	92	076	177	857	4	321	5	437	592	489	804	37	058	9397	055	2447
	03					5							691				603	5	093	747		98	8	3	
H2- Ob	168.	24.407	29.007	2432.	2250.	82.4	15.7300	401.85	230.094	15.257	20.851	15.043	81.	93.9217	288.32	107.7462	14.	74.8	15.	45.	13.4835	100.	18.3	76.1	82.38
	342	323	432	8908	1171	9767	77	905	03	592	885	24	301	58	035	6	907	588	130	558	46	401	0129	163	4579
	2					2							915				977	13	558	992		37	9	28	
Asgr 2	20.4	24.401	22.193	32.04	27.92	18.4	26.0796	35.098	25.3053	33.873	30.847	26.635	24.	41.7404	24.672	24.62700	21.	23.2	23.	27.	21.0484	32.4	29.3	97.8	694.2
	429	25	163	2781	0555	3588	81	398	47	883	549	659	140	28	736	5	693	170	443	561	62	743	2340	078	9412
	18					9							578				957	16	4	739		01	4	61	
Lyzl4	22.5	24.224	34.621	20.37	34.77	27.6	27.1612	25.138	26.5535	108.03	27.484	428.32	24.	25.9248	26.144	22.38977	30.	29.0	27.	22.	24.4116	26.9	24.9	30.2	33.09
	670	48	118	6104	9882	7330	7	95	88	399	103	354	612	96	95	7	041	184	226	673	16	572	7079	326	325
	48					4							018				241	92	789	557		65	6	72	

Atp6	149.645	24.176	424.77	25.98	22.87	22.2	19.3488	20.184	38.6802	3481.4	270.20	4778.6	27.314	28.7276	20.316	50.70680	28.068	81.6278	25.211	16.598	20.6474	20.5382	18.85442	751.354	1231.2658
v0d2	75	529	104	1357	8929	5	54	286	27	843	948	36	769	77	715	3	799	7	171	182	35	43	4	21	
Cyslt	19.2025	24.158	33.100	22.47	24.76	20.3	36.0888	18.051	16.9799	321.69	259.64	201.91	26.299	17.4298	17.463	21.45530	94.796	1005.00	1921.3	174.13	16.0115	20.8161	18.61927	328.680	484.23083
r1	08	518	196	5042	3204	7	49	97	47	369	448	466	407	67	112	7	417	1	936	588	56	99	9	22	
Klk1	17.8140	24.019	21.515	14.51	16.92	21.8	13.8456	17.186	15.5574	20.426	21.198	20.949	18.076	21.7186	19.210		26.536	19.8064	20.733	24.710	24.9984	21.1302	18.97583	757.474	982.19646
b1	53	198	978	6485	136	7	84	148	75	488	647	957	516	1	069		541	12	48	767	68	94	7	36	
Cd70	27.0261	23.893	21.794	16.04	19.20	20.7	181.089	22.664	24.8853	23.839	24.505	21.195	42.645	30.1496	24.903		800.92	34.9322	27.161	20.735	24.2772	28.3638	26.54385	506.986	40.326398
	05	957	775	4814	154	1	46	346	88	123	238	687	82	33	205		268	74	087	925	35	99	6	56	
Cxcr5	20.3324	23.878	16.434	2510.	2414.	19.7	201.697	111.27	568.209	17.187	27.745	18.626	228.99	805.956	30.798		17.459	40.7962	16.865	18.464	17.5354	41.1576	22.38503	33.6842	17.704959
	49	42	678	2009	8578	6	87	706	56	155	656	056	698	5	598		324	9	44	355	08	25	6	31	
Cyp1	9835.12	23.816	5862.6	40.83	26.61	33.1	24.8460	21.067	20.8025	23.665	25.500	20.789	77.062	19.1613	21.248	23.24961	33.310	56.9670	5507.2	18.744	22.2819	17.9215	20.32976	28.8561	30.3367
1a1	61	949	723	6808	1666	9	76	834	81	92	703	684	817	63	681	2	077	18	512	231	25	05	5	27	
Nxpe	23.1657	23.719	26.713	239.7	263.6	29.7	23.5992	28.842	26.4377	21.269	25.397	23.532	21.609	23.2565	24.214	22.27471	25.666	24.7539	22.513	26.030	23.8011	26.0247	24.71259	22.9281	21.859002
2	19	502	32	6646	175	9	92	871	87	606	735	068	586	01	671	3	394	51	713	415	11	85	7	51	
Timd	24.3286	23.528	20.134	68.59	27.47	268.	20.9655	21.744	21.3164	20.872	22.019	21.567	25.659	21.6861	23.138	23.87190	102.17	127.263	22.964	26.459	26.2079	20.8383	19.81335	24.2155	24.672534
2	87	194	86	3827	9782	3	03	779	71	464	227	001	811	51	923	6	731	94	298	816	17	14	2	5	
Tnfrs	16.2247	23.517	18.196	19.20	21.51	123.	21.3975	19.336	18.6398	22.638	16.576	22.109	19.339	19.1331	19.939	18.36636	18.184	21.9967	22.119	20.290	21.744	24.5596	21.63531	21.1317	21.067457
f17	7	121	961	4973	1491	5	68	547	31	29	1	799	459	25	427	5	572	09	19	134		03	5	94	



Ppp3	40.5	23.452	41.593	264.6	246.4	555.	196.879	235.43	481.467	39.688	32.664	32.707	110	111.960	162.22	140.3714	176	306.	286	18.	319.282	291.	372.	29.1	25.38
cc	801	339	013	8832	9704	0101	47	092	08	34	886	298	.56	96	688	7	.75	248	.89	436	35	968	8022	062	6667
	72					4							204				932	86	099	476		1	6	74	
Gbp2	22.1	23.282	20.119	20.66	28.97	26.7	19.6223	22.012	19.7640	28.839	2703.4	26.409	92.	133.144	25.538		25.	18.8	25.	26.	28.3306	25.3	22.6	188.	128.1
b	007	074	181	8062	2551	2183	31	333	48	412	043	501	419	52	924	53.34005	699	680	174	128	2	205	2709	213	435
	96					4							762				405	66	709	942			1	21	
Eome	41.0	23.104	22.656	20.69	21.50	20.6	1230.57	422.80	2973.82	19.327	21.644	20.904	52.	77.8681	55.287	72.19137	89.	26.5	29.	19.	18.7713	206	1827	19.4	19.10
s	630	903	782	023	1429	6326	1	567	02	558	299	09	064	72	375	1	292	788	483	033	44	7.60	.960	406	392
	56					4							265				871	93	812	252		72	3	83	
Gima	116.	22.742	29.683	642.8	436.2	57.8	157.656	506.04	482.654	30.044	30.890	34.348	119	628.063	382.71	367.2807	182	151.	114	27.	326.464	929.	484.	21.5	20.89
p5	268	692	006	8427	3411	3111	18	766	1	519	183	925	.87	45	509	4	.19	906	.15	489	44	462	2916	747	251
	82					2							974				465	3	359	298		84	3	04	
25000	47.4	22.594	18.123	12.62	12.74	19.8	30.6869	16.760	21.8828	35.951	47.512	22.833	22.	12.1155	18.134	18.10419	16.	50.8	67.	23.	13.9325	12.4	13.0	21.2	17.27
02B1	577	616	319	6697	6599	8316	67	515	19	548	433	526	719	68	683	4	255	379	507	039	87	096	4452	095	3637
3Rik	99												827				34	48	945	367		67	3	57	
	21.9	22.540	25.640	36.72	48.57	31.6	21.9606	21.911	22.8168	299.49	109.20	226.53	25.	26.1156	25.191	25.52646	25.	22.2	23.	30.	32.2741	26.2	25.1	75.0	33.11
Htr2b	065	763	6	2816	6489	0858	15	624	27	663	94	11	589	83	318	1	388	634	152	419	03	112	6168	316	4683
	43					2							989				03	64	095	618		79	3	08	
Il12rb	35.4	22.506	37.548	23.76	20.68	28.2	87.1022	25.555	28.3944	25.736	23.617	23.415	27.	30.6292	26.879	28.76571	707	92.2	25.	37.	57.5753	68.6	65.2	158.	77.71
2	157	093	055	3039	7991	7741	51	846	87	823	539	083	825	98	771	6	.02	380	628	448	44	772	9607	870	3465
	23					6							356				863	13	172	506		78	4	8	
Gm1	289.	22.466	24.004	14.34	17.94	13.4	13.1551	13.348	12.6160	12.583	15.582	12.371	14.	15.6133	12.912	13.38667	13.	11.8	13.	15.	14.5881	12.3	13.3	35.2	15.36
4047	076	33	157	1727	1801	1021	53	464	73	795	932	374	722	97	632	8	158	710	391	056	31	595	0343	925	5386
	92					8							299				896	07	598	518		87	5	09	
Catsp	115.	22.114	32.961	20.10	18.01	21.4	26.2930	25.603	34.8476	23.937	24.934	22.680	35.	44.6859	46.258	65.64594	23.	107.	198	22.	46.3062	66.6	33.0	28.1	28.72
erd	343	629	966	0972	4927	12	89	222	46	823	952	401	770	97	124	2	862	994	.03	189	9	075	7601	502	1464
	93												877				413	19	421	708		32	3	39	

Lta	25.4 407 19	22.100 189	21.527 116	83.37 7587	82.13 7066	21.5 3293 1	2321.63 16	143.22 561	102.810 56	20.528 877	33.662 365	24.273 495	219 5.2 586	184.115 08	239.52 569	204.5731 9	314 9.3 079	546. 927 35	53. 539 06	18. 239 569	23.3749 72	31.5 204 01	81.4 7531	126. 161 52	24.88 1557
Pglyr p3	25.7 569 59	22.075 8	19.360 846	102.8 5881	55.56 3665	185. 0407 6	20.0482 45	30.022 74	30.9192 73	17.644 982	28.012 841	20.255 911	23. 330 125	37.5840 81	39.708 684	28.63925 7	39. 563 902	23.7 425 19	17. 082 174	26. 238 141	25.0655 54	77.7 701 74	47.0 0800 2	22.8 009 08	23.06 5837
Cd8b 1	15.6 813 07	22.041 827	18.318 087	18.02 8003	16.82 7216	18.3 4919 4	1333.69 66	8644.6 081	6393.71 25	18.231 281	22.885 796	16.211 878	112 .03 789	31.9142 09	212.61 309	82.55403 2	36. 294 819	136. 570 95	152. .44 06	25. 859 97	21.7950 28	21.5 959 29	20.6 6566 6	19.2 606 71	17.59 8019
Mcpt 2	364. 001 49	21.973 52	16.558 27	23.52 7608	16.39 7958	22.3 0140 8	14.7088 72	18.951 288	19.3088 28	15.012 696	13.478 183	14.900 307	19. 666 958	17.2958 57	17.499 602	18.52260 7	19. 843 708	17.6 245 65	16. 724 007	22. 423 146	27.4708 13	19.8 367 89	19.9 2267 1	21.4 487 2	21.81 0535
Calca	225 1.32 03	21.865 043	22.957 857	18.93 5776	19.54 8088	24.1 5940 8	17.4740 63	17.223 189	17.1540 07	18.417 398	20.630 689	19.622 778	25. 674 904	20.6285 17	19.366 038	18.94237 7	18. 272 771	18.7 445 5	245 .18 546	22. 518 386	21.9301 15	25.5 240 35	22.9 0254 5	24.1 909 49	23.07 462
Oosp 1	21.9 542 93	21.719 758	35.798 392	35.31 1286	25.17 201	326. 3893 6	24.6356 56	25.306 425	23.0622 75	22.503 685	19.012 933	24.393 696	21. 879 798	22.4579 84	21.740 088	19.39313 9	21. 518 124	19.1 902 71	17. 991 817	21. 696 923	24.8689 31	21.8 431 17	35.5 751 16	34.38 7281	
Egr2	158. 844 12	21.678 951	709.53 617	304.3 1487	336.7 0265	39.7 2889 5	416.009 61	197.10 064	78.9728 44	433.27 856	21.693 28	2436.3 216	464 .17 362	960.483 04	186.29 946	1024.231 3	393 .42 554	51.2 891 03	105 .35 359	21. 815 45	256.479 43	279. 972 69	635. 7993 7	448. 419 39	906.5 5111
Trdc	22.1 207 28	21.660 18	68.416 39	15.12 9279	14.86 7748	20.9 3705 5	49.4234 76	94.418 574	185.907 5	15.868 894	17.268 5	21.143 029	60. 351 314	57.4431 83	92.982 069	55.43129 9	106 5.2 145	103. 156 4	130 .12 549	15. 389 45	8537.20 45	785. 207 83	775. 9467 6	18.2 217 47	17.97 757
Pdcd 1	19.1 868 44	21.629 23	20.619 87	19.64 4708	19.06 5815	17.7 7154 7	342.381 64	31.736 276	48.0950 69	17.834 02	23.101 345	19.779 684	429 .91 457	712.265 98	54.592 78	2935.401 9	100 0.3 984	111. 239 118	77. 459 084	18. 459 084	24.9340 81	19.7 506 55	20.5 1293 1	18.3 849 57	22.99 2339

Cxcl1	21.5	21.603	19.504	27.52	23.26	22.7	21.5873	24.901	19.9306	22.920	1561.8	20.165	20.	17.8338	18.480	20.73083	18.	20.6	17.	17.	17.5828	19.5	18.2	184.	16.75
1	622	284	565	5888	3529	8876	17	262	33	032	416	625	004	17	691	8	991	287	582	824	91	354	0659	936	746
	65					4							359				791	68	648	133		06	4	52	
Cd5	18.9	21.537	15.448	20.04	22.19	24.4	1148.51	1563.2	1731.71	16.726	15.770	16.925	424	5469.58	3298.9	4555.672	493	303	699	20.	22.2998	18.6	17.9	21.9	21.73
	889	072	51	7391	0413	416	55	581	82	992	954	689	2.3	73	718	8	3.3	3.80	.15	709	53	261	1043	649	6809
	67												569				211	27	701	424		28	41	41	
Gbp8	37.1	21.518	12.147	757.7	163.5	36.9	197.620	2643.5	1887.36	13.226	1203.6	24.283	163	1646.10	1237.3	923.5565	120	802.	151	19.	1310.25	124	662.	688.	148.3
	098	528	245	3657	0677	7856	77	98	63	841	362	146	.46	41	778	3	.86	883	3.0	537	66	6.74	4869	097	745
	2												661				445	62	012	115		8	2	21	
Pkd2l	22.4	21.370	21.957	24.89	25.95	275.	21.9408	22.717	21.4614	28.222	32.062	27.388	24.	20.3435	23.789	20.85369	22.	21.6	21.	22.		21.9	20.3	22.0	23.11
2	692	599	503	2159	3609	7029	21	033	52	154	098	737	166	77	498	5	732	886	047	650	23.588	503	9665	658	3925
	6					4							878				178	06	381	249		9	6	85	
Cr2	19.9	21.345	20.702	1999.	1634.	51.1	18.0468	19.753	19.4745	23.247	21.699	24.584	18.	67.1937	24.247	21.82901	20.	21.1	19.	24.	18.4434	50.4	20.4	18.8	18.45
	671	753	758	497	6221	9416	78	071	83	284	923	546	396	16	1	8	848	252	011	636	19	995	7113	482	6923
	25					2							814				361	95	37	211		82	81	81	
Ptger	347.	21.338	37.064	21.25	19.08	18.9	25.0067	18.301	18.0544	22.857	20.595	18.425	20.	18.8932	19.207	15.26294	42.	20.7	376	16.	17.6879	18.8	45.9	17.7	22.72
3	064	368	812	4469	3958	0863	37	592	91	605	187	742	495	02	899	7	404	178	.07	438	05	450	6128	984	0308
	95					2							132				951	44	869	67		84	3	29	
Myl1	285.	21.238	406.49	14.98	16.91	15.5	18.1161	28.838	20.7907	19.647	16.920	17.726	24.	26.7757	87.657	22.78953	23.	50.9	58.	18.	17.6517	22.6	24.6	23.3	30.56
0	091	864	119	0022	4179	4772	74	462	88	909	41	546	938	79	089	5	505	927	939	533	65	807	6166	302	6056
	27					8							272				983	47	821	368		28	3	64	
St8sia	25.4	21.103	30.896	21.19	22.28	20.4	29.7085	99.411	42.5960	21.872	23.814	40.835	86.	42.9879	160.59	78.48118	28.	151.	69.	22.	20.9244	19.6	20.8	19.8	19.77
1	840	069	557	7454	2536	5587	77	933	68	776	121	039	489	54	455	5	777	954	066	840	23	439	3486	118	2016
	59					5							806				415	14	751	873		06	86	86	
64305	28.5	21.087	25.204	21.16	21.38	20.9	35.9981	20.284	20.6570	22.499	22.281	23.558	59.	25.6221	22.695	24.81440	49.	70.5	115	22.	22.3843	19.1	20.1	26.1	24.47
71L1	539	932	982	4149	7875	6781	9	23	75	071	826	213	855	48	619	8	208	191	.50	246	24	470	4295	154	181
3Rik	8												201				779	45	06	323		49	7	51	

II2	19.8	21.024	17.433	18.61	18.06	21.9	75.9892	18.179	46.6679	19.646	16.976	18.574	84.	44.0233	22.576	72.35725	462	47.8	19.	23.	26.7257	30.9	20.7	26.4	24.02
	401	468	775	4674	2411	4080	57	158	86	654	831	066	442	87	62	3	2.7	784	764	448	1	643	20.7	341	5302
	34					4							651				172	03	778	033		85	2745	55	
Ccr8	14.6	20.977	19.463	16.64	20.65	19.6	19.8134	18.620	19.3263	17.714	23.036	18.505	384	37.1638	21.963	50.45906	32.	89.0	518	20.	23.6149	31.5	31.1	30.2	23.47
	246	664	995	7874	3408	1401	03	276	19	207	248	273	.66	64	735	5	169	479	.35	214	07	703	1346	703	499
	72					9							006				447	62	793	184		53	1	3	
20101 09A1 2Rik	24.5	20.974	31.497	18.30	28.82	46.0	20.5603	32.700	35.1125	17.641	16.638	16.412	24.	18.9588	30.915	27.66073	19.	55.1	34.	15.	16.1033	24.4	21.6	15.9	16.59
	708	964	614	5502	3688	9218	71	541	05	373	358	538	210	64	546	8	167	481	633	889	03	432	6459	012	4135
	09					6							131				081	33	503	023		03	1	3	
Fam1 67a	21.4	20.952	24.599	168.7	206.1	22.5	19.3474	17.418	19.3583	17.174	18.511	20.458	22.	24.0954	20.143	24.89852	18.	18.0	19.	19.	21.8252	18.5	16.8	22.6	23.15
	612	509	805	8929	9592	2303	38	38	2	718	715	751	100	97	809	8	560	535	919	401	9	387	6525	811	2325
	5					6							141				192	81	589	326		19	9	21	
49304 28O2 1Rik	22.6	20.791	20.909	20.06	22.59	117.	25.7123	19.355	18.8468	20.897	20.452	21.437	21.	25.5770	23.526	28.31096	22.	21.7	25.	20.	20.8324	25.4	22.8	20.7	19.54
	224	978	817	4008	7201	7280	55	402	71	387	281	232	036	69	539	3	176	656	343	626	42	419	1053	448	4884
	78					5							3				458	63	604	756		55	9	28	
Cd2	14.3	20.557	16.437	546.9	998.3	66.1	1503.32	3242.6	3678.55	18.904	19.830	19.313	520	2179.02	3785.3	5079.669	108	507	292	30.	18.9727	281	1324	12.7	15.79
	272	349	472	0318	3044	9179	41	765	94	637	207	747	4.0	82	789	6	4.6	3.48	4.0	115	62	4.19	.549	839	8417
	49					8							503				416	34	908	948		35	5	89	
Ccr4	20.8	20.183	18.556	21.26	18.37	21.2	28.8109	19.901	19.9460	16.560	18.845	19.503	92.	36.9600	24.122	78.92716	77.	102.	65.	22.	23.3538	24.4	23.0	29.5	25.32
	730	051	739	7319	7945	3384	06	04	64	995	3	107	871	5	726	4	154	906	427	277	86	794	0259	172	3379
	65					5							864				192	54	64	132		52	8	81	
Cdkn 2a	454.	20.036	1136.0	18.15	25.47	24.8	43.7465	21.819	21.5976	27.747	26.897	27.896	21.	25.4734	20.837	44.27583	61.	27.5	61.	22.	26.5821	21.4		23.5	21.69
	769	838	06	7435	3629	7329	39	112	98	132	911	907	775	62	303	6	544	947	304	458	47	869	21.3	930	3964
	13					2							262				057	13	932	595		24	2393	35	
Amp d1	23.9	19.982	16.908	24.48	27.93	38.4	17.8847	178.76	32.7275	17.372	21.168	17.986	35.	22.4734	212.46	22.74905	21.	21.4	24.	17.	22.7008	23.8	23.1	25.1	23.82
	263	228	872	3843	3677	4779	76	974	61	884	403	769	409	93	047	2	129	321	876	603	83	189	2366	779	1187
	97					3							044				056	92	847	107		07	1	86	

Plau	179.22607	19.972103	41.922563	17.98567	16.805032	18.727093	16.736909	17.161628	16.378945	182.09404	64.527042	187.78915	25.544383	19.027174	18.977275	18.625401	18.863838	18.202051	18.550557	19.487492	19.924425	17.523916	21.285003	29.546115	29.624872	
	Itk	202.27543	19.959028	18.572266	17.264639	19.175929	15.642337	673.37442	168.76688	136.23327	15.271969	15.971181	15.837168	118.00061	30.181739	172.73652	113.1833	416.83	216.400	331.42	15.435	19.203654	19.5965	27.06020	14.0666	13.951729
		Cd247	20.57787	19.924964	19.801539	20.740808	23.709695	19.018352	153.43213	257.21133	252.15809	20.603657	20.89932	20.284883	183.69802	55.086761	423.6787	277.30831	55.015	356.069	127.48	19.556	37.572207	47.1056	37.94529	21.4436
Gima p7	18.16973		19.814079	14.938041	2588.6156	1358.8403	241.17539	943.36748	1282.3755	1799.0754	14.89703	14.948096	17.189248	572.9457	1661.1765	1099.2725	2421.1329	247.11	156.007	793.73	18.666	6603.7317	978.777	574.5409	19.1288	18.98658
	Reg3b	18.788134	19.732673	18.681581	20.87583	19.69388	18.380406	24.766791	21.588724	20.308336	20.638281	17.722277	22.10074	20.722413	18.602401	20.335737	21.369924	19.546	19.6326	19.167	21.234	397.34267	18.1405	18.19750	25.3334	22.291112
Themis		23.166014	19.698419	18.392442	21.145654	21.986758	19.824192	287.64293	182.79577	190.29105	22.010834	22.136045	22.891976	63.53152	76.345356	150.45503	141.26784	270.88	691.409	419.78	20.278	58.872599	24.5062	20.36690	18.7321	19.316961
	Gm1110	115.34276	19.573259	62.632942	87.202671	47.529753	25.889529	78.768801	68.870388	83.780618	24.883485	99.812878	20.777083	138.26287	102.82785	119.6477	182.48743	50.531	354.87	246.877	30.54	79.412767	53.136	103.8666	86.5477	88.009237
Mcoln3		21.216373	19.424363	21.800021	22.932334	26.616518	27.893036	24.695218	51.055482	35.152806	126.42233	20.17192	103.93174	49.696694	22.709655	53.486689	41.534788	17.732	23.1576	18.710	17.705	51.686237	21.7089	19.74944	24.8652	28.675179
	Ncr1	25.026691	19.383909	17.521616	17.296352	16.966997	18.030001	17.747824	19.831587	21.554011	16.578103	16.433537	17.584849	21.954508	17.552228	16.274243	18.219351	14.083	16.2399	16.630	18.923	17.201403	846.871	689.4940	16.1336	15.751518
																		32	66	593	134		01	2	64	

Mx1	23.1	19.290	20.059	81.91	90.99	54.5	68.2451	81.252	342.066	149.14	5707.6	47.454	49.	134.345	42.992	149.5306	39.	32.5	93.	596	17.7035	51.2	30.3	418	674.8
	531	199	776	5848	6131	1498	38	972	64	823	753	644	270	34	324	9	905	733	737	.49	23	139	0302	9.48	8845
	88					8							216				917	39	247	712		8	8	24	
Cacn als	22.9	19.252	19.646	55.54	16.18	339.	53.9370	27.854	25.5589	18.757	20.362	20.116	33.	21.9690	19.429	108.6878	56.	40.5	21.	19.	17.6239	24.1	20.4	20.7	20.17
	274	311	673	5569	9194	5165	01	58	94	175	734	823	569	98	023	7	567	574	918	806	37	347	2031	320	2505
	04					2							859				49	57	256	06		34	28	28	
Cd27	16.3	19.237	15.336	13.88	16.32	14.6	424.032	1208.2	1665.93	16.474	17.213	16.049	559	796.311	1222.8		214	389.	202	12.	434.860	184.	110.	12.4	13.20
	393	96	196	2903	5437	1030	24	334	39	604	8	341	.98	61	091	1567.698	.37	460	.60	867	96	994	1271	382	6661
	04					7							845				581	56	926	675		08	2	6	
Mylk 3	76.7	19.198	369.26	22.80	25.57	20.1	14.9521	16.625	17.4911	19.121	21.752	18.367	18.	18.0899	16.423	16.90439	16.	16.2	16.	19.	16.8912	16.5	17.4	20.3	20.24
	155	694	449	1987	9715	8763	11	512	25	012	707	89	979	84	265	7	689	665	976	027	41	021	2928	884	171
	62					9							156				25	4	408	759		45	3	71	
Tbx2 1	14.3	19.112	16.583	59.64	67.40	21.6	1142.60	154.01	2456.19	15.114	15.859	15.230	149	585.369	70.365	326.4117	118	20.1	17.	13.	786.794	221	1006	15.6	16.30
	605	113	941	0984	7004	3351	78	054	45	893	617	808	.87	1	046	5	5.3	514	154	307	11	5.33	.737	235	1922
	39					4							65				673	35	515	258		84	7	25	
Ccr9	16.1	19.012	61.139	17.11	19.94	22.5	17.7667	487.52	28.7547	17.826	18.782	18.029	41.	26.2111	49.189	38.37955	17.	16.1	15.	19.	558.193	16.9	15.7	20.1	24.01
	305	992	25	4489	0453	5624	32	677	42	898	425	567	052	78	78	4	762	982	285	550	6	957	9176	206	4435
	76					7							335				263	36	761	317		16	9	64	
Ms4a 2	322	18.959	559.36	34.72	23.81	19.4	14.9786	14.470	14.1514	14.203	16.565	15.006	15.	15.5452	14.739	15.46338	14.	15.4	15.	16.	15.7070	15.4	15.1	17.4	17.47
	8.40	799	281	3445	3341	5924	29	562	87	88	017	195	384	25	781	2	884	463	396	965	92	535	8812	627	5085
	46												563				783	24	116	978		52	9	93	
Crtm	60.5	18.856	20.662	28.02	27.02	18.8	2172.20	684.06	970.391	24.247	26.805	22.287	54.	105.679	136.01	97.95488	819	37.7	24.	24.	994.888	612.	629.	20.3	17.42
	033	332	911	0061	2405	8251	76	65	1	457	946	432	550	94	991	2	.36	841	573	103	47	972	5304	823	0009
	76					3							789				364	37	654	459		38	21	21	
Ctla4	25.5	18.853	19.780	21.53	27.52	78.9	579.108	70.481	51.8173	20.253	27.811	22.580	162	1188.52	113.80	2825.083	107	431	387	21.	43.6135	30.2	25.2	21.2	20.58
	129	379	978	4995	0651	9645		044	2	744	174	546	2.9	08	531	7	5.6	3.87	.60	052	43	428	0646	690	6019
	59					8							511				778	62	686	503		09	81	81	

Mmp13	11.604006	18.851341	494.74524	13.217045	11.704522	12.845664	10.6821	10.77851	10.780177	226.21002	1370.8294	557.82819	10.678082	9.6884386	10.704086	11.092346	9.2755	14.7495	22.094	8.2624	10.268262	10.7344	10.37899	3681.27	715.29238
Trav12-3	24.923638	18.785845	21.466858	21.148636	15.90401	17.302598	34.369631	63.506226	46.540091	18.895764	20.723219	21.148374	43.287943	16.041999	142.90979	168.75176	32.574	179.450	142.35	21.115	20.099331	24.3651	27.39076	17.4692	18.045473
Fasl	19.519889	18.707264	14.977166	15.015672	16.029346	17.843248	782.82299	31.082736	358.8382	14.505012	16.718546	14.857929	71.921944	81.00705	87.363529	58.126195	330.57	30.6497	38.180	15.863	2561.1797	675.893	885.9848	16.2875	16.859231
Tph1	11616.598	18.656345	18.989193	17.679002	14.201016	19.663154	18.197892	20.348068	20.740535	15.464913	19.612095	18.157012	24.145388	21.595367	22.376974	17.498183	29.019	19.9446	23.594	24.102	26.795544	20.2883	22.32301	21.6572	20.642068
Bex6	13.263637	18.578761	24.423128	11.617948	10.194015	10.874608	10.770178	11.1692	11.61363	12.709448	11.359093	15.090354	10.385196	10.58015	10.80958	9.9891547	10.758	11.2670	9.9672	186.99	10.114758	12.6192	10.41216	14.0827	19.410631
Reg1	24.213233	18.572831	19.316711	20.687109	21.904142	19.94147	16.731777	21.503492	17.627232	20.66718	22.771884	20.015008	20.708299	24.349272	20.055533	19.142029	21.868	21.2585	21.761	22.918	708.12852	20.4260	17.05686	21.6194	23.751187
Spof2	17.992287	18.546259	19.108048	19.457548	16.07734	21.009755	32.234676	31.885588	43.120112	21.004558	16.545745	18.774724	22.553928	22.911842	38.57293	19.559927	23.374	61.5444	43.475	17.920	17.248946	21.0568	20.80433	17.7073	18.100025
Apoc3	23.573139	18.537051	27.094241	28.977813	27.445411	25.147634	24.872277	28.974852	32.72934	26.326418	22.158076	23.861212	23.415748	26.293934	25.182596	28.367738	28.262	26.3678	26.271	21.191	805.44568	23.6716	29.82125	20.5016	21.514031
Il5ra	21.421505	18.536181	265.88193	18.255755	43.073594	15.046541	17.79897	20.242145	18.015393	15.742312	14.908924	14.919959	15.775134	15.577902	17.626493	16.338804	16.300	14.3935	18.321	16.191	15.481026	17.5283	15.47419	17.4147	16.37537

Abcc2	20.951169	18.463755	337.95368	20.35982	21.905848	16.756681	22.94661	21.425478	20.015944	24.763559	21.973015	22.478467	18.709221	16.77164	18.679132	21.618761	17.878047	17.478514	19.464191	25.25526278	18.794551	18.45484	20.608143	20.38656	
Skap1	148.33456	18.46284	18.101854	18.434052	16.115752	17.418094	420.01298	2012.3592	2125.4542	17.934174	19.207041	18.94833	1276.5532	1281.5443	2496.4176	2158.5574	280.22	2897.51	3375.1	17.1103	1258.247	1147.60	1718.700	15.7802	15.254321
Lipn	13.470294	18.401014	20.392011	12.244872	11.232263	14.65739	15.590731	13.274917	15.393565	74.919376	112.70551	564.36906	12.752383	12.665843	13.380979	16.552458	13.787027	12.970206	13.519089	13.1344154	11.698666	14.18873	23.294702	23.849695	
Trbj2-2	20.76995	18.25742	23.200323	29.61194	23.048932	23.712932	365.76453	867.24774	649.45521	26.157548	28.336896	29.388525	658.52581	335.01686	1520.356	1396.5437	211.82	970.146	618.00	20.885	372.16276	27.2007	33.33291	25.9438	24.502467
A630023P12Rik	17.746229	18.224053	18.577608	147.46669	58.335424	21.000123	25.760008	271.76905	269.80862	18.969324	19.06246	15.620913	441.39527	1928.0704	935.95039	1081.2392	32.752417	1545.5578	282.62	18.821407	22.093683	21.4739	20.72357	16.1692	16.222366
Cdh17	18.736807	18.110431	308.10389	373.15155	69.378312	49.801085	14.145138	18.714979	17.614719	15.216502	16.876974	14.024065	20.704276	15.598353	18.369883	21.13162	29.985924	72.0766	83.309	21.567587	204.13857	27.55173	22.60663	36.51012	34.473534
Il12b	16.828346	18.073563	16.944851	19.890661	18.897413	19.259982	16.826894	20.617605	19.168244	17.830393	666.9992	18.075561	18.393616	15.868194	16.923386	17.724689	14.756369	17.4242	18.045	14.737	16.300472	17.0227	17.78397	6556.84	75.93121
Klre1	17.355822	18.043971	19.669749	16.434739	14.574847	14.001488	320.51089	48.605673	989.69728	19.126699	17.462116	16.696607	19.83968	22.599586	26.307004	19.525286	37.532785	18.929746	14.920	18.495437	23.769764	3241.20	1949.366	16.1125	18.015324
Pglyrp2	13.324474	17.975827	21.211185	108.35603	86.150493	15.55644	79.246558	354.164	519.74732	15.86796	17.635064	15.190705	262.49789	426.98452	534.03826	363.26294	28.906446	614.35419	1284.6	14.531417	398.65432	551.77963	368.64248	15.9264	15.261084



Foxp3	18.810917	17.9751	15.301126	21.373851	31.729626	23.366187	14.813428	20.154144	18.191783	20.828781	18.299741	18.784719	1241.4963	724.38587	51.78598	305.74963	16.63257	20.832071	21.683725	18.52787	18.432134	17.393832	17.30061	19.997459	19.359118
Il2ra	33.434612	17.947048	15.439696	18.52029	17.703393	18.87263	820.96889	16.973175	19.755645	17.4141	18.879031	15.909397	1371.3906	59.749035	35.777964	60.052336	3404.6388	779.4728	2921.6348	14.348857	17.166619	18.279067	28.257526	313.75027	45.307662
Txk	314.07258	17.585032	27.715731	19.224708	28.423617	17.260271	327.00631	655.94357	599.36577	18.481187	20.564052	18.85223	305.72237	156.71506	909.6349	157.47623	24.806107	297.28133	34.988298	17.434166	2114.3043	1362.4254	1758.6202	19.802020	20.217058
Ccl12	22.971778	17.443912	44.34287	14.877769	15.739117	13.854185	15.006728	14.293591	15.35987	28.673687	4231.9178	105.38936	14.865293	14.791558	15.945856	15.830611	16.019678	17.606389	13.614943	13.973751	14.76626	18.037761	17.403848	870.93952	28.502189
Tnfsf4	91.650783	17.366113	37.085909	25.763616	29.132424	19.442337	276.40424	27.045735	36.582113	19.246343	52.650517	17.841144	74.543163	29.442918	23.987773	33.135109	625.37365	124.24205	30.716103	23.049948	25.783339	24.353958	30.103402	735.45759	253.98749
S1pr5	15.218792	17.327289	15.80283	16.962133	15.668811	16.047721	19.741881	31.660561	303.20643	15.531826	16.03229	15.829432	17.857263	120.45334	47.027785	16.31168	18.363617	16.836232	16.779144	769.3289	15.973389	3529.3558	501.24688	14.563041	14.883787
Gpr34	536.30255	17.228795	438.91249	139.97265	15.111556	13.890171	38.610752	240.8318	36.272683	120.58511	9.8327717	33.864391	65.554543	17.1110377	135.40508	23.225012	18.517816	63.025809	216.96807	11.984422	1380.6981	18.247137	53.020622	13.261148	65.143052
Gm5547	201.8394	16.984335	40.96112	50.628824	22.941075	554.05693	50.376485	353.10441	440.78928	85.941042	27.732508	50.895497	67.124035	94.674254	203.66541	288.67483	22.360826	365.8481	287.34243	219.23378	156.72755	260.00136	94.12644	18.505419	37.579748
4930426D05Rik	15.522599	16.854196	14.99826	831.11054	491.60513	18.210887	14.327504	15.457699	19.522473	16.691435	15.760746	16.852853	14.831484	15.519697	15.856108	17.168584	16.811147	16.31132	14.43716	16.798771	17.308158	26.76584	15.907827	16.746481	16.706591

Clnk	346.	16.806	18.061	21.07	23.69	17.8	20.6150	15.879	36.3842	18.293	13.846	16.948	21.	17.6393	18.308	18.14192	19.	17.6	23.	18.	863.132	539.	1061	18.5	18.41
	397	43	828	2921	6565	4449	98	884	93	359	567	827	570	35	746	9	045	660	224	253	6	849	.169	782	4916
	96					3							943				958	34	258	788	1	9	78		
Nlrc3	93.9	16.683	16.883	373.5	232.7	15.4	116.253	790.52	714.234	40.742	19.967	28.190	188	1029.77	471.09	319.4649	58.	292.	277	16.	436.569	619.	488.	12.9	14.08
	132	79	075	7563	5407	0757	47	795	53	966	471	211	.49	82	264	4	065	571	.05	704	27	267	7764	857	8752
	97					5							572				68	65	691	317	65	8	29		
Trbv	19.4	16.630	17.069	21.32	19.55	15.9	273.578	899.65	636.814	15.098	17.294	14.874	214	58.3548	602.12	408.5301	66.	498.	293	19.	20.1593	17.0	16.9	17.0	17.54
	874	498	54	8614	1401	3558	53	74	52	234	439	95	.19	06	486	5	651	448	.66	123	97	405	6559	580	7158
	14	16				3							513				514	19	601	888	4	9	75		
Cyp3	16.8	16.553	14.413	20.94	25.01	24.8	11.9699	14.784	13.7557	16.858	14.688	17.323	18.	14.7823	16.034		15.	16.3	12.	18.	1037.26	12.5	14.0	43.4	32.75
	966	737	277	7781	6259	5568	72	693	22	957	736	849	091	6	488	15.72006	940	851	499	236	77	649	9731	343	707
	a11	41				4							947				031	86	55	829	86	86	79		
P2ry1	136	16.510	2670.2	17.08	15.47	50.9	22.3240	18.639	19.5852	417.34	1220.8	261.60	20.	17.0882	34.052	16.98562	95.	42.3	541	19.	14.7361	215.	1596	309	1024.
	8.92	095	026	3201	9007	0045	14	806	88	579	472	503	457	46	646	4	361	981	.59	203	9	440	.218	7.02	7664
	4	51											481				755	07	524	191	04	6	19		
Khdc	13.0	16.396	14.172	30.53	17.01	24.1	26.8011	15.813	15.6322	16.966	11.278	13.374	15.	17.7600	20.783	21.05712	14.	19.7	12.	20.	21.9727	136	511.	31.6	24.62
	719	528	594	3372	3404	1147	7	265	49	538	938	592	435	98	38	2	724	730	047	839	41	4.82	4023	354	6585
	1b	45											732				456	52	042	164		1	22		
Trat1	15.9	16.142	17.368	16.54	14.86	16.3	17.2970	98.587	44.5456	16.133	14.628	16.287	129	235.665	597.11	215.9893	18.	102.	167	13.	93.4078	19.8	16.3	14.7	15.38
	916	103	597	9144	0104	8497	33	794	09	56	653	586	.18	65	764	7	885	474	.91	647	59	741	6659	191	3574
	04					5							37				135	68	503	855	99	99	12		
Pth	16.4	16.082	14.617	14.85	13.83	16.9	14.1734	14.794	14.4886	17.376	15.806	14.881	15.	11.6997	12.852	13.99831	16.	15.0	166	14.	15.4413	13.0	13.8	15.4	14.53
	561	259	695	0374	1635	5470	59	13	49	128	397	847	613	66	609	4	063	347	2.6	841	36	106	7580	325	683
	77					3							372				308	71	284	493		54	1	98	
Kynu	16.6	16.071	24.531	370.4	250.8	17.3	18.9036	18.115	16.9535	24.833	384.92	37.552	31.	15.5414	17.333	16.84680	15.	16.2	13.	31.	15.1340	16.4	14.8	397.	305.4
	859	575	772	3799	1796	5037	54	163	07	768	924	162	550	96	675	2	340	692	737	314	5	617	4473	316	2387
	56					6							891				691	19	353	337		16	1	73	

Gpr171	878.08328	16.068909	124.26653	202.63534	248.00953	80.502017	1044.9538	713.72948	824.24819	12.553636	12.918159	12.242113	174.98634	181.49619	654.75394	471.21117	1379.7	1343.36	1652.8	13869	2390.7545	861.773	1585.018	153709	202.88033
Cd28	17.857683	16.010799	66.319346	14.307031	14.607893	746.56591	782.50101	901.94076	1782.7934	713.2474	15.542644	399.58133	894.92886	2617.9937	1550.5256	2959.5493	904.18	2569.61	1439.2	16199	15.855497	345.827	363.2038	25.3768	98.901781
Havc2	2038.3506	15.916346	124.52886	18.918338	16.176075	16.063883	112.60647	20.226949	19.894652	116.48367	51.624134	162.09883	35.449191	25.386166	18.401064	22.439273	259.25	24.6983	51.764	220.69	17.335229	16.0950	17.74135	18.6654	25.731919
Lax1	13.21019	15.908314	13.398211	28.028785	21.624718	34.826922	29.162081	129.78845	368.48092	13.566674	14.443776	14.374133	77.821684	73.290744	81.004285	239.05172	18.606	76.7976	28.281	11.431	74.179944	188.379	182.8154	12.3657	12.400951
Fabp1	15.952591	15.773511	15.649434	12.657176	14.307757	13.931732	16.575107	15.999839	16.944876	13.281296	15.395071	14.567757	15.133878	15.241111	14.839364	15.54748	16.149	16.9624	16.762	15.298	1025.1272	15.0102	15.82477	15.4419	15.873952
Dppa3	20.450295	15.710493	34.313227	13.784429	17.150441	13.555571	16.0962	16.546995	16.928412	94.379901	71.082965	56.285099	20.166056	15.639371	17.108586	20.161857	16.099	18.7549	19.785	17.887	13.800657	26.5269	19.94876	16.1839	22.637203
Il10	13.707357	15.705612	17.028249	15.204521	12.768029	20.193115	22.532341	17.549732	15.892919	29.950941	228.24878	34.556008	35.158621	15.771869	14.734681	132.61454	130.56	26.1825	2249.2	12.324	15.068392	13.4803	11.87472	194.460	14.672073
Klk1b11	16.272666	15.566137	85.393204	12.691831	13.001139	13.112456	16.012872	18.563995	17.372881	23.697519	19.164455	24.158704	17.472597	37.935485	21.952268	27.761162	17.469	19.2253	17.204	16.178	18.982026	18.6706	15.86278	2018.20	3311.111
Il5	18.238793	15.411515	16.529479	15.510331	15.729902	16.311958	15.045043	15.14252	14.92273	15.345637	14.125967	14.304013	14.569339	15.470035	16.34326	14.901902	14.150	17.2913	1148.9	15.2229	15.785368	16.0749	14.73952	15.2912	15.636624

Klra7	12.2	15.301	12.120	12.54	12.27	12.3	849.684	30.737	2321.19	12.109	11.988	11.960	15.	10.9736	11.726	13.14400	59.	11.3	11.	13.	12.1017	519	4402	13.4	12.42
	249					3562							022				827	961	302	074		.144	703	2468	
	9					6							46				211	63	099	049		199	347	93	
18100	18.9	15.052	16.680	21.50	23.63	18.0	23.8396	18.716	17.9695	19.538	17.360	18.151	31.	14.9324	17.762	25.51822	14.	47.8	18.	14.	14.2217	14.3	14.7	16.9	21.04
7300	505					4710							944				210	924	302	367		7695	644	7508	
8Rik	73					9							44				854	9	892	534		805	574	55	
Trbv	13.6	14.970	15.834	14.22	14.45	12.9	226.543	630.69	397.39	13.632	15.038	15.372	94.	46.8329	244.04	222.9268	39.	321.	91.	13.	39.4301	15.7	15.4	12.1	12.93
	168					8509							372				894	743	312	598		8140	964	2894	
	29					32							3				79	818	033	755		491	407	84	
Art2a	15.4	14.837	13.438	15.90	13.07	14.0	13.1944	13.154	14.4219	17.832	15.411	17.081	26.	18.1940	19.936	392.4096	13.	14.3	17.	14.	764.074	12.8	12.9	14.7	16.29
	120					6601							520				173	227	701	876		2789	227	0558	
	-ps					74							1				61	162	34	446		022	91	015	
Gm8	13.3	14.753	9.8307	828.1	1606.	15.7	410.199	631.87	536.036	17.139	69.616	13.494	178	357.975	353.27	709.2317	251	165.	39.	46.	11.5125	71.7	24.4	20.0	11.41
	157					4833							.74				727	699	586	071		0120	119	9395	
	369					71							5				61	408	22	405		999	174	376	
Klra5	15.4	14.629	14.438	19.85	29.96	23.8	64.9434	14.892	117.271	16.169	15.799	17.881	16.	13.2415	15.380	14.88504	268	14.9	23.	15.	5275.04	183.	187.	20.3	19.27
	684					0234							.56				205	114	908	355		4914	430	1185	
	27					1							51				076	21	128	189		707	721	52	
Il3	25.7	14.621	13.105	14.33	15.35	16.6	569.904	13.268	13.8859	12.174	11.519	12.735	23.	14.9137	14.625	13.29085	183	13.2	11.	13.	15.0635	13.8	16.0	14.5	13.70
	144					7869							5.8				295	796	063	256		6120	909	4669	
	46					4							77				173	43	666	578		55	43	53	
F9	14.7	14.407	15.696	37.92	45.23	163.	13.9865	14.616	15.9790	27.638	20.887	22.155	16.	14.8150	16.050	15.09373	18.	14.2	12.	18.	17.0602	17.6	15.2	37.5	34.34
	968					5273							010				462	894	166	996		6659	724	2751	
	19					6							71				003	05	951	866		071	535	37	
Ifng	14.3	14.258	14.775	16.80	24.31	18.0	15223.8	34.194	288.993	14.316	16.505	13.962	54.	386.090	48.146	701.1482	114	85.0	19.	12.	27.7804	274	1322	13.0	12.49
	350					3001							65.				932	672	979	1.34		.974	106	8287	
	18					4							04				022	85	084	93		844	657	19	

Tnfsf11	14.460759	14.246971	15.18181	17.243082	17.93346	14.79404	585.53704	17.250317	24.38072	15.226175	14.931055	15.310971	358.97418	191.9975	43.274776	983.96556	148.05	143.529	101.50	12.012	12.63115	15.7275	29.65	13.0232	13.485125
Ddx43	30.246236	14.239313	13.165208	16.775345	15.951258	16.788475	74.105122	63.154083	215.15374	19.402648	18.227488	16.483762	78.318065	110.5046	48.370533	156.79015	14.299	14.4435	18.842	15.625	460.03704	313.796	199.8346	15.6910	17.382296
Plac11	13.626651	13.91174	14.736425	18.118158	15.478859	111.5004	12.701435	13.076791	12.468234	13.191551	13.337248	14.114323	12.530929	12.494327	15.304446	12.755276	13.127	12.7395	14.109	14.735	16.022183	17.3823	14.03406	15.8958	15.403922
Klrc119	11.780419	13.896123	11.800904	11.208835	12.795422	12.425836	415.97076	16.220739	248.79042	12.733891	14.652451	12.200161	15.995223	12.130951	13.228776	14.976372	415.91	33.4304	14.381	13.323	21.243442	33.4335	28.23945	13.2256	13.480163
Mucl18	14.55748	13.854124	12.551343	10.081503	11.40983	11.505415	12.743199	13.752167	13.234433	12.216398	13.878078	13.944374	14.302402	16.08964	13.461137	13.516617	12.434	13.1742	13.456	14.211	11.966531	14.1478	13.16721	310.345	293.98524
Trbv5	13.199145	13.830367	12.278784	12.153416	14.94563	13.242727	217.99707	619.09977	387.61884	13.063112	12.566333	14.229355	729.33232	160.33669	2045.514	1792.5671	199.96	139.730	107.50	11.985	311.81601	13.7226	14.94152	12.8714	13.200118
Cd3g	13.203485	13.806092	13.107546	14.202284	13.84484	11.815965	1967.0873	7054.1791	7570.6178	12.269857	13.875262	11.849607	256.78971	2351.3656	8137.8997	8810.8355	225.48	819.189	731.12	18.229	14615.241	59.2812	43.76081	11.2854	11.754785
Mmp12	26.633851	13.586384	540.0487	15.175673	13.686839	14.105537	14.210802	14.466004	15.252087	2645.032	812.42854	2836.0348	14.528127	13.190981	14.917734	15.307857	13.423	136.634	98.074	12.681	13.164132	17.2432	16.68689	5286.50	6282.3889
Cd226	11.781276	13.523277	79.88461	12.009179	13.501266	12.679841	159.15102	737.9364	417.9014	12.161067	11.884094	11.643506	91.443393	283.95742	212.98271	113.06842	61.565	151.018	84.952	18.432	261.76558	424.056	253.2438	25.6487	18.576996



Ambn	14.153984	12.726078	13.378733	12.108703	16.620577	16.268968	13.619305	14.302234	13.262555	17.588121	16.456728	17.039647	14.648962	15.523599	13.633173	14.093836	13.983093	14.0136	113073	12.513884	13.795774	13.52907	13.520968	13.1466	13.140353
Il6	2266.7642	12.679228	1981.8223	21.298045	11.637017	14.497145	11.915943	9.6583924	9.6978146	11.551194	1316.8492	10.901481	12.025643	10.187517	9.8447758	18.645299	13.952935	12.6316	14.73796	9.9796	10.940808	11.2906	10.57295	9324.38	102.37709
Ahrr	418.48046	12.521974	85.013024	16.427633	15.829447	23.546315	17.630378	15.214603	16.732168	275.71695	192.52549	507.62599	18.437655	13.577496	15.5716	14.075369	27.483975	35.1564	36.502	20.509	178.91201	12.9125	145.4709	311.015	543.76051
Klra8	15.979265	12.517223	11.331079	12.036783	12.200559	10.129219	18.191349	11.901884	256.8079	11.14439	12.585953	11.684866	13.266431	20.90215	12.04778	11.409114	12.070398	11.6292	11.486	27.616	11.782043	10361.5	5190.190	11.3423	11.379761
2010106E10Rik	12.435715	12.406728	12.79981	13.755338	11.427274	12.834827	13.554425	14.832378	14.312405	11.431878	10.743458	11.116158	12.20744	11.502507	12.680813	13.076876	10.233	12.9763	14.367	11.145	255.66316	12.3300	12.27427	10.8990	11.052706
Htra4	13.138532	12.100633	12.283521	12.906985	13.018226	12.152942	14.031892	12.86348	12.333606	17.659726	24.065602	16.106077	12.885517	14.412018	12.925307	12.845642	13.669895	12.7448	12.878	11.350	12.071965	13.0808	14.32206	1004.35	15.555633
Serpinb7	10.974679	12.020513	11.001625	20.425771	52.590026	97.900338	10.309002	10.446318	10.444069	10.937132	10.201026	10.837949	12.592811	11.617777	11.539741	10.70375	11.882576	9.84379	10.257	12.993	13.442035	12.9974	13.94414	40.0161	13.867045
Sh2d1a	13.650779	11.94528	9.4823836	11.646592	12.220961	11.161438	1584.5327	688.12092	1727.4651	11.530924	11.809378	10.730792	476.72412	492.06863	929.43184	3977.4282	280.21	1388.04	235.80	9.2535	14.342076	649.751	567.6190	9.64432	9.7421534
Slc15a1	13.885538	11.880284	12.579584	18.909032	12.731832	13.451541	12.735696	12.009667	12.301581	14.428894	11.224432	13.323717	13.128892	12.38209	17.84381	13.168467	16.239923	33.2683	13.759	12.260	69.384739	12.5712	13.45968	12.7276	13.863094

A430	14.2					14.0							12.				13.	12.7	13.	11.			13.5	
108G	839	11.766	19.875	12.68	13.21	3551	13.1672	12.787	13.1355	64.721	16.222	35.211	012	10.5231	13.209	12.99807	660	705	508	649	13.1872	11.4	10.5	14.55
06Rik	52	876	919	5244	0112	4	98	522	61	742	795	444	612	25	933	8	493	51	242	985	97	95	7939	6651
Klrb1	10.8					11.1							14.				11.	10.6	11.	11.			22.2	
999		11.705	21.719	12.36	12.04	7577	11.5728	10.610	10.7431	11.409	11.981	11.712	652	12.1968	11.165	11.35296	036	300	405	247	11.4456	223.	262.	27.95
b	04	855	632	5695	9793	5	05	132	86	394	48	243	363	4	423	4	387	28	929	723	16	386	4984	3164
17000	11.6					11.2							10.				10.	9.77	398	10.			10.6	
61F12	035	11.426	10.468	12.46	10.49	6068	10.8642	10.732	9.96335	9.8476	10.826	10.518	909	12.2819	9.7962	10.63628	332	894	.47	708	11.0777	11.0	10.8	10.82
Rik	67	739	148	8588	8051	6	37	806	21	218	078	21	131	92	9	8	771	72	679	361	64	384	0457	1742
Sval1	12.8					11.8							11.				11.	12.9	382	11.			11.5	
250		11.300	11.355	11.92	13.00	4368	14.4865	12.639	11.7885	10.932	12.122	11.856	188	10.6719	10.682	12.18755	276	922	.61	436	11.8621	11.9	11.1	11.24
88		619	281	5902	8568	1	37	391	08	429	613	631	059	96	589	5	265	2	2	419	92	523	1050	3015
Otop	197.					12.1							11.				13.	11.2	12.	12.			12.8	
1	194	11.255	12.453	11.96	12.62	7211	11.7940	13.044	12.6078	11.233	12.093	11.586	728	12.1465	13.182	13.42878	682	341	460	531	13.0109	12.6	13.1	12.15
	21	106	235	2486	2279	7	78	115	34	996	215	509	244	47	008	3	286	72	531	841	7	831	6941	7212
Dmrt	11.3					10.5							10.				10.	11.1	10.	10.			10.4	
a1	582	11.084	11.754	11.50	11.54	7277	11.3290	37.083	531.970	11.518	12.434	10.940	084	13.2948	11.982	10.72343	925	541	010	298	10.8069	42.4	28.2	10.60
	59	011	522	4259	2186	6	17	012	49	596	595	531	73	37	493	4	398	33	988	456	27	386	1429	276
Gpr1	300.					36.9							150				171	248.	250	8.3			9.86	
74	971	10.760	22.825	292.3	351.1	9929	230.838	319.18	443.577	11.800	11.716	11.670	.65	267.629	279.67	360.6613	.78	796	.48	162	25.5253	527.	301.	10.24
	45	388	983	0036	906	6	71	227	89	645	147	346	314	85	339	9	59	48	251	995	43	793	5252	4661
Hsf2	13.8					13.1							32.				10.	12.2	11.	9.3			59.3	
959		10.504	12.959	12.54	15.30	2432	222.206	29.637	13.7553	62.355	58.970	39.429	964	11.0715	41.175	26.10008	835	021	120	563	16.6973	10.6	11.0	29.12
29		352	795	4794	8507	1	05	289	64	668	62	204	202	24	383	7	961	38	521	69	33	550	2665	6665
Rgs1	380.					10.5							9.8				10.	9.80	9.6	9.6			10.1	10.07
3	003	10.492	10.501	46.29	19.91	9627	9.98045	10.686	10.1490	9.9959	10.416	9.6896	315	9.98997	10.291		992	306	905	483	10.6864	10.2	9.37	
	57	961	534	1599	8337	4	27	044	96	945	528	426	23	09	444	10.39782	597	63	765	504	37	738	5801	8494



54304	11.0					10.4							10.				10.	10.2	10.	217		10.5	10.0	301.	
37J10	589	10.464	10.938	9.891	10.06	7005	9.61589	10.294	9.55452	20.417	25.511	13.680	427	10.0033	9.6192	9.790953	605	291	208	.40	12.6231	113	9120	257	227.5
Rik	07	007	549	5072	085	8	5	2	48	975	6	123	066	51	887	7	991	93	26	173	75	55	1	31	305
Klra1	649	10.275	9.8138	9.615	12.69	9.58	186.952	10.363	342.438	8.3932	9.8639	9.4440	10.	11.8675	8.9644	9.779765	11.	9.49	8.8	8.6	18.8200	136	1263	8.60	9.181
	25	622	559	1868	2564	9	29	292	96	316	691	59	803	3	718	7	859	16	039	917	01	5.02	.008	336	8655
Gzmc	911	10.251	23.449	9.981	11.26	11.5	743.759	11.937	11.6733	11.190	12.066	12.300	25.	15.9839	17.544	17.94767	188	23.1	573	10.	120.023	32.6	372.	11.5	11.86
	36	442	072	9114	576	5	02	407	29	253	367	667	904	14	404	2	601	54	995	732	21	517	9352	168	1351
Tcrg-V4	645	9.9155	9.7064	10.76	10.33	8.84	11.5338	9.3797	25.1722	8.8949	9.3474	9.2233	9.9	10.0617	9.6391		57.	19.0	17.	9.1	979.732	10.6	10.3	9.09	9.292
	27	2	307	9465	0714	1	37	258	95	735	011	124	758	61	35	9.123711	251	427	216	138	75	211	7672	540	8475
Cxcl3	725	9.8755	646.15	10.33	12.63	10.3	9.14871	10.292	9.54698	17.495	21.686	14.725	11.	11.7787	10.368	28.23345	9.9	85.7	55.	7.8	9.14931	10.4	10.2	637	2425.
	14	354	215	5024	3946	2	31	26	26	882	457	196	729	59	005	4	525	65	813	446	26	926	0279	5.52	2004
Gzme	132.	9.8184	9.5047	9.764	10.09	9.74	30.5229	9.3940	9.44459	9.1655	10.783	9.1693	10.	9.44804	10.334	9.673672	186	10.5	324	9.5	10.4508	10.4	10.5	10.3	9.626
	069	553	389	8081	9859	8	27	871	17	016	484	48	147	67	047	2	.57	498	.36	565	47	177	5417	062	9822
BC06	9.53	9.6561	10.297	10.11	12.86	56.7	9.56247	9.1207	10.1269	8.5920	10.116	8.9390	9.2	10.1633	8.8756	9.322886	9.4	9.32	9.3	9.4	8.92433	9.70	9.94	9.08	8.930
1194	765	071	162	2955	5095	3	7	132	58	318	261	174	517	1	152	7	863	601	487	076	08	524	0942	558	5873
	61												736				517	61	546	21		94	4	42	
A530	9.24	9.2902	9.4375	10.21	10.24	9.54	9.19983	21.411	10.7507	9.1951	9.0852	9.0460	9.9	10.0666	120.44	10.59571	8.9	10.3	9.1	8.9	8.62717	9.20	9.05	8.99	9.097
021J0	488	614	499	7261	0589	3	6	758	74	202	984	628	955	36	68	2	234	053	584	588	08	842	6798	681	7204
7Rik	61												073				394	76	549	737		67	1	19	
Gzmd	343.	8.8947	8.8871	9.924	10.07	9.32	36.8747	8.6973	8.52131	8.8267	8.7695	9.3138	9.2	9.21482	9.1549	9.196483	399	9.39	793	8.8	9.99586	9.05	8.90	10.3	10.15
	157	285	349	5596	6735	2	12	051	41	459	076	792	516	21	848	6	.29	072	.32	453	29	464	5615	367	0382
	14												924				761	45	589	306		95	2	22	

Supplementary Table 2 Detailed enrichment items of DEGs

Rank	Gene	Parent GO	Description	Enrichment Z-score	Total Genes	Gene In %	Gene Ontology	GeneID	Hits	Log (q-value)	Enrichment	Firmness	First	Best	URL
1	WPKM159625129	M101	Microglia phagocytosis pathway	9.8	204	10.5	GO:0005975	12259   12260   14129   16409   17972   18706   22177   22324   83433   170758	C1qa   C1qb   Fcgr1   Itgam   Ncf4   Pik3ca   Tyrobp   Vav1   Trem2   Rac3	2.8	0.1	1	1	1	7.28
2				7.3	10	5				0.8					
3				7.3	10	5				0.8					
4				7.3	10	5				0.8					
5				7.3	10	5				0.8					
6				7.3	10	5				0.8					
7				7.3	10	5				0.8					
8				7.3	10	5				0.8					
9				7.3	10	5				0.8					

1	-	4	9	3	8	0	1	7	0	1	1	0	1	0	9	phagocytosis	19_GO:0051179	localization	-	4	3	5	2	0.	1	-	-	-	-	-	-	-	7.	28.	11	62	95	08	95	79	12	12	9							
	-	4	7	1	4	0	1	5	1	1	0	1	0	9	microglial cell activation	19_GO:0002376	immune system process	-	4	8	6	1	0.	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7.	28.	11	62	95	08	95	79	12	12	9
1	-	4	5	7	4	1	1	0	1	1	0	1	0	9	synapse pruning	19_GO:0009987			-	4	1	8	20	5	0	0.	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7.	62	11	08		

	2	0		ol		cellular		5	0	9								3			95	79		
	2	9		og		process		2	8	0								3			95	12		
	5	8		ica				2	0	4								2			12			
	3	8		l				5	5	5								7			9			
	8	8		Pr				3	8	9								6						
	8	3		oc				8	6	8								7						
	5			es				8	0	4								9						
	8			se				5	8	3								0						
				s				8										1						
				G				-	1	8								-						
	4		G	O				4	9	.								1						
	5		O	Bi				.	.	3								.						
	2	:0		ol		regulation of	19_GO:005	5	0	9								3				-		
	2	1		og		hippocampal	0789	2	8	0	20	5						3			7.	28.		
	5	1	M	ica	1	neuron	regulation	2	0	4	83	8	4	4				2			11	62		
1	3	0	1	l	9	apoptotic	of	5	5	5	6				16409 16819 22177 83433			7	0	1	0	0	95	08
	8	0		Pr		process	biological	3	8	9								6			95	79		
	8	8		oc			process	8	8	9								7			12	12		
	8	8		es				8	6	8								7			9			
	5	9		se				8	0	4								9						
	8			s				5	8	3								0						
				G				8										1						
	-	G		O		leukocyte	19_GO:000	-	7	6								-				-		
	4	O		O		activation	2376	4	.	.	20	5						1				-		
	3	:0	M	Bi	1	involved in	immune	.	2	2	83	3	4	7				1			7.	62		
1	7	0	1	ol	9	inflammatory	system	3	1	1	6	7	6		11629 12259 12759 16189 16409 22177 83433			2	0	1	0	0	11	08
	1	0		og		response	process	7	9	1								7			95	79		
	9	2		ica				1	6	5								9			95	12		







	7	0		ol		localizatio	3	2	8		9	6				9		95	79
	0	4		og		n	7	5	6		8	1				4		95	12
	4	3		ica			0	4	3		9	5				0		12	
	4	2		l			4	4	6		0	2				3		9	
	7	7		Pr			4	8	9		1	7				4			
	9	7		oc			7	2	0		0	1				4			
	9			es			9	3	2		9	6				8			
	7			se			9	6	2		9					8			
				s			7									5			
	-			G			-		5		0					-			
	2	G		O			2	8								0			
	9	O		Bi			.	.	.		.	0.				.			
	7	:1		ol		19_GO:003	9	4	2							7			-
	2	9		og		2501	7	8	0		3	6				4		7.	28.
	5	0	M	ica	1	regulation of	2	0	8	20	1	5				2		11	62
1	8	0	1	l	9	amyloid-beta	5	2	1	83	1	4	4	12759   16189   83433   214384		6	9	95	08
	6	2		Pr		clearance	8	6	7	6		6				0	5	95	79
	3	2		oc		organisma	8	6	4		0	6				6		12	12
	8	1		es		l process	6	0	4		7	1				0			9
	7			se			3	4	4		3	4				6			
				s			8	8	1		3					8			
	-	G		G			-	9	4		0	0.				-			
	2	O		O		negative	2	.	.		.	3				0		-	28.
	4	:1	M	Bi	1	regulation of	8519	.	5	8	20	1	5			.		7.	62
1	8	9	1	ol	9	amyloid fibril	4	4	5	83	2	4	3	12759   12955   83433		5	4	11	08
	1	0		og		formation	8	0	4	6		6				0		95	79
	5	5		ica		of	1	2	3		4	5				7		95	12



2	9			l		biological	5	9	7			5	2					6		12				
7	0			Pr		process	2	3	5			0	7					8		9				
1	7			oc			7	0	5			5	2					7						
6				es			1	4	1			4	4					9						
				se			6		4			9						3						
				s														7						
				G			-	2	3			1						-						
				O			2						0.					0						
2.	G			Bi			.	.	.			.	5					.						
2	O			ol			2	7	1			6	4					3		-				
2	:0			og		19_GO:003	2	2	8			4	4					9		7. 28.				
2	0			ica	1	glial	2	5	7	20	1	5	8					9		11 62				
1	5	2	M	l	1	development	2	7	4	83	2	4	9	3	9	11652   12259   12759   14580   16409	Akt2   C1qa   Clu   Gfap   Itgam   P	1						
	7	1	1	Pr	1		5	9	0	6	6	6	5	0		18991   19058   83433   232232	ou3f1   Ppp3r1   Trem2   Hdac11	3	0	1	0	0	95	08
	9	7		oc		process	7	8	4				1	3				7		95	79			
	2	8		es			9	0	9				6	9				7		12	12			
	7	2		se			2	1	1				4	9				6		9				
	1			s			7	2	2				8	4				3						
				G			1											2						
				O			-	7	4				0					-						
2.	O			Bi			2	.				.	0.					0		-				
1	:1			ol		19_GO:000	.		0				5	3				.		7. 28.				
0	9			og	1	regulation of	1	1	4	20		5	4	1				3		11 62				
1	9	0	M	ica	1	amyloid fibril	0	5	0	83	1	4	3	9	6	12759   12955   83433	Clu   Cryab   Trem2	4	0	1	0	0	95	08
	5	5	1	l	1	formation	9	5	3	6	6	6	4	3				7		95	79			
	7	9		Pr			5	2					5	5				1		12	12			
	6	0		oc			7	1	5				0	2				2		9				
	9	6					6	9					5	7				9						

2			es				9	7	6			4	2			7						
2			se				2	8	5			9	4			5						
			s				2									2						
			G				-					0				-						
-			O				2		3			0	0.			0						
2.	G		Bi				.		.			.	4			.						
0	O		ol				0		3			9	0			3			-			
8	:0		og			19_GO:005	8	7	8			1	7			3			7.	28.		
5	0		ica	1	phagocytosis,	1179	5	5	5	20		5	5			7			11	62		
1	4	0	l	9	engulfment	localizatio	4	5	0	83	4	5	7	6	11629   14129   16409   83433   17075	3	7		95	08		
1	6	1	Pr			n	1	1	9	6	8	6	5	8	Aif1   Fcgr1   Itgam   Trem2   Rac3	0	1	0	0	95	79	
2	9		oc				2	2	6				0	7		4			12	12		
8	1		es				8	2	9				9	8		7			9			
2	1		se				2	1	3				1	1		2						
3			s				3						6			6						
			G				-						2			5						
-			O				5	4	6				0.			-						
5.	G		Bi				.		.				.	6		1						
6	O		ol				6	3	2				7	9		.			-			
5	:0		og			19_GO:005	5	0	7				4	9	12491   12512   12759   13645   14129	6			5.	7.6		
6	0		ica	1	positive	1179	6	3	0	20	1	5	7	5	Cd36   Cd63   Clu   Egf   Fcgr1   Ga	8			65	32		
1	7	4	l	9	regulation of	localizatio	7	8	2	83	3	4	15	2	14461   16189   19055   20379   2062	8			67	23		
5	5		Pr		endocytosis	n	5	9	8	6	3	6		2	0   22416   23892   30878   83433   192	8	0	2	1	1	57	44
7	8		oc				7	1	1					2	167	3			37	32		
3	0		es				7	5	2					7		5						
7	7		se				3	9	1					4		1						
4			s				7	7	7					7		6						
							4							7		7						



	3	0	ol	receptor	localizatio	5	3	4										3				67	44	
	7	0	og	internalization	n	3	2	1										3				57	32	
	2	2	ica			7	2	7										2				37		
	4	0	l			2	3	4										7				4		
	0	9	Pr			4	4	9										6						
	4	2	oc			0	4	5										7						
	6		es			4	3	2										9						
	7		se			6	2	9										0						
			s			7												1						
			G															-						
	-		O			-	5	5										1						
	4.	G	Bi			4	.	.										.						
	3	O	ol			.	3	7										6					-	
	8	:0	og	positive		3	6	3										4				2		
	0	0	ica	regulation	of 19_GO:005	8	6	8	20	5								8				4		
1	0	4	M 1 0	receptor-	1179	0	4	8	83	6	4	9		12512   12759   13645   16189   20379	Cd63   Clu   Egf   Il4   Sfrp4   Plk2		9	0	2	0	0	65	32	
	2	8	1 1 0	mediated	localizatio	2	1	8	6	4	6			20620   22416   23892   30878	Wnt3a   Grem1   Apln		0					57	44	
	1	2	Pr	endocytosis	n	1	4	9										8				37	32	
	2	6	oc			2	8	6										8						
	9	0	es			9	3	5										7				4		
	4		se			4	5	2										6						
			s															3						
	-	G	G			-	3	4										2						
	3.	O	O	regulation	of 19_GO:005	3	.	.										.	6				-	7.6
	7	:0	M 1 0	receptor-	1179	.	4	7	20	1	5			11812   12512   12759   13645   16189	Apoc1   Cd63   Clu   Egf   Il4   Ppp		1				5.	32		
1	5	0	1 1 0	mediated	localizatio	7	9	0	83	3	4	12		19058   20379   20620   22416   2389	3r1   Sfrp4   Plk2   Wnt3a   Grem1		.	0	2	0	0	65	23	
	8	4	og	endocytosis	n	5	5	0	6	1	6			2   30878   192199	Apln   Rspo1		0					67	44	
	7	8	ica			8	6	4										8				57	32	
																		0						







2	0	ol		ar	8	3	9		2	3	06   19225   20657   21333   21391   21	mp2   Pik3ca   Ptgs2   Sod3   Tac1	4						31	33	
8	0	og		organisma	2	9	4		8	9	924   30878   67451   75697   109648	Tbxas1   Tnnc1   Apln   Pkp2   C2c	0						65	02	
7	8	ica		l process	8	5	7		2	6	110809   240672   244911   319552	d4b   Npy   Srsf1   Dusp5   C2cd4a	4						71		
1	0	l			7	2	6		0	2		Spx	8						6		
4	1	Pr			1	6	5		5	9			5								
0	5	oc			4	9	7		1	1			9								
1		es			0	8	2		2	2			8								
7		se			1	7	6		8				5								
		s			7								4								
		G											-								
-		O			-	2	4		3				1								
4.	G	Bi			4	.	.		.	0.			.								
1	O	ol			.	8	7		2	7			2							-	
9	:0	og		19_GO:003	1	7	8		9	6			2								
3	0	ica	1	vascular process	2501	9	4	0	20	2	5	11541   11550   12491   13166   13616	Adora2b   Adra1d   Cd36   Dbh   E	2					5.	3.5	
8	0	l	1	in circulatory	multicellul	3	0	0	83	3	4	15559   16533   16598   17300   1739	dn3   Htr2b   Kcnmb1   Klf2   Foxc	2					08	09	
8	3	Pr	1	system	ar	8	6	5	6	9	6	0   19225   20537   20657   21391   308	1   Mmp2   Ptgs2   Slc5a1   Sod3   T	5	0	4	0	0	31	07	
1	0	oc			organisma	8	6	5	6	9	6	78   75697   240672   244911	bxas1   Apln   C2cd4b   Dusp5   C	9					65	33	
4	1	es			l process	8	3	8		3	4		2cd4a	5						71	02
6		se				1	1	8		2	7			9						6	
		s				4	7	4		9	2			2							
-	G	G				6	5	7		7				5							
3.	O	O			-	2	4		5	0.				0.							
8	:0	Bi	1	regulation of	19_GO:006	3	.	.		.	9	11541   11550   11858   13166   13616	Adora2b   Adra1d   Rnd2   Dbh   E	-						-	3.5
8	0	ol	1	anatomical	5007	.	0	2	20	5	5	13860   14260   15163   15559   1653	dn3   Eps8   Fmn1   Hcls1   Htr2b	1					5.	09	
9	9	og		structure size	biological	8	6	2	83	7	4	3   16598   17300   17390   18706   187	Kcnmb1   Klf2   Foxc1   Mmp2   Pi	.	0	4	0	0	08	07	
2	0	ica			regulation	8	0	8	6	4	6	54   18846   19225   20348   20359   20	k3ca   Prkce   Plxna3   Ptgs2   Sem	1					31	33	
						8	0	8		7	3	496   20657   21391   22362   22416   2	a3c   Sema6b   Slc12a2   Sod3   Tbx	4					65	02	
						9	9	3		6	6		as1   Vpreb1a   Wnt3a   Sema4g	2							



0	0	l					2	6	3					5	5	6456   30878   66333   107351   23079	Apln   Aqp11   Kank1   Wdpc1   D	4		71					
0	6	Pr					0	9	7					5	4	6   240672   382253	usp5   Cdkl5	7		6					
2	6	oc					0	2	3					6	8			4							
8		es					2	2	4					7	7			9							
7		se					8	8	6					8				5							
		s					7											1							
		G					-											-							
-		O					3	2	4					2				0							
3.	G	Bi					.	.	.					.				6							
5	O	ol					5	9	3					5				9		-					
5	:0	og					5	8	7					6				6		5. 3.5					
8	0	ica	1	regulation	of	5007	8	4	4	20	1	5		4		11541   11550   13166   13616   15559	Adora2b   Adra1d   Dbh   Edn3	6		08 09					
1	2	3	M	1	0		1	9	6	5	83	7	4	14	1	4	16533   16598   17300   17390   1922	Htr2b   Kcnmb1   Klf2   Foxc1   M	9	0	4	0	0	31	07
6	5	Pr					2	7	5	6	9	6		0		5   20657   21391   30878   240672	mp2   Ptgs2   Sod3   Tbxas1   Apln	9		65 33					
4	2	oc					6	2	4					2			Dusp5	7		71 02					
0	9	es					4	6	5					5				9		6					
9	6	se					0	8	1					6				5							
1		s					9	3	6					4				9							
		G					1											3							
-		O					-	2	4					2				-							
3.	O	Bi					3	.	.					.				0		-					
5	:0	ol					.	9	3					5				6							
5	0	og	1	blood	vessel	2501	5	8	7	20	1	5		6		11541   11550   13166   13616   15559	Adora2b   Adra1d   Dbh   Edn3	9		5. 3.5					
1	8	9	M	1	0		5	4	4	83	7	4	14	4		4	16533   16598   17300   17390   1922	Htr2b   Kcnmb1   Klf2   Foxc1   M	6	0	4	0	0	31	07
2	7	ica	9	diameter		ar	8	6	5	6	9	6		1		5   20657   21391   30878   240672	mp2   Ptgs2   Sod3   Tbxas1   Apln	9		65 33					
6	7	l					2	7	5					0			Dusp5	9		71 02					
4	4	Pr					6	2	4					2				7		6					
0	6	oc					l	process						4				9							











	-	G			-	4	3			0	0.		-											
	2.	G	O		2	.	.			.	4		0											
	3	O	Bi		.	6	8			9	0		4						-					
	7	:0	ol	phenol-	3	5	4			1	0		4						4.	15.				
	9	0	og	containing	19_GO:000	7	3	1	20	4	5		5						37	26				
1	4	4	ica	1	8152	9	8	5	83	4	5		6	13166   13195   53626   59012   21634	Dbh   Ddc   Insm1   Moxd1   Tph2	7								
	6	6	l	9	metabolic	4	0	7	6	1	6		5	3				0	5	0	0	98	44	
	6	1	Pr	biosynthetic	process	6	1	6					5					3				02	68	
	6	8	oc	process		6	4	3					9					8				81	86	
	1	9	es			6	4	3					9					8				4		
	5		se			1	8	0					1					8						
			s			5	3	5					6					9						
	-	G			-	4	3			0	0.		-											
	2.	G	O		2	.	.			.	4		0											
	1	O	Bi		.	0	4			9	0		3										-	
	2	:0	ol		1	5	4			1	0		3										4.	15.
	3	0	og	catecholamine	19_GO:000	2	9	4	20	4	5		5										37	26
1	9	0	ica	1	8152	3	6	7	83	4	5		6	13166   13195   53626   59012   23794	Dbh   Ddc   Insm1   Moxd1   Aoc2	4							98	44
	4	6	l	9	metabolic	9	9	9	6	7	6		5	0				6	0	5	0	0	02	68
	6	5	Pr	process	process	4	9	1					0					8					81	86
	9	8	oc			6	1	2					9					1					4	
	4	4	es			9	6	3					1					8						
	7		se			4	6	7					1					2						
			s			7							6					8						
	-	G	G	catechol-	19_GO:000	-	4	3	20	4	5		0	0.									-	15.
1	2.	O	O	containing	8152	2	.	.	83	7	4	5	.	4	13166   13195   53626   59012   23794	Dbh   Ddc   Insm1   Moxd1   Aoc2	0	0	5	0	0	4.	26	
	1	:0	Bi	compound		.	0	4	6	7	6		9	0				.					37	44













																						6 0	l						1 1 1						0 7				8	82
																						4 0	Pr						6 4 8					4 6				3	3	
																						3 3	oc						4 9 0				3 3				9			
																						8	es						3 8 2				9 4				2			
																						3	se						8 1 3				6				7			
																						-	s						3								2			
																						2. G	G						-				4	0.					-	
																						8 O	Bi						2	.	.		.	9				0		
																						7 :0	ol						8	8 4			9	2	12373   13616   15559   16819   17748	Casq2   Edn3   Htr2b   Lcn2   Mt1			.	-
																						4 0	og				19_GO:004	7	8 3			4	7	17750   18754   20203   20393   2049	Mt2   Prkce   S100b   Sgk1   Slc12a			6	4. 2.1	
																						1 4 5	ica	1	monoatomic ion	2592	4	3 5 20 5 5			5	8	6   20535   20855   21391   22042   274	2   Slc4a2   Stc1   Tbxas1   Tfrce   Ab			9	29 39		
1																					4 5	l	9	homeostasis	homeostati	4	6 5 83 4 4 27			0	8	21   59091   66333   68428   71753   73	cc6   Jph2   Aqp11   Steap3   Tmpr	3	0 7 0 0	68 07				
																					2 0	Pr				c process	2	4 1 6 7 6			5	7	649   76376   105243   109648   21080	ss6   Cybrd1   Slc24a2   Slc9a3   Np	1		99 91			
																					2 8	oc						2	1 0			4	4	8   214189   269356   270160	y   Lacc1   Scgn   Slc4a11   Rab39	9		82 57		
																					3 0	es						2	0 4			9				1	3			
																					7 1	se						3	3 1			4	8			8				
																					2	s						7	9 9			5	9			4				
																					- G	G						-	1 3			4	0.				-			
																					2. O	O						2	.	.		.	9	12373   13616   15559   16819   17748	Casq2   Edn3   Htr2b   Lcn2   Mt1			0	-	
																					7 :0	Bi					19_GO:004	.	8 2			7	1	17750   18754   20203   20393   2049	Mt2   Prkce   S100b   Sgk1   Slc12a			.	4. 2.1	
																					0 0	ol	1	monoatomic	2592	7	5 9 20 5 5			6	1	6   20535   20855   22042   27421   590	2   Slc4a2   Stc1   Tfrce   Abcc6   Jph	6		6	29 39			
																					1 6 5	og	9	cation	homeostati	0	8 5 83 3 4 26			1	3	91   66333   68428   71753   73649   76	2   Aqp11   Steap3   Tmprss6   Cyb	0	0 7 0 0	68 07				
																					4 5	ica				c process	6	0 0 6 4 6			9	7	376   105243   109648   210808   2141	rd1   Slc24a2   Slc9a3   Npy   Lacc1	5		99 91			
																					5 0	l						4	3 2			0	9	89   269356   270160	Scgn   Slc4a11   Rab39	3		82 57		
																					7 8	Pr						5	4 0			4	7			3	3			
																					8 0	oc						7	6 0			7				2				























9	0	ol	system	0	8	8			9	4	9   16768   17175   19885   54123   605	T23   Il4   Lag3   Masp2   Rorc   Irf7	3					83	40				
3	0	og	process	9	1	8			6	1	04   208154   240754   667277	Il21r   Btla   Lax1   C1rb	3					12	35				
1	2	ica		3	9	4			7	2			7					5					
0	2	l		1	2	2			0	4			3										
2	5	Pr		0	0	2			3	7			4										
2	0	oc		2	8	3			2	2			7										
5		es		2	1	0			9				2										
3		se		5	9	5			7				6										
		s		3									5										
		G											-										
-		O		-	4	3			0				0										
2.	G	Bi		2	.	.			.	0.			.										
0	O	ol		.	9	5			7	3			3										
7	:0	og	complement	19_GO:000	0	2	8		3	6			3					-	8.1				
7	0	ica	1	2376	7	4	6	20	3	5			2	4				4.	77				
1	0	M	1	1	1	0	1	9	3	4	4	6	9	12259   12260   17175   667277	C1qa   C1qb   Masp2   C1rb	7	0	1	0	0	0	07	39
1	6	1	1	0	1	0	1	9	1	6			0	5				83	40				
0	9	Pr	pathway	system	1	2	7	6	6				0	5				12	40				
2	5	oc		process	0	2	9						0	6				5	35				
7	5	es			2	2	7						7	1									
2	8	se			7	1	6						3	4									
		s			2	4	9						3										
-		Wi			-	6	3						0	0.				-					
2.	W	ki			2	.	.						.	3				4.	8.1				
0	P	Pa	2	Complement	activation,	.	7	8	20	1	5		5	1				4.	77				
1	2	M	1	1	0	1	7	7	83	1	4	3	5	1	12259   12260   625018	C1qa   C1qb   C4a	.	0	1	0	0	07	39
3	0	1	1	0	7	7	7	6	6	7	6		4	6				83	40				
3	0	th			3	4	9						9	3				12	40				
6	0	w			3	3	9						4	5				5	35				





8		es			5	3	8		8								1	
1		se			8	6	1		2								4	
		s			1												3	
					-		4		0								-	
2.					2	5			0.								0	
8		Wi			.	.	6		9								.	-
6	W	ki			8	9	0		1								6	4.
6	P	Pa			6	6			7								9	00
1	2	M	2	White fat cell differentiation	6	2	8	20	5								3	00
3	8	1	1	0	th	7	6	83	3	4	5		12608   14461   16598   19401   94187	Cebpb   Gata2   Klf2   Rara   Zfp42			3	0
5	7				w		6	6	2	6							1	1
6	2	ay			5	8			6								1	2
2	2	s			6	3			7								1	0
5					2	1			9								1	0
2					5	5			1								8	0
					2		6		6								4	0
		G			-		4		3								-	
3.	G	O			3				. 0.								1	
9	O	Bi			.	.			2								.	-
6	:0	ol			9	7	5		7								1	
6	0	og			6	5	7		9				11541   12317   12512   13036   13645	Adora2b   Calr   Cd63   Ctsh   Egf			4	3.
1	2	M	1	0	ica	1	regulation of	19_GO:004	6	8	9	20	2	5			4	96
2	1	1	1	0	l	9	epithelial cell	0011	6	6	6	83	4	4	18		4	62
2	0				Pr		migration	locomotio	2	3	4	6	9	6			4	14
1	6				oc			n	2	3	4	6	9	6			2	21
9	3				es				1	8	5						7	91
1	2				se				9	6							7	94
4					s				1	5	8						4	4
									4	1	9						3	

1	3.6140	6319	1101	0	G	Biological processes	positive regulation of cell migration	19_GO:0040011	1	1	9	8	1	20	5	5	31	5	0.	11541   11629   11652   12317   13036   13345   13616   13645   13653   14461   14828   15200   16189   16819   17390   18754   19055   19225   20348   20620   20620   21333   22411   26456   359   3626   69683   74048   83433   225631   227541   320924	Adora2b   Aif1   Akt2   Calr   Ctsh   Twist2   Edn3   Egf   Egr1   Gata2   Hspa5   Hbegf   Il4   Lcn2   Mmp2   Prkce   Ppp3ca   Ptgs2   Sema3c   Sema6b   Plk2   Tac1   Wnt11   Sema4g   Insm1   Emc10   Vsir   Trem2   Onecut2   Camk1d   Ccbe1	-	0	0	0	0	0	0	3.	3.0
1	3.6140	6319	1101	0	G	Biological processes	positive regulation of epithelial cell migration	19_GO:0040011	1	1	9	5	2	20	1	5	13	9	0.	11541   12317   13036   13645   14461   15200   16819   18754   19225   20620   21333   69683   320924	Adora2b   Calr   Ctsh   Egf   Gata2   Hbegf   Lcn2   Prkce   Ptgs2   Plk2   Tac1   Emc10   Ccbe1	-	0	0	0	0	0	0	3.	3.0
1	3.6140	6319	1101	0	G	Biological processes	positive regulation of cell motility	19_GO:0040011	1	1	9	3	7	6	2	6	6	9	0.	11541   11629   11652   12317   13036   13345   13616   13645   13653   14461   14828   15200   16189   16819   17390   18754   19055   19225   20348   20620   21333   22411   26456   359   3626   69683   74048   83433   225631   227541   320924	Adora2b   Aif1   Akt2   Calr   Ctsh   Twist2   Edn3   Egf   Egr1   Gata2   Hspa5   Hbegf   Il4   Lcn2   Mmp2   Prkce   Ppp3ca   Ptgs2   Sema3c   Sema6b   Plk2   Tac1   Wnt11   Sema4g   Insm1   Emc10   Vsir   Trem2   Onecut2   Camk1d   Ccbe1	-	0	0	0	0	0	0	3.	3.0







1	3	9	1	5	0	M	1	1	0	1	9	1	0	0	0	0	0	0	0	0	G	O	Bi	ol	og	ica	1	1	9	positive regulation of DNA-binding transcription factor activity	19_GO:0008152	metabolic process	1	5	2	6	83	7	4	19	3	8	5	9	7	4	4	12491   12759   15163   16189   18013   18761   19055   20128   20684   2204	Cd36   Clu   Hcls1   Il4   Neurod2   Prkcq   Ppp3ca   Trim30a   Sp100   Tfr1   Wnt3a   Grem1   Thap11   Fank1   Card14   Myocd   Rab7b   Camk1d   Stk36	1	4	2	0	1	5	1	1	1	3.	2.6	91	46	52	21	47	26	91	68	9
1	2	4	7	9	1	9	2	3	0	1	5	0	0	0	0	0	0	0	0	0	G	O	Bi	ol	og	ica	1	1	9	VEGF signaling pathway	-	2	4	5	20	5	4	8	5	8	4	1	0	5	1	0	5	4	11652   18706   18752   19055   19058   19225   170758   329502	Akt2   Pik3ca   Prkcg   Ppp3ca   Ppp3r1   Ptgs2   Rac3   Pla2g4e	1	0	1	0	6	1	1	3.	51	89	59								

9	0		G					8	6	3				6	4			1						32	60
3	4		Pa					9	3	3				5	2			4						04	23
2	3		th					3	6	8				2	1			2						90	
0	7		w					2	0	6				0	7			4						4	
4	0		ay					0	9	0				1	8			7							
9								4	9	3				4	7			4							
0								9	5	8				6	3			9							
4								0	3	1				5				5							
								4										1							
-								-						2				-							
3.								3		3	4			0.				0							
4	m		K					.	.	.				.	6			.							
4	m		E					4	4	4				0	0			9						-	
6	u		G					6	6	6				1	1			6						3.	5.4
3	0	M	G	2	Natural killer cell mediated			6	9	8	20	1	5	4	2	14972   15040   15896   16822   18706	H2-K1   H2-	6						89	51
1	8	1	Pa	4	cytotoxicity - Mus musculus			3	1	4	83	2	4	11	6	18752   19055   19058   22177   2232	T23   Icam2   Lcp2   Pik3ca   Prkcg	9	0	1	0	0		32	59
4	4	1	th		(house mouse)			8	9	6	6	1	6		5	4   170758	Ppp3ca   Ppp3r1   Tyrobp   Vav1	9	6					04	60
8	6		w					4	7	2					2		Rac3	7						90	23
3	5		ay					8	4	2					0			9						4	
6	0							3							9			5							
6								6	6	1					1			9							
								6	9	3					5			3							
-	m		K					-	2	4				2	0.			-							
3.	m		E					3	.	.				.	6	11541   11652   12388   13645   14065	Adora2b   Akt2   Ctnnd1   Egf   F2	0						-	5.4
2	u	M	G	2	Rap1 signaling pathway -			.	6	0	20	2	5	7	9	14677   16409   16822   18706   1875	rl3   Gnai1   Itgam   Lcp2   Pik3ca	.	0	1	0	0		3.	51
1	6	1	G	4	Mus musculus (house mouse)			2	7	3	83	1	4	15	4	2   22324   23880   53978   170758   22	Prkcg   Vav1   Fyb   Lpar2   Rac3	8	6					89	59
1	4		Pa					6	4	9	6	4	6		7	7377	Farp2	8						32	60
1	0		th					1	8	8					2			3						04	23



6	1		w			1	4	8												8			90	
4	5		ay			6	8	5												3			4	
5						4	5	7												9				
9						5	1	0												2				
9						9	6	5												7				
						9														2				
						-	4	4												-				
2.						2														0				
7	m		K			.	.	.												.			-	
7	m		E			7	0	0												2			4	
7	u		G			7	4	6												8			8	
6	0	M	G	2	Fc epsilon RI signaling	7	7	20	5											2			1	
1	9	4	1	1	0	6	3	5	83	6	4	7		11652	16189	16822	18706	22324	Akt2	Il4	Lcp2	Pik3ca	Vav1	R
8	6		Pa	4	pathway - Mus musculus	9	9	6	6	6	6			170758	329502				ac3	Pla2g4e				
4	6		th		(house mouse)	8	9	6	6	6	6								5					
4	6		w			8	7	7												1				5
9	4		ay			4	0	9												2				3
4	4					9	4	0												8				6
5						4	7	8												3				3
						5														1				1
						-	3	3												-				-
2.	m		K			2	.	.												.				0
2	m		E			.	2	3												2				4
7	u		G			.	2	3												2				8
1	2	0	M	G	2	B cell receptor signaling	2	9	9	20	5									8				1
5	4	1	1	0	Pa	4	7	7	9	83	8	4	7		11652	17060	18706	19055	19058	Akt2	Blnk	Pik3ca	Ppp3ca	Ppp
8	6		th		(house mouse)	2	8	0	6	1	6				22324	170758				3r1	Vav1	Rac3		
6	6		w			2	8	0	6	1	6									0				4
6	2		ay			5	7	7												2				5
4						8	9	1												1				6
						6	0	9												2				3





				G			-	3	3		1					-													
	2.	G		O			2	.	.		.	0.				0													
	2	O		Bi			.	2	3		2	4				4				-									
	4	:0		ol			2	5	6		8	8				0				3. 13.									
1	3	0	M	ica	1	response	19_GO:005	4	7	0	20	8	5			2	1	12919   12921   13166   13860   16533	Crhbp   Crhr1   Dbh   Eps8   Kcnm	4	1				87	87			
	4	4	1	l	9	ethanol	response	4	6	2	83	2	4	7		4	0	18754   19401	b1   Prkce   Rara	1	0	7	0	0	64	67			
	9	5		Pr		to stimulus		9	6	1	6	6				5				3						09	89		
	2	4		oc				2	1	3						1				3						21	88		
	1	7		es				1	0	0						2				6							7		
	8	1		se				8	3	0						8													
	4			s				4	8	5						2													
				G				-		6						0													
	3.	G		O			3	9	.							0													
	8	O		Bi			.	.	.							.													
	6	:0		ol			8	5	2							9													
	7	0	M	og		nitric oxide	19_GO:002	6	4	8	20	2	5			1											3.	9.5	
1	3	0	1	ica	1	mediated signal	3052	7	0	1	83	0	4	5		5	6	12491   17748   17750   19416   23488	Cd36   Mt1   Mt2   Rasd1   Gucy1a	2	0	1			86	40			
	5	7		l	9	transduction	signaling	3	2	7	6	0	6			7	5	9		2	4	0	8	1	1	73	29		
	9	2		Pr				5	9	5						5				6							10	4	
	1	6		oc				9	3	9						0				7									
	0	3		es				1	0	8						9				8								9	
	9			se				0	4	5						1				1									
				s				9								6													
	-	G		G		second-	19_GO:002	-	2	3	20	1	5			2	0.	11541   12373   12491   13616   15559	Adora2b   Casq2   Cd36   Edn3   H	-						-	9.5		
1	2.	O	M	O	1	messenger-	3052	2	.	.	83	9	4	12	.	6		17748   17750   19055   19058   1941	tr2b   Mt1   Mt2   Ppp3ca   Ppp3r1	0	0	1			3.	40			
	2	:0	1	Bi	9	signaling		.	3	1	6	5	6			1	2	6   54396   234889	Rasd1   Irgm2   Gucy1a2	.		8			86	29			

6	0		ol	mediated		2	4	0									4		73	30	
1	1		og	signaling		6	8	3									0		59	4	
3	9		ica			1	3	2									9		10		
9	9		l			3	7	4									0		9		
3	3		Pr			9	9	6									8				
8	2		oc			3	8	2									2				
6			es			8	2	1									1				
2			se			6	5	9									6				
			s			2											7				
			G														-				
-			O			-	5	3									0				
2.	G		Bi			2	.	.									.				
1	O		ol			.	0	6									3			-	
2	:0		og			1	8	7									5		3.	9.5	
8	0		ica	cGMP-	19_GO:002	2	8	5	20	5							2		4		
1	1	M	l	mediated	3052	8	1	7	83	3	4	4		11541   12491   15559   234889	Adora2b   Cd36   Htr2b   Gucy1a2	4	0	1	0	0	
1	1	1	l	signaling	signaling	1	5	4	6	0	6						7	0	8	0	
8	9		Pr			1	5	4	6								7				
1	9		oc			8	6	9									3			10	
5	3		es			1	2	1									7			9	
9	4		se			5	8	9									2				
			s			9	8	5									6				
-	m		K			-	3	4									-				
3.	m		E			3	.	.									1			-	
8	u	M	G	Osteoclast differentiation	-	.	5	7	20	1	5			11652   14129   14200   16477   16822	Akt2   Fcgr1   Fhl2   Junb   Lcp2   B	1				3.	
5	0	1	G	Mus musculus (house mouse)		8	7	9	83	2	4	12		17060   17972   18706   19055   1905	lnk   Ncf4   Pik3ca   Ppp3ca   Ppp3	.	0	1	1	1	85
4	4		Pa			5	7	8	6	8	6			8   22177   83433	r1   Tyrobp   Trem2	1		9			41
1	3		th			4	6	4									4				83
																	1				53

	8	8					1	0	9			0	0			5			91					
	3	0					8	9	6			2	1			3			8					
	9						3	8	1			1	2			4								
	1						9	9	0			9	3			2								
	8						1		2			8				1								
							8									6								
			R				-									-								
	-	-					2	5	4			0	0.			0								
	2.	M	Re				.	.	.			.	4			.			-					
	5	M	act				5	0	0			9	0			5								
	2	U	o				2	2	6			1	7			2			3. 5.2					
	5	-	m				5	1	9	20	5	5	6			2			85 63					
1	6	2	M	1	0	e	6	2	9	83	3	4	5	7	6	16822   18706   22177   23845   83433	Lcp2   Pik3ca   Tyrobp   Clec5a   Trem2	1	0	1	0	0	41	60
	4	1	1			Ge		6	0	5	6	8	6	5	5				83 99					
	6	7				ne		4	6	3				0	6				91 53					
	5	2				Se		6	8	7				9	7				8					
	4	1				ts		5	6	7				1	8									
	8	2						4	3	5				1	1				6					
								8						6					8					
	-		R				-	5	3					0	0.				-					
	2.	-	Re				2	.	.			.	3			0			3. 5.2					
	1	M	act				.	2	7			7	6			.			85 63					
1	8	M	M	1	0	o	1	6	6	20	2	5	3	4	4	16822   18706   22177   83433	Lcp2   Pik3ca   Tyrobp   Trem2	3	0	1	0	0	41	60
	1	U	1			m	6	8	3	8	9	6	6	2	9				83 99					
	4	-				e		1	6	9				6	5				91 53					
	0	2				Ge		4	0	7				0	6				3					
	1	4				ne		0	9	9				0					1					



























	2	0		ol	biosynthetic	regulation	7	7	5											6			32	92	
	5	4		og	process	of	2	9	6											1			01	41	
	3	5		ica		biological	5	3	7											4			59		
	3	4		l		process	3	4	5											7			2		
	5	2		Pr			3	0	6											4					
	2	9		oc			5	6	8											5					
	6			es			2	5	8											5					
	3			se			6	9	4											5					
				s			3													3					
				G			-	1	5											-					
	-			O			2	0	.											0					
	2.	G		Bi			.	.	1											.					
	5	O		ol		19_GO:003	5	.	1											5			-		
	9	:0		og	regulation	of 2501	9	4	1											5			3.	10.	
	7	0		ica	1 fibroblast	multicellul	7	0	9	20	1	5								9			74	40	
1	9	9	M	l	9 growth factor	ar	9	7	5	83	1	4	3	4	5	11629   19225   22411	Aif1   Ptgs2   Wnt11		3	0	2	0	0	32	75
	8	0	1	Pr	production	organisma	8	5	8	6	1	6								8	0	2	01	92	
	2	2		oc		l process	8	9	0											0			59	41	
	9	7		es			2	2	5											8			2		
	9	0		se			9	4	5											5					
	3			s			9	1	3											2					
							3													3					
	-	W		Wi			-	1	6											-			-	16.	
	3.	P		ki			3	2	.	20	1	5								1			3.	35	
1	7	2	M	Pa	2 Serotonin and anxiety-related	events	.	.	6	83	1	4	4	7	6	12918   12921   19055   192167	Crh   Crhr1   Ppp3ca   Nlgn1		.	0	2	1	1	70	47
	0	1	1	th	7		7	7	6	6	2	6								0	0	3	93	88	
	9	4		w			0	2	1											5			97	07	
	3	0					9	0	9											3					

9		ay			3	3	7								2		34
7		s			9	9	0								2		7
3					7	0	1								9		
4					3	7	9								0		
7					4	2	9								0		
					7										1		
		G			-										-		
		O			3	1									0		
3.	G	Bi			.	6									.		
2	O	ol			2	.									8		-
3	:2	og			3	3									7		3. 16.
7	0	ica	1	regulation of	19_GO:005	3	5	20	5						9		6
1	3	l	9	corticosterone	1179	7	4	83	7	4	3		12918   12921   21333	Crh   Crhr1   Tac1	6	2	70 35
5	0	Pr		secretion	localizatio	3	7	1	6	6					8	0	93 47
2	8	oc			n	5	8								8	3	97 88
3	5	es				2	8	1							5		34 07
4	2	se				3	0	6							1		7
8		s				4	7								6		
		G				8									4		
		O				-	1	5							-		
2.	:0	Bi				2	2	.							0		-
8	0	ol	1	regulation of	19_GO:005	.	.	7							.		3. 16.
7	5	og	9	corticotropin	1179	8	7	6	20	5					6		70 35
1	4	ica		secretion	localizatio	7	2	9	83	9	4	3	12918   12919   30878	Crh   Crhbp   Apln	9	0	93 47
1	4	l			n	4	0	0	6	6					3	2	97 88
8	5	Pr				1	3	1							1		34 07
7	9	oc				8	9	9							9		7
						7	0	8							1		





7	0	ol	systemic arterial	ar	0	2	8			3	4					3			93	88		
7	0	og	blood pressure	organisma	7	4	6			2	9					3			97	07		
1	3	ica		l process	7	0	5			6	5					7			34			
0	0	l			1	2	7			0	6					3			7			
2	8	Pr			0	2	9			0	1					4						
7	5	oc			2	2	7			7	4					7						
2		es			7	1	6			3						2						
		se			2	4	9			3						6						
		s														5						
		G			-											-						
		O			3		2	4			3					1						
3.	G	Bi			.	.	.	.		.	0.											
6	O	ol			.	6	3			2	7					.						
6	:0	og			19_GO:003	6	1	1		9	6					0				-		
9	0	ica			2501	6	1	5	20	2	5					2				3.	2.7	
1	8	M			multicellul	9	7	0	83	6	4	18				4				66	50	
7	1	1			ar	8	9	9	6	3	6					1	0	2	1	1	98	35
0	5	Pr			organisma	7	9	9	6	3	6					1					70	47
0	0	oc			l process	0	1	0								6					03	5
3	3	es				0	2	4								7					5	
5		se				0	5	6								1						
		s				3	1	8								2						
		G				5										3						
		O				-	2	3			1	0.				-						
2.	O	O			19_GO:003	2	.	.			.	5				0					-	2.7
0	:0	M			2502	.	7	0	20	1	5					0					3.	50
1	5	1			developm	0	7	0	83	1	4	8				.					66	35
3	0	og			ental	0	5	3	6	1	6					3	0	2	0	0	98	47
0	1	ica			process	5	0	3	6	1	6					2					70	5
						3	3	1								6						

8	6	1	0	5	3	0	7	5	03		
7	4	Pr	8	4	9	1	8	9	5		
7	9	oc	7	7	2	4	7	1			
3		es	7	5	4	6	3	6			
2		se	3			5		0			
		s	2					9			
-	R		-					-			
-	-		3	1	3	5	0.	0			
3.	M	Re	.	.	.	.	9	.			
5	M	act	5	9	9	6	9	11541   11652   12854   12918   12919	Adora2b   Akt2   Cort   Crh   Crhb	-	
3	M	o	3	6	5	7	0	12921   13616   13733   14065   1453	p   Crhr1   Edn3   Adgre1   F2rl3	3. 2.6	
9	U	m	3	8	1	20	6	5	9   14676   14677   14744   15200   155	Opn1mw   Gna15   Gnai1   Gpr65	53 71
1	5	-	1	0	e	6	Signaling by GPCR	31	59   18706   18752   18754   18761   20	Hbegf   Htr2b   Pik3ca   Prkcg   P	95 28
4	3	1	5	7	9	6	1	6	295   20308   21333   22324   23796   2	rkce   Prkcq   Ccl17   Ccl9   Tac1	43 20
3	7	ne	4	9	5	5	5	3919   30878   53978   66066   109648	Vav1   Aplnr   Insl5   Apln   Lpar2	31 51	
3	2	Se	3	9	3	6	4	216152   574402	Gng11   Npy   Plppr3   Gpr17	4	
1	7	ts	3	2	9	7	8				
4	9		1	8	7	8					
0			4								
-	R	Re	-	2	3	4	0.				
3.	-	act	3	.	.	.	8				
1	M	o	.	1	7	0	4	11541   12854   12918   12919   12921	Adora2b   Cort   Crh   Crhbp   Crh	3. 2.6	
1	M	m	1	3	1	20	3	5	13616   13733   14065   14539   1474	r1   Edn3   Adgre1   F2rl3   Opn1m	53 71
1	1	U	1	0	e	6	GPCR ligand binding	22	4   15559   20295   20308   21333   237	w   Gpr65   Htr2b   Ccl17   Ccl9   T	95 28
9	-	Ge	1	8	3	6	4	6	96   23919   30878   53978   66066   10	ac1   Aplnr   Insl5   Apln   Lpar2	43 20
9	5	ne	9	2	5	0	5	9648   216152   574402	Gng11   Npy   Plppr3   Gpr17	31 51	
1	0	Se	9	6	9	4	6				
7	0	ts	1	8	7	0					









7	0		ol		cellular	3	3	4												9			27	51
9	3		og		process	7	2	2												4			38	65
4	4		ica			9	2	9												3			99	
7	3		l			4	3	6												0			5	
2	6		Pr			7	4	3												2				
8	8		oc			2	4	8												9				
3			es			8	3	3												5				
4			se			3	2	8												4				
			s			4														4				
			G			-		7	5											-				
-			O			3														0				
3.	G		Bi			.	.	.												.				
3	O		ol		19_GO:003	3	6	4												9			-	
7	:0		og	plasma	2501	7	3	4												4			3.	11.
9	0	M	ica	1 lipoprotein	multicellul	9	2	2	20	2	5									5			51	44
1	4	3	1	1	0	ar	4	2	9	83	5	4	5	7	5	11812   15450   16816   16891   18830	Apoc1   Lipc   Lcat   Lipg   Pltp	0	0	2	0	0	27	83
7	4		Pr	9 particle	organisma	7	3	6	6	5	6									0	7		38	51
2	3		oc	remodeling	l process	2	4	3												2			99	65
8	6		es			2	4	8												9				
3	9		se			8	4	8												5			5	
4			s			3	3	3												4				
			G			4	2	8												4				
-	G		G			-		7	5											-				
3.	O		O	protein-	19_GO:000	3	.	.												0			-	11.
2	:0	M	Bi	1 containing	9987	.	0	1	20	2	5									.			3.	44
1	1	0	1	1	0	ol	9	complex	cellular	2	6	7	7	6	5	11812   15450   16816   16891   18830	Apoc1   Lipc   Lcat   Lipg   Pltp	0	0	2	0	0	51	83
6	3		og	remodeling	process	1	6	4												8	7		27	51
5	4		ica			6	8	5												6			38	65
						6	8	5												6				

















-		G		-	1	2			3		-															
2.	G	O		2	.	.			.	0.																
0	O	Bi		.	8	7			2	7									-							
2	:1	ol	regulation of	0	5	1			9	6									3							
4	9	og	monoatomic	19_GO:005	2	1	4	20	3	5				12373   12512   13616   14065   16189	Casq2   Cd63   Edn3   F2rl3   Il4   K	1			3.	4.1						
1	4	0	M	1	0	1	9		4	4	6	83	7	4	18	7	1		1	2	0	0	0	65	53	
8	4	1	1	0	1	9			4	4	6	83	7	4	18	7	1		8	0	9	0	0	65	53	
8	4	1	1	0	1	9			4	8	2	6	1	6		0	2		8					40	21	
4	0	Pr	transmembrane	n	8	5	8		3	4					91   83433   212933   237611	Jph2   Trem2   Pm20d1   Stac3	3							10	26	
4	6	oc	transport		4	4	2		2	7									4					6		
3	2	es			4	4	0		9	2									7							
4		se			3	2	8		7										3							
		s			4														2							
		R																								
-	-			-	4	4			1										-							
3.	M	Re		3	.	.			.	0.									0							
3	M	act		.	4	6			4										.						-	
6	U	o		3	2	7			6	1									9						3.	8.1
2	-	m		6	4	3	20		5	4									3						36	77
1	7	9	M	1	0	6			2	4	9	83	6	4	8	2	2		8	0	3	1	1	27	39	
0	0	1	1	0	6				2	4	9	83	6	4	8	2	2		8	0	3	1	1	27	39	
8	0	Ge	Extra-nuclear	estrogen	7	8	5	6	9	6					11652   13645   14677   15200   17390	Akt2   Egf   Gnai1   Hbegf   Mmp2	8		8	0	0	1	1	08	40	
8	0	ne	signaling		7	8	5	6	9	6					18706   66066   103573	Pik3ca   Gng11   Xpo1	8		8	0	0	1	1	08	40	
9	9	Se		8	3	8			1	8									5						90	35
0	3	ts		9	7	1			4	7									4						6	
6	9			0	2	6			6	3									4							
				6	9	9			5										3							
				6															3							









7	0	ol	apoptotic	regulation	0	3	3				8	1							3				91	77							
8	4	og	process	of	7	5	8				2	4							3				72	86							
6	3	ica		biological	8	5	9				0	5							7				43								
6	5	l		process	6	4	6				5	3							3				4								
8	2	Pr			6	7	5				1	6							4												
9	5	oc			8	7	6				2								7												
0		es			9	8	9				8								2												
7		se			0	6					2								6												
		s			7														5												
		G			-														-												
-		O			3	2	3				3								0												
3.	G	Bi			.	.					.								.												
2	O	ol			2	5	9				1								8				-								
8	:0	og		19_GO:003	8	0	9				1	4							9				3.	3.9							
9	0	ica	1	skeletal system	2502	4	7	20	2	5	3	2	12406	13345	13395	14260	15412	Serpinh1	Twist2	Dlx5	Fmn1		28	28							
1	4	4	M	1	0	9	7	4	83	5	4	17	5	9	17300	17390	18634	19401	2037	a	Sfrp4	Stc1	Osr1	Tmem107	3	0	3	1	1	94	35
8	8	Pr	1	morphogenesis	4	8	7	6	9	6	5	9	9	20855	23967	66910	79456	216	Recq14	Wnt9a	Tmem119	Mthf		84	59						
4	7	oc			8	7	7				3								0				74	58							
7	0	es			4	3	5				1								0					6							
4	5	se			7	6	9				1								9												
6		s			4	2	8				4								0												
		G			6														4												
-	G	O			-	3	3				1	0.							-				-	3.9							
2.	O	Bi	1	endochondral	19_GO:003	2	.	.	20	5	.	4							0				3.	28							
7	:0	ol	9	bone	2502	.	9	9	83	6	4	7	2	8	12406	13395	17300	18634	19401	Serpinh1	Dlx5	Foxc1	Pex7	Ra	.	0	3	0	0	28	35
0	0	og		morphogenesis	7	2	6	6	8	6	8	1	8	1	20855	231633			6				0	2	0	0	94	59			
1	6	ica			0	8	7				2	4							0												
3	0				1	3	6				0	5							5				84	58							









	9	0		ol		ental	5	6	2									5			79	90	
	3	0		og		process	9	2	4									5			39	72	
	1	1		ica			3	3	6									3			64		
	7	7		l			1	6	9									8			1		
	0	5		Pr			7	9	6									0					
	4	6		oc			0	0	3									8					
	9			es			4	8	5									5					
	7			se			9	6	6									2					
				s			7											3					
				G			-	8	4									-					
	2.	G		O			2	.	.									0					
	3	O		Bi			.	8	6									.					
	7	:0		ol		19_GO:003	3	0	1									4					
	6	0		og			7	6	8	20								5					
	0		M	ica	1	paraxial	2502	6	6	8	1	5						9					
1	0	4	1	l	9	mesoderm	developm	0	4	5	83	3	4	3	4	5	17300   22411   22416						
	5	8		Pr		morphogenesis	ental	5	2	3	6		6		5	2							
	5	3		oc			process	5	4	4					0	7							
	1	4		es				5	3	9					5	2							
	1	0		se				1	4	2					4	2							
	3			s				1	5	4					9								
				G				3															
	-	G		O			19_GO:003	-	2	3					1	0.							
	2.	O		O				2	.	.	20	1	5		.	5							
	1	:0	M	Bi	1	segmentation	2502	.	8	1	83	0	4	8	4	1	11308   12808   17285   17300   20348	Abi1   Cobl   Meox1   Foxc1   Sema	.	0	3	0	0
1	2	0	1	ol	9		developm	1	2	2	6	8	6		6	4	22416   23967   233826	3c   Wnt3a   Osr1   Palb2	3	0	3	0	0
	2	3		og			ental	2	6	2					5	2							
	1	5		ica			process	2	7	2					2	1							

8	2		l			1	5	3				0	7					2		64								
9	8		Pr			8	3	2				1	8					9		1								
4	2		oc			9	4	0				4	7					6										
7			es			4	9	2				6	3					5										
5			se			7	3	9				5						3										
			s			5												5										
			G			-						0						-										
			O			3	1	6				0	0.					0										
3.	G		Bi			.	6	.				.	3					.		-								
2	O		ol			2	.	6				5	1					8										
3	:2		og	regulation	of	19_GO:000	3	3	6			4	6					7		3. 16.								
7	0		ica	1	CD8-positive,	2376	3	5	6	20	5	9	6					6		23 35								
1	3	0	M	1	1	0	1	9	alpha-beta T cell	immune	3	4	83	7	4	3	4	5	19260   20535   74048	Ptpn22   Slc4a2   Vsir	6	0	3	1	1	73	47	
5	0		l	9	proliferation	system	3	7	1	6	6	5	5					8		52 88								
2	5		Pr			process	5	8	6			0	2					8		34 07								
3	6		oc				2	8	1			5	7					5										
4	4		es				3	0	6			4	2					1		8								
4	4		se				4	7	5			9	4					6										
8			s				8											4										
			G				-	7	4			0						-										
2.	O		O				2	.				.	0.					0		-								
1	:0		Bi			19_GO:000	.	1	0			5	3					.		3. 16.								
0	0		ol	negative	regulation	of	1	5	4	20	5	4	1					3		23 35								
1	9	4	M	1	1	0	1	9	alpha-beta T cell	immune	0	5	0	83	1	4	3	9	6	20535   74048   208154	Slc4a2   Vsir   Btla	4	0	3	0	0	73	47
5	6		ica	9	proliferation	system	9	5	3	6	6	4	3					7		52 88								
7	6		l			process	5	2	1			5	5					1		34 07								
6	4		Pr				7	1	5			0	2					2		8								
9	2		oc				6	9	1			5	7					9										

2		es			9	7	6				4	2							7								
2		se			2	8	5				9	4							5								
		s			2														2								
		G			-		4				1								-								
-		O			3	5					0.								0								
3.	G	Bi			.	.					.	4							.								
1	O	ol			1	5	8				0	4							8								
8	:0	og	regulation	of	19_GO:000	8	8	2			9	6							5								
7	0	ica	1	polysaccharide	8152	7	4	0	20	4	5	8	1	11652   13645   20411   53412   54646	Akt2   Egf   Sorbs1   Ppp1r3c   Ppp	2	3		18	62							
1	4	1	1	0	l	9	biosynthetic	metabolic		4	5	1	83	4	4	6	9	5	11652   13645   20411   53412   54646   76487	Akt2   Egf   Sorbs1   Ppp1r3c   Ppp1r3f   Ppp1r3g	2	0	3	1	1	74	68
2	2	Pr			process	process				2	6	6	6	1	6		0	2		22	31						
2	8	oc								2	1	9							8		20	5					
2	8	es								2	7	8							4			4					
0	5	se								0	8	9							5								
4		s								4		2							3								
		G			-		4					0							-								
-		O			2	5						0.							0								
2.	G	Bi			.	.					.	4							.								
8	O	ol			8	9	6				9	0							.								
6	:0	og	regulation	of	19_GO:000	6	6	0			1	7							6								
6	0	ica	1	glycogen	8152	6	2	8	20	3	5	5	6						9								
1	3	1	1	0	l	9	biosynthetic	metabolic		3	6	6	83	2	4	5	7	5	11652   20411   53412   54646   76487	Akt2   Sorbs1   Ppp1r3c   Ppp1r3f   Ppp1r3g	3	0	3	0	0	74	68
5	5	Pr			process	process				5	8	1	6	2	6		5	6		1	5	0	0	22	31		
6	9	oc								6	3	2							9		20	5					
2	7	es								2	1	1							1			4					
5	9	se								2	1	9							8								
2		s								5	5	6							4								



7	0		ol	metabolic	metabolic	4	9	9				1	7				5		74	31					
5	7		og	process	process	7	2	1				5	6				0		22	5					
3	0		ica			5	4	2				7	5				5		20						
6	8		l			3	5	4				5	6				2		4						
0	7		Pr			6	7	0				0	7				6								
5	3		oc			0	9	8				9	8				1								
4			es			5	6	8				1	1				4								
3			se			4	9	4				6					1								
			s			3											7								
			G			-	3	4				2					-								
-			O			3							0.				0								
3.	G		Bi			.	.	.				.	6				.								
1	O		ol			1	0	0				1	2				8		-						
6	:0		og	regulation	of	19_GO:000	1	1	8			9	7				3		3.	4.2					
6	0		ica	1	myeloid	2376	6	2	5	20	1	5	7	4	12608 14461 15163 16189 16409	Cebpb Gata2 Hcls1 Il4 Itgam	7		16	40					
1	5	0	M	1	0	immune	6	7	4	83	5	4	12	8	4	19055 19401 20308 22177 2276	Ppp3ca Rara Ccl9 Tyrobp Zf	0	3	65	13				
0	2		l	9	leukocyte	system	5	2	5	6	2	6	0	4	1 74511 83433	pm1 Lrrc17 Trem2	0	6	04	02					
4	7		Pr		differentiation	process	0	4	8			2	0				7		00	4					
0	6		oc				4	4	8			2	1				1								
0	1		es				0	1	7			1	2				0		6						
6			se				0	1	5			9	2				5								
			s				0	8	4			8	3				6								
-	G		G				-	2	3			3	0.				Abi1 Cebpb Twist2 Gata2 Hb	-	-	4.2					
3.	O		O			19_GO:003	3	.	.			.	7	11308 12608 13345 14461 15122	a-	0		3.	40						
0	:0	M	Bi	1	myeloid	cell	2502	.	2	7	20	3	5	4	8	15163 16189 16409 16477 1659	a1 Hcls1 Il4 Itgam Junb Klf2	.	0	3	0	0	16	13	
5	0	1	ol	9	differentiation	developm	ental	0	5	2	83	2	4	19	7	4	8 20535 22042 22177 22761 238	Slc4a2 Tfrc Tyrobp Zfpm1 C	7	0	6	0	0	65	02
8	3		og			process	5	8	8	6	1	6	9	3	45 83433 210710 227377 235505	lec5a Trem2 Gab3 Farp2 Cd1	8		04	4					
3	0		ica				8	7	3			8	1		09		5								



3	0		l				3	6	1			5	9			0		00	
2	9		Pr				3	0	0			3	7			1		6	
9	9		oc				2	9	4			4	3			5			
5			es				9	6	9			8	7			9			
4			se				5	9	9							4			
			s				4									7			
			G				-		4			1				-			
2.	G		O				2	4								0			
8	O		Bi				.	.	.			.	0.			.		-	
9	:0		ol				8	2	2			8	4			6		3. 4.2	
6	0		og				9	4	2			8	8			9		16 40	
1	2	3	ica	1	osteoclast	19_GO:0032502	6	0	0	20	6	5	2	1	16477   20535   22042   22177   83433	Junb   Slc4a2   Tfrc   Tyrobp   Tre	3	3	0 0 0 65 13
6	0	M	l	9	differentiation	developmental	2	1	8	6	3	6	5	4	227377   235505	m2   Farp2   Cd109	1	6	04 02
6	3		Pr			process	6	3	2				1	5		9		00 4	
9	1		oc				6	0	3				2	3		1		6	
2	6		es				9	2	8				8	6		8			
9			se				2	4	7				2			4			
			s				9												
-	G		G				-	2	3			2				-			
2.	O		O				2	.	.			.	0.			0		-	
8	:0		Bi			19_GO:000	.	4	6			7				.		3. 4.2	
6	0		ol		regulation of	2376	8	4	4	20	2	5	4	9	12608   12986   13345   14461   15163	Cebpb   Csf3r   Twist2   Gata2   Hc	6		16 40
1	6	4	og	1	myeloid cell immune	differentiation system	6	6	9	83	3	4	15	7	16189   16409   19055   19401   2030	ls1   Il4   Itgam   Ppp3ca   Rara   Cc	9	3	0 0 0 65 13
4	5	M	ica	9			6	2	5	6	4	6	2	5	8   22177   22761   74511   83433   226	l9   Tyrobp   Zfp1   Lrrc17   Tre	3	6	04 02
4	6		l			process	4	2	7				5	6	421	m2   Rab7b	1		00 4
7	3		Pr				4	8	5				2	1		9		6	
2	7		oc				7	9	4				7			1			



1	-	M	1	0	G	1	9	negative regulation of fat cell proliferation	19_GO:0048519	-	1	6	20	5	0	14461   16189   83433	Gata2   Il4   Trem2	-	3	0	0	0	88	04										
	3.				G					O	3	4	.	0.																				
	0				O					Bi	.	1	5	3	-																			
	4				:0					ol	0	3	7	4	1			7							3.	14.								
	1				0					og	4	1	6	20	5			8							07	31								
	7				7					ica	1	0	8	83	8			4							3	4	5	1	0	3	0	0	88	04
	6				0					l	9	4	3	6	6			5							2	30	39							
	1				3					Pr	6	3	0	0	7			9							09	56								
	1				4					oc	1	9	1	5	2			1							2									
	3				5					es	1	5	1	4	4			0																
6		se	3	6	7	9		6																										
		s	6																															
1	-	M	1	0	G	1	9	positive regulation of regulated secretory pathway	19_GO:0051179	-	4	4	20	6	5	0	11541   12921   14461   16189   16409   60510   192167	Adora2b   Crhr1   Gata2   Il4   Itgam   Syt9   Nlgn1	-	3	0	0	88	04										
	2.				G					O	2	.	.	0.																				
	8				O					Bi	.	1	1	2	4	.			-															
	5				:1					ol	8	7	7	8	8	6			3.						14.									
	5				9					og	5	3	1	20	5	9			07						31									
	6				0					ica	1	8	5	83	6	4			7						0	4	5	1	0	3	0	0	88	04
	9				3					l	9	7	0	6	4	6			5						30	39								
	9				3					Pr	9	8	8	1	3	9			09						56									
	5				0					oc	9	2	5	2	6	1			2															
	3				7					es	5	0	4	8		8																		
5		se	3	5	3	2		4																										
		s	5																															
1	-	M	1	0	G	1	9	positive regulation of	19_GO:0002376	-	5	4	20	3	5	0	11541   12921   14461   16189   16409	Adora2b   Crhr1   Gata2   Il4   Itgam	-	3	0	0	3.	31										
	2.				O					O	2	.	.	83	7	4			5						.	4	0	0	7	0	0	07	04	
	5				:0					Bi	.	1	1	6	6	9			0															

	7	0		ol	leukocyte	system	5	5	5										5		88	39			
	7	4		og	degranulation	process	7	6	1										4		30	56			
	6	3		ica			7	9	4										9		09				
	0	3		l			6	1	7										2		2				
	9	0		Pr			0	5	9										0						
	8	2		oc			9	1											6						
	9			es			8	5											9						
	5			se			9	7											4						
				s			5												1						
				G			-	6	4										-						
	-			O			2	.	.										0						
	2.	G		Bi			.	.											.						
	4	O		ol	positive		4	1	1										4		-				
	1	:0		og	regulation	of 19_GO:000	1	0	9										7		3.	14.			
	9	0		ica	mast	cell 2376	9	5	0	20	2	5							6		07	31			
1	1	3	M	l	activation	immune	9	7	2	83	2	4	4		11541   12921   14461   16189	Adora2b   Crhr1   Gata2   Il4	0	3	0	0	88	04			
	9	3	1	l	involved	in system	1	8	3	6	5	6							5	0	7	0	0	30	39
	4	0		Pr	immune	process	9	7	4										7					09	56
	3	0		oc	response		4	5	4										8					2	
	7	8		es			3	4	1										0						
	6			se			7	6	6										3						
				s			6												5						
	-	G		G			-	6	4										-						
	2.	O		O	positive	19_GO:000	2	.	.										0		-		14.		
	4	:0	M	Bi	regulation	of 2376	.	1	1	20	2	5							0		3.	31			
1	1	0	1	l	mast	cell	4	0	9	83	5	4	4		11541   12921   14461   16189	Adora2b   Crhr1   Gata2   Il4	0	3	0	0	07	04			
	9	4		og	degranulation	system	1	5	0	6	6								4	0	7	0	0	88	39
	1	3		ica	degranulation	process	9	7	2										7					30	56
																			6						











8	0	l		2	9	3			0	6		3									
4	9	Pr		8	4	7			0	1		3									
5	9	oc		4	6	7			7	4		2									
4		es		5	9	0			3			6									
2		se		4	7	8			3			4									
		s		2																	
		G		-	6	4			0			-									
-		O		2	.	.			.	0.		0									
2.	G	Bi		.	9	5			7	3		.									
6	O	ol	19_GO:005	6	3	7			3	6		5			-						
3	:1	og	0789	3	8	1	20	5	2	4		5			14.						
0	9	ica	1 regulation of	0	3	4	83	2	4	4	6	9	12491   14129   14461   83433	Cd36   Fcgr1   Gata2   Trem2	8	0	3	0	0	07	31
1	1	l	9 membrane	1	9	5	6	2	6		0	5			2	9	0	0	27	04	
3	5	Pr	1 invagination	3	4	7			0	6		4			4			00	39	56	
1	1	oc		1	9	5			7	1		6			6			54			
1	5	es		1	3	6			3	4		1			1						
7	3	se		7	8	7			3			5			5						
4		s		4																	
-	G	G		-	6	4			0	0.		-									
2.	O	O		2	.	.			.	3		0									
5	:0	Bi	19_GO:003	.	6	4			7	6		.							-	14.	
5	0	ol	2501	5	3	3	20	5	3	4		5			3.			31			
1	6	og	1 amyloid-beta	5	6	6	83	2	4	4	2	9	12491   16409   83433   228357	Cd36   Itgam   Trem2   Lrp4	3	0	3	0	0	07	31
1	7	ica	9 clearance	6	7	8	6	3	6		6	5			5	9	0	0	27	04	
4	2	l		1	2	5			0	6		1			5			00	39	56	
5	4	Pr		4	5	7			0	1		6			1			54			
2	2	oc		5	5	8			7	4		6			6						

6		es		2	9	9		3									3			
8		se		6	3	4		3									3			
		s		8													2			
		G		-	3	3		1									-			
2.	G	O		2				0.									0			
4	O	Bi		.	.	.		.	5								.			
0	:0	ol		4	1	4		4	1								4		-	14.
1	0	og		0	4	7		6	4								6		3.	31
1	5	ica	1	1	7	7	20	5	5	2	12317   12491   14129   14461   17175	Calr   Cd36   Fcgr1   Gata2   Masp	6	0	3	0	0	0	07	04
6	0	l	9	1	3	2	83	9	4	8	83433   94176   227541	2   Trem2   Dock2   Camk1d	6	0	9	0	0	27	39	
4	7	Pr		6	1	7	6	7	6				6				6		00	56
4	6	oc		4	3	7		1	8				6				6		54	
8	6	es		4	1	8		4	7				0				0			
4		se		8	6	8		6	3				3				3			
		s		4	8	8		5					2				2			
		G		-		3		1					-				-			
2.	G	O		2	2			0.					0				0			
1	O	Bi		.	.			.	5				.				.			
5	:0	ol		1	6	1		6	4				3				3		-	14.
7	0	og		1	6	0		4	4				6				6		3.	31
1	5	ica	1	5	2	6	20	1	5	8	12317   12491   14129   14461   17175	Calr   Cd36   Fcgr1   Gata2   Masp	9	0	3	0	0	07	04	
2	0	l	9	7	4	8	83	2	4	9	18752   83433   94176   227541	2   Prkcg   Trem2   Dock2   Camk1d	7	0	9	0	0	27	39	
3	7	Pr		2	0	8	6	9	6	5			2				2		00	56
2	6	oc		3	7	9		1	2				3				3		54	
7	4	es		2	7	2		6	9				1				1			
2		se		7	3	0		4	4				4				4			
		s		2	6	9		8					6				6			



	0	0		ol		ental	5	0	6											5				39	85
	2	0		og		process	0	5	6											1				18	41
	8	9		ica			2	9	1											0				44	
	8	8		l			8	6	4											8				2	
	2	5		Pr			8	8	3											3					
	8	5		oc			2	5	2											9					
	2			es			8	4	9											7					
	1			se			2	1	1											9					
				s			1													5					
				G			-	2	3											-					
	2.	G		O			2	.	.											0					
	4	O		Bi			.	7	4											.					
	7	:0		ol			4	8	3											5					
	9	0		og		19_GO:003	7	5	9	20	1	5								0				3.	2.8
	9	0	M	ica	1	specification of	2502	9	4	4	83	3	4	10	1	5	8	13590   20671   22416   23796   23892	Lefty1   Sox17   Wnt3a   Aplnr   Gr	7	4			04	05
1	9	0	1	l	9	symmetry	developm	9	4	4	83	3	4	10	5	4	8	54562   66910   71860   110082   381	em1   Dnaaf11   Tmem107   Cfap5	6	0	0	0	39	96
	7	9		Pr			ental	7	8	9	6	7	6		0	3	738		2   Dnah5   Drc1	8				18	85
	4	7		oc			process	4	7	2					1	4				7				44	41
	9	9		es				9	0	3					8	5				9				2	
	4	9		se				4	1	5					3	3				3					
	9			s				9	9	6					2					7					
				G				-	2	3					1	0.				-					
	2.	O		O			19_GO:003	2	.	.	20	1	5		.	5				0				-	2.8
	1	:0	M	Bi	1	determination	2502	.	6	0	83	3	4	9	6	4	8	13590   20671   22416   23796   54562	Lefty1   Sox17   Wnt3a   Aplnr   D	.	4			3.	05
1	3	0	1	ol	9	of left/right	developm	1	4	8	6	0	6		4	4	8	66910   71860   110082   381738	naaf11   Tmem107   Cfap52   Dna	3	0	0	0	04	96
	5	0		og		symmetry	ental	3	1	0					8	9			h5   Drc1	5				39	85
	9	7		ica			process	5	9	5					3	0				6				18	41















					G					-																							
-					O					2	1																						
2.	G			Bi						.	.			3	0.																		
1	O			ol						1	8			4	8																		
8	:	0			og						8	8	8		7	4	12918   12919   14409   15559   18610																
3	0	M		ica		1		trans-synaptic		19_GO:002	3		6	20	3	5	18752   18754   19055   21333   6051		Crh   Crhbp   Gabrr2   Htr2b   Pdy		7												
1	2	9	1	1	0	l		9		signaling	3		2	9	83	8	4	19	0   72585   75209   83762   109648   17		n   Prkcg   Prkce   Ppp3ca   Tac1   S		9	4	0			0	0	73	79		
2	9			Pr						2	7	6		6	5	6	0758   192167   237611   241770   380		yt9   Lypd1   Sv2c   Otof   Npy   Ra		3	3							56	71			
1	5			oc						2	8	0						702		c3   Nlgn1   Stac3   Rims4   Shisa6		1											
8	3			es						1	6	9										7											
4	7			se						8	2	9										0											
6					s						4	6											5										
					G					-																							
					O					2	1	2																					
2.	G			Bi						.	.			3	0.																		
1	O			ol						1	8	8				4	8																
3	:	1			og						3	6	2				7	4	11541   12918   12921   13616   14461	Adora2b   Crh   Crhr1   Edn3   Gat		5											
7	9	M		ica		1		positive		19_GO:005	3		3	1	20	3	5	16189   16409   17929   18754   1876		a2   Il4   Itgam   Myom1   Prkce   P		6	4	0			0	0	94	80			
1	2	0	1	1	0	l		9		regulation of	1179	7		9	5	83	8	4	19	rkcq   Rbp4   Slc12a2   Tac1   Apln		9	3	0			0	0	73	79			
8	3			Pr						2	1	6		9	6					1   19662   20496   21333   30878   605		9								56	71		
6	5			oc						8	3	3						10   83433   98170   192167   229593		1   Golph3l		5											
1	3			es						6	2	9										6											
1	2			se						1	9	9										3											
2					s						1	3	7										6										
					G					-																							
					O					2	.	.	83	5	4	21	.	8															
1	2.	O	1	1	0	O		9		positive	19_GO:005	-		1	2	20	4	5	3	0.	11541   11686   12918   12921   13616	Adora2b   Alox12b   Crh   Crhr1		-	4	0			0	0	2.	80	
0	:	0			Bi						.	7	7		6	3	6	4   18761   19055   19662   20496   213		Edn3   Gata2   Il4   Itgam   Myom1		.	3							94	79		















9	9			l				4	9	8					0	6		4						07
4	4			Pr				9	8	7					2	8		2						3
3	4			oc				4	3	0					9	4		1						
0				es				3	1	7					3	4		1						
3				se				0	3	4								8						
				s				3										7						
				G				-	2	3					2			-						
2	G			O				2										0						
5	O			Bi					.	.								.						-
9	:0			ol		19_GO:000		5	4	4					3	6		5						-
0	0			og	regulation of T	2376		9	8	0	20	2	5		0	2	11629   12524   12608   16189   18761	Aif1   Cd86   Cebpb   Il4   Prkcq   P						2. 2.9
1	7	M	1	ica	1	cell	immune	0	1	9	83	0	4	13	9	4	19055   19260   20535   22042   2697	pp3ca   Ptpn22   Slc4a2   Tfr3   Pla	3	0	4	0	0	85 35
8	2	1	0	l	9	proliferation	system	7	3	4	6	1	6		5	4	1   74048   170786   208154	2g2f   Vsir   Cd209a   Btla	8	0	9	0	0	49 47
0	1			Pr		process		8	5	6					2	8		0						34 47
2	2			oc				0	5	8					2	8		8						07 82
3	9			es				2	5	8					3	6		5						3
3				se				2	1	1					8	2		2						
				s				3	3	9					1			3						
				G				-	2	3					1			-						
2	O			O				2	.	.								0						-
5	:0			Bi		19_GO:000		.	8	4					8	5		.						2. 2.9
0	0			ol	negative	2376		5	0	6	20	1	5		3	7	12524   12608   16189   16768   19260	Cd86   Cebpb   Il4   Lag3   Ptpn22	5					85 35
1	2	M	1	og	1	regulation of T	immune	0	5	6	83	3	4	10	1	3	20535   26971   74048   208154   240	Slc4a2   Pla2g2f   Vsir   Btla   Lax	1	0	4	0	0	49 47
8	0	1	0	ica	9	cell activation	system	2	9	1	6	6	6		5	4	754	1	0					34 47
8	8			l		process		8	6	4					0	3		8						07 82
2	6			Pr				8	8	3					1	4		3						3
8	8			oc				2	5	2					8			9						







8	8		l			2	8	2				5	0					4			67
1	0		Pr			8	5	1				2	3					3			4
6	5		oc			1	4	5				0	9					4			
7			es			6	7	1				1	9					2			
4			se			7	4	8				5						7			
			s			4															
			G			-	2	3				2						-			
-			O			2	.	.				.	6					0			
2.	G		Bi			.	4	1				0	0					.			-
2	O		ol			2	6	5				1	1					4			2.
7	:0		og		19_GO:005	7	9	5	20	1	5	4	1					1			2.8
5	0		ica		1179	5	2	3	83	7	4	11	6	2		13616   15451   16508   16523   16533	Edn3   Hpn   Kcnd2   Kcnj8   Kcn	5	5	0	80
1	0	M	l	1	potassium ion	9	5	2	6	0	6	5	9	0		20496   56543   76376   105243   329	mb1   Slc12a2   Kcnd3   Slc24a2   Sl	5	0	0	82
9	6	1	Pr		transport	9	5	2	6	0	6	5	0		064   382571	c9a3   Pkd2l1   Kcnf1	5	0	0	81	
0	8		oc			9	2	9				2	0					9			54
5	1		es			0	2	9				2	3					2			67
5	3		se			5	3	2				0	9					9			74
2			s			5	1	4				1	9					8			4
			G			2	6	3				5						4			
-	G		O			-	2	3				2						-			
2.	O		Bi			2	.	.				.	6					0			-
2	:0		ol			.	3	0				1	2					.			2.
4	0		og		19_GO:005	2	3	8	20	1	5	9	2			12491   14580   16523   19662   20496	Cd36   Gfap   Kcnj8   Rbp4   Slc12a	4			80
1	4	M	ica	1	import into cell	1179	4	6	3	83	9	4	12	7	4	20537   56543   68428   76376   8343	2   Slc5a1   Kcnd3   Steap3   Slc24a	0	0	5	82
0	8	1	l			9	4	3	6	6	6	6	8	4		3   105243   319552	2   Trem2   Slc9a3   Spx	0	0	0	81
6	6		Pr			4	3	6	6	6	6	8	4					4			54
3	5		oc			0	9	2				0	0					1			67
8	7					6	8	2				2	1					3			74
						3	2	1				1						3			4









5	M					4	6	4			8	1					4			82	46	
8	U					5	1	5			2	4					9			84	97	
0	-					8	7	7			0	5					7			54		
4	2					0	0	6			5	3					3			2		
9	0					4	9	2			1	6					8					
5	2					9	4	8			2						6					
7	9					5	0	0			8						0					
4	4					7	2	5			2						0					
	8					4											8					
	0																					
-																						
2	G					2	2	3			2	0					0					
6	O						.	.			.	6					.					
6	:0					6	7	6			0	0					5			-		
8	0				19_GO:003	6	7	0			1	0					7			2	2.7	
1	3	M				6	9	0	20	1	5			14200   17300   19662   20348   21924	Fhl2   Foxc1   Rbp4   Sema3c   Tnn	8			66	79		
4	3	1				8	9	9	83	5	4	11		22411   22761   23796   67451   1167	c1   Wnt11   Zfpm1   Aplnr   Pkp2	3	0	5	1	1	83	95
5	2					3	5	8	6	1	6			01   268902	Fgfr1   Robo2	7			45	29		
4	0					4	2	4									0			48	39	
8	6					5	9	7									0				1	
1						4	3	4									2					
						8	9	2									2					
						1											6					
-	G																					
2	O					19_GO:003	-	1	2					4	0.							
1	2	M				2502	2	.	.	20	6	5		. 9	12180   13590   14200   15559   16523	Smyd1   Lefty1   Fhl2   Htr2b   Kc	0					
7	0	1				developm	.	7	8	83	0	4	27	17300   17390   17927   19058   1940	nj8   Foxc1   Mmp2   Myod1   Ppp	0		5	0	0	66	95
4	0					ental	2	0	7	6	5	6		1   19662   20348   20671   21924   224	3r1   Rara   Rbp4   Sema3c   Sox17	.	0	4			83	29
						process	7	3	8					11   22416   22761   23796   23892   23	Tnnc1   Wnt11   Wnt3a   Zfpm1	4					45	39
															Aplnr   Grem1   Osr1   Apln   Pkp	1						

6	7	ica			4	0	8			0	4	967		30878		67451		110082		116701	2		Dnah5		Fgfr1		Myocd		Robo2	5			48																								
1	5	l			6	6	1			5	7		214384		268902		381738					Drc1											5		1																						
2	0	Pr			1	0	5			4	4																							9																							
0	7	oc			2	5	3			9	8																								2																						
6		es			0	7	3			4	9																									9																					
3		se			6	6	9			5																											8																				
		s			3																																	4																			
		G			-																																		-																		
		O			2		2	3		2		0.																												0																	
2.	G	Bi			.	.	.			.		6																													.																
2	O	ol			2		3	0		1		2																														3		-													
0	:0	og		19_GO:003		1	4			9		7																															2.	2.7													
9	0	ica	1	cardiac chamber	2502		2	4	20	1	5			14200		17300		19662		20348		21924		Fhl2		Foxc1		Rbp4		Sema3c		Tnn									8		66	79													
1	8	0	M	1	1	0	l	9	development	developm		8	7	7	83	9	4	12	8	4																						3	0	5	0	0	83	95									
2	3	Pr			8		9	3	6	8	6			01		214384		268902																										3	4	0	0	45	29								
6	2	oc			2		8	0		2		0																																5		48	39										
6	0	es			6		3	4		1		1																																	4		1										
6	5	se			6		1	5		9		2																																	2												
8		s			6		3	4		8		3																																	3												
		G			8																																								5												
		O			-		1	2		5		0.																																		-											
2.	G	Bi			2	.	.			.		9		12388		12808		13036		13645		14260																										0		-							
1	O	ol			19_GO:003		6	7		1		4			15200		15412		17300		17390		1905																										2.	2.7							
7	:0	og	1	tissue	2502		1	5	7	20	6	5																																					.		66	79					
1	0	ica	1	morphogenesis	developm		1	5	7	83	4	4	28		8		19401		20348		20496		20671		208																									3	0	5	0	0	83	95	
1	4	l			7		4	0		8		9		55		21923		21924		22411		22416		22																											7	0	4	0	0	45	29
4	8	Pr			1		0	1		2		6		761		23796		23892		23967		67451		7																											3		48	39			
1	7	l			4		4	7		0		2		6905		231470		268902		270685																															7						
7		Pr			1		4	7		5		9																																									5		1		



													5					6																							
se												8					5																								
s												-	6	4			0	-																							
G												2	. .			. 0.	0																								
O												.	9	5			7 3	.																							
Bi												6	3	7			3 6	5																							
ol												3	8	1	20	5	2 4	5																							
:0												0	3	4	83	2	4 4	6 9																							
og												1	9	5	6	2	6	0 5																							
positive												3	4	7			0 6	4																							
19_GO:003												1	9	5	6			0 5																							
2502												3	4	7			0 6	6																							
1 regulation of												1	9	5	6			0 5																							
19 epidermal cell												1	9	5	6			0 5																							
developmental												3	4	7			0 6	6																							
Pr differentiation												1	9	5			7 1	4																							
process												1	3	6			3 4	1																							
oc												7	8	7			3	5																							
es												4																													
se												-	5	4			0	-																							
s												2	. .			. 0.	0																								
G												.	8	0			7 3	.																							
O												3	7	7			3 6	4																							
Bi												5	0	6	20	5	2 4	4																							
ol												5	9	7	83	2	4 4	6 9																							
:0												6	4	7	6	6	0 5	5																							
og												0	9	0			0 6	8																							
positive												6	5	9			7 1	9																							
19_GO:003												3	6	9			3 4	0																							
2502												6	3	8			3	1																							
1 regulation of												6	3	8			3	1																							
19 epidermis												6	3	8			3	1																							
developmental												6	3	8			3	1																							
Pr development												6	3	8			3	1																							
process												6	3	8			3	1																							
oc												6	3	8			3	1																							
es												6	3	8			3	1																							
se												6	3	8			3	1																							
s												6	3	8			3	1																							
1	-	2.	G	6	O	3	:0	0	0	1	4	1	1	0	M	1	1	0	1	9	1	9	positive regulation of epidermal cell differentiation process	19_GO:003	2502	developmental process	17300   20379   54200   55948	Foxc1   Sfrp4   Sult2b1   Sfn	8	0	5	1	1	01	39	31	49	17	38	4	5
1	-	2.	G	6	O	3	:0	5	0	1	4	1	1	0	M	1	1	0	1	9	1	9	positive regulation of epidermis development	19_GO:003	2502	developmental process	17300   20379   54200   55948	Foxc1   Sfrp4   Sult2b1   Sfn	4	0	5	0	0	01	39	31	49	17	38	4	5

	-	G				-	6	4		0						-																
	2.	G				2	.	.		.	0.					0																
	6	O				.	9	5		7	3					.			-													
	3	:0				6	3	7		3	6					5			2.	6.9												
	0	0			og	19_GO:005	3	8	1	20	5					5			63	38												
1	1	3	M	1	0	ica	1	response	to	0896	0	3	4	83	2	4	4	6	9	12491   15122   24110   319554	Cd36   Hba-a1   Usp18   Idi1	8	0	5	1	1	01	39				
	3	5	1			l	9	stilbenoid		response	1	9	5	6	2	6			0	5		6							31	49		
	1	6				Pr			to	stimulus	3	4	7									4							17	38		
	1	3				oc					1	9	5									6								4		
	7	4				es					1	3	6									1										
	4					se					7	8	7									5										
						s					4																					
						G					-	2	3									-										
	-	G				O					2	.	.									2										
	2.	O				Bi					.	7	5									.										
	6	:0				ol					6	4	5									5									-	3.3
	2	0				og				19_GO:000	2	3	0	20	1	5						5									2.	92
1	3	0	M	1	0	ica	1	spindle		9987	3	6	9	83	5	4	11	6	2	17865   20620   21335   50883   51944	Mybl2   Plk2   Tacc3   Chek2   Kns	6	0	5	1	1	62	10				
	5	7	1			l	9	organization		cellular	5	1	2	6	3	6					54141   66977   68519   78906   1108	trn   Spag5   Nuf2   Eml1   Misp   P	3		7			35	41			
	1	0				Pr				process	1	3	3								54   219072	tpa   Haus4	9						10	92		
	0	5				oc					0	6	1									9									51	
	5	1				es					5	8	1									6										
	1					se					1	5	2									3										
						s					1	5	2									7										
	-	G				G					-	3	3	20	9	5						-									-	3.3
1	2.	O	M	1	0	O	1	mitotic spindle		19_GO:000	2	.	.	83	0	4	8	.	5	17865   20620   21335   50883   66977	Mybl2   Plk2   Tacc3   Chek2   Nuf	0	0	5	0	0	2.	92				
	6	:0	1			Bi	9	organization		9987	.	3	7	6	0	6					68519   78906   110854	2   Eml1   Misp   Ptpa	.		7			62	10			















4	2		l			6	0	5			5	6				5		54																																			
6	8		Pr			4	6	3			0	7				1		8																																			
5	6		oc			6	8	7			9	8				2																																					
4			es			5	6	7			1	1				1																																					
8			se			4	3	5			6					6																																					
			s			8										8																																					
			G			-	1				4					-																																					
2	G		O			2		3			0.					0																																					
4	O		Bi			.	.	.			.	8				.																																					
8	:0		ol			4	8	1			0	4				5		-																																			
7	0		og			8	9	3			2	1	11629		17152		54562		56226		64099		Aif1		Mak		Dnaaf11		Espn		Parv		5		2.	5.0																	
1	0	M	ica	1	cell projection	9987	7	9	20	4	5	9	1	66713		66910		75050		83922		9418		g		Actr2		Tmem107		Kif27		Cep4		0		52	21																
0	0	1	l	9	assembly	cellular	0	4	83	4	4	22	3	7		110082		110084		114602		170758		1		Zfp423		Dnah5		Dnah1		Zmy		8	6	0	0	56	20														
4	0		Pr			process	0	2	6	2	6	0	6		212892		225631		229474		232943		0	3	nd10		Rac3		Rsph4a		Onecut2		F		3	0	3	0	0	46	68												
8	3		oc				0	4				4	5	269209		381738		382571		432516		4	6	hdc1		Klc3		Stk36		Drc1		Kcnf1		9		54	63																
1	1		es				4	8				0	6									0	8	Myo1a		7								2		8																	
3			se				1	9	4			2	7									9	7												2																		
			s				3					9												3															3														
-	G		G				-	4	3			0												-																													
2	O		O				2	.	.			.4											0.																														
2	:0		Bi		epithelial cilium		.	4	7			9	0																															2.	5.0								
8	0		ol		movement		2	3	0	20	4	5	1																															4		52	21						
1	9	M	og	1	involved in		8	7	1	83	3	4	5	5	7	54562		75050		110082		110084		269																							1	0	6	0	0	56	20
2	3	1	ica	9	extracellular	localizatio	9	3	2	6	6	7	5	6	209																																		5		46	68	
8	3		l		fluid movement	n	2	4	7			5	6																																		5		54	63			
6	5		Pr				8	5	1			0	7																																				9		8		
6	1		oc				6	6	1			9																																						2			



1	-	2. G	1 O	:0	M	1	1	0	G	O	Bi	ol	og	ica	1	extracellular	1179	19_GO:005	localization	6	7	6	20	4	5	5	5	54562   75050   110082   110084   269	Dnaaf11   Kif27   Dnah5   Dnah1	3	0	6	0	0	56	21																									
																				3	9	1	83	6	4	5	7										209	Stk36	1	3	0	0	0	46	68																
																				5	5	6	6	6			6												6			4					54	63													
																				4	3	2					0												7			4																			
																				9	4	4					9												8			2						8													
																				9	9	1					1												1			4																			
																				5	8						5										6	1	6			3																			
																				-	-	-	-	-	-	-	-										2	3				1																			
																				-	2. G	-	1 O	-																								1													
																				-	4 :0	-	4 O	-													1					8																			
																				-	4 0	-	4 O	-													4			19 GO:000	cilium	or	9987	19_GO:000	4	4	2	20	1	5	1	3	18830   54562   71860   110082   1100	Pltp   Dnaaf11   Cfpap52   Dnah5	6					52	21
																				1	4 0	M	1	1	0	1	9										1	9	83	5	4	10	5	84   212892   224661   232943   26970	Dnah1   Rsph4a   Slc26a8   Klc3	2	0	6	0	0	56	20	1   381738	Wdr66   Drc1	5	3	0	0	46	68	
																				1	1 5	1	1	1													1	4	2				1																		
9	3							1	2	7				8																																															
8	9							9	5	4				3																																															
5								8	9	9				2																																															
-	-	G	1	M	1	0	1	G	O	9	cilium- dependent	cell		19_GO:000	9987	2	.	.	83	5	4	10	.	5	84   212892   224661   232943   26970	Dnah1   Rsph4a   Slc26a8   Klc3	0	0	6	0	0	2.	21																												
1	2. O	1	1	:0				Bi	motility		19_GO:000	9987				.	4	0	6	3	6	8	7	1   381738	Wdr66   Drc1	.	3				52	20																													















6		es		3	6	9		3		0		
6		se		6	3	8		3		1		
		s		6								
		G		-	8	4		0		-		
2.	G	O		2	.	.		.	0.	0		
2	O	Bi		.	1	4		5	3	.		
7	:0	ol		2	7	0		4	1	4	-	
9	0	og	19_GO:000	7	7	6	20	5	6	1	2.	8.1
1	7	ica	1 actin crosslink	9	7	6		1	5	9	35	77
7	5	M	1 9 formation	9	3	7	83	4	3	4	56	39
7	1	1	cellular	7	9	8	6	4	6	5	06	40
9	7	Pr	process	7	4	2		0	2	9	36	35
4	6	oc		9	0	7		5	7	2	6	
1	4	es		4	3	0		4	2	9		
7		se		1	5	6		9	4	8		
		s		7						4		
		G		-	7	4		0		-		
2.	G	O		2	.	.		.	0.	0		
1	O	Bi	19_GO:004	.	6	2		5	3	.	-	
9	:1	ol	8518	1	3	1		4	1	3	2.	8.1
1	9	og	positive	9	2	5	20	5	6	7	35	77
1	3	ica	1 positive	1	2	0	83	1	5	9	56	39
1	0	M	1 9 regulation of	3	3	8	6	5	6	3	07	39
7	0	1	ruffle assembly	1	3	8	6	5	6	5	06	40
7	0	Pr	of	1	4	9		0	2	1	36	35
3	2	oc	biological	7	4	0		5	7	7	6	
5	9	es	process	3	3	7		4	2	0		
6		se		5	2	4		9	4	5		
		s		6						5		



	2	0		G		3	5	5		3	3		4			62	72					
	6	4		Pa		2	0	9		1	8		1			74	16					
	2	2		th		6	0	3		5	4		9			76						
	7	7		w		2	8	9		0	3		5			6						
	4	0		ay		7	1	8		1	4		3									
	7					4	4	2		8	5		4									
	6					7		6		3	3		4									
	6					6		7		2			7									
						6							1									
	-					-	3	3		1	0.		-									
	2.					2	.	.		.	4		.									
	3			Wi		.	8	5		0	4		4			-						
	2	W		ki		3	1	8		9	6		1			2.	3.8					
	2	P		Pa		2	6	3	20	8	5		9			32	16					
1	2	4	M	th	2	2	1	4	83	6	4	6	9	5	18752   18754   18761   20379   22411   22416	Prkcg   Prkce   Prkcq   Sfrp4   Wnt11   Wnt3a	9	7	0	0	62	11
	2	0	1	w	7	2	1	1	6	0	6		0	2				74	72			
	2	3		ay		2	7	7		1	7		3					76	16			
	6			s		6	2	7		0	7		4					6				
	2					2	1	0		9	1		4									
	1					1	6	2		9	6		7									
	-					-	3	3		1	0.		-									
	2.	W		Wi		2	.	.		.	4		0			-	3.8					
	0	P		ki		.	0	1	20	8	5		2	8	14676   14677   18752   18754   18761	Gna15   Gnai1   Prkcg   Prkce   Prkcq   Ppp3ca   Gng11	.	7	0	0	2.	16
1	5	2	M	Pa	2	0	0	0	83	9	4	7	8	1	19055   66066		3	1	0	0	32	11
	2	3	1	th	7	0	0	0	6	6			2	4				62	72			
	2	2		w		5	1	3		2	4		2					74	16			
	7					2	4	9		0	5		6									



1		ay			7	4	3			5	3				5				76								
8		s			1	0	1			1	6				9				6								
3					8	5	1			2					1												
8					3	0	9			8					6												
4					8	7	2			2					0												
					4										9												
-		G			-	1	2			3					-												
2.	G	O			2					0.					0												
3	O	Bi			.	.	.			.	8				.												
0	:0	ol			3	8	9			8	2				4				-								
5	0	og			0	6	6			4	3	11686   12352   13166   14261   15360	Alox12b   Car5a   Dbh   Fmo1   H		1			2.	1.8								
1	4	M			19_GO:000	small molecule	8152			5	6	20	4	5	6	0			30	63							
8	4	1			1	0	1			4	6	83	3	4	21	1	0	9   21391   23887   59012   71275   836	Scd1   Tbxas1   Ggt5   Moxd1   No	5	7			54	68		
2	2	1			1	0	1			8	8	7	6	0	6	5	0	03   106861   192156   216134   23169	xred1   Elovl4   Abhd3   Mvd   Pd	5	0	2	1	1	82	51	
4	8	Pr			process					3	0				1   270685   328035			xk   Sds   Mthfd11   Fads6	9						41	52	
1	3	oc			2	1	9			8	9									2							3
3		es			4	5	2			4	4									9							
		se			1	2	4			6	7									8							
		s			3															4							
-	G	G			-	5	3			0	0.									-							
2.	O	O			2	.	.			.	3									0							
2	:2	Bi			19_GO:003	positive	2502			.	6	9								.						2.	5.6
9	0	ol			2	5	6	20	5	3	4									4						29	53
1	4	M			1	0	1			9	3	9	83	2	4	4	2	9	15412   17300   20671   74048	Hoxb4   Foxc1   Sox17   Vsir	1	0	7	1	1	49	50
9	0	1			1	0	1			4	5	0	6	7	6	6	5			5						24	69
2	7	ica			9					4	5	0	6		6	5				5						45	87
4	3	l			process					9	0	6								5							
4	8	Pr			2	6	9			0	1									9							6
		oc			4	9	4			7	4									2							





	3	0		ol		ental	2	5	6									4		69	60			
	6	3		og		process	3	1	6									0		23	23			
	9	1		ica			6	5	6									4		00				
	2	1		l			9	9	2									1		6				
	3	0		Pr			2	6	1									3						
	0	2		oc			3	0	3									3						
	0			es			0	2	2									4						
	6			se			0	3	7									5						
				s			6											1						
				G			-											-						
	2.	G		O			2	5	3									0						
	2	O		Bi			.	.										.						
	3	:0		ol			2	4	8									4		-				
	6	0		og		19_GO:000	3	5	6									0		2.	5.4			
	9	4	M	ica	1	peptide	6	1	6	20	5							4	7		23	51		
1	2	3	1	l	9	catabolic	9	5	6	83	8	4	4	6	9	13036   23887   54381   237553	Ctsh   Ggt5   Cpq   Trhde	1	0	7	1	1	69	59
	3	1		Pr		process	2	9	2	6	6			0	5			3		23	60			
	0	7		oc			2	6	1					0	6			3		00	23			
	0	1		es			3	0	3					7	1			3		6				
	0			se			0	2	2					3	4			4						
	6			s			0	3	7					3				5						
				G			6											1						
	-	G		O		19_GO:003	-	4	3					0	0.			-		-	4.2			
	2.	O		Bi	1	regulation of	2	.	.	20	5			.	4			0		-	4.2			
	2	:0	M	ol	9	myotube	.	2	5	83	4	5		9	0	12180   17927   214384   231633   234	Smyd1   Myod1   Myocd   Tmem1	.	0	7	1	1	2.	40
1	0	0	1	ol		developmental	2	4	6	6	5	6		1	7	839	19   Piezo1	3	0	8	1	1	20	13
	4	1		og		process	0	0	9					5	6			8		42	02			
	2	0		ica			4	1	3					7	5			0		71	4			

7	8		l				2	3	0			5	6				9		48
1	3		Pr				7	0	0			0	7				2		4
4	0		oc				1	2	2			9	8				3		
8			es				4	4	7			1	1				4		
4			se				8		4			6					8		
			s				4										5		
			G				-					0					-		
-			O				2	7	4			0	0.				0		
2.	G		Bi				.	.	.			.	3				.		
1	O		ol				1	6	2			5	1				3		-
9	:0		og	C-terminal	19_GO:000		9	3	1			4	1				7		2. 7.6
1	0	M	ica	1	protein amino	8152	1	2	5	20	5	9	6				9		19 32
1	3	1	l	9	acid	metabolic	3	2	0	83	1	4	3	4	5	54396   67526   78933	3	0	7 1 1 13 23
1	8	1	Pr		modification	process	1	3	8	6	5	6	5	2			3	9	17 44
7	4		oc				7	4	9			0	2				1		35 32
3	1		es				3	4	0			5	2				7		6
5	0		se				5	3	7			4	4				0		
6			s				6	2	4			9					5		
			G				-	5	3			0	0.				-		
2.	O		O				2	.	.			.	3				0		-
1	:0		Bi				.	2	7			7	6				.		2. 5.2
8	0	M	ol			19_GO:005	1	6	6	20	5	3	4				3		18 63
1	1	4	og	1	response	to 0896	8	3	8	83	2	4	4	2	9	16816   17748   17750   20657	7	0	8 1 1 14 60
4	6	1	ica	9	copper ion	response	1	6	9	6	9	6	5				9	0	01 99
0	6		l			to stimulus	4	0	7			0	6				3		63 53
1	8		Pr				0	9	9			0	1				1		7
6	8		oc				1	9	5			7	4				7		





3	0	ol	signaling																					3		18	19				
1	4	og	pathway																					5		30	2				
8	6	ica																						4		39					
3	6	l																						7		4					
0	2	Pr																						7							
3	6	oc																						3							
9		es																						7							
4		se																						2							
		s																						6							
-		G																						-							
2.	G	O																						0							
0	O	Bi																						.							
2	:1	ol																						3		-					
7	9	og	regulation	of	19_GO:005	2	6	6																8	1	2.	3.1				
1	1	ica	1	cellular	0896	7	8	9	20	9	5													2	1	13	06				
7	0	l	9	response	to	response	1	0	3	83	0	4	7										3	0	8	0	18	14			
4	0	Pr		insulin stimulus	to	stimulus	7	9	8	6	0	6												3	0	3	0	0	30	19	
8	7	oc																							1				39	2	
4	6	es																							7				4		
7		se																							0						
		s																							9						
-	G	G																							4						
2.	O	O		neuroendocrine	19_GO:003	2	.	.																	-		-	7.1			
1	:0	Bi	1	cell	2502	.	1	0	20	1	5													0				2.	55		
0	0	ol	9	developmental	differentiation	1	5	4	83	6	6	3												.	0	8	1	1	10	21	
9	6	og			process	0	5	0	6	6														3	0	4				95	97
5	1	ica																							4					76	8
																									7						



7	1		l					5	1	1												1						92
6	0		Pr					7	9	5												2						2
9	1		oc					6	7	1												9						
2			es					9	8	6												7						
2			se					2		5												5						
			s					2														2						
			G					-														-						
-			O					2	6	3												0						
2.	G		O					.	.	.												.						
0	O		Bi					.	7	8												3						-
3	:0		ol				19_GO:003	0	3	7												1						2. 7.1
3	0		og				2502	3	4	9	20		5									3						10 55
1	6	4	M	1	0		cell migration	3	4	9	20		1	5								4	8					95 21
1	8	2	1	1	0		involved in developm	6	3	9	83		7	4	3							3	0	4	0	0		76 97
0	0		l	9			gastrulation	8	2	7	6		6									8						92 8
4	7		Pr				process	0	4	4												2						2
2	4		oc					4	4	2												5						
2	4		es					4	9	5												7						
5			se					2	9	5												5						
			s					5														5						
-	G		G					-	7	4												-						
2.	O		O					2	.	.												0						-
1	:0		Bi				19_GO:003	.	.	0												.						2. 7.1
0	0		ol				2502	1	1	4	20		5									3						10 55
1	9	1	M	1	0		neuron	0	5	0	83		1	4	3							4	0	8				95 21
5	6		1	1	0		remodeling	0	5	0	83		6	4	3							7	5	1	1			76 97
7	3		ica	9				9	5	3	6		6									1						92 8
7	3		l				process	5	2	1												1						
6	2		Pr					7	1	5												2						2
9	2		oc					6	9	1												9						

13590 | 20671 | 22411

Lefty1 | Sox17 | Wnt11

12259 | 227377 | 380713

C1qa | Farp2 | Scarf1





7	0	ol		ar	0	7	3		6	6		Ppp3ca   Tnnc1   Pkp2   Srsf1   My	3					47	12							
4	0	og		organisma	7	0	8		4	4		ocd   Stac3	3					66	8							
7	3	ica		l process	4	7	9		1	4			7					06								
6	0	l			7	6	1		0	2			3					5								
6	1	Pr			6	1	8		2	4			4													
0	2	oc			6	2	8		5	7			7													
6		es			0	8	6		6	5			2													
5		se			6				4				6													
		s			5								5													
		G			-								-													
-		O		19_GO:004	2	2	2		1	0.			0													
2.	G	Bi		4419	.	.			.	5			.													
0	O	ol		biological	0	5	9		6	4			3					-								
5	:0	og		process	5	6	7		4	4			2					2.	2.5							
3	0	ica	1	response to type	3	3	7	20	1	5			8					05	63							
1	2	3	M	1	9	II interferon			3	0	6	83	3	4	9	3	0	17472   20295   20308   20684   21822	Gbp4   Ccl17   Ccl9   Sp100   Tgtp1	6	9	0	1	1	32	06
1	4	Pr			2	6	5	6	4	6			5				54396   55932   66713   226421	Irgm2   Gbp3   Actr2   Rab7b	5	0				11	38	
1	3	oc		s	1	3	9		1	3			9						73	02						
7	4	es		interaction	1	8	2		6	2			1						4							
3	1	se		between	7	0	8		4	9			6													
4		s		organisms	3	2	7		4	4			0													
		G			4				8				9													
-	G	G		positive	-	2	3		1	0.			-													
2.	O	O		regulation of	2	.	.	20	1	5			.	5					-	2.7						
0	:1	Bi	1	protein	1179	.	7	0	83	1	4	8	4	1			11652   16409   20411   22416   58801	Akt2   Itgam   Sorbs1   Wnt3a   Pm	.	9	0	1	1	05	35	
5	9	ol	9	localization to	0	5	3	6	1	6			6	4			83433   228357   237611	aip1   Trem2   Lrp4   Stac3	3	1				30	47	
3	0	og		membrane	5	0	3		5	2			2													
0	5	ica			3	3	1		2	1			6													

8	4		l				0	5	3			0	7			5			73	
7	7		Pr				8	4	9			1	8			9			2	
7	7		oc				7	7	2			4	7			1				
3			es				7	5	4			6	3			6				
2			se				3					5				0				
			s				2									9				
-							-	3	3			1				-				
2.							2									0				
0	m		K				.	.	.			.	0.			.			-	
5	m		E				0	0	1			2	4			3				
2	u		G				5	0	0			8	8			2			2. 3.0	
0	M		G	2	PPAR signaling pathway -		2	1	3	20	5	2	1	11520   12140   12491   15360   18830	Plin2   Fabp7   Cd36   Hmgcs2   Plt	6	9		05 01	
1	7	3	1	1	0	Pa	4	4	9	83	8	4	7	20249   20411	p   Scd1   Sorbs1	5	0	1	27 44	
1	3		th				7	4	3	6	9	6				9			18 05	
8			w				1	0	1							1			38 07	
3	2		ay				8	5	1							2			4	
8	0						3	0	9							6				
4							8	7	2							0				
							4									9				
-	G		G				-	6	3							-				
2.	O		O				2	.	.							0			-	
0	:0		Bi				.	7	8							.			2. 6.7	
3	0		ol		cellular	19_GO:004	0	3	7	20	5	4	1			3			03 34	
1	3	3	M	1	0	og	1	3	4	9	83	1	4	3	20496   20855   21391	Slc12a2   Stc1   Tbxas1	1	0	9	36 32
6	0	1	1	0		ica	9	3	3	9	6	7	6			4			80 44	
8	0		l		homeostasis			6	2	7						3			42 99	
0	0		Pr					8	4	4						8			5	
4	2		oc					0	4	2						2				



Supplementary Table 3 Detailed enrichment items of all the genes by GSEA

ID	Description	setSize	enrichmentScore	NES	pv	p.adjust	qvalue	rank	leadingEdge	core_enrichment
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	135	-0.55	1.964	8.4E-03	0.043	0.042	20	tags=41 %, list=14% ,	Oprk1/Bdkrb2/Prokr2/Rxfp2/Ccl21a/Avpr2/Sstr1/Rxfp1/Tac2/Cckbr/Edn3/Agtr2/Gal/Sstr2/Ccr6/Npy/Npbwr1/F2r11/Hc/Ece2/Mc1r/F2r13/Ghsr/Pmch/Pnoc/Mc5r/Penk/Insl5/Tacr1/Oprm1/Pf4/Ccl5/Ccl3/Tac1/Ccr5/Kiss1/Pdyn/Trhr/Cort/Ccl28/Oxtr/Tacr2/Cxcl10/Ccl9/Npsr1/Trh/Galr1/Mc3r/Sstr5/Apln/Aplnr/Avpr1a/Pomc/Ghrl/Prhr
LEIN_CHOROID_PLEXUS_MARKERS	LEIN_CHOROID_PLEXUS_MARKERS	93	0.60	2.043	2.5E-06	0.0065	0.0063	25	tags=55 %, list=18% ,	Cab39l/Slco1c1/Kif9/Slc39a12/Slc4a5/Pcolce/4932438H23Rik/Rbm47/Ttr/Itgb5/Vwa3a/Spata17/Slc6a20a/Cldn1/Col9a3/Nid2/Pltp/Sostdc1/Otx2/Tcn2/Cpq/Efs/Cfh/F13a1/Lgals3bp/Slc26a11/Dnali1/Tgfbi/Cdh3/Trpv4/Tbc1d9/Rnaset2a/Prlr/Cfap44/Lbp/Wfdc2/Tpsb2/Ace/Cldn2/Slc24a5/Col8a1/Abca4/Tmem72/Sulf1/Col8a2/F5/Folr1/Ttc21a/Lepr/Calml4/Kcne2
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	373	0.42	1.636	1.0E-08	0.0177	0.0177	27	tags=30 %, list=20% ,	Tub/Cep128/Spata6/Paqr8/Pitpnm1/Saxo2/Prr29/Eml6/Ngef/Meig1/Dzip1/700030J22Rik/Cfap126/Frmd8/Rabl2/Kif9/Odf2/Arntl2/Kif3a/Map6/Morn5/Tekt1/Ppp1r32/Bbs12/Cfap157/Ccdc40/BC051019/Ttc7b/Rasal2/Fam149a/Rfx2/Cfap45/Casc1/Coprs/Tsga10/Anks1/Mdh1b/Cfap69/Rint1/Tmem231/Pask/Spata17/Ccdc121/Rsph1/Nacc2/Cep41/Iqch/Neto2/Drc1/Ppp6r3/Zbbx/Iqub/Pomt1/Eml1/Efhc1/Dnah12/Nod2/Znfx1/Akap14/Zmynd10/Efcab12/Adgb/Fank1/Dnaaf1/Spaca9/Ttc29/Ranbp9/Sntn/Nek5/Dnali1/Coch/Mlf1/Wdr49/W

REACTOME_GPCR_LIGAND_BINDING	REACTOME_GPCR_LIGAND_BINDING	3	-	-	3.3	0.0	0.0	2	tags=36	dr66/Dnaaf3/Kif24/Cfap53/Dnajb13/1700016K19Rik/Rsph4a/Rsad2/Map3k19/Dnah5/Dynlrb2/Armc3/Ttll6/Ly6h/Oasl1/Lrrc23/Ak9/Fam81b/Zhx3/Iqcg/Ak7/Mak/Dnah7b/Pifo/Cfap221/Cfap57/Rab36/Cfap46/Cfap206/Jhy/Ston2/Ttc21a/Dnah11/Dzank1/Dnah6/2410004P03Rik/Foxj1/Ptpn22/Cfap52/Dnal1Ednrb/Tacr3/Wnt2b/Ccl2/Wnt7b/Gpr4/Opn4/Pth1r/Gnb4/Adra2a/Smo/P2ry13/Cmklr1/Oprk1/Bdkrb2/Fzd9/Wnt7a/Prokr2/Rxfp2/Chrm5/P2ry12/Cysltr1/Ccl21a/Avpr2/Lpar1/Ptafr/Sstr1/Calcb/Crhbp/Fzd10/Rxfp1/Plppr3/Tac2/Cckbr/Gngt2/Ptger2/Crhr2/Ihh/Ptch1/Edn3/Agtr2/Pth2r/Gal/Sstr2/Lpar3/C
		1	0.43	1.6	89	04	04	3	list=17%	rhr1/Adcyap1/Ccr6/Npy/Adora2b/Calca/Npbwr1/F2r11/Adcyap1r1/Hc/Ece2
		7	9319	55	8E	38	26	9	,	/Mc1r/F2r13/Ghsr/Rho/Pmch/Pnoc/Ptger3/Mc5r/Gng11/Penk/Insl5/Grm8/
			04	15	-	64	05	2	signal=3	Pth2/Tacr1/Oprm1/Opn3/Hrh1/Gpr35/Adora2a/Pf4/Ptgfr/Ccl5/Drd2/Ccl3/Gpr39/Vipr2/Crh/Tac1/Ccr5/Gpr17/Kiss1/Pdyn/Trhr/Cort/Ccl28/Adra2b/O
				64	06	6			1%	xtr/Wnt16/Tacr2/Lpar2/Cxcl10/Ccl9/Npsr1/Adgre1/Trh/Galr1/Mc3r/Sstr5/Apln/Aplnr/Glp1r/Glp2r/Avpr1a/Opn1mw/Pomc/Ghrl/Ucn2/Casr/Prhr
										Htr2c/P2ry6/Galr2/Sstr4/Npffr1/Ednrb/Tacr3/Ccl2/Gpr4/Opn4/Adra2a/P2r
										y13/Cmklr1/Oprk1/Bdkrb2/Prokr2/Rxfp2/Chrm5/P2ry12/Cysltr1/Ccl21a/Av
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	2	-	-	4.8	0.0	0.0	2	tags=39	pr2/Lpar1/Ptafr/Sstr1/Rxfp1/Plppr3/Tac2/Cckbr/Ptger2/Edn3/Agtr2/Gal/Sst
		2	0.47	1.7	92	05	04	5	list=18%	r2/Lpar3/Ccr6/Npy/Adora2b/Npbwr1/F2r11/Hc/Ece2/Mc1r/F2r13/Ghsr/Rho
		8	0279	34	4E	06	91	6	,	/Pmch/Pnoc/Ptger3/Mc5r/Penk/Insl5/Tacr1/Oprm1/Opn3/Hrh1/Gpr35/Ado
			9	82	-	45	91	0	signal=3	ra2a/Pf4/Ptgfr/Ccl5/Drd2/Ccl3/Gpr39/Tac1/Ccr5/Gpr17/Kiss1/Pdyn/Trhr/
				5	06	9	6		3%	Cort/Ccl28/Adra2b/Oxtr/Tacr2/Lpar2/Cxcl10/Ccl9/Npsr1/Trh/Galr1/Mc3r/
										Sstr5/Apln/Aplnr/Avpr1a/Opn1mw/Pomc/Ghrl/Prhr
REACTOME_COLLAGEN_FOR	REACTOME_COLLAGEN_FOR	8	-	-	7.9	0.0	0.0	2	tags=44	P3h2/Loxl3/Col6a2/Pcolce/P4ha1/Col11a2/Crtap/Col22a1/Col6a3/Col14a1/Tl
		1	0.59	1.9	59	06	06	3	,	l1/Col6a5/Col9a3/Itgb4/Col2a1/Col26a1/Serpinh1/Col6a1/Col5a1/Col20a1/C
			3599	46	5E	86	66	0	list=16%	ol18a1/P4ha3/Col12a1/Col28a1/Lamc2/Loxl2/Col7a1/Col23a1/Col17a1/Loxl4
			58	36				5	,	/Col10a1/Col8a1/Col6a6/Col16a1/Col8a2/Col24a1



				23	-	64	92		signal=3	
				5	06	4	6		7%	
									tags=49	
				-	9.7	0.0	0.0			
REACTOME_COLLAGEN_BIOS	REACTOME_COLLAGEN_BIOS			-	1.9	95	07	07	2	%, P3h2/Col6a2/Pcolce/P4ha1/Col11a2/Crtap/Col22a1/Col6a3/Col14a1/Tll1/Col
YNTHESES_AND_MODIFYING_	YNTHESES_AND_MODIFYING_	6	0.61	43	7E	24	03		3	list=16% 6a5/Col9a3/Col2a1/Col26a1/Serpinh1/Col6a1/Col5a1/Col20a1/Col18a1/P4ha3
ENZYMES	ENZYMES	3	4201	25	-	32	52		0	, /Col12a1/Col28a1/Col7a1/Col23a1/Col17a1/Col10a1/Col8a1/Col6a6/Col16a1/
				45	17	06	4	4	5	signal=4 Col8a2/Col24a1
										1%
										tags=68
					2.1	2.2	0.0	0.0	3	%,
AMIT_EGF_RESPONSE_40_HEL	AMIT_EGF_RESPONSE_40_HEL	3	0.65	25	18	13	13		3	list=24% Sgk1/Klf2/Cebpb/Nr4a1/Junb/Egr1/Rnf141/Dusp5/Ptgs2/Dusp1/Slc2a3/Mbn
A	A	8	3338	01	5E	67	28		8	, l1/Pias1/Bcl3/Cbx4/Hes1/Mbnl2/Btg2/Cdkn2aip/Klf6/Nfib/Zfp36/Camkmt/
				91	-	-	70		1	Ier2/Sec23a/Ube4b
					75	05	8			signal=5
										2%
										Icam5/Efemp1/Dag1/Serpine1/Itga1/Tgfb3/Mmp24/Sdc3/Fn1/Scube1/Vtn/Lt
										bp4/Col3a1/Adamts2/Lama2/Col1a1/Timp2/Adam19/Pxdn/F11r/Trappc4/Pl
										od1/Nid1/Adam17/Lamc3/P3h3/Adam8/Dcn/Mmp25/Adamts16/Col5a2/Ltb
										p1/Adamts18/Cd151/Fbln1/Bmp7/Cdh1/Htra1/Pecam1/Vcan/P3h2/Adamts1
					-	2.3	0.0	0.0	3	%,
REACTOME_EXTRACELLULAR	REACTOME_EXTRACELLULAR	2	-	1.6	78	13	13		0	list=21%
_MATRIX_ORGANIZATION	_MATRIX_ORGANIZATION	6	0.44	51	7E	67	28		2	, l1a2/Ttr/Ltbp3/Crtap/Itgb5/Capn3/Emilin2/Col22a1/Ddr2/Itgb2/Matn4/Sdc
		2	1242	77	-	99	70		5	signal=3 Col2a1/Itgal/Ctsd/Adamts5/Col26a1/Dmp1/Serpinh1/Ltbp2/Col6a1/Col5a1/I
				33	55	05	8			9%
										tga9/Icam2/Fbln2/Itgam/Itga3/Col20a1/Casp3/Col18a1/Adamts4/Cma1/Mm
										p17/Mmp2/Cd44/P4ha3/Col12a1/Col28a1/Mmp11/Lamc2/Mmp15/Tnc/Loxl2
										/Vcam1/Col7a1/Ntn4/Timp1/Col23a1/Tpsb2/Col17a1/Loxl4/Capn11/Col10a1
										/Col8a1/Col6a6/Capns2/Itgb8/Aspn/Col16a1/Prkca/Col8a2/Gdf5/Col24a1



FLORIO_NEOCORTEX_BASAL_	FLORIO_NEOCORTEX_BASAL_	2	-	-	7.8	0.0	0.0	2	tags=38	Tmem212/Pde7b/Morc4/Olfm1/Slc14a2/Pcdh11x/Cpt1a/Slc38a11/Gpr83/Eml
RADIAL_GLIA_UP	RADIAL_GLIA_UP	4	0.43	1.6	02	28	28	9	%,	6/Cdhr4/Shisa9/Htr2c/Slc17a6/Sfmbt2/Ttc6/Npffr1/Marveld2/Ccdc190/Tmc7
		4	6712	20	9E	84	01	5	list=21%	/Abca9/Gimap1/Pde3a/Wwtr1/Chdh/Zfp57/Oprk1/Parp14/Yes1/Synpo2/Cn
		4	47	07	-	83	99	0	,	ksr3/Pla2r1/Ankrd55/Prrg4/Gbp9/Ttc39b/Cfap54/Adgr14/Vstm4/Cenpi/Acot
				84	05	6	7	0	signal=3	11/Icam2/Arhgap28/Pcdh18/Rhoh/Crb1/Kcng3/Ppp1r3b/Tm4sf1/Mfsd4b1/A
									0%	damts4/Nnmt/Chrdl1/Sult1c2/Gadl1/Dmc1/C1qtnf7/Col28a1/Dock5/Cux2/St
										c1/Penk/Cdcp1/Bnipl/Rsad2/Lamc2/Axdnd1/Ptpn14/Dsc3/Foxp2/Neurod4/
										Mrap2/Crabp1/Clmn/Greb1/Col8a1/Cobl/Fblim1/Syt9/Gbp8/Slc10a1/Cgnl1/
										Myocd/Gdf5/Oas2/2410004P03Rik/Wdr93/Gbp4/Apol9a/Abcc9/Lax1/Sv2c
										Grm3/Htr2c/P2ry6/Galr2/Sstr4/Grik1/Npffr1/Ednrb/Tacr3/Chrn1/Grin2c/P
										th1r/Gabra3/Chrn3/Adra2a/P2ry13/Oprk1/Bdkrb2/Rxfp2/Chrm5/Grik3/Cy
KEGG_NEUROACTIVE_LIGAN	KEGG_NEUROACTIVE_LIGAN	2	-	-	0.0	0.0	0.0	2	tags=40	sltr1/Avpr2/Chrna7/Lpar1/Ptafr/Gabrd/Sstr1/Gria4/Rxfp1/Cckbr/Ptger2/Cr
D_RECEPTOR_INTERACTION	D_RECEPTOR_INTERACTION	0	0.44	1.6	00	69	67	5	%,	hr2/Ghr/Agtr2/Pth2r/Glra3/Sstr2/Lpar3/Crhr1/Adora2b/Npbwr1/F2rl1/Chr
		9	3701	24	20	60	60	8	list=18%	na3/Adcyap1r1/Mc1r/F2rl3/Gpr50/Ghsr/Ptger3/Mc5r/Grm8/Grin3a/Tacr1/P
		9	93	93	17	26	39	7	,	rlr/Oprm1/Hrh1/Gpr35/Adora2a/Ptgfr/Drd2/Vipr2/Trhr/Gabrq/Chrn4/Ga
					1	2	5	7	signal=3	brg3/Adra2b/Oxtr/Tacr2/Lpar2/Chrna4/Grin2d/Galr1/Mc3r/Sstr5/Lepr/Apl
					8				3%	nr/Glp1r/Glp2r/Avpr1a/Chrna10/Gh/Prlhr
										tags=49
										%,
PID_SYNDECAN_1_PATHWAY	PID_SYNDECAN_1_PATHWAY	4	0.64	1.9	00	73	71	2	list=15%	Col6a2/Tgfb1/Col11a2/Hpse/Sdc1/Col6a3/Col14a1/Col9a3/Col2a1/Met/Col6
		3	0707	11	22	52	41	0	,	a1/Col5a1/Col12a1/Col7a1/Hgf/Ccl5/Col17a1/Col10a1/Col8a1/Col16a1/Col8
					72	39	26	4	signal=4	a2
					8	4	6		1%	
										tags=58
VILIMAS_NOTCH1_TARGETS_	VILIMAS_NOTCH1_TARGETS_	1	-	-	0.0	0.0	0.0	1	%,	Itgb2/Csf3r/Itgam/Cma1/Ncf4/Clec10a/Trem2/Tpsb2/Lrrc25/Ccl9/Vpreb1
DN	DN	9	0.75	1.8	00	89	87	8	list=13%	
					31	91	33			

			4110	78	43	82	62	4	,	
			76	48	3	6	1	4	signal=5	
									0%	
				1.5	0.0	0.0	0.0		tags=32	Nup107/Srsf1/Elavl2/Polr2l/Eif4e/Magohb/Zc3h11a/Cpsf6/Cwc27/Wbp11/C
REACTOME_PROCESSING_OF_	REACTOME_PROCESSING_OF_	2	0.34	28	00	89	87	3	%,	wc22/Hnrnpa0/Nup93/Wtap/Cdc40/Gcfc2/Aaas/Cstf3/Prpf40a/Zmat5/Pqbp
CAPPED_INTRON_CONTAININ	CAPPED_INTRON_CONTAININ	2	6536	93	33	91	33	5	list=25%	1/Seh11/Ppnh/Nup11/Smndc1/Clp1/Nup43/Sf3b4/Lsm8/Srsf11/Snrnp40/Thoc
G_PRE_MRNA	G_PRE_MRNA	3	51	77	00	82	62	0	,	7/Lsm5/Eif4a3/Polr2f/Thoc2/Upf3b/Srsf5/Hnrnp1/Isy1/Zcrb1/Sugp1/Nxt1/
				9	7	6	1	9	signal=2	Magoh/Rae1/Cdc5l/Usp39/Snrpb2/Hnrnp2/Rbm22/Gtf2f2/Nup37/Snrpf/Sf
									5%	1/Nupl2/Ppil6/Snrpd1/Pcbp1/Cwc25/Sec13/Lsm7/Plrg1/Cstf2t/Syf2/Dnajc8/
										Wbp4/Nup88/Eftud2/Sf3a3/Prpf38a/Sf3b2/Snrpa1
										P3h2/Adamts1/Loxl3/Angptl4/Sdc2/Wnt7b/Ctsk/Muc13/Bmp4/Adamts7/P4
										ha1/Tgfb1/Fgf11/Sema3g/Mmp21/Grifin/Clec3b/Angpt2/Anxa9/Kitl/Hpse/
										Wnt7a/Lgals9/Sema6d/Megf6/Inhba/Ccl21a/Ctsz/Plxnb3/Tpo/Sdc1/C1qc/Cb
										ln2/Ptn/Mmp28/Tll1/Crhbp/Anxa5/Hbegf/S100b/Pspn/Cstl1/C1qtnf2/Ihh/C
				-	0.0	0.0	0.0	2	%,	1qtnf5/Gpc3/Ctsd/Adamts5/Nrg1/Adamtsl4/Gpc6/Serpinh1/Brinp3/Il11/Se
NABA_MATRISOME_ASSOCIAT	NABA_MATRISOME_ASSOCIAT	4	0.37	1.4	00	89	87	3	list=16%	ma4g/Sema3f/F13a1/Sema3a/Nodal/Clec4a3/C1qa/Sema4d/Megf11/Epgn/Cl
ED	ED	7	7533	52	31	91	33	0	,	ec5a/Plxna3/C1qb/Adamts4/Chrdl1/Inha/Mmp17/Mmp2/Ctsh/Lgals12/Fam
		1	99	72	06	82	62	5	signal=2	20a/P4ha3/C1qtnf7/Bmp6/Bmp3/Ntf5/Insl5/Mmp11/Tgm4/Igf2/Mmp15/Cbl
				6	8	6	1		5%	n1/Wfikkn2/Clec10a/Hhip/Loxl2/Gdnf/Ccl12/Btc/Adamts15/Ccl6/Hgf/Ada
										mtsl1/Timp1/Pf4/Ccl5/Sema3b/Sema6b/Ccl3/Plxnd1/Loxl4/Serpind1/Elfn2/
										Adamts12/Gdf15/Ccl28/Angptl2/Wnt16/Cd209b/Cxcl10/Fasl/Masp2/Adamts
										13/Sulf1/Ccl9/Pappa2/Ctsw/Il1b/Bmp8a/Serpinh1a/Sfrp5/Tgm6/Il7/Gdf5/C
										1qtnf3/Adam33/Chrdl2/Adamts19/Gh/Il4
SMID_BREAST_CANCER_NOR	SMID_BREAST_CANCER_NOR	3	-	-	0.0	0.0	0.0	2	tags=31	Cdkn1c/Pecam1/Baalc/Mrc1/Plcb2/Gimap6/Lamp3/P3h2/Lime1/Sym/Lyn/
MAL_LIKE_UP	MAL_LIKE_UP	4	0.39	1.4	00	98	95	4	%,	Rasgrp2/Jchain/Arhgap25/Clec3b/St6gal1/Angpt2/Ly9/Reln/Cd180/Ccl21a/L
		5		90	38	37	55		list=17%	y96/Trat1/Ptn/Il33/Ptprc/Col14a1/Tnfrsf1b/Trf/Il27ra/Clu/Pltp/Arid5a/Sost

			4353	22	01	61	12	2	,	dc1/S100b/Git2/Dpp4/Fyb/Cd72/Cnn1/Met/Syne3/Edn3/Rasa4/Itgal/Tnfrsf
			99	53	2	5	3	3	signal=2	25/Folr2/Cfh/Dok2/Icam2/Prkcq/F13a1/Acap1/Ccr6/Clec4a3/Nlrp3/Lcp2/Sp
				6					7%	110/Dock2/Col18a1/Gmip/Cma1/Nrip2/Chrd11/Chil1/Cd6/Pnoc/Ciita/Ggt5
										/Mef2c/Tnfaip8/Des/Gng11/Ncf4/Doc2b/Cryab/Aif1/Clec10a/Vcam1/Fcmr/
										Hgf/Ccl5/Mzb1/Wipf1/Col17a1/Svep1/Bbox1/Meox1/Mall/Acta2/Oxtr/Vill/
										Il1r2/Srpx/Il21r/Enpp2/Zeb1/Rnase6/Ctsw/Fcrls/Lepr/Il7/Aplnr/Cd4/Ptpn2
										2/Aqp1/Adarb1/Kctd12
										tags=48
			-		0.0	0.1	0.1	2	%,	
				1.8	00	09	06	0	list=14%	Lrrtm3/Calcb/Neurl3/Rnf112/Cnn1/Cplx3/Tlr9/Parvg/Kcng4/Xirp1/Th/Mzb
MIKKELSEN_ES_ICP_WITH_H3	MIKKELSEN_ES_ICP_WITH_H3	3	0.65	33	46	41	27	4	,	1/Kcnj9/Cfap57/Mc3r/Col24a1
K27ME3	K27ME3	3	2039	18	01	26	07	5	signal=4	
			21	87	2	3	9		2%	
										tags=26
			-		0.0	0.1	0.1	2	%,	Ppp1r1b/Gnb4/Adra2a/P2ry13/Oprk1/Rgs1/Bdkrb2/Rgs22/P2ry12/Ccl21a/L
				1.5	00	09	06	2	list=16%	par1/Sstr1/Gngt2/Agtr2/Gal/Sstr2/Lpar3/Ccr6/Adcy1/Npy/Camk2d/Npbwr
REACTOME_G_ALPHA_I_SIGN	REACTOME_G_ALPHA_I_SIGN	2	0.42	71	47	41	27	1	,	1/Hc/Rho/Pmch/Pnoc/Ptger3/Gng11/Penk/Ins15/Grm8/Gna15/Oprm1/Opn
ALLING_EVENTS	ALLING_EVENTS	1	7787	70	17	26	07	1	signal=2	3/Pf4/Ccl5/Rgs6/Ccr5/Gpr17/Pdyn/Adcy8/Cort/Ccl28/Adra2b/Lpar2/Cxcl1
		8	69	69	9	3	9	1	2%	0/Itpr2/Ccl9/Prkca/Galr1/Sstr5/Apln/Aplnr/Opn1mw/Pomc/Casr
										tags=29
			-		0.0	0.1	0.1	2	%,	Fam149a/Cfap45/AA986860/Casc1/Tsga10/Dhcr24/Mdh1b/Tmem231/Smim22
				1.5	00	09	06	0	list=14%	/Spata17/Tmem40/Rsph1/Cgn/B3gnt7/Tcea3/Drc1/Clic3/Zbbx/Tlcd2/Impa2
SENGUPTA_NASOPHARYNGE	SENGUPTA_NASOPHARYNGE	2	0.40	30	48	41	27	3	,	/Efhc1/Dnah12/Spag17/Akap14/Morn3/Dnah2/Fank1/Dnaaf1/Ccdc81/Tox3/
AL_CARCINOMA_DN	AL_CARCINOMA_DN	5	9678	93	61	26	07	4	signal=2	Ttc29/Ankrd35/Sntn/Nek5/Dnali1/Wdr66/Stoml3/Tspan1/Cfap53/Bnip1/Rsp
		6	58	84	8	3	9		6%	h4a/Map3k19/Dnah5/Chst9/Rrad/Dynlrb2/Armc3/Myo1d/Dmkn/Wfdc2/Ak
										9/Tmc5/Il20ra/Lrrc34/Fam81b/Clic6/Daw1/Dnah10/Hydin/Cobl/Iqcg/Ak7/



				-	0.0	0.1	0.1		tags=39	
			-	1.7	01	75	70	1	%,	
WP_VITAMIN_A_AND_CAROT	WP_VITAMIN_A_AND_CAROT	3	0.64	91	00	41	38	7	list=12%	Rlbp1/Cyp26b1/Bco1/Awat2/Rxrg/Rbp4/Aldh1a3/Npc1l1/Crabp1/Cd36/Cyp
ENOID_METABOLISM	ENOID_METABOLISM	1	4588	89	90	78	06	7	,	26a1/Rpe65
			78	50	2	8	6	0	signal=3	
				3					4%	
				-	0.0	0.1	0.1		tags=27	
			-	1.5	01	75	70	1	%,	Sdc1/Chn2/Cda/Mmp28/Itgb4/Fzd10/Fhod3/Zfp750/Cyp26b1/Clic3/Impa2/
JAEGER_METASTASIS_DN	JAEGER_METASTASIS_DN	1	0.42	25	04	41	38	8	list=13%	Krt19/Ptch1/Jag1/Sfn/Fgfr2/Efs/Cfh/Cdhr1/F2rl1/Zfp185/Tm4sf1/Cdh3/Scel
		9	1046	15	54	78	06	2	,	/Cd24a/Lamc2/Bicd2/Gna15/Chp2/Esrp2/Evpl/Col7a1/Ctnnd1/Tpsb2/Col17
		1	1	43	7	8	6	8	signal=2	a1/Dsc3/Bbox1/Nlrx1/Car12/Abhd2/Cobl/Ephx3/Il1r2/Enpp2/Dio2/Krt23/T
				1					4%	fap2c/Tyrp1/Fat2/Krt15/Prss8/Cpa3
				-	0.0	0.1	0.1		tags=36	Dcn/Vwa3b/Ntn3/Col5a2/Ltbp1/Ecm2/Fbln1/Lgi4/Ntn1/Crim1/Vcan/Mmrn
			-	1.5	01	75	70	2	%,	2/Hspg2/Col6a2/Vwa1/Pcolce/Aebp1/Prelp/Ogn/Egflam/Col11a2/Ltbp3/Vw
NABA_CORE_MATRISOME	NABA_CORE_MATRISOME	2	0.41	20	05	41	38	8	list=20%	a5b2/Reln/Emilin2/Col22a1/Creld2/Igfbp5/Vwa3a/Matn4/Col6a3/Col14a1/C
		2	3351	62	06	78	06	1	,	ol6a5/Col9a3/Nid2/Col2a1/Hmcn2/Tinagl1/Col26a1/Dmp1/Ltbp2/Col6a1/Fr
		0	78	53	1	8	6	1	signal=2	as1/Col5a1/Papln/Fbln2/Abi3bp/Col20a1/Coch/Tgfbi/Mfge8/Sbspon/Col18a
				1					9%	1/Emid1/Col12a1/Col28a1/Fndc8/Lamc2/Tnc/Esm1/Igfbp1/Col7a1/Ntn4/Col
										23a1/Col17a1/Svep1/Col10a1/Rspo1/Hmcn1/Col8a1/Col6a6/Igfbp2/Srpx/Nd
										nf/Aspn/Col16a1/Col8a2/Impg2/Col24a1
				-	0.0	0.1	0.1		tags=27	Mcam/Bmp7/Aldh1l2/Efcab1/Cdh13/Htra1/Plpp1/Fam184a/Pla2g7/Lgals1/E
LIM_MAMMARY_STEM_CELL_	LIM_MAMMARY_STEM_CELL_	4	0.36	03	00	41	38	2	%,	dnrb/Slc1a3/Sox11/Prx/Vcan/P3h2/Adamts1/Hspg2/Lims2/Synm/Gnb4/Pcol
UP	UP	3	6943	97	99	78	06	5	list=18%	ce/Jam2/Sntb2/Aebp1/Hdac4/Cacnb4/Arhgap25/Lrp1/Ngfr/Rfx2/Pdpn/Ths
		8	62	71	1	8	6	1	,	d1/Reln/Bag3/Plekha4/Scn4b/Upp1/Tshz3/Col14a1/Map3k7cl/Slc1a5/Itgb4/
				9				3	signal=2	Neto2/Fhod3/Lrp4/Rcsd1/Rarres2/Cnn1/Gpc3/Tinagl1/Jag1/Nrg1/Scml2/Ser
									3%	pinh1/Lcat/Col5a1/Itga9/Abi3bp/Adgra2/Pcdh18/Heg1/Card10/Vsir/Sbspon

/Col18a1/Btbd11/Zfp423/Edaradd/Nnmt/Cdh3/Tm7sf3/Psd2/Tro/Mpdz/Mmp2/Tmem255b/Mamdc2/Fgfr11/Qrich2/Mef2c/Col12a1/Gng11/Amotl1/Cryab/Phldb1/Tagln/Col7a1/Col23a1/Eid3/Ppp1r3c/Wipf1/Col17a1/Svep1/Kcnmb1/Vgll3/Acta2/Ssh1/Has2/Mia/Angptl2/Adgr1/Oxtr/Igfbp2/Srpx/Enpp2/Sulf1/Tenm3/Col16a1/Lag3/Il1b/Myocd/Cd36/Tns4/Ucn2/Soga1/Adarb1

				-	0.0	0.1	tags=26	
			-	1.8	0.1	1	%,	
HANSON_HRAS_SIGNALING_VIA_NFKB	HANSON_HRAS_SIGNALING_VIA_NFKB	1	0.72	04	83	0	list=7%,	Col18a1/Aldh1a3/Oas1a/Tslp/Sox5
		9	4582	92	40	3	signal=2	
			52	55	57	7	4%	
				4	2	1		
								Srsf1/Elavl2/Polr2l/Magohb/Cpsf6/Cwc27/Wbp11/Cwc22/Hnrnpa0/Cdc40/Gcfc2/Cstf3/Prpf40a/Zmat5/Pqbp1/Ppih/Smndc1/Clp1/Sf3b4/Lsm8/Srsf11/Snrnp40/Lsm5/Eif4a3/Polr2f/Upf3b/Srsf5/Hnrnpl/Isy1/Zcrb1/Sugp1/Magoh/Cdc51/Usp39/Snrpb2/Hnrnph2/Rbm22/Gtf2f2/Snrpf/Sf1/Ppil6/Snrpd1/Pcbp1/Cwc25/Lsm7/Plrg1/Cstf2t/Syf2/Dnajc8/Wbp4/Eftud2/Sf3a3/Prpf38a/Sf3b2/Snrpa1/Papola/Ppie/Prcc/Cpsf3/U2af1/Hnrnpu/Crnkl1/Cstf2/Ncbp1/Sf3b5/Snrpd2/Fus/Polr2d/Ddx42/Polr2j/Gtf2f1/Cwc15/Cpsf2/Prpf3/Lsm2/Bcas2/Prpf8/Bud31/Prpf31/Tra2b/Snrpn/Polr2c
				1.5	0.0	0.1	tags=46	
		1	0.35	06	83	4	%,	
REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	7	0924	98	13	13	list=35%	
		8	78	77	47	91	,	
				5	7	1	signal=3	
							0%	
							tags=38	
			-	1.6	0.1	1	%,	Trim21/B2m/Trim14/H2-D1/Gbp2/Ptafr/Gbp9/Socs1/Sp100/H2-M3/Gbp7/H2-Q1/Camk2d/Pml/Cd44/Ciita/Trim6/H2-T23/Vcam1/Gbp5/Oasl1/Irf7/Fcgr1/Gbp3/Oas1a/Gbp8/Oas2/Gbp4
REACTOME_INTERFERON_GAMMA_SIGNALING	REACTOME_INTERFERON_GAMMA_SIGNALING	7	0.52	90	94	5	list=11%	
		3	1945	43	96	3	,	
			67	07	36	3	signal=3	
				8	7	2	4%	



























			G																																									
	-	G	O				-	1	3			3																																
	2	O	Bi				2	.	.			.																																
	.	:0	ol		19_GO		.	7	0			1																																
	4	0	og	regulation of	:00230		4	0	1	20	3	9	6	5	14169		14580		14805		14813		4		Gfap		Grik1		Grin2c		Grin2			2.4										
	1	3	4	M	1	0	ica	1	9	synaptic	52		3	8	4	83	8	1	29	5	7	14814		15465		17260		18013		d		Hrh1		Mef2c		Neurod2		Pe		-	23			
	5	8	l	plasticity	signali		5	9	8	6	6	6	9	8	18619		19699		76376		110891		nk		Reln		Slc24a2		Slc8a2		Gri		0.68	0	2	0	0	9.14	83					
	5	1	Pr	ng			5	5	3				3	5		170935		192167		210274		24	d2ip		Nlgn1		Shank2		Rims4				5075			2085	13							
	1	6	oc				1	0	0				8	1	1770		246317		260297		31922		Neto1		Prprt1		Sctr		Shisa6		Vg													
	3	7	ess				3	8	7				9	9	9		380702		381677				f																					
			es																																									
															11516		11931		12043		12048		11516		11931		12043		12048		Adcyap1		Atp1b1		Bcl2		Bcl2l							
															12313		12404		12638		12669		12313		12404		12638		12669		1		Calm1		Cbln1		Cftr		Chrm1					
															13048		13179		13488		14167		13048		13179		13488		14167			Cux2		Dcn		Drd1		Fgf12		Fg				
															14169		14401		14403		14466		14169		14401		14403		14466		f14		Gabrb2		Gabrd		Gba		Gri					
															14805		14813		14814		15165		14805		14813		14814		15165		k1		Grin2c		Grin2d		Hcn1		Hc					
															15168		16485		16518		16522		15168		16485		16518		16522		n3		Kcna1		Kcnj2		Kcnj6		Mef				3.7	
															17260		17926		18216		19055		17260		17926		18216		19055		2c		Myoc		Ntsr1		Ppp3ca		Rel					
															19699		20265		20271		21336		19699		20265		20271		21336		n		Scn1a		Scn5a		Tacr1		Bok					
															51800		52882		58801		64378		51800		52882		58801		64378		Rgs7bp		Pmaip1		Gpr88		Cnt							
															66797		67451		70357		71653		66797		67451		70357		71653		nap2		Pkp2		Kcnip1		Shtn1							
															93692		108058		110784		1108		93692		108058		110784		1108		Glrx		Camk2d		Nr3c2		Gabra							
															86		110891		192167		192287		86		110891		192167		192287		5		Slc8a2		Nlgn1		Slc25a36		N					
															230899		238384		241770		243		230899		238384		241770		243		ppa		Slc24a4		Rims4		Grip2							
															547		246317		380728				547		246317		380728				Neto1		Kcnh4											







						11516   11931   12043   12313		Adcyap1   Atp1b1   Bcl2   Cal															
						12638   12669   12733   13167		m1   Cftr   Chrm1   Clnka   Db															
						13367   13488   13489   14167		i   Diaph1   Drd1   Drd2   Fgf12															
		G				14169   14813   14814   15165		Fgf14   Grin2c   Grin2d   Hcn															
	-	G	O		-	2	6	0															
	7	O	Bi		7	.	.	6															
	.	:0	ol		19_GO	.	1	0															
	2	0	og		regulation of	:00511	2	1	9	20	6	9	4	1						2.7			
1	6	4	ica	1	monoatomic	79	6	0	7	83	3	1	4	1	19092   19699   20265   20271	Prkg2   Reln   Scn1a   Scn5a   Tr	-					-	57
	6	3	l	9	ion transport	localiz	6	1	2	6	6	6	1	0	22065   30955   54377   56808	pc3   Pik3cg   Cacng4   Cacna2	4.17	0	5	0	0	8.42	17
	4	2	Pr		ation		4	5	6				0	0	58237   59091   70357   74513	d2   Nkain4   Jph2   Kcnip1   Ne	355					0132	88
	1	6	oc				1	2	6				4	7	77574   80334   81905   93692	to2   Tcaf1   Kcnip4   Cacng8							
	1	9	ess				1	2	8				8	8	98660   100102   107589   1080	Glrx   Atp1a2   Pcsk9   Mylk   C							
			es												58   110784   223864   229709	amk2d   Nr3c2   Rapgef3   Ahc							
															230899   241794   246317   269	yl1   Nppa   Kcng1   Neto1   Dp							
															109   269587   382427   382571	p10   Epb41   Best3   Kcnf1   Gr							
															546134	amd2							
															11931   12043   12313   12638	Atp1b1   Bcl2   Calm1   Cftr   Cl							
	-	G	G			-	2	6	5				0		12733   13167   13367   13488	cnka   Db1   Diaph1   Drd1   Dr							
	7	O	O		regulation of	19_GO	7	.	.				.		13489   14167   14169   14813	d2   Fgf12   Fgf14   Grin2c   Gri							
	.	:0	Bi		monoatomic	:00511	.	2	0				3		14814   15165   15168   15444	n2d   Hcn1   Hcn3   Hpca   Cxcl							2.7
	0	0	ol		ion	79	0	6	9	20	4	9	4	4	15945   16485   16504   16517	10   Kcna1   Kcnc3   Kcnj16   Kc	-					-	57
1	5	3	og	1	transmembr	79	5	5	1	83	9	1	4	3	16518   16522   18216   18854	nj2   Kcnj6   Ntsr1   Pml   Ppp3c	4.06	0	5	0	0	8.42	17
	7	4	ica	9	ane	localiz	7	4	1	6	2	6	9	4	19055   19699   20265   20271	a   Reln   Scn1a   Scn5a   Trpc3	1448					0132	88
	0	7	l		transport	ation	0	2	7				3	7	22065   30955   54377   56808	Pik3cg   Cacng4   Cacna2d2   J							
	3	6	Pr				3	5	2				4	1	59091   70357   74513   77574	ph2   Kcnip1   Neto2   Tcaf1   K							
	6	5	oc				6	9	6				5	6	80334   81905   93692   98660	cnip4   Cacng8   Glrx   Atp1a2							



				ess								100102   108058   110784   223	Pcsk9   Camk2d   Nr3c2   Rap											
				es								864   230899   241794   246317	gef3   Nppa   Kcng1   Neto1   D											
												269109   382571	pp10   Kcnf1											
				G																				
	-	G		O			-	2	5			3	0	11931   12043   12313   12638	Atp1b1   Bcl2   Calm1   Cftr   C									
	6	O		Bi			6	.	.			.	.	12671   13489   14167   14169	hrm3   Drd2   Fgf12   Fgf14   Hc									
	.	:	0	ol	regulation of	19_GO	.	5	8			7	6	15165   15168   15444   16485	n1   Hcn3   Hpca   Kcna1   Mef2									
	2	0		og	transmembr	:00511	2	5	3	20	3	9	1	2	17260   18216   19055   19699	c   Ntsr1   Ppp3ca   Reln   Cacn	-		-	2.7				
1	4	2	M	ica	ane	79	4	2	7	83	0	1	34	1	4	54377   59091   74513   77574	g4   Jph2   Neto2   Tcaf1   Cacn	3.43	0	5	0	0	8.42	57
	4	2	1	l	transporter	localiz	4	4	2	6	3	6	7	6	81905   93692   98660   100102	g8   Glrx   Atp1a2   Pcsk9   Cam	5312					0132	17	
	3	8		Pr	activity	ation	3	3	6					9	4	108058   110784   192167   22	k2d   Nr3c2   Nlgn1   Rapgef3							88
	8	9		oc			8	7	1					0	1	3864   229709   230899   24179	Ahcyl1   Nppa   Kcng1   Neto1							
	6	8		ess			6	8	3					4	1	4   246317   260297   380702	Prrt1   Shisa6							
				es																				
				G																				
	-	G		O			-	2	5					3	0	11931   12043   12313   12638	Atp1b1   Bcl2   Calm1   Cftr   C							
	6	O		Bi		19_GO	6	.	.					.	.	12671   13489   14167   14169	hrm3   Drd2   Fgf12   Fgf14   Hc							
	.	:	0	ol		:00650	.	.	8					8	6	15165   15168   15444   16337	n1   Hcn3   Hpca   Insr   Kcna1							2.7
	2	0		og	regulation of	07	2	1	20	3	9	2	6	16485   17260   18216   19055	Mef2c   Ntsr1   Ppp3ca   Reln	-		-						
1	4	3	M	ica	transporter	biologi	4	1	5	83	1	1	35	0	3	19699   54377   59091   74513	Cacng4   Jph2   Neto2   Tcaf1	3.43	0	5	0	0	8.42	57
	1	2	1	l	activity	cal	1	1	0	6	7	6	9	3	77574   81905   93692   98660	Cacng8   Glrx   Atp1a2   Pcsk	5312					0132	17	
	8	4		Pr		regulat	8	4	0					4	4	100102   108058   110784   192	9   Camk2d   Nr3c2   Nlgn1   R							88
	6	0		oc		ion	6	6	8					0	0	167   223864   229709   230899	apgef3   Ahcyl1   Nppa   Kcng							
	6	9		ess			6	8	2					1	7	241794   246317   260297   38	1   Neto1   Prrt1   Shisa6							
				es												0702								







				G																																								
-	G			O	-	2	4									1	0																											
3	O			Bi	3	.	.									.	.																											
.	:	0			ol		19_GO	.	5	0									7	4	11931		12313		12638		14169																	
3	0			og	positive		:	00511	3	9	7	20	1	9	4	3	15165		16485		18216		19055		Atp1b1		Calm1		Cftr		Fgf14				2.7									
1	5	3	M	1	0	ica	1	9	regulation of														Hcn1		Kcna1		Ntsr1		Ppp3ca				-		57									
2	2			l	9	transporter	localiz	2	6	2	6	0	6	7	8	19699		54377		59091		77574		Reln		Cacng4		Jph2		Tcaf1		C		1.31	0	5	0	0	8.42	17				
8	4			Pr		activity	ation	2	6	2	6	0	6	7	8	81905		93692		223864		23089		acng8		Glrx		Rapgef3		Nppa		1747				0132	88							
1	1			oc				1	5	2									4	0																								
2	1			ess				2	7	9									9	6																								
				es																																								
				G																																								
-	G			O	-	2	3									2	0																											
3	O			Bi	3	.	.									.	.																											
.	:	1			ol	regulation of	19_GO	.	2	8									1	4	11931		12043		12313		13167		Atp1b1		Bcl2		Calm1		Dbi		Di			2.7				
2	9			og	calcium ion		:	00511	2	6	5	20	2	9	8	8	13367		13488		13489		14169		aph1		Drd1		Drd2		Fgf14		Hp				-		57					
1	3	0	M	1	0	ica	1	9	transmembr	79	3	3	9	83	0	1	20	3	2	15444		15945		18216		18854		ca		Cxcl10		Ntsr1		Pml		Ppp3		1.24	0	5	0	0	8.42	17
8	3			l	9	ane	localiz	8	3	4	6	1	6	4	8	19055		22065		30955		59091		ca		Trpc3		Pik3cg		Jph2		Atp1		0185				0132	88					
2	1			Pr		transport	ation	2	5	1									0	6	98660		108058		223864		230899		a2		Camk2d		Rapgef3		Nppa									
5	6			oc				5	5	3									6	5																								
7	9			ess				7	7	1									1	1																								
				es																																								
-	G			G		regulation of	19_GO	-	1	3	20	2	9	2	0	11931		12043		12313		13167		Atp1b1		Bcl2		Calm1		Dbi		Di							2.7					
2	O	M	1	0	O	1		2	.	.	83	9	1	24	.	.	13367		13488		13489		14169		aph1		Drd1		Drd2		Fgf14		Hp									57		
.	:	0	1			Bi	9	transport	79	.	8	1	6	4	6	6	5	15444		15945		16170		18216		ca		Cxcl10		Il16		Ntsr1		Pml		0.77	0	5	0	0	8.42	17		
5	0			ol				5	5	7									2	2	18854		19055		22065		30955		Ppp3ca		Trpc3		Pik3cg		Jph2				7141				0132	88











			G																													
	-	G	O	19_GO	-	2	4				2	0																				
	3	O	Bi	:00325	3	.	.				.	.	11516	11550 11551 11556	Adcyap1		Adra1d		Adra2a		A											
	.	:0	ol	01	.	5	4				1	4	12638	12671 13488 13618	drb3		Cftr		Chrm3		Drd1		Ed		3.0							
	9	0	og	blood vessel	multic	9	4	4	20	1	9	8	8	15465	15559 15560 21336	nrb		Hrh1		Htr2b		Htr2c		Tac		-						
1	0	9	M	1	0	1	9	1	20	3	2		22339	30878 74617 98660	r1		Vegfa		Apln		Scpep1		Atp	1.70	0	6	0	0	8.40	19		
	5	7	1	1	0	9	1	9	1	20	3	2		22339	30878 74617 98660	r1		Vegfa		Apln		Scpep1		Atp	1.70	0	6	0	0	8.40	19	
	8	7	Pr	1	9	1	9	1	20	3	2		22339	30878 74617 98660	r1		Vegfa		Apln		Scpep1		Atp	1.70	0	6	0	0	8.40	19		
	5	4	oc	maintenace	organi	5	5	6	6	9	6	4	8	230899	240672 242202 243	1a2		Nppa		Dusp5		Pde5a		Gr	8781				3773	47		
	2	6	ess	smal	8	3	6					0	6	547		ip2													68			
	5	4	oc	proces	5	3	3					6	5																			
	2	6	ess	s	2	5	8					1	1																			
			es																													
			G																													
	-	G	O	19_GO	-	3						1	0																			
	3	O	Bi	:00325	3	.	.					.	.																			
	.	:0	ol	01	.	0						6	4																			
	8	0	og	multic	8	1			20	1	9	3	1	12313	12671 13489 13618	Calm1		Chrm3		Drd2		Ednrb								3.0		
	1	9	M	1	0	1	9	1	15	7	9			15165	15168 16392 16518		Hcn1		Hcn3		Isl1		Kcnj2		Sc	1.70	0	6	0	0	8.40	19
	3	2	1	1	0	9	1	9	1	15	7	9		15165	15168 16392 16518		Hcn1		Hcn3		Isl1		Kcnj2		Sc	1.70	0	6	0	0	8.40	19
	6	0	Pr	1	9	1	9	1	15	7	9			20271	20346 22003 30878	n5a		Sema3a		Tpm1		Apln		P	745				3773	47		
	1	2	oc	organi	3	4			6	3	6	5	3	67451	230899 319552	kp2		Nppa		Spx												
	7	7	ess	smal	6	7						5	3																			
	1	2	oc	proces	1	6						4	8																			
	7	7	ess	s	7	8						6	6																			
			es																													
	-	G	G	19_GO	-	2	4					2	0	11516	11550 11551 11556	Adcyap1		Adra1d		Adra2a		A								3.0		
	3	O	M	1	0	1	9	1	20	3	2			12638	12671 13488 13618	drb3		Cftr		Chrm3		Drd1		Ed								
1	.	:0	1	1	0	9	1	9	1	20	3	2		12638	12671 13488 13618	drb3		Cftr		Chrm3		Drd1		Ed	1.69	0	6	0	0	8.40	19	
	8	0	ol	Bi	9	1	9	1	20	3	2			15465	15559 15560 21336	nrb		Hrh1		Htr2b		Htr2c		Tac	0021				3773	47		
	8	0	ol	biologi	8	2	1					8	8	22339	30878 74617 98660	r1		Vegfa		Apln		Scpep1		Atp						68		





































7	0	ol	develo	7	6	7	6	3	13869		14466		14828		15208		rbb4		Gba		Hspa5		Hes5		Ela	17	
0	6	og	pment	0	0	5	8	0	15572		16392		16485		16568		vl4		Isl1		Kcna1		Kif3a		Neur	83	
3	0	ica	al	3	5	4	5	0	18013		18032		18080		18111		od2		Nfix		Nin		Nnat		Ntf3		P
3	3	l	proces	3	5	7	5	0	18205		18516		18846		18991		bx3		Plxna3		Pou3f1		Med1				
4	2	Pr	s	4	0	6	9	6	19014		19699		20346		20359		Reln		Sema3a		Sema6b		Sema				
4	2	oc		4	1	5	6		20361		22026		22062		30841		7a		Nr2c2		Trp73		Kdm2b		Zb		
		ess							30928		56747		66797		68169		tb18		Sez6l		Cntnap2		Ndnf				
		es							73750		74653		75050		78801		Whrn		Pomk		Kif27		Ak7		Sm		
									93761		98660		104001		11008		arca1		Atp1a2		Rtn1		Dnah5				
									2		170758		171167		211323		2		Rac3		Fut10		Nrg1		Ptchd1		S
									11612		214968		239857		2410		ema6d		Cadm2		Pgap1		Dmrt				
									62		242620		252838		268902		a2		Tox		Robo2		Nfasc		Sctr		
									269116		319229		320191		545		Hook3		Ccdc141								
									428																		
									11819		11922		12140		13167		Nr2f2		Neurod6		Fabp7		Dbi				
									4	0																	
									13395		13488		13489		13869			Dlx5		Drd1		Drd2		Erb4		H	
									15208		15572		16392		16485		es5		Elav14		Isl1		Kcna1		Kif3a		
									16568		18032		18080		18846			Nfix		Nin		Plxna3		Pou3f1			2.8
									18991		19699		20346		20359		Reln		Sema3a		Sema6b		Sema				
									20361		22062		30841		30928		7a		Trp73		Kdm2b		Zbtb18		C		18
									66797		68169		98660		110082		ntnap2		Ndnf		Atp1a2		Dnah			17	
										170758		171167		211323		21		5		Rac3		Fut10		Nrg1		Ptchd1	
									1612		241062		242620		25283			Pgap1		Dmrta2		Tox		Robo2			83
									8		268902		320191		545428			Hook3		Ccdc141							

- G  
 4 O  
 . :0  
 7 0  
 1 8 3 M 1 0  
 1 1 9  
 8 0  
 5 9  
 8 0  
 8 0  
 es  
 es

19\_GO  
 :00325  
 02  
 forebrain  
 1 developmen  
 9 t  
 develo  
 pment  
 al  
 proces  
 s

- 2 4  
 4 . .  
 . 0 7  
 7 8 9 20 4 9  
 8 7 4 83 1 1 38  
 8 8 3 6 4 6  
 5 6 0  
 8 3 1  
 8 6 2

-  
 -  
 2.32 0 10 0 0 6.94  
 5815 7715  
 83







































































6	0			ol		locom	6	5	6			3	4	19699	20346	20348	20359	Sema3a	Sema3c	Sema6b	Se								12		
2	0			og		otion	2	4	8			8	8	20361	22339	26456	53870	ma7a	Vegfa	Sema4g	Cntn6								28		
3	7			ica			3	0	4			4	7	67784	170758	214968	2689	Plxnd1	Rac3	Sema6d	Rob										
7	4			l			7	0	7			2	0	02	269116	269784		o2	Nfasc	Cntn4											
4	1			Pr			4	3	4			7	4																		
8	1			oc			8	5	5			9	4																		
				ess																											
				es																											
				G																											
-	G			O			-		4			2	0																		
4	O			Bi			4		.				.	11658	12561	13395	13640	Alcam	Cdh4	Dlx5	Efna5	E									
.	:0			ol		19_GO	.		8			8	5	13800	13841	13842	16392	nah	Epha7	Epha8	Isl1	Mef									
5	0			og	neuron	:00400	5	4	4	20	2	9	3	4	17260	18205	18209	18846	2c	Ntf3	Ntn3	Plxna3	Reln	-					-		
1	9	9	M	ica	projection	11	9	4	83	4	1	26	8	8	19699	20346	20348	20359	Sema3a	Sema3c	Sema6b	Se	2.18	0	19	0	0	5.41	39		
2	7	1	0	l	guidance	locom	2	3	6	6	2	6	4	7	20361	22339	26456	53870	ma7a	Vegfa	Sema4g	Cntn6	6863					3066	12		
4	4			Pr		otion	4	8	5				2	0	67784	170758	214968	2689	Plxnd1	Rac3	Sema6d	Rob							28		
9	8			oc			9	6	8				7	4	02	269116	269784		o2	Nfasc	Cntn4										
2	5			ess			2	3	2				9	4																	
				es																											
-	G			G			-	2	4				4	0	11658	12043	12561	12808	Alcam	Bcl2	Cdh4	Cobl	Dlx								
4	O			O		19_GO	4	.	.					.	13395	13489	13640	13800	5	Drd2	Efna5	Enah	Epha7						2.6		
.	:0			Bi	axon	:00325	.	0	5	20	4	9	1	6	13841	13842	16392	17260	Epha8	Isl1	Mef2c	Map1b	-						-		
1	4	0	M	ol	developmen	02	4	1	5	83	2	1	38	4	5	17755	18032	18080	18205	Nfix	Nin	Ntf3	Ntn3	Plxna	2.08	0	19	0	0	5.41	39
4	6	1	0	og	t	develo	4	4	4	6	9	6	8	8	18209	18846	19699	20346	3	Reln	Sema3a	Sema3c	Se	0867					3066	12	
7	1			ica		pment	7	8	5				4	8	20348	20359	20361	21923	ma6b	Sema7a	Tnc	Vegfa	S						28		
3	5			l		al	3	6	5				7	6	22339	26456	53870	66797	ema4g	Cntn6	Cntnap2	Plxn									

















































R																																					
-	-	Re	-	2	3			1	0																												
2	M	act	2	.	.			.	.																												
.	M	o	.	4	4			4	3	12313		13590		13601		18751		Calm1		Lefty1		Ecm1		Prkcb	2.4												
5	U	m	Response to elevated	5	4	20	1	9	4	3	12313		13590		13601		18751		Calm1		Lefty1		Ecm1		Prkcb	-	-	2.4									
1	8	M	e	6	4	1			1	9	19039		20692		22339		54216		Lgals3bp		Sparc		Vegfa		Pcdh	0.80	0	25	0	0	4.49	43					
8	7	1	Ge	Ca2+	8	3	5			9	0	66866		68038		71660		104009	7	Nhlrc2		Chid1		Rarres2		Qs	1914	0	25	0	0	4.49	86				
7	6	ne			8	8	6			6	1	6			2	8				240334			ox1		Pcyox1l					9999	3						
0	0	Set			7	6	7			1	1																										
3	0	s			0	3	1			4	6																										
5					3																																
R																																					
-	-	Re	-	2	3			1	0																												
2	M	act	2	.	.			.	.																												
.	M	o	.	3	1			3	3																												
2	U	m	2	5	3	20	1	9	1	7	12313		13590		13601		19039		Calm1		Lefty1		Ecm1		Lgals3	-	-	-	-	2.4							
1	9	M	e	6	9	3	3	83	1	1	12	0	5	20692		22339		54216		66866		bp		Sparc		Vegfa		Pcdh	7	Nhl	0.61	0	25	0	0	4.49	43
7	1	1	Ge	Platelet degranulation	7	1	7	6	6	6	0	6	4	68038		71660		104009		24033	rc2		Chid1		Rarres2		Qsox1		P	2047	0	25	0	0	4.49	86	
8	4	ne			8	0	6			4	9																										
0	6	Set			0	9	8			3	1																										
1	0	s			1	5	2			7	7																										
8																																					
-	G	G	extracellular	19_GO	-	2	4	20	2	9	3	0	12406		12815		12822		12836		Serpinh1		Col11a2		Col18a1	-	-	-	-	-	-	2.4					
1	4	O	matrix	:00099	4	.	.	83	7	1	28	.	.	13406		14114		14115		14580		Col7a1		Dmp1		Fbln1		Fbln2	2.11	0	26	1	1	4.49	02		
.	:0	Bi	organization	87	.	3	7	6	4	6	0	5	17385		17388		17389		50706		Gfap		Mmp11		Mmp15		Mm	0025	0	26	1	1	4.49	8163			





G																						
- G O 19_GO - 1 7 0 0																						
4 O Bi :00325 4 1 . . .																						
. :0 ol 01 . . 0 5 2																						
4 0 og relaxation of multic 4 3 3 20 9 4 4																						
1 6 5 M 1 0 ica 1 cardiac ellular 6 7 5 83 1 1 5 5 3 11931   16518   18706   108058 Atp1b1   Kcnj2   Pik3ca   Camk - .																						
8 5 1 9 muscle organi 8 3 8 6 6 8 4  242202 2d   Pde5a 2.09 0 27 1 1 4.46 37																						
1 1 Pr smal 1 3 4 5 4 132 8178 62																						
7 1 oc proces 7 6 7 1 5																						
8 9 ess s 8 2 9 5 1																						
es																						
G																						
- G O 19_GO - 5 4 0 0																						
2 O Bi :00325 2 . . .																						
. :0 ol 01 . 4 . 5 2																						
7 0 og relaxation of multic 7 1 4 20 9 4 4																						
1 3 9 M 1 0 ica 1 muscle ellular 3 5 1 83 1 1 5 5 3 11931   16518   18706   108058 Atp1b1   Kcnj2   Pik3ca   Camk - .																						
6 0 1 9 muscle organi 6 8 1 6 6 8 4  242202 2d   Pde5a 0.88 0 27 0 0 4.46 37																						
4 0 Pr smal 4 8 4 5 4 4505 8178 62																						
3 7 oc proces 3 6 9 1 5																						
4 5 ess s 4 9 4 5 1																						
es																						
- G G actin- 19_GO - 3 3 20 9 0 0																						
1 2 O M 1 0 1 mediated :00099 2 . . 83 6 1 8 . . 16518   18706   20265   20271   Kcnj2   Pik3ca   Scn1a   Scn5a   - .																						
. :0 1 Bi 9 cell 87 . 0 3 6 0 6 8 3 22003   67451   71653   108058 Tpm1   Pkp2   Shtn1   Camk2d 0.64 0 27 0 0 4.46 37																						
3 0 ol contraction cellula 3 3 8 7 0 2098 8178 62																						













			G																															
	-	G	O					-	6	4					0	0																		
	3	O	Bi		19_GO	3	.	.							.	.																		
	.	:0	ol		:00099	.	3	8							5	2																		
	0	0	og	1	inner dynein	87	0	1	4	20	9			4	4													6.3						
1	6	3	ica	1	arm	cellula	6	8	0	83	1	5	5	3	54562   68270   110084   22705		Dnaaf11   Dnaaf1   Dnah1   Dnah7b   Dnah2									-	-	18						
	4	6	l	9	assembly	r	4	5	7	6	6			8	4	8   327954									1.11	0	30	0	0	4.29	53			
	4	1	Pr		proces	s	4	3	0					5	4															47				
	8	5	oc		s		8	4	4					1	5																			
	4	9	ess				4	7	5					5	1																			
			es																															
			G																															
	-	G	O						-	2	3				1	0																		
	2	O	Bi		19_GO	2	.	.							.	.																		
	.	:0	ol		:00099	.	3	6						7	4	13206   13411   18830   54562	Ddx4   Dnah11   Pltp   Dnaaf11																	
	9	0	og	1	cilium or	87	9	7	7	20	1	9		4	3	68708   69329   74711   110082	Rabl2   Cfap206   Ttl9   Dnah									-	-	18						
1	3	0	ica	1	flagellum-	cellula	3	8	0	83	5	1	16	6	2	110084   207686   212892   22	5   Dnah1   Cfap69   Rsph4a   Sl	1.03	0	30	0	0	0	4.29										
	1	1	l	9	dependent	r	1	7	4	6	3	6		7	8	4661   232943   269701   32795	c26a8   Klc3   Wdr66   Dnah2	1636									8993							
	3	5	Pr		cell motility	proces	3	4	7					2	5	4   380654	Cfap54																	
	7	3	oc			s	7	2	2					4	0																			
	2	9	ess				2	5	1					9	6																			
			es																															
	-	G	G		19_GO	-	2	3							1	0																		
	2	O	O	1	cilium-	:00099	2	.	.	20	1	9			.	.	13206   13411   18830   54562	Ddx4   Dnah11   Pltp   Dnaaf11									-	-	18					
1	.	:0	Bi	9	dependent	87	.	3	6	83	5	1	16		7	4	68708   69329   74711   110082	Rabl2   Cfap206   Ttl9   Dnah	1.03	0	30	0	0	0	4.29									
	9	0	ol		cell motility	cellula	9	7	7	6	3	6		4	3	110084   207686   212892   22	5   Dnah1   Cfap69   Rsph4a   Sl	1636										8993						











			G																																										
-	G		O			19_GO	-	3	4					1	0																														
3	O		Bi			:00325	3	.	.					.	.																														
.	:0		ol			01	.	6	4					0	3																														
4	0	M	og	1	smooth	multic	4	1	4	20			9	9	4	12671		13488		13489		13618		Chrm3		Drd1		Drd2		Ednr	rb		-		-	4.9									
1	0	0	1	0	ica	9	muscle	ellular	0	0	9	83	6	1	10	1	3	15559		20606		21336		72043		Htr2b		Sstr2		Tacr1		Sulf2		M		1.34	0	32	0	0	4.12	44			
3	6		l		contraction	organi	3	5	9	6		3	6	7	3	107589		243547								ylk		Grip2				7339			0.23	94									
6	9		Pr			smal	6	9	9																												0.02								
0	3		oc			proces	0	1	3																																				
9	9		ess			s	9	3	4																																				
			es																																										
			G																																										
-	G		O			19_GO	-	4	4																																				
2	O		Bi			:00325	2	.	.																																				
.	:0		ol			01	.	9	0																																				
5	0	M	og	1	phasic	multic	5	4	5	20			9	4	4																								4.9						
1	4	1	1	0	ica	9	smooth	ellular	4	4	9	83	2	1	5	5	3	13488		13489		13618		15559		Drd1		Drd2		Ednr	rb		Htr2b		S		0.77	0	32	0	0	4.12	44		
9	4		l		muscle	organi	9	9	1	6		3	6	8	4																								94						
6	8		Pr		contraction	smal	6	4	6																														0.02						
5	2		oc			proces	5	0	6																																				
1	1		ess			s	1	2	1																																				
			es																																										
-	G		G		muscle	19_GO	-	1	4									11819		12023		12043		12675		Nr2f2		Barx2		Bcl2		Chuk		Dy		-		-		2.7					
1	4	O	M	1	0	O	1	structure	:00325	4	.	.	20	5	9			.	.	13549		13618		14106		16392		rk1b		Ednr	rb		Foxh1		Isl1		Mef		1.84	0	33	1	1	4.10	73
.	:0	1	1		Bi	9	developmen	02	.	8	2	83	4	1	44			8	7	17260		17261		17932		18032		2c		Mef2d		Myt1		Nfix		Ntf3									
1	0		ol		t	develo	1	3	5											18205		18209		19014		19055		Ntn3		Med1		Ppp3ca		Ptgfrn								3712	08		







GO		Molecular Function		Biological Process		GO ID		GO Count		Gene Count		Gene Name		Expression									
1	00019	cardiac ventricle development	1	00019	1	00019	02325	2013	2013	69	22	Bcl2	Ctnnd1	Cd44	Chuk	2.7							
1	00099	morphogenesis	1	00099	9	00099	02325	8341	8341	461	11	Cobl	Ctssl	Enah	Epha7	73							
1	00099	proliferation	1	00099	9	00099	02325	666	666	88	8	Erbp4	Foxh1	Brd2	Gpc3	99							
1	00099	cellular process	1	00099	9	00099	02325	666	666	88	8	Hes5	Isl1	Kif3a	Mef2c	Pgr	08						
1	00099	cellular process	1	00099	9	00099	02325	666	666	88	8	Pml	Med1	Sema3a	Sema3	-	-	73					
1	00099	cellular process	1	00099	9	00099	02325	666	666	88	8	Tal1	Tnc	Tnnc1	Tpm1	1.09	0	33	0	0	4.10	99	
1	00099	cellular process	1	00099	9	00099	02325	666	666	88	8	Vegfa	Yap1	Kdm2b	Sirt6	0379	-	-	-	-	3712	08	
1	00099	cellular process	1	00099	9	00099	02325	666	666	88	8	Nckap1	Heyl	Pkp2	Plxnd1	-	-	-	-	-	-	-	
1	00099	cellular process	1	00099	9	00099	02325	666	666	88	8	Dnaaf1	Ptk7	Lrg1	Mylk	-	-	-	-	-	-	-	
1	00099	cellular process	1	00099	9	00099	02325	666	666	88	8	Hectd1	Nrg1	Mtss1	Gcnt4	-	-	-	-	-	-	-	
1	00099	cellular process	1	00099	9	00099	02325	666	666	88	8	Kdm2a	Car9	Robo2	-	-	-	-	-	-	-	-	
1	00099	cardiac ventricle development	1	00099	9	00099	02325	8351	8351	166	62	Foxh1	Isl1	Mef2c	Med1	Scn5a	Sema3c	Tnnc1	Tpm1	-	-	2.7	
1	00099	cellular process	1	00099	9	00099	02325	666	666	88	8	Heyl	Pkp2	Ptk7	Ap2b1	Fgf	1.04	0	33	0	0	4.10	99
1	00099	cellular process	1	00099	9	00099	02325	666	666	88	8	rl1	Hectd1	Nrg1	Robo2	6861	-	-	-	-	-	-	08















		G																									
-	G	O		- 2 4 1 0																							
4	O	Bi		19_GO 4 . . . . .																							
		ol		:00508 . 8 6 8 4 11514   12313   15165   15444   Adcy8   Calm1   Hcn1   Hpca   J																							
0	0	og		96 0 4 2 20 1 9 5 4 16477   17260   18013   19055   unb   Mef2c   Neurod2   Ppp3c																							
1	0	M	1		response to		respon 0 3 4 83 3 1 17 5 5 19395   20271   22065   54153   a   Rasgrp2   Scn5a   Trpc3   Ras																				
0	1	1		9		calcium ion		se to 0 3 7 6 6 6 8 9 54524   66871   107589   19216 a4   Syt6   Cpne8   Mylk   Nlgn																			
9	5	Pr		stimul 9 4 6 9 2 7   229709 1   Ahcy11																							
3	9	oc		us 3 0 5 5 4																							
9	2	ess		9 6 3 2 3																							
		es																									
		G																									
-	G	O		- 3 4 1 0																							
3	O	Bi		19_GO 3 . . . . .																							
		ol		:00508 . 3 5 3 3 11514   15444   16477   17260   Adcy8   Hpca   Junb   Mef2c																							
6	0	og		cellular		96 6 6 8 20 8 9 1 7 18013   19395   20271   54153   Neurod2   Rasgrp2   Scn5a   Ra																					
1	7	M	1		response to		respon 7 9 2 83 1 12 0 5 54524   66871   107589   19216 sa4   Syt6   Cpne8   Mylk   Nlgn																				
8	1	1		9		calcium ion		se to 8 8 5 6 6 0 6 7 1 3548																			
9	2	Pr		stimul 9 8 6 4 9																							
6	7	oc		us 6 5 1 3 1																							
1	7	ess		1 2 1 7 7																							
		es																									
-	G	G		19_GO - 2 3 2 0 11514   12043   12313   12576   Adcy8   Bcl2   Calm1   Cdkn1b																							
3	O	M	1		response to		:00508 3 . . 20 3 9 . . 12675   15165   15444   16477     Chuk   Hcn1   Hpca   Junb   K																				
1	.	:0		1		9		metal ion		96 . 0 8 83 0 1 27 9 5 16485   16816   17260   18013   cna1   Lcat   Mef2c   Neurod2																	
3	0	ol		respon 3 0 0 4 5 19055   19395   20271   21924   Ppp3ca   Rasgrp2   Scn5a   Tnn																							
				8504																							
																		-	-								
																		1.28	0	36	0	0	4.00				
																		0939	0939								
																		3.3	3.3								
																		69	69								
																		88	88								
																		52	52								





									40332   243616   243634   2685	4   Slc6a7   Slc6a11   Ano2   Slc2								
									12   329178   382427   433926	6a11   Unc80   Best3   Lrrc8b								
R																		
-																		
-	M		Re			-	1	2										
2			act			2	.	.										
	M		o			.	8	8										
	U		m	SLC-mediated		1	8	1	20	2	9							
1			e	transmembrane		2	6	6	83	1	1	18	5					
1	M	1	0															
2		4	1			3	8	0	6	7	6		0					
3		2		Ge	transport													
3		5		ne		3	2	0					6					
0		4		Set		0	5	7										
1		0		s		1	1	9										
7																		
				G														
	G			O			-	6	5									
3				Bi	adenylate	3	.	.										
				ol	cyclase-	19_GO	.	8	5									
7				og	activating	:00230	7	2	8	20	9		5	6				
1	M	1	0	ica	adrenergic	52	9	4	7	83	2	1	6	5	6			
9		1		l	receptor	signali	0	0	7	6	6		0	5				
0				Pr	signaling	ng	7	1	7									
7				oc	pathway		7	7	4									
7				ess			2	5	2									
2				es														

12313   15203   20499   20503	Calm1   Heph   Slc12a7   Slc16a								
20519   28253   74338   76376	7   Slc22a3   Slco1b2   Slc6a19								1.8
107566   108115   110891   110	Slc24a2   Arl2bp   Slco4a1   Slc8								86
895   117591   234967   238384	a2   Slc9a4   Slc2a9   Slc36a4   Sl	0.51	0	38	0	0	0	3.84	82
240332   243616   268512	c24a4   Slc6a7   Slc6a11   Slc26a	6153						7113	51
	11								

11550   11551   11556   13488	Adra1d   Adra2a   Adrb3   Drd								
13489   245424	1   Drd2   Gpr101	1.62	0	39	1	1	1	3.79	24
		5624						0772	01









		G																																														
-	G	O										-	5	4	0										0																							
2	O	Bi										19_GO	2	.	.	.										.																						
.	:	0	ol										:	00650	.	6	0	4										2																				
3	0	og										activation of	07	3	8	2	20	9	3	1											-											6.8						
1	5	0	M	1	0	ica										1	adenylate	biologi	5	6	1	83	1	4	6	7	11516   11556   13488   210044	Adcyap1   Adrb3   Drd1   Adcy2	0.64	0	39	0	0	3.79	-											24		
4	7	l										9	cyclase	cal	4	6	4	6	6	6	8											5217											0772	01				
5	1	Pr										activity	regulat	5	8	7	8										6																					
5	9	oc											ion	5	1	0	1										3																					
1	0	ess												1	2	3	2										4																					
		es																																														
		G																																														
-	G	O										19_GO	-	2	3	0										0																						
2	O	Bi										:	00325	2	.	.	.										.																					
.	:	0	ol										01	.	8	1	8										3																					
1	0	og										multic	1	4	6	20	9	7	0											-											6.8							
1	6	4	M	1	0	ica										1	vasodilation	ellular	6	3	7	83	6	1	8	3	7	11516   11551   11556   12638   13488   13618   22339   230899	Adcyap1   Adra2a   Adrb3   Cftr   Drd1   Ednrb   Vegfa   Nppa	0.54	0	39	0	0	3.79	-											24	
9	2	l										9	organi	organi	9	3	0	6	6	3	4											0615											0772	01				
0	3	Pr										smal	0	4	5	6										2																						
4	1	oc										proces	4	0	9	2										8																						
6	1	ess										s	6	6	7	4										9																						
		es																																														
-	G	G										19_GO	-	3	3	0										0																						
2	O	O										regulation of	:00650	2	.	.	20	9	.	.	11516   11556   13488   13489	Adcyap1   Adrb3   Drd1   Drd2	-											-														
1	.	:	0	M	1	0	Bi										1	cyclase	07	.	0	1	83	5	1	7	7	2	15444   21858   210044	Hpca   Timp2   Adcy2	0.50	0	39	0	0	3.79	0772											01
0	0	ol										biologi	0	0	3	6	6	6	8											2919											0772	01						





































3	4		og	localiz	3	7	9	5	8	18751 19055 19662 21336	Ppp3ca Rbp4 Tacr1 Trh													
1	6		ica	ation	1	4	7	9	5	22044 30878 50721 67623	Apln Sirt6 Tm7sf3 Nrg1 R													
5	8		l		5	3	6	3	1	211323 215445 230899 238	ab11fip3 Nppa Gpr68 Baia													
3	8		Pr		3	3	7	8	9	377 545192	p3													
5	3		oc		5	3		9																
			ess																					
			es																					
			G																					
-	G		O		-	2	3	1	0															
3	O		Bi		3	.	.	.	.															
.	:0		ol	positive	19_GO	.	4	8	7	4	11514 11516 12426 12638	Adcy8 Adcyap1 Cckbr Cftr							2.4					
0	0		og	regulation of	:00511	0	5	1	20	1	9	4	3	12671 13489 16392 18111	Chrm3 Drd2 Isl1 Nnat Pr	-				-				
1	8	9	M	ica	peptide	79	8	9	9	83	4	1	16	6	2	18751 19662 22044 30878	kcb Rbp4 Trh Apln Sirt6	1.13	0	49	0	0	3.33	10
6	0		1	l	hormone	localiz	6	1	9	6	8	6	7	8	50721 67623 238377 54519	Tm7sf3 Gpr68 Baia	7569					1535	54	
3	2		Pr	secretion	ation	3	0	5	2	5	2													
7	7		oc			7	5	3	4	0														
5	7		ess			5	4	6	9	6														
			es																					
			G																					
-	G		O		19_GO	-	1	3	4	0	11514 11516 11551 12426	Adcy8 Adcyap1 Adra2a Cc												
3	O		Bi		:00650	3	.	.	.	.	12638 12671 12903 12921	kbr Cftr Chrm3 Crabp1 Cr												
.	:0		ol	regulation of	07	.	6	4	20	6	9	9	7	13039 13371 13489 13618	hr1 Ctsl Dio2 Drd2 Ednrb	-				-	2.4			
1	0	0	M	og	hormone	biologi	0	2	2	83	2	1	45	1	1	13640 15560 15893 16322	Efna5 Htr2c Ica1 Inha Isl	1.08	0	49	0	0	3.33	59
1	1		1	og	levels	cal	1	7	5	6	9	6	2	4	16392 16522 17202 17932	1 Kcnj6 Mc4r Myt1 Nnat	6889					1535	10	
6	0		ica		regulat	6	3	9	6	1	18111 18751 19014 19055	Prkcb Med1 Ppp3ca Rbp4												
6	8		l		ion	6	4	6	6	2	19662 19699 21336 22044	Reln Tacr1 Trh Apln Sirt6												
			Pr								30878 50721 56448 67623	Cyp2d22 Tm7sf3 Akr1c18												

3	1	oc			3	9	9			3	1	105349   107522   107585   108	Ece2   Dio3   Slco4a1   Nrg1												
8	7	ess			8	2	9			8	5	115   211323   215445   218476	Rab11fip3   Gcnt4   Nppa   Cpl												
		es										230899   235415   238377   38	x3   Gpr68   Vgf   Baiap3   Plb1												
												1677   545192   665270													
												11514   11516   11551   12048	Adcy8   Adcyap1   Adra2a   Bc												
		G										12426   12638   12671   12921	l2l1   Cckbr   Cftr   Chrm3   Crh												
		O										0	13489   13640   14158   15560	r1   Drd2   Efna5   Fer   Htr2c   I											
		Bi										5	. 15893   16322   16392   16504	ca1   Inha   Isl1   Kcnc3   Kcnj6											
		ol											7	16522   17260   17932   18111	Mef2c   Myt1   Nnat   Ntsr1   Pr										
		og	regulation of	19_GO									3	4	18216   18751   19055   19662	kcb   Ppp3ca   Rbp4   Syk   Sdc1				2.4					
		ica	secretion by	:00511	0	8	0	20	7	9			4	3	20963   20969   21336   21463	Tacr1   Tcp11   Trh   Apln   Sir	1.08	0	49	0	0	3.33	59		
1	1	0	1	0	79	1	9	7	83	0	1	49	9	4	22044   30878   50721   54524	t6   Syt6   Ptges   Tm7sf3   Fbxl2	6889					1535	10		
		l	cell	localiz	5	9	4	6	1	6			3	4	7	64292   67623   72194   75209	0   Sv2c   Stxbp5   Npy   Rap1a						54		
		Pr		ation	3	9	8						4	1	78808   109648   109905   1921	Nlgn1   Nrg1   Rab11fip3   Go									
		oc			9	9	9						5	6	67   211323   215445   229593	lph3l   Nppa   Cplx3   Gpr68   R									
		ess			7	3	5								230899   235415   238377   241	ims4   Pram1   Baiap3									
		es													770   378460   545192										
															1	0									
		G													2	.	.								
		O													7	4	11514   11516   12426   12638	Adcy8   Adcyap1   Cckbr   Cftr						2.4	
		Bi	positive	19_GO											4	3	12671   13489   16392   18111	Chrm3   Drd2   Isl1   Nnat   Pr						59	
		ol	regulation of	:00511	9	9	9	20	1	9					6	2	18751   19662   22044   30878	kcb   Rbp4   Trh   Apln   Sirt6	1.04	0	49	0	0	3.33	10
1	6	0	1	0	79	6	4	9	83	5	1	16	6	7	8	50721   67623   238377   54519	Tm7sf3   Gpr68   Baiap3	6861					1535	54	
		ica	peptide	localiz	1	3	8	6	2	6															
		l	secretion	ation	7	9	9								2	5	2								
		Pr			0	2	3								4	0									
		oc			4	1	8								9	6									



| 235415 | 238377 | 241770 | 31

9552 | 378460 | 545192

		G																			
-	G	O		-	1	3															
2	O	Bi		2	.	.															
.	:0	ol		19_GO	.	9	3														
7	0	og	regulation of	:00511	7	4	4	20	2	9											
1	2	0	M	1	0	ica	1	9	peptide	79	2	4	4	83	6	1	23				
7	2	1	1	9	l	secretion	localiz	7	8	8	6	9	6								
4	7	Pr		ation	4	8	0														
3	9	oc			3	7	2														
8	1	ess			8	3	5														
		es																			
		G																			
-	G	O		-	1	3															
2	O	Bi		2	.	.															
.	:0	ol		19_GO	.	9	3														
6	0	og	regulation of	:00511	6	3	0	20	2	9											
1	8	9	M	1	0	ica	1	9	peptide	79	8	0	6	83	7	1	23				
6	0	1	1	9	l	transport	localiz	6	5	3	6	1	6								
0	0	Pr		ation	0	3	7														
2	8	oc			2	3	6														
7	7	ess			7	8	3														
		es																			

11514 | 11516 | 11551 | 12426 | Adcy8 | Adcyap1 | Adra2a | Cc  
12638 | 12671 | 13489 | 13640 | kbr | Cftr | Chrm3 | Drd2 | Efna 2.4  
15560 | 15893 | 16392 | 16522 | 5 | Htr2c | Ica1 | Isl1 | Kcnj6 | M -  
17932 | 18111 | 18751 | 19055 | yt1 | Nnat | Prkcb | Ppp3ca | Rb 0.88 0 49 0 0 3.33 59  
19662 | 22044 | 30878 | 50721 | p4 | Trh | Apln | Sirt6 | Tm7sf3 | 0497 1535 10  
67623 | 238377 | 545192 Gpr68 | Baiap3 54

11514 | 11516 | 11551 | 12426 | Adcy8 | Adcyap1 | Adra2a | Cc  
12638 | 12671 | 13489 | 13640 | kbr | Cftr | Chrm3 | Drd2 | Efna 2.4  
15560 | 15893 | 16392 | 16522 | 5 | Htr2c | Ica1 | Isl1 | Kcnj6 | M -  
17932 | 18111 | 18751 | 19055 | yt1 | Nnat | Prkcb | Ppp3ca | Rb 0.84 0 49 0 0 3.33 10  
19662 | 22044 | 30878 | 50721 | p4 | Trh | Apln | Sirt6 | Tm7sf3 | 8438 1535 54  
67623 | 238377 | 545192 Gpr68 | Baiap3































													G																							
													O	19_GO	- 2 2								1 0													
													Bi	:00325	2 . .								. .													
													ol	02	. 0 7								4 3	13367 13860 16568 17909	Diaph1 Eps8 Kif3a Myo10					-					2.0	
													og	1	0 8 7 20 1 9								1 9	18846 22003 22339 22379	Plxna3 Tpm1 Vegfa Fmnl3					-					82	
1	0	0	M	1	0	ica	1	9	regulation of	develo	0 2 5 83 4 1 13								9 0	27418 67784 170758 26958	Mkln1 Plxnd1 Rac3 Epb4					0.44	0	56	0	0	3.20	44				
													l	al	4 4 4 6 2 6								2 8 7	320609	1 Strip2					0384					5246	66
													Pr	proces	3 4 1								1 1													
													oc	s	2 6 7								4 6													
													ess		8 6 2																					
													es																							
													G	11308 11856 12043 12317																						
													O	12808 13367 13644 13800																						
													Bi	19_GO	- 1 3								4 0	13860 14158 16518 18706	Abi1 Arhgap6 Bcl2 Calr C											
													ol	:00099	3 . .								. .	19240 20265 20271 20410	Fer Kcnj2 Pik3ca Tmsb10											
													og	actin	. 6 5								6 6	21927 22003 22376 22379	Scn1a Scn5a Sorbs3 Tnfai									1.8		
1	0	0	M	1	0	ica	1	9	regulation of	develo	87 . 7 5 20 5 9								9 9	23970 26554 27418 50875	p1 Tpm1 Was Fmnl3 Pacsi					-					73					
1	6	0	1	1	0	l	9	9	actin	cellula	1 7 9 83 8 1 43								4 8	50884 59069 67451 68794	n2 Cul3 Mkln1 Tmod3 Nc					1.18	0	57	1	1	3.16	25				
													l	r	6 7 0 6 3 6								3 8	69693 71461 71584 71653	kap1 Tpm3 Pkp2 Flnc Pof					6465					986	
													Pr	proces	9 1 8								2 7	108058 109270 170758 170	1b Ptk7 Gdpd2 Shtn1 Cam									97		
													oc	s	8 7 1								3 2	935 211401 215789 225288	k2d Prr5 Rac3 Grid2ip Mts											
													ess		6 3 8								1 8	269587 333605 432516 54	s1 Phactr2 Fhod3 Epb41 Fr											
													es		4963																					
													G	actin	19_GO	- 1 3 20 5 9								4 0	11308 11856 12043 12317	Abi1 Arhgap6 Bcl2 Calr C					-					1.8
1	2	0	M	1	0	O	1	9	cytoskeleton	:00099	2 . . 83 3 1 38								. .	12808 13367 13644 13800	obl Diaph1 Efs Enah Eps8					0.82	0	57	0	0	3.16	73				
													Bi	organization	87 . 6 1 6 0 6								1 6	13860 14158 18706 19240	Fer Pik3ca Tmsb10 Sorbs3					2944					986	













































											7				5															
											G																			
											- G O				19_GO - 4 3				0 0											
											2 O Bi				:00325 2 . .				. .											
											. :0 ol				02 . 2 9				6 2											
											6 0 M og				1 1 6 1 0 1 9 innervation				develo 6 6 6 20 3 9 5 6				14401   16392   20346   72043   Gabrb2   Isl1   Sema3a   Sulf2				- 4.2			
											1 1 6 1 0 1 9				pment 1 5 3 83 2 1 6 5 6				77018   110886 Col25a1   Gabra5				0.80 0 74 1 1 2.61 01							
											7 0 l				al 7 0 5 6 6 0 5				1914 7561 09											
											5 3 Pr				proces 5 1 6				2 3											
											6 8 oc				s 6 0 5				1 4											
											1 4 ess				s 1 9 4				8 3											
											es																			
											G																			
											- G O				19_GO - 3 3				0 0											
											2 O Bi				:00507 2 . .				. .											
											. :0 ol				89 . 7 8				7 2											
											6 0 M og				1 1 0 0 1 9 regulation of				regulat 6 0 0 20 4 9 6 8				13411   21334   21336   68270   Dnah11   Tac2   Tacr1   Dnaaf1				- 3.7			
											1 0 0 1 0 1 9				cilium 0 2 4 83 3 1 7 4 7				69329   207686   212892   Cfap206   Cfap69   Rsph4a				0.80 0 75 1 1 2.60 02							
											1 3 l				movement 1 9 6 6 6 1 7				1914 1555 52											
											5 3 Pr				cal 5 5 4				9 3											
											5 5 oc				proces 5 5 6				2 1											
											5 2 ess				s 5 2 6				1 7											
											es																			















2	0	ol	developmen	develo	2	9	2			5	6														06			
3	2	og	t	pment	3	1	8			5	6														43			
0	1	ica		al	0	5	8			0	5																	
7	5	l		proces	7	8	3			2	3																	
4	9	Pr		s	4	8	6			1	4																	
1	1	oc			1	1	8			8	3																	
		ess																										
		es																										
		G																										
	-	G	O				-	6	4		0	0																
2	O	Bi		19_GO	2	.	.			.	.																	
.	:	ol	CD8-	:00023	.	4	4			4	2																	
5	0	M	og	76	5	9	1	20	9	3	1														6.4			
1	8	1	1	1	0	ica	1	alpha-beta T	immu	8	9	3	83	1	9	4	6	7	12043   20230   252838   54503	Bcl2   Satb1   Tox   Wdfy4	0.80	0	83	1	1	2.58	99	
3	6	1	l	9	cell	ne	3	0	5	6	6	6	8	0							1914				3728	06		
7	0	Pr	activation	system	7	6	8			8	6														43			
2	3	oc		proces	2	4	4			1	3																	
8	7	ess		s	8	3	2			2	4																	
		es																										
	-	m	KE		-	2	3			1	0																	
2	m	G	Cell adhesion		2	.	.			.	.										11658   12524   12561   14961	Alcam   Cd86   Cdh4   H2-						
.	u	M	G	2	.	1	2	20	1	9	8	4									14964   14972   15040   15042	Ab1   H2-D1   H2-K1   H2-	-				2.1	
1	5	0	1	1	0	Pa	2	molecules - Mus	muscu	5	2	6	83	8	1	17	5	4	15896   19266   19268   20969	T23   H2-	0.77	0	84	1	1	2.54	24	
4	4	th	4	musculus (house	4	4	7	6	2	6	5	5									66797   75677   192167   24544	T24   Icam2   Ptpird   Ptparf   Sdc	3206				6852	69
6	4	wa		mouse)	6	6	8			8	9	6									6   269116	1   Cntnap2   Cldn22   Nlgn1   S						41
8	5	y			8	9	9			9	2										litrk4   Nfasc							





					G																	
-	G				O	19_GO		-	3		2	0										
2	O				Bi	:00507		2	1				.	.	12043	12048	12608	13841				
.	:0				ol	89		.	1		6	5			14401	14466	15183	15505				
5	0				og	regulation of		8							14401	14466	15183	15505				2.0
1	1	M			ica	1 neuron		1	4		2	2			16392	17260	18032	18205				
1	4	1	1	0	l	9 apoptotic		1	7		83	9	1	24	0	7	18706	19268	22062	22339		-
8	3				Pr	process		8	3	6	6	6			0	7	30841	51800	58801	67784		0.74
3	5				oc			3	0						8	7	68169	100102	110886	2378		0
4	2				ess			4	2						7	0	68					1
2	3				es			2	2						3	2						1
					G	19_GO																
-	G				O	:00485		-	2	3					1							
2	O				Bi	19		2	.	.					.							
.	:0				ol	negative		.	0	1					9	.	12043	12048	12608	14401		
4	0				og	regulation of		4	3	6	20	2	9		6	4	14466	15505	16392	17260		2.0
1	6	M			ica	1 neuron		6	7	7	83	0	1	18	5	5	18032	18205	18706	22062		-
1	4	1	1	0	l	9 apoptotic		5	0	9	6	1	6		0	8	22339	30841	51800	67784		0.71
5	3				Pr	process		7	2	8					6	5	68169	110886				0
7	5				oc			8	0	2					5	7						0
8	2				ess			6	1	7					5							0
6	4				es			s														0
-	m				KE	Regulation of		-	3	3					0	0	11514	11556	16337	18706		3.1
2	m	M			G	2 lipolysis in adipocytes		2	.	.	20		5	9		.	11514	11556	16337	18706		-
1	.	u	1	1	G	- Mus musculus		.	1	5	83	7	1	8	.	.	19092	109648	210044	2308		0.72
4	0				Pa	(house mouse)		4	9	5	6	6			8	3	99					0
								4	9	5	6	6			7	0						0.072





															G																																										
-	G			O																-	3			0	0																																
2	O			Bi																2	4			.	.																																
.	:	2			ol	19_GO																.	9			5	2																														
4	0			og	positive	:00400	4	7	2	20	9	4	4																-	-	4.7																										
1	6	0	M	1	0	ica	1	9	regulation of	11	6	9	83	2	9	4	4	13488		19699		20346		71653		Drd1		Reln		Sema3a		Shtn1		-	-	38																					
3	1			l	neuron	9	8	9	83	4	6	5	5	3																0.71	0	90	1	1	2.46	90																					
9	2			Pr	migration	9	9	9																						091					3988	1																					
8	2			oc																8	0			9	1																5	4															
8	4			ess																8	1			6																	5	1															
															es																																										
															G																																										
-	G			O																-	3	3			0	0																															
2	O			Bi																2	.	.			.	.																															
.	:	0			ol	19_GO																.	8	6			6	2																													
4	0			og	potassium	92	4	9	8	20	9	5	6																-	-	3.8																										
1	4	5	M	1	0	ica	1	9	ion	4	9	1	83	3	1	6	5	6	11931		20499		98660		108058		Atp1b1		Slc12a7		Atp1a2		Ca	0.67	0	91	1	1	2.41	99																	
1	1	5			l	homeostasis	1	4	3	6	6	0	5																	110784		110895		mk2d		Nr3c2		Slc9a4	0367					298	43												
2	0			Pr																2	3	3			2	3																															
9	7			oc																9	8	7			1	4																															
8	5			ess																8	6	6			8	3																															
															es																																										
-	m			KE																-	3	3			0	0																															
2	m	M			G	2	2	.	.	20	9								11931		16337		18706		18751		Atp1b1		Insr		Pik3ca		Prkcb	-	-	99																					
1	.	u	1	1	0	G	4	.	5	4	83	8	1	6	6	2			98660		110784		Atp1a2		Nr3c2	0.58	0	91	0	0	2.41	43																									
2	0			Pa	reabsorption - Mus	2	9	2	6	6	6	5	6																5038					298	86																						













ess  
es  
G  
- G O - 2 3 1 0  
2 O Bi 2 . . . .  
. :0 ol 19\_GO . 0 1 7 4 12675 | 13860 | 18032 | 19395 | Chuk | Eps8 | Nfix | Rasgrp2 |  
3 0 M og 1 Ras protein :00230 3 9 0 20 1 9 4 3 19419 | 22376 | 50884 | 67425 | Rasgrp1 | Was | Nckap1 | Eps8l - - 2.8  
1 6 0 1 1 0 1 9 ica 9 signal 52 6 1 0 83 7 1 16 6 2 69632 | 71653 | 74055 | 74563 | 1 | Arhgef12 | Shtn1 | Plce1 | Ra 0.64 0 97 1 1 2.36 43  
3 7 1 l 9 transduction signali 3 6 7 6 4 6 7 8 109905 | 170758 | 223864 | 269 sgef1c | Rap1a | Rac3 | Rapgef3 5217 3096 34  
0 2 Pr ng 0 5 9 2 5 608 | Plekhhg5 06  
9 6 oc 9 2 3 4 0  
6 5 ess 6 9 4 9 6  
es  
G  
- G O - 2 3 0 0  
2 O Bi 2 . . . .  
. :0 ol 19\_GO . 8 1 8 3  
1 0 M og 1 Rho protein :00230 1 4 6 20 9 7 0 12675 | 13860 | 18032 | 22376 | Chuk | Eps8 | Nfix | Was | Eps8 - - 2.8  
1 6 0 1 1 0 1 9 ica 9 signal 52 6 3 7 83 6 1 8 3 7 67425 | 69632 | 71653 | 269608 11 | Arhgef12 | Shtn1 | Plekhhg5 0.54 0 97 0 0 2.36 43  
9 7 1 l 9 transduction signali 9 3 0 6 4 6 3 4 0615 3096 34  
0 2 Pr ng 0 4 5 6 2  
4 6 oc 4 0 9 2 8  
6 6 ess 6 6 7 4 9  
es





											ess															
											es															
											G															
	-	G	O	19_GO	-	1					3	0														
	2	O	Bi	:00507	2	.					.	.	11819   12192   12576   12822   Nr2f2   Zfp3611   Cdkn1b   Col													
	.	:0	ol	89	.	6					3	5	13039   13395   13489   13601   18a1   Ctst1   Dlx5   Drd2   Ecm1													
	3	0	og	regulation of	regulat	3	4	20	4	9	8	9	13618   13869   14734   15208     Ednrb   Erbb4   Gpc3   Hes5					1.9								
1	1	5	M	1	0	1	1	1	1	1	1	1	15559   16392   16568   17260   Htr2b   Isl1   Kif3a   Mef2c   Pgr					-	-	13						
	5	0	1	9	cell	ion of	1	3	83	2	1	31	4	7	18667   19014   19302   20271     Med1   Pex2   Scn5a   Sparc					0.62	0	103	1	1	2.31	27
	9	6	Pr	proliferation	biologi	5	7	8	6	9	6	2	4	20692   21336   22339   22601   Tacr1   Vegfa   Yap1   Apln   Sir					6813					5981	59	
	8	7	oc	cal	proces	8	2	4					7	6	30878   50721   69683   72043   t6   Emc10   Sulf2   Lrg1   Mtss1											
	1	8	ess	s	1	7					5	6	76905   211401   238328   Vash1													
											es															
											G															
	-	G	O		-	1					1															
	2	O	Bi	19_GO	2	.					.	0														
	.	:0	ol	:00099	.	9					9	.	12048   12140   12576   12608   Bcl2l1   Fabp7   Cdkn1b   Cebp							1.9						
	1	0	M	1	0	1	1	1	1	1	1	1	12675   12822   13039   13134   b   Chuk   Col18a1   Ctst1   Dach					-	-	13						
1	8	5	1	9	cell	cellula	8	3	83	1	1	18	5	8	13489   14734   16568   17260   1   Drd2   Gpc3   Kif3a   Mef2c					0.54	0	103	0	0	2.31	27
	3	0	1	9	proliferation	r	3	2	6	4	6	0	5	8	19014   19108   22339   22601   Med1   Prkx   Vegfa   Yap1   Mt					5337					5981	59
	8	6	Pr	proliferation	proces	8	7	7					6	9	211401   241639   ss1   Fermt1											
	6	7	oc	s	6	5					5	7														
	1	3	ess	s	1	9					5															
											es															









			G																				
	-	G	O		-	5	3			0	0												
	2	O	Bi		2	.	.			.	.												
	.	:0	ol		19_GO	.	0	6			4	2											
	1	0	og		:00400	1	5	9	20		9	3	1			-			-	5.0			
1	5	4	M	1	collateral	07	5	4	0	83	1	4	6	7	12808   13640   18032   18080	Cobl   Efna5   Nfix   Nin	0.54	0	106	0	0	2.28	54
	9	8	1	1	sprouting	growt	9	8	5	6	8	6	8					0615				4617	82
	2	6			Pr	h	2	2	3			8	6										78
	5	6			oc		5	7	2			1	3										
	9	8			ess		9	8	1			2	4										
			es																				
			G																				
	-	G	O		-	2	2			1	0												
	2	O	Bi		2	.	.																
	.	:0	ol		19_GO	.	1	8															
	1	0	og		:00400	1	4	8	20	1	9	4	3	12043   12561   12808   13640	Bcl2   Cdh4   Cobl   Efna5   Ma	-					-	5.0	
1	0	1	M	1	cell growth	07	0	2	8	83	3	1	13	1 9 17755   18032   18080   18846	p1b   Nfix   Nin   Plxna3   Sema	0.50	0	106	0	0	2.28	54	
	4	6	1	1		growt	4	8	3	6	8	6		9 0 20346   20361   50706   50721	3a   Sema7a   Postn   Sirt6   Ca	7933					4617	82	
	0	0			Pr	h	0	0	3			2	8	108058	mk2d								78
	0	4			oc		0	7	9			1	1										
	9	9			ess		9	4	4			4	6										
			es																				
	-	G	G		19_GO	-	2	3		1	0	12043   12313   12325   12576	Bcl2   Calm1   Camk2g   Cdkn1								-	2.1	
	2	O	M	1	cell cycle	:00099	2	.	.	20	1	9		. . 13860   18032   18557   19055	b   Eps8   Nfix   Cdk18   Ppp3ca	0.60	0	107	1	1	2.27	08	
1	.	:0	1	1	phase	87	.	1	0	83	6	1	15	6 4 50875   57775   66131   68431	Tmod3   Usp29   Tipin   Fbxl1							96	
	2	0			transition	cellula	2	0	3	6	2	6		3 1 108058   217232   244879	5   Camk2d   Cdc27   Npat	2139					6746	79	





















3	U	e		3	2	2				4	7									
1	-	Ge		1	0	5				1	7									
2	9	ne		2	5	5				9	3									
7	8	Set		7	9	2				2	1									
8	3	s		8	1	4				1	7									
1																				
8																				
9																				
	R																			
-	-																			
-	M	Re		-	1	2				4	0	11308	11856	12313	12638	Abi1	Arhgap6	Calm1	Cftr	
2	M	act		2	.	.				.	.	13367	17931	17978	18706	Diaph1	Ppp1r12a	Ncoa2	Pi	
.	M	o		.	5	6				1	6	18751	19387	21927	22042	k3ca	Prkcb	Rangap1	Tnfaip	
1	U	m		1	1	6	20	5	9	4	5	22143	22379	26554	50875	1	Tfrc	Tuba1b	Fmnl3	Cul3
1	-	M	6	1	1	6	20	5	9	4	5	22143	22379	26554	50875		Tmod3	Nckap1	Ddx39b	P
1	2	1	1	1	0	e	6	6	6	1	6	50884	53817	54216	59069					
1	2	1	1	1	0	e	6	6	6	1	6	50884	53817	54216	59069	cdh7	Tpm3	Cpne8	Itgb3bp	0.51
2	9	Ge		2	7	5	6	1	6	4	8	66871	67733	67784	68097		Plxnd1	Dynll2	Steap3	Lbr
2	9	ne		2	7	5	6	1	6	4	8	66871	67733	67784	68097		Plxnd1	Dynll2	Steap3	Lbr
2	4	ne		2	9	1				7	6	68428	98386	109904	17075		Mcf2	Rac3	Tor1aip1	Senp
8	4	Set		8	2	5				1	4	8	208263	223870	232943	2	1	Klc3	Arhgef9	Pde5a
8	3	Set		8	2	5				1	4	8	208263	223870	232943	2	1	Klc3	Arhgef9	Pde5a
7	3	s		7	5	1				6	1	36915	242202	269608	2699	hg5	Nup98	Scai	Ccdc187	I
7	1	s		7	5	1				6	1	36915	242202	269608	2699	hg5	Nup98	Scai	Ccdc187	I
5												66	320271	329366	544963	qgap2				
-	R	Re		-	1	2				3	0	11308	11856	12638	13367	Abi1	Arhgap6	Cftr	Diaph1	
2	-	act		2	.	.				.	.	18706	21927	22042	22143		Pik3ca	Tnfaip1	Tfrc	Tuba
.	M	o		.	6	6	20	3	9	0	5	22379	26554	50875	50884	1b	Fmnl3	Cul3	Tmod3	Nc
1	0	M	6	1	0	m	6	6	6	5	6	22379	26554	50875	50884	kap1	Ddx39b	Pcdh7	Tpm3	
1	0	M	1	1	0	m	6	6	6	5	6	53817	54216	59069	66871		Cpne8	Plxnd1	Steap3	Lbr
5	U	e		5	6	9				6	8	67784	68428	98386	109904		Cpne8	Plxnd1	Steap3	Lbr
1	-	Ge		1	5	3				7	7	170758	208263	223870	23		Mcf2	Rac3	Tor1aip1	Senp























ron reg  
proj ulat  
ecti ion  
on of  
dev biol  
elop ogi  
me cal  
nt pro  
ces  
s

neg  
ativ

e

reg

ulat

ion

of

axo

n

gro

wth

exte

nsio

n

neg

ativ

e

reg

ion

of

1  
G  
- O:  
4.9 00  
880 30  
52 51  
7

M1 1 0

GO  
Bio  
log  
ical  
Pro  
ces  
ses

19

19\_  
GO  
:00  
400  
07  
gro  
wth

-  
4.9 29.5  
8 42 07 20836 48 59  
8 93 82  
5 8  
2

4  
77 3.2  
96 729  
61 044

18846 | 20348 | 20359 |  
26456

Plxna3 | Sema3c |  
Sema6b | Sema4g

-  
2.0  
0  
2 0 1 0 0  
0  
1  
3

7.37  
47

52.318  
895

1  
- G  
4.5 O:  
295 00  
58 32

M1 1 0

GO  
Bio  
log  
ical

19

19\_  
GO  
:00  
485

-  
6.4  
4.94 17 20836 43 59  
5 75 16  
2 94

8  
.5 570  
59 968

12140 | 18846 | 20348 |  
20359 | 26456 | 109648  
| 268902 | 574402

Fabp7 | Plxna3 | Se  
ma3c | Sema6b | Se  
ma4g | Npy | Robo  
2 | Gpr17

-  
1.6  
8  
0 1 0 0  
7.37  
47

52.318  
895



ID	Gene	M	D	C	GO	Term	Count		Log2	P	FDR	Biomarkers	Pathway	Enrichment					P	FDR
							Observed	Expected						Min	Max	Mean	SD	CI		
1	G-4.00	M1	1	0	GO:19019	biological processes	4.4	1.4	13.68	0.0007	5.9e-05	Plxna3   Rbp4   Sema3c   Sema6b   Sema4g	1.68	0.0	1.0	0.0	7.37	52.318		
1	G-4.00	M1	1	0	GO:19019	biological processes	4.4	1.4	13.68	0.0007	5.9e-05	Gfap   Hspa5   H2-K1   Plxna3   Ppp3ca   Sema3c   Sema6b   Sema4g   Robo2	1.68	0.0	1.0	0.0	7.37	52.318		





1	4.2	01	M1	1	0	ical	19	regulation of plasma membrane	19_	GO	507	89	4.	2	4.5	5.	38	77	59	10	49	844	13860   14580   14828	5   H2-	1.	5	3	6	1	3	3	0	1	0	0	7.37	52.318	895
1	4.2	00	M1	1	0	log	19	regulation of biological processes	19_	GO	400	11	4.	2	8.8	6.	51	23	59	6	69	349	12317   18846   20348	Calr   Plxna3   Sema3c   Sema6b   Sema4g   Robo2	1.	5	3	5	9	0	1	0	0	7.37	52.318	895		









1	3.5	00	M1	1	0	ical	19	on	elo	5	64	72	20836	75	59	9	54	808	26456   170758   26890	Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895	
	859	31				Pro		dev	pm	8	98	77				9	54	808	26456   170758   26890	Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895	
	97	17				ces		elop	ent	9	32	7				7			2	Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895	
		5				ses		me	al	9											Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895
								nt	pro	7											Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895
								ces													Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895
								s													Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895
								reg													Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895
								ulat	19_	3.											Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895
								ion	GO	5	12.	6.									Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895
								of	:00	1	39	49									Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895
								axo	400	3	13	30									Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895
								n	07	2	17	3									Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895
								exte	gro	0											Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895
								nsio	wth	8											Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895
								n													Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Tnc   Sema4g   Rac3   Robo2	1	5	7	0	1	0	0	7.37	52.318	895

1	3.40038957	M1	1	0	19	GO	Biological Processes	regulation of neuroprogenitor cell proliferation	325	3.4	5.16094	20836	479	59	7	64	099	20348   20359   26456	Gfap   Plxna3   Pp3ca   Sema3c   Sema6b   Sema4g   Robo2	0	6	9	4	4	1	-	0	1	0	0	7.37	52.318	895
1	3.30567	M1	1	0	19	GO	Biological Processes	angioblast cell migration	099	3.78	5.5033	20836	225	59	5	45	258	13590   20348   20359   26456   320924	Lefty1   Sema3c   Sema6b   Sema4g   Ccbe1	0	3	4	4	8	-	0	1	0	0	7.37	52.318	895	



1	3.3	00	M1	1	0	ical	19	cell mor pho gen esis inv olve d in neu ron al diff ere ntia tion reg ulat ion of exte nt of cell gro wth	19_ GO :00 325 02 5 0 2 0 1	3. 3 5 0 35 34 9 1	4. 83 57 54 9	20836	48 9	59	7	64 40 7	099 087	18846   19055   20348   20359   26456   170758   268902	Plxna3   Ppp3ca   S ema3c   Sema6b   S ema4g   Rac3   Ro bo2	0 3 0 6 3 9	0 1 0 0 0	0 0 0 0 0	7.37 47	52.318 895
1	3.3	00	M1	1	0	ical	19	cell mor pho gen esis inv olve d in neu ron al diff ere ntia tion reg ulat ion of exte nt of cell gro wth	19_ GO :00 325 02 5 0 2 0 1	3. 3 5 0 35 34 9 1	4. 83 57 54 9	20836	48 9	59	7	64 40 7	099 087	18846   19055   20348   20359   26456   170758   268902	Plxna3   Ppp3ca   S ema3c   Sema6b   S ema4g   Rac3   Ro bo2	0 3 0 6 3 9	0 1 0 0 0	0 0 0 0 0	7.37 47	52.318 895
1	3.3	00	M1	1	0	ical	19	cell mor pho gen esis inv olve d in neu ron al diff ere ntia tion reg ulat ion of exte nt of cell gro wth	19_ GO :00 325 02 5 0 2 0 1	3. 3 5 0 35 34 9 1	6. 04 10 30 7	20836	12 9	59	4	6. 77 96 61	3.2 729 044	18846   20348   20359   26456	Plxna3   Sema3c   Sema6b   Sema4g	0 0 8 9 8	0 1 0 0 0	0 0 0 0 0	7.37 47	52.318 895

19_		GO		:00		neu		-		325		-		-										
G		GO		neu		325		-		-		-		-										
- O:		Bio		ral		02		3.		6.		5.		0.										
3.1 00		log		cres		dev		1 17.		82		08 2.8		9										
1	607 01	M1	1	0	ical	19	t	elo	6 36	22	20836	61	59	3	47 600	20348   20359   26456	Sema3c   Sema6b	1	0	1	0	0	7.37	52.318
	35 75				Pro		cell	pm	0 81	17					45 697		Sema4g	2					47	895
	5				ces		mig	ent	7 58	2					8			9						
					ses		rati	al	3									7						
					on		pro	ces	5									2						

19_		GO		:00		neu		-		325		-		-										
G		GO		ron		325		-		-		-		-										
- O:		Bio		proj		02		3.		4.		11		0.										
3.1 00		log		ecti		dev		1 4.6		56		.8 4.2		18846   19055   20348										
1	477 48	M1	1	0	ical	19	on	elo	4 73	00	20836	52	59	7	64 099	20359   26456   170758	Plxna3   Ppp3ca   S	9	0	1	0	0	7.37	52.318
	98 81				Pro		mor	pm	7 09	39					40 087	268902	ema3c   Sema6b   S	0					47	895
	2				ces		pho	ent	7 6	2					7		ema4g   Rac3   Ro	4						
					ses		gen	al	9								bo2	1						
					esis		pro	ces	8									5						
					ces		ces	s										2						

ID	Gene	Chromosome	Start	End	Strand	GO Term	GO ID	Count	Gene Count	Other Count	Pathway	Gene Count	Other Count	Score	Other Score										
1	G - O: 3.1 197 49 7	M1	1	0	ical	19	mesencymal cell migration processes	GO:0009987	16.81	6.69	20836	63	59	3	47	600	20348   20359   26456	Sema3c   Sema6b   Sema4g	9	0	1	0	0	7.37	52.318
1	G - O: 3.1 190 23 9	M1	1	0	ical	19	plasma membrane morphogenesis	GO:0032502	4.6	4.52	20836	53	59	7	64	099	18846   19055   20348   20359   26456   170758   268902	Plxna3   Ppp3ca   Sema3c   Sema6b   Sema4g   Rac3   Robo2	8	0	1	0	0	7.37	52.318















				ces								s																				
				posi	19_								GO																			
				19_	GO								:00																			
1	GO	19_	GO	:00																												
1	G	-	O:	2.6	00	M1	1	0	ical	19	ion	11	5	68	47	20836	63	59	7	64	099	12317 14828 19055 20348 20359 26456 320924	Calr Hspa5 Ppp3ca Sema3c Sema6b Sema4g Ccb	5	9	3	6	6	2	7.37	52.318	895
1	G	-	O:	2.5	00	M1	1	0	ical	19	ion	11	5	68	47	20836	97	59	3	47	600	20348 20359 26456	Sema3c Sema6b Sema4g	5	2	2	8	5	6	7.37	52.318	895
	G	-	O:	2.5	00	M1	1	0	ical	19	ion	11	5	68	47	20836	97	59	3	47	600	20348 20359 26456	Sema3c Sema6b Sema4g	5	2	2	8	5	6	7.37	52.318	895
	G	-	O:	2.5	00	M1	1	0	ical	19	ion	11	5	68	47	20836	97	59	3	47	600	20348 20359 26456	Sema3c Sema6b Sema4g	5	2	2	8	5	6	7.37	52.318	895
	G	-	O:	2.5	00	M1	1	0	ical	19	ion	11	5	68	47	20836	97	59	3	47	600	20348 20359 26456	Sema3c Sema6b Sema4g	5	2	2	8	5	6	7.37	52.318	895
	G	-	O:	2.5	00	M1	1	0	ical	19	ion	11	5	68	47	20836	97	59	3	47	600	20348 20359 26456	Sema3c Sema6b Sema4g	5	2	2	8	5	6	7.37	52.318	895
	G	-	O:	2.5	00	M1	1	0	ical	19	ion	11	5	68	47	20836	97	59	3	47	600	20348 20359 26456	Sema3c Sema6b Sema4g	5	2	2	8	5	6	7.37	52.318	895
	G	-	O:	2.5	00	M1	1	0	ical	19	ion	11	5	68	47	20836	97	59	3	47	600	20348 20359 26456	Sema3c Sema6b Sema4g	5	2	2	8	5	6	7.37	52.318	895
	G	-	O:	2.5	00	M1	1	0	ical	19	ion	11	5	68	47	20836	97	59	3	47	600	20348 20359 26456	Sema3c Sema6b Sema4g	5	2	2	8	5	6	7.37	52.318	895

1	2.5	00	M1	1	0	ical	19	neg ativ e reg ulat ion of cell gro wth	19_	-	2.	5	6.8	4.	50	20	59	4	6.	3.2	18846   20348   20359	Plxna3   Sema3c	5	0	1	0	0	7.37	52.318	
	587	30				Pro		ces	GO	cell	:00	400	8	33	99	6			77	729	26456	Sema6b   Sema4g	8	0				47	895	
	72	30				ses		gro	GO	ular	325	7	09	6					61	044			2							
	8							wth	GO	com	02	2									18846   20348   20359		5	0	1	0	0			
									cell	pon	dev	4	3.6	3.					11	.8	4.2	18846   19055   20348	Plxna3   Ppp3ca   S	5	0					
1	2.5	00	M1	1	0	ical	19	ular	GO	ent	elo	9	73	65	20836	67	59	7	64	099	20359   26456   170758	ema3c   Sema6b   S	0	0	1	0	0	7.37	52.318	
	490	32				Pro		com	GO	mor	pm	0	20	89		3			40	087	268902	ema4g   Rac3   Ro	5					47	895	
	88	98				ces		dev	GO	pho	ent	8	62	7					7			bo2	4							
	9					ses		ent	GO	gen	al	8											4							
								al	GO	esis	pro	8											5							
								pro	GO	ces	s																			
1	2.5	00	M1	1	0	Bio	19	ces	GO	neural	19_	-	10.	5.	10	59	3	5.	2.8		20348   20359   26456	Sema3c   Sema6b	5	0	1	0	0	7.37	52.318	
						log		ses	GO	res	:00	2.	59	50	0				47	697		Sema4g	5					47	895	







1	G	- O:	2.0 00	071 01	59 55	8	M1	1	0	ical	19	GO	reg	19_	-	2.	3.8	3.	26	20836	46	59	5	47	3.6	18846   20348   20359	21923   26456	Plxna3   Sema3c   Sema6b   Tnc   Sema4g	1	1	0	1	0	0	7.37	-	52.318									
																																						07	7	99	86	2	45	258	76	002
												GO	reg	19_	-	2.	3.8	3.	26	20836	46	59	5	47	3.6	18846   20348   20359	21923   26456	Plxna3   Sema3c   Sema6b   Tnc   Sema4g	1	1	0	1	0	0	7.37	-	52.318									
												GO	reg	19_	-	6.	6.5	7.	63	20836	64	59	12	38	403	15042   16768   17060	22042   240754   62501	22259   12260   12524	12921   14972   15040	15042   16768   17060	22042   240754   62501	C1qa   C1qb   Cd86   Crhr1   H2-K1   H2-T23   H2-T24   Lag3   Blnk   Tfrcl   Lax1   C4a	2.	6	9	4	8	9	2	0	2	1	1	6.66	-	34.453
												GO	reg	19_	-	6.	6.5	7.	63	20836	64	59	12	38	403	15042   16768   17060	22042   240754   62501	22259   12260   12524	12921   14972   15040	15042   16768   17060	22042   240754   62501	C1qa   C1qb   Cd86   Crhr1   H2-K1   H2-T23   H2-T24   Lag3   Blnk   Tfrcl   Lax1   C4a	2.	6	9	4	8	9	2	0	2	1	1	6.66	-	34.453





							(house	0													8								
							mouse)	2													4								
								4													4								
							Human	-													-								
							immunod	5.													2.								
						KE	efficiency	2	7.				11								1								
						GG	virus 1	9	10.				.8	4.2	12317		14972		15040		Calr		H2-K1		H2-	1			
1						Pat	infection -	6	30				7	64	099	15042		18706		19055		T23		H2-	2				
						hw	Mus	6	02	22	20836	24	59	40	087	170758					9	0	2	0	0	6.66	34.453		
						ay	musculus	6	82	10			7								8					2814	907		
							(house	4													4								
							mouse)	4													4								
							Antigen																						
							Presentati	-													-								
						Rea	on:	5.													2.								
						cto	Folding,	2	34.				6.								1								
						me	assembly	6	45				3.2								2								
1						Ge	and	5	39	25	20836	41	59	4	77	729	12317		14828		14972		Calr		Hspa5		H2-	2	
						ne	peptide	2	07	90					96	044	15040				9	0	2	0	0	6.66	34.453		
						Set	loading of	5		6					61						8					2814	907		
						s	class I	4													4								
							MHC																						
							Antigen	-	19.												-								
						KE	processin	5.	61	9.			8.	3.6							2.								
1						GG	g and	2	95	43	20836	90	59	5	47	258	12317		14828		14972		Calr		Hspa5		H2-	2.	
						Pat	presentati	5	86	31					45	002	15040		15042		1	0	2	0	0	6.66	34.453		
																					2						2814	907	

















1	3.6550145	000270	M1	1	0	GO	19	023	76	19	59	5	47	3.6258	14972   15040   15042   16768   22042	H2-K1   H2-T23   H2-T24   Lag3   Tfr	1	8	7	0	2	0	0	6.66	2814	34.453	907
1	3.619757	0002	M1	1	0	GO	19	023	76	31	59	6	10	3.9349	12921   14972   15040   15042   16768   22042	Crhr1   H2-K1   H2-T23   H2-T24   Lag3   Tfr	1	1	1	0	2	0	0	6.66	2814	34.453	907



gen		via		MH		C		clas		s I		via		ER		pat		hwa		y,		TA		P-		ind		epe		nde		nt		posi		19_																																				
1	3.5	724	53	00	31	M1	1	0	GO	19	0	ical	19	ion	18	2	4	5	3	GO	19_	00	485	18	pos	itiv	killi	ng	reg	3.	5	7	2	4	5	3	6.	84	57	20836	11	0	59	4	6.	77	96	61	3.2	729	044	14972	15040	15042	16768	H2-K1	H2-T23	H2-T24	Lag3	1.	1	5	7	0	2	0	0	0	6.66	2814	34.453	907



1	3.500	M1	1	0	ical	19	GO	Biological processes	19_023	-	76	3.5	23.54	8.06	20836	45	59	3	47	600	14972   15040   15042	H2-K1   H2-T23   H2-T24	5	0	2	0	0	6.66	34.453
	509				Pro		GO	log	023	-	76	3.5	23.54	8.06	20836	45	59	3	47	600	14972   15040   15042	H2-K1   H2-T23   H2-T24	7					2814	907
	848				ses		GO	log	023	-	76	3.5	23.54	8.06	20836	45	59	3	47	600	14972   15040   15042	H2-K1   H2-T23   H2-T24	8						
	4				ses		GO	log	023	-	76	3.5	23.54	8.06	20836	45	59	3	47	600	14972   15040   15042	H2-K1   H2-T23   H2-T24	9						

















ID	Gene	Region	Chromosome	Start	End	GO	Regulation	Transcription	Chromatin	Score	Score	Score	Score	Score	Score	Score	Score	Score	Score	Score						
1	G-107341	M1	1	0	19	GO:0190005	regulation of cell killing	regulation of cell killing	H2-K1 H2-T23 H2-T24 Lag3	3.00	9.13	5.40	20836	155	59	4	6.77	3.2729	14972 15040 15042 16768	H2-K1 H2-T23 H2-T24 Lag3	0	2	0	0	6.66	34.453
1	G-199524	M1	1	0	19	GO:0190005	regulation of cell killing	regulation of cell killing	H2-K1 H2-T23 H2-T24 Tfrc	2.90	8.61	5.21	20836	164	59	4	6.77	3.2729	14972 15040 15042 22042	H2-K1 H2-T23 H2-T24 Tfrc	0	2	0	0	6.66	34.453

e syst  
im em  
mu pro  
ne ces  
resp s  
ons  
e  
bas  
ed  
on  
som  
atic  
reco  
mbi  
nati  
on  
of  
im  
mu  
ne  
rece  
ptor  
s  
buil  
t  
fro









ons ces

e s

bas

ed

on

som

atic

reco

mbi

nati

on

of

in

mu

ne

rece

ptor

s

buil

t

fro

m

in

mu

nog

lob







1	-	W	M1	1	0	ath	27	activation	Wi kiP ath pathway	Complement, classical pathway	4.845979	62.321037	13.478307	208361759	5.0847458	60012259 12260 625018	C1qa C1qb C4a	1	0	3	0	0	5.265254	62.321037			
1	-	O:	M1	1	0	ical	19	effector	GO Biological Processes	immune system process	4.7283732	62.321037	6.440274	2083640859	13.548322	12259 12260 12608 14972 15040 16768 20442 625018	C1qa C1qb Cebpb H2-K1 H2-T23 Lag3 St3gal1 C4a	8	2	1	1	0	3	0	0	5.265254	62.321037





















adh biol  
esio ogi  
n cal  
pro  
ces  
s

19\_

GO

:00

reg  
ulat  
ion  
of T  
cell  
ne  
acti  
vati  
on  
pro  
ces  
s

19\_

GO

:00

leuk  
ocyt  
e  
acti  
vati  
on  
mu

-  
3.  
9  
9  
0  
3  
6  
6  
1  
2

-  
6.4  
37  
67  
66  
6

5.  
73  
11  
58  
6

20836  
38  
4

59  
7

11  
.8  
64  
40  
7

4.2  
099  
087

12524 | 12608 | 15505 |  
16768 | 19055 | 22042 |  
240754

Cd86 | Cebpb | Hs  
ph1 | Lag3 | Ppp3c  
a | Tfrc | Lax1

1.  
3  
9  
3  
4  
5  
8

-  
0  
5  
0  
0

4.01  
8593

18.266  
511

1

G  
- O:  
3.9 00  
903 50  
12 86  
3

M1

1

0

GO  
Bio  
log  
ical  
Pro  
ces  
ses

19

1

G  
- O:  
3.9 00  
151 45  
15 32  
1

M1

1

0

GO  
Bio  
log  
ical  
Pro  
ces  
ses

19

leuk  
ocyt  
e  
acti  
vati  
on  
mu

19\_  
GO  
:00

-  
3.  
9  
1  
5  
1

4.6  
46  
74  
4  
7

5.  
16  
77  
98  
7

20836  
68  
4

59  
9

15  
.2  
54  
23  
7

4.6  
808  
879

12259 | 12524 | 12608 |  
16768 | 17060 | 20442 |  
109648 | 114570 | 2407  
54

C1qa | Cd86 | Ceb  
pb | Lag3 | Blnk | S  
t3gal1 | Npy | Crip  
3 | Lax1

1.  
3  
5  
3  
7

-  
0  
5  
0  
0

4.01  
8593

18.266  
511



					ne	1																		3
					syst	5																		3
					em																			
					pro																			
					ces																			
					s																			
					19_																			
					GO																			
					:00																			
					485																			
					neg																			
					ativ																			
					neg	-																		-
				GO	e	3.																		1.
	G			Bio	reg	5	6.6						10											
	- O:			log	ulat	6	63						.1	3.9										1
1	3.5	00		ical	ion	0	25						6	69	349	12524   12608   16768								1
	603	07	M1	1	19	0	25	30	20836							18846   21923   240754								5
	97	16		Pro	of	3	55																	0
				ces	cell	9		2					49	167										0
				ses	adh	7							2											8
					esio																			9
					n																			
					ogi																			
					cal																			
					pro																			
					ces																			
					s																			

Cd86 | Cebpb | Lax1  
g3 | Plxna3 | Tnc |

18.266  
511  
8593  
4.01





1		M1	1	0	ical	19	ion	mu	2	68	13	6	59	4													
					GO		neg	ativ	19_																		
	G				Bio		ativ	GO																			
	- O:				log		ativ	:00																			
	3.2 00				ical	19	ion	mu	2	38	24	20836	13	59	4	6.	3.2	12524   12608   16768	Cd86   Cebpb   La	5	0	5	0	0	4.01	18.266	
	229 50	M1	1	0	Pro	19	of T	ne	2	68	13							240754	g3   Lax1	4	0	5	0	0	4.01	511	
	79 86				ces		cell	syst	9	39	6							044		0					8593		
	8				ses		acti	em	7									61		0							
							vati	pro	9											0							
							on	ces												0							
								s												0							
	G				GO		neg	ativ	19_																		
	- O:				Bio		ativ	GO																			
	3.1 00				log		ativ	:00																			
	867 02	M1	1	0	ical	19	reg	023	3.	4.7	4.								11	0.	0.						18.266
	82 68				Pro	19	ulat	76	1	44	29	20836	52	59	7	.8	4.2	12524   12608   16768	Cd86   Cebpb   La	9	0	5	0	0	4.01	511	
	3				ces		ion	im	8	85	25							74511   109648   24075	g3   Lrrc17   Npy	3	0	5	0	0	4.01	511	
					ses		of	mu	6	18	3							4   574402	Lax1   Gpr17	0					8593		
									7											6							

























1	2.1	19	M1	1	0	ical	19	leuk	reg	0	81	06	20836	27	59	4	6.	3.2	12524	15505	19055	Cd86	Hsph1	Pp	8	0	5	0	0	4.01	18.266	
	000	03				Pro		ocyt	ulat	0	33	07		8			77	729	22042			p3ca	Tfrc	1					8593	511		
	03	03				ces		e	ion	0	15	8					61	044						2								
	9					ses		cell-	of	0													9									
								cell	biol	3													9									
								adh	ogi																							
								esio	cal																							
								n	pro																							
								ces																								
								s																								
								reg	19_	-	4.9						6.															
								ulat	GO	2.	21	3.					77	3.2	12524	12608	19055	Cd86	Cebpb	Pp	0.							
								ion	:00	0	98	51					96	729	22042			p3ca	Tfrc	1								
								of	507	5	67						61	044						3								











1	2.7	193	37	89	52	76	M1	1	0	6	Peptide ligand-binding receptors	7	7.5	41	20836	18	59	4	6.	3.2	77	729	044	61	12854   23919   30878   109648	Cort   Insl5   Apln   Npy	2	4	2	8	4	0	6	0	0	3.92	106	24.638	549
1	2.4	706	63	1			M1	1	0	19	GO Biological Processes	2.	4.	74	20836	10	59	3	5.	2.8	08	600	45	8	12921   30878   109648	Crhr1   Apln   Npy	4	9	6	2	7	0	6	0	0	3.92	106	24.638	549











1	3.4676356	0042596	M1	1	0	ical	19	resp	ons	e	to	org	ani	sm	al	pro	ces	s	19_	GO	:00	325	01	-	mu	3.	7.	5.	08	2.8	600	12921 18013 72585	Crhr1 Neurod2 Lypd1	0	1	0	8	0	0	0	3.64	9852	22.072	034
1	2.1	00	M1	1	0	Bio	19	resp	ons	e	to	org	ani	sm	al	pro	ces	s	19_	GO	:00	1	-	mu	2.	7.7	4.	5.	2.8	600	16477 18013 19055	Junb Neurod2 Ppp3ca	0.	1	0	8	0	0	0	3.64	9852	22.072	034	



1	2.5796583	0046883	M1	1	0	ical	19	GO	Biological Processes	regulation of hormone production	19_0051179	-	2.5796583	4.1812	20836	337	59	5	45	258	12921   16322   19055   19662   30878	Crhr1   Inha   Ppp3ca   Rbp4   Apln	2	0	9	0	0	3.24	18.586	976
1	2.1177230	0046660	M1	1	0	ical	19	GO	Biological Processes	female sex differentiation	19_0022414	-	2.1177230	4.1167	20836	142	59	3	47	600	12608   16322   19662	Cebpb   Inha   Rbp4	9	0	9	0	0	3.24	18.586	976
1	2.066308	00010	M1	1	0	ical	19	GO	Biological Processes	regulation of	19_00650	-	2.066308	3.7045	20836	629	59	6	169	349	12921   16322   19055   19662   30878   105349	Crhr1   Inha   Ppp3ca   Rbp4   Apln   Akr1c18	0	0	9	0	0	3.24	18.586	976











inte  
rsp  
ecie  
s  
inte  
ract  
ion  
bet  
we  
en  
org  
ani  
sms  
19\_  
defe  
nse  
:00  
resp  
ons  
e to  
biol  
ogi  
cal  
pro  
ces  
bact  
eriu  
m  
olv

1	2.8	00	M1	1	0	ical	19	444	-	2.	8.0	4.	17	59	4	6.	3.2	17472   55932   78416	Gbp4   Gbp3   Rna	9	0	11	0	0	3.20	8.0261
	071	50				Pro		19	19	8	19	81	20836	6	77	729	109648		se6   Npy	9					5875	941
		83				ces		444		7	41	86			61	044				5						
		0				ses		19		1		2								1						
								19												6						











ID	Gene	M	C	GO	Term	P	Gene					Pathway	P	Q	R	S	T	U	V	W							
							1	2	3	4	5										6	7	8	9			
1	G-0:3.00045362541	M1	1	0	ical	19	em	elo	325	3.0	6.6	4.95	20836	26	59	5	45	258	12654 19662 21923 116701 320924	Chil1 Rbp4 Tnc Fgfrl1 Ccbe1	5	0	13	1	1	3.04	6.6884
1	G-0:2.300678394	M1	1	0	ical	19	elop	me	325	2.3	6.0	4.14	20836	23	59	4	77	729	12654 19662 21923 320924	Chil1 Rbp4 Tnc Ccbe1	8	0	13	0	0	3.04	6.6884













1	2.0	766	4	10	1	M1	1	0	ical	19	GO	Biological Processes	hway negative regulation of transcription	GO	19_00230	230	52	52	230	20836	14	7	59	3	47	600	13590	14828	71753	Lefty1   Hspa5   Tmprss6	1	5	9	8	7	0	16	0	0	0	2.67	6921	9.9948	833
---	-----	-----	---	----	---	----	---	---	------	----	----	----------------------	---	----	----------	-----	----	----	-----	-------	----	---	----	---	----	-----	-------	-------	-------	--------------------------	---	---	---	---	---	---	----	---	---	---	------	------	--------	-----















**Supplementary Table 6 Sequence of all primers used**

---

<b>Primer name</b>	<b>Primer sequence(5'to3')</b>
H2-T24 forward	GCAACATGAGGCACTAACGCAG
H2-T24 reverse	GGAAACGCAAGGACACTCAGCA
Tfrc forward	GAAGTCCAGTGTGGGAACAGGT
Tfrc reverse	CAACCACTCAGTGGCACCAACA
Rac3 forward	ACACACCCATCCTTCTGGTG
Rac3 reverse	AGGTACTIONGACGGAACCAATCTC
$\beta$ -Actin forward	CATTGCTGACAGGATGCAGAAGG
$\beta$ -Actin reverse	TGCTGGAAGGTGGACAGTGAGG

---