Supplementary File S1: Comprehensive details about the different steps of pre-processing and ana

Geo_accession_number	Sample_ID	Sample_description	Raw_reads	Clean_reads
GSM1254084	Milk-mRNA-TC-1-001	0_hour_control_animal_1	20,718,878	19111093.07
GSM1254085	Milk-mRNA-TC-1-002	12_hour_control_animal_1	19,811,944	18514261.67
GSM1254086	Milk-mRNA-TC-1-003	24_hour_control_animal_1	25,858,517	24257874.8
GSM1254087	Milk-mRNA-TC-1-004	36_hour_control_animal_1	18,640,732	17559569.54
GSM1254088	Milk-mRNA-TC-1-005	48_hour_control_animal_1	17,609,857	16202829.43
GSM1254089	Milk-mRNA-TC-2-001	0_hour_control_animal_2	33,798,892	31879114.93
GSM1254090	Milk-mRNA-TC-2-002	12_hour_control_animal_2	17,280,881	16356353.87
GSM1254091	Milk-mRNA-TC-2-003	24_hour_control_animal_2	52,006,852	49130873.08
GSM1254092	Milk-mRNA-TC-2-004	36_hour_control_animal_2	27,355,722	25252066.98
GSM1254093	Milk-mRNA-TC-2-005	48_hour_control_animal_2	9,829,401	9306476.867
GSM1254094	Milk-mRNA-TC-3-001	0_hour_control_animal_3	17,143,701	16283087.21
GSM1254095	Milk-mRNA-TC-3-002	12_hour_control_animal_3	18,841,300	17742852.21
GSM1254096	Milk-mRNA-TC-3-003	24_hour_control_animal_3	12,573,120	11782270.75
GSM1254097	Milk-mRNA-TC-3-004	36_hour_control_animal_3	15,470,012	14275727.07
GSM1254098	Milk-mRNA-TC-3-005	48_hour_control_animal_3	36,051,781	33373133.67
GSM1254099	Milk-mRNA-TC-4-001	0_hour_control_animal_4	17,968,186	16785879.36
GSM1254100	Milk-mRNA-TC-4-002	12_hour_control_animal_4	12,002,000	11182263.4
GSM1254101	Milk-mRNA-TC-4-003	24_hour_control_animal_4	19,366,295	18080373.01
GSM1254102	Milk-mRNA-TC-4-004	36_hour_control_animal_4	45,770,860	43395352.37
GSM1254103	Milk-mRNA-TC-4-005	48_hour_control_animal_4	43,264,871	40141147.31
GSM1254104	Milk-mRNA-TC-5-001	0_hour_control_animal_5	24,902,268	23490309.4
GSM1254105	Milk-mRNA-TC-5-002	12_hour_control_animal_5	38,440,720	36334168.54
GSM1254106	Milk-mRNA-TC-5-003	24_hour_control_animal_5	70,750,168	67134834.42
GSM1254107	Milk-mRNA-TC-5-004	36_hour_control_animal_5	66,078,829	61552429.21
GSM1254108	Milk-mRNA-TC-5-005	48_hour_control_animal_5	77,385,014	72502019.62
GSM1254109	Milk-mRNA-TI-1-001	0_hour_infected_animal_1	18,370,591	17110368.46
GSM1254110	Milk-mRNA-TI-1-002	12_hour_infected_animal_1	24,563,421	22689231.98
GSM1254111	Milk-mRNA-TI-1-003	24_hour_infected_animal_1	70,796,017	65606668.95
GSM1254112	Milk-mRNA-TI-1-004	36_hour_infected_animal_1	38,934,888	36587114.25
GSM1254113	Milk-mRNA-TI-1-005	48_hour_infected_animal_1	116,133,346	108120145.1
GSM1254119	Milk-mRNA-TI-3-001	0_hour_infected_animal_3	55,867,931	52258862.66
GSM1254120	Milk-mRNA-TI-3-002	12_hour_infected_animal_3	44,902,024	42423432.28
GSM1254122	Milk-mRNA-TI-3-004	36_hour_infected_animal_3	53,998,739	51234003.56
GSM1254123	Milk-mRNA-TI-3-005	48_hour_infected_animal_3	39,319,518	36810932.75
GSM1254124	Milk-mRNA-TI-4-001	0_hour_infected_animal_4	49,159,957	45949811.81
GSM1254125	Milk-mRNA-TI-4-002	12_hour_infected_animal_4	66,381,407	61920576.45
GSM1254126	Milk-mRNA-TI-4-003	24_hour_infected_animal_4	38,731,025	36267731.81
GSM1254127	Milk-mRNA-TI-4-004	36_hour_infected_animal_4	86,666,760	80756086.97
GSM1254128	Milk-mRNA-TI-4-005	48_hour_infected_animal_4	54,446,900	51283535.11
GSM1254129	Milk-mRNA-TI-5-001	0_hour_infected_animal_5	83,696,307	78875399.72
GSM1254130	Milk-mRNA-TI-5-002	12_hour_infected_animal_5	72,428,423	68705602.06
GSM1254131	Milk-mRNA-TI-5-003	24_hour_infected_animal_5	61,824,286	58578510.99
GSM1254132	Milk-mRNA-TI-5-004	36_hour_infected_animal_5	41,858,195	39489021.16
GSM1254133	Milk-mRNA-TI-5-005	48_hour_infected_animal_5	50,193,787	46891035.82

lysis of RNA-seq data

Clean_reads (%)	uniquely_aligned_reads	uniquely_aligned_reads (%)	Overall_mapping_rate (%)
92.24%	17964427.48	94.00%	96.00%
93.45%	17403405.97	94.00%	98.00%
93.81%	22559823.56	93.00%	97.00%
94.20%	16330399.68	93.00%	99.00%
92.01%	15230659.66	94.00%	99.00%
94.32%	29328785.74	92.00%	98.00%
94.65%	15211409.1	93.00%	96.00%
94.47%	45691711.97	93.00%	97.00%
92.31%	23484422.29	93.00%	97.00%
94.68%	8561958.717	92.00%	98.00%
94.98%	14980440.23	92.00%	97.00%
94.17%	16678281.08	94.00%	96.00%
93.71%	11075334.51	94.00%	99.00%
92.28%	13276426.18	93.00%	98.00%
92.57%	31370745.65	94.00%	98.00%
93.42%	15778726.6	94.00%	96.00%
93.17%	10287682.33	92.00%	96.00%
93.36%	16814746.9	93.00%	96.00%
94.81%	40357677.7	93.00%	96.00%
92.78%	36929855.53	92.00%	97.00%
94.33%	21845987.75	93.00%	98.00%
94.52%	33790776.75	93.00%	98.00%
94.89%	62435396.01	93.00%	99.00%
93.15%	56628234.88	92.00%	99.00%
93.69%	67426878.24	93.00%	97.00%
93.14%	16083746.35	94.00%	96.00%
92.37%	21327878.06	94.00%	98.00%
92.67%	60358135.44	92.00%	99.00%
93.97%	34026016.26	93.00%	99.00%
93.10%	99470533.52	92.00%	96.00%
93.54%	49123330.9	94.00%	98.00%
94.48%	39878026.34	94.00%	97.00%
94.88%	47135283.28	92.00%	98.00%
93.62%	34234167.46	93.00%	96.00%
93.47%	42733324.98	93.00%	98.00%
93.28%	58205341.86	94.00%	98.00%
93.64%	33366313.27	92.00%	99.00%
93.18%	75103160.88	93.00%	97.00%
94.19%	48206523	94.00%	97.00%
94.24%	74142875.73	94.00%	97.00%
94.86%	63896209.91	93.00%	96.00%
94.75%	54478015.22	93.00%	98.00%
94.34%	36724789.68	93.00%	98.00%
93.42%	43139752.95	92.00%	96.00%

Supplementary_File_S1: Comprehensive details about the different steps of pre-processing and an

Geo_accession_number	Sample_ID	Sample_description	Raw_reads	Clean_reads
GSM1253773	Milk-miRNA-TC-1-001	0_hour_control_animal_1	17,331,105	14,877,021
GSM1253774	Milk-miRNA-TC-1-002	12_hour_control_animal_1	28,014,725	23,902,163
GSM1253775	Milk-miRNA-TC-1-003	24_hour_control_animal_1	20,528,511	17,246,002
GSM1253776	Milk-miRNA-TC-1-004	36_hour_control_animal_1	26,412,904	22,810,184
GSM1253777	Milk-miRNA-TC-1-005	48_hour_control_animal_1	17,831,552	15,504,534
GSM1253778	Milk-miRNA-TC-2-001	0_hour_control_animal_2	25,328,242	21,328,913
GSM1253779	Milk-miRNA-TC-2-002	12_hour_control_animal_2	14,583,126	12,271,701
GSM1253780	Milk-miRNA-TC-2-003	24_hour_control_animal_2	11,852,859	10,136,565
GSM1253781	Milk-miRNA-TC-2-004	36_hour_control_animal_2	7,941,655	6,805,204
GSM1253782	Milk-miRNA-TC-2-005	48_hour_control_animal_2	18,391,794	15,763,607
GSM1253783	Milk-miRNA-TC-3-001	0_hour_control_animal_3	40,359,797	34,019,273
GSM1253784	Milk-miRNA-TC-3-002	12_hour_control_animal_3	22,496,712	19,153,701
GSM1253785	Milk-miRNA-TC-3-003	24_hour_control_animal_3	22,180,912	19,155,436
GSM1253786	Milk-miRNA-TC-3-004	36_hour_control_animal_3	11,916,844	10,234,186
GSM1253787	Milk-miRNA-TC-3-005	48_hour_control_animal_3	16,974,932	14,515,264
GSM1253788	Milk-miRNA-TC-4-001	0_hour_control_animal_4	19,737,101	17,001,539
GSM1253789	Milk-miRNA-TC-4-002	12_hour_control_animal_4	53,992,816	46,779,376
GSM1253790	Milk-miRNA-TC-4-003	24_hour_control_animal_4	42,174,080	36,602,884
GSM1253791	Milk-miRNA-TC-4-004	36_hour_control_animal_4	19,631,471	16,722,087
GSM1253792	Milk-miRNA-TC-4-005	48_hour_control_animal_4	24,263,976	20,580,704
GSM1253793	Milk-miRNA-TC-5-001	0_hour_control_animal_5	16,258,605	13,912,488
GSM1253794	Milk-miRNA-TC-5-002	12_hour_control_animal_5	14,296,183	12,010,223
GSM1253795	Milk-miRNA-TC-5-003	24_hour_control_animal_5	17,382,527	14,663,900
GSM1253796	Milk-miRNA-TC-5-004	36_hour_control_animal_5	12,605,875	10,834,750
GSM1253797	Milk-miRNA-TC-5-005	48_hour_control_animal_5	17,434,308	14,935,972
GSM1253798	Milk-miRNA-TI-1-001	0_hour_infected_animal_1	18,912,613	15,969,810
GSM1253799	Milk-miRNA-TI-1-002	12_hour_infected_animal_1	11,261,766	9,766,203
GSM1253800	Milk-miRNA-TI-1-003	24_hour_infected_animal_1	36,023,074	30,331,428
GSM1253801	Milk-miRNA-TI-1-004	36_hour_infected_animal_1	24,112,155	20,649,650
GSM1253802	Milk-miRNA-TI-1-005	48_hour_infected_animal_1	4,579,416	3,979,970
GSM1253808	Milk-miRNA-TI-3-001	0_hour_infected_animal_3	651,418	547,973
GSM1253809	Milk-miRNA-TI-3-002	12_hour_infected_animal_3	532,806	462,049
GSM1253811	Milk-miRNA-TI-3-004	36_hour_infected_animal_3	25,093,076	21,534,878
GSM1253812	Milk-miRNA-TI-3-005	48_hour_infected_animal_3	24,657,275	21,064,710
GSM1253813	Milk-miRNA-TI-4-001	0_hour_infected_animal_4	61,575,773	51,920,692
GSM1253814	Milk-miRNA-TI-4-002	12_hour_infected_animal_4	30,843,483	26,429,781
GSM1253815	Milk-miRNA-TI-4-003	24_hour_infected_animal_4	11,136,199	9,388,929
GSM1253816	Milk-miRNA-TI-4-004	36_hour_infected_animal_4	13,095,699	11,208,609
GSM1253817	Milk-miRNA-TI-4-005	48_hour_infected_animal_4	19,698,731	17,031,523
GSM1253818	Milk-miRNA-TI-5-001	0_hour_infected_animal_5	20,994,557	18,103,607
GSM1253819	Milk-miRNA-TI-5-002	12_hour_infected_animal_5	38,614,345	32,656,152
GSM1253820	Milk-miRNA-TI-5-003	24_hour_infected_animal_5	12,954,574	11,073,570
GSM1253821	Milk-miRNA-TI-5-004	36_hour_infected_animal_5	24,631,897	21,368,171
GSM1253822	Milk-miRNA-TI-5-005	48_hour_infected_animal_5	7,068,913	6,052,403

alysis of miRNA-seq data

Clean_reads (%)	uniquely_aligned_reads	uniquely_aligned_reads (%)	Overall_mapping_rate (%)
85.84%	13091778.07	88.00%	96.00%
85.32%	21033903.77	88.00%	96.00%
84.01%	15004021.82	87.00%	97.00%
86.36%	20072961.83	88.00%	98.00%
86.95%	13799035.67	89.00%	98.00%
84.21%	18556153.95	87.00%	95.00%
84.15%	10799096.47	88.00%	95.00%
85.52%	9021542.865	89.00%	96.00%
85.69%	5988579.669	88.00%	97.00%
85.71%	13871973.84	88.00%	98.00%
84.29%	30277152.87	89.00%	97.00%
85.14%	17046793.53	89.00%	97.00%
86.36%	16665228.97	87.00%	98.00%
85.88%	9006083.352	88.00%	98.00%
85.51%	12628279.99	87.00%	98.00%
86.14%	15131369.53	89.00%	95.00%
86.64%	41633644.45	89.00%	96.00%
86.79%	32210537.95	88.00%	95.00%
85.18%	14548215.69	87.00%	96.00%
84.82%	18316826.95	89.00%	96.00%
85.57%	12242989.7	88.00%	97.00%
84.01%	10568996.54	88.00%	97.00%
84.36%	12904231.8	88.00%	95.00%
85.95%	9642927.111	89.00%	98.00%
85.67%	13293014.78	89.00%	96.00%
84.44%	13893735.06	87.00%	98.00%
86.72%	8594259.058	88.00%	95.00%
84.20%	26994971.19	89.00%	96.00%
85.64%	18378188.09	89.00%	95.00%
86.91%	3462574.288	87.00%	95.00%
84.12%	487695.8112	89.00%	97.00%
86.72%	401982.946	87.00%	97.00%
85.82%	18950692.48	88.00%	96.00%
85.43%	18536944.83	88.00%	98.00%
84.32%	45690208.78	88.00%	96.00%
85.69%	23522504.72	89.00%	95.00%
84.31%	8168368.558	87.00%	98.00%
85.59%	9863575.721	88.00%	98.00%
86.46%	14987740.08	88.00%	95.00%
86.23%	16112209.79	89.00%	95.00%
84.57%	28410851.86	87.00%	97.00%
85.48%	9634005.774	87.00%	96.00%
86.75%	18803990.17	88.00%	96.00%
85.62%	5326114.913	88.00%	95.00%

Supplementary File S2: Information about identifying and removing outliers of RNA-seq d

Sample	Outlier_color	Standardized_connectivity_score
CN_00H_01	black	0.587585589
CN_00H_02	black	0.182584432
CN_00H_03	black	0.598669536
CN_00H_04	black	0.56761654
CN_00H_05	black	0.642335621
CN_12H_01	black	0.600621986
CN_12H_02	black	0.37379024
CN_12H_03	black	0.63376144
CN_12H_04	black	0.400496108
CN_12H_05	black	0.564408509
CN_24H_01	red	-4.993607921
CN_24H_02	black	0.219212374
CN_24H_03	black	0.604887696
CN_24H_04	black	0.099484033
CN_24H_05	black	0.654066893
CN_36H_01	black	0.380765988
CN_36H_02	black	0.345497506
CN_36H_03	black	0.723367876
CN_36H_04	black	-0.519991927
CN_36H_05	black	0.103122047
CN_48H_01	black	0.535926774
CN_48H_02	black	0.31397123
CN_48H_03	black	0.51140855
CN_48H_04	black	0.44339452
CN_48H_05	black	0.681020323
INF_00H_01	black	-0.448461887
INF_00H_03	black	-0.485562444
INF_00H_04	black	0.464510726
INF_00H_05	black	0.607730931
INF_12H_01	black	-0.856200677
INF_12H_03	black	-0.401676515
INF_12H_04	black	0.629825902
INF_12H_05	black	0.555584571
INF_24H_01	black	-0.661985948
INF_24H_04	black	0.603374867
INF_24H_05	black	0.637767057
INF_36H_01	black	-1.253586742
INF_36H_03	black	-1.761281576
INF_36H_04	black	-1.60290013
INF_36H_05	black	-0.086094493
INF_48H_01	black	-0.164702656
INF_48H_03	black	-0.232846883
INF_48H_04	black	-0.900073636
INF_48H_05	black	0.102183568

data (samples with a standardized connectivity score < −2.5 were highlighted).

Supplementary File S2: Information about identifying and removing outliers of miRNA-seq data (sa

Sample	Outlier_color	Standardized_connectivity_score
CN_00H_01	black	0.342795086
CN_00H_02	red	-4.299823069
CN_00H_03	black	0.504906398
CN_00H_04	black	0.475546353
CN_00H_05	black	-0.241731243
CN_12H_01	black	0.468979478
CN_12H_02	black	-0.120882373
CN_12H_03	black	0.573135815
CN_12H_04	black	0.227452125
CN_12H_05	black	0.521643287
CN_24H_01	black	0.446643586
CN_24H_02	red	-2.952312951
CN_24H_03	black	0.486472693
CN_24H_04	black	-1.231344463
CN_24H_05	black	0.568491068
CN_36H_01	black	0.480401137
CN_36H_02	black	0.455921545
CN_36H_03	black	0.537696531
CN_36H_04	black	0.145889204
CN_36H_05	black	0.370949844
CN_48H_01	black	0.087321734
CN_48H_02	black	0.425308726
CN_48H_03	black	0.452389742
CN_48H_04	black	0.4656504
CN_48H_05	black	0.447834403
INF_00H_01	black	-0.234468252
INF_00H_03	black	-1.949638241
INF_00H_04	black	0.405147896
INF_00H_05	black	0.519524721
INF_12H_01	black	-0.183842322
INF_12H_03	black	-2.072777047
INF_12H_04	black	0.071738776
INF_12H_05	black	0.450945595
INF_24H_01	black	0.523253206
INF_24H_04	black	0.32582699
INF_24H_05	black	0.52396831
INF_36H_01	black	0.322969537
INF_36H_03	black	-0.039153803
INF_36H_04	black	-0.105765596
INF_36H_05	black	0.355691181
INF_48H_01	black	0.500038343
INF_48H_03	black	0.353844529
INF_48H_04	black	0.279711663
INF_48H_05	black	0.313649458

amples with a standardized connectivity score < −2.5 were highlighted).

Supplementary File S3: appropriate soft threshold powers for RNA-seq-based matrix

Power	SFT.R.sq	slope	uncated.R.s	mean.k.	median.k.	max.k.
1	0.101854	9.143898	0.944886	4697.058	4679.898	5090.602
2	0.175488	4.971992	0.915615	2732.366	2750.128	3188.629
3	0.085777	1.350864	0.87585	1740.856	1741.237	2349.288
4	0.013307	0.291977	0.790292	1183.296	1167.863	1855.334
5	0.079213	-0.51252	0.776381	844.2439	819.6119	1549.651
6	0.308867	-0.89472	0.821611	625.4011	594.7772	1325.455
7	0.481716	-1.08513	0.857493	477.3329	442.6908	1152.702
8	0.587929	-1.17837	0.891056	373.2521	335.5577	1016.872
9	0.651775	-1.25902	0.907466	297.7516	256.8224	905.56
10	0.690744	-1.32064	0.919791	241.5234	200.5027	812.5448
11	0.720931	-1.35379	0.931776	198.7062	157.6355	733.6391
12	0.74556	-1.37787	0.942856	165.4763	125.4166	665.8934
13	0.762416	-1.41504	0.949222	139.2616	100.114	607.1533
14	0.778003	-1.4395	0.955717	118.2847	80.60785	555.7985
15	0.787671	-1.46186	0.96152	101.2888	65.44997	510.5816
16	0.798155	-1.47793	0.967343	87.36592	53.47542	470.5232
18	0.807496	-1.51513	0.97065	66.23707	36.00195	402.9059
19	0.810826	-1.53791	0.970439	58.15294	29.78609	374.1977
20	0.815668	-1.55254	0.973513	51.30475	24.90469	348.2898
21	0.824861	-1.55928	0.977894	45.46578	20.75476	324.8253
22	0.830408	-1.56795	0.979832	40.4577	17.59585	303.5041
23	0.833691	-1.57189	0.981647	36.13883	14.92471	284.0721
24	0.836964	-1.58016	0.982806	32.39556	12.68326	266.3125
25	0.839541	-1.58514	0.983845	29.13607	10.80145	250.0395
26	0.839272	-1.59452	0.983276	26.28556	9.254207	235.0926
27	0.840414	-1.59978	0.982982	23.78267	7.92939	221.3331
28	0.841379	-1.60386	0.982483	21.57674	6.815265	208.6401
29	0.841804	-1.60989	0.981738	19.62567	5.874364	196.9077
30	0.845777	-1.61138	0.981928	17.89429	5.066654	186.0431

Supplementary File S3: appropriate soft threshold powers for miRNA-seq-based matrix

Power	SFT.R.sq	slope	uncated.R.s	mean.k.	median.k.	max.k.
1	0.740675	5.482195	0.81684	174.3791	178.879	199.8511
2	0.128873	0.785777	0.654867	99.67238	102.6416	132.9855
3	0.222015	-0.76164	0.732618	60.142	60.96055	93.50137
4	0.611841	-1.3123	0.843632	37.92397	37.25778	68.067
5	0.767718	-1.42591	0.955712	24.81595	23.24931	50.85509
7	0.86888	-1.52346	0.928604	11.64748	9.889038	30.127
8	0.844447	-1.46306	0.849317	8.295858	6.693764	23.75244
9	0.835298	-1.41904	0.819336	6.041869	4.564141	18.97823
10	0.897584	-1.38973	0.89501	4.489613	3.318213	15.3433
11	0.928728	-1.35897	0.923971	3.397388	2.45043	12.53472
12	0.946152	-1.33701	0.945757	2.613652	1.79006	10.33557
13	0.956992	-1.34338	0.953245	2.041101	1.334426	8.781388
14	0.967039	-1.37141	0.968737	1.615884	0.999564	7.573914
15	0.916614	-1.43016	0.917148	1.295268	0.773255	6.580455
16	0.947355	-1.4484	0.960851	1.050123	0.595531	5.753756
17	0.893118	-1.49125	0.917821	0.860256	0.462213	5.05892
18	0.817353	-1.55469	0.818221	0.711444	0.375304	4.469751
19	0.893672	-1.53036	0.927377	0.593523	0.307761	3.966281
20	0.867478	-1.55842	0.898552	0.499126	0.242412	3.533078
21	0.256888	-2.87182	0.16351	0.42285	0.198273	3.158053
22	0.255675	-2.8229	0.168756	0.360676	0.160171	2.831621
23	0.257	-2.79572	0.170686	0.309587	0.129662	2.5461
24	0.256954	-2.74545	0.17274	0.267292	0.102721	2.295267
25	0.256739	-2.70682	0.170031	0.232032	0.082876	2.074034
26	0.904043	-1.44425	0.93868	0.202445	0.068348	1.878209
27	0.915388	-1.42744	0.953174	0.177468	0.057258	1.704304
28	0.894149	-1.4045	0.915066	0.156263	0.047482	1.549404
29	0.890335	-1.39136	0.899743	0.138165	0.039113	1.411052
30	0.897387	-1.36778	0.908717	0.122641	0.032177	1.287165

Supplementary File S4: Details about RNA-seq modules

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ENSBTAG00000009101	SH2B3	5	green
ENSBTAG00000009112	TRAM2	5	green
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ENSBTAG00000039601	SAP25	11	greenyellow
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ENSBTAG00000000524	CSTB	0	grey
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ENSBTAG00000000581	DOCK10	0	grey
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ENSBTAG00000000833	TAX1BP3	0	grey
ENSBTAG00000000897	IQGAP2	0	grey
ENSBTAG00000000959	ZSWIM1	0	grey
ENSBTAG00000001066	PILRA	0	grey
ENSBTAG00000001083	MAP3K20	0	grey
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ENSBTAG00000004297	ACOXL	0	grey
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ENSBTAG00000046700	NA	1	turquoise
ENSBTAG00000046701	FRAT2	1	turquoise
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ENSBTAG00000046724	CBX6	1	turquoise
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ENSBTAG00000046765	POLR2A	1	turquoise
ENSBTAG00000046773	MCOLN2	1	turquoise
ENSBTAG00000046841	IRF2BP2	1	turquoise
ENSBTAG00000046862	MARCKSL1	1	turquoise
ENSBTAG00000046885	NA	1	turquoise
ENSBTAG00000046900	GGT1	1	turquoise
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ENSBTAG00000046941	LOC786015	1	turquoise
ENSBTAG00000046956	STYX	1	turquoise
ENSBTAG00000046981	NA	1	turquoise
ENSBTAG00000047030	LOC515276	1	turquoise
ENSBTAG00000047055	NA	1	turquoise
ENSBTAG00000047059	TIMM17A	1	turquoise
ENSBTAG00000047077	ENTPD7	1	turquoise
ENSBTAG00000047088	NA	1	turquoise
ENSBTAG00000047093	NA	1	turquoise
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ENSBTAG00000047128	NA	1	turquoise
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ENSBTAG00000047158	LRFN1	1	turquoise
ENSBTAG00000047166	SH2D7	1	turquoise
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ENSBTAG00000047206	H1-4	1	turquoise
ENSBTAG00000047213	GPRASP1	1	turquoise
ENSBTAG00000047238	ITGAM	1	turquoise
ENSBTAG00000047275	NA	1	turquoise
ENSBTAG00000047293	NRIP1	1	turquoise
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ENSBTAG00000047338	DCBLD1	1	turquoise
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ENSBTAG00000047341	LOC100299503	1	turquoise
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ENSBTAG00000047367	CMTR2	1	turquoise
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ENSBTAG00000047383	LOC784305	1	turquoise
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ENSBTAG00000047432	LOC781224	1	turquoise
ENSBTAG00000047448	C25H16orf54	1	turquoise
ENSBTAG00000047473	LOC100301263	1	turquoise

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ENSBTAG00000047495	CD81	1	turquoise
ENSBTAG00000047502	FKBP5	1	turquoise
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ENSBTAG00000047534	NA	1	turquoise
ENSBTAG00000047538	RIMBP3B	1	turquoise
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ENSBTAG00000047676	PRODH	1	turquoise
ENSBTAG00000047680	IRF7	1	turquoise
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ENSBTAG00000048184	NA	1	turquoise
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ENSBTAG00000001231	CDHR1	4	yellow
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ENSBTAG00000001298	STAMBPL1	4	yellow
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ENSBTAG00000001471	POC1A	4	yellow
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ENSBTAG00000001631	KIFC1	4	yellow
ENSBTAG00000001635	CUTA	4	yellow
ENSBTAG00000001694	TYRO3	4	yellow
ENSBTAG00000001717	AURKB	4	yellow

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ENSBTAG00000001842	GSTM3	4	yellow
ENSBTAG00000001872	ORC6	4	yellow
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ENSBTAG00000002292	SMARCA1	4	yellow
ENSBTAG00000002298	CKAP2L	4	yellow
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ENSBTAG00000005560	ST18	4	yellow
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ENSBTAG00000016467	SLC22A17	4	yellow
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ENSBTAG00000020227	FAM72A	4	yellow
ENSBTAG00000020352	PAQR5	4	yellow
ENSBTAG00000020394	TNFAIP8L2	4	yellow
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ENSBTAG00000026505	LOC539789	4	yellow
ENSBTAG00000026580	HTR1E	4	yellow
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ENSBTAG00000026613	MSTO1	4	yellow
ENSBTAG00000026704	CENPW	4	yellow
ENSBTAG00000026768	TH	4	yellow
ENSBTAG00000026851	FMNL2	4	yellow
ENSBTAG00000026963	NCALD	4	yellow
ENSBTAG00000026971	CDCA5	4	yellow
ENSBTAG00000027386	SOX12	4	yellow
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ENSBTAG00000027728	NUDT12	4	yellow
ENSBTAG00000027923	NA	4	yellow
ENSBTAG00000030393	RDH13	4	yellow
ENSBTAG00000030593	RFTN1	4	yellow
ENSBTAG00000030646	KCTD17	4	yellow
ENSBTAG00000030757	ELFN1	4	yellow
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ENSBTAG00000030897	XRCC2	4	yellow
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ENSBTAG00000033441	SHCBP1	4	yellow
ENSBTAG00000033545	EBD	4	yellow
ENSBTAG00000033690	BARD1	4	yellow
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ENSBTAG00000034323	LOC107131287	4	yellow
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ENSBTAG00000037389	TRIM44	4	yellow
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ENSBTAG00000037640	PID1	4	yellow
ENSBTAG00000037757	EBF4	4	yellow
ENSBTAG00000037856	MGC152281	4	yellow
ENSBTAG00000037951	KLHL6	4	yellow
ENSBTAG00000038085	NA	4	yellow
ENSBTAG00000038322	LOC510613	4	yellow
ENSBTAG00000038384	KRT5	4	yellow
ENSBTAG00000038496	CR2	4	yellow
ENSBTAG00000038532	FOLR3	4	yellow
ENSBTAG00000039071	ANKRD16	4	yellow
ENSBTAG00000039163	NA	4	yellow
ENSBTAG00000039190	SLC9A5	4	yellow
ENSBTAG00000039234	LIPK	4	yellow
ENSBTAG00000039329	RAET1G	4	yellow
ENSBTAG00000039462	PCLAF	4	yellow
ENSBTAG00000039686	NA	4	yellow
ENSBTAG00000039709	PARPBP	4	yellow
ENSBTAG00000040028	OBSCN	4	yellow
ENSBTAG00000040065	RAD51AP1	4	yellow
ENSBTAG00000040512	PCP4L1	4	yellow
ENSBTAG00000042753	LOC112443378	4	yellow
ENSBTAG00000043545	NA	4	yellow
ENSBTAG00000044000	PRIM1	4	yellow
ENSBTAG00000044006	GINS2	4	yellow
ENSBTAG00000044033	EDIL3	4	yellow
ENSBTAG00000044063	B4GALT6	4	yellow
ENSBTAG00000044150	UCK2	4	yellow
ENSBTAG00000044175	CENPK	4	yellow
ENSBTAG00000045604	TTC9	4	yellow
ENSBTAG00000045770	KRT77	4	yellow
ENSBTAG00000045795	KIR2DS1	4	yellow
ENSBTAG00000045892	NA	4	yellow
ENSBTAG00000046264	NA	4	yellow
ENSBTAG00000046556	NA	4	yellow
ENSBTAG00000046594	NA	4	yellow
ENSBTAG00000046766	NA	4	yellow
ENSBTAG00000046866	NA	4	yellow
ENSBTAG00000046910	NA	4	yellow
ENSBTAG00000047103	IDNK	4	yellow
ENSBTAG00000047265	PPP1R14B	4	yellow
ENSBTAG00000047322	NA	4	yellow
ENSBTAG00000047347	NA	4	yellow

ENSBTAG00000047462	NA	4	yellow
ENSBTAG00000047536	NA	4	yellow
ENSBTAG00000047598	NA	4	yellow
ENSBTAG00000047739	TSC22D1	4	yellow
ENSBTAG00000047755	FNDC10	4	yellow
ENSBTAG00000047807	SAPCD2	4	yellow
ENSBTAG00000048271	MICAL3	4	yellow

black	7	190
blue	2	2530
brown	3	1045
cyan	14	53
green	5	448
greenyellow	11	123
grey	0	231
grey60	17	43
lightcyan	16	49
magenta	9	178
midnightblue	15	53
pink	8	179
purple	10	139
red	6	216
salmon	13	75
tan	12	117
turquoise	1	2980
yellow	4	614

Supplementary File S4: Details about miRNA-seq-based modules

miRNA_id	Module_label	Module_color
bta-miR-100	2	blue
bta-miR-10b	2	blue
bta-miR-125a	2	blue
bta-miR-127	2	blue
bta-miR-1388-5p	2	blue
bta-miR-141	2	blue
bta-miR-143	2	blue
bta-miR-148a	2	blue
bta-miR-150	2	blue
bta-miR-151-3p	2	blue
bta-miR-152/bta-miR-2957	2	blue
bta-miR-182	2	blue
bta-miR-183	2	blue
bta-miR-193b	2	blue
bta-miR-200a	2	blue
bta-miR-200b	2	blue
bta-miR-200c	2	blue
bta-miR-204	2	blue
bta-miR-205	2	blue
bta-miR-224	2	blue
bta-miR-2285t	2	blue
bta-miR-27b	2	blue
bta-miR-29a	2	blue
bta-miR-30a-5p	2	blue
bta-miR-31	2	blue
bta-miR-335	2	blue
bta-miR-3431	2	blue
bta-miR-375	2	blue
bta-miR-429	2	blue
bta-miR-450b	2	blue
bta-miR-451	2	blue
bta-miR-455-5p	2	blue
bta-miR-486	2	blue
bta-miR-504	2	blue
bta-miR-615	2	blue
bta-miR-96	2	blue
bta-miR-99a-3p	2	blue
bta-miR-99a-5p	2	blue
bta-miR-10a	3	brown
bta-miR-126-5p	3	brown
bta-miR-142-3p	3	brown
bta-miR-142-5p	3	brown
bta-miR-15a	3	brown
bta-miR-16a	3	brown

bta-miR-16b	3	brown
bta-miR-181c	3	brown
bta-miR-181d	3	brown
bta-miR-186	3	brown
bta-miR-191	3	brown
bta-miR-192	3	brown
bta-miR-19a	3	brown
bta-miR-19b	3	brown
bta-miR-223	3	brown
bta-miR-2284w	3	brown
bta-miR-2284x	3	brown
bta-miR-23a	3	brown
bta-miR-25	3	brown
bta-miR-29c	3	brown
bta-miR-301a	3	brown
bta-miR-30b-5p	3	brown
bta-miR-32	3	brown
bta-miR-338	3	brown
bta-miR-342	3	brown
bta-miR-361	3	brown
bta-miR-362-5p	3	brown
bta-miR-363	3	brown
bta-miR-374a	3	brown
bta-miR-374b	3	brown
bta-miR-410	3	brown
bta-miR-425-5p	3	brown
bta-miR-660	3	brown
bta-miR-101	0	grey
bta-miR-106b	0	grey
bta-miR-107	0	grey
bta-miR-125b	0	grey
bta-miR-1296	0	grey
bta-miR-1388-3p	0	grey
bta-miR-145	0	grey
bta-miR-1468	0	grey
bta-miR-146a	0	grey
bta-miR-15b	0	grey
bta-miR-188	0	grey
bta-miR-194	0	grey
bta-miR-196b	0	grey
bta-miR-208b	0	grey
bta-miR-21-3p	0	grey
bta-miR-21-5p	0	grey
bta-miR-215	0	grey
bta-miR-22-3p/bta-miR-3600	0	grey
bta-miR-2284i	0	grey
bta-miR-2285b	0	grey

bta-miR-2285h	0	grey
bta-miR-2285k	0	grey
bta-miR-2285q	0	grey
bta-miR-2285v	0	grey
bta-miR-2299-5p	0	grey
bta-miR-2313-3p	0	grey
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bta-miR-2316	0	grey
bta-miR-2319a	0	grey
bta-miR-2336	0	grey
bta-miR-2339	0	grey
bta-miR-2357	0	grey
bta-miR-2388-3p	0	grey
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bta-miR-2411-3p	0	grey
bta-miR-2424	0	grey
bta-miR-2450a	0	grey
bta-miR-2478	0	grey
bta-miR-2483-5p	0	grey
bta-miR-26a	0	grey
bta-miR-26a/bta-miR-26c	0	grey
bta-miR-26b	0	grey
bta-miR-27a-3p	0	grey
bta-miR-2898	0	grey
bta-miR-292	0	grey
bta-miR-30e-5p	0	grey
bta-miR-30f	0	grey
bta-miR-331	0	grey
bta-miR-339a	0	grey
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bta-miR-340	0	grey
bta-miR-345-3p	0	grey
bta-miR-345-5p	0	grey
bta-miR-34c	0	grey
bta-miR-3613	0	grey
bta-miR-362-3p	0	grey
bta-miR-369-3p	0	grey
bta-miR-4286	0	grey
bta-miR-454	0	grey
bta-miR-505	0	grey
bta-miR-532	0	grey
bta-miR-6119-3p	0	grey
bta-miR-6119-5p	0	grey
bta-miR-6120-3p	0	grey
bta-miR-6520	0	grey
bta-miR-6524	0	grey

bta-miR-6530	0	grey
bta-miR-6533	0	grey
bta-miR-664	0	grey
bta-miR-769	0	grey
bta-miR-874	0	grey
bta-miR-935	0	grey
bta-miR-98	0	grey
bta-let-7a	1	turquoise
bta-let-7a-5p	1	turquoise
bta-let-7b/bta-miR-3596	1	turquoise
bta-let-7c	1	turquoise
bta-let-7d	1	turquoise
bta-let-7e	1	turquoise
bta-let-7f	1	turquoise
bta-let-7g	1	turquoise
bta-let-7i	1	turquoise
bta-miR-103	1	turquoise
bta-miR-106a	1	turquoise
bta-miR-1246	1	turquoise
bta-miR-1249	1	turquoise
bta-miR-126-3p	1	turquoise
bta-miR-1271	1	turquoise
bta-miR-1277	1	turquoise
bta-miR-128	1	turquoise
bta-miR-129-3p	1	turquoise
bta-miR-1291	1	turquoise
bta-miR-1306	1	turquoise
bta-miR-1307	1	turquoise
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bta-miR-130b	1	turquoise
bta-miR-132	1	turquoise
bta-miR-1343-3p	1	turquoise
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bta-miR-17-3p	1	turquoise
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bta-miR-193a-5p	1	turquoise
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bta-miR-219-5p	1	turquoise
bta-miR-22-5p	1	turquoise
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bta-miR-452	1	turquoise
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bta-miR-491	1	turquoise
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bta-miR-500	1	turquoise
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bta-miR-503-3p	1	turquoise
bta-miR-503-5p	1	turquoise
bta-miR-542-5p/bta-miR-3601	1	turquoise
bta-miR-545-3p	1	turquoise
bta-miR-545-5p	1	turquoise
bta-miR-6123	1	turquoise
bta-miR-628	1	turquoise
bta-miR-6517	1	turquoise
bta-miR-6518	1	turquoise
bta-miR-652	1	turquoise
bta-miR-6521	1	turquoise
bta-miR-6522	1	turquoise
bta-miR-6523	1	turquoise
bta-miR-6525	1	turquoise
bta-miR-6527	1	turquoise
bta-miR-6529	1	turquoise
bta-miR-6531	1	turquoise
bta-miR-671	1	turquoise
bta-miR-677	1	turquoise
bta-miR-744	1	turquoise
bta-miR-760-3p	1	turquoise
bta-miR-760-5p	1	turquoise
bta-miR-877	1	turquoise
bta-miR-885	1	turquoise
bta-miR-92a	1	turquoise
bta-miR-92b	1	turquoise

bta-miR-93	1	turquoise
bta-miR-99b	1	turquoise

blue	2	38
brown	3	33
turquoise	1	183
grey	0	74

Supplementary File S5: Comprehensive information from the module-trai

RNA-seq-based Modules	R_Milk_volume (in Litres)	P_Milk_volume (in Litres)
MEmidnightblue	0.266826804	0.083691788
MEsalmon	-0.075499909	0.630384984
MEpink	-0.263818804	0.087371242
MEyellow	0.038674102	0.805510269
MEblue	0.192266291	0.216761239
MEred	0.209245812	0.17809405
MEbrown	-0.123424523	0.430391768
MEgreenyellow	-0.238218238	0.123972471
MEblack	-0.233585543	0.131674988
MElightcyan	-0.281852798	0.067086922
MEgrey60	-0.215957931	0.164262696
MEpurple	-0.379037561	0.01219027
MEgreen	-0.324236179	0.033906212
MEturquoise	-0.107651539	0.492008434
MEcyan	-0.137323203	0.379876321
MEmagenta	0.23178803	0.134757851
MEtan	0.183698931	0.238332263
MEgrey	-0.251371792	0.10394731

t relationships analysis result (R = correlation; P = p-value)

R_Rectal_tempreature (in Farenheit)	P_Rectal_tempreature (in Farenheit)
-0.442496997	0.002966311
-0.068481731	0.662586431
0.520484855	0.000346411
0.347039559	0.022607361
-0.101892669	0.51558771
-0.284088612	0.064856823
-0.152079722	0.330282267
0.073803399	0.638110219
-0.120735778	0.440579251
-0.104549072	0.504641585
0.244011579	0.114822667
0.670228647	8.82E-07
0.43633481	0.003443629
0.00928522	0.952876996
0.654898615	1.89E-06
-0.11316074	0.469984409
-0.367793542	0.015247753
-0.112175956	0.473882327

R_Ambient_temperature (in Celsius)	P_Ambient_temperature (in Celsius)	R_Humidity (%)	P_Humidity (%)
-0.358663929	0.018186873	0.321584632	0.035478908
-0.049271645	0.753698972	0.263469087	0.08780705
0.545594118	0.000154447	0.28525189	0.063720033
0.227728963	0.141916565	0.004837921	0.97543726
-0.078709749	0.61587511	0.031233299	0.842400676
-0.109354446	0.485144382	0.256427062	0.096946798
-0.095593134	0.542011664	-0.150138389	0.336565267
0.157010573	0.314655091	0.233063692	0.132564527
-0.007294893	0.962970073	-0.149958729	0.337150442
0.148254414	0.342732898	-0.155316625	0.319970003
0.057665441	0.713394605	-0.269788223	0.080188443
0.498655722	0.000665583	-0.031851223	0.839323241
0.451418866	0.002378291	0.228190722	0.141088301
-0.015537596	0.921225291	-0.016228056	0.917736412
0.280762802	0.068195946	-0.023097485	0.883118804
-0.205280081	0.186648067	-0.147846788	0.344076452
-0.410358334	0.006273411	-0.323081834	0.03458368
0.132387003	0.397400674	-0.046091256	0.769147321

R_Total_bacterial_counts (TBC; Per 10mL)	P_Total_bacterial_counts (TBC; Per 10mL)
0.175623718	0.259958677
0.018190078	0.907830902
-0.141322082	0.366020958
-0.413970312	0.005787278
-0.777108635	8.93E-10
-0.569640981	6.69E-05
-0.188775006	0.2253822
-0.019029971	0.903594722
-0.138850221	0.374549268
-0.102594571	0.512683927
0.505936669	0.000537905
0.561080297	9.08E-05
0.521197772	0.000338848
0.72688445	3.40E-08
0.22954044	0.138687808
-0.491822602	0.0008094
-0.018575946	0.905884376
-0.1309517	0.402582928

R_Somatic_cell_counts (SCC; Per mL)	P_Somatic_cell_counts (SCC; Per mL)	R_CD14_cell_number (Per mL)
-0.005036622	0.974428757	-0.251603113
-0.035585914	0.820775315	-0.639160425
0.029199986	0.852543288	-0.553401627
-0.443348346	0.002905163	-0.249221376
-0.673523696	7.44E-07	-0.257210283
-0.54437482	0.000160864	-0.573593276
-0.312723784	0.041174754	-0.090947223
0.039157009	0.803129529	-0.39010217
-0.275153919	0.074134086	-0.09688273
-0.229420417	0.138900034	-0.182912468
0.40560248	0.006967192	0.518114994
0.589130206	3.24E-05	0.170097421
0.518846066	0.000364376	-0.252727102
0.586031746	3.64E-05	0.308495358
0.177461306	0.254926169	0.270261933
-0.313456016	0.040677447	0.428011859
-0.086821106	0.579856137	0.469801662
-0.014228759	0.927842763	0.077611988

P_CD14_cell_number (Per mL)
0.103618763
3.97E-06
0.00011856
0.10703982
0.09589548
5.80E-05
0.561906941
0.009708307
0.536549861
0.240383017
0.000372658
0.275490095
0.102033649
0.044144413
0.079638848
0.004194445
0.001480192
0.620821586

Supplementary File S6: Comprehensive details of the results of functional enrichment analysis of si

BP	Term	Overlap	P-value	Adjusted P-value
	cytokine-mediated signaling pathway (GO:0019221)	219/621	8.06E-46	4.19E-42
	cellular response to cytokine stimulus (GO:0071345)	177/482	9.01E-40	2.34E-36
	positive regulation of cytokine production (GO:0001819)	126/335	1.03E-29	1.79E-26
	inflammatory response (GO:0006954)	94/230	1.38E-25	1.80E-22
	response to cytokine (GO:0034097)	70/150	2.06E-23	2.14E-20
	response to lipopolysaccharide (GO:0032496)	72/159	4.55E-23	3.51E-20
	positive regulation of intracellular signal transduction (GO	159/546	4.73E-23	3.51E-20
	neutrophil mediated immunity (GO:0002446)	145/488	5.01E-22	3.25E-19
	neutrophil degranulation (GO:0043312)	141/481	7.51E-21	4.34E-18
	neutrophil activation involved in immune response (GO:0	141/485	1.73E-20	8.99E-18
	response to molecule of bacterial origin (GO:0002237)	43/73	6.48E-20	3.06E-17
	regulation of interleukin-8 production (GO:0032677)	45/81	2.28E-19	9.85E-17
	regulation of inflammatory response (GO:0050727)	78/206	4.44E-19	1.77E-16
	regulation of I-kappaB kinase/NF-kappaB signaling (GO:00	81/224	2.42E-18	8.97E-16
	cellular response to lipopolysaccharide (GO:0071222)	54/120	1.68E-17	5.81E-15
	negative regulation of cytokine production (GO:0001818)	69/182	4.50E-17	1.46E-14
	positive regulation of DNA-binding transcription factor ac	82/246	3.83E-16	1.17E-13
	positive regulation of interleukin-8 production (GO:0032	35/61	5.71E-16	1.65E-13
	regulation of interleukin-6 production (GO:0032675)	49/110	8.55E-16	2.34E-13
	cellular response to molecule of bacterial origin (GO:007	50/115	1.46E-15	3.80E-13
	positive regulation of NF-kappaB transcription factor acti	59/155	6.76E-15	1.67E-12
	positive regulation of I-kappaB kinase/NF-kappaB signalir	62/171	1.97E-14	4.64E-12
	innate immune response (GO:0045087)	90/302	3.08E-14	6.79E-12
	regulation of cytokine-mediated signaling pathway (GO:0	37/74	3.13E-14	6.79E-12
	defense response to symbiont (GO:0140546)	50/124	5.49E-14	1.10E-11
	regulation of tumor necrosis factor production (GO:0032	50/124	5.49E-14	1.10E-11
	positive regulation of phagocytosis (GO:0050766)	30/53	1.14E-13	2.20E-11
	regulation of innate immune response (GO:0045088)	33/64	2.47E-13	4.58E-11
	defense response to virus (GO:0051607)	51/133	3.23E-13	5.78E-11
	positive regulation of response to external stimulus (GO:	52/139	5.95E-13	1.03E-10
	regulation of type I interferon production (GO:0032479)	39/89	1.39E-12	2.33E-10
	positive regulation of T cell activation (GO:0050870)	35/75	2.06E-12	3.34E-10
	positive regulation of defense response (GO:0031349)	41/98	2.38E-12	3.66E-10
	response to lipid (GO:0033993)	45/114	2.40E-12	3.66E-10
	regulation of phagocytosis (GO:0050764)	30/58	2.70E-12	3.97E-10
	regulation of defense response (GO:0031347)	37/83	2.75E-12	3.97E-10
	toll-like receptor signaling pathway (GO:0002224)	39/91	3.27E-12	4.55E-10
	positive regulation of interleukin-6 production (GO:0032	35/76	3.33E-12	4.55E-10
	positive regulation of cellular process (GO:0048522)	145/625	4.52E-12	6.02E-10
	positive regulation of inflammatory response (GO:00507	38/89	7.10E-12	9.22E-10
	regulation of interferon-gamma production (GO:0032649	37/86	1.02E-11	1.29E-09
	positive regulation of transcription, DNA-templated (GO:	237/1183	1.43E-11	1.77E-09
	cellular response to lipid (GO:0071396)	67/219	1.61E-11	1.93E-09
	regulation of interleukin-12 production (GO:0032655)	27/51	1.63E-11	1.93E-09

regulation of cell adhesion (GO:0030155)	48/133	2.05E-11	2.36E-09
positive regulation of type I interferon production (GO:0(	34/77	2.90E-11	3.27E-09
regulation of cell population proliferation (GO:0042127)	166/764	3.60E-11	3.96E-09
cellular response to tumor necrosis factor (GO:0071356)	61/194	3.66E-11	3.96E-09
MyD88-independent toll-like receptor signaling pathway	20/31	5.19E-11	5.50E-09
regulation of cytokine production (GO:0001817)	51/150	6.19E-11	6.44E-09
positive regulation of transport (GO:0051050)	37/91	7.57E-11	7.71E-09
positive regulation of peptidyl-tyrosine phosphorylation (	47/134	1.03E-10	1.02E-08
cellular response to interferon-gamma (GO:0071346)	44/121	1.04E-10	1.02E-08
cellular response to type I interferon (GO:0071357)	30/65	1.09E-10	1.02E-08
type I interferon signaling pathway (GO:0060337)	30/65	1.09E-10	1.02E-08
regulation of peptidyl-tyrosine phosphorylation (GO:005(	37/92	1.10E-10	1.02E-08
cellular response to oxygen-containing compound (GO:1(	85/323	2.16E-10	1.97E-08
positive regulation of transcription by RNA polymerase II	187/908	2.34E-10	2.06E-08
response to interleukin-1 (GO:0070555)	35/86	2.37E-10	2.06E-08
cellular response to interleukin-1 (GO:0071347)	51/155	2.38E-10	2.06E-08
TRIF-dependent toll-like receptor signaling pathway (GO:	19/30	2.55E-10	2.15E-08
cellular protein modification process (GO:0006464)	206/1025	2.57E-10	2.15E-08
regulation of interferon-beta production (GO:0032648)	25/49	2.62E-10	2.16E-08
positive regulation of interleukin-1 beta production (GO:(	27/56	2.68E-10	2.17E-08
negative regulation of intracellular signal transduction (G	60/198	2.78E-10	2.22E-08
positive regulation of interferon-gamma production (GO:	27/57	4.45E-10	3.50E-08
response to interferon-gamma (GO:0034341)	33/80	5.05E-10	3.88E-08
positive regulation of protein phosphorylation (GO:0001(	93/371	5.08E-10	3.88E-08
positive regulation of interleukin-12 production (GO:003	20/34	5.71E-10	4.30E-08
response to tumor necrosis factor (GO:0034612)	40/110	7.28E-10	5.37E-08
positive regulation of tumor necrosis factor production ((	32/77	7.34E-10	5.37E-08
positive regulation of interleukin-1 production (GO:0032	28/62	8.45E-10	6.09E-08
programmed necrotic cell death (GO:0097300)	14/18	9.17E-10	6.53E-08
necroptotic process (GO:0070266)	13/16	1.45E-09	1.02E-07
regulation of interleukin-1 beta production (GO:0032651	33/83	1.58E-09	1.08E-07
positive regulation of lymphocyte proliferation (GO:0050	31/75	1.58E-09	1.08E-07
regulation of apoptotic process (GO:0042981)	156/742	1.72E-09	1.16E-07
regulation of tyrosine phosphorylation of STAT protein ((	29/68	2.21E-09	1.47E-07
regulation of NIK/NF-kappaB signaling (GO:1901222)	32/80	2.32E-09	1.53E-07
pattern recognition receptor signaling pathway (GO:0002	27/61	2.92E-09	1.90E-07
positive regulation of tumor necrosis factor superfamily (	32/81	3.35E-09	2.15E-07
I-kappaB kinase/NF-kappaB signaling (GO:0007249)	27/62	4.52E-09	2.86E-07
regulation of response to external stimulus (GO:0032101	43/130	4.97E-09	3.11E-07
positive regulation of immune response (GO:0050778)	30/75	7.30E-09	4.51E-07
regulation of programmed necrotic cell death (GO:00620	14/20	8.94E-09	5.46E-07
interferon-gamma-mediated signaling pathway (GO:006(	28/68	1.07E-08	6.48E-07
regulation of interferon-gamma-mediated signaling path	15/23	1.14E-08	6.82E-07
positive regulation of chemokine production (GO:003272	24/53	1.26E-08	7.40E-07
protein phosphorylation (GO:0006468)	111/496	1.27E-08	7.40E-07
positive regulation of interferon-beta production (GO:00	19/36	1.80E-08	1.04E-06
negative regulation of type I interferon production (GO:0	21/43	1.94E-08	1.11E-06

regulation of interleukin-17 production (GO:0032660)	18/33	2.17E-08	1.22E-06
positive regulation of tyrosine phosphorylation of STAT p	25/59	3.28E-08	1.83E-06
regulation of interleukin-10 production (GO:0032653)	22/48	3.88E-08	2.14E-06
receptor signaling pathway via JAK-STAT (GO:0007259)	17/31	4.83E-08	2.64E-06
regulation of response to interferon-gamma (GO:006033	44879	5.43E-08	2.94E-06
phosphorylation (GO:0016310)	92/400	5.81E-08	3.11E-06
receptor signaling pathway via STAT (GO:0097696)	15/25	5.86E-08	3.11E-06
regulation of chemokine production (GO:0032642)	20/42	7.26E-08	3.81E-06
positive regulation of cell migration (GO:0030335)	68/269	7.41E-08	3.85E-06
regulation of intracellular signal transduction (GO:19025	98/437	8.05E-08	4.14E-06
negative regulation of viral process (GO:0048525)	27/70	1.00E-07	5.10E-06
positive regulation of cell population proliferation (GO:0(	104/474	1.04E-07	5.24E-06
negative regulation of DNA-binding transcription factor a	43/143	1.14E-07	5.71E-06
lipopolysaccharide-mediated signaling pathway (GO:0031	13/20	1.19E-07	5.90E-06
regulation of necroptotic process (GO:0060544)	14/23	1.27E-07	6.23E-06
regulation of MAP kinase activity (GO:0043405)	33/97	1.39E-07	6.73E-06
apoptotic process (GO:0006915)	60/231	1.55E-07	7.44E-06
interleukin-27-mediated signaling pathway (GO:0070106	44880	1.79E-07	8.53E-06
regulation of T cell proliferation (GO:0042129)	28/76	1.82E-07	8.62E-06
defense response to bacterium (GO:0042742)	49/176	2.21E-07	1.03E-05
positive regulation of macromolecule metabolic process	87/384	2.66E-07	1.23E-05
cellular response to interleukin-15 (GO:0071350)	44847	3.24E-07	1.47E-05
interleukin-15-mediated signaling pathway (GO:0035723	44847	3.24E-07	1.47E-05
cellular defense response (GO:0006968)	21/49	3.24E-07	1.47E-05
positive regulation of NIK/NF-kappaB signaling (GO:1901	22/53	3.36E-07	1.51E-05
regulation of immune response (GO:0050776)	49/179	3.85E-07	1.71E-05
positive regulation of T cell proliferation (GO:0042102)	25/66	4.44E-07	1.96E-05
cellular response to virus (GO:0098586)	17/35	4.87E-07	2.11E-05
positive regulation of lymphocyte activation (GO:005125	17/35	4.87E-07	2.11E-05
tumor necrosis factor-mediated signaling pathway (GO:0(	36/116	5.12E-07	2.20E-05
interleukin-35-mediated signaling pathway (GO:0070757	44815	5.36E-07	2.27E-05
positive regulation of nitric-oxide synthase biosynthetic p	44815	5.36E-07	2.27E-05
negative regulation of cell population proliferation (GO:0	85/379	5.72E-07	2.39E-05
vascular endothelial growth factor receptor signaling pat	25/67	6.20E-07	2.56E-05
negative regulation of apoptotic process (GO:0043066)	103/485	6.21E-07	2.56E-05
positive regulation of immune effector process (GO:0002	16/32	6.42E-07	2.62E-05
positive regulation of apoptotic signaling pathway (GO:2(	23/59	7.02E-07	2.85E-05
regulation of calcidiol 1-monooxygenase activity (GO:006	44749	7.18E-07	2.89E-05
cellular response to interleukin-9 (GO:0071355)	44782	7.54E-07	2.98E-05
interleukin-9-mediated signaling pathway (GO:0038113)	44782	7.54E-07	2.98E-05
positive regulation of MAPK cascade (GO:0043410)	66/274	7.57E-07	2.98E-05
extrinsic apoptotic signaling pathway (GO:0097191)	26/72	7.79E-07	3.04E-05
negative regulation of toll-like receptor signaling pathwa	17/36	8.08E-07	3.11E-05
positive regulation of myeloid leukocyte differentiation (	17/36	8.08E-07	3.11E-05
regulation of response to biotic stimulus (GO:0002831)	15/29	8.22E-07	3.14E-05
positive regulation of gene expression (GO:0010628)	102/482	8.36E-07	3.17E-05
MAPK cascade (GO:0000165)	71/303	8.86E-07	3.33E-05

regulation of extrinsic apoptotic signaling pathway (GO:2	24/64	9.31E-07	3.48E-05
regulation of nitric-oxide synthase biosynthetic process ((	44848	9.98E-07	3.70E-05
positive regulation of cysteine-type endopeptidase activi	36/119	1.02E-06	3.75E-05
positive regulation of interleukin-17 production (GO:003	13/23	1.19E-06	4.36E-05
positive regulation of interferon-alpha production (GO:0(	44915	1.30E-06	4.68E-05
toll-like receptor 4 signaling pathway (GO:0034142)	44915	1.30E-06	4.68E-05
negative regulation of transcription, DNA-templated (GO	176/948	1.51E-06	5.41E-05
regulation of angiogenesis (GO:0045765)	52/203	1.59E-06	5.66E-05
negative regulation of transcription by RNA polymerase I	134/684	1.62E-06	5.71E-05
negative regulation of NF-kappaB transcription factor act	27/79	1.67E-06	5.88E-05
positive regulation of cell death (GO:0010942)	24/66	1.78E-06	6.19E-05
cellular response to vascular endothelial growth factor st	16/34	1.81E-06	6.26E-05
positive regulation of toll-like receptor signaling pathway	14/27	1.85E-06	6.37E-05
positive regulation of T-helper 1 type immune response (	44816	1.89E-06	6.42E-05
positive regulation of T-helper 17 type immune response	44816	1.89E-06	6.42E-05
stress-activated MAPK cascade (GO:0051403)	23/62	1.95E-06	6.56E-05
negative regulation of innate immune response (GO:004	17/38	2.08E-06	6.97E-05
negative regulation of viral genome replication (GO:0045	21/54	2.22E-06	7.40E-05
interleukin-1-mediated signaling pathway (GO:0070498)	30/94	2.33E-06	7.71E-05
negative regulation of interleukin-6 production (GO:0032	15/31	2.45E-06	8.01E-05
positive regulation of leukocyte cell-cell adhesion (GO:19	15/31	2.45E-06	8.01E-05
negative regulation of defense response (GO:0031348)	28/85	2.49E-06	8.09E-05
regulation of gene expression (GO:0010468)	195/1079	2.64E-06	8.47E-05
negative regulation of programmed cell death (GO:0043(	83/381	2.64E-06	8.47E-05
positive regulation of T cell cytokine production (GO:000	44916	2.66E-06	8.47E-05
negative regulation of inflammatory response (GO:00507	53/212	2.79E-06	8.84E-05
regulation of cytokine production involved in inflammato	18/43	3.38E-06	1.06E-04
positive regulation of neuron death (GO:1901216)	19/47	3.40E-06	1.06E-04
negative regulation of multicellular organismal process ((	53/214	3.76E-06	1.17E-04
regulation of cell migration (GO:0030334)	87/408	3.82E-06	1.18E-04
positive regulation of interleukin-10 production (GO:003	15/32	4.05E-06	1.25E-04
regulation of interferon-alpha production (GO:0032647)	13/25	4.18E-06	1.28E-04
negative regulation of cellular process (GO:0048523)	113/566	4.25E-06	1.29E-04
positive regulation of cellular catabolic process (GO:0031	39/141	4.34E-06	1.30E-04
regulation of small GTPase mediated signal transduction	39/141	4.34E-06	1.30E-04
cell chemotaxis (GO:0060326)	24/69	4.39E-06	1.30E-04
regulation of protein-containing complex assembly (GO:(	34/116	4.39E-06	1.30E-04
negative regulation of gene expression (GO:0010629)	72/322	4.55E-06	1.34E-04
positive regulation of cytokine-mediated signaling pathw	16/36	4.61E-06	1.35E-04
negative regulation of immune response (GO:0050777)	46/178	4.81E-06	1.40E-04
negative regulation of MAP kinase activity (GO:0043407)	19/48	4.93E-06	1.42E-04
negative regulation of tumor necrosis factor superfamily	19/48	4.93E-06	1.42E-04
regulation of interleukin-2 production (GO:0032663)	19/48	4.93E-06	1.42E-04
calcium-mediated signaling (GO:0019722)	31/102	5.02E-06	1.43E-04
cellular response to interleukin-21 (GO:0098757)	44750	5.08E-06	1.43E-04
interleukin-21-mediated signaling pathway (GO:0038114	44750	5.08E-06	1.43E-04
regulation of MyD88-independent toll-like receptor signa	44750	5.08E-06	1.43E-04

positive regulation of adaptive immune response based c	44817	5.42E-06	1.49E-04
response to muramyl dipeptide (GO:0032495)	44817	5.42E-06	1.49E-04
cellular response to lipoteichoic acid (GO:0071223)	44718	5.42E-06	1.49E-04
response to lipoteichoic acid (GO:0070391)	44718	5.42E-06	1.49E-04
myeloid cell activation involved in immune response (GO	44884	5.93E-06	1.62E-04
positive regulation of protein kinase activity (GO:004586(	41/154	7.05E-06	1.91E-04
regulation of smooth muscle cell proliferation (GO:00486	19/49	7.06E-06	1.91E-04
negative regulation of MAPK cascade (GO:0043409)	29/94	7.24E-06	1.95E-04
positive regulation of interleukin-2 production (GO:0032	13/26	7.34E-06	1.96E-04
positive regulation of signal transduction (GO:0009967)	59/252	7.37E-06	1.96E-04
positive regulation of programmed cell death (GO:00430(	65/286	7.42E-06	1.97E-04
positive regulation of apoptotic process (GO:0043065)	69/310	8.39E-06	2.21E-04
positive regulation of small GTPase mediated signal trans	14/30	9.08E-06	2.38E-04
negative regulation of tumor necrosis factor production (	18/46	1.06E-05	2.76E-04
cellular response to interleukin-2 (GO:0071352)	44784	1.08E-05	2.76E-04
interleukin-2-mediated signaling pathway (GO:0038110)	44784	1.08E-05	2.76E-04
negative regulation of programmed necrotic cell death (G	44784	1.08E-05	2.76E-04
positive regulation of production of molecular mediator (	16/38	1.08E-05	2.76E-04
regulation of toll-like receptor signaling pathway (GO:00	13/27	1.24E-05	3.17E-04
positive regulation of cytokine production involved in infl	44851	1.32E-05	3.35E-04
defense response to protozoan (GO:0042832)	44818	1.34E-05	3.37E-04
cellular response to chemokine (GO:1990869)	21/60	1.54E-05	3.86E-04
peptidyl-tyrosine dephosphorylation (GO:0035335)	15/35	1.57E-05	3.93E-04
protein dephosphorylation (GO:0006470)	37/139	1.94E-05	4.82E-04
interleukin-23-mediated signaling pathway (GO:0038155	44751	2.02E-05	4.97E-04
negative regulation of lipid localization (GO:1905953)	44751	2.02E-05	4.97E-04
cellular response to interleukin-6 (GO:0071354)	13/28	2.04E-05	5.00E-04
regulation of protein phosphorylation (GO:0001932)	60/266	2.08E-05	5.07E-04
cellular response to interleukin-12 (GO:0071349)	18/48	2.10E-05	5.11E-04
regulation of ERK1 and ERK2 cascade (GO:0070372)	55/238	2.20E-05	5.31E-04
macrophage activation (GO:0042116)	15/36	2.36E-05	5.69E-04
regulation of GTPase activity (GO:0043087)	46/189	2.57E-05	6.14E-04
myeloid leukocyte differentiation (GO:0002573)	23/71	2.61E-05	6.21E-04
negative regulation of interleukin-8 production (GO:0032	44852	2.62E-05	6.21E-04
positive regulation of B cell activation (GO:0050871)	19/53	2.63E-05	6.21E-04
positive regulation of cysteine-type endopeptidase activi	21/62	2.72E-05	6.39E-04
protein mono-ADP-ribosylation (GO:0140289)	44785	2.85E-05	6.68E-04
cellular response to mechanical stimulus (GO:0071260)	18/49	2.92E-05	6.79E-04
activation of cysteine-type endopeptidase activity involve	25/81	3.00E-05	6.96E-04
regulation of viral genome replication (GO:0045069)	22/67	3.06E-05	7.07E-04
regulation of tumor necrosis factor-mediated signaling pa	20/58	3.13E-05	7.18E-04
zymogen activation (GO:0031638)	17/45	3.18E-05	7.27E-04
positive regulation of angiogenesis (GO:0045766)	32/116	3.21E-05	7.32E-04
MyD88-dependent toll-like receptor signaling pathway (G	13/29	3.25E-05	7.37E-04
negative regulation of MyD88-independent toll-like recep	44719	3.36E-05	7.53E-04
positive regulation of T-helper 17 cell differentiation (GO	44719	3.36E-05	7.53E-04
regulation of protein deubiquitination (GO:0090085)	44719	3.36E-05	7.53E-04

positive regulation of signaling receptor activity (GO:200(	15/37	3.49E-05	7.78E-04
positive regulation of protein modification process (GO:0	50/214	3.75E-05	8.32E-04
osteoclast differentiation (GO:0030316)	44887	3.77E-05	8.34E-04
intrinsic apoptotic signaling pathway (GO:0097193)	29/102	4.04E-05	8.89E-04
monocyte extravasation (GO:0035696)	44686	4.09E-05	8.97E-04
cellular response to organic substance (GO:0071310)	33/123	4.50E-05	9.82E-04
negative regulation of protein serine/threonine kinase ac	24/78	4.54E-05	9.87E-04
metal ion transport (GO:0030001)	26/88	4.86E-05	0.00105119
regulation of peptidyl-serine phosphorylation (GO:00331	28/98	4.95E-05	0.001065956
positive regulation of MAP kinase activity (GO:0043406)	22/69	5.10E-05	0.001091459
negative regulation of macromolecule metabolic process	46/194	5.13E-05	0.001091459
regulation of programmed cell death (GO:0043067)	46/194	5.13E-05	0.001091459
Fc receptor mediated stimulatory signaling pathway (GO:	23/74	5.45E-05	0.001154643
dendritic cell chemotaxis (GO:0002407)	44820	5.94E-05	0.001242686
positive regulation of toll-like receptor 4 signaling pathw	44752	5.96E-05	0.001242686
regulation of T-helper 17 cell differentiation (GO:200315	44752	5.96E-05	0.001242686
regulation of T-helper 17 type immune response (GO:20(	44752	5.96E-05	0.001242686
regulation of cysteine-type endopeptidase activity involv	26/89	6.00E-05	0.001242686
second-messenger-mediated signaling (GO:0019932)	26/89	6.00E-05	0.001242686
hemopoiesis (GO:0030097)	27/94	6.05E-05	0.001246689
regulation of T cell activation (GO:0050863)	17/47	6.07E-05	0.001246689
regulation of toll-like receptor 4 signaling pathway (GO:0	44888	6.36E-05	0.001301622
mature B cell differentiation involved in immune respons	44786	6.55E-05	0.001335247
integrin-mediated signaling pathway (GO:0007229)	23/75	6.88E-05	0.001395703
myeloid cell differentiation (GO:0030099)	18/52	7.26E-05	0.001451666
regulation of intrinsic apoptotic signaling pathway (GO:2(	18/52	7.26E-05	0.001451666
cytoplasmic pattern recognition receptor signaling pathw	44922	7.27E-05	0.001451666
regulation of vascular endothelial growth factor producti	44922	7.27E-05	0.001451666
cellular response to growth factor stimulus (GO:0071363	39/158	7.36E-05	0.001465249
cellular response to hydrogen peroxide (GO:0070301)	14/35	7.57E-05	0.001501427
Fc-epsilon receptor signaling pathway (GO:0038095)	30/111	8.45E-05	0.00166878
growth hormone receptor signaling pathway (GO:006039	44854	8.59E-05	0.001684714
negative regulation of lipid storage (GO:0010888)	44854	8.59E-05	0.001684714
positive regulation of cell motility (GO:2000147)	50/221	8.99E-05	0.001754987
positive regulation of nucleic acid-templated transcriptio	98/511	9.17E-05	0.001784575
regulation of nitric oxide biosynthetic process (GO:00454	15/40	1.02E-04	0.001967529
regulation of cytokine production involved in immune res	44889	1.03E-04	0.001997466
Fc-gamma receptor signaling pathway (GO:0038094)	22/72	1.04E-04	0.002005203
positive regulation of vasculature development (GO:1904	28/102	1.07E-04	0.002051766
neutrophil migration (GO:1990266)	23/77	1.08E-04	0.00206015
positive regulation of cellular component biogenesis (GO	26/92	1.10E-04	0.002097564
response to hydrogen peroxide (GO:0042542)	17/49	1.11E-04	0.002097564
negative regulation of interleukin-10 production (GO:003	44821	1.11E-04	0.002097564
positive regulation of defense response to virus by host (	44923	1.12E-04	0.002097564
regulation of B cell activation (GO:0050864)	44923	1.12E-04	0.002097564
positive regulation of protein-containing complex assemb	31/118	1.15E-04	0.002155633
cellular response to reactive oxygen species (GO:003461	20/63	1.18E-04	0.002182959

leukocyte aggregation (GO:0070486)	44720	1.19E-04	0.002182959
positive regulation of apoptotic cell clearance (GO:20004	44720	1.19E-04	0.002182959
positive regulation of cysteine-type endopeptidase activi	44720	1.19E-04	0.002182959
regulation of apoptotic cell clearance (GO:2000425)	44720	1.19E-04	0.002182959
T-helper cell lineage commitment (GO:0002295)	44720	1.19E-04	0.002182959
positive regulation of macromolecule biosynthetic proce	33/129	1.23E-04	0.002247627
positive regulation of Notch signaling pathway (GO:0045	16/45	1.26E-04	0.002284719
regulation of humoral immune response (GO:0002920)	18/54	1.27E-04	0.002295807
granulocyte chemotaxis (GO:0071621)	22/73	1.31E-04	0.002357322
growth hormone receptor signaling pathway via JAK-STA	44787	1.35E-04	0.002403545
positive regulation of granulocyte macrophage colony-sti	44787	1.35E-04	0.002403545
positive regulation of T-helper cell differentiation (GO:00	44787	1.35E-04	0.002403545
positive regulation of type 2 immune response (GO:0002	44787	1.35E-04	0.002403545
purinergic nucleotide receptor signaling pathway (GO:00	44855	1.45E-04	0.002553451
PERK-mediated unfolded protein response (GO:0036499)	44753	1.45E-04	0.002553451
T cell chemotaxis (GO:0010818)	44753	1.45E-04	0.002553451
negative regulation of ERK1 and ERK2 cascade (GO:00703	17/50	1.47E-04	0.002570988
regulation of complement activation (GO:0030449)	17/50	1.47E-04	0.002570988
regulation of autophagy (GO:0010506)	51/231	1.47E-04	0.002570988
negative regulation of intrinsic apoptotic signaling pathw	20/64	1.50E-04	0.002613699
platelet degranulation (GO:0002576)	32/125	1.53E-04	0.002641089
positive regulation of GTPase activity (GO:0043547)	48/214	1.53E-04	0.002641089
antigen processing and presentation of peptide antigen v	13/33	1.64E-04	0.002818356
negative regulation of cysteine-type endopeptidase activ	18/55	1.65E-04	0.002835348
positive regulation of extrinsic apoptotic signaling pathwa	44924	1.68E-04	0.002859056
protein ADP-ribosylation (GO:0006471)	44924	1.68E-04	0.002859056
interleukin-12-mediated signaling pathway (GO:0035722	16/46	1.69E-04	0.00287425
response to organic cyclic compound (GO:0014070)	19/60	1.80E-04	0.003041746
regulation of extrinsic apoptotic signaling pathway via de	15/42	1.92E-04	0.003238996
dendritic cell migration (GO:0036336)	44822	1.97E-04	0.003273682
interleukin-6-mediated signaling pathway (GO:0070102)	44822	1.97E-04	0.003273682
regulation of adaptive immune response (GO:0002819)	44822	1.97E-04	0.003273682
T cell migration (GO:0072678)	44822	1.97E-04	0.003273682
neutrophil chemotaxis (GO:0030593)	21/70	1.98E-04	0.003282891
receptor-mediated endocytosis (GO:0006898)	35/143	2.00E-04	0.003316188
positive regulation of hydrolase activity (GO:0051345)	36/149	2.16E-04	0.003537951
regulation of NK T cell activation (GO:0051133)	44687	2.19E-04	0.003537951
regulation of vitamin D biosynthetic process (GO:006055	44687	2.19E-04	0.003537951
response to peptidoglycan (GO:0032494)	44687	2.19E-04	0.003537951
T-helper 17 cell lineage commitment (GO:0072540)	44687	2.19E-04	0.003537951
vesicle fusion with endoplasmic reticulum-Golgi intermec	44687	2.19E-04	0.003537951
positive regulation of protein serine/threonine kinase act	28/106	2.19E-04	0.003537951
cellular response to chemical stress (GO:0062197)	27/101	2.27E-04	0.003667672
negative regulation of extrinsic apoptotic signaling pathw	13/34	2.33E-04	0.003734465
regulation of activated T cell proliferation (GO:0046006)	13/34	2.33E-04	0.003734465
regulation of lipid storage (GO:0010883)	44856	2.34E-04	0.003734465
positive regulation of phosphorylation (GO:0042327)	54/253	2.39E-04	0.00380571

Fc-gamma receptor signaling pathway involved in phagoc	21/71	2.46E-04	0.003910869
Fc receptor signaling pathway (GO:0038093)	29/112	2.47E-04	0.003912636
positive regulation of acute inflammatory response (GO:(	44788	2.56E-04	0.004026938
positive regulation of osteoclast differentiation (GO:0045	44788	2.56E-04	0.004026938
cellular response to peptide (GO:1901653)	18/57	2.74E-04	0.004302193
negative regulation of response to external stimulus (GO:	30/118	2.75E-04	0.004306374
antigen receptor-mediated signaling pathway (GO:00508	42/185	2.92E-04	0.004547806
regulation of viral entry into host cell (GO:0046596)	14/39	2.94E-04	0.004551847
response to peptide (GO:1901652)	14/39	2.94E-04	0.004551847
positive regulation of phosphatidylinositol 3-kinase signa	22/77	3.06E-04	0.004711699
positive regulation of protein modification by small prote	22/77	3.06E-04	0.004711699
cellular response to muramyl dipeptide (GO:0071225)	44721	3.18E-04	0.004813168
negative regulation of glycoprotein biosynthetic process	44721	3.18E-04	0.004813168
negative regulation of necroptotic process (GO:0060546)	44721	3.18E-04	0.004813168
positive regulation of protein polyubiquitination (GO:190	44721	3.18E-04	0.004813168
regulation of T-helper 1 type immune response (GO:0002	44721	3.18E-04	0.004813168
positive regulation of cellular biosynthetic process (GO:0(	41/180	3.18E-04	0.004813168
negative regulation of cysteine-type endopeptidase activ	17/53	3.27E-04	0.004918656
regulation of immune effector process (GO:0002697)	17/53	3.27E-04	0.004918656
cellular response to interleukin-7 (GO:0098761)	44823	3.30E-04	0.004921342
interleukin-7-mediated signaling pathway (GO:0038111)	44823	3.30E-04	0.004921342
leukocyte adhesion to vascular endothelial cell (GO:0061	44823	3.30E-04	0.004921342
positive regulation of peptidyl-serine phosphorylation (G	25/93	3.48E-04	0.00517847
negative regulation of peptidyl-tyrosine phosphorylation	44926	3.53E-04	0.005246353
negative regulation of inflammatory response to antigeni	33/136	3.56E-04	0.005261845
regulation of Notch signaling pathway (GO:0008593)	23/83	3.68E-04	0.005423795
positive regulation of nitric oxide biosynthetic process (G	44892	3.69E-04	0.005429344
dephosphorylation (GO:0016311)	36/153	3.73E-04	0.005472526
defense response to Gram-negative bacterium (GO:0050	21/73	3.75E-04	0.005485714
protein autophosphorylation (GO:0046777)	37/159	3.92E-04	0.005723792
negative regulation of I-kappaB kinase/NF-kappaB signali	14/40	3.97E-04	0.00577598
calcium ion transport (GO:0006816)	29/115	3.99E-04	0.005796975
regulation of cytosolic calcium ion concentration (GO:005	35/148	4.04E-04	0.005840093
regulation of inflammatory response to antigenic stimulu	33/137	4.10E-04	0.005911627
positive regulation of leukocyte chemotaxis (GO:000269(	17/54	4.18E-04	0.006021815
regulation of protein kinase activity (GO:0045859)	28/110	4.24E-04	0.006061192
response to endoplasmic reticulum stress (GO:0034976)	28/110	4.24E-04	0.006061192
negative regulation of autophagy (GO:0010507)	18/59	4.40E-04	0.00628436
positive regulation of innate immune response (GO:0045	13/36	4.49E-04	0.006376629
regulation of defense response to virus by host (GO:0050	13/36	4.49E-04	0.006376629
positive regulation of alpha-beta T cell proliferation (GO:(	44789	4.52E-04	0.00638319
regulation of granulocyte macrophage colony-stimulating	44789	4.52E-04	0.00638319
positive regulation of response to biotic stimulus (GO:00(	15/45	4.55E-04	0.006405658
protein polyubiquitination (GO:0000209)	63/314	4.60E-04	0.006464644
negative regulation of nucleic acid-templated transcriptic	87/464	4.74E-04	0.006636169
regulation of protein serine/threonine kinase activity (GC	28/111	4.96E-04	0.006923082
regulation of chemotaxis (GO:0050920)	12024	4.98E-04	0.006923082

regulation of protein kinase B signaling (GO:0051896)	45/207	4.99E-04	0.006923082
regulation of cellular component movement (GO:005127	16/50	5.00E-04	0.006923082
positive regulation of protein kinase B signaling (GO:0051	37/161	5.07E-04	0.006998137
cellular response to organic cyclic compound (GO:00714(	35/150	5.26E-04	0.007243679
adaptive immune response based on somatic recombinat	44824	5.29E-04	0.007243679
regulation of T cell migration (GO:2000404)	44824	5.29E-04	0.007243679
cortical cytoskeleton organization (GO:0030865)	14/41	5.30E-04	0.007243679
nucleotide-binding oligomerization domain containing sig	44893	5.35E-04	0.0072794
positive regulation of nitric oxide metabolic process (GO:	44893	5.35E-04	0.0072794
negative regulation of extrinsic apoptotic signaling pathw	22/80	5.48E-04	0.007431382
negative regulation of NIK/NF-kappaB signaling (GO:1901	44858	5.51E-04	0.007448473
Notch signaling pathway (GO:0007219)	18/60	5.52E-04	0.007448473
macrophage activation involved in immune response (GC	44755	5.91E-04	0.007881934
negative regulation of endoplasmic reticulum unfolded p	44755	5.91E-04	0.007881934
positive regulation of mRNA metabolic process (GO:1903	44755	5.91E-04	0.007881934
toll-like receptor 9 signaling pathway (GO:0034162)	44755	5.91E-04	0.007881934
positive regulation of smooth muscle cell proliferation (G	15/46	5.93E-04	0.007881934
regulation of B cell proliferation (GO:0030888)	15/46	5.93E-04	0.007881934
regulation of p38MAPK cascade (GO:1900744)	13/37	6.09E-04	0.008074049
regulation of Ras protein signal transduction (GO:004657	23/86	6.37E-04	0.008411456
intrinsic apoptotic signaling pathway in response to DNA	16/51	6.40E-04	0.008411456
regulation of protein modification process (GO:0031399)	16/51	6.40E-04	0.008411456
death-inducing signaling complex assembly (GO:0071550	44688	6.81E-04	0.008774451
marginal zone B cell differentiation (GO:0002315)	44688	6.81E-04	0.008774451
negative regulation of p38MAPK cascade (GO:1903753)	44688	6.81E-04	0.008774451
positive regulation of chemokine (C-X-C motif) ligand 2 p	44688	6.81E-04	0.008774451
positive regulation of NK T cell activation (GO:0051135)	44688	6.81E-04	0.008774451
regulation of natural killer cell proliferation (GO:0032817	44688	6.81E-04	0.008774451
regulation of prostaglandin biosynthetic process (GO:003	44688	6.81E-04	0.008774451
T-helper 17 cell differentiation (GO:0072539)	44688	6.81E-04	0.008774451
positive regulation of cytokine production involved in im	12389	6.89E-04	0.008854533
granulocyte activation (GO:0036230)	44722	7.05E-04	0.008994136
positive regulation of tissue remodeling (GO:0034105)	44722	7.05E-04	0.008994136
regulation of neutrophil migration (GO:1902622)	44722	7.05E-04	0.008994136
T cell receptor signaling pathway (GO:0050852)	36/158	7.08E-04	0.009019137
innate immune response activating cell surface receptor	29/119	7.29E-04	0.009256443
positive regulation of transcription of Notch receptor tar	44790	7.55E-04	0.009543891
regulation of leukocyte migration (GO:0002685)	44790	7.55E-04	0.009543891
epidermal growth factor receptor signaling pathway (GO:	15/47	7.66E-04	0.009654603
regulation of cell growth (GO:0001558)	46/217	7.73E-04	0.009718419
regulation of phosphorylation (GO:0042325)	30/125	7.81E-04	0.009797173
positive regulation of T cell migration (GO:2000406)	44859	8.10E-04	0.01008499
positive regulation of vascular endothelial growth factor	44859	8.10E-04	0.01008499
regulation of heterotypic cell-cell adhesion (GO:0034114	44859	8.10E-04	0.01008499
response to peptide hormone (GO:0043434)	16/52	8.11E-04	0.01008499
positive regulation of protein metabolic process (GO:005	28/115	9.05E-04	0.01121854
positive regulation of pri-miRNA transcription by RNA pol	12754	9.37E-04	0.011589326

transmembrane receptor protein tyrosine kinase signalin	76/404	9.47E-04	0.011684899
positive regulation of stress-activated MAPK cascade (GO	25/99	9.51E-04	0.011701612
protein homooligomerization (GO:0051260)	29/121	9.69E-04	0.011896567
positive regulation of epithelial cell migration (GO:00106	24/94	0.001008061	0.012292612
negative regulation of cell adhesion (GO:0007162)	20/73	0.001010384	0.012292612
positive regulation of JNK cascade (GO:0046330)	20/73	0.001010384	0.012292612
regulation of actin filament-based process (GO:0032970)	20/73	0.001010384	0.012292612
regulation of JNK cascade (GO:0046328)	26/105	0.001039865	0.012530394
actin cytoskeleton reorganization (GO:0031532)	18/63	0.001044496	0.012530394
positive regulation of Ras protein signal transduction (GO	18/63	0.001044496	0.012530394
activation of cysteine-type endopeptidase activity (GO:0(	44756	0.001046812	0.012530394
microvillus organization (GO:0032528)	44756	0.001046812	0.012530394
myeloid dendritic cell activation (GO:0001773)	44756	0.001046812	0.012530394
regulation of IRE1-mediated unfolded protein response ((	44756	0.001046812	0.012530394
positive regulation of B cell proliferation (GO:0030890)	44895	0.001057173	0.012596359
regulation of type I interferon-mediated signaling pathwa	44895	0.001057173	0.012596359
negative regulation of cellular macromolecule biosynthet	98/547	0.001068245	0.01269916
membrane protein proteolysis (GO:0033619)	13/39	0.001075325	0.012754143
peptidyl-serine phosphorylation (GO:0018105)	35/156	0.001114018	0.013182967
leukocyte tethering or rolling (GO:0050901)	44791	0.001201823	0.014157528
positive regulation of amyloid-beta formation (GO:19020	44791	0.001201823	0.014157528
regulation of phosphatidylinositol 3-kinase signaling (GO:	26/106	0.00120697	0.014185991
negative regulation of B cell activation (GO:0050869)	44826	0.00122166	0.014229875
peptidyl-threonine dephosphorylation (GO:0035970)	44826	0.00122166	0.014229875
positive regulation of amyloid precursor protein catabolic	44826	0.00122166	0.014229875
regulation of platelet activation (GO:0010543)	44826	0.00122166	0.014229875
positive regulation of reactive oxygen species metabolic p	15/49	0.001239925	0.014378144
receptor internalization (GO:0031623)	15/49	0.001239925	0.014378144
negative regulation of protein kinase activity (GO:000646	23/90	0.001253687	0.014462528
positive regulation of cell cycle G1/S phase transition (GC	13119	0.001255553	0.014462528
regulation of JUN kinase activity (GO:0043506)	13119	0.001255553	0.014462528
regulation of cytoskeleton organization (GO:0051493)	27/112	0.001297108	0.014908132
copper ion transport (GO:0006825)	44723	0.001376217	0.015138789
negative regulation of interleukin-17 production (GO:003	44723	0.001376217	0.015138789
negative regulation of T-helper cell differentiation (GO:0(	44723	0.001376217	0.015138789
positive regulation of epidermal growth factor-activated	44723	0.001376217	0.015138789
regulation of cysteine-type endopeptidase activity involv	44723	0.001376217	0.015138789
tryptophan metabolic process (GO:0006568)	44723	0.001376217	0.015138789
cadmium ion transmembrane transport (GO:0070574)	44656	0.001381287	0.015138789
cadmium ion transport (GO:0015691)	44656	0.001381287	0.015138789
cellular response to nicotine (GO:0071316)	44656	0.001381287	0.015138789
copper ion import (GO:0015677)	44656	0.001381287	0.015138789
endothelin receptor signaling pathway (GO:0086100)	44656	0.001381287	0.015138789
negative regulation of PERK-mediated unfolded protein r	44656	0.001381287	0.015138789
negative regulation of vitamin D biosynthetic process (GC	44656	0.001381287	0.015138789
p38MAPK cascade (GO:0038066)	44656	0.001381287	0.015138789
positive regulation of natural killer cell proliferation (GO:(	44656	0.001381287	0.015138789

positive regulation of prostaglandin biosynthetic process	44656	0.001381287	0.015138789
positive regulation of T-helper 1 cell cytokine production	44656	0.001381287	0.015138789
positive regulation of transcription from RNA polymerase	44656	0.001381287	0.015138789
regulation of receptor catabolic process (GO:2000644)	44656	0.001381287	0.015138789
regulation of sodium:proton antiporter activity (GO:0032	44656	0.001381287	0.015138789
regulation of T-helper 1 cell cytokine production (GO:200	44656	0.001381287	0.015138789
toll-like receptor 2 signaling pathway (GO:0034134)	44656	0.001381287	0.015138789
cellular response to starvation (GO:0009267)	35/158	0.001409532	0.015415828
negative regulation of response to biotic stimulus (GO:00	11628	0.001444216	0.015728938
positive regulation of mononuclear cell migration (GO:00	11628	0.001444216	0.015728938
positive regulation of RNA metabolic process (GO:00512	14/45	0.001500297	0.01622914
regulation of pri-miRNA transcription by RNA polymerase	14/45	0.001500297	0.01622914
regulation of receptor signaling pathway via JAK-STAT (G	14/45	0.001500297	0.01622914
positive regulation of cytosolic calcium ion concentration	33/147	0.00150264	0.01622914
establishment of protein localization to membrane (GO:0	19/70	0.001506937	0.016241775
cellular calcium ion homeostasis (GO:0006874)	31/136	0.001588285	0.017065799
actin filament reorganization (GO:0090527)	44689	0.001616241	0.017065799
antigen processing and presentation of endogenous pept	44689	0.001616241	0.017065799
positive regulation of glial cell migration (GO:1903977)	44689	0.001616241	0.017065799
positive regulation of MHC class II biosynthetic process ((	44689	0.001616241	0.017065799
regulation of activation of Janus kinase activity (GO:0010	44689	0.001616241	0.017065799
regulation of dendritic cell chemotaxis (GO:2000508)	44689	0.001616241	0.017065799
regulation of interleukin-18 production (GO:0032661)	44689	0.001616241	0.017065799
regulation of protein K63-linked ubiquitination (GO:1900	44689	0.001616241	0.017065799
regulation of toll-like receptor 3 signaling pathway (GO:0	44689	0.001616241	0.017065799
positive regulation of T cell mediated immunity (GO:0002	13485	0.001658707	0.017431891
regulation of cell cycle G1/S phase transition (GO:190280	13485	0.001658707	0.017431891
cellular response to oxidative stress (GO:0034599)	29/125	0.001660979	0.017431891
cellular response to arsenic-containing substance (GO:00	44757	0.00173895	0.017995708
integrated stress response signaling (GO:0140467)	44757	0.00173895	0.017995708
membrane raft organization (GO:0031579)	44757	0.00173895	0.017995708
microvillus assembly (GO:0030033)	44757	0.00173895	0.017995708
prostanoid biosynthetic process (GO:0046457)	44757	0.00173895	0.017995708
protein homotrimerization (GO:0070207)	44757	0.00173895	0.017995708
protein trimerization (GO:0070206)	44757	0.00173895	0.017995708
artery development (GO:0060840)	44827	0.001772765	0.018272842
regulation of cysteine-type endopeptidase activity (GO:2(	44827	0.001772765	0.018272842
regulation of G1/S transition of mitotic cell cycle (GO:200	19/71	0.001805949	0.018514201
JNK cascade (GO:0007254)	13/41	0.001806872	0.018514201
negative regulation of cell-cell adhesion (GO:0022408)	13/41	0.001806872	0.018514201
regulation of glucose transmembrane transport (GO:001(	44792	0.00183612	0.018776853
regulation of protein ubiquitination (GO:0031396)	26/109	0.001854511	0.018927668
positive regulation of response to stimulus (GO:0048584)	14/46	0.001897139	0.019324778
regulation of cellular biosynthetic process (GO:0031326)	11994	0.001939974	0.019681782
chemokine-mediated signaling pathway (GO:0070098)	16/56	0.001943552	0.019681782
peptidyl-tyrosine modification (GO:0018212)	16/56	0.001943552	0.019681782
cellular response to lectin (GO:1990858)	27/115	0.001961665	0.019788056

stimulatory C-type lectin receptor signaling pathway (GO	27/115	0.001961665	0.019788056
protein modification by small protein removal (GO:0070(	54/276	0.002017868	0.020315549
RNA metabolic process (GO:0016070)	30/133	0.002220237	0.022170324
leukocyte cell-cell adhesion (GO:0007159)	44862	0.002231969	0.022170324
positive regulation of monooxygenase activity (GO:00327	44862	0.002231969	0.022170324
regulation of calcium-mediated signaling (GO:0050848)	44862	0.002231969	0.022170324
regulation of DNA damage response, signal transduction	44862	0.002231969	0.022170324
regulation of immunoglobulin production (GO:0002637)	44862	0.002231969	0.022170324
response to interferon-beta (GO:0035456)	44862	0.002231969	0.022170324
regulation of epidermal growth factor receptor signaling	18/67	0.002245456	0.022261721
regulated exocytosis (GO:0045055)	38/180	0.002273632	0.022498128
positive regulation of cellular metabolic process (GO:003	25/105	0.002304917	0.022764337
carboxylic acid transport (GO:0046942)	16/57	0.002374753	0.02334464
positive regulation of proteolysis (GO:0045862)	16/57	0.002374753	0.02334464
negative regulation of cold-induced thermogenesis (GO:(	14/47	0.002377154	0.02334464
antigen processing and presentation of exogenous peptic	20/78	0.002420848	0.023691525
adipose tissue development (GO:0060612)	44724	0.0024444	0.023691525
mRNA transcription (GO:0009299)	44724	0.0024444	0.023691525
positive regulation of leukocyte proliferation (GO:00706(	44724	0.0024444	0.023691525
positive regulation of neuroinflammatory response (GO:(	44724	0.0024444	0.023691525
protein auto-ADP-ribosylation (GO:0070213)	44724	0.0024444	0.023691525
regulation of MHC class II biosynthetic process (GO:0045	44724	0.0024444	0.023691525
regulation of transcription by RNA polymerase II (GO:000	336/2206	0.002471123	0.023905928
nucleotide-binding domain, leucine rich repeat containin	44828	0.002505952	0.024108183
positive regulation of transcription from RNA polymerase	44828	0.002505952	0.024108183
regulation of vascular endothelial growth factor receptor	44828	0.002505952	0.024108183
negative regulation of smooth muscle cell proliferation ((	12359	0.002565668	0.024637051
negative regulation of protein phosphorylation (GO:0001	33/152	0.002673682	0.025626896
cortical actin cytoskeleton organization (GO:0030866)	44793	0.002707479	0.02585543
positive regulation of activated T cell proliferation (GO:0(	44793	0.002707479	0.02585543
filopodium assembly (GO:0046847)	44758	0.002739784	0.025878506
negative regulation of epithelial cell differentiation (GO:(	44758	0.002739784	0.025878506
neutrophil activation (GO:0042119)	44758	0.002739784	0.025878506
positive regulation of leukocyte adhesion to vascular end	44758	0.002739784	0.025878506
positive regulation of myeloid leukocyte cytokine produc	44758	0.002739784	0.025878506
regulation of hormone secretion (GO:0046883)	44758	0.002739784	0.025878506
fat cell differentiation (GO:0045444)	16/58	0.002882576	0.027128591
receptor metabolic process (GO:0043112)	16/58	0.002882576	0.027128591
positive regulation of T cell differentiation (GO:0045582)	13/43	0.002907053	0.027309481
intrinsic apoptotic signaling pathway in response to endo	44863	0.003006796	0.028195495
peptidyl-tyrosine phosphorylation (GO:0018108)	18/69	0.003186985	0.029629276
ATF6-mediated unfolded protein response (GO:0036500)	44690	0.003239544	0.029629276
endothelial cell chemotaxis (GO:0035767)	44690	0.003239544	0.029629276
kynurenine metabolic process (GO:0070189)	44690	0.003239544	0.029629276
positive regulation of macrophage cytokine production ((	44690	0.003239544	0.029629276
positive regulation of NLRP3 inflammasome complex ass	44690	0.003239544	0.029629276
positive regulation of smooth muscle cell apoptotic proc	44690	0.003239544	0.029629276

regulation of endothelial cell development (GO:1901550)	44690	0.003239544	0.029629276
regulation of endothelial cell differentiation (GO:004560:	44690	0.003239544	0.029629276
regulation of interleukin-23 production (GO:0032667)	44690	0.003239544	0.029629276
regulation of leukocyte mediated cytotoxicity (GO:00019	44690	0.003239544	0.029629276
regulation of PERK-mediated unfolded protein response (	44690	0.003239544	0.029629276
regulation of tumor necrosis factor superfamily cytokine	44690	0.003239544	0.029629276
response to vitamin (GO:0033273)	44690	0.003239544	0.029629276
positive regulation of cell adhesion (GO:0045785)	20/80	0.003329452	0.030398074
positive regulation of epidermal growth factor receptor s	12724	0.003344616	0.03048295
regulation of neutrophil chemotaxis (GO:0090022)	44829	0.003460168	0.031480865
response to reactive oxygen species (GO:0000302)	16/59	0.003476971	0.031578431
negative regulation of secretion by cell (GO:1903531)	14580	0.003544105	0.032076004
regulation of peptidyl-threonine phosphorylation (GO:00	14580	0.003544105	0.032076004
regulation of cyclin-dependent protein kinase activity (G(	15/54	0.003580179	0.032346139
negative regulation of phosphorylation (GO:0042326)	21/86	0.003611181	0.032513145
positive regulation of endothelial cell migration (GO:001(	21/86	0.003611181	0.032513145
lymphocyte chemotaxis (GO:0048247)	13/44	0.003633362	0.03254365
protein K63-linked ubiquitination (GO:0070534)	13/44	0.003633362	0.03254365
regulation of endothelial cell apoptotic process (GO:2000	13/44	0.003633362	0.03254365
cellular response to bacterial lipopeptide (GO:0071221)	44657	0.003706861	0.032583995
ISG15-protein conjugation (GO:0032020)	44657	0.003706861	0.032583995
negative regulation of amyloid precursor protein biosynth	44657	0.003706861	0.032583995
negative regulation of toll-like receptor 2 signaling pathw	44657	0.003706861	0.032583995
positive regulation of killing of cells of other organism (G(	44657	0.003706861	0.032583995
positive regulation of toll-like receptor 7 signaling pathwa	44657	0.003706861	0.032583995
purine ribonucleoside catabolic process (GO:0046130)	44657	0.003706861	0.032583995
regulation of interleukin-1-mediated signaling pathway ((	44657	0.003706861	0.032583995
regulation of T-helper 17 cell lineage commitment (GO:2(	44657	0.003706861	0.032583995
regulation of type 2 immune response (GO:0002828)	44657	0.003706861	0.032583995
response to angiotensin (GO:1990776)	44657	0.003706861	0.032583995
protein stabilization (GO:0050821)	37/179	0.003741757	0.032835185
negative regulation of growth (GO:0045926)	28/126	0.003819284	0.033458991
positive regulation of phosphatase activity (GO:0010922)	44794	0.003870569	0.033794293
positive regulation of transcription from RNA polymerase	44794	0.003870569	0.033794293
positive regulation of endopeptidase activity (GO:001095	44864	0.00398161	0.034647342
regulation of macrophage activation (GO:0043030)	44864	0.00398161	0.034647342
negative regulation of macrophage derived foam cell diff	44725	0.004033074	0.034803683
regulation of chemokine (C-X-C motif) ligand 2 productio	44725	0.004033074	0.034803683
regulation of receptor signaling pathway via STAT (GO:19	44725	0.004033074	0.034803683
relaxation of cardiac muscle (GO:0055119)	44725	0.004033074	0.034803683
response to UV-B (GO:0010224)	44725	0.004033074	0.034803683
negative regulation of chemokine production (GO:00326(	44759	0.004129095	0.035338797
negative regulation of peptidyl-threonine phosphorylatio	44759	0.004129095	0.035338797
negative regulation of phagocytosis (GO:0050765)	44759	0.004129095	0.035338797
regulation of establishment of endothelial barrier (GO:19	44759	0.004129095	0.035338797
regulation of NLRP3 inflammasome complex assembly (G	44759	0.004129095	0.035338797
cellular response to hormone stimulus (GO:0032870)	19/76	0.004157063	0.035519639

positive regulation of immunoglobulin production (GO:0(	13089	0.004302106	0.036698587
regulation of blood vessel endothelial cell migration (GO:	15/55	0.004330342	0.036878892
negative regulation of ERBB signaling pathway (GO:1901:	14946	0.004462168	0.037815599
positive regulation of intrinsic apoptotic signaling pathwa	14946	0.004462168	0.037815599
positive regulation of wound healing (GO:0090303)	14946	0.004462168	0.037815599
positive regulation of chemotaxis (GO:0050921)	13/45	0.004499922	0.038073445
peptidyl-serine modification (GO:0018209)	35/169	0.004562848	0.038543079
regulation of monocyte chemotaxis (GO:0090025)	44830	0.004677686	0.039385058
regulation of regulatory T cell differentiation (GO:004558	44830	0.004677686	0.039385058
ERBB signaling pathway (GO:0038127)	17/66	0.004708621	0.039581365
positive regulation of multicellular organismal process (G	63/345	0.004944946	0.041500796
enzyme linked receptor protein signaling pathway (GO:0(	30/140	0.004953683	0.04150707
B cell differentiation (GO:0030183)	16/61	0.004968821	0.041566872
negative regulation of response to DNA damage stimulus	44865	0.005189895	0.043276897
regulation of macrophage derived foam cell differentiatic	44865	0.005189895	0.043276897
negative regulation of metabolic process (GO:0009892)	15/56	0.005203559	0.043321294
protein localization to membrane (GO:0072657)	39/195	0.005357799	0.044534028
negative regulation of phosphate metabolic process (GO:	44795	0.005384235	0.04456957
positive regulation of granulocyte chemotaxis (GO:00716	44795	0.005384235	0.04456957
positive regulation of fat cell differentiation (GO:004560(	14/51	0.005396393	0.04456957
regulation of epithelial cell migration (GO:0010632)	14/51	0.005396393	0.04456957
membrane assembly (GO:0071709)	13455	0.005465204	0.044994823
regulation of osteoclast differentiation (GO:0045670)	13455	0.005465204	0.044994823
erythrocyte differentiation (GO:0030218)	13/46	0.005525263	0.045376696
proteasome-mediated ubiquitin-dependent protein catat	59/321	0.005529057	0.045376696
T cell differentiation (GO:0030217)	15311	0.005560913	0.04556616
cellular response to interleukin-4 (GO:0071353)	44691	0.005774455	0.046436987
cytoplasmic pattern recognition receptor signaling pathw	44691	0.005774455	0.046436987
immunoglobulin mediated immune response (GO:00160(	44691	0.005774455	0.046436987
indolalkylamine catabolic process (GO:0046218)	44691	0.005774455	0.046436987
negative regulation of cholesterol storage (GO:0010887)	44691	0.005774455	0.046436987
negative regulation of heterotypic cell-cell adhesion (GO:	44691	0.005774455	0.046436987
positive regulation of cell activation (GO:0050867)	44691	0.005774455	0.046436987
positive regulation of vascular endothelial growth factor	44691	0.005774455	0.046436987
protein poly-ADP-ribosylation (GO:0070212)	44691	0.005774455	0.046436987
regulation of axon guidance (GO:1902667)	44691	0.005774455	0.046436987
regulation of cell-cell adhesion involved in gastrulation (G	44691	0.005774455	0.046436987
response to laminar fluid shear stress (GO:0034616)	44691	0.005774455	0.046436987
regulation of protein binding (GO:0043393)	26/118	0.005825327	0.046773687
establishment of vesicle localization (GO:0051650)	44760	0.00599191	0.047962979
positive regulation of lymphocyte chemotaxis (GO:01401	44760	0.00599191	0.047962979
antigen processing and presentation of exogenous peptic	18/73	0.006059521	0.04842956
protein localization to plasma membrane (GO:0072659)	29/136	0.006081906	0.048486743
positive regulation of ERK1 and ERK2 cascade (GO:00703	35/172	0.006085343	0.048486743
regulation of MAPK cascade (GO:0043408)	34/166	0.006119885	0.048639015
Ras protein signal transduction (GO:0007265)	30/142	0.006123179	0.048639015
positive regulation of intracellular protein transport (GO:	31/148	0.006145802	0.048744186

negative regulation of insulin receptor signaling pathway	44831	0.006203531	0.048783043
amyloid precursor protein catabolic process (GO:004298	44726	0.006272776	0.048783043
manganese ion transport (GO:0006828)	44726	0.006272776	0.048783043
negative regulation of bone mineralization (GO:0030502)	44726	0.006272776	0.048783043
negative regulation of DNA damage response, signal tran	44726	0.006272776	0.048783043
negative regulation of interleukin-12 production (GO:003	44726	0.006272776	0.048783043
negative regulation of viral transcription (GO:0032897)	44726	0.006272776	0.048783043
nuclear migration (GO:0007097)	44726	0.006272776	0.048783043
positive regulation of lymphocyte migration (GO:200040	44726	0.006272776	0.048783043
regulation of macrophage cytokine production (GO:0010	44726	0.006272776	0.048783043
regulation of protein kinase C signaling (GO:0090036)	44726	0.006272776	0.048783043
relaxation of muscle (GO:0090075)	44726	0.006272776	0.048783043
T cell differentiation in thymus (GO:0033077)	44726	0.006272776	0.048783043
positive regulation of autophagy (GO:0010508)	21/90	0.006334832	0.049192005
superoxide metabolic process (GO:0006801)	11963	0.006667135	0.051695177
monocyte chemotaxis (GO:0002548)	15676	0.006863837	0.053061957
positive regulation of protein tyrosine kinase activity (GO	15676	0.006863837	0.053061957
B cell activation (GO:0042113)	20/85	0.006898547	0.053251041
negative regulation of signal transduction (GO:0009968)	50/267	0.007007681	0.053933193
protein deubiquitination (GO:0016579)	50/267	0.007007681	0.053933193
NIK/NF-kappaB signaling (GO:0038061)	18/74	0.007036799	0.053997295
proteolysis involved in cellular protein catabolic process (	18/74	0.007036799	0.053997295
regulation of actin cytoskeleton organization (GO:00329	21/91	0.007230006	0.055398057
positive regulation of JUN kinase activity (GO:0043507)	44796	0.007310357	0.055848976
regulation of B cell receptor signaling pathway (GO:0050	44796	0.007310357	0.055848976
negative regulation of cellular catabolic process (GO:003	17/69	0.007584189	0.05696687
cellular response to interleukin-18 (GO:0071351)	44658	0.007741792	0.05696687
chemical homeostasis within a tissue (GO:0048875)	44658	0.007741792	0.05696687
complement activation, alternative pathway (GO:000695	44658	0.007741792	0.05696687
interleukin-18-mediated signaling pathway (GO:0035655	44658	0.007741792	0.05696687
macropinocytosis (GO:0044351)	44658	0.007741792	0.05696687
negative regulation of interferon-gamma-mediated signa	44658	0.007741792	0.05696687
negative regulation of neurotransmitter secretion (GO:0(	44658	0.007741792	0.05696687
negative regulation of response to interferon-gamma (G(	44658	0.007741792	0.05696687
negative regulation of T-helper 17 type immune respons	44658	0.007741792	0.05696687
nucleotide-binding oligomerization domain containing 2 s	44658	0.007741792	0.05696687
positive regulation of activation of Janus kinase activity (	44658	0.007741792	0.05696687
positive regulation of fibroblast apoptotic process (GO:2(	44658	0.007741792	0.05696687
positive regulation of interleukin-23 production (GO:003	44658	0.007741792	0.05696687
positive regulation of miRNA metabolic process (GO:200(	44658	0.007741792	0.05696687
positive regulation of oxidative stress-induced cell death	44658	0.007741792	0.05696687
positive regulation of receptor catabolic process (GO:200	44658	0.007741792	0.05696687
positive regulation of unsaturated fatty acid biosynthetic	44658	0.007741792	0.05696687
protein desumoylation (GO:0016926)	44658	0.007741792	0.05696687
regulation of necrotic cell death (GO:0010939)	44658	0.007741792	0.05696687
regulation of T-helper 1 cell differentiation (GO:0045625)	44658	0.007741792	0.05696687
regulation of toll-like receptor 7 signaling pathway (GO:0	44658	0.007741792	0.05696687

release of sequestered calcium ion into cytosol by endop	44658	0.007741792	0.05696687
sphingosine-1-phosphate receptor signaling pathway (GC	44658	0.007741792	0.05696687
surfactant homeostasis (GO:0043129)	44658	0.007741792	0.05696687
synaptic vesicle budding from presynaptic endocytic zone	44658	0.007741792	0.05696687
negative regulation of cellular response to insulin stimulu	44832	0.008084801	0.059406709
negative regulation of mitotic cell cycle (GO:0045930)	13/48	0.008131475	0.059581116
positive regulation of blood vessel endothelial cell migrat	13/48	0.008131475	0.059581116
positive regulation of neutrophil chemotaxis (GO:009002	44761	0.008416127	0.060978776
positive regulation of oxidoreductase activity (GO:00513	44761	0.008416127	0.060978776
prostaglandin biosynthetic process (GO:0001516)	44761	0.008416127	0.060978776
pyroptosis (GO:0070269)	44761	0.008416127	0.060978776
regulation of leukocyte chemotaxis (GO:0002688)	44761	0.008416127	0.060978776
regulation of lymphocyte proliferation (GO:0050670)	44761	0.008416127	0.060978776
regulation of neuroinflammatory response (GO:0150077)	44761	0.008416127	0.060978776
regulation of T cell cytokine production (GO:0002724)	44761	0.008416127	0.060978776
apoptotic cell clearance (GO:0043277)	12328	0.008450386	0.061056681
regulation of sprouting angiogenesis (GO:1903670)	12328	0.008450386	0.061056681
connective tissue development (GO:0061448)	14185	0.008523955	0.061417399
regulation of cell communication (GO:0010646)	14185	0.008523955	0.061417399
positive regulation of cellular amide metabolic process (G	19/81	0.008609164	0.061945438
cellular metal ion homeostasis (GO:0006875)	23/104	0.008717488	0.062638102
regulation of cell cycle (GO:0051726)	54/296	0.008906919	0.063910835
protein localization to cell periphery (GO:1990778)	29/140	0.009183471	0.065648
macrophage differentiation (GO:0030225)	44727	0.009295335	0.065648
negative regulation of leukocyte activation (GO:0002695)	44727	0.009295335	0.065648
positive regulation of cell killing (GO:0031343)	44727	0.009295335	0.065648
positive regulation of natural killer cell activation (GO:00	44727	0.009295335	0.065648
regulation of macrophage differentiation (GO:0045649)	44727	0.009295335	0.065648
regulation of triglyceride biosynthetic process (GO:00108	44727	0.009295335	0.065648
regulation of RNA splicing (GO:0043484)	18/76	0.00937316	0.065648
negative regulation of oxidative stress-induced neuron de	44692	0.009439664	0.065648
negative regulation of platelet-derived growth factor rec	44692	0.009439664	0.065648
nucleus localization (GO:0051647)	44692	0.009439664	0.065648
positive regulation of DNA methylation-dependent heter	44692	0.009439664	0.065648
positive regulation of integrin activation (GO:0033625)	44692	0.009439664	0.065648
positive regulation of macrophage differentiation (GO:00	44692	0.009439664	0.065648
pyrimidine nucleoside catabolic process (GO:0046135)	44692	0.009439664	0.065648
rDNA heterochromatin assembly (GO:0000183)	44692	0.009439664	0.065648
regulation of CD4-positive, alpha-beta T cell proliferation	44692	0.009439664	0.065648
regulation of T cell apoptotic process (GO:0070232)	44692	0.009439664	0.065648
regulation of T-helper 2 cell cytokine production (GO:200	44692	0.009439664	0.065648
regulation of toll-like receptor 2 signaling pathway (GO:0	44692	0.009439664	0.065648
response to sterol (GO:0036314)	44692	0.009439664	0.065648
T cell homeostasis (GO:0043029)	44692	0.009439664	0.065648
tryptophan catabolic process (GO:0006569)	44692	0.009439664	0.065648
heterochromatin assembly (GO:0031507)	44797	0.009712565	0.067007667
leukotriene metabolic process (GO:0006691)	44797	0.009712565	0.067007667

long-chain fatty-acyl-CoA metabolic process (GO:003533(	44797	0.009712565	0.067007667
negative regulation of ossification (GO:0030279)	44797	0.009712565	0.067007667
positive regulation of neuron apoptotic process (GO:004:	44797	0.009712565	0.067007667
regulation of cell size (GO:0008361)	44797	0.009712565	0.067007667
positive regulation of protein ubiquitination (GO:003139(	19/82	0.009846577	0.067752277
regulation of cyclin-dependent protein serine/threonine	19/82	0.009846577	0.067752277
positive regulation of mRNA catabolic process (GO:0061(	16407	0.010181302	0.069962786
cellular protein catabolic process (GO:0044257)	15/60	0.010217284	0.070117295
negative regulation of interferon-gamma production (GO	44833	0.010369908	0.070977172
positive regulation of leukocyte migration (GO:0002687)	44833	0.010369908	0.070977172
endothelial cell migration (GO:0043542)	14550	0.010480328	0.071544417
protein acylation (GO:0043543)	14550	0.010480328	0.071544417
B cell receptor signaling pathway (GO:0050853)	12693	0.010577794	0.071926227
regulation of amyloid-beta formation (GO:1902003)	12693	0.010577794	0.071926227
regulation of cell adhesion mediated by integrin (GO:003	12693	0.010577794	0.071926227
negative regulation of cytokine-mediated signaling pathw	14/55	0.010929946	0.07422362
small GTPase mediated signal transduction (GO:0007264	23/106	0.010981793	0.074478345
protein-containing complex subunit organization (GO:00(	24/112	0.011113499	0.075273305
modulation by symbiont of entry into host (GO:0052372)	44762	0.011490022	0.077419796
positive regulation of alpha-beta T cell activation (GO:00(	44762	0.011490022	0.077419796
positive regulation of protein processing (GO:0010954)	44762	0.011490022	0.077419796
regulation of protein modification by small protein conju	44762	0.011490022	0.077419796
transforming growth factor beta receptor signaling pathw	20/89	0.01159966	0.0780573
transcription by RNA polymerase II (GO:0006366)	57/320	0.011939845	0.080242554
proteasomal protein catabolic process (GO:0010498)	39/205	0.012301853	0.082568636
negative regulation of cell junction assembly (GO:190188	44798	0.012654875	0.084719166
positive regulation of release of cytochrome c from mito(	44798	0.012654875	0.084719166
lymphocyte differentiation (GO:0030098)	19/84	0.012746783	0.085005824
nuclear export (GO:0051168)	19/84	0.012746783	0.085005824
vascular transport (GO:0010232)	19/84	0.012746783	0.085005824
ubiquitin-dependent protein catabolic process (GO:0006(	62/354	0.012890963	0.085857121
regulation of T cell receptor signaling pathway (GO:0050(	13058	0.013088073	0.086443981
positive regulation of binding (GO:0051099)	20/90	0.013103899	0.086443981
extrinsic apoptotic signaling pathway via death domain re	44834	0.013107755	0.086443981
activation of NF-kappaB-inducing kinase activity (GO:000	44728	0.013228675	0.086443981
cellular polysaccharide catabolic process (GO:0044247)	44728	0.013228675	0.086443981
negative regulation of anoikis (GO:2000811)	44728	0.013228675	0.086443981
negative regulation of macrophage activation (GO:00430	44728	0.013228675	0.086443981
negative regulation of type I interferon-mediated signalir	44728	0.013228675	0.086443981
platelet-derived growth factor receptor signaling pathwa	44728	0.013228675	0.086443981
positive regulation of double-strand break repair via nonl	44728	0.013228675	0.086443981
positive regulation of TORC1 signaling (GO:1904263)	44728	0.013228675	0.086443981
protein localization to endoplasmic reticulum (GO:00709	44728	0.013228675	0.086443981
regulation of establishment of cell polarity (GO:2000114)	44728	0.013228675	0.086443981
regulation of interleukin-1 production (GO:0032652)	44728	0.013228675	0.086443981
regulation of isotype switching (GO:0045191)	44728	0.013228675	0.086443981
regulation of hydrolase activity (GO:0051336)	17/73	0.01344732	0.08765223

regulation of Rho protein signal transduction (GO:003502	17/73	0.01344732	0.08765223
blood circulation (GO:0008015)	13/51	0.013747201	0.08785481
negative regulation of protein ubiquitination (GO:003139	13/51	0.013747201	0.08785481
negative regulation of transport (GO:0051051)	13/51	0.013747201	0.08785481
macroautophagy (GO:0016236)	25/120	0.013785473	0.08785481
coronary vasculature morphogenesis (GO:0060977)	44659	0.013867362	0.08785481
cytoplasmic sequestering of NF-kappaB (GO:0007253)	44659	0.013867362	0.08785481
fusion of virus membrane with host plasma membrane ((	44659	0.013867362	0.08785481
membrane fusion involved in viral entry into host cell (GO	44659	0.013867362	0.08785481
myeloid leukocyte mediated immunity (GO:0002444)	44659	0.013867362	0.08785481
negative regulation of regulated secretory pathway (GO::	44659	0.013867362	0.08785481
negative regulation of T-helper 17 cell differentiation (GO	44659	0.013867362	0.08785481
positive regulation of adaptive immune response (GO:00(	44659	0.013867362	0.08785481
positive regulation of dendritic cell chemotaxis (GO:2000	44659	0.013867362	0.08785481
positive regulation of extracellular matrix disassembly (G	44659	0.013867362	0.08785481
positive regulation of T-helper 2 cell cytokine production	44659	0.013867362	0.08785481
regulation of extracellular matrix constituent secretion ((	44659	0.013867362	0.08785481
regulation of nitrogen compound metabolic process (GO:	44659	0.013867362	0.08785481
regulation of oxidative stress-induced neuron death (GO:	44659	0.013867362	0.08785481
regulation of pattern recognition receptor signaling path	44659	0.013867362	0.08785481
regulation of T-helper 2 cell differentiation (GO:0045628)	44659	0.013867362	0.08785481
regulation of transcription from RNA polymerase II prom(	44659	0.013867362	0.08785481
regulation of vascular wound healing (GO:0061043)	44659	0.013867362	0.08785481
synaptic vesicle budding (GO:0070142)	44659	0.013867362	0.08785481
histone H3-K9 demethylation (GO:0033169)	44693	0.014436294	0.090794852
nucleoside catabolic process (GO:0009164)	44693	0.014436294	0.090794852
regulation of glycogen metabolic process (GO:0070873)	44693	0.014436294	0.090794852
regulation of myoblast fusion (GO:1901739)	44693	0.014436294	0.090794852
regulation of natural killer cell activation (GO:0032814)	44693	0.014436294	0.090794852
synaptic vesicle fusion to presynaptic active zone membr	44693	0.014436294	0.090794852
calcium ion homeostasis (GO:0055074)	21/97	0.014995535	0.094085279
protein K48-linked ubiquitination (GO:0070936)	14/57	0.01499569	0.094085279
chondroitin sulfate biosynthetic process (GO:0030206)	44763	0.015299756	0.095302434
NAD biosynthetic process (GO:0009435)	44763	0.015299756	0.095302434
nuclear-transcribed mRNA poly(A) tail shortening (GO:00	44763	0.015299756	0.095302434
positive regulation of antigen receptor-mediated signalin	44763	0.015299756	0.095302434
regulation of anoikis (GO:2000209)	44763	0.015299756	0.095302434
regulation of fibroblast migration (GO:0010762)	44763	0.015299756	0.095302434
DNA damage response, signal transduction by p53 class n	17/74	0.015359232	0.095558336
keratinocyte differentiation (GO:0030216)	15281	0.01540388	0.095607117
regulation of filopodium assembly (GO:0051489)	15281	0.01540388	0.095607117
skin development (GO:0043588)	18/80	0.01588458	0.098473025
actin filament organization (GO:0007015)	30/152	0.015926303	0.098613999
membrane fusion (GO:0061025)	13424	0.01601995	0.098957955
transition metal ion transport (GO:0000041)	13424	0.01601995	0.098957955
histone lysine demethylation (GO:0070076)	44799	0.016200298	0.099598279
negative regulation of intrinsic apoptotic signaling pathw	44799	0.016200298	0.099598279

positive regulation of G1/S transition of mitotic cell cycle	44799	0.016200298	0.099598279
positive regulation of T cell mediated cytotoxicity (GO:00	44799	0.016200298	0.099598279
transport across blood-brain barrier (GO:0150104)	19/86	0.016283763	0.099993082
prostaglandin metabolic process (GO:0006693)	11567	0.016346885	0.100143948
protein palmitoylation (GO:0018345)	11567	0.016346885	0.100143948
cellular response to fibroblast growth factor stimulus (GC	20/92	0.016573202	0.101410819
positive regulation of cell-cell adhesion (GO:0022409)	17502	0.01732515	0.105887242
membrane organization (GO:0061024)	44/242	0.017810975	0.108535905
negative regulation of cytokine production involved in im	44729	0.018192091	0.108535905
negative regulation of viral entry into host cell (GO:0046	44729	0.018192091	0.108535905
pyrimidine-containing compound catabolic process (GO:(	44729	0.018192091	0.108535905
synaptic vesicle membrane organization (GO:0048499)	44729	0.018192091	0.108535905
negative regulation of angiogenesis (GO:0016525)	19/87	0.018317725	0.108535905
regulation of transcription from RNA polymerase II prom	19/87	0.018317725	0.108535905
nucleic acid-templated transcription (GO:0097659)	15646	0.018434222	0.108535905
regulation of transcription, DNA-templated (GO:0006355	330/2244	0.018657623	0.108535905
cellular divalent inorganic cation homeostasis (GO:00725	23/111	0.01874298	0.108535905
regulation of signal transduction (GO:0009966)	37/198	0.018858469	0.108535905
IRE1-mediated unfolded protein response (GO:0036498)	13/53	0.018886702	0.108535905
alpha-beta T cell differentiation (GO:0046632)	44625	0.018928495	0.108535905
bone marrow development (GO:0048539)	44625	0.018928495	0.108535905
cellular response to sodium arsenite (GO:1903936)	44625	0.018928495	0.108535905
cellular response to vitamin D (GO:0071305)	44625	0.018928495	0.108535905
chronic inflammatory response (GO:0002544)	44625	0.018928495	0.108535905
DNA catabolic process, exonucleolytic (GO:0000738)	44625	0.018928495	0.108535905
glucose import across plasma membrane (GO:0098708)	44625	0.018928495	0.108535905
inosine metabolic process (GO:0046102)	44625	0.018928495	0.108535905
mature ribosome assembly (GO:0042256)	44625	0.018928495	0.108535905
negative regulation of CREB transcription factor activity (	44625	0.018928495	0.108535905
negative regulation of hydrogen peroxide metabolic proc	44625	0.018928495	0.108535905
negative regulation of IRE1-mediated unfolded protein re	44625	0.018928495	0.108535905
negative regulation of lipid transport (GO:0032369)	44625	0.018928495	0.108535905
negative regulation of myosin-light-chain-phosphatase ac	44625	0.018928495	0.108535905
negative regulation of pinocytosis (GO:0048550)	44625	0.018928495	0.108535905
peptidyl-cysteine S-nitrosylation (GO:0018119)	44625	0.018928495	0.108535905
positive regulation of CD4-positive, alpha-beta T cell prol	44625	0.018928495	0.108535905
positive regulation of cell fate commitment (GO:0010455	44625	0.018928495	0.108535905
positive regulation of glial cell proliferation (GO:0060252	44625	0.018928495	0.108535905
positive regulation of heat generation (GO:0031652)	44625	0.018928495	0.108535905
positive regulation of interleukin-18 production (GO:003	44625	0.018928495	0.108535905
positive regulation of leukocyte mediated immunity (GO:	44625	0.018928495	0.108535905
positive regulation of leukocyte tethering or rolling (GO:1	44625	0.018928495	0.108535905
positive regulation of MHC class I biosynthetic process (G	44625	0.018928495	0.108535905
positive regulation of mononuclear cell proliferation (GO	44625	0.018928495	0.108535905
positive regulation of oxidative stress-induced neuron de	44625	0.018928495	0.108535905
postsynaptic endocytosis (GO:0140239)	44625	0.018928495	0.108535905
postsynaptic neurotransmitter receptor internalization (G	44625	0.018928495	0.108535905

regulation of core promoter binding (GO:1904796)	44625	0.018928495	0.108535905
regulation of dendritic cell cytokine production (GO:0002	44625	0.018928495	0.108535905
regulation of Fc-gamma receptor signaling pathway invol	44625	0.018928495	0.108535905
regulation of fever generation (GO:0031620)	44625	0.018928495	0.108535905
regulation of glial cell migration (GO:1903975)	44625	0.018928495	0.108535905
regulation of miRNA catabolic process (GO:2000625)	44625	0.018928495	0.108535905
regulation of miRNA metabolic process (GO:2000628)	44625	0.018928495	0.108535905
regulation of mononuclear cell proliferation (GO:003294	44625	0.018928495	0.108535905
regulation of NK T cell proliferation (GO:0051140)	44625	0.018928495	0.108535905
regulation of nucleotide-binding oligomerization domain	44625	0.018928495	0.108535905
regulation of platelet-derived growth factor receptor-bet	44625	0.018928495	0.108535905
regulation of retinal ganglion cell axon guidance (GO:009	44625	0.018928495	0.108535905
regulation of type B pancreatic cell apoptotic process (GC	44625	0.018928495	0.108535905
response to sodium arsenite (GO:1903935)	44625	0.018928495	0.108535905
Toll signaling pathway (GO:0008063)	44625	0.018928495	0.108535905
tryptophan catabolic process to kynurenine (GO:0019441	44625	0.018928495	0.108535905
negative regulation of epithelial cell apoptotic process (G	13789	0.019411593	0.110695091
phagocytosis, engulfment (GO:0006911)	13789	0.019411593	0.110695091
positive regulation of myeloid cell differentiation (GO:00	13789	0.019411593	0.110695091
regulation of erythrocyte differentiation (GO:0045646)	13789	0.019411593	0.110695091
regulation of intracellular pH (GO:0051453)	13789	0.019411593	0.110695091
regulation of epithelial to mesenchymal transition (GO:0(	17/76	0.019810553	0.112767753
membrane protein intracellular domain proteolysis (GO:(	44764	0.019927006	0.112767753
microglial cell activation (GO:0001774)	44764	0.019927006	0.112767753
negative regulation of interleukin-2 production (GO:0032	44764	0.019927006	0.112767753
positive regulation of neutrophil migration (GO:1902624)	44764	0.019927006	0.112767753
regulation of membrane protein ectodomain proteolysis	44764	0.019927006	0.112767753
regulation of viral release from host cell (GO:1902186)	44764	0.019927006	0.112767753
cellular response to topologically incorrect protein (GO:0	11933	0.020134619	0.113818655
regulation of gene expression, epigenetic (GO:0040029)	18/82	0.020246096	0.114253438
regulation of protein metabolic process (GO:0051246)	17868	0.020389713	0.114253438
cellular senescence (GO:0090398)	44800	0.020409469	0.114253438
chondroitin sulfate proteoglycan biosynthetic process (G	44800	0.020409469	0.114253438
positive regulation of erythrocyte differentiation (GO:00	44800	0.020409469	0.114253438
positive regulation of nuclear division (GO:0051785)	44800	0.020409469	0.114253438
protein export from nucleus (GO:0006611)	44800	0.020409469	0.114253438
release of sequestered calcium ion into cytosol (GO:0051	44800	0.020409469	0.114253438
stress-activated protein kinase signaling cascade (GO:003	44800	0.020409469	0.114253438
negative regulation of binding (GO:0051100)	19/88	0.020543059	0.114877492
DNA catabolic process (GO:0006308)	44694	0.02093832	0.115471947
entry into host (GO:0044409)	44694	0.02093832	0.115471947
icosanoid secretion (GO:0032309)	44694	0.02093832	0.115471947
negative regulation of hippo signaling (GO:0035331)	44694	0.02093832	0.115471947
negative regulation of viral release from host cell (GO:19	44694	0.02093832	0.115471947
positive regulation of calcium-mediated signaling (GO:00	44694	0.02093832	0.115471947
positive regulation of CD4-positive, alpha-beta T cell activ	44694	0.02093832	0.115471947
positive regulation of heterochromatin assembly (GO:00	44694	0.02093832	0.115471947

positive regulation of protein localization to cell surface (	44694	0.02093832	0.115471947
purine-containing compound salvage (GO:0043101)	44694	0.02093832	0.115471947
regulation of antigen receptor-mediated signaling pathw	44694	0.02093832	0.115471947
regulation of homotypic cell-cell adhesion (GO:0034110)	44694	0.02093832	0.115471947
response to interleukin-6 (GO:0070741)	44694	0.02093832	0.115471947
DNA-templated transcription, initiation (GO:0006352)	32/168	0.02135201	0.117628519
cellular response to DNA damage stimulus (GO:0006974)	60/350	0.021501842	0.118328465
cellular response to glucose starvation (GO:0042149)	16011	0.021885037	0.120055723
positive regulation of leukocyte mediated cytotoxicity (G	16011	0.021885037	0.120055723
regulation of cell-cell adhesion (GO:0022407)	16011	0.021885037	0.120055723
regulation of cell differentiation (GO:0045595)	30/156	0.022329713	0.120550061
CD40 signaling pathway (GO:0023035)	44660	0.022369636	0.120550061
cellular response to leptin stimulus (GO:0044320)	44660	0.022369636	0.120550061
IMP metabolic process (GO:0046040)	44660	0.022369636	0.120550061
negative regulation of leukocyte degranulation (GO:0043	44660	0.022369636	0.120550061
negative regulation of production of molecular mediator	44660	0.022369636	0.120550061
positive regulation of memory T cell differentiation (GO:(	44660	0.022369636	0.120550061
protein O-linked glycosylation via threonine (GO:001824:	44660	0.022369636	0.120550061
regulation of cell adhesion molecule production (GO:006	44660	0.022369636	0.120550061
regulation of dendritic cell antigen processing and presen	44660	0.022369636	0.120550061
regulation of epidermis development (GO:0045682)	44660	0.022369636	0.120550061
regulation of fibroblast apoptotic process (GO:2000269)	44660	0.022369636	0.120550061
regulation of glial cell proliferation (GO:0060251)	44660	0.022369636	0.120550061
regulation of pinocytosis (GO:0048548)	44660	0.022369636	0.120550061
regulation of smooth muscle cell apoptotic process (GO:(	44660	0.022369636	0.120550061
response to vitamin D (GO:0033280)	44660	0.022369636	0.120550061
T-helper 1 type immune response (GO:0042088)	44660	0.022369636	0.120550061
regulation of apoptotic signaling pathway (GO:2001233)	14154	0.023300041	0.125433898
negative regulation of catabolic process (GO:0009895)	18233	0.023839115	0.12820311
positive regulation of cell cycle (GO:0045787)	15/66	0.024062254	0.128773405
cellular response to alkaloid (GO:0071312)	44730	0.024292192	0.128773405
cellular response to dsRNA (GO:0071359)	44730	0.024292192	0.128773405
long-chain fatty-acyl-CoA biosynthetic process (GO:0035:	44730	0.024292192	0.128773405
negative regulation of signal transduction by p53 class m	44730	0.024292192	0.128773405
positive regulation of extracellular matrix organization (G	44730	0.024292192	0.128773405
positive regulation of fatty acid metabolic process (GO:0(	44730	0.024292192	0.128773405
positive regulation of interleukin-4 production (GO:0032	44730	0.024292192	0.128773405
positive regulation of response to endoplasmic reticulum	44730	0.024292192	0.128773405
regulation of brown fat cell differentiation (GO:0090335)	44730	0.024292192	0.128773405
regulation of establishment or maintenance of cell polari	44730	0.024292192	0.128773405
regulation of platelet aggregation (GO:0090330)	44730	0.024292192	0.128773405
regulation of transforming growth factor beta productior	44730	0.024292192	0.128773405
response to interferon-alpha (GO:0035455)	44730	0.024292192	0.128773405
negative regulation of cell growth (GO:0030308)	25/126	0.024498067	0.129432642
positive regulation of ATP metabolic process (GO:190358	12298	0.024516212	0.129432642
positive regulation of receptor signaling pathway via JAK-	12298	0.024516212	0.129432642
signal transduction by p53 class mediator (GO:0072331)	12298	0.024516212	0.129432642

cellular response to transforming growth factor beta stim	23/114	0.025138059	0.132312278
positive regulation of cellular component organization (G	23/114	0.025138059	0.132312278
positive regulation of kinase activity (GO:0033674)	23/114	0.025138059	0.132312278
negative regulation of apoptotic signaling pathway (GO:2	17/78	0.025187069	0.132436055
protein-containing complex assembly (GO:0065003)	47/267	0.025231498	0.132535524
positive regulation of phosphatidylinositol 3-kinase activi	44801	0.025339342	0.132565845
positive regulation of protein import into nucleus (GO:00	44801	0.025339342	0.132565845
positive regulation of response to wounding (GO:190303	44801	0.025339342	0.132565845
regulation of protein transport (GO:0051223)	44801	0.025339342	0.132565845
membrane protein ectodomain proteolysis (GO:0006509	44765	0.025446798	0.132727026
positive regulation of epithelial cell apoptotic process (G	44765	0.025446798	0.132727026
regulation of interleukin-4 production (GO:0032673)	44765	0.025446798	0.132727026
negative regulation of epidermal growth factor receptor	16377	0.025786287	0.134228217
positive regulation of stress fiber assembly (GO:0051496)	16377	0.025786287	0.134228217
glycerophospholipid biosynthetic process (GO:0046474)	33/177	0.026189068	0.136188395
axon guidance (GO:0007411)	37/203	0.02691506	0.139823735
anion transmembrane transport (GO:0098656)	15/67	0.027321711	0.141794494
actin polymerization or depolymerization (GO:0008154)	18598	0.027698242	0.143292246
regulation of generation of precursor metabolites and en	18598	0.027698242	0.143292246
cellular response to ketone (GO:1901655)	14519	0.027720637	0.143292246
protein monoubiquitination (GO:0006513)	14519	0.027720637	0.143292246
regulation of actin filament polymerization (GO:0030833	16/73	0.027895075	0.144050609
transcription initiation from RNA polymerase II promoter	27/140	0.028069866	0.144809287
glycosaminoglycan biosynthetic process (GO:0006024)	20/97	0.02839031	0.146317124
positive regulation of protein catabolic process (GO:0045	18/85	0.028438113	0.146418233
negative regulation of cell differentiation (GO:0045596)	35/191	0.028573466	0.146969462
protein ubiquitination (GO:0016567)	85/525	0.028720837	0.147271963
antigen processing and presentation of endogenous pept	44695	0.029085858	0.147271963
cardiolipin metabolic process (GO:0032048)	44695	0.029085858	0.147271963
cytoplasmic sequestering of transcription factor (GO:004	44695	0.029085858	0.147271963
detection of bacterium (GO:0016045)	44695	0.029085858	0.147271963
NAD biosynthesis via nicotinamide riboside salvage pathv	44695	0.029085858	0.147271963
negative regulation of secretion (GO:0051048)	44695	0.029085858	0.147271963
positive regulation of leukocyte degranulation (GO:0043	44695	0.029085858	0.147271963
positive regulation of regulatory T cell differentiation (GC	44695	0.029085858	0.147271963
regulation of DNA methylation-dependent heterochroma	44695	0.029085858	0.147271963
regulation of response to endoplasmic reticulum stress ((	44695	0.029085858	0.147271963
regulation of trophoblast cell migration (GO:1901163)	44695	0.029085858	0.147271963
response to chemokine (GO:1990868)	44695	0.029085858	0.147271963
substrate-dependent cell migration (GO:0006929)	44695	0.029085858	0.147271963
T-helper cell differentiation (GO:0042093)	44695	0.029085858	0.147271963
vascular endothelial growth factor signaling pathway (GO	44695	0.029085858	0.147271963
blood vessel morphogenesis (GO:0048514)	13/56	0.029133516	0.147369635
autophagosome maturation (GO:0097352)	12663	0.029534048	0.148960562
protein destabilization (GO:0031648)	12663	0.029534048	0.148960562
regulation of transmembrane transport (GO:0034762)	12663	0.029534048	0.148960562
negative regulation of T cell activation (GO:0050868)	16742	0.030166564	0.151855912

regulation of insulin receptor signaling pathway (GO:004(	16742	0.030166564	0.151855912
positive regulation of protein localization to nucleus (GO:	15/68	0.030896844	0.154538414
regulation of myeloid cell differentiation (GO:0045637)	15/68	0.030896844	0.154538414
actin filament polymerization (GO:0030041)	44802	0.031041991	0.154538414
establishment of endothelial barrier (GO:0061028)	44802	0.031041991	0.154538414
positive regulation of dephosphorylation (GO:0035306)	44802	0.031041991	0.154538414
regulation of T cell mediated cytotoxicity (GO:0001914)	44802	0.031041991	0.154538414
mRNA transport (GO:0051028)	21/104	0.03107154	0.154538414
cellular response to amino acid starvation (GO:0034198)	16/74	0.031353241	0.154538414
regulation of stress fiber assembly (GO:0051492)	16/74	0.031353241	0.154538414
regulation of endothelial cell proliferation (GO:0001936)	19/92	0.031572432	0.154538414
negative regulation of cellular component organization ((	17/80	0.031593083	0.154538414
DNA alkylation (GO:0006305)	44731	0.031619617	0.154538414
DNA methylation or demethylation (GO:0044728)	44731	0.031619617	0.154538414
leukotriene biosynthetic process (GO:0019370)	44731	0.031619617	0.154538414
maintenance of protein localization in organelle (GO:007	44731	0.031619617	0.154538414
negative regulation of RNA metabolic process (GO:00512	44731	0.031619617	0.154538414
positive regulation of leukocyte activation (GO:0002696)	44731	0.031619617	0.154538414
positive regulation of monocyte chemotaxis (GO:009002(	44731	0.031619617	0.154538414
regulation of cell-cell adhesion mediated by cadherin (GC	44731	0.031619617	0.154538414
regulation of epithelial cell differentiation (GO:0030856)	44731	0.031619617	0.154538414
response to cholesterol (GO:0070723)	44731	0.031619617	0.154538414
phosphate-containing compound metabolic process (GO:	38/212	0.031864143	0.154538414
amino acid import across plasma membrane (GO:008971	44766	0.031925609	0.154538414
defense response to fungus (GO:0050832)	44766	0.031925609	0.154538414
dendritic cell differentiation (GO:0097028)	44766	0.031925609	0.154538414
immune response-activating cell surface receptor signalir	44766	0.031925609	0.154538414
negative regulation of synaptic transmission (GO:005080	44766	0.031925609	0.154538414
positive regulation of carbohydrate metabolic process (G	44766	0.031925609	0.154538414
positive regulation of cell-substrate junction organization	44766	0.031925609	0.154538414
positive regulation of p38MAPK cascade (GO:1900745)	44766	0.031925609	0.154538414
protein K48-linked deubiquitination (GO:0071108)	44766	0.031925609	0.154538414
regulation of axon extension involved in axon guidance ((	44766	0.031925609	0.154538414
regulation of monooxygenase activity (GO:0032768)	44766	0.031925609	0.154538414
positive regulation of actin filament bundle assembly (GC	18963	0.031990874	0.154538414
positive regulation of epithelial cell proliferation (GO:005	24/123	0.032478735	0.154538414
lymphocyte migration (GO:0072676)	14885	0.032706494	0.154538414
negative regulation of blood coagulation (GO:0030195)	14885	0.032706494	0.154538414
chromatin organization (GO:0006325)	27/142	0.033030888	0.154538414
regulation of bone mineralization (GO:0030500)	13/57	0.033310605	0.154538414
arachidonate transport (GO:1903963)	44661	0.03343311	0.154538414
arachidonic acid secretion (GO:0050482)	44661	0.03343311	0.154538414
B cell homeostasis (GO:0001782)	44661	0.03343311	0.154538414
I-kappaB phosphorylation (GO:0007252)	44661	0.03343311	0.154538414
iron ion transmembrane transport (GO:0034755)	44661	0.03343311	0.154538414
myeloid dendritic cell differentiation (GO:0043011)	44661	0.03343311	0.154538414
negative regulation of cell-cell adhesion mediated by cad	44661	0.03343311	0.154538414

negative regulation of hormone secretion (GO:0046888)	44661	0.03343311	0.154538414
negative regulation of interferon-beta production (GO:0(	44661	0.03343311	0.154538414
negative regulation of transcription by competitive prom	44661	0.03343311	0.154538414
negative regulation of transmembrane transport (GO:00	44661	0.03343311	0.154538414
negative regulation of tyrosine phosphorylation of STAT	44661	0.03343311	0.154538414
negative regulation of vascular endothelial growth factor	44661	0.03343311	0.154538414
negative regulation of voltage-gated calcium channel acti	44661	0.03343311	0.154538414
peptidyl-lysine acetylation (GO:0018394)	44661	0.03343311	0.154538414
phosphatidylcholine catabolic process (GO:0034638)	44661	0.03343311	0.154538414
pinocytosis (GO:0006907)	44661	0.03343311	0.154538414
positive regulation of coagulation (GO:0050820)	44661	0.03343311	0.154538414
positive regulation of hemostasis (GO:1900048)	44661	0.03343311	0.154538414
positive regulation of myoblast fusion (GO:1901741)	44661	0.03343311	0.154538414
regulation of endoplasmic reticulum unfolded protein res	44661	0.03343311	0.154538414
regulation of granulocyte differentiation (GO:0030852)	44661	0.03343311	0.154538414
regulation of hydrogen peroxide-induced cell death (GO::	44661	0.03343311	0.154538414
regulation of macrophage migration (GO:1905521)	44661	0.03343311	0.154538414
regulation of memory T cell differentiation (GO:0043380)	44661	0.03343311	0.154538414
regulation of podosome assembly (GO:0071801)	44661	0.03343311	0.154538414
regulation of tau-protein kinase activity (GO:1902947)	44661	0.03343311	0.154538414
response to interleukin-4 (GO:0070670)	44661	0.03343311	0.154538414
astrocyte development (GO:0014002)	44626	0.034150164	0.154538414
cellular response to salt (GO:1902075)	44626	0.034150164	0.154538414
cellular triglyceride homeostasis (GO:0035356)	44626	0.034150164	0.154538414
chitin catabolic process (GO:0006032)	44626	0.034150164	0.154538414
chitin metabolic process (GO:0006030)	44626	0.034150164	0.154538414
contact inhibition (GO:0060242)	44626	0.034150164	0.154538414
detection of virus (GO:0009597)	44626	0.034150164	0.154538414
ear development (GO:0043583)	44626	0.034150164	0.154538414
hexose import across plasma membrane (GO:0140271)	44626	0.034150164	0.154538414
leukocyte chemotaxis involved in inflammatory response	44626	0.034150164	0.154538414
membrane raft assembly (GO:0001765)	44626	0.034150164	0.154538414
multinuclear osteoclast differentiation (GO:0072674)	44626	0.034150164	0.154538414
negative regulation of CD8-positive, alpha-beta T cell acti	44626	0.034150164	0.154538414
negative regulation of cytosolic calcium ion concentratio	44626	0.034150164	0.154538414
negative regulation of lens fiber cell differentiation (GO:1	44626	0.034150164	0.154538414
negative regulation of myeloid cell apoptotic process (GC	44626	0.034150164	0.154538414
negative regulation of myeloid leukocyte mediated immu	44626	0.034150164	0.154538414
negative regulation of relaxation of muscle (GO:1901078	44626	0.034150164	0.154538414
negative regulation of transporter activity (GO:0032410)	44626	0.034150164	0.154538414
negative regulation of vitamin metabolic process (GO:00	44626	0.034150164	0.154538414
neutrophil extravasation (GO:0072672)	44626	0.034150164	0.154538414
norepinephrine transport (GO:0015874)	44626	0.034150164	0.154538414
positive regulation of antigen processing and presentatio	44626	0.034150164	0.154538414
positive regulation of deacetylase activity (GO:0090045)	44626	0.034150164	0.154538414
positive regulation of dendritic cell antigen processing an	44626	0.034150164	0.154538414
positive regulation of fever generation (GO:0031622)	44626	0.034150164	0.154538414

positive regulation of focal adhesion disassembly (GO:01	44626	0.034150164	0.154538414
positive regulation of granulocyte differentiation (GO:00	44626	0.034150164	0.154538414
positive regulation of hemoglobin biosynthetic process (G	44626	0.034150164	0.154538414
positive regulation of microglial cell migration (GO:19041	44626	0.034150164	0.154538414
positive regulation of natural killer cell mediated cytotoxi	44626	0.034150164	0.154538414
positive regulation of natural killer cell mediated immune	44626	0.034150164	0.154538414
positive regulation of non-membrane spanning protein ty	44626	0.034150164	0.154538414
positive regulation of plasminogen activation (GO:00107	44626	0.034150164	0.154538414
positive regulation of receptor binding (GO:1900122)	44626	0.034150164	0.154538414
positive regulation of sterol transport (GO:0032373)	44626	0.034150164	0.154538414
positive regulation of T-helper 2 cell differentiation (GO:(	44626	0.034150164	0.154538414
positive regulation of toll-like receptor 3 signaling pathwa	44626	0.034150164	0.154538414
regulation of centriole elongation (GO:1903722)	44626	0.034150164	0.154538414
regulation of focal adhesion disassembly (GO:0120182)	44626	0.034150164	0.154538414
regulation of hormone biosynthetic process (GO:004688	44626	0.034150164	0.154538414
regulation of immunoglobulin mediated immune respons	44626	0.034150164	0.154538414
regulation of macrophage apoptotic process (GO:200010	44626	0.034150164	0.154538414
regulation of nucleotide-binding oligomerization domain	44626	0.034150164	0.154538414
regulation of pro-B cell differentiation (GO:2000973)	44626	0.034150164	0.154538414
regulation of type B pancreatic cell proliferation (GO:006	44626	0.034150164	0.154538414
release of sequestered calcium ion into cytosol by sarcop	44626	0.034150164	0.154538414
ruffle assembly (GO:0097178)	44626	0.034150164	0.154538414
TORC2 signaling (GO:0038203)	44626	0.034150164	0.154538414
positive regulation of nucleocytoplasmic transport (GO:0	17107	0.035052715	0.158170874
regulation of transcription from RNA polymerase II prom	16/75	0.035116599	0.158170874
response to amino acid starvation (GO:1990928)	16/75	0.035116599	0.158170874
protein targeting to membrane (GO:0006612)	18/87	0.035134851	0.158170874
negative regulation of protein modification process (GO:(	17/81	0.035213504	0.158170874
phospholipase C-activating G protein-coupled receptor si	17/81	0.035213504	0.158170874
bicarbonate transport (GO:0015701)	13028	0.035226891	0.158170874
cellular response to amyloid-beta (GO:1904646)	13028	0.035226891	0.158170874
positive regulation of lipid biosynthetic process (GO:0046	13028	0.035226891	0.158170874
regulation of canonical Wnt signaling pathway (GO:00608	44/253	0.035370538	0.15867871
nitrogen compound transport (GO:0071705)	27/143	0.035747488	0.160231408
negative regulation of protein metabolic process (GO:005	19329	0.03673941	0.164535548
transcription, DNA-templated (GO:0006351)	39/221	0.03726422	0.16674214
cellular response to peptide hormone stimulus (GO:0071	21/106	0.037450002	0.166788531
peptidyl-lysine modification (GO:0018205)	21/106	0.037450002	0.166788531
cell projection organization (GO:0030030)	44803	0.037563538	0.166788531
chondroitin sulfate metabolic process (GO:0030204)	44803	0.037563538	0.166788531
negative regulation of gene expression, epigenetic (GO:0	44803	0.037563538	0.166788531
negative regulation of interleukin-1 production (GO:0032	44803	0.037563538	0.166788531
plasma membrane invagination (GO:0099024)	44803	0.037563538	0.166788531
positive regulation of lipid kinase activity (GO:0090218)	44803	0.037563538	0.166788531
positive regulation of protein import (GO:1904591)	44803	0.037563538	0.166788531
positive regulation of protein binding (GO:0032092)	13/58	0.03790118	0.168144004
nucleobase-containing compound catabolic process (GO:	15250	0.038287987	0.169178771

positive regulation of TOR signaling (GO:0032008)	15250	0.038287987	0.169178771
regulation of viral transcription (GO:0046782)	15250	0.038287987	0.169178771
androgen receptor signaling pathway (GO:0030521)	44696	0.038981134	0.169178771
cellular response to estrogen stimulus (GO:0071391)	44696	0.038981134	0.169178771
cellular response to exogenous dsRNA (GO:0071360)	44696	0.038981134	0.169178771
fibrinolysis (GO:0042730)	44696	0.038981134	0.169178771
glucan catabolic process (GO:0009251)	44696	0.038981134	0.169178771
glycogen catabolic process (GO:0005980)	44696	0.038981134	0.169178771
intracellular cholesterol transport (GO:0032367)	44696	0.038981134	0.169178771
myoblast differentiation (GO:0045445)	44696	0.038981134	0.169178771
negative regulation of ubiquitin-protein transferase activ	44696	0.038981134	0.169178771
neurotrophin TRK receptor signaling pathway (GO:00480	44696	0.038981134	0.169178771
positive regulation of exosomal secretion (GO:1903543)	44696	0.038981134	0.169178771
positive regulation of heterotypic cell-cell adhesion (GO:(	44696	0.038981134	0.169178771
positive regulation of membrane protein ectodomain prc	44696	0.038981134	0.169178771
positive regulation of pattern recognition receptor signal	44696	0.038981134	0.169178771
positive regulation of sprouting angiogenesis (GO:190367	44696	0.038981134	0.169178771
pyrimidine nucleoside metabolic process (GO:0006213)	44696	0.038981134	0.169178771
regulation of dephosphorylation (GO:0035303)	44696	0.038981134	0.169178771
regulation of extracellular matrix disassembly (GO:00107	44696	0.038981134	0.169178771
regulation of integrin activation (GO:0033623)	44696	0.038981134	0.169178771
regulation of nuclear-transcribed mRNA poly(A) tail short	44696	0.038981134	0.169178771
regulation of T cell chemotaxis (GO:0010819)	44696	0.038981134	0.169178771
response to acidic pH (GO:0010447)	44696	0.038981134	0.169178771
T cell proliferation (GO:0042098)	44696	0.038981134	0.169178771
carbohydrate homeostasis (GO:0033500)	15/70	0.039054893	0.169357402
RNA transport (GO:0050658)	16/76	0.039198214	0.169837132
negative regulation of actin filament polymerization (GO:	44767	0.039419792	0.170087889
negative regulation of antigen receptor-mediated signalir	44767	0.039419792	0.170087889
peptide catabolic process (GO:0043171)	44767	0.039419792	0.170087889
phosphatidylglycerol metabolic process (GO:0046471)	44767	0.039419792	0.170087889
regulation of epidermal cell differentiation (GO:0045604)	44767	0.039419792	0.170087889
endoplasmic reticulum calcium ion homeostasis (GO:003	44732	0.040246596	0.172509132
eye morphogenesis (GO:0048592)	44732	0.040246596	0.172509132
glucose transmembrane transport (GO:1904659)	44732	0.040246596	0.172509132
granulocyte differentiation (GO:0030851)	44732	0.040246596	0.172509132
myeloid cell development (GO:0061515)	44732	0.040246596	0.172509132
negative regulation of viral life cycle (GO:1903901)	44732	0.040246596	0.172509132
regulation of acute inflammatory response (GO:0002673	44732	0.040246596	0.172509132
regulation of tissue remodeling (GO:0034103)	44732	0.040246596	0.172509132
polyol metabolic process (GO:0019751)	17472	0.040469475	0.173178686
regulation of DNA binding (GO:0051101)	17472	0.040469475	0.173178686
positive regulation of mitotic nuclear division (GO:00458	13394	0.041629211	0.177848481
regulation of protein import into nucleus (GO:0042306)	13394	0.041629211	0.177848481
cellular macromolecule catabolic process (GO:0044265)	19694	0.041964597	0.178986931
epidermal cell differentiation (GO:0009913)	19694	0.041964597	0.178986931
regulation of cellular component organization (GO:00511	26/139	0.042866621	0.182625075

protein polymerization (GO:0051258)	13/59	0.042923045	0.182625075
regulation of secretion by cell (GO:1903530)	13/59	0.042923045	0.182625075
mitotic G1 DNA damage checkpoint signaling (GO:00315	14/65	0.043460399	0.184277925
regulation of cellular catabolic process (GO:0031329)	14/65	0.043460399	0.184277925
regulation of RNA metabolic process (GO:0051252)	14/65	0.043460399	0.184277925
cellular response to UV (GO:0034644)	16/77	0.043610453	0.184277925
phosphatidylcholine metabolic process (GO:0046470)	16/77	0.043610453	0.184277925
gland development (GO:0048732)	15/71	0.043666242	0.184277925
regulation of endopeptidase activity (GO:0052548)	15/71	0.043666242	0.184277925
regulation of glycolytic process (GO:0006110)	15/71	0.043666242	0.184277925
regulation of TOR signaling (GO:0032006)	15/71	0.043666242	0.184277925
snRNA transcription (GO:0009301)	15/71	0.043666242	0.184277925
activation of protein kinase activity (GO:0032147)	22/114	0.043783746	0.184474096
histone modification (GO:0016570)	22/114	0.043783746	0.184474096
positive regulation of epithelial to mesenchymal transitio	15615	0.044492294	0.18730751
phospholipid translocation (GO:0045332)	44804	0.044943251	0.18874712
positive regulation of RNA splicing (GO:0033120)	44804	0.044943251	0.18874712
regulation of cellular component size (GO:0032535)	44804	0.044943251	0.18874712
inositol phosphate metabolic process (GO:0043647)	17838	0.046439139	0.194374098
B cell mediated immunity (GO:0019724)	44662	0.04714367	0.194374098
cellular response to increased oxygen levels (GO:003629	44662	0.04714367	0.194374098
fatty acid homeostasis (GO:0055089)	44662	0.04714367	0.194374098
Golgi to lysosome transport (GO:0090160)	44662	0.04714367	0.194374098
hepatocyte growth factor receptor signaling pathway (GO	44662	0.04714367	0.194374098
induction of positive chemotaxis (GO:0050930)	44662	0.04714367	0.194374098
miRNA mediated inhibition of translation (GO:0035278)	44662	0.04714367	0.194374098
negative regulation of translation, ncRNA-mediated (GO:	44662	0.04714367	0.194374098
positive regulation of cellular respiration (GO:1901857)	44662	0.04714367	0.194374098
positive regulation of ceramide biosynthetic process (GO	44662	0.04714367	0.194374098
positive regulation of leukocyte apoptotic process (GO:2	44662	0.04714367	0.194374098
positive regulation of lipid localization (GO:1905954)	44662	0.04714367	0.194374098
positive regulation of sphingolipid biosynthetic process (	44662	0.04714367	0.194374098
positive regulation of transcription from RNA polymerase	44662	0.04714367	0.194374098
positive regulation of triglyceride biosynthetic process (G	44662	0.04714367	0.194374098
regulation of amyloid precursor protein biosynthetic proc	44662	0.04714367	0.194374098
regulation of lamellipodium morphogenesis (GO:200039	44662	0.04714367	0.194374098
regulation of lymphocyte migration (GO:2000401)	44662	0.04714367	0.194374098
regulation of T cell mediated immunity (GO:0002709)	44662	0.04714367	0.194374098
regulation of toll-like receptor 9 signaling pathway (GO:0	44662	0.04714367	0.194374098
response to corticosteroid (GO:0031960)	44662	0.04714367	0.194374098
synaptic vesicle transport (GO:0048489)	44662	0.04714367	0.194374098
endothelial cell development (GO:0001885)	44768	0.047974351	0.197329178
positive regulation of filopodium assembly (GO:0051491)	44768	0.047974351	0.197329178
positive regulation of ion transmembrane transporter act	44768	0.047974351	0.197329178
negative regulation of blood vessel morphogenesis (GO:2	16/78	0.048364878	0.198778118
response to ionizing radiation (GO:0010212)	15/72	0.048649877	0.199791391
negative regulation of G1/S transition of mitotic cell cycle	13759	0.048770595	0.20012894

extrinsic apoptotic signaling pathway in absence of ligand	44733	0.050225343	0.204804284
intrinsic apoptotic signaling pathway in response to DNA	44733	0.050225343	0.204804284
neurotrophin signaling pathway (GO:0038179)	44733	0.050225343	0.204804284
positive regulation of glycolytic process (GO:0045821)	44733	0.050225343	0.204804284
positive regulation of immune system process (GO:0002	44733	0.050225343	0.204804284
positive regulation of lipid storage (GO:0010884)	44733	0.050225343	0.204804284
positive regulation of purine nucleotide metabolic proces	44733	0.050225343	0.204804284
regulation of transcription by RNA polymerase III (GO:00	44733	0.050225343	0.204804284
aromatic amino acid family catabolic process (GO:00090	44697	0.05068681	0.205076308
B cell activation involved in immune response (GO:00023	44697	0.05068681	0.205076308
negative regulation of receptor signaling pathway via JAK	44697	0.05068681	0.205076308
positive regulation of endothelial cell apoptotic process (	44697	0.05068681	0.205076308
positive regulation of syncytium formation by plasma me	44697	0.05068681	0.205076308
regulation of amyloid-beta clearance (GO:1900221)	44697	0.05068681	0.205076308
regulation of cholesterol storage (GO:0010885)	44697	0.05068681	0.205076308
regulation of defense response to virus (GO:0050688)	44697	0.05068681	0.205076308
regulation of intrinsic apoptotic signaling pathway in resp	44697	0.05068681	0.205076308
regulation of mast cell degranulation (GO:0043304)	44697	0.05068681	0.205076308
regulation of cellular protein metabolic process (GO:003	18203	0.052981256	0.210438348
ERBB2 signaling pathway (GO:0038128)	11902	0.053212802	0.210438348
gene silencing by miRNA (GO:0035195)	11902	0.053212802	0.210438348
hematopoietic progenitor cell differentiation (GO:00022	11902	0.053212802	0.210438348
negative regulation of chemotaxis (GO:0050922)	11902	0.053212802	0.210438348
positive regulation of receptor signaling pathway via STA	11902	0.053212802	0.210438348
positive regulation of proteasomal ubiquitin-dependent p	16/79	0.053472145	0.210438348
negative regulation of protein modification by small prot	20424	0.05391816	0.210438348
astrocyte differentiation (GO:0048708)	44627	0.053956473	0.210438348
autophagosome membrane docking (GO:0016240)	44627	0.053956473	0.210438348
catecholamine uptake (GO:0090493)	44627	0.053956473	0.210438348
cellular response to laminar fluid shear stress (GO:00714	44627	0.053956473	0.210438348
cellular response to platelet-derived growth factor stimul	44627	0.053956473	0.210438348
detection of molecule of bacterial origin (GO:0032490)	44627	0.053956473	0.210438348
glial cell migration (GO:0008347)	44627	0.053956473	0.210438348
hyaluronan biosynthetic process (GO:0030213)	44627	0.053956473	0.210438348
hyperosmotic response (GO:0006972)	44627	0.053956473	0.210438348
mRNA transcription by RNA polymerase II (GO:0042789)	44627	0.053956473	0.210438348
negative regulation of oligodendrocyte differentiation (G	44627	0.053956473	0.210438348
negative regulation of type 2 immune response (GO:000	44627	0.053956473	0.210438348
positive regulation of B cell receptor signaling pathway (G	44627	0.053956473	0.210438348
positive regulation of gliogenesis (GO:0014015)	44627	0.053956473	0.210438348
positive regulation of histone H3-K9 methylation (GO:005	44627	0.053956473	0.210438348
positive regulation of humoral immune response (GO:00(	44627	0.053956473	0.210438348
positive regulation of IRE1-mediated unfolded protein re	44627	0.053956473	0.210438348
positive regulation of lipopolysaccharide-mediated signal	44627	0.053956473	0.210438348
positive regulation of lymphocyte apoptotic process (GO:	44627	0.053956473	0.210438348
positive regulation of protein deubiquitination (GO:1903(	44627	0.053956473	0.210438348
positive regulation of respiratory burst (GO:0060267)	44627	0.053956473	0.210438348

positive regulation of trophoblast cell migration (GO:190	44627	0.053956473	0.210438348
posttranslational protein targeting to membrane, translo	44627	0.053956473	0.210438348
protein catabolic process in the vacuole (GO:0007039)	44627	0.053956473	0.210438348
regulation of glial cell apoptotic process (GO:0034350)	44627	0.053956473	0.210438348
regulation of hemoglobin biosynthetic process (GO:0046	44627	0.053956473	0.210438348
regulation of histone deacetylase activity (GO:1901725)	44627	0.053956473	0.210438348
regulation of I-kappaB phosphorylation (GO:1903719)	44627	0.053956473	0.210438348
regulation of inositol phosphate biosynthetic process (GC	44627	0.053956473	0.210438348
regulation of lens fiber cell differentiation (GO:1902746)	44627	0.053956473	0.210438348
regulation of MHC class I biosynthetic process (GO:00453	44627	0.053956473	0.210438348
regulation of microglial cell migration (GO:1904139)	44627	0.053956473	0.210438348
regulation of myosin-light-chain-phosphatase activity (GC	44627	0.053956473	0.210438348
regulation of natural killer cell chemotaxis (GO:2000501)	44627	0.053956473	0.210438348
regulation of natural killer cell mediated cytotoxicity dire	44627	0.053956473	0.210438348
regulation of non-membrane spanning protein tyrosine k	44627	0.053956473	0.210438348
ribonucleoprotein complex disassembly (GO:0032988)	44627	0.053956473	0.210438348
substrate-dependent cell migration, cell extension (GO:0(	44627	0.053956473	0.210438348
T cell apoptotic process (GO:0070231)	44627	0.053956473	0.210438348
vascular associated smooth muscle cell development (GC	44627	0.053956473	0.210438348
positive regulation of catabolic process (GO:0009896)	14/67	0.054325583	0.211718983
cellular component assembly (GO:0022607)	44/261	0.054889604	0.213756741
acute inflammatory response (GO:0002526)	44769	0.057622068	0.222728156
cellular lipid catabolic process (GO:0044242)	44769	0.057622068	0.222728156
cellular response to unfolded protein (GO:0034620)	44769	0.057622068	0.222728156
entrainment of circadian clock by photoperiod (GO:0043	44769	0.057622068	0.222728156
L-alpha-amino acid transmembrane transport (GO:19024	44769	0.057622068	0.222728156
negative regulation of endothelial cell apoptotic process	44769	0.057622068	0.222728156
positive regulation of gene silencing by miRNA (GO:2000	44769	0.057622068	0.222728156
positive regulation of mitotic cell cycle (GO:0045931)	44769	0.057622068	0.222728156
regulation of epidermal growth factor-activated receptor	44769	0.057622068	0.222728156
response to glucocorticoid (GO:0051384)	44769	0.057622068	0.222728156
glucose homeostasis (GO:0042593)	17/86	0.0579411	0.223628541
regulation of neuron death (GO:1901214)	17/86	0.0579411	0.223628541
negative regulation of protein binding (GO:0032091)	15/74	0.059779604	0.230553115
iron ion transport (GO:0006826)	18568	0.060112367	0.231664501
negative regulation of transforming growth factor beta re	14/68	0.060399704	0.232599305
adenylate cyclase-activating G protein-coupled receptor s	22/118	0.060530017	0.232928475
response to UV (GO:0009411)	19/99	0.060603115	0.232978711
DNA damage response, signal transduction by p53 class n	20790	0.060677612	0.232978711
protein-containing complex disassembly (GO:0032984)	20790	0.060677612	0.232978711
glutamate metabolic process (GO:0006536)	44734	0.061587229	0.235427267
negative regulation of biomineral tissue development (G	44734	0.061587229	0.235427267
negative regulation of lymphocyte activation (GO:00512	44734	0.061587229	0.235427267
positive regulation of DNA-templated transcription, initia	44734	0.061587229	0.235427267
positive regulation of signal transduction by p53 class me	44734	0.061587229	0.235427267
regulation of response to cytokine stimulus (GO:0060759	44734	0.061587229	0.235427267
regulation of macroautophagy (GO:0016241)	21/112	0.062320964	0.238056918

protein targeting (GO:0006605)	23/125	0.063324829	0.239556183
regulation of protein secretion (GO:0050708)	23/125	0.063324829	0.239556183
ERAD pathway (GO:0036503)	17/87	0.063479764	0.239556183
cellular response to growth hormone stimulus (GO:0071	44663	0.063497375	0.239556183
inositol phosphate catabolic process (GO:0071545)	44663	0.063497375	0.239556183
negative regulation of B cell proliferation (GO:0030889)	44663	0.063497375	0.239556183
negative regulation of cellular response to vascular endo	44663	0.063497375	0.239556183
negative regulation of heart contraction (GO:0045822)	44663	0.063497375	0.239556183
negative regulation of JUN kinase activity (GO:0043508)	44663	0.063497375	0.239556183
negative regulation of production of miRNAs involved in	44663	0.063497375	0.239556183
phospholipid efflux (GO:0033700)	44663	0.063497375	0.239556183
positive regulation of cellular senescence (GO:2000774)	44663	0.063497375	0.239556183
positive regulation of endoplasmic reticulum unfolded pr	44663	0.063497375	0.239556183
regulation of amyloid precursor protein catabolic process	44663	0.063497375	0.239556183
regulation of B cell apoptotic process (GO:0002902)	44663	0.063497375	0.239556183
regulation of plasminogen activation (GO:0010755)	44663	0.063497375	0.239556183
toll-like receptor 3 signaling pathway (GO:0034138)	44663	0.063497375	0.239556183
protein processing (GO:0016485)	20/106	0.064115159	0.240385859
negative regulation of ATPase activity (GO:0032780)	44698	0.064226289	0.240385859
negative regulation of intrinsic apoptotic signaling pathw	44698	0.064226289	0.240385859
positive regulation of blood coagulation (GO:0030194)	44698	0.064226289	0.240385859
positive regulation of macrophage activation (GO:00430	44698	0.064226289	0.240385859
positive regulation of muscle hypertrophy (GO:0014742)	44698	0.064226289	0.240385859
positive regulation of positive chemotaxis (GO:0050927)	44698	0.064226289	0.240385859
regulation of cell killing (GO:0031341)	44698	0.064226289	0.240385859
regulation of cellular respiration (GO:0043457)	44698	0.064226289	0.240385859
retrograde protein transport, ER to cytosol (GO:0030970	44698	0.064226289	0.240385859
vasculature development (GO:0001944)	44698	0.064226289	0.240385859
negative regulation of lymphocyte proliferation (GO:005	14489	0.065361646	0.243932294
negative regulation of protein secretion (GO:0050709)	14489	0.065361646	0.243932294
regulation of nitric-oxide synthase activity (GO:0050999)	14489	0.065361646	0.243932294
regulation of T cell differentiation (GO:0045580)	14489	0.065361646	0.243932294
negative regulation of canonical Wnt signaling pathway (	29/165	0.067705382	0.252316684
regulation of neuron projection development (GO:00109	29/165	0.067705382	0.252316684
regulation of axonogenesis (GO:0050770)	18933	0.067845782	0.252477679
regulation of substrate adhesion-dependent cell spreadir	18933	0.067845782	0.252477679
icosanoid metabolic process (GO:0006690)	21155	0.067975485	0.252598458
regulation of reactive oxygen species metabolic process (	21155	0.067975485	0.252598458
negative regulation of oxidative stress-induced cell death	44770	0.068382984	0.253749715
photoperiodism (GO:0009648)	44770	0.068382984	0.253749715
transmembrane receptor protein serine/threonine kinase	24/133	0.07075088	0.26234891
positive regulation of cytoskeleton organization (GO:005	16/82	0.071002079	0.263092583
protein transport (GO:0015031)	59/369	0.072091267	0.266938085
cellular response to amino acid stimulus (GO:0071230)	12632	0.072507006	0.268095301
positive regulation of protein dephosphorylation (GO:00	12632	0.072507006	0.268095301
defense response to Gram-positive bacterium (GO:00508	14/70	0.073880313	0.272747351
snRNA transcription by RNA polymerase II (GO:0042795)	14/70	0.073880313	0.272747351

diacylglycerol metabolic process (GO:0046339)	44735	0.074342685	0.272747351
DNA methylation (GO:0006306)	44735	0.074342685	0.272747351
hexose transmembrane transport (GO:0008645)	44735	0.074342685	0.272747351
hyaluronan metabolic process (GO:0030212)	44735	0.074342685	0.272747351
negative regulation of G protein-coupled receptor signali	44735	0.074342685	0.272747351
peptidyl-L-cysteine S-palmitoylation (GO:0018230)	44735	0.074342685	0.272747351
peptidyl-S-diacylglycerol-L-cysteine biosynthetic process	44735	0.074342685	0.272747351
positive regulation of cholesterol efflux (GO:0010875)	44735	0.074342685	0.272747351
regulation of mononuclear cell migration (GO:0071675)	44735	0.074342685	0.272747351
gene expression (GO:0010467)	57/356	0.074406549	0.272789007
plasma membrane organization (GO:0007009)	13/64	0.075009566	0.274805849
autophagosome assembly (GO:0000045)	21520	0.07582096	0.277192039
positive regulation of mitochondrion organization (GO:0(	21520	0.07582096	0.277192039
positive regulation of mitotic cell cycle phase transition (	21520	0.07582096	0.277192039
positive regulation of organelle assembly (GO:1902117)	17076	0.075947975	0.27719684
regulation of fibroblast proliferation (GO:0048145)	17076	0.075947975	0.27719684
negative regulation of cellular biosynthetic process (GO:(	19299	0.076191399	0.27719684
positive regulation of protein localization to plasma mem	19299	0.076191399	0.27719684
sprouting angiogenesis (GO:0002040)	19299	0.076191399	0.27719684
positive regulation of cellular protein metabolic process (	19/102	0.077421024	0.27719684
regulation of protein catabolic process (GO:0042176)	19/102	0.077421024	0.27719684
positive regulation of plasma membrane bounded cell pr	16/83	0.077606054	0.27719684
alpha-beta T cell activation (GO:0046631)	44628	0.078009967	0.27719684
basic amino acid transport (GO:0015802)	44628	0.078009967	0.27719684
benzene-containing compound metabolic process (GO:0(	44628	0.078009967	0.27719684
cellular response to angiotensin (GO:1904385)	44628	0.078009967	0.27719684
cellular response to UV-B (GO:0071493)	44628	0.078009967	0.27719684
dopamine uptake (GO:0090494)	44628	0.078009967	0.27719684
dynamin family protein polymerization involved in memb	44628	0.078009967	0.27719684
dynamin family protein polymerization involved in mitocl	44628	0.078009967	0.27719684
negative regulation of amyloid-beta clearance (GO:19002	44628	0.078009967	0.27719684
negative regulation of CD4-positive, alpha-beta T cell pro	44628	0.078009967	0.27719684
negative regulation of glial cell apoptotic process (GO:00	44628	0.078009967	0.27719684
negative regulation of monooxygenase activity (GO:0032	44628	0.078009967	0.27719684
peptidyl-tyrosine dephosphorylation involved in inactivat	44628	0.078009967	0.27719684
positive regulation of dendritic cell cytokine production (	44628	0.078009967	0.27719684
positive regulation of execution phase of apoptosis (GO:1	44628	0.078009967	0.27719684
positive regulation of fibroblast migration (GO:0010763)	44628	0.078009967	0.27719684
positive regulation of homotypic cell-cell adhesion (GO:0(	44628	0.078009967	0.27719684
positive regulation of monocyte chemotactic protein-1 pr	44628	0.078009967	0.27719684
purine ribonucleoside monophosphate catabolic process	44628	0.078009967	0.27719684
regulation of CD8-positive, alpha-beta T cell proliferation	44628	0.078009967	0.27719684
regulation of chemokine (C-C motif) ligand 5 production (	44628	0.078009967	0.27719684
regulation of lymphocyte apoptotic process (GO:007022	44628	0.078009967	0.27719684
regulation of nitric oxide metabolic process (GO:0080164	44628	0.078009967	0.27719684
regulation of protein ADP-ribosylation (GO:0010835)	44628	0.078009967	0.27719684
regulation of RNA biosynthetic process (GO:2001141)	44628	0.078009967	0.27719684

RNA secondary structure unwinding (GO:0010501)	44628	0.078009967	0.27719684
stress-induced premature senescence (GO:0090400)	44628	0.078009967	0.27719684
translocation of molecules into host (GO:0044417)	44628	0.078009967	0.27719684
tyrosine phosphorylation of STAT protein (GO:0007260)	44628	0.078009967	0.27719684
vascular associated smooth muscle contraction (GO:0014	44628	0.078009967	0.27719684
ventricular trabecula myocardium morphogenesis (GO:0(	44628	0.078009967	0.27719684
viral mRNA export from host cell nucleus (GO:0046784)	44628	0.078009967	0.27719684
wound healing, spreading of epidermal cells (GO:003531	44628	0.078009967	0.27719684
cation transport (GO:0006812)	30/174	0.078332699	0.278153365
3'-UTR-mediated mRNA stabilization (GO:0070935)	44699	0.079585569	0.279356103
amyloid precursor protein metabolic process (GO:00429	44699	0.079585569	0.279356103
carbohydrate derivative transport (GO:1901264)	44699	0.079585569	0.279356103
intracellular estrogen receptor signaling pathway (GO:00	44699	0.079585569	0.279356103
negative regulation of fibroblast proliferation (GO:00481	44699	0.079585569	0.279356103
negative regulation of lipid catabolic process (GO:00509	44699	0.079585569	0.279356103
negative regulation of Rho protein signal transduction (G	44699	0.079585569	0.279356103
positive regulation of cardiac muscle hypertrophy (GO:0(	44699	0.079585569	0.279356103
positive regulation of cell cycle phase transition (GO:190	44699	0.079585569	0.279356103
positive regulation of CREB transcription factor activity (G	44699	0.079585569	0.279356103
positive regulation of glial cell differentiation (GO:00456	44699	0.079585569	0.279356103
positive regulation of phosphoprotein phosphatase activi	44699	0.079585569	0.279356103
positive regulation of stress-activated protein kinase sign	44699	0.079585569	0.279356103
regulation of B cell differentiation (GO:0045577)	44699	0.079585569	0.279356103
regulation of production of miRNAs involved in gene siler	44699	0.079585569	0.279356103
regulation of protein-containing complex disassembly (G	44699	0.079585569	0.279356103
regulation of single stranded viral RNA replication via dou	44699	0.079585569	0.279356103
regulation of vesicle-mediated transport (GO:0060627)	18/96	0.079817218	0.279980045
negative regulation of epithelial to mesenchymal transiti	44771	0.080264216	0.280789633
negative regulation of transferase activity (GO:0051348)	44771	0.080264216	0.280789633
regulation of double-strand break repair via nonhomolog	44771	0.080264216	0.280789633
response to cadmium ion (GO:0046686)	44771	0.080264216	0.280789633
cholesterol homeostasis (GO:0042632)	14/71	0.081301316	0.282409682
positive regulation of cellular protein localization (GO:19	14/71	0.081301316	0.282409682
protein complex oligomerization (GO:0051259)	17/90	0.082217292	0.282409682
AMP metabolic process (GO:0046033)	44664	0.082412527	0.282409682
antifungal innate immune response (GO:0061760)	44664	0.082412527	0.282409682
cellular biogenic amine metabolic process (GO:0006576)	44664	0.082412527	0.282409682
cellular potassium ion homeostasis (GO:0030007)	44664	0.082412527	0.282409682
intracellular sterol transport (GO:0032366)	44664	0.082412527	0.282409682
negative regulation by host of viral transcription (GO:004	44664	0.082412527	0.282409682
negative regulation of alcohol biosynthetic process (GO:1	44664	0.082412527	0.282409682
negative regulation of CD4-positive, alpha-beta T cell acti	44664	0.082412527	0.282409682
negative regulation of histone methylation (GO:0031061	44664	0.082412527	0.282409682
negative regulation of hydrogen peroxide-induced cell de	44664	0.082412527	0.282409682
negative regulation of intrinsic apoptotic signaling pathw	44664	0.082412527	0.282409682
negative regulation of vascular endothelial growth factor	44664	0.082412527	0.282409682
positive regulation of cell aging (GO:0090343)	44664	0.082412527	0.282409682

positive regulation of fatty acid biosynthetic process (GO	44664	0.082412527	0.282409682
positive regulation of nuclear-transcribed mRNA poly(A) t	44664	0.082412527	0.282409682
positive regulation of protein exit from endoplasmic retic	44664	0.082412527	0.282409682
positive regulation of reactive oxygen species biosynthet	44664	0.082412527	0.282409682
positive regulation of transporter activity (GO:0032411)	44664	0.082412527	0.282409682
purine-containing compound catabolic process (GO:0072	44664	0.082412527	0.282409682
regulation of fibrinolysis (GO:0051917)	44664	0.082412527	0.282409682
regulation of leukocyte adhesion to vascular endothelial	44664	0.082412527	0.282409682
regulation of lysosomal lumen pH (GO:0035751)	44664	0.082412527	0.282409682
regulation of oxidoreductase activity (GO:0051341)	44664	0.082412527	0.282409682
regulation of platelet-derived growth factor receptor sign	44664	0.082412527	0.282409682
regulation of protein exit from endoplasmic reticulum (G	44664	0.082412527	0.282409682
regulation of response to stress (GO:0080134)	44664	0.082412527	0.282409682
semaphorin-plexin signaling pathway involved in neuron	44664	0.082412527	0.282409682
synaptic vesicle localization (GO:0097479)	44664	0.082412527	0.282409682
negative regulation of cell cycle G1/S phase transition (G	12997	0.083552973	0.285376524
regulation of lipid biosynthetic process (GO:0046890)	12997	0.083552973	0.285376524
regulation of TORC1 signaling (GO:1903432)	12997	0.083552973	0.285376524
response to exogenous dsRNA (GO:0043330)	12997	0.083552973	0.285376524
semaphorin-plexin signaling pathway (GO:0071526)	12997	0.083552973	0.285376524
chromatin remodeling (GO:0006338)	19/103	0.083654841	0.285536726
phospholipid transport (GO:0015914)	21885	0.084220432	0.287278491
histone deacetylation (GO:0016575)	17441	0.085536763	0.291194943
regulation of protein localization to nucleus (GO:190018	17441	0.085536763	0.291194943
regulation of wound healing (GO:0061041)	17441	0.085536763	0.291194943
histone monoubiquitination (GO:0010390)	44736	0.088481719	0.299845095
lipid translocation (GO:0034204)	44736	0.088481719	0.299845095
mammary gland development (GO:0030879)	44736	0.088481719	0.299845095
phospholipid catabolic process (GO:0009395)	44736	0.088481719	0.299845095
protein kinase B signaling (GO:0043491)	44736	0.088481719	0.299845095
regulation of cardiac muscle hypertrophy (GO:0010611)	44736	0.088481719	0.299845095
wound healing, spreading of cells (GO:0044319)	44736	0.088481719	0.299845095
sterol homeostasis (GO:0055092)	14/72	0.089182701	0.301840602
positive regulation of supramolecular fiber organization (	17/91	0.08918678	0.301840602
plasma membrane bounded cell projection assembly (GC	45/278	0.089817462	0.303777157
artery morphogenesis (GO:0048844)	44772	0.093260082	0.314397227
negative regulation of cytoskeleton organization (GO:005	44772	0.093260082	0.314397227
phosphatidylcholine acyl-chain remodeling (GO:0036151	44772	0.093260082	0.314397227
positive regulation of phosphate metabolic process (GO:(	44772	0.093260082	0.314397227
regulation of natural killer cell mediated cytotoxicity (GO	44772	0.093260082	0.314397227
positive regulation of ubiquitin-dependent protein catab	15/79	0.094777436	0.319305304
intrinsic apoptotic signaling pathway by p53 class mediat	13363	0.095531196	0.320638839
mitochondrion disassembly (GO:0061726)	13363	0.095531196	0.320638839
platelet aggregation (GO:0070527)	13363	0.095531196	0.320638839
positive regulation of substrate adhesion-dependent cell	13363	0.095531196	0.320638839
regulation of cardiac muscle contraction (GO:0055117)	13363	0.095531196	0.320638839
cellular response to alcohol (GO:0097306)	17807	0.095825616	0.320638839

nucleus organization (GO:0006997)	17807	0.095825616	0.320638839
cellular response to hypoxia (GO:0071456)	23/131	0.095979966	0.320638839
heterophilic cell-cell adhesion via plasma membrane cell	15585	0.096204173	0.320638839
potassium ion import across plasma membrane (GO:199(	15585	0.096204173	0.320638839
regulation of ubiquitin-dependent protein catabolic proc	15585	0.096204173	0.320638839
cardiac muscle cell contraction (GO:0086003)	44700	0.096716277	0.320638839
histone deubiquitination (GO:0016578)	44700	0.096716277	0.320638839
negative regulation of cytokine production involved in inf	44700	0.096716277	0.320638839
negative regulation of nervous system development (GO:	44700	0.096716277	0.320638839
negative regulation of T cell receptor signaling pathway (	44700	0.096716277	0.320638839
neuromuscular process (GO:0050905)	44700	0.096716277	0.320638839
positive regulation of focal adhesion assembly (GO:0051(	44700	0.096716277	0.320638839
positive regulation of triglyceride metabolic process (GO:	44700	0.096716277	0.320638839
Rac protein signal transduction (GO:0016601)	44700	0.096716277	0.320638839
regulation of bicellular tight junction assembly (GO:2000(	44700	0.096716277	0.320638839
regulation of exosomal secretion (GO:1903541)	44700	0.096716277	0.320638839
regulation of oligodendrocyte differentiation (GO:00487(	44700	0.096716277	0.320638839
regulation of synaptic vesicle exocytosis (GO:2000300)	44700	0.096716277	0.320638839
regulation of vascular endothelial growth factor signaling	44700	0.096716277	0.320638839
positive regulation of synaptic transmission (GO:0050806	14/73	0.097526988	0.322914407
ubiquitin-dependent ERAD pathway (GO:0030433)	14/73	0.097526988	0.322914407
organonitrogen compound biosynthetic process (GO:190	27/158	0.098803784	0.326933542
positive regulation of proteasomal protein catabolic proc	16/86	0.099767811	0.32991329
peptidyl-threonine modification (GO:0018210)	13/67	0.10018754	0.331090501
phosphatidylinositol metabolic process (GO:0046488)	20/112	0.100485657	0.331629784
adenylate cyclase-modulating G protein-coupled recepto	28/165	0.100604457	0.331629784
mRNA-containing ribonucleoprotein complex export fron	18/99	0.100606071	0.331629784
organic anion transport (GO:0015711)	18/99	0.100606071	0.331629784
regulation of DNA-templated transcription, initiation (GO	22616	0.102692514	0.335032088
negative regulation of cell cycle (GO:0045786)	15/80	0.103047174	0.335032088
regulation of protein localization to plasma membrane (G	15/80	0.103047174	0.335032088
cellular response to low-density lipoprotein particle stim	44665	0.103743209	0.335032088
dicarboxylic acid catabolic process (GO:0043649)	44665	0.103743209	0.335032088
heterochromatin organization (GO:0070828)	44665	0.103743209	0.335032088
positive regulation of brown fat cell differentiation (GO:0	44665	0.103743209	0.335032088
positive regulation of cyclase activity (GO:0031281)	44665	0.103743209	0.335032088
positive regulation of sodium ion transmembrane transp	44665	0.103743209	0.335032088
positive regulation of T cell chemotaxis (GO:0010820)	44665	0.103743209	0.335032088
positive regulation of T cell receptor signaling pathway (G	44665	0.103743209	0.335032088
positive regulation of transmembrane transport (GO:003	44665	0.103743209	0.335032088
regulation of intrinsic apoptotic signaling pathway in resp	44665	0.103743209	0.335032088
regulation of retinoic acid receptor signaling pathway (GO	44665	0.103743209	0.335032088
renal absorption (GO:0070293)	44665	0.103743209	0.335032088
smooth muscle contraction (GO:0006939)	44665	0.103743209	0.335032088
endosome transport via multivesicular body sorting path	44737	0.103974967	0.335032088
glycolytic process through glucose-6-phosphate (GO:006	44737	0.103974967	0.335032088
negative regulation of cellular carbohydrate metabolic pr	44737	0.103974967	0.335032088

negative regulation of endocytosis (GO:0045806)	44737	0.103974967	0.335032088
negative regulation of response to endoplasmic reticulun	44737	0.103974967	0.335032088
negative regulation of sequestering of calcium ion (GO:0(	44737	0.103974967	0.335032088
negative regulation of signaling (GO:0023057)	44737	0.103974967	0.335032088
organophosphate ester transport (GO:0015748)	44737	0.103974967	0.335032088
positive regulation of ERBB signaling pathway (GO:19011	44737	0.103974967	0.335032088
positive regulation of peptidyl-threonine phosphorylatior	44737	0.103974967	0.335032088
regulation of cholesterol transport (GO:0032374)	44737	0.103974967	0.335032088
regulation of myotube differentiation (GO:0010830)	44737	0.103974967	0.335032088
regulation of epithelial cell proliferation (GO:0050678)	17/93	0.104228744	0.335032088
actin-mediated cell contraction (GO:0070252)	44629	0.105830155	0.335032088
bone resorption (GO:0045453)	44629	0.105830155	0.335032088
glucosamine-containing compound catabolic process (GC	44629	0.105830155	0.335032088
leukotriene D4 biosynthetic process (GO:1901750)	44629	0.105830155	0.335032088
leukotriene D4 metabolic process (GO:1901748)	44629	0.105830155	0.335032088
negative regulation of alpha-beta T cell activation (GO:00	44629	0.105830155	0.335032088
negative regulation of bone resorption (GO:0045779)	44629	0.105830155	0.335032088
negative regulation of glial cell differentiation (GO:00456	44629	0.105830155	0.335032088
negative regulation of protein activation cascade (GO:20(	44629	0.105830155	0.335032088
negative regulation of protein-containing complex disass	44629	0.105830155	0.335032088
negative regulation of RNA catabolic process (GO:19023(	44629	0.105830155	0.335032088
neurotransmitter receptor transport to postsynaptic mer	44629	0.105830155	0.335032088
Notch receptor processing (GO:0007220)	44629	0.105830155	0.335032088
peptidyl-cysteine modification (GO:0018198)	44629	0.105830155	0.335032088
phosphatidylglycerol biosynthetic process (GO:0006655)	44629	0.105830155	0.335032088
positive regulation of B cell differentiation (GO:0045579)	44629	0.105830155	0.335032088
positive regulation of extracellular matrix assembly (GO:1	44629	0.105830155	0.335032088
positive regulation of mitochondrial calcium ion concentr	44629	0.105830155	0.335032088
positive regulation of phagocytosis, engulfment (GO:006(	44629	0.105830155	0.335032088
positive regulation of protein kinase C signaling (GO:009(	44629	0.105830155	0.335032088
positive regulation of tumor necrosis factor-mediated sig	44629	0.105830155	0.335032088
postsynaptic membrane assembly (GO:0097104)	44629	0.105830155	0.335032088
quaternary ammonium group transport (GO:0015697)	44629	0.105830155	0.335032088
regulation of cellular extravasation (GO:0002691)	44629	0.105830155	0.335032088
regulation of DNA-templated transcription in response to	44629	0.105830155	0.335032088
regulation of glucan biosynthetic process (GO:0010962)	44629	0.105830155	0.335032088
regulation of lipid transport (GO:0032368)	44629	0.105830155	0.335032088
regulation of protein deacetylation (GO:0090311)	44629	0.105830155	0.335032088
regulation of respiratory burst (GO:0060263)	44629	0.105830155	0.335032088
regulation of RNA polymerase II regulatory region sequer	44629	0.105830155	0.335032088
regulation of skeletal muscle cell differentiation (GO:200	44629	0.105830155	0.335032088
regulation of vesicle fusion (GO:0031338)	44629	0.105830155	0.335032088
response to leptin (GO:0044321)	44629	0.105830155	0.335032088
response to misfolded protein (GO:0051788)	44629	0.105830155	0.335032088
response to type I interferon (GO:0034340)	44629	0.105830155	0.335032088
semaphorin-plexin signaling pathway involved in axon gu	44629	0.105830155	0.335032088
circulatory system development (GO:0072359)	22/126	0.10637321	0.336546179

positive regulation of actin filament polymerization (GO:(	18172	0.106811353	0.337726707
aminoglycan catabolic process (GO:0006026)	44773	0.107352498	0.338819092
peptide cross-linking (GO:0018149)	44773	0.107352498	0.338819092
positive regulation of proteolysis involved in cellular prot	44773	0.107352498	0.338819092
regulation of cell-substrate adhesion (GO:0010810)	15950	0.108079199	0.340905549
negative regulation of endothelial cell proliferation (GO:(	13728	0.108430678	0.340979038
negative regulation of stress-activated MAPK cascade (G(	13728	0.108430678	0.340979038
phagosome maturation (GO:0090382)	13728	0.108430678	0.340979038
positive regulation of exocytosis (GO:0045921)	13728	0.108430678	0.340979038
regulation of vascular associated smooth muscle cell prol	13728	0.108430678	0.340979038
regulation of neurogenesis (GO:0050767)	22981	0.11276335	0.354175092
response to retinoic acid (GO:0032526)	22981	0.11276335	0.354175092
modification-dependent protein catabolic process (GO:0(	33/201	0.113156563	0.355195376
regulation of nucleic acid-templated transcription (GO:19	66/430	0.113345219	0.355572713
cardiac epithelial to mesenchymal transition (GO:006031	44701	0.115539514	0.358559005
cellular monovalent inorganic cation homeostasis (GO:0(	44701	0.115539514	0.358559005
cellular response to interferon-beta (GO:0035458)	44701	0.115539514	0.358559005
embryonic digestive tract development (GO:0048566)	44701	0.115539514	0.358559005
establishment of epithelial cell polarity (GO:0090162)	44701	0.115539514	0.358559005
maintenance of protein location in nucleus (GO:0051457	44701	0.115539514	0.358559005
mesoderm development (GO:0007498)	44701	0.115539514	0.358559005
negative regulation of axon extension involved in axon gu	44701	0.115539514	0.358559005
negative regulation of dephosphorylation (GO:0035305)	44701	0.115539514	0.358559005
nucleobase-containing compound biosynthetic process ((	44701	0.115539514	0.358559005
organic cation transport (GO:0015695)	44701	0.115539514	0.358559005
positive regulation of cyclin-dependent protein kinase ac	44701	0.115539514	0.358559005
positive regulation of natural killer cell mediated cytotoxi	44701	0.115539514	0.358559005
positive regulation of nitrogen compound metabolic proc	44701	0.115539514	0.358559005
post-transcriptional gene silencing by RNA (GO:0035194)	44701	0.115539514	0.358559005
regulation of granulocyte chemotaxis (GO:0071622)	44701	0.115539514	0.358559005
regulation of hippo signaling (GO:0035330)	44701	0.115539514	0.358559005
regulation of lymphocyte differentiation (GO:0045619)	44701	0.115539514	0.358559005
autophagosome organization (GO:1905037)	20760	0.115768041	0.359053715
positive regulation of protein polymerization (GO:00322	13/69	0.119499037	0.370183362
RNA 3'-end processing (GO:0031123)	13/69	0.119499037	0.370183362
intracellular steroid hormone receptor signaling pathway	16316	0.120735655	0.371478362
positive regulation of receptor-mediated endocytosis (GC	16316	0.120735655	0.371478362
response to amyloid-beta (GO:1904645)	16316	0.120735655	0.371478362
lamellipodium assembly (GO:0030032)	44738	0.120775159	0.371478362
mononuclear cell differentiation (GO:1903131)	44738	0.120775159	0.371478362
negative regulation of interleukin-1 beta production (GO:	44738	0.120775159	0.371478362
negative regulation of macroautophagy (GO:0016242)	44738	0.120775159	0.371478362
negative regulation of protein transport (GO:0051224)	44738	0.120775159	0.371478362
negative regulation of receptor-mediated endocytosis (G	44738	0.120775159	0.371478362
purine-containing compound biosynthetic process (GO:0(	44738	0.120775159	0.371478362
regulation of viral life cycle (GO:1903900)	44738	0.120775159	0.371478362
TOR signaling (GO:0031929)	44738	0.120775159	0.371478362

lysosome organization (GO:0007040)	14093	0.122232129	0.375515025
negative regulation of TOR signaling (GO:0032007)	14093	0.122232129	0.375515025
amyloid fibril formation (GO:1990000)	23346	0.123384616	0.377515428
positive regulation of cell growth (GO:0030307)	18/102	0.124495244	0.377515428
regulation of proteasomal ubiquitin-dependent protein c	18/102	0.124495244	0.377515428
regulation of endothelial cell migration (GO:0010594)	16/89	0.125483771	0.377515428
regulation of mRNA catabolic process (GO:0061013)	21/122	0.125549407	0.377515428
external encapsulating structure organization (GO:00452	35/217	0.126349171	0.377515428
positive regulation of gene expression, epigenetic (GO:0(	21125	0.127196699	0.377515428
cellular sodium ion homeostasis (GO:0006883)	44666	0.127293066	0.377515428
engulfment of apoptotic cell (GO:0043652)	44666	0.127293066	0.377515428
establishment of apical/basal cell polarity (GO:0035089)	44666	0.127293066	0.377515428
ganglioside biosynthetic process (GO:0001574)	44666	0.127293066	0.377515428
histone H3 deacetylation (GO:0070932)	44666	0.127293066	0.377515428
histone mRNA catabolic process (GO:0071044)	44666	0.127293066	0.377515428
macrophage migration (GO:1905517)	44666	0.127293066	0.377515428
modulation by host of viral genome replication (GO:0044	44666	0.127293066	0.377515428
negative regulation of chondrocyte differentiation (GO:0(	44666	0.127293066	0.377515428
negative regulation of single stranded viral RNA replicatic	44666	0.127293066	0.377515428
peptidyl-arginine modification (GO:0018195)	44666	0.127293066	0.377515428
positive regulation of chromatin organization (GO:19052(	44666	0.127293066	0.377515428
positive regulation of DNA damage response, signal trans	44666	0.127293066	0.377515428
positive regulation of endothelial cell chemotaxis (GO:20(	44666	0.127293066	0.377515428
regulation of extracellular matrix organization (GO:1903(	44666	0.127293066	0.377515428
regulation of microglial cell activation (GO:1903978)	44666	0.127293066	0.377515428
response to muscle stretch (GO:0035994)	44666	0.127293066	0.377515428
superoxide anion generation (GO:0042554)	44666	0.127293066	0.377515428
proteolysis (GO:0006508)	45/287	0.13083209	0.377515428
cellular response to organonitrogen compound (GO:0071	18/103	0.133143802	0.377515428
regulation of anatomical structure morphogenesis (GO:0(	21/123	0.133451625	0.377515428
AMP biosynthetic process (GO:0006167)	44597	0.13373725	0.377515428
anion homeostasis (GO:0055081)	44597	0.13373725	0.377515428
cardiac muscle cell myoblast differentiation (GO:006037(	44597	0.13373725	0.377515428
CD4-positive, alpha-beta T cell activation (GO:0035710)	44597	0.13373725	0.377515428
chromatin maintenance (GO:0070827)	44597	0.13373725	0.377515428
ciliary neurotrophic factor-mediated signaling pathway ((	44597	0.13373725	0.377515428
coronary artery morphogenesis (GO:0060982)	44597	0.13373725	0.377515428
DNA ligation involved in DNA repair (GO:0051103)	44597	0.13373725	0.377515428
dopamine catabolic process (GO:0042420)	44597	0.13373725	0.377515428
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA tra	44597	0.13373725	0.377515428
endonucleolytic cleavage to generate mature 5'-end of S(	44597	0.13373725	0.377515428
fatty acid omega-oxidation (GO:0010430)	44597	0.13373725	0.377515428
fructose 2,6-bisphosphate metabolic process (GO:00060(	44597	0.13373725	0.377515428
glomerular visceral epithelial cell migration (GO:0090521	44597	0.13373725	0.377515428
glutathione transport (GO:0034635)	44597	0.13373725	0.377515428
His-Purkinje system development (GO:0003164)	44597	0.13373725	0.377515428
histone citrullination (GO:0036414)	44597	0.13373725	0.377515428

histone H3-K27 demethylation (GO:0071557)	44597	0.13373725	0.377515428
histone H4-K20 methylation (GO:0034770)	44597	0.13373725	0.377515428
histone H4-K20 trimethylation (GO:0034773)	44597	0.13373725	0.377515428
immature B cell differentiation (GO:0002327)	44597	0.13373725	0.377515428
intracellular sequestering of iron ion (GO:0006880)	44597	0.13373725	0.377515428
kidney morphogenesis (GO:0060993)	44597	0.13373725	0.377515428
L-aspartate transmembrane transport (GO:0070778)	44597	0.13373725	0.377515428
lymph node development (GO:0048535)	44597	0.13373725	0.377515428
lysosomal protein catabolic process (GO:1905146)	44597	0.13373725	0.377515428
meiotic sister chromatid segregation (GO:0045144)	44597	0.13373725	0.377515428
microtubule nucleation by microtubule organizing center	44597	0.13373725	0.377515428
mRNA cleavage involved in gene silencing by miRNA (GO:	44597	0.13373725	0.377515428
negative regulation of blood coagulation, intrinsic pathw	44597	0.13373725	0.377515428
negative regulation of calcium ion-dependent exocytosis	44597	0.13373725	0.377515428
negative regulation of cysteine-type endopeptidase activ	44597	0.13373725	0.377515428
negative regulation of histone H3-K27 methylation (GO:0	44597	0.13373725	0.377515428
negative regulation of histone H4 acetylation (GO:00902	44597	0.13373725	0.377515428
negative regulation of hydrogen peroxide-induced neuro	44597	0.13373725	0.377515428
negative regulation of immunoglobulin production (GO:0	44597	0.13373725	0.377515428
negative regulation of mast cell activation involved in im	44597	0.13373725	0.377515428
negative regulation of organ growth (GO:0046621)	44597	0.13373725	0.377515428
negative regulation of RNA polymerase II regulatory regic	44597	0.13373725	0.377515428
negative regulation of T cell migration (GO:2000405)	44597	0.13373725	0.377515428
negative regulation of vascular endothelial cell proliferati	44597	0.13373725	0.377515428
neuroinflammatory response (GO:0150076)	44597	0.13373725	0.377515428
ornithine transport (GO:0015822)	44597	0.13373725	0.377515428
oxidative RNA demethylation (GO:0035513)	44597	0.13373725	0.377515428
positive regulation of axon extension involved in axon gu	44597	0.13373725	0.377515428
positive regulation of CD4-positive, CD25-positive, alpha-	44597	0.13373725	0.377515428
positive regulation of cell proliferation involved in heart r	44597	0.13373725	0.377515428
positive regulation of DNA demethylation (GO:1901537)	44597	0.13373725	0.377515428
positive regulation of endothelial cell chemotaxis by VEG	44597	0.13373725	0.377515428
positive regulation of histone H3-K27 methylation (GO:0(	44597	0.13373725	0.377515428
positive regulation of mast cell activation involved in imn	44597	0.13373725	0.377515428
positive regulation of mast cell chemotaxis (GO:0060754)	44597	0.13373725	0.377515428
positive regulation of metallopeptidase activity (GO:1905	44597	0.13373725	0.377515428
positive regulation of natural killer cell chemotaxis (GO:2	44597	0.13373725	0.377515428
positive regulation of necrotic cell death (GO:0010940)	44597	0.13373725	0.377515428
positive regulation of nucleotide-binding oligomerization	44597	0.13373725	0.377515428
positive regulation of protein catabolic process in the vac	44597	0.13373725	0.377515428
positive regulation of toll-like receptor 9 signaling pathw	44597	0.13373725	0.377515428
positive regulation of vascular associated smooth muscle	44597	0.13373725	0.377515428
prostaglandin transport (GO:0015732)	44597	0.13373725	0.377515428
protein citrullination (GO:0018101)	44597	0.13373725	0.377515428
protein localization to membrane raft (GO:1903044)	44597	0.13373725	0.377515428
pyridine-containing compound metabolic process (GO:00	44597	0.13373725	0.377515428
quinone catabolic process (GO:1901662)	44597	0.13373725	0.377515428

receptor-mediated virion attachment to host cell (GO:00	44597	0.13373725	0.377515428
regulation of antifungal innate immune response (GO:19	44597	0.13373725	0.377515428
regulation of astrocyte activation (GO:0061888)	44597	0.13373725	0.377515428
regulation of blood coagulation, intrinsic pathway (GO:2(	44597	0.13373725	0.377515428
regulation of caveolin-mediated endocytosis (GO:200128	44597	0.13373725	0.377515428
regulation of cell maturation (GO:1903429)	44597	0.13373725	0.377515428
regulation of cellular response to osmotic stress (GO:010	44597	0.13373725	0.377515428
regulation of cyclase activity (GO:0031279)	44597	0.13373725	0.377515428
regulation of germinal center formation (GO:0002634)	44597	0.13373725	0.377515428
regulation of guanyl-nucleotide exchange factor activity (	44597	0.13373725	0.377515428
regulation of histone H3-K9 trimethylation (GO:1900112)	44597	0.13373725	0.377515428
regulation of histone H4-K16 acetylation (GO:2000618)	44597	0.13373725	0.377515428
regulation of hormone metabolic process (GO:0032350)	44597	0.13373725	0.377515428
regulation of hydrogen peroxide biosynthetic process (G(	44597	0.13373725	0.377515428
regulation of inositol trisphosphate biosynthetic process	44597	0.13373725	0.377515428
regulation of microvillus assembly (GO:0032534)	44597	0.13373725	0.377515428
regulation of natural killer cell mediated immunity (GO:0(	44597	0.13373725	0.377515428
regulation of neutrophil activation (GO:1902563)	44597	0.13373725	0.377515428
regulation of phosphatidylinositol dephosphorylation (G(	44597	0.13373725	0.377515428
regulation of respiratory burst involved in inflammatory r	44597	0.13373725	0.377515428
regulation of synaptic vesicle priming (GO:0010807)	44597	0.13373725	0.377515428
regulation of synaptic vesicle recycling (GO:1903421)	44597	0.13373725	0.377515428
regulation of systemic arterial blood pressure by endothe	44597	0.13373725	0.377515428
regulation of vascular associated smooth muscle contract	44597	0.13373725	0.377515428
regulation of vitamin D receptor signaling pathway (GO:0	44597	0.13373725	0.377515428
response to fructose (GO:0009750)	44597	0.13373725	0.377515428
response to salt stress (GO:0009651)	44597	0.13373725	0.377515428
ribose phosphate metabolic process (GO:0019693)	44597	0.13373725	0.377515428
RNA phosphodiester bond hydrolysis, exonucleolytic (GO	44597	0.13373725	0.377515428
rRNA 5'-end processing (GO:0000967)	44597	0.13373725	0.377515428
Schwann cell differentiation (GO:0014037)	44597	0.13373725	0.377515428
serotonin transport (GO:0006837)	44597	0.13373725	0.377515428
serotonin uptake (GO:0051610)	44597	0.13373725	0.377515428
sulfide oxidation (GO:0019418)	44597	0.13373725	0.377515428
sulfide oxidation, using sulfide:quinone oxidoreductase ((	44597	0.13373725	0.377515428
T cell extravasation (GO:0072683)	44597	0.13373725	0.377515428
negative regulation of Wnt signaling pathway (GO:00301	31/191	0.135101031	0.377515428
positive regulation of endothelial cell proliferation (GO:0(	14/77	0.135513727	0.377515428
beta-catenin destruction complex disassembly (GO:1904	44702	0.1359502	0.377515428
calcium-mediated signaling using intracellular calcium so	44702	0.1359502	0.377515428
cellular response to steroid hormone stimulus (GO:0071	44702	0.1359502	0.377515428
focal adhesion assembly (GO:0048041)	44702	0.1359502	0.377515428
histone ubiquitination (GO:0016574)	44702	0.1359502	0.377515428
negative regulation of cell communication (GO:0010648)	44702	0.1359502	0.377515428
negative regulation of reproductive process (GO:200024	44702	0.1359502	0.377515428
positive regulation of vascular associated smooth muscle	44702	0.1359502	0.377515428
regulation of lipid catabolic process (GO:0050994)	44702	0.1359502	0.377515428

regulation of lipopolysaccharide-mediated signaling path	44702	0.1359502	0.377515428
sterol transport (GO:0015918)	44702	0.1359502	0.377515428
vacuolar acidification (GO:0007035)	44702	0.1359502	0.377515428
adherens junction assembly (GO:0034333)	44630	0.136857477	0.377515428
arginine metabolic process (GO:0006525)	44630	0.136857477	0.377515428
aromatic amino acid family metabolic process (GO:0009(	44630	0.136857477	0.377515428
cAMP biosynthetic process (GO:0006171)	44630	0.136857477	0.377515428
cellular response to dopamine (GO:1903351)	44630	0.136857477	0.377515428
cellular response to leucine (GO:0071233)	44630	0.136857477	0.377515428
cellular response to oxidised low-density lipoprotein part	44630	0.136857477	0.377515428
cellular response to purine-containing compound (GO:00	44630	0.136857477	0.377515428
dicarboxylic acid biosynthetic process (GO:0043650)	44630	0.136857477	0.377515428
endothelial tube morphogenesis (GO:0061154)	44630	0.136857477	0.377515428
ESCRT complex disassembly (GO:1904896)	44630	0.136857477	0.377515428
ESCRT III complex disassembly (GO:1904903)	44630	0.136857477	0.377515428
granulocyte migration (GO:0097530)	44630	0.136857477	0.377515428
histone H2B ubiquitination (GO:0033523)	44630	0.136857477	0.377515428
histone H3-K36 demethylation (GO:0070544)	44630	0.136857477	0.377515428
ionotropic glutamate receptor signaling pathway (GO:00	44630	0.136857477	0.377515428
leptin-mediated signaling pathway (GO:0033210)	44630	0.136857477	0.377515428
modulation by symbiont of host process (GO:0044003)	44630	0.136857477	0.377515428
monocyte activation (GO:0042117)	44630	0.136857477	0.377515428
negative regulation of alpha-beta T cell proliferation (GO	44630	0.136857477	0.377515428
negative regulation of extracellular matrix organization ((	44630	0.136857477	0.377515428
negative regulation of humoral immune response mediat	44630	0.136857477	0.377515428
negative regulation of protein autophosphorylation (GO:(	44630	0.136857477	0.377515428
negative regulation of protein exit from endoplasmic reti	44630	0.136857477	0.377515428
negative regulation of receptor binding (GO:1900121)	44630	0.136857477	0.377515428
negative regulation of toll-like receptor 4 signaling pathw	44630	0.136857477	0.377515428
neuron remodeling (GO:0016322)	44630	0.136857477	0.377515428
positive regulation by symbiont of entry into host (GO:00	44630	0.136857477	0.377515428
positive regulation of keratinocyte migration (GO:005154	44630	0.136857477	0.377515428
positive regulation of monocyte differentiation (GO:0045	44630	0.136857477	0.377515428
positive regulation of skeletal muscle tissue developmen	44630	0.136857477	0.377515428
positive regulation of T cell apoptotic process (GO:00702	44630	0.136857477	0.377515428
positive regulation of viral entry into host cell (GO:00465	44630	0.136857477	0.377515428
protein K11-linked deubiquitination (GO:0035871)	44630	0.136857477	0.377515428
regulation of actin filament-based movement (GO:19031	44630	0.136857477	0.377515428
regulation of cell activation (GO:0050865)	44630	0.136857477	0.377515428
regulation of epithelial cell apoptotic process (GO:19040	44630	0.136857477	0.377515428
regulation of high voltage-gated calcium channel activity	44630	0.136857477	0.377515428
regulation of leukocyte tethering or rolling (GO:1903236)	44630	0.136857477	0.377515428
regulation of mast cell activation (GO:0033003)	44630	0.136857477	0.377515428
regulation of organ growth (GO:0046620)	44630	0.136857477	0.377515428
regulation of peptidyl-lysine acetylation (GO:2000756)	44630	0.136857477	0.377515428
regulation of phagocytosis, engulfment (GO:0060099)	44630	0.136857477	0.377515428
regulation of phospholipid metabolic process (GO:19037	44630	0.136857477	0.377515428

response to dopamine (GO:1903350)	44630	0.136857477	0.377515428
response to leucine (GO:0043201)	44630	0.136857477	0.377515428
retinoic acid receptor signaling pathway (GO:0048384)	44630	0.136857477	0.377515428
sarcoplasmic reticulum calcium ion transport (GO:00702	44630	0.136857477	0.377515428
secretory granule organization (GO:0033363)	44630	0.136857477	0.377515428
toxin transport (GO:1901998)	44630	0.136857477	0.377515428
regulation of receptor-mediated endocytosis (GO:00482	14458	0.136908386	0.377515428
apoptotic mitochondrial changes (GO:0008637)	12236	0.138696674	0.380160367
negative chemotaxis (GO:0050919)	12236	0.138696674	0.380160367
negative regulation of JNK cascade (GO:0046329)	12236	0.138696674	0.380160367
positive regulation of cholesterol transport (GO:0032376	12236	0.138696674	0.380160367
positive regulation of organelle organization (GO:001063	12236	0.138696674	0.380160367
regulation of neurotransmitter secretion (GO:0046928)	12236	0.138696674	0.380160367
regulation of protein localization to cell surface (GO:200	12236	0.138696674	0.380160367
cellular response to cadmium ion (GO:0071276)	44739	0.138818906	0.380160367
negative regulation of cation channel activity (GO:20012	44739	0.138818906	0.380160367
negative regulation of protein polymerization (GO:00322	44739	0.138818906	0.380160367
positive regulation of cellular component movement (GO	44739	0.138818906	0.380160367
positive regulation of striated muscle cell differentiation	44739	0.138818906	0.380160367
regulation of blood coagulation (GO:0030193)	44739	0.138818906	0.380160367
positive regulation of cell projection organization (GO:00	20/117	0.139139186	0.380836707
regulation of mitotic cell cycle (GO:0007346)	29/178	0.139668664	0.38208463
response to insulin (GO:0032868)	15/84	0.140365474	0.383788757
negative regulation of protein-containing complex assem	19268	0.143848361	0.392511969
positive regulation of protein localization to cell peripher	19268	0.143848361	0.392511969
protein homotetramerization (GO:0051289)	19268	0.143848361	0.392511969
cellular response to metal ion (GO:0071248)	22/131	0.143858092	0.392511969
protein autoubiquitination (GO:0051865)	24077	0.146242713	0.398808868
RNA processing (GO:0006396)	29/179	0.146605573	0.399588643
regulation of cellular response to stress (GO:0080135)	20/118	0.147775071	0.40256502
activation of GTPase activity (GO:0090630)	18/105	0.151449873	0.411583216
autophagy of mitochondrion (GO:0000422)	14824	0.152424941	0.411583216
negative regulation of protein kinase B signaling (GO:005	14824	0.152424941	0.411583216
positive regulation of cation channel activity (GO:200125	14824	0.152424941	0.411583216
response to organonitrogen compound (GO:0010243)	14824	0.152424941	0.411583216
digestive tract morphogenesis (GO:0048546)	44667	0.152828494	0.411583216
eosinophil chemotaxis (GO:0048245)	44667	0.152828494	0.411583216
eosinophil migration (GO:0072677)	44667	0.152828494	0.411583216
glutamine family amino acid catabolic process (GO:0009(	44667	0.152828494	0.411583216
negative regulation of immune effector process (GO:000	44667	0.152828494	0.411583216
negative regulation of transcription regulatory region DN	44667	0.152828494	0.411583216
nucleotide catabolic process (GO:0009166)	44667	0.152828494	0.411583216
polyol biosynthetic process (GO:0046173)	44667	0.152828494	0.411583216
positive regulation of immunoglobulin mediated immune	44667	0.152828494	0.411583216
positive regulation of isotype switching (GO:0045830)	44667	0.152828494	0.411583216
regulation of blood vessel endothelial cell proliferation in	44667	0.152828494	0.411583216
regulation of ceramide biosynthetic process (GO:200030	44667	0.152828494	0.411583216

regulation of monocyte differentiation (GO:0045655)	44667	0.152828494	0.411583216
regulation of oxidative phosphorylation (GO:0002082)	44667	0.152828494	0.411583216
regulation of rRNA processing (GO:2000232)	44667	0.152828494	0.411583216
sphingolipid catabolic process (GO:0030149)	44667	0.152828494	0.411583216
T cell mediated immunity (GO:0002456)	44667	0.152828494	0.411583216
T cell activation (GO:0042110)	16/92	0.154694461	0.416176967
Wnt signaling pathway (GO:0016055)	16/92	0.154694461	0.416176967
regulation of myoblast differentiation (GO:0045661)	12601	0.155856962	0.419087431
mRNA 3'-end processing (GO:0031124)	14/79	0.157203195	0.421436928
cell projection assembly (GO:0030031)	44703	0.157821668	0.421436928
positive regulation of peptidase activity (GO:0010952)	44703	0.157821668	0.421436928
proteasomal ubiquitin-independent protein catabolic pro	44703	0.157821668	0.421436928
regulation of endoplasmic reticulum stress-induced intrin	44703	0.157821668	0.421436928
regulation of vacuole organization (GO:0044088)	44703	0.157821668	0.421436928
regulation of voltage-gated calcium channel activity (GO:	44703	0.157821668	0.421436928
cellular response to acid chemical (GO:0071229)	44740	0.158028708	0.421436928
cellular response to epidermal growth factor stimulus (G	44740	0.158028708	0.421436928
internal peptidyl-lysine acetylation (GO:0018393)	44740	0.158028708	0.421436928
L-amino acid transport (GO:0015807)	44740	0.158028708	0.421436928
negative regulation of calcium ion transmembrane transp	44740	0.158028708	0.421436928
neutral amino acid transport (GO:0015804)	44740	0.158028708	0.421436928
positive regulation of cytosolic calcium ion concentration	44740	0.158028708	0.421436928
regulation of insulin secretion involved in cellular respons	44740	0.158028708	0.421436928
regulation of neuron migration (GO:2001222)	44740	0.158028708	0.421436928
cellular response to nutrient levels (GO:0031669)	24442	0.158454663	0.422139473
regulation of protein localization (GO:0032880)	24442	0.158454663	0.422139473
phosphatidylinositol biosynthetic process (GO:0006661)	21/126	0.158854484	0.422987721
RNA export from nucleus (GO:0006405)	18/106	0.161097131	0.428739546
epithelial to mesenchymal transition (GO:0001837)	17411	0.163181867	0.434065439
extracellular structure organization (GO:0043062)	34/216	0.163653216	0.434945165
positive regulation of metabolic process (GO:0009893)	19/113	0.163680038	0.434945165
positive regulation of cell differentiation (GO:0045597)	40/258	0.164412546	0.436668292
cytoskeleton organization (GO:0007010)	20/120	0.165924648	0.440459145
regulation of fat cell differentiation (GO:0045598)	14/80	0.168690837	0.444429687
epithelial cell migration (GO:0010631)	15189	0.168740554	0.444429687
regulation of release of cytochrome c from mitochondria	15189	0.168740554	0.444429687
cellular glucan metabolic process (GO:0006073)	44631	0.170500167	0.444429687
chromatin-mediated maintenance of transcription (GO:0	44631	0.170500167	0.444429687
complement receptor mediated signaling pathway (GO:0	44631	0.170500167	0.444429687
desensitization of G protein-coupled receptor signaling p	44631	0.170500167	0.444429687
establishment of epithelial cell apical/basal polarity (GO:	44631	0.170500167	0.444429687
glutamine family amino acid biosynthetic process (GO:00	44631	0.170500167	0.444429687
hematopoietic stem cell proliferation (GO:0071425)	44631	0.170500167	0.444429687
humoral immune response mediated by circulating immu	44631	0.170500167	0.444429687
inositol phosphate dephosphorylation (GO:0046855)	44631	0.170500167	0.444429687
isotype switching (GO:0045190)	44631	0.170500167	0.444429687
lipoprotein biosynthetic process (GO:0042158)	44631	0.170500167	0.444429687

negative regulation of activated T cell proliferation (GO:0	44631	0.170500167	0.444429687
negative regulation of bone remodeling (GO:0046851)	44631	0.170500167	0.444429687
negative regulation of receptor signaling pathway via STA	44631	0.170500167	0.444429687
negative regulation of response to cytokine stimulus (GO	44631	0.170500167	0.444429687
negative regulation of steroid biosynthetic process (GO:0	44631	0.170500167	0.444429687
Notch signaling involved in heart development (GO:0061	44631	0.170500167	0.444429687
organophosphate catabolic process (GO:0046434)	44631	0.170500167	0.444429687
phosphorylated carbohydrate dephosphorylation (GO:00	44631	0.170500167	0.444429687
positive regulation of alcohol biosynthetic process (GO:1	44631	0.170500167	0.444429687
positive regulation of cellular extravasation (GO:0002693	44631	0.170500167	0.444429687
positive regulation of interleukin-13 production (GO:003	44631	0.170500167	0.444429687
positive regulation of myelination (GO:0031643)	44631	0.170500167	0.444429687
positive regulation of posttranscriptional gene silencing (	44631	0.170500167	0.444429687
positive regulation of production of miRNAs involved in g	44631	0.170500167	0.444429687
positive regulation of transforming growth factor beta pr	44631	0.170500167	0.444429687
postsynapse assembly (GO:0099068)	44631	0.170500167	0.444429687
regulation of cytoplasmic transport (GO:1903649)	44631	0.170500167	0.444429687
regulation of ERAD pathway (GO:1904292)	44631	0.170500167	0.444429687
regulation of gene expression by genetic imprinting (GO:(	44631	0.170500167	0.444429687
regulation of monocyte chemotactic protein-1 productio	44631	0.170500167	0.444429687
regulation of stress-activated protein kinase signaling cas	44631	0.170500167	0.444429687
vasoconstriction (GO:0042310)	44631	0.170500167	0.444429687
mRNA export from nucleus (GO:0006406)	18/107	0.171065251	0.445679027
regulation of gene silencing by miRNA (GO:0060964)	24807	0.171167491	0.445721863
regulation of focal adhesion assembly (GO:0051893)	19998	0.171760776	0.446595211
regulation of megakaryocyte differentiation (GO:004565	19998	0.171760776	0.446595211
regulation of proteolysis (GO:0030162)	19998	0.171760776	0.446595211
intracellular pH reduction (GO:0051452)	12966	0.173932962	0.451114198
negative regulation of neurogenesis (GO:0050768)	12966	0.173932962	0.451114198
negative regulation of T cell proliferation (GO:0042130)	12966	0.173932962	0.451114198
regulation of phosphatidylinositol 3-kinase activity (GO:0	12966	0.173932962	0.451114198
response to estrogen (GO:0043627)	12966	0.173932962	0.451114198
regulation of peptide hormone secretion (GO:0090276)	13/74	0.17629986	0.451226966
protein modification by small protein conjugation (GO:00	61/409	0.178016587	0.451226966
production of miRNAs involved in gene silencing by miRN	44741	0.1783151	0.451226966
regulation of DNA biosynthetic process (GO:2000278)	44741	0.1783151	0.451226966
regulation of fatty acid biosynthetic process (GO:004230	44741	0.1783151	0.451226966
transition metal ion homeostasis (GO:0055076)	44741	0.1783151	0.451226966
iron ion homeostasis (GO:0055072)	22586	0.178696506	0.451226966
protein lipidation (GO:0006497)	22586	0.178696506	0.451226966
cellular response to ionizing radiation (GO:0071479)	17777	0.17872562	0.451226966
positive regulation of endocytosis (GO:0045807)	17777	0.17872562	0.451226966
positive regulation of protein localization to membrane (	17/101	0.178898729	0.451226966
cellular response to fatty acid (GO:0071398)	44668	0.180090717	0.451226966
diol biosynthetic process (GO:0034312)	44668	0.180090717	0.451226966
establishment of protein localization to endoplasmic reti	44668	0.180090717	0.451226966
histone H2A ubiquitination (GO:0033522)	44668	0.180090717	0.451226966

midbody abscission (GO:0061952)	44668	0.180090717	0.451226966
modified amino acid transport (GO:0072337)	44668	0.180090717	0.451226966
negative regulation of ATP metabolic process (GO:19035	44668	0.180090717	0.451226966
negative regulation of vascular associated smooth muscl	44668	0.180090717	0.451226966
positive regulation of cardiac muscle tissue growth (GO:0	44668	0.180090717	0.451226966
positive regulation of cyclin-dependent protein serine/th	44668	0.180090717	0.451226966
positive regulation of DNA replication (GO:0045740)	44668	0.180090717	0.451226966
positive regulation of smooth muscle cell migration (GO:(	44668	0.180090717	0.451226966
regulation of osteoblast proliferation (GO:0033688)	44668	0.180090717	0.451226966
response to purine-containing compound (GO:0014074)	44668	0.180090717	0.451226966
ruffle organization (GO:0031529)	44668	0.180090717	0.451226966
acylglycerol biosynthetic process (GO:0046463)	44704	0.181010279	0.451226966
blood vessel endothelial cell migration (GO:0043534)	44704	0.181010279	0.451226966
glucose 6-phosphate metabolic process (GO:0051156)	44704	0.181010279	0.451226966
negative regulation of intracellular protein transport (GO	44704	0.181010279	0.451226966
negative regulation of phosphoprotein phosphatase activ	44704	0.181010279	0.451226966
positive regulation of mRNA processing (GO:0050685)	44704	0.181010279	0.451226966
activation of Janus kinase activity (GO:0042976)	44598	0.183530814	0.451226966
adherens junction maintenance (GO:0034334)	44598	0.183530814	0.451226966
aromatic amino acid transport (GO:0015801)	44598	0.183530814	0.451226966
B cell chemotaxis (GO:0035754)	44598	0.183530814	0.451226966
chromatin organization involved in negative regulation of	44598	0.183530814	0.451226966
cobalamin transport (GO:0015889)	44598	0.183530814	0.451226966
dehydroascorbic acid transport (GO:0070837)	44598	0.183530814	0.451226966
gamma-aminobutyric acid transport (GO:0015812)	44598	0.183530814	0.451226966
histone H4-K12 acetylation (GO:0043983)	44598	0.183530814	0.451226966
imitative learning (GO:0098596)	44598	0.183530814	0.451226966
IMP biosynthetic process (GO:0006188)	44598	0.183530814	0.451226966
intracellular pH elevation (GO:0051454)	44598	0.183530814	0.451226966
isoleucine metabolic process (GO:0006549)	44598	0.183530814	0.451226966
L-arginine transmembrane transport (GO:1903400)	44598	0.183530814	0.451226966
L-ornithine transmembrane transport (GO:1903352)	44598	0.183530814	0.451226966
leucine transport (GO:0015820)	44598	0.183530814	0.451226966
lipoxin metabolic process (GO:2001300)	44598	0.183530814	0.451226966
lymphocyte apoptotic process (GO:0070227)	44598	0.183530814	0.451226966
molybdopterin cofactor biosynthetic process (GO:003232	44598	0.183530814	0.451226966
monoubiquitinated protein deubiquitination (GO:003552	44598	0.183530814	0.451226966
morphogenesis of an endothelium (GO:0003159)	44598	0.183530814	0.451226966
negative regulation of actin filament depolymerization (G	44598	0.183530814	0.451226966
negative regulation of B cell receptor signaling pathway (	44598	0.183530814	0.451226966
negative regulation of blood vessel endothelial cell prolif	44598	0.183530814	0.451226966
negative regulation of cardiac muscle cell apoptotic proc	44598	0.183530814	0.451226966
negative regulation of cellular response to hypoxia (GO:1	44598	0.183530814	0.451226966
negative regulation of fibroblast migration (GO:0010764)	44598	0.183530814	0.451226966
negative regulation of mast cell activation (GO:0033004)	44598	0.183530814	0.451226966
negative regulation of monocyte chemotaxis (GO:009002	44598	0.183530814	0.451226966
negative regulation of protein targeting to membrane (G	44598	0.183530814	0.451226966

negative regulation of trophoblast cell migration (GO:190	44598	0.183530814	0.451226966
nucleotide transport (GO:0006862)	44598	0.183530814	0.451226966
oxygen homeostasis (GO:0032364)	44598	0.183530814	0.451226966
pentose-phosphate shunt, non-oxidative branch (GO:000	44598	0.183530814	0.451226966
peptide antigen assembly with MHC protein complex (GC	44598	0.183530814	0.451226966
positive regulation of centriole replication (GO:0046601)	44598	0.183530814	0.451226966
positive regulation of cholesterol metabolic process (GO:	44598	0.183530814	0.451226966
positive regulation of endoplasmic reticulum stress-induc	44598	0.183530814	0.451226966
positive regulation of gluconeogenesis (GO:0045722)	44598	0.183530814	0.451226966
positive regulation of histone phosphorylation (GO:0033	44598	0.183530814	0.451226966
positive regulation of I-kappaB phosphorylation (GO:190	44598	0.183530814	0.451226966
positive regulation of immune response to tumor cell (GC	44598	0.183530814	0.451226966
positive regulation of osteoblast proliferation (GO:00336	44598	0.183530814	0.451226966
positive regulation of T cell mediated immune response t	44598	0.183530814	0.451226966
positive regulation of tau-protein kinase activity (GO:190	44598	0.183530814	0.451226966
protein geranylgeranylation (GO:0018344)	44598	0.183530814	0.451226966
protein insertion into mitochondrial membrane involved	44598	0.183530814	0.451226966
protein K29-linked ubiquitination (GO:0035519)	44598	0.183530814	0.451226966
protein-DNA complex subunit organization (GO:0071824)	44598	0.183530814	0.451226966
pteridine-containing compound biosynthetic process (GO	44598	0.183530814	0.451226966
purine nucleobase transport (GO:0006863)	44598	0.183530814	0.451226966
radial glial cell differentiation (GO:0060019)	44598	0.183530814	0.451226966
regulation of adiponectin secretion (GO:0070163)	44598	0.183530814	0.451226966
regulation of adipose tissue development (GO:1904177)	44598	0.183530814	0.451226966
regulation of blood vessel remodeling (GO:0060312)	44598	0.183530814	0.451226966
regulation of DNA demethylation (GO:1901535)	44598	0.183530814	0.451226966
regulation of extracellular exosome assembly (GO:19035	44598	0.183530814	0.451226966
regulation of hematopoietic stem cell proliferation (GO:1	44598	0.183530814	0.451226966
regulation of immature T cell proliferation in thymus (GO	44598	0.183530814	0.451226966
regulation of keratinocyte apoptotic process (GO:190217	44598	0.183530814	0.451226966
regulation of macromolecule biosynthetic process (GO:0(	44598	0.183530814	0.451226966
regulation of mast cell chemotaxis (GO:0060753)	44598	0.183530814	0.451226966
regulation of membrane tubulation (GO:1903525)	44598	0.183530814	0.451226966
regulation of neutrophil extravasation (GO:2000389)	44598	0.183530814	0.451226966
regulation of protein autoubiquitination (GO:1902498)	44598	0.183530814	0.451226966
regulation of response to reactive oxygen species (GO:19	44598	0.183530814	0.451226966
regulation of resting membrane potential (GO:0060075)	44598	0.183530814	0.451226966
regulation of sarcomere organization (GO:0060297)	44598	0.183530814	0.451226966
regulation of superoxide metabolic process (GO:0090322	44598	0.183530814	0.451226966
regulation of T cell activation via T cell receptor contact v	44598	0.183530814	0.451226966
renal system process involved in regulation of blood volu	44598	0.183530814	0.451226966
replication-born double-strand break repair via sister chr	44598	0.183530814	0.451226966
retinal ganglion cell axon guidance (GO:0031290)	44598	0.183530814	0.451226966
signal complex assembly (GO:0007172)	44598	0.183530814	0.451226966
taurine metabolic process (GO:0019530)	44598	0.183530814	0.451226966
tRNA pseudouridine synthesis (GO:0031119)	44598	0.183530814	0.451226966
vesicle localization (GO:0051648)	44598	0.183530814	0.451226966

vocal learning (GO:0042297)	44598	0.183530814	0.451226966
canonical Wnt signaling pathway (GO:0060070)	25173	0.184362254	0.45305672
calcium ion transmembrane import into cytosol (GO:009	15554	0.18580794	0.455962327
negative regulation of protein catabolic process (GO:004	15554	0.18580794	0.455962327
regulation of DNA recombination (GO:0000018)	15554	0.18580794	0.455962327
positive regulation of response to DNA damage stimulus	20363	0.186608349	0.457062883
pyruvate metabolic process (GO:0006090)	20363	0.186608349	0.457062883
regulation of gene silencing by RNA (GO:0060966)	20363	0.186608349	0.457062883
regulation of posttranscriptional gene silencing (GO:0060	20363	0.186608349	0.457062883
cellular response to insulin stimulus (GO:0032869)	21/129	0.186713524	0.457104975
organic substance transport (GO:0071702)	22/136	0.187984786	0.460000453
regulation of cell death (GO:0010941)	17/102	0.189779426	0.464173314
activation of adenylate cyclase activity (GO:0007190)	13332	0.192857529	0.470077773
establishment of protein localization to plasma membran	13332	0.192857529	0.470077773
regulation of mRNA processing (GO:0050684)	13332	0.192857529	0.470077773
regulation of ossification (GO:0030278)	13332	0.192857529	0.470077773
regulation of receptor internalization (GO:0002090)	13332	0.192857529	0.470077773
transferrin transport (GO:0033572)	13332	0.192857529	0.470077773
regulation of G protein-coupled receptor signaling pathw	14/82	0.192886654	0.470077773
negative regulation of kinase activity (GO:0033673)	22951	0.192917384	0.470077773
sphingolipid metabolic process (GO:0006665)	19/116	0.193741801	0.471865287
response to unfolded protein (GO:0006986)	18142	0.194906332	0.474256859
RNA catabolic process (GO:0006401)	18142	0.194906332	0.474256859
positive regulation of canonical Wnt signaling pathway (G	21/130	0.196519182	0.477957468
positive regulation of protein transport (GO:0051222)	25538	0.198017668	0.481376597
negative regulation of cell migration (GO:0030336)	23/144	0.19840888	0.482102026
alpha-amino acid catabolic process (GO:1901606)	44742	0.199578858	0.483362315
fatty-acyl-CoA biosynthetic process (GO:0046949)	44742	0.199578858	0.483362315
Golgi to plasma membrane protein transport (GO:00430(	44742	0.199578858	0.483362315
heterotypic cell-cell adhesion (GO:0034113)	44742	0.199578858	0.483362315
maintenance of blood-brain barrier (GO:0035633)	44742	0.199578858	0.483362315
respiratory tube development (GO:0030323)	44742	0.199578858	0.483362315
termination of RNA polymerase I transcription (GO:0006	44742	0.199578858	0.483362315
regulation of macromolecule metabolic process (GO:006	31/200	0.200490765	0.485344606
positive regulation of establishment of protein localizatio	20729	0.202008418	0.488391048
regulation of ATP metabolic process (GO:1903578)	20729	0.202008418	0.488391048
positive regulation of growth (GO:0045927)	13/76	0.202169484	0.488391048
positive regulation of axonogenesis (GO:0050772)	15919	0.20357451	0.488391048
regulation of carbohydrate catabolic process (GO:004347	15919	0.20357451	0.488391048
regulation of purine nucleotide metabolic process (GO:19	15919	0.20357451	0.488391048
canonical glycolysis (GO:0061621)	44705	0.205359904	0.488391048
cardiac muscle cell differentiation (GO:0055007)	44705	0.205359904	0.488391048
cellular response to catecholamine stimulus (GO:007187(	44705	0.205359904	0.488391048
cholesterol efflux (GO:0033344)	44705	0.205359904	0.488391048
glucose catabolic process to pyruvate (GO:0061718)	44705	0.205359904	0.488391048
negative regulation of lipid metabolic process (GO:00458	44705	0.205359904	0.488391048
negative regulation of neuron differentiation (GO:00456(	44705	0.205359904	0.488391048

positive regulation of cellular response to transforming g	44705	0.205359904	0.488391048
positive regulation of transforming growth factor beta re	44705	0.205359904	0.488391048
positive regulation of viral life cycle (GO:1903902)	44705	0.205359904	0.488391048
potassium ion homeostasis (GO:0055075)	44705	0.205359904	0.488391048
purine ribonucleotide catabolic process (GO:0009154)	44705	0.205359904	0.488391048
regulation of keratinocyte proliferation (GO:0010837)	44705	0.205359904	0.488391048
cardiocyte differentiation (GO:0035051)	44632	0.206167771	0.488391048
cellular response to fluid shear stress (GO:0071498)	44632	0.206167771	0.488391048
cellular response to nitrogen levels (GO:0043562)	44632	0.206167771	0.488391048
cellular response to nitrogen starvation (GO:0006995)	44632	0.206167771	0.488391048
cellular response to thyroid hormone stimulus (GO:0097(	44632	0.206167771	0.488391048
fat-soluble vitamin catabolic process (GO:0042363)	44632	0.206167771	0.488391048
glycine metabolic process (GO:0006544)	44632	0.206167771	0.488391048
intrinsic apoptotic signaling pathway in response to oxida	44632	0.206167771	0.488391048
maintenance of protein localization in endoplasmic retic	44632	0.206167771	0.488391048
mitotic G1/S transition checkpoint signaling (GO:004481(	44632	0.206167771	0.488391048
mitotic nuclear membrane disassembly (GO:0007077)	44632	0.206167771	0.488391048
negative regulation by host of viral process (GO:0044793	44632	0.206167771	0.488391048
negative regulation of complement activation (GO:00459	44632	0.206167771	0.488391048
negative regulation of glucose transmembrane transport	44632	0.206167771	0.488391048
negative regulation of leukocyte apoptotic process (GO:2	44632	0.206167771	0.488391048
negative regulation of vascular permeability (GO:004311(	44632	0.206167771	0.488391048
nuclear body organization (GO:0030575)	44632	0.206167771	0.488391048
organic hydroxy compound catabolic process (GO:19016(	44632	0.206167771	0.488391048
phagolysosome assembly (GO:0001845)	44632	0.206167771	0.488391048
positive regulation of myeloid leukocyte mediated immu	44632	0.206167771	0.488391048
positive regulation of protein maturation (GO:1903319)	44632	0.206167771	0.488391048
posttranslational protein targeting to endoplasmic reticu	44632	0.206167771	0.488391048
presynapse organization (GO:0099172)	44632	0.206167771	0.488391048
pyrimidine-containing compound metabolic process (GO:	44632	0.206167771	0.488391048
regulation of astrocyte differentiation (GO:0048710)	44632	0.206167771	0.488391048
regulation of chromatin binding (GO:0035561)	44632	0.206167771	0.488391048
regulation of hemopoiesis (GO:1903706)	44632	0.206167771	0.488391048
regulation of keratinocyte migration (GO:0051547)	44632	0.206167771	0.488391048
anterior/posterior pattern specification (GO:0009952)	23316	0.20762624	0.489066569
cell cycle G1/S phase transition (GO:0044843)	23316	0.20762624	0.489066569
acidic amino acid transport (GO:0015800)	44669	0.208806477	0.489066569
alternative mRNA splicing, via spliceosome (GO:0000380)	44669	0.208806477	0.489066569
cell migration involved in sprouting angiogenesis (GO:00(	44669	0.208806477	0.489066569
cellular response to glucocorticoid stimulus (GO:0071385	44669	0.208806477	0.489066569
hyaluronan catabolic process (GO:0030214)	44669	0.208806477	0.489066569
maintenance of gastrointestinal epithelium (GO:0030277	44669	0.208806477	0.489066569
mitochondrial fission (GO:0000266)	44669	0.208806477	0.489066569
negative regulation of leukocyte cell-cell adhesion (GO:1(	44669	0.208806477	0.489066569
neuron maturation (GO:0042551)	44669	0.208806477	0.489066569
positive chemotaxis (GO:0050918)	44669	0.208806477	0.489066569
positive regulation of cell adhesion mediated by integrin	44669	0.208806477	0.489066569

positive regulation of macrophage derived foam cell diffe	44669	0.208806477	0.489066569
positive regulation of mRNA splicing, via spliceosome (GC	44669	0.208806477	0.489066569
positive regulation of myoblast differentiation (GO:0045(	44669	0.208806477	0.489066569
positive regulation of nitric-oxide synthase activity (GO:0	44669	0.208806477	0.489066569
positive regulation of synaptic transmission, glutamaterg	44669	0.208806477	0.489066569
regulation of catabolic process (GO:0009894)	44669	0.208806477	0.489066569
regulation of mitochondrial outer membrane permeabiliz	44669	0.208806477	0.489066569
regulation of oxidative stress-induced intrinsic apoptotic	44669	0.208806477	0.489066569
regulation of protein sumoylation (GO:0033233)	44669	0.208806477	0.489066569
regulation of transcription by RNA polymerase I (GO:000(	44669	0.208806477	0.489066569
release of cytochrome c from mitochondria (GO:000183(	44669	0.208806477	0.489066569
triglyceride biosynthetic process (GO:0019432)	44669	0.208806477	0.489066569
wound healing (GO:0042060)	25903	0.212110295	0.496580884
glutamine family amino acid metabolic process (GO:0009	13697	0.212557129	0.496955124
positive regulation of calcium ion transport (GO:0051928	13697	0.212557129	0.496955124
regulation of protein autophosphorylation (GO:0031952)	13697	0.212557129	0.496955124
supramolecular fiber organization (GO:0097435)	52/351	0.214301289	0.500807555
monocarboxylic acid transport (GO:0015718)	21094	0.217925805	0.509048812
cellular nitrogen compound biosynthetic process (GO:00(	11475	0.221713185	0.515512937
multivesicular body organization (GO:0036257)	11475	0.221713185	0.515512937
negative regulation of DNA binding (GO:0043392)	11475	0.221713185	0.515512937
positive regulation of protein targeting to mitochondrion	11475	0.221713185	0.515512937
protein acetylation (GO:0006473)	11475	0.221713185	0.515512937
regulation of cellular pH (GO:0030641)	11475	0.221713185	0.515512937
regulation of cellular senescence (GO:2000772)	11475	0.221713185	0.515512937
triglyceride homeostasis (GO:0070328)	11475	0.221713185	0.515512937
homotypic cell-cell adhesion (GO:0034109)	16285	0.221983146	0.515512937
mRNA catabolic process (GO:0006402)	16285	0.221983146	0.515512937
mRNA stabilization (GO:0048255)	16285	0.221983146	0.515512937
positive regulation of biosynthetic process (GO:0009891)	16285	0.221983146	0.515512937
positive regulation of cell-matrix adhesion (GO:0001954)	16285	0.221983146	0.515512937
regulation of cilium assembly (GO:1902017)	23682	0.222793403	0.516932438
regulation of transcription initiation from RNA polymeras	23682	0.222793403	0.516932438
histone acetylation (GO:0016573)	26268	0.226614722	0.516997084
regulation of hematopoietic stem cell differentiation (GO	26268	0.226614722	0.516997084
mesenchymal cell differentiation (GO:0048762)	18872	0.229005241	0.516997084
protein modification process (GO:0036211)	13/78	0.229622642	0.516997084
phosphatidylinositol dephosphorylation (GO:0046856)	44706	0.230706139	0.516997084
positive regulation of DNA-templated transcription, elon	44706	0.230706139	0.516997084
positive regulation of lipid metabolic process (GO:00458:	44706	0.230706139	0.516997084
regulation of protein processing (GO:0070613)	44706	0.230706139	0.516997084
regulation of proteolysis involved in cellular protein catal	44706	0.230706139	0.516997084
response to dsRNA (GO:0043331)	44706	0.230706139	0.516997084
sodium ion homeostasis (GO:0055078)	44706	0.230706139	0.516997084
G1/S transition of mitotic cell cycle (GO:0000082)	14/85	0.231986233	0.516997084
mRNA destabilization (GO:0061157)	14062	0.232953097	0.516997084
negative regulation of ubiquitin-dependent protein catab	14062	0.232953097	0.516997084

positive regulation of cell development (GO:0010720)	14062	0.232953097	0.516997084
positive regulation of signaling (GO:0023056)	14062	0.232953097	0.516997084
response to cAMP (GO:0051591)	14062	0.232953097	0.516997084
response to estradiol (GO:0032355)	14062	0.232953097	0.516997084
synaptic vesicle endocytosis (GO:0048488)	14062	0.232953097	0.516997084
negative regulation of mitotic cell cycle phase transition (	15/92	0.233831325	0.516997084
muscle organ development (GO:0007517)	21459	0.234322679	0.516997084
regulation of calcium ion transport (GO:0051924)	21459	0.234322679	0.516997084
aldehyde biosynthetic process (GO:0046184)	44599	0.235360559	0.516997084
angiotensin-activated signaling pathway (GO:0038166)	44599	0.235360559	0.516997084
arginine catabolic process (GO:0006527)	44599	0.235360559	0.516997084
bleb assembly (GO:0032060)	44599	0.235360559	0.516997084
calcium ion export (GO:1901660)	44599	0.235360559	0.516997084
cardiolipin acyl-chain remodeling (GO:0035965)	44599	0.235360559	0.516997084
cardiolipin biosynthetic process (GO:0032049)	44599	0.235360559	0.516997084
catecholamine catabolic process (GO:0042424)	44599	0.235360559	0.516997084
cellular protein complex disassembly (GO:0043624)	44599	0.235360559	0.516997084
cellular response to caffeine (GO:0071313)	44599	0.235360559	0.516997084
cellular response to monoamine stimulus (GO:0071868)	44599	0.235360559	0.516997084
cleavage furrow formation (GO:0036089)	44599	0.235360559	0.516997084
dendrite arborization (GO:0140059)	44599	0.235360559	0.516997084
dopamine transport (GO:0015872)	44599	0.235360559	0.516997084
dorsal aorta development (GO:0035907)	44599	0.235360559	0.516997084
dorsal aorta morphogenesis (GO:0035912)	44599	0.235360559	0.516997084
endosome to lysosome transport via multivesicular body	44599	0.235360559	0.516997084
establishment of centrosome localization (GO:0051660)	44599	0.235360559	0.516997084
fatty acid elongation, monounsaturated fatty acid (GO:0(	44599	0.235360559	0.516997084
fatty acid elongation, polyunsaturated fatty acid (GO:003	44599	0.235360559	0.516997084
fatty acid elongation, saturated fatty acid (GO:0019367)	44599	0.235360559	0.516997084
fatty acid elongation, unsaturated fatty acid (GO:001936	44599	0.235360559	0.516997084
gamma-delta T cell activation (GO:0046629)	44599	0.235360559	0.516997084
gap junction assembly (GO:0016264)	44599	0.235360559	0.516997084
gas homeostasis (GO:0033483)	44599	0.235360559	0.516997084
gland morphogenesis (GO:0022612)	44599	0.235360559	0.516997084
glutamine transport (GO:0006868)	44599	0.235360559	0.516997084
glutathione catabolic process (GO:0006751)	44599	0.235360559	0.516997084
glyceraldehyde-3-phosphate metabolic process (GO:001	44599	0.235360559	0.516997084
hemostasis (GO:0007599)	44599	0.235360559	0.516997084
histone H3-K14 acetylation (GO:0044154)	44599	0.235360559	0.516997084
inhibition of cysteine-type endopeptidase activity (GO:00	44599	0.235360559	0.516997084
iron coordination entity transport (GO:1901678)	44599	0.235360559	0.516997084
iron import into cell (GO:0033212)	44599	0.235360559	0.516997084
lipoxin biosynthetic process (GO:2001301)	44599	0.235360559	0.516997084
lymphoid progenitor cell differentiation (GO:0002320)	44599	0.235360559	0.516997084
lysosomal microautophagy (GO:0016237)	44599	0.235360559	0.516997084
membrane invagination (GO:0010324)	44599	0.235360559	0.516997084
miRNA loading onto RISC involved in gene silencing by mi	44599	0.235360559	0.516997084

mitochondrion-endoplasmic reticulum membrane tether	44599	0.235360559	0.516997084
modulation by symbiont of host defense response (GO:0(	44599	0.235360559	0.516997084
monoacylglycerol biosynthetic process (GO:0006640)	44599	0.235360559	0.516997084
negative regulation by host of viral genome replication (G	44599	0.235360559	0.516997084
negative regulation of acute inflammatory response (GO:	44599	0.235360559	0.516997084
negative regulation of cell cycle phase transition (GO:190	44599	0.235360559	0.516997084
negative regulation of digestive system process (GO:006(	44599	0.235360559	0.516997084
negative regulation of low-density lipoprotein receptor a	44599	0.235360559	0.516997084
negative regulation of membrane protein ectodomain pr	44599	0.235360559	0.516997084
negative regulation of protein K63-linked ubiquitination (	44599	0.235360559	0.516997084
negative regulation of retinoic acid receptor signaling pat	44599	0.235360559	0.516997084
negative regulation of T cell apoptotic process (GO:00702	44599	0.235360559	0.516997084
neuron projection arborization (GO:0140058)	44599	0.235360559	0.516997084
nicotinamide nucleotide biosynthetic process (GO:00193	44599	0.235360559	0.516997084
nodal signaling pathway (GO:0038092)	44599	0.235360559	0.516997084
nucleobase catabolic process (GO:0046113)	44599	0.235360559	0.516997084
parallel actin filament bundle assembly (GO:0030046)	44599	0.235360559	0.516997084
peptide transport (GO:0015833)	44599	0.235360559	0.516997084
piecemeal microautophagy of the nucleus (GO:0034727)	44599	0.235360559	0.516997084
positive regulation of amyloid-beta clearance (GO:19002	44599	0.235360559	0.516997084
positive regulation of aspartic-type endopeptidase activit	44599	0.235360559	0.516997084
positive regulation of cilium movement (GO:0003353)	44599	0.235360559	0.516997084
positive regulation of cilium-dependent cell motility (GO:	44599	0.235360559	0.516997084
positive regulation of ER-associated ubiquitin-dependent	44599	0.235360559	0.516997084
positive regulation of flagellated sperm motility (GO:190	44599	0.235360559	0.516997084
positive regulation of hormone metabolic process (GO:0(	44599	0.235360559	0.516997084
positive regulation of icosanoid secretion (GO:0032305)	44599	0.235360559	0.516997084
positive regulation of interleukin-5 production (GO:0032	44599	0.235360559	0.516997084
positive regulation of lamellipodium morphogenesis (GO:	44599	0.235360559	0.516997084
positive regulation of mast cell activation (GO:0033005)	44599	0.235360559	0.516997084
positive regulation of miRNA mediated inhibition of trans	44599	0.235360559	0.516997084
positive regulation of pinocytosis (GO:0048549)	44599	0.235360559	0.516997084
positive regulation of podosome assembly (GO:0071803)	44599	0.235360559	0.516997084
positive regulation of type I interferon-mediated signalin	44599	0.235360559	0.516997084
positive regulation of urine volume (GO:0035810)	44599	0.235360559	0.516997084
positive regulation of vesicle fusion (GO:0031340)	44599	0.235360559	0.516997084
protein localization to endoplasmic reticulum exit site (G	44599	0.235360559	0.516997084
receptor-mediated endocytosis of virus by host cell (GO:(	44599	0.235360559	0.516997084
regulation by virus of viral protein levels in host cell (GO:(	44599	0.235360559	0.516997084
regulation of chromatin assembly or disassembly (GO:00(	44599	0.235360559	0.516997084
regulation of endothelial cell chemotaxis to fibroblast grc	44599	0.235360559	0.516997084
regulation of entry of bacterium into host cell (GO:20005	44599	0.235360559	0.516997084
regulation of extracellular matrix assembly (GO:1901201	44599	0.235360559	0.516997084
regulation of histone H3-K27 methylation (GO:0061085)	44599	0.235360559	0.516997084
regulation of ketone biosynthetic process (GO:0010566)	44599	0.235360559	0.516997084
regulation of MDA-5 signaling pathway (GO:0039533)	44599	0.235360559	0.516997084
regulation of miRNA mediated inhibition of translation (G	44599	0.235360559	0.516997084

regulation of muscle organ development (GO:0048634)	44599	0.235360559	0.516997084
regulation of NAD(P)H oxidase activity (GO:0033860)	44599	0.235360559	0.516997084
regulation of oxidative stress-induced neuron intrinsic ap	44599	0.235360559	0.516997084
regulation of relaxation of muscle (GO:1901077)	44599	0.235360559	0.516997084
regulation of skeletal muscle contraction (GO:0014819)	44599	0.235360559	0.516997084
regulation of striated muscle cell differentiation (GO:005	44599	0.235360559	0.516997084
regulation of transforming growth factor beta2 productic	44599	0.235360559	0.516997084
regulation of vascular associated smooth muscle cell apo	44599	0.235360559	0.516997084
response to caffeine (GO:0031000)	44599	0.235360559	0.516997084
response to host defenses (GO:0052200)	44599	0.235360559	0.516997084
response to increased oxygen levels (GO:0036296)	44599	0.235360559	0.516997084
ribose phosphate biosynthetic process (GO:0046390)	44599	0.235360559	0.516997084
ribosomal small subunit export from nucleus (GO:000005	44599	0.235360559	0.516997084
RIG-I signaling pathway (GO:0039529)	44599	0.235360559	0.516997084
succinate transport (GO:0015744)	44599	0.235360559	0.516997084
tachykinin receptor signaling pathway (GO:0007217)	44599	0.235360559	0.516997084
tRNA threonylcarbamoyladenosine metabolic process (G	44599	0.235360559	0.516997084
white fat cell differentiation (GO:0050872)	44599	0.235360559	0.516997084
axonogenesis (GO:0007409)	36/240	0.23787727	0.521240836
dopamine metabolic process (GO:0042417)	44670	0.238697199	0.521240836
establishment of skin barrier (GO:0061436)	44670	0.238697199	0.521240836
establishment or maintenance of apical/basal cell polarit	44670	0.238697199	0.521240836
heart trabecula morphogenesis (GO:0061384)	44670	0.238697199	0.521240836
negative regulation of amyloid precursor protein catabol	44670	0.238697199	0.521240836
negative regulation of oxidative stress-induced intrinsic a	44670	0.238697199	0.521240836
positive regulation of actin cytoskeleton reorganization (	44670	0.238697199	0.521240836
positive regulation of cellular protein catabolic process (9	44670	0.238697199	0.521240836
positive regulation of cilium assembly (GO:0045724)	44670	0.238697199	0.521240836
positive regulation of macrophage migration (GO:190552	44670	0.238697199	0.521240836
regulation of RIG-I signaling pathway (GO:0039535)	44670	0.238697199	0.521240836
regulation of water loss via skin (GO:0033561)	44670	0.238697199	0.521240836
sphingosine metabolic process (GO:0006670)	44670	0.238697199	0.521240836
protein deacetylation (GO:0006476)	16650	0.240972983	0.522494473
negative regulation of epithelial cell proliferation (GO:00	26634	0.241503771	0.522494473
negative regulation of supramolecular fiber organization	26634	0.241503771	0.522494473
positive regulation of secretion by cell (GO:1903532)	26634	0.241503771	0.522494473
central nervous system neuron axonogenesis (GO:00219	44633	0.243294347	0.522494473
chromatin organization involved in regulation of transcrip	44633	0.243294347	0.522494473
endonucleolytic cleavage of tricistronic rRNA transcript (9	44633	0.243294347	0.522494473
establishment of protein localization to chromosome (GC	44633	0.243294347	0.522494473
fatty acid elongation (GO:0030497)	44633	0.243294347	0.522494473
glucose import (GO:0046323)	44633	0.243294347	0.522494473
high-density lipoprotein particle assembly (GO:0034380)	44633	0.243294347	0.522494473
lymphocyte mediated immunity (GO:0002449)	44633	0.243294347	0.522494473
negative regulation of autophagosome assembly (GO:19(	44633	0.243294347	0.522494473
negative regulation of gluconeogenesis (GO:0045721)	44633	0.243294347	0.522494473
negative regulation of myotube differentiation (GO:0010	44633	0.243294347	0.522494473

pathway-restricted SMAD protein phosphorylation (GO:0	44633	0.243294347	0.522494473
pentose-phosphate shunt (GO:0006098)	44633	0.243294347	0.522494473
positive regulation of ERAD pathway (GO:1904294)	44633	0.243294347	0.522494473
positive regulation of histone deacetylation (GO:003106	44633	0.243294347	0.522494473
positive regulation of neuron migration (GO:2001224)	44633	0.243294347	0.522494473
positive regulation of protein acetylation (GO:1901985)	44633	0.243294347	0.522494473
positive regulation of purine nucleotide biosynthetic pro	44633	0.243294347	0.522494473
positive regulation of ruffle assembly (GO:1900029)	44633	0.243294347	0.522494473
protein localization to mitochondrion (GO:0070585)	44633	0.243294347	0.522494473
purine nucleotide catabolic process (GO:0006195)	44633	0.243294347	0.522494473
purine ribonucleoside triphosphate metabolic process (G	44633	0.243294347	0.522494473
regulation of autophagosome maturation (GO:1901096)	44633	0.243294347	0.522494473
regulation of cell communication by electrical coupling (	44633	0.243294347	0.522494473
regulation of interleukin-5 production (GO:0032674)	44633	0.243294347	0.522494473
regulation of mRNA metabolic process (GO:1903311)	44633	0.243294347	0.522494473
regulation of protein acetylation (GO:1901983)	44633	0.243294347	0.522494473
regulation of retrograde protein transport, ER to cytosol	44633	0.243294347	0.522494473
response to iron ion (GO:0010039)	44633	0.243294347	0.522494473
response to thyroid hormone (GO:0097066)	44633	0.243294347	0.522494473
ribosomal subunit export from nucleus (GO:0000054)	44633	0.243294347	0.522494473
sodium ion export across plasma membrane (GO:003637	44633	0.243294347	0.522494473
sphingoid biosynthetic process (GO:0046520)	44633	0.243294347	0.522494473
sphingosine biosynthetic process (GO:0046512)	44633	0.243294347	0.522494473
spinal cord development (GO:0021510)	44633	0.243294347	0.522494473
very long-chain fatty acid biosynthetic process (GO:0042	44633	0.243294347	0.522494473
7-methylguanosine mRNA capping (GO:0006370)	11841	0.244605855	0.522717983
7-methylguanosine RNA capping (GO:0009452)	11841	0.244605855	0.522717983
activation of phospholipase C activity (GO:0007202)	11841	0.244605855	0.522717983
modulation by host of symbiont process (GO:0051851)	11841	0.244605855	0.522717983
negative regulation of cell-matrix adhesion (GO:0001953	11841	0.244605855	0.522717983
negative regulation of DNA biosynthetic process (GO:200	11841	0.244605855	0.522717983
positive regulation of lamellipodium organization (GO:19	11841	0.244605855	0.522717983
protein K63-linked deubiquitination (GO:0070536)	11841	0.244605855	0.522717983
regulation of cellular amide metabolic process (GO:0034	11841	0.244605855	0.522717983
regulation of centrosome duplication (GO:0010824)	11841	0.244605855	0.522717983
regulation of intracellular protein transport (GO:0033157	11841	0.244605855	0.522717983
regulation of NMDA receptor activity (GO:2000310)	11841	0.244605855	0.522717983
plasma membrane bounded cell projection morphogene	19238	0.246828773	0.527034722
signal transduction in response to DNA damage (GO:004	19238	0.246828773	0.527034722
regulation of transforming growth factor beta receptor si	16/100	0.247998346	0.529314465
protein localization to organelle (GO:0033365)	22/142	0.248813665	0.530836545
negative regulation of cellular metabolic process (GO:00	14427	0.253962878	0.540490434
organophosphate biosynthetic process (GO:0090407)	14427	0.253962878	0.540490434
phospholipid dephosphorylation (GO:0046839)	14427	0.253962878	0.540490434
regulation of cellular component biogenesis (GO:004408	14427	0.253962878	0.540490434
regulation of intracellular transport (GO:0032386)	14427	0.253962878	0.540490434
regulation of protein targeting to mitochondrion (GO:19	14427	0.253962878	0.540490434

glial cell development (GO:0021782)	44707	0.256880182	0.544246551
hippo signaling (GO:0035329)	44707	0.256880182	0.544246551
membrane depolarization during action potential (GO:00	44707	0.256880182	0.544246551
mRNA polyadenylation (GO:0006378)	44707	0.256880182	0.544246551
negative regulation of cell development (GO:0010721)	44707	0.256880182	0.544246551
negative regulation of protein localization to membrane	44707	0.256880182	0.544246551
organelle fission (GO:0048285)	44707	0.256880182	0.544246551
phosphatidylethanolamine acyl-chain remodeling (GO:00	44707	0.256880182	0.544246551
proteoglycan metabolic process (GO:0006029)	44707	0.256880182	0.544246551
regulation of biomineral tissue development (GO:007016	44707	0.256880182	0.544246551
RNA polyadenylation (GO:0043631)	44707	0.256880182	0.544246551
calcium ion transmembrane transport (GO:0070588)	14/87	0.259698691	0.549769642
sodium ion transmembrane transport (GO:0035725)	14/87	0.259698691	0.549769642
regulation of synaptic transmission, glutamatergic (GO:0(	17015	0.260480209	0.551199465
cellular protein metabolic process (GO:0044267)	60/417	0.267209464	0.565208943
regulation of cellular macromolecule biosynthetic proces	67/468	0.267771658	0.566167589
phosphatidylcholine biosynthetic process (GO:0006656)	12206	0.268141228	0.566487872
regulation of cholesterol efflux (GO:0010874)	12206	0.268141228	0.566487872
peptidyl-threonine phosphorylation (GO:0018107)	22190	0.268392537	0.566565354
cellular response to misfolded protein (GO:0071218)	44671	0.26948662	0.566565354
cellular response to nitrogen compound (GO:1901699)	44671	0.26948662	0.566565354
energy reserve metabolic process (GO:0006112)	44671	0.26948662	0.566565354
ganglioside metabolic process (GO:0001573)	44671	0.26948662	0.566565354
hepaticobiliary system development (GO:0061008)	44671	0.26948662	0.566565354
miRNA metabolic process (GO:0010586)	44671	0.26948662	0.566565354
mitotic cytokinetic process (GO:1902410)	44671	0.26948662	0.566565354
positive regulation of lymphocyte differentiation (GO:00	44671	0.26948662	0.566565354
protein targeting to lysosome (GO:0006622)	44671	0.26948662	0.566565354
regulation of smooth muscle cell migration (GO:0014910	44671	0.26948662	0.566565354
xenobiotic transport (GO:0042908)	44671	0.26948662	0.566565354
positive regulation of neuron projection development (G	14/88	0.273983709	0.575657443
lipid transport (GO:0006869)	17/109	0.274032889	0.575657443
fatty acid derivative biosynthetic process (GO:1901570)	14793	0.275501226	0.576398178
positive regulation of catalytic activity (GO:0043085)	14793	0.275501226	0.576398178
positive regulation of double-strand break repair (GO:20(	14793	0.275501226	0.576398178
antiviral innate immune response (GO:0140374)	44634	0.281353746	0.576398178
branching involved in blood vessel morphogenesis (GO:0(	44634	0.281353746	0.576398178
cAMP metabolic process (GO:0046058)	44634	0.281353746	0.576398178
covalent chromatin modification (GO:0016569)	44634	0.281353746	0.576398178
immune response-regulating cell surface receptor signali	44634	0.281353746	0.576398178
low-density lipoprotein particle remodeling (GO:003437	44634	0.281353746	0.576398178
negative regulation of cartilage development (GO:00610	44634	0.281353746	0.576398178
negative regulation of neuroinflammatory response (GO:	44634	0.281353746	0.576398178
negative regulation of smooth muscle cell migration (GO:	44634	0.281353746	0.576398178
neuron fate commitment (GO:0048663)	44634	0.281353746	0.576398178
nuclear membrane disassembly (GO:0051081)	44634	0.281353746	0.576398178
nucleoside phosphate catabolic process (GO:1901292)	44634	0.281353746	0.576398178

peptidyl-serine dephosphorylation (GO:0070262)	44634	0.281353746	0.576398178
polarized epithelial cell differentiation (GO:0030859)	44634	0.281353746	0.576398178
positive regulation of cardiac muscle cell proliferation (G	44634	0.281353746	0.576398178
positive regulation of insulin secretion involved in cellula	44634	0.281353746	0.576398178
positive regulation of long-term synaptic potentiation (G	44634	0.281353746	0.576398178
positive regulation of protein-containing complex disasse	44634	0.281353746	0.576398178
positive regulation of superoxide anion generation (GO:0	44634	0.281353746	0.576398178
pre-miRNA processing (GO:0031054)	44634	0.281353746	0.576398178
protein modification by small protein conjugation or rem	44634	0.281353746	0.576398178
regulation of cell projection organization (GO:0031344)	44634	0.281353746	0.576398178
regulation of histone methylation (GO:0031060)	44634	0.281353746	0.576398178
response to X-ray (GO:0010165)	44634	0.281353746	0.576398178
sodium-independent organic anion transport (GO:00432	44634	0.281353746	0.576398178
steroid catabolic process (GO:0006706)	44634	0.281353746	0.576398178
thymus development (GO:0048538)	44634	0.281353746	0.576398178
camera-type eye development (GO:0043010)	44708	0.283712288	0.576398178
negative regulation of catalytic activity (GO:0043086)	44708	0.283712288	0.576398178
peptide hormone secretion (GO:0030072)	44708	0.283712288	0.576398178
regulation of cell junction assembly (GO:1901888)	44708	0.283712288	0.576398178
regulation of vasculature development (GO:1901342)	44708	0.283712288	0.576398178
cytoplasmic microtubule organization (GO:0031122)	19968	0.283769051	0.576398178
negative regulation of response to stimulus (GO:0048585	22555	0.285979993	0.576398178
regulation of translational initiation (GO:0006446)	25143	0.287382649	0.576398178
aromatic compound biosynthetic process (GO:0019438)	44600	0.287810755	0.576398178
aromatic compound catabolic process (GO:0019439)	44600	0.287810755	0.576398178
autophagosome-lysosome fusion (GO:0061909)	44600	0.287810755	0.576398178
axon extension involved in axon guidance (GO:0048846)	44600	0.287810755	0.576398178
cellular response to hepatocyte growth factor stimulus (G	44600	0.287810755	0.576398178
chromatin silencing at telomere (GO:0006348)	44600	0.287810755	0.576398178
commissural neuron axon guidance (GO:0071679)	44600	0.287810755	0.576398178
cysteine metabolic process (GO:0006534)	44600	0.287810755	0.576398178
endonucleolytic cleavage in ITS1 to separate SSU-rRNA fr	44600	0.287810755	0.576398178
entry of bacterium into host cell (GO:0035635)	44600	0.287810755	0.576398178
establishment of protein localization to chromatin (GO:0(	44600	0.287810755	0.576398178
immunological synapse formation (GO:0001771)	44600	0.287810755	0.576398178
lymphatic endothelial cell differentiation (GO:0060836)	44600	0.287810755	0.576398178
mast cell activation involved in immune response (GO:00	44600	0.287810755	0.576398178
mast cell degranulation (GO:0043303)	44600	0.287810755	0.576398178
meiotic sister chromatid cohesion (GO:0051177)	44600	0.287810755	0.576398178
monoamine transport (GO:0015844)	44600	0.287810755	0.576398178
myoblast migration (GO:0051451)	44600	0.287810755	0.576398178
natural killer cell differentiation (GO:0001779)	44600	0.287810755	0.576398178
negative regulation of complement activation, classical p	44600	0.287810755	0.576398178
negative regulation of keratinocyte proliferation (GO:001	44600	0.287810755	0.576398178
negative regulation of microglial cell activation (GO:1903	44600	0.287810755	0.576398178
negative regulation of muscle cell apoptotic process (GO:	44600	0.287810755	0.576398178
negative regulation of muscle cell differentiation (GO:005	44600	0.287810755	0.576398178

negative regulation of osteoblast proliferation (GO:0033(	44600	0.287810755	0.576398178
negative regulation of phospholipase activity (GO:00105(	44600	0.287810755	0.576398178
negative regulation of response to reactive oxygen specie	44600	0.287810755	0.576398178
negative regulation of striated muscle cell apoptotic proc	44600	0.287810755	0.576398178
negative regulation of T cell mediated cytotoxicity (GO:0(	44600	0.287810755	0.576398178
neuron projection extension involved in neuron projectio	44600	0.287810755	0.576398178
neurotransmitter reuptake (GO:0098810)	44600	0.287810755	0.576398178
osteoblast development (GO:0002076)	44600	0.287810755	0.576398178
peptidyl-lysine deacetylation (GO:0034983)	44600	0.287810755	0.576398178
peptidyl-serine autophosphorylation (GO:0036289)	44600	0.287810755	0.576398178
phosphatidylinositol-3-phosphate biosynthetic process (G	44600	0.287810755	0.576398178
plasma membrane phospholipid scrambling (GO:001712(	44600	0.287810755	0.576398178
platelet activating factor metabolic process (GO:0046469	44600	0.287810755	0.576398178
positive regulation of aspartic-type peptidase activity (GC	44600	0.287810755	0.576398178
positive regulation of astrocyte differentiation (GO:0048(	44600	0.287810755	0.576398178
positive regulation of cell migration by vascular endothel	44600	0.287810755	0.576398178
positive regulation of endocytic recycling (GO:2001137)	44600	0.287810755	0.576398178
positive regulation of isomerase activity (GO:0010912)	44600	0.287810755	0.576398178
positive regulation of lipoprotein lipase activity (GO:0051	44600	0.287810755	0.576398178
positive regulation of membrane invagination (GO:19051	44600	0.287810755	0.576398178
positive regulation of muscle contraction (GO:0045933)	44600	0.287810755	0.576398178
positive regulation of myeloid cell apoptotic process (GO	44600	0.287810755	0.576398178
positive regulation of myotube differentiation (GO:00108	44600	0.287810755	0.576398178
positive regulation of oligodendrocyte differentiation (GC	44600	0.287810755	0.576398178
positive regulation of protein localization to early endoso	44600	0.287810755	0.576398178
positive regulation of protein localization to endosome ((	44600	0.287810755	0.576398178
positive regulation of steroid biosynthetic process (GO:0(	44600	0.287810755	0.576398178
positive regulation of vascular associated smooth muscle	44600	0.287810755	0.576398178
protein localization to microtubule (GO:0035372)	44600	0.287810755	0.576398178
protein localization to microtubule cytoskeleton (GO:007	44600	0.287810755	0.576398178
proximal/distal pattern formation (GO:0009954)	44600	0.287810755	0.576398178
pyrimidine nucleobase catabolic process (GO:0006208)	44600	0.287810755	0.576398178
regulation of alpha-beta T cell differentiation (GO:00466(	44600	0.287810755	0.576398178
regulation of alpha-beta T cell proliferation (GO:0046640	44600	0.287810755	0.576398178
regulation of ATPase-coupled calcium transmembrane tr	44600	0.287810755	0.576398178
regulation of CD4-positive, alpha-beta T cell activation (G	44600	0.287810755	0.576398178
regulation of Cdc42 protein signal transduction (GO:0032	44600	0.287810755	0.576398178
regulation of chemokine-mediated signaling pathway (GC	44600	0.287810755	0.576398178
regulation of collateral sprouting (GO:0048670)	44600	0.287810755	0.576398178
regulation of dendritic spine maintenance (GO:1902950)	44600	0.287810755	0.576398178
regulation of endodeoxyribonuclease activity (GO:00320(	44600	0.287810755	0.576398178
regulation of intrinsic apoptotic signaling pathway by p53	44600	0.287810755	0.576398178
regulation of metaphase/anaphase transition of cell cycle	44600	0.287810755	0.576398178
regulation of microvillus organization (GO:0032530)	44600	0.287810755	0.576398178
regulation of mitochondrial gene expression (GO:006212	44600	0.287810755	0.576398178
regulation of positive chemotaxis (GO:0050926)	44600	0.287810755	0.576398178
regulation of protein localization to early endosome (GO:	44600	0.287810755	0.576398178

regulation of proton transport (GO:0010155)	44600	0.287810755	0.576398178
regulation of response to wounding (GO:1903034)	44600	0.287810755	0.576398178
regulation of translational termination (GO:0006449)	44600	0.287810755	0.576398178
response to hepatocyte growth factor (GO:0035728)	44600	0.287810755	0.576398178
response to hydroperoxide (GO:0033194)	44600	0.287810755	0.576398178
single strand break repair (GO:0000012)	44600	0.287810755	0.576398178
skeletal muscle tissue regeneration (GO:0043403)	44600	0.287810755	0.576398178
snRNA transcription by RNA polymerase III (GO:0042796)	44600	0.287810755	0.576398178
spleen development (GO:0048536)	44600	0.287810755	0.576398178
SREBP signaling pathway (GO:0032933)	44600	0.287810755	0.576398178
store-operated calcium entry (GO:0002115)	44600	0.287810755	0.576398178
vascular associated smooth muscle cell differentiation (G	44600	0.287810755	0.576398178
fibroblast growth factor receptor signaling pathway (GO:(	27729	0.288184804	0.576924876
positive regulation of Wnt signaling pathway (GO:003017	23/153	0.291806057	0.583949332
cell-substrate junction assembly (GO:0007044)	12571	0.29220214	0.584066993
positive regulation of mitochondrial outer membrane pe	12571	0.29220214	0.584066993
transcription by RNA polymerase I (GO:0006360)	12571	0.29220214	0.584066993
import into cell (GO:0098657)	15158	0.297481363	0.594162122
regulation of protein dephosphorylation (GO:0035304)	15158	0.297481363	0.594162122
cognition (GO:0050890)	17746	0.300781484	0.596645652
Golgi to plasma membrane transport (GO:0006893)	17746	0.300781484	0.596645652
actin filament-based transport (GO:0099515)	44672	0.300906951	0.596645652
epithelial cell development (GO:0002064)	44672	0.300906951	0.596645652
linoleic acid metabolic process (GO:0043651)	44672	0.300906951	0.596645652
long-term synaptic potentiation (GO:0060291)	44672	0.300906951	0.596645652
mitotic spindle assembly checkpoint signaling (GO:00070	44672	0.300906951	0.596645652
mitotic spindle checkpoint signaling (GO:0071174)	44672	0.300906951	0.596645652
negative regulation of peptidyl-serine phosphorylation (G	44672	0.300906951	0.596645652
neuron apoptotic process (GO:0051402)	44672	0.300906951	0.596645652
poly(A)+ mRNA export from nucleus (GO:0016973)	44672	0.300906951	0.596645652
positive regulation of transcription regulatory region DN	44672	0.300906951	0.596645652
regulation of cardiac muscle cell proliferation (GO:00600	44672	0.300906951	0.596645652
regulation of dendritic spine development (GO:0060998)	44672	0.300906951	0.596645652
regulation of ubiquitin protein ligase activity (GO:190466	44672	0.300906951	0.596645652
response to glucagon (GO:0033762)	44672	0.300906951	0.596645652
sensory perception of pain (GO:0019233)	44672	0.300906951	0.596645652
spindle assembly checkpoint signaling (GO:0071173)	44672	0.300906951	0.596645652
zinc ion transport (GO:0006829)	44672	0.300906951	0.596645652
regulation of insulin secretion (GO:0050796)	16/104	0.301417515	0.597429985
positive regulation of cold-induced thermogenesis (GO:0	15/97	0.302437748	0.599223531
protein sumoylation (GO:0016925)	20333	0.302778752	0.599670459
regulation of mRNA splicing, via spliceosome (GO:004802	14/90	0.303293419	0.600460866
cellular response to calcium ion (GO:0071277)	25508	0.304331178	0.602056538
cellular response to decreased oxygen levels (GO:003629	25508	0.304331178	0.602056538
glycerophospholipid catabolic process (GO:0046475)	44709	0.311034802	0.611360498
glycogen metabolic process (GO:0005977)	44709	0.311034802	0.611360498
histone mRNA metabolic process (GO:0008334)	44709	0.311034802	0.611360498

keratan sulfate biosynthetic process (GO:0018146)	44709	0.311034802	0.611360498
negative regulation of phosphatase activity (GO:0010923	44709	0.311034802	0.611360498
phagosome acidification (GO:0090383)	44709	0.311034802	0.611360498
positive regulation of cell communication (GO:0010647)	44709	0.311034802	0.611360498
positive regulation of fibroblast proliferation (GO:004814	44709	0.311034802	0.611360498
protein localization to lysosome (GO:0061462)	44709	0.311034802	0.611360498
regulation of calcineurin-NFAT signaling cascade (GO:007	44709	0.311034802	0.611360498
regulation of DNA-templated transcription, elongation (G	44709	0.311034802	0.611360498
regulation of extrinsic apoptotic signaling pathway in abs	44709	0.311034802	0.611360498
regulation of multicellular organismal development (GO::	44709	0.311034802	0.611360498
regulation of phosphatase activity (GO:0010921)	44709	0.311034802	0.611360498
regulation of plasma membrane bounded cell projection	44709	0.311034802	0.611360498
RNA phosphodiester bond hydrolysis (GO:0090501)	44709	0.311034802	0.611360498
T cell activation involved in immune response (GO:00022	44709	0.311034802	0.611360498
negative regulation of organelle assembly (GO:1902116)	12936	0.316671621	0.619120341
negative regulation of Ras protein signal transduction (G	12936	0.316671621	0.619120341
regulation of autophagosome assembly (GO:2000785)	12936	0.316671621	0.619120341
regulation of mitotic spindle organization (GO:0060236)	12936	0.316671621	0.619120341
regulation of neuron apoptotic process (GO:0043523)	15/98	0.316832268	0.619120341
histone H3 acetylation (GO:0043966)	15523	0.319816044	0.619120341
phosphatidylinositol phosphate biosynthetic process (GO	15523	0.319816044	0.619120341
acute-phase response (GO:0006953)	44635	0.319868912	0.619120341
cellular response to ATP (GO:0071318)	44635	0.319868912	0.619120341
central nervous system neuron development (GO:00219	44635	0.319868912	0.619120341
contractile actin filament bundle assembly (GO:0030038)	44635	0.319868912	0.619120341
endoderm development (GO:0007492)	44635	0.319868912	0.619120341
endoplasmic reticulum to cytosol transport (GO:1903513	44635	0.319868912	0.619120341
establishment of spindle localization (GO:0051293)	44635	0.319868912	0.619120341
GTP metabolic process (GO:0046039)	44635	0.319868912	0.619120341
heterocycle biosynthetic process (GO:0018130)	44635	0.319868912	0.619120341
histone H4-K5 acetylation (GO:0043981)	44635	0.319868912	0.619120341
histone H4-K8 acetylation (GO:0043982)	44635	0.319868912	0.619120341
icosanoid biosynthetic process (GO:0046456)	44635	0.319868912	0.619120341
lipoxygenase pathway (GO:0019372)	44635	0.319868912	0.619120341
mRNA methylation (GO:0080009)	44635	0.319868912	0.619120341
negative regulation of endoplasmic reticulum stress-indu	44635	0.319868912	0.619120341
negative regulation of leukocyte mediated cytotoxicity (G	44635	0.319868912	0.619120341
nitric oxide biosynthetic process (GO:0006809)	44635	0.319868912	0.619120341
nucleobase-containing small molecule catabolic process (	44635	0.319868912	0.619120341
peptidyl-tyrosine autophosphorylation (GO:0038083)	44635	0.319868912	0.619120341
phosphatidylethanolamine biosynthetic process (GO:000	44635	0.319868912	0.619120341
positive regulation of chromosome organization (GO:200	44635	0.319868912	0.619120341
positive regulation of nuclear-transcribed mRNA catabol	44635	0.319868912	0.619120341
positive regulation of response to cytokine stimulus (GO:	44635	0.319868912	0.619120341
protein localization to cell-cell junction (GO:0150105)	44635	0.319868912	0.619120341
regulation of clathrin-dependent endocytosis (GO:20003	44635	0.319868912	0.619120341
regulation of neuron projection arborization (GO:015001	44635	0.319868912	0.619120341

regulation of nuclear-transcribed mRNA catabolic proces	44635	0.319868912	0.619120341
regulation of secretion (GO:0051046)	44635	0.319868912	0.619120341
regulation of superoxide anion generation (GO:0032928)	44635	0.319868912	0.619120341
RNA phosphodiester bond hydrolysis, endonucleolytic (G	44635	0.319868912	0.619120341
stress fiber assembly (GO:0043149)	44635	0.319868912	0.619120341
synaptonemal complex assembly (GO:0007130)	44635	0.319868912	0.619120341
synaptonemal complex organization (GO:0070193)	44635	0.319868912	0.619120341
vitamin D metabolic process (GO:0042359)	44635	0.319868912	0.619120341
inorganic cation import across plasma membrane (GO:00	28460	0.320670285	0.620440273
aminoglycan biosynthetic process (GO:0006023)	18111	0.321440047	0.620937491
negative regulation of cell projection organization (GO:0(	18111	0.321440047	0.620937491
cellular response to light stimulus (GO:0071482)	25873	0.321524899	0.620937491
positive regulation of cell-substrate adhesion (GO:00108:	25873	0.321524899	0.620937491
regulation of plasma membrane bounded cell projection	25873	0.321524899	0.620937491
positive regulation of DNA metabolic process (GO:00510	23285	0.322037098	0.621695549
post-translational protein modification (GO:0043687)	49/345	0.325199867	0.627568094
sulfur compound biosynthetic process (GO:0044272)	17/113	0.327218677	0.631229494
nuclear-transcribed mRNA catabolic process (GO:000095	25/171	0.332208729	0.634311188
amino acid import (GO:0043090)	44673	0.332703675	0.634311188
heme biosynthetic process (GO:0006783)	44673	0.332703675	0.634311188
membrane lipid metabolic process (GO:0006643)	44673	0.332703675	0.634311188
mitochondrial calcium ion homeostasis (GO:0051560)	44673	0.332703675	0.634311188
natural killer cell mediated cytotoxicity (GO:0042267)	44673	0.332703675	0.634311188
negative regulation of cyclin-dependent protein kinase a	44673	0.332703675	0.634311188
negative regulation of DNA recombination at telomere (G	44673	0.332703675	0.634311188
negative regulation of mitotic metaphase/anaphase tran	44673	0.332703675	0.634311188
positive regulation of axon extension (GO:0045773)	44673	0.332703675	0.634311188
positive regulation of lipid catabolic process (GO:005099	44673	0.332703675	0.634311188
regulation of centrosome cycle (GO:0046605)	44673	0.332703675	0.634311188
regulation of DNA recombination at telomere (GO:00726	44673	0.332703675	0.634311188
regulation of macrophage chemotaxis (GO:0010758)	44673	0.332703675	0.634311188
ubiquitin-dependent protein catabolic process via the mu	44673	0.332703675	0.634311188
zinc ion transmembrane transport (GO:0071577)	44673	0.332703675	0.634311188
beta-catenin-TCF complex assembly (GO:1904837)	44710	0.338684735	0.634311188
dicarboxylic acid transport (GO:0006835)	44710	0.338684735	0.634311188
glycolytic process (GO:0006096)	44710	0.338684735	0.634311188
lamellipodium organization (GO:0097581)	44710	0.338684735	0.634311188
negative regulation of myeloid leukocyte differentiation (	44710	0.338684735	0.634311188
regulation of gluconeogenesis (GO:0006111)	44710	0.338684735	0.634311188
regulation of protein targeting to membrane (GO:009031	44710	0.338684735	0.634311188
regulation of ubiquitin-protein transferase activity (GO:0(	44710	0.338684735	0.634311188
nucleic acid metabolic process (GO:0090304)	26238	0.338925095	0.634311188
adenosine metabolic process (GO:0046085)	44601	0.339805204	0.634311188
alpha-amino acid biosynthetic process (GO:1901607)	44601	0.339805204	0.634311188
amyloid-beta formation (GO:0034205)	44601	0.339805204	0.634311188
anoikis (GO:0043276)	44601	0.339805204	0.634311188
astral microtubule organization (GO:0030953)	44601	0.339805204	0.634311188

basement membrane assembly (GO:0070831)	44601	0.339805204	0.634311188
bone cell development (GO:0098751)	44601	0.339805204	0.634311188
cellular response to forskolin (GO:1904322)	44601	0.339805204	0.634311188
cellular response to interleukin-17 (GO:0097398)	44601	0.339805204	0.634311188
cellular response to sterol depletion (GO:0071501)	44601	0.339805204	0.634311188
complement activation, classical pathway (GO:0006958)	44601	0.339805204	0.634311188
embryonic digestive tract morphogenesis (GO:0048557)	44601	0.339805204	0.634311188
epithelial cell apoptotic process (GO:1904019)	44601	0.339805204	0.634311188
epithelial to mesenchymal transition involved in endocar	44601	0.339805204	0.634311188
glycerolipid biosynthetic process (GO:0045017)	44601	0.339805204	0.634311188
inositol metabolic process (GO:0006020)	44601	0.339805204	0.634311188
interleukin-17-mediated signaling pathway (GO:0097400	44601	0.339805204	0.634311188
intestinal epithelial cell differentiation (GO:0060575)	44601	0.339805204	0.634311188
L-ascorbic acid metabolic process (GO:0019852)	44601	0.339805204	0.634311188
lipoprotein metabolic process (GO:0042157)	44601	0.339805204	0.634311188
mast cell mediated immunity (GO:0002448)	44601	0.339805204	0.634311188
mitochondrial respirasome assembly (GO:0097250)	44601	0.339805204	0.634311188
negative regulation of exocytosis (GO:0045920)	44601	0.339805204	0.634311188
negative regulation of leukocyte proliferation (GO:00706	44601	0.339805204	0.634311188
negative regulation of lipase activity (GO:0060192)	44601	0.339805204	0.634311188
negative regulation of nitric oxide biosynthetic process (G	44601	0.339805204	0.634311188
negative regulation of nitric oxide metabolic process (GO	44601	0.339805204	0.634311188
negative regulation of pathway-restricted SMAD protein	44601	0.339805204	0.634311188
negative regulation of platelet aggregation (GO:0090331)	44601	0.339805204	0.634311188
negative regulation of retrograde protein transport, ER to	44601	0.339805204	0.634311188
negative regulation of systemic arterial blood pressure (G	44601	0.339805204	0.634311188
negative regulation of T cell cytokine production (GO:00(	44601	0.339805204	0.634311188
negative regulation of ubiquitin protein ligase activity (G(	44601	0.339805204	0.634311188
nuclear RNA surveillance (GO:0071027)	44601	0.339805204	0.634311188
nucleoside diphosphate catabolic process (GO:0009134)	44601	0.339805204	0.634311188
organic cyclic compound catabolic process (GO:1901361)	44601	0.339805204	0.634311188
ornithine metabolic process (GO:0006591)	44601	0.339805204	0.634311188
peripheral nervous system axon ensheathment (GO:0032	44601	0.339805204	0.634311188
plasminogen activation (GO:0031639)	44601	0.339805204	0.634311188
positive regulation of ATP biosynthetic process (GO:2001	44601	0.339805204	0.634311188
positive regulation of blood vessel endothelial cell prolife	44601	0.339805204	0.634311188
positive regulation of cell-cell adhesion mediated by cadh	44601	0.339805204	0.634311188
positive regulation of chromatin binding (GO:0035563)	44601	0.339805204	0.634311188
positive regulation of inositol phosphate biosynthetic pro	44601	0.339805204	0.634311188
positive regulation of ligase activity (GO:0051351)	44601	0.339805204	0.634311188
positive regulation of mast cell degranulation (GO:00433	44601	0.339805204	0.634311188
positive regulation of sequestering of triglyceride (GO:00	44601	0.339805204	0.634311188
positive regulation of triglyceride lipase activity (GO:0061	44601	0.339805204	0.634311188
purine nucleobase metabolic process (GO:0006144)	44601	0.339805204	0.634311188
regulation of actin filament organization (GO:0110053)	44601	0.339805204	0.634311188
regulation of aspartic-type endopeptidase activity involve	44601	0.339805204	0.634311188
regulation of CD8-positive, alpha-beta T cell activation (G	44601	0.339805204	0.634311188

regulation of complement activation, classical pathway ((	44601	0.339805204	0.634311188
regulation of complement-dependent cytotoxicity (GO:19	44601	0.339805204	0.634311188
regulation of ER-associated ubiquitin-dependent protein	44601	0.339805204	0.634311188
regulation of fertilization (GO:0080154)	44601	0.339805204	0.634311188
regulation of transmembrane transporter activity (GO:00	44601	0.339805204	0.634311188
response to forskolin (GO:1904321)	44601	0.339805204	0.634311188
response to UV-C (GO:0010225)	44601	0.339805204	0.634311188
Schwann cell development (GO:0014044)	44601	0.339805204	0.634311188
sensory organ morphogenesis (GO:0090596)	44601	0.339805204	0.634311188
small RNA loading onto RISC (GO:0070922)	44601	0.339805204	0.634311188
somatic recombination of immunoglobulin genes involve	44601	0.339805204	0.634311188
synapse pruning (GO:0098883)	44601	0.339805204	0.634311188
tetrahydrofolate interconversion (GO:0035999)	44601	0.339805204	0.634311188
lipid homeostasis (GO:0055088)	23651	0.340415557	0.634994189
protein catabolic process (GO:0030163)	23651	0.340415557	0.634994189
endoderm formation (GO:0001706)	13302	0.341434435	0.635081907
negative regulation of cellular protein localization (GO:19	13302	0.341434435	0.635081907
Wnt signaling pathway, calcium modulating pathway (GO	13302	0.341434435	0.635081907
arachidonic acid metabolic process (GO:0019369)	21064	0.341603203	0.635081907
positive regulation of cell junction assembly (GO:190189(	21064	0.341603203	0.635081907
regulation of mitotic nuclear division (GO:0007088)	21064	0.341603203	0.635081907
amino acid transport (GO:0006865)	18476	0.342346433	0.635081907
organic hydroxy compound biosynthetic process (GO:190	18476	0.342346433	0.635081907
positive regulation of cell morphogenesis involved in diff	18476	0.342346433	0.635081907
cellular glucose homeostasis (GO:0001678)	15888	0.34241856	0.635081907
cellular response to retinoic acid (GO:0071300)	15888	0.34241856	0.635081907
DNA synthesis involved in DNA repair (GO:0000731)	15888	0.34241856	0.635081907
natural killer cell activation (GO:0030101)	15888	0.34241856	0.635081907
negative regulation of proteolysis (GO:0045861)	15888	0.34241856	0.635081907
positive regulation of phospholipase C activity (GO:00108	15888	0.34241856	0.635081907
substantia nigra development (GO:0021762)	15888	0.34241856	0.635081907
cell morphogenesis involved in differentiation (GO:00009	26604	0.356492872	0.657476948
positive regulation of neurogenesis (GO:0050769)	26604	0.356492872	0.657476948
positive regulation of protein secretion (GO:0050714)	26604	0.356492872	0.657476948
3'-UTR-mediated mRNA destabilization (GO:0061158)	44636	0.358416692	0.657476948
apoptotic DNA fragmentation (GO:0006309)	44636	0.358416692	0.657476948
autophagy of nucleus (GO:0044804)	44636	0.358416692	0.657476948
cellular response to corticosteroid stimulus (GO:0071384	44636	0.358416692	0.657476948
cellular response to sterol (GO:0036315)	44636	0.358416692	0.657476948
ceramide catabolic process (GO:0046514)	44636	0.358416692	0.657476948
epiboly involved in wound healing (GO:0090505)	44636	0.358416692	0.657476948
glycosphingolipid biosynthetic process (GO:0006688)	44636	0.358416692	0.657476948
Golgi to endosome transport (GO:0006895)	44636	0.358416692	0.657476948
male meiosis I (GO:0007141)	44636	0.358416692	0.657476948
membrane repolarization (GO:0086009)	44636	0.358416692	0.657476948
mitotic sister chromatid cohesion (GO:0007064)	44636	0.358416692	0.657476948
motor neuron axon guidance (GO:0008045)	44636	0.358416692	0.657476948

negative regulation of cell-substrate junction organizatio	44636	0.358416692	0.657476948
negative regulation of focal adhesion assembly (GO:0051	44636	0.358416692	0.657476948
neuron cell-cell adhesion (GO:0007158)	44636	0.358416692	0.657476948
nitric oxide metabolic process (GO:0046209)	44636	0.358416692	0.657476948
nucleoside diphosphate metabolic process (GO:0009132)	44636	0.358416692	0.657476948
positive regulation by host of viral transcription (GO:004	44636	0.358416692	0.657476948
protein localization to microtubule organizing center (GO	44636	0.358416692	0.657476948
purine ribonucleoside monophosphate biosynthetic proc	44636	0.358416692	0.657476948
regulation of ATP biosynthetic process (GO:2001169)	44636	0.358416692	0.657476948
regulation of chromatin silencing (GO:0031935)	44636	0.358416692	0.657476948
regulation of ERBB signaling pathway (GO:1901184)	44636	0.358416692	0.657476948
regulation of interleukin-13 production (GO:0032656)	44636	0.358416692	0.657476948
regulation of mitotic sister chromatid separation (GO:001	44636	0.358416692	0.657476948
regulation of neurotransmitter transport (GO:0051588)	44636	0.358416692	0.657476948
regulation of Rac protein signal transduction (GO:003502	44636	0.358416692	0.657476948
chemical homeostasis (GO:0048878)	24016	0.358966188	0.658020236
regulation of cell-matrix adhesion (GO:0001952)	24016	0.358966188	0.658020236
cellular iron ion homeostasis (GO:0006879)	21429	0.361307785	0.661612246
membrane lipid biosynthetic process (GO:0046467)	21429	0.361307785	0.661612246
negative regulation of neuron projection development (G	21429	0.361307785	0.661612246
regulation of primary metabolic process (GO:0080090)	19/130	0.361845566	0.662363537
cholesterol transport (GO:0030301)	18841	0.363433161	0.664666745
inositol lipid-mediated signaling (GO:0048017)	18841	0.363433161	0.664666745
negative regulation of cellular protein metabolic process	14/94	0.364172339	0.664666745
DNA catabolic process, endonucleolytic (GO:0000737)	44674	0.364639119	0.664666745
negative regulation of extrinsic apoptotic signaling pathw	44674	0.364639119	0.664666745
negative regulation of signal transduction in absence of li	44674	0.364639119	0.664666745
nucleotide metabolic process (GO:0009117)	44674	0.364639119	0.664666745
positive regulation of natural killer cell mediated immuni	44674	0.364639119	0.664666745
positive regulation of protein autophosphorylation (GO:0	44674	0.364639119	0.664666745
positive regulation of receptor internalization (GO:00020	44674	0.364639119	0.664666745
positive regulation of transcription by RNA polymerase I (	44674	0.364639119	0.664666745
vesicle transport along microtubule (GO:0047496)	44674	0.364639119	0.664666745
cation transmembrane transport (GO:0098655)	16254	0.365203634	0.665462251
lysosome localization (GO:0032418)	13667	0.366378424	0.665500934
neural crest cell migration (GO:0001755)	13667	0.366378424	0.665500934
regulation of actin cytoskeleton reorganization (GO:2000	13667	0.366378424	0.665500934
regulation of microtubule cytoskeleton organization (GO:	13667	0.366378424	0.665500934
mRNA splice site selection (GO:0006376)	44711	0.366505904	0.665500934
multivesicular body assembly (GO:0036258)	44711	0.366505904	0.665500934
regulation of protein localization to membrane (GO:1905	44711	0.366505904	0.665500934
regulation of striated muscle contraction (GO:0006942)	44711	0.366505904	0.665500934
response to alcohol (GO:0097305)	44711	0.366505904	0.665500934
zinc ion homeostasis (GO:0055069)	44711	0.366505904	0.665500934
cytosolic transport (GO:0016482)	17/116	0.368669676	0.669196006
insulin receptor signaling pathway (GO:0008286)	26969	0.374189414	0.678740923
neurotransmitter transport (GO:0006836)	26969	0.374189414	0.678740923

cell-cell junction assembly (GO:0007043)	24381	0.377643442	0.68476708
glycolipid metabolic process (GO:0006664)	19207	0.384633954	0.690090587
regulation of exocytosis (GO:0017157)	19207	0.384633954	0.690090587
cellular response to radiation (GO:0071478)	16619	0.388088222	0.690090587
neural crest cell development (GO:0014032)	16619	0.388088222	0.690090587
positive regulation of nervous system development (GO:(	16619	0.388088222	0.690090587
adrenal gland development (GO:0030325)	44602	0.390542122	0.690090587
calcium import into the mitochondrion (GO:0036444)	44602	0.390542122	0.690090587
cellular response to acidic pH (GO:0071468)	44602	0.390542122	0.690090587
cellular response to oxygen levels (GO:0071453)	44602	0.390542122	0.690090587
cellular response to prostaglandin stimulus (GO:0071379	44602	0.390542122	0.690090587
chloride ion homeostasis (GO:0055064)	44602	0.390542122	0.690090587
chondroitin sulfate proteoglycan metabolic process (GO:(	44602	0.390542122	0.690090587
complement activation, lectin pathway (GO:0001867)	44602	0.390542122	0.690090587
defense response to tumor cell (GO:0002357)	44602	0.390542122	0.690090587
ectoderm development (GO:0007398)	44602	0.390542122	0.690090587
endothelium development (GO:0003158)	44602	0.390542122	0.690090587
ether lipid biosynthetic process (GO:0008611)	44602	0.390542122	0.690090587
formation of translation preinitiation complex (GO:00017	44602	0.390542122	0.690090587
fructose 6-phosphate metabolic process (GO:0006002)	44602	0.390542122	0.690090587
genetic imprinting (GO:0071514)	44602	0.390542122	0.690090587
L-glutamate transmembrane transport (GO:0015813)	44602	0.390542122	0.690090587
L-serine metabolic process (GO:0006563)	44602	0.390542122	0.690090587
lactation (GO:0007595)	44602	0.390542122	0.690090587
lipid droplet formation (GO:0140042)	44602	0.390542122	0.690090587
lipid phosphorylation (GO:0046834)	44602	0.390542122	0.690090587
lipoprotein transport (GO:0042953)	44602	0.390542122	0.690090587
membrane lipid catabolic process (GO:0046466)	44602	0.390542122	0.690090587
microtubule anchoring at centrosome (GO:0034454)	44602	0.390542122	0.690090587
modification-dependent macromolecule catabolic proces	44602	0.390542122	0.690090587
monovalent inorganic anion homeostasis (GO:0055083)	44602	0.390542122	0.690090587
negative regulation of cAMP-mediated signaling (GO:004	44602	0.390542122	0.690090587
negative regulation of cell adhesion mediated by integrin	44602	0.390542122	0.690090587
negative regulation of cellular protein catabolic process (	44602	0.390542122	0.690090587
negative regulation of circadian rhythm (GO:0042754)	44602	0.390542122	0.690090587
negative regulation of glycolytic process (GO:0045820)	44602	0.390542122	0.690090587
negative regulation of inclusion body assembly (GO:0090	44602	0.390542122	0.690090587
negative regulation of leukocyte migration (GO:0002686)	44602	0.390542122	0.690090587
negative regulation of lymphocyte apoptotic process (GO	44602	0.390542122	0.690090587
negative regulation of purine nucleotide metabolic proce	44602	0.390542122	0.690090587
negative regulation of sodium ion transmembrane transp	44602	0.390542122	0.690090587
negative regulation of sodium ion transmembrane transp	44602	0.390542122	0.690090587
negative regulation of telomerase activity (GO:0051974)	44602	0.390542122	0.690090587
negative regulation of viral-induced cytoplasmic pattern	44602	0.390542122	0.690090587
nerve growth factor signaling pathway (GO:0038180)	44602	0.390542122	0.690090587
neuron projection maintenance (GO:1990535)	44602	0.390542122	0.690090587
nuclear mRNA surveillance (GO:0071028)	44602	0.390542122	0.690090587

peptidyl-amino acid modification (GO:0018193)	44602	0.390542122	0.690090587
phagosome-lysosome fusion (GO:0090385)	44602	0.390542122	0.690090587
positive regulation of behavior (GO:0048520)	44602	0.390542122	0.690090587
positive regulation of epidermis development (GO:00456	44602	0.390542122	0.690090587
positive regulation of mesenchymal cell proliferation (GO	44602	0.390542122	0.690090587
positive regulation of protein sumoylation (GO:0033235)	44602	0.390542122	0.690090587
positive regulation of receptor recycling (GO:0001921)	44602	0.390542122	0.690090587
positive regulation of RIG-I signaling pathway (GO:19002	44602	0.390542122	0.690090587
positive regulation of rRNA processing (GO:2000234)	44602	0.390542122	0.690090587
positive regulation of transcription by RNA polymerase III	44602	0.390542122	0.690090587
presynaptic membrane assembly (GO:0097105)	44602	0.390542122	0.690090587
primary miRNA processing (GO:0031053)	44602	0.390542122	0.690090587
protein localization to endosome (GO:0036010)	44602	0.390542122	0.690090587
protein O-linked glycosylation via serine (GO:0018242)	44602	0.390542122	0.690090587
protein prenylation (GO:0018342)	44602	0.390542122	0.690090587
Rap protein signal transduction (GO:0032486)	44602	0.390542122	0.690090587
regulation of DNA methylation (GO:0044030)	44602	0.390542122	0.690090587
regulation of hair cycle (GO:0042634)	44602	0.390542122	0.690090587
regulation of histone phosphorylation (GO:0033127)	44602	0.390542122	0.690090587
regulation of long-term synaptic depression (GO:190045	44602	0.390542122	0.690090587
regulation of protein neddylation (GO:2000434)	44602	0.390542122	0.690090587
regulation of receptor binding (GO:1900120)	44602	0.390542122	0.690090587
regulation of store-operated calcium entry (GO:2001256)	44602	0.390542122	0.690090587
regulation of urine volume (GO:0035809)	44602	0.390542122	0.690090587
removal of superoxide radicals (GO:0019430)	44602	0.390542122	0.690090587
rRNA pseudouridine synthesis (GO:0031118)	44602	0.390542122	0.690090587
sequestering of actin monomers (GO:0042989)	44602	0.390542122	0.690090587
smooth muscle tissue development (GO:0048745)	44602	0.390542122	0.690090587
urea cycle (GO:0000050)	44602	0.390542122	0.690090587
lymphocyte proliferation (GO:0046651)	14032	0.391395666	0.690659133
negative regulation of proteasomal protein catabolic pro	14032	0.391395666	0.690659133
positive regulation of insulin secretion (GO:0032024)	14032	0.391395666	0.690659133
regulation of phosphoprotein phosphatase activity (GO:0	14032	0.391395666	0.690659133
'de novo' posttranslational protein folding (GO:0051084)	44712	0.39435065	0.691439491
cellular response to cAMP (GO:0071320)	44712	0.39435065	0.691439491
negative regulation of axon extension (GO:0030517)	44712	0.39435065	0.691439491
negative regulation of proteasomal ubiquitin-dependent	44712	0.39435065	0.691439491
positive regulation of Rho protein signal transduction (GO	44712	0.39435065	0.691439491
regulation of developmental growth (GO:0048638)	44712	0.39435065	0.691439491
vitamin transport (GO:0051180)	44712	0.39435065	0.691439491
cellular transition metal ion homeostasis (GO:0046916)	14/96	0.39533073	0.691439491
apoptotic nuclear changes (GO:0030262)	44675	0.396494953	0.691439491
axon extension (GO:0048675)	44675	0.396494953	0.691439491
endocrine system development (GO:0035270)	44675	0.396494953	0.691439491
extracellular matrix assembly (GO:0085029)	44675	0.396494953	0.691439491
negative regulation of protein depolymerization (GO:190	44675	0.396494953	0.691439491
negative regulation of protein tyrosine kinase activity (GO	44675	0.396494953	0.691439491

porphyrin-containing compound biosynthetic process (G(	44675	0.396494953	0.691439491
positive regulation of lamellipodium assembly (GO:00105	44675	0.396494953	0.691439491
protein alpha-1,2-demannosylation (GO:0036508)	44675	0.396494953	0.691439491
purine nucleotide metabolic process (GO:0006163)	44675	0.396494953	0.691439491
response to gamma radiation (GO:0010332)	44675	0.396494953	0.691439491
activation of protein kinase A activity (GO:0034199)	44637	0.39662939	0.691439491
cell communication by electrical coupling involved in carc	44637	0.39662939	0.691439491
cell surface receptor signaling pathway involved in heart	44637	0.39662939	0.691439491
cellular modified amino acid catabolic process (GO:00422	44637	0.39662939	0.691439491
copper ion homeostasis (GO:0055070)	44637	0.39662939	0.691439491
histone H2A monoubiquitination (GO:0035518)	44637	0.39662939	0.691439491
membrane depolarization during cardiac muscle cell actic	44637	0.39662939	0.691439491
monosaccharide transmembrane transport (GO:0015749	44637	0.39662939	0.691439491
negative regulation of insulin secretion (GO:0046676)	44637	0.39662939	0.691439491
protein autoprocessing (GO:0016540)	44637	0.39662939	0.691439491
regulation of neuroblast proliferation (GO:1902692)	44637	0.39662939	0.691439491
regulation of receptor recycling (GO:0001919)	44637	0.39662939	0.691439491
regulation of steroid biosynthetic process (GO:0050810)	44637	0.39662939	0.691439491
regulation of transferase activity (GO:0051338)	44637	0.39662939	0.691439491
reverse cholesterol transport (GO:0043691)	44637	0.39662939	0.691439491
stabilization of membrane potential (GO:0030322)	44637	0.39662939	0.691439491
stem cell development (GO:0048864)	44637	0.39662939	0.691439491
neuron projection morphogenesis (GO:0048812)	20/140	0.397145089	0.692106253
regulation of cell motility (GO:2000145)	19/133	0.401543528	0.699536764
heart morphogenesis (GO:0003007)	19572	0.40588425	0.706624892
positive regulation of macroautophagy (GO:0016239)	19572	0.40588425	0.706624892
regulation of hematopoietic progenitor cell differentiatio	27699	0.409815375	0.713229773
alpha-amino acid metabolic process (GO:1901605)	16984	0.410992217	0.714333221
spliceosomal complex assembly (GO:0000245)	16984	0.410992217	0.714333221
vesicle organization (GO:0016050)	16984	0.410992217	0.714333221
protein maturation (GO:0051604)	14/97	0.410999422	0.714333221
sodium ion transport (GO:0006814)	13/90	0.416233125	0.722723676
positive regulation of intracellular transport (GO:003238	14397	0.416383438	0.722723676
regulation of protein tyrosine kinase activity (GO:006109	14397	0.416383438	0.722723676
vesicle cytoskeletal trafficking (GO:0099518)	14397	0.416383438	0.722723676
regulation of endocytosis (GO:0030100)	22525	0.420942757	0.729202401
heart development (GO:0007507)	23/164	0.421020885	0.729202401
glycoprotein biosynthetic process (GO:0009101)	30651	0.421772819	0.729202401
long-chain fatty acid metabolic process (GO:0001676)	30651	0.421772819	0.729202401
establishment or maintenance of epithelial cell apical/ba	11810	0.422081159	0.729202401
liver development (GO:0001889)	11810	0.422081159	0.729202401
metal ion export (GO:0070839)	11810	0.422081159	0.729202401
negative regulation of developmental growth (GO:00486	11810	0.422081159	0.729202401
negative regulation of intracellular steroid hormone rece	11810	0.422081159	0.729202401
regulation of cell migration involved in sprouting angioge	11810	0.422081159	0.729202401
regulation of transcription involved in G1/S transition of	11810	0.422081159	0.729202401
response to amino acid (GO:0043200)	11810	0.422081159	0.729202401

RNA biosynthetic process (GO:0032774)	11810	0.422081159	0.729202401
transcription initiation from RNA polymerase I promoter	11810	0.422081159	0.729202401
negative regulation of neuron death (GO:1901215)	14/98	0.426693943	0.736615835
glycosaminoglycan metabolic process (GO:0030203)	19937	0.427121669	0.736615835
mitotic cell cycle phase transition (GO:0044772)	29/209	0.427385276	0.736615835
cellular polysaccharide biosynthetic process (GO:003369	44676	0.428073764	0.736615835
divalent inorganic cation homeostasis (GO:0072507)	44676	0.428073764	0.736615835
fat-soluble vitamin metabolic process (GO:0006775)	44676	0.428073764	0.736615835
in utero embryonic development (GO:0001701)	44676	0.428073764	0.736615835
negative regulation of ion transport (GO:0043271)	44676	0.428073764	0.736615835
regulation of calcium ion import (GO:0090279)	44676	0.428073764	0.736615835
regulation of microtubule depolymerization (GO:003111	44676	0.428073764	0.736615835
regulation of mitochondrial fission (GO:0090140)	44676	0.428073764	0.736615835
regulation of spindle assembly (GO:0090169)	44676	0.428073764	0.736615835
glycosphingolipid metabolic process (GO:0006687)	17349	0.43383905	0.738800143
cellular response to pH (GO:0071467)	44638	0.434193959	0.738800143
endothelial cell proliferation (GO:0001935)	44638	0.434193959	0.738800143
phosphatidylglycerol acyl-chain remodeling (GO:003614	44638	0.434193959	0.738800143
phosphatidylinositol acyl-chain remodeling (GO:003614	44638	0.434193959	0.738800143
positive regulation of cell migration involved in sprouting	44638	0.434193959	0.738800143
positive regulation of excitatory postsynaptic potential (	44638	0.434193959	0.738800143
positive regulation of nervous system process (GO:0031	44638	0.434193959	0.738800143
presynapse assembly (GO:0099054)	44638	0.434193959	0.738800143
protein localization to centrosome (GO:0071539)	44638	0.434193959	0.738800143
pulmonary valve development (GO:0003177)	44638	0.434193959	0.738800143
regulation of cellular protein catabolic process (GO:1903	44638	0.434193959	0.738800143
regulation of early endosome to late endosome transpor	44638	0.434193959	0.738800143
regulation of fatty acid metabolic process (GO:0019217)	44638	0.434193959	0.738800143
regulation of multicellular organism growth (GO:004001	44638	0.434193959	0.738800143
regulation of spindle organization (GO:0090224)	44638	0.434193959	0.738800143
regulation of vascular endothelial cell proliferation (GO:1	44638	0.434193959	0.738800143
RNA destabilization (GO:0050779)	44638	0.434193959	0.738800143
rRNA catabolic process (GO:0016075)	44638	0.434193959	0.738800143
aminoglycan metabolic process (GO:0006022)	44603	0.439440316	0.738800143
angiogenesis involved in wound healing (GO:0060055)	44603	0.439440316	0.738800143
camera-type eye morphogenesis (GO:0048593)	44603	0.439440316	0.738800143
cardiac muscle cell membrane repolarization (GO:009962	44603	0.439440316	0.738800143
carnitine shuttle (GO:0006853)	44603	0.439440316	0.738800143
cell differentiation in spinal cord (GO:0021515)	44603	0.439440316	0.738800143
cell proliferation in forebrain (GO:0021846)	44603	0.439440316	0.738800143
cell-cell junction maintenance (GO:0045217)	44603	0.439440316	0.738800143
cellular response to cholesterol (GO:0071397)	44603	0.439440316	0.738800143
cellular response to superoxide (GO:0071451)	44603	0.439440316	0.738800143
cyclooxygenase pathway (GO:0019371)	44603	0.439440316	0.738800143
DNA damage response, signal transduction resulting in tr	44603	0.439440316	0.738800143
embryonic eye morphogenesis (GO:0048048)	44603	0.439440316	0.738800143
glutathione biosynthetic process (GO:0006750)	44603	0.439440316	0.738800143

glycerol metabolic process (GO:0006071)	44603	0.439440316	0.738800143
glycerolipid metabolic process (GO:0046486)	44603	0.439440316	0.738800143
Golgi inheritance (GO:0048313)	44603	0.439440316	0.738800143
intestinal lipid absorption (GO:0098856)	44603	0.439440316	0.738800143
lipoprotein localization (GO:0044872)	44603	0.439440316	0.738800143
midbrain dopaminergic neuron differentiation (GO:1904	44603	0.439440316	0.738800143
monocyte differentiation (GO:0030224)	44603	0.439440316	0.738800143
negative regulation of cholesterol transport (GO:003237	44603	0.439440316	0.738800143
negative regulation of defense response to virus (GO:005	44603	0.439440316	0.738800143
negative regulation of homotypic cell-cell adhesion (GO:(	44603	0.439440316	0.738800143
negative regulation of lymphocyte migration (GO:20004(	44603	0.439440316	0.738800143
negative regulation of protein localization to cell surface	44603	0.439440316	0.738800143
negative regulation of sprouting angiogenesis (GO:19036	44603	0.439440316	0.738800143
positive regulation by host of viral process (GO:0044794)	44603	0.439440316	0.738800143
positive regulation of bone resorption (GO:0045780)	44603	0.439440316	0.738800143
positive regulation of histone exchange (GO:1900051)	44603	0.439440316	0.738800143
positive regulation of keratinocyte proliferation (GO:001(	44603	0.439440316	0.738800143
positive regulation of phospholipid transport (GO:20011	44603	0.439440316	0.738800143
positive regulation of transcription elongation from RNA	44603	0.439440316	0.738800143
positive regulation of vacuole organization (GO:0044090)	44603	0.439440316	0.738800143
presynaptic membrane organization (GO:0097090)	44603	0.439440316	0.738800143
protein kinase C signaling (GO:0070528)	44603	0.439440316	0.738800143
protein kinase C-activating G protein-coupled receptor si	44603	0.439440316	0.738800143
protein oxidation (GO:0018158)	44603	0.439440316	0.738800143
pyrimidine nucleoside salvage (GO:0043097)	44603	0.439440316	0.738800143
pyrimidine-containing compound salvage (GO:0008655)	44603	0.439440316	0.738800143
regulation of cardiac muscle cell apoptotic process (GO:0	44603	0.439440316	0.738800143
regulation of dendritic cell apoptotic process (GO:20006(	44603	0.439440316	0.738800143
regulation of histone exchange (GO:1900049)	44603	0.439440316	0.738800143
regulation of inclusion body assembly (GO:0090083)	44603	0.439440316	0.738800143
regulation of mast cell activation involved in immune res	44603	0.439440316	0.738800143
regulation of mesenchymal cell proliferation (GO:001046	44603	0.439440316	0.738800143
regulation of microtubule-based movement (GO:006063	44603	0.439440316	0.738800143
regulation of mitochondrial depolarization (GO:0051900)	44603	0.439440316	0.738800143
regulation of phospholipase activity (GO:0010517)	44603	0.439440316	0.738800143
tetrahydrobiopterin metabolic process (GO:0046146)	44603	0.439440316	0.738800143
tetrahydrofolate metabolic process (GO:0046653)	44603	0.439440316	0.738800143
urate metabolic process (GO:0046415)	44603	0.439440316	0.738800143
bone development (GO:0060348)	14763	0.441244997	0.741114697
carboxylic acid metabolic process (GO:0019752)	14763	0.441244997	0.741114697
regulation of sodium ion transmembrane transporter act	14763	0.441244997	0.741114697
extracellular matrix organization (GO:0030198)	41/300	0.443945671	0.745409748
negative regulation of cell motility (GO:2000146)	16/114	0.445160893	0.747208672
regulation of organelle assembly (GO:1902115)	28430	0.445502899	0.747541201
muscle contraction (GO:0006936)	18/129	0.447368582	0.750429379
glycoprotein metabolic process (GO:0009100)	20302	0.448286414	0.751483679
regulation of cardiac conduction (GO:1903779)	20302	0.448286414	0.751483679

regulation of lipid metabolic process (GO:0019216)	13/92	0.448874049	0.75217982
actin filament bundle assembly (GO:0051017)	12175	0.449570422	0.75217982
actin filament bundle organization (GO:0061572)	12175	0.449570422	0.75217982
keratan sulfate metabolic process (GO:0042339)	12175	0.449570422	0.75217982
muscle cell development (GO:0055001)	12175	0.449570422	0.75217982
very long-chain fatty acid metabolic process (GO:000003	12175	0.449570422	0.75217982
kidney development (GO:0001822)	25842	0.452734157	0.757229216
myelination (GO:0042552)	17715	0.456556187	0.762493641
purine ribonucleotide biosynthetic process (GO:0009152	17715	0.456556187	0.762493641
regulation of mitochondrion organization (GO:0010821)	17715	0.456556187	0.762493641
substrate adhesion-dependent cell spreading (GO:00344	17715	0.456556187	0.762493641
cell-matrix adhesion (GO:0007160)	14/100	0.458061549	0.762493641
cellular response to drug (GO:0035690)	44677	0.459199858	0.762493641
chaperone cofactor-dependent protein refolding (GO:00	44677	0.459199858	0.762493641
clathrin-dependent endocytosis (GO:0072583)	44677	0.459199858	0.762493641
meiosis I (GO:0007127)	44677	0.459199858	0.762493641
negative regulation of proteolysis involved in cellular pro	44677	0.459199858	0.762493641
positive regulation of histone methylation (GO:0031062)	44677	0.459199858	0.762493641
positive regulation of protein insertion into mitochondria	44677	0.459199858	0.762493641
positive regulation of viral transcription (GO:0050434)	44677	0.459199858	0.762493641
regulation of actin filament bundle assembly (GO:003223	44677	0.459199858	0.762493641
regulation of chondrocyte differentiation (GO:0032330)	44677	0.459199858	0.762493641
regulation of mitotic metaphase/anaphase transition (GC	44677	0.459199858	0.762493641
regulation of myelination (GO:0031641)	44677	0.459199858	0.762493641
regulation of protein insertion into mitochondrial membr	44677	0.459199858	0.762493641
organonitrogen compound catabolic process (GO:190156	23255	0.460619361	0.762493641
acylglycerol metabolic process (GO:0006639)	15128	0.465890181	0.762493641
carbohydrate catabolic process (GO:0016052)	15128	0.465890181	0.762493641
regulation of response to DNA damage stimulus (GO:200	15128	0.465890181	0.762493641
response to growth factor (GO:0070848)	15128	0.465890181	0.762493641
negative regulation of transmembrane receptor protein s	15/108	0.466516173	0.762493641
glycosaminoglycan catabolic process (GO:0006027)	20668	0.469321609	0.762493641
mitochondrial transport (GO:0006839)	20668	0.469321609	0.762493641
nuclear-transcribed mRNA catabolic process, deadenylati	20668	0.469321609	0.762493641
actin filament capping (GO:0051693)	44639	0.470849586	0.762493641
activin receptor signaling pathway (GO:0032924)	44639	0.470849586	0.762493641
barbed-end actin filament capping (GO:0051016)	44639	0.470849586	0.762493641
cellular response to glucagon stimulus (GO:0071377)	44639	0.470849586	0.762493641
cytoplasmic translational initiation (GO:0002183)	44639	0.470849586	0.762493641
diol metabolic process (GO:0034311)	44639	0.470849586	0.762493641
epoxygenase P450 pathway (GO:0019373)	44639	0.470849586	0.762493641
fatty acid transmembrane transport (GO:1902001)	44639	0.470849586	0.762493641
folic acid metabolic process (GO:0046655)	44639	0.470849586	0.762493641
histone H4-K16 acetylation (GO:0043984)	44639	0.470849586	0.762493641
long-term memory (GO:0007616)	44639	0.470849586	0.762493641
mitochondrion localization (GO:0051646)	44639	0.470849586	0.762493641
negative regulation of calcium ion transport (GO:005192	44639	0.470849586	0.762493641

negative regulation of protein localization to nucleus (GO	44639	0.470849586	0.762493641
negative regulation of RNA splicing (GO:0033119)	44639	0.470849586	0.762493641
negative regulation of striated muscle cell differentiation	44639	0.470849586	0.762493641
NLS-bearing protein import into nucleus (GO:0006607)	44639	0.470849586	0.762493641
positive regulation of establishment of protein localizatio	44639	0.470849586	0.762493641
postsynaptic membrane organization (GO:0001941)	44639	0.470849586	0.762493641
regulation of collagen biosynthetic process (GO:0032965)	44639	0.470849586	0.762493641
regulation of mitochondrial membrane permeability (GO	44639	0.470849586	0.762493641
regulation of mitotic spindle assembly (GO:1901673)	44639	0.470849586	0.762493641
response to ATP (GO:0033198)	44639	0.470849586	0.762493641
striated muscle cell differentiation (GO:0051146)	44639	0.470849586	0.762493641
negative regulation of neuron apoptotic process (GO:004	26207	0.471391373	0.762493641
phosphatidylinositol-mediated signaling (GO:0048015)	26207	0.471391373	0.762493641
protein tetramerization (GO:0051262)	26207	0.471391373	0.762493641
cardiac muscle contraction (GO:0060048)	12540	0.476702873	0.762493641
epithelial tube morphogenesis (GO:0060562)	12540	0.476702873	0.762493641
negative regulation of blood vessel endothelial cell migra	12540	0.476702873	0.762493641
phosphatidylinositol 3-kinase signaling (GO:0014065)	12540	0.476702873	0.762493641
positive regulation of DNA binding (GO:0043388)	12540	0.476702873	0.762493641
regulation of keratinocyte differentiation (GO:0045616)	12540	0.476702873	0.762493641
response to steroid hormone (GO:0048545)	12540	0.476702873	0.762493641
adherens junction organization (GO:0034332)	18080	0.479075535	0.762493641
protein secretion (GO:0009306)	23621	0.480289067	0.762493641
regulation of cellular ketone metabolic process (GO:0010	23621	0.480289067	0.762493641
inorganic cation transmembrane transport (GO:0098662)	37/274	0.48045763	0.762493641
regulation of kinase activity (GO:0043549)	13/94	0.481352558	0.762493641
non-canonical Wnt signaling pathway (GO:0035567)	17/124	0.481654965	0.762493641
autophagy of peroxisome (GO:0030242)	44604	0.486094803	0.762493641
C-terminal protein amino acid modification (GO:0018410	44604	0.486094803	0.762493641
cell cycle checkpoint signaling (GO:0000075)	44604	0.486094803	0.762493641
dosage compensation by inactivation of X chromosome (	44604	0.486094803	0.762493641
energy coupled proton transport, down electrochemical g	44604	0.486094803	0.762493641
exit from mitosis (GO:0010458)	44604	0.486094803	0.762493641
eye photoreceptor cell differentiation (GO:0001754)	44604	0.486094803	0.762493641
glutamine metabolic process (GO:0006541)	44604	0.486094803	0.762493641
macrophage chemotaxis (GO:0048246)	44604	0.486094803	0.762493641
microtubule anchoring at microtubule organizing center (	44604	0.486094803	0.762493641
mitochondrion distribution (GO:0048311)	44604	0.486094803	0.762493641
modulation by host of viral process (GO:0044788)	44604	0.486094803	0.762493641
morphogenesis of a polarized epithelium (GO:0001738)	44604	0.486094803	0.762493641
motile cilium assembly (GO:0044458)	44604	0.486094803	0.762493641
negative regulation of cell division (GO:0051782)	44604	0.486094803	0.762493641
negative regulation of cilium assembly (GO:1902018)	44604	0.486094803	0.762493641
negative regulation of gene silencing by miRNA (GO:0060	44604	0.486094803	0.762493641
negative regulation of hemostasis (GO:1900047)	44604	0.486094803	0.762493641
negative regulation of leukocyte chemotaxis (GO:000268	44604	0.486094803	0.762493641
negative regulation of receptor internalization (GO:0002(	44604	0.486094803	0.762493641

negative regulation of release of sequestered calcium ion	44604	0.486094803	0.762493641
negative regulation of ryanodine-sensitive calcium-releas	44604	0.486094803	0.762493641
neurotransmitter uptake (GO:0001504)	44604	0.486094803	0.762493641
nonribosomal peptide biosynthetic process (GO:0019184	44604	0.486094803	0.762493641
nucleoside salvage (GO:0043174)	44604	0.486094803	0.762493641
phasic smooth muscle contraction (GO:0014821)	44604	0.486094803	0.762493641
phosphate ion transmembrane transport (GO:0035435)	44604	0.486094803	0.762493641
phospholipid homeostasis (GO:0055091)	44604	0.486094803	0.762493641
poly-N-acetyllactosamine biosynthetic process (GO:0030	44604	0.486094803	0.762493641
positive regulation of actin filament depolymerization (G	44604	0.486094803	0.762493641
positive regulation of sodium ion transmembrane transp	44604	0.486094803	0.762493641
positive regulation of ubiquitin protein ligase activity (GO	44604	0.486094803	0.762493641
pyrimidine nucleobase metabolic process (GO:0006206)	44604	0.486094803	0.762493641
regulation of actin filament depolymerization (GO:00308	44604	0.486094803	0.762493641
regulation of actin nucleation (GO:0051125)	44604	0.486094803	0.762493641
regulation of cell communication by electrical coupling in	44604	0.486094803	0.762493641
regulation of cholesterol esterification (GO:0010872)	44604	0.486094803	0.762493641
regulation of dendritic cell differentiation (GO:2001198)	44604	0.486094803	0.762493641
regulation of feeding behavior (GO:0060259)	44604	0.486094803	0.762493641
regulation of flagellated sperm motility (GO:1901317)	44604	0.486094803	0.762493641
regulation of histone H3-K9 methylation (GO:0051570)	44604	0.486094803	0.762493641
regulation of leukocyte cell-cell adhesion (GO:1903037)	44604	0.486094803	0.762493641
regulation of oxidative stress-induced cell death (GO:190	44604	0.486094803	0.762493641
regulation of RNA export from nucleus (GO:0046831)	44604	0.486094803	0.762493641
regulation of vascular associated smooth muscle cell mig	44604	0.486094803	0.762493641
serine family amino acid biosynthetic process (GO:00090	44604	0.486094803	0.762493641
tricarboxylic acid metabolic process (GO:0072350)	44604	0.486094803	0.762493641
modulation of excitatory postsynaptic potential (GO:009	44678	0.489719421	0.762493641
negative regulation of plasma membrane bounded cell pi	44678	0.489719421	0.762493641
positive regulation of muscle cell differentiation (GO:005	44678	0.489719421	0.762493641
cell junction organization (GO:0034330)	26573	0.489923383	0.762493641
negative regulation of DNA recombination (GO:0045910)	21033	0.490173585	0.762493641
ceramide biosynthetic process (GO:0046513)	15493	0.490235861	0.762493641
regulation of nervous system development (GO:0051960	15493	0.490235861	0.762493641
lipid biosynthetic process (GO:0008610)	29526	0.4985318	0.762493641
regulation of translation (GO:0006417)	24/178	0.499173098	0.762493641
G protein-coupled receptor signaling pathway, coupled to	23986	0.499787379	0.762493641
positive regulation of ion transport (GO:0043270)	18445	0.501333751	0.762493641
lung development (GO:0030324)	12905	0.503374736	0.762493641
positive regulation of reproductive process (GO:2000243	12905	0.503374736	0.762493641
regulation of muscle cell differentiation (GO:0051147)	12905	0.503374736	0.762493641
regulation of trans-synaptic signaling (GO:0099177)	12905	0.503374736	0.762493641
respiratory system development (GO:0060541)	12905	0.503374736	0.762493641
retrograde transport, endosome to Golgi (GO:0042147)	32478	0.506327298	0.762493641
cardiac ventricle development (GO:0003231)	44640	0.50638421	0.762493641
cellular modified amino acid biosynthetic process (GO:00	44640	0.50638421	0.762493641
dopaminergic neuron differentiation (GO:0071542)	44640	0.50638421	0.762493641

inositol phosphate-mediated signaling (GO:0048016)	44640	0.50638421	0.762493641
natural killer cell mediated immunity (GO:0002228)	44640	0.50638421	0.762493641
negative regulation of cyclin-dependent protein serine/t	44640	0.50638421	0.762493641
negative regulation of osteoclast differentiation (GO:004	44640	0.50638421	0.762493641
negative regulation of telomere maintenance via telome	44640	0.50638421	0.762493641
positive regulation of epidermal cell differentiation (GO:(	44640	0.50638421	0.762493641
positive regulation of epithelial cell differentiation (GO:0(	44640	0.50638421	0.762493641
purine ribonucleoside monophosphate metabolic proces	44640	0.50638421	0.762493641
regulation of protein localization to cell periphery (GO:19	44640	0.50638421	0.762493641
regulation of smooth muscle contraction (GO:0006940)	44640	0.50638421	0.762493641
chromatin assembly (GO:0031497)	26938	0.508293846	0.762493641
5-phosphoribose 1-diphosphate biosynthetic process (GC	44566	0.509160816	0.762493641
5-phosphoribose 1-diphosphate metabolic process (GO:0	44566	0.509160816	0.762493641
adenosine 5'-(hexahydrogen pentaphosphate) catabolic p	44566	0.509160816	0.762493641
adenosine 5'-(hexahydrogen pentaphosphate) metabolic	44566	0.509160816	0.762493641
anterograde dendritic transport (GO:0098937)	44566	0.509160816	0.762493641
anterograde dendritic transport of neurotransmitter rece	44566	0.509160816	0.762493641
antigen processing and presentation of lipid antigen via M	44566	0.509160816	0.762493641
antigen processing and presentation, endogenous lipid ar	44566	0.509160816	0.762493641
antigen processing and presentation, exogenous lipid ant	44566	0.509160816	0.762493641
apoptotic chromosome condensation (GO:0030263)	44566	0.509160816	0.762493641
beta-catenin destruction complex assembly (GO:190488	44566	0.509160816	0.762493641
bile acid secretion (GO:0032782)	44566	0.509160816	0.762493641
C-terminal protein deglutamylation (GO:0035609)	44566	0.509160816	0.762493641
C-terminal protein lipidation (GO:0006501)	44566	0.509160816	0.762493641
cannabinoid signaling pathway (GO:0038171)	44566	0.509160816	0.762493641
cardiac endothelial cell differentiation (GO:0003348)	44566	0.509160816	0.762493641
cell fate commitment involved in formation of primary ge	44566	0.509160816	0.762493641
cellular response to antibiotic (GO:0071236)	44566	0.509160816	0.762493641
cellular response to erythropoietin (GO:0036018)	44566	0.509160816	0.762493641
cellular response to heparin (GO:0071504)	44566	0.509160816	0.762493641
cellular response to macrophage colony-stimulating factc	44566	0.509160816	0.762493641
cellular response to nutrient (GO:0031670)	44566	0.509160816	0.762493641
cellular response to testosterone stimulus (GO:0071394)	44566	0.509160816	0.762493641
cerebellar Purkinje cell differentiation (GO:0021702)	44566	0.509160816	0.762493641
cerebral cortex neuron differentiation (GO:0021895)	44566	0.509160816	0.762493641
chemokine (C-X-C motif) ligand 12 signaling pathway (GO	44566	0.509160816	0.762493641
cyclic-GMP-AMP transmembrane import across plasma n	44566	0.509160816	0.762493641
dephosphorylation of RNA polymerase II C-terminal dom	44566	0.509160816	0.762493641
determination of dorsal/ventral asymmetry (GO:004826	44566	0.509160816	0.762493641
diadenosine hexaphosphate catabolic process (GO:19019	44566	0.509160816	0.762493641
diadenosine hexaphosphate metabolic process (GO:1901	44566	0.509160816	0.762493641
diadenosine pentaphosphate catabolic process (GO:1901	44566	0.509160816	0.762493641
diadenosine pentaphosphate metabolic process (GO:190	44566	0.509160816	0.762493641
diaphragm development (GO:0060539)	44566	0.509160816	0.762493641
diphosphoinositol polyphosphate metabolic process (GO	44566	0.509160816	0.762493641
disaccharide biosynthetic process (GO:0046351)	44566	0.509160816	0.762493641

DNA protection (GO:0042262)	44566	0.509160816	0.762493641
dopamine biosynthetic process (GO:0042416)	44566	0.509160816	0.762493641
drug transport (GO:0015893)	44566	0.509160816	0.762493641
embryonic viscerocranium morphogenesis (GO:0048703)	44566	0.509160816	0.762493641
enamel mineralization (GO:0070166)	44566	0.509160816	0.762493641
endocardial cell differentiation (GO:0060956)	44566	0.509160816	0.762493641
endothelial cell apoptotic process (GO:0072577)	44566	0.509160816	0.762493641
establishment of monopolar cell polarity (GO:0061162)	44566	0.509160816	0.762493641
establishment of protein localization to telomere (GO:00	44566	0.509160816	0.762493641
exocyst localization (GO:0051601)	44566	0.509160816	0.762493641
extracellular exosome biogenesis (GO:0097734)	44566	0.509160816	0.762493641
female genitalia development (GO:0030540)	44566	0.509160816	0.762493641
forebrain regionalization (GO:0021871)	44566	0.509160816	0.762493641
fructose catabolic process (GO:0006001)	44566	0.509160816	0.762493641
fructose catabolic process to hydroxyacetone phosphate	44566	0.509160816	0.762493641
fructose transmembrane transport (GO:0015755)	44566	0.509160816	0.762493641
G protein-coupled opioid receptor signaling pathway (GO	44566	0.509160816	0.762493641
glial cell-derived neurotrophic factor receptor signaling p	44566	0.509160816	0.762493641
glucose-6-phosphate transport (GO:0015760)	44566	0.509160816	0.762493641
glucosylceramide metabolic process (GO:0006678)	44566	0.509160816	0.762493641
glutamate catabolic process (GO:0006538)	44566	0.509160816	0.762493641
glycerol biosynthetic process (GO:0006114)	44566	0.509160816	0.762493641
glycerol ether metabolic process (GO:0006662)	44566	0.509160816	0.762493641
hemoglobin metabolic process (GO:0020027)	44566	0.509160816	0.762493641
hexose phosphate transport (GO:0015712)	44566	0.509160816	0.762493641
histone-threonine phosphorylation (GO:0035405)	44566	0.509160816	0.762493641
insulin metabolic process (GO:1901142)	44566	0.509160816	0.762493641
intracellular distribution of mitochondria (GO:0048312)	44566	0.509160816	0.762493641
isocitrate metabolic process (GO:0006102)	44566	0.509160816	0.762493641
isopentenyl diphosphate biosynthetic process (GO:00092	44566	0.509160816	0.762493641
L-arginine import across plasma membrane (GO:009763	44566	0.509160816	0.762493641
leukotriene B4 metabolic process (GO:0036102)	44566	0.509160816	0.762493641
mammary gland duct morphogenesis (GO:0060603)	44566	0.509160816	0.762493641
mannose trimming involved in glycoprotein ERAD pathwa	44566	0.509160816	0.762493641
mature conventional dendritic cell differentiation (GO:00	44566	0.509160816	0.762493641
medium-chain fatty acid catabolic process (GO:0051793)	44566	0.509160816	0.762493641
membrane raft distribution (GO:0031580)	44566	0.509160816	0.762493641
menaquinone metabolic process (GO:0009233)	44566	0.509160816	0.762493641
metanephric mesenchymal cell differentiation (GO:0072	44566	0.509160816	0.762493641
mitochondrial RNA 3'-end processing (GO:0000965)	44566	0.509160816	0.762493641
modulation by symbiont of host autophagy (GO:0075071	44566	0.509160816	0.762493641
mRNA 3'-end processing by stem-loop binding and cleava	44566	0.509160816	0.762493641
negative regulation of adaptive immune response (GO:0(	44566	0.509160816	0.762493641
negative regulation of autophagosome maturation (GO:1	44566	0.509160816	0.762493641
negative regulation of B cell differentiation (GO:0045578	44566	0.509160816	0.762493641
negative regulation of cellular respiration (GO:1901856)	44566	0.509160816	0.762493641
negative regulation of ceramide biosynthetic process (GC	44566	0.509160816	0.762493641

negative regulation of dendritic cell differentiation (GO:2	44566	0.509160816	0.762493641
negative regulation of histone deacetylation (GO:003106	44566	0.509160816	0.762493641
negative regulation of interferon-alpha production (GO:0	44566	0.509160816	0.762493641
negative regulation of leukocyte adhesion to vascular en	44566	0.509160816	0.762493641
negative regulation of leukocyte differentiation (GO:1902	44566	0.509160816	0.762493641
negative regulation of macrophage chemotaxis (GO:0010	44566	0.509160816	0.762493641
negative regulation of macrophage cytokine production (	44566	0.509160816	0.762493641
negative regulation of macrophage differentiation (GO:0	44566	0.509160816	0.762493641
negative regulation of organelle organization (GO:00106	44566	0.509160816	0.762493641
negative regulation of oxidative stress-induced neuron in	44566	0.509160816	0.762493641
negative regulation of plasminogen activation (GO:00107	44566	0.509160816	0.762493641
negative regulation of protein acetylation (GO:1901984)	44566	0.509160816	0.762493641
negative regulation of protein polyubiquitination (GO:19	44566	0.509160816	0.762493641
negative regulation of regulatory T cell differentiation (G	44566	0.509160816	0.762493641
negative regulation of smooth muscle contraction (GO:0	44566	0.509160816	0.762493641
negative regulation of synapse organization (GO:190580	44566	0.509160816	0.762493641
negative regulation of tubulin deacetylation (GO:190442	44566	0.509160816	0.762493641
nucleoside transport (GO:0015858)	44566	0.509160816	0.762493641
nucleoside triphosphate catabolic process (GO:0009143)	44566	0.509160816	0.762493641
oocyte development (GO:0048599)	44566	0.509160816	0.762493641
oxaloacetate transport (GO:0015729)	44566	0.509160816	0.762493641
oxidative DNA demethylation (GO:0035511)	44566	0.509160816	0.762493641
peptidyl-lysine oxidation (GO:0018057)	44566	0.509160816	0.762493641
peristalsis (GO:0030432)	44566	0.509160816	0.762493641
phenol-containing compound metabolic process (GO:001	44566	0.509160816	0.762493641
PML body organization (GO:0030578)	44566	0.509160816	0.762493641
positive regulation by host of viral genome replication (G	44566	0.509160816	0.762493641
positive regulation of 3'-UTR-mediated mRNA stabilizatio	44566	0.509160816	0.762493641
positive regulation of amine transport (GO:0051954)	44566	0.509160816	0.762493641
positive regulation of AMPA receptor activity (GO:20009	44566	0.509160816	0.762493641
positive regulation of anoikis (GO:2000210)	44566	0.509160816	0.762493641
positive regulation of basement membrane assembly inv	44566	0.509160816	0.762493641
positive regulation of bicellular tight junction assembly (G	44566	0.509160816	0.762493641
positive regulation of cAMP-dependent protein kinase ac	44566	0.509160816	0.762493641
positive regulation of cardiac muscle contraction (GO:00	44566	0.509160816	0.762493641
positive regulation of dendritic cell differentiation (GO:2	44566	0.509160816	0.762493641
positive regulation of deoxyribonuclease activity (GO:003	44566	0.509160816	0.762493641
positive regulation of DNA ligation (GO:0051106)	44566	0.509160816	0.762493641
positive regulation of dopamine receptor signaling pathw	44566	0.509160816	0.762493641
positive regulation of endothelial cell-matrix adhesion via	44566	0.509160816	0.762493641
positive regulation of epithelial to mesenchymal transitio	44566	0.509160816	0.762493641
positive regulation of feeding behavior (GO:2000253)	44566	0.509160816	0.762493641
positive regulation of fertilization (GO:1905516)	44566	0.509160816	0.762493641
positive regulation of fibroblast growth factor receptor si	44566	0.509160816	0.762493641
positive regulation of gamma-delta T cell activation (GO:0	44566	0.509160816	0.762493641
positive regulation of Golgi to plasma membrane protein	44566	0.509160816	0.762493641
positive regulation of histone H3-K9 acetylation (GO:200	44566	0.509160816	0.762493641

positive regulation of intrinsic apoptotic signaling pathwa	44566	0.509160816	0.762493641
positive regulation of long-term synaptic depression (GO:	44566	0.509160816	0.762493641
positive regulation of low-density lipoprotein receptor ac	44566	0.509160816	0.762493641
positive regulation of macrophage proliferation (GO:012(	44566	0.509160816	0.762493641
positive regulation of maintenance of mitotic sister chror	44566	0.509160816	0.762493641
positive regulation of maintenance of sister chromatid co	44566	0.509160816	0.762493641
positive regulation of membrane permeability (GO:19057	44566	0.509160816	0.762493641
positive regulation of myoblast proliferation (GO:200028	44566	0.509160816	0.762493641
positive regulation of neurotransmitter transport (GO:00	44566	0.509160816	0.762493641
positive regulation of neutrophil extravasation (GO:2000	44566	0.509160816	0.762493641
positive regulation of nucleobase-containing compound t	44566	0.509160816	0.762493641
positive regulation of prostaglandin secretion (GO:00323	44566	0.509160816	0.762493641
positive regulation of protein localization to cell cortex (G	44566	0.509160816	0.762493641
positive regulation of protein monoubiquitination (GO:19	44566	0.509160816	0.762493641
positive regulation of protein neddylation (GO:2000436)	44566	0.509160816	0.762493641
positive regulation of RNA export from nucleus (GO:0046	44566	0.509160816	0.762493641
positive regulation of the force of heart contraction (GO:(	44566	0.509160816	0.762493641
positive regulation of translation in response to stress (G	44566	0.509160816	0.762493641
postsynaptic density protein 95 clustering (GO:0097119)	44566	0.509160816	0.762493641
protein deglycosylation involved in glycoprotein catabolic	44566	0.509160816	0.762493641
protein K29-linked deubiquitination (GO:0035523)	44566	0.509160816	0.762493641
protein localization to microtubule end (GO:1905725)	44566	0.509160816	0.762493641
protein localization to microtubule plus-end (GO:190482	44566	0.509160816	0.762493641
protein localization to site of double-strand break (GO:19	44566	0.509160816	0.762493641
pulmonary artery morphogenesis (GO:0061156)	44566	0.509160816	0.762493641
pyrimidine deoxyribonucleotide biosynthetic process (GC	44566	0.509160816	0.762493641
pyrimidine nucleoside transport (GO:0015864)	44566	0.509160816	0.762493641
pyrimidine nucleotide metabolic process (GO:0006220)	44566	0.509160816	0.762493641
receptor transactivation (GO:0035624)	44566	0.509160816	0.762493641
reelin-mediated signaling pathway (GO:0038026)	44566	0.509160816	0.762493641
regulation of adherens junction organization (GO:190339	44566	0.509160816	0.762493641
regulation of basement membrane assembly involved in	44566	0.509160816	0.762493641
regulation of cell proliferation involved in heart morphog	44566	0.509160816	0.762493641
regulation of cellular response to vascular endothelial gro	44566	0.509160816	0.762493641
regulation of cytochrome-c oxidase activity (GO:1904959	44566	0.509160816	0.762493641
regulation of endothelial tube morphogenesis (GO:19015	44566	0.509160816	0.762493641
regulation of glomerular mesangial cell proliferation (GO:	44566	0.509160816	0.762493641
regulation of glycoprotein metabolic process (GO:190301	44566	0.509160816	0.762493641
regulation of growth hormone receptor signaling pathwa	44566	0.509160816	0.762493641
regulation of guanylate cyclase activity (GO:0031282)	44566	0.509160816	0.762493641
regulation of heart growth (GO:0060420)	44566	0.509160816	0.762493641
regulation of hippocampal neuron apoptotic process (GO	44566	0.509160816	0.762493641
regulation of homophilic cell adhesion (GO:1903385)	44566	0.509160816	0.762493641
regulation of integrin biosynthetic process (GO:0045113)	44566	0.509160816	0.762493641
regulation of interleukin-1 alpha production (GO:003265(	44566	0.509160816	0.762493641
regulation of low-density lipoprotein particle receptor ca	44566	0.509160816	0.762493641
regulation of maintenance of mitotic sister chromatid col	44566	0.509160816	0.762493641

regulation of metaphase plate congression (GO:0090235)	44566	0.509160816	0.762493641
regulation of microglial cell mediated cytotoxicity (GO:19	44566	0.509160816	0.762493641
regulation of morphogenesis of a branching structure (GO	44566	0.509160816	0.762493641
regulation of mRNA binding (GO:1902415)	44566	0.509160816	0.762493641
regulation of myoblast proliferation (GO:2000291)	44566	0.509160816	0.762493641
regulation of natural killer cell differentiation (GO:00328	44566	0.509160816	0.762493641
regulation of neutrophil degranulation (GO:0043313)	44566	0.509160816	0.762493641
regulation of plasma membrane organization (GO:19037	44566	0.509160816	0.762493641
regulation of protein monoubiquitination (GO:1902525)	44566	0.509160816	0.762493641
regulation of respiratory gaseous exchange by nervous sy	44566	0.509160816	0.762493641
regulation of ribonuclease activity (GO:0060700)	44566	0.509160816	0.762493641
regulation of skeletal muscle tissue development (GO:00	44566	0.509160816	0.762493641
regulation of snRNA transcription by RNA polymerase II (	44566	0.509160816	0.762493641
regulation of sterol transport (GO:0032371)	44566	0.509160816	0.762493641
regulation of triglyceride metabolic process (GO:0090207	44566	0.509160816	0.762493641
renal tubule development (GO:0061326)	44566	0.509160816	0.762493641
response to cocaine (GO:0042220)	44566	0.509160816	0.762493641
response to denervation involved in regulation of muscle	44566	0.509160816	0.762493641
response to macrophage colony-stimulating factor (GO:0	44566	0.509160816	0.762493641
response to mitochondrial depolarisation (GO:0098780)	44566	0.509160816	0.762493641
response to morphine (GO:0043278)	44566	0.509160816	0.762493641
retina vasculature development in camera-type eye (GO:	44566	0.509160816	0.762493641
ribosome localization (GO:0033750)	44566	0.509160816	0.762493641
RNA import into mitochondrion (GO:0035927)	44566	0.509160816	0.762493641
rRNA transport (GO:0051029)	44566	0.509160816	0.762493641
sensory perception of sour taste (GO:0050915)	44566	0.509160816	0.762493641
serotonin metabolic process (GO:0042428)	44566	0.509160816	0.762493641
stress granule disassembly (GO:0035617)	44566	0.509160816	0.762493641
thorax and anterior abdomen determination (GO:000735	44566	0.509160816	0.762493641
tight junction organization (GO:0120193)	44566	0.509160816	0.762493641
tonic smooth muscle contraction (GO:0014820)	44566	0.509160816	0.762493641
trophoblast giant cell differentiation (GO:0060707)	44566	0.509160816	0.762493641
ubiquitin-dependent glycoprotein ERAD pathway (GO:00	44566	0.509160816	0.762493641
ubiquitin-dependent SMAD protein catabolic process (GO	44566	0.509160816	0.762493641
ubiquitin-independent protein catabolic process via the n	44566	0.509160816	0.762493641
uridine transport (GO:0015862)	44566	0.509160816	0.762493641
vascular endothelial growth factor receptor-2 signaling p	44566	0.509160816	0.762493641
vesicle tethering to Golgi (GO:0099041)	44566	0.509160816	0.762493641
vitamin D3 metabolic process (GO:0070640)	44566	0.509160816	0.762493641
zygotic determination of anterior/posterior axis, embryo	44566	0.509160816	0.762493641
zymogen inhibition (GO:0097341)	44566	0.509160816	0.762493641
negative regulation of hydrolase activity (GO:0051346)	21398	0.510792104	0.764495817
RNA modification (GO:0009451)	21398	0.510792104	0.764495817
anion transport (GO:0006820)	15858	0.514206222	0.768941084
lipid modification (GO:0030258)	15858	0.514206222	0.768941084
spermatid development (GO:0007286)	15858	0.514206222	0.768941084
cellular component disassembly (GO:0022411)	24351	0.519073255	0.773517746

extracellular matrix disassembly (GO:0022617)	24351	0.519073255	0.773517746
negative regulation of G2/M transition of mitotic cell cyc	24351	0.519073255	0.773517746
amide transport (GO:0042886)	44679	0.519500176	0.773517746
calcium ion import (GO:0070509)	44679	0.519500176	0.773517746
carbohydrate derivative biosynthetic process (GO:19011	44679	0.519500176	0.773517746
cellular zinc ion homeostasis (GO:0006882)	44679	0.519500176	0.773517746
cytosolic calcium ion transport (GO:0060401)	44679	0.519500176	0.773517746
positive regulation of synapse assembly (GO:0051965)	44679	0.519500176	0.773517746
protein localization to Golgi apparatus (GO:0034067)	44679	0.519500176	0.773517746
receptor clustering (GO:0043113)	44679	0.519500176	0.773517746
regulation of muscle contraction (GO:0006937)	44679	0.519500176	0.773517746
regulation of reactive oxygen species biosynthetic proces	44679	0.519500176	0.773517746
sulfur compound transport (GO:0072348)	44679	0.519500176	0.773517746
transcription by RNA polymerase III (GO:0006383)	44679	0.519500176	0.773517746
SCF-dependent proteasomal ubiquitin-dependent protein	32843	0.522910307	0.778372219
regulation of cellular amine metabolic process (GO:0033	18810	0.523272471	0.778465203
sensory perception (GO:0007600)	18810	0.523272471	0.778465203
sphingolipid biosynthetic process (GO:0030148)	27303	0.526468466	0.780118505
aortic valve development (GO:0003176)	13271	0.529494126	0.780118505
dendrite morphogenesis (GO:0048813)	13271	0.529494126	0.780118505
negative regulation of DNA metabolic process (GO:00510	13271	0.529494126	0.780118505
negative regulation of fat cell differentiation (GO:004559	13271	0.529494126	0.780118505
regulation of androgen receptor signaling pathway (GO:0	13271	0.529494126	0.780118505
cardiac cell development (GO:0055006)	44605	0.530240316	0.780118505
cellular component maintenance (GO:0043954)	44605	0.530240316	0.780118505
chondroitin sulfate catabolic process (GO:0030207)	44605	0.530240316	0.780118505
cytoplasmic sequestering of protein (GO:0051220)	44605	0.530240316	0.780118505
embryonic hemopoiesis (GO:0035162)	44605	0.530240316	0.780118505
Golgi ribbon formation (GO:0090161)	44605	0.530240316	0.780118505
mitochondrial outer membrane permeabilization (GO:00	44605	0.530240316	0.780118505
muscle tissue development (GO:0060537)	44605	0.530240316	0.780118505
myelination in peripheral nervous system (GO:0022011)	44605	0.530240316	0.780118505
negative regulation of adenylate cyclase activity (GO:000	44605	0.530240316	0.780118505
negative regulation of chromatin organization (GO:19052	44605	0.530240316	0.780118505
negative regulation of chromatin silencing (GO:0031936)	44605	0.530240316	0.780118505
negative regulation of gene silencing (GO:0060969)	44605	0.530240316	0.780118505
negative regulation of locomotion (GO:0040013)	44605	0.530240316	0.780118505
negative regulation of macromolecule biosynthetic proce	44605	0.530240316	0.780118505
negative regulation of mononuclear cell migration (GO:0	44605	0.530240316	0.780118505
negative regulation of myoblast differentiation (GO:0045	44605	0.530240316	0.780118505
negative regulation of potassium ion transport (GO:0043	44605	0.530240316	0.780118505
negative regulation of reactive oxygen species biosynthet	44605	0.530240316	0.780118505
negative regulation of stem cell differentiation (GO:2000	44605	0.530240316	0.780118505
plasma membrane tubulation (GO:0097320)	44605	0.530240316	0.780118505
poly-N-acetyllactosamine metabolic process (GO:003030	44605	0.530240316	0.780118505
polyamine metabolic process (GO:0006595)	44605	0.530240316	0.780118505
positive regulation of calcium ion import (GO:0090280)	44605	0.530240316	0.780118505

positive regulation of cellular carbohydrate metabolic pr	44605	0.530240316	0.780118505
pseudouridine synthesis (GO:0001522)	44605	0.530240316	0.780118505
pteridine-containing compound metabolic process (GO:0	44605	0.530240316	0.780118505
regulation of actomyosin structure organization (GO:011	44605	0.530240316	0.780118505
regulation of cell aging (GO:0090342)	44605	0.530240316	0.780118505
regulation of short-term neuronal synaptic plasticity (GO	44605	0.530240316	0.780118505
regulation of tube diameter (GO:0035296)	44605	0.530240316	0.780118505
UV-damage excision repair (GO:0070914)	44605	0.530240316	0.780118505
vascular process in circulatory system (GO:0003018)	44605	0.530240316	0.780118505
ephrin receptor signaling pathway (GO:0048013)	30256	0.533172586	0.784210527
embryonic organ morphogenesis (GO:0048562)	16224	0.537732935	0.789264492
neurogenesis (GO:0022008)	16224	0.537732935	0.789264492
positive regulation of osteoblast differentiation (GO:004	16224	0.537732935	0.789264492
positive regulation of potassium ion transmembrane tran	16224	0.537732935	0.789264492
transcription elongation from RNA polymerase II promot	24716	0.538108385	0.789264492
cellular amino acid catabolic process (GO:0009063)	33208	0.539322173	0.789264492
cyclic purine nucleotide metabolic process (GO:0052652)	44641	0.5406304	0.789264492
intracellular lipid transport (GO:0032365)	44641	0.5406304	0.789264492
mitochondrial calcium ion transmembrane transport (GO	44641	0.5406304	0.789264492
negative regulation of ion transmembrane transporter ac	44641	0.5406304	0.789264492
negative regulation of microtubule depolymerization (GC	44641	0.5406304	0.789264492
negative regulation of protein localization to cell periphe	44641	0.5406304	0.789264492
negative regulation of protein localization to plasma mem	44641	0.5406304	0.789264492
negative regulation of small GTPase mediated signal tran	44641	0.5406304	0.789264492
regulation of cell-substrate junction assembly (GO:00901	44641	0.5406304	0.789264492
regulation of mitochondrial translation (GO:0070129)	44641	0.5406304	0.789264492
response to progesterone (GO:0032570)	44641	0.5406304	0.789264492
rRNA modification (GO:0000154)	44641	0.5406304	0.789264492
stress granule assembly (GO:0034063)	44641	0.5406304	0.789264492
ameboidal-type cell migration (GO:0001667)	19176	0.544838452	0.789264492
positive regulation of developmental growth (GO:004863	19176	0.544838452	0.789264492
RNA splicing (GO:0008380)	13/98	0.545016552	0.789264492
aggrephagy (GO:0035973)	44680	0.54843063	0.789264492
negative regulation of mRNA catabolic process (GO:1902	44680	0.54843063	0.789264492
positive regulation of viral genome replication (GO:0045	44680	0.54843063	0.789264492
response to zinc ion (GO:0010043)	44680	0.54843063	0.789264492
regulation of osteoblast differentiation (GO:0045667)	30621	0.550191986	0.789264492
chromosome organization (GO:0051276)	14/106	0.550330184	0.789264492
glutamate receptor signaling pathway (GO:0007215)	13636	0.55498094	0.789264492
regulation of transport (GO:0051049)	13636	0.55498094	0.789264492
skeletal muscle tissue development (GO:0007519)	13636	0.55498094	0.789264492
regulation of stem cell differentiation (GO:2000736)	33573	0.555539129	0.789264492
regulation of cell division (GO:0051302)	28034	0.562103777	0.789264492
water-soluble vitamin metabolic process (GO:0006767)	28034	0.562103777	0.789264492
regulation of DNA replication (GO:0006275)	19541	0.565983645	0.789264492
cellular protein localization (GO:0034613)	43/329	0.566797621	0.789264492
O-glycan processing (GO:0016266)	22494	0.570799254	0.789264492

bone morphogenesis (GO:0060349)	44606	0.571721384	0.789264492
C4-dicarboxylate transport (GO:0015740)	44606	0.571721384	0.789264492
calcium ion import across plasma membrane (GO:00987(	44606	0.571721384	0.789264492
cellular copper ion homeostasis (GO:0006878)	44606	0.571721384	0.789264492
ceramide transport (GO:0035627)	44606	0.571721384	0.789264492
coenzyme A metabolic process (GO:0015936)	44606	0.571721384	0.789264492
endothelial cell differentiation (GO:0045446)	44606	0.571721384	0.789264492
genitalia development (GO:0048806)	44606	0.571721384	0.789264492
membrane repolarization during action potential (GO:00	44606	0.571721384	0.789264492
monoacylglycerol metabolic process (GO:0046462)	44606	0.571721384	0.789264492
negative regulation of cell migration involved in sproutin	44606	0.571721384	0.789264492
negative regulation of coagulation (GO:0050819)	44606	0.571721384	0.789264492
negative regulation of cyclase activity (GO:0031280)	44606	0.571721384	0.789264492
negative regulation of pri-miRNA transcription by RNA pc	44606	0.571721384	0.789264492
negative regulation of T cell mediated immunity (GO:000	44606	0.571721384	0.789264492
negative regulation of TORC1 signaling (GO:1904262)	44606	0.571721384	0.789264492
negative regulation of translational initiation (GO:004594	44606	0.571721384	0.789264492
neuromuscular process controlling balance (GO:0050885	44606	0.571721384	0.789264492
nuclear pore organization (GO:0006999)	44606	0.571721384	0.789264492
nucleoside phosphate biosynthetic process (GO:1901293	44606	0.571721384	0.789264492
nucleoside triphosphate metabolic process (GO:0009141	44606	0.571721384	0.789264492
positive regulation of alpha-beta T cell differentiation (G(	44606	0.571721384	0.789264492
positive regulation of glucose metabolic process (GO:001	44606	0.571721384	0.789264492
positive regulation of glycoprotein biosynthetic process (	44606	0.571721384	0.789264492
positive regulation of macrophage chemotaxis (GO:0010	44606	0.571721384	0.789264492
positive regulation of potassium ion transmembrane tran	44606	0.571721384	0.789264492
positive regulation of protein deacetylation (GO:0090312	44606	0.571721384	0.789264492
positive regulation of SMAD protein signal transduction (	44606	0.571721384	0.789264492
protein localization to vacuole (GO:0072665)	44606	0.571721384	0.789264492
pyrimidine nucleoside biosynthetic process (GO:0046134	44606	0.571721384	0.789264492
regulation of integrin-mediated signaling pathway (GO:2(	44606	0.571721384	0.789264492
regulation of lamellipodium organization (GO:1902743)	44606	0.571721384	0.789264492
regulation of vasculogenesis (GO:2001212)	44606	0.571721384	0.789264492
ribonucleoside monophosphate biosynthetic process (GC	44606	0.571721384	0.789264492
sequestering of extracellular ligand from receptor (GO:0(	44606	0.571721384	0.789264492
tRNA wobble base modification (GO:0002097)	44606	0.571721384	0.789264492
vasodilation (GO:0042311)	44606	0.571721384	0.789264492
ribosome biogenesis (GO:0042254)	25/192	0.572281691	0.789264492
regulation of mRNA stability (GO:0043488)	19/146	0.572822863	0.789264492
cellular response to osmotic stress (GO:0071470)	44642	0.573460914	0.789264492
fatty-acyl-CoA metabolic process (GO:0035337)	44642	0.573460914	0.789264492
lipid droplet organization (GO:0034389)	44642	0.573460914	0.789264492
mRNA modification (GO:0016556)	44642	0.573460914	0.789264492
negative regulation of myeloid cell differentiation (GO:0(	44642	0.573460914	0.789264492
negative regulation of protein dephosphorylation (GO:00	44642	0.573460914	0.789264492
negative regulation of small molecule metabolic process	44642	0.573460914	0.789264492
phosphatidylserine acyl-chain remodeling (GO:0036150)	44642	0.573460914	0.789264492

positive regulation of calcium ion transmembrane transp	44642	0.573460914	0.789264492
regulation of adenylate cyclase activity (GO:0045761)	44642	0.573460914	0.789264492
regulation of execution phase of apoptosis (GO:1900117)	44642	0.573460914	0.789264492
activation of transmembrane receptor protein tyrosine ki	44567	0.574286772	0.789264492
alditol metabolic process (GO:0019400)	44567	0.574286772	0.789264492
amino-acid betaine transport (GO:0015838)	44567	0.574286772	0.789264492
aminophospholipid transport (GO:0015917)	44567	0.574286772	0.789264492
amylin receptor signaling pathway (GO:0097647)	44567	0.574286772	0.789264492
aspartate metabolic process (GO:0006531)	44567	0.574286772	0.789264492
blood vessel endothelial cell proliferation involved in spr	44567	0.574286772	0.789264492
carnitine transport (GO:0015879)	44567	0.574286772	0.789264492
cellular hyperosmotic response (GO:0071474)	44567	0.574286772	0.789264492
cellular response to cold (GO:0070417)	44567	0.574286772	0.789264492
cellular response to granulocyte macrophage colony-stim	44567	0.574286772	0.789264492
cellular response to iron ion (GO:0071281)	44567	0.574286772	0.789264492
cellular response to X-ray (GO:0071481)	44567	0.574286772	0.789264492
cellular water homeostasis (GO:0009992)	44567	0.574286772	0.789264492
cholesterol import (GO:0070508)	44567	0.574286772	0.789264492
choline transport (GO:0015871)	44567	0.574286772	0.789264492
dermatan sulfate proteoglycan metabolic process (GO:00	44567	0.574286772	0.789264492
diadenosine polyphosphate catabolic process (GO:00159	44567	0.574286772	0.789264492
double-strand break repair via classical nonhomologous e	44567	0.574286772	0.789264492
embryonic hindlimb morphogenesis (GO:0035116)	44567	0.574286772	0.789264492
embryonic skeletal joint development (GO:0072498)	44567	0.574286772	0.789264492
enzyme-directed rRNA pseudouridine synthesis (GO:000	44567	0.574286772	0.789264492
epithelial tube branching involved in lung morphogenesis	44567	0.574286772	0.789264492
erythrose 4-phosphate/phosphoenolpyruvate family ami	44567	0.574286772	0.789264492
establishment of planar polarity (GO:0001736)	44567	0.574286772	0.789264492
foam cell differentiation (GO:0090077)	44567	0.574286772	0.789264492
free ubiquitin chain polymerization (GO:0010994)	44567	0.574286772	0.789264492
gastrulation with mouth forming second (GO:0001702)	44567	0.574286772	0.789264492
glandular epithelial cell differentiation (GO:0002067)	44567	0.574286772	0.789264492
glomerular epithelial cell differentiation (GO:0072311)	44567	0.574286772	0.789264492
glomerulus vasculature development (GO:0072012)	44567	0.574286772	0.789264492
glycerol-3-phosphate metabolic process (GO:0006072)	44567	0.574286772	0.789264492
glycolipid transport (GO:0046836)	44567	0.574286772	0.789264492
glycosylceramide catabolic process (GO:0046477)	44567	0.574286772	0.789264492
glycosylceramide metabolic process (GO:0006677)	44567	0.574286772	0.789264492
growth hormone secretion (GO:0030252)	44567	0.574286772	0.789264492
guanine nucleotide transmembrane transport (GO:19037	44567	0.574286772	0.789264492
hepatocyte differentiation (GO:0070365)	44567	0.574286772	0.789264492
histamine metabolic process (GO:0001692)	44567	0.574286772	0.789264492
hydrogen peroxide biosynthetic process (GO:0050665)	44567	0.574286772	0.789264492
hydrogen sulfide metabolic process (GO:0070813)	44567	0.574286772	0.789264492
indolalkylamine metabolic process (GO:0006586)	44567	0.574286772	0.789264492
inner ear auditory receptor cell differentiation (GO:0042	44567	0.574286772	0.789264492
L-serine biosynthetic process (GO:0006564)	44567	0.574286772	0.789264492

macromolecule biosynthetic process (GO:0009059)	44567	0.574286772	0.789264492
macrophage derived foam cell differentiation (GO:00107	44567	0.574286772	0.789264492
maintenance of DNA repeat elements (GO:0043570)	44567	0.574286772	0.789264492
medium-chain fatty acid biosynthetic process (GO:00517	44567	0.574286772	0.789264492
meiotic DNA double-strand break formation (GO:004213	44567	0.574286772	0.789264492
mesenchymal cell differentiation involved in kidney deve	44567	0.574286772	0.789264492
mesodermal cell fate commitment (GO:0001710)	44567	0.574286772	0.789264492
metaphase/anaphase transition of cell cycle (GO:004478	44567	0.574286772	0.789264492
metaphase/anaphase transition of mitotic cell cycle (GO:	44567	0.574286772	0.789264492
mRNA 5'-splice site recognition (GO:0000395)	44567	0.574286772	0.789264492
negative regulation of anion transport (GO:1903792)	44567	0.574286772	0.789264492
negative regulation of astrocyte differentiation (GO:0048	44567	0.574286772	0.789264492
negative regulation of endoplasmic reticulum calcium ior	44567	0.574286772	0.789264492
negative regulation of ERAD pathway (GO:1904293)	44567	0.574286772	0.789264492
negative regulation of erythrocyte differentiation (GO:00	44567	0.574286772	0.789264492
negative regulation of establishment of protein localizati	44567	0.574286772	0.789264492
negative regulation of excitatory postsynaptic potential (	44567	0.574286772	0.789264492
negative regulation of fat cell proliferation (GO:0070345)	44567	0.574286772	0.789264492
negative regulation of glial cell proliferation (GO:006025	44567	0.574286772	0.789264492
negative regulation of glucocorticoid receptor signaling p	44567	0.574286772	0.789264492
negative regulation of glycogen biosynthetic process (GO	44567	0.574286772	0.789264492
negative regulation of hematopoietic progenitor cell diffe	44567	0.574286772	0.789264492
negative regulation of histone H3-K9 methylation (GO:00	44567	0.574286772	0.789264492
negative regulation of meiotic cell cycle (GO:0051447)	44567	0.574286772	0.789264492
negative regulation of morphogenesis of an epithelium ((	44567	0.574286772	0.789264492
negative regulation of neuron migration (GO:2001223)	44567	0.574286772	0.789264492
negative regulation of SMAD protein signal transduction	44567	0.574286772	0.789264492
negative regulation of T cell differentiation in thymus (GC	44567	0.574286772	0.789264492
negative regulation of triglyceride metabolic process (GO	44567	0.574286772	0.789264492
nephron tubule development (GO:0072080)	44567	0.574286772	0.789264492
neurotransmitter receptor transport, endosome to posts	44567	0.574286772	0.789264492
peptidyl-diphthamide biosynthetic process from peptidyl	44567	0.574286772	0.789264492
peptidyl-diphthamide metabolic process (GO:0017182)	44567	0.574286772	0.789264492
peptidyl-glutamine methylation (GO:0018364)	44567	0.574286772	0.789264492
peroxisome proliferator activated receptor signaling path	44567	0.574286772	0.789264492
piRNA biosynthetic process (GO:1990511)	44567	0.574286772	0.789264492
plasma membrane raft assembly (GO:0044854)	44567	0.574286772	0.789264492
positive regulation of activin receptor signaling pathway	44567	0.574286772	0.789264492
positive regulation of anion transport (GO:1903793)	44567	0.574286772	0.789264492
positive regulation of autophagosome maturation (GO:19	44567	0.574286772	0.789264492
positive regulation of autophagy of mitochondrion in res	44567	0.574286772	0.789264492
positive regulation of cell-cell adhesion mediated by inte	44567	0.574286772	0.789264492
positive regulation of endothelial cell development (GO:1	44567	0.574286772	0.789264492
positive regulation of epithelial cell differentiation involv	44567	0.574286772	0.789264492
positive regulation of establishment of endothelial barrie	44567	0.574286772	0.789264492
positive regulation of extrinsic apoptotic signaling pathw	44567	0.574286772	0.789264492
positive regulation of ion transmembrane transport (GO:	44567	0.574286772	0.789264492

positive regulation of lipoprotein particle clearance (GO:(	44567	0.574286772	0.789264492
positive regulation of microglial cell activation (GO:19035	44567	0.574286772	0.789264492
positive regulation of neurotransmitter secretion (GO:00(	44567	0.574286772	0.789264492
positive regulation of protein glycosylation (GO:0060050)	44567	0.574286772	0.789264492
positive regulation of RNA binding (GO:1905216)	44567	0.574286772	0.789264492
positive regulation of skeletal muscle fiber development	44567	0.574286772	0.789264492
positive regulation of toll-like receptor 2 signaling pathwa	44567	0.574286772	0.789264492
positive regulation of Wnt signaling pathway, planar cell	44567	0.574286772	0.789264492
postsynaptic density assembly (GO:0097107)	44567	0.574286772	0.789264492
presynaptic active zone organization (GO:1990709)	44567	0.574286772	0.789264492
pronephros development (GO:0048793)	44567	0.574286772	0.789264492
protection from natural killer cell mediated cytotoxicity (	44567	0.574286772	0.789264492
protein deubiquitination involved in ubiquitin-dependent	44567	0.574286772	0.789264492
protein K27-linked ubiquitination (GO:0044314)	44567	0.574286772	0.789264492
protein localization to non-motile cilium (GO:0097499)	44567	0.574286772	0.789264492
protein localization to perinuclear region of cytoplasm (G	44567	0.574286772	0.789264492
protein repair (GO:0030091)	44567	0.574286772	0.789264492
protein-DNA covalent cross-linking repair (GO:0106300)	44567	0.574286772	0.789264492
proton-transporting V-type ATPase complex assembly (G	44567	0.574286772	0.789264492
purine deoxyribonucleotide catabolic process (GO:00091	44567	0.574286772	0.789264492
regulation of 3'-UTR-mediated mRNA stabilization (GO:19	44567	0.574286772	0.789264492
regulation of digestive system process (GO:0044058)	44567	0.574286772	0.789264492
regulation of endoplasmic reticulum tubular network org	44567	0.574286772	0.789264492
regulation of endothelial cell-matrix adhesion via fibrone	44567	0.574286772	0.789264492
regulation of excitatory synapse assembly (GO:1904889)	44567	0.574286772	0.789264492
regulation of glomerular filtration (GO:0003093)	44567	0.574286772	0.789264492
regulation of glucagon secretion (GO:0070092)	44567	0.574286772	0.789264492
regulation of glucokinase activity (GO:0033131)	44567	0.574286772	0.789264492
regulation of glutamate receptor signaling pathway (GO:1	44567	0.574286772	0.789264492
regulation of hepatocyte proliferation (GO:2000345)	44567	0.574286772	0.789264492
regulation of hyaluronan biosynthetic process (GO:19001	44567	0.574286772	0.789264492
regulation of hydrogen peroxide metabolic process (GO:(	44567	0.574286772	0.789264492
regulation of long-chain fatty acid import across plasma r	44567	0.574286772	0.789264492
regulation of macrophage proliferation (GO:0120040)	44567	0.574286772	0.789264492
regulation of mitotic sister chromatid segregation (GO:0(	44567	0.574286772	0.789264492
regulation of mitotic spindle checkpoint (GO:1903504)	44567	0.574286772	0.789264492
regulation of mRNA export from nucleus (GO:0010793)	44567	0.574286772	0.789264492
regulation of nitric oxide mediated signal transduction (G	44567	0.574286772	0.789264492
regulation of nuclease activity (GO:0032069)	44567	0.574286772	0.789264492
regulation of protein depolymerization (GO:1901879)	44567	0.574286772	0.789264492
regulation of protein lipidation (GO:1903059)	44567	0.574286772	0.789264492
regulation of relaxation of cardiac muscle (GO:1901897)	44567	0.574286772	0.789264492
regulation of retrograde transport, endosome to Golgi (G	44567	0.574286772	0.789264492
regulation of ribonucleoprotein complex localization (GO	44567	0.574286772	0.789264492
regulation of saliva secretion (GO:0046877)	44567	0.574286772	0.789264492
regulation of SNARE complex assembly (GO:0035542)	44567	0.574286772	0.789264492
regulation of T-helper cell differentiation (GO:0045622)	44567	0.574286772	0.789264492

regulation of thymocyte apoptotic process (GO:0070243)	44567	0.574286772	0.789264492
regulation of tooth mineralization (GO:0070170)	44567	0.574286772	0.789264492
regulation of translational elongation (GO:0006448)	44567	0.574286772	0.789264492
regulation of transmission of nerve impulse (GO:005196	44567	0.574286772	0.789264492
regulation of ventricular cardiac muscle cell membrane d	44567	0.574286772	0.789264492
regulation of very-low-density lipoprotein particle remod	44567	0.574286772	0.789264492
renal filtration cell differentiation (GO:0061318)	44567	0.574286772	0.789264492
response to catecholamine (GO:0071869)	44567	0.574286772	0.789264492
response to granulocyte macrophage colony-stimulating	44567	0.574286772	0.789264492
response to heparin (GO:0071503)	44567	0.574286772	0.789264492
response to manganese ion (GO:0010042)	44567	0.574286772	0.789264492
response to testosterone (GO:0033574)	44567	0.574286772	0.789264492
snoRNA localization (GO:0048254)	44567	0.574286772	0.789264492
sterol import (GO:0035376)	44567	0.574286772	0.789264492
succinate transmembrane transport (GO:0071422)	44567	0.574286772	0.789264492
T-tubule organization (GO:0033292)	44567	0.574286772	0.789264492
telencephalon cell migration (GO:0022029)	44567	0.574286772	0.789264492
trigeminal nerve development (GO:0021559)	44567	0.574286772	0.789264492
type B pancreatic cell proliferation (GO:0044342)	44567	0.574286772	0.789264492
venous blood vessel morphogenesis (GO:0048845)	44567	0.574286772	0.789264492
ventricular cardiac muscle cell development (GO:005501	44567	0.574286772	0.789264492
ventricular compact myocardium morphogenesis (GO:00	44567	0.574286772	0.789264492
xenobiotic transport across blood-brain barrier (GO:1990	44567	0.574286772	0.789264492
DNA-templated transcription, elongation (GO:0006354)	25447	0.575287372	0.790313242
organic acid transport (GO:0015849)	13/100	0.57584131	0.790313242
cardiac muscle cell action potential (GO:0086001)	44681	0.576419032	0.790313242
microtubule polymerization (GO:0046785)	44681	0.576419032	0.790313242
morphogenesis of an epithelium (GO:0002009)	44681	0.576419032	0.790313242
ncRNA catabolic process (GO:0034661)	44681	0.576419032	0.790313242
negative regulation of Notch signaling pathway (GO:0045	44681	0.576419032	0.790313242
peptidyl-lysine trimethylation (GO:0018023)	44681	0.576419032	0.790313242
positive regulation of DNA recombination (GO:0045911)	44681	0.576419032	0.790313242
purine ribonucleotide metabolic process (GO:0009150)	28399	0.579506883	0.794064683
positive regulation of potassium ion transport (GO:00432	14001	0.579766572	0.794064683
tRNA aminoacylation (GO:0043039)	14001	0.579766572	0.794064683
ventricular septum development (GO:0003281)	14001	0.579766572	0.794064683
rRNA metabolic process (GO:0016072)	21/162	0.580464654	0.794811249
establishment of protein localization to extracellular regi	16954	0.583219617	0.79816278
regulation of DNA metabolic process (GO:0051052)	16954	0.583219617	0.79816278
Wnt signaling pathway, planar cell polarity pathway (GO:	31352	0.583500553	0.798336943
regulation of alternative mRNA splicing, via spliceosome	19906	0.586665203	0.801822081
regulation of cellular amino acid metabolic process (GO:0	19906	0.586665203	0.801822081
regulation of proteasomal protein catabolic process (GO:	19906	0.586665203	0.801822081
unsaturated fatty acid metabolic process (GO:0033559)	19906	0.586665203	0.801822081
regulation of heart contraction (GO:0008016)	34304	0.587300666	0.802268462
visual perception (GO:0007601)	34304	0.587300666	0.802268462
fatty acid metabolic process (GO:0006631)	16/124	0.587520885	0.802358306

positive regulation of cell cycle process (GO:0090068)	13/101	0.590932339	0.806805125
DNA-templated transcription, termination (GO:0006353)	25812	0.593368984	0.809706296
sterol metabolic process (GO:0016125)	25812	0.593368984	0.809706296
negative regulation of cellular amide metabolic process (	31717	0.599743958	0.815751343
phosphatidylethanolamine metabolic process (GO:00463	11414	0.603392107	0.815751343
positive regulation of locomotion (GO:0040017)	11414	0.603392107	0.815751343
positive regulation of ubiquitin-protein transferase activit	11414	0.603392107	0.815751343
proteoglycan biosynthetic process (GO:0030166)	11414	0.603392107	0.815751343
regulation of calcium ion-dependent exocytosis (GO:001	11414	0.603392107	0.815751343
renal water homeostasis (GO:0003091)	11414	0.603392107	0.815751343
regulation of ion transmembrane transporter activity (GC	14366	0.603793488	0.815751343
cilium-dependent cell motility (GO:0060285)	44643	0.604784161	0.815751343
cytoskeleton-dependent intracellular transport (GO:0030	44643	0.604784161	0.815751343
ERK1 and ERK2 cascade (GO:0070371)	44643	0.604784161	0.815751343
mitotic cell cycle checkpoint signaling (GO:0007093)	44643	0.604784161	0.815751343
negative regulation of GTPase activity (GO:0034260)	44643	0.604784161	0.815751343
oligosaccharide biosynthetic process (GO:0009312)	44643	0.604784161	0.815751343
positive regulation of histone acetylation (GO:0035066)	44643	0.604784161	0.815751343
positive regulation of transcription initiation from RNA p	44643	0.604784161	0.815751343
protein deacylation (GO:0035601)	44643	0.604784161	0.815751343
regulation of calcium ion transmembrane transport (GO::	44643	0.604784161	0.815751343
regulation of neural precursor cell proliferation (GO:200	44643	0.604784161	0.815751343
regulation of peptidase activity (GO:0052547)	44643	0.604784161	0.815751343
regulation of release of sequestered calcium ion into cyt	44643	0.604784161	0.815751343
regulation of SMAD protein signal transduction (GO:0060	44643	0.604784161	0.815751343
regulation of steroid metabolic process (GO:0019218)	44643	0.604784161	0.815751343
response to copper ion (GO:0046688)	44643	0.604784161	0.815751343
regulation of cellular metabolic process (GO:0031323)	17319	0.605080174	0.815751343
triglyceride metabolic process (GO:0006641)	20271	0.606845431	0.815751343
negative regulation of endopeptidase activity (GO:00109	23224	0.608882159	0.815751343
positive regulation of viral process (GO:0048524)	23224	0.608882159	0.815751343
acetyl-CoA metabolic process (GO:0006084)	44607	0.610467888	0.815751343
C21-steroid hormone biosynthetic process (GO:0006700)	44607	0.610467888	0.815751343
calcium ion import into cytosol (GO:1902656)	44607	0.610467888	0.815751343
cardiac myofibril assembly (GO:0055003)	44607	0.610467888	0.815751343
clathrin coat assembly (GO:0048268)	44607	0.610467888	0.815751343
dermatan sulfate proteoglycan biosynthetic process (GO:	44607	0.610467888	0.815751343
embryonic cranial skeleton morphogenesis (GO:0048701	44607	0.610467888	0.815751343
mammary gland epithelium development (GO:0061180)	44607	0.610467888	0.815751343
membrane repolarization during cardiac muscle cell actio	44607	0.610467888	0.815751343
mitochondrial RNA metabolic process (GO:0000959)	44607	0.610467888	0.815751343
negative regulation of androgen receptor signaling pathw	44607	0.610467888	0.815751343
negative regulation of blood pressure (GO:0045776)	44607	0.610467888	0.815751343
negative regulation of protein processing (GO:0010955)	44607	0.610467888	0.815751343
nucleosome positioning (GO:0016584)	44607	0.610467888	0.815751343
placenta development (GO:0001890)	44607	0.610467888	0.815751343
positive regulation of keratinocyte differentiation (GO:00	44607	0.610467888	0.815751343

positive regulation of lyase activity (GO:0051349)	44607	0.610467888	0.815751343
positive regulation of protein export from nucleus (GO:0(	44607	0.610467888	0.815751343
positive regulation of secretion (GO:0051047)	44607	0.610467888	0.815751343
protein hydroxylation (GO:0018126)	44607	0.610467888	0.815751343
regulation of aerobic respiration (GO:1903715)	44607	0.610467888	0.815751343
regulation of amyloid fibril formation (GO:1905906)	44607	0.610467888	0.815751343
regulation of endothelial cell chemotaxis (GO:2001026)	44607	0.610467888	0.815751343
regulation of lymphocyte activation (GO:0051249)	44607	0.610467888	0.815751343
regulation of sequestering of triglyceride (GO:0010889)	44607	0.610467888	0.815751343
regulation of synaptic transmission, GABAergic (GO:0032	44607	0.610467888	0.815751343
response to ethanol (GO:0045471)	44607	0.610467888	0.815751343
cellular response to BMP stimulus (GO:0071773)	26177	0.6110754	0.815751343
fatty acid biosynthetic process (GO:0006633)	26177	0.6110754	0.815751343
response to metal ion (GO:0010038)	26177	0.6110754	0.815751343
regulation of neuron differentiation (GO:0045664)	29129	0.613357321	0.815751343
ciliary basal body-plasma membrane docking (GO:00977	35034	0.618035005	0.815751343
regulation of cell cycle phase transition (GO:1901987)	35034	0.618035005	0.815751343
sensory perception of light stimulus (GO:0050953)	35034	0.618035005	0.815751343
rRNA processing (GO:0006364)	22/173	0.618429881	0.815751343
regulation of Wnt signaling pathway (GO:0030111)	14/111	0.622729728	0.815751343
histone H4 acetylation (GO:0043967)	17685	0.626297871	0.815751343
phosphatidic acid biosynthetic process (GO:0006654)	17685	0.626297871	0.815751343
Rho protein signal transduction (GO:0007266)	20637	0.626491678	0.815751343
digestive tract development (GO:0048565)	14732	0.627014684	0.815751343
nucleocytoplasmic transport (GO:0006913)	14732	0.627014684	0.815751343
ribosomal small subunit biogenesis (GO:0042274)	14732	0.627014684	0.815751343
sulfur compound catabolic process (GO:0044273)	14732	0.627014684	0.815751343
synaptic vesicle exocytosis (GO:0016079)	14732	0.627014684	0.815751343
antimicrobial humoral immune response mediated by an	23590	0.627252588	0.815751343
B cell proliferation (GO:0042100)	11780	0.629293652	0.815751343
endodermal cell differentiation (GO:0035987)	11780	0.629293652	0.815751343
negative regulation of double-strand break repair (GO:20	11780	0.629293652	0.815751343
negative regulation of microtubule polymerization or dep	11780	0.629293652	0.815751343
positive regulation of glucose transmembrane transport (	11780	0.629293652	0.815751343
positive regulation of telomere maintenance (GO:00322(	11780	0.629293652	0.815751343
regulation of cell morphogenesis (GO:0022604)	11780	0.629293652	0.815751343
skeletal muscle organ development (GO:0060538)	11780	0.629293652	0.815751343
negative regulation of cellular response to growth factor	29495	0.629760957	0.815751343
acylglycerol acyl-chain remodeling (GO:0036155)	44568	0.630774426	0.815751343
adenylate cyclase-activating dopamine receptor signaling	44568	0.630774426	0.815751343
aldehyde catabolic process (GO:0046185)	44568	0.630774426	0.815751343
atrioventricular valve formation (GO:0003190)	44568	0.630774426	0.815751343
AV node cell action potential (GO:0086016)	44568	0.630774426	0.815751343
axon ensheathment in central nervous system (GO:0032	44568	0.630774426	0.815751343
calcitonin family receptor signaling pathway (GO:009764(	44568	0.630774426	0.815751343
cellular response to prostaglandin E stimulus (GO:00713(	44568	0.630774426	0.815751343
chylomicron remnant clearance (GO:0034382)	44568	0.630774426	0.815751343

citrulline metabolic process (GO:0000052)	44568	0.630774426	0.815751343
collagen-activated tyrosine kinase receptor signaling pathl	44568	0.630774426	0.815751343
creatine metabolic process (GO:0006600)	44568	0.630774426	0.815751343
cyclic nucleotide transport (GO:0070729)	44568	0.630774426	0.815751343
detection of muscle stretch (GO:0035995)	44568	0.630774426	0.815751343
detection of stimulus involved in sensory perception of p	44568	0.630774426	0.815751343
DNA ligation (GO:0006266)	44568	0.630774426	0.815751343
exocrine system development (GO:0035272)	44568	0.630774426	0.815751343
flavin-containing compound metabolic process (GO:0042	44568	0.630774426	0.815751343
G protein-coupled receptor internalization (GO:0002031)	44568	0.630774426	0.815751343
ganglioside catabolic process (GO:0006689)	44568	0.630774426	0.815751343
glandular epithelial cell development (GO:0002068)	44568	0.630774426	0.815751343
glycosylceramide biosynthetic process (GO:0046476)	44568	0.630774426	0.815751343
Golgi disassembly (GO:0090166)	44568	0.630774426	0.815751343
heme transport (GO:0015886)	44568	0.630774426	0.815751343
hexose catabolic process (GO:0019320)	44568	0.630774426	0.815751343
hindlimb morphogenesis (GO:0035137)	44568	0.630774426	0.815751343
histone H3-K9 methylation (GO:0051567)	44568	0.630774426	0.815751343
inhibitory postsynaptic potential (GO:0060080)	44568	0.630774426	0.815751343
keratinocyte proliferation (GO:0043616)	44568	0.630774426	0.815751343
late nucleophagy (GO:0044805)	44568	0.630774426	0.815751343
long-term synaptic depression (GO:0060292)	44568	0.630774426	0.815751343
maintenance of protein location in extracellular region (G	44568	0.630774426	0.815751343
malate metabolic process (GO:0006108)	44568	0.630774426	0.815751343
miRNA catabolic process (GO:0010587)	44568	0.630774426	0.815751343
modulation by symbiont of host apoptotic process (GO:0	44568	0.630774426	0.815751343
negative regulation of centriole replication (GO:0046600)	44568	0.630774426	0.815751343
negative regulation of cytoplasmic translation (GO:20007	44568	0.630774426	0.815751343
negative regulation of dendritic spine development (GO:(	44568	0.630774426	0.815751343
negative regulation of DNA repair (GO:0045738)	44568	0.630774426	0.815751343
negative regulation of double-strand break repair via non	44568	0.630774426	0.815751343
negative regulation of epidermal cell differentiation (GO:	44568	0.630774426	0.815751343
negative regulation of glycogen metabolic process (GO:0(	44568	0.630774426	0.815751343
negative regulation of heart rate (GO:0010459)	44568	0.630774426	0.815751343
negative regulation of intracellular transport (GO:003238	44568	0.630774426	0.815751343
negative regulation of lymphocyte differentiation (GO:00	44568	0.630774426	0.815751343
negative regulation of meiotic nuclear division (GO:0045	44568	0.630774426	0.815751343
negative regulation of mitochondrial outer membrane pe	44568	0.630774426	0.815751343
negative regulation of NLRP3 inflammasome complex ass	44568	0.630774426	0.815751343
negative regulation of protein import (GO:1904590)	44568	0.630774426	0.815751343
negative regulation of protein import into nucleus (GO:0(	44568	0.630774426	0.815751343
negative regulation of protein kinase activity by regulatio	44568	0.630774426	0.815751343
negative regulation of RIG-I signaling pathway (GO:00395	44568	0.630774426	0.815751343
negative regulation of striated muscle tissue developmer	44568	0.630774426	0.815751343
neurotransmitter receptor transport, endosome to plasm	44568	0.630774426	0.815751343
norepinephrine metabolic process (GO:0042415)	44568	0.630774426	0.815751343
nose development (GO:0043584)	44568	0.630774426	0.815751343

Notch receptor processing, ligand-dependent (GO:00353	44568	0.630774426	0.815751343
nuclear-transcribed mRNA catabolic process, deadenylati	44568	0.630774426	0.815751343
oxygen transport (GO:0015671)	44568	0.630774426	0.815751343
pantothenate metabolic process (GO:0015939)	44568	0.630774426	0.815751343
pentose metabolic process (GO:0019321)	44568	0.630774426	0.815751343
pexophagy (GO:0000425)	44568	0.630774426	0.815751343
pharyngeal arch artery morphogenesis (GO:0061626)	44568	0.630774426	0.815751343
photoreceptor cell differentiation (GO:0046530)	44568	0.630774426	0.815751343
platelet dense granule organization (GO:0060155)	44568	0.630774426	0.815751343
polyamine biosynthetic process (GO:0006596)	44568	0.630774426	0.815751343
positive regulation by symbiont of host autophagy (GO:0	44568	0.630774426	0.815751343
positive regulation of adenylate cyclase activity (GO:004	44568	0.630774426	0.815751343
positive regulation of cAMP-mediated signaling (GO:004	44568	0.630774426	0.815751343
positive regulation of cardiac epithelial to mesenchymal t	44568	0.630774426	0.815751343
positive regulation of catecholamine secretion (GO:0033	44568	0.630774426	0.815751343
positive regulation of histone H4 acetylation (GO:009024	44568	0.630774426	0.815751343
positive regulation of intracellular estrogen receptor sign	44568	0.630774426	0.815751343
positive regulation of microtubule nucleation (GO:00900	44568	0.630774426	0.815751343
positive regulation of mitophagy in response to mitochor	44568	0.630774426	0.815751343
positive regulation of mRNA binding (GO:1902416)	44568	0.630774426	0.815751343
positive regulation of multicellular organism growth (GO:	44568	0.630774426	0.815751343
positive regulation of phospholipid biosynthetic process (	44568	0.630774426	0.815751343
positive regulation of potassium ion import across plasm	44568	0.630774426	0.815751343
positive regulation of striated muscle contraction (GO:00	44568	0.630774426	0.815751343
positive regulation of synaptic plasticity (GO:0031915)	44568	0.630774426	0.815751343
positive regulation of vascular associated smooth muscle	44568	0.630774426	0.815751343
proline metabolic process (GO:0006560)	44568	0.630774426	0.815751343
protection from non-homologous end joining at telomere	44568	0.630774426	0.815751343
protein localization to ciliary membrane (GO:1903441)	44568	0.630774426	0.815751343
protein localization to cytoplasmic stress granule (GO:19	44568	0.630774426	0.815751343
purine ribonucleoside metabolic process (GO:0046128)	44568	0.630774426	0.815751343
regulation of bile acid metabolic process (GO:1904251)	44568	0.630774426	0.815751343
regulation of blood-brain barrier permeability (GO:19056	44568	0.630774426	0.815751343
regulation of cardiac muscle cell membrane potential (GO	44568	0.630774426	0.815751343
regulation of CD8-positive, alpha-beta T cell differentiatio	44568	0.630774426	0.815751343
regulation of cGMP-mediated signaling (GO:0010752)	44568	0.630774426	0.815751343
regulation of cytoplasmic mRNA processing body assemb	44568	0.630774426	0.815751343
regulation of dopamine metabolic process (GO:0042053)	44568	0.630774426	0.815751343
regulation of fat cell proliferation (GO:0070344)	44568	0.630774426	0.815751343
regulation of glial cell differentiation (GO:0045685)	44568	0.630774426	0.815751343
regulation of glucocorticoid receptor signaling pathway (	44568	0.630774426	0.815751343
regulation of glycogen (starch) synthase activity (GO:200	44568	0.630774426	0.815751343
regulation of lysosomal protein catabolic process (GO:19	44568	0.630774426	0.815751343
regulation of mitochondrial membrane permeability invo	44568	0.630774426	0.815751343
regulation of morphogenesis of an epithelium (GO:19053	44568	0.630774426	0.815751343
regulation of norepinephrine secretion (GO:0014061)	44568	0.630774426	0.815751343
regulation of phospholipid transport (GO:2001138)	44568	0.630774426	0.815751343

regulation of Rab protein signal transduction (GO:003248	44568	0.630774426	0.815751343
regulation of respiratory system process (GO:0044065)	44568	0.630774426	0.815751343
regulation of skeletal muscle satellite cell proliferation (G	44568	0.630774426	0.815751343
regulation of smooth muscle cell differentiation (GO:005	44568	0.630774426	0.815751343
regulation of T cell mediated immune response to tumor	44568	0.630774426	0.815751343
regulation of T cell tolerance induction (GO:0002664)	44568	0.630774426	0.815751343
regulation of transcription from RNA polymerase II prom	44568	0.630774426	0.815751343
regulation of transforming growth factor beta activation	44568	0.630774426	0.815751343
regulation of tubulin deacetylation (GO:0090043)	44568	0.630774426	0.815751343
regulation of vesicle size (GO:0097494)	44568	0.630774426	0.815751343
response to alkaloid (GO:0043279)	44568	0.630774426	0.815751343
riboflavin metabolic process (GO:0006771)	44568	0.630774426	0.815751343
rRNA-containing ribonucleoprotein complex export from	44568	0.630774426	0.815751343
serine transport (GO:0032329)	44568	0.630774426	0.815751343
sinoatrial node development (GO:0003163)	44568	0.630774426	0.815751343
SMAD protein complex assembly (GO:0007183)	44568	0.630774426	0.815751343
somatic recombination of immunoglobulin gene segment	44568	0.630774426	0.815751343
synaptic transmission, dopaminergic (GO:0001963)	44568	0.630774426	0.815751343
synaptic vesicle docking (GO:0016081)	44568	0.630774426	0.815751343
thiamine-containing compound metabolic process (GO:0	44568	0.630774426	0.815751343
thyroid hormone transport (GO:0070327)	44568	0.630774426	0.815751343
TRAIL-activated apoptotic signaling pathway (GO:003646	44568	0.630774426	0.815751343
type B pancreatic cell development (GO:0003323)	44568	0.630774426	0.815751343
vascular wound healing (GO:0061042)	44568	0.630774426	0.815751343
zinc ion import across plasma membrane (GO:0071578)	44568	0.630774426	0.815751343
regulation of establishment of planar polarity (GO:00901	32448	0.63130875	0.816239163
carbohydrate biosynthetic process (GO:0016051)	44644	0.634539739	0.818989799
cardiac muscle cell development (GO:0055013)	44644	0.634539739	0.818989799
lymphocyte activation involved in immune response (GO	44644	0.634539739	0.818989799
negative regulation of stress fiber assembly (GO:0051497	44644	0.634539739	0.818989799
positive regulation of protein targeting to membrane (GC	44644	0.634539739	0.818989799
protein exit from endoplasmic reticulum (GO:0032527)	44644	0.634539739	0.818989799
regulation of ruffle assembly (GO:1900027)	44644	0.634539739	0.818989799
BMP signaling pathway (GO:0030509)	23955	0.645142429	0.828689627
dicarboxylic acid metabolic process (GO:0043648)	21002	0.645576197	0.828689627
negative regulation of cell cycle G2/M phase transition (G	21002	0.645576197	0.828689627
renal system development (GO:0072001)	21002	0.645576197	0.828689627
basement membrane organization (GO:0071711)	44608	0.646475171	0.828689627
body fluid secretion (GO:0007589)	44608	0.646475171	0.828689627
histone H2A acetylation (GO:0043968)	44608	0.646475171	0.828689627
late endosome to vacuole transport via multivesicular bo	44608	0.646475171	0.828689627
N-terminal protein amino acid acetylation (GO:0006474)	44608	0.646475171	0.828689627
negative regulation of DNA replication (GO:0008156)	44608	0.646475171	0.828689627
negative regulation of lyase activity (GO:0051350)	44608	0.646475171	0.828689627
negative regulation of natural killer cell mediated cytoto	44608	0.646475171	0.828689627
negative regulation of platelet activation (GO:0010544)	44608	0.646475171	0.828689627
neuron projection organization (GO:0106027)	44608	0.646475171	0.828689627

nuclear transport (GO:0051169)	44608	0.646475171	0.828689627
oogenesis (GO:0048477)	44608	0.646475171	0.828689627
positive regulation of small molecule metabolic process (	44608	0.646475171	0.828689627
regulation of activin receptor signaling pathway (GO:003	44608	0.646475171	0.828689627
regulation of fatty acid oxidation (GO:0046320)	44608	0.646475171	0.828689627
regulation of leukocyte activation (GO:0002694)	44608	0.646475171	0.828689627
regulation of phosphate metabolic process (GO:0019220	44608	0.646475171	0.828689627
regulation of systemic arterial blood pressure by hormon	44608	0.646475171	0.828689627
response to organophosphorus (GO:0046683)	44608	0.646475171	0.828689627
serine family amino acid metabolic process (GO:0009069	44608	0.646475171	0.828689627
sympathetic nervous system development (GO:0048485)	44608	0.646475171	0.828689627
mitotic cytokinesis (GO:0000281)	18050	0.646840507	0.828689627
regulation of cellular localization (GO:0060341)	18050	0.646840507	0.828689627
regulation of stress-activated MAPK cascade (GO:003287	18050	0.646840507	0.828689627
response to glucose (GO:0009749)	18050	0.646840507	0.828689627
secondary alcohol metabolic process (GO:1902652)	18050	0.646840507	0.828689627
carboxylic acid transmembrane transport (GO:1905039)	15097	0.64939307	0.830730607
endosome organization (GO:0007032)	15097	0.64939307	0.830730607
positive regulation of cation transmembrane transport (G	15097	0.64939307	0.830730607
regulation of cell development (GO:0060284)	15097	0.64939307	0.830730607
regulation of G0 to G1 transition (GO:0070316)	15097	0.64939307	0.830730607
regulation of mitochondrial membrane potential (GO:005	15097	0.64939307	0.830730607
lytic vacuole organization (GO:0080171)	12145	0.654083043	0.835906865
neuron projection extension (GO:1990138)	12145	0.654083043	0.835906865
positive regulation of histone modification (GO:0031058)	12145	0.654083043	0.835906865
RNA stabilization (GO:0043489)	12145	0.654083043	0.835906865
negative regulation of translation (GO:0017148)	33178	0.66153251	0.838039437
positive regulation of developmental process (GO:00510	22/177	0.662174195	0.838039437
embryonic organ development (GO:0048568)	24320	0.662531268	0.838039437
protein localization to nucleus (GO:0034504)	13/106	0.662533774	0.838039437
acylglycerol homeostasis (GO:0055090)	44645	0.662694165	0.838039437
cellular response to hexose stimulus (GO:0071331)	44645	0.662694165	0.838039437
chemical synaptic transmission, postsynaptic (GO:00995	44645	0.662694165	0.838039437
energy derivation by oxidation of organic compounds (GO	44645	0.662694165	0.838039437
peripheral nervous system development (GO:0007422)	44645	0.662694165	0.838039437
protein quality control for misfolded or incompletely syn	44645	0.662694165	0.838039437
receptor catabolic process (GO:0032801)	44645	0.662694165	0.838039437
regulation of cAMP-mediated signaling (GO:0043949)	44645	0.662694165	0.838039437
response to hexose (GO:0009746)	44645	0.662694165	0.838039437
ventricular cardiac muscle tissue development (GO:0003	44645	0.662694165	0.838039437
phosphatidic acid metabolic process (GO:0046473)	18415	0.666682322	0.838039437
ncRNA processing (GO:0034470)	25/201	0.666979978	0.838039437
skeletal system morphogenesis (GO:0048705)	15462	0.670900782	0.838039437
translesion synthesis (GO:0019985)	15462	0.670900782	0.838039437
nucleic acid phosphodiester bond hydrolysis (GO:009030	27638	0.67771588	0.838039437
central nervous system neuron differentiation (GO:0021	12510	0.677733711	0.838039437
female gamete generation (GO:0007292)	12510	0.677733711	0.838039437

organelle disassembly (GO:1903008)	12510	0.677733711	0.838039437
organic cyclic compound biosynthetic process (GO:19013	12510	0.677733711	0.838039437
positive regulation of release of sequestered calcium ion	12510	0.677733711	0.838039437
regulation of lamellipodium assembly (GO:0010591)	12510	0.677733711	0.838039437
tRNA export from nucleus (GO:0006409)	12510	0.677733711	0.838039437
tRNA-containing ribonucleoprotein complex export from	12510	0.677733711	0.838039437
ventricular cardiac muscle tissue morphogenesis (GO:005	12510	0.677733711	0.838039437
adenosine to inosine editing (GO:0006382)	44569	0.679769188	0.838039437
anterograde axonal protein transport (GO:0099641)	44569	0.679769188	0.838039437
antigen processing and presentation of exogenous peptic	44569	0.679769188	0.838039437
axo-dendritic protein transport (GO:0099640)	44569	0.679769188	0.838039437
box C/D snoRNP assembly (GO:0000492)	44569	0.679769188	0.838039437
brown fat cell differentiation (GO:0050873)	44569	0.679769188	0.838039437
carbohydrate phosphorylation (GO:0046835)	44569	0.679769188	0.838039437
cardiac atrium development (GO:0003230)	44569	0.679769188	0.838039437
cardiac muscle hypertrophy (GO:0003300)	44569	0.679769188	0.838039437
cell migration involved in heart development (GO:00609	44569	0.679769188	0.838039437
cellular response to epinephrine stimulus (GO:0071872)	44569	0.679769188	0.838039437
cellular response to interferon-alpha (GO:0035457)	44569	0.679769188	0.838039437
dendritic spine maintenance (GO:0097062)	44569	0.679769188	0.838039437
diacylglycerol biosynthetic process (GO:0006651)	44569	0.679769188	0.838039437
elastic fiber assembly (GO:0048251)	44569	0.679769188	0.838039437
endosomal vesicle fusion (GO:0034058)	44569	0.679769188	0.838039437
ER overload response (GO:0006983)	44569	0.679769188	0.838039437
establishment of Golgi localization (GO:0051683)	44569	0.679769188	0.838039437
establishment of protein localization to peroxisome (GO:	44569	0.679769188	0.838039437
folic acid transport (GO:0015884)	44569	0.679769188	0.838039437
forebrain neuron development (GO:0021884)	44569	0.679769188	0.838039437
forebrain neuron differentiation (GO:0021879)	44569	0.679769188	0.838039437
fructose metabolic process (GO:0006000)	44569	0.679769188	0.838039437
galactosylceramide metabolic process (GO:0006681)	44569	0.679769188	0.838039437
histidine catabolic process (GO:0006548)	44569	0.679769188	0.838039437
histidine metabolic process (GO:0006547)	44569	0.679769188	0.838039437
histone H2A-K119 monoubiquitination (GO:0036353)	44569	0.679769188	0.838039437
histone H3-K4 demethylation (GO:0034720)	44569	0.679769188	0.838039437
immune response-inhibiting cell surface receptor signalin	44569	0.679769188	0.838039437
internal protein amino acid acetylation (GO:0006475)	44569	0.679769188	0.838039437
lens fiber cell development (GO:0070307)	44569	0.679769188	0.838039437
lens fiber cell differentiation (GO:0070306)	44569	0.679769188	0.838039437
macromolecule depalmitoylation (GO:0098734)	44569	0.679769188	0.838039437
macromolecule modification (GO:0043412)	44569	0.679769188	0.838039437
mammary gland epithelial cell differentiation (GO:00606	44569	0.679769188	0.838039437
mitochondrial respiratory chain complex III assembly (GO	44569	0.679769188	0.838039437
mitochondrial RNA processing (GO:0000963)	44569	0.679769188	0.838039437
mitophagy (GO:0000423)	44569	0.679769188	0.838039437
negative regulation by symbiont of host apoptotic proces	44569	0.679769188	0.838039437
negative regulation by symbiont of host programmed cel	44569	0.679769188	0.838039437

negative regulation of actin nucleation (GO:0051126)	44569	0.679769188	0.838039437
negative regulation of alpha-beta T cell differentiation (G	44569	0.679769188	0.838039437
negative regulation of B cell apoptotic process (GO:0002	44569	0.679769188	0.838039437
negative regulation of calcium ion import (GO:0090281)	44569	0.679769188	0.838039437
negative regulation of cAMP-dependent protein kinase a	44569	0.679769188	0.838039437
negative regulation of macrophage migration (GO:19055	44569	0.679769188	0.838039437
negative regulation of mitochondrial membrane potentia	44569	0.679769188	0.838039437
negative regulation of mRNA polyadenylation (GO:19003	44569	0.679769188	0.838039437
negative regulation of muscle hypertrophy (GO:0014741)	44569	0.679769188	0.838039437
negative regulation of neural precursor cell proliferation	44569	0.679769188	0.838039437
negative regulation of nitrogen compound metabolic pro	44569	0.679769188	0.838039437
negative regulation of potassium ion transmembrane tra	44569	0.679769188	0.838039437
neuron fate specification (GO:0048665)	44569	0.679769188	0.838039437
peptidyl-lysine hydroxylation (GO:0017185)	44569	0.679769188	0.838039437
peptidyl-proline hydroxylation to 4-hydroxy-L-proline (GC	44569	0.679769188	0.838039437
positive regulation of CD4-positive, alpha-beta T cell diffe	44569	0.679769188	0.838039437
positive regulation of early endosome to late endosome t	44569	0.679769188	0.838039437
positive regulation of epithelial cell proliferation involved	44569	0.679769188	0.838039437
positive regulation of intracellular steroid hormone recep	44569	0.679769188	0.838039437
positive regulation of leukocyte differentiation (GO:1902	44569	0.679769188	0.838039437
positive regulation of meiotic nuclear division (GO:00458	44569	0.679769188	0.838039437
positive regulation of melanin biosynthetic process (GO:0	44569	0.679769188	0.838039437
positive regulation of neuron projection arborization (GO	44569	0.679769188	0.838039437
positive regulation of ryanodine-sensitive calcium-releas	44569	0.679769188	0.838039437
positive regulation of secondary metabolite biosynthetic	44569	0.679769188	0.838039437
positive regulation of triglyceride catabolic process (GO:0	44569	0.679769188	0.838039437
postsynaptic density organization (GO:0097106)	44569	0.679769188	0.838039437
progesterone receptor signaling pathway (GO:0050847)	44569	0.679769188	0.838039437
protein deglutamylation (GO:0035608)	44569	0.679769188	0.838039437
protein deglycosylation (GO:0006517)	44569	0.679769188	0.838039437
protein depalmitoylation (GO:0002084)	44569	0.679769188	0.838039437
protein localization to presynapse (GO:1905383)	44569	0.679769188	0.838039437
regulation of acetyl-CoA biosynthetic process from pyruv	44569	0.679769188	0.838039437
regulation of actin filament length (GO:0030832)	44569	0.679769188	0.838039437
regulation of acyl-CoA biosynthetic process (GO:0050812	44569	0.679769188	0.838039437
regulation of chaperone-mediated autophagy (GO:19047	44569	0.679769188	0.838039437
regulation of cyclic-nucleotide phosphodiesterase activity	44569	0.679769188	0.838039437
regulation of cytoplasmic translational elongation (GO:19	44569	0.679769188	0.838039437
regulation of dopamine receptor signaling pathway (GO:0	44569	0.679769188	0.838039437
regulation of epithelial to mesenchymal transition involv	44569	0.679769188	0.838039437
regulation of extent of cell growth (GO:0061387)	44569	0.679769188	0.838039437
regulation of Golgi to plasma membrane protein transpo	44569	0.679769188	0.838039437
regulation of myeloid leukocyte differentiation (GO:0002	44569	0.679769188	0.838039437
regulation of phospholipase A2 activity (GO:0032429)	44569	0.679769188	0.838039437
regulation of potassium ion import (GO:1903286)	44569	0.679769188	0.838039437
regulation of protein glycosylation (GO:0060049)	44569	0.679769188	0.838039437
regulation of protein localization to cell cortex (GO:19047	44569	0.679769188	0.838039437

regulation of protein localization to chromatin (GO:1905(	44569	0.679769188	0.838039437
regulation of protein localization to nucleolus (GO:19047	44569	0.679769188	0.838039437
regulation of skeletal muscle fiber development (GO:004	44569	0.679769188	0.838039437
regulation of stem cell division (GO:2000035)	44569	0.679769188	0.838039437
regulation of striated muscle tissue development (GO:00	44569	0.679769188	0.838039437
respiratory chain complex III assembly (GO:0017062)	44569	0.679769188	0.838039437
response to epinephrine (GO:0071871)	44569	0.679769188	0.838039437
ribosome disassembly (GO:0032790)	44569	0.679769188	0.838039437
self proteolysis (GO:0097264)	44569	0.679769188	0.838039437
skeletal myofibril assembly (GO:0014866)	44569	0.679769188	0.838039437
spermidine metabolic process (GO:0008216)	44569	0.679769188	0.838039437
sulfur amino acid biosynthetic process (GO:0000097)	44569	0.679769188	0.838039437
T cell mediated cytotoxicity (GO:0001913)	44569	0.679769188	0.838039437
thyroid gland development (GO:0030878)	44569	0.679769188	0.838039437
TORC1 signaling (GO:0038202)	44569	0.679769188	0.838039437
venous blood vessel development (GO:0060841)	44569	0.679769188	0.838039437
vitamin K metabolic process (GO:0042373)	44569	0.679769188	0.838039437
water homeostasis (GO:0030104)	44569	0.679769188	0.838039437
amyloid-beta metabolic process (GO:0050435)	44609	0.679787909	0.838039437
aorta morphogenesis (GO:0035909)	44609	0.679787909	0.838039437
DNA biosynthetic process (GO:0071897)	44609	0.679787909	0.838039437
mesenchyme morphogenesis (GO:0072132)	44609	0.679787909	0.838039437
negative regulation of amyloid-beta formation (GO:1902	44609	0.679787909	0.838039437
pharyngeal system development (GO:0060037)	44609	0.679787909	0.838039437
phosphate ion transport (GO:0006817)	44609	0.679787909	0.838039437
positive regulation of collagen metabolic process (GO:00	44609	0.679787909	0.838039437
positive regulation of regulated secretory pathway (GO:1	44609	0.679787909	0.838039437
positive regulation of stem cell proliferation (GO:200064	44609	0.679787909	0.838039437
positive regulation of telomere capping (GO:1904355)	44609	0.679787909	0.838039437
regulation of cardiac muscle contraction by regulation of	44609	0.679787909	0.838039437
regulation of cholesterol biosynthetic process (GO:00455	44609	0.679787909	0.838039437
regulation of metal ion transport (GO:0010959)	44609	0.679787909	0.838039437
regulation of stem cell proliferation (GO:0072091)	44609	0.679787909	0.838039437
RNA interference (GO:0016246)	44609	0.679787909	0.838039437
neuron projection development (GO:0031175)	21/171	0.681960435	0.840333693
selective autophagy (GO:0061912)	21732	0.681972445	0.840333693
intracellular protein transport (GO:0006886)	42/336	0.685576646	0.844574502
ion transport (GO:0006811)	14/116	0.68899611	0.847074891
metanephros development (GO:0001656)	44646	0.689236875	0.847074891
negative regulation of signaling receptor activity (GO:200	44646	0.689236875	0.847074891
negative regulation of telomere maintenance via telomer	44646	0.689236875	0.847074891
negative regulation of transposition (GO:0010529)	44646	0.689236875	0.847074891
positive regulation of microtubule polymerization or dep	44646	0.689236875	0.847074891
regulation of glycogen biosynthetic process (GO:0005979	44646	0.689236875	0.847074891
regulation of potassium ion transmembrane transporter	44646	0.689236875	0.847074891
regulation of synapse organization (GO:0050807)	44646	0.689236875	0.847074891
regulation of telomere maintenance (GO:0032204)	44646	0.689236875	0.847074891

regulation of signal transduction by p53 class mediator (G	19/156	0.690877801	0.84889077
tRNA aminoacylation for protein translation (GO:000641	15827	0.691518469	0.84947705
cell morphogenesis involved in neuron differentiation (G	28004	0.693245852	0.851196455
phospholipid metabolic process (GO:0006644)	28004	0.693245852	0.851196455
RNA splicing, via transesterification reactions with bulgec	31/251	0.693878306	0.851771692
regulation of mitotic cell cycle phase transition (GO:1901	23/188	0.694105678	0.851849514
adenylate cyclase-inhibiting G protein-coupled receptor s	22098	0.699251401	0.857556899
ribonucleoprotein complex biogenesis (GO:0022613)	22098	0.699251401	0.857556899
RNA methylation (GO:0001510)	22098	0.699251401	0.857556899
blood vessel diameter maintenance (GO:0097746)	12875	0.700231621	0.857948885
negative regulation of epithelial cell migration (GO:0010(	12875	0.700231621	0.857948885
regulation of ion transmembrane transport (GO:0034765	12875	0.700231621	0.857948885
regulation of regulated secretory pathway (GO:1903305)	12875	0.700231621	0.857948885
amide biosynthetic process (GO:0043604)	19146	0.704190363	0.862392488
cartilage development (GO:0051216)	19146	0.704190363	0.862392488
negative regulation of developmental process (GO:0051(	28369	0.708299526	0.862963381
chromatin disassembly (GO:0031498)	44610	0.710487119	0.862963381
DNA conformation change (GO:0071103)	44610	0.710487119	0.862963381
embryonic digit morphogenesis (GO:0042733)	44610	0.710487119	0.862963381
epithelial structure maintenance (GO:0010669)	44610	0.710487119	0.862963381
G protein-coupled acetylcholine receptor signaling pathw	44610	0.710487119	0.862963381
glycoprotein catabolic process (GO:0006516)	44610	0.710487119	0.862963381
high-density lipoprotein particle remodeling (GO:003437	44610	0.710487119	0.862963381
intermediate filament organization (GO:0045109)	44610	0.710487119	0.862963381
melanosome transport (GO:0032402)	44610	0.710487119	0.862963381
negative regulation of biosynthetic process (GO:0009890	44610	0.710487119	0.862963381
negative regulation of cation transmembrane transport (	44610	0.710487119	0.862963381
negative regulation of double-strand break repair via hon	44610	0.710487119	0.862963381
nucleosome disassembly (GO:0006337)	44610	0.710487119	0.862963381
nucleotide biosynthetic process (GO:0009165)	44610	0.710487119	0.862963381
outer dynein arm assembly (GO:0036158)	44610	0.710487119	0.862963381
pigment granule transport (GO:0051904)	44610	0.710487119	0.862963381
positive regulation of cartilage development (GO:006103	44610	0.710487119	0.862963381
positive regulation of peptidyl-serine phosphorylation of	44610	0.710487119	0.862963381
prostanoid metabolic process (GO:0006692)	44610	0.710487119	0.862963381
regulation of chromosome segregation (GO:0051983)	44610	0.710487119	0.862963381
regulation of membrane depolarization (GO:0003254)	44610	0.710487119	0.862963381
response to axon injury (GO:0048678)	44610	0.710487119	0.862963381
water transport (GO:0006833)	44610	0.710487119	0.862963381
branching morphogenesis of an epithelial tube (GO:0048	16193	0.711234544	0.862963381
hexose biosynthetic process (GO:0019319)	16193	0.711234544	0.862963381
metal ion homeostasis (GO:0055065)	16193	0.711234544	0.862963381
monocarboxylic acid catabolic process (GO:0072329)	44647	0.71417653	0.862963381
negative regulation of actin filament bundle assembly (G	44647	0.71417653	0.862963381
presynaptic endocytosis (GO:0140238)	44647	0.71417653	0.862963381
regulation of transcription elongation from RNA polymer	44647	0.71417653	0.862963381
nucleosome organization (GO:0034728)	34639	0.717552974	0.862963381

calcium-dependent cell-cell adhesion via plasma membra	13241	0.721573785	0.862963381
cellular response to heat (GO:0034605)	13241	0.721573785	0.862963381
embryonic limb morphogenesis (GO:0030326)	13241	0.721573785	0.862963381
positive regulation of bone mineralization (GO:0030501)	13241	0.721573785	0.862963381
regulation of embryonic development (GO:0045995)	13241	0.721573785	0.862963381
regulation of microtubule-based process (GO:0032886)	13241	0.721573785	0.862963381
retina homeostasis (GO:0001895)	13241	0.721573785	0.862963381
acid secretion (GO:0046717)	44570	0.722264636	0.862963381
associative learning (GO:0008306)	44570	0.722264636	0.862963381
cholesterol catabolic process (GO:0006707)	44570	0.722264636	0.862963381
chylomicron remodeling (GO:0034371)	44570	0.722264636	0.862963381
cilium movement involved in cell motility (GO:0060294)	44570	0.722264636	0.862963381
collagen-activated signaling pathway (GO:0038065)	44570	0.722264636	0.862963381
DNA cytosine deamination (GO:0070383)	44570	0.722264636	0.862963381
DNA topological change (GO:0006265)	44570	0.722264636	0.862963381
embryonic forelimb morphogenesis (GO:0035115)	44570	0.722264636	0.862963381
endochondral ossification (GO:0001958)	44570	0.722264636	0.862963381
estrogen biosynthetic process (GO:0006703)	44570	0.722264636	0.862963381
fucose catabolic process (GO:0019317)	44570	0.722264636	0.862963381
hepoxilin biosynthetic process (GO:0051122)	44570	0.722264636	0.862963381
hepoxilin metabolic process (GO:0051121)	44570	0.722264636	0.862963381
histone phosphorylation (GO:0016572)	44570	0.722264636	0.862963381
hormone transport (GO:0009914)	44570	0.722264636	0.862963381
icosanoid transport (GO:0071715)	44570	0.722264636	0.862963381
inner ear receptor cell development (GO:0060119)	44570	0.722264636	0.862963381
intestinal cholesterol absorption (GO:0030299)	44570	0.722264636	0.862963381
ketone biosynthetic process (GO:0042181)	44570	0.722264636	0.862963381
kinetochore assembly (GO:0051382)	44570	0.722264636	0.862963381
L-fucose catabolic process (GO:0042355)	44570	0.722264636	0.862963381
L-fucose metabolic process (GO:0042354)	44570	0.722264636	0.862963381
L-phenylalanine metabolic process (GO:0006558)	44570	0.722264636	0.862963381
lysosomal lumen acidification (GO:0007042)	44570	0.722264636	0.862963381
maintenance of apical/basal cell polarity (GO:0035090)	44570	0.722264636	0.862963381
maintenance of epithelial cell apical/basal polarity (GO:0	44570	0.722264636	0.862963381
mesodermal cell differentiation (GO:0048333)	44570	0.722264636	0.862963381
mitochondrial tRNA modification (GO:0070900)	44570	0.722264636	0.862963381
mitral valve morphogenesis (GO:0003183)	44570	0.722264636	0.862963381
negative regulation of biomineralization (GO:0110150)	44570	0.722264636	0.862963381
negative regulation of fibrinolysis (GO:0051918)	44570	0.722264636	0.862963381
negative regulation of membrane potential (GO:0045837	44570	0.722264636	0.862963381
negative regulation of mRNA 3'-end processing (GO:0031	44570	0.722264636	0.862963381
negative regulation of smooth muscle cell differentiation	44570	0.722264636	0.862963381
nucleoside diphosphate phosphorylation (GO:0006165)	44570	0.722264636	0.862963381
nucleoside triphosphate biosynthetic process (GO:00091	44570	0.722264636	0.862963381
nucleotide phosphorylation (GO:0046939)	44570	0.722264636	0.862963381
oligosaccharide catabolic process (GO:0009313)	44570	0.722264636	0.862963381
peroxisomal transport (GO:0043574)	44570	0.722264636	0.862963381

peroxisome fission (GO:0016559)	44570	0.722264636	0.862963381
phosphorylation of RNA polymerase II C-terminal domain	44570	0.722264636	0.862963381
positive regulation of autophagosome assembly (GO:200	44570	0.722264636	0.862963381
positive regulation of autophagy of mitochondrion (GO:1	44570	0.722264636	0.862963381
positive regulation of blood pressure (GO:0045777)	44570	0.722264636	0.862963381
positive regulation of CD8-positive, alpha-beta T cell acti	44570	0.722264636	0.862963381
positive regulation of cholesterol esterification (GO:0010	44570	0.722264636	0.862963381
positive regulation of megakaryocyte differentiation (GO	44570	0.722264636	0.862963381
positive regulation of membrane potential (GO:0045838)	44570	0.722264636	0.862963381
positive regulation of smooth muscle contraction (GO:00	44570	0.722264636	0.862963381
protein hexamerization (GO:0034214)	44570	0.722264636	0.862963381
protein K6-linked ubiquitination (GO:0085020)	44570	0.722264636	0.862963381
regulation of cellular response to oxidative stress (GO:19	44570	0.722264636	0.862963381
regulation of ER to Golgi vesicle-mediated transport (GO:	44570	0.722264636	0.862963381
regulation of gap junction assembly (GO:1903596)	44570	0.722264636	0.862963381
regulation of helicase activity (GO:0051095)	44570	0.722264636	0.862963381
regulation of histone H4 acetylation (GO:0090239)	44570	0.722264636	0.862963381
regulation of leukocyte degranulation (GO:0043300)	44570	0.722264636	0.862963381
regulation of nephron tubule epithelial cell differentiatio	44570	0.722264636	0.862963381
regulation of nuclear cell cycle DNA replication (GO:0033	44570	0.722264636	0.862963381
regulation of peroxisome proliferator activated receptor	44570	0.722264636	0.862963381
regulation of Wnt signaling pathway, planar cell polarity	44570	0.722264636	0.862963381
skeletal muscle fiber development (GO:0048741)	44570	0.722264636	0.862963381
sterol catabolic process (GO:0016127)	44570	0.722264636	0.862963381
sympathetic ganglion development (GO:0061549)	44570	0.722264636	0.862963381
type B pancreatic cell differentiation (GO:0003309)	44570	0.722264636	0.862963381
unsaturated fatty acid biosynthetic process (GO:0006636	44570	0.722264636	0.862963381
monocarboxylic acid metabolic process (GO:0032787)	17/143	0.722950392	0.863385583
neuron development (GO:0048666)	17/143	0.722950392	0.863385583
action potential (GO:0001508)	16558	0.730044444	0.871256808
amino acid transmembrane transport (GO:0003333)	16558	0.730044444	0.871256808
mitotic G2/M transition checkpoint (GO:0044818)	16558	0.730044444	0.871256808
mRNA metabolic process (GO:0016071)	35004	0.730585077	0.871701763
glucose metabolic process (GO:0006006)	22828	0.73191952	0.873093435
cellular protein-containing complex assembly (GO:00346	20/168	0.732181704	0.873205682
plasma membrane bounded cell projection organization	15/128	0.735411221	0.874929601
mucosal immune response (GO:0002385)	44648	0.737537665	0.874929601
positive regulation of microtubule polymerization (GO:0(	44648	0.737537665	0.874929601
protein localization to cell surface (GO:0034394)	44648	0.737537665	0.874929601
regulation of microtubule polymerization or depolymeriz	44648	0.737537665	0.874929601
regulation of postsynapse organization (GO:0099175)	44648	0.737537665	0.874929601
ventricular septum morphogenesis (GO:0060412)	44648	0.737537665	0.874929601
aspartate family amino acid catabolic process (GO:00090	44611	0.738679736	0.874929601
aspartate family amino acid metabolic process (GO:0009(	44611	0.738679736	0.874929601
ATP synthesis coupled proton transport (GO:0015986)	44611	0.738679736	0.874929601
carbohydrate derivative catabolic process (GO:1901136)	44611	0.738679736	0.874929601
cellular response to copper ion (GO:0071280)	44611	0.738679736	0.874929601

detection of mechanical stimulus (GO:0050982)	44611	0.738679736	0.874929601
endocardial cushion morphogenesis (GO:0003203)	44611	0.738679736	0.874929601
endoplasmic reticulum mannose trimming (GO:1904380)	44611	0.738679736	0.874929601
establishment of melanosome localization (GO:0032401)	44611	0.738679736	0.874929601
excitatory postsynaptic potential (GO:0060079)	44611	0.738679736	0.874929601
glycerolipid catabolic process (GO:0046503)	44611	0.738679736	0.874929601
mesenchymal cell development (GO:0014031)	44611	0.738679736	0.874929601
N-glycan processing (GO:0006491)	44611	0.738679736	0.874929601
negative regulation of immune system process (GO:0002	44611	0.738679736	0.874929601
neural crest cell differentiation (GO:0014033)	44611	0.738679736	0.874929601
pore complex assembly (GO:0046931)	44611	0.738679736	0.874929601
regulation of autophagy of mitochondrion (GO:1903146)	44611	0.738679736	0.874929601
regulation of centriole replication (GO:0046599)	44611	0.738679736	0.874929601
regulation of histone H3-K4 methylation (GO:0051569)	44611	0.738679736	0.874929601
regulation of peptidyl-serine phosphorylation of STAT pr	44611	0.738679736	0.874929601
regulation of stem cell population maintenance (GO:200	44611	0.738679736	0.874929601
response to fatty acid (GO:0070542)	44611	0.738679736	0.874929601
vesicle transport along actin filament (GO:0030050)	44611	0.738679736	0.874929601
ncRNA metabolic process (GO:0034660)	13606	0.741766835	0.877785582
phospholipid biosynthetic process (GO:0008654)	13606	0.741766835	0.877785582
regulation of intracellular steroid hormone receptor sign	13606	0.741766835	0.877785582
tRNA transport (GO:0051031)	13606	0.741766835	0.877785582
COPII vesicle coating (GO:0048208)	23193	0.747299175	0.883310154
negative regulation of peptidase activity (GO:0010466)	23193	0.747299175	0.883310154
vesicle coating (GO:0006901)	23193	0.747299175	0.883310154
vesicle targeting, rough ER to cis-Golgi (GO:0048207)	23193	0.747299175	0.883310154
postreplication repair (GO:0006301)	16923	0.747949891	0.883310154
posttranscriptional regulation of gene expression (GO:00	16923	0.747949891	0.883310154
regulation of double-strand break repair via homologous	16923	0.747949891	0.883310154
regulation of telomerase activity (GO:0051972)	16923	0.747949891	0.883310154
glycerophospholipid metabolic process (GO:0006650)	29465	0.750536445	0.883310154
regulation of organelle organization (GO:0033043)	29465	0.750536445	0.883310154
mRNA splicing, via spliceosome (GO:0000398)	33/274	0.751240615	0.883310154
ceramide metabolic process (GO:0006672)	20241	0.754878897	0.883310154
G2/M transition of mitotic cell cycle (GO:0000086)	15/130	0.756840064	0.883310154
Golgi organization (GO:0007030)	15/130	0.756840064	0.883310154
post-Golgi vesicle-mediated transport (GO:0006892)	32782	0.759121977	0.883310154
alanine transport (GO:0032328)	44571	0.759122642	0.883310154
apical protein localization (GO:0045176)	44571	0.759122642	0.883310154
cell differentiation involved in metanephros developmen	44571	0.759122642	0.883310154
cellular response to hydroxyurea (GO:0072711)	44571	0.759122642	0.883310154
cellular response to leucine starvation (GO:1990253)	44571	0.759122642	0.883310154
chylomicron assembly (GO:0034378)	44571	0.759122642	0.883310154
DNA damage response, signal transduction by p53 class n	44571	0.759122642	0.883310154
DNA dealkylation (GO:0035510)	44571	0.759122642	0.883310154
DNA dealkylation involved in DNA repair (GO:0006307)	44571	0.759122642	0.883310154
dosage compensation (GO:0007549)	44571	0.759122642	0.883310154

endodermal cell fate commitment (GO:0001711)	44571	0.759122642	0.883310154
forelimb morphogenesis (GO:0035136)	44571	0.759122642	0.883310154
glycine transport (GO:0015816)	44571	0.759122642	0.883310154
glycosphingolipid catabolic process (GO:0046479)	44571	0.759122642	0.883310154
hematopoietic stem cell differentiation (GO:0060218)	44571	0.759122642	0.883310154
histone H4 deacetylation (GO:0070933)	44571	0.759122642	0.883310154
long-chain fatty acid import into cell (GO:0044539)	44571	0.759122642	0.883310154
low-density lipoprotein particle receptor catabolic proces	44571	0.759122642	0.883310154
low-density lipoprotein receptor particle metabolic proce	44571	0.759122642	0.883310154
lung epithelium development (GO:0060428)	44571	0.759122642	0.883310154
muscle cell migration (GO:0014812)	44571	0.759122642	0.883310154
myelin maintenance (GO:0043217)	44571	0.759122642	0.883310154
negative regulation of establishment of protein localizati	44571	0.759122642	0.883310154
negative regulation of lipopolysaccharide-mediated signa	44571	0.759122642	0.883310154
negative regulation of peptidyl-lysine acetylation (GO:20	44571	0.759122642	0.883310154
negative regulation of phosphatidylinositol 3-kinase signa	44571	0.759122642	0.883310154
negative regulation of transcription from RNA polymeras	44571	0.759122642	0.883310154
neuron projection fasciculation (GO:0106030)	44571	0.759122642	0.883310154
nuclear pore complex assembly (GO:0051292)	44571	0.759122642	0.883310154
nucleic acid transport (GO:0050657)	44571	0.759122642	0.883310154
nucleoside metabolic process (GO:0009116)	44571	0.759122642	0.883310154
omega-hydroxylase P450 pathway (GO:0097267)	44571	0.759122642	0.883310154
positive regulation of lipase activity (GO:0060193)	44571	0.759122642	0.883310154
positive regulation of mRNA 3'-end processing (GO:0031	44571	0.759122642	0.883310154
positive regulation of transcription of nucleolar large rRN	44571	0.759122642	0.883310154
positive regulation of vasculogenesis (GO:2001214)	44571	0.759122642	0.883310154
production of siRNA involved in RNA interference (GO:00	44571	0.759122642	0.883310154
receptor recycling (GO:0001881)	44571	0.759122642	0.883310154
regulation of bile acid biosynthetic process (GO:0070857	44571	0.759122642	0.883310154
regulation of cell-cell adhesion mediated by integrin (GO:	44571	0.759122642	0.883310154
regulation of cilium movement (GO:0003352)	44571	0.759122642	0.883310154
regulation of DNA damage checkpoint (GO:2000001)	44571	0.759122642	0.883310154
regulation of low-density lipoprotein particle clearance ((	44571	0.759122642	0.883310154
regulation of microtubule nucleation (GO:0010968)	44571	0.759122642	0.883310154
regulation of RNA polymerase II transcription preinitiatio	44571	0.759122642	0.883310154
RNA polymerase II preinitiation complex assembly (GO:0(	44571	0.759122642	0.883310154
serine family amino acid catabolic process (GO:0009071)	44571	0.759122642	0.883310154
small nucleolar ribonucleoprotein complex assembly (GO	44571	0.759122642	0.883310154
SNARE complex assembly (GO:0035493)	44571	0.759122642	0.883310154
telomere maintenance in response to DNA damage (GO:(	44571	0.759122642	0.883310154
Wnt signaling pathway involved in midbrain dopaminergi	44571	0.759122642	0.883310154
establishment of mitotic spindle localization (GO:004000	44649	0.75935768	0.883310154
homologous chromosome pairing at meiosis (GO:000712	44649	0.75935768	0.883310154
hydrogen peroxide metabolic process (GO:0042743)	44649	0.75935768	0.883310154
limb development (GO:0060173)	44649	0.75935768	0.883310154
lipid catabolic process (GO:0016042)	44649	0.75935768	0.883310154
negative regulation of wound healing (GO:0061045)	44649	0.75935768	0.883310154

protein K11-linked ubiquitination (GO:0070979)	44649	0.75935768	0.883310154
protein targeting to peroxisome (GO:0006625)	44649	0.75935768	0.883310154
regulation of actin polymerization or depolymerization (G	44649	0.75935768	0.883310154
regulation of neuronal synaptic plasticity (GO:0048168)	44649	0.75935768	0.883310154
ncRNA export from nucleus (GO:0097064)	13971	0.760825666	0.884621605
negative regulation of G0 to G1 transition (GO:0070317)	13971	0.760825666	0.884621605
epithelial cilium movement involved in extracellular fluid	44612	0.764490315	0.885908361
folic acid-containing compound metabolic process (GO:0(	44612	0.764490315	0.885908361
gastrulation (GO:0007369)	44612	0.764490315	0.885908361
insulin secretion (GO:0030073)	44612	0.764490315	0.885908361
mesoderm formation (GO:0001707)	44612	0.764490315	0.885908361
microtubule nucleation (GO:0007020)	44612	0.764490315	0.885908361
mitochondrial cytochrome c oxidase assembly (GO:0033(	44612	0.764490315	0.885908361
positive regulation of embryonic development (GO:0040(	44612	0.764490315	0.885908361
positive regulation of G2/M transition of mitotic cell cycl	44612	0.764490315	0.885908361
positive regulation of heart contraction (GO:0045823)	44612	0.764490315	0.885908361
positive regulation of peptidyl-lysine acetylation (GO:200	44612	0.764490315	0.885908361
production of small RNA involved in gene silencing by RN	44612	0.764490315	0.885908361
protein-DNA complex disassembly (GO:0032986)	44612	0.764490315	0.885908361
regulation of fibroblast growth factor receptor signaling p	44612	0.764490315	0.885908361
regulation of protein kinase A signaling (GO:0010738)	44612	0.764490315	0.885908361
mRNA processing (GO:0006397)	36/300	0.766452823	0.887984482
response to calcium ion (GO:0051592)	12/107	0.775017366	0.897706848
steroid biosynthetic process (GO:0006694)	23924	0.77615024	0.898618341
tRNA modification (GO:0006400)	23924	0.77615024	0.898618341
regulation of dendrite development (GO:0050773)	14336	0.778772176	0.900069388
establishment of spindle orientation (GO:0051294)	44650	0.779684168	0.900069388
ion homeostasis (GO:0050801)	44650	0.779684168	0.900069388
long-chain fatty acid biosynthetic process (GO:0042759)	44650	0.779684168	0.900069388
primary neural tube formation (GO:0014020)	44650	0.779684168	0.900069388
regulation of long-term synaptic potentiation (GO:19002	44650	0.779684168	0.900069388
mitotic nuclear division (GO:0140014)	27242	0.782225705	0.900069388
regulation of G2/M transition of mitotic cell cycle (GO:00	17/149	0.782472147	0.900069388
acetylcholine receptor signaling pathway (GO:0095500)	44613	0.78805448	0.900069388
anterior/posterior axis specification (GO:0009948)	44613	0.78805448	0.900069388
autonomic nervous system development (GO:0048483)	44613	0.78805448	0.900069388
cellular response to estradiol stimulus (GO:0071392)	44613	0.78805448	0.900069388
cobalamin metabolic process (GO:0009235)	44613	0.78805448	0.900069388
endocardial cushion development (GO:0003197)	44613	0.78805448	0.900069388
heparan sulfate proteoglycan metabolic process (GO:003	44613	0.78805448	0.900069388
hydrogen peroxide catabolic process (GO:0042744)	44613	0.78805448	0.900069388
melanosome localization (GO:0032400)	44613	0.78805448	0.900069388
natural killer cell activation involved in immune response	44613	0.78805448	0.900069388
nucleotide-excision repair, DNA incision, 3'-to lesion (GO:	44613	0.78805448	0.900069388
nucleotide-excision repair, preincision complex stabilizati	44613	0.78805448	0.900069388
positive regulation of smoothened signaling pathway (GC	44613	0.78805448	0.900069388
protein localization to chromatin (GO:0071168)	44613	0.78805448	0.900069388

regulation of cardiac muscle contraction by calcium ion si	44613	0.78805448	0.900069388
regulation of lipoprotein lipase activity (GO:0051004)	44613	0.78805448	0.900069388
peptide metabolic process (GO:0006518)	30560	0.78833741	0.900069388
positive regulation of translation (GO:0045727)	11/100	0.789708786	0.900069388
actin filament depolymerization (GO:0030042)	44572	0.791090823	0.900069388
actin filament network formation (GO:0051639)	44572	0.791090823	0.900069388
alcohol catabolic process (GO:0046164)	44572	0.791090823	0.900069388
axonal transport of mitochondrion (GO:0019896)	44572	0.791090823	0.900069388
calcineurin-NFAT signaling cascade (GO:0033173)	44572	0.791090823	0.900069388
cellular response to UV-A (GO:0071492)	44572	0.791090823	0.900069388
central nervous system myelination (GO:0022010)	44572	0.791090823	0.900069388
coenzyme A biosynthetic process (GO:0015937)	44572	0.791090823	0.900069388
detection of light stimulus involved in sensory perceptior	44572	0.791090823	0.900069388
detection of light stimulus involved in visual perception (	44572	0.791090823	0.900069388
ER-associated misfolded protein catabolic process (GO:0(	44572	0.791090823	0.900069388
erythrocyte development (GO:0048821)	44572	0.791090823	0.900069388
establishment of endothelial intestinal barrier (GO:00905	44572	0.791090823	0.900069388
glucocorticoid biosynthetic process (GO:0006704)	44572	0.791090823	0.900069388
glucocorticoid metabolic process (GO:0008211)	44572	0.791090823	0.900069388
inositol phosphate biosynthetic process (GO:0032958)	44572	0.791090823	0.900069388
lipoprotein catabolic process (GO:0042159)	44572	0.791090823	0.900069388
metanephric mesenchyme development (GO:0072075)	44572	0.791090823	0.900069388
mitochondrial transcription (GO:0006390)	44572	0.791090823	0.900069388
mitochondrion morphogenesis (GO:0070584)	44572	0.791090823	0.900069388
myotube cell development (GO:0014904)	44572	0.791090823	0.900069388
negative regulation of calcium ion transmembrane transp	44572	0.791090823	0.900069388
negative regulation of centrosome duplication (GO:0010{	44572	0.791090823	0.900069388
negative regulation of intracellular estrogen receptor sigr	44572	0.791090823	0.900069388
negative regulation of natural killer cell mediated immun	44572	0.791090823	0.900069388
negative regulation of potassium ion transmembrane tra	44572	0.791090823	0.900069388
negative regulation of protein maturation (GO:1903318)	44572	0.791090823	0.900069388
peptidyl-proline hydroxylation (GO:0019511)	44572	0.791090823	0.900069388
positive regulation of actin nucleation (GO:0051127)	44572	0.791090823	0.900069388
positive regulation of chondrocyte differentiation (GO:00	44572	0.791090823	0.900069388
positive regulation of cytoplasmic transport (GO:190365{	44572	0.791090823	0.900069388
positive regulation of neuroblast proliferation (GO:00020	44572	0.791090823	0.900069388
positive regulation of non-canonical Wnt signaling pathw	44572	0.791090823	0.900069388
positive regulation of viral release from host cell (GO:190	44572	0.791090823	0.900069388
protein localization to phagophore assembly site (GO:00{	44572	0.791090823	0.900069388
protein polyglutamylation (GO:0018095)	44572	0.791090823	0.900069388
purine nucleoside bisphosphate biosynthetic process (GC	44572	0.791090823	0.900069388
regulation of biosynthetic process (GO:0009889)	44572	0.791090823	0.900069388
regulation of endocytic recycling (GO:2001135)	44572	0.791090823	0.900069388
regulation of histone H3-K9 acetylation (GO:2000615)	44572	0.791090823	0.900069388
regulation of melanin biosynthetic process (GO:0048021)	44572	0.791090823	0.900069388
regulation of mRNA 3'-end processing (GO:0031440)	44572	0.791090823	0.900069388
regulation of myeloid leukocyte mediated immunity (GO:	44572	0.791090823	0.900069388

response to hydroxyurea (GO:0072710)	44572	0.791090823	0.900069388
response to prostaglandin E (GO:0034695)	44572	0.791090823	0.900069388
rhodopsin mediated signaling pathway (GO:0016056)	44572	0.791090823	0.900069388
ribonucleoside bisphosphate biosynthetic process (GO:0(	44572	0.791090823	0.900069388
signal peptide processing (GO:0006465)	44572	0.791090823	0.900069388
skeletal muscle cell differentiation (GO:0035914)	44572	0.791090823	0.900069388
sphingomyelin metabolic process (GO:0006684)	44572	0.791090823	0.900069388
telomere maintenance via recombination (GO:0000722)	44572	0.791090823	0.900069388
UDP-N-acetylglucosamine biosynthetic process (GO:0006	44572	0.791090823	0.900069388
V(D)J recombination (GO:0033151)	44572	0.791090823	0.900069388
positive regulation of transmembrane receptor protein s(	33878	0.794388653	0.903623616
negative regulation of cell-substrate adhesion (GO:00108	14702	0.795634096	0.904248332
organic hydroxy compound transport (GO:0015850)	14702	0.795634096	0.904248332
positive regulation of ossification (GO:0045778)	14702	0.795634096	0.904248332
stem cell differentiation (GO:0048863)	14702	0.795634096	0.904248332
modulation of chemical synaptic transmission (GO:00508	12/109	0.796117511	0.90459984
oligosaccharide metabolic process (GO:0009311)	18019	0.796336069	0.904650313
activation of protein kinase B activity (GO:0032148)	44651	0.798572574	0.905390564
cardiac muscle cell action potential involved in contractic	44651	0.798572574	0.905390564
negative regulation of osteoblast differentiation (GO:004	44651	0.798572574	0.905390564
organelle transport along microtubule (GO:0072384)	44651	0.798572574	0.905390564
purine nucleoside bisphosphate metabolic process (GO:0	44651	0.798572574	0.905390564
regulation of transmembrane receptor protein serine/thr	44651	0.798572574	0.905390564
ribonucleoside bisphosphate metabolic process (GO:003	44651	0.798572574	0.905390564
steroid hormone biosynthetic process (GO:0120178)	44651	0.798572574	0.905390564
tube closure (GO:0060606)	44651	0.798572574	0.905390564
eye development (GO:0001654)	21337	0.798904783	0.905390564
nucleosome assembly (GO:0006334)	21337	0.798904783	0.905390564
anaphase-promoting complex-dependent catabolic proce	30926	0.799958444	0.90638694
regulation of BMP signaling pathway (GO:0030510)	27973	0.806640768	0.909894729
cellular response to nerve growth factor stimulus (GO:19	44614	0.8095138	0.909894729
maturation of 5.8S rRNA from tricistronic rRNA transcript	44614	0.8095138	0.909894729
neuronal action potential (GO:0019228)	44614	0.8095138	0.909894729
nucleotide-excision repair, DNA duplex unwinding (GO:0(	44614	0.8095138	0.909894729
positive regulation of dendritic spine development (GO:0	44614	0.8095138	0.909894729
positive regulation of neural precursor cell proliferation (	44614	0.8095138	0.909894729
protein import into peroxisome membrane (GO:0045046	44614	0.8095138	0.909894729
protein localization to cell junction (GO:1902414)	44614	0.8095138	0.909894729
regulation of chromosome organization (GO:0033044)	44614	0.8095138	0.909894729
rRNA methylation (GO:0031167)	44614	0.8095138	0.909894729
tetrapyrrole metabolic process (GO:0033013)	44614	0.8095138	0.909894729
cell junction assembly (GO:0034329)	11/102	0.81054318	0.909894729
mitotic sister chromatid segregation (GO:0000070)	11/102	0.81054318	0.909894729
neuron migration (GO:0001764)	18384	0.81074202	0.909894729
ribosome assembly (GO:0042255)	18384	0.81074202	0.909894729
gluconeogenesis (GO:0006094)	15067	0.811443912	0.909894729
heart contraction (GO:0060047)	15067	0.811443912	0.909894729

hexose metabolic process (GO:0019318)	15067	0.811443912	0.909894729
positive regulation of biomineral tissue development (GC	15067	0.811443912	0.909894729
protein methylation (GO:0006479)	15067	0.811443912	0.909894729
visual system development (GO:0150063)	15067	0.811443912	0.909894729
aortic valve morphogenesis (GO:0003180)	11749	0.816084158	0.909894729
axonemal dynein complex assembly (GO:0070286)	11749	0.816084158	0.909894729
cellular response to glucose stimulus (GO:0071333)	11749	0.816084158	0.909894729
membrane depolarization (GO:0051899)	11749	0.816084158	0.909894729
regulation of dendrite morphogenesis (GO:0048814)	11749	0.816084158	0.909894729
microtubule cytoskeleton organization involved in mitosi	14/128	0.817203705	0.909894729
cholesterol metabolic process (GO:0008203)	28338	0.818042635	0.909894729
actin crosslink formation (GO:0051764)	44573	0.818817682	0.909894729
amino sugar biosynthetic process (GO:0046349)	44573	0.818817682	0.909894729
ATP transport (GO:0015867)	44573	0.818817682	0.909894729
attachment of mitotic spindle microtubules to kinetocho	44573	0.818817682	0.909894729
axonal fasciculation (GO:0007413)	44573	0.818817682	0.909894729
calcineurin-mediated signaling (GO:0097720)	44573	0.818817682	0.909894729
catecholamine biosynthetic process (GO:0042423)	44573	0.818817682	0.909894729
cell differentiation in hindbrain (GO:0021533)	44573	0.818817682	0.909894729
cochlea morphogenesis (GO:0090103)	44573	0.818817682	0.909894729
dermatan sulfate biosynthetic process (GO:0030208)	44573	0.818817682	0.909894729
digestive system development (GO:0055123)	44573	0.818817682	0.909894729
early endosome to Golgi transport (GO:0034498)	44573	0.818817682	0.909894729
endoplasmic reticulum membrane organization (GO:009(	44573	0.818817682	0.909894729
epithelial cell-cell adhesion (GO:0090136)	44573	0.818817682	0.909894729
ethanol oxidation (GO:0006069)	44573	0.818817682	0.909894729
ganglion development (GO:0061548)	44573	0.818817682	0.909894729
gas transport (GO:0015669)	44573	0.818817682	0.909894729
glomerular visceral epithelial cell differentiation (GO:007	44573	0.818817682	0.909894729
Golgi localization (GO:0051645)	44573	0.818817682	0.909894729
hemidesmosome assembly (GO:0031581)	44573	0.818817682	0.909894729
magnesium ion transport (GO:0015693)	44573	0.818817682	0.909894729
megakaryocyte differentiation (GO:0030219)	44573	0.818817682	0.909894729
melanocyte differentiation (GO:0030318)	44573	0.818817682	0.909894729
mesoderm morphogenesis (GO:0048332)	44573	0.818817682	0.909894729
mitochondrial genome maintenance (GO:0000002)	44573	0.818817682	0.909894729
negative regulation of amyloid fibril formation (GO:1905(	44573	0.818817682	0.909894729
negative regulation of calcineurin-mediated signaling (GC	44573	0.818817682	0.909894729
negative regulation of calcineurin-NFAT signaling cascade	44573	0.818817682	0.909894729
negative regulation of cardiac muscle hypertrophy (GO:0(	44573	0.818817682	0.909894729
negative regulation of fatty acid biosynthetic process (GC	44573	0.818817682	0.909894729
negative regulation of histone acetylation (GO:0035067)	44573	0.818817682	0.909894729
negative regulation of microtubule polymerization (GO:0(	44573	0.818817682	0.909894729
negative regulation of oxidoreductase activity (GO:00513	44573	0.818817682	0.909894729
negative regulation of transcription elongation from RNA	44573	0.818817682	0.909894729
P-body assembly (GO:0033962)	44573	0.818817682	0.909894729
peptidyl-methionine modification (GO:0018206)	44573	0.818817682	0.909894729

positive regulation of branching involved in ureteric bud	44573	0.818817682	0.909894729
positive regulation of fatty acid oxidation (GO:0046321)	44573	0.818817682	0.909894729
positive regulation of metaphase/anaphase transition of	44573	0.818817682	0.909894729
positive regulation of mitotic metaphase/anaphase trans	44573	0.818817682	0.909894729
positive regulation of mitotic sister chromatid separation	44573	0.818817682	0.909894729
positive regulation of protein depolymerization (GO:1901	44573	0.818817682	0.909894729
positive regulation of vascular permeability (GO:0043117	44573	0.818817682	0.909894729
protein localization to condensed chromosome (GO:1903	44573	0.818817682	0.909894729
protein localization to synapse (GO:0035418)	44573	0.818817682	0.909894729
purine nucleoside monophosphate biosynthetic process (	44573	0.818817682	0.909894729
purine nucleotide biosynthetic process (GO:0006164)	44573	0.818817682	0.909894729
regulation of axon regeneration (GO:0048679)	44573	0.818817682	0.909894729
regulation of CD4-positive, alpha-beta T cell differentiatic	44573	0.818817682	0.909894729
regulation of DNA-dependent DNA replication (GO:00903	44573	0.818817682	0.909894729
regulation of muscle system process (GO:0090257)	44573	0.818817682	0.909894729
regulation of response to oxidative stress (GO:1902882)	44573	0.818817682	0.909894729
regulation of sensory perception (GO:0051931)	44573	0.818817682	0.909894729
regulation of sequestering of calcium ion (GO:0051282)	44573	0.818817682	0.909894729
regulation of triglyceride catabolic process (GO:0010896)	44573	0.818817682	0.909894729
replicative senescence (GO:0090399)	44573	0.818817682	0.909894729
sensory perception of taste (GO:0050909)	44573	0.818817682	0.909894729
sno(s)RNA 3'-end processing (GO:0031126)	44573	0.818817682	0.909894729
sphingoid metabolic process (GO:0046519)	44573	0.818817682	0.909894729
thyroid hormone generation (GO:0006590)	44573	0.818817682	0.909894729
urogenital system development (GO:0001655)	44573	0.818817682	0.909894729
mitotic metaphase plate congression (GO:0007080)	18749	0.824322259	0.915815684
regulation of double-strand break repair (GO:2000779)	15432	0.8262379	0.917747679
ear morphogenesis (GO:0042471)	44615	0.829011825	0.919060271
positive regulation of cell cycle G2/M phase transition (G	44615	0.829011825	0.919060271
positive regulation of morphogenesis of an epithelium (G	44615	0.829011825	0.919060271
protein alkylation (GO:0008213)	44615	0.829011825	0.919060271
regulation of protein export from nucleus (GO:0046825)	44615	0.829011825	0.919060271
regulation of supramolecular fiber organization (GO:1902	44615	0.829011825	0.919060271
regulation of telomere capping (GO:1904353)	44615	0.829011825	0.919060271
respiratory chain complex IV assembly (GO:0008535)	44615	0.829011825	0.919060271
response to nutrient levels (GO:0031667)	44615	0.829011825	0.919060271
bile acid metabolic process (GO:0008206)	12114	0.83228424	0.922097809
mitotic G2 DNA damage checkpoint signaling (GO:00070	12114	0.83228424	0.922097809
vasculogenesis (GO:0001570)	12114	0.83228424	0.922097809
positive regulation of DNA biosynthetic process (GO:200	22433	0.836553051	0.923189446
response to light stimulus (GO:0009416)	22433	0.836553051	0.923189446
endocytic recycling (GO:0032456)	19115	0.837102227	0.923189446
negative regulation of BMP signaling pathway (GO:00305	19115	0.837102227	0.923189446
regulation of release of sequestered calcium ion into cyto	19115	0.837102227	0.923189446
regulation of telomere maintenance via telomerase (GO:	19115	0.837102227	0.923189446
COPII-coated vesicle budding (GO:0090114)	25750	0.837459294	0.923189446
potassium ion transport (GO:0006813)	13/122	0.838080885	0.923189446

potassium ion transmembrane transport (GO:0071805)	15/139	0.838611243	0.923189446
axon development (GO:0061564)	29068	0.839282433	0.923189446
regulation of cellular response to heat (GO:1900034)	29068	0.839282433	0.923189446
regulation of ion transport (GO:0043269)	29068	0.839282433	0.923189446
glutathione metabolic process (GO:0006749)	15797	0.840055253	0.923189446
cell cycle G2/M phase transition (GO:0044839)	14/131	0.842189917	0.923189446
alpha-linolenic acid metabolic process (GO:0036109)	44574	0.842865744	0.923189446
cell part morphogenesis (GO:0032990)	44574	0.842865744	0.923189446
central nervous system projection neuron axonogenesis (	44574	0.842865744	0.923189446
cranial nerve development (GO:0021545)	44574	0.842865744	0.923189446
dermatan sulfate metabolic process (GO:0030205)	44574	0.842865744	0.923189446
detection of calcium ion (GO:0005513)	44574	0.842865744	0.923189446
DNA deamination (GO:0045006)	44574	0.842865744	0.923189446
DNA replication-independent nucleosome organization ((	44574	0.842865744	0.923189446
endochondral bone morphogenesis (GO:0060350)	44574	0.842865744	0.923189446
extracellular transport (GO:0006858)	44574	0.842865744	0.923189446
inner dynein arm assembly (GO:0036159)	44574	0.842865744	0.923189446
kinetochore organization (GO:0051383)	44574	0.842865744	0.923189446
lipid oxidation (GO:0034440)	44574	0.842865744	0.923189446
microtubule-based transport (GO:0099111)	44574	0.842865744	0.923189446
mitochondrion transport along microtubule (GO:004749	44574	0.842865744	0.923189446
negative regulation of cell morphogenesis involved in dif	44574	0.842865744	0.923189446
negative regulation of cellular senescence (GO:2000773)	44574	0.842865744	0.923189446
negative regulation of DNA-dependent DNA replication ((	44574	0.842865744	0.923189446
negative regulation of epidermal growth factor-activated	44574	0.842865744	0.923189446
negative regulation of nucleocytoplasmic transport (GO:(	44574	0.842865744	0.923189446
negative regulation of substrate adhesion-dependent cel	44574	0.842865744	0.923189446
plasma membrane repair (GO:0001778)	44574	0.842865744	0.923189446
positive regulation of calcineurin-mediated signaling (GO	44574	0.842865744	0.923189446
positive regulation of calcineurin-NFAT signaling cascade	44574	0.842865744	0.923189446
positive regulation of insulin receptor signaling pathway (	44574	0.842865744	0.923189446
positive regulation of lipid transport (GO:0032370)	44574	0.842865744	0.923189446
positive regulation of sodium ion transport (GO:0010765	44574	0.842865744	0.923189446
positive regulation of steroid metabolic process (GO:004	44574	0.842865744	0.923189446
positive regulation of vascular endothelial cell proliferati	44574	0.842865744	0.923189446
protein neddylation (GO:0045116)	44574	0.842865744	0.923189446
regulation of histone modification (GO:0031056)	44574	0.842865744	0.923189446
regulation of membrane repolarization (GO:0060306)	44574	0.842865744	0.923189446
regulation of mitotic cell cycle spindle assembly checkpoi	44574	0.842865744	0.923189446
regulation of nucleocytoplasmic transport (GO:0046822)	44574	0.842865744	0.923189446
regulation of T cell differentiation in thymus (GO:003308	44574	0.842865744	0.923189446
reticulophagy (GO:0061709)	44574	0.842865744	0.923189446
spliceosomal tri-snRNP complex assembly (GO:0000244)	44574	0.842865744	0.923189446
transcription preinitiation complex assembly (GO:007089	44574	0.842865744	0.923189446
triglyceride-rich lipoprotein particle remodeling (GO:003	44574	0.842865744	0.923189446
UDP-N-acetylglucosamine metabolic process (GO:000604	44574	0.842865744	0.923189446
C21-steroid hormone metabolic process (GO:0008207)	44616	0.846691068	0.92427877

dorsal/ventral pattern formation (GO:0009953)	44616	0.846691068	0.92427877
establishment of mitotic spindle orientation (GO:000013	44616	0.846691068	0.92427877
inner ear morphogenesis (GO:0042472)	44616	0.846691068	0.92427877
neuromuscular junction development (GO:0007528)	44616	0.846691068	0.92427877
nucleotide-excision repair, DNA gap filling (GO:0006297)	44616	0.846691068	0.92427877
positive regulation of phospholipase activity (GO:001051	44616	0.846691068	0.92427877
protein insertion into mitochondrial membrane (GO:005	44616	0.846691068	0.92427877
regulation of cellular response to transforming growth fa	44616	0.846691068	0.92427877
negative regulation of mitochondrion organization (GO:0	12479	0.847240713	0.92427877
neural tube closure (GO:0001843)	12479	0.847240713	0.92427877
phosphatidylserine metabolic process (GO:0006658)	12479	0.847240713	0.92427877
positive regulation of calcium ion transport into cytosol (	12479	0.847240713	0.92427877
positive regulation of telomerase activity (GO:0051973)	12479	0.847240713	0.92427877
protein insertion into membrane (GO:0051205)	12479	0.847240713	0.92427877
regulation of glucose metabolic process (GO:0010906)	12479	0.847240713	0.92427877
sister chromatid segregation (GO:0000819)	12479	0.847240713	0.92427877
striated muscle tissue development (GO:0014706)	12479	0.847240713	0.92427877
synaptic vesicle recycling (GO:0036465)	12479	0.847240713	0.92427877
endomembrane system organization (GO:0010256)	22/199	0.848768455	0.925751024
intracellular protein transmembrane transport (GO:0065	16163	0.852937299	0.930102701
cytoskeleton-dependent cytokinesis (GO:0061640)	26481	0.857901329	0.93246898
monocarboxylic acid biosynthetic process (GO:0072330)	23163	0.858338968	0.93246898
striated muscle contraction (GO:0006941)	19845	0.860372532	0.93246898
embryonic skeletal system development (GO:0048706)	12844	0.861022786	0.93246898
muscle cell differentiation (GO:0042692)	12844	0.861022786	0.93246898
regulation of blood circulation (GO:1903522)	12844	0.861022786	0.93246898
regulation of postsynaptic membrane potential (GO:006	12844	0.861022786	0.93246898
regulation of protein polymerization (GO:0032271)	12844	0.861022786	0.93246898
smoothened signaling pathway (GO:0007224)	12844	0.861022786	0.93246898
cAMP-mediated signaling (GO:0019933)	44617	0.862690762	0.93246898
regulation of rhodopsin mediated signaling pathway (GO	44617	0.862690762	0.93246898
regulation of ryanodine-sensitive calcium-release channe	44617	0.862690762	0.93246898
ribosomal large subunit assembly (GO:0000027)	44617	0.862690762	0.93246898
RNA splicing, via transesterification reactions (GO:00003	44617	0.862690762	0.93246898
atrial septum development (GO:0003283)	44575	0.863722951	0.93246898
atrioventricular valve development (GO:0003171)	44575	0.863722951	0.93246898
cardiac left ventricle morphogenesis (GO:0003214)	44575	0.863722951	0.93246898
cell junction maintenance (GO:0034331)	44575	0.863722951	0.93246898
COPII-coated vesicle cargo loading (GO:0090110)	44575	0.863722951	0.93246898
ether lipid metabolic process (GO:0046485)	44575	0.863722951	0.93246898
heart process (GO:0003015)	44575	0.863722951	0.93246898
histone H3-K4 trimethylation (GO:0080182)	44575	0.863722951	0.93246898
intestinal absorption (GO:0050892)	44575	0.863722951	0.93246898
ncRNA transcription (GO:0098781)	44575	0.863722951	0.93246898
negative regulation of cell activation (GO:0050866)	44575	0.863722951	0.93246898
negative regulation of DNA-templated transcription, elon	44575	0.863722951	0.93246898
negative regulation of fibroblast growth factor receptor s	44575	0.863722951	0.93246898

negative regulation of mRNA splicing, via spliceosome (G	44575	0.863722951	0.93246898
negative regulation of T cell differentiation (GO:0045581	44575	0.863722951	0.93246898
neurotransmitter biosynthetic process (GO:0042136)	44575	0.863722951	0.93246898
ovarian follicle development (GO:0001541)	44575	0.863722951	0.93246898
pancreas development (GO:0031016)	44575	0.863722951	0.93246898
positive regulation of cellular response to insulin stimulu	44575	0.863722951	0.93246898
positive regulation of mitochondrial translation (GO:007(	44575	0.863722951	0.93246898
protein localization to kinetochore (GO:0034501)	44575	0.863722951	0.93246898
protein maturation by iron-sulfur cluster transfer (GO:00	44575	0.863722951	0.93246898
quinone biosynthetic process (GO:1901663)	44575	0.863722951	0.93246898
regulation of cAMP-dependent protein kinase activity (G(	44575	0.863722951	0.93246898
regulation of gastrulation (GO:0010470)	44575	0.863722951	0.93246898
regulation of histone deacetylation (GO:0031063)	44575	0.863722951	0.93246898
regulation of lipase activity (GO:0060191)	44575	0.863722951	0.93246898
regulation of sensory perception of pain (GO:0051930)	44575	0.863722951	0.93246898
regulation of transcription of nucleolar large rRNA by RN/	44575	0.863722951	0.93246898
respiratory electron transport chain (GO:0022904)	44575	0.863722951	0.93246898
response to UV-A (GO:0070141)	44575	0.863722951	0.93246898
retinal metabolic process (GO:0042574)	44575	0.863722951	0.93246898
sulfate transport (GO:0008272)	44575	0.863722951	0.93246898
tRNA wobble uridine modification (GO:0002098)	44575	0.863722951	0.93246898
microtubule bundle formation (GO:0001578)	16528	0.86492682	0.933574658
protein-DNA complex assembly (GO:0065004)	15/143	0.867495849	0.936153082
diterpenoid metabolic process (GO:0016101)	23529	0.868300732	0.936438095
negative regulation of cell cycle process (GO:0010948)	23529	0.868300732	0.936438095
pre-replicative complex assembly (GO:0036388)	23529	0.868300732	0.936438095
regulation of sodium ion transport (GO:0002028)	13210	0.873699938	0.942065416
regulation of cellular protein localization (GO:1903827)	16893	0.876067455	0.944344708
global genome nucleotide-excision repair (GO:0070911)	44618	0.877145215	0.944344708
histone methylation (GO:0016571)	44618	0.877145215	0.944344708
epithelial cell differentiation (GO:0030855)	10/101	0.877257949	0.944344708
ribonucleoprotein complex assembly (GO:0022618)	14/136	0.877925158	0.944344708
aflatoxin metabolic process (GO:0046222)	44576	0.881812547	0.944344708
catecholamine metabolic process (GO:0006584)	44576	0.881812547	0.944344708
detection of mechanical stimulus involved in sensory per	44576	0.881812547	0.944344708
electron transport chain (GO:0022900)	44576	0.881812547	0.944344708
eye photoreceptor cell development (GO:0042462)	44576	0.881812547	0.944344708
G protein-coupled glutamate receptor signaling pathway	44576	0.881812547	0.944344708
glucosamine-containing compound metabolic process (G(	44576	0.881812547	0.944344708
medium-chain fatty acid metabolic process (GO:0051791	44576	0.881812547	0.944344708
mitotic recombination (GO:0006312)	44576	0.881812547	0.944344708
mycotoxin metabolic process (GO:0043385)	44576	0.881812547	0.944344708
myoblast fusion (GO:0007520)	44576	0.881812547	0.944344708
negative regulation of cellular component movement (G(	44576	0.881812547	0.944344708
negative regulation of mRNA processing (GO:0050686)	44576	0.881812547	0.944344708
organic heteropentacyclic compound metabolic process (	44576	0.881812547	0.944344708
photoreceptor cell development (GO:0042461)	44576	0.881812547	0.944344708

phototransduction, visible light (GO:0007603)	44576	0.881812547	0.944344708
positive regulation of double-strand break repair via hom	44576	0.881812547	0.944344708
positive regulation of glycogen metabolic process (GO:00	44576	0.881812547	0.944344708
positive regulation of histone H3-K4 methylation (GO:00	44576	0.881812547	0.944344708
protein kinase A signaling (GO:0010737)	44576	0.881812547	0.944344708
protein localization to chromosome, telomeric region (G	44576	0.881812547	0.944344708
regulation of branching involved in ureteric bud morpho	44576	0.881812547	0.944344708
regulation of cytoplasmic translation (GO:2000765)	44576	0.881812547	0.944344708
regulation of establishment of protein localization (GO:0	44576	0.881812547	0.944344708
regulation of non-canonical Wnt signaling pathway (GO:2	44576	0.881812547	0.944344708
regulation of phospholipase C activity (GO:1900274)	44576	0.881812547	0.944344708
ubiquinone biosynthetic process (GO:0006744)	44576	0.881812547	0.944344708
ubiquinone metabolic process (GO:0006743)	44576	0.881812547	0.944344708
protein O-linked glycosylation (GO:0006493)	10/102	0.884509539	0.947037728
acyl-CoA metabolic process (GO:0006637)	13575	0.885341064	0.947395415
proton transmembrane transport (GO:1902600)	13575	0.885341064	0.947395415
organelle organization (GO:0006996)	48/420	0.88539071	0.947395415
bile acid biosynthetic process (GO:0006699)	44619	0.890182673	0.950565054
microtubule polymerization or depolymerization (GO:00	44619	0.890182673	0.950565054
monovalent inorganic cation homeostasis (GO:0055067)	44619	0.890182673	0.950565054
peptidyl-lysine methylation (GO:0018022)	44619	0.890182673	0.950565054
peroxisomal membrane transport (GO:0015919)	44619	0.890182673	0.950565054
positive regulation of BMP signaling pathway (GO:00305	44619	0.890182673	0.950565054
positive regulation of calcium ion transmembrane transp	44619	0.890182673	0.950565054
protein peptidyl-prolyl isomerization (GO:0000413)	44619	0.890182673	0.950565054
regulation of cardiac muscle cell contraction (GO:008600	44619	0.890182673	0.950565054
regulation of transcription regulatory region DNA binding	44619	0.890182673	0.950565054
regulation of cell cycle G2/M phase transition (GO:19027	31260	0.891389363	0.951657982
actomyosin structure organization (GO:0031032)	27942	0.892495251	0.952447171
establishment of protein localization to organelle (GO:00	27942	0.892495251	0.952447171
establishment of protein localization to mitochondrion (G	17624	0.895977855	0.954066113
actin-myosin filament sliding (GO:0033275)	13940	0.896013783	0.954066113
muscle filament sliding (GO:0030049)	13940	0.896013783	0.954066113
negative regulation of endothelial cell migration (GO:001	13940	0.896013783	0.954066113
regulation of axon extension (GO:0030516)	13940	0.896013783	0.954066113
sterol biosynthetic process (GO:0016126)	13940	0.896013783	0.954066113
heme catabolic process (GO:0042167)	44577	0.897501654	0.954066113
mesenchyme development (GO:0060485)	44577	0.897501654	0.954066113
mRNA cis splicing, via spliceosome (GO:0045292)	44577	0.897501654	0.954066113
N-acetylglucosamine metabolic process (GO:0006044)	44577	0.897501654	0.954066113
negative regulation of histone modification (GO:0031057	44577	0.897501654	0.954066113
negative regulation of release of cytochrome c from mito	44577	0.897501654	0.954066113
neural tube development (GO:0021915)	44577	0.897501654	0.954066113
oligodendrocyte development (GO:0014003)	44577	0.897501654	0.954066113
porphyrin-containing compound catabolic process (GO:0	44577	0.897501654	0.954066113
positive regulation of collagen biosynthetic process (GO:(	44577	0.897501654	0.954066113
regulation of cellular carbohydrate metabolic process (G	44577	0.897501654	0.954066113

retrograde axonal transport (GO:0008090)	44577	0.897501654	0.954066113
transepithelial transport (GO:0070633)	44577	0.897501654	0.954066113
chordate embryonic development (GO:0043009)	21306	0.898596813	0.954839526
regulation of pathway-restricted SMAD protein phosphor	21306	0.898596813	0.954839526
bile acid and bile salt transport (GO:0015721)	44620	0.90192456	0.957005328
macromolecule catabolic process (GO:0009057)	44620	0.90192456	0.957005328
negative regulation of axonogenesis (GO:0050771)	44620	0.90192456	0.957005328
protein depolymerization (GO:0051261)	44620	0.90192456	0.957005328
regulation of small molecule metabolic process (GO:0062	44620	0.90192456	0.957005328
regulation of sodium ion transmembrane transport (GO:1	44620	0.90192456	0.957005328
sarcomere organization (GO:0045214)	44620	0.90192456	0.957005328
mitochondrion organization (GO:0007005)	18/175	0.903148542	0.958108368
regulation of exit from mitosis (GO:0007096)	14305	0.905783887	0.960707899
mitotic DNA damage checkpoint signaling (GO:0044773)	21671	0.90660183	0.961379161
adenylate cyclase-activating adrenergic receptor signalin	44578	0.911108712	0.962230079
cellular biogenic amine biosynthetic process (GO:004240	44578	0.911108712	0.962230079
cellular response to gamma radiation (GO:0071480)	44578	0.911108712	0.962230079
detection of visible light (GO:0009584)	44578	0.911108712	0.962230079
embryo development ending in birth or egg hatching (GO	44578	0.911108712	0.962230079
epithelial cell morphogenesis (GO:0003382)	44578	0.911108712	0.962230079
gliogenesis (GO:0042063)	44578	0.911108712	0.962230079
maturation of 5.8S rRNA (GO:0000460)	44578	0.911108712	0.962230079
mitochondrial ATP synthesis coupled proton transport (G	44578	0.911108712	0.962230079
negative regulation of cell aging (GO:0090344)	44578	0.911108712	0.962230079
positive regulation of dendrite extension (GO:1903861)	44578	0.911108712	0.962230079
positive regulation of heart rate (GO:0010460)	44578	0.911108712	0.962230079
preassembly of GPI anchor in ER membrane (GO:001625	44578	0.911108712	0.962230079
protein heterooligomerization (GO:0051291)	44578	0.911108712	0.962230079
protein localization to chromosome, centromeric region	44578	0.911108712	0.962230079
pulmonary valve morphogenesis (GO:0003184)	44578	0.911108712	0.962230079
purine ribonucleotide transport (GO:0015868)	44578	0.911108712	0.962230079
regulation of cellular response to growth factor stimulus	44578	0.911108712	0.962230079
ribosomal small subunit assembly (GO:0000028)	44578	0.911108712	0.962230079
snRNA metabolic process (GO:0016073)	44578	0.911108712	0.962230079
determination of bilateral symmetry (GO:0009855)	47150	0.912485033	0.962900619
glial cell differentiation (GO:0010001)	47150	0.912485033	0.962900619
nucleotide-excision repair, preincision complex assembly	47150	0.912485033	0.962900619
telomere maintenance via telomerase (GO:0007004)	47150	0.912485033	0.962900619
regulation of microtubule polymerization (GO:0031113)	14671	0.914714921	0.96505768
collagen fibril organization (GO:0030199)	32721	0.917619283	0.967925314
maturation of SSU-rRNA from tricistronic rRNA transcript	10990	0.921970773	0.969372644
protein N-linked glycosylation via asparagine (GO:001827	10990	0.921970773	0.969372644
regulation of catecholamine secretion (GO:0050433)	10990	0.921970773	0.969372644
regulation of vasoconstriction (GO:0019229)	10990	0.921970773	0.969372644
RNA-dependent DNA biosynthetic process (GO:0006278)	10990	0.921970773	0.969372644
snRNA 3'-end processing (GO:0034472)	10990	0.921970773	0.969372644
adenine nucleotide transport (GO:0051503)	44579	0.922909932	0.969372644

base conversion or substitution editing (GO:0016553)	44579	0.922909932	0.969372644
cellular response to zinc ion (GO:0071294)	44579	0.922909932	0.969372644
embryonic heart tube development (GO:0035050)	44579	0.922909932	0.969372644
fluid transport (GO:0042044)	44579	0.922909932	0.969372644
negative regulation of peptide hormone secretion (GO:0(	44579	0.922909932	0.969372644
negative regulation of tumor necrosis factor-mediated si	44579	0.922909932	0.969372644
nitric oxide mediated signal transduction (GO:0007263)	44579	0.922909932	0.969372644
regulation of cartilage development (GO:0061035)	44579	0.922909932	0.969372644
regulation of delayed rectifier potassium channel activity	44579	0.922909932	0.969372644
regulation of dendrite extension (GO:1903859)	44579	0.922909932	0.969372644
regulation of mRNA polyadenylation (GO:1900363)	44579	0.922909932	0.969372644
regulation of ventricular cardiac muscle cell membrane r	44579	0.922909932	0.969372644
sodium ion import across plasma membrane (GO:009871	44579	0.922909932	0.969372644
tRNA metabolic process (GO:0006399)	44579	0.922909932	0.969372644
organelle assembly (GO:0070925)	47/425	0.926099855	0.972526531
antigen processing and presentation of peptide antigen v	9/100	0.926970963	0.973244574
determination of left/right symmetry (GO:0007368)	15401	0.930300912	0.975782553
positive regulation of ATPase activity (GO:0032781)	15401	0.930300912	0.975782553
embryonic skeletal system morphogenesis (GO:0048704)	11355	0.930480957	0.975782553
peptidyl-asparagine modification (GO:0018196)	11355	0.930480957	0.975782553
regulation of potassium ion transport (GO:0043266)	11355	0.930480957	0.975782553
cell-cell junction organization (GO:0045216)	30133	0.930900899	0.975782553
central nervous system development (GO:0007417)	28/268	0.931605505	0.975782553
atrioventricular valve morphogenesis (GO:0003181)	44580	0.933144894	0.975782553
DNA double-strand break processing (GO:0000729)	44580	0.933144894	0.975782553
ethanol metabolic process (GO:0006067)	44580	0.933144894	0.975782553
heparan sulfate proteoglycan biosynthetic process (GO:0	44580	0.933144894	0.975782553
nuclear membrane organization (GO:0071763)	44580	0.933144894	0.975782553
nucleotide-sugar biosynthetic process (GO:0009226)	44580	0.933144894	0.975782553
piRNA metabolic process (GO:0034587)	44580	0.933144894	0.975782553
positive regulation of G protein-coupled receptor signalir	44580	0.933144894	0.975782553
positive regulation of mitochondrial fission (GO:0090141	44580	0.933144894	0.975782553
protein import into mitochondrial matrix (GO:0030150)	44580	0.933144894	0.975782553
purine ribonucleoside bisphosphate metabolic process (G	44580	0.933144894	0.975782553
synaptic transmission, cholinergic (GO:0007271)	44580	0.933144894	0.975782553
telomere capping (GO:0016233)	44580	0.933144894	0.975782553
retinoid metabolic process (GO:0001523)	33817	0.933536564	0.975995663
cardiac muscle tissue development (GO:0048738)	19450	0.933921409	0.976201553
endoplasmic reticulum organization (GO:0007029)	26816	0.934229287	0.976326925
epidermis development (GO:0008544)	30498	0.935971864	0.977430368
development of primary male sexual characteristics (GO:	15766	0.937069307	0.977430368
male gonad development (GO:0008584)	15766	0.937069307	0.977430368
myofibril assembly (GO:0030239)	15766	0.937069307	0.977430368
positive regulation of neuron differentiation (GO:004566	15766	0.937069307	0.977430368
positive regulation of peptide hormone secretion (GO:00	15766	0.937069307	0.977430368
signal release from synapse (GO:0099643)	15766	0.937069307	0.977430368
positive regulation of transferase activity (GO:0051347)	14/148	0.937694707	0.977430368

cardiac muscle tissue morphogenesis (GO:0055008)	11720	0.938107375	0.977430368
intra-Golgi vesicle-mediated transport (GO:0006891)	11720	0.938107375	0.977430368
long-chain fatty acid transport (GO:0015909)	11720	0.938107375	0.977430368
mitochondrial membrane organization (GO:0007006)	11720	0.938107375	0.977430368
peptidyl-proline modification (GO:0018208)	11720	0.938107375	0.977430368
regulation of dendritic spine morphogenesis (GO:006100	11720	0.938107375	0.977430368
regulation of intracellular estrogen receptor signaling pat	11720	0.938107375	0.977430368
inorganic anion transport (GO:0015698)	19815	0.939805294	0.978806837
regulation of potassium ion transmembrane transport (G	19815	0.939805294	0.978806837
protein targeting to ER (GO:0045047)	9/103	0.940723179	0.979543872
cellular macromolecule biosynthetic process (GO:003464	33/314	0.94128834	0.979543872
adrenergic receptor signaling pathway (GO:0071875)	44581	0.942021403	0.979543872
early endosome to late endosome transport (GO:004502	44581	0.942021403	0.979543872
fatty acid transport (GO:0015908)	44581	0.942021403	0.979543872
neuromuscular synaptic transmission (GO:0007274)	44581	0.942021403	0.979543872
oligodendrocyte differentiation (GO:0048709)	44581	0.942021403	0.979543872
positive regulation of hormone secretion (GO:0046887)	44581	0.942021403	0.979543872
negative regulation of cell death (GO:0060548)	34547	0.942592359	0.979941426
detection of chemical stimulus involved in sensory perce	16132	0.94322528	0.979967596
neurotransmitter secretion (GO:0007269)	16132	0.94322528	0.979967596
positive regulation of cell division (GO:0051781)	16132	0.94322528	0.979967596
nuclear-transcribed mRNA catabolic process, nonsense-m	10/113	0.943372079	0.979967596
inorganic anion transmembrane transport (GO:0098661)	23863	0.943952369	0.980374362
steroid metabolic process (GO:0008202)	9/104	0.944774424	0.980610358
positive regulation of telomere maintenance via telomer	12086	0.944934639	0.980610358
primary alcohol metabolic process (GO:0034308)	12086	0.944934639	0.980610358
regulation of histone acetylation (GO:0035065)	12086	0.944934639	0.980610358
protein import into nucleus (GO:0006606)	27912	0.948535755	0.982823805
nucleotide-excision repair (GO:0006289)	9/105	0.948580032	0.982823805
chromosome condensation (GO:0030261)	16497	0.948817998	0.982823805
regulation of DNA repair (GO:0006282)	16497	0.948817998	0.982823805
calcium ion transport into cytosol (GO:0060402)	44582	0.949719701	0.982823805
cellular response to inorganic substance (GO:0071241)	44582	0.949719701	0.982823805
error-prone translesion synthesis (GO:0042276)	44582	0.949719701	0.982823805
innate immune response in mucosa (GO:0002227)	44582	0.949719701	0.982823805
negative regulation of response to wounding (GO:190303	44582	0.949719701	0.982823805
nuclear envelope organization (GO:0006998)	44582	0.949719701	0.982823805
regulation of cholesterol metabolic process (GO:009018	44582	0.949719701	0.982823805
regulation of transposition (GO:0010528)	44582	0.949719701	0.982823805
retinol metabolic process (GO:0042572)	44582	0.949719701	0.982823805
sensory organ development (GO:0007423)	20546	0.95016323	0.982823805
tight junction assembly (GO:0120192)	20546	0.95016323	0.982823805
cellular amide metabolic process (GO:0043603)	10/115	0.950646144	0.982823805
cell-cell adhesion via plasma-membrane adhesion molec	16/170	0.950832033	0.982823805
histone lysine methylation (GO:0034968)	12451	0.951040475	0.982823805
secondary alcohol biosynthetic process (GO:1902653)	12451	0.951040475	0.982823805
termination of RNA polymerase II transcription (GO:0006	12451	0.951040475	0.982823805

tRNA methylation (GO:0030488)	12451	0.951040475	0.982823805
ribosomal large subunit biogenesis (GO:0042273)	20911	0.954703624	0.985325605
chaperone-mediated protein complex assembly (GO:005	44583	0.956396126	0.985325605
exogenous drug catabolic process (GO:0042738)	44583	0.956396126	0.985325605
female gonad development (GO:0008585)	44583	0.956396126	0.985325605
glutathione derivative biosynthetic process (GO:1901687	44583	0.956396126	0.985325605
glutathione derivative metabolic process (GO:1901685)	44583	0.956396126	0.985325605
homologous chromosome segregation (GO:0045143)	44583	0.956396126	0.985325605
limb morphogenesis (GO:0035108)	44583	0.956396126	0.985325605
negative regulation of lipid biosynthetic process (GO:005	44583	0.956396126	0.985325605
organelle fusion (GO:0048284)	44583	0.956396126	0.985325605
positive regulation of translational initiation (GO:004594	44583	0.956396126	0.985325605
regulation of cardiac muscle cell membrane repolarizatio	44583	0.956396126	0.985325605
acylglycerol catabolic process (GO:0046464)	12816	0.956496059	0.985325605
cholesterol biosynthetic process (GO:0006695)	12816	0.956496059	0.985325605
maturation of SSU-rRNA (GO:0030490)	12816	0.956496059	0.985325605
oxoacid metabolic process (GO:0043436)	12816	0.956496059	0.985325605
embryonic heart tube morphogenesis (GO:0003143)	17227	0.958495182	0.986557785
positive regulation of pathway-restricted SMAD protein p	17227	0.958495182	0.986557785
regulation of synapse assembly (GO:0051963)	17227	0.958495182	0.986557785
telomere organization (GO:0032200)	17227	0.958495182	0.986557785
DNA replication (GO:0006260)	9/108	0.958641713	0.986557785
double-strand break repair (GO:0006302)	15/164	0.95897263	0.986702874
neuron differentiation (GO:0030182)	16/174	0.961159508	0.988187252
axonal transport (GO:0098930)	13181	0.961366385	0.988187252
cyclic-nucleotide-mediated signaling (GO:0019935)	13181	0.961366385	0.988187252
positive regulation of telomere maintenance via telomer	13181	0.961366385	0.988187252
telomere maintenance via telomere lengthening (GO:001	13181	0.961366385	0.988187252
cilium organization (GO:0044782)	22/228	0.961759153	0.988395411
drug catabolic process (GO:0042737)	44584	0.962186276	0.988443287
nucleotide-excision repair, DNA damage recognition (GO	44584	0.962186276	0.988443287
fatty acid oxidation (GO:0019395)	21641	0.962660207	0.988734633
mitotic spindle organization (GO:0007052)	14/157	0.964138003	0.990056716
centromere complex assembly (GO:0034508)	13547	0.965710657	0.990692508
nucleotide-excision repair, DNA incision, 5'-to lesion (GO	13547	0.965710657	0.990692508
positive regulation of cytokinesis (GO:0032467)	13547	0.965710657	0.990692508
protein insertion into ER membrane (GO:0045048)	13547	0.965710657	0.990692508
regulation of glucose import (GO:0046324)	13547	0.965710657	0.990692508
skeletal system development (GO:0001501)	14/158	0.966352157	0.991054108
protein glycosylation (GO:0006486)	11/130	0.966507526	0.991054108
DNA packaging (GO:0006323)	44585	0.967207762	0.991054108
ncRNA 3'-end processing (GO:0043628)	44585	0.967207762	0.991054108
peptidyl-glutamic acid modification (GO:0018200)	44585	0.967207762	0.991054108
sulfur amino acid metabolic process (GO:0000096)	44585	0.967207762	0.991054108
spliceosomal snRNP assembly (GO:0000387)	13912	0.969582673	0.992713514
chloride transmembrane transport (GO:1902476)	18323	0.969843949	0.992713514
epithelium development (GO:0060429)	10/122	0.97002591	0.992713514

cytoplasmic translation (GO:0002181)	34151	0.971180376	0.992713514
antigen processing and presentation of exogenous peptic	8/103	0.97119871	0.992713514
3'-phosphoadenosine 5'-phosphosulfate metabolic proce	44586	0.971562594	0.992713514
cardiac conduction system development (GO:0003161)	44586	0.971562594	0.992713514
outflow tract septum morphogenesis (GO:0003148)	44586	0.971562594	0.992713514
peroxisome organization (GO:0007031)	44586	0.971562594	0.992713514
regulation of AMPA receptor activity (GO:2000311)	44586	0.971562594	0.992713514
regulation of cardiac muscle cell action potential (GO:00	44586	0.971562594	0.992713514
double-strand break repair via nonhomologous end joinir	22737	0.972192342	0.992713514
transcription-coupled nucleotide-excision repair (GO:000	26785	0.972761476	0.992713514
DNA duplex unwinding (GO:0032508)	18688	0.972923839	0.992713514
gonad development (GO:0008406)	18688	0.972923839	0.992713514
mitotic nuclear membrane organization (GO:0101024)	18688	0.972923839	0.992713514
mitotic nuclear membrane reassembly (GO:0007084)	18688	0.972923839	0.992713514
regulation of smoothened signaling pathway (GO:000858	18688	0.972923839	0.992713514
DNA recombination (GO:0006310)	14277	0.973031225	0.992713514
DNA replication-independent nucleosome assembly (GO:	14277	0.973031225	0.992713514
nucleotide-excision repair, DNA incision (GO:0033683)	14277	0.973031225	0.992713514
regulation of heart rate by cardiac conduction (GO:0086(	14277	0.973031225	0.992713514
cotranslational protein targeting to membrane (GO:0006	34516	0.973480545	0.992976916
regulation of cytokinesis (GO:0032465)	30834	0.974015702	0.993312564
neuropeptide signaling pathway (GO:0007218)	23102	0.974826245	0.993312564
DNA geometric change (GO:0032392)	44587	0.975339247	0.993312564
DNA modification (GO:0006304)	44587	0.975339247	0.993312564
maturation of LSU-rRNA (GO:0000470)	44587	0.975339247	0.993312564
positive regulation of glucose import (GO:0046326)	44587	0.975339247	0.993312564
retinoic acid metabolic process (GO:0042573)	44587	0.975339247	0.993312564
snRNA processing (GO:0016180)	44587	0.975339247	0.993312564
cilium movement (GO:0003341)	19054	0.975703609	0.993488877
detection of chemical stimulus involved in sensory perce	14642	0.976100473	0.993698208
tRNA processing (GO:0008033)	23468	0.97722438	0.9945799
regulation of cell cycle process (GO:0010564)	8/106	0.977349449	0.9945799
bicellular tight junction assembly (GO:0070830)	19419	0.978210516	0.994698124
calcium-ion regulated exocytosis (GO:0017156)	44588	0.978614459	0.994698124
dendritic spine organization (GO:0097061)	44588	0.978614459	0.994698124
melanosome organization (GO:0032438)	44588	0.978614459	0.994698124
mitotic chromosome condensation (GO:0007076)	44588	0.978614459	0.994698124
nucleobase-containing small molecule interconversion (G	44588	0.978614459	0.994698124
sensory perception of bitter taste (GO:0050913)	15008	0.97883032	0.994722909
double-strand break repair via homologous recombinatic	35612	0.979406268	0.994947904
chloride transport (GO:0006821)	27881	0.979434761	0.994947904
nuclear membrane reassembly (GO:0031468)	19784	0.980469622	0.995637104
antigen processing and presentation of exogenous peptic	35977	0.98109167	0.995637104
ATP-dependent chromatin remodeling (GO:0043044)	15373	0.98125676	0.995637104
cellular respiration (GO:0045333)	15373	0.98125676	0.995637104
cristae formation (GO:0042407)	44589	0.981454785	0.995637104
GPI anchor metabolic process (GO:0006505)	44589	0.981454785	0.995637104

response to ketone (GO:1901654)	44589	0.981454785	0.995637104
sensory perception of mechanical stimulus (GO:0050954)	32295	0.981800814	0.99579368
protein targeting to mitochondrion (GO:0006626)	20149	0.982503928	0.996256221
cilium assembly (GO:0060271)	30/314	0.9826404	0.996256221
protein N-linked glycosylation (GO:0006487)	24563	0.983191202	0.996261011
protein import (GO:0017038)	32660	0.983373923	0.996261011
DNA-dependent DNA replication maintenance of fidelity	15738	0.983412216	0.996261011
heart looping (GO:0001947)	15738	0.983412216	0.996261011
mismatch repair (GO:0006298)	44590	0.983917951	0.996384748
regulation of calcium ion transmembrane transporter act	44590	0.983917951	0.996384748
nervous system development (GO:0007399)	45/447	0.984212687	0.996418118
telomere maintenance (GO:0000723)	20515	0.98433451	0.996418118
recombinational repair (GO:0000725)	28976	0.984552234	0.996444352
cardiac ventricle morphogenesis (GO:0003208)	16103	0.985325852	0.996504099
mitotic spindle assembly (GO:0090307)	16103	0.985325852	0.996504099
CENP-A containing chromatin organization (GO:0061641)	44591	0.986054023	0.996504099
CENP-A containing nucleosome assembly (GO:0034080)	44591	0.986054023	0.996504099
estrogen metabolic process (GO:0008210)	44591	0.986054023	0.996504099
histone H3-K4 methylation (GO:0051568)	44591	0.986054023	0.996504099
non-motile cilium assembly (GO:1905515)	44591	0.986054023	0.996504099
sensory perception of sound (GO:0007605)	33390	0.986145828	0.996504099
peptide biosynthetic process (GO:0043043)	13/162	0.986491135	0.996659169
fatty acid catabolic process (GO:0009062)	25659	0.987655146	0.99764116
chondrocyte differentiation (GO:0002062)	11689	0.989512806	0.998631205
chromatin remodeling at centromere (GO:0031055)	11689	0.989512806	0.998631205
GPI anchor biosynthetic process (GO:0006506)	11689	0.989512806	0.998631205
protein transmembrane import into intracellular organell	11689	0.989512806	0.998631205
determination of heart left/right asymmetry (GO:006137	17199	0.9898646	0.998631205
apical junction assembly (GO:0043297)	21976	0.989980887	0.998631205
homophilic cell adhesion via plasma membrane adhesion	21976	0.989980887	0.998631205
DNA repair (GO:0006281)	27/298	0.990375997	0.998835819
exonucleolytic catabolism of deadenylated mRNA (GO:0(	12055	0.990905839	0.999124875
positive regulation of DNA repair (GO:0045739)	17564	0.991047253	0.999124875
axoneme assembly (GO:0035082)	12420	0.992113846	0.99981211
protein localization to chromosome (GO:0034502)	12420	0.992113846	0.99981211
brain development (GO:0007420)	11/150	0.992461046	0.999968024
base-excision repair, gap-filling (GO:0006287)	12785	0.993161394	0.999993541
nuclear-transcribed mRNA catabolic process, exonucleoly	12785	0.993161394	0.999993541
protein localization to cilium (GO:0061512)	12785	0.993161394	0.999993541
import into nucleus (GO:0051170)	28216	0.994093592	0.999993541
translation (GO:0006412)	17/214	0.994709089	0.999993541
mitochondrial respiratory chain complex assembly (GO:0	32994	0.994794772	0.999993541
SRP-dependent cotranslational protein targeting to mem	32994	0.994794772	0.999993541
anterograde axonal transport (GO:0008089)	13516	0.994857513	0.999993541
histone exchange (GO:0043486)	13881	0.995540586	0.999993541
odontogenesis (GO:0042476)	14246	0.996132907	0.999993541
replication fork processing (GO:0031297)	14246	0.996132907	0.999993541

synapse assembly (GO:0007416)	25263	0.996425339	0.999993541
glycolipid biosynthetic process (GO:0009247)	14611	0.99664653	0.999993541
intraciliary transport involved in cilium assembly (GO:003	14611	0.99664653	0.999993541
DNA-dependent DNA replication (GO:0006261)	8/129	0.996887486	0.999993541
generation of neurons (GO:0048699)	15/202	0.996967891	0.999993541
spindle assembly (GO:0051225)	30773	0.997231848	0.999993541
regulation of neurotransmitter receptor activity (GO:009	21217	0.997453905	0.999993541
mitochondrial gene expression (GO:0140053)	15342	0.997478102	0.999993541
endoplasmic reticulum to Golgi vesicle-mediated transpo	13/185	0.99764184	0.999993541
regulation of cation channel activity (GO:2001257)	32599	0.9984062	0.999993541
synapse organization (GO:0050808)	7/126	0.998560586	0.999993541
base-excision repair (GO:0006284)	17533	0.998926876	0.999993541
DNA metabolic process (GO:0006259)	21/277	0.999023591	0.999993541
inner mitochondrial membrane organization (GO:000700	17899	0.999069191	0.999993541
fatty acid beta-oxidation (GO:0006635)	18994	0.999392339	0.999993541
translational elongation (GO:0006414)	4/104	0.999707547	0.999993541
mitochondrial respiratory chain complex I assembly (GO:	21186	0.999740219	0.999993541
NADH dehydrogenase complex assembly (GO:0010257)	21186	0.999740219	0.999993541
anterograde trans-synaptic signaling (GO:0098916)	15/244	0.999896446	0.999993541
retrograde vesicle-mediated transport, Golgi to endoplas	31079	0.999920333	0.999993541
aerobic electron transport chain (GO:0019646)	25569	0.9999506	0.999993541
mitochondrial translational elongation (GO:0070125)	32540	0.999951628	0.999993541
mitochondrial ATP synthesis coupled electron transport (	25934	0.999956746	0.999993541
translational termination (GO:0006415)	35096	0.999978765	0.999993541
sensory perception of chemical stimulus (GO:0007606)	36192	0.999984578	0.999993541
chemical synaptic transmission (GO:0007268)	18/306	0.999987317	0.999993541
mitochondrial translation (GO:0032543)	2/105	0.999991068	0.999993541
mitochondrial translational termination (GO:0070126)	32509	0.999993541	0.999993541

gnificant highly-correlated RNA-seq-based modules (turquoise; Significant tern

Old P-value	Old Adjusted P-value	Odds Ratio	Combined Score	Genes	KEGG
0	0	3.792617643	393.7961679	IFITM3;IL1	.
0	0	3.994324532	359.1120712	RIPOR2;CS	.
0	0	4.088642659	272.8887854	FCN1;IL23I	.
0	0	4.648627681	266.0853869	IL1RN;CD4	.
0	0	5.849254743	305.555873	IFITM3;CSI	.
0	0	5.534342476	284.7111431	CXCL8;CD8	.
0	0	2.793930239	143.6253436	CSF3;NCF1	.
0	0	2.866140304	140.5712103	FCN1;RAB3	.
0	0	2.807684292	130.1022442	FCN1;RAB3	.
0	0	2.774384119	126.2438106	FCN1;RAB3	.
0	0	9.509974457	420.1752391	CXCL8;IL23	.
0	0	8.297066718	356.1670308	FCN1;C5AI	.
0	0	4.074884709	172.202669	TNFAIP6;SI	.
0	0	3.788850341	153.6903072	CD40;TRAI	.
0	0	5.440169296	210.1388236	CXCL8;CD8	.
0	0	4.072529384	153.288873	IL23R;TNFA	.
0	0	3.341695838	118.6269927	CD40;CRTC	.
0	0	8.906314274	312.6007125	FCN1;SERP	.
0	0	5.332363829	185.0102778	TNFAIP3;P	.
0	0	5.107124915	174.4546693	CXCL8;CD8	.
0	0	4.087192399	133.3583609	CD40;IL1RA	.
0	0	3.784292133	119.4332716	CD40;TRAI	.
0	0	2.83819448	88.29932046	IFITM3;FCN	.
0	0	6.616972477	205.7457209	RNF31;RNA	.
0	0	4.483651919	136.9034726	IFITM3;RTI	.
0	0	4.483651919	136.9034726	TNFAIP3;P	.
0	0	8.614762386	256.7272305	PTPRJ;PLA2	.
0	0	7.035557744	204.2476701	RNASEL;TN	.
0	0	4.126820832	118.6956021	IFITM3;RTI	.
0	0	3.966290596	111.6518866	SERPINE1;I	.
0	0	5.16130834	140.9168011	ILRUN;UBA	.
0	0	5.784425134	155.6593984	CD274;CD8	.
0	0	4.761357836	127.4271181	SERPINE1;I	.
0	0	4.320652174	115.6040485	RARG;IL23I	.
0	0	7.074369588	188.4342842	DYSF;PLA2	.
0	0	5.319580176	141.6071227	SEMA7A;XI	.
0	0	4.962222647	131.2369056	ITGAM;UBI	.
0	0	5.643015521	149.1381495	NOD2;TNF	.
0	0	2.03159473	53.07117817	CSF3;CSF1;	.
0	0	4.928189555	126.5108449	CD81;SERP	.
0	0	4.993025651	126.3899519	CD274;IL23	.
0	0	1.700711343	42.46611478	ZNF296;MA	.
0	0	2.930926141	72.84464771	RET;CXCL8	.
0	0	7.421315689	184.3224556	CD40;IL23I	.

0	0	3.742016484	92.10063244	ACVRL1;RE
0	0	5.224220144	126.7652076	DDX3X;CG
0	0	1.869476462	44.95478939	CSF3;CSF1;
0	0	3.045965608	73.19832625	CD40;CXCL
0	0	11.97113559	283.5005197	CD40;TICA
0	0	3.414809121	80.26408156	TNF;PIK3C
0	0	4.529398856	105.5566126	FMR1;PLA2
0	0	3.578038302	82.28751979	NRP1;CSF3
0	0	3.782511088	86.93312188	CCL14;CIIT
0	0	5.657208213	129.7983209	IFITM3;RN
0	0	5.657208213	129.7983209	IFITM3;RN
0	0	4.446788991	101.9479932	NRP1;CSF3
0	0	2.379422563	52.95891615	RET;CXCL8
0	0	1.748642565	38.77636765	ZNF296;CR
0	0	4.53392052	100.4818787	CCL14;HDA
0	0	3.249693283	72.011883	IL1RN;CD4
0	0	11.3682612	251.1278018	CD40;TICA
0	0	1.698907186	37.51728929	TP53RK;UB
0	0	6.866359082	151.4786705	DDX3X;REL
0	0	6.140005778	135.3302154	NLRC4;NOL
0	0	2.885527926	63.49107078	DGKG;DGK
0	0	5.934996192	127.8026677	IL23R;CEBP
0	0	4.636186454	99.24587846	IFITM3;CCL
0	0	2.23052074	47.73515741	ACVRL1;BC
0	0	9.404264554	200.1513251	CD40;RIPK
0	0	3.778251599	79.49808349	CCL14;CD4
0	0	4.694255797	98.73357182	LY96;PTPR
0	0	5.431529412	113.4763211	NLRC4;NOL
0	0	23.00132626	478.6579551	TICAM2;M
0	0	28.46868687	579.3552668	TICAM2;M
0	0	4.357259542	88.31401028	TNFAIP3;N
0	0	4.649408848	94.21464668	CD274;CD4
0	0	1.786933399	36.05824039	FCMR;STEA
0	0	4.904745153	97.75185156	CD40;IL23F
0	0	4.400101742	87.47725706	NFAT5;DDX
0	0	5.235551723	102.8906235	FCN1;LY96
0	0	4.310054583	84.10391307	LY96;PTPR
0	0	5.085670765	97.72232857	RNF31;ROC
0	0	3.268507509	62.49039516	SEMA7A;C
0	0	4.397509213	82.38959256	ITGAM;CD8
0	0	15.33244916	284.1606597	ASAH1;ML
0	0	4.6152	84.69290215	CIITA;PTAF
0	0	12.32396702	225.3700004	IFNGR1;ST
0	0	5.451554938	99.14798538	CD74;EGR1
0	0	1.923817017	34.98275873	CCNT1;TP5
0	0	7.353387824	131.1131964	DDX3X;DDX
0	0	6.283244681	111.5624178	ILRUN;IL10

0	0	7.89313093	139.2935848	IL15;IL23R;
0	0	4.844043782	83.47806333	CD40;IL23I
0	0	5.570593223	95.05988349	CD274;IL2
0	0	7.984527423	134.5140591	IFNAR2;ST
0	0	24.07065355	402.6662415	SOCS3;SO
0	0	1.987337536	33.11168883	RET;DGKG;
0	0	9.858036391	164.1648506	IFNAR2;ST
0	0	5.981769844	98.33083889	CD74;EGR1
0	0	2.243960084	36.83958575	RET;NRP1;
0	0	1.924370631	31.43472635	FAM13B;TI
0	0	4.137586567	66.68083248	IFITM3;RN
0	0	1.872072779	30.10236393	CSF3;CSF1;
0	0	2.84145977	45.41784302	HDAC4;GFI
0	0	12.19805195	194.4594389	LYN;PRKCE
0	0	10.21986443	162.2660984	ZBP1;MLKI
0	0	3.401353769	53.71318128	TENM1;CD
0	0	2.324206196	36.44904116	CSRNP1;FA
0	0	18.05194928	280.446109	STAT1;OAS
0	0	3.844222222	59.6495006	CD274;SDC
0	0	2.551435103	39.10500437	IL23R;SERF
0	0	1.946393003	29.46841562	CXCL8;DDX
0	0	21.87413293	326.8647358	STAT5A;IL1
0	0	21.87413293	326.8647358	STAT5A;IL1
0	0	4.93512538	73.73802363	LGALS3BP;
0	0	4.670761761	69.62036134	NFAT5;DDX
0	0	2.492121588	36.80602039	CD40;CD81
0	0	4.015387757	58.73241418	CD274;CD8
0	0	6.208754847	90.24681705	DDX3X;DDX
0	0	6.208754847	90.24681705	NOD2;CYR
0	0	2.969105846	43.00715588	CD40;TNF;
0	0	29.52061271	426.2249839	STAT1;CAM
0	0	29.52061271	426.2249839	FCER2;IFNG
0	0	1.919894515	27.59832778	ACVRL1;BT
0	0	3.919556788	56.02519478	NRP1;FLT1
0	0	1.793855867	25.63625228	FCMR;ZFAI
0	0	6.572241183	93.71646441	IL10;XBP1;
0	0	4.205249261	59.58853151	TRAF2;TNF
0	0	121429	1717887.119	CYP27B1;IF
0	0	52.46427221	739.6139063	STAT5A;ST
0	0	52.46427221	739.6139063	STAT5A;ST
0	0	2.102178793	29.62773488	RET;BCAR3
0	0	3.722430943	52.35692962	DDX3X;BCI
0	0	5.881638847	82.50899042	OTUD4;LYN
0	0	5.881638847	82.50899042	CCR1;CD74
0	0	7.039829958	98.63541247	ERAP1;XIAI
0	0	1.785299882	24.98389128	CSF1;FMR1
0	0	2.028574815	28.27163519	RET;LRRK2

0	0	3.94986687	54.85101476	TCF7L2;SR(
0	0	16.4046538	226.6762593	FCER2;EDN
0	0	2.861291555	39.48181266	PRR7;DDX3
0	0	8.537159091	116.4482374	IL15;IL23R;
0	0	9.847974252	133.4972357	IFIH1;DDX3
0	0	9.847974252	133.4972357	ITGAM;TIC
0	0	1.525537536	20.44649407	NAB1;GFI1
0	0	2.276740225	30.39839287	CD40;BTG1
0	0	1.624597062	21.66481417	GFI1;WWC
0	0	3.419686273	45.48229044	GFI1;NLRC
0	0	3.761343259	49.80504947	EGR1;PRR7
0	0	5.841317996	77.23975642	MAP2K3;N
0	0	7.073658437	93.36749658	TASL;DDX3
0	0	19.67927383	259.3390014	IL1R1;IL23A
0	0	19.67927383	259.3390014	CLEC7A;IL2
0	0	3.881095837	51.03692374	MAP2K3;R
0	0	5.32086856	69.61588885	USP15;STA
0	0	4.186170213	54.49173974	IFITM3;RN
0	0	3.088603222	40.05833405	IL1RN;PELI
0	0	6.159140447	79.56608782	IL10;GHSR;
0	0	6.159140447	79.56608782	NFAT5;CYR
0	0	3.235555556	41.74658565	ILRUN;TNF
0	0	1.477438616	18.97922884	JMJD1C;RB
0	0	1.84768365	23.72983118	FCMR;TNFA
0	0	8.753250032	112.3711161	IL6;RSAD2;
0	0	2.203589744	28.18145515	TNFAIP6;TI
0	0	4.73314611	59.6203676	GBP5;NOS
0	0	4.461723072	56.17755644	EGR1;DAX
0	0	2.175962733	27.17837075	PTPRO;WV
0	0	1.798333345	22.43518411	RET;ACVRL
0	0	5.79650359	71.97317188	CD274;STA
0	0	7.113478535	88.10456194	IL10;DDX3
0	0	1.659124646	20.52177413	RIPOR2;AD
0	0	2.522447005	31.14495575	AMER1;PFI
0	0	2.522447005	31.14495575	ARHGAP9;I
0	0	3.509978446	43.29780294	CCR1;NRP1
0	0	2.733355684	33.71677301	DDX3X;SR(
0	0	1.907762883	23.46688352	ACVRL1;BT
0	0	5.256579446	64.58666779	ZBP1;CD74
0	0	2.30117632	28.17858821	ILRUN;RAN
0	0	4.307621816	52.63638125	LYN;PTPN1
0	0	4.307621816	52.63638125	ILRUN;IL10
0	0	4.307621816	52.63638125	ANXA1;CD
0	0	2.876827709	35.10111636	PTGFR;PRK
0	0	45.88888889	559.4253085	STAT1;STA
0	0	45.88888889	559.4253085	STAT1;STA
0	0	45.88888889	559.4253085	TICAM2;IR

0	0	14.75860439	178.9599366	CLEC7A;IL2
0	0	14.75860439	178.9599366	RIPK2;ERBI
0	0	104082	1262017.68	CD14;LBP;I
0	0	104082	1262017.68	CD14;LBP;I
0	0	9.023892884	108.6033112	PYCARD;SE
0	0	2.393967936	28.39864942	CDKN1A;D
0	0	4.163793976	49.38648895	TCF7L2;ED
0	0	2.93842636	34.78005615	RGS14;PTP
0	0	6.565909091	77.62242997	ANXA1;CD
0	0	2.021576296	23.89039973	NRP1;MAN
0	0	1.946313301	22.98934825	RARG;PRR
0	0	1.895343833	22.15452089	RARG;PRR
0	0	5.746352785	66.70960511	LYN;SRC;EF
0	0	4.225291407	48.41598289	ILRUN;IL10
0	0	17.48607435	200.0109323	STAT5A;ST
0	0	17.48607435	200.0109323	STAT5A;ST
0	0	17.48607435	200.0109323	CASP8;RIPI
0	0	4.778156997	54.64331046	IL10;XBP1;
0	0	6.096563853	68.85915997	OTUD4;GF
0	0	9.372466353	105.2796455	GBP5;IL6;C
0	0	11.80620272	132.4912678	GBP6;BATF
0	0	3.54091653	39.24315735	CCL14;CCR
0	0	4.926175133	54.48753127	DUSP5;PTF
0	0	2.391261168	25.94570365	PPP1R15A;
0	0	22.94312169	248.0055853	IL23A;IL23I
0	0	22.94312169	248.0055853	NFKBIA;IL6
0	0	5.68979798	61.4496381	SELPLG;SR
0	0	1.925385373	20.75894169	CD40;FMR
0	0	3.943149905	42.46430778	IL10;SERPI
0	0	1.985596318	21.29747468	NRP1;FLT4
0	0	4.691324597	49.97313119	ITGAM;IFN
0	0	2.122805465	22.44006512	ARHGAP9;I
0	0	3.151750634	33.26729584	BATF2;CDK
0	0	8.200435112	86.50536721	IL10;ANXA
0	0	3.67308723	38.73726847	CD74;CD4(
0	0	3.367799689	35.40302719	DDX3X;RIP
0	0	13.11379962	137.2244587	PARP10;PA
0	0	3.815731162	39.84719616	MAP3K2;C
0	0	2.937289356	30.59088823	FASLG;NOI
0	0	3.215034419	33.41753421	IFITM3;RN
0	0	3.459931637	35.89081745	RNF31;SPP
0	0	3.989039129	41.3164326	C1R;RIPK2;
0	0	2.50911139	25.9584746	CD40;RAM
0	0	5.333877841	55.12304381	MAP3K1;L
0	0	39.31847374	404.9702418	TICAM2;SA
0	0	39.31847374	404.9702418	IL23A;IL23I
0	0	39.31847374	404.9702418	OTUD4;ITC

0	0	4.477824109	45.95452013	NLGN3;IL1
0	0	2.012569924	20.51254832	CD40;DDX
0	0	6.561695685	66.83241063	DCSTAMP;
0	0	2.615195874	26.45665121	ERO1A;PPI
0	0	86735	876329.3346	JAML;PECA
0	0	2.415101781	24.17405648	ACVRL1;NI
0	0	2.923460547	29.23410548	HEXIM1;LY
0	0	2.759249481	27.40664608	RYR1;SLC2
0	0	2.632685714	26.10186411	BCAR3;TEN
0	0	3.07786862	30.42323038	TENM1;CD
0	0	2.050492956	20.25584378	ACVRL1;PR
0	0	2.050492956	20.25584378	USP36;RAI
0	0	2.965839111	29.11907693	LYN;FCER1
0	0	8.432029393	82.0487652	CCR1;CXCR
0	0	15.29453263	148.7873055	TICAM2;NI
0	0	15.29453263	148.7873055	TBX21;NFK
0	0	15.29453263	148.7873055	CLEC7A;IL2
0	0	2.715294772	26.39396577	DDX3X;SRC
0	0	2.715294772	26.39396577	CXCL8;DGK
0	0	2.651782974	25.7575117	FLT1;WNT2
0	0	3.722673242	36.14464948	LAPTM5;IL
0	0	6.014540752	58.11406517	LYN;TICAM
0	0	10.49043478	101.0525498	LFNG;DOCI
0	0	2.908635566	27.87819984	NRP1;SEM
0	0	3.478446255	33.15177873	KMT2E;LYN
0	0	3.478446255	33.15177873	URI1;DDX3
0	0	5.250132526	50.03278464	IFIH1;CYLD
0	0	5.250132526	50.03278464	C3;IL1A;IL6
0	0	2.159966052	20.55566599	ACVRL1;NI
0	0	4.376910446	41.5300818	ANXA1;RIP
0	0	2.437977436	22.86569349	MALT1;PSN
0	0	6.559591373	61.41011804	LYN;STAT5
0	0	6.559591373	61.41011804	ABCA1;NFK
0	0	1.929397704	17.97667965	RET;FLT1;C
0	0	1.572695612	14.62100224	NCF1;CD8(
0	0	3.939802881	36.22822846	EDN1;SMA
0	0	5.551563501	50.94456811	IL10;SLC7A
0	0	2.892694793	26.52323467	LYN;FCER1
0	0	2.489801802	22.76273329	CD40;RAM
0	0	2.800584425	25.58229203	CCL14;EDN
0	0	2.591422408	23.60954806	SDC4;VPS4
0	0	3.489603092	31.78264231	ANXA1;RIP
0	0	7.377600227	67.15267245	CD274;IL2
0	0	4.921715259	44.7797986	TRAF3IP2;I
0	0	4.921715259	44.7797986	IL10;IL6;TH
0	0	2.345581595	21.26856451	DDX3X;SRC
0	0	3.056730761	27.64795875	JUN;ANXA1

0	0	19.65810351	177.5824918	SEMA4D;IL
0	0	19.65810351	177.5824918	C3;C4A;CC
0	0	19.65810351	177.5824918	PRR7;CASP
0	0	19.65810351	177.5824918	C3;C4A;CC
0	0	19.65810351	177.5824918	SPN;IL6;ST
0	0	2.263370706	20.37224462	BCAR3;CIIT
0	0	3.623344187	32.54115353	CREBBP;M
0	0	3.284819734	29.47350731	CPB2;C1S;(
0	0	2.835811329	25.35986811	CCL14;EDN
0	0	8.74152489	77.88269094	LYN;STAT5
0	0	8.74152489	77.88269094	DDX58;IL2
0	0	8.74152489	77.88269094	ANXA1;CD
0	0	8.74152489	77.88269094	CD74;IL6;R
0	0	5.962920923	52.72220503	C3;PYCARD
0	0	11.4702381	101.382982	CXCL8;HSP
0	0	11.4702381	101.382982	CXCL10;CX
0	0	3.383662114	29.85422234	LYN;PTPN1
0	0	3.383662114	29.85422234	CPB2;C1S;(
0	0	1.869324878	16.49085416	USP36;LRR
0	0	2.987086973	26.29233088	CDKN2D;U
0	0	2.265112635	19.90299077	CFD;LGALS
0	0	1.907101727	16.75370863	CCL14;BCA
0	0	4.266117424	37.1861526	PDIA3;SEC
0	0	3.195856198	27.82730996	CDKN2D;D
0	0	4.631935319	40.26265328	RET;PYCAR
0	0	4.631935319	40.26265328	ART1;PARP
0	0	3.502363797	30.41393346	IL10;SERPI
0	0	3.044743226	26.25764552	PAQR8;CDI
0	0	3.647544436	31.21511654	DDX3X;SEP
0	0	6.557488654	55.96350071	CCR1;CXCR
0	0	6.557488654	55.96350071	SOCS3;IL6;
0	0	6.557488654	55.96350071	PYCARD;RI
0	0	6.557488654	55.96350071	CXCL10;CX
0	0	2.816652193	24.02119737	CCL14;EDN
0	0	2.133962171	18.17068435	NLGN3;RAI
0	0	2.098004538	17.71247351	BCAR3;CCL
0	0	32.75302115	276.0651384	CD300A;IL
0	0	32.75302115	276.0651384	IFNG;GFI1;
0	0	32.75302115	276.0651384	IL6;IRAK3;I
0	0	32.75302115	276.0651384	IL6;STAT3;S
0	0	32.75302115	276.0651384	TAP2;TAP1
0	0	2.36157265	19.90384976	TENM1;CD
0	0	2.399966036	20.13355153	ERO1A;PRI
0	0	4.062734488	33.97833084	DDX3X;SEP
0	0	4.062734488	33.97833084	CD274;RIP
0	0	5.465695548	45.70293032	C3;NFKBIA
0	0	1.79039097	14.93151544	RET;NRP1;

0	0	2.760159574	22.93551093	LYN;SRC;PI
0	0	2.298780488	19.09363013	MALT1;PSI
0	0	7.492303538	61.96965342	IL6;IL1B;OS
0	0	7.492303538	61.96965342	CCR1;CSF1
0	0	3.031615823	24.86520377	XBP1;RIPK
0	0	2.243137629	18.38918815	ILRUN;TNF
0	0	1.93524438	15.75370175	RNF31;PTP
0	0	3.675755968	29.89692099	FCN1;IFITM
0	0	3.675755968	29.89692099	STAT5A;ST
0	0	2.628962372	21.27639119	LYN;CSF3;F
0	0	2.628962372	21.27639119	AMER1;HD
0	0	13.10464677	105.5540031	RIPK2;NOD
0	0	13.10464677	105.5540031	SLC2A10;A
0	0	13.10464677	105.5540031	CASP8;PEL
0	0	13.10464677	105.5540031	DDX3X;MA
0	0	13.10464677	105.5540031	IL23A;IL23I
0	0	1.943239283	15.65108484	BCAR3;CXC
0	0	3.101152841	24.8917984	CAST;CDKN
0	0	3.101152841	24.8917984	CPB2;C1S;C
0	0	5.901399395	47.31401819	STAT5A;ST
0	0	5.901399395	47.31401819	STAT5A;ST
0	0	5.901399395	47.31401819	SELP;SPN;S
0	0	2.417265422	19.25019703	BCAR3;TEN
0	0	4.143884892	32.93452325	SOCS3;SOC
0	0	2.108693397	16.74711481	RAMP2;SR
0	0	2.519651458	19.92736962	GALNT11;N
0	0	4.509864686	35.65012314	EDN1;SMA
0	0	2.025807589	15.99206936	MTMR3;PF
0	0	2.653692717	20.93482814	GSDMD;NC
0	0	1.996932496	15.6632293	SMG1;FLT1
0	0	3.534176699	27.6788361	RIOK3;STA
0	0	2.218204942	17.35820346	RYR1;SLC2
0	0	2.038947518	15.93465628	RYR1;PTGF
0	0	2.088296389	16.28909201	RAMP2;CD
0	0	3.017163598	23.47033601	CCR1;CSF1
0	0	2.245853659	17.44331595	CDKN1A;CS
0	0	2.245853659	17.44331595	ERO1A;PPF
0	0	2.883398899	22.28287584	IL10;USP36
0	0	3.709025033	28.58892128	ZBP1;AKIRI
0	0	3.709025033	28.58892128	TRAF3IP2;I
0	0	6.555387524	50.48603007	CD81;IL23A
0	0	6.555387524	50.48603007	DDX58;IL23
0	0	3.28222138	25.2574445	AKIRIN2;GI
0	0	1.656767524	12.7295351	TRAF3IP2;F
0	0	1.526170634	11.68202779	CIITA;CDKN
0	0	2.218666667	16.88246938	DIRAS3;CD
0	0	3.936463461	29.93825705	P2RY12;GP

0	0	1.830372359	13.91455562	RET;CSF3;S.
0	0	3.089607174	23.48540211	LYN;ROCK1.
0	0	1.964495783	14.90654317	RET;CSF3;S.
0	0	2.003255057	15.12396891	URI1;INSIG.
0	0	5.364599092	40.47247611	STAT3;IL18.
0	0	5.364599092	40.47247611	PYCARD;SF.
0	0	3.403084782	25.66915084	ROCK1;PLE.
0	0	4.244333615	31.97145357	CYLD;ITCH;.
0	0	4.244333615	31.97145357	EDN1;SMA.
0	0	2.49254905	18.71769826	TCF7L2;DD.
0	0	4.684341387	35.1520318	ADGRG3;C.
0	0	2.814583898	21.11488108	GALNT11;M.
0	0	7.645943563	56.83820175	SBNO2;IFN.
0	0	7.645943563	56.83820175	PPP1R15A;.
0	0	7.645943563	56.83820175	MOV10;PM.
0	0	7.645943563	56.83820175	IRAK2;TNIF.
0	0	3.176159847	23.5986337	IL10;EDN1;.
0	0	3.176159847	23.5986337	IL10;LYN;C.
0	0	3.554277146	26.31334555	NCF1;GADI.
0	0	2.399251614	17.65457584	LYN;STARD.
0	0	3.001159326	22.07270709	BCL2A1;CII.
0	0	3.001159326	22.07270709	PPP1R16B;.
0	0	16.37556647	119.4176137	CASP8;RIPI.
0	0	16.37556647	119.4176137	LFNG;DOCI.
0	0	16.37556647	119.4176137	CYLD;DUSF.
0	0	16.37556647	119.4176137	CD74;MBP.
0	0	16.37556647	119.4176137	IL23A;IL23I.
0	0	16.37556647	119.4176137	IL23A;IL23I.
0	0	16.37556647	119.4176137	CD74;ANXA.
0	0	16.37556647	119.4176137	IL6;STAT3;S.
0	0	3.748796452	27.29447259	SLC7A5;CLI.
0	0	9.827918398	71.329274	KMT2E;PRI.
0	0	9.827918398	71.329274	ROCK1;IL1S.
0	0	9.827918398	71.329274	BST1;RAC2.
0	0	1.942218909	14.08612009	RNF31;PTP.
0	0	2.119126863	15.3089374	FCN1;SRC;C.
0	0	5.826675068	41.88629299	NOTCH3;KA.
0	0	5.826675068	41.88629299	BST1;ANXA.
0	0	3.076727161	22.07474533	DGKD;SRC;.
0	0	1.77232238	12.69999541	ACVRL1;OC.
0	0	2.077011056	14.86152779	NRP1;CDKI.
0	0	4.371799723	31.12286429	PYCARD;SF.
0	0	4.371799723	31.12286429	C3;IL1A;IL6.
0	0	4.371799723	31.12286429	IL10;IL1RN.
0	0	2.917625248	20.76379802	STAT5A;ST.
0	0	2.116168582	14.82961951	CDKN1B;CS.
0	0	3.57819008	24.95024708	IL10;FOSL1.

0	0	1.530239359	10.65395036	RET;BCAR3	.
0	0	2.220499609	15.45129157	NCF1;FLT4	.
0	0	2.072818631	14.38450129	RYR1;STEA	.
0	0	2.253154377	15.54615001	NRP1;EDN	.
0	0	2.478555919	17.0956529	ACVRL1;RI	.
0	0	2.478555919	17.0956529	NCF1;GADI	.
0	0	2.478555919	17.0956529	ROCK1;PRI	.
0	0	2.163357153	14.85937401	NCF1;FLT4	.
0	0	2.626489564	18.02880375	NRP1;PTPN	.
0	0	2.626489564	18.02880375	LYN;GPR35	.
0	0	6.553287982	44.96869783	CASP8;IFI1	.
0	0	6.553287982	44.96869783	RAP1B;SLC	.
0	0	6.553287982	44.96869783	PYCARD;BA	.
0	0	6.553287982	44.96869783	PTPN1;BCL	.
0	0	3.797123391	26.01848606	CD74;BST1	.
0	0	3.797123391	26.01848606	IFNAR2;ZBI	.
0	0	1.443524423	9.876216118	FMR1;NAB	.
0	0	3.280492424	22.42259919	RET;NAPSA	.
0	0	1.903257171	12.9417341	SMG1;ROC	.
0	0	5.243705104	35.25823158	SELP;SPN;S	.
0	0	5.243705104	35.25823158	IFNG;IFNGI	.
0	0	2.136191473	14.3544428	CSF3;FLT1;	.
0	0	4.538752473	30.44388468	IL10;LYN;P	.
0	0	4.538752473	30.44388468	PDP1;DUSI	.
0	0	4.538752473	30.44388468	LYN;IFNG;I	.
0	0	4.538752473	30.44388468	LYN;SELP;C	.
0	0	2.895408732	19.37811562	CDKN1A;IT	.
0	0	2.895408732	19.37811562	RAMP2;CX	.
0	0	2.255490608	15.07043592	PTPN1;CDI	.
0	0	3.422419044	22.86237123	KMT2E;AD	.
0	0	3.422419044	22.86237123	PAK1;EDN	.
0	0	2.088051611	13.88056988	PHLDB1;CL	.
0	0	7.861881375	51.7973519	STEAP3;STI	.
0	0	7.861881375	51.7973519	IFNG;DDIT	.
0	0	7.861881375	51.7973519	ANXA1;TBX	.
0	0	7.861881375	51.7973519	ADAM17;N	.
0	0	7.861881375	51.7973519	PRR7;GSN;	.
0	0	7.861881375	51.7973519	HAAO;KYN	.
0	0	26.19252548	172.47096	SLC11A1;SI	.
0	0	26.19252548	172.47096	SLC11A1;SI	.
0	0	26.19252548	172.47096	B2M;TNF;N	.
0	0	26.19252548	172.47096	STEAP3;STI	.
0	0	26.19252548	172.47096	BCAR3;EDN	.
0	0	26.19252548	172.47096	PPP1R15A;	.
0	0	26.19252548	172.47096	CYP27B1;G	.
0	0	26.19252548	172.47096	MAP2K3;ZI	.
0	0	26.19252548	172.47096	IL23A;IL23I	.

0	0	26.19252548	172.47096	CD74;ANX
0	0	26.19252548	172.47096	IL1R1;IL1B
0	0	26.19252548	172.47096	RBPJ;HIF1
0	0	26.19252548	172.47096	PTPN1;ITC
0	0	26.19252548	172.47096	SLC9A3R1;
0	0	26.19252548	172.47096	IL1R1;IL1B
0	0	26.19252548	172.47096	RIPK2;TNI
0	0	1.872092518	12.28934682	CDKN1A;PI
0	0	3.607059046	23.59084605	ILRUN;ITC
0	0	3.607059046	23.59084605	CCR1;CXCL
0	0	2.963292547	19.26760192	UTP15;DD
0	0	2.963292547	19.26760192	IL10;EGR1;
0	0	2.963292547	19.26760192	IL10;IL10R
0	0	1.904007634	12.37706159	PTGFR;GP
0	0	2.446320366	15.89539826	RTP4;NCF1
0	0	1.941455087	12.51287361	RYR1;CCL1
0	0	10.9164149	70.16691693	GSN;CASS4
0	0	10.9164149	70.16691693	ERAP2;ERA
0	0	10.9164149	70.16691693	P2RY12;CS
0	0	10.9164149	70.16691693	CIITA;XBP1
0	0	10.9164149	70.16691693	CD300A;IL
0	0	10.9164149	70.16691693	SLAMF8;IL
0	0	10.9164149	70.16691693	IL10;GBP5;
0	0	10.9164149	70.16691693	PARP10;D
0	0	10.9164149	70.16691693	FLOT1;FLO
0	0	3.279628928	20.99525568	IL23A;IL23
0	0	3.279628928	20.99525568	MN1;CDK
0	0	1.985990695	12.71103171	ERO1A;PR
0	0	5.733796296	36.43525817	DAXX;DDX
0	0	5.733796296	36.43525817	CXCL8;HSP
0	0	5.733796296	36.43525817	CLN3;ANX
0	0	5.733796296	36.43525817	RAP1B;SLC
0	0	5.733796296	36.43525817	CD74;EDN
0	0	5.733796296	36.43525817	PNPT1;STE
0	0	5.733796296	36.43525817	PNPT1;STE
0	0	4.21431273	26.69857732	ACVRL1;NF
0	0	4.21431273	26.69857732	PYCARD;NI
0	0	2.399137025	15.15455487	KMT2E;CD
0	0	3.045819805	19.23787955	RIPK2;SH2I
0	0	3.045819805	19.23787955	IL10;IL1RN
0	0	4.766729679	30.03087766	C3;NR4A3;
0	0	2.058622002	12.94900906	AMER1;PR
0	0	2.870523873	17.9907453	ARG2;RSA
0	0	3.435096067	21.45245136	C3;CXCL8;I
0	0	2.625255973	16.39009758	CCL14;CCR
0	0	2.625255973	16.39009758	LYN;FLT1;S
0	0	2.016517517	12.57089312	SRC;CLEC1

0	0	2.016517517	12.57089312	SRC;CLEC1	.
0	0	1.602747418	9.946191862	OTUD4;US	.
0	0	1.914801476	11.69970747	RNASEH2B	.
0	0	3.642535839	22.23721168	SELP;ROCK	.
0	0	3.642535839	22.23721168	CYP27B1;F	.
0	0	3.642535839	22.23721168	BST1;P2RX	.
0	0	3.642535839	22.23721168	SPRED2;CD	.
0	0	3.642535839	22.23721168	IL10;XBP1;	.
0	0	3.642535839	22.23721168	IFITM3;IFN	.
0	0	2.41152461	14.70751929	BCAR3;DGI	.
0	0	1.760671101	10.71610779	CFD;LGALS	.
0	0	2.053248668	12.46878539	CDKN1A;C	.
0	0	2.561077351	15.47623622	SLC13A3;S	.
0	0	2.561077351	15.47623622	RHBDD1;N	.
0	0	2.783377542	16.81675329	TLE3;IL15;I	.
0	0	2.264232487	13.63891554	PDIA3;FCE	.
0	0	6.551190026	39.3985662	XBP1;DGA	.
0	0	6.551190026	39.3985662	DDX5;C5AI	.
0	0	6.551190026	39.3985662	LYN;CSF1;C	.
0	0	6.551190026	39.3985662	IL6;IL1B;CC	.
0	0	6.551190026	39.3985662	PARP10;PA	.
0	0	6.551190026	39.3985662	IL10;CIITA;	.
0	0	1.200213258	7.204979362	ZNF296;M	.
0	0	3.933131619	23.55586627	CYLD;ITCH;	.
0	0	3.933131619	23.55586627	HSPA5;DDI	.
0	0	3.933131619	23.55586627	PTPN1;HHI	.
0	0	3.278766086	19.5595986	IL10;CDKN	.
0	0	1.823478094	10.80282901	PPP1R15B;	.
0	0	4.369250158	25.82985908	FMNL3;IKB	.
0	0	4.369250158	25.82985908	PYCARD;IL	.
0	0	5.096413874	30.06821065	FGD3;FGD	.
0	0	5.096413874	30.06821065	SPRED2;SP	.
0	0	5.096413874	30.06821065	KMT2E;PRI	.
0	0	5.096413874	30.06821065	SELP;NFAT	.
0	0	5.096413874	30.06821065	CD74;SEM	.
0	0	5.096413874	30.06821065	EDN1;ANX	.
0	0	2.499954855	14.62241331	TCF7L2;EG	.
0	0	2.499954855	14.62241331	RAMP2;CX	.
0	0	2.842436869	16.60158014	XBP1;IL23F	.
0	0	3.450624291	20.03736219	ERO1A;PPF	.
0	0	2.31668713	13.31789257	LYN;FLT1;I	.
0	0	8.186839124	46.92960497	XBP1;HSPA	.
0	0	8.186839124	46.92960497	NR4A1;NRI	.
0	0	8.186839124	46.92960497	KYNU;KYA	.
0	0	8.186839124	46.92960497	CD74;SEM	.
0	0	8.186839124	46.92960497	GBP5;DDX	.
0	0	8.186839124	46.92960497	IFNG;IL12B	.

0	0	8.186839124	46.92960497	IKBKB;ROC
0	0	8.186839124	46.92960497	BTG1;NOT
0	0	8.186839124	46.92960497	IFNG;CLEC
0	0	8.186839124	46.92960497	NCR1;NOS
0	0	8.186839124	46.92960497	PPP1R15A;
0	0	8.186839124	46.92960497	CD274;ZFP
0	0	8.186839124	46.92960497	CDKN2D;C
0	0	2.188504874	12.48530542	RET;P2RY1
0	0	3.136030017	17.87663586	BCAR3;AD/
0	0	3.687098147	20.89271337	RIPOR2;CD
0	0	2.441675265	13.82377373	PLK3;JUN;I
0	0	2.914720855	16.44622378	PNKD;ANX
0	0	2.914720855	16.44622378	SPRED2;SP
0	0	2.523473494	14.21306693	DIRAS3;CD
0	0	2.121358429	11.92992678	HDAC4;CD
0	0	2.121358429	11.92992678	MAP2K3;S
0	0	2.75058651	15.45168601	CCL14;HSD
0	0	2.75058651	15.45168601	TRAF3IP2;(
0	0	2.75058651	15.45168601	IL10;CD40;
0	0	13.09550774	73.3030207	CD14;TLR6
0	0	13.09550774	73.3030207	HERC5;UB/
0	0	13.09550774	73.3030207	AGO2;ABC
0	0	13.09550774	73.3030207	LYN;ACOD
0	0	13.09550774	73.3030207	FCER2;IFN(
0	0	13.09550774	73.3030207	TASL;DDX3
0	0	13.09550774	73.3030207	PNP;ADA2;
0	0	13.09550774	73.3030207	OTUD4;ZBI
0	0	13.09550774	73.3030207	IL23A;IL23I
0	0	13.09550774	73.3030207	CD74;NLRF
0	0	13.09550774	73.3030207	ROCK1;PRI
0	0	1.713682323	9.576399392	USP36;CDI
0	0	1.877442177	10.45302024	ACVRL1;CD
0	0	4.032921332	22.40027211	PPP1R15A;
0	0	4.032921332	22.40027211	XBP1;SESN
0	0	3.277903897	18.1139233	PYCARD;LY
0	0	3.277903897	18.1139233	CD74;IL6;T
0	0	5.61498192	30.9566673	ABCA1;NFI
0	0	5.61498192	30.9566673	CD74;MBP
0	0	5.61498192	30.9566673	IL6;PTPRC;
0	0	5.61498192	30.9566673	RGS2;GSN;
0	0	5.61498192	30.9566673	CDKN1A;H
0	0	4.586507937	25.17853871	IL10;IL6;SII
0	0	4.586507937	25.17853871	SPRED2;SP
0	0	4.586507937	25.17853871	CD300A;D
0	0	4.586507937	25.17853871	IKBKB;ROC
0	0	4.586507937	25.17853871	GBP5;DDX
0	0	2.188053657	11.99698127	NCOA1;ST/

0	0	3.00518862	16.37422296	IL10;MAD2	.
0	0	2.460244503	13.38891843	ACVRL1;M	.
0	0	2.810461405	15.21055592	ZFYVE28;R	.
0	0	2.810461405	15.21055592	SLC9A3R1;	.
0	0	2.810461405	15.21055592	XBP1;ANX/	.
0	0	2.664476799	14.3980205	P2RY12;NF	.
0	0	1.717315827	9.256003188	SMG1;ROC	.
0	0	3.470009789	18.61643479	CCR1;LYN;(	.
0	0	3.470009789	18.61643479	DUSP10;SC	.
0	0	2.276687003	12.19930924	DGKD;SRC;	.
0	0	1.471966647	7.815243974	SERPINE1;I	.
0	0	1.792222646	9.512443821	RET;FLT1;C	.
0	0	2.332886698	12.37496687	IL10;HDAC	.
0	0	3.121633065	16.42304184	CDKN2D;CI	.
0	0	3.121633065	16.42304184	ABCA1;NFI	.
0	0	2.400099854	12.6207151	TLE3;IL15;I	.
0	0	1.644127774	8.597476184	RAMP2;RC	.
0	0	3.744639482	19.56304545	CDKN2D;CI	.
0	0	3.744639482	19.56304545	CD74;RIPO	.
0	0	2.481898344	12.96053417	XBP1;SYAP	.
0	0	2.481898344	12.96053417	SRC;PRKCE	.
0	0	2.884814534	15.02801977	NLGN3;UG	.
0	0	2.884814534	15.02801977	CCR1;CSF1	.
0	0	2.583585859	13.43057588	KMT2E;LYI	.
0	0	1.48318639	7.709214395	UBE2D1;HI	.
0	0	2.713392263	14.08791337	LFNG;ADAI	.
0	0	6.549093656	33.75606817	DCSTAMP;	.
0	0	6.549093656	33.75606817	IFIH1;IRF3;	.
0	0	6.549093656	33.75606817	CD74;FCER	.
0	0	6.549093656	33.75606817	HAAO;KYN	.
0	0	6.549093656	33.75606817	ABCA1;NR1	.
0	0	6.549093656	33.75606817	IL10;IL1RN	.
0	0	6.549093656	33.75606817	SELP;SOX1	.
0	0	6.549093656	33.75606817	PRKCB;IL1I	.
0	0	6.549093656	33.75606817	PARP10;PA	.
0	0	6.549093656	33.75606817	NRP1;MYC	.
0	0	6.549093656	33.75606817	IL10;IL1RN	.
0	0	6.549093656	33.75606817	ABCA1;KLF	.
0	0	1.856266861	9.551495557	HDAC4;CSI	.
0	0	4.169312169	21.33580885	CCDC186;S	.
0	0	4.169312169	21.33580885	ADAM17;C	.
0	0	2.147703985	10.96644383	PDIA3;NCF	.
0	0	1.780687258	9.085844809	RAMP2;RC	.
0	0	1.67941762	8.568174083	CCL14;NRP	.
0	0	1.693076238	8.628275345	BCAR3;RET	.
0	0	1.760014433	8.968459517	CDKN1A;G	.
0	0	1.741118869	8.865752948	RNF31;TEN	.

0	0	3.27704236	16.6560155	PTPN1;PTP.
0	0	4.912825841	24.91557424	ADAM19;C.
0	0	4.912825841	24.91557424	TRPC5;TRP.
0	0	4.912825841	24.91557424	CCR1;SRGN.
0	0	4.912825841	24.91557424	CD74;MDN.
0	0	4.912825841	24.91557424	IL10;TLR8;I.
0	0	4.912825841	24.91557424	HEXIM1;IFI.
0	0	4.912825841	24.91557424	DYNC1H1;S.
0	0	4.912825841	24.91557424	PYCARD;SF.
0	0	4.912825841	24.91557424	CD74;SEMA.
0	0	4.912825841	24.91557424	DGKG;CD4 .
0	0	4.912825841	24.91557424	RGS2;GSN; .
0	0	4.912825841	24.91557424	ADAM17;P.
0	0	1.997918594	10.11284861	PLK3;PRKA.
0	0	2.979568672	14.92932245	PREX1;NRF.
0	0	2.622794396	13.06542042	CCL14;IL6;I.
0	0	2.622794396	13.06542042	PTPN1;ADA.
0	0	2.019574045	10.05029815	IL10;HDAC.
0	0	1.516329085	7.522127058	OTUD4;CX.
0	0	1.516329085	7.522127058	OTUD4;US .
0	0	2.109230144	10.45461427	TRAF2;TIRA.
0	0	2.109230144	10.45461427	HM13;VPS.
0	0	1.969262918	9.707511844	ROCK1;PRK.
0	0	3.494795211	17.18902159	EDN1;PAK1.
0	0	3.494795211	17.18902159	LYN;ELF1;C.
0	0	2.144967608	10.47106612	IL10;KDM4.
0	0	8.729835158	42.43679444	IL18RAP;IL .
0	0	8.729835158	42.43679444	NAPSA;ABC.
0	0	8.729835158	42.43679444	C3;CFD;CFI.
0	0	8.729835158	42.43679444	IL18RAP;IL .
0	0	8.729835158	42.43679444	PYCARD;M.
0	0	8.729835158	42.43679444	NR1H2;NR .
0	0	8.729835158	42.43679444	RAP1B;PNI.
0	0	8.729835158	42.43679444	NR1H2;NR .
0	0	8.729835158	42.43679444	TBX21;ZC3 .
0	0	8.729835158	42.43679444	RIPK2;NOD.
0	0	8.729835158	42.43679444	IL23A;IL23I.
0	0	8.729835158	42.43679444	BCL2L11;B.
0	0	8.729835158	42.43679444	IFNG;CLEC.
0	0	8.729835158	42.43679444	PNPT1;ZC3.
0	0	8.729835158	42.43679444	SFPQ;RIPK.
0	0	8.729835158	42.43679444	PTPN1;ITCI.
0	0	8.729835158	42.43679444	CD74;ANXA.
0	0	8.729835158	42.43679444	SENP7;USP.
0	0	8.729835158	42.43679444	SLC6A6;AS.
0	0	8.729835158	42.43679444	ANXA1;CD.
0	0	8.729835158	42.43679444	TASL;DDX3.

0	0	8.729835158	42.43679444	RYR1;CCL3 .
0	0	8.729835158	42.43679444	S1PR1;S1P .
0	0	8.729835158	42.43679444	NAPSA;AB(.
0	0	8.729835158	42.43679444	MX2;MX1; .
0	0	3.104387292	14.95622196	PTPN1;PTP .
0	0	2.435670996	11.72048046	IL10;BTG3; .
0	0	2.435670996	11.72048046	MAP2K3;S .
0	0	3.82164903	18.25833134	CD74;RIPO .
0	0	3.82164903	18.25833134	PDP1;EDN .
0	0	3.82164903	18.25833134	CD74;EDN .
0	0	3.82164903	18.25833134	GSDMD;ZB .
0	0	3.82164903	18.25833134	LYN;ADAM .
0	0	3.82164903	18.25833134	IL12B;TNF .
0	0	3.82164903	18.25833134	IL6;IL1B;IL .
0	0	3.82164903	18.25833134	TRAF2;TNF .
0	0	2.849857705	13.60391883	FCN1;XKR8 .
0	0	2.849857705	13.60391883	PPP1R16B; .
0	0	2.670816161	12.72610484	XBP1;SPTL .
0	0	2.670816161	12.72610484	UGCG;PTPI .
0	0	2.011015994	9.562236405	NIBAN1;DI .
0	0	1.864141201	8.840548349	CCR1;CCL1 .
0	0	1.468571828	6.933020232	CDKN1A;CI .
0	0	1.716120083	8.049203853	RAMP2;RC .
0	0	4.366704445	20.42850275	CASP8;CSF .
0	0	4.366704445	20.42850275	CD300A;ZC .
0	0	4.366704445	20.42850275	FCER2;MA .
0	0	4.366704445	20.42850275	LAMP1;IL2 .
0	0	4.366704445	20.42850275	CASP8;CSF .
0	0	4.366704445	20.42850275	C3;NR1H2; .
0	0	2.036262514	9.509152552	FUS;CLK4;F .
0	0	5.457263343	25.44631774	IL10;NR4A .
0	0	5.457263343	25.44631774	SLC9A3R1; .
0	0	5.457263343	25.44631774	DYNC1H1;S .
0	0	5.457263343	25.44631774	ATF7IP;SET .
0	0	5.457263343	25.44631774	P2RY12;RA .
0	0	5.457263343	25.44631774	CASP8;CSF .
0	0	5.457263343	25.44631774	NT5C3A;DI .
0	0	5.457263343	25.44631774	MBD2;BAZ .
0	0	5.457263343	25.44631774	CD274;CD8 .
0	0	5.457263343	25.44631774	CD274;RIP .
0	0	5.457263343	25.44631774	IL6;RSAD2; .
0	0	5.457263343	25.44631774	LYN;ACOD .
0	0	5.457263343	25.44631774	INSIG1;PM .
0	0	5.457263343	25.44631774	RIPK3;TNF .
0	0	5.457263343	25.44631774	HAAO;KYN .
0	0	3.276181474	15.18292217	ZNFX1;MB .
0	0	3.276181474	15.18292217	GGT5;CYP4 .

0	0	3.276181474	15.18292217	DGAT2;ELC
0	0	3.276181474	15.18292217	CCR1;SRGN
0	0	3.276181474	15.18292217	ITGAM;DD
0	0	3.276181474	15.18292217	RAP1GAP2
0	0	1.978980608	9.144139866	ARRDC4;AI
0	0	1.978980608	9.144139866	DIRAS3;CD
0	0	2.458585763	11.27803036	MOV10;BT
0	0	2.186252211	10.0210684	MYLIP;DEN
0	0	2.948997731	13.47351972	CD274;DDI
0	0	2.948997731	13.47351972	ADAM17;II
0	0	2.575281172	11.73878918	NRP1;NR4A
0	0	2.575281172	11.73878918	ING5;KAT2
0	0	2.730955984	12.42311446	LAT2;PTPR
0	0	2.730955984	12.42311446	ROCK1;IFN
0	0	2.730955984	12.42311446	RET;LYN;P2
0	0	2.239244355	10.11298489	OTUD4;IL1
0	0	1.819011407	8.206500153	DIRAS3;JUI
0	0	1.790414606	8.056140296	CD74;CREB
0	0	3.527472527	15.75466694	CXCL8;TRIM
0	0	3.527472527	15.75466694	PNP;IL23A;
0	0	3.527472527	15.75466694	CLEC3B;GS
0	0	3.527472527	15.75466694	EGR1;DAXX
0	0	1.902056947	8.477048325	ACVRL1;US
0	0	1.426277338	6.31537658	RARG;MAM
0	0	1.544185157	6.791334674	PSMB10;AT
0	0	3.083287001	13.47307868	ACVRL1;IKI
0	0	3.083287001	13.47307868	PYCARD;BC
0	0	1.917866947	8.366649217	IL10;HDAC
0	0	1.917866947	8.366649217	WASHC4;E
0	0	1.917866947	8.366649217	SLC22A3;SI
0	0	1.397633008	6.081420903	RNF13;RNF
0	0	2.621566402	11.36725331	CD81;CD3C
0	0	1.874776192	8.126865076	TCF7L2;CSI
0	0	2.808407175	12.17318472	DAXX;DDX
0	0	3.929807329	16.99786475	CHI3L1;TRA
0	0	3.929807329	16.99786475	MGAM;PH
0	0	3.929807329	16.99786475	PIK3CA;SRC
0	0	3.929807329	16.99786475	PTPRC;ZC3
0	0	3.929807329	16.99786475	CNOT7;STA
0	0	3.929807329	16.99786475	NRP1;PTPN
0	0	3.929807329	16.99786475	MAD2L2;P
0	0	3.929807329	16.99786475	FLCN;SEH1
0	0	3.929807329	16.99786475	PPP1R15A;
0	0	3.929807329	16.99786475	RAP1B;RIP
0	0	3.929807329	16.99786475	IL10;NLRP1
0	0	3.929807329	16.99786475	IL10;MAD2
0	0	1.991294982	8.580441194	ARHGAP9;

0	0	1.991294982	8.580441194	ABCA1;NRI.
0	0	2.242992424	9.615529155	ACVRL1;RC.
0	0	2.242992424	9.615529155	IVNS1ABP;.
0	0	2.242992424	9.615529155	PXK;NDFIP.
0	0	1.727549467	7.401063613	ILRUN;PRK.
0	0	6.546998867	28.00948369	NRP1;SPRE.
0	0	6.546998867	28.00948369	IL10;NFKBI.
0	0	6.546998867	28.00948369	HYAL2;CXC.
0	0	6.546998867	28.00948369	HYAL2;CXC.
0	0	6.546998867	28.00948369	KMT2E;AD.
0	0	6.546998867	28.00948369	RAP1B;STX.
0	0	6.546998867	28.00948369	TBX21;ZC3.
0	0	6.546998867	28.00948369	PYCARD;CI.
0	0	6.546998867	28.00948369	IL12A;CALF.
0	0	6.546998867	28.00948369	IL6;PDPN;F.
0	0	6.546998867	28.00948369	IL6;RSAD2;.
0	0	6.546998867	28.00948369	RGCC;RIC1.
0	0	6.546998867	28.00948369	IFNG;ABCA.
0	0	6.546998867	28.00948369	TLR6;FBXO.
0	0	6.546998867	28.00948369	GFI1;XIAP;.
0	0	6.546998867	28.00948369	ANXA1;IL1.
0	0	6.546998867	28.00948369	SESN2;ANK.
0	0	6.546998867	28.00948369	XBP1;SERP.
0	0	6.546998867	28.00948369	MX2;MX1;.
0	0	4.677384549	19.82280163	KDM4A;KD.
0	0	4.677384549	19.82280163	NT5C3A;DI.
0	0	4.677384549	19.82280163	PPP1R3B;P.
0	0	4.677384549	19.82280163	CD53;RIPO.
0	0	4.677384549	19.82280163	IL23A;IL12I.
0	0	4.677384549	19.82280163	STX1B;STX.
0	0	1.813164894	7.615297555	CCR1;CCL1.
0	0	2.134846709	8.96634003	HACE1;DTX.
0	0	3.27532124	13.69057561	VCAN;CHST.
0	0	3.27532124	13.69057561	PARP10;HA.
0	0	3.27532124	13.69057561	ZFP36;TUT.
0	0	3.27532124	13.69057561	PTPRC;CD8.
0	0	3.27532124	13.69057561	PIK3CA;SR(.
0	0	3.27532124	13.69057561	CLN3;PRKC.
0	0	1.956246839	8.169362205	PLK3;BTG2.
0	0	2.403318193	10.0293733	TGM1;BCR.
0	0	2.403318193	10.0293733	PPP1R16B;.
0	0	1.904450021	7.889006005	RYR1;CLIC4.
0	0	1.614813472	6.684977752	AVIL;NEDD.
0	0	2.520591403	10.41992436	DCSTAMP;.
0	0	2.520591403	10.41992436	TRPC5;TRP.
0	0	2.911825247	12.00465669	KDM5A;KD.
0	0	2.911825247	12.00465669	CDKN2D;CI.

0	0	2.911825247	12.00465669	KMT2E;AD	.
0	0	2.911825247	12.00465669	IL23A;IL23	.
0	0	1.860401863	7.660366186	SLC22A3;S	.
0	0	2.680597579	11.02722229	CD74;EDN	.
0	0	2.680597579	11.02722229	GOLGA7B;	.
0	0	1.822488079	7.472143189	CXCL8;EGR	.
0	0	2.247460378	9.114791449	IL10;ADAM	.
0	0	1.460670329	5.883493073	RTP4;VPS4	.
0	0	3.572346052	14.313563	IL10;APOA	.
0	0	3.572346052	14.313563	FCN1;IFITM	.
0	0	3.572346052	14.313563	NT5C3A;DI	.
0	0	3.572346052	14.313563	STX1B;SYN	.
0	0	1.832936933	7.331538971	SEMA6A;N	.
0	0	1.832936933	7.331538971	CREBBP;EG	.
0	0	2.325657493	9.287621232	MEF2A;NR	.
0	0	1.14544213	4.560578375	ZNF296;GF	.
0	0	1.715161597	6.821087878	CCR1;CCL1	.
0	0	1.509777385	5.995013765	GALNT11;F	.
0	0	2.130596591	8.456971124	ZBTB17;XB	.
0	0	9.817924528	38.94855912	ANXA1;RSA	.
0	0	9.817924528	38.94855912	PTPRC;LRP	.
0	0	9.817924528	38.94855912	DAXX;ZC3H	.
0	0	9.817924528	38.94855912	CYP24A1;V	.
0	0	9.817924528	38.94855912	CXCL13;S1	.
0	0	9.817924528	38.94855912	ISG20;TRE	.
0	0	9.817924528	38.94855912	SLC2A10;S	.
0	0	9.817924528	38.94855912	PNP;ADA2	.
0	0	9.817924528	38.94855912	DDX3X;EIF	.
0	0	9.817924528	38.94855912	ADGRG3;D	.
0	0	9.817924528	38.94855912	MPV17L;H	.
0	0	9.817924528	38.94855912	HSPA5;DNA	.
0	0	9.817924528	38.94855912	NR1H2;NR	.
0	0	9.817924528	38.94855912	IKBKB;ROC	.
0	0	9.817924528	38.94855912	STX1B;NR1	.
0	0	9.817924528	38.94855912	NOS2;S10	.
0	0	9.817924528	38.94855912	CD81;LGAL	.
0	0	9.817924528	38.94855912	IL23A;IL23	.
0	0	9.817924528	38.94855912	IL6;IL1B;TN	.
0	0	9.817924528	38.94855912	IL1B;PTGS2	.
0	0	9.817924528	38.94855912	GBP5;TLR9	.
0	0	9.817924528	38.94855912	NOS2;CLEC	.
0	0	9.817924528	38.94855912	SELP;SELE;	.
0	0	9.817924528	38.94855912	CIITA;NLRP	.
0	0	9.817924528	38.94855912	CSF1;IL12B	.
0	0	9.817924528	38.94855912	TLR6;TLR4;	.
0	0	9.817924528	38.94855912	MX2;MX1;	.
0	0	9.817924528	38.94855912	MX2;MX1;	.

0	0	9.817924528	38.94855912	IFNG;GTF2 .
0	0	9.817924528	38.94855912	CLEC7A;PL .
0	0	9.817924528	38.94855912	PTPRC;PTP .
0	0	9.817924528	38.94855912	IL1B;PTGS2 .
0	0	9.817924528	38.94855912	P2RY12;GP .
0	0	9.817924528	38.94855912	PNPT1;ZC3 .
0	0	9.817924528	38.94855912	NFKB1;RC3 .
0	0	9.817924528	38.94855912	CSF1;IL12B .
0	0	9.817924528	38.94855912	IL23A;IL18 .
0	0	9.817924528	38.94855912	XIAP;BIRC2 .
0	0	9.817924528	38.94855912	HIP1R;PTPI .
0	0	9.817924528	38.94855912	NRP1;PTPR .
0	0	9.817924528	38.94855912	CAST;TCF7 .
0	0	9.817924528	38.94855912	DAXX;ZC3H .
0	0	9.817924528	38.94855912	PELI2;PELI1 .
0	0	9.817924528	38.94855912	KYNU;IDO2 .
0	0	2.427096033	9.567332934	CAST;IL10;T .
0	0	2.427096033	9.567332934	XKR8;ITGA .
0	0	2.427096033	9.567332934	STAT5B;MA .
0	0	2.427096033	9.567332934	LYN;STAT5 .
0	0	2.427096033	9.567332934	SLC4A7;CLI .
0	0	1.889714771	7.410593046	PHLDB1;SM .
0	0	3.056790123	11.96941002	ADAM17;H .
0	0	3.056790123	11.96941002	ITGAM;IFN .
0	0	3.056790123	11.96941002	ZFP36;PTPI .
0	0	3.056790123	11.96941002	CD74;RIPO .
0	0	3.056790123	11.96941002	IL10;ROCK1 .
0	0	3.056790123	11.96941002	TRIM8;CHM .
0	0	2.563901861	10.01284344	ATXN3;PTP .
0	0	1.844722486	7.194036378	DIRAS3;HD .
0	0	2.184904708	8.50523272	SERPINB4;I .
0	0	2.758412098	10.73506774	CDKN1A;ID .
0	0	2.758412098	10.73506774	VCAN;CHST .
0	0	2.758412098	10.73506774	STAT5B;MA .
0	0	2.758412098	10.73506774	IL1A;EDN1 .
0	0	2.758412098	10.73506774	EGR2;DESI .
0	0	2.758412098	10.73506774	ERO1A;RYR .
0	0	2.758412098	10.73506774	IKBKB;MAP .
0	0	1.806268088	7.017770879	ILRUN;CDK .
0	0	4.092475453	15.82222339	ISG20;DFFI .
0	0	4.092475453	15.82222339	SRC;CXCR4 .
0	0	4.092475453	15.82222339	ANXA1;NO .
0	0	4.092475453	15.82222339	MAP2K3;W .
0	0	4.092475453	15.82222339	TRIM8;TRI .
0	0	4.092475453	15.82222339	P2RX5;CLE .
0	0	4.092475453	15.82222339	SOCS1;CD8 .
0	0	4.092475453	15.82222339	ATF7IP;SET .

0	0	4.092475453	15.82222339	ABCA7;STX
0	0	4.092475453	15.82222339	PNP;AMPD
0	0	4.092475453	15.82222339	LYN;ELF1;P
0	0	4.092475453	15.82222339	LYN;CELA2
0	0	4.092475453	15.82222339	SBNO2;SEL
0	0	1.545077092	5.943308048	NOTCH3;R
0	0	1.360985146	5.225661232	BTG2;CDKI
0	0	2.252850587	8.610287025	PRKAA1;XE
0	0	2.252850587	8.610287025	ITGAM;LAI
0	0	2.252850587	8.610287025	SRC;RNASE
0	0	1.563186464	5.942980246	PHLDB1;DI
0	0	5.237297093	19.90199489	RNF31;CD4
0	0	5.237297093	19.90199489	UGCG;NR4
0	0	5.237297093	19.90199489	PNP;AMPD
0	0	5.237297093	19.90199489	CD300A;LG
0	0	5.237297093	19.90199489	IL10;APOA
0	0	5.237297093	19.90199489	IL23A;IL23I
0	0	5.237297093	19.90199489	GALNT11;C
0	0	5.237297093	19.90199489	CXCL8;IL1B
0	0	5.237297093	19.90199489	SLC11A1;N
0	0	5.237297093	19.90199489	KLF7;MAFF
0	0	5.237297093	19.90199489	BCL2L11;B
0	0	5.237297093	19.90199489	IL6;IL1B;HE
0	0	5.237297093	19.90199489	CLN3;NR1H
0	0	5.237297093	19.90199489	IFNG;IL12B
0	0	5.237297093	19.90199489	CDKN2D;C
0	0	5.237297093	19.90199489	IL18;IL12B;
0	0	2.340278904	8.797810875	BCL2L12;P
0	0	2.125730426	7.942637715	HDAC4;MA
0	0	1.928377113	7.187275328	CDKN1B;U
0	0	3.274461655	12.17313963	RYR1;CASP
0	0	3.274461655	12.17313963	IFIH1;DDX5
0	0	3.274461655	12.17313963	ELOVL5;AC
0	0	3.274461655	12.17313963	CD74;MDM
0	0	3.274461655	12.17313963	IL6;SMAD3
0	0	3.274461655	12.17313963	NR4A3;ELC
0	0	3.274461655	12.17313963	SLC7A5;FC
0	0	3.274461655	12.17313963	ATXN3;XBF
0	0	3.274461655	12.17313963	FLCN;SOX1
0	0	3.274461655	12.17313963	RAP1B;RIP
0	0	3.274461655	12.17313963	LYN;CELA2
0	0	3.274461655	12.17313963	SMAD3;ITC
0	0	3.274461655	12.17313963	IFITM3;IFN
0	0	1.624357641	6.025004084	ACVRL1;CD
0	0	2.456930787	9.111332942	PFKFB4;PR
0	0	2.456930787	9.111332942	IL10;IL6;IL1
0	0	2.456930787	9.111332942	PYCARD;DI

0	0	1.658329503	6.108244905	ACVRL1;JU	.
0	0	1.658329503	6.108244905	PPP1R15A;	.
0	0	1.658329503	6.108244905	MAP2K3;R	.
0	0	1.827545461	6.727970751	TCF7L2;UR	.
0	0	1.40404835	5.166423553	AMER1;CD	.
0	0	2.620340265	9.630790886	P2RY12;FG	.
0	0	2.620340265	9.630790886	SMAD3;IFN	.
0	0	2.620340265	9.630790886	ANXA1;CLE	.
0	0	2.620340265	9.630790886	PTPN1;NDI	.
0	0	2.865575397	10.52000108	ADAM19;A	.
0	0	2.865575397	10.52000108	CD40;IL6;G	.
0	0	2.865575397	10.52000108	SLC7A5;FC	.
0	0	2.18445622	7.990549593	ZFYVE28;R	.
0	0	2.18445622	7.990549593	NRP1;PAK1	.
0	0	1.504715331	5.480795014	DGKG;SLC4	.
0	0	1.463876147	5.292013734	RET;NRP1;	.
0	0	1.891183589	6.808400144	SLC13A3;P	.
0	0	2.069670579	7.422638305	PREX1;GHS	.
0	0	2.069670579	7.422638305	RANBP2;SE	.
0	0	2.259449163	8.101431523	MAP4K1;P	.
0	0	2.259449163	8.101431523	RNF126;DT	.
0	0	1.840475288	6.58762266	VASP;TENM	.
0	0	1.568110589	5.602951146	NOTCH3;R	.
0	0	1.703651457	6.067907973	SDC4;CHPF	.
0	0	1.7618171	6.272112974	AMER1;PLI	.
0	0	1.473244892	5.237793307	NOTCH4;LF	.
0	0	1.27185553	4.515255514	RNF13;FBX	.
0	0	3.637546156	12.86783113	ERAP2;ERA	.
0	0	3.637546156	12.86783113	PGS1;PNPL	.
0	0	3.637546156	12.86783113	IL10;NFKBI	.
0	0	3.637546156	12.86783113	NOD1;CD1	.
0	0	3.637546156	12.86783113	PARP10;NA	.
0	0	3.637546156	12.86783113	CD74;TIFAI	.
0	0	3.637546156	12.86783113	FGR;ITGAM	.
0	0	3.637546156	12.86783113	DUSP10;SC	.
0	0	3.637546156	12.86783113	ATF7IP;SET	.
0	0	3.637546156	12.86783113	NR1H2;NR	.
0	0	3.637546156	12.86783113	AGO2;ARH	.
0	0	3.637546156	12.86783113	RIPOR2;LR	.
0	0	3.637546156	12.86783113	P2RY12;NF	.
0	0	3.637546156	12.86783113	IL6;GPR183	.
0	0	3.637546156	12.86783113	NRP1;PIK3	.
0	0	1.981606765	7.006696023	NRP1;RAM	.
0	0	2.358517398	8.307197131	VMP1;CLN	.
0	0	2.358517398	8.307197131	CREBBP;GS	.
0	0	2.358517398	8.307197131	KCNJ12;PR	.
0	0	2.120085051	7.422462532	SPN;IL10;C	.

0	0	2.120085051	7.422462532	PTPN1;PTP.
0	0	1.855393594	6.45139134	SMAD3;DT.
0	0	1.855393594	6.45139134	KMT2E;LYN.
0	0	2.495418129	8.665125958	PREX1;PST.
0	0	2.495418129	8.665125958	RAP1B;PPF.
0	0	2.495418129	8.665125958	PPP1R16B;.
0	0	2.495418129	8.665125958	PTPRC;RIPI.
0	0	1.659574468	5.761151336	UPF2;RANI.
0	0	1.808638343	6.262297468	CDKN1A;A.
0	0	1.808638343	6.262297468	NRP1;ROCI.
0	0	1.706899242	5.898140741	ACVRL1;PP.
0	0	1.76932341	6.112688712	DDX3X;HSI.
0	0	3.022405626	10.43932124	ATF7IP;KM.
0	0	3.022405626	10.43932124	ATF7IP;KM.
0	0	3.022405626	10.43932124	GGT5;ALO.
0	0	3.022405626	10.43932124	MORC3;HS.
0	0	3.022405626	10.43932124	KAT2B;ZC3.
0	0	3.022405626	10.43932124	CLEC7A;TN.
0	0	3.022405626	10.43932124	CCR1;CXCL.
0	0	3.022405626	10.43932124	ADAM19;M.
0	0	3.022405626	10.43932124	KLF7;IFNG;.
0	0	3.022405626	10.43932124	GRAMD1C.
0	0	1.434197051	4.942635931	ISYNA1;PFI.
0	0	2.69685652	9.288909133	SLC6A6;SL.
0	0	2.69685652	9.288909133	CLEC7A;CL.
0	0	2.69685652	9.288909133	LYN;BATF2.
0	0	2.69685652	9.288909133	LYN;FCER1.
0	0	2.69685652	9.288909133	ATAD1;SLC.
0	0	2.69685652	9.288909133	PFKFB4;PR.
0	0	2.69685652	9.288909133	NRP1;ROCI.
0	0	2.69685652	9.288909133	GADD45B;.
0	0	2.69685652	9.288909133	OTUB2;OTI.
0	0	2.69685652	9.288909133	NRP1;SEM.
0	0	2.69685652	9.288909133	IL1A;LYPLA.
0	0	2.016485597	6.941357677	NRP1;PAK1.
0	0	1.590465323	5.45079457	PPP1R16B;.
0	0	2.184008072	7.469704308	CCL14;RET.
0	0	2.184008072	7.469704308	CPB2;EDN1.
0	0	1.540660287	5.254132488	KDM5A;HD.
0	0	1.936458333	6.587597866	SRGN;CCR1.
0	0	4.364162577	14.83033461	ANXA1;PNI.
0	0	4.364162577	14.83033461	ANXA1;PNI.
0	0	4.364162577	14.83033461	LYN;DOCK1.
0	0	4.364162577	14.83033461	TLR9;TLR4;.
0	0	4.364162577	14.83033461	SLC25A37;.
0	0	4.364162577	14.83033461	BATF2;DCS.
0	0	4.364162577	14.83033461	MAD2L2;R.

0	0	4.364162577	14.83033461	RAB11FIP1 .
0	0	4.364162577	14.83033461	PYCARD;RE .
0	0	4.364162577	14.83033461	MAD2L2;H .
0	0	4.364162577	14.83033461	PRKCB;IL1E .
0	0	4.364162577	14.83033461	SOCS3;SOC .
0	0	4.364162577	14.83033461	SEMA6A;IL .
0	0	4.364162577	14.83033461	GPR35;FM .
0	0	4.364162577	14.83033461	KAT2B;CRE .
0	0	4.364162577	14.83033461	PNPLA8;EN .
0	0	4.364162577	14.83033461	PYCARD;M .
0	0	4.364162577	14.83033461	F12;SERPIN .
0	0	4.364162577	14.83033461	F12;SERPIN .
0	0	4.364162577	14.83033461	CD53;RIPO .
0	0	4.364162577	14.83033461	XBP1;FICD; .
0	0	4.364162577	14.83033461	TESC;RARA .
0	0	4.364162577	14.83033461	LRRK2;STK .
0	0	4.364162577	14.83033461	P2RY12;CS .
0	0	4.364162577	14.83033461	IL23A;IL23I .
0	0	4.364162577	14.83033461	HCK;GSN;F .
0	0	4.364162577	14.83033461	EGR1;IFNG .
0	0	4.364162577	14.83033461	DCSTAMP; .
0	0	6.54490566	22.10206724	NF1;DLL1;S .
0	0	6.54490566	22.10206724	DAXX;ZC3H .
0	0	6.54490566	22.10206724	XBP1;DGAT .
0	0	6.54490566	22.10206724	OVGP1;CH .
0	0	6.54490566	22.10206724	OVGP1;CH .
0	0	6.54490566	22.10206724	PAK1;FAP;I .
0	0	6.54490566	22.10206724	IFIH1;DDX5 .
0	0	6.54490566	22.10206724	NIPBL;ECE1 .
0	0	6.54490566	22.10206724	SLC2A10;SI .
0	0	6.54490566	22.10206724	NINJ1;SLAM .
0	0	6.54490566	22.10206724	ANXA2;FLC .
0	0	6.54490566	22.10206724	DCSTAMP; .
0	0	6.54490566	22.10206724	CD274;SOC .
0	0	6.54490566	22.10206724	SMAD3;AT .
0	0	6.54490566	22.10206724	SPRED2;SP .
0	0	6.54490566	22.10206724	MAEA;IRF7 .
0	0	6.54490566	22.10206724	CD300A;LG .
0	0	6.54490566	22.10206724	GRK2;TIFAI .
0	0	6.54490566	22.10206724	NDFIP2;PP .
0	0	6.54490566	22.10206724	GFI1;SNAI1 .
0	0	6.54490566	22.10206724	JAML;PECA .
0	0	6.54490566	22.10206724	SLC22A3;SI .
0	0	6.54490566	22.10206724	SLC11A1;N .
0	0	6.54490566	22.10206724	MAPK8;PR .
0	0	6.54490566	22.10206724	SLC11A1;N .
0	0	6.54490566	22.10206724	IL1B;PTGS2 .

0	0	6.54490566	22.10206724	IQSEC1;AR .
0	0	6.54490566	22.10206724	TESC;HCLS .
0	0	6.54490566	22.10206724	SLC25A37; .
0	0	6.54490566	22.10206724	P2RY12;CS .
0	0	6.54490566	22.10206724	IL12B;IL12 .
0	0	6.54490566	22.10206724	IL12B;IL12 .
0	0	6.54490566	22.10206724	DOCK3;SR(.
0	0	6.54490566	22.10206724	CLEC3B;F1 .
0	0	6.54490566	22.10206724	NRP1;ANX .
0	0	6.54490566	22.10206724	NR1H2;NR .
0	0	6.54490566	22.10206724	IL18;RARA; .
0	0	6.54490566	22.10206724	FLOT1;PTP .
0	0	6.54490566	22.10206724	VPS4B;CEP .
0	0	6.54490566	22.10206724	IQSEC1;AR .
0	0	6.54490566	22.10206724	EGR1;FFAR .
0	0	6.54490566	22.10206724	IL10;SUPT6 .
0	0	6.54490566	22.10206724	IRF7;NOD2 .
0	0	6.54490566	22.10206724	ERBIN;PTP .
0	0	6.54490566	22.10206724	FLCN;HES1 .
0	0	6.54490566	22.10206724	NR4A1;NR .
0	0	6.54490566	22.10206724	RYR1;CCL3 .
0	0	6.54490566	22.10206724	INPP5K;AIF .
0	0	6.54490566	22.10206724	SYAP1;PRR .
0	0	2.059392235	6.900821999	TCF7L2;SM .
0	0	1.777880617	5.954266843	CREBBP;EG .
0	0	1.777880617	5.954266843	CDKN1A;A .
0	0	1.710551935	5.727888762	RTP4;ATAD .
0	0	1.741576963	5.827883618	PPP1R16B; .
0	0	1.741576963	5.827883618	P2RY12;P2 .
0	0	2.26767427	7.587514575	CA12;SLC4 .
0	0	2.26767427	7.587514575	CASP4;ATP .
0	0	2.26767427	7.587514575	CREB1;ELO .
0	0	1.382905328	4.621498207	AMER1;DR .
0	0	1.527290096	5.087823729	SLC22A3;R .
0	0	1.965959864	6.495345129	MAD2L2;E .
0	0	1.407120997	4.629036409	DDX5;NFIX .
0	0	1.620337922	5.322402566	XBP1;PKLR .
0	0	1.620337922	5.322402566	HDAC4;RA .
0	0	2.381852552	7.816576561	P2RY12;GS .
0	0	2.381852552	7.816576561	VCAN;CHS .
0	0	2.381852552	7.816576561	AEBP2;PHF .
0	0	2.381852552	7.816576561	IL10;GHSR; .
0	0	2.381852552	7.816576561	SNX18;ITG .
0	0	2.381852552	7.816576561	P2RY12;FG .
0	0	2.381852552	7.816576561	SMAD3;IFN .
0	0	1.893316498	6.196395191	TCF7L2;CSI .
0	0	2.113434147	6.895330586	ISG20;DFFI .

0	0	2.113434147	6.895330586	FLCN;SEH1 .
0	0	2.113434147	6.895330586	IFITM3;HE) .
0	0	3.273602719	10.62178509	DDX17;DA) .
0	0	3.273602719	10.62178509	OCSTAMP; .
0	0	3.273602719	10.62178509	IFIH1;DDX5 .
0	0	3.273602719	10.62178509	CPB2;SERP .
0	0	3.273602719	10.62178509	MGAM;PH .
0	0	3.273602719	10.62178509	PHKG1;RB1 .
0	0	3.273602719	10.62178509	ABCA1;NP(.
0	0	3.273602719	10.62178509	DDX17;TCF .
0	0	3.273602719	10.62178509	MAD2L2;D .
0	0	3.273602719	10.62178509	CASP3;DDI .
0	0	3.273602719	10.62178509	SDCBP;SD(.
0	0	3.273602719	10.62178509	IL10;IL1B;F .
0	0	3.273602719	10.62178509	IFNG;IL1B;5 .
0	0	3.273602719	10.62178509	USP15;DH) .
0	0	3.273602719	10.62178509	ITGA5;KLF4 .
0	0	3.273602719	10.62178509	NT5C3A;DI .
0	0	3.273602719	10.62178509	PPP1R16B; .
0	0	3.273602719	10.62178509	IL6;FAP;PD .
0	0	3.273602719	10.62178509	RAP1B;SEL .
0	0	3.273602719	10.62178509	BTG2;ZFP3 .
0	0	3.273602719	10.62178509	CXCL10;AD .
0	0	3.273602719	10.62178509	GPR65;GPI .
0	0	3.273602719	10.62178509	TNFSF14;D .
0	0	1.787717968	5.797188797	TCF7L2;CR1 .
0	0	1.748148148	5.662468794	PNPT1;FM .
0	0	2.546884186	8.23531756	GSN;TMSB .
0	0	2.546884186	8.23531756	CD300A;LA .
0	0	2.546884186	8.23531756	GGT5;NPEI .
0	0	2.546884186	8.23531756	PGS1;PNPL .
0	0	2.546884186	8.23531756	KLF7;ZFP36 .
0	0	2.806357602	9.016068808	PSEN1;BAK .
0	0	2.806357602	9.016068808	RARG;NIPB .
0	0	2.806357602	9.016068808	SLC2A9;SL(.
0	0	2.806357602	9.016068808	CDKN1A;C5 .
0	0	2.806357602	9.016068808	ALAS1;NRF .
0	0	2.806357602	9.016068808	FCN1;IFITM .
0	0	2.806357602	9.016068808	IL6;F12;OS .
0	0	2.806357602	9.016068808	IL15;IL23A; .
0	0	2.002071242	6.421057474	INPP4A;ISY .
0	0	2.002071242	6.421057474	ILRUN;NFK .
0	0	2.183560262	6.9414358	IL1A;EDN1 .
0	0	2.183560262	6.9414358	SMAD3;IFN .
0	0	1.9178988	6.08152081	ISG20;DFFI .
0	0	1.9178988	6.08152081	TGM1;BCR .
0	0	1.509457607	4.754280989	OGFR;URI1 .

0	0	1.852050395	5.830896248	GSN;MID1I.
0	0	1.852050395	5.830896248	ANXA1;RIC.
0	0	1.799136631	5.641921774	PLK3;BTG2.
0	0	1.799136631	5.641921774	MTMR3;RC.
0	0	1.799136631	5.641921774	USP36;FUS.
0	0	1.719390515	5.385919274	H2AW;CDK.
0	0	1.719390515	5.385919274	SLC44A3;C.
0	0	1.755692895	5.497390435	XBP1;ANXA.
0	0	1.755692895	5.497390435	SERPINB10.
0	0	1.755692895	5.497390435	HDAC4;RAI.
0	0	1.755692895	5.497390435	PRKAA1;SE.
0	0	1.755692895	5.497390435	ZNF143;US.
0	0	1.568299374	4.90641303	RIPK3;SLC1.
0	0	1.568299374	4.90641303	HDAC4;USI.
0	0	2.047271093	6.372006957	SDCBP;TCF.
0	0	2.278162242	7.0676673	ABCA1;ATF.
0	0	2.278162242	7.0676673	RBM3;SET.
0	0	2.278162242	7.0676673	PPP1R15A;.
0	0	1.947848681	5.979140969	INPP4A;ISY.
0	0	3.740495066	11.42554993	CD74;FCER.
0	0	3.740495066	11.42554993	ATP6V1G1.
0	0	3.740495066	11.42554993	PRKAA1;XE.
0	0	3.740495066	11.42554993	CLN3;LAMI.
0	0	3.740495066	11.42554993	NRP1;PAK1.
0	0	3.740495066	11.42554993	CXCL8;VEG.
0	0	3.740495066	11.42554993	ZFP36;EIF6.
0	0	3.740495066	11.42554993	ZFP36;EIF6.
0	0	3.740495066	11.42554993	IFNG;IL10R.
0	0	3.740495066	11.42554993	PRKCD;TNI.
0	0	3.740495066	11.42554993	LYN;ANXA1.
0	0	3.740495066	11.42554993	C3;ZC3H12.
0	0	3.740495066	11.42554993	PRKCD;TNI.
0	0	3.740495066	11.42554993	HSPA5;DDI.
0	0	3.740495066	11.42554993	CNEP1R1;N.
0	0	3.740495066	11.42554993	AGO2;ABC.
0	0	3.740495066	11.42554993	SRC;PDPN;.
0	0	3.740495066	11.42554993	SPN;STK10.
0	0	3.740495066	11.42554993	RIPK3;IL1B.
0	0	3.740495066	11.42554993	RSAD2;TLR.
0	0	3.740495066	11.42554993	IL10;IL1RN.
0	0	3.740495066	11.42554993	SYNJ1;KIF5.
0	0	2.412698413	7.327579254	RAP1B;PPF.
0	0	2.412698413	7.327579254	NRP1;RIPO.
0	0	2.412698413	7.327579254	TRPC6;SLC.
0	0	1.691560547	5.12370542	SEMA6A;N.
0	0	1.724791509	5.214227565	CDKN1A;PI.
0	0	2.105454398	6.359793915	CDKN2D;PI.

0	0	2.61911598	7.834392797	BCL2A1;CA.
0	0	2.61911598	7.834392797	PYCARD;IF.
0	0	2.61911598	7.834392797	CASP3;DDI.
0	0	2.61911598	7.834392797	PFKFB4;PR.
0	0	2.61911598	7.834392797	ANXA1;RS/.
0	0	2.61911598	7.834392797	C3;ZC3H12.
0	0	2.61911598	7.834392797	PFKFB4;PR.
0	0	2.61911598	7.834392797	TENM1;ZN.
0	0	2.975830816	8.874193995	HAAO;KYN.
0	0	2.975830816	8.874193995	GPR183;CD.
0	0	2.975830816	8.874193995	SOCS3;SOC.
0	0	2.975830816	8.874193995	CD40;RGC.
0	0	2.975830816	8.874193995	CD53;RIPO.
0	0	2.975830816	8.874193995	ROCK1;IFN.
0	0	2.975830816	8.874193995	ABCA1;NR.
0	0	2.975830816	8.874193995	ILRUN;HER.
0	0	2.975830816	8.874193995	CDKN2D;N.
0	0	2.975830816	8.874193995	LYN;FGR;C.
0	0	1.896479939	5.571511173	RBM3;NFK.
0	0	2.183112791	6.40406593	PIK3CA;SR.
0	0	2.183112791	6.40406593	MOV10;ZF.
0	0	2.183112791	6.40406593	FLT1;PTPR.
0	0	2.183112791	6.40406593	SEMA4A;SI.
0	0	2.183112791	6.40406593	IL10;IL6;IL.
0	0	1.66461407	4.874979458	PLK3;LRRK.
0	0	1.828482869	5.339696473	IVNS1ABP;.
0	0	4.908396226	14.3304437	STAT3;DLL.
0	0	4.908396226	14.3304437	VMP1;CAL.
0	0	4.908396226	14.3304437	SLC22A3;S.
0	0	4.908396226	14.3304437	KLF4;ASS1;.
0	0	4.908396226	14.3304437	HYAL1;HAS.
0	0	4.908396226	14.3304437	LY96;LBP;T.
0	0	4.908396226	14.3304437	P2RY12;CC.
0	0	4.908396226	14.3304437	HYAL1;HAS.
0	0	4.908396226	14.3304437	ARHGEF2;I.
0	0	4.908396226	14.3304437	C5AR1;SUF.
0	0	4.908396226	14.3304437	DAAM2;NF.
0	0	4.908396226	14.3304437	ANXA1;TB.
0	0	4.908396226	14.3304437	CD81;PRK.
0	0	4.908396226	14.3304437	IL6;IL1B;TN.
0	0	4.908396226	14.3304437	ZNF304;JA.
0	0	4.908396226	14.3304437	IL1B;ACOD.
0	0	4.908396226	14.3304437	PTPN1;BCL.
0	0	4.908396226	14.3304437	CD180;LY8.
0	0	4.908396226	14.3304437	IL10;FNIP1.
0	0	4.908396226	14.3304437	TNIP1;ZC3I.
0	0	4.908396226	14.3304437	CAMK1D;C.

0	0	4.908396226	14.3304437	AGO2;ACV
0	0	4.908396226	14.3304437	HSPA5;SEC
0	0	4.908396226	14.3304437	CLN3;LAMI
0	0	4.908396226	14.3304437	PRKCD;CCL
0	0	4.908396226	14.3304437	SLC25A37;
0	0	4.908396226	14.3304437	KDM5A;PR
0	0	4.908396226	14.3304437	PLCG2;SIRI
0	0	4.908396226	14.3304437	PLEK;PTK2
0	0	4.908396226	14.3304437	SPRED2;SP
0	0	4.908396226	14.3304437	CIITA;NLRP
0	0	4.908396226	14.3304437	P2RY12;CS
0	0	4.908396226	14.3304437	IKBKB;ROC
0	0	4.908396226	14.3304437	CCL4;CCL3
0	0	4.908396226	14.3304437	IL12B;IL12
0	0	4.908396226	14.3304437	DOCK3;SR(
0	0	4.908396226	14.3304437	DHX8;TFIP
0	0	4.908396226	14.3304437	P2RY12;NF
0	0	4.908396226	14.3304437	FAS;FASLG
0	0	4.908396226	14.3304437	RAMP2;HE
0	0	1.731044492	5.042117192	CDKN1B;H
0	0	1.331300903	3.864009429	NLGN3;CD
0	0	2.291931217	6.540827137	IL6;HP;LBP
0	0	2.291931217	6.540827137	ENPP2;AP(
0	0	2.291931217	6.540827137	PTPN1;DA)
0	0	2.291931217	6.540827137	ID2;USP2;E
0	0	2.291931217	6.540827137	SLC7A5;SL(
0	0	2.291931217	6.540827137	IL10;RAMP
0	0	2.291931217	6.540827137	DDX5;ZFP3
0	0	2.291931217	6.540827137	KLHL18;PP
0	0	2.291931217	6.540827137	ZFYVE28;A
0	0	2.291931217	6.540827137	IL10;IL1RN
0	0	1.614908403	4.599789298	TCF7L2;CR
0	0	1.614908403	4.599789298	EGR1;DAX)
0	0	1.66613125	4.693642913	CDKN1A;R(
0	0	1.847745492	5.195009771	STEAP3;AT
0	0	1.698889871	4.768394953	NRROS;SM
0	0	1.502605156	4.214230283	ABCA1;PTG
0	0	1.556914389	4.364667786	CDKN2D;CI
0	0	1.786823173	5.007001008	PLK3;BTG2
0	0	1.786823173	5.007001008	AMER1;FZI
0	0	2.455279562	6.843602553	GCLC;MTH
0	0	2.455279562	6.843602553	CCR1;SRGN
0	0	2.455279562	6.843602553	LAPTM5;TI
0	0	2.455279562	6.843602553	FOSL1;SET)
0	0	2.455279562	6.843602553	HEXIM1;SF
0	0	2.455279562	6.843602553	IFIH1;ELF1
0	0	1.512976385	4.199201517	USP36;ATP

0	0	1.478546932	4.080017399	RTP4;NCF1 .
0	0	1.478546932	4.080017399	CELA2A;RS .
0	0	1.591746152	4.388498427	HSPA5;RHE .
0	0	3.272744432	9.022160169	PXN;STAT3 .
0	0	3.272744432	9.022160169	SYNJ1;INPF .
0	0	3.272744432	9.022160169	IL10;LYN;C .
0	0	3.272744432	9.022160169	SEMA6A;IL .
0	0	3.272744432	9.022160169	GRK2;ZC3H .
0	0	3.272744432	9.022160169	DUSP10;PT .
0	0	3.272744432	9.022160169	IL6;STAT3;J .
0	0	3.272744432	9.022160169	ABCA1;APO .
0	0	3.272744432	9.022160169	ARG2;CGAS .
0	0	3.272744432	9.022160169	PTPN1;XBP .
0	0	3.272744432	9.022160169	ROCK1;FLC .
0	0	3.272744432	9.022160169	IL10;LYN;B .
0	0	3.272744432	9.022160169	CLEC3B;F1 .
0	0	3.272744432	9.022160169	CASP8;TNI .
0	0	1.524567431	4.188100251	SRGN;C1R; .
0	0	2.727687563	7.488437037	PXK;PPIF;T .
0	0	2.727687563	7.488437037	CD74;MDM .
0	0	2.727687563	7.488437037	F12;SERPIN .
0	0	2.727687563	7.488437037	TNIP2;CCL3 .
0	0	2.727687563	7.488437037	MEF2A;EDI .
0	0	2.727687563	7.488437037	CXCL8;VEG .
0	0	2.727687563	7.488437037	IL10;MAPK .
0	0	2.727687563	7.488437037	PNPT1;NOS .
0	0	2.727687563	7.488437037	HM13;RHB .
0	0	2.727687563	7.488437037	ACVRL1;PII .
0	0	1.964863843	5.359794177	SPN;IL10;L .
0	0	1.964863843	5.359794177	MIDN;RAB .
0	0	1.964863843	5.359794177	FCER2;IL1A .
0	0	1.964863843	5.359794177	XBP1;IFNG .
0	0	1.398625247	3.765923807	AMER1;DR .
0	0	1.398625247	3.765923807	RET;RETRE .
0	0	1.801447767	4.84682774	TIAM2;PAK .
0	0	1.801447767	4.84682774	NRP1;PDPI .
0	0	1.74701502	4.697038825	GGT5;PNPI .
0	0	1.74701502	4.697038825	BST1;CDKN .
0	0	2.182665659	5.855287122	LRRK2;FYN .
0	0	2.182665659	5.855287122	ID2;USP2;E .
0	0	1.443713555	3.823805719	ACVRL1;DI .
0	0	1.588673998	4.202115993	VASP;NRP1 .
0	0	1.250009949	3.287304118	STEAP3;SY .
0	0	2.014948379	5.287369785	XBP1;SESN .
0	0	2.014948379	5.287369785	PPP1R15A; .
0	0	1.638025767	4.267563095	GBP6;GSDI .
0	0	1.638025767	4.267563095	ZNF143;CC .

0	0	2.310718016	6.005717866	DGKG;PGS .
0	0	2.310718016	6.005717866	ATF7IP;KM .
0	0	2.310718016	6.005717866	SLC2A9;SL(.
0	0	2.310718016	6.005717866	HYAL1;HAS .
0	0	2.310718016	6.005717866	RGS2;CXCL .
0	0	2.310718016	6.005717866	GOLGA7B;.
0	0	2.310718016	6.005717866	GOLGA7B;.
0	0	2.310718016	6.005717866	NFKBIA;AB .
0	0	2.310718016	6.005717866	LYN;STK10 .
0	0	1.251908004	3.252721538	MRPS15;SI .
0	0	1.669994058	4.325517791	OSBPL2;DY .
0	0	1.708937655	4.408000478	VMP1;GAB .
0	0	1.708937655	4.408000478	PYCARD;B(.
0	0	1.708937655	4.408000478	KLHL18;KM .
0	0	1.81937613	4.68981807	SDCBP;DYN .
0	0	1.81937613	4.68981807	PARP10;CD .
0	0	1.757408467	4.524459868	GFI1;MPV1 .
0	0	1.757408467	4.524459868	CLN3;IFNG .
0	0	1.757408467	4.524459868	ACVRL1;NF .
0	0	1.500379651	3.838716696	NIBAN1;AN .
0	0	1.500379651	3.838716696	HACE1;CDI .
0	0	1.564871886	3.999984429	P2RY12;NF .
0	0	3.926490566	10.0161581	ANXA1;RSA .
0	0	3.926490566	10.0161581	CLN3;SLC6 .
0	0	3.926490566	10.0161581	KYNU;KYA .
0	0	3.926490566	10.0161581	PRKCD;NFH .
0	0	3.926490566	10.0161581	CDKN1A;H .
0	0	3.926490566	10.0161581	SLC22A3;SI .
0	0	3.926490566	10.0161581	MX2;MX1; .
0	0	3.926490566	10.0161581	MX2;MX1; .
0	0	3.926490566	10.0161581	IFNG;IFNGI .
0	0	3.926490566	10.0161581	CD274;LGA .
0	0	3.926490566	10.0161581	PRKCD;CCL .
0	0	3.926490566	10.0161581	CYP27B1;G .
0	0	3.926490566	10.0161581	PTPN1;DUS .
0	0	3.926490566	10.0161581	CLEC7A;DD .
0	0	3.926490566	10.0161581	FAP;DLC1;.
0	0	3.926490566	10.0161581	PRKCE;PTK .
0	0	3.926490566	10.0161581	PDPN;PLA(.
0	0	3.926490566	10.0161581	CLEC7A;IL1 .
0	0	3.926490566	10.0161581	PNP;AMPD .
0	0	3.926490566	10.0161581	IRF1;PTPN .
0	0	3.926490566	10.0161581	IL10;DDX3 .
0	0	3.926490566	10.0161581	LYN;CD274 .
0	0	3.926490566	10.0161581	SIRPA;CD4 .
0	0	3.926490566	10.0161581	KAT2B;IFN .
0	0	3.926490566	10.0161581	IL1B;ACTN .

0	0	3.926490566	10.0161581	DDX3X;DD
0	0	3.926490566	10.0161581	CDKN1A;M
0	0	3.926490566	10.0161581	DDX39B;AI
0	0	3.926490566	10.0161581	IL15;JAK2;J
0	0	3.926490566	10.0161581	ACTA2;EDI
0	0	3.926490566	10.0161581	NRG1;RBPJ
0	0	3.926490566	10.0161581	DDX39B;AI
0	0	3.926490566	10.0161581	ACVRL1;AD
0	0	1.366358495	3.479828355	SLC22A3;K
0	0	2.517720195	6.372154673	ZFP36;MAI
0	0	2.517720195	6.372154673	ADAM19;C
0	0	2.517720195	6.372154673	CLN3;SLC2
0	0	2.517720195	6.372154673	DDX17;DD
0	0	2.517720195	6.372154673	PARP10;M
0	0	2.517720195	6.372154673	PRKAA1;IL
0	0	2.517720195	6.372154673	RIPOR2;FL(
0	0	2.517720195	6.372154673	MEF2A;ED
0	0	2.517720195	6.372154673	KLHL18;PL(
0	0	2.517720195	6.372154673	CRTC2;CAI
0	0	2.517720195	6.372154673	EGR2;ID2;(
0	0	2.517720195	6.372154673	PPP1R15A;
0	0	2.517720195	6.372154673	LYN;RNF13
0	0	2.517720195	6.372154673	XBP1;PPP2
0	0	2.517720195	6.372154673	DDX5;IL6;Z
0	0	2.517720195	6.372154673	CLN3;IRAK
0	0	2.517720195	6.372154673	CXCL8;SETI
0	0	1.512392351	3.823352118	NRP1;PTPN
0	0	2.083333333	5.255065375	MAD2L2;SI
0	0	2.083333333	5.255065375	ZFP36;CDK
0	0	2.083333333	5.255065375	MAD2L2;P
0	0	2.083333333	5.255065375	MAPK8;MT
0	0	1.609195402	4.038425642	ABCA1;XBF
0	0	1.609195402	4.038425642	PRKAA1;DT
0	0	1.526066893	3.812709711	GSDMD;PN
0	0	2.908938383	7.260762061	AMPD1;AM
0	0	2.908938383	7.260762061	CLEC7A;CL
0	0	2.908938383	7.260762061	SLC22A3;M
0	0	2.908938383	7.260762061	ATP1A3;AT
0	0	2.908938383	7.260762061	ABCA1;NP(
0	0	2.908938383	7.260762061	JUN;CCL4;(
0	0	2.908938383	7.260762061	CYP27B1;G
0	0	2.908938383	7.260762061	CD274;TAF
0	0	2.908938383	7.260762061	PHF1;BCOF
0	0	2.908938383	7.260762061	IL10;NR4A
0	0	2.908938383	7.260762061	CD74;MAR
0	0	2.908938383	7.260762061	PTPN1;HHI
0	0	2.908938383	7.260762061	ARG2;CGA

0	0	2.908938383	7.260762061	ELOVL5;MI.
0	0	2.908938383	7.260762061	BTG2;ZFP3.
0	0	2.908938383	7.260762061	SEC16B;CD.
0	0	2.908938383	7.260762061	PLCG2;RAE.
0	0	2.908938383	7.260762061	TRPC6;NR1.
0	0	2.908938383	7.260762061	PNP;GDA;D.
0	0	2.908938383	7.260762061	FAP;F12;F1.
0	0	2.908938383	7.260762061	NFAT5;IL6;.
0	0	2.908938383	7.260762061	TASL;CLN3.
0	0	2.908938383	7.260762061	HP;SLAMF8.
0	0	2.908938383	7.260762061	SLC9A3R1;.
0	0	2.908938383	7.260762061	SEC16B;CD.
0	0	2.908938383	7.260762061	IL10;ADCY8.
0	0	2.908938383	7.260762061	NRP1;PLXN.
0	0	2.908938383	7.260762061	SYNJ1;KIF5.
0	0	1.94020864	4.816130324	CDKN2D;CI.
0	0	1.94020864	4.816130324	C3;ASAH1;.
0	0	1.94020864	4.816130324	FLCN;SEH1.
0	0	1.94020864	4.816130324	IFIH1;DDX5.
0	0	1.94020864	4.816130324	NRP1;SEM.
0	0	1.482432115	3.677997074	KDM5A;KD.
0	0	1.672480605	4.138248417	ABCA1;ATF.
0	0	1.770101543	4.352341639	HDAC4;ELK.
0	0	1.770101543	4.352341639	ILRUN;FLCI.
0	0	1.770101543	4.352341639	ANXA1;CLE.
0	0	2.182218864	5.291791954	RYBP;DTX3.
0	0	2.182218864	5.291791954	ABCA1;ATF.
0	0	2.182218864	5.291791954	GPAT4;NO.
0	0	2.182218864	5.291791954	APOA2;EN.
0	0	2.182218864	5.291791954	SETX;PLK3;.
0	0	2.182218864	5.291791954	MEF2A;ED.
0	0	2.182218864	5.291791954	ACVRL1;AD.
0	0	1.581359188	3.822252998	ABCA1;XBF.
0	0	1.505357216	3.638482189	VASP;TENN.
0	0	1.267361568	3.0543108	NRP1;GALN.
0	0	1.992638601	4.727262304	NRP1;NF1;.
0	0	1.992638601	4.727262304	PIK3CA;PR.
0	0	1.992638601	4.727262304	PNPLA8;NF.
0	0	1.992638601	4.727262304	NRP1;SDCE.
0	0	1.992638601	4.727262304	NCR1;LAM.
0	0	1.535520517	3.61803017	SMURF1;LI.
0	0	1.870807453	4.393221679	PYCARD;DI.
0	0	1.870807453	4.393221679	GABARAPL.
0	0	1.870807453	4.393221679	P2RY12;ST.
0	0	1.870807453	4.393221679	NRP1;TESK.
0	0	1.870807453	4.393221679	RGS2;ZC3H.
0	0	1.723420356	4.04180892	GRAMD1C.

0	0	1.723420356	4.04180892	USP36;SUI .
0	0	1.395919589	3.2714992	PLK3;CREB .
0	0	1.785930408	4.181367682	SELP;TENM .
0	0	1.785930408	4.181367682	KCNK9;KCI .
0	0	1.785930408	4.181367682	NUB1;DESI .
0	0	2.337748166	5.46091791	GSN;PIK3C .
0	0	2.337748166	5.46091791	USP36;USF .
0	0	2.337748166	5.46091791	PYCARD;ZC .
0	0	2.337748166	5.46091791	IL6;IL1B;TN .
0	0	2.337748166	5.46091791	LAPTM5;P' .
0	0	2.337748166	5.46091791	CLN3;TIFAI .
0	0	2.337748166	5.46091791	NRP1;ROCI .
0	0	2.337748166	5.46091791	NR1H2;CNI .
0	0	2.337748166	5.46091791	HACE1;RHC .
0	0	2.337748166	5.46091791	IKBKB;ROC .
0	0	2.337748166	5.46091791	SDCBP;SDC .
0	0	2.337748166	5.46091791	DAAM2;NF .
0	0	2.337748166	5.46091791	RAP1B;FM .
0	0	2.337748166	5.46091791	SEMA6A;IL .
0	0	1.554466574	3.618217023	NLGN3;SLC .
0	0	1.554466574	3.618217023	HSPA5;RHE .
0	0	1.351232246	3.12758833	SLC44A3;A .
0	0	1.497545913	3.451708072	FMR1;LRRI .
0	0	1.576943042	3.628090918	GALNT11;F .
0	0	1.424643736	3.273461292	MTMR3;PL .
0	0	1.339951338	3.077276923	PTGFR;RAI .
0	0	1.456124816	3.344052775	UPF2;RANI .
0	0	1.456124816	3.344052775	CA12;SLC2 .
0	0	1.604030632	3.650799473	FOSL1;SET .
0	0	1.511809646	3.435690819	IL10;HEXI .
0	0	1.511809646	3.435690819	PRKCE;RHC .
0	0	2.617893545	5.931718959	ABCA1;FCE .
0	0	2.617893545	5.931718959	PM20D2;M .
0	0	2.617893545	5.931718959	SETDB1;SN .
0	0	2.617893545	5.931718959	SOX13;PIM .
0	0	2.617893545	5.931718959	MAPK8;NC .
0	0	2.617893545	5.931718959	TESC;CHP1 .
0	0	2.617893545	5.931718959	ADAM17;C .
0	0	2.617893545	5.931718959	CD81;PRKI .
0	0	2.617893545	5.931718959	C3;NR4A3; .
0	0	2.617893545	5.931718959	CD74;MAR .
0	0	2.617893545	5.931718959	CTBP2;CAL .
0	0	2.617893545	5.931718959	SLC9A3R1; .
0	0	2.617893545	5.931718959	ACTA2;RO(.
0	0	2.067245939	4.679428466	VPS4B;TMI .
0	0	2.067245939	4.679428466	HK3;PKLR;/ .
0	0	2.067245939	4.679428466	HDAC4;PLE .

0	0	2.067245939	4.679428466	CD300A;NI
0	0	2.067245939	4.679428466	USP25;XBP
0	0	2.067245939	4.679428466	ERO1A;RYF
0	0	2.067245939	4.679428466	PTPN1;NLF
0	0	2.067245939	4.679428466	SLC25A19;
0	0	2.067245939	4.679428466	BCAR3;DGI
0	0	2.067245939	4.679428466	RIPK2;PRK
0	0	2.067245939	4.679428466	NR1H2;AP(
0	0	2.067245939	4.679428466	HDAC4;XBI
0	0	1.465572838	3.313905425	ACVRL1;TC
0	0	3.271886792	7.348395267	GSN;PIK3C
0	0	3.271886792	7.348395267	SRC;RAB3I
0	0	3.271886792	7.348395267	OVGP1;CH
0	0	3.271886792	7.348395267	GGT5;GGT
0	0	3.271886792	7.348395267	GGT5;GGT
0	0	3.271886792	7.348395267	CD274;CD3
0	0	3.271886792	7.348395267	IL6;TMEM1
0	0	3.271886792	7.348395267	DAAM2;NF
0	0	3.271886792	7.348395267	F12;SERPIN
0	0	3.271886792	7.348395267	PHF23;IRAI
0	0	3.271886792	7.348395267	FMR1;TEN
0	0	3.271886792	7.348395267	GRIPAP1;S
0	0	3.271886792	7.348395267	GALNT11;A
0	0	3.271886792	7.348395267	NOS2;S10(
0	0	3.271886792	7.348395267	PGS1;CRLS
0	0	3.271886792	7.348395267	IL10;XBP1;
0	0	3.271886792	7.348395267	PHLDB1;RC
0	0	3.271886792	7.348395267	MICU1;MC
0	0	3.271886792	7.348395267	C3;RAB31;
0	0	3.271886792	7.348395267	CD40;FLT4
0	0	3.271886792	7.348395267	ADAM17;C
0	0	3.271886792	7.348395267	NLGN3;LRF
0	0	3.271886792	7.348395267	SLC22A3;SI
0	0	3.271886792	7.348395267	BST1;OLFM
0	0	3.271886792	7.348395267	RGS14;DDI
0	0	3.271886792	7.348395267	PPP1R3B;P
0	0	3.271886792	7.348395267	NR1H2;NR
0	0	3.271886792	7.348395267	SPRED2;SP
0	0	3.271886792	7.348395267	CAMK1D;C
0	0	3.271886792	7.348395267	DDIT3;TMS
0	0	3.271886792	7.348395267	DDX17;DD
0	0	3.271886792	7.348395267	ANXA1;AN
0	0	3.271886792	7.348395267	NR4A3;STA
0	0	3.271886792	7.348395267	ATXN3;F12
0	0	3.271886792	7.348395267	MX1;ISG15
0	0	3.271886792	7.348395267	PLXNA2;PL
0	0	1.386376926	3.106595521	MEF2A;AC

0	0	1.679133075	3.755701929	PYCARD;VA.
0	0	1.909501764	4.26131572	OVGP1;SD(.
0	0	1.909501764	4.26131572	TGM1;FCG.
0	0	1.909501764	4.26131572	SMURF1;FI.
0	0	1.733302928	3.856410077	ATXN3;BST.
0	0	1.806192556	4.012717262	FLT1;RGCC.
0	0	1.806192556	4.012717262	CYLD;ITCH;.
0	0	1.806192556	4.012717262	ATP6V1G1.
0	0	1.806192556	4.012717262	SDCBP;SDC.
0	0	1.806192556	4.012717262	IL10;CDKN.
0	0	1.571859144	3.430525845	IL6;IFNG;R.
0	0	1.571859144	3.430525845	RET;CDKN2.
0	0	1.287956652	2.806435524	RNF13;RNF.
0	0	1.190311235	2.591684986	ZNF331;AC.
0	0	2.181772407	4.708576187	ACVRL1;SN.
0	0	2.181772407	4.708576187	ATP1A3;AT.
0	0	2.181772407	4.708576187	PNPT1;IFI1.
0	0	2.181772407	4.708576187	NIPBL;CXCI.
0	0	2.181772407	4.708576187	SLC9A3R1;.
0	0	2.181772407	4.708576187	SUN2;MOF.
0	0	2.181772407	4.708576187	HCK;SECTM.
0	0	2.181772407	4.708576187	SEMA4A;SI.
0	0	2.181772407	4.708576187	PPP1R15A;.
0	0	2.181772407	4.708576187	PNP;AMPD.
0	0	2.181772407	4.708576187	SLC22A3;SI.
0	0	2.181772407	4.708576187	ADAM17;C.
0	0	2.181772407	4.708576187	LAMP1;IL1.
0	0	2.181772407	4.708576187	MAPK8;IFN.
0	0	2.181772407	4.708576187	MOV10;CN.
0	0	2.181772407	4.708576187	BST1;CAMI.
0	0	2.181772407	4.708576187	MAP2K3;W.
0	0	2.181772407	4.708576187	TBX21;SLA.
0	0	1.600824291	3.45164409	VMP1;GAB.
0	0	1.520447781	3.230110675	VASP;TENM.
0	0	1.520447781	3.230110675	TUT7;PNPT.
0	0	1.683682732	3.559560861	DDX17;DD.
0	0	1.683682732	3.559560861	C3;ATAD1;.
0	0	1.683682732	3.559560861	CASP4;ATP.
0	0	1.963770306	4.151066078	P2RY12;PT.
0	0	1.963770306	4.151066078	LYN;BATF3.
0	0	1.963770306	4.151066078	GHSR;SERF.
0	0	1.963770306	4.151066078	USP36;SM(.
0	0	1.963770306	4.151066078	NDFIP2;RS.
0	0	1.963770306	4.151066078	SDCBP;ITG.
0	0	1.963770306	4.151066078	PRPSAP1;P.
0	0	1.963770306	4.151066078	TRIM25;TR.
0	0	1.963770306	4.151066078	FLCN;SMG.

0	0	1.745885318	3.669559986	ABCA1;CLN
0	0	1.745885318	3.669559986	FLCN;PRKA
0	0	1.540949284	3.224357543	TSPAN14;G
0	0	1.403876389	2.92495928	SEMA7A;EI
0	0	1.403876389	2.92495928	DESI1;LRRI
0	0	1.435753581	2.980019752	ACVRL1;NF
0	0	1.362386771	2.827028732	PNPT1;FMI
0	0	1.260871481	2.608372404	ITGAM;ELN
0	0	1.565933252	3.228986597	KAT2B;H1-
0	0	2.379765949	4.905324086	ATP1A3;AT
0	0	2.379765949	4.905324086	XKR8;RHOG
0	0	2.379765949	4.905324086	SLC9A3R1;
0	0	2.379765949	4.905324086	B4GALNT1
0	0	2.379765949	4.905324086	HDAC4;ELK
0	0	2.379765949	4.905324086	TUT7;XRN1
0	0	2.379765949	4.905324086	P2RY12;CC
0	0	2.379765949	4.905324086	CCL8;FMR1
0	0	2.379765949	4.905324086	EFEMP1;RI
0	0	2.379765949	4.905324086	SETDB1;IN
0	0	2.379765949	4.905324086	ART1;PADI
0	0	2.379765949	4.905324086	DAXX;TAL1
0	0	2.379765949	4.905324086	SPRED2;DI
0	0	2.379765949	4.905324086	TMSB4X;FC
0	0	2.379765949	4.905324086	RIC1;FAP;S
0	0	2.379765949	4.905324086	IL6;PTPRC;
0	0	2.379765949	4.905324086	GSN;PIK3C
0	0	2.379765949	4.905324086	NCF1;NCF4
0	0	1.219586587	2.480444635	RET;CPB2;I
0	0	1.38727983	2.797207723	P2RY12;EG
0	0	1.348951815	2.716810847	PHLDB1;SE
0	0	4.361624544	8.775057436	ADSS2;APR
0	0	4.361624544	8.775057436	GLS;KCTD7
0	0	4.361624544	8.775057436	NRG1;RBPJ
0	0	4.361624544	8.775057436	RSAD2;CDI
0	0	4.361624544	8.775057436	SIRT1;SUPT
0	0	4.361624544	8.775057436	IL6ST;IL6R
0	0	4.361624544	8.775057436	TGFBR1;VE
0	0	4.361624544	8.775057436	POLB;LIG4
0	0	4.361624544	8.775057436	MAOB;MA
0	0	4.361624544	8.775057436	ABT1;NOP9
0	0	4.361624544	8.775057436	ABT1;NOP9
0	0	4.361624544	8.775057436	CYP24A1;C
0	0	4.361624544	8.775057436	PFKFB4;PFI
0	0	4.361624544	8.775057436	ROCK1;TES
0	0	4.361624544	8.775057436	SLC9A3R1;
0	0	4.361624544	8.775057436	ID2;HOPX
0	0	4.361624544	8.775057436	PADI3;PAD

0	0	4.361624544	8.775057436	KDM6B;KD
0	0	4.361624544	8.775057436	KMT5C;KM
0	0	4.361624544	8.775057436	KMT5C;KM
0	0	4.361624544	8.775057436	IRF2BP2;FM
0	0	4.361624544	8.775057436	FTH1;SRI
0	0	4.361624544	8.775057436	LRRK2;PRK
0	0	4.361624544	8.775057436	SLC1A2;SL(
0	0	4.361624544	8.775057436	RIPK3;PDP
0	0	4.361624544	8.775057436	CLN3;LAMI
0	0	4.361624544	8.775057436	HORMAD1
0	0	4.361624544	8.775057436	NIN;CEP19
0	0	4.361624544	8.775057436	MOV10;AG
0	0	4.361624544	8.775057436	F12;SERPIN
0	0	4.361624544	8.775057436	STXBP3;CB
0	0	4.361624544	8.775057436	PIH1D1;PL
0	0	4.361624544	8.775057436	PHF1;SUPT
0	0	4.361624544	8.775057436	PIH1D1;SIF
0	0	4.361624544	8.775057436	IL10;NR4A
0	0	4.361624544	8.775057436	PARP3;FCG
0	0	4.361624544	8.775057436	CD300A;LG
0	0	4.361624544	8.775057436	WWC2;WV
0	0	4.361624544	8.775057436	DDIT3;TMS
0	0	4.361624544	8.775057436	RIPOR2;LR
0	0	4.361624544	8.775057436	FLT1;CCL2
0	0	4.361624544	8.775057436	IFNG;ADCY
0	0	4.361624544	8.775057436	SLC25A29;
0	0	4.361624544	8.775057436	ALKBH1;JM
0	0	4.361624544	8.775057436	NRP1;VEGI
0	0	4.361624544	8.775057436	IFNG;LGAL
0	0	4.361624544	8.775057436	PIM1;RBPJ
0	0	4.361624544	8.775057436	OTUD4;TO
0	0	4.361624544	8.775057436	PRKD2;VEC
0	0	4.361624544	8.775057436	PHF1;ZNF3
0	0	4.361624544	8.775057436	FGR;GAB2
0	0	4.361624544	8.775057436	VEGFC;VEG
0	0	4.361624544	8.775057436	STAT3;MBI
0	0	4.361624544	8.775057436	CCL4;CCL3
0	0	4.361624544	8.775057436	SLC6A6;RIF
0	0	4.361624544	8.775057436	SLC46A2;SI
0	0	4.361624544	8.775057436	CD81;LDLR
0	0	4.361624544	8.775057436	RSAD2;PTF
0	0	4.361624544	8.775057436	E2F3;SOD2
0	0	4.361624544	8.775057436	NOS2;SLCC
0	0	4.361624544	8.775057436	PADI3;PAD
0	0	4.361624544	8.775057436	FLOT1;FLO
0	0	4.361624544	8.775057436	PDXK;HAA(
0	0	4.361624544	8.775057436	NQO2;CYP

0	0	4.361624544	8.775057436	CD81;ICAM
0	0	4.361624544	8.775057436	USP15;PLA
0	0	4.361624544	8.775057436	IL6;LDLR
0	0	4.361624544	8.775057436	F12;SERPIN
0	0	4.361624544	8.775057436	CLN3;SRC
0	0	4.361624544	8.775057436	CLEC7A;LR
0	0	4.361624544	8.775057436	CLN3;MICU
0	0	4.361624544	8.775057436	MAPK8;MA
0	0	4.361624544	8.775057436	BCL6;TNFA
0	0	4.361624544	8.775057436	CCPG1;PBX
0	0	4.361624544	8.775057436	PIH1D1;ZN
0	0	4.361624544	8.775057436	PIH1D1;SIR
0	0	4.361624544	8.775057436	TCF7L2;FFA
0	0	4.361624544	8.775057436	MPV17L;FY
0	0	4.361624544	8.775057436	P2RY6;PTK
0	0	4.361624544	8.775057436	FSCN1;RAP
0	0	4.361624544	8.775057436	NCR1;PIK3
0	0	4.361624544	8.775057436	CD300A;FC
0	0	4.361624544	8.775057436	MTMR3;M
0	0	4.361624544	8.775057436	SLAMF8;LE
0	0	4.361624544	8.775057436	STX1B;STX
0	0	4.361624544	8.775057436	GRIPAP1;R
0	0	4.361624544	8.775057436	EDN1;ECE1
0	0	4.361624544	8.775057436	DOCK4;ATI
0	0	4.361624544	8.775057436	CYP27B1;N
0	0	4.361624544	8.775057436	XBP1;KHK
0	0	4.361624544	8.775057436	KMO;TNF
0	0	4.361624544	8.775057436	RNASEH2B
0	0	4.361624544	8.775057436	TRIR;XRN1
0	0	4.361624544	8.775057436	ABT1;NOP5
0	0	4.361624544	8.775057436	EGR2;NF1
0	0	4.361624544	8.775057436	SLC22A3;SL
0	0	4.361624544	8.775057436	SLC22A3;SL
0	0	4.361624544	8.775057436	TSTD1;SQC
0	0	4.361624544	8.775057436	TSTD1;SQC
0	0	4.361624544	8.775057436	CCL2;ITGAL
0	0	1.270015732	2.542231641	AMER1;DR
0	0	1.455433455	2.908949142	PPP1R16B;
0	0	2.045293618	4.081315177	AMER1;FZI
0	0	2.045293618	4.081315177	SELP;PTGFI
0	0	2.045293618	4.081315177	URI1;SRC;A
0	0	2.045293618	4.081315177	BCR;ACTN2
0	0	2.045293618	4.081315177	DTX3L;UBE
0	0	2.045293618	4.081315177	PTPN1;NLR
0	0	2.045293618	4.081315177	ASTL;DUSP
0	0	2.045293618	4.081315177	IL10;JUN;P
0	0	2.045293618	4.081315177	PRKAA1;IL2

0	0	2.045293618	4.081315177	CD180;LY8	.
0	0	2.045293618	4.081315177	STARD3;NI	.
0	0	2.045293618	4.081315177	CLN3;SLC1	.
0	0	2.804312668	5.577259685	RAMP2;AC	.
0	0	2.804312668	5.577259685	NOS2;SLC3	.
0	0	2.804312668	5.577259685	KYNU;ATP	.
0	0	2.804312668	5.577259685	ADCY4;AD	.
0	0	2.804312668	5.577259685	LRRK2;ATF	.
0	0	2.804312668	5.577259685	SESN2;KLH	.
0	0	2.804312668	5.577259685	TLR6;TLR4	.
0	0	2.804312668	5.577259685	RYR1;P2RY	.
0	0	2.804312668	5.577259685	HAAO;KYN	.
0	0	2.804312668	5.577259685	ACVRL1;PR	.
0	0	2.804312668	5.577259685	VPS4B;CHM	.
0	0	2.804312668	5.577259685	VPS4B;CHM	.
0	0	2.804312668	5.577259685	ANXA1;CCI	.
0	0	2.804312668	5.577259685	DTX3L;WA	.
0	0	2.804312668	5.577259685	KDM4A;KD	.
0	0	2.804312668	5.577259685	CLN3;GRIN	.
0	0	2.804312668	5.577259685	UGCG;STA	.
0	0	2.804312668	5.577259685	ENO1;B2M	.
0	0	2.804312668	5.577259685	CSF1;HYAL	.
0	0	2.804312668	5.577259685	CD274;LGA	.
0	0	2.804312668	5.577259685	FAP;TNFRS	.
0	0	2.804312668	5.577259685	CD46;FCGF	.
0	0	2.804312668	5.577259685	NLRP12;TE	.
0	0	2.804312668	5.577259685	INSIG1;UBA	.
0	0	2.804312668	5.577259685	IL10;ADAM	.
0	0	2.804312668	5.577259685	LYN;ACOD	.
0	0	2.804312668	5.577259685	C3;SCARF1	.
0	0	2.804312668	5.577259685	CD74;LGAL	.
0	0	2.804312668	5.577259685	IQSEC1;AR	.
0	0	2.804312668	5.577259685	CD74;DCST	.
0	0	2.804312668	5.577259685	NIBAN2;FL	.
0	0	2.804312668	5.577259685	CD274;LGA	.
0	0	2.804312668	5.577259685	CD74;LGAL	.
0	0	2.804312668	5.577259685	OTUB2;VCI	.
0	0	2.804312668	5.577259685	PDPN;PDE4	.
0	0	2.804312668	5.577259685	IL6;FCER1G	.
0	0	2.804312668	5.577259685	ZFP36;NUP	.
0	0	2.804312668	5.577259685	PDE4B;SRI	.
0	0	2.804312668	5.577259685	SELP;SELE;	.
0	0	2.804312668	5.577259685	LYN;CD300	.
0	0	2.804312668	5.577259685	WWC2;WW	.
0	0	2.804312668	5.577259685	FLCN;PRKA	.
0	0	2.804312668	5.577259685	C3;RAB31;	.
0	0	2.804312668	5.577259685	MTMR3;AE	.

0	0	2.804312668	5.577259685	LRRK2;ATF
0	0	2.804312668	5.577259685	SESN2;KLH
0	0	2.804312668	5.577259685	RARG;RAR
0	0	2.804312668	5.577259685	RYR1;CCL3
0	0	2.804312668	5.577259685	ABCA1;SRC
0	0	2.804312668	5.577259685	SLC22A3;SI
0	0	1.68946887	3.35941304	C3;SERPINI
0	0	1.762413512	3.481587857	NAIF1;SFN
0	0	1.762413512	3.481587857	SEMA4A;SI
0	0	1.762413512	3.481587857	CYLD;ITCH
0	0	1.762413512	3.481587857	NFKBIA;AB
0	0	1.762413512	3.481587857	ANXA1;AN
0	0	1.762413512	3.481587857	STX1B;PNK
0	0	1.762413512	3.481587857	ACTN2;STX
0	0	1.870149495	3.692769199	MAPK8;MT
0	0	1.870149495	3.692769199	SLC6A9;GP
0	0	1.870149495	3.692769199	PRKCD;HIP
0	0	1.870149495	3.692769199	LYN;ADAM
0	0	1.870149495	3.692769199	EDN1;NIBA
0	0	1.870149495	3.692769199	EDN1;FAP;
0	0	1.350816951	2.664189945	FZD1;LYN;I
0	0	1.275633287	2.511061603	BTG3;BTG2
0	0	1.423838877	2.79571579	CELA2A;XB
0	0	1.558924743	3.022748186	DDX3X;HSI
0	0	1.558924743	3.022748186	IFNG;PRKC
0	0	1.558924743	3.022748186	RYR1;GBP5
0	0	1.322398084	2.564034587	MEF2A;RYI
0	0	1.482628793	2.8503355	ITCH;RNF1
0	0	1.267055386	2.432758343	RNASEL;TU
0	0	1.336955595	2.5563446	RANBP2;CI
0	0	1.355231303	2.557999866	RAP1GAP2
0	0	1.63657845	3.078539888	GABARAPL
0	0	1.63657845	3.078539888	FLCN;SLC9
0	0	1.63657845	3.078539888	NLGN3;P2I
0	0	1.63657845	3.078539888	IL6;KYNU;I
0	0	2.181326287	4.097488245	NIPBL;ID2;
0	0	2.181326287	4.097488245	CCL8;CCL4
0	0	2.181326287	4.097488245	CCL8;CCL4
0	0	2.181326287	4.097488245	NOS2;PRO
0	0	2.181326287	4.097488245	CD300A;SL
0	0	2.181326287	4.097488245	MAD2L2;D
0	0	2.181326287	4.097488245	PNP;GDA;X
0	0	2.181326287	4.097488245	CYP27B1;IS
0	0	2.181326287	4.097488245	MAD2L2;K
0	0	2.181326287	4.097488245	MAD2L2;C
0	0	2.181326287	4.097488245	PPP1R16B;
0	0	2.181326287	4.097488245	PRKCD;TNI

0	0	2.181326287	4.097488245	CD74;DCST.
0	0	2.181326287	4.097488245	PPIF;NUPR.
0	0	2.181326287	4.097488245	UTP15;USF.
0	0	2.181326287	4.097488245	ASAH1;ACE.
0	0	2.181326287	4.097488245	CTSH;CD46.
0	0	1.37883959	2.573332919	CD74;TNFS.
0	0	1.37883959	2.573332919	AMER1;FZI.
0	0	1.697040956	3.154487908	XKR8;RIPO.
0	0	1.410487656	2.609706936	ZNF473;AL.
0	0	1.924871157	3.553869531	GSN;RHOG.
0	0	1.924871157	3.553869531	PSME1;CTS.
0	0	1.924871157	3.553869531	PSMA2;PSI.
0	0	1.924871157	3.553869531	XBP1;BCL2.
0	0	1.924871157	3.553869531	MTMR3;AN.
0	0	1.924871157	3.553869531	GPR35;FM.
0	0	1.785039668	3.29335993	XBP1;SESN.
0	0	1.785039668	3.29335993	STAT5B;ZFI.
0	0	1.785039668	3.29335993	KAT2B;CRE.
0	0	1.785039668	3.29335993	SLC7A5;PR.
0	0	1.785039668	3.29335993	GPR35;FM.
0	0	1.785039668	3.29335993	SLC6A6;SL(
0	0	1.785039668	3.29335993	P2RY8;GPF.
0	0	1.785039668	3.29335993	KLF7;LRP5;.
0	0	1.785039668	3.29335993	IGSF10;NIP.
0	0	1.455088561	2.6806904	KLF10;FLCN.
0	0	1.455088561	2.6806904	MAPK8;RA.
0	0	1.310182371	2.410429886	SMG1;MTN.
0	0	1.339753321	2.446051677	UPF2;RANI.
0	0	1.550491679	2.810870781	DDX17;DD.
0	0	1.224378905	2.216132707	ITGAM;ELN.
0	0	1.323959192	2.396156614	KDM6B;DY.
0	0	1.202807417	2.171520223	ACVRL1;RI.
0	0	1.310064565	2.353166167	SEMA6A;SI.
0	0	1.389036251	2.472050602	XBP1;SMA.
0	0	1.58689351	2.82370709	NRP1;ROC.
0	0	1.58689351	2.82370709	PYCARD;BC.
0	0	2.453632075	4.340521773	PHKG2;PRI.
0	0	2.453632075	4.340521773	SERTAD1;Z.
0	0	2.453632075	4.340521773	C5AR2;C5A.
0	0	2.453632075	4.340521773	GRK2;ADRI.
0	0	2.453632075	4.340521773	SLC9A3R1;.
0	0	2.453632075	4.340521773	GLUL;ASS1.
0	0	2.453632075	4.340521773	WNT2B;AR.
0	0	2.453632075	4.340521773	C1S;C1R;CI.
0	0	2.453632075	4.340521773	SYNJ1;INPF.
0	0	2.453632075	4.340521773	LIG4;CCR6;.
0	0	2.453632075	4.340521773	UGCG;WDI.

0	0	2.453632075	4.340521773	CD274;LGA.
0	0	2.453632075	4.340521773	IL6;TMEM.
0	0	2.453632075	4.340521773	SOCS3;SOC.
0	0	2.453632075	4.340521773	PTPRC;IRA.
0	0	2.453632075	4.340521773	GFI1;SNAI1.
0	0	2.453632075	4.340521773	GALNT11;S.
0	0	2.453632075	4.340521773	APOA2;EN.
0	0	2.453632075	4.340521773	SYNJ1;INPF.
0	0	2.453632075	4.340521773	PRKAA1;AE.
0	0	2.453632075	4.340521773	RIPOR2;CC.
0	0	2.453632075	4.340521773	IL18;RARA;.
0	0	2.453632075	4.340521773	EGR2;PARD.
0	0	2.453632075	4.340521773	ZFP36;FMF.
0	0	2.453632075	4.340521773	DDX5;IL6;F.
0	0	2.453632075	4.340521773	LGALS9;CD.
0	0	2.453632075	4.340521773	NLGN3;LRF.
0	0	2.453632075	4.340521773	SRC;LRRK2.
0	0	2.453632075	4.340521773	ATXN3;USF.
0	0	2.453632075	4.340521773	DIRAS3;DN.
0	0	2.453632075	4.340521773	CLEC7A;IL1.
0	0	2.453632075	4.340521773	LYN;RNF13.
0	0	2.453632075	4.340521773	ACTA2;EDN.
0	0	1.324623158	2.338900635	UPF2;RANI.
0	0	1.428549792	2.52155141	RANBP2;ZF.
0	0	1.487892546	2.621149782	ACVRL1;NF.
0	0	1.487892546	2.621149782	KMT2E;KA.
0	0	1.487892546	2.621149782	SERPINB4;.
0	0	1.636337868	2.862094558	ATP6V1G1.
0	0	1.636337868	2.862094558	IL6;GDI1;IL.
0	0	1.636337868	2.862094558	SPN;IL10;C.
0	0	1.636337868	2.862094558	P2RY12;FG.
0	0	1.636337868	2.862094558	CYP27B1;C.
0	0	1.395417288	2.421842965	CELA2A;NC.
0	0	1.149579387	1.984034402	FBXO25;UB.
0	0	1.707330694	2.943784819	PUS10;TUT.
0	0	1.707330694	2.943784819	ACVRL1;CD.
0	0	1.707330694	2.943784819	EIF6;ELOVL.
0	0	1.707330694	2.943784819	SLC11A1;X.
0	0	1.440325511	2.480336179	ATP6V1G1.
0	0	1.440325511	2.480336179	UGCG;ZDH.
0	0	1.510648202	2.601190424	CDKN1A;N.
0	0	1.510648202	2.601190424	C3;CLN3;R.
0	0	1.325380266	2.280893812	ITGAM;CD.
0	0	2.013415803	3.451587782	DGAT2;ZC.
0	0	2.013415803	3.451587782	ASAH1;GCI.
0	0	2.013415803	3.451587782	EDEM1;SE.
0	0	2.013415803	3.451587782	RYBP;DTX.

0	0	2.013415803	3.451587782	VPS4B;CHM
0	0	2.013415803	3.451587782	SLC9A3R1;
0	0	2.013415803	3.451587782	HDAC4;FLC
0	0	2.013415803	3.451587782	IL10;CDKN
0	0	2.013415803	3.451587782	EDN1;PIM1
0	0	2.013415803	3.451587782	ADAM17;C
0	0	2.013415803	3.451587782	BCAR3;BRF
0	0	2.013415803	3.451587782	NRP1;DOC
0	0	2.013415803	3.451587782	MN1;TMEM
0	0	2.013415803	3.451587782	RYR1;P2RY
0	0	2.013415803	3.451587782	PLEK;INPP5
0	0	1.817828969	3.107035923	DGAT2;GPA
0	0	1.817828969	3.107035923	NRP1;NR4A
0	0	1.817828969	3.107035923	RPIA;HK3;T
0	0	1.817828969	3.107035923	GDI1;INSIG
0	0	1.817828969	3.107035923	PPP1R15A;
0	0	1.817828969	3.107035923	RBM3;CELF
0	0	3.2710298	5.545614628	PTK2B;JAK
0	0	3.2710298	5.545614628	KIFC3;INAV
0	0	3.2710298	5.545614628	SLC25A29;
0	0	3.2710298	5.545614628	HSD3B7;CY
0	0	3.2710298	5.545614628	SIRT1;EZH1
0	0	3.2710298	5.545614628	CBLIF;TCN1
0	0	3.2710298	5.545614628	SLC2A10;SI
0	0	3.2710298	5.545614628	SLC6A6;SLC
0	0	3.2710298	5.545614628	JADE3;JAD
0	0	3.2710298	5.545614628	NRXN2;STF
0	0	3.2710298	5.545614628	AMPD1;AM
0	0	3.2710298	5.545614628	CLN3;CFTR
0	0	3.2710298	5.545614628	SDS;SDSL
0	0	3.2710298	5.545614628	SLC25A29;
0	0	3.2710298	5.545614628	SLC25A29;
0	0	3.2710298	5.545614628	SLC7A5;SLC
0	0	3.2710298	5.545614628	ALOX5AP;A
0	0	3.2710298	5.545614628	FASLG;RIPK
0	0	3.2710298	5.545614628	MOCOS;MC
0	0	3.2710298	5.545614628	ATXN3;USP
0	0	3.2710298	5.545614628	ACVRL1;PR
0	0	3.2710298	5.545614628	GSN;PIK3C
0	0	3.2710298	5.545614628	CD300A;FC
0	0	3.2710298	5.545614628	IL12B;IL12A
0	0	3.2710298	5.545614628	PPP1R10;M
0	0	3.2710298	5.545614628	HYOU1;EN
0	0	3.2710298	5.545614628	HAS1;HYAL
0	0	3.2710298	5.545614628	CD300A;CD
0	0	3.2710298	5.545614628	DUSP1;SLA
0	0	3.2710298	5.545614628	GDI1;INPP5

0	0	3.2710298	5.545614628	ARHGDIB;C .
0	0	3.2710298	5.545614628	SLC25A19; .
0	0	3.2710298	5.545614628	SOD2;HIF1 .
0	0	3.2710298	5.545614628	RPIA;TKT .
0	0	3.2710298	5.545614628	CALR;TAPB .
0	0	3.2710298	5.545614628	VPS4B;CEP .
0	0	3.2710298	5.545614628	PRKAA1;AE .
0	0	3.2710298	5.545614628	BCL2L11;D .
0	0	3.2710298	5.545614628	SIRT1;PTPN .
0	0	3.2710298	5.545614628	FMR1;IL1B .
0	0	3.2710298	5.545614628	PLCG2;TNF .
0	0	3.2710298	5.545614628	CD274;FBX .
0	0	3.2710298	5.545614628	TMEM119; .
0	0	3.2710298	5.545614628	FBXO38;M .
0	0	3.2710298	5.545614628	EGR1;NAB2 .
0	0	3.2710298	5.545614628	CHM;RABG .
0	0	3.2710298	5.545614628	BCL2L11;B .
0	0	3.2710298	5.545614628	ITCH;UBE2 .
0	0	3.2710298	5.545614628	TCF4;SUPT .
0	0	3.2710298	5.545614628	GCH1;MTH .
0	0	3.2710298	5.545614628	VDAC3;SLC .
0	0	3.2710298	5.545614628	STAT3;HES .
0	0	3.2710298	5.545614628	RAB11FIP1 .
0	0	3.2710298	5.545614628	KLF7;SIRT1 .
0	0	3.2710298	5.545614628	FLT4;TMBI .
0	0	3.2710298	5.545614628	OTUD4;TO .
0	0	3.2710298	5.545614628	SDCBP;SDC .
0	0	3.2710298	5.545614628	EIF2AK2;N4 .
0	0	3.2710298	5.545614628	IL1A;IL1B .
0	0	3.2710298	5.545614628	ZFP36;GSN .
0	0	3.2710298	5.545614628	TNFRSF1B; .
0	0	3.2710298	5.545614628	VEGFC;VEC .
0	0	3.2710298	5.545614628	PLEKHM2;I .
0	0	3.2710298	5.545614628	RIPOR2;OL .
0	0	3.2710298	5.545614628	LRRK2;MAI .
0	0	3.2710298	5.545614628	GCH1;STK2 .
0	0	3.2710298	5.545614628	ATP1A3;KC .
0	0	3.2710298	5.545614628	EDN1;MYL .
0	0	3.2710298	5.545614628	BST1;GCH1 .
0	0	3.2710298	5.545614628	CD81;LGAL .
0	0	3.2710298	5.545614628	CYP4F2;PT .
0	0	3.2710298	5.545614628	NIPBL;REC8 .
0	0	3.2710298	5.545614628	NRP1;ALCA .
0	0	3.2710298	5.545614628	SRC;PXN .
0	0	3.2710298	5.545614628	STAT5A;ST .
0	0	3.2710298	5.545614628	RPUSD4;PU .
0	0	3.2710298	5.545614628	LIMK2;TES .

0	0	3.2710298	5.545614628	NRXN2;STF.
0	0	1.402958836	2.372196719	AMER1;FZI.
0	0	1.540131213	2.592105089	ERO1A;RYF.
0	0	1.540131213	2.592105089	IL10;MAD2.
0	0	1.540131213	2.592105089	IL10;H1-4;I.
0	0	1.454744188	2.442141981	SPRED2;SP.
0	0	1.454744188	2.442141981	HK3;SDS;SI.
0	0	1.454744188	2.442141981	RANBP2;SE.
0	0	1.454744188	2.442141981	RANBP2;SE.
0	0	1.273566785	2.137274045	BCAR3;ATF.
0	0	1.26403142	2.112694842	ARRDC4;AI.
0	0	1.309711684	2.176600413	PRR7;CDKN.
0	0	1.579821201	2.600075348	P2RY11;AD.
0	0	1.579821201	2.600075348	SYS1;RAB3.
0	0	1.579821201	2.600075348	CWC22;SA.
0	0	1.579821201	2.600075348	CYP27B1;C.
0	0	1.579821201	2.600075348	ATAD1;SDC.
0	0	1.579821201	2.600075348	STEAP3;AT.
0	0	1.348026213	2.218382769	EDN1;CXCL.
0	0	1.412002197	2.323440072	SPRED1;CD.
0	0	1.282788906	2.105350263	ASAH1;ELC.
0	0	1.472796899	2.408370784	PTPN1;DAX.
0	0	1.472796899	2.408370784	ISG20;ZFP3.
0	0	1.261809487	2.052958019	AMER1;DD.
0	0	1.378265808	2.231962296	TENM1;IL1.
0	0	1.245005185	2.013702917	ACVRL1;CD.
0	0	1.636097469	2.636646077	HAAO;KYN.
0	0	1.636097469	2.636646077	ELOVL5;AC.
0	0	1.636097469	2.636646077	SYS1;RAB3.
0	0	1.636097469	2.636646077	RNASE10;N.
0	0	1.636097469	2.636646077	IL6;GJB6;PI.
0	0	1.636097469	2.636646077	ABCA3;PDI.
0	0	1.636097469	2.636646077	TAF1A;UBT.
0	0	1.201752129	1.931200161	MTMR3;M.
0	0	1.423037063	2.276070811	RNF31;USF.
0	0	1.423037063	2.276070811	RANBP2;SE.
0	0	1.350962001	2.159713922	DDX3X;KLH.
0	0	1.496041048	2.38128324	TIAM2;SEM.
0	0	1.496041048	2.38128324	RANBP2;SE.
0	0	1.496041048	2.38128324	RANBP2;SE.
0	0	1.722054381	2.72599695	HK3;PKLR;I.
0	0	1.722054381	2.72599695	KDM6B;NR.
0	0	1.722054381	2.72599695	NR4A3;LRF.
0	0	1.722054381	2.72599695	ABCA1;NPC.
0	0	1.722054381	2.72599695	HK3;PKLR;I.
0	0	1.722054381	2.72599695	PRKAA1;IL1.
0	0	1.722054381	2.72599695	HES1;CALR.

0	0	1.722054381	2.72599695	FLCN;SDCB.
0	0	1.722054381	2.72599695	FLCN;SDCB.
0	0	1.722054381	2.72599695	CD74;FMR.
0	0	1.722054381	2.72599695	ATP1A3;AT.
0	0	1.722054381	2.72599695	NUDT7;PN.
0	0	1.722054381	2.72599695	TGM1;ZFP.
0	0	2.180880503	3.443752116	KDM6B;NR.
0	0	2.180880503	3.443752116	KLF4;ASS1;.
0	0	2.180880503	3.443752116	GABARAPL.
0	0	2.180880503	3.443752116	GABARAPL.
0	0	2.180880503	3.443752116	KLF9;LMO.
0	0	2.180880503	3.443752116	CYP27B1;C.
0	0	2.180880503	3.443752116	RIDA;SDS;S.
0	0	2.180880503	3.443752116	PRKCD;PR.
0	0	2.180880503	3.443752116	HSPA5;INS.
0	0	2.180880503	3.443752116	PLK3;SDE2.
0	0	2.180880503	3.443752116	PRKCB;CNE.
0	0	2.180880503	3.443752116	CCL8;ZC3H.
0	0	2.180880503	3.443752116	SERPING1;.
0	0	2.180880503	3.443752116	PRKCB;IL1E.
0	0	2.180880503	3.443752116	IRF7;HCLS1.
0	0	2.180880503	3.443752116	RAMP2;PT.
0	0	2.180880503	3.443752116	USPL1;PMI.
0	0	2.180880503	3.443752116	CYP27B1;C.
0	0	2.180880503	3.443752116	CLN3;PLA2.
0	0	2.180880503	3.443752116	ITGAM;DD.
0	0	2.180880503	3.443752116	ASTL;RHBD.
0	0	2.180880503	3.443752116	HSPA5;SEC.
0	0	2.180880503	3.443752116	FZD1;NLGN.
0	0	2.180880503	3.443752116	NT5C3A;SL.
0	0	2.180880503	3.443752116	IL6;ID2;HE.
0	0	2.180880503	3.443752116	DTX3L;ZNF.
0	0	2.180880503	3.443752116	CREBBP;PR.
0	0	2.180880503	3.443752116	IQSEC1;AR.
0	0	1.384768241	2.176877469	HHEX;TIFA.
0	0	1.384768241	2.176877469	CDKN2D;C.
0	0	1.869492531	2.928274767	SLC6A6;SL.
0	0	1.869492531	2.928274767	DDX17;DD.
0	0	1.869492531	2.928274767	NRP1;NR4.
0	0	1.869492531	2.928274767	ZFP36;ANX.
0	0	1.869492531	2.928274767	HYAL1;HYA.
0	0	1.869492531	2.928274767	TLR9;NOD.
0	0	1.869492531	2.928274767	MTFP1;MX.
0	0	1.869492531	2.928274767	LAPTM5;P.
0	0	1.869492531	2.928274767	C3;SCARF1.
0	0	1.869492531	2.928274767	NRP1;PTPR.
0	0	1.869492531	2.928274767	P2RY12;RE.

0	0	1.869492531	2.928274767	CSF1;IL18;I
0	0	1.869492531	2.928274767	RBM3;CELI
0	0	1.869492531	2.928274767	XKR8;RIPO
0	0	1.869492531	2.928274767	FCER2;GCH
0	0	1.869492531	2.928274767	NLGN3;CCI
0	0	1.869492531	2.928274767	FAP;ODC1;
0	0	1.869492531	2.928274767	MPV17L;H
0	0	1.869492531	2.928274767	SFPQ;SOD2
0	0	1.869492531	2.928274767	HDAC4;EGI
0	0	1.869492531	2.928274767	UTP15;UBT
0	0	1.869492531	2.928274767	SFN;BAK1;S
0	0	1.869492531	2.928274767	DGAT2;GP/
0	0	1.354424265	2.100236469	PAK1;SMA
0	0	1.52707231	2.364739403	GCLC;SLC3
0	0	1.52707231	2.364739403	CCR1;P2RX
0	0	1.52707231	2.364739403	NLRP12;DI
0	0	1.139896027	1.755864335	AVIL;UBE2I
0	0	1.392679177	2.121886852	NCOA1;SLC
0	0	1.570562901	2.365849921	ASAH1;ARC
0	0	1.570562901	2.365849921	VPS4B;CHM
0	0	1.570562901	2.365849921	ILRUN;MAI
0	0	1.570562901	2.365849921	RNF31;USP
0	0	1.570562901	2.365849921	ING5;KAT2
0	0	1.570562901	2.365849921	SLC4A7;CLI
0	0	1.570562901	2.365849921	ARG2;PNP
0	0	1.570562901	2.365849921	XBP1;DGAT
0	0	1.454400336	2.189096223	P2RY12;ST
0	0	1.454400336	2.189096223	DDX5;RIDA
0	0	1.454400336	2.189096223	ZFP36;FUS
0	0	1.454400336	2.189096223	CXCL8;CRE
0	0	1.454400336	2.189096223	NRP1;CSF1
0	0	1.358561981	2.039894917	CYLD;LIMK
0	0	1.358561981	2.039894917	ATF7IP;TCF
0	0	1.331390909	1.976455081	ING5;KAT2
0	0	1.331390909	1.976455081	ITCH;PSMA
0	0	1.402501621	2.067301961	DDX17;DDI
0	0	1.309242424	1.926311951	ERO1A;USI
0	0	1.635857251	2.399165426	MTMR3;SY
0	0	1.635857251	2.399165426	CCNT1;ELL
0	0	1.635857251	2.399165426	CREB1;IL1E
0	0	1.635857251	2.399165426	CLN3;ASTL
0	0	1.635857251	2.399165426	NUB1;PSM
0	0	1.635857251	2.399165426	DDX58;RIC
0	0	1.635857251	2.399165426	CYP4F2;AT
0	0	1.290843202	1.886021637	CDK17;CDI
0	0	1.477726575	2.152926659	MOV10;RII
0	0	1.477726575	2.152926659	SDCBP;RYE

0	0	1.477726575	2.152926659	NIBAN2;RG
0	0	1.477726575	2.152926659	EDN1;ANX
0	0	1.477726575	2.152926659	RAP1B;VGI
0	0	1.477726575	2.152926659	GGT5;STAT
0	0	1.477726575	2.152926659	NLGN3;SYN
0	0	1.275316798	1.853233309	CDKN2D;CI
0	0	1.363586203	1.978640134	MEF2A;CX(
0	0	1.363586203	1.978640134	CCR1;TRPC
0	0	2.616672954	3.785374989	KDM3A;TK
0	0	2.616672954	3.785374989	ACTN2;SRC
0	0	2.616672954	3.785374989	ARG2;NOS
0	0	2.616672954	3.785374989	EMP1;EMF
0	0	2.616672954	3.785374989	ATP2B1;SL
0	0	2.616672954	3.785374989	PLA2G4A;F
0	0	2.616672954	3.785374989	PGS1;CRLS
0	0	2.616672954	3.785374989	MAOB;MA
0	0	2.616672954	3.785374989	VPS4B;ETF
0	0	2.616672954	3.785374989	RYR1;SLC8
0	0	2.616672954	3.785374989	NR4A3;TGI
0	0	2.616672954	3.785374989	SNX18;SNX
0	0	2.616672954	3.785374989	NRP1;PHA(
0	0	2.616672954	3.785374989	SLC22A3;SI
0	0	2.616672954	3.785374989	ACVRL1;RB
0	0	2.616672954	3.785374989	ACVRL1;RB
0	0	2.616672954	3.785374989	VPS4B;LYS
0	0	2.616672954	3.785374989	PARD3;EZR
0	0	2.616672954	3.785374989	ELOVL4;EL(
0	0	2.616672954	3.785374989	ELOVL4;EL(
0	0	2.616672954	3.785374989	ELOVL4;EL(
0	0	2.616672954	3.785374989	ELOVL4;EL(
0	0	2.616672954	3.785374989	JAML;SOX1
0	0	2.616672954	3.785374989	GJB2;GJB6
0	0	2.616672954	3.785374989	SOD2;HIF1
0	0	2.616672954	3.785374989	SLC9A3R1;
0	0	2.616672954	3.785374989	SLC1A5;SL(
0	0	2.616672954	3.785374989	GGT5;GGT
0	0	2.616672954	3.785374989	TKT;KHK
0	0	2.616672954	3.785374989	P2RY12;NF
0	0	2.616672954	3.785374989	ING5;BRPF
0	0	2.616672954	3.785374989	BCL2L12;C
0	0	2.616672954	3.785374989	FLVCR1;LC
0	0	2.616672954	3.785374989	SLC11A2;SI
0	0	2.616672954	3.785374989	ALOX5AP;A
0	0	2.616672954	3.785374989	LIG4;BATF
0	0	2.616672954	3.785374989	RB1CC1;AT
0	0	2.616672954	3.785374989	SMURF1;C
0	0	2.616672954	3.785374989	AGO2;ADA

0	0	2.616672954	3.785374989	VMP1;CAL
0	0	2.616672954	3.785374989	B2M;TLR2
0	0	2.616672954	3.785374989	DGAT2;PL
0	0	2.616672954	3.785374989	CCL8;ZC3H
0	0	2.616672954	3.785374989	NLRP3;FC
0	0	2.616672954	3.785374989	RGCC;SUS
0	0	2.616672954	3.785374989	TIFAB;NR1
0	0	2.616672954	3.785374989	ITGAV;PSE
0	0	2.616672954	3.785374989	IL10;ROCK
0	0	2.616672954	3.785374989	OTUB2;PA
0	0	2.616672954	3.785374989	CALR;EZH2
0	0	2.616672954	3.785374989	PRKCQ;JA
0	0	2.616672954	3.785374989	ROCK1;PH
0	0	2.616672954	3.785374989	HAAO;KYN
0	0	2.616672954	3.785374989	SMAD3;AC
0	0	2.616672954	3.785374989	DPYS;DPY
0	0	2.616672954	3.785374989	FSCN1;AIF
0	0	2.616672954	3.785374989	TAP2;TAP1
0	0	2.616672954	3.785374989	RB1CC1;AT
0	0	2.616672954	3.785374989	ROCK1;AB
0	0	2.616672954	3.785374989	LYN;PICAL
0	0	2.616672954	3.785374989	RNASE10;
0	0	2.616672954	3.785374989	RNASE10;
0	0	2.616672954	3.785374989	HERPUD1;
0	0	2.616672954	3.785374989	RNASE10;
0	0	2.616672954	3.785374989	EGR1;HIF1
0	0	2.616672954	3.785374989	CYP4F2;IL1
0	0	2.616672954	3.785374989	IL9;RARA
0	0	2.616672954	3.785374989	SRC;ENPP2
0	0	2.616672954	3.785374989	NR4A3;NE
0	0	2.616672954	3.785374989	AGO2;STA
0	0	2.616672954	3.785374989	CLN3;ANK
0	0	2.616672954	3.785374989	FSCN1;TNF
0	0	2.616672954	3.785374989	ZBP1;NLRC
0	0	2.616672954	3.785374989	HYAL2;INP
0	0	2.616672954	3.785374989	ANXA1;AN
0	0	2.616672954	3.785374989	SEC16B;LR
0	0	2.616672954	3.785374989	SIGLEC1;TF
0	0	2.616672954	3.785374989	STAU1;STA
0	0	2.616672954	3.785374989	PARP10;TA
0	0	2.616672954	3.785374989	FGF18;CXC
0	0	2.616672954	3.785374989	CXCL8;ITG
0	0	2.616672954	3.785374989	RGCC;SMA
0	0	2.616672954	3.785374989	PHF1;SUPT
0	0	2.616672954	3.785374989	EGR1;PPTC
0	0	2.616672954	3.785374989	RIOK3;DHX
0	0	2.616672954	3.785374989	AGO2;STA

0	0	2.616672954	3.785374989	TIFAB;SFM
0	0	2.616672954	3.785374989	RFK;SLAMF
0	0	2.616672954	3.785374989	HIF1A;MCL
0	0	2.616672954	3.785374989	TIFAB;SRI
0	0	2.616672954	3.785374989	SCN4A;KCN
0	0	2.616672954	3.785374989	NRG1;SIK1
0	0	2.616672954	3.785374989	SMAD3;HIF
0	0	2.616672954	3.785374989	E2F3;SOD2
0	0	2.616672954	3.785374989	RYR1;SLC8
0	0	2.616672954	3.785374989	B2M;TLR2
0	0	2.616672954	3.785374989	ATP6V1G1
0	0	2.616672954	3.785374989	PRPSAP1;T
0	0	2.616672954	3.785374989	LTV1;NOPS
0	0	2.616672954	3.785374989	DDX58;TRI
0	0	2.616672954	3.785374989	SLC13A3;SI
0	0	2.616672954	3.785374989	GRK2;GRK5
0	0	2.616672954	3.785374989	TP53RK;OS
0	0	2.616672954	3.785374989	CTBP2;SIRT
0	0	1.155993616	1.66000731	RET;NLGN3
0	0	1.744759029	2.499471086	GCH1;MAC
0	0	1.744759029	2.499471086	UGCG;TME
0	0	1.744759029	2.499471086	CLIC4;PARI
0	0	1.744759029	2.499471086	S1PR1;NRC
0	0	1.744759029	2.499471086	ROCK1;FLC
0	0	1.744759029	2.499471086	SOD2;HIF1
0	0	1.744759029	2.499471086	NRP1;HCK;
0	0	1.744759029	2.499471086	AMER1;CD
0	0	1.744759029	2.499471086	CEP120;ZM
0	0	1.744759029	2.499471086	P2RY12;CS
0	0	1.744759029	2.499471086	USP15;DHX
0	0	1.744759029	2.499471086	UGCG;TME
0	0	1.744759029	2.499471086	ASAH1;SPT
0	0	1.415010474	2.013659601	HDAC4;MII
0	0	1.309125331	1.86009716	DUSP10;RC
0	0	1.309125331	1.86009716	PIK3CA;ATI
0	0	1.309125331	1.86009716	IL1A;STX1B
0	0	1.962679245	2.77421427	MYCBP2;A
0	0	1.962679245	2.77421427	SERTAD1;Z
0	0	1.962679245	2.77421427	ABT1;RCL1
0	0	1.962679245	2.77421427	NIPBL;PIH1
0	0	1.962679245	2.77421427	ELOVL4;EL
0	0	1.962679245	2.77421427	SLC2A10;SI
0	0	1.962679245	2.77421427	ABCA1;APC
0	0	1.962679245	2.77421427	CD46;GNL3
0	0	1.962679245	2.77421427	LRRK2;PHF
0	0	1.962679245	2.77421427	PGP;SIK1;C
0	0	1.962679245	2.77421427	HDAC4;XBI

0	0	1.962679245	2.77421427	USP15;TGF.
0	0	1.962679245	2.77421427	RPIA;TKT;R.
0	0	1.962679245	2.77421427	ATXN3;HEF.
0	0	1.962679245	2.77421427	NIPBL;PRK.
0	0	1.962679245	2.77421427	NIPBL;SEM.
0	0	1.962679245	2.77421427	PRKAA1;DI.
0	0	1.962679245	2.77421427	NOS2;TMS.
0	0	1.962679245	2.77421427	P2RY12;DE.
0	0	1.962679245	2.77421427	LRRK2;ISG.
0	0	1.962679245	2.77421427	PNP;GDA;X.
0	0	1.962679245	2.77421427	LRRK2;ENT.
0	0	1.962679245	2.77421427	CLN3;CALC.
0	0	1.962679245	2.77421427	SRI;CALM1.
0	0	1.962679245	2.77421427	IL9;RARA;L.
0	0	1.962679245	2.77421427	SAFB2;SAF.
0	0	1.962679245	2.77421427	DDX3X;KA.
0	0	1.962679245	2.77421427	EDEM1;UB.
0	0	1.962679245	2.77421427	SLC11A2;H.
0	0	1.962679245	2.77421427	LMO2;KLF.
0	0	1.962679245	2.77421427	LTV1;EIF6;I.
0	0	1.962679245	2.77421427	ATP1A3;AT.
0	0	1.962679245	2.77421427	ASAH1;SPT.
0	0	1.962679245	2.77421427	ASAH1;SPT.
0	0	1.962679245	2.77421427	NF1;DLL1;Z.
0	0	1.962679245	2.77421427	ELOVL4;EL.
0	0	1.510069455	2.126339549	POLR2A;PC.
0	0	1.510069455	2.126339549	POLR2A;PC.
0	0	1.510069455	2.126339549	P2RY12;P2.
0	0	1.510069455	2.126339549	JUN;CCNT1.
0	0	1.510069455	2.126339549	ACVRL1;AD.
0	0	1.510069455	2.126339549	ACVRL1;CD.
0	0	1.510069455	2.126339549	PIK3CA;SR.
0	0	1.510069455	2.126339549	OTUB2;OT.
0	0	1.510069455	2.126339549	RBM3;ROC.
0	0	1.510069455	2.126339549	VPS4B;CEP.
0	0	1.510069455	2.126339549	TENM1;PLI.
0	0	1.510069455	2.126339549	IFNG;SLC6A.
0	0	1.369806143	1.916441541	PAK1;LRRK.
0	0	1.369806143	1.916441541	MAD2L2;SI.
0	0	1.246943677	1.73865497	CREBBP;SM.
0	0	1.200411757	1.669833973	PPP1R15A;.
0	0	1.431464947	1.961918867	SDCBP;EDN.
0	0	1.431464947	1.961918867	GK5;IPMK;.
0	0	1.431464947	1.961918867	MTMR3;SY.
0	0	1.431464947	1.961918867	RAP1B;PAF.
0	0	1.431464947	1.961918867	DYNC1H1;C.
0	0	1.431464947	1.961918867	RNF31;USF.

0	0	1.557869371	2.11737118	NRROS;NF
0	0	1.557869371	2.11737118	CASP3;DVL
0	0	1.557869371	2.11737118	SCN9A;SCN
0	0	1.557869371	2.11737118	PNPT1;PAF
0	0	1.557869371	2.11737118	IL6;IL1B;RF
0	0	1.557869371	2.11737118	GDI1;TMBI
0	0	1.557869371	2.11737118	SEC16B;M
0	0	1.557869371	2.11737118	PNPLA8;M
0	0	1.557869371	2.11737118	CHST11;CS
0	0	1.557869371	2.11737118	CYP27B1;R
0	0	1.557869371	2.11737118	PNPT1;PAF
0	0	1.255332292	1.692480673	SLC24A1;T
0	0	1.255332292	1.692480673	SLC24A1;S
0	0	1.377693762	1.853312765	NLGN3;AT/
0	0	1.101219508	1.453304074	ERO1A;GA
0	0	1.094886527	1.442645133	ZNF331;AC
0	0	1.454057004	1.913890126	SLC44A3;C
0	0	1.454057004	1.913890126	NFKBIA;AB
0	0	1.308891411	1.721590997	MAPK8;RO
0	0	1.635617214	2.144681054	ATXN3;RNI
0	0	1.635617214	2.144681054	DAXX;RIOK
0	0	1.635617214	2.144681054	ADRB3;PHI
0	0	1.635617214	2.144681054	NEU1;B4G/
0	0	1.635617214	2.144681054	XBP1;NIPB
0	0	1.635617214	2.144681054	DDX17;TU
0	0	1.635617214	2.144681054	VPS4B;CHM
0	0	1.635617214	2.144681054	XBP1;PPP2
0	0	1.635617214	2.144681054	ZFYVE16;N
0	0	1.635617214	2.144681054	NRP1;PLAU
0	0	1.635617214	2.144681054	SLC22A3;S
0	0	1.238296652	1.603206118	RET;FZD1;I
0	0	1.209569011	1.565795731	ABCA1;NC(
0	0	1.388007055	1.789367615	GGT5;ALO)
0	0	1.388007055	1.789367615	MAPK8;MI
0	0	1.388007055	1.789367615	MAD2L2;P
0	0	1.784150943	2.262557668	CXCL10;DD
0	0	1.784150943	2.262557668	NRP1;NOT
0	0	1.784150943	2.262557668	ADCY4;AD(
0	0	1.784150943	2.262557668	MBD2;CHD
0	0	1.784150943	2.262557668	LYN;FGR;C
0	0	1.784150943	2.262557668	APOA2;PL/
0	0	1.784150943	2.262557668	EFEMP1;T(
0	0	1.784150943	2.262557668	PTPRC;TNF
0	0	1.784150943	2.262557668	SERPINE1;
0	0	1.784150943	2.262557668	ID2;DLL1;T
0	0	1.784150943	2.262557668	PRKCB;NEK
0	0	1.784150943	2.262557668	ENTPD1;EN

0	0	1.784150943	2.262557668	PPP1R15B;
0	0	1.784150943	2.262557668	SLC9A3R1;
0	0	1.784150943	2.262557668	PIM1;GLI1;
0	0	1.784150943	2.262557668	STX4;ADCY
0	0	1.784150943	2.262557668	ADCY8;ZDH
0	0	1.784150943	2.262557668	SETX;CALC
0	0	1.784150943	2.262557668	ITGAM;CLE
0	0	1.784150943	2.262557668	TUT7;AGO
0	0	1.784150943	2.262557668	DESI1;UBA
0	0	1.784150943	2.262557668	MOV10;SE
0	0	1.784150943	2.262557668	PIH1D1;PA
0	0	1.784150943	2.262557668	NIPBL;ANX
0	0	1.784150943	2.262557668	SLCO3A1;S
0	0	1.784150943	2.262557668	HSD11B1;C
0	0	1.784150943	2.262557668	RIPK3;HES
0	0	1.486971299	1.87327845	EFEMP1;NI
0	0	1.486971299	1.87327845	CLN3;TMB
0	0	1.486971299	1.87327845	GHSR;EDN
0	0	1.486971299	1.87327845	RAP1B;RO(
0	0	1.486971299	1.87327845	IL6;NF1;PR
0	0	1.308774584	1.648525362	CCDC88B;D
0	0	1.283152686	1.606293422	LYN;PTPN1
0	0	1.262932122	1.574801439	PPP1R15B;
0	0	2.180435056	2.715627452	GCH1;PSAT
0	0	2.180435056	2.715627452	EPHX2;TET
0	0	2.180435056	2.715627452	CLN3;RUB(
0	0	2.180435056	2.715627452	NRP1;ALCA
0	0	2.180435056	2.715627452	NRP1;BCAI
0	0	2.180435056	2.715627452	EZH1;EZH2
0	0	2.180435056	2.715627452	NRP1;VEGI
0	0	2.180435056	2.715627452	GCLC;GGT1
0	0	2.180435056	2.715627452	ABT1;NOP5
0	0	2.180435056	2.715627452	SRC;GRB2
0	0	2.180435056	2.715627452	NIPBL;PIH1
0	0	2.180435056	2.715627452	CD81;COR(
0	0	2.180435056	2.715627452	ACVRL1;PD
0	0	2.180435056	2.715627452	NR4A3;PIK
0	0	2.180435056	2.715627452	NR4A3;PIK
0	0	2.180435056	2.715627452	HORMAD1
0	0	2.180435056	2.715627452	SLC22A3;SI
0	0	2.180435056	2.715627452	ANXA1;RO
0	0	2.180435056	2.715627452	PTPRC;TOX
0	0	2.180435056	2.715627452	CD46;CD55
0	0	2.180435056	2.715627452	VDR;KLF9
0	0	2.180435056	2.715627452	PTPRC;LDL
0	0	2.180435056	2.715627452	ZC3H12A;A
0	0	2.180435056	2.715627452	ID2;EREG

0	0	2.180435056	2.715627452	MN1;EIF2A .
0	0	2.180435056	2.715627452	RGS2;ANXA .
0	0	2.180435056	2.715627452	LRRK2;NFE .
0	0	2.180435056	2.715627452	PPP1R10;M .
0	0	2.180435056	2.715627452	PTPRC;FCG .
0	0	2.180435056	2.715627452	NRP1;ALCA .
0	0	2.180435056	2.715627452	SLC22A3;SI .
0	0	2.180435056	2.715627452	CLEC5A;LR .
0	0	2.180435056	2.715627452	HDAC4;SIR .
0	0	2.180435056	2.715627452	RIPK1;MAF .
0	0	2.180435056	2.715627452	PIK3CA;PIK .
0	0	2.180435056	2.715627452	PLSCR2;PLS .
0	0	2.180435056	2.715627452	LPCAT2;PL .
0	0	2.180435056	2.715627452	LYN;PICALI .
0	0	2.180435056	2.715627452	ID2;HES1 .
0	0	2.180435056	2.715627452	PRKD2;VEC .
0	0	2.180435056	2.715627452	ACTN2;ZDH .
0	0	2.180435056	2.715627452	ITGAM;NO .
0	0	2.180435056	2.715627452	NR1H2;NR .
0	0	2.180435056	2.715627452	C3;RAB31 .
0	0	2.180435056	2.715627452	PROK2;EN(.
0	0	2.180435056	2.715627452	ANXA1;SIR .
0	0	2.180435056	2.715627452	ATP11A;M .
0	0	2.180435056	2.715627452	CXCR4;TNF .
0	0	2.180435056	2.715627452	DTX3L;EZR .
0	0	2.180435056	2.715627452	DTX3L;EZR .
0	0	2.180435056	2.715627452	IFNG;TNF .
0	0	2.180435056	2.715627452	DOCK4;NR .
0	0	2.180435056	2.715627452	MAPRE1;M .
0	0	2.180435056	2.715627452	MAPRE1;M .
0	0	2.180435056	2.715627452	HOXC9;DLI .
0	0	2.180435056	2.715627452	DPYS;DPYD .
0	0	2.180435056	2.715627452	PNP;PRDM .
0	0	2.180435056	2.715627452	IRF1;CCR2 .
0	0	2.180435056	2.715627452	VMP1;TLR .
0	0	2.180435056	2.715627452	TARM1;CD .
0	0	2.180435056	2.715627452	ABCA1;NRI .
0	0	2.180435056	2.715627452	EDN1;HIF1 .
0	0	2.180435056	2.715627452	SEMA4D;N .
0	0	2.180435056	2.715627452	FYN;FCGR2 .
0	0	2.180435056	2.715627452	PRKCD;SIR .
0	0	2.180435056	2.715627452	RPS7;MDM .
0	0	2.180435056	2.715627452	HECW2;NE .
0	0	2.180435056	2.715627452	FSCN1;CDH .
0	0	2.180435056	2.715627452	TSFM;ALKB .
0	0	2.180435056	2.715627452	F3;VEGFA .
0	0	2.180435056	2.715627452	DTX3L;EZR .

0	0	2.180435056	2.715627452	SLC9A3R1;
0	0	2.180435056	2.715627452	IL10;PLAU
0	0	2.180435056	2.715627452	ETF1;SHFL
0	0	2.180435056	2.715627452	NRP1;BCAI
0	0	2.180435056	2.715627452	GPX3;PRK(
0	0	2.180435056	2.715627452	LIG4;SIRT1
0	0	2.180435056	2.715627452	ANXA1;CFL
0	0	2.180435056	2.715627452	ELL;SNAPC
0	0	2.180435056	2.715627452	ADAM17;R
0	0	2.180435056	2.715627452	INSIG1;ARI
0	0	2.180435056	2.715627452	CRACR2B;(
0	0	2.180435056	2.715627452	RAMP2;HE
0	0	1.246569662	1.55092379	SETX;SPRE
0	0	1.158207078	1.426524148	AMER1;DD
0	0	1.402045442	1.724949768	BCR;LAMB
0	0	1.402045442	1.724949768	MAPK8;CA
0	0	1.402045442	1.724949768	TAF1A;UBT
0	0	1.347105509	1.633235707	SLC6A6;SL(
0	0	1.347105509	1.633235707	PPP1R15A;
0	0	1.308657845	1.572183904	NIPBL;DOP
0	0	1.308657845	1.572183904	SYS1;RAB3
0	0	1.539315613	1.848647545	SUN2;ACTI
0	0	1.539315613	1.848647545	ACTA2;SLC
0	0	1.539315613	1.848647545	ELOVL5;PN
0	0	1.539315613	1.848647545	SLC24A1;R
0	0	1.539315613	1.848647545	MAD2L2;IK
0	0	1.539315613	1.848647545	MAD2L2;IK
0	0	1.539315613	1.848647545	RASSF2;DD
0	0	1.539315613	1.848647545	TRPC5;LIG4
0	0	1.539315613	1.848647545	NXF1;DDX1
0	0	1.539315613	1.848647545	NIBAN2;IFI
0	0	1.539315613	1.848647545	PIM1;GLI1;
0	0	1.539315613	1.848647545	GRIN3A;FN
0	0	1.539315613	1.848647545	MAD2L2;F1
0	0	1.539315613	1.848647545	CREB1;AD(
0	0	1.539315613	1.848647545	SCN9A;CCL
0	0	1.539315613	1.848647545	MAD2L2;IK
0	0	1.539315613	1.848647545	SLC30A1;S
0	0	1.189988623	1.427104427	TCF7L2;MI
0	0	1.197206864	1.431715524	KDM6B;DY
0	0	1.280248964	1.529581205	IFIH1;RANI
0	0	1.205570292	1.438311136	DDX17;DD1
0	0	1.241085646	1.476443601	RYR1;MEF2
0	0	1.241085646	1.476443601	NPEPPS;EG
0	0	1.422238277	1.660961639	PNPLA8;EN
0	0	1.422238277	1.660961639	PHKG1;PHI
0	0	1.422238277	1.660961639	ZNF473;TU

0	0	1.422238277	1.660961639	B3GNT3;B3
0	0	1.422238277	1.660961639	PPP1R15A;
0	0	1.422238277	1.660961639	ATP6V1G1
0	0	1.422238277	1.660961639	EDN1;CD8(
0	0	1.422238277	1.660961639	CD74;CDKI
0	0	1.422238277	1.660961639	ZFYVE16;C
0	0	1.422238277	1.660961639	CLEC7A;PL
0	0	1.422238277	1.660961639	TSFM;CCN
0	0	1.422238277	1.660961639	RET;IL1A;IL
0	0	1.422238277	1.660961639	NIPBL;OAS
0	0	1.422238277	1.660961639	URI1;RIPK3
0	0	1.422238277	1.660961639	MBOAT1;P
0	0	1.422238277	1.660961639	TRIR;ZC3H
0	0	1.422238277	1.660961639	CD74;FCER
0	0	1.353620885	1.556515035	KAT2B;LRR
0	0	1.353620885	1.556515035	RIPOR2;FL(
0	0	1.353620885	1.556515035	MTMR3;LR
0	0	1.353620885	1.556515035	DYNC1H1;I
0	0	1.182714177	1.359391296	EGLN3;AG/
0	0	1.308541194	1.491749145	ING5;KAT2
0	0	1.308541194	1.491749145	SOCS3;SM(
0	0	1.635377358	1.864075099	IL6;LBP;IL6
0	0	1.635377358	1.864075099	P2RY12;P2
0	0	1.635377358	1.864075099	ATP7A;ARI
0	0	1.635377358	1.864075099	SRC;ZYX;PI
0	0	1.635377358	1.864075099	DUSP5;DU
0	0	1.635377358	1.864075099	TMEM129;
0	0	1.635377358	1.864075099	DYNC1H1;I
0	0	1.635377358	1.864075099	LRRK2;ENT
0	0	1.635377358	1.864075099	GCH1;MO(
0	0	1.635377358	1.864075099	KAT8;JADE
0	0	1.635377358	1.864075099	KAT8;JADE
0	0	1.635377358	1.864075099	ALOX5AP;I
0	0	1.635377358	1.864075099	ALOX5AP;/
0	0	1.635377358	1.864075099	WTAP;TRM
0	0	1.635377358	1.864075099	XBP1;LRRK
0	0	1.635377358	1.864075099	PTPRC;LGA
0	0	1.635377358	1.864075099	ARG2;GCH
0	0	1.635377358	1.864075099	ENTPD1;EN
0	0	1.635377358	1.864075099	TEC;PTK2B
0	0	1.635377358	1.864075099	CHKA;ETNI
0	0	1.635377358	1.864075099	PPP1R10;L
0	0	1.635377358	1.864075099	ZFP36;CNC
0	0	1.635377358	1.864075099	IFIH1;CD74
0	0	1.635377358	1.864075099	ACTB;ACTG
0	0	1.635377358	1.864075099	DGKD;HIP1
0	0	1.635377358	1.864075099	MOV10;DV

0	0	1.635377358	1.864075099	ZFP36;CNC
0	0	1.635377358	1.864075099	OAS2;NRG
0	0	1.635377358	1.864075099	ITGAM;CLE
0	0	1.635377358	1.864075099	ZC3H12C;K
0	0	1.635377358	1.864075099	SRC;ZYX;PH
0	0	1.635377358	1.864075099	SYCP1;HOF
0	0	1.635377358	1.864075099	SYCP1;HOF
0	0	1.635377358	1.864075099	CYP27B1;C
0	0	1.208073865	1.373992943	SLC24A1;K
0	0	1.276665591	1.448944247	SDC4;HAS1
0	0	1.276665591	1.448944247	MYLIP;STX
0	0	1.219979728	1.384286953	CREBBP;FM
0	0	1.219979728	1.384286953	NRP1;CSF1
0	0	1.219979728	1.384286953	PPP1R16B;
0	0	1.234589053	1.398898695	OTUD4;DN
0	0	1.083959968	1.217628828	CSF1;CHM;
0	0	1.158901587	1.294639783	GGT5;CHPI
0	0	1.120767394	1.235076485	DDX5;SMG
0	0	1.45371419	1.599816901	SLC6A6;SL(
0	0	1.45371419	1.599816901	ALAS1;FLV(
0	0	1.45371419	1.599816901	TEX2;SMPI
0	0	1.45371419	1.599816901	MICU1;SLC
0	0	1.45371419	1.599816901	CEBPG;PLE
0	0	1.45371419	1.599816901	HEXIM1;CI
0	0	1.45371419	1.599816901	DAXX;POLI
0	0	1.45371419	1.599816901	MAD2L2;IK
0	0	1.45371419	1.599816901	NRP1;SEM
0	0	1.45371419	1.599816901	IL1B;PRKCI
0	0	1.45371419	1.599816901	VPS4B;CHM
0	0	1.45371419	1.599816901	DAXX;POLI
0	0	1.45371419	1.599816901	CSF1;SLAM
0	0	1.45371419	1.599816901	RNF126;VP
0	0	1.45371419	1.599816901	SLC30A1;SI
0	0	1.362899673	1.475591836	TLE4;TCF7I
0	0	1.362899673	1.475591836	SLC13A3;P
0	0	1.362899673	1.475591836	HK3;PKLR;I
0	0	1.362899673	1.475591836	P2RY12;PT
0	0	1.362899673	1.475591836	CCL3;RARA
0	0	1.362899673	1.475591836	PGP;SIK1;S
0	0	1.362899673	1.475591836	ITGAM;GD
0	0	1.362899673	1.475591836	ARRDC4;D
0	0	1.19957734	1.297914077	DUSP11;PC
0	0	1.868836558	2.017189951	ADA2;XDH
0	0	1.868836558	2.017189951	SDS;SDSL
0	0	1.868836558	2.017189951	ABCA7;PSE
0	0	1.868836558	2.017189951	PIK3CA;BM
0	0	1.868836558	2.017189951	LIMK2;EZR

0	0	1.868836558	2.017189951	RAMP2;LA	.
0	0	1.868836558	2.017189951	ANXA2;SR(	.
0	0	1.868836558	2.017189951	ADCY8;CFT	.
0	0	1.868836558	2.017189951	TRAF3IP2;I	.
0	0	1.868836558	2.017189951	INSIG1;ARI	.
0	0	1.868836558	2.017189951	C1S;C1R	.
0	0	1.868836558	2.017189951	NIPBL;ID2	.
0	0	1.868836558	2.017189951	IL10;GSN	.
0	0	1.868836558	2.017189951	SNAI1;RBP	.
0	0	1.868836558	2.017189951	CLN3;CRLS	.
0	0	1.868836558	2.017189951	ISYNA1;ITP	.
0	0	1.868836558	2.017189951	TRAF3IP2;I	.
0	0	1.868836558	2.017189951	SRC;IL6ST	.
0	0	1.868836558	2.017189951	SLC2A1;SL(	.
0	0	1.868836558	2.017189951	APOA2;OLI	.
0	0	1.868836558	2.017189951	NR4A3;PIK	.
0	0	1.868836558	2.017189951	HIGD1A;CC	.
0	0	1.868836558	2.017189951	ANXA1;VPS	.
0	0	1.868836558	2.017189951	LYN;TNFAI	.
0	0	1.868836558	2.017189951	RGS2;APOA	.
0	0	1.868836558	2.017189951	ZC3H12A;S	.
0	0	1.868836558	2.017189951	ZC3H12A;S	.
0	0	1.868836558	2.017189951	LDLRAD4;S	.
0	0	1.868836558	2.017189951	PRKCD;ALC	.
0	0	1.868836558	2.017189951	UBAC2;UBI	.
0	0	1.868836558	2.017189951	ADRB3;SOI	.
0	0	1.868836558	2.017189951	TBX21;SMA	.
0	0	1.868836558	2.017189951	MAD2L2;R	.
0	0	1.868836558	2.017189951	XRN1;DXO	.
0	0	1.868836558	2.017189951	ENTPD1;EN	.
0	0	1.868836558	2.017189951	HSD11B1;E	.
0	0	1.868836558	2.017189951	ARG2;ODC	.
0	0	1.868836558	2.017189951	PARD3;NF1	.
0	0	1.868836558	2.017189951	PLAU;F11	.
0	0	1.868836558	2.017189951	TMSB4X;EN	.
0	0	1.868836558	2.017189951	PPP1R16B;	.
0	0	1.868836558	2.017189951	ADAM19;F	.
0	0	1.868836558	2.017189951	DTX3L;PAR	.
0	0	1.868836558	2.017189951	P2RY6;CD2	.
0	0	1.868836558	2.017189951	MID1IP1;T	.
0	0	1.868836558	2.017189951	FGR;GAB2	.
0	0	1.868836558	2.017189951	FITM1;OSB	.
0	0	1.868836558	2.017189951	NR1H2;NR	.
0	0	1.868836558	2.017189951	GDA;DPYD	.
0	0	1.868836558	2.017189951	PIK3CA;AR	.
0	0	1.868836558	2.017189951	LYN;PICALI	.
0	0	1.868836558	2.017189951	CD274;IRF1	.

0	0	1.868836558	2.017189951	CD46;CD5
0	0	1.868836558	2.017189951	IL10;CD55
0	0	1.868836558	2.017189951	HERPUD1;
0	0	1.868836558	2.017189951	RNASE10;
0	0	1.868836558	2.017189951	PIM1;ACTE
0	0	1.868836558	2.017189951	ADCY8;CFT
0	0	1.868836558	2.017189951	DCUN1D3;
0	0	1.868836558	2.017189951	PARD3;NF
0	0	1.868836558	2.017189951	NIPBL;STR
0	0	1.868836558	2.017189951	AGO2;ADA
0	0	1.868836558	2.017189951	LIG4;BATF
0	0	1.868836558	2.017189951	C3;ITGAM
0	0	1.868836558	2.017189951	MTHFD2;M
0	0	1.211656227	1.305666431	ABCA1;PRK
0	0	1.211656227	1.305666431	CELA2A;RA
0	0	1.308424632	1.406032598	DUSP5;DU
0	0	1.308424632	1.406032598	ILRUN;RIP(
0	0	1.308424632	1.406032598	TCF7L2;MC
0	0	1.226763427	1.317673272	PNPLA8;CY
0	0	1.226763427	1.317673272	NLGN3;NR
0	0	1.226763427	1.317673272	IL1A;EDN1
0	0	1.246196777	1.335838321	SLC7A5;SL(
0	0	1.246196777	1.335838321	HSD3B7;PS
0	0	1.246196777	1.335838321	NRP1;TESK
0	0	1.272119342	1.363357559	HK3;PRKA
0	0	1.272119342	1.363357559	RET;LYN;SE
0	0	1.272119342	1.363357559	CDKN2D;P
0	0	1.272119342	1.363357559	NCR1;CASF
0	0	1.272119342	1.363357559	IL10;CLN3;
0	0	1.272119342	1.363357559	P2RY12;P2
0	0	1.272119342	1.363357559	CNP;MAOE
0	0	1.179843884	1.216939395	NRP1;RILP
0	0	1.179843884	1.216939395	TIAM2;IFN
0	0	1.179843884	1.216939395	IL1A;TCF7L
0	0	1.509492017	1.548827907	MOV10;ZF
0	0	1.509492017	1.548827907	DFFB;CASP
0	0	1.509492017	1.548827907	RB1CC1;W
0	0	1.509492017	1.548827907	ZFP36;ANX
0	0	1.509492017	1.548827907	GRAMD1C
0	0	1.509492017	1.548827907	ASAH1;ACE
0	0	1.509492017	1.548827907	PDPN;ARH
0	0	1.509492017	1.548827907	B4GALNT1
0	0	1.509492017	1.548827907	SYS1;DOP1
0	0	1.509492017	1.548827907	DNMT3L;F
0	0	1.509492017	1.548827907	ATP1B3;AT
0	0	1.509492017	1.548827907	NIPBL;POG
0	0	1.509492017	1.548827907	RHOG;RAC

0	0	1.509492017	1.548827907	ACVRL1;SR.
0	0	1.509492017	1.548827907	ACVRL1;SR.
0	0	1.509492017	1.548827907	NLGN3;RE.
0	0	1.509492017	1.548827907	ARG2;GCH.
0	0	1.509492017	1.548827907	ENTPD1;EN.
0	0	1.509492017	1.548827907	JUN;CCNT1.
0	0	1.509492017	1.548827907	CEP83;SNX.
0	0	1.509492017	1.548827907	AMPD1;AN.
0	0	1.509492017	1.548827907	FLCN;TMSE.
0	0	1.509492017	1.548827907	H1-4;MIER.
0	0	1.509492017	1.548827907	RHBDF2;P.
0	0	1.509492017	1.548827907	IL18;RARA;.
0	0	1.509492017	1.548827907	NEK6;HEC.
0	0	1.509492017	1.548827907	FMR1;FLO.
0	0	1.509492017	1.548827907	ARHGAP17.
0	0	1.189557321	1.218733686	SLC4A7;SL.
0	0	1.189557321	1.218733686	BST1;CSF1;.
0	0	1.20165797	1.223317969	ATP6V1G1.
0	0	1.20165797	1.223317969	SPTLC2;EL.
0	0	1.20165797	1.223317969	MYLIP;STX.
0	0	1.120085917	1.138609641	NCOA1;CR.
0	0	1.217145118	1.231945449	ABCA1;STA.
0	0	1.217145118	1.231945449	PIK3CA;PT.
0	0	1.145026525	1.156623429	BTG2;EDN.
0	0	1.377123443	1.389307031	DFFB;CASP.
0	0	1.377123443	1.389307031	IL1A;IL1B;T.
0	0	1.377123443	1.389307031	IL1A;IL1B;T.
0	0	1.377123443	1.389307031	RNASEH2B.
0	0	1.377123443	1.389307031	LAMP1;IL1.
0	0	1.377123443	1.389307031	DDX3X;RA.
0	0	1.377123443	1.389307031	ATAD1;FM.
0	0	1.377123443	1.389307031	UTP15;PIH.
0	0	1.377123443	1.389307031	DYNC1H1;.
0	0	1.237666238	1.246701424	SLC7A5;SL.
0	0	1.266144266	1.271320939	FLCN;NR4A.
0	0	1.266144266	1.271320939	NRP1;SEM.
0	0	1.266144266	1.271320939	NRP1;HCK;.
0	0	1.266144266	1.271320939	CYLD;PHLD.
0	0	1.308308157	1.313202078	SETX;CELF3.
0	0	1.308308157	1.313202078	VPS4B;CHM.
0	0	1.308308157	1.313202078	CLN3;GSN;.
0	0	1.308308157	1.313202078	GRK2;MYB.
0	0	1.308308157	1.313202078	GRIN3A;PM.
0	0	1.308308157	1.313202078	MT2A;TMC.
0	0	1.123587928	1.121176958	SYS1;RIC1;.
0	0	1.16074699	1.141006347	BCAR3;ATF.
0	0	1.16074699	1.141006347	SLC22A3;S.

0	0	1.168247662	1.137645184	FLCN;RAM	.
0	0	1.189413989	1.136441255	GALC;UGC	.
0	0	1.189413989	1.136441255	ANXA1;RA	.
0	0	1.205026455	1.140584761	CDKN1A;IF	.
0	0	1.205026455	1.140584761	SEMA4A;SI	.
0	0	1.205026455	1.140584761	NLGN3;RG	.
0	0	1.635137684	1.537388251	NF1;STRA6	.
0	0	1.635137684	1.537388251	MICU1;MC	.
0	0	1.635137684	1.537388251	CHP1;PKD1	.
0	0	1.635137684	1.537388251	ATP6V1G1	.
0	0	1.635137684	1.537388251	PTGFR;PTG	.
0	0	1.635137684	1.537388251	CA12;SLC1	.
0	0	1.635137684	1.537388251	CSGALNAC	.
0	0	1.635137684	1.537388251	FCN1;MAS	.
0	0	1.635137684	1.537388251	LAPTM5;KI	.
0	0	1.635137684	1.537388251	ITGAM;SM	.
0	0	1.635137684	1.537388251	KDM6B;PE	.
0	0	1.635137684	1.537388251	LPCAT2;PL	.
0	0	1.635137684	1.537388251	EIF5;DENR	.
0	0	1.635137684	1.537388251	HK3;HK2	.
0	0	1.635137684	1.537388251	DIRAS3;DN	.
0	0	1.635137684	1.537388251	PRAF2;SLC	.
0	0	1.635137684	1.537388251	SDS;PSAT1	.
0	0	1.635137684	1.537388251	GPAT4;VEC	.
0	0	1.635137684	1.537388251	FITM1;CDS	.
0	0	1.635137684	1.537388251	DGKG;DGK	.
0	0	1.635137684	1.537388251	VMP1;PRK	.
0	0	1.635137684	1.537388251	ENPP2;SM	.
0	0	1.635137684	1.537388251	NIN;NINL	.
0	0	1.635137684	1.537388251	TUT7;ISG1	.
0	0	1.635137684	1.537388251	CA12;SLC1	.
0	0	1.635137684	1.537388251	UBE2B;PDI	.
0	0	1.635137684	1.537388251	PDE3B;SER	.
0	0	1.635137684	1.537388251	RIC1;ANXA	.
0	0	1.635137684	1.537388251	SFPQ;CRY2	.
0	0	1.635137684	1.537388251	HDAC4;NU	.
0	0	1.635137684	1.537388251	DNAJB6;HS	.
0	0	1.635137684	1.537388251	CD300A;SL	.
0	0	1.635137684	1.537388251	BCL6;PRKC	.
0	0	1.635137684	1.537388251	HDAC4;NU	.
0	0	1.635137684	1.537388251	HECW2;PR	.
0	0	1.635137684	1.537388251	HECW2;PR	.
0	0	1.635137684	1.537388251	PARP3;SRC	.
0	0	1.635137684	1.537388251	RIOK3;DHX	.
0	0	1.635137684	1.537388251	RAPGEF1;N	.
0	0	1.635137684	1.537388251	ATP1A3;PS	.
0	0	1.635137684	1.537388251	XRN1;DXO	.

0	0	1.635137684	1.537388251	APOA2;ATI.
0	0	1.635137684	1.537388251	CLN3;PLA2.
0	0	1.635137684	1.537388251	NR4A3;STF.
0	0	1.635137684	1.537388251	TMEM79;S.
0	0	1.635137684	1.537388251	STAT1;LRP.
0	0	1.635137684	1.537388251	HDAC4;PIA.
0	0	1.635137684	1.537388251	ANXA2;ECE.
0	0	1.635137684	1.537388251	USP15;DH).
0	0	1.635137684	1.537388251	UTP15;RIO.
0	0	1.635137684	1.537388251	ZNF143;EL.
0	0	1.635137684	1.537388251	NLGN3;LRF.
0	0	1.635137684	1.537388251	PUS10;SM/.
0	0	1.635137684	1.537388251	NRP1;ARF6.
0	0	1.635137684	1.537388251	GALNT3;G/.
0	0	1.635137684	1.537388251	CHM;RABG.
0	0	1.635137684	1.537388251	RAP1B;RAF.
0	0	1.635137684	1.537388251	DNMT3L;M.
0	0	1.635137684	1.537388251	NIPBL;HPSI.
0	0	1.635137684	1.537388251	FMR1;IL1B.
0	0	1.635137684	1.537388251	FMR1;ADC.
0	0	1.635137684	1.537388251	DCUN1D3;.
0	0	1.635137684	1.537388251	ADAM15;B.
0	0	1.635137684	1.537388251	EFHB;SLC8.
0	0	1.635137684	1.537388251	HYAL2;INP.
0	0	1.635137684	1.537388251	ATP7A;SOI.
0	0	1.635137684	1.537388251	RPUSD4;G/.
0	0	1.635137684	1.537388251	GSN;TMSB.
0	0	1.635137684	1.537388251	NF1;STRA6.
0	0	1.635137684	1.537388251	ARG2;ASS1.
0	0	1.226506422	1.150507542	IL10;CD40;.
0	0	1.226506422	1.150507542	SDCBP;USF.
0	0	1.226506422	1.150507542	TCF7L2;ST).
0	0	1.226506422	1.150507542	PPP1R15A;.
0	0	1.257915989	1.170509433	ERO1A;HSF.
0	0	1.257915989	1.170509433	RAP1B;RAF.
0	0	1.257915989	1.170509433	SEMA4A;SI.
0	0	1.257915989	1.170509433	SDCBP;RYB.
0	0	1.257915989	1.170509433	P2RY8;GPF.
0	0	1.257915989	1.170509433	STAT5A;ST.
0	0	1.257915989	1.170509433	CBLIF;SLC2.
0	0	1.116969658	1.036584226	ATP6V1G1.
0	0	1.30819177	1.210197697	DFFB;CASP.
0	0	1.30819177	1.210197697	NLGN3;NR.
0	0	1.30819177	1.210197697	TG;NF1;TG.
0	0	1.30819177	1.210197697	RAMP2;LA.
0	0	1.30819177	1.210197697	PIK3CA;AT.
0	0	1.30819177	1.210197697	ZFYVE28;P.

0	0	1.30819177	1.210197697	ALAS1;FLV
0	0	1.30819177	1.210197697	PIK3CA;AV
0	0	1.30819177	1.210197697	MAN1A2;E
0	0	1.30819177	1.210197697	PRPSAP1;P
0	0	1.30819177	1.210197697	PRKAA1;D(
0	0	1.401590296	1.296124775	ADCY4;AD(
0	0	1.401590296	1.296124775	ATP1A3;AT
0	0	1.401590296	1.296124775	GALNT11;S
0	0	1.401590296	1.296124775	GGT5;GGT
0	0	1.401590296	1.296124775	MT2A;XIAF
0	0	1.401590296	1.296124775	RYBP;PCGF
0	0	1.401590296	1.296124775	SCN4B;SLC
0	0	1.401590296	1.296124775	SLC2A9;SL(
0	0	1.401590296	1.296124775	KLF7;MIDN
0	0	1.401590296	1.296124775	F12;CASP4
0	0	1.401590296	1.296124775	LRRK2;NF1
0	0	1.401590296	1.296124775	ANXA2;ECE
0	0	1.401590296	1.296124775	EGR1;ASAH
0	0	1.401590296	1.296124775	NLRC5;NAE
0	0	1.401590296	1.296124775	ABCA1;AP(
0	0	1.401590296	1.296124775	KCNK9;KCN
0	0	1.401590296	1.296124775	PTPRC;NR(
0	0	1.090454488	1.006984123	MEF2A;RO
0	0	1.090420147	0.994942236	HACE1;RO(
0	0	1.162915354	1.048585958	ACVRL1;NI
0	0	1.162915354	1.048585958	SPTLC2;CA
0	0	1.124343537	1.002968994	ITCH;PSMA
0	0	1.174060507	1.043952297	FOLH1B;KY
0	0	1.174060507	1.043952297	SETX;GCFC
0	0	1.174060507	1.043952297	WASHC4;S
0	0	1.103448276	0.981145899	SRGN;TESC
0	0	1.104437229	0.968050032	SLC24A1;SI
0	0	1.189270873	1.041978148	TENM1;DY
0	0	1.189270873	1.041978148	PTPN1;PTP
0	0	1.189270873	1.041978148	CLN3;CCDC
0	0	1.132135168	0.979589491	PTPN1;ZFY
0	0	1.067168244	0.923178263	MEF2A;AC'
0	0	1.105599138	0.954450971	NPC1;CHST
0	0	1.105599138	0.954450971	ELOVL5;PN
0	0	1.211256574	1.044778641	SLC9A3R1;
0	0	1.211256574	1.044778641	XBP1;IL6;A
0	0	1.211256574	1.044778641	SLC11A1;A
0	0	1.211256574	1.044778641	CDKN1A;CI
0	0	1.211256574	1.044778641	CNOT2;CR'
0	0	1.211256574	1.044778641	ANXA1;MM
0	0	1.211256574	1.044778641	CDK17;GFI
0	0	1.211256574	1.044778641	XBP1;SESN

0	0	1.211256574	1.044778641	SETX;BRF2
0	0	1.211256574	1.044778641	TAF1A;UBT
0	0	1.090248832	0.928552156	CSF1;LRRK
0	0	1.137568834	0.967714298	SDC4;HYAL
0	0	1.054037517	0.896005025	CDKN1A;CI
0	0	1.245825019	1.057032387	HAS1;CSGA
0	0	1.245825019	1.057032387	CYP27B1;T
0	0	1.245825019	1.057032387	CYP27B1;C
0	0	1.245825019	1.057032387	FLCN;LIG4;
0	0	1.245825019	1.057032387	PXK;ACTN2
0	0	1.245825019	1.057032387	CCL3;CCL2
0	0	1.245825019	1.057032387	ATXN7;MII
0	0	1.245825019	1.057032387	LRRK2;STA
0	0	1.245825019	1.057032387	DYNC1H1;\
0	0	1.144642857	0.955870264	GALC;UGC
0	0	1.308075472	1.091280188	HYAL1;CHF
0	0	1.308075472	1.091280188	ACVRL1;PR
0	0	1.308075472	1.091280188	PLA2G4A;F
0	0	1.308075472	1.091280188	PLA2G4A;F
0	0	1.308075472	1.091280188	ANXA1;PTC
0	0	1.308075472	1.091280188	NLGN3;STX
0	0	1.308075472	1.091280188	EGR2;PARI
0	0	1.308075472	1.091280188	FZD1;NLGN
0	0	1.308075472	1.091280188	CEP83;SNX
0	0	1.308075472	1.091280188	TNFRSF1B;
0	0	1.308075472	1.091280188	AMER1;RIC
0	0	1.308075472	1.091280188	SRC;DENNI
0	0	1.308075472	1.091280188	EIF6;PRKAC
0	0	1.308075472	1.091280188	STAT5A;GH
0	0	1.308075472	1.091280188	DYNC1H1;I
0	0	1.308075472	1.091280188	ADAM17;F
0	0	1.308075472	1.091280188	RIDA;ROCK
0	0	1.308075472	1.091280188	TRIR;XRN1
0	0	1.453371893	1.195039938	XYLT1;B3G
0	0	1.453371893	1.195039938	HPSE;VEGF
0	0	1.453371893	1.195039938	NF1;VEGFA
0	0	1.453371893	1.195039938	ATP1A1;KC
0	0	1.453371893	1.195039938	MID1IP1;P
0	0	1.453371893	1.195039938	DRAXIN;SC
0	0	1.453371893	1.195039938	CEP120;NU
0	0	1.453371893	1.195039938	MYADM;IN
0	0	1.453371893	1.195039938	GRAMD1C
0	0	1.453371893	1.195039938	ATP7A;SOI
0	0	1.453371893	1.195039938	TBXAS1;PT
0	0	1.453371893	1.195039938	MAD2L2;K
0	0	1.453371893	1.195039938	RARG;EFEM
0	0	1.453371893	1.195039938	GCLC;GGT1

0	0	1.453371893	1.195039938	GK5;PGP .
0	0	1.453371893	1.195039938	DGKG;PGP .
0	0	1.453371893	1.195039938	PLK3;VCPI .
0	0	1.453371893	1.195039938	UGCG;LDLI .
0	0	1.453371893	1.195039938	VMP1;PRK .
0	0	1.453371893	1.195039938	FZD1;NR4A .
0	0	1.453371893	1.195039938	IFI16;VEGF .
0	0	1.453371893	1.195039938	APOA2;NFI .
0	0	1.453371893	1.195039938	ILRUN;ITCH .
0	0	1.453371893	1.195039938	PRKCD;ALC .
0	0	1.453371893	1.195039938	RIPOR2;LR .
0	0	1.453371893	1.195039938	ACTN2;PIC .
0	0	1.453371893	1.195039938	SEMA6A;E .
0	0	1.453371893	1.195039938	YTHDC2;IG .
0	0	1.453371893	1.195039938	DCSTAMP; .
0	0	1.453371893	1.195039938	DAXX;H3-3 .
0	0	1.453371893	1.195039938	TGM1;ARE .
0	0	1.453371893	1.195039938	ABCA3;AB .
0	0	1.453371893	1.195039938	ELL;SUPT6 .
0	0	1.453371893	1.195039938	ANXA2;RA .
0	0	1.453371893	1.195039938	NLGN3;LRF .
0	0	1.453371893	1.195039938	PLEK;FLOT .
0	0	1.453371893	1.195039938	DGKD;PAR .
0	0	1.453371893	1.195039938	APOA2;LO .
0	0	1.453371893	1.195039938	UPP1;DCK .
0	0	1.453371893	1.195039938	UPP1;DCK .
0	0	1.453371893	1.195039938	PPP1R10;N .
0	0	1.453371893	1.195039938	LYN;LGALS .
0	0	1.453371893	1.195039938	DAXX;H3-3 .
0	0	1.453371893	1.195039938	DNAJB6;HS .
0	0	1.453371893	1.195039938	LYN;CD30 .
0	0	1.453371893	1.195039938	STAT1;LRP .
0	0	1.453371893	1.195039938	LAMP1;CC .
0	0	1.453371893	1.195039938	SRC;LRRK2 .
0	0	1.453371893	1.195039938	RGS2;PLA2 .
0	0	1.453371893	1.195039938	GCH1;CALM .
0	0	1.453371893	1.195039938	MTHFD2;M .
0	0	1.453371893	1.195039938	SLC2A9;PN .
0	0	1.154225649	0.944335498	PTPRC;SH3 .
0	0	1.154225649	0.944335498	CYP4F2;CY .
0	0	1.154225649	0.944335498	SLC9A3R1; .
0	0	1.035624117	0.840981761	ITGAM;ELN .
0	0	1.06794208	0.864306355	ACVRL1;CD .
0	0	1.090146354	0.881439497	HCK;CYLD; .
0	0	1.06073132	0.853223056	RYR1;ARHG .
0	0	1.113300889	0.893226836	TNIP1;MAN .
0	0	1.113300889	0.893226836	RYR1;ITPR .

0	0	1.076352129	0.86217199	NCOA1;CR
0	0	1.167929974	0.933716532	FSCN1;NE
0	0	1.167929974	0.933716532	RFLNB;FSC
0	0	1.167929974	0.933716532	B3GNT3;B
0	0	1.167929974	0.933716532	RAMP2;DY
0	0	1.167929974	0.933716532	ELOVL4;EL
0	0	1.090112246	0.863859641	NIPBL;HYA
0	0	1.116660214	0.875510186	PLLP;PARD
0	0	1.116660214	0.875510186	SLC25A16;
0	0	1.116660214	0.875510186	USP36;FLC
0	0	1.116660214	0.875510186	NRP1;LAM
0	0	1.064770835	0.831321658	ACTN2;SR
0	0	1.189127973	0.925462322	IL1B;PDE4
0	0	1.189127973	0.925462322	ERO1A;HS
0	0	1.189127973	0.925462322	CANX;SIGL
0	0	1.189127973	0.925462322	DNMT3L;B
0	0	1.189127973	0.925462322	RPS7;MAR
0	0	1.189127973	0.925462322	PHF1;PAF1
0	0	1.189127973	0.925462322	MAPK8;CA
0	0	1.189127973	0.925462322	CCNT1;POL
0	0	1.189127973	0.925462322	ROCK1;PLE
0	0	1.189127973	0.925462322	ACVRL1;EF
0	0	1.189127973	0.925462322	DUSP1;NE
0	0	1.189127973	0.925462322	EGR2;PAR
0	0	1.189127973	0.925462322	MAPK8;CA
0	0	1.090078164	0.845010342	NPEPPS;RI
0	0	1.12118301	0.856365565	DGKG;GK5
0	0	1.12118301	0.856365565	HK3;PKLR;I
0	0	1.12118301	0.856365565	SMG1;FXR
0	0	1.12118301	0.856365565	ACVRL1;ST
0	0	1.054929199	0.804344051	SMAD3;SM
0	0	1.090044108	0.824582409	VCAN;SDC
0	0	1.090044108	0.824582409	SLC25A16;
0	0	1.090044108	0.824582409	ZFP36;TUT
0	0	1.22625	0.923631838	SVIL;GSN;A
0	0	1.22625	0.923631838	SMAD3;AC
0	0	1.22625	0.923631838	SVIL;GSN;A
0	0	1.22625	0.923631838	ADCY4;AD
0	0	1.22625	0.923631838	EIF4A1;EIF
0	0	1.22625	0.923631838	GCH1;CAL
0	0	1.22625	0.923631838	CYP4F2;EP
0	0	1.22625	0.923631838	MID1IP1;S
0	0	1.22625	0.923631838	PM20D2;M
0	0	1.22625	0.923631838	KAT8;JADE
0	0	1.22625	0.923631838	RGS14;SG
0	0	1.22625	0.923631838	MEF2A;LR
0	0	1.22625	0.923631838	INPP5K;SL

0	0	1.22625	0.923631838	ILRUN;FLCI.
0	0	1.22625	0.923631838	PTBP2;PTB.
0	0	1.22625	0.923631838	HDAC4;XBI.
0	0	1.22625	0.923631838	RANBP2;KI.
0	0	1.22625	0.923631838	CEP120;CH.
0	0	1.22625	0.923631838	NLGN3;LRI.
0	0	1.22625	0.923631838	CIITA;IL6;R.
0	0	1.22625	0.923631838	NAIF1;PPIF.
0	0	1.22625	0.923631838	VPS4B;CHM.
0	0	1.22625	0.923631838	P2RY12;P2.
0	0	1.22625	0.923631838	KDM6B;NR.
0	0	1.072179528	0.8063504	CLN3;AGAI.
0	0	1.072179528	0.8063504	EDN1;PIK3.
0	0	1.072179528	0.8063504	RYR1;GBP5.
0	0	1.127591416	0.835389507	GRK2;GSN;.
0	0	1.127591416	0.835389507	ACVRL1;PA.
0	0	1.127591416	0.835389507	ACVRL1;RC.
0	0	1.127591416	0.835389507	EDN1;PIK3.
0	0	1.127591416	0.835389507	NIBAN2;CE.
0	0	1.127591416	0.835389507	CYP27B1;Z.
0	0	1.127591416	0.835389507	PAQR8;UR.
0	0	1.090010078	0.802135147	RAMP2;CD.
0	0	1.070196672	0.784847065	ABCA1;STE.
0	0	1.070196672	0.784847065	PSMA2;OD.
0	0	1.021093821	0.748478347	SLC24A1;SI.
0	0	1.049653947	0.767460055	RET;CD74;I.
0	0	1.039099173	0.759090274	FZD1;TCF7.
0	0	1.307959261	0.943498513	RB1CC1;SC.
0	0	1.307959261	0.943498513	FOLH1B;AT.
0	0	1.307959261	0.943498513	NABP2;NA.
0	0	1.307959261	0.943498513	PCGF5;LRII.
0	0	1.307959261	0.943498513	VPS9D1;AT.
0	0	1.307959261	0.943498513	UBE2S;CHM.
0	0	1.307959261	0.943498513	STAT3;VEG.
0	0	1.307959261	0.943498513	GLUL;GLS .
0	0	1.307959261	0.943498513	CCL3;CCL2.
0	0	1.307959261	0.943498513	NIN;NINL .
0	0	1.307959261	0.943498513	MEF2A;LRI.
0	0	1.307959261	0.943498513	PTX3;IGF2I.
0	0	1.307959261	0.943498513	ACTB;ACTC.
0	0	1.307959261	0.943498513	ZMYND10;.
0	0	1.307959261	0.943498513	SUSD2;TXM.
0	0	1.307959261	0.943498513	LIMK2;TES.
0	0	1.307959261	0.943498513	ZC3H12A;T.
0	0	1.307959261	0.943498513	EDN1;SERI.
0	0	1.307959261	0.943498513	DUSP1;SLA.
0	0	1.307959261	0.943498513	SDCBP;ANI.

0	0	1.307959261	0.943498513	SRI;CALM1	.
0	0	1.307959261	0.943498513	SRI;CALM1	.
0	0	1.307959261	0.943498513	SLC22A3;G	.
0	0	1.307959261	0.943498513	GCLC;GGT1	.
0	0	1.307959261	0.943498513	UPP1;DCK	.
0	0	1.307959261	0.943498513	EDN1;TIFA	.
0	0	1.307959261	0.943498513	SLC37A1;S	.
0	0	1.307959261	0.943498513	ABCA1;AB	.
0	0	1.307959261	0.943498513	B3GNT3;B3	.
0	0	1.307959261	0.943498513	ACTN2;PLE	.
0	0	1.307959261	0.943498513	ATP1B3;GL	.
0	0	1.307959261	0.943498513	FZR1;UBE2	.
0	0	1.307959261	0.943498513	DPYS;DPYD	.
0	0	1.307959261	0.943498513	PIK3CA;PLE	.
0	0	1.307959261	0.943498513	GSN;CORO	.
0	0	1.307959261	0.943498513	SRI;CALM1	.
0	0	1.307959261	0.943498513	APOA2;AB	.
0	0	1.307959261	0.943498513	LGALS9;FC	.
0	0	1.307959261	0.943498513	NR4A3;STA	.
0	0	1.307959261	0.943498513	RNASE10;C	.
0	0	1.307959261	0.943498513	JARID2;SIR	.
0	0	1.307959261	0.943498513	ASS1;FUT4	.
0	0	1.307959261	0.943498513	STK26;FYN	.
0	0	1.307959261	0.943498513	NRDE2;SUI	.
0	0	1.307959261	0.943498513	DOCK4;NR	.
0	0	1.307959261	0.943498513	PSAT1;GGT	.
0	0	1.307959261	0.943498513	ASS1;IDH3	.
0	0	1.137361104	0.811987866	NLGN3;ST	.
0	0	1.137361104	0.811987866	LIMK2;PRK	.
0	0	1.137361104	0.811987866	MEF2A;MA	.
0	0	1.054825284	0.752624446	NLGN3;VA	.
0	0	1.067736584	0.761291588	MAD2L2;H	.
0	0	1.089976074	0.777009778	ASAH1;SPT	.
0	0	1.089976074	0.777009778	IL1B;BHLH	.
0	0	1.042567664	0.725718736	PRKAA1;XE	.
0	0	1.019181655	0.708129812	NIBAN1;TS	.
0	0	1.051025232	0.728962211	CCR1;PTGI	.
0	0	1.064599483	0.735088089	CCR1;TRPC	.
0	0	1.089942095	0.748158472	ABCA3;PDI	.
0	0	1.089942095	0.748158472	RNASE10;A	.
0	0	1.089942095	0.748158472	MEF2A;MA	.
0	0	1.089942095	0.748158472	NLGN3;BCI	.
0	0	1.089942095	0.748158472	ABCA3;PDI	.
0	0	1.032563423	0.702733738	RNF126;RI	.
0	0	1.154051054	0.785285107	HES1;MDM	.
0	0	1.154051054	0.785285107	GCLC;MTH	.
0	0	1.154051054	0.785285107	NR4A2;MA	.

0	0	1.154051054	0.785285107	NFAT5;EDN	.
0	0	1.154051054	0.785285107	CEBPG;PLE	.
0	0	1.154051054	0.785285107	HEXIM1;HI	.
0	0	1.154051054	0.785285107	CCL3;TLR4	.
0	0	1.154051054	0.785285107	XRN1;SRC;	.
0	0	1.154051054	0.785285107	CYP27B1;V	.
0	0	1.154051054	0.785285107	BTG1;VEZF	.
0	0	1.154051054	0.785285107	AMPD1;AN	.
0	0	1.154051054	0.785285107	CLN3;ZDHH	.
0	0	1.154051054	0.785285107	NMUR2;PR	.
0	0	1.038021969	0.702424859	H1-4;DAXX	.
0	0	1.63489819	1.103542165	PRPSAP1	.
0	0	1.63489819	1.103542165	PRPSAP1	.
0	0	1.63489819	1.103542165	NUDT3	.
0	0	1.63489819	1.103542165	NUDT3	.
0	0	1.63489819	1.103542165	KIF5C	.
0	0	1.63489819	1.103542165	KIF5C	.
0	0	1.63489819	1.103542165	CD1D	.
0	0	1.63489819	1.103542165	CD1D	.
0	0	1.63489819	1.103542165	CD1D	.
0	0	1.63489819	1.103542165	DFFB	.
0	0	1.63489819	1.103542165	AMER1	.
0	0	1.63489819	1.103542165	SLC9A3R1	.
0	0	1.63489819	1.103542165	FOLH1B	.
0	0	1.63489819	1.103542165	ATG7	.
0	0	1.63489819	1.103542165	DAGLB	.
0	0	1.63489819	1.103542165	NRG1	.
0	0	1.63489819	1.103542165	PAF1	.
0	0	1.63489819	1.103542165	MDM2	.
0	0	1.63489819	1.103542165	MT2A	.
0	0	1.63489819	1.103542165	EGR1	.
0	0	1.63489819	1.103542165	DCSTAMP	.
0	0	1.63489819	1.103542165	XBP1	.
0	0	1.63489819	1.103542165	NCOA4	.
0	0	1.63489819	1.103542165	ATP7A	.
0	0	1.63489819	1.103542165	TOX	.
0	0	1.63489819	1.103542165	CXCR4	.
0	0	1.63489819	1.103542165	LRRC8C	.
0	0	1.63489819	1.103542165	RPRD1A	.
0	0	1.63489819	1.103542165	AIDA	.
0	0	1.63489819	1.103542165	NUDT3	.
0	0	1.63489819	1.103542165	NUDT3	.
0	0	1.63489819	1.103542165	NUDT3	.
0	0	1.63489819	1.103542165	NUDT3	.
0	0	1.63489819	1.103542165	STRA6	.
0	0	1.63489819	1.103542165	NUDT3	.
0	0	1.63489819	1.103542165	SLC2A1	.

0	0	1.63489819	1.103542165	NUDT1	.
0	0	1.63489819	1.103542165	GCH1	.
0	0	1.63489819	1.103542165	ABCA3	.
0	0	1.63489819	1.103542165	NIPBL	.
0	0	1.63489819	1.103542165	FAM20A	.
0	0	1.63489819	1.103542165	NRG1	.
0	0	1.63489819	1.103542165	IL10	.
0	0	1.63489819	1.103542165	FSCN1	.
0	0	1.63489819	1.103542165	NABP2	.
0	0	1.63489819	1.103542165	TNFAIP2	.
0	0	1.63489819	1.103542165	RAB27A	.
0	0	1.63489819	1.103542165	STRA6	.
0	0	1.63489819	1.103542165	WNT2B	.
0	0	1.63489819	1.103542165	KHK	.
0	0	1.63489819	1.103542165	KHK	.
0	0	1.63489819	1.103542165	SLC2A6	.
0	0	1.63489819	1.103542165	ADCY8	.
0	0	1.63489819	1.103542165	RET	.
0	0	1.63489819	1.103542165	SLC37A1	.
0	0	1.63489819	1.103542165	UGCG	.
0	0	1.63489819	1.103542165	GLUL	.
0	0	1.63489819	1.103542165	PGP	.
0	0	1.63489819	1.103542165	LIPE	.
0	0	1.63489819	1.103542165	ALAS1	.
0	0	1.63489819	1.103542165	SLC37A1	.
0	0	1.63489819	1.103542165	PRKCB	.
0	0	1.63489819	1.103542165	CELA2A	.
0	0	1.63489819	1.103542165	LRRK2	.
0	0	1.63489819	1.103542165	IDH3A	.
0	0	1.63489819	1.103542165	PMVK	.
0	0	1.63489819	1.103542165	SLC7A1	.
0	0	1.63489819	1.103542165	CYP4F2	.
0	0	1.63489819	1.103542165	LRP5	.
0	0	1.63489819	1.103542165	EDEM1	.
0	0	1.63489819	1.103542165	LGALS9	.
0	0	1.63489819	1.103542165	ABHD1	.
0	0	1.63489819	1.103542165	PTPRC	.
0	0	1.63489819	1.103542165	CYP4F2	.
0	0	1.63489819	1.103542165	STAT1	.
0	0	1.63489819	1.103542165	PNPT1	.
0	0	1.63489819	1.103542165	ATG7	.
0	0	1.63489819	1.103542165	ZNF473	.
0	0	1.63489819	1.103542165	SAMSN1	.
0	0	1.63489819	1.103542165	PHF23	.
0	0	1.63489819	1.103542165	ID2	.
0	0	1.63489819	1.103542165	PPIF	.
0	0	1.63489819	1.103542165	PRKAA1	.

0	0	1.63489819	1.103542165	FCGR2B	.
0	0	1.63489819	1.103542165	KDM5A	.
0	0	1.63489819	1.103542165	IL10	.
0	0	1.63489819	1.103542165	KLF4	.
0	0	1.63489819	1.103542165	FCGR2B	.
0	0	1.63489819	1.103542165	SLAMF8	.
0	0	1.63489819	1.103542165	IRAK3	.
0	0	1.63489819	1.103542165	PTPN2	.
0	0	1.63489819	1.103542165	FLCN	.
0	0	1.63489819	1.103542165	HIF1A	.
0	0	1.63489819	1.103542165	SERPINE1	.
0	0	1.63489819	1.103542165	SIRT1	.
0	0	1.63489819	1.103542165	PARP10	.
0	0	1.63489819	1.103542165	IRF1	.
0	0	1.63489819	1.103542165	DOCK4	.
0	0	1.63489819	1.103542165	TLR2	.
0	0	1.63489819	1.103542165	PRKAA1	.
0	0	1.63489819	1.103542165	SLC28A3	.
0	0	1.63489819	1.103542165	SMPDL3A	.
0	0	1.63489819	1.103542165	YTHDC2	.
0	0	1.63489819	1.103542165	SLC13A5	.
0	0	1.63489819	1.103542165	ALKBH1	.
0	0	1.63489819	1.103542165	LOXL1	.
0	0	1.63489819	1.103542165	TIFAB	.
0	0	1.63489819	1.103542165	ATP7A	.
0	0	1.63489819	1.103542165	PML	.
0	0	1.63489819	1.103542165	YTHDC2	.
0	0	1.63489819	1.103542165	TENT4B	.
0	0	1.63489819	1.103542165	GRK2	.
0	0	1.63489819	1.103542165	NLGN3	.
0	0	1.63489819	1.103542165	SIK1	.
0	0	1.63489819	1.103542165	PHLDB1	.
0	0	1.63489819	1.103542165	NPHP1	.
0	0	1.63489819	1.103542165	SIRT1	.
0	0	1.63489819	1.103542165	RGS2	.
0	0	1.63489819	1.103542165	LGALS9	.
0	0	1.63489819	1.103542165	PRKCD	.
0	0	1.63489819	1.103542165	PARP3	.
0	0	1.63489819	1.103542165	LRRK2	.
0	0	1.63489819	1.103542165	RIN2	.
0	0	1.63489819	1.103542165	TGFBR1	.
0	0	1.63489819	1.103542165	NR4A3	.
0	0	1.63489819	1.103542165	CFAP69	.
0	0	1.63489819	1.103542165	PRKD2	.
0	0	1.63489819	1.103542165	NOD2	.
0	0	1.63489819	1.103542165	CLN3	.
0	0	1.63489819	1.103542165	PIH1D1	.

0	0	1.63489819	1.103542165	RPS7	.
0	0	1.63489819	1.103542165	ADCY8	.
0	0	1.63489819	1.103542165	ANXA2	.
0	0	1.63489819	1.103542165	PTK2	.
0	0	1.63489819	1.103542165	NSMCE2	.
0	0	1.63489819	1.103542165	NSMCE2	.
0	0	1.63489819	1.103542165	LAPTM5	.
0	0	1.63489819	1.103542165	SOX15	.
0	0	1.63489819	1.103542165	STX1B	.
0	0	1.63489819	1.103542165	RIPOR2	.
0	0	1.63489819	1.103542165	NRDE2	.
0	0	1.63489819	1.103542165	IL1B	.
0	0	1.63489819	1.103542165	EPB41L2	.
0	0	1.63489819	1.103542165	BIRC2	.
0	0	1.63489819	1.103542165	DCUN1D3	.
0	0	1.63489819	1.103542165	NRDE2	.
0	0	1.63489819	1.103542165	SLC8A1	.
0	0	1.63489819	1.103542165	DDX3X	.
0	0	1.63489819	1.103542165	NRXN2	.
0	0	1.63489819	1.103542165	EDEM1	.
0	0	1.63489819	1.103542165	TNFAIP3	.
0	0	1.63489819	1.103542165	MAPRE1	.
0	0	1.63489819	1.103542165	MAPRE1	.
0	0	1.63489819	1.103542165	PARP3	.
0	0	1.63489819	1.103542165	STRA6	.
0	0	1.63489819	1.103542165	CMPK2	.
0	0	1.63489819	1.103542165	SLC28A3	.
0	0	1.63489819	1.103542165	DCK	.
0	0	1.63489819	1.103542165	ADAM17	.
0	0	1.63489819	1.103542165	STAT5A	.
0	0	1.63489819	1.103542165	VEGFA	.
0	0	1.63489819	1.103542165	PHLDB1	.
0	0	1.63489819	1.103542165	RBPJ	.
0	0	1.63489819	1.103542165	DLL1	.
0	0	1.63489819	1.103542165	COX17	.
0	0	1.63489819	1.103542165	CXCL10	.
0	0	1.63489819	1.103542165	IL6R	.
0	0	1.63489819	1.103542165	PTX3	.
0	0	1.63489819	1.103542165	JAK2	.
0	0	1.63489819	1.103542165	NOS2	.
0	0	1.63489819	1.103542165	DUSP6	.
0	0	1.63489819	1.103542165	ITGAM	.
0	0	1.63489819	1.103542165	PTPRG	.
0	0	1.63489819	1.103542165	S100A9	.
0	0	1.63489819	1.103542165	IL16	.
0	0	1.63489819	1.103542165	ANXA2	.
0	0	1.63489819	1.103542165	NSMCE2	.

0	0	1.63489819	1.103542165	DYNC1H1	.
0	0	1.63489819	1.103542165	ITGAM	.
0	0	1.63489819	1.103542165	LRRK2	.
0	0	1.63489819	1.103542165	FMR1	.
0	0	1.63489819	1.103542165	SOX15	.
0	0	1.63489819	1.103542165	PRDM1	.
0	0	1.63489819	1.103542165	ITGAM	.
0	0	1.63489819	1.103542165	GSN	.
0	0	1.63489819	1.103542165	BIRC2	.
0	0	1.63489819	1.103542165	NLGN3	.
0	0	1.63489819	1.103542165	OAS2	.
0	0	1.63489819	1.103542165	FLOT1	.
0	0	1.63489819	1.103542165	ZNF143	.
0	0	1.63489819	1.103542165	TSPO	.
0	0	1.63489819	1.103542165	C3	.
0	0	1.63489819	1.103542165	STAT1	.
0	0	1.63489819	1.103542165	TGM2	.
0	0	1.63489819	1.103542165	HDAC4	.
0	0	1.63489819	1.103542165	DCSTAMP	.
0	0	1.63489819	1.103542165	SQSTM1	.
0	0	1.63489819	1.103542165	ADCY8	.
0	0	1.63489819	1.103542165	ACVRL1	.
0	0	1.63489819	1.103542165	EIF6	.
0	0	1.63489819	1.103542165	PNPT1	.
0	0	1.63489819	1.103542165	PNPT1	.
0	0	1.63489819	1.103542165	PKD1L3	.
0	0	1.63489819	1.103542165	ATP7A	.
0	0	1.63489819	1.103542165	ZFAND1	.
0	0	1.63489819	1.103542165	TIFAB	.
0	0	1.63489819	1.103542165	ACTG1	.
0	0	1.63489819	1.103542165	EDN1	.
0	0	1.63489819	1.103542165	SOX15	.
0	0	1.63489819	1.103542165	EDEM1	.
0	0	1.63489819	1.103542165	SMURF1	.
0	0	1.63489819	1.103542165	VPS4B	.
0	0	1.63489819	1.103542165	SLC28A3	.
0	0	1.63489819	1.103542165	VEGFA	.
0	0	1.63489819	1.103542165	TBC1D23	.
0	0	1.63489819	1.103542165	CYP27B1	.
0	0	1.63489819	1.103542165	TIFAB	.
0	0	1.63489819	1.103542165	CAST	.
0	0	1.046321361	0.702910961	SERPINB4;I	.
0	0	1.046321361	0.702910961	METTL1;Al	.
0	0	1.060455998	0.705342035	SLC22A3;SI	.
0	0	1.060455998	0.705342035	DGKG;DGK	.
0	0	1.060455998	0.705342035	YTHDC2;RI	.
0	0	1.032526475	0.677038202	SCUBE3;GS	.

0	0	1.032526475	0.677038202	SCUBE3;GS	.
0	0	1.032526475	0.677038202	GPR132;PS	.
0	0	1.089908141	0.713767904	PDPN;TAP2	.
0	0	1.089908141	0.713767904	CACNA1A;I	.
0	0	1.089908141	0.713767904	GK5;TNIP1	.
0	0	1.089908141	0.713767904	MT2A;SLC3	.
0	0	1.089908141	0.713767904	ATP2B1;M	.
0	0	1.089908141	0.713767904	NLGN3;SEM	.
0	0	1.089908141	0.713767904	GBP5;ARL5	.
0	0	1.089908141	0.713767904	LRP4;NRXN	.
0	0	1.089908141	0.713767904	MYBPH;NM	.
0	0	1.089908141	0.713767904	PLCG2;RAB	.
0	0	1.089908141	0.713767904	SLC9A3R1;	.
0	0	1.089908141	0.713767904	IVNS1ABP;	.
0	0	1.019094499	0.660725156	CUL4A;PSM	.
0	0	1.040343915	0.67378183	PSMA2;OD	.
0	0	1.040343915	0.67378183	GNAL;ADO	.
0	0	1.021743757	0.655513852	ASAH1;SPT	.
0	0	1.054721762	0.670627121	ROCK1;ELN	.
0	0	1.054721762	0.670627121	MEF2A;KLF	.
0	0	1.054721762	0.670627121	ACVRL1;H1	.
0	0	1.054721762	0.670627121	FLCN;IL6;SI	.
0	0	1.054721762	0.670627121	DDX5;SAFB	.
0	0	1.188985289	0.754321931	SLC8A1;VE	.
0	0	1.188985289	0.754321931	FYN;SUPT6	.
0	0	1.188985289	0.754321931	VCAN;HYA	.
0	0	1.188985289	0.754321931	NFKBIA;NF	.
0	0	1.188985289	0.754321931	TAL1;ATF4	.
0	0	1.188985289	0.754321931	STX6;OPTN	.
0	0	1.188985289	0.754321931	BCL2L11;B	.
0	0	1.188985289	0.754321931	NF1;STRA6	.
0	0	1.188985289	0.754321931	PARD3;NF2	.
0	0	1.188985289	0.754321931	LTB4R2;CC	.
0	0	1.188985289	0.754321931	H1-4;ATAD	.
0	0	1.188985289	0.754321931	H1-4;ATAD	.
0	0	1.188985289	0.754321931	H1-4;ATAD	.
0	0	1.188985289	0.754321931	ELANE;PTP	.
0	0	1.188985289	0.754321931	IL10;EDN1	.
0	0	1.188985289	0.754321931	DUSP1;SLA	.
0	0	1.188985289	0.754321931	ANKRD2;D	.
0	0	1.188985289	0.754321931	ACTN2;PTK	.
0	0	1.188985289	0.754321931	MPV17L;FY	.
0	0	1.188985289	0.754321931	HES1;N4BP	.
0	0	1.188985289	0.754321931	BIN2;SNX9	.
0	0	1.188985289	0.754321931	B3GNT3;B3	.
0	0	1.188985289	0.754321931	ODC1;SAT1	.
0	0	1.188985289	0.754321931	CCL3;CCL2	.

0	0	1.188985289	0.754321931	PRKCE;CD2
0	0	1.188985289	0.754321931	PUS10;GAI
0	0	1.188985289	0.754321931	GCH1;CALI
0	0	1.188985289	0.754321931	ROCK1;AC
0	0	1.188985289	0.754321931	PNPT1;NEI
0	0	1.188985289	0.754321931	CLN3;RAB3
0	0	1.188985289	0.754321931	GCLC;ROCI
0	0	1.188985289	0.754321931	H2AW;SIR
0	0	1.188985289	0.754321931	GCLC;ROCI
0	0	1.013082279	0.637137684	LYN;SDCBP
0	0	1.032489611	0.640549581	RARG;NIPB
0	0	1.032489611	0.640549581	ANXA1;BTI
0	0	1.032489611	0.640549581	IL6;LRP5;TI
0	0	1.032489611	0.640549581	ACTN2;KCI
0	0	1.014665606	0.628783487	CCNT1;ELL
0	0	1.005970932	0.621128867	HAL;SDS;N
0	0	1.089874214	0.670293799	ADCY4;AD(
0	0	1.089874214	0.670293799	MID1IP1;P
0	0	1.089874214	0.670293799	MICU1;SLC
0	0	1.089874214	0.670293799	ACTN2;PRI
0	0	1.089874214	0.670293799	ATXN7;MII
0	0	1.089874214	0.670293799	TMBIM1;N
0	0	1.089874214	0.670293799	TMBIM1;N
0	0	1.089874214	0.670293799	SPRY1;CYR
0	0	1.089874214	0.670293799	ROCK1;PTI
0	0	1.089874214	0.670293799	RPUSD4;TS
0	0	1.089874214	0.670293799	SRC;ACOD1
0	0	1.089874214	0.670293799	GAR1;TFB1
0	0	1.089874214	0.670293799	DYNC1H1;I
0	0	1.017166373	0.6176905	SEMA4A;SI
0	0	1.017166373	0.6176905	GHSR;SEM
0	0	1.000026738	0.606955342	IVNS1ABP;
0	0	1.046251416	0.628477449	DYNC1H1;/
0	0	1.046251416	0.628477449	FUS;FMR1;
0	0	1.046251416	0.628477449	DDX3X;CN(
0	0	1.046251416	0.628477449	MT2A;HAA
0	0	0.998953865	0.596862942	DDX5;IL6;S
0	0	0.994983278	0.594240674	TCF7L2;PH
0	0	1.0217027	0.601600525	CLN3;GRIN
0	0	1.0217027	0.601600525	NRP1;YRD(
0	0	1.0217027	0.601600525	RYR1;IGSF8
0	0	0.993179607	0.583807096	ITCH;PSMA
0	0	0.990667171	0.570692439	FLCN;PLK3
0	0	0.990667171	0.570692439	PDXK;VNN
0	0	0.994996549	0.566342183	ACVRL1;BC
0	0	0.982802829	0.557989223	FCN1;RTP4
0	0	0.986924421	0.553385991	GALNT11;(

0	0	1.089840312	0.609333531	LRP5;IFITM
0	0	1.089840312	0.609333531	SLC1A2;SL(
0	0	1.089840312	0.609333531	SLC24A1;S
0	0	1.089840312	0.609333531	MT2A;ATP
0	0	1.089840312	0.609333531	ABCA13;SC
0	0	1.089840312	0.609333531	SLC25A16;
0	0	1.089840312	0.609333531	ACVRL1;KD
0	0	1.089840312	0.609333531	TIFAB;STR/
0	0	1.089840312	0.609333531	ATP1A1;KC
0	0	1.089840312	0.609333531	DGAT2;PL/
0	0	1.089840312	0.609333531	MMRN2;KI
0	0	1.089840312	0.609333531	EDN1;SERF
0	0	1.089840312	0.609333531	LTB4R2;CC
0	0	1.089840312	0.609333531	RELA;PPAR
0	0	1.089840312	0.609333531	PTPRC;SM/
0	0	1.089840312	0.609333531	SESN2;DEP
0	0	1.089840312	0.609333531	FMR1;AGC
0	0	1.089840312	0.609333531	CLN3;TIFAI
0	0	1.089840312	0.609333531	SEH1L;NUF
0	0	1.089840312	0.609333531	PNP;CMPK
0	0	1.089840312	0.609333531	CMPK2;SM
0	0	1.089840312	0.609333531	PNP;SOCS1
0	0	1.089840312	0.609333531	SIRT1;PTPN
0	0	1.089840312	0.609333531	SLC2A10;C
0	0	1.089840312	0.609333531	CSF1;PTK2
0	0	1.089840312	0.609333531	ACTN2;ATF
0	0	1.089840312	0.609333531	NIPBL;IFNG
0	0	1.089840312	0.609333531	JAK2;TGFB
0	0	1.089840312	0.609333531	CD81;LAM
0	0	1.089840312	0.609333531	UPP1;DCK
0	0	1.089840312	0.609333531	BST1;SLC2/
0	0	1.089840312	0.609333531	PDPN;CD4
0	0	1.089840312	0.609333531	RIN2;XDH
0	0	1.089840312	0.609333531	RFK;ADSS2
0	0	1.089840312	0.609333531	NRROS;CD
0	0	1.089840312	0.609333531	ALKBH1;DF
0	0	1.089840312	0.609333531	ADRB3;SOI
0	0	0.978636335	0.546200369	LTV1;RPL1(
0	0	0.978063961	0.544956454	ROCK1;FU
0	0	1.03245283	0.574111396	DDX3X;ZFA
0	0	1.03245283	0.574111396	DGAT2;AC
0	0	1.03245283	0.574111396	FITM1;RAB
0	0	1.03245283	0.574111396	WTAP;TRM
0	0	1.03245283	0.574111396	ZFP36;PAF
0	0	1.03245283	0.574111396	PPP1R15A;
0	0	1.03245283	0.574111396	PGP;SIK1;C
0	0	1.03245283	0.574111396	MBOAT1;P

0	0	1.03245283	0.574111396	VMP1;P2R	.
0	0	1.03245283	0.574111396	LTB4R2;NF	.
0	0	1.03245283	0.574111396	FAP;DLC1;7	.
0	0	1.307843137	0.725364338	NRG1	.
0	0	1.307843137	0.725364338	GK5	.
0	0	1.307843137	0.725364338	SLC25A29	.
0	0	1.307843137	0.725364338	ATP11B	.
0	0	1.307843137	0.725364338	RAMP2	.
0	0	1.307843137	0.725364338	ASS1	.
0	0	1.307843137	0.725364338	ACVRL1	.
0	0	1.307843137	0.725364338	SLC25A29	.
0	0	1.307843137	0.725364338	ARHGEF2	.
0	0	1.307843137	0.725364338	NFKBIA	.
0	0	1.307843137	0.725364338	ZFP36	.
0	0	1.307843137	0.725364338	B2M	.
0	0	1.307843137	0.725364338	NIPBL	.
0	0	1.307843137	0.725364338	CLN3	.
0	0	1.307843137	0.725364338	LDLR	.
0	0	1.307843137	0.725364338	SLC44A2	.
0	0	1.307843137	0.725364338	CSGALNAC	.
0	0	1.307843137	0.725364338	NUDT3	.
0	0	1.307843137	0.725364338	LIG4	.
0	0	1.307843137	0.725364338	RARG	.
0	0	1.307843137	0.725364338	SLC2A10	.
0	0	1.307843137	0.725364338	RPUSD4	.
0	0	1.307843137	0.725364338	CTSH	.
0	0	1.307843137	0.725364338	ASRGL1	.
0	0	1.307843137	0.725364338	NPHP1	.
0	0	1.307843137	0.725364338	STAT1	.
0	0	1.307843137	0.725364338	UBE2S	.
0	0	1.307843137	0.725364338	LRP5	.
0	0	1.307843137	0.725364338	WDR77	.
0	0	1.307843137	0.725364338	PTPRO	.
0	0	1.307843137	0.725364338	PECAM1	.
0	0	1.307843137	0.725364338	GK5	.
0	0	1.307843137	0.725364338	CLN3	.
0	0	1.307843137	0.725364338	GALC	.
0	0	1.307843137	0.725364338	ST6GALNA	.
0	0	1.307843137	0.725364338	GHSR	.
0	0	1.307843137	0.725364338	LRRC8C	.
0	0	1.307843137	0.725364338	ANXA1	.
0	0	1.307843137	0.725364338	SLC22A3	.
0	0	1.307843137	0.725364338	MAOB	.
0	0	1.307843137	0.725364338	SQOR	.
0	0	1.307843137	0.725364338	ATP7A	.
0	0	1.307843137	0.725364338	SLC4A7	.
0	0	1.307843137	0.725364338	PSAT1	.

0	0	1.307843137	0.725364338	SLC11A1	.
0	0	1.307843137	0.725364338	STAT1	.
0	0	1.307843137	0.725364338	TCF7L2	.
0	0	1.307843137	0.725364338	ABHD1	.
0	0	1.307843137	0.725364338	HORMAD1	.
0	0	1.307843137	0.725364338	STAT1	.
0	0	1.307843137	0.725364338	KLF4	.
0	0	1.307843137	0.725364338	TACC3	.
0	0	1.307843137	0.725364338	TACC3	.
0	0	1.307843137	0.725364338	SRSF12	.
0	0	1.307843137	0.725364338	CYP4F2	.
0	0	1.307843137	0.725364338	LDLR	.
0	0	1.307843137	0.725364338	TGM2	.
0	0	1.307843137	0.725364338	USP25	.
0	0	1.307843137	0.725364338	ZFP36	.
0	0	1.307843137	0.725364338	LRRK2	.
0	0	1.307843137	0.725364338	LRRK2	.
0	0	1.307843137	0.725364338	E2F3	.
0	0	1.307843137	0.725364338	HES1	.
0	0	1.307843137	0.725364338	CRY2	.
0	0	1.307843137	0.725364338	INPP5K	.
0	0	1.307843137	0.725364338	N4BP2L2	.
0	0	1.307843137	0.725364338	PIH1D1	.
0	0	1.307843137	0.725364338	DUSP1	.
0	0	1.307843137	0.725364338	TNF	.
0	0	1.307843137	0.725364338	SRGAP2	.
0	0	1.307843137	0.725364338	SLC2A10	.
0	0	1.307843137	0.725364338	PTPN2	.
0	0	1.307843137	0.725364338	SIK1	.
0	0	1.307843137	0.725364338	HNF1B	.
0	0	1.307843137	0.725364338	GRIPAP1	.
0	0	1.307843137	0.725364338	DPH3	.
0	0	1.307843137	0.725364338	DPH3	.
0	0	1.307843137	0.725364338	CREBBP	.
0	0	1.307843137	0.725364338	ACTN4	.
0	0	1.307843137	0.725364338	MYBL1	.
0	0	1.307843137	0.725364338	FLOT1	.
0	0	1.307843137	0.725364338	ACVR1B	.
0	0	1.307843137	0.725364338	CYP4F2	.
0	0	1.307843137	0.725364338	CALCOCO2	.
0	0	1.307843137	0.725364338	HK2	.
0	0	1.307843137	0.725364338	CXCL13	.
0	0	1.307843137	0.725364338	S1PR2	.
0	0	1.307843137	0.725364338	LIF	.
0	0	1.307843137	0.725364338	S1PR2	.
0	0	1.307843137	0.725364338	ATF3	.
0	0	1.307843137	0.725364338	TRPC6	.

0	0	1.307843137	0.725364338	ANXA2	.
0	0	1.307843137	0.725364338	CCL3	.
0	0	1.307843137	0.725364338	STX1B	.
0	0	1.307843137	0.725364338	CHP1	.
0	0	1.307843137	0.725364338	FMR1	.
0	0	1.307843137	0.725364338	NIBAN2	.
0	0	1.307843137	0.725364338	TIRAP	.
0	0	1.307843137	0.725364338	PLEKHA4	.
0	0	1.307843137	0.725364338	NRXN2	.
0	0	1.307843137	0.725364338	CAST	.
0	0	1.307843137	0.725364338	HNF1B	.
0	0	1.307843137	0.725364338	SERPINB4	.
0	0	1.307843137	0.725364338	TNFAIP3	.
0	0	1.307843137	0.725364338	UBE2S	.
0	0	1.307843137	0.725364338	ARL13B	.
0	0	1.307843137	0.725364338	SQSTM1	.
0	0	1.307843137	0.725364338	MSRB3	.
0	0	1.307843137	0.725364338	VCPIP1	.
0	0	1.307843137	0.725364338	TM9SF4	.
0	0	1.307843137	0.725364338	PNP	.
0	0	1.307843137	0.725364338	TENT4B	.
0	0	1.307843137	0.725364338	SGK1	.
0	0	1.307843137	0.725364338	RAB3GAP1	.
0	0	1.307843137	0.725364338	RIN2	.
0	0	1.307843137	0.725364338	SEMA4A	.
0	0	1.307843137	0.725364338	PTPRO	.
0	0	1.307843137	0.725364338	IL6	.
0	0	1.307843137	0.725364338	MIDN	.
0	0	1.307843137	0.725364338	FYN	.
0	0	1.307843137	0.725364338	XBP1	.
0	0	1.307843137	0.725364338	NFKB1	.
0	0	1.307843137	0.725364338	RAC2	.
0	0	1.307843137	0.725364338	ACSL5	.
0	0	1.307843137	0.725364338	PTK2	.
0	0	1.307843137	0.725364338	DUSP1	.
0	0	1.307843137	0.725364338	DUSP1	.
0	0	1.307843137	0.725364338	SUPT6H	.
0	0	1.307843137	0.725364338	VEGFA	.
0	0	1.307843137	0.725364338	OAS2	.
0	0	1.307843137	0.725364338	MAP1B	.
0	0	1.307843137	0.725364338	RAB3GAP1	.
0	0	1.307843137	0.725364338	PDE4B	.
0	0	1.307843137	0.725364338	LRRK2	.
0	0	1.307843137	0.725364338	SUPT6H	.
0	0	1.307843137	0.725364338	TIFAB	.
0	0	1.307843137	0.725364338	STXBP1	.
0	0	1.307843137	0.725364338	IL27	.

0	0	1.307843137	0.725364338	JAK3	.
0	0	1.307843137	0.725364338	BCOR	.
0	0	1.307843137	0.725364338	ALKBH1	.
0	0	1.307843137	0.725364338	FMR1	.
0	0	1.307843137	0.725364338	SMAD7	.
0	0	1.307843137	0.725364338	APOA2	.
0	0	1.307843137	0.725364338	PTPRO	.
0	0	1.307843137	0.725364338	NR4A3	.
0	0	1.307843137	0.725364338	ZFP36	.
0	0	1.307843137	0.725364338	EGR1	.
0	0	1.307843137	0.725364338	LRRK2	.
0	0	1.307843137	0.725364338	NCOA4	.
0	0	1.307843137	0.725364338	PIH1D1	.
0	0	1.307843137	0.725364338	LDLR	.
0	0	1.307843137	0.725364338	SLC13A3	.
0	0	1.307843137	0.725364338	DYSF	.
0	0	1.307843137	0.725364338	LRRK2	.
0	0	1.307843137	0.725364338	TIFAB	.
0	0	1.307843137	0.725364338	SERPINB1	.
0	0	1.307843137	0.725364338	VEGFA	.
0	0	1.307843137	0.725364338	MEF2A	.
0	0	1.307843137	0.725364338	TGFBR1	.
0	0	1.307843137	0.725364338	SLC22A1	.
0	0	0.980729955	0.542231455	CCNT1;ELL	.
0	0	0.976924417	0.539187212	NCOA1;SL(	.
0	0	1.005952899	0.55419997	ATP1A1;SC	.
0	0	1.005952899	0.55419997	TPPP3;NDE	.
0	0	1.005952899	0.55419997	SLC9A3R1;	.
0	0	1.005952899	0.55419997	TRIR;XRN1	.
0	0	1.005952899	0.55419997	LFNG;NOT(	.
0	0	1.005952899	0.55419997	KMT5C;TE	.
0	0	1.005952899	0.55419997	MAD2L2;F	.
0	0	0.975824623	0.53238819	ACOT9;GP/	.
0	0	0.990684794	0.540051722	ACTN2;KCI	.
0	0	0.990684794	0.540051722	SARS1;PPA	.
0	0	0.990684794	0.540051722	HES1;MDM	.
0	0	0.973630602	0.529583357	TRIR;UTP1	.
0	0	0.980751794	0.528812994	ABCA1;STE	.
0	0	0.980751794	0.528812994	SMG1;ALYI	.
0	0	0.971842584	0.523541201	FZD1;PSM/	.
0	0	0.973770123	0.519312555	DDX17;DD	.
0	0	0.973770123	0.519312555	PSMA2;OD	.
0	0	0.973770123	0.519312555	DESI1;FMR	.
0	0	0.973770123	0.519312555	ELOVL5;PN	.
0	0	0.968544463	0.515477167	RYR1;KCNJ	.
0	0	0.968544463	0.515477167	SLC24A1;E	.
0	0	0.968496749	0.515088686	GGT5;XBP1	.

0	0	0.965767045	0.50804538	DYNC1H1;S.
0	0	0.964596612	0.503460438	SETX;ZNF4 .
0	0	0.964596612	0.503460438	ABCA1;STA.
0	0	0.95882917	0.490203763	BTG2;RIDA.
0	0	0.968639459	0.489345062	CHKA;PNPI.
0	0	0.968639459	0.489345062	P2RY12;ST.
0	0	0.968639459	0.489345062	ARRDC4;FZ.
0	0	0.968639459	0.489345062	CHST11;CS.
0	0	0.968639459	0.489345062	STXBP3;ST.
0	0	0.968639459	0.489345062	CYP4F2;AD.
0	0	0.96149147	0.485094606	TRPC6;PPII.
0	0	0.980773585	0.493214993	DNAH17;C.
0	0	0.980773585	0.493214993	CCDC88B;C.
0	0	0.980773585	0.493214993	CTSH;ITGA.
0	0	0.980773585	0.493214993	PLK3;NABP.
0	0	0.980773585	0.493214993	LRCH1;FICD.
0	0	0.980773585	0.493214993	FUT4;ST3G.
0	0	0.980773585	0.493214993	PIH1D1;IL1.
0	0	0.980773585	0.493214993	MED13;ME.
0	0	0.980773585	0.493214993	HDAC4;LYP.
0	0	0.980773585	0.493214993	PTK2B;FYN.
0	0	0.980773585	0.493214993	LRRK2;ID2;.
0	0	0.980773585	0.493214993	SERPINB4;.
0	0	0.980773585	0.493214993	SRI;CALM1.
0	0	0.980773585	0.493214993	SLC2A10;JA.
0	0	0.980773585	0.493214993	ASAH1;EPH.
0	0	0.980773585	0.493214993	IL1A;DAXX.
0	0	0.956775733	0.480678685	PM20D2;E .
0	0	0.953428131	0.476219393	GK5;DGAT.
0	0	0.950926276	0.471783557	SERPINB10.
0	0	0.950926276	0.471783557	DDX3X;CN.
0	0	1.005948408	0.496465301	NUDT7;PM.
0	0	1.005948408	0.496465301	STARD3;TS.
0	0	1.005948408	0.496465301	SLC24A1;S.
0	0	1.005948408	0.496465301	MEF2A;MY.
0	0	1.005948408	0.496465301	HIP1R;PICA.
0	0	1.005948408	0.496465301	VCAN;CSGA.
0	0	1.005948408	0.496465301	NIPBL;TGFI.
0	0	1.005948408	0.496465301	ID2;JAK2 .
0	0	1.005948408	0.496465301	ATP1A1;KC.
0	0	1.005948408	0.496465301	PNPT1;TFB.
0	0	1.005948408	0.496465301	SIRT1;PIAS.
0	0	1.005948408	0.496465301	NOS2;FFAR.
0	0	1.005948408	0.496465301	LRRK2;SER.
0	0	1.005948408	0.496465301	H1-4;PAF1 .
0	0	1.005948408	0.496465301	ADAM19;P.
0	0	1.005948408	0.496465301	CYP27B1;V.

0	0	1.005948408	0.496465301	NOS2;NF1	.
0	0	1.005948408	0.496465301	TCF7L2;IL1	.
0	0	1.005948408	0.496465301	XBP1;CYP4	.
0	0	1.005948408	0.496465301	EGLN3;JMJ	.
0	0	1.005948408	0.496465301	ATP7A;CO	.
0	0	1.005948408	0.496465301	PSEN1;LDL	.
0	0	1.005948408	0.496465301	TMSB4X;PI	.
0	0	1.005948408	0.496465301	THEMIS2;C	.
0	0	1.005948408	0.496465301	FITM1;OSB	.
0	0	1.005948408	0.496465301	CLN3;STXB	.
0	0	1.005948408	0.496465301	GRIN3A;AD	.
0	0	0.9489837	0.467407614	ACVRL1;DI	.
0	0	0.9489837	0.467407614	XBP1;ELOV	.
0	0	0.9489837	0.467407614	IL1A;MT2A	.
0	0	0.947430182	0.46311108	ROCK1;LRF	.
0	0	0.945096554	0.454790083	DYNC1H1;I	.
0	0	0.945096554	0.454790083	MN1;CDKN	.
0	0	0.945096554	0.454790083	SLC24A1;E	.
0	0	0.952252939	0.457625588	UTP15;RPS	.
0	0	0.943422024	0.446844934	AMER1;LRI	.
0	0	0.933941389	0.437018436	ING5;MOR	.
0	0	0.933941389	0.437018436	DGKG;DGK	.
0	0	0.933916424	0.436717801	ARHGEF11	.
0	0	0.933966336	0.435961774	NIPBL;CXCI	.
0	0	0.933966336	0.435961774	ATXN1;RGS	.
0	0	0.933966336	0.435961774	LTV1;NOM	.
0	0	0.933966336	0.435961774	GGT5;NUD	.
0	0	0.933966336	0.435961774	STX1B;STX	.
0	0	0.933891439	0.43557254	CXCL10;CX	.
0	0	0.933991264	0.432584849	IL10;CD40;	.
0	0	0.933991264	0.432584849	LAMB3;PA	.
0	0	0.933991264	0.432584849	OTUB2;MA	.
0	0	0.933991264	0.432584849	ATXN7;MII	.
0	0	0.933991264	0.432584849	C3;NR4A3;	.
0	0	0.933991264	0.432584849	PPP1R10;N	.
0	0	0.933991264	0.432584849	MOV10;PD	.
0	0	0.933991264	0.432584849	IGSF8;SVIL	.
0	0	0.933841414	0.431822245	SPART;PTP	.
0	0	1.089806435	0.502190397	DGAT2	.
0	0	1.089806435	0.502190397	GNAL	.
0	0	1.089806435	0.502190397	ALDH3B1	.
0	0	1.089806435	0.502190397	DCHS1	.
0	0	1.089806435	0.502190397	SCN4B	.
0	0	1.089806435	0.502190397	B4GALT5	.
0	0	1.089806435	0.502190397	RAMP2	.
0	0	1.089806435	0.502190397	PTGER2	.
0	0	1.089806435	0.502190397	LDLR	.

0	0	1.089806435	0.502190397	ASS1	.
0	0	1.089806435	0.502190397	DDR2	.
0	0	1.089806435	0.502190397	SLC6A8	.
0	0	1.089806435	0.502190397	LRRC8C	.
0	0	1.089806435	0.502190397	PTK2	.
0	0	1.089806435	0.502190397	TMEM120A	.
0	0	1.089806435	0.502190397	LIG4	.
0	0	1.089806435	0.502190397	IGSF3	.
0	0	1.089806435	0.502190397	RFK	.
0	0	1.089806435	0.502190397	SAG	.
0	0	1.089806435	0.502190397	NEU1	.
0	0	1.089806435	0.502190397	DLL1	.
0	0	1.089806435	0.502190397	UGCG	.
0	0	1.089806435	0.502190397	PLK3	.
0	0	1.089806435	0.502190397	FLVCR1	.
0	0	1.089806435	0.502190397	LRP5	.
0	0	1.089806435	0.502190397	RARG	.
0	0	1.089806435	0.502190397	SETDB1	.
0	0	1.089806435	0.502190397	NLGN3	.
0	0	1.089806435	0.502190397	EREG	.
0	0	1.089806435	0.502190397	ATG7	.
0	0	1.089806435	0.502190397	SLC24A1	.
0	0	1.089806435	0.502190397	NRROS	.
0	0	1.089806435	0.502190397	ME2	.
0	0	1.089806435	0.502190397	TENT4B	.
0	0	1.089806435	0.502190397	SFPQ	.
0	0	1.089806435	0.502190397	KAT2B	.
0	0	1.089806435	0.502190397	FMR1	.
0	0	1.089806435	0.502190397	GRIN3A	.
0	0	1.089806435	0.502190397	OTUB2	.
0	0	1.089806435	0.502190397	TFIP11	.
0	0	1.089806435	0.502190397	DLL1	.
0	0	1.089806435	0.502190397	INPP5K	.
0	0	1.089806435	0.502190397	SRI	.
0	0	1.089806435	0.502190397	INSIG1	.
0	0	1.089806435	0.502190397	ID2	.
0	0	1.089806435	0.502190397	HORMAD1	.
0	0	1.089806435	0.502190397	MPV17L	.
0	0	1.089806435	0.502190397	MEFV	.
0	0	1.089806435	0.502190397	CHP1	.
0	0	1.089806435	0.502190397	CHP1	.
0	0	1.089806435	0.502190397	ADAR	.
0	0	1.089806435	0.502190397	DHX58	.
0	0	1.089806435	0.502190397	SOX15	.
0	0	1.089806435	0.502190397	GRIPAP1	.
0	0	1.089806435	0.502190397	ATP7A	.
0	0	1.089806435	0.502190397	STRA6	.

0	0	1.089806435	0.502190397	PSEN1	.
0	0	1.089806435	0.502190397	ZFP36	.
0	0	1.089806435	0.502190397	IPCEF1	.
0	0	1.089806435	0.502190397	VNN2	.
0	0	1.089806435	0.502190397	RPIA	.
0	0	1.089806435	0.502190397	SQSTM1	.
0	0	1.089806435	0.502190397	HES1	.
0	0	1.089806435	0.502190397	STAT3	.
0	0	1.089806435	0.502190397	ABCA1	.
0	0	1.089806435	0.502190397	SAT1	.
0	0	1.089806435	0.502190397	ATG7	.
0	0	1.089806435	0.502190397	NF1	.
0	0	1.089806435	0.502190397	CGAS	.
0	0	1.089806435	0.502190397	TGFBR1	.
0	0	1.089806435	0.502190397	GRK2	.
0	0	1.089806435	0.502190397	PIH1D1	.
0	0	1.089806435	0.502190397	PAK1	.
0	0	1.089806435	0.502190397	PAK1	.
0	0	1.089806435	0.502190397	OPTN	.
0	0	1.089806435	0.502190397	FMR1	.
0	0	1.089806435	0.502190397	GHSR	.
0	0	1.089806435	0.502190397	CHP1	.
0	0	1.089806435	0.502190397	ATP1B3	.
0	0	1.089806435	0.502190397	RGS2	.
0	0	1.089806435	0.502190397	ADCY8	.
0	0	1.089806435	0.502190397	SOD2	.
0	0	1.089806435	0.502190397	PRODH	.
0	0	1.089806435	0.502190397	TFIP11	.
0	0	1.089806435	0.502190397	ARL13B	.
0	0	1.089806435	0.502190397	DDX3X	.
0	0	1.089806435	0.502190397	ENPP4	.
0	0	1.089806435	0.502190397	SIRT1	.
0	0	1.089806435	0.502190397	VEGFA	.
0	0	1.089806435	0.502190397	SLC8B1	.
0	0	1.089806435	0.502190397	SOCS1	.
0	0	1.089806435	0.502190397	CGAS	.
0	0	1.089806435	0.502190397	CNOT2	.
0	0	1.089806435	0.502190397	ITGAM	.
0	0	1.089806435	0.502190397	E2F3	.
0	0	1.089806435	0.502190397	NF1	.
0	0	1.089806435	0.502190397	CRY2	.
0	0	1.089806435	0.502190397	INPP5K	.
0	0	1.089806435	0.502190397	LDLR	.
0	0	1.089806435	0.502190397	NAIF1	.
0	0	1.089806435	0.502190397	CXCL10	.
0	0	1.089806435	0.502190397	FFAR3	.
0	0	1.089806435	0.502190397	ABCA3	.

0	0	1.089806435	0.502190397	DENND3	.
0	0	1.089806435	0.502190397	NLGN3	.
0	0	1.089806435	0.502190397	CFLAR	.
0	0	1.089806435	0.502190397	EREG	.
0	0	1.089806435	0.502190397	FBXO38	.
0	0	1.089806435	0.502190397	IL2RA	.
0	0	1.089806435	0.502190397	RBPJ	.
0	0	1.089806435	0.502190397	ITGAV	.
0	0	1.089806435	0.502190397	PRKAA1	.
0	0	1.089806435	0.502190397	PICALM	.
0	0	1.089806435	0.502190397	RYR1	.
0	0	1.089806435	0.502190397	RFK	.
0	0	1.089806435	0.502190397	EIF6	.
0	0	1.089806435	0.502190397	SLC38A2	.
0	0	1.089806435	0.502190397	GJB6	.
0	0	1.089806435	0.502190397	SMAD3	.
0	0	1.089806435	0.502190397	LIG4	.
0	0	1.089806435	0.502190397	SLC6A2	.
0	0	1.089806435	0.502190397	STX1B	.
0	0	1.089806435	0.502190397	SLC25A19	.
0	0	1.089806435	0.502190397	SLC7A5	.
0	0	1.089806435	0.502190397	CASP8	.
0	0	1.089806435	0.502190397	DLL1	.
0	0	1.089806435	0.502190397	VEGFA	.
0	0	1.089806435	0.502190397	SLC39A8	.
0	0	0.933816373	0.429518397	FZD1;PSM	.
0	0	0.934016173	0.424842266	FUT4;ST3G	.
0	0	0.934016173	0.424842266	MYLK3;SLC	.
0	0	0.934016173	0.424842266	CD74;GPR	.
0	0	0.934016173	0.424842266	DLC1;INPP	.
0	0	0.934016173	0.424842266	ITGAM;CHI	.
0	0	0.934016173	0.424842266	TMEM129	.
0	0	0.934016173	0.424842266	P2RY12;DE	.
0	0	0.917454316	0.4021057	ACVRL1;DI	.
0	0	0.915185185	0.400496049	GCLC;MTH	.
0	0	0.915185185	0.400496049	GPR132;PS	.
0	0	0.915185185	0.400496049	STAT1;HYA	.
0	0	0.934041063	0.407447847	RAMP2;LA	.
0	0	0.934041063	0.407447847	GPAT4;VEC	.
0	0	0.934041063	0.407447847	MORF4L2;I	.
0	0	0.934041063	0.407447847	TMEM50B	.
0	0	0.934041063	0.407447847	KAT2B;CRE	.
0	0	0.934041063	0.407447847	SLFN11;GT	.
0	0	0.934041063	0.407447847	LTB4R2;CC	.
0	0	0.934041063	0.407447847	SERPINB4;I	.
0	0	0.934041063	0.407447847	PRKCD;ALC	.
0	0	0.934041063	0.407447847	ATP1A3;PS	.

0	0	0.934041063	0.407447847	RGS14;NUI.
0	0	0.934041063	0.407447847	STRA8;HOI.
0	0	0.934041063	0.407447847	PRKCE;PPA.
0	0	0.934041063	0.407447847	ACVR1B;SM.
0	0	0.934041063	0.407447847	NR4A3;PRI.
0	0	0.934041063	0.407447847	LYN;CD74 .
0	0	0.934041063	0.407447847	IKBKB;PSEI.
0	0	0.934041063	0.407447847	EDN1;ECE1.
0	0	0.934041063	0.407447847	VGF;STAT1.
0	0	0.934041063	0.407447847	GCLC;SARS.
0	0	0.934041063	0.407447847	NRP1;NF1 .
0	0	0.912169108	0.397391512	SNX18;RO(.
0	0	0.912169108	0.397391512	LYN;DYNC1.
0	0	0.912169108	0.397391512	EIF2AK2;FA.
0	0	0.912169108	0.397391512	TCF7L2;PRI.
0	0	0.912169108	0.397391512	ABCA1;STA.
0	0	0.907970376	0.39198633	SLC7A5;SL(.
0	0	0.907970376	0.39198633	WASHC4;R.
0	0	0.907970376	0.39198633	ACTN2;KCI.
0	0	0.907970376	0.39198633	IL1B;BHLHI.
0	0	0.907970376	0.39198633	RYBP;MAX.
0	0	0.907970376	0.39198633	SPART;LRR.
0	0	0.901732599	0.382804388	ABCA1;CLI.
0	0	0.901732599	0.382804388	NLGN3;NR.
0	0	0.901732599	0.382804388	NIPBL;FMR.
0	0	0.901732599	0.382804388	FUS;SLC11.
0	0	0.910070047	0.376037441	BTG2;RIDA.
0	0	0.927462881	0.382324892	PHLDB1;XE.
0	0	0.901583991	0.371170882	CXCL8;RPL.
0	0	0.913579342	0.376105763	MORC3;PP.
0	0	0.891509434	0.366804143	PNPLA8;IL1.
0	0	0.891509434	0.366804143	PRKAA1;XE.
0	0	0.891509434	0.366804143	NLGN3;LRF.
0	0	0.891509434	0.366804143	NR4A3;ADI.
0	0	0.891509434	0.366804143	EGR2;NF1;.
0	0	0.891509434	0.366804143	ATXN3;NG.
0	0	0.891509434	0.366804143	MYLIP;SMI.
0	0	0.891509434	0.366804143	UBE2B;PDI.
0	0	0.891509434	0.366804143	TCF7L2;AP.
0	0	0.891509434	0.366804143	ID2;HOPX;.
0	0	0.891386475	0.361405182	DGKG;DGK.
0	0	0.928105974	0.375878512	PUS10;TUT.
0	0	0.883379603	0.352586851	LRP5;RFLN.
0	0	0.883379603	0.352586851	MAD2L2;P.
0	0	0.891263238	0.346725583	CUL4A;ISG.
0	0	0.871624512	0.339062655	NR4A2;DR.
0	0	0.871624512	0.339062655	STRA8;DIA.

0	0	0.871624512	0.339062655	PLK3;RB1C	.
0	0	0.871624512	0.339062655	GCH1;HSD	.
0	0	0.871624512	0.339062655	CXCL10;P2	.
0	0	0.871624512	0.339062655	PIK3CA;AV	.
0	0	0.871624512	0.339062655	RANBP2;SE	.
0	0	0.871624512	0.339062655	RANBP2;SE	.
0	0	0.871624512	0.339062655	NRG1;RBP	.
0	0	0.934065934	0.360551289	ADAR	.
0	0	0.934065934	0.360551289	KIF5C	.
0	0	0.934065934	0.360551289	B2M	.
0	0	0.934065934	0.360551289	KIF5C	.
0	0	0.934065934	0.360551289	PIH1D1	.
0	0	0.934065934	0.360551289	METRNL	.
0	0	0.934065934	0.360551289	ITPK1	.
0	0	0.934065934	0.360551289	MDM4	.
0	0	0.934065934	0.360551289	HDAC4	.
0	0	0.934065934	0.360551289	DCHS1	.
0	0	0.934065934	0.360551289	PDE4B	.
0	0	0.934065934	0.360551289	IFNAR1	.
0	0	0.934065934	0.360551289	FYN	.
0	0	0.934065934	0.360551289	DGAT2	.
0	0	0.934065934	0.360551289	ATP7A	.
0	0	0.934065934	0.360551289	ANKFY1	.
0	0	0.934065934	0.360551289	DDIT3	.
0	0	0.934065934	0.360551289	SLC9A3R1	.
0	0	0.934065934	0.360551289	ZFAND6	.
0	0	0.934065934	0.360551289	PDPN	.
0	0	0.934065934	0.360551289	ATP7A	.
0	0	0.934065934	0.360551289	ZSWIM6	.
0	0	0.934065934	0.360551289	KHK	.
0	0	0.934065934	0.360551289	GALC	.
0	0	0.934065934	0.360551289	HAL	.
0	0	0.934065934	0.360551289	HAL	.
0	0	0.934065934	0.360551289	PCGF5	.
0	0	0.934065934	0.360551289	KDM5A	.
0	0	0.934065934	0.360551289	LYN	.
0	0	0.934065934	0.360551289	KAT2B	.
0	0	0.934065934	0.360551289	ATF4	.
0	0	0.934065934	0.360551289	TDRD7	.
0	0	0.934065934	0.360551289	LYPLA1	.
0	0	0.934065934	0.360551289	CHD1	.
0	0	0.934065934	0.360551289	ID2	.
0	0	0.934065934	0.360551289	TTC19	.
0	0	0.934065934	0.360551289	PNPT1	.
0	0	0.934065934	0.360551289	SQSTM1	.
0	0	0.934065934	0.360551289	SFPQ	.
0	0	0.934065934	0.360551289	SFPQ	.

0	0	0.934065934	0.360551289	CORO1A	.
0	0	0.934065934	0.360551289	SOCS1	.
0	0	0.934065934	0.360551289	BCL6	.
0	0	0.934065934	0.360551289	SLC30A1	.
0	0	0.934065934	0.360551289	SIRT1	.
0	0	0.934065934	0.360551289	SLAMF8	.
0	0	0.934065934	0.360551289	RNF122	.
0	0	0.934065934	0.360551289	CCNT1	.
0	0	0.934065934	0.360551289	RGS2	.
0	0	0.934065934	0.360551289	NF1	.
0	0	0.934065934	0.360551289	LDLR	.
0	0	0.934065934	0.360551289	ACTN2	.
0	0	0.934065934	0.360551289	DLL1	.
0	0	0.934065934	0.360551289	JMJD6	.
0	0	0.934065934	0.360551289	EGLN3	.
0	0	0.934065934	0.360551289	SOCS1	.
0	0	0.934065934	0.360551289	EZR	.
0	0	0.934065934	0.360551289	JAML	.
0	0	0.934065934	0.360551289	PAK1	.
0	0	0.934065934	0.360551289	LGALS9	.
0	0	0.934065934	0.360551289	STRA8	.
0	0	0.934065934	0.360551289	ATP7A	.
0	0	0.934065934	0.360551289	DVL2	.
0	0	0.934065934	0.360551289	CALM1	.
0	0	0.934065934	0.360551289	ATP7A	.
0	0	0.934065934	0.360551289	DAGLB	.
0	0	0.934065934	0.360551289	NRXN2	.
0	0	0.934065934	0.360551289	SRC	.
0	0	0.934065934	0.360551289	FOLH1B	.
0	0	0.934065934	0.360551289	NGLY1	.
0	0	0.934065934	0.360551289	LYPLA1	.
0	0	0.934065934	0.360551289	KIF5C	.
0	0	0.934065934	0.360551289	PDP1	.
0	0	0.934065934	0.360551289	ARHGAP35	.
0	0	0.934065934	0.360551289	PDP1	.
0	0	0.934065934	0.360551289	PLK3	.
0	0	0.934065934	0.360551289	CALM1	.
0	0	0.934065934	0.360551289	DPH3	.
0	0	0.934065934	0.360551289	LRRK2	.
0	0	0.934065934	0.360551289	TGFBR1	.
0	0	0.934065934	0.360551289	DNM2	.
0	0	0.934065934	0.360551289	CLN3	.
0	0	0.934065934	0.360551289	IRF7	.
0	0	0.934065934	0.360551289	ANXA1	.
0	0	0.934065934	0.360551289	ATP1B3	.
0	0	0.934065934	0.360551289	CHP1	.
0	0	0.934065934	0.360551289	EPB41L2	.

0	0	0.934065934	0.360551289	VCPIP1	.
0	0	0.934065934	0.360551289	GLUL	.
0	0	0.934065934	0.360551289	NIBAN2	.
0	0	0.934065934	0.360551289	EVI2B	.
0	0	0.934065934	0.360551289	SOX15	.
0	0	0.934065934	0.360551289	TTC19	.
0	0	0.934065934	0.360551289	PDE4B	.
0	0	0.934065934	0.360551289	DENR	.
0	0	0.934065934	0.360551289	CASP8	.
0	0	0.934065934	0.360551289	CFLAR	.
0	0	0.934065934	0.360551289	SAT1	.
0	0	0.934065934	0.360551289	GGT1	.
0	0	0.934065934	0.360551289	CTSH	.
0	0	0.934065934	0.360551289	TG	.
0	0	0.934065934	0.360551289	SMG1	.
0	0	0.934065934	0.360551289	ACVRL1	.
0	0	0.934065934	0.360551289	CYP4F2	.
0	0	0.934065934	0.360551289	CLN3	.
0	0	0.871721363	0.336462154	ABCA7;PSE	.
0	0	0.871721363	0.336462154	ACVRL1;RE	.
0	0	0.871721363	0.336462154	CDKN2D;SI	.
0	0	0.871721363	0.336462154	ACVRL1;M	.
0	0	0.871721363	0.336462154	ROCK1;AB(	.
0	0	0.871721363	0.336462154	HES1;TGFB	.
0	0	0.871721363	0.336462154	SLC37A1;SI	.
0	0	0.871721363	0.336462154	RGCC;VSIR	.
0	0	0.871721363	0.336462154	RAB3D;RAI	.
0	0	0.871721363	0.336462154	PTPRC;N4E	.
0	0	0.871721363	0.336462154	NABP2;PRI	.
0	0	0.871721363	0.336462154	CALM1;SLC	.
0	0	0.871721363	0.336462154	PRKAA1;AE	.
0	0	0.871721363	0.336462154	IL16;SRI	.
0	0	0.871721363	0.336462154	PTPRC;EIF2	.
0	0	0.871721363	0.336462154	AGO2;NRD	.
0	0	0.914734043	0.350145223	LYN;BTG2;	.
0	0	0.879884005	0.336789703	DYNC1H1;/	.
0	0	0.933030585	0.352214358	STXBP3;PP	.
0	0	0.896915795	0.334118761	SLC24A1;T	.
0	0	0.852698934	0.317349194	NIPBL;NF1	.
0	0	0.852698934	0.317349194	ZFYVE28;SI	.
0	0	0.852698934	0.317349194	XRN1;SRC;	.
0	0	0.852698934	0.317349194	MOV10;TU	.
0	0	0.852698934	0.317349194	PAK1;CLIP1	.
0	0	0.852698934	0.317349194	PPP1R3B;P	.
0	0	0.852698934	0.317349194	KCNS1;ACT	.
0	0	0.852698934	0.317349194	CLN3;GRIP	.
0	0	0.852698934	0.317349194	SMG1;PPP	.

0	0	0.906145908	0.335085793	HEXIM1;PL
0	0	0.860083082	0.317254907	SARS1;PPA
0	0	0.877909996	0.321640393	MEF2A;KLF
0	0	0.877909996	0.321640393	ENPP2;APC
0	0	0.920423341	0.336376704	DDX5;DHX
0	0	0.910671736	0.332514534	KLHL18;DY
0	0	0.863232505	0.308817064	P2RY12;GN
0	0	0.863232505	0.308817064	LTV1;CUL4
0	0	0.863232505	0.308817064	WTAP;MET
0	0	0.843458883	0.300561606	EDN1;GCLC
0	0	0.843458883	0.300561606	ACVRL1;DL
0	0	0.843458883	0.300561606	KCNJ12;KC
0	0	0.843458883	0.300561606	LRRK2;RAB
0	0	0.852531989	0.298988559	ARG2;ASAH
0	0	0.852531989	0.298988559	WNT2B;HY
0	0	0.864949497	0.298310889	KLF7;PARP
0	0	0.817191626	0.279319743	H2AW;NFE
0	0	0.817191626	0.279319743	HHEX;TOP1
0	0	0.817191626	0.279319743	CREBBP;EC
0	0	0.817191626	0.279319743	TLR9;NOD2
0	0	0.817191626	0.279319743	GRK2;RGS1
0	0	0.817191626	0.279319743	EDEM1;NG
0	0	0.817191626	0.279319743	APOA2;AB
0	0	0.817191626	0.279319743	BFSP2;DNA
0	0	0.817191626	0.279319743	MREG;RAB
0	0	0.817191626	0.279319743	CIITA;IL6
0	0	0.817191626	0.279319743	PPIF;CBARI
0	0	0.817191626	0.279319743	MAD2L2;C
0	0	0.817191626	0.279319743	H2AW;NFE
0	0	0.817191626	0.279319743	PRPSAP1;P
0	0	0.817191626	0.279319743	DNAH17;ZI
0	0	0.817191626	0.279319743	MREG;RAB
0	0	0.817191626	0.279319743	ACVRL1;TA
0	0	0.817191626	0.279319743	IFNG;LIF
0	0	0.817191626	0.279319743	CYP2S1;GS
0	0	0.817191626	0.279319743	ZNF207;HC
0	0	0.817191626	0.279319743	LRRK2;SMA
0	0	0.817191626	0.279319743	P2RY12;SA
0	0	0.817191626	0.279319743	PDPN;CFTR
0	0	0.837981253	0.285544647	NRP1;PAK1
0	0	0.837981253	0.285544647	CRTC2;CHS
0	0	0.837981253	0.285544647	CYP27B1;C
0	0	0.817122642	0.275063996	CYP4F2;LPI
0	0	0.817122642	0.275063996	DLC1;INPP
0	0	0.817122642	0.275063996	NLGN3;SYN
0	0	0.817122642	0.275063996	HEXIM1;EL
0	0	0.866010598	0.287436281	H2AW;NFE

0	0	0.817053605	0.266621455	SELP;SELL;	.
0	0	0.817053605	0.266621455	ATXN3;IL1	.
0	0	0.817053605	0.266621455	RARG;NIPB	.
0	0	0.817053605	0.266621455	TMEM119;	.
0	0	0.817053605	0.266621455	PHLDB1;NI	.
0	0	0.817053605	0.266621455	CYLD;PHLD	.
0	0	0.817053605	0.266621455	LYZ;B2M;A	.
0	0	0.817260558	0.265906899	SLC9A3R1	.
0	0	0.817260558	0.265906899	CLN3	.
0	0	0.817260558	0.265906899	SCARF1	.
0	0	0.817260558	0.265906899	APOA2	.
0	0	0.817260558	0.265906899	CFAP54	.
0	0	0.817260558	0.265906899	DDR2	.
0	0	0.817260558	0.265906899	CDADC1	.
0	0	0.817260558	0.265906899	TOP1	.
0	0	0.817260558	0.265906899	NIPBL	.
0	0	0.817260558	0.265906899	TMEM119	.
0	0	0.817260558	0.265906899	HSD17B1	.
0	0	0.817260558	0.265906899	FUT4	.
0	0	0.817260558	0.265906899	ALOX12	.
0	0	0.817260558	0.265906899	ALOX12	.
0	0	0.817260558	0.265906899	PRKCD	.
0	0	0.817260558	0.265906899	SLC7A5	.
0	0	0.817260558	0.265906899	SLCO3A1	.
0	0	0.817260558	0.265906899	SLC4A7	.
0	0	0.817260558	0.265906899	LDLR	.
0	0	0.817260558	0.265906899	HSD17B1	.
0	0	0.817260558	0.265906899	POGZ	.
0	0	0.817260558	0.265906899	FUT4	.
0	0	0.817260558	0.265906899	FUT4	.
0	0	0.817260558	0.265906899	ASRGL1	.
0	0	0.817260558	0.265906899	CLN3	.
0	0	0.817260558	0.265906899	SLC9A3R1	.
0	0	0.817260558	0.265906899	SLC9A3R1	.
0	0	0.817260558	0.265906899	KDM6B	.
0	0	0.817260558	0.265906899	RPUSD4	.
0	0	0.817260558	0.265906899	DCHS1	.
0	0	0.817260558	0.265906899	ROCK1	.
0	0	0.817260558	0.265906899	SERPINE1	.
0	0	0.817260558	0.265906899	RNF122	.
0	0	0.817260558	0.265906899	CCNT1	.
0	0	0.817260558	0.265906899	EREG	.
0	0	0.817260558	0.265906899	CMPK2	.
0	0	0.817260558	0.265906899	CMPK2	.
0	0	0.817260558	0.265906899	CMPK2	.
0	0	0.817260558	0.265906899	NEU1	.
0	0	0.817260558	0.265906899	ZFAND6	.

0	0	0.817260558	0.265906899	SEC16B	.
0	0	0.817260558	0.265906899	GTF2H1	.
0	0	0.817260558	0.265906899	RAB3GAP1	.
0	0	0.817260558	0.265906899	FBXO7	.
0	0	0.817260558	0.265906899	ID2	.
0	0	0.817260558	0.265906899	PTPN22	.
0	0	0.817260558	0.265906899	APOA2	.
0	0	0.817260558	0.265906899	TESC	.
0	0	0.817260558	0.265906899	GLRX	.
0	0	0.817260558	0.265906899	PROK2	.
0	0	0.817260558	0.265906899	LRRC8C	.
0	0	0.817260558	0.265906899	UBE2S	.
0	0	0.817260558	0.265906899	GCH1	.
0	0	0.817260558	0.265906899	LRRK2	.
0	0	0.817260558	0.265906899	IL1B	.
0	0	0.817260558	0.265906899	SIRT1	.
0	0	0.817260558	0.265906899	PIH1D1	.
0	0	0.817260558	0.265906899	LYN	.
0	0	0.817260558	0.265906899	LIF	.
0	0	0.817260558	0.265906899	NUGGC	.
0	0	0.817260558	0.265906899	SIRT1	.
0	0	0.817260558	0.265906899	PLEKHA4	.
0	0	0.817260558	0.265906899	RYR1	.
0	0	0.817260558	0.265906899	SCARF1	.
0	0	0.817260558	0.265906899	NRP1	.
0	0	0.817260558	0.265906899	DLL1	.
0	0	0.817260558	0.265906899	ALOX12	.
0	0	0.881437122	0.285951137	GGT5;SLC1	.
0	0	0.881437122	0.285951137	LYN;TENM	.
0	0	0.816984517	0.257064067	CLN3;SCN9	.
0	0	0.816984517	0.257064067	SLC6A6;SL(	.
0	0	0.816984517	0.257064067	CDKN1A;FZ	.
0	0	0.855651382	0.268597175	ZNF473;ZF	.
0	0	0.831746032	0.259575224	CRTC2;ADF	.
0	0	0.882715226	0.275165786	SMAD3;SR(	.
0	0	0.867209672	0.266515604	LYN;BTG2;I	.
0	0	0.784392453	0.238798964	NOS2;FFAF	.
0	0	0.784392453	0.238798964	PAK1;CLIP1	.
0	0	0.784392453	0.238798964	FCN1;SMU	.
0	0	0.784392453	0.238798964	MAP1B;SK/	.
0	0	0.784392453	0.238798964	SIPA1L1;LR	.
0	0	0.784392453	0.238798964	HES1;TGFB	.
0	0	0.769077152	0.232946415	SDS;SDSL	.
0	0	0.769077152	0.232946415	FOLH1B;AS	.
0	0	0.769077152	0.232946415	VPS9D1;AT	.
0	0	0.769077152	0.232946415	NGLY1;AO/	.
0	0	0.769077152	0.232946415	DAXX;MT2	.

0	0	0.769077152	0.232946415	PKD1L3;PT	.
0	0	0.769077152	0.232946415	ACVRL1;M	.
0	0	0.769077152	0.232946415	UGGT1;MA	.
0	0	0.769077152	0.232946415	MREG;RAB	.
0	0	0.769077152	0.232946415	LRRK2;RAB	.
0	0	0.769077152	0.232946415	PLA2G4A;C	.
0	0	0.769077152	0.232946415	NRG1;TAP	.
0	0	0.769077152	0.232946415	MAN1A2;G	.
0	0	0.769077152	0.232946415	LYN;FCGR2	.
0	0	0.769077152	0.232946415	NRG1;TAP	.
0	0	0.769077152	0.232946415	GSDMD;NU	.
0	0	0.769077152	0.232946415	USP36;FBX	.
0	0	0.769077152	0.232946415	KAT2B;CEP	.
0	0	0.769077152	0.232946415	PIH1D1;BC	.
0	0	0.769077152	0.232946415	IFNG;LIF	.
0	0	0.769077152	0.232946415	CNOT2;TAI	.
0	0	0.769077152	0.232946415	FFAR3;FFA	.
0	0	0.769077152	0.232946415	ACTN4;MY	.
0	0	0.792248647	0.236660773	DDX17;TU	.
0	0	0.792248647	0.236660773	CLN3;MBO	.
0	0	0.792248647	0.236660773	DDX5;SAFE	.
0	0	0.792248647	0.236660773	RANBP2;SE	.
0	0	0.816846183	0.237938857	ANKRD28;S	.
0	0	0.816846183	0.237938857	SERPINB10	.
0	0	0.816846183	0.237938857	ANKRD28;S	.
0	0	0.816846183	0.237938857	ANKRD28;S	.
0	0	0.797012011	0.231467666	PARP10;UB	.
0	0	0.797012011	0.231467666	RBM3;RPL	.
0	0	0.797012011	0.231467666	MAD2L2;P	.
0	0	0.797012011	0.231467666	PARM1;SR	.
0	0	0.828258507	0.237682916	CLN3;SYNJ	.
0	0	0.828258507	0.237682916	CLN3;CLIC4	.
0	0	0.894013493	0.255714041	DDX5;DHX	.
0	0	0.800197374	0.225013857	ASAH1;SPT	.
0	0	0.852028876	0.237378077	PLK3;DYNC	.
0	0	0.852028876	0.237378077	PLK3;SEC1	.
0	0	0.827023377	0.227921694	SYS1;DOP1	.
0	0	0.726411932	0.200193267	SLC6A6	.
0	0	0.726411932	0.200193267	ACTB	.
0	0	0.726411932	0.200193267	STAT1	.
0	0	0.726411932	0.200193267	FMR1	.
0	0	0.726411932	0.200193267	SESN2	.
0	0	0.726411932	0.200193267	APOA2	.
0	0	0.726411932	0.200193267	KAT5	.
0	0	0.726411932	0.200193267	ALKBH1	.
0	0	0.726411932	0.200193267	ALKBH1	.
0	0	0.726411932	0.200193267	LRIF1	.

0	0	0.726411932	0.200193267	PAF1	.
0	0	0.726411932	0.200193267	NIPBL	.
0	0	0.726411932	0.200193267	SLC6A9	.
0	0	0.726411932	0.200193267	NEU1	.
0	0	0.726411932	0.200193267	BATF	.
0	0	0.726411932	0.200193267	HDAC4	.
0	0	0.726411932	0.200193267	SLC2A1	.
0	0	0.726411932	0.200193267	MYLIP	.
0	0	0.726411932	0.200193267	MYLIP	.
0	0	0.726411932	0.200193267	STRA6	.
0	0	0.726411932	0.200193267	ROCK1	.
0	0	0.726411932	0.200193267	CXCR4	.
0	0	0.726411932	0.200193267	NDFIP2	.
0	0	0.726411932	0.200193267	TRIB1	.
0	0	0.726411932	0.200193267	SIRT1	.
0	0	0.726411932	0.200193267	SLC9A3R1	.
0	0	0.726411932	0.200193267	JUN	.
0	0	0.726411932	0.200193267	ARHGAP35	.
0	0	0.726411932	0.200193267	NUP98	.
0	0	0.726411932	0.200193267	SIDT2	.
0	0	0.726411932	0.200193267	NT5C3A	.
0	0	0.726411932	0.200193267	CYP4F2	.
0	0	0.726411932	0.200193267	PLA2G5	.
0	0	0.726411932	0.200193267	PAF1	.
0	0	0.726411932	0.200193267	PIH1D1	.
0	0	0.726411932	0.200193267	RIN2	.
0	0	0.726411932	0.200193267	AGO2	.
0	0	0.726411932	0.200193267	LMTK2	.
0	0	0.726411932	0.200193267	SIRT1	.
0	0	0.726411932	0.200193267	CXCL13	.
0	0	0.726411932	0.200193267	CCDC65	.
0	0	0.726411932	0.200193267	DDX39B	.
0	0	0.726411932	0.200193267	ANXA2	.
0	0	0.726411932	0.200193267	PAK1	.
0	0	0.726411932	0.200193267	ATF7IP	.
0	0	0.726411932	0.200193267	GTF2B	.
0	0	0.726411932	0.200193267	SDS	.
0	0	0.726411932	0.200193267	PIH1D1	.
0	0	0.726411932	0.200193267	STXBP1	.
0	0	0.726411932	0.200193267	TFIP11	.
0	0	0.726411932	0.200193267	FZD1	.
0	0	0.754179971	0.207612443	NDE1;NUS	.
0	0	0.754179971	0.207612443	SYCP1;HOF	.
0	0	0.754179971	0.207612443	PRDX5;MA	.
0	0	0.754179971	0.207612443	KAT2B;KRE	.
0	0	0.754179971	0.207612443	HSD11B1;L	.
0	0	0.754179971	0.207612443	EDN1;SERF	.

0	0	0.754179971	0.207612443	FZR1;UBE2 .
0	0	0.754179971	0.207612443	ATAD1;ZFA .
0	0	0.754179971	0.207612443	COTL1;HCL .
0	0	0.754179971	0.207612443	CLN3;ZDHH .
0	0	0.768902805	0.210180376	RANBP2;SE .
0	0	0.768902805	0.210180376	RYBP;MAX .
0	0	0.72630873	0.195047248	SLC9A3R1; .
0	0	0.72630873	0.195047248	MTHFD2;M .
0	0	0.72630873	0.195047248	NR4A3;LRF .
0	0	0.72630873	0.195047248	ANXA1;FAI .
0	0	0.72630873	0.195047248	KDM6B;SN .
0	0	0.72630873	0.195047248	NDE1;NDE .
0	0	0.72630873	0.195047248	COX17;CO .
0	0	0.72630873	0.195047248	NIBAN2;B4 .
0	0	0.72630873	0.195047248	VPS4B;STO .
0	0	0.72630873	0.195047248	EDN1;RGS .
0	0	0.72630873	0.195047248	PRKAA1;IL .
0	0	0.72630873	0.195047248	AGO2;SNIP .
0	0	0.72630873	0.195047248	H2AW;NFE .
0	0	0.72630873	0.195047248	PRKD2;SPR .
0	0	0.72630873	0.195047248	LRRK2;AKA .
0	0	0.890141383	0.236761702	DDX5;DHX .
0	0	0.825141992	0.210303809	MEF2A;RYI .
0	0	0.788587849	0.199835392	HSD11B1;H .
0	0	0.788587849	0.199835392	PUS10;ME .
0	0	0.74689101	0.186750188	CAMK1D;S .
0	0	0.726205451	0.180728103	NDE1;LLGL .
0	0	0.726205451	0.180728103	SLC4A7;SL(.
0	0	0.726205451	0.180728103	EPHX2;ALC .
0	0	0.726205451	0.180728103	VASP;DLC1 .
0	0	0.726205451	0.180728103	ADCY8;ZDH .
0	0	0.791934468	0.194508572	UBE2S;NDI .
0	0	0.841078655	0.206314031	DYNC1H1;\ .
0	0	0.688042248	0.163883444	GRK2;RGS1 .
0	0	0.688042248	0.163883444	DDIT3;WLS .
0	0	0.688042248	0.163883444	NRP1;NF1 .
0	0	0.688042248	0.163883444	KAT5;NRIP .
0	0	0.688042248	0.163883444	CBLIF;TCN1 .
0	0	0.688042248	0.163883444	ACVRL1;M .
0	0	0.688042248	0.163883444	XYLT1;HPS .
0	0	0.688042248	0.163883444	PRDX5;GP) .
0	0	0.688042248	0.163883444	MREG;RAB .
0	0	0.688042248	0.163883444	CORO1A;C .
0	0	0.688042248	0.163883444	CUL4A;GTF .
0	0	0.688042248	0.163883444	CUL4A;GTF .
0	0	0.688042248	0.163883444	PDCL;GLI1 .
0	0	0.688042248	0.163883444	NIPBL;PIH1 .

0	0	0.688042248	0.163883444	CALM1;SLC	.
0	0	0.688042248	0.163883444	NR1H2;NR	.
0	0	0.794542462	0.188965315	NPEPPS;DN	.
0	0	0.807347175	0.190607423	NIBAN1;RB	.
0	0	0.653733032	0.153197431	GSN	.
0	0	0.653733032	0.153197431	ACTN1	.
0	0	0.653733032	0.153197431	SCARF1	.
0	0	0.653733032	0.153197431	HIF1A	.
0	0	0.653733032	0.153197431	NFAT5	.
0	0	0.653733032	0.153197431	MMP1	.
0	0	0.653733032	0.153197431	B4GALT5	.
0	0	0.653733032	0.153197431	SLC25A16	.
0	0	0.653733032	0.153197431	GNAT2	.
0	0	0.653733032	0.153197431	GNAT2	.
0	0	0.653733032	0.153197431	UGGT1	.
0	0	0.653733032	0.153197431	ALAS1	.
0	0	0.653733032	0.153197431	RAPGEF6	.
0	0	0.653733032	0.153197431	HSD11B1	.
0	0	0.653733032	0.153197431	HSD11B1	.
0	0	0.653733032	0.153197431	IPMK	.
0	0	0.653733032	0.153197431	LYPLA1	.
0	0	0.653733032	0.153197431	STAT1	.
0	0	0.653733032	0.153197431	TFB1M	.
0	0	0.653733032	0.153197431	PNPT1	.
0	0	0.653733032	0.153197431	RYR1	.
0	0	0.653733032	0.153197431	CBARP	.
0	0	0.653733032	0.153197431	KAT2B	.
0	0	0.653733032	0.153197431	CNOT2	.
0	0	0.653733032	0.153197431	LGALS9	.
0	0	0.653733032	0.153197431	ACTN2	.
0	0	0.653733032	0.153197431	LRRK2	.
0	0	0.653733032	0.153197431	EGLN3	.
0	0	0.653733032	0.153197431	GSN	.
0	0	0.653733032	0.153197431	ACVRL1	.
0	0	0.653733032	0.153197431	EZR	.
0	0	0.653733032	0.153197431	VEGFA	.
0	0	0.653733032	0.153197431	PLEKHA4	.
0	0	0.653733032	0.153197431	CHMP2A	.
0	0	0.653733032	0.153197431	WDR45	.
0	0	0.653733032	0.153197431	TTLL7	.
0	0	0.653733032	0.153197431	SLC25A16	.
0	0	0.653733032	0.153197431	MID1IP1	.
0	0	0.653733032	0.153197431	ACTN2	.
0	0	0.653733032	0.153197431	PIH1D1	.
0	0	0.653733032	0.153197431	ATP7A	.
0	0	0.653733032	0.153197431	PAF1	.
0	0	0.653733032	0.153197431	LYN	.

0	0	0.653733032	0.153197431	FMR1	.
0	0	0.653733032	0.153197431	PTGER2	.
0	0	0.653733032	0.153197431	SAG	.
0	0	0.653733032	0.153197431	SLC25A16	.
0	0	0.653733032	0.153197431	HM13	.
0	0	0.653733032	0.153197431	EGR2	.
0	0	0.653733032	0.153197431	SMPDL3A	.
0	0	0.653733032	0.153197431	NSMCE2	.
0	0	0.653733032	0.153197431	UAP1	.
0	0	0.653733032	0.153197431	LIG4	.
0	0	0.796628	0.183369785	ACVRL1;FL	.
0	0	0.726102093	0.165998467	ADAM15;P	.
0	0	0.726102093	0.165998467	NCOA1;SL(	.
0	0	0.726102093	0.165998467	TMEM119;	.
0	0	0.726102093	0.165998467	DNMT3L;P	.
0	0	0.80803507	0.184238846	BCR;NLGN	.
0	0	0.742541541	0.169101944	NEU1;ST6(	.
0	0	0.700229111	0.157502133	IL18;RICTO	.
0	0	0.700229111	0.157502133	ATP1A1;SC	.
0	0	0.700229111	0.157502133	SEMA4D;LI	.
0	0	0.700229111	0.157502133	CLN3;NDE1	.
0	0	0.700229111	0.157502133	ACOT9;GP/	.
0	0	0.700229111	0.157502133	SMAD3;XIA	.
0	0	0.700229111	0.157502133	ACOT9;GP/	.
0	0	0.700229111	0.157502133	STARD3;HS	.
0	0	0.700229111	0.157502133	VASP;DLC1	.
0	0	0.753901369	0.169261043	NIPBL;EFEI	.
0	0	0.753901369	0.169261043	DAXX;H2B(	.
0	0	0.783903177	0.174963659	FZR1;PSM/	.
0	0	0.768553319	0.16514432	ACVRL1;SP	.
0	0	0.653602414	0.138120215	RAPGEF1;N	.
0	0	0.653602414	0.138120215	ABT1;NOP9	.
0	0	0.653602414	0.138120215	SCN9A;SCN	.
0	0	0.653602414	0.138120215	CUL4A;GTF	.
0	0	0.653602414	0.138120215	FMR1;PSEN	.
0	0	0.653602414	0.138120215	TOX;VEGFA	.
0	0	0.653602414	0.138120215	ATAD1;RAI	.
0	0	0.653602414	0.138120215	HEG1;JAK1	.
0	0	0.653602414	0.138120215	SMG1;LIG4	.
0	0	0.653602414	0.138120215	TFB1M;MR	.
0	0	0.653602414	0.138120215	CBLIF;TCN1	.
0	0	0.789511775	0.165837472	VASP;NLGN	.
0	0	0.789511775	0.165837472	EML4;NIPB	.
0	0	0.725998657	0.152318422	NR4A2;NR1	.
0	0	0.725998657	0.152318422	TRAF7;DDX	.
0	0	0.706436901	0.147602934	CRTC2;ENC	.
0	0	0.706436901	0.147602934	GRK2;PIK3(	.

0	0	0.706436901	0.147602934	ADPGK;CH	.
0	0	0.706436901	0.147602934	TMEM119;	.
0	0	0.706436901	0.147602934	VCPKMT;E	.
0	0	0.706436901	0.147602934	C3;ITGAM;	.
0	0	0.676044242	0.137397741	ROCK1;ELN	.
0	0	0.676044242	0.137397741	DNAH17;C	.
0	0	0.676044242	0.137397741	PRKAA1;XE	.
0	0	0.676044242	0.137397741	SCN9A;CA(	.
0	0	0.676044242	0.137397741	SEMA4D;H	.
0	0	0.801945181	0.161886173	RANBP2;SU	.
0	0	0.757371031	0.152111021	ABCA1;STA	.
0	0	0.594268477	0.118790602	AIF1	.
0	0	0.594268477	0.118790602	UAP1	.
0	0	0.594268477	0.118790602	CD47	.
0	0	0.594268477	0.118790602	SEH1L	.
0	0	0.594268477	0.118790602	ARHGAP35	.
0	0	0.594268477	0.118790602	NFAT5	.
0	0	0.594268477	0.118790602	GCH1	.
0	0	0.594268477	0.118790602	ATP7A	.
0	0	0.594268477	0.118790602	TIFAB	.
0	0	0.594268477	0.118790602	VCAN	.
0	0	0.594268477	0.118790602	NIPBL	.
0	0	0.594268477	0.118790602	SNX8	.
0	0	0.594268477	0.118790602	VCPIP1	.
0	0	0.594268477	0.118790602	KIFC3	.
0	0	0.594268477	0.118790602	ALDH2	.
0	0	0.594268477	0.118790602	NRP1	.
0	0	0.594268477	0.118790602	IPCEF1	.
0	0	0.594268477	0.118790602	PTPRO	.
0	0	0.594268477	0.118790602	SLC9A3R1	.
0	0	0.594268477	0.118790602	LAMB3	.
0	0	0.594268477	0.118790602	NIPAL4	.
0	0	0.594268477	0.118790602	TAL1	.
0	0	0.594268477	0.118790602	MREG	.
0	0	0.594268477	0.118790602	SNAI1	.
0	0	0.594268477	0.118790602	MEF2A	.
0	0	0.594268477	0.118790602	LDLR	.
0	0	0.594268477	0.118790602	CHP1	.
0	0	0.594268477	0.118790602	CHP1	.
0	0	0.594268477	0.118790602	RGS2	.
0	0	0.594268477	0.118790602	SIRT1	.
0	0	0.594268477	0.118790602	SIRT1	.
0	0	0.594268477	0.118790602	MAPRE1	.
0	0	0.594268477	0.118790602	HP	.
0	0	0.594268477	0.118790602	HEXIM1	.
0	0	0.594268477	0.118790602	DYNC1H1	.
0	0	0.594268477	0.118790602	APOA2	.

0	0	0.594268477	0.118790602	VEGFA	.
0	0	0.594268477	0.118790602	NR4A3	.
0	0	0.594268477	0.118790602	NSMCE2	.
0	0	0.594268477	0.118790602	NSMCE2	.
0	0	0.594268477	0.118790602	NSMCE2	.
0	0	0.594268477	0.118790602	PLEK	.
0	0	0.594268477	0.118790602	VEGFA	.
0	0	0.594268477	0.118790602	IK	.
0	0	0.594268477	0.118790602	NRXN2	.
0	0	0.594268477	0.118790602	ADSS2	.
0	0	0.594268477	0.118790602	PRPSAP1	.
0	0	0.594268477	0.118790602	SCARF1	.
0	0	0.594268477	0.118790602	SOCS1	.
0	0	0.594268477	0.118790602	NUGGC	.
0	0	0.594268477	0.118790602	SRI	.
0	0	0.594268477	0.118790602	STOX1	.
0	0	0.594268477	0.118790602	CCL3	.
0	0	0.594268477	0.118790602	PTK2B	.
0	0	0.594268477	0.118790602	DAGLB	.
0	0	0.594268477	0.118790602	SERPINE1	.
0	0	0.594268477	0.118790602	PKD1L3	.
0	0	0.594268477	0.118790602	TENT4B	.
0	0	0.594268477	0.118790602	SGPP1	.
0	0	0.594268477	0.118790602	TG	.
0	0	0.594268477	0.118790602	ANXA1	.
0	0	0.71017503	0.137201366	EML4;SEH1	.
0	0	0.68780672	0.13128341	OTUB2;PPI	.
0	0	0.622442564	0.116720965	NIPBL;TIFA	.
0	0	0.622442564	0.116720965	VPS4B;STO	.
0	0	0.622442564	0.116720965	LIF;VEGFA	.
0	0	0.622442564	0.116720965	VCPKMT;E	.
0	0	0.622442564	0.116720965	TCF7L2;IL1	.
0	0	0.622442564	0.116720965	PIK3CA;MA	.
0	0	0.622442564	0.116720965	NABP2;PRI	.
0	0	0.622442564	0.116720965	COX17;CO	.
0	0	0.622442564	0.116720965	PRKAA1;AT	.
0	0	0.653471698	0.119965159	HSD3B7;NI	.
0	0	0.653471698	0.119965159	CDKN1A;FZ	.
0	0	0.653471698	0.119965159	RAMP2;SPI	.
0	0	0.712655837	0.127184366	PARM1;RG	.
0	0	0.712655837	0.127184366	CDKN2D;SI	.
0	0	0.695024748	0.123581712	EHD4;STX6	.
0	0	0.695024748	0.123581712	SPART;SMI	.
0	0	0.695024748	0.123581712	CXCL10;CX	.
0	0	0.695024748	0.123581712	XRN1;SRC;	.
0	0	0.725791551	0.128742807	ANKRD28;S	.
0	0	0.778753128	0.137559468	SLC24A1;K	.

0	0	0.789775367	0.139006813	SLC24A1;K	.
0	0	0.735951436	0.128944578	KLF7;MAP1	.
0	0	0.735951436	0.128944578	RANBP2;CI	.
0	0	0.735951436	0.128944578	PXK;KCNJ1	.
0	0	0.670131932	0.116795694	GGT5;GCL(	.
0	0	0.781246458	0.134178873	PLK3;DYNC	.
0	0	0.544714681	0.093117664	ELOVL5	.
0	0	0.544714681	0.093117664	PNPT1	.
0	0	0.544714681	0.093117664	MYCBP2	.
0	0	0.544714681	0.093117664	TIFAB	.
0	0	0.544714681	0.093117664	VCAN	.
0	0	0.544714681	0.093117664	CALM1	.
0	0	0.544714681	0.093117664	CDADC1	.
0	0	0.544714681	0.093117664	H3-3A	.
0	0	0.544714681	0.093117664	TMEM119	.
0	0	0.544714681	0.093117664	CABYR	.
0	0	0.544714681	0.093117664	ZMYND10	.
0	0	0.544714681	0.093117664	POGZ	.
0	0	0.544714681	0.093117664	ALOX12	.
0	0	0.544714681	0.093117664	CABYR	.
0	0	0.544714681	0.093117664	HIF1A	.
0	0	0.544714681	0.093117664	ACTN4	.
0	0	0.544714681	0.093117664	SIRT1	.
0	0	0.544714681	0.093117664	SLFN11	.
0	0	0.544714681	0.093117664	ZFYVE28	.
0	0	0.544714681	0.093117664	CHP1	.
0	0	0.544714681	0.093117664	ACTN4	.
0	0	0.544714681	0.093117664	DYSF	.
0	0	0.544714681	0.093117664	TNF	.
0	0	0.544714681	0.093117664	TNF	.
0	0	0.544714681	0.093117664	SIRT1	.
0	0	0.544714681	0.093117664	ABCA3	.
0	0	0.544714681	0.093117664	SCN4B	.
0	0	0.544714681	0.093117664	APOA2	.
0	0	0.544714681	0.093117664	ADAM17	.
0	0	0.544714681	0.093117664	DCUN1D3	.
0	0	0.544714681	0.093117664	FLCN	.
0	0	0.544714681	0.093117664	KCNJ2	.
0	0	0.544714681	0.093117664	DUSP1	.
0	0	0.544714681	0.093117664	MX2	.
0	0	0.544714681	0.093117664	TOX	.
0	0	0.544714681	0.093117664	RB1CC1	.
0	0	0.544714681	0.093117664	SRSF12	.
0	0	0.544714681	0.093117664	GTF2B	.
0	0	0.544714681	0.093117664	APOA2	.
0	0	0.544714681	0.093117664	UAP1	.
0	0	0.594115428	0.098872326	STARD3;TS	.

0	0	0.594115428	0.098872326	ACVRL1;AI	.
0	0	0.594115428	0.098872326	NDE1;NDE	.
0	0	0.594115428	0.098872326	TIFAB;TTC	.
0	0	0.594115428	0.098872326	LRRK2;LRP	.
0	0	0.594115428	0.098872326	POLB;LIG4	.
0	0	0.594115428	0.098872326	FLT1;PLA2	.
0	0	0.594115428	0.098872326	BCL2L11;B	.
0	0	0.594115428	0.098872326	SMAD3;SM	.
0	0	0.632355447	0.104825834	FLCN;MPV	.
0	0	0.632355447	0.104825834	VASP;DLC1	.
0	0	0.632355447	0.104825834	MBOAT1;P	.
0	0	0.632355447	0.104825834	CXCL10;CX	.
0	0	0.632355447	0.104825834	PARM1;PR	.
0	0	0.632355447	0.104825834	RTP4;SEC6	.
0	0	0.632355447	0.104825834	RUBCNL;SI	.
0	0	0.632355447	0.104825834	NUSAP1;ZM	.
0	0	0.632355447	0.104825834	IGSF8;SVIL	.
0	0	0.632355447	0.104825834	NLGN3;SYN	.
0	0	0.811145684	0.13300263	WASHC4;S	.
0	0	0.653340883	0.103926438	HSPA5;SEC	.
0	0	0.703378103	0.10780408	SNX18;RO(	.
0	0	0.687570835	0.105030701	HSD3B7;XE	.
0	0	0.666579321	0.100246735	ARHGEF11	.
0	0	0.612558962	0.091659838	SLC2A10;X	.
0	0	0.612558962	0.091659838	FBXO40;NI	.
0	0	0.612558962	0.091659838	KCNJ12;EC	.
0	0	0.612558962	0.091659838	NLGN3;LRF	.
0	0	0.612558962	0.091659838	TPPP3;COT	.
0	0	0.612558962	0.091659838	ARL13B;GL	.
0	0	0.568251521	0.083930171	KSR1;PDE7	.
0	0	0.568251521	0.083930171	SAG;CALM	.
0	0	0.568251521	0.083930171	SRI;CALM1	.
0	0	0.568251521	0.083930171	TRAF7;RPL	.
0	0	0.568251521	0.083930171	SF3B1;SMN	.
0	0	0.502784546	0.073659555	MDM4	.
0	0	0.502784546	0.073659555	MDM4	.
0	0	0.502784546	0.073659555	RBPJ	.
0	0	0.502784546	0.073659555	MYADM	.
0	0	0.502784546	0.073659555	SEC24B	.
0	0	0.502784546	0.073659555	LIPE	.
0	0	0.502784546	0.073659555	FYN	.
0	0	0.502784546	0.073659555	TET2	.
0	0	0.502784546	0.073659555	UGCG	.
0	0	0.502784546	0.073659555	USPL1	.
0	0	0.502784546	0.073659555	LDLR	.
0	0	0.502784546	0.073659555	HEXIM1	.
0	0	0.502784546	0.073659555	SPRY1	.

0	0	0.502784546	0.073659555	SRSF12	.
0	0	0.502784546	0.073659555	IRF1	.
0	0	0.502784546	0.073659555	DAGLB	.
0	0	0.502784546	0.073659555	VEGFA	.
0	0	0.502784546	0.073659555	TCF7L2	.
0	0	0.502784546	0.073659555	SIRT1	.
0	0	0.502784546	0.073659555	RPUSD4	.
0	0	0.502784546	0.073659555	IK	.
0	0	0.502784546	0.073659555	LTO1	.
0	0	0.502784546	0.073659555	COQ10B	.
0	0	0.502784546	0.073659555	SIRT1	.
0	0	0.502784546	0.073659555	PHLDB1	.
0	0	0.502784546	0.073659555	NIPBL	.
0	0	0.502784546	0.073659555	APOA2	.
0	0	0.502784546	0.073659555	CCL3	.
0	0	0.502784546	0.073659555	PIH1D1	.
0	0	0.502784546	0.073659555	GPD2	.
0	0	0.502784546	0.073659555	MMP1	.
0	0	0.502784546	0.073659555	DHRS13	.
0	0	0.502784546	0.073659555	SLC26A11	.
0	0	0.502784546	0.073659555	DPH3	.
0	0	0.63736891	0.092488843	CLIP1;TPPF	.
0	0	0.764917196	0.108728812	DAXX;H2B(	.
0	0	0.675677084	0.095417198	SDC4;CYP4	.
0	0	0.675677084	0.095417198	RYBP;PPP1	.
0	0	0.675677084	0.095417198	PSMA2;PSI	.
0	0	0.593962264	0.080195765	SIK1;ATP1A	.
0	0	0.622157508	0.082319021	VCPIP1;PTI	.
0	0	0.54454294	0.071380169	CUL4A;GTF	.
0	0	0.54454294	0.071380169	CREBBP;EZ	.
0	0	0.717466416	0.093955243	KDM6B;AN	.
0	0	0.749010741	0.097516652	ABT1;RPL1	.
0	0	0.46684443	0.058717721	GGT1	.
0	0	0.46684443	0.058717721	ATP7A	.
0	0	0.46684443	0.058717721	TMEM120A	.
0	0	0.46684443	0.058717721	POR	.
0	0	0.46684443	0.058717721	VEGFA	.
0	0	0.46684443	0.058717721	DAGLB	.
0	0	0.46684443	0.058717721	CHST3	.
0	0	0.46684443	0.058717721	ABHD1	.
0	0	0.46684443	0.058717721	NSMCE2	.
0	0	0.46684443	0.058717721	GGT1	.
0	0	0.46684443	0.058717721	CD81	.
0	0	0.46684443	0.058717721	ACTN1	.
0	0	0.46684443	0.058717721	SRSF12	.
0	0	0.46684443	0.058717721	GGT1	.
0	0	0.46684443	0.058717721	VEGFA	.

0	0	0.46684443	0.058717721	SAG	.
0	0	0.46684443	0.058717721	FUS	.
0	0	0.46684443	0.058717721	PHKG2	.
0	0	0.46684443	0.058717721	KMT2E	.
0	0	0.46684443	0.058717721	EZR	.
0	0	0.46684443	0.058717721	NABP2	.
0	0	0.46684443	0.058717721	VEGFA	.
0	0	0.46684443	0.058717721	FMR1	.
0	0	0.46684443	0.058717721	CEP120	.
0	0	0.46684443	0.058717721	DAAM2	.
0	0	0.46684443	0.058717721	FLT1	.
0	0	0.46684443	0.058717721	COQ10B	.
0	0	0.46684443	0.058717721	COQ10B	.
0	0	0.709626742	0.087086799	GALNT11;C	.
0	0	0.576459489	0.070202577	ACOT9;GP/	.
0	0	0.576459489	0.070202577	ATP1A3;AT	.
0	0	0.84081481	0.102349235	ALAS1;LRR	.
0	0	0.522731045	0.060808564	HSD3B7;O9	.
0	0	0.522731045	0.060808564	TPPP3;ZNF	.
0	0	0.522731045	0.060808564	CYP4F2;SL(	.
0	0	0.522731045	0.060808564	VCPKMT;EI	.
0	0	0.522731045	0.060808564	ATAD1;RAI	.
0	0	0.522731045	0.060808564	ACVRL1;RB	.
0	0	0.522731045	0.060808564	CXCL10;CX	.
0	0	0.522731045	0.060808564	PPIF;FKBP5	.
0	0	0.522731045	0.060808564	PDE4B;SRI	.
0	0	0.522731045	0.060808564	MAD2L2;N	.
0	0	0.67836889	0.077994752	DYNC1H1;I	.
0	0	0.662449199	0.075343055	ROCK1;AC1	.
0	0	0.662449199	0.075343055	LAMP1;PPI	.
0	0	0.593808985	0.06522373	TIMM17A;1	.
0	0	0.559956873	0.061482976	MYBPC2;TI	.
0	0	0.559956873	0.061482976	MYBPC2;TI	.
0	0	0.559956873	0.061482976	ACVRL1;RC	.
0	0	0.559956873	0.061482976	SEMA7A;LI	.
0	0	0.559956873	0.061482976	INSIG1;PM	.
0	0	0.43569633	0.047116339	GSTA1	.
0	0	0.43569633	0.047116339	TGFBR1	.
0	0	0.43569633	0.047116339	SRSF12	.
0	0	0.43569633	0.047116339	CHST3	.
0	0	0.43569633	0.047116339	JARID2	.
0	0	0.43569633	0.047116339	PPIF	.
0	0	0.43569633	0.047116339	ARL13B	.
0	0	0.43569633	0.047116339	B4GALT5	.
0	0	0.43569633	0.047116339	GSTA1	.
0	0	0.43569633	0.047116339	RGCC	.
0	0	0.43569633	0.047116339	SIRT1	.

0	0	0.43569633	0.047116339	DYNC1H1	.
0	0	0.43569633	0.047116339	SLC1A2	.
0	0	0.61612894	0.065877017	FLCN;XYLT	.
0	0	0.61612894	0.065877017	ACVRL1;SD	.
0	0	0.502596988	0.051880272	NCOA1;SL(	.
0	0	0.502596988	0.051880272	SMURF1;EI	.
0	0	0.502596988	0.051880272	GDI1;LRP4	.
0	0	0.502596988	0.051880272	GSN;VPS4E	.
0	0	0.502596988	0.051880272	EPHX2;SIR	.
0	0	0.502596988	0.051880272	FXYD5;SCN	.
0	0	0.502596988	0.051880272	ACTN2;MY	.
0	0	0.747942325	0.076191569	MEF2A;PN	.
0	0	0.544371069	0.053867987	RGCC;UBE	.
0	0	0.604684178	0.059290446	CDKN1A;F	.
0	0	0.408441742	0.03802309	ADRB3	.
0	0	0.408441742	0.03802309	SAT1	.
0	0	0.408441742	0.03802309	MDM2	.
0	0	0.408441742	0.03802309	GNAT2	.
0	0	0.408441742	0.03802309	RICTOR	.
0	0	0.408441742	0.03802309	RILPL2	.
0	0	0.408441742	0.03802309	ANXA1	.
0	0	0.408441742	0.03802309	EIF6	.
0	0	0.408441742	0.03802309	ATP5PB	.
0	0	0.408441742	0.03802309	SIRT1	.
0	0	0.408441742	0.03802309	SMURF1	.
0	0	0.408441742	0.03802309	EDN1	.
0	0	0.408441742	0.03802309	PIGH	.
0	0	0.408441742	0.03802309	TMEM120	.
0	0	0.408441742	0.03802309	IK	.
0	0	0.408441742	0.03802309	STRA6	.
0	0	0.408441742	0.03802309	LRRC8C	.
0	0	0.408441742	0.03802309	XIAP	.
0	0	0.408441742	0.03802309	ABT1	.
0	0	0.408441742	0.03802309	INTS6	.
0	0	0.483954343	0.044322279	GALNT11;I	.
0	0	0.483954343	0.044322279	EGR2;STAT	.
0	0	0.483954343	0.044322279	CUL4A;GTF	.
0	0	0.483954343	0.044322279	ANKRD28;(	.
0	0	0.529627741	0.047212512	PAK1;CLIP1	.
0	0	0.64471983	0.055428304	ADAMTS2;	.
0	0	0.466643315	0.037910922	ABT1;NOP9	.
0	0	0.466643315	0.037910922	UGGT1;UB	.
0	0	0.466643315	0.037910922	GRK2;FFAR	.
0	0	0.466643315	0.037910922	ECE1;ATP2	.
0	0	0.466643315	0.037910922	ANKRD28;(	.
0	0	0.466643315	0.037910922	USB1;INTS	.
0	0	0.384393576	0.030837448	LRRC8C	.

0	0	0.384393576	0.030837448	ADAR	.
0	0	0.384393576	0.030837448	MT2A	.
0	0	0.384393576	0.030837448	HES1	.
0	0	0.384393576	0.030837448	PDPN	.
0	0	0.384393576	0.030837448	MIDN	.
0	0	0.384393576	0.030837448	PTPN2	.
0	0	0.384393576	0.030837448	NOS2	.
0	0	0.384393576	0.030837448	TAPT1	.
0	0	0.384393576	0.030837448	KCNS1	.
0	0	0.384393576	0.030837448	SMURF1	.
0	0	0.384393576	0.030837448	CCNT1	.
0	0	0.384393576	0.030837448	SCN4B	.
0	0	0.384393576	0.030837448	SLC8A1	.
0	0	0.384393576	0.030837448	SARS1	.
0	0	0.809632431	0.062158085	GALNT11;[	.
0	0	0.645475553	0.048948372	CD74;DYN(	.
0	0	0.502409289	0.036297656	GALNT11;[	.
0	0	0.502409289	0.036297656	VMP1;DNA	.
0	0	0.450526151	0.032462062	HOXC9;TG[	.
0	0	0.450526151	0.032462062	UGGT1;UB	.
0	0	0.450526151	0.032462062	ACTN2;PTK	.
0	0	0.609241623	0.043623195	FLCN;SMA[	.
0	0	0.760311111	0.053864873	ITGAM;SLC	.
0	0	0.363017429	0.025118915	MDM4	.
0	0	0.363017429	0.025118915	KAT5	.
0	0	0.363017429	0.025118915	ALDH2	.
0	0	0.363017429	0.025118915	XYLT1	.
0	0	0.363017429	0.025118915	CHMP2A	.
0	0	0.363017429	0.025118915	UAP1	.
0	0	0.363017429	0.025118915	MYBL1	.
0	0	0.363017429	0.025118915	C3	.
0	0	0.363017429	0.025118915	MCU	.
0	0	0.363017429	0.025118915	TIMM17A	.
0	0	0.363017429	0.025118915	BPNT1	.
0	0	0.363017429	0.025118915	CHRNE	.
0	0	0.363017429	0.025118915	TFIP11	.
0	0	0.621586101	0.042749676	DHRS13;SD	.
0	0	0.533062149	0.036441722	KDM6B;GJ[	.
0	0	0.584610006	0.039772996	VCPIP1;SE(	.
0	0	0.601190476	0.039780691	UGCG;LAM	.
0	0	0.489820755	0.031837385	WNT2B;SO	.
0	0	0.489820755	0.031837385	WNT2B;SO	.
0	0	0.489820755	0.031837385	ACTN2;CFL	.
0	0	0.489820755	0.031837385	TCF4;ARHG	.
0	0	0.489820755	0.031837385	TCF7L2;AC	.
0	0	0.489820755	0.031837385	STXBP3;ST	.
0	0	0.681460074	0.043838909	ARRDC4;RI	.

0	0	0.435483465	0.027823415	S1PR1;SM/	.
0	0	0.435483465	0.027823415	GOSR1;CO	.
0	0	0.435483465	0.027823415	MID1IP1;P	.
0	0	0.435483465	0.027823415	PPIF;BAK1	.
0	0	0.435483465	0.027823415	PPIF;FKBP5	.
0	0	0.435483465	0.027823415	SIPA1L1;LR	.
0	0	0.435483465	0.027823415	PAK1;CNO	.
0	0	0.522370706	0.03243011	CLIC5;CLIC	.
0	0	0.522370706	0.03243011	KCNJ12;KC	.
0	0	0.624766633	0.038177215	RPS9;RPS7	.
0	0	0.764958844	0.046284422	MRPS15;A	.
0	0	0.343891403	0.0205397	ADRB3	.
0	0	0.343891403	0.0205397	LMTK2	.
0	0	0.343891403	0.0205397	PPARD	.
0	0	0.343891403	0.0205397	RIMBP3B	.
0	0	0.343891403	0.0205397	SOX13	.
0	0	0.343891403	0.0205397	EDN1	.
0	0	0.607060272	0.035890236	CSF1;LRRK	.
0	0	0.477846295	0.027930177	RTP4;GNA	.
0	0	0.477846295	0.027930177	STXBP3;ST	.
0	0	0.477846295	0.027930177	SVIL;TAL1;I	.
0	0	0.63343729	0.036925913	UPF2;CTIF;	.
0	0	0.544026939	0.03137924	GABRR2;SL	.
0	0	0.618154312	0.035116781	HSD11B1;S	.
0	0	0.421411275	0.023868532	FBXO4;PRK	.
0	0	0.421411275	0.023868532	GPD2;DHR	.
0	0	0.421411275	0.023868532	FLCN;IL1B	.
0	0	0.559458147	0.029559415	RANBP2;PI	.
0	0	0.611679747	0.032290033	POLB;CUL4	.
0	0	0.466442049	0.024506064	DFFB;H1-4	.
0	0	0.466442049	0.024506064	CEBPG;SIR	.
0	0	0.326677979	0.016852791	SLC8A1	.
0	0	0.326677979	0.016852791	FMR1	.
0	0	0.326677979	0.016852791	MAD2L2	.
0	0	0.326677979	0.016852791	NOS2	.
0	0	0.326677979	0.016852791	SERPINE1	.
0	0	0.326677979	0.016852791	SUN2	.
0	0	0.326677979	0.016852791	EPHX2	.
0	0	0.326677979	0.016852791	MYBL1	.
0	0	0.326677979	0.016852791	DHRS3	.
0	0	0.502221448	0.025674308	SH3PXD2B	.
0	0	0.502221448	0.025674308	RAMP2;PA	.
0	0	0.62129975	0.031446077	ACOT9;DN	.
0	0	0.677393142	0.034152708	CD164;TEN	.
0	0	0.408218597	0.020492025	SETDB1;EZ	.
0	0	0.408218597	0.020492025	INSIG1;PM	.
0	0	0.408218597	0.020492025	SETX;ZNF4	.

0	0	0.408218597	0.020492025	METTL1;M	.
0	0	0.492717081	0.022839569	TRAF7;RPL	.
0	0	0.311103929	0.013869976	HOPX	.
0	0	0.311103929	0.013869976	CYP2S1	.
0	0	0.311103929	0.013869976	VEGFA	.
0	0	0.311103929	0.013869976	GSTA1	.
0	0	0.311103929	0.013869976	GSTA1	.
0	0	0.311103929	0.013869976	SYCP1	.
0	0	0.311103929	0.013869976	NIPBL	.
0	0	0.311103929	0.013869976	SIK1	.
0	0	0.311103929	0.013869976	STX4	.
0	0	0.311103929	0.013869976	DDX3X	.
0	0	0.311103929	0.013869976	SCN4B	.
0	0	0.395825475	0.017605767	LIPE;APOA	.
0	0	0.395825475	0.017605767	INSIG1;PM	.
0	0	0.395825475	0.017605767	RIOK3;RIOI	.
0	0	0.395825475	0.017605767	PPA1;BPNT	.
0	0	0.445188679	0.018871879	TBX21;HES	.
0	0	0.445188679	0.018871879	ACVRL1;SD	.
0	0	0.445188679	0.018871879	NLGN3;IL1	.
0	0	0.445188679	0.018871879	PARP3;LTC	.
0	0	0.593040847	0.025048787	FAM111B;I	.
0	0	0.656308674	0.027494572	KDM4A;PA	.
0	0	0.66009034	0.026149414	FZD1;TENM	.
0	0	0.38416136	0.015135838	DYNC1H1;I	.
0	0	0.38416136	0.015135838	KSR1;PDE7	.
0	0	0.38416136	0.015135838	FBXO4;PRK	.
0	0	0.38416136	0.015135838	ANKRD28;(	.
0	0	0.69577812	0.027129238	GALNT11;C	.
0	0	0.296945701	0.011446429	CYP2S1	.
0	0	0.296945701	0.011446429	CUL4A	.
0	0	0.474745187	0.018066323	CYP24A1;C	.
0	0	0.638237094	0.023308954	RANBP2;SU	.
0	0	0.373163766	0.013020063	POGZ;OIP5	.
0	0	0.373163766	0.013020063	CUL4A;GTF	.
0	0	0.373163766	0.013020063	SVIL;PRKCE	.
0	0	0.373163766	0.013020063	SEC61G;UE	.
0	0	0.373163766	0.013020063	PRKAG2;CF	.
0	0	0.633768052	0.021691954	RFLNB;XYL	.
0	0	0.602764649	0.020533897	NPC1;GALN	.
0	0	0.284018624	0.009469736	H1-4	.
0	0	0.284018624	0.009469736	INTS6	.
0	0	0.284018624	0.009469736	TTLL7	.
0	0	0.284018624	0.009469736	GCLC	.
0	0	0.362777149	0.011206017	SRSF12;WI	.
0	0	0.41670012	0.012759398	GABRR2;CI	.
0	0	0.582232042	0.017718775	SLC9A3R1;	.

0	0	0.53097699	0.015527394	EIF4A1;RPS	.
0	0	0.54926276	0.016051758	CD74;DYNC	.
0	0	0.272168803	0.007851956	BPNT1	.
0	0	0.272168803	0.007851956	GJB6	.
0	0	0.272168803	0.007851956	NRP1	.
0	0	0.272168803	0.007851956	SEC16B	.
0	0	0.272168803	0.007851956	NLGN3	.
0	0	0.272168803	0.007851956	CALM1	.
0	0	0.450111298	0.012693864	POLB;KAT5	.
0	0	0.479801626	0.013250379	CUL4A;POL	.
0	0	0.407995283	0.011199256	CUL4A;AND	.
0	0	0.407995283	0.011199256	WNT2B;SO	.
0	0	0.407995283	0.011199256	SEH1L;CHM	.
0	0	0.407995283	0.011199256	SEH1L;CHM	.
0	0	0.407995283	0.011199256	CREBBP;PD	.
0	0	0.352951971	0.009649391	TREX1;LIG4	.
0	0	0.352951971	0.009649391	OIP5;H3-3A	.
0	0	0.352951971	0.009649391	CUL4A;GTF	.
0	0	0.352951971	0.009649391	SCN4B;KCN	.
0	0	0.524843398	0.014106446	RPS9;RPS7	.
0	0	0.50184534	0.013212511	FLCN;PLK3	.
0	0	0.442456699	0.011280891	LTB4R2;NM	.
0	0	0.261266968	0.006523816	ANXA1	.
0	0	0.261266968	0.006523816	PARP3	.
0	0	0.261266968	0.006523816	EIF6	.
0	0	0.261266968	0.006523816	CREBL2	.
0	0	0.261266968	0.006523816	CYP2S1	.
0	0	0.261266968	0.006523816	INTS6	.
0	0	0.399645745	0.009829854	CABYR;DNA	.
0	0	0.343643908	0.008312662	RTP4;GNAT	.
0	0	0.435057254	0.01002328	SARS1;MET	.
0	0	0.532356005	0.012196817	PLK3;FLCN	.
0	0	0.391630189	0.008627762	RAMP2;PA	.
0	0	0.251203736	0.005430403	ARHGAP17	.
0	0	0.251203736	0.005430403	FYN	.
0	0	0.251203736	0.005430403	LYST	.
0	0	0.251203736	0.005430403	NUSAP1	.
0	0	0.251203736	0.005430403	GLRX	.
0	0	0.334813181	0.007163988	RTP4;GNAT	.
0	0	0.507260435	0.01055545	NIPBL;SFPC	.
0	0	0.459448534	0.009547179	CLIC5;GAB	.
0	0	0.383928968	0.007572468	SEH1L;CHM	.
0	0	0.501657073	0.009576322	CD74;DYNC	.
0	0	0.326423991	0.006176308	MBD2;ACT	.
0	0	0.326423991	0.006176308	NR4A3;CO	.
0	0	0.241885928	0.004527943	ATP5PB	.
0	0	0.241885928	0.004527943	PIGH	.

0	0	0.241885928	0.004527943	NR1H3	.
0	0	0.477254508	0.008765652	CLIC5;RIPC	.
0	0	0.376523948	0.006646001	TIMM17A;	.
0	0	0.687163392	0.012033636	GALNT11;A	.
0	0	0.414268337	0.00702254	SLC39A8;U	.
0	0	0.471477144	0.007904711	ATAD1;PPI	.
0	0	0.318444029	0.005326582	SLFN11;AL	.
0	0	0.318444029	0.005326582	TBX21;DLL	.
0	0	0.233233678	0.003781364	TREX1	.
0	0	0.233233678	0.003781364	CALM1	.
0	0	0.727311487	0.011573897	HDAC4;NL(	.
0	0	0.369398362	0.005832612	PARP3;NSM	.
0	0	0.440745693	0.006861672	SFPQ;NSM	.
0	0	0.310844066	0.00459517	RBPJ;SMAI	.
0	0	0.310844066	0.00459517	ZNF207;CE	.
0	0	0.225178135	0.003162432	OIP5	.
0	0	0.225178135	0.003162432	OIP5	.
0	0	0.225178135	0.003162432	HSD17B1	.
0	0	0.225178135	0.003162432	TET2	.
0	0	0.225178135	0.003162432	ARL13B	.
0	0	0.46033023	0.006422084	CLIC5;RIPC	.
0	0	0.568369941	0.007730366	GGT5;RPS9	.
0	0	0.395369322	0.004911153	NUDT7;AB	.
0	0	0.210626186	0.002220542	WNT2B	.
0	0	0.210626186	0.002220542	OIP5	.
0	0	0.210626186	0.002220542	PIGH	.
0	0	0.210626186	0.002220542	TIMM17A	.
0	0	0.290070833	0.002954984	TBX21;DLL	.
0	0	0.343396226	0.003457877	RAMP2;PA	.
0	0	0.343396226	0.003457877	PECAM1;C	.
0	0	0.647867057	0.006265272	H2AW;BTG	.
0	0	0.204032334	0.001863992	CNOT7	.
0	0	0.283748544	0.002551769	CEBPG;SIR	.
0	0	0.19783811	0.001566366	CCDC65	.
0	0	0.19783811	0.001566366	PARP3	.
0	0	0.515436856	0.003900576	EGR2;NIPB	.
0	0	0.192008251	0.001317579	POLB	.
0	0	0.192008251	0.001317579	CNOT7	.
0	0	0.192008251	0.001317579	SNX10	.
0	0	0.3573124	0.00211669	PPP1R10;S	.
0	0	0.561437496	0.002978402	TSFM;MRP	.
0	0	0.383463657	0.002001229	SDHAF2;C(	.
0	0	0.383463657	0.002001229	RPS9;RPS7	.
0	0	0.181320178	9.35E-04	KIF5C	.
0	0	0.176409441	7.88E-04	OIP5	.
0	0	0.171757164	6.65E-04	BCOR	.
0	0	0.171757164	6.65E-04	ALYREF	.

0	0	0.296415094	0.001061482	NLGN3;FZD	.
0	0	0.167343466	5.62E-04	PIGH	.
0	0	0.167343466	5.62E-04	IFT52	.
0	0	0.430589448	0.001342306	POLB;PSM	.
0	0	0.521785667	0.001584515	FZD1;NRP1	.
0	0	0.32591544	9.03E-04	NEK6;ZNF2	.
0	0	0.232944441	5.94E-04	ACTN2;PTK	.
0	0	0.159161976	4.02E-04	MRPS15	.
0	0	0.49170851	0.001160897	SEC16B;DY	.
0	0	0.30665512	4.89E-04	KCNS1;ACT	.
0	0	0.382997644	5.52E-04	CAST;NLGN	.
0	0	0.138795289	1.49E-04	POLB	.
0	0	0.532673288	5.20E-04	DFFB;TCF7	.
0	0	0.135895865	1.27E-04	ATP5PB	.
0	0	0.12787981	7.77E-05	PPARD	.
0	0	0.260430351	7.62E-05	TSFM;MRP	.
0	0	0.114379085	2.97E-05	FOXRED1	.
0	0	0.114379085	2.97E-05	FOXRED1	.
0	0	0.425044115	4.40E-05	NLGN3;CN	.
0	0	0.156921916	1.25E-05	COPZ1;TAF	.
0	0	0.094421492	4.66E-06	SDHAF2	.
0	0	0.149672429	7.24E-06	TSFM;MRP	.
0	0	0.093067227	4.03E-06	SDHAF2	.
0	0	0.138470429	2.94E-06	MRPS15;ET	.
0	0	0.134164505	2.07E-06	GNAL;C5AI	.
0	0	0.404625237	5.13E-06	NLGN3;STX	.
0	0	0.12630515	1.13E-06	TSFM;MRP	.
0	0	0.07395362	4.78E-07	MRPS15	.

ns were highlighted)

Term	Overlap	P-value	Adjusted P-value	Old P-value	Old Adjusted P-value
TNF signaling pathway	57/112	1.20E-21	2.76E-19	0	0
Lipid and atherosclerosis	84/215	1.79E-21	2.76E-19	0	0
NOD-like receptor signaling pathw	73/181	8.96E-20	9.23E-18	0	0
NF-kappa B signaling pathway	52/104	1.99E-19	1.54E-17	0	0
Hepatitis B	67/162	5.91E-19	3.65E-17	0	0
C-type lectin receptor signaling pat	51/104	1.31E-18	6.74E-17	0	0
Pertussis	42/76	4.68E-18	2.07E-16	0	0
Influenza A	68/172	5.73E-18	2.21E-16	0	0
Toll-like receptor signaling pathwa	49/104	5.03E-17	1.73E-15	0	0
Measles	58/139	8.19E-17	2.53E-15	0	0
Tuberculosis	68/180	9.41E-17	2.64E-15	0	0
Epstein-Barr virus infection	73/202	1.19E-16	3.05E-15	0	0
Chemokine signaling pathway	70/192	2.95E-16	6.99E-15	0	0
Coronavirus disease	79/232	3.39E-16	6.99E-15	0	0
Osteoclast differentiation	54/127	3.53E-16	6.99E-15	0	0
Necroptosis	62/159	3.62E-16	6.99E-15	0	0
Kaposi sarcoma-associated herpes	70/193	4.04E-16	7.34E-15	0	0
Human cytomegalovirus infection	75/225	6.94E-15	1.19E-13	0	0
Toxoplasmosis	48/112	1.06E-14	1.72E-13	0	0
JAK-STAT signaling pathway	60/162	1.71E-14	2.64E-13	0	0
Pathways in cancer	135/531	1.90E-14	2.80E-13	0	0
Leishmaniasis	38/77	2.43E-14	3.42E-13	0	0
Cytokine-cytokine receptor interac	87/295	1.59E-13	2.14E-12	0	0
Shigellosis	76/246	4.06E-13	5.23E-12	0	0
Th17 cell differentiation	44/107	7.81E-13	9.65E-12	0	0
Viral protein interaction with cytol	42/100	1.10E-12	1.31E-11	0	0
Yersinia infection	51/137	1.24E-12	1.41E-11	0	0
IL-17 signaling pathway	40/94	2.28E-12	2.52E-11	0	0
Salmonella infection	73/249	1.93E-11	2.00E-10	0	0
MAPK signaling pathway	82/294	1.94E-11	2.00E-10	0	0
Apoptosis	50/142	2.23E-11	2.23E-10	0	0
Th1 and Th2 cell differentiation	38/92	2.39E-11	2.31E-10	0	0
Chagas disease	40/102	4.98E-11	4.66E-10	0	0
Inflammatory bowel disease	30/65	1.09E-10	9.86E-10	0	0
PD-L1 expression and PD-1 checkp	36/89	1.62E-10	1.43E-09	0	0
AGE-RAGE signaling pathway in dia	38/100	4.43E-10	3.71E-09	0	0
Legionellosis	27/57	4.45E-10	3.71E-09	0	0
RIG-I-like receptor signaling pathw	30/70	1.02E-09	8.26E-09	0	0
Hepatitis C	50/157	1.27E-09	1.01E-08	0	0
Pathogenic Escherichia coli infectic	58/197	1.85E-09	1.43E-08	0	0
FoxO signaling pathway	44/131	1.93E-09	1.45E-08	0	0
Viral carcinogenesis	59/203	2.31E-09	1.70E-08	0	0
Human T-cell leukemia virus 1 infe	61/219	7.53E-09	5.41E-08	0	0
Fluid shear stress and atherosclero	43/139	4.62E-08	3.25E-07	0	0

Malaria	22/50	9.63E-08	6.61E-07	0	0
Human immunodeficiency virus 1 i	56/212	2.17E-07	1.46E-06	0	0
Transcriptional misregulation in ca	51/192	6.17E-07	4.06E-06	0	0
African trypanosomiasis	17/37	1.31E-06	8.44E-06	0	0
Epithelial cell signaling in Helicoba	25/70	1.60E-06	1.01E-05	0	0
Rheumatoid arthritis	30/93	1.81E-06	1.12E-05	0	0
Cytosolic DNA-sensing pathway	23/63	2.68E-06	1.62E-05	0	0
Neurotrophin signaling pathway	35/119	2.93E-06	1.74E-05	0	0
HIF-1 signaling pathway	32/109	8.00E-06	4.65E-05	0	0
Growth hormone synthesis, secret	34/119	8.13E-06	4.65E-05	0	0
Chronic myeloid leukemia	25/76	8.71E-06	4.89E-05	0	0
Non-small cell lung cancer	24/72	1.02E-05	5.56E-05	0	0
Rap1 signaling pathway	51/210	1.03E-05	5.56E-05	0	0
Notch signaling pathway	21/59	1.14E-05	6.08E-05	0	0
Fc gamma R-mediated phagocytos	29/97	1.42E-05	7.46E-05	0	0
Amoebiasis	30/102	1.46E-05	7.50E-05	0	0
Platelet activation	34/124	2.12E-05	1.08E-04	0	0
Complement and coagulation casc	26/85	2.50E-05	1.24E-04	0	0
Neutrophil extracellular trap forma	46/189	2.57E-05	1.26E-04	0	0
Pancreatic cancer	24/76	2.82E-05	1.36E-04	0	0
B cell receptor signaling pathway	25/81	3.00E-05	1.43E-04	0	0
Fc epsilon RI signaling pathway	22/68	3.96E-05	1.84E-04	0	0
Small cell lung cancer	27/92	4.00E-05	1.84E-04	0	0
Human papillomavirus infection	70/331	4.29E-05	1.95E-04	0	0
Proteoglycans in cancer	48/205	5.01E-05	2.24E-04	0	0
Adipocytokine signaling pathway	22/69	5.10E-05	2.25E-04	0	0
Leukocyte transendothelial migrat	31/114	5.72E-05	2.49E-04	0	0
T cell receptor signaling pathway	29/104	5.97E-05	2.56E-04	0	0
Prolactin signaling pathway	22/70	6.51E-05	2.76E-04	0	0
Natural killer cell mediated cytoto	34/131	7.20E-05	3.01E-04	0	0
Acute myeloid leukemia	21/67	9.89E-05	4.08E-04	0	0
Non-alcoholic fatty liver disease	38/155	1.06E-04	4.29E-04	0	0
Insulin resistance	29/108	1.25E-04	5.00E-04	0	0
Ferroptosis	15/41	1.41E-04	5.57E-04	0	0
Sphingolipid signaling pathway	30/119	3.22E-04	0.001259411	0	0
GnRH signaling pathway	25/93	3.48E-04	0.001343723	0	0
Focal adhesion	44/201	4.91E-04	0.001871406	0	0
Phagosome	35/152	6.81E-04	0.002565683	0	0
Inflammatory mediator regulation	25/98	8.11E-04	0.003019282	0	0
Protein processing in endoplasmic	38/171	8.50E-04	0.003126036	0	0
Apelin signaling pathway	32/137	8.74E-04	0.003141814	0	0
Insulin signaling pathway	32/137	8.74E-04	0.003141814	0	0
VEGF signaling pathway	17/59	0.001285144	0.004564476	0	0
ErbB signaling pathway	22/85	0.00132402	0.004649115	0	0
Colorectal cancer	22/86	0.001560102	0.005416533	0	0
Gastric acid secretion	20/76	0.001730431	0.005941146	0	0
Bladder cancer	13/41	0.001806872	0.006135422	0	0

Cellular senescence	34/156	0.002176199	0.00730919	0	0
PI3K-Akt signaling pathway	66/354	0.002466201	0.00819415	0	0
p53 signaling pathway	19/73	0.002555804	0.008401525	0	0
Parathyroid hormone synthesis, se	25/106	0.00264379	0.008599274	0	0
Relaxin signaling pathway	29/129	0.00274344	0.008830448	0	0
Renal cell carcinoma	18/69	0.003186985	0.010152356	0	0
Prostate cancer	23/97	0.003566402	0.011245085	0	0
Adherens junction	18/71	0.004435084	0.013842838	0	0
Hematopoietic cell lineage	23/99	0.00467053	0.014431938	0	0
mTOR signaling pathway	32/154	0.006151656	0.018820411	0	0
Aldosterone synthesis and secretic	22/98	0.008498157	0.025494471	0	0
Choline metabolism in cancer	22/98	0.008498157	0.025494471	0	0
Calcium signaling pathway	45/240	0.009883261	0.029364689	0	0
Oxytocin signaling pathway	31/154	0.010982979	0.032310195	0	0
Phospholipase D signaling pathwa	30/148	0.011083756	0.032310195	0	0
Staphylococcus aureus infection	21/95	0.011895661	0.03435289	0	0
Ras signaling pathway	43/232	0.013903582	0.039779692	0	0
Type II diabetes mellitus	17137	0.014619736	0.041444939	0	0
Glioma	17/75	0.017475871	0.048649046	0	0
Thyroid hormone synthesis	17/75	0.017475871	0.048649046	0	0
Regulation of actin cytoskeleton	40/218	0.020030366	0.055262348	0	0
MicroRNAs in cancer	54/310	0.021156267	0.057852092	0	0
Endocytosis	45/252	0.02239656	0.060706466	0	0
Antigen processing and presentati	17/78	0.025187069	0.067676559	0	0
Pancreatic secretion	21/102	0.025544643	0.068045644	0	0
Thyroid hormone signaling pathwa	24/121	0.027215693	0.071877344	0	0
Breast cancer	28/147	0.029768873	0.077954082	0	0
Cell adhesion molecules	28/148	0.032221539	0.083667693	0	0
Intestinal immune network for IgA	17838	0.046439139	0.119580783	0	0
Mineral absorption	13/60	0.048392494	0.123525522	0	0
Thyroid cancer	13759	0.048770595	0.123525522	0	0
Phosphatidylinositol signaling syste	19/97	0.050909266	0.126919854	0	0
Systemic lupus erythematosus	25/135	0.051325159	0.126919854	0	0
Type I diabetes mellitus	15980	0.051342983	0.126919854	0	0
Inositol phosphate metabolism	15/73	0.054017501	0.132471491	0	0
Allograft rejection	14124	0.056675255	0.136817608	0	0
Primary immunodeficiency	14124	0.056675255	0.136817608	0	0
Signaling pathways regulating pluri	26/143	0.057525927	0.137794664	0	0
Autophagy	25/137	0.059416554	0.141228577	0	0
Pathways of neurodegeneration	75/475	0.060334663	0.141390216	0	0
Mitophagy	14/68	0.060399704	0.141390216	0	0
SNARE interactions in vesicular tra	12267	0.062395717	0.144964486	0	0
Nitrogen metabolism	44698	0.064226289	0.148103906	0	0
Cholinergic synapse	21/113	0.067373637	0.154210769	0	0
Chemical carcinogenesis	40/239	0.070615443	0.159576803	0	0
Vascular smooth muscle contractic	24/133	0.07075088	0.159576803	0	0
Longevity regulating pathway	19/102	0.077421024	0.173355771	0	0

Glycosaminoglycan biosynthesis	19664	0.085155566	0.18930266	0	0
cAMP signaling pathway	36/216	0.08654631	0.19102007	0	0
Viral myocarditis	22251	0.09317742	0.203097441	0	0
Glycerophospholipid metabolism	18/98	0.093332805	0.203097441	0	0
Tryptophan metabolism	15585	0.096204173	0.207881745	0	0
Wnt signaling pathway	28/166	0.106396229	0.228308575	0	0
Circadian rhythm	44773	0.107352498	0.228771874	0	0
Aldosterone-regulated sodium rea	13728	0.108430678	0.229486845	0	0
Ubiquitin mediated proteolysis	24/140	0.11123807	0.233826963	0	0
cGMP-PKG signaling pathway	28/167	0.112397595	0.234667952	0	0
Arginine and proline metabolism	18537	0.118486103	0.244081373	0	0
Vibrio cholerae infection	18537	0.118486103	0.244081373	0	0
Herpes simplex virus 1 infection	75/498	0.130178799	0.266392377	0	0
Neomycin, kanamycin and gentam	44597	0.13373725	0.27094079	0	0
ABC transporters	16681	0.134155149	0.27094079	0	0
Bacterial invasion of epithelial cells	14/77	0.135513727	0.271023302	0	0
Pantothenate and CoA biosynthesi	44702	0.1359502	0.271023302	0	0
Estrogen signaling pathway	23/137	0.137930805	0.273209095	0	0
Arginine biosynthesis	44703	0.157821668	0.308651237	0	0
Histidine metabolism	44703	0.157821668	0.308651237	0	0
Salivary secretion	16/93	0.165180845	0.32101183	0	0
Hepatocellular carcinoma	27/168	0.167102137	0.322716003	0	0
Axon guidance	29/182	0.168594139	0.323575087	0	0
Glucagon signaling pathway	18/107	0.171065251	0.326291127	0	0
Tight junction	27/169	0.175101776	0.331941403	0	0
Proximal tubule bicarbonate reclar	44704	0.181010279	0.341049856	0	0
Vitamin B6 metabolism	44598	0.183530814	0.343703161	0	0
Graft-versus-host disease	15554	0.18580794	0.345871406	0	0
Spinocerebellar ataxia	23/143	0.189050741	0.349800472	0	0
Cocaine addiction	18142	0.194906332	0.358488431	0	0
Hypertrophic cardiomyopathy	15/90	0.208343277	0.37953648	0	0
Fatty acid biosynthesis	44669	0.208806477	0.37953648	0	0
Central carbon metabolism in canc	25903	0.212110295	0.383287024	0	0
Asthma	11475	0.221713185	0.398310316	0	0
Endometrial cancer	21459	0.234322679	0.418530104	0	0
Glycosphingolipid biosynthesis	16650	0.240972983	0.426426658	0	0
Melanoma	26634	0.241503771	0.426426658	0	0
RNA degradation	13/79	0.243887078	0.428188109	0	0
Lysosome	20/128	0.249242688	0.43511859	0	0
Long-term depression	22190	0.268392537	0.465917382	0	0
Long-term potentiation	24777	0.270717586	0.467328124	0	0
Carbohydrate digestion and absorp	17380	0.280438842	0.481420012	0	0
Arachidonic acid metabolism	22555	0.285979993	0.488219988	0	0
Amphetamine addiction	25508	0.304331178	0.516694142	0	0
Nicotinate and nicotinamide metal	12936	0.316671621	0.53448409	0	0
Morphine addiction	14/91	0.318268843	0.53448409	0	0
Pyrimidine metabolism	20699	0.322075196	0.537952624	0	0

Serotonergic synapse	17/113	0.327218677	0.542547848	0	0
Gastric cancer	22/149	0.328338018	0.542547848	0	0
Synaptic vesicle cycle	28825	0.3372244	0.553848417	0	0
Alzheimer disease	52/369	0.340659772	0.553848417	0	0
Mucin type O-glycan biosynthesis	13302	0.341434435	0.553848417	0	0
Cholesterol metabolism	18476	0.342346433	0.553848417	0	0
Progesterone-mediated oocyte ma	15/100	0.346117809	0.557033348	0	0
Purine metabolism	19/129	0.34877101	0.558395037	0	0
TGF-beta signaling pathway	14/94	0.364172339	0.577807777	0	0
Protein export	44674	0.364639119	0.577807777	0	0
beta-Alanine metabolism	44711	0.366505904	0.577807777	0	0
Gap junction	13/88	0.383648262	0.601763009	0	0
Dopaminergic synapse	19/132	0.388247557	0.605901491	0	0
Sulfur metabolism	44602	0.390542122	0.606419677	0	0
RNA polymerase	44712	0.39435065	0.609271754	0	0
Phenylalanine metabolism	44637	0.39662939	0.60974369	0	0
GABAergic synapse	13/89	0.399919616	0.611758224	0	0
Peroxisome	30286	0.404736581	0.614795261	0	0
Endocrine and other factor-regulat	19572	0.40588425	0.614795261	0	0
Hippo signaling pathway	23/163	0.408934683	0.616394229	0	0
Proteasome	16984	0.410992217	0.616488326	0	0
Adrenergic signaling in cardiomyoc	21/150	0.430893645	0.64321805	0	0
Other types of O-glycan biosynthes	17349	0.43383905	0.644501281	0	0
Taurine and hypotaurine metaboli	44603	0.439440316	0.649260495	0	0
Glycine, serine and threonine meta	14763	0.441244997	0.649260495	0	0
Glutamatergic synapse	16/114	0.445160893	0.651918085	0	0
Regulation of lipolysis in adipocyte	20302	0.448286414	0.652193711	0	0
Fructose and mannose metabolism	12175	0.449570422	0.652193711	0	0
Folate biosynthesis	44677	0.459199858	0.658941586	0	0
Maturity onset diabetes of the you	44677	0.459199858	0.658941586	0	0
Basal cell carcinoma	23255	0.460619361	0.658941586	0	0
Glycosaminoglycan degradation	44639	0.470849586	0.670472452	0	0
Melanogenesis	14/101	0.473686597	0.671418157	0	0
Sphingolipid metabolism	18080	0.479075535	0.675955892	0	0
Collecting duct acid secretion	44678	0.489719421	0.687833187	0	0
Cortisol synthesis and secretion	23986	0.499787379	0.698797738	0	0
Alcoholism	25/186	0.504506854	0.702218999	0	0
D-Glutamine and D-glutamate met	44566	0.509160816	0.705518799	0	0
Dilated cardiomyopathy	13/96	0.513463217	0.70830417	0	0
Phototransduction	44679	0.519500176	0.713446909	0	0
Ovarian steroidogenesis	18810	0.523272471	0.715447759	0	0
Starch and sucrose metabolism	13271	0.529494126	0.71933336	0	0
Parkinson disease	33/249	0.530770246	0.71933336	0	0
Bile secretion	33208	0.539322173	0.727731666	0	0
Prion disease	36/273	0.542584218	0.728950101	0	0
Alanine, aspartate and glutamate r	13636	0.55498094	0.742377102	0	0
Glycerolipid metabolism	22494	0.570799254	0.759674351	0	0

Caffeine metabolism	44567	0.574286772	0.759674351	0	0
Renin secretion	25447	0.575287372	0.759674351	0	0
Arrhythmogenic right ventricular c	28399	0.579506883	0.761989902	0	0
Cushing syndrome	20/155	0.58893817	0.771109722	0	0
Insulin secretion	31717	0.599743958	0.781944655	0	0
Galactose metabolism	11414	0.603392107	0.783395635	0	0
ECM-receptor interaction	32448	0.63130875	0.816210894	0	0
Glutathione metabolism	21002	0.645576197	0.830334537	0	0
Circadian entrainment	35765	0.647607195	0.830334537	0	0
Amyotrophic lateral sclerosis	46/364	0.662427986	0.84582747	0	0
Glycolysis / Gluconeogenesis	24685	0.679402154	0.857365159	0	0
Riboflavin metabolism	44569	0.679769188	0.857365159	0	0
Selenocompound metabolism	44609	0.679787909	0.857365159	0	0
Cell cycle	15/124	0.689072515	0.865542306	0	0
Biosynthesis of unsaturated fatty a	44647	0.71417653	0.889840919	0	0
Fatty acid elongation	44647	0.71417653	0.889840919	0	0
Autoimmune thyroid disease	19511	0.721833756	0.895769601	0	0
Protein digestion and absorption	12/103	0.728372401	0.900268287	0	0
Thermogenesis	28/232	0.733516171	0.903013931	0	0
Lysine degradation	23193	0.747299175	0.916331131	0	0
GnRH secretion	23559	0.762041721	0.926382381	0	0
One carbon pool by folate	44612	0.764490315	0.926382381	0	0
Steroid biosynthesis	44612	0.764490315	0.926382381	0	0
Pentose phosphate pathway	44650	0.779684168	0.940497054	0	0
PPAR signaling pathway	27242	0.782225705	0.940497054	0	0
Ether lipid metabolism	18019	0.796336069	0.953751339	0	0
Cysteine and methionine metaboli	18384	0.81074202	0.967255923	0	0
Mannose type O-glycan biosynthes	44615	0.829011825	0.985248668	0	0
Fatty acid degradation	15797	0.840055253	0.990393154	0	0
Non-homologous end-joining	44574	0.842865744	0.990393154	0	0
Retrograde endocannabinoid signa	16/148	0.842955985	0.990393154	0	0
Vasopressin-regulated water reabs	16163	0.852937299	0.994942981	0	0
mRNA surveillance pathway	36069	0.853268252	0.994942981	0	0
alpha-Linolenic acid metabolism	44617	0.862690762	0.999671977	0	0
Ribosome biogenesis in eukaryotes	11/108	0.863794233	0.999671977	0	0
RNA transport	20/186	0.871216099	0.999994349	0	0
Tyrosine metabolism	13210	0.873699938	0.999994349	0	0
Hedgehog signaling pathway	20576	0.880788178	0.999994349	0	0
Thiamine metabolism	44576	0.881812547	0.999994349	0	0
AMPK signaling pathway	12/120	0.886925275	0.999994349	0	0
Primary bile acid biosynthesis	44578	0.911108712	0.999994349	0	0
Linoleic acid metabolism	47150	0.912485033	0.999994349	0	0
Nicotine addiction	14671	0.914714921	0.999994349	0	0
Drug metabolism	10/108	0.920966686	0.999994349	0	0
Glyoxylate and dicarboxylate meta	10990	0.921970773	0.999994349	0	0
Other glycan degradation	44579	0.922909932	0.999994349	0	0
Fat digestion and absorption	15766	0.937069307	0.999994349	0	0

Diabetic cardiomyopathy	20/203	0.94363422	0.999994349	0	0
Spliceosome	14/150	0.944704931	0.999994349	0	0
Base excision repair	12086	0.944934639	0.999994349	0	0
Basal transcription factors	16497	0.948817998	0.999994349	0	0
Terpenoid backbone biosynthesis	44583	0.956396126	0.999994349	0	0
Pyruvate metabolism	17227	0.958495182	0.999994349	0	0
Amino sugar and nucleotide sugar	17593	0.962662976	0.999994349	0	0
Oocyte meiosis	11/129	0.964092285	0.999994349	0	0
Vitamin digestion and absorption	44585	0.967207762	0.999994349	0	0
Various types of N-glycan biosynth	14277	0.973031225	0.999994349	0	0
Neuroactive ligand-receptor intera	34/341	0.974180439	0.999994349	0	0
Glycosylphosphatidylinositol (GPI)-	44587	0.975339247	0.999994349	0	0
Taste transduction	31564	0.978229476	0.999994349	0	0
Cardiac muscle contraction	31929	0.980089605	0.999994349	0	0
Aminoacyl-tRNA biosynthesis	24198	0.981389503	0.999994349	0	0
Porphyrin and chlorophyll metabo	15738	0.983412216	0.999994349	0	0
Ascorbate and aldarate metabolisr	44591	0.986054023	0.999994349	0	0
Citrate cycle (TCA cycle)	44591	0.986054023	0.999994349	0	0
Nucleotide excision repair	17199	0.9898646	0.999994349	0	0
Valine, leucine and isoleucine degr	17564	0.991047253	0.999994349	0	0
Metabolism of xenobiotics by cyto	27851	0.993428764	0.999994349	0	0
DNA replication	13150	0.994069791	0.999994349	0	0
Huntington disease	26/306	0.996537216	0.999994349	0	0
Oxidative phosphorylation	8/133	0.99784414	0.999994349	0	0
Steroid hormone biosynthesis	22313	0.998262528	0.999994349	0	0
N-Glycan biosynthesis	18264	0.999192586	0.999994349	0	0
Retinol metabolism	24869	0.999292156	0.999994349	0	0
Fanconi anemia pathway	19725	0.9995425	0.999994349	0	0
Ribosome	7/158	0.999941635	0.999994349	0	0
Olfactory transduction	5/440	0.999994349	0.999994349	0	0

Odds Ratio	Combined Score	Genes
6.903235747	332.5341705	CSF1;TNFAIP3;TNF;CXCL2;ICAM1;IKBKB;CASP7;CASP8;CASP3;MAP3K8;JUNB;M
4.297106725	205.2890892	ERO1A;CD40;CXCL8;NCF1;NCF4;FASLG;TNF;CXCL2;ICAM1;IKBKB;PYCARD;CASF
4.516390324	198.0833205	CXCL8;TNFAIP3;ANTXR2;TNF;CXCL2;PYCARD;IKBKB;PANX1;PSTPIP1;CASP8;NA
6.649365629	286.3163338	CD40;CXCL8;TNFAIP3;TNF;CXCL2;ICAM1;TNFSF13B;IKBKB;PLAU;TRIM25;LBP;E
4.705027069	197.4828464	CDKN1A;CXCL8;DDX3X;FASLG;TNF;IFIH1;IKBKB;CASP8;CASP3;JAK2;IKBKE;JAK3
6.395617305	263.3543186	LSP1;TNF;PYCARD;IKBKB;CASP8;IL12B;IL12A;IKBKE;IL10;FCER1G;KSR1;PRKCD;F
8.190979341	326.841345	CXCL8;ITGAM;C1S;C1R;LY96;NOD1;TNF;RELA;C2;PYCARD;C3;C4A;CASP7;MAPK
4.361419432	173.1518025	CIITA;CXCL8;CALCOCO2;ADAR;FASLG;TNF;ACTB;ACTG1;ICAM1;PYCARD;IFIH1;I
5.916129032	222.0222883	CD40;CXCL8;CD80;TNF;IKBKB;CASP8;IL12B;IL12A;MAP3K8;LBP;IKBKE;IFNAR2;I
4.764280787	176.4712071	CDKN1B;TNFAIP3;ADAR;FASLG;IFIH1;IKBKB;CCND2;CASP8;CASP3;IL12B;IL12A;
4.0480105	149.3806289	CIITA;ITGAM;LSP1;TCIRG1;TNF;FCGR3A;CASP8;LAMP1;CASP3;LAMP2;IL12B;IL1
3.776557899	138.4895053	CD40;CDKN1A;CDKN1B;TNFAIP3;RBPJ;ITGAL;TNF;ICAM1;IKBKB;CCND2;CASP8;
3.826247279	136.8244908	CXCL8;NCF1;CXCL13;CXCL2;PIK3CG;CRKL;CXCL16;IKBKB;PREX1;RAC2;CCR6;CCI
3.449086135	122.8590688	NRP1;CSF3;CXCL8;RPLP1;F13A1;CGAS;ADAR;TNF;IFIH1;IKBKB;C4A;C3AR1;IL12I
4.91651689	174.9307634	CSF1;NCF1;NCF4;TNF;SIRPB1;IKBKB;FCGR3A;SIRPA;JUNB;JAK1;IFNAR2;IL1R1;IF
4.255412272	151.3010884	H2AW;TNFAIP3;FASLG;PYGM;TNF;PYCARD;CASP8;FTH1;CAPN2;TNFSF10;JAK2;
3.79491925	134.5140861	CDKN1A;CXCL8;CXCL2;PIK3CG;ICAM1;IKBKB;PREX1;ZFP36;CASP8;CASP3;CCR5;
3.335337471	108.7352046	CDKN1A;CXCL8;CGAS;FASLG;TNF;CRKL;IKBKB;CASP8;CASP3;RAC2;ITGAV;CCR5;
4.975911708	160.1119006	CD40;CIITA;LY96;XIAP;TNF;PIK3R6;PIK3CG;RELA;PIK3R5;IKBKB;MAPK8;SOCS1;(
3.912116331	124.0213913	CSF3;CDKN1A;IL23R;IL27RA;CCND2;PIM1;IL12B;IL12A;JAK2;IL6R;JAK3;IL13RA1
2.294976172	72.50532224	IL23R;ITGA2B;CRKL;FRAT1;RASSF1;FRAT2;CCND2;RASSF5;PIM1;IL12B;IL12A;IL(
6.449026818	202.1610444	ITGAM;NCF1;NCF4;PTGS2;TNF;RELA;C3;FCGR3A;IL12B;IL12A;JAK2;JAK1;IL10;JU
2.793732013	82.3263216	ACVRL1;IL1RN;CD40;CSF3;CXCL8;CSF1;IL23R;IL27;FASLG;IL1RAP;CXCL13;TNF;C
2.979871716	85.0218662	CXCL8;CALCOCO2;UBE2D1;CGAS;TNF;ACTB;HK2;CRKL;ACTG1;IKBKB;PYCARD;H
4.626816818	128.9868547	IL23R;IL1RAP;IL2RG;HIF1A;RELA;IL27RA;IKBKB;MAPK8;TBX21;IL21R;STAT6;JAK
4.79495239	132.0219491	CCL14;CXCL8;CSF1;IL20RA;CXCR4;CXCL13;IL2RG;TNF;CXCL2;IL18RAP;CCL8;CXC
3.933964035	107.8667528	CXCL8;TNF;ACTB;ACTG1;CRKL;PYCARD;IKBKB;RAC2;MAP2K3;IL10;IL18;RHOG;T
4.90226928	131.4114428	CSF3;CXCL8;TRAF3IP2;TNFAIP3;PTGS2;CXCL2;TNF;RELA;HSP90B1;IKBKB;MAPK
2.760489341	68.09880583	CXCL8;TNF;ACTB;PIK3CG;ACTG1;IKBKB;PYCARD;CASP7;CASP8;KIF5C;CASP3;TU
2.57786413	63.58813302	FLT1;CSF1;FLT4;FASLG;IL1RAP;AREG;TNF;DUSP16;CRKL;ELK4;IKBKB;DUSP10;CA
3.602657469	88.35297598	FASLG;TNF;ACTB;ACTG1;LMNB1;IKBKB;CASP7;CASP8;CASP6;CASP3;CAPN2;TN
4.653593938	113.812853	RBPJL;NOTCH3;MAML2;RBPJ;IL2RG;DLL1;RELA;IKBKB;MAPK8;TBX21;STAT4;IL1
4.26774317	101.2442283	CXCL8;SERPINE1;FASLG;TNF;RELA;C3;IKBKB;MAPK8;CASP8;CCL3;IL12B;CCL2;IL
5.657208213	129.7983209	IL23R;NOD2;IL2RG;TNF;RELA;IL18RAP;TBX21;IL21R;STAT4;IL12B;IL12A;STAT6;
4.488677082	101.189453	CD274;HIF1A;RELA;IKBKB;JAK2;JAK1;MAP2K3;BATF2;BATF3;JUN;TICAM2;IFNG
4.051255166	87.2498826	CDKN1B;CXCL8;SERPINE1;TNF;RELA;ICAM1;MAPK8;CASP3;PIM1;PLCG2;CCL2;J
5.934996192	127.8026677	CXCL8;ITGAM;NLRC4;CXCL2;TNF;RELA;PYCARD;C3;CASP7;CASP8;CASP3;IL12B;
4.948627526	102.4763668	CXCL8;DDX3X;TNF;TANK;RELA;IFIH1;IKBKB;MAPK8;CASP8;DHX58;IL12B;TRIM2
3.094919234	63.38833755	CDKN1A;CD81;FASLG;TNF;IKBKB;CASP8;CASP3;IKBKE;JAK1;IFNAR2;RSAD2;DDX
2.766981328	55.63967986	CXCL8;FASLG;TNF;ACTB;ACTG1;IKBKB;PYCARD;CASP7;CASP8;CASP3;TUBB1;CA
3.345801227	67.14010984	CDKN1A;PRKAA1;CDKN1B;FBXO25;AGAP2;PRKAG2;FASLG;NLK;STK4;IKBKB;MA
2.717213334	54.03042628	CDKN1A;CDKN1B;DDX3X;GTF2B;HDAC11;RBPJ;POLB;CCND2;CASP8;CASP3;CCF
2.560285298	47.8901587	NRP1;CD40;CDKN1A;CRTC2;SLC2A1;ITGAL;TNF;ETS2;ICAM1;ELK4;IKBKB;POLB;
2.96054039	50.0021337	PRKAA1;NCF1;SDC4;SRC;ITGA2B;TNF;ACTB;RELA;ACTG1;ICAM1;HSP90B1;IKBK

5.172096433	83.56035219	IL10;CD40;CSF3;CXCL8;GYPC;CD81;IL18;ITGAL;TNF;SELE;ICAM1;SELP;IL6;IFNG;
2.376252678	36.45869742	CGAS;FASLG;TNF;CRKL;IKBKB;CASP8;CASP3;RAC2;CCR5;B2M;MAP2K3;PDIA3;F
2.391793547	34.1981952	CD40;CDKN1A;CDKN1B;CXCL8;FLT1;ITGAM;CCNT1;JMJD1C;ELK4;HHEX;CCND2
5.587234446	75.67836758	IL10;PRKCB;IL18;FASLG;TNF;SELE;ICAM1;IL6;IFNG;IL1B;TLR9;IL12B;FAS;IL12A;I
3.657618806	48.81197434	CXCL8;SRC;NOD1;TCIRG1;CXCL2;RELA;IKBKB;MAPK8;PAK1;CXCR1;CASP3;CXCR
3.137810214	41.48071425	CXCL8;FLT1;CSF1;CD80;TCIRG1;ITGAL;CXCL2;TNF;ICAM1;TNFSF13B;CCL3;CCL2
3.78384981	48.54392195	ZBP1;RIPK3;DDX58;TREX1;IL18;CGAS;ADAR;RELA;NFKB1;IKBKB;PYCARD;NFKBI
2.747485358	35.00245914	FASLG;PSEN1;RELA;CRKL;RAP1B;IKBKB;MAPK8;IRAK2;ARHGDIB;PLCG2;SH2B2;
2.738322342	32.13789536	CDKN1A;PFKFB3;CDKN1B;FLT1;SERPINE1;SLC2A1;ENO1;ENO3;HIF1A;HK2;RELA
2.636426117	30.89892338	ITPR1;ADCY4;ITPR2;ADCY8;ADCY7;CRKL;SOCS3;MAPK8;SOCS1;PLCG2;JAK2;JUI
3.226191542	37.58787459	CDKN1A;CDKN1B;CTBP2;RELA;CRKL;IKBKB;E2F2;E2F3;BAK1;STAT5A;STAT5B;SI
3.290034234	37.82862754	RET;STAT5A;STAT5B;CDKN1A;GADD45B;PRKCB;STAT3;TGFA;BRAF;STK4;GADD
2.118805563	24.34101572	DOCK4;FLT1;ITGAM;CSF1;FLT4;ITGA2B;ITGAL;ACTB;CRKL;ACTG1;SIPA1L1;RASS
3.634308511	41.36191225	TLE4;RBPJL;TLE3;NOTCH3;CREBBP;MAML2;DTX3L;CTBP2;NOTCH4;PSEN1;RBP
2.808302322	31.33950978	NCF1;CRKL;FCGR3A;PAK1;INPP5D;PLCG2;RAC2;PIP5K1B;LYN;VASP;MARCKSL1;
2.744154276	30.55993772	SERPINB10;CXCL8;ITGAM;CD1D;TNF;CXCL2;RELA;CASP3;IL12B;IL12A;CD14;IL1
2.489236774	26.78325742	ROCK1;SRC;ITGA2B;ITPR1;ADCY4;ITPR2;RASGRP2;ADCY8;ADCY7;ACTB;ARHGA
2.900053551	30.73357056	CFD;CPB2;ITGAM;C1S;C1R;SERPINE1;C5AR1;F13A1;C2;C3;C4A;C7;PLAU;C3AR1
2.122805465	22.44006512	HDAC4;H2AW;ITGAM;SELPLG;NCF1;SRC;HDAC11;ITGA2B;NCF4;C5AR1;ITGAL;A
3.03625245	31.80461572	CDKN1A;SMAD3;GADD45B;STAT1;STAT3;TGFA;BRAF;TGFBR1;RELA;NFKB1;GAI
2.937289356	30.59088823	CD81;DAPP1;MALT1;RELA;IKBKB;INPP5D;RAC2;PLCG2;LYN;JUN;CD72;PRKCB;F
3.144960587	31.87702283	MAP2K3;LYN;FCER1G;PLA2G4A;GAB2;MAPK14;TNF;VAV1;MAPK13;MAPK11;M
2.733692659	27.68623255	CDKN1A;CDKN1B;MAX;ITGA2B;XIAP;PTGS2;RELA;IKBKB;CASP3;E2F2;ITGAV;E2
1.774081342	17.84272792	CDKN1A;CDKN1B;WNT2B;MAML2;ITGA2B;FASLG;TCIRG1;RBPJ;TNF;IKBKB;LFN
2.017482304	19.97800628	CDKN1A;DDX5;WNT2B;SDC4;ROCK1;SRC;PXN;ITPR1;ITPR2;FASLG;HIF1A;TNF;A
3.07786862	30.42323038	PRKAA1;STAT3;SLC2A1;ACSL6;PRKAG2;ACSL5;ACSL4;TRAF2;TNFRSF1B;TNF;PR
2.459191457	24.02439151	ITGAM;NCF1;ROCK1;NCF4;PXN;CXCR4;ITGAL;ACTB;ARHGAP35;ACTG1;ICAM1;
2.545162602	24.75577399	TNF;MALT1;RELA;IKBKB;MAPK8;PAK1;MAP3K8;FYN;IL10;JUN;FOS;MAPK14;NF
3.013572153	29.04999916	STAT5A;STAT5B;CISH;SRC;STAT1;STAT3;FOS;MAPK14;RELA;NFKB1;MAPK13;SC
2.308664281	22.02257242	FASLG;ITGAL;TNF;ICAM1;FCGR3A;PAK1;CASP3;SH3BP2;TNFSF10;PLCG2;RAC2;
3.000867253	27.67160549	STAT5A;STAT5B;TCF7L2;ITGAM;BCL2A1;CEBPE;STAT3;BRAF;DUSP6;RELA;NFKB
2.139987907	19.595052	PRKAA1;CXCL8;PRKAG2;FASLG;TNF;COX7A1;RELA;IKBKB;SOCS3;CASP7;MAPK8
2.415734023	21.71679581	CRTC2;PRKAA1;SLC2A1;PRKAG2;PYGM;TNF;RELA;IKBKB;SOCS3;MAPK8;PPARG
3.788053304	33.59956099	STEAP3;NCOA4;SLC11A2;ACSL6;ACSL5;CYBB;SLC3A2;ACSL4;SAT1;GCLC;MAP1L
2.217805326	17.83338273	ASAH1;ROCK1;TNF;RELA;MAPK8;SPTLC2;PPP2R3C;RAC2;S1PR1;FCER1A;FYN;S
2.417265422	19.25019703	SRC;ADCY4;ITPR1;ITPR2;ADCY8;ADCY7;MAPK8;PTK2B;MAP2K3;MAP3K2;EGR1
1.846523426	14.07042951	FLT1;ROCK1;SRC;FLT4;ITGA2B;PXN;XIAP;ACTB;ARHGAP35;MYLK3;CRKL;ACTG1
1.968782851	14.35666463	ITGAM;NCF1;C1R;NCF4;TCIRG1;CORO1A;ACTB;FCAR;ACTG1;C3;FCGR3A;LAMP
2.251047726	16.02124012	SRC;PTGER2;ITPR1;ADCY4;ITPR2;ALOX12;IL1RAP;ADCY8;ADCY7;MAPK8;PLCG2
1.880797596	13.29820555	ERO1A;PPP1R15A;ERO1B;NGLY1;UBE2D1;UBE2J2;HSP90B1;UBE2J1;HERPUD1;
2.004847296	14.11803216	RYR1;HDAC4;NOTCH3;PRKAA1;SERPINE1;PDE3B;ITPR1;ADCY4;ITPR2;PRKAG2;A
2.004847296	14.11803216	PRKAA1;PDE3B;PRKAG2;PYGM;HK2;CRKL;IKBKB;LIPE;SOCS3;HK3;MAPK8;SOCS
2.657209697	17.68873856	PRKCB;SRC;PXN;PLA2G4A;PTGS2;MAPK14;PTK2;MAPK13;VEGFA;MAPK11;MA
2.294064059	15.20295264	STAT5A;STAT5B;CDKN1A;JUN;CDKN1B;PRKCB;SRC;TGFA;NRG1;BRAF;AREG;PTI
2.258088655	14.59403667	TCF7L2;CDKN1A;JUN;SMAD3;GADD45B;TGFA;BRAF;FOS;AREG;TGFBR1;EREG;C
2.345369215	14.9151056	PRKCB;ADCY4;ITPR1;KCNJ15;ATP1A3;ITPR2;KCNJ16;ATP1B3;SLC4A2;ATP1A1;A
3.045819805	19.23787955	CDKN1A;CXCL8;SRC;MMP1;BRAF;VEGFA;RASSF1;MDM2;E2F2;E2F3;KRAS;RAF1

1.832917081	11.23610346	CDKN1A;CXCL8;TRAF3IP2;SERPINE1;ITPR1;ITPR2;RELA;CCND2;RASSF5;CAPN2;
1.511153524	9.07459257	CDKN1A;CRTC2;CSF3;CDKN1B;FLT1;CSF1;FLT4;ITGA2B;FASLG;AREG;PIK3CG;IKI
2.310012936	13.78936475	CDKN1A;STEAP3;CD82;GADD45B;SERPINE1;SHISA5;PPM1D;GADD45G;COP1;C
2.027782476	12.03598791	CDKN1A;ITPR1;ADCY4;LRP5;ITPR2;ADCY8;ADCY7;CYP27B1;SLC9A3R1;MMP25;
1.906108994	11.24326507	SRC;ADCY4;ADCY8;ADCY7;RELA;MAPK8;GNG4;INSL3;JUN;EDN1;NOS2;MMP1;
2.31668713	13.31789257	CDKN1A;CREBBP;EGLN3;JUN;SLC2A1;TGFA;BRAF;HIF1A;CRKL;VEGFA;RAP1B;FL
2.041306135	11.5052055	TCF7L2;CREBBP;CDKN1A;CDKN1B;IL1R2;TGFA;BRAF;NFKB1;RELA;HSP90B1;NFI
2.229007196	12.07722616	PTPN1;TCF7L2;CREBBP;SMAD3;SRC;ACTN1;PTPRJ;ACTN4;NLK;ACTB;TGFBR1;A
1.987357414	10.66511914	CSF3;IL4R;ITGAM;CSF1;IL1R1;IL1R2;ITGA2B;CD1D;TNF;FCER2;IL1A;IL6;CD5;IL1
1.723782063	8.775833165	PRKAA1;SEH1L;WNT2B;LRP5;SLC3A2;TNF;IKBKB;FLCN;SESN2;DVL2;RICTOR;ATI
1.90022805	9.060108622	CAMK1D;KCNK9;PRKCB;PRKCE;ITPR1;ADCY4;ITPR2;ATP1A3;ATP1B3;ATP1A1;A
1.90022805	9.060108622	DGKG;SLC22A3;JUN;SLC44A3;LYPLA1;DGKD;CHKA;PRKCB;SLC44A2;SLC22A1;PI
1.517697027	7.007074775	RET;RYR1;PTGFR;FLT1;FLT4;PTAFR;ADCY4;ITPR1;CXCR4;CACNA1A;ITPR2;MST1
1.655609508	7.469130893	RYR1;CDKN1A;PRKAA1;ROCK1;SRC;ITPR1;ADCY4;ITPR2;PRKAG2;ADCY8;PTGS2
1.669940617	7.518531311	DGKG;PTGFR;DGKD;CXCL8;ADCY4;LPAR3;ADCY8;ADCY7;PIK3R6;PIK3CG;PIK3R
1.862384991	8.253311016	IL10;CFD;ITGAM;SELPLG;C1S;C1R;C5AR1;PTAFR;ITGAL;FCAR;ICAM1;C2;C3;SELI
1.495659754	6.394856018	FLT1;CSF1;FLT4;TGFA;FASLG;PLA2G5;RASGRP2;STK4;RELA;ETS2;RASGRP4;IKBK
2.313695793	9.77625063	IKBKB;HK3;SOCS3;MAPK8;SOCS1;PKLR;PIK3CA;PRKCE;PRKCD;CACNA1A;TNF;H
1.922407252	7.779855585	CDKN1A;CAMK1D;GADD45B;PRKCB;TGFA;BRAF;GADD45G;PIK3CA;PLCG2;MDI
1.922407252	7.779855585	HSPA5;GPX3;PRKCB;ADCY4;ITPR1;ATP1A3;ITPR2;ATP1B3;ATP1A1;TTF1;ADCY8
1.476541235	5.774023176	ITGAM;ROCK1;SRC;ITGA2B;PXN;CXCR4;ITGAL;ACTB;ARHGAP35;MYLK3;CRKL;A
1.387123052	5.348495593	CDKN1A;CDKN1B;MIR146A;CRKL;GLS;IKBKB;RASSF1;CCND2;PLAU;CASP3;PIM1
1.428714324	5.427468399	WASHC4;SRC;VPS4B;AGAP2;CXCR4;IL2RG;RAB11FIP1;GRK2;CYTH4;CXCR1;GRK
1.827545461	6.727970751	PDIA3;CD74;CIITA;HSPA5;TAP2;TAP1;HSPA2;TNF;TAPBP;CREB1;IFNG;CANX;RF
1.700748621	6.23720243	CPB2;CELA2A;PRKCB;RAB3D;ITPR1;ADCY4;ITPR2;ATP1A3;ATP1B3;SLC4A2;PLA
1.623446648	5.850839234	NCOA1;NOTCH3;CREBBP;PRKCB;SRC;STAT1;NOTCH4;SLC2A1;ATP1A3;ATP1B3;
1.544246499	5.426933064	NOTCH3;CDKN1A;WNT2B;NOTCH4;FLT4;LRP5;DLL1;FRAT1;FRAT2;DVL2;E2F2;E
1.531288889	5.260161319	NLGN3;CD274;CD40;ITGAM;SELPLG;SDC4;CD80;SDC3;ICAM3;NRXN2;ITGAL;VS
1.947848681	5.979140969	IL10;IL15RA;CD40;IL6;IL15;CD80;CXCR4;ITGB7;LTBR;ICOSLG;TNFSF13B
1.812540297	5.48911619	VDR;SLC11A2;ATP1A3;ATP1B3;SLC30A1;ATP1A1;ATP2B1;SLC8A1;MT2A;FTH1;
2.105454398	6.359793915	RET;TCF7L2;CDKN1A;GADD45B;NCOA4;BRAF;KRAS;BAK1;GADD45G
1.597020229	4.755463636	DGKG;DGKD;MTMR3;PRKCB;INPP1;IPMK;ITPK1;ITPR1;ITPR2;MTMR7;INPP4A;S
1.490677321	4.426676949	H2AW;CD40;C1S;C1R;CD80;TNF;C2;C3;C4A;FCGR3A;C7;TRIM21;ELANE;H3-3A;
1.985117922	5.894265737	IL1A;IFNG;CD80;IL1B;LTA;IL12B;FAS;FASLG;IL12A;TNF
1.694955687	4.94663866	ISYNA1;MTMR3;INPP1;IPMK;ITPK1;PIK3CG;MTMR7;INPP4A;PIK3CA;SYNJ1;INP
2.032735145	5.8347987	IL10;CD40;IFNG;CD80;IL12B;FAS;FASLG;IL12A;TNF
2.032735145	5.8347987	CD40;CIITA;PTPRC;RFX5;TAP2;TAP1;IL2RG;IL7R;JAK3
1.457513852	4.161959255	WNT2B;ACVR1B;DVL2;JAK2;JARID2;SKIL;JAK3;JAK1;FZD1;SMAD3;SETDB1;PCGI
1.463888209	4.132823445	PRKAA1;MTMR3;ITPR1;HIF1A;TANK;MAPK8;LAMP1;ATG101;RB1CC1;TP53INP
1.232568852	3.460866604	RYR1;WNT2B;CSF1;LRRK2;FASLG;UBE2L6;TNF;FRAT1;CASP7;FRAT2;CASP8;KIF5
1.698889871	4.768394953	GABARAPL1;USP15;JUN;CALCOCO2;SRC;HIF1A;RELA;MAPK8;FUNDC1;PGAM5;
2.095667297	5.813923109	STX1B;GOSR1;STX6;STX4;STX3;SNAP29;VAMP5;STX11
2.727687563	7.488437037	CA12;CA5B;CA4;CA9;GLUL
1.496444265	4.036660617	PRKCB;KCNJ12;ITPR1;ADCY4;CACNA1A;ITPR2;FOS;ADCY8;GNG11;ADCY7;PIK3I
1.319109901	3.496309255	SRC;NR1I3;ADCY4;XIAP;CACNA1A;ADCY8;PTGS2;ADCY7;DLL1;RELA;HSP90B1;H
1.443713555	3.823805719	ARHGEF11;EDN1;PTGIR;RAMP2;ROCK1;PRKCB;PRKCE;PRKCD;ITPR1;ADCY4;ITP
1.500379651	3.838716696	PRKAA1;ADCY4;PRKAG2;HSPA2;ADCY8;SOD2;PRKAB1;SIRT1;ADCY7;NFKB1;REI

1.715466277	4.225666073	CHST11;CHSY1;CHPF2;CSGALNACT2;CHST15;XYLT1;B3GNT2;B3GALT6;B4GALT
1.31196026	3.210465981	ROCK1;PTGER2;PDE3B;ADCY4;ATP1A3;ATP1A1;GLI1;ADCY8;ADCY7;RELA;RAP1
1.637542598	3.886297748	CD40;CASP8;CD80;CASP3;RAC2;FYN;ITGAL;BID;ACTB;CD55;ACTG1;ICAM1
1.474411765	3.496690803	DGKG;LYPLA1;DGKD;CHKA;MBOAT1;PLD4;PLA2G4A;PLA2G5;GPCPD1;CRLS1;P
1.785930408	4.181367682	MAOB;ALDH2;MAOA;HAAO;KYNU;KYAT3;KMO;IDO2;IDO1
1.330164251	2.980346257	WNT2B;CTBP2;LRP5;PRICKLE3;PSEN1;NLK;FRAT1;MAPK8;CCND2;FRAT2;DVL2;
1.909501764	4.26131572	PRKAA1;CREB1;BHLHE40;CRY2;PRKAG2;FBXL3;PRKAB1
1.806192556	4.012717262	PIK3CA;PRKCB;ATP1A3;SFN;ATP1B3;KRAS;ATP1A1;SGK1
1.356042025	2.977980299	MAP3K1;UBA7;UBE2B;SMURF1;UBE2D1;XIAP;UBE2L6;UBE2G1;UBE2J2;PIAS2;
1.320517986	2.886272979	ROCK1;PDE3B;ITPR1;ADCY4;ITPR2;ATP1A3;ATP1A1;ADCY8;ADCY7;MYLK3;SLC8
1.637060159	3.491783175	ARG2;ALDH2;MAOB;NOS2;MAOA;ODC1;LAP3;PRODH;SAT1;AGMAT
1.637060159	3.491783175	ERO1A;ATP6V1G1;SEC61G;PLCG2;TCIRG1;ATP6V1E1;ATP6V0D1;ACTB;CFTR;AC
1.16396789	2.373151737	ZNF331;CGAS;FASLG;TNF;IFIH1;IKBKB;CASP8;CASP3;IL12B;IL12A;JAK2;IKBKE;B
4.361624544	8.775057436	HK3;HK2
1.636819213	3.287974218	ABCA1;ABCA6;ABCA3;TAP2;TAP1;ABCA7;ABCA13;ABCG1;CFTR
1.455433455	2.908949142	SRC;PXN;RHOG;ACTB;PTK2;ACTG1;CRKL;DNM2;MAD2L2;PIK3CA;ELMO2;HCLS
2.045293618	4.081315177	ALDH2;VNN2;DPYS;DPYD;UPB1
1.321989861	2.618866054	NCOA1;JUN;SRC;PRKCD;ITPR1;ADCY4;ITPR2;TGFA;HSPA2;FOS;ADCY8;ADCY7;H
1.924871157	3.553869531	ARG2;NOS2;GLUL;ASS1;GLS
1.924871157	3.553869531	HAL;MAOB;ALDH2;MAOA;ALDH3B1
1.360853784	2.450508975	PRKCB;ADCY4;ITPR1;ATP1A3;ITPR2;ATP1B3;SLC4A2;ATP1A1;ATP2B1;ADCY8;L
1.254670966	2.244794625	CDKN1A;WNT2B;LRP5;TGFA;ACTB;ACTG1;FRAT1;FRAT2;DVL2;PLCG2;E2F2;E2F
1.24199446	2.211074296	NRP1;SEMA7A;ROCK1;SRC;CXCR4;RND1;PAK1;PLCG2;PLXNA2;RAC2;PLXNA1;F
1.324623158	2.338900635	CRTC2;CREBBP;PRKAA1;PDE3B;ITPR1;SLC2A1;ITPR2;PRKAG2;PYGM;PRKAB1;SI
1.245762848	2.170602111	PRKAA1;ROCK1;SRC;PRKAG2;ARHGAP17;CD1D;ACTB;ACTG1;SLC9A3R1;MAPK8
1.817828969	3.107035923	CA4;ATP1A3;ATP1B3;ATP1A1;GLS
3.2710298	5.545614628	PDXK;PSAT1
1.540131213	2.592105089	IL1A;IL6;IFNG;CD80;IL1B;FAS;FASLG;TNF
1.255453105	2.091258243	RYR1;RBPJL;XBP1;PRKCB;GTF2B;ITPR1;CACNA1A;ITPR2;TRAF2;RBPJ;ATXN3;MA
1.472796899	2.408370784	JUN;CREB1;GRIN3A;MAOB;MAOA;FOSB;RELA;NFKB1;ATF4
1.309476876	2.054003775	EDN1;PRKAA1;TPM4;ITGA2B;PRKAG2;TNF;PRKAB1;ACTB;SLC8A1;ACTG1;IL6;IT
1.869492531	2.928274767	ACSL6;ACSL5;ACSL4;ACSF3
1.354424265	2.100236469	RET;HK3;SLC7A5;PIK3CA;SLC2A1;KRAS;SLC1A5;RAF1;SLC16A3;HIF1A;HK2;GLS
1.570562901	2.365849921	IL10;CD40;FCER1G;IL9;FCER1A;TNF
1.363586203	1.978640134	TCF7L2;CDKN1A;PIK3CA;GADD45B;BRAF;GRB2;KRAS;BAK1;RAF1;GADD45G
1.415010474	2.013659601	B3GNT3;B3GNT2;B4GALNT1;ST6GALNAC4;FUT4;B4GALT4;ST3GAL3;ST6GALNA
1.309125331	1.86009716	CDKN1A;PIK3CA;GADD45B;FGF18;MDM2;E2F2;E2F3;BRAF;KRAS;BAK1;RAF1;G
1.289330808	1.819310178	BTG3;BTG2;BTG1;PNPT1;ENO1;TOB2;ENO3;TENT4B;CNOT7;PAN3;XRN1;CNOT
1.212460086	1.684505	CD164;NAPSA;ASAH1;SLC11A1;SLC11A2;LAPTM5;TCIRG1;LITAF;IGF2R;GALC;CI
1.308891411	1.721590997	RYR1;LYN;PRKCB;ITPR1;PLA2G4A;CACNA1A;ITPR2;BRAF;KRAS;RAF1
1.28555883	1.679812879	RAP1B;CREBBP;PRKCB;ITPR1;ITPR2;BRAF;KRAS;RAF1;ADCY8;CALM1;ATF4
1.342290728	1.706587908	HK3;MGAM;PIK3CA;PRKCB;ATP1A3;ATP1B3;ATP1A1;HK2
1.283152686	1.606293422	GGT5;GPX3;CYP4F2;EPHX2;TBXAS1;PLA2G4A;ALOX12;PLA2G5;GGT1;PTGS2
1.241085646	1.476443601	JUN;CREB1;GRIN3A;MAOB;PRKCB;MAOA;FOSB;FOS;CALM1;SIRT1;ATF4
1.353620885	1.556515035	BST1;PNP;NAPRT;NAMPT;CD38;SIRT1
1.189844638	1.362204145	PRKCB;PDE3B;ADCY4;CACNA1A;ADCY8;ADCY7;GNG11;GABRR2;GRK2;GRK5;GI
1.2529372	1.419540553	NT5C3A;ENTPD1;PNP;DPYS;DPYD;CMPK2;UPP1;DCK;UPB1

1.158901587	1.294639783	MAOB;PRKCB;MAOA;DUSP1;ITPR1;CACNA1A;ITPR2;PLA2G4A;ALOX12;BRAF;P
1.133786441	1.262711178	FZD1;TCF7L2;CDKN1A;SMAD3;CDKN1B;WNT2B;GADD45B;LRP5;BRAF;TGFBR1;
1.189700871	1.293212813	STX1B;ATP6V1G1;SLC6A9;STXBP1;SLC1A2;CACNA1A;TCIRG1;STX3;ATP6V1E1;A
1.074034859	1.15659703	WNT2B;CSF1;TNF;IKBKB;FRAT1;CASP7;FRAT2;CASP8;KIF5C;CASP3;RB1CC1;TUI
1.308424632	1.406032598	GALNT11;GALNT3;GALNT1;B3GNT3;ST6GALNAC4;B4GALT5
1.246196777	1.335838321	ABCA1;MYLIP;STARD3;NPC1;APOA2;VDAC3;TSPO;LDLR
1.154751817	1.22516405	PDE3B;ADCY4;BRAF;ADCY8;MAPK14;ADCY7;MAPK13;MAD2L2;STK10;MAPK11
1.130334093	1.190625778	ENTPD1;PKLR;GDA;PDE3B;ADCY4;AMPD1;ADA2;AMPD3;ADCY8;DCK;ADCY7;A
1.145026525	1.156623429	TGIF1;CREBBP;SMAD3;ROCK1;SMURF1;ACVR1B;TNF;TGFBR1;SMAD7;ZFYVE16
1.377123443	1.389307031	HSPA5;SEC61G;SRPRA;SEC62
1.308308157	1.313202078	ALDH2;DPYS;ALDH3B1;DPYD;UPB1
1.134020202	1.08642439	MAP3K2;PRKCB;SRC;ADCY4;ITPR1;ITPR2;ADCY8;ADCY7;TUBA4A;TUBB1;GRB2;
1.100133718	1.040849832	MAOB;PRKCB;MAOA;ITPR1;CACNA1A;ITPR2;FOS;MAPK14;GNG11;MAPK13;MA
1.635137684	1.537388251	SQOR;BPNT1
1.257915989	1.170509433	POLR3A;POLR2A;POLR2C;POLR1F;POLR2K
1.401590296	1.296124775	MAOB;MAOA;ALDH3B1
1.119034091	1.025585471	GABARAPL1;PRKCB;SRC;ADCY4;CACNA1A;ADCY8;ADCY7;GNG11;GLS;GABRR2;
1.121458322	1.014380182	PRDX5;NUDT7;NOS2;EPHX2;MPV17L;PMVK;ACSL6;ACSL5;ACSL4;FAR2;SOD2;X
1.162915354	1.048585958	PRKCB;VDR;ATP1A3;ATP1B3;ATP1A1;ATP2B1;SLC8A1;DNM2
1.074853341	0.961133681	FZD1;TCF7L2;SMAD3;WNT2B;SERPINE1;AREG;ACTB;TGFBR1;ACTG1;STK3;SMA
1.174060507	1.043952297	IFNG;PSMA2;PSME1;PSME2;PSMB10;PSMB8;PSMB9
1.064943097	0.896569186	TPM4;CREM;ADCY4;ATP1A3;ATP1B3;ATP1A1;ATP2B1;ADCY8;MAPK14;ADCY7;
1.144642857	0.955870264	LFNG;GALNT11;GALNT3;GALNT1;MFNG;EOGT;ST3GAL3
1.453371893	1.195039938	GGT5;GGT1
1.154225649	0.944335498	ALAS1;SDS;MAOB;MAOA;PSAT1;SDSL
1.06794208	0.864306355	PRKCB;ITPR1;SLC1A2;ADCY4;CACNA1A;ITPR2;PLA2G4A;ADCY8;GNG11;ADCY7;
1.113300889	0.893226836	LIPE;ADRB3;PIK3CA;PDE3B;ADCY4;ADCY8;PTGS2;ADCY7
1.167929974	0.933716532	HK3;PFKFB4;PFKFB3;HK2;KHK
1.189127973	0.925462322	GCH1;MOCOS;ALPL;MOCS1
1.189127973	0.925462322	HHEX;PKLR;HES1;HNF1B
1.090078164	0.845010342	FZD1;TCF7L2;CDKN1A;WNT2B;GADD45B;DVL2;BAK1;GLI1;GADD45G
1.22625	0.923631838	HYAL1;HYAL2;HPSE
1.052471112	0.786416271	FZD1;TCF7L2;CREBBP;EDN1;WNT2B;PRKCB;ADCY4;ADCY8;ADCY7;CREB1;DVL2
1.090010078	0.802135147	GALC;UGCG;ASAH1;SPTLC2;NEU1;ACER3;SGPP1
1.137361104	0.811987866	ATP6V1G1;TCIRG1;ATP6V1E1;ATP6V0D1
1.051025232	0.728962211	NR4A1;CREB1;ADCY4;ITPR1;ITPR2;ADCY8;ADCY7;LDLR;ATF4
1.015461773	0.694752395	HDAC4;H2AW;MAOB;MAOA;HDAC11;GNG4;H3-3A;H3-3B;H2AC6;H2BC5;BRAF
1.63489819	1.103542165	GLS
1.024242424	0.682736324	TPM4;ITGA2B;ADCY4;ADCY8;TNF;ADCY7;ACTB;SLC8A1;ACTG1;ITGAV;ITGB7;IT
1.089908141	0.713767904	SLC24A1;GNAT2;SAG;CALM1
1.040343915	0.67378183	HSD17B1;ADCY4;PLA2G4A;ADCY8;PTGS2;ADCY7;LDLR
1.054721762	0.670627121	HK3;MGAM;PYGM;HK2;GANC
0.998945081	0.63275782	MAOB;UBA7;MAOA;LRRK2;ITPR1;ITPR2;UBE2L6;UBE2J2;COX7A1;UBE2J1;MAF
1.005970932	0.621128867	SLC10A1;SLC22A1;SLC2A1;ADCY4;ATP1A3;ATP1B3;SLC4A2;ATP1A1;ADCY8;AD
0.993117058	0.607203652	RYR1;NCF1;NCF4;ITPR1;ITPR2;TNF;COX7A1;MAPK8;C7;KIF5C;CASP3;TUBB1;RA
1.0217027	0.601600525	ADSS2;GLUL;ASRGL1;ASS1;GLS
0.986924421	0.553385991	DGKG;DGKD;DGAT2;ALDH2;GPAT4;MBOAT1;GPAT3;LPIN2

1.307843137	0.725364338	XDH
0.980729955	0.542231455	EDN1;CREB1;ADRB3;PTGER2;PDE3B;ITPR1;ITPR2;CALM1;KCNJ2
0.975824623	0.53238819	TCF7L2;ACTN2;ITGA2B;ITGAV;ITGB7;ITGA5;ACTB;SLC8A1;ACTG1;ITGA9
0.968448889	0.512729843	FZD1;TCF7L2;CDKN1A;CDKN1B;WNT2B;ITPR1;ADCY4;ITPR2;BRAF;ADCY8;ADC
0.95882917	0.490203763	CCKAR;CREB1;PRKCB;SLC2A1;ADCY4;ATP1A3;ATP1B3;ATP1A1;ADCY8;ADCY7;A
0.968639459	0.489345062	HK3;MGAM;HK2;GANC
0.933816373	0.429518397	SDC4;LAMB3;ITGA2B;COL6A3;ITGAV;ITGB7;CD47;ITGA5;FREM1;CD44;ITGA9
0.915185185	0.400496049	GGT5;GCLC;GPX3;ODC1;GSTA1;LAP3;GGT1
0.922752077	0.400908968	RYR1;CREB1;RASD1;PRKCB;GNG4;ITPR1;ADCY4;FOS;CALM1;ADCY8;GNG11;AD
0.94488472	0.389144562	SEH1L;SLC1A2;TANK;TNF;COX7A1;ACTB;ACTG1;NXF1;KIF5C;ATG101;CASP3;RB
0.886251642	0.342573529	HK3;ALDH2;PKLR;ADPGK;ALDH3B1;ENO1;ENO3;HK2
0.934065934	0.360551289	RFK
0.871721363	0.336462154	KYAT3;SCLY
0.899242545	0.334885807	CDKN2D;ZBTB17;CREBBP;CDKN1A;SMAD3;CDKN1B;GADD45B;GADD45G;MAD
0.817122642	0.275063996	ELOVL4;ELOVL5;HACD2
0.817122642	0.275063996	ELOVL4;ELOVL5;HACD2
0.834344782	0.271963377	IL10;CD40;TG;CD80;FAS;FASLG
0.861611694	0.273081642	CPB2;CELA2A;ELN;COL6A3;ATP1A3;ATP1B3;SLC3A2;SLC1A5;ATP1A1;SLC38A2;
0.896366013	0.277788879	KDM3A;PRKAA1;KDM3B;COX17;ADCY4;PRKAG2;ADCY8;ADCY7;COX7A1;ACTB;
0.816846183	0.237938857	KMT2E;ALDH2;SETDB1;KMT5C;KMT5B;EZH1;EZH2
0.802469136	0.218074175	TRPC5;PIK3CA;PRKCB;ITPR1;ITPR2;KRAS;RAF1
0.72630873	0.195047248	MTHFD2;MTHFS
0.72630873	0.195047248	CYP27B1;CYP24A1
0.726205451	0.180728103	RPIA;TKT;RBKS
0.791934468	0.194508572	MMP1;ACSL6;APOA2;OLR1;ACSL5;NR1H3;ACSL4;PPARD
0.742541541	0.169101944	LPCAT2;ENPP2;PLA2G4A;PLD4;PLA2G5
0.725998657	0.152318422	GCLC;SDS;PSAT1;KYAT3;SDSL
0.622442564	0.116720965	FUT4;ST3GAL3
0.670131932	0.116795694	ALDH2;ACSL6;ACSL5;ACSL4
0.544714681	0.093117664	LIG4
0.791303249	0.13518667	PRKCB;ITPR1;ADCY4;CACNA1A;ITPR2;ADCY8;PTGS2;MAPK14;GNG11;ADCY7;M
0.653340883	0.103926438	DYNC1H1;CREB1;ARHGDIB;STX4
0.742054484	0.11775017	UPF2;NXF1;SMG1;DDX19B;DDX39B;FUS;PPP2R3C;PAPOLG;ALYREF;ETF1
0.568251521	0.083930171	PLA2G4A;PLA2G5
0.740418458	0.108412585	RCL1;UTP15;NXF1;XRN1;EIF6;XRN2;SBDS;GAR1;RIOK1;UTP14A;GTPBP4
0.786175465	0.10838626	UPF2;RANBP2;EIF4A1;SEH1L;NUP210;FUS;FMR1;ALYREF;THOC2;SENP2;EIF1;N
0.593962264	0.080195765	MAOB;MAOA;ALDH3B1
0.640364907	0.081286715	SCUBE2;CCND2;GRK2;SMURF1;GLI1
0.46684443	0.058717721	ALPL
0.725272414	0.087028733	LIPE;CRTC2;PFKFB4;PRKAA1;PFKFB3;CREB1;PIK3CA;PPP2R3C;PRKAG2;PRKAB1
0.408441742	0.03802309	HSD3B7
0.483954343	0.044322279	PLA2G4A;PLA2G5
0.529627741	0.047212512	GABRR2;GRIN3A;CACNA1A
0.665948559	0.054828487	MAOB;MAOA;ALDH3B1;DPYS;DPYD;GSTA1;FMO2;UPP1;UPB1;XDH
0.466643315	0.037910922	PGP;GLUL
0.384393576	0.030837448	NEU1
0.489820755	0.031837385	ABCA1;DGAT2;PLA2G5

0.712437142	0.041333228	SMAD3;NCF1;PRKCB;ATP5PB;PRKCD;NCF4;SLC2A1;CYBB;MAPK14;COX7A1;REI
0.671360587	0.038188764	DDX5;DHX8;FUS;ALYREF;THOC2;HSPA2;PQBP1;U2AF1L4;DDX39B;TRA2A;SRSF
0.421411275	0.023868532	POLB;PARP3
0.466442049	0.024506064	GTF2B;GTF2H1;TAF5L
0.311103929	0.013869976	PMVK
0.445188679	0.018871879	ALDH2;PKLR;ME2
0.43527044	0.016562868	HK3;UAP1;HK2
0.607908108	0.02223014	MAD2L2;MAPK11;ITPR1;ADCY4;ITPR2;CALM1;ADCY8;MAPK14;ADCY7;REC8;M
0.284018624	0.009469736	CBLIF
0.352951971	0.009649391	MAN1A2;ST3GAL3
0.720567439	0.018849134	PTGFR;PTGER2;PTAFR;C5AR1;LPAR3;LTB4R;C3;P2RY8;GABRR2;P2RY6;HTR7;CC
0.261266968	0.006523816	PIGH
0.489242539	0.010768717	SCN9A;ADCY4;CACNA1A;PKD1L3;ADCY8;TRPM5
0.483174523	0.009717257	TPM4;ATP1A3;ATP1B3;ATP1A1;COX7A1;SLC8A1
0.42097444	0.007908363	SARS1;CARS1;TARS1;WARS1
0.318444029	0.005326582	ALAS1;CPOX
0.225178135	0.003162432	ALDH2
0.225178135	0.003162432	IDH3A
0.290070833	0.002954984	CUL4A;GTF2H1
0.283748544	0.002551769	ALDH2;ACSF3
0.362296045	0.002388589	HSD11B1;ALDH3B1;CYP2S1;GSTA1
0.186511528	0.001109345	RNASEH2B
0.603270977	0.002092623	ITPR1;SLC1A2;COX7A1;MAPK8;CASP8;POLR2A;KIF5C;ATG101;CASP3;RB1CC1;F
0.4167138	8.99E-04	ATP6V1G1;PPA1;ATP5PB;COX17;TCIRG1;ATP6V1E1;ATP6V0D1;COX7A1
0.221061448	3.84E-04	HSD11B1;HSD17B1
0.133114784	1.08E-04	MAN1A2
0.197535521	1.40E-04	CYP2S1;DHRS3
0.123039927	5.63E-05	HES1
0.301271944	1.76E-05	RPS9;MRPS15;RPS7;RPL10;RPLP1;FAU;RPL18
0.073410425	4.15E-07	RGS2;GRK2;GNAL;CALM1;SLC8A1

IAP3K5;MAP2K3;EDN1;RIPK3;IL15;TRAF2;FOS;TRAF1;TNFRSF1B;TNFRSF1A;CREB1;PIK3CA;TRAF3;IL1B;IRF1;LTA;P
?7;CASP8;CASP6;CASP3;TNFSF10;IL12B;OLR1;IL12A;LBP;JAK2;IKBKE;MAP3K5;MAP2K3;TICAM2;MMP1;IL18;CYBB
MPT;CASP4;IKBKE;JAK1;IFNAR2;GBP5;GABARAPL1;RIPK3;RIPK2;PRKCD;IL18;CYBB;TRAF2;IRAK4;TYK2;IRF3;OAS2;
DARADD;TICAM2;IL1R1;PRKCB;DDX58;TRAF2;IRAK4;TRAF1;TIRAP;TNFRSF1A;TRAF3;IL1B;LTA;PRKCQ;LTB;TLR4;B
;JAK1;MAP2K3;TICAM2;PRKCB;DDX58;FOS;IRAK4;TYK2;TGFBR1;TIRAP;CREB1;IRF3;PIK3CA;TRAF3;VDAC3;IRF7;RA
PIK3CA;IL23A;IL1B;IRF1;MAPKAPK2;CLEC4E;RAF1;IRF9;SRC;ITPR1;ITPR2;PTGS2;MALT1;RELA;RELB;MAPK8;PAK1;(
K8;CASP3;IL12B;NLRP3;IL12A;CD14;IL10;JUN;TICAM2;NOS2;FOS;IRAK4;MAPK14;TIRAP;NFKB1;MAPK13;IL1A;MAI
KBKB;CASP8;CASP3;TNFSF10;IL12B;TRIM25;IL12A;JAK2;IKBKE;KPNA1;JAK1;IFNAR2;RSAD2;PRKCB;DDX58;IFNGR1
MAP2K3;TICAM2;FOS;IRAK4;TIRAP;IRF3;PIK3CA;TRAF3;IL1B;IRF7;TLR9;TLR8;IRF5;TLR6;TLR4;TLR3;IFNAR1;TLR2;L
IKBKE;JAK3;JAK1;IFNAR2;DDX58;FOS;IRAK4;TYK2;IL1A;IRF3;PIK3CA;OAS2;TRAF3;IL1B;IRF7;TLR9;CD46;TLR4;IRF9;
12A;LBP;JAK2;JAK1;IL10;FCER1G;KSR1;IFNGR1;RIPK2;IFNGR2;IL18;IRAK4;TIRAP;TNFRSF1A;IL1A;CREB1;IFNG;IL23A
;CASP3;B2M;IKBKE;JAK3;JAK1;IFNAR2;MAP2K3;PDIA3;ENTPD1;DDX58;TAP2;TAP1;TRAF2;TYK2;IRAK4;TAPBP;FCE
R5;JAK2;JAK3;CCR3;CCR2;PRKCB;PRKCD;VAV1;FGR;HCK;PIK3CA;PARD3;RAF1;DOCK2;CCL14;ROCK1;SRC;PXN;ADC
B;IL12A;IKBKE;IL6R;JAK1;IFNAR2;RPS9;RPS7;PRKCB;DDX58;MMP1;CYBB;FOS;TYK2;IRAK4;TNFRSF1A;ADAM17;IRF
FNGR1;IFNGR2;TRAF2;FOS;GAB2;TYK2;TGFBR1;TNFRSF1A;IL1A;CREB1;IFNG;PIK3CA;IL1B;LCP2;SQSTM1;IRF9;IFNA
;GLUL;JAK3;JAK1;IFNAR2;ZBP1;TICAM2;H2AC6;RIPK3;IFNGR1;IFNGR2;CYBB;PLA2G4A;TRAF2;TYK2;TNFRSF1A;IL1A
;JAK2;IKBKE;CCR3;JAK1;IFNAR2;GABARAPL1;IFNGR1;TRAF2;FOS;TYK2;TNFRSF1A;HCK;CREB1;IRF3;PIK3CA;TRAF3;
;B2M;IL6R;CCR3;JAK1;PDIA3;ARHGEF11;IL1R1;PRKCB;TAP2;TAP1;TRAF2;TAPBP;TNFRSF1A;CREB1;IRF3;PIK3CA;IL
CASP8;CASP3;IL12B;IL12A;CCR5;JAK2;LDLR;JAK1;MAP2K3;IL10;LAMB3;NOS2;IFNGR1;IL10RB;STAT1;IFNGR2;IL10
.;JAK1;IFNAR2;IL10;IL15RA;IL4R;CISH;IFNGR1;IL15;IFNGR2;TYK2;PIAS2;PIAS1;IFNG;PIK3CA;IL23A;IL6ST;RAF1;STAI
6R;IL13RA1;IFNAR2;IL15RA;IL4R;PRKCB;BCR;EML4;IL23A;IL6ST;RAF1;IFNAR1;NOTCH3;CTBP2;MAX;NOTCH4;TGFA
UN;MARCKSL1;NOS2;IFNGR1;PRKCB;STAT1;IFNGR2;CYBB;FOS;IRAK4;MAPK14;NFKB1;MAPK13;NFKBIA;IL1A;MAP
CXCL2;IL27RA;CXCL16;TNFSF13B;IL18RAP;TNFSF10;IL12B;IL12A;CCR6;CCR5;IL6R;TNFRSF4;CCR3;CCR2;IL13RA1;IL1
IK3;CASP4;CAPN2;H3-3A;H3-3B;CAST;GABARAPL1;FNBP1;IL1R1;RIPK2;ACTN1;PRKCE;PRKCD;IL18;TRAF2;ACTN4;T
C2;IL6R;JAK3;JAK1;STAT5A;STAT5B;JUN;IL4R;SMAD3;IL1R1;IFNGR1;STAT1;IFNGR2;STAT3;FOS;TYK2;MAPK14;NFKI
CR1;CCL4;CXCR2;TNFSF10;CCL3;CCL2;CCR6;CCR5;IL6R;CCR3;CCR2;CCR1;IL10;XCR1;TNFSF14;CCL20;IL10RB;IL10RA
TRAF2;FOS;IRAK4;VAV1;IRF3;PIK3CA;IL1B;ELMO2;ARHGEF1;LCP2;ITGA5;TLR4;SKAP2;ARF6;ROCK1;SRC;PXN;NLRC
C8;CASP8;CASP3;CCL2;MAPK6;IKBKE;USP25;JUN;MMP1;CCL20;TRAF2;FOS;MAPK14;IL17RC;NFKB1;MAPK13;FOSL
IBB1;CASP4;TNFSF10;KPNA3;KPNA1;MAP2K3;ANXA2;RIPK3;RIPK2;IL18;RHOG;RHOH;TRAF2;FOS;IRAK4;TUBA4A;T
ASP3;RAC2;MAP3K8;MAP3K5;MAP4K1;MAP2K3;DUSP5;DAXX;DUSP2;IL1R1;PRKCB;DUSP1;PLA2G4A;TRAF2;FOS;
FSF10;CTSH;CTSC;MAP3K5;DFFB;DAXX;PARP3;TRAF2;FOS;TRAF1;NGF;TUBA4A;TNFRSF1A;PIK3CA;DDIT3;RAF1;BI
L2B;IL12A;STAT6;JAK2;JAK3;JAK1;STAT5A;STAT5B;JUN;IL4R;IFNGR1;STAT1;IFNGR2;FOS;TYK2;MAPK14;NFKB1;MA
.12A;IL10;JUN;NOS2;IFNGR1;IFNGR2;FOS;IRAK4;CFLAR;MAPK14;NFKB1;TGFBR1;TNFRSF1A;MAPK13;NFKBIA;MAI
IL10;JUN;IL4R;SMAD3;IFNGR1;STAT1;IFNGR2;STAT3;IL18;NFKB1;IL1A;IL6;IFNG;IL23A;IL1B;TLR4;IL18R1;TLR2
R1;STAT1;IFNGR2;STAT3;FOS;MAPK14;TIRAP;NFKB1;BATF;MAPK13;EML4;NFKBIA;MAPK11;IFNG;PIK3CA;TLR9;P
IAK2;STAT5A;EGR1;STAT5B;JUN;EDN1;SMAD3;PRKCB;STAT1;PRKCE;PRKCD;STAT3;CYBB;VEGFC;MAPK14;SELE;F3

25;IL12A;RIPK1;IKBKE;MAP3K1;DDX58;TRAF2;ISG15;MAPK14;NFKB1;MAPK13;NFKBIA;CXCL10;CYLD;MAPK11;IRF
K58;TRAF2;TYK2;PIAS1;TNFRSF1A;IFNG;IRF3;PIK3CA;OAS2;TRAF3;IRF7;RAF1;IRF9;TLR3;IFNAR1;RNASEL;RELA;SOC
ASP4;TNFSF10;ARHGEF11;IL1R1;IL18;TRAF2;FOS;IRAK4;TUBA4A;TIRAP;TNFRSF1A;IL1B;HCLS1;ARHGEF1;ARHGEF2
APK8;CCND2;BCL2L11;TNFSF10;S1PR1;S1PR4;IL10;CDKN2D;PLK3;GABARAPL1;CREBBP;SMAD3;GADD45B;STAT3;I
R5;JAK3;CCR3;JAK1;ACTN1;TRAF2;ACTN4;TRAF1;KAT2B;CREB1;H2BC15;IRF3;PIK3CA;TRAF3;MAPKAPK2;RASA2;VI
ZFP36;CCND2;KAT5;TSPO;B2M;JAK3;JAK1;IL15RA;IL1R1;IL15;IL1R2;FOS;TGFBR1;TNFRSF1A;KAT2B;CREB1;PIK3CA
B;MAPK8;RAC2;CCL2;ITGAV;MAP3K5;MEF2A;JUN;EDN1;IL1R1;DUSP1;IL1R2;FOS;MAPK14;SELE;NFKB1;PTK2;ASS

PRKCB;TAP2;TAP1;TRAF2;FOS;IRAK4;TNFRSF1B;TAPBP;TNFRSF1A;IRF3;PIK3CA;RAF1;TLR4;TLR2;PXN;ITPR1;CXCR4
;PLAU;NFKBIZ;ITGB7;H3-3A;H3-3B;IL1R2;LMO2;TRAF1;DUSP6;ETV6;DDIT3;BMP2K;RARA;ERG;NUPR1;BIRC2;BIRC

2;PLCG2;ATP6V1E1;LYN;ATP6V1G1;JUN;MAPK14;NFKB1;MAPK13;NFKBIA;MAPK11;ADAM17;ATP6V0D1;HBEGF
;ATP6V1E1;ATP6V1G1;JUN;IL15;MMP1;CCL20;IL18;FOS;VEGFA;IL1A;IL6;IFNG;IL23A;IL1B;LTB;ATP6V0D1;TLR4;TL

MAP3K5;JUN;MAP3K1;RIPK2;PRKCD;BRAF;IRAK3;IRAK4;NGF;MAPK14;NFKB1;MAPK13;NFKBIA;MAPK11;PIK3CA;
A;HK3;MKNK1;PLCG2;IL6R;EIF4E;CREBBP;EDN1;EGLN3;NOS2;PRKCB;IFNGR1;IFNGR2;STAT3;CYBB;NFKB1;VEGFA;I
NB;MAP2K3;STAT5A;GHSR;STAT5B;CREBBP;MAP3K1;PRKCB;STAT1;STAT3;FOS;MAPK14;PTK2;MAPK13;MAPK11;
MAD3;GADD45B;BRAF;GAB2;TGFBR1;NFKB1;GADD45G;BCR;NFKBIA;PIK3CA;MDM2;GRB2;KRAS;RAF1

SF5;RAC2;MAP2K3;PRKCB;ARAP3;NGF;VAV1;APBB1IP;ADORA2A;PIK3CA;ADORA2B;PARD3;RAPGEF1;PRKD2;LCP2

;GSN;PRKCB;PRKCE;LIMK2;PRKCD;LIMK1;PLA2G4A;GAB2;VAV1;DNM2;HCK;MARCKS;PTPRC;FCGR2A;PIK3CA;RAF
0;SERPINB4;ARG2;LAMB3;NOS2;IL1R1;PRKCB;ACTN1;IL1R2;ACTN4;NFKB1;PTK2;IL6;GNAL;IFNG;PIK3CA;IL1B;TLR
P35;MYLK3;PIK3R6;PIK3CG;ACTG1;PIK3R5;RAP1B;PLCG2;FYN;LYN;VASP;P2RY12;PTGIR;FCER1G;PLA2G4A;MAPK

ACTB;RELA;ACTG1;C3;FCGR3A;CLEC7A;CASP4;PLCG2;RAC2;ATG7;ELANE;H3-3A;H3-3B;GSDMD;H2AC6;H2BC5;PRI

F3;BAK1;ZBTB17;GADD45B;LAMB3;NOS2;TRAF2;TRAF1;NFKB1;PTK2;GADD45G;NFKBIA;PIK3CA;TRAF3;BIRC2;BIR
G;CCND2;CASP8;CASP3;ITGAV;ITGB7;ATP6V1E1;IKBKE;JAK1;IFNAR2;ATP6V1G1;TYK2;TNFRSF1A;CREB1;IRF3;PIK3
ACTB;ACTG1;PAK1;PLAU;CASP3;PLCG2;IL12B;ITGAV;FZD1;PRKCB;STAT3;PLAUR;BRAF;MIR21;MAPK14;PTK2;VAV1

RAP1B;RASSF5;PLCG2;RAC2;PTK2B;VASP;PRKCB;ACTN1;CYBB;RHOH;ACTN4;MAPK14;PTK2;VAV1;MAPK13;MAPK
KB1;VAV1;MAPK13;NFKBIA;MAPK11;PTPRC;TEC;IFNG;PIK3CA;PRKCQ;GRB2;LCP2;KRAS;PTPN6;RAF1;NFKBIE;NFK

PTK2B;FYN;BID;IFNAR2;FCER1G;PRKCB;IFNGR1;IFNGR2;BRAF;VAV1;NCR1;IFNG;PIK3CA;FAS;GRB2;CD48;LCP2;KR

3;BCL2L11;CASP8;CASP3;BID;IL6R;MAP3K5;MLXIP;JUN;XBP1;PKLR;NR1H3;TRAF2;FOS;MAPK14;PRKAB1;NFKB1;TN
C1B;MLXIP;PTPN1;PRKCB;PRKCE;NR1H2;PRKCD;STAT3;NR1H3;PRKAB1;NFKB1;TNFRSF1A;NFKBIA;IL6;CREB1;PIK3

1PR2;BID;S1PR4;MAP3K5;FCER1G;PRKCB;PRKCE;TRAF2;GAB2;MAPK14;NFKB1;SGPP1;TNFRSF1A;MAPK13;MAPK
.;JUN;MAP3K1;PRKCB;PRKCD;PLA2G4A;MAPK14;MAPK13;MAPK11;GRB2;KRAS;RAF1;CALM1;ATF4;HBEGF
.;RAP1B;PAK1;MAPK8;CCND2;RAC2;CAPN2;PIP5K1B;ITGAV;ITGB7;FYN;VASP;JUN;LAMB3;PRKCB;ACTN1;VEGFC;B
1;CLEC7A;SEC61G;LAMP2;TUBB1;OLR1;ITGAV;CD14;ATP6V1E1;DYNC1H1;ATP6V1G1;TAP2;CYBB;TAP1;TUBA4A;
;MAP2K3;IL1R1;PRKCB;PRKCE;PRKCD;PLA2G4A;NGF;MAPK14;MAPK13;MAPK11;PIK3CA;IL1B;PRKCQ;CALM1
;ATXN3;MAPK8;MAN1A2;SEC61G;CAPN2;BAK1;SEC62;UGGT1;MARCHF6;MAP3K5;PDIA3;XBP1;SEC24B;HSPA5;EI
ADCY8;ADCY7;MYLK3;SLC8A1;PIK3R6;PIK3CG;PIK3R5;LIPE;GNG4;MEF2A;EGR1;GABARAPL1;SMAD3;NOS2;PRKCE
1;PHKG1;MKNK1;PHKG2;FLOT1;FLOT2;EIF4E;SH2B2;PTPN1;PKLR;BRAF;PRKAB1;PIK3CA;PPP1R3B;PPP1R3D;RAP

E2F2;E2F3;MAP2K3;SMAD3;GADD45B;MAPK14;SIRT1;NFKB1;TGFBR1;HIPK3;GADD45G;MAPK13;IL1A;MAPK11;I
BKB;CCND2;ITGAV;ITGB7;JAK2;JAK3;IL6R;JAK1;IFNAR2;IL4R;NGF;EREG;CREB1;PIK3CA;DDIT4;COL6A3;SGK3;ITGA5

;PDE4B;MEF2A;ARHGEF11;EGR1;PRKCB;VDR;BRAF;FOS;NR4A2;CREB1;CYP24A1;ARHGEF1;RAF1;ATF4;HBEGF
VEGFC;FOS;MAPK14;GNG11;NFKB1;TGFBR1;MAPK13;VEGFA;NFKBIA;ACTA2;MAPK11;CREB1;PIK3CA;GRB2;KRAS

P6V1E1;FNIP1;EIF4E;FNIP2;FZD1;ATP6V1G1;PRKCB;BRAF;TNFRSF1A;SLC7A5;CLIP1;PIK3CA;DDIT4;GRB2;KRAS;RA

.R;ADCY8;ADCY7;MYLK3;SLC8A1;HTR7;CCKAR;PHKG1;HRH2;PHKG2;PLCG2;CD38;PTK2B;CAMK1D;NOS2;PRKCB;V
;ADCY7;ACTB;MYLK3;PIK3R6;PIK3CG;ACTG1;PIK3R5;RGS2;CD38;KCNJ2;JUN;CAMK1D;PRKCB;KCNJ12;PLA2G4A;F
5;CYTH4;CXCR1;CXCR2;PLCG2;FCER1A;PTK2B;PIP5K1B;FYN;RALGDS;CYTH1;FCER1G;PLA2G4A;GAB2;DNM2;PIK3C

KB;RAP1B;RASSF1;PAK1;MAPK8;HTR7;GNG4;RASSF5;PLCG2;RAC2;SHOC2;RALGDS;KSR1;PRKCB;VEGFC;PLA2G4A;

ACTG1;FGD3;PAK1;TMSB4X;RAC2;PIP5K1B;ITGAV;ITGB7;GSN;ACTN1;LIMK2;LIMK1;BRAF;ACTN4;SSH2;PTK2;VAV1
L;PRKCB;MIR23A;PRKCE;MIR27A;MIRLET7I;MIR21;SIRT1;PIK3CA;DDIT4;MIR101-1;FSCN1;ITGA5;EZR;RAF1;CD44;I
K5;KIF5C;CXCR2;GRK6;PIP5K1B;CCR5;LDLR;RAB11FIP4;CYTH1;SMAD3;IQSEC1;SMURF1;IQSEC3;ARAP3;VPS37A;HS

;ATP1A1;HIF1A;ACTB;MED12L;ACTG1;KAT2B;MED13;MED30;PIK3CA;PLCG2;MDM2;ITGAV;KRAS;RAF1
E2F3;HES1;BAK1;FZD1;NCOA1;TCF7L2;JUN;GADD45B;BRAF;FOS;GADD45G;NFKB2;PIK3CA;FGF18;GRB2;KRAS;RAF
SIR;ICAM1;SPN;ALCAM;ITGAV;ITGB7;ICOSLG;PDCD1LG2;SELE;SELP;VCAN;PTPRC;SELL;PECAM1;SIGLEC1;NECTIN2;

2;LAMP2;ATG7;SNAP29;GABARAPL1;PRKCD;CFLAR;VMP1;ATG16L2;PIK3CA;ATG16L1;DDIT4;PRKCQ;KRAS;RAF1;S
5C;CASP3;RB1CC1;TUBB1;CAPN2;MAP3K5;MAP2K3;DAXX;GABARAPL1;PRKCB;GPX3;CYBB;TRAF2;TNFRSF1B;TUBA

HSD11B1;JAK2;IKBKE;KPNA3;KPNA1;PAQR8;STAT5A;STAT5B;JUN;PRKCB;VDR;EPHX2;STAT3;MIRLET7I;FOS;KLF4;N
PR2;PLA2G4A;BRAF;PLA2G5;ADCY8;ADCY7;MYLK3;ACTA2;ADORA2A;ADORA2B;PRKCQ;ARHGEF1;RAF1;CALM1

LB;LIPE;PAK1;MAPK8;RAC2;PDE4B;FFAR2;GHSR;CREBBP;JUN;EDN1;ARAP3;BRAF;ATP1B3;FOS;ATP2B1;VAV1;NFK

RAC2;TBL1X;TLE4;FZD1;TLE3;TCF7L2;CREBBP;JUN;SMAD3;PRKCB;SENP2;DKK4;FOSL1;DAAM2;ROR2;LGR6;PPARI

8A1;PIK3R6;PIK3CG;PIK3R5;RGS2;MEF2A;VASP;TRPC6;PRKCE;ATP1B3;ATP2B1;CREB1;ADRB3;PPIF;VDAC3;RAF1;(

2M;JAK1;IFNAR2;PDIA3;DAXX;IFNGR1;DDX58;IFNGR2;TAP2;TAP1;TRAF2;TYK2;IRAK4;TNFRSF1A;TAPBP;PIK3CA;IF

3;BAK1;FZD1;TCF7L2;SMAD3;GADD45B;PRKCB;BRAF;TGFBR1;GADD45G;PIK3CA;GSTA1;GRB2;KRAS;RAF1;NFE2L
YN;SRGAP2;PLXNA4;SEMA4A;TRPC5;SEMA6A;TRPC6;UNC5A;SEMA4D;LIMK2;SEMA4B;LIMK1;SSH2;PTK2;PIK3CA

3;MAP3K5;RAB8B;VASP;JUN;MAP3K1;ACTN1;PRKCE;ACTN4;PRKAB1;TUBA4A;PARD3;HCLS1;ARHGEF2;EZR;RAPG

3B1;CAPN2;MAP3K5;CYBB;TRAF2;TUBA4A;TNFRSF1A;DKK4;IL1A;ADAM17;PIK3CA;PSMA2;DDIT3;IL1B;VDAC3;PP

F;GNG11;H2AJ;H3-5;GRIN3A;CREB1;H2BC15;ADORA2A;ADORA2B;FOSB;GRB2;KRAS;RAF1;CALM1;ATF4

PK8;KIF5C;CASP3;TUBB1;MAP3K5;DAXX;XBP1;HSPA5;DUSP1;ATP5PB;SEPTIN5;UBE2G1;TUBA4A;GNAL;ADORA2A

AC2;FYN;EGR1;HSPA5;ATP5PB;PRKCD;CYBB;HSPA2;MAPK14;TUBA4A;MAPK13;IL1A;MAPK11;IL6;GRIN3A;CREB1;I

3;1CC1;TUBB1;BID;MAP3K5;RANBP2;MAP2K3;DAXX;GABARAPL1;XBP1;NUP210;DNAH17;HSPA5;NOS2;ATP5PB;FL

;ACTG1;LIPE;SLC25A29;MAP3K5;MAP2K3;ATP5PB;ACSL6;ACSL5;ACSL4;MAPK14;PRKAB1;MAPK13;MAPK11;CREB

CKAR;HRH2;CHRNE;C3AR1;S1PR1;TSPO;S1PR2;INSL3;S1PR4;GHSR;EDN1;PTGIR;P2RY11;GPR35;P2RY14;P2RX5;GF

POLR2C;TUBB1;POLR2K;MAP3K5;TGM2;CREBBP;DNAH17;ATP5PB;GPX3;TRAF2;SOD2;TUBA4A;CREB1;PSMA2;VD

'GAM5;BIRC2;ATF4;BIRC3;NOD2;PTGS2;RELA;SOCS3;MAPK8;CCL2;RIPK1;JUN;MLKL;CCL20;LIF;VEGFC;CFLAR;MAF
;TRAF2;FOS;IRAK4;VAV1;TIRAP;TNFRSF1A;IRF3;PIK3CA;TRAF3;DDIT3;IL1B;IRF7;ARHGEF1;TLR6;TLR4;ABCG1;ATF4
TRAF3;IL1B;VDAC3;IRF7;TXNIP;RBCK1;TLR4;NAIP;BIRC2;IRF9;IFNAR1;BIRC3;RNF31;RNASEL;ITPR1;ITPR2;XIAP;NC
IRC2;BIRC3;BCL2A1;LY96;XIAP;PTGS2;MALT1;RELA;RELB;CCL4;PLCG2;RIPK1;CD14;LYN;GADD45B;TNFSF14;CFLAF
AF1;TLR4;TLR3;ATF4;IFNAR1;TLR2;SRC;RELA;MAPK8;STAT4;E2F2;PTK2B;E2F3;STAT6;BID;STAT5A;STAT5B;CREBBF
CLEC7A;PLCG2;NLRP3;PLK3;EGR2;JUN;EGR3;STAT1;STAT2;MAPK14;NFKB1;NFKB2;MAPK13;NFKBIA;CYLD;MAPK1

L;IFNGR2;IL18;IRAK4;TYK2;TNFRSF1A;IL1A;IFNG;IRF3;PIK3CA;OAS2;TRAF3;IL1B;IRF7;NUP98;RAF1;TLR4;IRF9;TLR3
Y96;RELA;MAPK8;CCL4;CCL3;RIPK1;CD14;JUN;STAT1;MAPK14;NFKB1;MAPK13;NFKBIA;CXCL10;MAPK11;CXCL11
;IFNAR1;TLR2;IL2RG;RELA;MAPK8;BAK1;BID;SLAMF1;STAT5A;STAT5B;JUN;STAT1;MX2;STAT2;MX1;STAT3;EIF2AK
A;IL1B;RFX5;TLR9;TLR6;ATP6V0D1;CLEC4E;RAF1;TLR4;TLR2;SRC;CEBPG;NOD2;CORO1A;MALT1;RELA;C3;CYP27B1
R2;IRF3;PIK3CA;OAS2;TRAF3;IRF7;CD44;IRF9;TLR2;IFNAR1;RBPJL;RELA;RELB;MAPK8;BCL2L11;PLCG2;E2F2;RIPK1
CY4;CXCR4;RASGRP2;ADCY8;ADCY7;PIK3R6;RELA;PIK3R5;RAP1B;PAK1;GRK2;CCL8;GRK5;CXCR1;GNG4;GRK6;CCL4
F3;PIK3CA;OAS2;TRAF3;IL1B;TLR8;MASP2;IL6ST;TLR4;CFB;TLR3;IRF9;HBEGF;TLR2;IFNAR1;CFD;RPL10;C1S;C1R;C5
AR1;RELA;RELB;SOCS3;MAPK8;SOCS1;PLCG2;FYN;JUN;STAT1;STAT2;MAPK14;NFKB1;FOSL2;NFKB2;MAPK13;FOSL
A;H2AJ;IFNG;IL1B;VDAC3;PGAM5;RBCK1;SQSTM1;TLR4;BIRC2;IRF9;TLR3;IFNAR1;BIRC3;CHMP5;RNF31;VPS4B;XIA
;MAPKAPK2;IRF7;IL6ST;RAF1;TLR3;IRF9;IFNAR1;SRC;ITPR1;ITPR2;PTGS2;HIF1A;PIK3R6;RELA;PIK3R5;C3;MAPK8;G
1B;ARHGEF1;RAF1;ATF4;ROCK1;SRC;PTGER2;PXN;ADCY4;ITPR1;CXCR4;ITPR2;ADCY8;PTGS2;ADCY7;RELA;GNG4;(
RA;STAT3;HSPA2;IRAK4;TYK2;MAPK14;NFKB1;TNFRSF1A;MAPK13;NFKBIA;MAPK11;IFNG;PPIF;TAB2;TLR4;MYD88
M2;IRF9;IFNAR1;IL20RA;CSF2RB;IL2RG;IL22RA2;SOCS3;SOCS1;IL21R;STAT4;STAT6;MCL1;STAT5A;STAT5B;CREBBF
A;LPAR3;CSF2RB;RASGRP2;STK4;HIF1A;RASGRP4;HSP90B1;BCL2L11;PLCG2;DVL2;RALGDS;FZD1;STAT5A;ZBTB17;S

10;IFNAR2;IL15RA;IL4R;IL1R1;IFNGR1;IL15;IL1R2;IFNGR2;TNFRSF18;IL18;IL16;NGF;TNFRSF1B;IL17RC;TGFBR1;TNF
TNFRSF1A;IRF3;PIK3CA;IL1B;HCLS1;ELMO2;PRKCQ;RBCK1;ARHGEF2;ITGA5;TLR4;SQSTM1;NAIP;CD44;ARF6;RNF3
B1;TGFBR1;MAPK13;NFKBIA;MAPK11;IL6;IFNG;IL23A;IL1B;IL2RA;IL2RB;RARA;PRKCQ;IL6ST;NFKBIE;NFKBIB

4;MEFV;RELA;MAPK8;NLRP3;CCL2;PTK2B;PIP5K1B;JUN;FYB1;LIMK1;MAPK14;NFKB1;PTK2;MAPK13;NFKBIA;MAF

TIRAP;DNM2;TNFRSF1A;PIK3CA;IL1B;TLR9;ELMO2;TLR6;RAF1;TLR4;NAIP;BIRC2;ARF6;TLR2;BIRC3;LY96;NOD1;NLI
IRAK4;NGF;DUSP6;TGFBR1;EREG;TNFRSF1A;IL1A;MAPKAPK3;DDIT3;IL1B;MAPKAPK2;RASA2;RAF1;ATF4;MAX;TG
RC2;ATF4;BIRC3;BCL2A1;ITPR1;ITPR2;XIAP;CSF2RB;RELA;MAPK8;BCL2L11;RIPK1;BAK1;BID;MCL1;JUN;GADD45B;

CS3;E2F2;RIPK1;E2F3;BAK1;BID;LDLR;STAT1;MX2;STAT2;MX1;STAT3;EIF2AK2;NR1H3;BRAF;CFLAR;NFKB1;NFKBIA
;EZR;TLR4;NAIP;ARF6;ROCK1;SRC;RELA;SLC9A3R1;PAK1;MAPK8;CYTH4;NLRP3;RIPK1;FYN;BAK1;CYTH1;JUN;SEC2
BRAF;MAPK14;SOD2;PRKAB1;SIRT1;TGFBR1;GADD45G;MAPK13;MAPK11;IL6;BCL6;PIK3CA;CCNG2;MDM2;GRB2;
DAC3;IRF7;ATP6V0D1;IL6ST;IRF9;ATF4;HDAC4;RBPJL;SRC;PXN;RELA;C3;BAK1;LYN;STAT5A;STAT5B;CREBBP;EGR2
A;CANX;VDAC3;LTA;ATF4;ADCY4;XIAP;ADCY8;IL2RG;ADCY7;RELA;RELB;MAPK8;E2F2;E2F3;STAT5A;EGR1;STAT5B;
1;TNFRSF1A;MAPK13;VEGFA;IL1A;MAPK11;IFNG;PIK3CA;IL1B;GSTA1;PECAM1;ARHGEF2;CALM1;SQSTM1;NFE2L

I;ITPR2;RELA;PAK1;MAPK8;GNG4;PLCG2;PTK2B;RIPK1;BAK1;BID;JUN;LIMK2;LIMK1;MAPK14;GNG11;PTK2;NFKB1
C3;DDX5;BCL2A1;MAX;CEBPE;RELA;CD14;BAK1;ELANE;ZBTB17;GADD45B;FUS;NFKB1;PTK2;PML;GADD45G;IL6;H3

2;RAF1;RAPGEF6;RGS14;SRC;ADCY4;LPAR3;ADCY8;RASGRP2;ADCY7;RAP1GAP;RAP1B;RALGDS;VASP;FYB1;VEGFC

KCB;CYBB;MAPK14;NFKB1;MAPK13;SELP;MAPK11;H2AJ;H3-5;H2BC15;FCGR2A;PIK3CA;PPIF;VDAC3;TLR8;PADI4;I

3CA;TRAF3;PARD3;MFNG;IRF1;COL6A3;MAML3;ITGA5;ATP6V0D1;RAF1;LLGL1;TLR3;IRF9;IFNAR1;ITGA9;RBPJL;NC
.;VEGFA;MAPK13;MAPK11;PIK3CA;MDM2;HCLS1;FAS;GRB2;ARHGEF1;KRAS;PTPN6;HPSE;ITGA5;EZR;RAF1;TLR4;C

RAF;ACTN4;PTK2;VAV1;VEGFA;PIK3CA;RAPGEF1;ZYX;COL6A3;GRB2;ITGA5;RAF1;BIRC2;BCAR1;BIRC3;ITGA9

DEM1;DNAJB12;EIF2AK2;TRAF2;UBE2G1;HSPA2;PDIA6;DNAJC1;DDIT3;DNAJB11;CANX;HYOU1;CALR;ATF4;NFE2L2

5;SGK1;RAF1;TLR4;ATF4;TLR2;IFNAR1;ITGA9;PRKAA1;TGFA;LPAR3;IL2RG;PIK3R6;RELA;PIK3R5;HSP90B1;BCL2L11

'EGFC;ATP2B1;NGF;MCOLN2;TPCN2;VEGFA;P2RX5;GNAL;ADRB3;LTB4R2;ADORA2A;ADORA2B;FGF18;ORAI2;VDA

GAB2;NGF;GNG11;NFKB1;VEGFA;PIK3CA;RASA3;FGF18;RASA2;REL;NF1;GRB2;KRAS;CALM1;RAF1;ARF6

HDAC4;NOTCH3;ROCK1;NOTCH4;PTGS2;SLC7A1;BCL2L11;SOCS1;PLCG2;E2F2;BMF;E2F3;BAK1;MCL1;CREBBP;STA
SPA2;ARAP1;IGF2R;TGFBR1;PML;RNF41;DNM2;SPART;ITCH;ZFYVE16;EHD4;RAB31;PARD3;IL2RA;IL2RB;CHMP2A;

A4A;TNFRSF1A;DKK4;IL1A;PSMA2;DDIT3;IL1B;VDAC3;PPIF;RAF1;SQSTM1;OPTN;ATF4;UBA7;ITPR1;LRP5;ITPR2;PS

FNG;IRF3;TRAF3;OAS2;IL1B;TLR9;IRF7;LTA;SRSF3;SRSF5;ITGA5;BIRC2;TLR3;IRF9;IFNAR1;BIRC3;TLR2;ZNF473;RNA

IF;RAF1;ATF4;ITPR1;LRP5;ITPR2;PSEN1;PTGS2;COX7A1;RELA;MAPK8;ATG101;DVL2;BID;FZD1;XBP1;NOS2;ATP5PI

JS;GPX3;ALYREF;NRG1;TRAF2;TNFRSF1B;MAPK14;TUBA4A;TNFRSF1A;MAPK13;SETX;MAPK11;NUP210L;PSMA2;I

4;TLR2;SRC;ITPR1;LY96;TANK;RELA;HSP90B1;RAP1B;MAPK8;CCL3;NLRP3;CCL2;CD14;BID;LDLR;ABCA1;LYN;JUN;X
)D1;NLRC4;NOD2;MEFV;TANK;RELA;MAPK8;IFI16;NLRP3;CCL2;RIPK1;GBP4;GSDMD;JUN;STAT1;STAT2;ERBIN;MA

?;EGR2;JUN;EGR3;SMAD3;MAP3K1;SLC10A1;STAT1;STAT2;STAT3;BRAF;MAPK14;NFKB1;MAPK13;NFKBIA;MAPK1

3;IFNAR1;RNASEL;RELA;SOCS3;NXF1;NLRP3;CCL2;BAK1;BID;CREBBP;STAT1;MX2;STAT2;MX1;EIF2AK2;NFKB1;PMI

1;MAPK8;CLEC7A;IRAK2;CD14;BID;PLK3;CD74;CREBBP;NOS2;VDR;IL10RB;STAT1;IL10RA;MAPK14;NFKB1;MAPK13
;E2F3;HES1;BAK1;BID;LYN;JUN;GADD45B;STAT1;STAT2;STAT3;EIF2AK2;ISG15;MAPK14;NFKB1;GADD45G;NFKB2;
4;CXCR2;PLCG2;CCL3;CCL2;PTK2B;CCR1;LYN;STAT5B;XCR1;CCL20;STAT1;STAT2;STAT3;BRAF;GNG11;NFKB1;PTK2;
AR1;RELA;C2;C3;MAPK8;C7;PLCG2;NLRP3;CCL2;RPL18;JUN;STAT1;STAT2;MX2;STAT3;MX1;EIF2AK2;ISG15;MAPK

AP;MAPK8;STAT4;NLRP3;RIPK1;STAT6;BID;STAT5A;STAT5B;MLKL;STAT1;STAT2;STAT3;EIF2AK2;CFLAR;SPATA2L;C
NG4;PLCG2;E2F2;E2F3;BAK1;BID;CCR1;LYN;TCF7L2;CREBBP;JUN;STAT1;STAT2;STAT3;EIF2AK2;MAPK14;GNG11;
CXCR2;CCL4;CCL3;CCL2;E2F2;PTK2B;RIPK1;E2F3;BAK1;BID;CCR1;IL10RB;IL10RA;STAT3;MAPK14;GNG11;PTK2;NFI

STAT5B;CREBBP;JUN;SMAD3;GADD45B;BRAF;GNG11;NFKB1;PTK2;NFKB2;GADD45G;NFKBIA;IL6;FGF18;MDM2;G

FRSF1A;IL1A;IFNG;IL23A;IL1B;LTA;LTB;IL6ST;IFNAR1;CCL14;IL20RA;CXCR4;CSF2RB;ACVR1B;IL2RG;CCL8;CXCR1;CX
1;ROCK1;SRC;PXN;ITPR1;ITPR2;NOD1;NLRC4;RELA;MALT1;U2AF1L4;C3;MAPK8;CYTH4;PLCG2;NLRP3;RIPK1;CD1

RC4;RELA;HSP90B1;PAK1;MAPK8;CYTH4;NLRP3;SNX9;RIPK1;CD14;BAK1;CYTH1;GSDMD;DYNC1H1;TCF7L2;JUN;M
FA;CACNA1A;NLK;RASGRP2;STK4;RELA;RASGRP4;RELB;STK3;RAP1B;PAK1;MAPK8;MKNK1;CD14;MAP4K4;MAP3K

4B;MAPK14;NFKB1;MAPK13;NFKBIA;MAPK11;IL6;FCGR2A;ABI1;FAS;TAB2;PTPN6;MYD88;MYO1F;NFKBIB

OTCH3;NOTCH4;PXN;PSEN1;PTGS2;RELA;SLC9A3R1;PPP2R3C;DVL2;HES1;BAK1;HES4;FZD1;TCF7L2;CREBBP;LAMB

;GNG4;PPP2R3C;EIF4E;MCL1;LAMB3;OSM;VEGFC;GNG11;PTK2;NFKB1;VEGFA;NR4A1;IL6;IL2RA;FGF18;IL2RB;MD

SEN1;PTGS2;UBE2J2;TANK;COX7A1;RELA;UBE2J1;ATXN3;MAPK8;ATXN1;ATG101;DVL2;BAK1;BID;FZD1;XBP1;DNA

SEL;SRC;CFP;RELA;C3;SOCS3;NXF1;CCL2;ZNF304;BAK1;BID;ZNF300;CD74;TNFSF14;STAT1;STAT2;ALYREF;EIF2AK2

BP1;HSPA5;STAT3;HSPA2;POU2F2;MAPK14;SOD2;SELE;PTK2;NFKB1;MAPK13;NFKBIA;SELP;MAPK11;IL6;FAS;TAB

RB2;CALM1;IL7R;NFE2L2;RET;CDKN1A;CDKN1B;CXCL8;WNT2B;FLT4;SLC2A1;FASLG;GLI1;IKBKB;CASP7;CASP8;CA

CR2;CCL4;CCL3;IL21R;CCL2;RELT;CCR1;XCR1;TNFSF14;CCL20;IL10RB;IL10RA;LIF;OSM;CXCL10;CXCL11;IL6;IL2RA;I
4;CYTH1;JUN;MAPK14;PTK2;NFKB1;MAPK13;NFKBIA;MAPK11;H3-5;TNIP1;ATG16L1;MDM2;TAB2;MYD88;BCAR1

2;JUN;MAP3K1;GADD45B;VEGFC;BRAF;HSPA2;MAPK14;NFKB1;GADD45G;VEGFA;NFKB2;MAPK13;NR4A1;MAPK

AH17;HSPA5;NOS2;FUS;ATP5PB;SEPTIN5;BRAF;UBE2G1;MAPK14;NFKB1;MAPK13;MAPK11;IL6;FAS;KRAS;CALM1;

SP3;RAC2;ITGAV;JAK2;JAK3;JAK1;NCOA1;ARHGEF11;EDN1;IFNGR1;IL15;MMP1;IFNGR2;NCOA4;TRAF2;FOS;TRAF

1;TGFBR1;PIK3CA;IFNG;TRAF3;RARA;ARHGEF1;BIRC2;PPARD;BIRC3;ROCK1;PTGER2;ADCY4;LRP5;CXCR4;XIAP;AD

CY8;PTGS2;IL2RG;ADCY7;DLL1;RELA;MAPK8;GNG4;STAT4;E2F2;STAT6;E2F3;HES1;BAK1;BID;TCF7L2;EGLN3;LAMI

B3;NOS2;STAT1;STAT2;STAT3;VEGFC;PML;VEGFA;IL2RA;IL2RB;GSTA1;FAS;KRAS

Supplementary File S6: Comprehensive details of the results of functional enrichment an

BP	Term	Overlap	P-value	Adjusted P-value
	fatty acid catabolic process (GO:0009062)	37/70	2.76E-17	1.25E-13
	cilium assembly (GO:0060271)	87/314	1.90E-15	2.96E-12
	DNA repair (GO:0006281)	84/298	1.96E-15	2.96E-12
	fatty acid beta-oxidation (GO:0006635)	29/52	1.16E-14	1.30E-11
	interstrand cross-link repair (GO:0036297)	27/55	5.47E-12	4.94E-09
	DNA metabolic process (GO:0006259)	72/277	1.43E-11	1.07E-08
	cilium organization (GO:0044782)	62/228	4.90E-11	3.16E-08
	recombinational repair (GO:0000725)	31/79	2.02E-10	1.10E-07
	double-strand break repair via homologous r	35/97	2.18E-10	1.10E-07
	fatty acid oxidation (GO:0019395)	26/59	2.81E-10	1.27E-07
	double-strand break repair (GO:0006302)	47/164	1.62E-09	6.67E-07
	intraciliary transport involved in cilium assem	20/40	2.06E-09	7.77E-07
	plasma membrane bounded cell projection a	67/278	2.28E-09	7.92E-07
	cellular response to DNA damage stimulus (G	78/350	5.28E-09	1.70E-06
	base-excision repair (GO:0006284)	21/48	1.70E-08	5.12E-06
	cellular amide metabolic process (GO:00436(	35/115	3.62E-08	1.02E-05
	base-excision repair, gap-filling (GO:0006287	17/35	5.86E-08	1.56E-05
	ciliary basal body-plasma membrane docking	30/95	1.35E-07	3.40E-05
	short-chain fatty acid metabolic process (GO:	44782	2.42E-07	5.76E-05
	DNA replication (GO:0006260)	31/108	8.96E-07	2.02E-04
	regulation of cell cycle G2/M phase transitior	26/85	1.79E-06	3.86E-04
	protein localization to ciliary transition zone (	44718	2.28E-06	4.61E-04
	nucleotide-excision repair, DNA incision (GO:	16/39	2.45E-06	4.61E-04
	replication fork processing (GO:0031297)	16/39	2.45E-06	4.61E-04
	branched-chain amino acid catabolic process	44885	2.79E-06	4.80E-04
	branched-chain amino acid metabolic proces	44885	2.79E-06	4.80E-04
	organelle assembly (GO:0070925)	81/425	2.87E-06	4.80E-04
	DNA-dependent DNA replication (GO:000626	33/129	6.57E-06	0.00106058
	fatty acid metabolic process (GO:0006631)	32/124	7.40E-06	0.001153151
	fatty acid beta-oxidation using acyl-CoA oxid	44819	8.96E-06	0.001348763
	mitotic cell cycle phase transition (GO:00447	46/209	9.78E-06	0.001424826
	nucleotide-excision repair (GO:0006289)	28/105	1.39E-05	0.001965622
	nucleobase-containing small molecule interc	44922	1.69E-05	0.002313987
	cellular amino acid catabolic process (GO:00(	25/90	1.85E-05	0.002430527
	glucuronate catabolic process (GO:0006064)	44686	1.99E-05	0.002430527
	glucuronate catabolic process to xylulose 5-p	44686	1.99E-05	0.002430527
	xylulose 5-phosphate biosynthetic process (G	44686	1.99E-05	0.002430527
	pyrimidine deoxyribonucleotide catabolic pro	44786	2.26E-05	0.002519851
	fatty acid beta-oxidation using acyl-CoA dehy	44752	2.29E-05	0.002519851
	myelin assembly (GO:0032288)	44752	2.29E-05	0.002519851
	telomeric loop disassembly (GO:0090657)	44752	2.29E-05	0.002519851
	nucleotide-excision repair, DNA incision, 5'-to	14/37	3.11E-05	0.003294719
	DNA duplex unwinding (GO:0032508)	17/51	3.14E-05	0.003294719
	DNA-dependent DNA replication maintenanc	15/43	4.98E-05	0.005103993

depyrimidination (GO:0045008)	44720	5.20E-05	0.005103993
short-chain fatty acid catabolic process (GO:(	44720	5.20E-05	0.005103993
regulation of G2/M transition of mitotic cell c	34/149	6.30E-05	0.005969413
monocarboxylic acid metabolic process (GO:(	33/143	6.34E-05	0.005969413
protein localization to cilium (GO:0061512)	13/35	7.47E-05	0.006889515
regulation of sequestering of triglyceride (GO	44788	9.12E-05	0.008104908
water-soluble vitamin metabolic process (GO	21/76	9.15E-05	0.008104908
nucleotide-sugar biosynthetic process (GO:0(	44823	1.07E-04	0.009335882
hexose metabolic process (GO:0019318)	14/41	1.15E-04	0.009824897
telomere maintenance (GO:0000723)	17/56	1.19E-04	0.00993236
protein N-linked glycosylation (GO:0006487)	19/67	1.34E-04	0.01077101
G2/M transition of mitotic cell cycle (GO:000	30/130	1.34E-04	0.01077101
biotin metabolic process (GO:0006768)	44721	1.41E-04	0.01077101
positive regulation of DNA-directed DNA poly	44721	1.41E-04	0.01077101
regulation of DNA-directed DNA polymerase	44721	1.41E-04	0.01077101
cell cycle G2/M phase transition (GO:004483	30/131	1.55E-04	0.011641678
regulation of mitotic cell cycle phase transitic	39/188	1.72E-04	0.012720089
glutathione metabolic process (GO:0006749)	14/43	2.05E-04	0.014967367
mismatch repair (GO:0006298)	44894	2.15E-04	0.015406286
nucleic acid phosphodiester bond hydrolysis	20/75	2.26E-04	0.015948073
intraciliary retrograde transport (GO:003572	44755	2.39E-04	0.016596916
acyl-CoA biosynthetic process (GO:0071616)	44790	2.79E-04	0.019078137
cellular response to leucine starvation (GO:1	44722	3.17E-04	0.021399395
mitotic spindle organization (GO:0007052)	33/157	4.08E-04	0.027104032
DNA strand elongation (GO:0022616)	44791	4.51E-04	0.029549131
organonitrogen compound biosynthetic proc	33/158	4.60E-04	0.029677461
monocarboxylic acid biosynthetic process (G	17/63	5.61E-04	0.035701239
long-chain fatty acid transport (GO:0015909)	11994	5.78E-04	0.036193618
sphingolipid metabolic process (GO:0006665	26/116	5.85E-04	0.036193618
protein glycosylation (GO:0006486)	28/130	7.22E-04	0.044070059
lipid transport across blood-brain barrier (GO	44656	7.88E-04	0.046624772
folic acid transport (GO:0015884)	44689	8.26E-04	0.046624772
glycoside catabolic process (GO:0016139)	44689	8.26E-04	0.046624772
regulation of acetyl-CoA biosynthetic process	44689	8.26E-04	0.046624772
regulation of acyl-CoA biosynthetic process ((	44689	8.26E-04	0.046624772
telomeric D-loop disassembly (GO:0061820)	44689	8.26E-04	0.046624772
nucleotide-excision repair, DNA gap filling (G	44828	8.91E-04	0.049680693
nucleotide-excision repair, preincision compl	44863	9.95E-04	0.054843374
DNA recombination (GO:0006310)	14580	0.001019996	0.054861192
DNA replication-independent nucleosome as	14580	0.001019996	0.054861192
fatty acid transport (GO:0015908)	44793	0.001051912	0.055912234
carboxylic acid catabolic process (GO:004639	44724	0.001138084	0.059101858
carnitine metabolic process (GO:0009437)	44724	0.001138084	0.059101858
non-motile cilium assembly (GO:1905515)	44864	0.001340974	0.068846816
mitotic nuclear division (GO:0140014)	18/74	0.001469567	0.074302376
error-prone translesion synthesis (GO:00422	44794	0.001529465	0.074302376
intracellular lipid transport (GO:0032365)	44794	0.001529465	0.074302376

nucleotide-excision repair, DNA incision, 3'-tc	44794	0.001529465	0.074302376
nucleotide-excision repair, preincision compl	44794	0.001529465	0.074302376
L-phenylalanine metabolic process (GO:0006	44690	0.001681744	0.0799802
phosphatidylglycerol biosynthetic process (G	44690	0.001681744	0.0799802
DNA modification (GO:0006304)	44830	0.001720341	0.080963563
establishment of protein localization to plasn	13455	0.001745659	0.081308125
histone H2A monoubiquitination (GO:00355	44759	0.001784707	0.082278631
carboxylic acid biosynthetic process (GO:004	44725	0.00190892	0.086245023
UV-damage excision repair (GO:0070914)	44725	0.00190892	0.086245023
regulation of DNA recombination (GO:00000	15676	0.002080826	0.088870052
attachment of GPI anchor to protein (GO:001	44657	0.002148854	0.088870052
N-acetylneuraminate catabolic process (GO:0	44657	0.002148854	0.088870052
negative regulation of sequestering of triglyc	44657	0.002148854	0.088870052
regulation of protein localization to cilium (G	44657	0.002148854	0.088870052
regulation of t-circle formation (GO:1904429	44657	0.002148854	0.088870052
glutathione derivative biosynthetic process ((	44795	0.002163724	0.088870052
glutathione derivative metabolic process (GO	44795	0.002163724	0.088870052
nucleotide-excision repair, DNA duplex unwir	44795	0.002163724	0.088870052
protein mannosylation (GO:0035268)	44795	0.002163724	0.088870052
positive regulation of cytokinesis (GO:00324(	13820	0.002229948	0.090764908
DNA damage checkpoint signaling (GO:0000(	11963	0.002323579	0.093214386
Golgi to plasma membrane transport (GO:00	13/48	0.002341162	0.093214386
peptide metabolic process (GO:0006518)	19/83	0.002352023	0.093214386
DNA strand elongation involved in DNA replic	44760	0.002633253	0.101765675
protein O-linked mannosylation (GO:003526	44760	0.002633253	0.101765675
microtubule cytoskeleton organization involv	26/128	0.002635366	0.101765675
DNA replication initiation (GO:0006270)	14185	0.002817607	0.106974367
histone exchange (GO:0043486)	14185	0.002817607	0.106974367
very long-chain fatty acid metabolic process (	12328	0.002995546	0.107519584
cardiolipin metabolic process (GO:0032048)	44726	0.003017953	0.107519584
ribonucleoside monophosphate biosynthetic	44726	0.003017953	0.107519584
cellular response to acidic pH (GO:0071468)	44691	0.00304615	0.107519584
cellular response to oxidised low-density lipo	44691	0.00304615	0.107519584
mitotic DNA replication (GO:1902969)	44691	0.00304615	0.107519584
N-acetylneuraminate metabolic process (GO:	44691	0.00304615	0.107519584
regulation of glycoprotein biosynthetic proce	44691	0.00304615	0.107519584
serine family amino acid catabolic process (G	44691	0.00304615	0.107519584
positive regulation of cell division (GO:00517	16407	0.003194405	0.111878451
phosphatidic acid metabolic process (GO:004	13/50	0.003462302	0.120328327
fatty acid transmembrane transport (GO:190	44761	0.003760206	0.128701598
regulation of centriole replication (GO:00465	44761	0.003760206	0.128701598
sister chromatid segregation (GO:0000819)	12693	0.003813673	0.12955017
cellular response to oxidative stress (GO:003	25/125	0.003898866	0.131455795
dicarboxylic acid transport (GO:0006835)	44833	0.004011886	0.133091094
hydrogen peroxide metabolic process (GO:0(	44833	0.004011886	0.133091094
peptidyl-glutamic acid modification (GO:0018	44797	0.004035741	0.133091094
small GTPase mediated signal transduction ((	22/106	0.004111353	0.134602112

dicarboxylic acid metabolic process (GO:0043	14/57	0.004320163	0.140085944
organonitrogen compound catabolic process	15/63	0.004387231	0.140085944
mitotic recombination (GO:0006312)	44727	0.004545362	0.140085944
response to acidic pH (GO:0010447)	44727	0.004545362	0.140085944
ubiquinone metabolic process (GO:0006743)	44727	0.004545362	0.140085944
amino sugar catabolic process (GO:0046348)	44658	0.004557909	0.140085944
cardiolipin biosynthetic process (GO:003204	44658	0.004557909	0.140085944
regulation of vascular associated smooth mu	44658	0.004557909	0.140085944
xenobiotic catabolic process (GO:0042178)	44658	0.004557909	0.140085944
positive regulation of cell cycle process (GO:(	21/101	0.004872614	0.148284802
glycolipid metabolic process (GO:0006664)	13/52	0.004983824	0.148284802
formation of extrachromosomal circular DNA	44692	0.005059434	0.148284802
ketone body metabolic process (GO:190222	44692	0.005059434	0.148284802
t-circle formation (GO:0090656)	44692	0.005059434	0.148284802
telomere maintenance via telomere trimmin	44692	0.005059434	0.148284802
UDP-N-acetylglucosamine biosynthetic proce	44692	0.005059434	0.148284802
membrane lipid biosynthetic process (GO:00	14/58	0.005105213	0.148284802
CENP-A containing chromatin organization (G	44834	0.005156566	0.148284802
CENP-A containing nucleosome assembly (GO	44834	0.005156566	0.148284802
base-excision repair, AP site formation (GO:0	44762	0.005218522	0.148284802
cellular modified amino acid biosynthetic pro	44762	0.005218522	0.148284802
telomere organization (GO:0032200)	17502	0.005720406	0.16152997
organic substance transport (GO:0071702)	26/136	0.006136363	0.172199309
phosphate-containing compound metabolic p	37/212	0.006202729	0.172987207
translesion synthesis (GO:0019985)	15646	0.006520379	0.175743114
phosphatidylethanolamine metabolic proces	11567	0.006538655	0.175743114
purine nucleoside bisphosphate metabolic pr	11567	0.006538655	0.175743114
ribonucleoside bisphosphate metabolic proc	11567	0.006538655	0.175743114
DNA unwinding involved in DNA replication ((	44728	0.006573835	0.175743114
nuclear transport (GO:0051169)	44728	0.006573835	0.175743114
nucleoside diphosphate metabolic process (G	44728	0.006573835	0.175743114
cellular response to ionizing radiation (GO:00	17868	0.006846823	0.180900273
phosphatidic acid biosynthetic process (GO:0	17868	0.006846823	0.180900273
DNA geometric change (GO:0032392)	44799	0.006957664	0.181703629
global genome nucleotide-excision repair (GO	44799	0.006957664	0.181703629
proton transmembrane transport (GO:19026	13789	0.007359585	0.191095435
amino sugar biosynthetic process (GO:00463	44693	0.007860407	0.199799129
glycine metabolic process (GO:0006544)	44693	0.007860407	0.199799129
purine nucleoside monophosphate biosynthe	44693	0.007860407	0.199799129
DNA synthesis involved in DNA repair (GO:00	16011	0.007871679	0.199799129
protein transport (GO:0015031)	58/369	0.008177276	0.202461342
chromatin remodeling at centromere (GO:00	11933	0.008188036	0.202461342
diacylglycerol biosynthetic process (GO:0006	44659	0.00829025	0.202461342
negative regulation of macrophage migration	44659	0.00829025	0.202461342
negative regulation of sodium ion transport (	44659	0.00829025	0.202461342
negative regulation of vascular associated sm	44659	0.00829025	0.202461342
postsynapse organization (GO:0099173)	44659	0.00829025	0.202461342

sphingolipid biosynthetic process (GO:00301	16/74	0.008897801	0.215272937
bile acid biosynthetic process (GO:0006699)	44800	0.008910146	0.215272937
negative regulation of G0 to G1 transition (G	14154	0.008981723	0.215848007
dolichol-linked oligosaccharide biosynthetic p	44729	0.009186093	0.219591373
error-free translesion synthesis (GO:0070987	44764	0.009349416	0.22231927
cellular protein modification process (GO:00(	142/1025	0.009598322	0.227043019
bile acid metabolic process (GO:0008206)	12298	0.010135224	0.238494493
cellular response to chemical stress (GO:0062	20/101	0.010245178	0.23983272
DNA integrity checkpoint signaling (GO:0031!	14519	0.010863764	0.25300251
amide transport (GO:0042886)	44801	0.011243917	0.259183763
carbohydrate derivative biosynthetic process	44801	0.011243917	0.259183763
oligosaccharide-lipid intermediate biosynthet	44694	0.011580095	0.260915345
UDP-N-acetylglucosamine metabolic process	44694	0.011580095	0.260915345
nucleotide metabolic process (GO:0009117)	44765	0.012132809	0.260915345
nucleotide-excision repair, DNA damage reco	44765	0.012132809	0.260915345
cellular response to pH (GO:0071467)	44730	0.012462521	0.260915345
regulation of establishment or maintenance (	44730	0.012462521	0.260915345
response to axon injury (GO:0048678)	44730	0.012462521	0.260915345
amino-acid betaine biosynthetic process (GO	44625	0.012647291	0.260915345
carnitine biosynthetic process (GO:0045329)	44625	0.012647291	0.260915345
DNA replication, synthesis of RNA primer (GC	44625	0.012647291	0.260915345
double-strand break repair via synthesis-dep	44625	0.012647291	0.260915345
erythrose 4-phosphate/phosphoenolpyruvat	44625	0.012647291	0.260915345
ethanolamine-containing compound metabo	44625	0.012647291	0.260915345
fatty acid derivative catabolic process (GO:19	44625	0.012647291	0.260915345
folate transmembrane transport (GO:009883	44625	0.012647291	0.260915345
L-phenylalanine catabolic process (GO:00065	44625	0.012647291	0.260915345
leucine catabolic process (GO:0006552)	44625	0.012647291	0.260915345
N-acylethanolamine metabolic process (GO:0	44625	0.012647291	0.260915345
negative regulation of macrophage chemotax	44625	0.012647291	0.260915345
positive regulation of dendritic cell differenti	44625	0.012647291	0.260915345
positive regulation of DNA ligation (GO:0051:	44625	0.012647291	0.260915345
positive regulation of protein localization to (	44625	0.012647291	0.260915345
regulation of inflammatory response to wour	44625	0.012647291	0.260915345
phosphorylation (GO:0016310)	61/400	0.012766164	0.262170588
regulation of protein kinase activity (GO:004!	21/110	0.013058547	0.263266958
signal transduction in response to DNA dama	19329	0.013188814	0.263266958
exonucleolytic trimming involved in rRNA pro	44660	0.01357707	0.263266958
exonucleolytic trimming to generate mature	44660	0.01357707	0.263266958
fatty acid alpha-oxidation (GO:0001561)	44660	0.01357707	0.263266958
galactose metabolic process (GO:0006012)	44660	0.01357707	0.263266958
ketone body biosynthetic process (GO:00469	44660	0.01357707	0.263266958
L-ascorbic acid metabolic process (GO:00198	44660	0.01357707	0.263266958
N-acylphosphatidylethanolamine metabolic p	44660	0.01357707	0.263266958
nucleoside diphosphate phosphorylation (GO	44660	0.01357707	0.263266958
nucleoside triphosphate biosynthetic process	44660	0.01357707	0.263266958
nucleotide phosphorylation (GO:0046939)	44660	0.01357707	0.263266958

positive regulation of sequestering of triglyce	44660	0.01357707	0.263266958
regulation of cytokinesis (GO:0032465)	17/84	0.013837236	0.267165091
transition metal ion homeostasis (GO:00550	44802	0.013998982	0.269137866
platelet degranulation (GO:0002576)	23/125	0.01491913	0.285612841
negative regulation of organelle assembly (G	13028	0.015045952	0.286825362
regulation of G0 to G1 transition (GO:00703	15250	0.015505089	0.293994873
glycosphingolipid metabolic process (GO:000	17472	0.015552186	0.293994873
ether lipid metabolic process (GO:0046485)	44695	0.016336852	0.300040228
nucleoside phosphate biosynthetic process ((	44695	0.016336852	0.300040228
nucleoside triphosphate metabolic process ((	44695	0.016336852	0.300040228
pre-miRNA processing (GO:0031054)	44695	0.016336852	0.300040228
protein localization to vacuole (GO:0072665)	44695	0.016336852	0.300040228
quinone biosynthetic process (GO:1901663)	44695	0.016336852	0.300040228
respiratory electron transport chain (GO:002	44695	0.016336852	0.300040228
sphingosine metabolic process (GO:0006670)	44731	0.016478981	0.300209829
telomere capping (GO:0016233)	44731	0.016478981	0.300209829
Golgi to plasma membrane protein transport	44803	0.017214411	0.312348223
transcription-coupled nucleotide-excision rep	15/73	0.017515908	0.316547498
telomere maintenance via telomere lengther	13394	0.018070209	0.325263759
glycerophospholipid metabolic process (GO:(	16/80	0.018495147	0.330652233
anion transmembrane transport (GO:009865	14/67	0.01851594	0.330652233
glycerophospholipid biosynthetic process (G(	30/177	0.018728048	0.333123313
peroxisome organization (GO:0007031)	44767	0.019402744	0.342289081
iron ion homeostasis (GO:0055072)	13/61	0.019470627	0.342289081
positive regulation of DNA biosynthetic proce	13/61	0.019470627	0.342289081
regulation of mitotic cell cycle (GO:0007346)	30/178	0.020126271	0.351171338
acetyl-CoA biosynthetic process (GO:000608	44661	0.020597699	0.351171338
glycosphingolipid catabolic process (GO:0046	44661	0.020597699	0.351171338
long-chain fatty acid import into cell (GO:004	44661	0.020597699	0.351171338
membrane lipid catabolic process (GO:00464	44661	0.020597699	0.351171338
removal of superoxide radicals (GO:0019430)	44661	0.020597699	0.351171338
rRNA 3'-end processing (GO:0031125)	44661	0.020597699	0.351171338
UV protection (GO:0009650)	44661	0.020597699	0.351171338
cellular nitrogen compound biosynthetic proc	44804	0.020927722	0.352803916
regulation of cellular senescence (GO:200077	44804	0.020927722	0.352803916
steroid hormone biosynthetic process (GO:01	44804	0.020927722	0.352803916
folic acid-containing compound metabolic pr	44732	0.021304901	0.356026906
microtubule nucleation (GO:0007020)	44732	0.021304901	0.356026906
acyl-CoA metabolic process (GO:0006637)	13759	0.021512914	0.356026906
centromere complex assembly (GO:0034508)	13759	0.021512914	0.356026906
regulation of vascular associated smooth mu	13759	0.021512914	0.356026906
protein phosphorylation (GO:0006468)	72/496	0.021597291	0.35611884
medium-chain fatty acid metabolic process ((	44696	0.022232608	0.356902842
regulation of establishment of protein localiz	44696	0.022232608	0.356902842
ubiquinone biosynthetic process (GO:000674	44696	0.022232608	0.356902842
protein O-linked glycosylation (GO:0006493)	19/102	0.022436798	0.356902842
lipid transport (GO:0006869)	20/109	0.022737234	0.356902842

cellular carbohydrate catabolic process (GO:(	44626	0.023145758	0.356902842
cellular response to X-ray (GO:0071481)	44626	0.023145758	0.356902842
erythrose 4-phosphate/phosphoenolpyruvat(	44626	0.023145758	0.356902842
galactose catabolic process (GO:0019388)	44626	0.023145758	0.356902842
GDP-mannose metabolic process (GO:00196	44626	0.023145758	0.356902842
glycoside metabolic process (GO:0016137)	44626	0.023145758	0.356902842
glycosyl compound catabolic process (GO:19(	44626	0.023145758	0.356902842
histone-serine phosphorylation (GO:0035404	44626	0.023145758	0.356902842
isoleucine metabolic process (GO:0006549)	44626	0.023145758	0.356902842
negative regulation of lamellipodium organiz	44626	0.023145758	0.356902842
purine nucleobase biosynthetic process (GO:(	44626	0.023145758	0.356902842
regulation of cell cycle checkpoint (GO:19019	44626	0.023145758	0.356902842
regulation of hydrogen peroxide metabolic p(	44626	0.023145758	0.356902842
regulation of peptidyl-cysteine S-nitrosylatior	44626	0.023145758	0.356902842
negative regulation of receptor-mediated en(	44768	0.023987781	0.368628548
iron ion transport (GO:0006826)	18568	0.024254961	0.371470902
phospholipid metabolic process (GO:000664	15/76	0.024704813	0.377082254
GPI anchor biosynthetic process (GO:000650(	11902	0.02517429	0.382954351
hydrogen peroxide catabolic process (GO:00	44733	0.027001647	0.406091332
sterol transport (GO:0015918)	44733	0.027001647	0.406091332
vacuolar acidification (GO:0007035)	44733	0.027001647	0.406091332
cellular response to UV (GO:0034644)	15/77	0.02753235	0.406091332
purine ribonucleotide metabolic process (GO	15/77	0.02753235	0.406091332
cholesterol transport (GO:0030301)	18933	0.027818858	0.406091332
intrinsic apoptotic signaling pathway in respo	18933	0.027818858	0.406091332
lipid homeostasis (GO:0055088)	13/64	0.028228691	0.406091332
microtubule bundle formation (GO:0001578)	16711	0.028963314	0.406091332
monocarboxylic acid catabolic process (GO:0(	44769	0.02926496	0.406091332
negative regulation of plasma membrane bo(	44769	0.02926496	0.406091332
peroxisomal membrane transport (GO:00159	44769	0.02926496	0.406091332
ceramide catabolic process (GO:0046514)	44697	0.029350243	0.406091332
heme catabolic process (GO:0042167)	44697	0.029350243	0.406091332
negative regulation of telomere maintenance	44697	0.029350243	0.406091332
porphyrin-containing compound catabolic pr(	44697	0.029350243	0.406091332
purine ribonucleoside monophosphate biosy(	44697	0.029350243	0.406091332
regulation of cellular carbohydrate metabolic	44697	0.029350243	0.406091332
regulation of ceramide biosynthetic process (	44697	0.029350243	0.406091332
regulation of establishment of cell polarity (G	44697	0.029350243	0.406091332
regulation of fatty acid oxidation (GO:004632	44697	0.029350243	0.406091332
resolution of meiotic recombination interme(	44697	0.029350243	0.406091332
cellular glucan metabolic process (GO:00060	44662	0.029476725	0.406091332
cellular response to superoxide (GO:007145	44662	0.029476725	0.406091332
central nervous system myelination (GO:002	44662	0.029476725	0.406091332
negative regulation of centrosome duplicatio	44662	0.029476725	0.406091332
nuclear DNA replication (GO:0033260)	44662	0.029476725	0.406091332
positive regulation of ceramide biosynthetic	44662	0.029476725	0.406091332
positive regulation of sphingolipid biosynthet	44662	0.029476725	0.406091332

telomere maintenance via recombination (G	44662	0.029476725	0.406091332
peptidyl-serine modification (GO:0018209)	28/169	0.02948162	0.406091332
cellular iron ion homeostasis (GO:0006879)	21520	0.030013856	0.412165966
chemical homeostasis (GO:0048878)	13/65	0.03170316	0.431986054
positive regulation of protein localization to c	19299	0.031743995	0.431986054
protein homotetramerization (GO:0051289)	19299	0.031743995	0.431986054
postreplication repair (GO:0006301)	17076	0.033327814	0.452177369
fatty-acyl-CoA metabolic process (GO:00353	44734	0.033621243	0.454792738
fatty acid derivative biosynthetic process (GC	14855	0.034621406	0.46415285
glycolipid biosynthetic process (GO:0009247)	14855	0.034621406	0.46415285
sulfur compound catabolic process (GO:0044	14855	0.034621406	0.46415285
positive regulation of fibroblast proliferation	44770	0.035271981	0.464750579
protein localization to lysosome (GO:006146	44770	0.035271981	0.464750579
regulation of small molecule metabolic proce	44770	0.035271981	0.464750579
positive regulation of DNA binding (GO:0043	12632	0.035394744	0.464750579
cardiolipin acyl-chain remodeling (GO:00359(	44627	0.037086672	0.464750579
ganglioside catabolic process (GO:0006689)	44627	0.037086672	0.464750579
heme transport (GO:0015886)	44627	0.037086672	0.464750579
hemostasis (GO:0007599)	44627	0.037086672	0.464750579
left/right pattern formation (GO:0060972)	44627	0.037086672	0.464750579
leucine metabolic process (GO:0006551)	44627	0.037086672	0.464750579
miRNA loading onto RISC involved in gene sil	44627	0.037086672	0.464750579
negative regulation of centriole replication (G	44627	0.037086672	0.464750579
negative regulation of protein import (GO:19	44627	0.037086672	0.464750579
negative regulation of protein import into nu	44627	0.037086672	0.464750579
negative regulation of ruffle assembly (GO:19	44627	0.037086672	0.464750579
nucleobase biosynthetic process (GO:004611	44627	0.037086672	0.464750579
positive regulation of integrin-mediated signa	44627	0.037086672	0.464750579
positive regulation of potassium ion import a	44627	0.037086672	0.464750579
protein localization to ciliary membrane (GO:	44627	0.037086672	0.464750579
regulation of defense response to bacterium	44627	0.037086672	0.464750579
regulation of Rab protein signal transduction	44627	0.037086672	0.464750579
regulation of vascular associated smooth mu	44627	0.037086672	0.464750579
very long-chain fatty acid catabolic process (G	44627	0.037086672	0.464750579
regulation of protein localization to plasma m	15/80	0.037448347	0.464750579
diol biosynthetic process (GO:0034312)	44698	0.037751984	0.464750579
DNA biosynthetic process (GO:0071897)	44698	0.037751984	0.464750579
histone H2A ubiquitination (GO:0033522)	44698	0.037751984	0.464750579
modified amino acid transport (GO:0072337)	44698	0.037751984	0.464750579
negative regulation of cell aging (GO:009034	44698	0.037751984	0.464750579
positive regulation of muscle hypertrophy (G	44698	0.037751984	0.464750579
peptidyl-threonine phosphorylation (GO:001	22251	0.038079803	0.467512368
keratan sulfate catabolic process (GO:00423	44663	0.0402849	0.481500472
lysine catabolic process (GO:0006554)	44663	0.0402849	0.481500472
lysine metabolic process (GO:0006553)	44663	0.0402849	0.481500472
mitochondrial genome maintenance (GO:000	44663	0.0402849	0.481500472
negative regulation of cilium assembly (GO:1	44663	0.0402849	0.481500472

negative regulation of leukocyte chemotaxis	44663	0.0402849	0.481500472
negative regulation of microtubule polymeriz	44663	0.0402849	0.481500472
nonribosomal peptide biosynthetic process ((	44663	0.0402849	0.481500472
regulation of actin nucleation (GO:0051125)	44663	0.0402849	0.481500472
sphingoid metabolic process (GO:0046519)	44663	0.0402849	0.481500472
cellular response to amino acid starvation (G	14/74	0.040591451	0.482354979
glycosaminoglycan metabolic process (GO:00	20029	0.04074242	0.482354979
cytoskeleton-dependent intracellular transpc	44735	0.041205405	0.482354979
hyaluronan metabolic process (GO:0030212)	44735	0.041205405	0.482354979
positive regulation of cell cycle G2/M phase t	44735	0.041205405	0.482354979
protein deacylation (GO:0035601)	44735	0.041205405	0.482354979
proteolysis (GO:0006508)	43/287	0.041361752	0.482354979
oxoacid metabolic process (GO:0043436)	12997	0.041424022	0.482354979
regulation of TORC1 signaling (GO:1903432)	12997	0.041424022	0.482354979
smoothened signaling pathway (GO:0007224	12997	0.041424022	0.482354979
protein targeting to peroxisome (GO:000662	44771	0.04204067	0.488276984
response to amino acid starvation (GO:19905	14/75	0.044835447	0.519401405
cellular respiration (GO:0045333)	15585	0.045911987	0.529159079
regulation of double-strand break repair (GO	15585	0.045911987	0.529159079
amyloid precursor protein metabolic process	44699	0.047478712	0.537189726
dendritic cell migration (GO:0036336)	44699	0.047478712	0.537189726
hyaluronan catabolic process (GO:0030214)	44699	0.047478712	0.537189726
outer dynein arm assembly (GO:0036158)	44699	0.047478712	0.537189726
positive regulation of cardiac muscle hypertr	44699	0.047478712	0.537189726
prostanoid metabolic process (GO:0006692)	44699	0.047478712	0.537189726
regulation of telomere maintenance via telor	44699	0.047478712	0.537189726
glucose metabolic process (GO:0006006)	22981	0.047559958	0.537189726
regulation of sodium ion transport (GO:0002	13363	0.048096546	0.541895749
secondary alcohol metabolic process (GO:190	18172	0.049125909	0.55211656
alpha-amino acid catabolic process (GO:1901	44772	0.049596495	0.55264925
microtubule polymerization (GO:0046785)	44772	0.049596495	0.55264925
regulation of cation transmembrane transpor	44772	0.049596495	0.55264925
regulation of cardiac muscle hypertrophy (GO	44736	0.049784915	0.55264925
regulation of ruffle assembly (GO:1900027)	44736	0.049784915	0.55264925
glycosaminoglycan catabolic process (GO:000	20760	0.051366231	0.554444792
alpha-linolenic acid metabolic process (GO:0(	44664	0.053042607	0.554444792
DNA replication-independent nucleosome or	44664	0.053042607	0.554444792
myelination in peripheral nervous system (GO	44664	0.053042607	0.554444792
negative regulation of cellular senescence (G	44664	0.053042607	0.554444792
negative regulation of DNA-dependent DNA r	44664	0.053042607	0.554444792
negative regulation of nucleocytoplasmic tra	44664	0.053042607	0.554444792
positive regulation of calcineurin-mediated si	44664	0.053042607	0.554444792
positive regulation of calcineurin-NFAT signal	44664	0.053042607	0.554444792
positive regulation of calcium ion import (GO	44664	0.053042607	0.554444792
regulation of cell aging (GO:0090342)	44664	0.053042607	0.554444792
spindle assembly (GO:0051225)	15/84	0.054347524	0.554444792
aromatic compound catabolic process (GO:0(	44628	0.054364551	0.554444792

cellular response to epinephrine stimulus (G(	44628	0.054364551	0.554444792
cellular response to hepatocyte growth facto	44628	0.054364551	0.554444792
DNA damage induced protein phosphorylatio	44628	0.054364551	0.554444792
elastic fiber assembly (GO:0048251)	44628	0.054364551	0.554444792
establishment of protein localization to pero	44628	0.054364551	0.554444792
fructose metabolic process (GO:0006000)	44628	0.054364551	0.554444792
histone H2A-K119 monoubiquitination (GO:0	44628	0.054364551	0.554444792
lipid import into cell (GO:0140354)	44628	0.054364551	0.554444792
methionine metabolic process (GO:0006555)	44628	0.054364551	0.554444792
mitochondrial DNA replication (GO:0006264)	44628	0.054364551	0.554444792
negative regulation of glial cell apoptotic pro	44628	0.054364551	0.554444792
peptidyl-lysine deacetylation (GO:0034983)	44628	0.054364551	0.554444792
platelet activating factor metabolic process ((	44628	0.054364551	0.554444792
positive regulation of chromosome segregati	44628	0.054364551	0.554444792
positive regulation of leukocyte differentiatic	44628	0.054364551	0.554444792
positive regulation of triglyceride catabolic pı	44628	0.054364551	0.554444792
pre-replicative complex assembly involved in	44628	0.054364551	0.554444792
regulation of mitochondrial gene expression	44628	0.054364551	0.554444792
regulation of potassium ion import (GO:1903	44628	0.054364551	0.554444792
replication fork protection (GO:0048478)	44628	0.054364551	0.554444792
response to epinephrine (GO:0071871)	44628	0.054364551	0.554444792
response to hepatocyte growth factor (GO:0(	44628	0.054364551	0.554444792
somatic hypermutation of immunoglobulin g	44628	0.054364551	0.554444792
positive regulation of calcium ion transport ((	13728	0.055429968	0.561508059
regulation of actin cytoskeleton reorganizatic	13728	0.055429968	0.561508059
regulation of protein autophosphorylation (G	13728	0.055429968	0.561508059
sulfur compound biosynthetic process (GO:0(	19/113	0.056649554	0.572578718
prostaglandin metabolic process (GO:000669	44773	0.057958227	0.576051414
vitamin transport (GO:0051180)	44773	0.057958227	0.576051414
negative regulation of cell cycle process (GO:	23712	0.058542524	0.576051414
aspartate family amino acid catabolic proces	44700	0.058550055	0.576051414
aspartate family amino acid metabolic proce	44700	0.058550055	0.576051414
diol metabolic process (GO:0034311)	44700	0.058550055	0.576051414
DNA double-strand break processing (GO:00(	44700	0.058550055	0.576051414
folic acid metabolic process (GO:0046655)	44700	0.058550055	0.576051414
heparan sulfate proteoglycan biosynthetic pr	44700	0.058550055	0.576051414
positive regulation of actin cytoskeleton reor	44700	0.058550055	0.576051414
prostaglandin biosynthetic process (GO:0001	44700	0.058550055	0.576051414
regulated exocytosis (GO:0045055)	28/180	0.058880491	0.576051414
protein tetramerization (GO:0051262)	13/71	0.059195565	0.576051414
retrograde vesicle-mediated transport, Golgi	15/85	0.059280714	0.576051414
regulation of calcium ion import (GO:009027	44737	0.059379293	0.576051414
cation transmembrane transport (GO:00986	16316	0.059415662	0.576051414
hexose biosynthetic process (GO:0019319)	16316	0.059415662	0.576051414
mitotic spindle assembly (GO:0090307)	16316	0.059415662	0.576051414
positive regulation of receptor-mediated end	16316	0.059415662	0.576051414
protein-DNA complex assembly (GO:006500	23/143	0.059755921	0.578109744

regulation of protein modification process (G	18902	0.062057019	0.599088912
negative regulation of TOR signaling (GO:003	14093	0.063437456	0.611109649
epithelium development (GO:0060429)	20/122	0.064124123	0.616410189
regulation of cellular catabolic process (GO:0	24077	0.064619364	0.619851992
axonemal dynein complex assembly (GO:007	11871	0.067137737	0.629590959
positive regulation of telomere maintenance	11871	0.067137737	0.629590959
regulation of centrosome duplication (GO:00	11871	0.067137737	0.629590959
regulation of intracellular protein transport (	11871	0.067137737	0.629590959
regulation of transcription involved in G1/S t	11871	0.067137737	0.629590959
calcium ion import across plasma membrane	44665	0.067724924	0.629590959
dicarboxylic acid catabolic process (GO:0043	44665	0.067724924	0.629590959
negative regulation of cell activation (GO:005	44665	0.067724924	0.629590959
negative regulation of TORC1 signaling (GO:1	44665	0.067724924	0.629590959
nuclear pore organization (GO:0006999)	44665	0.067724924	0.629590959
positive regulation of sodium ion transmemb	44665	0.067724924	0.629590959
protein maturation by iron-sulfur cluster tran	44665	0.067724924	0.629590959
regulation of cAMP-dependent protein kinas	44665	0.067724924	0.629590959
regulation of gastrulation (GO:0010470)	44665	0.067724924	0.629590959
response to X-ray (GO:0010165)	44665	0.067724924	0.629590959
mitochondrion organization (GO:0007005)	27/175	0.067963679	0.630513143
post-translational protein modification (GO:0	49/345	0.068356195	0.632855101
cilium movement (GO:0003341)	19268	0.06927441	0.640044546
mononuclear cell differentiation (GO:190313	44738	0.069996755	0.641138017
negative regulation of telomere maintenance	44738	0.069996755	0.641138017
calcium ion transmembrane transport (GO:0(	15/87	0.070040139	0.641138017
lipid biosynthetic process (GO:0008610)	14/80	0.070727646	0.641138017
ganglioside metabolic process (GO:0001573)	44701	0.070965117	0.641138017
negative regulation of lipid storage (GO:0010	44701	0.070965117	0.641138017
positive regulation of G2/M transition of mit	44701	0.070965117	0.641138017
production of small RNA involved in gene sile	44701	0.070965117	0.641138017
purine ribonucleoside monophosphate meta	44701	0.070965117	0.641138017
regulation of nuclear division (GO:0051783)	44701	0.070965117	0.641138017
regulation of protein localization to cell perip	44701	0.070965117	0.641138017
positive regulation of cell cycle (GO:0045787	24442	0.07109565	0.641138017
neutrophil degranulation (GO:0043312)	66/481	0.071362521	0.642262686
positive regulation of intracellular transport (	14458	0.072127551	0.6433487
positive regulation of protein kinase activity (	24/154	0.074398979	0.6433487
amyloid-beta formation (GO:0034205)	44629	0.074758315	0.6433487
axon regeneration (GO:0031103)	44629	0.074758315	0.6433487
estrogen biosynthetic process (GO:0006703)	44629	0.074758315	0.6433487
fructose 1,6-bisphosphate metabolic process	44629	0.074758315	0.6433487
hepoxilin biosynthetic process (GO:0051122)	44629	0.074758315	0.6433487
hepoxilin metabolic process (GO:0051121)	44629	0.074758315	0.6433487
negative regulation of bone resorption (GO:0	44629	0.074758315	0.6433487
negative regulation of platelet aggregation (G	44629	0.074758315	0.6433487
negative regulation of smooth muscle cell dif	44629	0.074758315	0.6433487
peroxisomal transport (GO:0043574)	44629	0.074758315	0.6433487

positive regulation of chromatin binding (GO:	44629	0.074758315	0.6433487
positive regulation of extracellular matrix ass	44629	0.074758315	0.6433487
positive regulation of mitochondrial calcium i	44629	0.074758315	0.6433487
protein K6-linked ubiquitination (GO:008502(	44629	0.074758315	0.6433487
purine nucleobase metabolic process (GO:00	44629	0.074758315	0.6433487
regulation of ER to Golgi vesicle-mediated tra	44629	0.074758315	0.6433487
regulation of fibroblast apoptotic process (G(	44629	0.074758315	0.6433487
regulation of mammary gland epithelial cell p	44629	0.074758315	0.6433487
regulation of skeletal muscle cell differentiati	44629	0.074758315	0.6433487
response to misfolded protein (GO:0051788)	44629	0.074758315	0.6433487
small RNA loading onto RISC (GO:0070922)	44629	0.074758315	0.6433487
alpha-amino acid metabolic process (GO:190	17046	0.075226284	0.644919072
regulation of fibroblast proliferation (GO:004	17046	0.075226284	0.644919072
regulation of DNA replication (GO:0006275)	19633	0.07700177	0.657581423
keratan sulfate metabolic process (GO:00423	12236	0.077139919	0.657581423
positive regulation of organelle organization	12236	0.077139919	0.657581423
positive regulation of protein-containing com	19/118	0.080489786	0.684845295
neutrophil activation involved in immune res	66/485	0.081220796	0.688105037
nucleocytoplasmic transport (GO:0006913)	14824	0.081504093	0.688105037
positive regulation of catalytic activity (GO:0(	14824	0.081504093	0.688105037
regulation of microtubule polymerization (GO	14824	0.081504093	0.688105037
cellular lipid catabolic process (GO:0044242)	44739	0.081634418	0.688105037
phosphatidylinositol biosynthetic process (GO	20/126	0.08358516	0.692027786
regulation of DNA binding (GO:0051101)	17411	0.084011767	0.692027786
acetyl-CoA metabolic process (GO:0006084)	44666	0.084267598	0.692027786
C21-steroid hormone biosynthetic process (G	44666	0.084267598	0.692027786
calcium ion import into cytosol (GO:1902656	44666	0.084267598	0.692027786
cellular response to ATP (GO:0071318)	44666	0.084267598	0.692027786
electron transport chain (GO:0022900)	44666	0.084267598	0.692027786
icosanoid biosynthetic process (GO:0046456)	44666	0.084267598	0.692027786
nitric oxide biosynthetic process (GO:000680	44666	0.084267598	0.692027786
protein localization to chromosome, telomer	44666	0.084267598	0.692027786
regulation of clathrin-dependent endocytosis	44666	0.084267598	0.692027786
T cell proliferation (GO:0042098)	44666	0.084267598	0.692027786
androgen metabolic process (GO:0008209)	44702	0.084703711	0.692027786
heparan sulfate proteoglycan metabolic proc	44702	0.084703711	0.692027786
positive regulation of lipid storage (GO:0010(	44702	0.084703711	0.692027786
positive regulation of vascular associated sm	44702	0.084703711	0.692027786
regulation of cholesterol metabolic process (	44702	0.084703711	0.692027786
protein maturation (GO:0051604)	16/97	0.086594321	0.699984745
axoneme assembly (GO:0035082)	12601	0.087962748	0.699984745
negative regulation of mitochondrion organiz	12601	0.087962748	0.699984745
neural tube closure (GO:0001843)	12601	0.087962748	0.699984745
protein localization to chromosome (GO:003	12601	0.087962748	0.699984745
positive regulation of cellular biosynthetic pr	27/180	0.089001589	0.699984745
neutrophil mediated immunity (GO:0002446)	66/488	0.089221768	0.699984745
mitochondrial translation (GO:0032543)	17/105	0.090674654	0.699984745

cellular response to organic cyclic compound	23/150	0.09124038	0.699984745
carbohydrate catabolic process (GO:0016052	15189	0.091566212	0.699984745
carboxylic acid transmembrane transport (GO	15189	0.091566212	0.699984745
import into cell (GO:0098657)	15189	0.091566212	0.699984745
positive regulation of DNA repair (GO:00457	17777	0.093385324	0.699984745
positive regulation of endocytosis (GO:00458	17777	0.093385324	0.699984745
double-strand break repair via nonhomologo	22951	0.093774297	0.699984745
negative regulation of kinase activity (GO:00	22951	0.093774297	0.699984745
ceramide metabolic process (GO:0006672)	20363	0.093997595	0.699984745
glycogen metabolic process (GO:0005977)	44740	0.094278726	0.699984745
GPI anchor metabolic process (GO:0006505)	44740	0.094278726	0.699984745
macromolecule catabolic process (GO:00090	44740	0.094278726	0.699984745
regulation of calcineurin-NFAT signaling casc	44740	0.094278726	0.699984745
regulation of neuron migration (GO:2001222	44740	0.094278726	0.699984745
regulation of plasma membrane bounded cel	44740	0.094278726	0.699984745
transcription by RNA polymerase III (GO:000	44740	0.094278726	0.699984745
cellular macromolecule biosynthetic process	44/314	0.094724208	0.699984745
peptidyl-lysine modification (GO:0018205)	17/106	0.097005332	0.699984745
aromatic amino acid family metabolic proces	44630	0.097970027	0.699984745
calcium import into the mitochondrion (GO:0	44630	0.097970027	0.699984745
cellular response to leucine (GO:0071233)	44630	0.097970027	0.699984745
DNA replication-dependent nucleosome asse	44630	0.097970027	0.699984745
DNA replication-dependent nucleosome orga	44630	0.097970027	0.699984745
ether lipid biosynthetic process (GO:0008611	44630	0.097970027	0.699984745
L-glutamate transmembrane transport (GO:0	44630	0.097970027	0.699984745
lipoprotein transport (GO:0042953)	44630	0.097970027	0.699984745
negative regulation of transcription from RN	44630	0.097970027	0.699984745
neuron projection regeneration (GO:003110	44630	0.097970027	0.699984745
nuclear pore complex assembly (GO:005129	44630	0.097970027	0.699984745
nucleic acid transport (GO:0050657)	44630	0.097970027	0.699984745
phosphatidylcholine catabolic process (GO:0	44630	0.097970027	0.699984745
pinocytosis (GO:0006907)	44630	0.097970027	0.699984745
production of siRNA involved in RNA interfer	44630	0.097970027	0.699984745
regulation of attachment of spindle microtub	44630	0.097970027	0.699984745
regulation of DNA damage checkpoint (GO:2	44630	0.097970027	0.699984745
regulation of hair cycle (GO:0042634)	44630	0.097970027	0.699984745
regulation of low-density lipoprotein particle	44630	0.097970027	0.699984745
regulation of macrophage migration (GO:190	44630	0.097970027	0.699984745
regulation of microtubule nucleation (GO:00	44630	0.097970027	0.699984745
regulation of RNA polymerase II transcription	44630	0.097970027	0.699984745
response to leucine (GO:0043201)	44630	0.097970027	0.699984745
telomere maintenance in response to DNA da	44630	0.097970027	0.699984745
urea cycle (GO:0000050)	44630	0.097970027	0.699984745
phosphatidylcholine metabolic process (GO:0	13/77	0.099352045	0.699984745
response to UV (GO:0009411)	16/99	0.099683529	0.699984745
heme biosynthetic process (GO:0006783)	44703	0.099727975	0.699984745
positive regulation of axon extension (GO:00	44703	0.099727975	0.699984745

regulation of macrophage chemotaxis (GO:0(	44703	0.099727975	0.699984745
regulation of vacuole organization (GO:0044(	44703	0.099727975	0.699984745
sterol metabolic process (GO:0016125)	25903	0.101071666	0.699984745
calcium ion transmembrane import into cyto	15554	0.102308387	0.699984745
determination of left/right symmetry (GO:00	15554	0.102308387	0.699984745
positive regulation of ATPase activity (GO:00	15554	0.102308387	0.699984745
apoptotic DNA fragmentation (GO:0006309)	44667	0.102573395	0.699984745
aromatic amino acid family catabolic process	44667	0.102573395	0.699984745
N-acetylglucosamine metabolic process (GO:(	44667	0.102573395	0.699984745
negative regulation of platelet activation (GO	44667	0.102573395	0.699984745
negative regulation of release of cytochrome	44667	0.102573395	0.699984745
neural tube development (GO:0021915)	44667	0.102573395	0.699984745
nitric oxide metabolic process (GO:0046209)	44667	0.102573395	0.699984745
positive regulation of TORC1 signaling (GO:19	44667	0.102573395	0.699984745
sphingolipid catabolic process (GO:0030149)	44667	0.102573395	0.699984745
aggresome assembly (GO:0070842)	44597	0.104114597	0.699984745
alditol phosphate metabolic process (GO:005	44597	0.104114597	0.699984745
CD4-positive, alpha-beta T cell activation (GO	44597	0.104114597	0.699984745
cellular response to salt stress (GO:0071472)	44597	0.104114597	0.699984745
cellular response to vitamin (GO:0071295)	44597	0.104114597	0.699984745
de novo centriole assembly (GO:0097742)	44597	0.104114597	0.699984745
de novo centriole assembly involved in multi-	44597	0.104114597	0.699984745
deoxyribonucleotide metabolic process (GO:(	44597	0.104114597	0.699984745
DNA double-strand break processing involve(	44597	0.104114597	0.699984745
DNA protection (GO:0042262)	44597	0.104114597	0.699984745
double-strand break repair via single-strand a	44597	0.104114597	0.699984745
drug transport (GO:0015893)	44597	0.104114597	0.699984745
establishment of protein localization to telon	44597	0.104114597	0.699984745
establishment of T cell polarity (GO:0001768)	44597	0.104114597	0.699984745
glucose import in response to insulin stimulu	44597	0.104114597	0.699984745
histone-threonine phosphorylation (GO:0035	44597	0.104114597	0.699984745
L-methionine salvage from methylthioadeno	44597	0.104114597	0.699984745
left/right axis specification (GO:0070986)	44597	0.104114597	0.699984745
meiotic mismatch repair (GO:0000710)	44597	0.104114597	0.699984745
mitochondrial DNA repair (GO:0043504)	44597	0.104114597	0.699984745
negative regulation of cardiac muscle cell pro	44597	0.104114597	0.699984745
negative regulation of cholesterol biosynthet	44597	0.104114597	0.699984745
negative regulation of cholesterol metabolic	44597	0.104114597	0.699984745
negative regulation of cysteine-type endopep	44597	0.104114597	0.699984745
negative regulation of hydrogen peroxide me	44597	0.104114597	0.699984745
negative regulation of regulatory T cell differ	44597	0.104114597	0.699984745
negative regulation of smooth muscle cell ap	44597	0.104114597	0.699984745
negative regulation of sphingolipid biosynthe	44597	0.104114597	0.699984745
negative regulation of sterol biosynthetic pro	44597	0.104114597	0.699984745
plus-end-directed vesicle transport along mic	44597	0.104114597	0.699984745
positive regulation of basement membrane a	44597	0.104114597	0.699984745
positive regulation of glycoprotein metabolic	44597	0.104114597	0.699984745

positive regulation of low-density lipoprotein	44597	0.104114597	0.699984745
positive regulation of toll-like receptor 9 sign	44597	0.104114597	0.699984745
positive regulation of translation in response	44597	0.104114597	0.699984745
positive regulation of vascular associated sm	44597	0.104114597	0.699984745
protein lipoylation (GO:0009249)	44597	0.104114597	0.699984745
protein processing involved in protein targeti	44597	0.104114597	0.699984745
pyrimidine ribonucleotide metabolic process	44597	0.104114597	0.699984745
regulation of adenylate cyclase-activating G p	44597	0.104114597	0.699984745
regulation of barbed-end actin filament capp	44597	0.104114597	0.699984745
regulation of basement membrane assembly	44597	0.104114597	0.699984745
regulation of cellular response to vascular en	44597	0.104114597	0.699984745
regulation of intestinal lipid absorption (GO:1	44597	0.104114597	0.699984745
regulation of intracellular cholesterol transpo	44597	0.104114597	0.699984745
RNA import into mitochondrion (GO:003592	44597	0.104114597	0.699984745
rRNA transport (GO:0051029)	44597	0.104114597	0.699984745
succinyl-CoA metabolic process (GO:000610	44597	0.104114597	0.699984745
transcription initiation from RNA polymerase	44597	0.104114597	0.699984745
G1/S transition of mitotic cell cycle (GO:0000	14/85	0.104895879	0.704189569
Golgi organization (GO:0007030)	20/130	0.106581096	0.714441232
calcium ion transport (GO:0006816)	18/115	0.107080165	0.716723239
determination of bilateral symmetry (GO:000	44741	0.107906051	0.717996378
production of miRNAs involved in gene silenc	44741	0.107906051	0.717996378
protein ADP-ribosylation (GO:0006471)	44741	0.107906051	0.717996378
regulation of neuronal synaptic plasticity (GO	44741	0.107906051	0.717996378
regulation of TOR signaling (GO:0032006)	26268	0.109588842	0.728121161
negative regulation of DNA metabolic proces	13332	0.11202869	0.738898716
negative regulation of fat cell differentiation	13332	0.11202869	0.738898716
regulation of receptor internalization (GO:00	13332	0.11202869	0.738898716
transferrin transport (GO:0033572)	13332	0.11202869	0.738898716
transition metal ion transport (GO:0000041)	13332	0.11202869	0.738898716
transport across blood-brain barrier (GO:015	14/86	0.112748709	0.742563657
regulation of mitotic nuclear division (GO:00	21094	0.113041405	0.743407671
organic hydroxy compound biosynthetic proc	18507	0.113880295	0.747836008
acylglycerol biosynthetic process (GO:00464	44704	0.115984253	0.75181758
diacylglycerol metabolic process (GO:004633	44704	0.115984253	0.75181758
hexose transmembrane transport (GO:00086	44704	0.115984253	0.75181758
mitotic cell cycle checkpoint signaling (GO:00	44704	0.115984253	0.75181758
negative regulation of reactive oxygen specie	44704	0.115984253	0.75181758
positive regulation of protein autophosphory	44704	0.115984253	0.75181758
positive regulation of receptor internalizatior	44704	0.115984253	0.75181758
regulation of steroid metabolic process (GO:(	44704	0.115984253	0.75181758
regulation of telomere capping (GO:1904353	44704	0.115984253	0.75181758
regulation of programmed cell death (GO:00	28/194	0.120576483	0.7559857
protein autoubiquitination (GO:0051865)	24047	0.121095688	0.7559857
intrinsic apoptotic signaling pathway (GO:00	16/102	0.121496337	0.7559857
cellular protein localization (GO:0034613)	45/329	0.122208935	0.7559857
protein N-linked glycosylation via asparagine	44742	0.122483446	0.7559857

amyloid-beta metabolic process (GO:005043	44668	0.122518455	0.7559857
monosaccharide transmembrane transport (	44668	0.122518455	0.7559857
negative regulation of vascular associated sm	44668	0.122518455	0.7559857
positive regulation of cyclin-dependent prote	44668	0.122518455	0.7559857
positive regulation of telomere capping (GO:	44668	0.122518455	0.7559857
protein heterooligomerization (GO:0051291)	44668	0.122518455	0.7559857
regulation of cellular response to growth fact	44668	0.122518455	0.7559857
RNA interference (GO:0016246)	44668	0.122518455	0.7559857
mitochondrial respiratory chain complex I ass	21459	0.123319248	0.7559857
NADH dehydrogenase complex assembly (GC	21459	0.123319248	0.7559857
positive regulation of mitochondrion organiz	21459	0.123319248	0.7559857
calcineurin-NFAT signaling cascade (GO:0033	44631	0.123655031	0.7559857
cellular response to UV-A (GO:0071492)	44631	0.123655031	0.7559857
cyclooxygenase pathway (GO:0019371)	44631	0.123655031	0.7559857
glutathione biosynthetic process (GO:000675	44631	0.123655031	0.7559857
glycerolipid metabolic process (GO:0046486)	44631	0.123655031	0.7559857
hepatocyte growth factor receptor signaling	44631	0.123655031	0.7559857
lipoprotein catabolic process (GO:0042159)	44631	0.123655031	0.7559857
lipoprotein localization (GO:0044872)	44631	0.123655031	0.7559857
mitochondrial protein processing (GO:00349	44631	0.123655031	0.7559857
mitochondrion morphogenesis (GO:0070584	44631	0.123655031	0.7559857
monocyte differentiation (GO:0030224)	44631	0.123655031	0.7559857
negative regulation of bone remodeling (GO:	44631	0.123655031	0.7559857
negative regulation of homotypic cell-cell adl	44631	0.123655031	0.7559857
peptidyl-proline hydroxylation (GO:0019511)	44631	0.123655031	0.7559857
positive regulation of bone resorption (GO:0(	44631	0.123655031	0.7559857
protein kinase C-activating G protein-couplec	44631	0.123655031	0.7559857
protein polyglutamylation (GO:0018095)	44631	0.123655031	0.7559857
regulation of biosynthetic process (GO:00098	44631	0.123655031	0.7559857
regulation of histone H3-K9 acetylation (GO:2	44631	0.123655031	0.7559857
regulation of lamellipodium morphogenesis (	44631	0.123655031	0.7559857
regulation of lipid kinase activity (GO:004355	44631	0.123655031	0.7559857
regulation of long-term neuronal synaptic pla	44631	0.123655031	0.7559857
regulation of melanin biosynthetic process (G	44631	0.123655031	0.7559857
regulation of mitochondrial fusion (GO:0010(	44631	0.123655031	0.7559857
regulation of pH (GO:0006885)	44631	0.123655031	0.7559857
response to prostaglandin E (GO:0034695)	44631	0.123655031	0.7559857
negative regulation of cellular component or	13/80	0.124425464	0.759667898
regulation of smoothened signaling pathway	18872	0.124985286	0.76050002
phospholipid biosynthetic process (GO:0008(	13697	0.125235063	0.76050002
regulation of intracellular steroid hormone re	13697	0.125235063	0.76050002
tRNA transport (GO:0051031)	13697	0.125235063	0.76050002
peptidyl-serine phosphorylation (GO:001810	23/156	0.125589354	0.761627787
apoptotic nuclear changes (GO:0030262)	44705	0.133405138	0.79670546
C21-steroid hormone metabolic process (GO:	44705	0.133405138	0.79670546
cellular response to catecholamine stimulus (	44705	0.133405138	0.79670546
extracellular matrix assembly (GO:0085029)	44705	0.133405138	0.79670546

histone monoubiquitination (GO:0010390)	44705	0.133405138	0.79670546
porphyrin-containing compound biosynthetic	44705	0.133405138	0.79670546
positive regulation of carbohydrate metaboli	44705	0.133405138	0.79670546
sulfur amino acid metabolic process (GO:000	44705	0.133405138	0.79670546
positive regulation of cellular amide metabol	13/81	0.133514168	0.79670546
cellular transition metal ion homeostasis (GO	15/96	0.133776799	0.79670546
mitotic DNA damage checkpoint signaling (G(	21824	0.134089676	0.79670546
positive regulation of protein localization to p	19238	0.136645706	0.79670546
activation of protein kinase B activity (GO:00	11475	0.137969504	0.79670546
aminoglycan catabolic process (GO:0006026)	11475	0.137969504	0.79670546
negative regulation of response to DNA dam	11475	0.137969504	0.79670546
peptidyl-asparagine modification (GO:00181	11475	0.137969504	0.79670546
proteoglycan biosynthetic process (GO:0030	11475	0.137969504	0.79670546
regulation of transmembrane receptor prote	11475	0.137969504	0.79670546
tube closure (GO:0060606)	11475	0.137969504	0.79670546
SCF-dependent proteasomal ubiquitin-depen	14/89	0.138321379	0.79670546
regulation of axon extension (GO:0030516)	14062	0.139189366	0.79670546
regulation of macroautophagy (GO:0016241)	17/112	0.140659677	0.79670546
peptidyl-threonine modification (GO:001821	24777	0.141529857	0.79670546
regulation of cyclin-dependent protein serine	13/82	0.142960123	0.79670546
acidic amino acid transport (GO:0015800)	44669	0.14395839	0.79670546
cellular response to alkaloid (GO:0071312)	44669	0.14395839	0.79670546
melanosome transport (GO:0032402)	44669	0.14395839	0.79670546
microtubule depolymerization (GO:0007019)	44669	0.14395839	0.79670546
negative regulation of tumor necrosis factor-	44669	0.14395839	0.79670546
nucleotide biosynthetic process (GO:000916	44669	0.14395839	0.79670546
pigment granule transport (GO:0051904)	44669	0.14395839	0.79670546
positive regulation of fatty acid metabolic pr	44669	0.14395839	0.79670546
protein localization to centrosome (GO:0071	44669	0.14395839	0.79670546
regulation of platelet aggregation (GO:00903	44669	0.14395839	0.79670546
regulation of vascular endothelial cell prolife	44669	0.14395839	0.79670546
sodium ion import across plasma membrane	44669	0.14395839	0.79670546
3'-phosphoadenosine 5'-phosphosulfate bios	44598	0.144599043	0.79670546
activation of cysteine-type endopeptidase ac	44598	0.144599043	0.79670546
carnitine transport (GO:0015879)	44598	0.144599043	0.79670546
cellular hyperosmotic response (GO:007147	44598	0.144599043	0.79670546
cellular lipid biosynthetic process (GO:00973	44598	0.144599043	0.79670546
cholesterol import (GO:0070508)	44598	0.144599043	0.79670546
establishment of lymphocyte polarity (GO:00	44598	0.144599043	0.79670546
gastrulation with mouth forming second (GO	44598	0.144599043	0.79670546
glycerol ether biosynthetic process (GO:0046	44598	0.144599043	0.79670546
hydrogen peroxide biosynthetic process (GO:	44598	0.144599043	0.79670546
inclusion body assembly (GO:0070841)	44598	0.144599043	0.79670546
melanosome assembly (GO:1903232)	44598	0.144599043	0.79670546
mitochondrial proton-transporting ATP synth	44598	0.144599043	0.79670546
mitotic DNA replication initiation (GO:19029	44598	0.144599043	0.79670546
negative regulation of cardiac muscle tissue g	44598	0.144599043	0.79670546

negative regulation of fat cell proliferation (G	44598	0.144599043	0.79670546
negative regulation of glucocorticoid recepto	44598	0.144599043	0.79670546
negative regulation of histone H3-K9 methyla	44598	0.144599043	0.79670546
neuroblast proliferation (GO:0007405)	44598	0.144599043	0.79670546
nuclear cell cycle DNA replication initiation (G	44598	0.144599043	0.79670546
plus-end-directed organelle transport along r	44598	0.144599043	0.79670546
positive regulation of cholesterol metabolic p	44598	0.144599043	0.79670546
positive regulation of ion transmembrane tra	44598	0.144599043	0.79670546
positive regulation of lipoprotein particle cle	44598	0.144599043	0.79670546
positive regulation of microglial cell activatio	44598	0.144599043	0.79670546
positive regulation of nuclear cell cycle DNA r	44598	0.144599043	0.79670546
positive regulation of T-helper 2 cell differen	44598	0.144599043	0.79670546
protein K27-linked ubiquitination (GO:00443	44598	0.144599043	0.79670546
protein K29-linked ubiquitination (GO:00355	44598	0.144599043	0.79670546
protein localization to non-motile cilium (GO	44598	0.144599043	0.79670546
protein repair (GO:0030091)	44598	0.144599043	0.79670546
pteridine-containing compound biosynthetic	44598	0.144599043	0.79670546
purine ribonucleoside bisphosphate biosynth	44598	0.144599043	0.79670546
regulation of endoplasmic reticulum tubular	44598	0.144599043	0.79670546
regulation of glomerular filtration (GO:00030	44598	0.144599043	0.79670546
regulation of T cell activation via T cell recept	44598	0.144599043	0.79670546
sterol import (GO:0035376)	44598	0.144599043	0.79670546
tyrosine catabolic process (GO:0006572)	44598	0.144599043	0.79670546
valine metabolic process (GO:0006573)	44598	0.144599043	0.79670546
positive regulation of apoptotic process (GO:	42/310	0.145286377	0.799517479
activation of GTPase activity (GO:0090630)	16/105	0.145891195	0.801869125
mitochondrial respiratory chain complex asse	14/90	0.147503526	0.805559425
IRE1-mediated unfolded protein response (G	19603	0.148845604	0.805559425
protein homooligomerization (GO:0051260)	18/121	0.151407477	0.805559425
calcineurin-mediated signaling (GO:0097720)	44632	0.151445088	0.805559425
double-strand break repair via break-induced	44632	0.151445088	0.805559425
exit from mitosis (GO:0010458)	44632	0.151445088	0.805559425
inorganic ion transmembrane transport (GO:	44632	0.151445088	0.805559425
intrinsic apoptotic signaling pathway in respo	44632	0.151445088	0.805559425
microtubule anchoring (GO:0034453)	44632	0.151445088	0.805559425
negative regulation of JUN kinase activity (GO	44632	0.151445088	0.805559425
negative regulation of leukocyte apoptotic pr	44632	0.151445088	0.805559425
negative regulation of receptor internalizatio	44632	0.151445088	0.805559425
negative regulation of release of sequestered	44632	0.151445088	0.805559425
negative regulation of ryanodine-sensitive ca	44632	0.151445088	0.805559425
nucleotide-sugar metabolic process (GO:000	44632	0.151445088	0.805559425
positive regulation of actin filament depolym	44632	0.151445088	0.805559425
positive regulation of sodium ion transmemb	44632	0.151445088	0.805559425
protein import into peroxisome matrix (GO:0	44632	0.151445088	0.805559425
protein localization to condensed chromosor	44632	0.151445088	0.805559425
pyrimidine-containing compound metabolic p	44632	0.151445088	0.805559425
regulation of chromatin binding (GO:003556	44632	0.151445088	0.805559425

regulation of dendritic cell differentiation (G(	44632	0.151445088	0.805559425
regulation of DNA-dependent DNA replicatio	44632	0.151445088	0.805559425
regulation of oxidative stress-induced cell de	44632	0.151445088	0.805559425
regulation of triglyceride catabolic process (G	44632	0.151445088	0.805559425
replicative senescence (GO:0090399)	44632	0.151445088	0.805559425
regulation of double-strand break repair via h	17015	0.151812432	0.805559425
3'-phosphoadenosine 5'-phosphosulfate met	44706	0.151911605	0.805559425
peripheral nervous system development (GO	44706	0.151911605	0.805559425
regulation of cholesterol transport (GO:0032	44706	0.151911605	0.805559425
long-chain fatty acid metabolic process (GO:(	13/83	0.152756531	0.80909028
muscle contraction (GO:0006936)	19/129	0.153578061	0.812074298
negative regulation of cellular metabolic proc	14427	0.153859141	0.812074298
organophosphate biosynthetic process (GO:(	14427	0.153859141	0.812074298
negative regulation of microtubule polymeriz	11841	0.154315301	0.812094828
superoxide metabolic process (GO:0006801)	11841	0.154315301	0.812094828
protein processing (GO:0016485)	16/106	0.154582017	0.812094828
regulation of cell cycle process (GO:0010564)	16/106	0.154582017	0.812094828
negative regulation of response to stimulus ((	22555	0.157060065	0.823198812
response to light stimulus (GO:0009416)	22555	0.157060065	0.823198812
cytoplasmic microtubule organization (GO:0(	19968	0.161566221	0.844856695
regulation of proteasomal protein catabolic p	19968	0.161566221	0.844856695
endoplasmic reticulum to Golgi vesicle-media	26/185	0.161761054	0.84489762
positive regulation of protein transport (GO:(	25508	0.163658213	0.853819637
regulation of apoptotic process (GO:0042981	94/742	0.165342052	0.858955526
polyol metabolic process (GO:0019751)	17380	0.165720263	0.858955526
establishment of melanosome localization (G	44670	0.166733952	0.858955526
mitochondrion localization (GO:0051646)	44670	0.166733952	0.858955526
N-glycan processing (GO:0006491)	44670	0.166733952	0.858955526
negative regulation of protein localization to	44670	0.166733952	0.858955526
NLS-bearing protein import into nucleus (GO:	44670	0.166733952	0.858955526
pore complex assembly (GO:0046931)	44670	0.166733952	0.858955526
positive regulation of triglyceride metabolic p	44670	0.166733952	0.858955526
regulation of neuroinflammatory response (G	44670	0.166733952	0.858955526
response to ATP (GO:0033198)	44670	0.166733952	0.858955526
regulation of anatomical structure morphoge	18/123	0.168141153	0.865218372
carboxylic acid metabolic process (GO:00197	14793	0.169207185	0.869328112
organic acid transport (GO:0015849)	15/100	0.170073371	0.869328112
cellular response to drug (GO:0035690)	44707	0.171415145	0.869328112
hippo signaling (GO:0035329)	44707	0.171415145	0.869328112
purine-containing compound biosynthetic pr	44707	0.171415145	0.869328112
apoptotic cell clearance (GO:0043277)	12206	0.17146539	0.869328112
apoptotic mitochondrial changes (GO:00086	12206	0.17146539	0.869328112
lytic vacuole organization (GO:0080171)	12206	0.17146539	0.869328112
mitotic G2 DNA damage checkpoint signaling	12206	0.17146539	0.869328112
phosphatidylcholine biosynthetic process (G(	12206	0.17146539	0.869328112
positive regulation of ATP metabolic process	12206	0.17146539	0.869328112
primary alcohol metabolic process (GO:0034	12206	0.17146539	0.869328112

regulation of cholesterol efflux (GO:0010874	12206	0.17146539	0.869328112
glycoprotein metabolic process (GO:0009100	20333	0.174786171	0.869328112
cellular response to alcohol (GO:0097306)	17746	0.180187254	0.869328112
inositol phosphate metabolic process (GO:00	17746	0.180187254	0.869328112
substrate adhesion-dependent cell spreading	17746	0.180187254	0.869328112
negative regulation of apoptotic signaling pat	28825	0.180217884	0.869328112
cell part morphogenesis (GO:0032990)	44633	0.18096584	0.869328112
cellular component maintenance (GO:00439	44633	0.18096584	0.869328112
cytoplasmic sequestering of protein (GO:005	44633	0.18096584	0.869328112
fatty acid elongation (GO:0030497)	44633	0.18096584	0.869328112
glucan biosynthetic process (GO:0009250)	44633	0.18096584	0.869328112
glucose import (GO:0046323)	44633	0.18096584	0.869328112
glycogen biosynthetic process (GO:0005978)	44633	0.18096584	0.869328112
intracellular sterol transport (GO:0032366)	44633	0.18096584	0.869328112
macrophage activation involved in immune r	44633	0.18096584	0.869328112
negative regulation of hydrogen peroxide-inc	44633	0.18096584	0.869328112
negative regulation of macrophage derived f	44633	0.18096584	0.869328112
positive regulation of neuron migration (GO:2	44633	0.18096584	0.869328112
positive regulation of protein acetylation (GC	44633	0.18096584	0.869328112
positive regulation of ruffle assembly (GO:19	44633	0.18096584	0.869328112
positive regulation of vascular endothelial ce	44633	0.18096584	0.869328112
protein heterotetramerization (GO:0051290)	44633	0.18096584	0.869328112
regulation of actomyosin structure organizati	44633	0.18096584	0.869328112
regulation of mitotic cell cycle spindle assem	44633	0.18096584	0.869328112
regulation of protein acetylation (GO:190198	44633	0.18096584	0.869328112
response to nitric oxide (GO:0071731)	44633	0.18096584	0.869328112
sphingoid biosynthetic process (GO:0046520	44633	0.18096584	0.869328112
sphingosine biosynthetic process (GO:00465	44633	0.18096584	0.869328112
very long-chain fatty acid biosynthetic proces	44633	0.18096584	0.869328112
regulation of signal transduction by p53 class	22/156	0.18137285	0.869328112
cell cycle G1/S phase transition (GO:0044843	23285	0.181834349	0.869328112
positive regulation of DNA metabolic process	23285	0.181834349	0.869328112
positive regulation of endothelial cell migrati	13/86	0.184162653	0.869328112
gluconeogenesis (GO:0006094)	15158	0.185192093	0.869328112
positive regulation of TOR signaling (GO:003	15158	0.185192093	0.869328112
regulation of release of cytochrome c from m	15158	0.185192093	0.869328112
fatty acid biosynthetic process (GO:0006633)	26238	0.187378869	0.869328112
myeloid leukocyte differentiation (GO:00025	26238	0.187378869	0.869328112
aldehyde catabolic process (GO:0046185)	44599	0.187604008	0.869328112
amino-acid betaine metabolic process (GO:0(	44599	0.187604008	0.869328112
autophagosome membrane docking (GO:001	44599	0.187604008	0.869328112
bleb assembly (GO:0032060)	44599	0.187604008	0.869328112
cellular hypotonic response (GO:0071476)	44599	0.187604008	0.869328112
cellular nitrogen compound catabolic process	44599	0.187604008	0.869328112
cellular response to interleukin-18 (GO:0071	44599	0.187604008	0.869328112
cellular response to prostaglandin E stimulus	44599	0.187604008	0.869328112
cyclic nucleotide transport (GO:0070729)	44599	0.187604008	0.869328112

flavin-containing compound metabolic proce	44599	0.187604008	0.869328112
G-quadruplex DNA unwinding (GO:0044806)	44599	0.187604008	0.869328112
glomerular epithelial cell development (GO:0	44599	0.187604008	0.869328112
hexose catabolic process (GO:0019320)	44599	0.187604008	0.869328112
interleukin-18-mediated signaling pathway (G	44599	0.187604008	0.869328112
L-methionine salvage (GO:0071267)	44599	0.187604008	0.869328112
membrane fission (GO:0090148)	44599	0.187604008	0.869328112
mitochondrial DNA metabolic process (GO:0(	44599	0.187604008	0.869328112
negative regulation of dendritic cell apoptoti	44599	0.187604008	0.869328112
negative regulation of low-density lipoprotei	44599	0.187604008	0.869328112
nicotinamide nucleotide biosynthetic process	44599	0.187604008	0.869328112
Notch receptor processing, ligand-dependent	44599	0.187604008	0.869328112
pentose metabolic process (GO:0019321)	44599	0.187604008	0.869328112
peptide transport (GO:0015833)	44599	0.187604008	0.869328112
photoreceptor cell differentiation (GO:00465	44599	0.187604008	0.869328112
positive regulation of helicase activity (GO:0(	44599	0.187604008	0.869328112
positive regulation of lipopolysaccharide-me	44599	0.187604008	0.869328112
positive regulation of mitophagy in response	44599	0.187604008	0.869328112
positive regulation of mitotic cell cycle spindl	44599	0.187604008	0.869328112
positive regulation of oxidative stress-induce	44599	0.187604008	0.869328112
positive regulation of spindle checkpoint (GO	44599	0.187604008	0.869328112
positive regulation of striated muscle contrac	44599	0.187604008	0.869328112
protection from non-homologous end joining	44599	0.187604008	0.869328112
proton-transporting ATP synthase complex a	44599	0.187604008	0.869328112
pyrimidine ribonucleotide biosynthetic proce	44599	0.187604008	0.869328112
pyrimidine-containing compound biosynthetic	44599	0.187604008	0.869328112
regulation by virus of viral protein levels in h	44599	0.187604008	0.869328112
regulation of fat cell proliferation (GO:00703	44599	0.187604008	0.869328112
regulation of glial cell apoptotic process (GO:	44599	0.187604008	0.869328112
regulation of glucocorticoid receptor signalin	44599	0.187604008	0.869328112
regulation of metallopeptidase activity (GO:1	44599	0.187604008	0.869328112
regulation of microtubule binding (GO:19045	44599	0.187604008	0.869328112
regulation of mitochondrial membrane perm	44599	0.187604008	0.869328112
regulation of oxidative stress-induced neuror	44599	0.187604008	0.869328112
regulation of T-helper 1 cell differentiation (G	44599	0.187604008	0.869328112
riboflavin metabolic process (GO:0006771)	44599	0.187604008	0.869328112
serine transport (GO:0032329)	44599	0.187604008	0.869328112
thiamine-containing compound metabolic pr	44599	0.187604008	0.869328112
phosphatidylserine metabolic process (GO:0(	12571	0.189358815	0.873874492
positive regulation of mitochondrial outer m	12571	0.189358815	0.873874492
tRNA export from nucleus (GO:0006409)	12571	0.189358815	0.873874492
tRNA-containing ribonucleoprotein complex	12571	0.189358815	0.873874492
energy reserve metabolic process (GO:00061	44671	0.190676166	0.874796407
eye morphogenesis (GO:0048592)	44671	0.190676166	0.874796407
miRNA metabolic process (GO:0010586)	44671	0.190676166	0.874796407
positive regulation of cyclin-dependent prote	44671	0.190676166	0.874796407
skeletal muscle contraction (GO:0003009)	44671	0.190676166	0.874796407

positive regulation of programmed cell death	38/286	0.190720332	0.874796407
dendritic spine organization (GO:0097061)	44708	0.191819859	0.875396085
negative regulation of cation channel activity	44708	0.191819859	0.875396085
negative regulation of protein polymerization	44708	0.191819859	0.875396085
peptidyl-lysine methylation (GO:0018022)	44708	0.191819859	0.875396085
positive regulation of mitotic cell cycle (GO:0	44708	0.191819859	0.875396085
pre-replicative complex assembly (GO:00363	23651	0.194852164	0.88536978
protein catabolic process (GO:0030163)	23651	0.194852164	0.88536978
regulation of cilium assembly (GO:1902017)	23651	0.194852164	0.88536978
aminoglycan biosynthetic process (GO:00060	18111	0.19518112	0.88536978
oligosaccharide metabolic process (GO:0009	18111	0.19518112	0.88536978
response to hydrogen peroxide (GO:0042542	18111	0.19518112	0.88536978
negative regulation of supramolecular fiber o	26604	0.199797502	0.904494102
response to ionizing radiation (GO:0010212)	26604	0.199797502	0.904494102
monocarboxylic acid transport (GO:0015718)	21064	0.20262671	0.91638386
organelle organization (GO:0006996)	54/420	0.205930171	0.923651142
intracellular pH reduction (GO:0051452)	12936	0.207930137	0.923651142
negative regulation of cell cycle G1/S phase t	12936	0.207930137	0.923651142
positive regulation of immunoglobulin produ	12936	0.207930137	0.923651142
regulation of phosphatidylinositol 3-kinase a	12936	0.207930137	0.923651142
steroid biosynthetic process (GO:0006694)	24016	0.208262433	0.923651142
translational termination (GO:0006415)	14/96	0.20902445	0.923651142
translational elongation (GO:0006414)	15/104	0.210835728	0.923651142
2-oxoglutarate metabolic process (GO:00061	44634	0.211849732	0.923651142
amyloid precursor protein catabolic process (	44634	0.211849732	0.923651142
cellular response to low-density lipoprotein p	44634	0.211849732	0.923651142
coenzyme A metabolic process (GO:0015936	44634	0.211849732	0.923651142
COPII-coated vesicle cargo loading (GO:0090	44634	0.211849732	0.923651142
covalent chromatin modification (GO:00165	44634	0.211849732	0.923651142
cytoplasmic sequestering of transcription fac	44634	0.211849732	0.923651142
negative regulation of DNA damage response	44634	0.211849732	0.923651142
negative regulation of neuroinflammatory re	44634	0.211849732	0.923651142
negative regulation of pri-miRNA transcriptio	44634	0.211849732	0.923651142
negative regulation of T cell differentiation (G	44634	0.211849732	0.923651142
nucleoside phosphate catabolic process (GO:	44634	0.211849732	0.923651142
peptidyl-serine dephosphorylation (GO:0070	44634	0.211849732	0.923651142
positive regulation of cellular response to ins	44634	0.211849732	0.923651142
positive regulation of glucose metabolic proc	44634	0.211849732	0.923651142
positive regulation of glycoprotein biosynthe	44634	0.211849732	0.923651142
positive regulation of SMAD protein signal tra	44634	0.211849732	0.923651142
positive regulation of T-helper cell differentia	44634	0.211849732	0.923651142
positive regulation of type 2 immune respons	44634	0.211849732	0.923651142
protein localization to kinetochore (GO:0034	44634	0.211849732	0.923651142
pyrimidine nucleoside biosynthetic process (G	44634	0.211849732	0.923651142
regulation of cell projection organization (GO	44634	0.211849732	0.923651142
regulation of integrin-mediated signaling pat	44634	0.211849732	0.923651142
regulation of response to endoplasmic reticu	44634	0.211849732	0.923651142

response to UV-A (GO:0070141)	44634	0.211849732	0.923651142
steroid catabolic process (GO:0006706)	44634	0.211849732	0.923651142
sulfate transport (GO:0008272)	44634	0.211849732	0.923651142
phosphatidylinositol metabolic process (GO:(	16/112	0.212208859	0.923651142
endoplasmic reticulum organization (GO:000	26969	0.212564792	0.923651142
calcium ion import (GO:0070509)	44709	0.213024456	0.923651142
L-amino acid transport (GO:0015807)	44709	0.213024456	0.923651142
phagosome acidification (GO:0090383)	44709	0.213024456	0.923651142
positive regulation of phosphatidylinositol 3-	44709	0.213024456	0.923651142
regulation of sodium ion transmembrane tra	44709	0.213024456	0.923651142
sulfur compound transport (GO:0072348)	44709	0.213024456	0.923651142
calcium ion transport into cytosol (GO:00604	44672	0.215610864	0.92615706
cellular response to estradiol stimulus (GO:0(	44672	0.215610864	0.92615706
extrinsic apoptotic signaling pathway in abse	44672	0.215610864	0.92615706
intrinsic apoptotic signaling pathway in respo	44672	0.215610864	0.92615706
melanosome localization (GO:0032400)	44672	0.215610864	0.92615706
positive regulation of glycolytic process (GO:(	44672	0.215610864	0.92615706
positive regulation of purine nucleotide meta	44672	0.215610864	0.92615706
positive regulation of smoothened signaling p	44672	0.215610864	0.92615706
activation of cysteine-type endopeptidase ac	29921	0.215857323	0.92615706
negative regulation of protein modification p	29921	0.215857323	0.92615706
positive regulation of tumor necrosis factor s	29921	0.215857323	0.92615706
mitochondrial translational termination (GO:1	13/89	0.218367714	0.936039213
cellular response to glucose starvation (GO:0	15888	0.218889334	0.936498118
negative regulation of proteolysis (GO:00458	15888	0.218889334	0.936498118
dephosphorylation (GO:0016311)	21/153	0.223672235	0.94267407
regulation of peptide hormone secretion (GO	27334	0.225661505	0.94267407
mitotic nuclear membrane organization (GO:1	18841	0.226607776	0.94267407
mitotic nuclear membrane reassembly (GO:0	18841	0.226607776	0.94267407
intrinsic apoptotic signaling pathway by p53 (	13302	0.227110428	0.94267407
positive regulation of telomere maintenance	13302	0.227110428	0.94267407
regulation of protein import into nucleus (GO	13302	0.227110428	0.94267407
Wnt signaling pathway, calcium modulating p	13302	0.227110428	0.94267407
antigen processing and presentation of exoge	14/98	0.231748171	0.94267407
aspartate family amino acid biosynthetic pro(	44600	0.232017168	0.94267407
benzene-containing compound metabolic pro	44600	0.232017168	0.94267407
chromatin silencing at telomere (GO:000634(	44600	0.232017168	0.94267407
dendritic spine maintenance (GO:0097062)	44600	0.232017168	0.94267407
ER overload response (GO:0006983)	44600	0.232017168	0.94267407
glyoxylate metabolic process (GO:0046487)	44600	0.232017168	0.94267407
heparan sulfate proteoglycan biosynthetic pr	44600	0.232017168	0.94267407
isoprenoid metabolic process (GO:0006720)	44600	0.232017168	0.94267407
macromolecule depalmitoylation (GO:00987:	44600	0.232017168	0.94267407
macromolecule modification (GO:0043412)	44600	0.232017168	0.94267407
mitotic spindle elongation (GO:0000022)	44600	0.232017168	0.94267407
mitotic spindle midzone assembly (GO:00512	44600	0.232017168	0.94267407
multi-ciliated epithelial cell differentiation (G	44600	0.232017168	0.94267407

negative regulation of actin nucleation (GO:0	44600	0.232017168	0.94267407
negative regulation of appetite (GO:0032099	44600	0.232017168	0.94267407
negative regulation of cAMP-dependent prot	44600	0.232017168	0.94267407
negative regulation of mitochondrial fusion (	44600	0.232017168	0.94267407
negative regulation of mitotic nuclear divisio	44600	0.232017168	0.94267407
negative regulation of monooxygenase activi	44600	0.232017168	0.94267407
negative regulation of neural precursor cell p	44600	0.232017168	0.94267407
negative regulation of response to reactive o	44600	0.232017168	0.94267407
peptidyl-lysine hydroxylation (GO:0017185)	44600	0.232017168	0.94267407
peptidyl-proline hydroxylation to 4-hydroxy-l	44600	0.232017168	0.94267407
positive regulation of adaptive immune respo	44600	0.232017168	0.94267407
positive regulation of execution phase of apo	44600	0.232017168	0.94267407
positive regulation of insulin-like growth fact	44600	0.232017168	0.94267407
positive regulation of melanin biosynthetic p	44600	0.232017168	0.94267407
positive regulation of membrane invaginatio	44600	0.232017168	0.94267407
positive regulation of neuron projection arbo	44600	0.232017168	0.94267407
positive regulation of secondary metabolite b	44600	0.232017168	0.94267407
protein deglutamylation (GO:0035608)	44600	0.232017168	0.94267407
protein depalmitoylation (GO:0002084)	44600	0.232017168	0.94267407
pyrimidine nucleobase catabolic process (GO	44600	0.232017168	0.94267407
regulation of extracellular matrix constituent	44600	0.232017168	0.94267407
regulation of oxidative stress-induced neuror	44600	0.232017168	0.94267407
regulation of protein ADP-ribosylation (GO:0(	44600	0.232017168	0.94267407
regulation of protein glycosylation (GO:0060(	44600	0.232017168	0.94267407
regulation of T-helper 2 cell differentiation (G	44600	0.232017168	0.94267407
response to hydroperoxide (GO:0033194)	44600	0.232017168	0.94267407
ribosome disassembly (GO:0032790)	44600	0.232017168	0.94267407
single strand break repair (GO:0000012)	44600	0.232017168	0.94267407
skeletal muscle tissue regeneration (GO:0043	44600	0.232017168	0.94267407
spermidine metabolic process (GO:0008216)	44600	0.232017168	0.94267407
stress-induced premature senescence (GO:0(	44600	0.232017168	0.94267407
T cell mediated cytotoxicity (GO:0001913)	44600	0.232017168	0.94267407
tubulin complex assembly (GO:0007021)	44600	0.232017168	0.94267407
vitamin K metabolic process (GO:0042373)	44600	0.232017168	0.94267407
chromosome organization (GO:0051276)	15/106	0.232716597	0.944666292
glycolytic process (GO:0006096)	44710	0.234924124	0.950212348
negative regulation of myeloid leukocyte diff	44710	0.234924124	0.950212348
protein K11-linked ubiquitination (GO:00709	44710	0.234924124	0.950212348
telomere maintenance via telomerase (GO:0(	44710	0.234924124	0.950212348
supramolecular fiber organization (GO:00974	45/351	0.236447296	0.954036368
positive regulation of potassium ion transme	16254	0.236503039	0.954036368
response to amyloid-beta (GO:1904645)	16254	0.236503039	0.954036368
cellular response to osmotic stress (GO:0071	44673	0.241362618	0.955938473
maturation of 5.8S rRNA from tricistronic rRN	44673	0.241362618	0.955938473
mitochondrial calcium ion homeostasis (GO:(	44673	0.241362618	0.955938473
positive regulation of calcium ion transmemb	44673	0.241362618	0.955938473
positive regulation of lipid catabolic process (	44673	0.241362618	0.955938473

protein import into peroxisome membrane ((	44673	0.241362618	0.955938473
regulation of execution phase of apoptosis (G	44673	0.241362618	0.955938473
ameboidal-type cell migration (GO:0001667)	19207	0.242964516	0.955938473
negative regulation of protein metabolic proc	19207	0.242964516	0.955938473
negative regulation of protein-containing cor	19207	0.242964516	0.955938473
glucan catabolic process (GO:0009251)	44635	0.243745268	0.955938473
glucosamine-containing compound metaboli	44635	0.243745268	0.955938473
glycogen catabolic process (GO:0005980)	44635	0.243745268	0.955938473
intracellular cholesterol transport (GO:00323	44635	0.243745268	0.955938473
mitochondrial RNA metabolic process (GO:0(	44635	0.243745268	0.955938473
modulation by host of viral genome replicati	44635	0.243745268	0.955938473
negative regulation of leukocyte activation (G	44635	0.243745268	0.955938473
phosphatidylethanolamine biosynthetic proc	44635	0.243745268	0.955938473
photoreceptor cell development (GO:004246	44635	0.243745268	0.955938473
placenta development (GO:0001890)	44635	0.243745268	0.955938473
positive regulation of chromosome organizat	44635	0.243745268	0.955938473
positive regulation of histone H3-K4 methyla	44635	0.243745268	0.955938473
positive regulation of protein export from nu	44635	0.243745268	0.955938473
prostanoid biosynthetic process (GO:004645	44635	0.243745268	0.955938473
protein hydroxylation (GO:0018126)	44635	0.243745268	0.955938473
regulation of lymphocyte activation (GO:005	44635	0.243745268	0.955938473
regulation of microglial cell activation (GO:19	44635	0.243745268	0.955938473
regulation of neuron projection arborization	44635	0.243745268	0.955938473
RNA phosphodiester bond hydrolysis, endon	44635	0.243745268	0.955938473
synaptonemal complex assembly (GO:00071	44635	0.243745268	0.955938473
synaptonemal complex organization (GO:007	44635	0.243745268	0.955938473
tRNA splicing, via endonucleolytic cleavage a	44635	0.243745268	0.955938473
glutamine family amino acid metabolic proce	13667	0.24682824	0.965515142
negative regulation of G1/S transition of mito	13667	0.24682824	0.965515142
phagosome maturation (GO:0090382)	13667	0.24682824	0.965515142
positive regulation of intracellular protein tra	20/148	0.252540837	0.98700649
regulation of intracellular signal transduction	55/437	0.253168118	0.988602902
vascular transport (GO:0010232)	31017	0.254170292	0.990603611
amino acid transmembrane transport (GO:0(	16619	0.254557502	0.990603611
cellular response to radiation (GO:0071478)	16619	0.254557502	0.990603611
mitotic G2/M transition checkpoint (GO:004	16619	0.254557502	0.990603611
positive regulation of cellular component bio	13/92	0.255015349	0.991404918
ion transport (GO:0006811)	16/116	0.255265561	0.991404918
antigen processing and presentation of pepti	14/100	0.255421719	0.991404918
fatty-acyl-CoA biosynthetic process (GO:004	44711	0.257412259	0.993158487
long-chain fatty acid biosynthetic process (G(	44711	0.257412259	0.993158487
negative regulation of gene expression, epige	44711	0.257412259	0.993158487
positive regulation of lipid kinase activity (GC	44711	0.257412259	0.993158487
primary neural tube formation (GO:0014020)	44711	0.257412259	0.993158487
regulation of protein localization to membra	44711	0.257412259	0.993158487
RNA-dependent DNA biosynthetic process (G	44711	0.257412259	0.993158487
regulation of protein secretion (GO:0050708)	17/125	0.26569081	0.999994883

positive regulation of tumor necrosis factor p	28430	0.266719991	0.999994883
regulation of organelle assembly (GO:190211	28430	0.266719991	0.999994883
lysosome organization (GO:0007040)	14032	0.267010528	0.999994883
ncRNA export from nucleus (GO:0097064)	14032	0.267010528	0.999994883
positive regulation of protein localization to r	14/101	0.267580297	0.999994883
DNA catabolic process, endonucleolytic (GO:(	44674	0.267758063	0.999994883
DNA methylation (GO:0006306)	44674	0.267758063	0.999994883
membrane protein ectodomain proteolysis ((	44674	0.267758063	0.999994883
negative regulation of intracellular protein tr	44674	0.267758063	0.999994883
peptidyl-L-cysteine S-palmitoylation (GO:001	44674	0.267758063	0.999994883
peptidyl-S-diacylglycerol-L-cysteine biosynthe	44674	0.267758063	0.999994883
protein alkylation (GO:0008213)	44674	0.267758063	0.999994883
regulation of interleukin-4 production (GO:0(	44674	0.267758063	0.999994883
regulation of protein export from nucleus (G(	44674	0.267758063	0.999994883
regulation of SMAD protein signal transducti	44674	0.267758063	0.999994883
cellular response to starvation (GO:0009267)	21/158	0.27087078	0.999994883
protein localization to organelle (GO:003336!	19/142	0.273942893	0.999994883
inorganic cation transmembrane transport (G	35/274	0.27623423	0.999994883
cellular polysaccharide catabolic process (GO	44636	0.276323392	0.999994883
dendritic cell chemotaxis (GO:0002407)	44636	0.276323392	0.999994883
negative regulation of immune effector proc	44636	0.276323392	0.999994883
polyol biosynthetic process (GO:0046173)	44636	0.276323392	0.999994883
positive regulation of immunoglobulin media	44636	0.276323392	0.999994883
positive regulation of small molecule metabo	44636	0.276323392	0.999994883
protein localization to microtubule organizing	44636	0.276323392	0.999994883
regulation of ATP biosynthetic process (GO:2	44636	0.276323392	0.999994883
regulation of cholesterol storage (GO:001088	44636	0.276323392	0.999994883
regulation of ERBB signaling pathway (GO:19	44636	0.276323392	0.999994883
response to organophosphorus (GO:0046683	44636	0.276323392	0.999994883
RNA splicing, via endonucleolytic cleavage an	44636	0.276323392	0.999994883
serine family amino acid metabolic process ((	44636	0.276323392	0.999994883
T cell mediated immunity (GO:0002456)	44636	0.276323392	0.999994883
nuclear membrane reassembly (GO:0031468	19937	0.276762947	0.999994883
unsaturated fatty acid metabolic process (GC	19937	0.276762947	0.999994883
alpha-amino acid biosynthetic process (GO:1!	44601	0.27694827	0.999994883
bone resorption (GO:0045453)	44601	0.27694827	0.999994883
cilium movement involved in cell motility (GC	44601	0.27694827	0.999994883
endosome to melanosome transport (GO:00:	44601	0.27694827	0.999994883
endosome to pigment granule transport (GO	44601	0.27694827	0.999994883
glomerular filtration (GO:0003094)	44601	0.27694827	0.999994883
glucosamine-containing compound catabolic	44601	0.27694827	0.999994883
inositol metabolic process (GO:0006020)	44601	0.27694827	0.999994883
kynurenine metabolic process (GO:0070189)	44601	0.27694827	0.999994883
lipoprotein metabolic process (GO:0042157)	44601	0.27694827	0.999994883
lysosomal lumen acidification (GO:0007042)	44601	0.27694827	0.999994883
negative regulation of nitric oxide biosynthet	44601	0.27694827	0.999994883
negative regulation of nitric oxide metabolic	44601	0.27694827	0.999994883

neuronal ion channel clustering (GO:004516	44601	0.27694827	0.999994883
Notch receptor processing (GO:0007220)	44601	0.27694827	0.999994883
nucleoside diphosphate catabolic process (G	44601	0.27694827	0.999994883
oligosaccharide catabolic process (GO:00093	44601	0.27694827	0.999994883
organic cyclic compound catabolic process (G	44601	0.27694827	0.999994883
peptidyl-cysteine modification (GO:0018198)	44601	0.27694827	0.999994883
peripheral nervous system axon ensheathme	44601	0.27694827	0.999994883
peroxisome fission (GO:0016559)	44601	0.27694827	0.999994883
positive regulation of autophagy of mitochon	44601	0.27694827	0.999994883
positive regulation of ligase activity (GO:005	44601	0.27694827	0.999994883
positive regulation of megakaryocyte differe	44601	0.27694827	0.999994883
positive regulation of phagocytosis, engulfme	44601	0.27694827	0.999994883
positive regulation of smooth muscle cell apo	44601	0.27694827	0.999994883
protein hexamerization (GO:0034214)	44601	0.27694827	0.999994883
regulation of cellular response to oxidative st	44601	0.27694827	0.999994883
regulation of dendritic cell antigen processing	44601	0.27694827	0.999994883
regulation of ER-associated ubiquitin-depend	44601	0.27694827	0.999994883
regulation of fertilization (GO:0080154)	44601	0.27694827	0.999994883
regulation of helicase activity (GO:0051095)	44601	0.27694827	0.999994883
regulation of mitotic centrosome separation	44601	0.27694827	0.999994883
regulation of nuclear cell cycle DNA replicatio	44601	0.27694827	0.999994883
response to UV-C (GO:0010225)	44601	0.27694827	0.999994883
response to vitamin (GO:0033273)	44601	0.27694827	0.999994883
Schwann cell development (GO:0014044)	44601	0.27694827	0.999994883
synapse pruning (GO:0098883)	44601	0.27694827	0.999994883
tetrahydrofolate interconversion (GO:00359	44601	0.27694827	0.999994883
unsaturated fatty acid biosynthetic process ((	44601	0.27694827	0.999994883
regulation of protein phosphorylation (GO:0(	34/266	0.278501736	0.999994883
mitotic sister chromatid segregation (GO:000	14/102	0.279934011	0.999994883
regulation of proteasomal ubiquitin-depende	14/102	0.279934011	0.999994883
embryonic skeletal system morphogenesis (G	44712	0.280382019	0.999994883
positive regulation of locomotion (GO:00400	44712	0.280382019	0.999994883
positive regulation of mononuclear cell migra	44712	0.280382019	0.999994883
positive regulation of proteolysis involved in	44712	0.280382019	0.999994883
regulation of macrophage derived foam cell d	44712	0.280382019	0.999994883
regulation of exit from mitosis (GO:0007096)	14397	0.287583506	0.999994883
positive regulation of cysteine-type endopep	16/119	0.289541528	0.999994883
determination of heart left/right asymmetry	17349	0.291772687	0.999994883
embryonic heart tube morphogenesis (GO:0(	17349	0.291772687	0.999994883
antigen processing and presentation of exoge	14/103	0.292467759	0.999994883
negative regulation of protein phosphorylatio	20/152	0.292878915	0.999994883
regulation of cell cycle phase transition (GO:1	13/95	0.293685661	0.999994883
negative regulation of cytokine-mediated sig	20302	0.294120694	0.999994883
pyruvate metabolic process (GO:0006090)	20302	0.294120694	0.999994883
triglyceride metabolic process (GO:0006641)	20302	0.294120694	0.999994883
canonical glycolysis (GO:0061621)	44675	0.294628646	0.999994883
cholesterol efflux (GO:0033344)	44675	0.294628646	0.999994883

dendritic cell differentiation (GO:0097028)	44675	0.294628646	0.999994883
glucose catabolic process to pyruvate (GO:00	44675	0.294628646	0.999994883
leukotriene metabolic process (GO:0006691)	44675	0.294628646	0.999994883
positive regulation of viral life cycle (GO:190	44675	0.294628646	0.999994883
protein kinase B signaling (GO:0043491)	44675	0.294628646	0.999994883
purine ribonucleotide catabolic process (GO:(	44675	0.294628646	0.999994883
cellular response to reactive oxygen species (	23255	0.295268062	0.999994883
positive regulation of cellular protein localiza	26207	0.295595341	0.999994883
regulation of glycolytic process (GO:0006110	26207	0.295595341	0.999994883
negative regulation of macromolecule metab	25/194	0.300390018	0.999994883
protein-containing complex subunit organiza	15/112	0.303267863	0.999994883
negative regulation of double-strand break re	11810	0.303727704	0.999994883
protein transmembrane import into intracell	11810	0.303727704	0.999994883
regulation of cell morphogenesis (GO:00226(	11810	0.303727704	0.999994883
regulation of dendrite morphogenesis (GO:0(	11810	0.303727704	0.999994883
regulation of dendritic spine morphogenesis	11810	0.303727704	0.999994883
regulation of intracellular estrogen receptor s	11810	0.303727704	0.999994883
RNA biosynthetic process (GO:0032774)	11810	0.303727704	0.999994883
organic hydroxy compound transport (GO:00	14763	0.308473443	0.999994883
regulation of nitric oxide biosynthetic proces	14763	0.308473443	0.999994883
cellular response to gamma radiation (GO:00	44637	0.30928159	0.999994883
copper ion homeostasis (GO:0055070)	44637	0.30928159	0.999994883
negative regulation of amyloid-beta formatio	44637	0.30928159	0.999994883
preassembly of GPI anchor in ER membrane (	44637	0.30928159	0.999994883
protein localization to chromosome, centron	44637	0.30928159	0.999994883
purine ribonucleotide transport (GO:001586	44637	0.30928159	0.999994883
regulation of cholesterol biosynthetic proces	44637	0.30928159	0.999994883
response to purine-containing compound (G(	44637	0.30928159	0.999994883
reverse cholesterol transport (GO:0043691)	44637	0.30928159	0.999994883
tail-anchored membrane protein insertion in	44637	0.30928159	0.999994883
purine ribonucleotide biosynthetic process ((	17715	0.310823856	0.999994883
cell morphogenesis involved in differentiatio	26573	0.311046603	0.999994883
regulation of extrinsic apoptotic signaling pat	23621	0.311699752	0.999994883
cellular biogenic amine catabolic process (GC	44602	0.321692826	0.999994883
cellular response to hydroxyurea (GO:00727	44602	0.321692826	0.999994883
cellular response to oxygen levels (GO:00714	44602	0.321692826	0.999994883
cellular response to prostaglandin stimulus ((	44602	0.321692826	0.999994883
defense response to tumor cell (GO:0002357	44602	0.321692826	0.999994883
DNA damage response, signal transduction b	44602	0.321692826	0.999994883
fructose 6-phosphate metabolic process (GO	44602	0.321692826	0.999994883
histone H4 deacetylation (GO:0070933)	44602	0.321692826	0.999994883
iron ion transmembrane transport (GO:0034	44602	0.321692826	0.999994883
L-serine metabolic process (GO:0006563)	44602	0.321692826	0.999994883
lipid droplet formation (GO:0140042)	44602	0.321692826	0.999994883
microtubule anchoring at centrosome (GO:0(	44602	0.321692826	0.999994883
myelin maintenance (GO:0043217)	44602	0.321692826	0.999994883
negative regulation of cell adhesion mediate	44602	0.321692826	0.999994883

negative regulation of cholesterol storage (G	44602	0.321692826	0.999994883
negative regulation of extracellular matrix or	44602	0.321692826	0.999994883
negative regulation of heterotypic cell-cell ad	44602	0.321692826	0.999994883
negative regulation of leukocyte migration (G	44602	0.321692826	0.999994883
negative regulation of phosphatidylinositol 3-	44602	0.321692826	0.999994883
negative regulation of telomerase activity (G	44602	0.321692826	0.999994883
peptidyl-amino acid modification (GO:00181!	44602	0.321692826	0.999994883
positive regulation of epidermis developmen	44602	0.321692826	0.999994883
protein O-linked glycosylation via serine (GO:	44602	0.321692826	0.999994883
protein poly-ADP-ribosylation (GO:0070212)	44602	0.321692826	0.999994883
Rap protein signal transduction (GO:0032486	44602	0.321692826	0.999994883
regulation of cell activation (GO:0050865)	44602	0.321692826	0.999994883
regulation of cell-cell adhesion involved in ga	44602	0.321692826	0.999994883
regulation of cilium movement (GO:0003352	44602	0.321692826	0.999994883
regulation of epithelial cell apoptotic process	44602	0.321692826	0.999994883
regulation of histone phosphorylation (GO:0(	44602	0.321692826	0.999994883
regulation of hydrogen peroxide-induced cell	44602	0.321692826	0.999994883
regulation of organ growth (GO:0046620)	44602	0.321692826	0.999994883
regulation of peptidyl-lysine acetylation (GO:	44602	0.321692826	0.999994883
regulation of phagocytosis, engulfment (GO:(	44602	0.321692826	0.999994883
regulation of type B pancreatic cell developm	44602	0.321692826	0.999994883
renal filtration (GO:0097205)	44602	0.321692826	0.999994883
SNARE complex assembly (GO:0035493)	44602	0.321692826	0.999994883
cellular polysaccharide biosynthetic process (	44676	0.321812841	0.999994883
energy derivation by oxidation of organic cor	44676	0.321812841	0.999994883
fat-soluble vitamin metabolic process (GO:00	44676	0.321812841	0.999994883
glycolytic process through glucose-6-phospha	44676	0.321812841	0.999994883
in utero embryonic development (GO:00017(	44676	0.321812841	0.999994883
negative regulation of endocytosis (GO:0045!	44676	0.321812841	0.999994883
negative regulation of response to endoplasr	44676	0.321812841	0.999994883
negative regulation of sequestering of calciur	44676	0.321812841	0.999994883
phosphatidylglycerol metabolic process (GO:(	44676	0.321812841	0.999994883
positive regulation of ERBB signaling pathwa	44676	0.321812841	0.999994883
mitochondrial translational elongation (GO:0	32843	0.322620228	0.999994883
post-Golgi vesicle-mediated transport (GO:0(	32843	0.322620228	0.999994883
regulation of hydrolase activity (GO:0051336	26938	0.326678635	0.999994883
neuron projection extension (GO:1990138)	12175	0.327345971	0.999994883
positive regulation of telomere maintenance	12175	0.327345971	0.999994883
regulation of protein localization to cell surfa	12175	0.327345971	0.999994883
positive regulation of kinase activity (GO:003	15/114	0.328073392	0.999994883
mitotic G1 DNA damage checkpoint signaling	23986	0.328323605	0.999994883
negative regulation of DNA recombination (G	21033	0.329539519	0.999994883
regulation of reactive oxygen species metabo	21033	0.329539519	0.999994883
regulation of response to DNA damage stimu	15128	0.329607385	0.999994883
mitotic cytokinesis (GO:0000281)	18080	0.330097643	0.999994883
regulation of stress-activated MAPK cascade	18080	0.330097643	0.999994883
regulation of autophagy (GO:0010506)	29/231	0.333474195	0.999994883

negative regulation of neuron death (GO:190	13/98	0.333913963	0.999994883
regulation of neuron apoptotic process (GO:(	13/98	0.333913963	0.999994883
negative regulation of protein kinase activity	33208	0.336818446	0.999994883
positive regulation of transferase activity (GC	19/148	0.338597248	0.999994883
positive regulation of cytoskeleton organizati	30256	0.339680802	0.999994883
regulation of neuron projection developmen	21/165	0.342276015	0.999994883
adenine nucleotide transport (GO:0051503)	44638	0.342346224	0.999994883
embryonic heart tube development (GO:003	44638	0.342346224	0.999994883
intracellular estrogen receptor signaling path	44638	0.342346224	0.999994883
negative regulation of biosynthetic process ((	44638	0.342346224	0.999994883
negative regulation of cation transmembrane	44638	0.342346224	0.999994883
negative regulation of leukocyte cell-cell adh	44638	0.342346224	0.999994883
negative regulation of signal transduction by	44638	0.342346224	0.999994883
positive regulation of CREB transcription fact	44638	0.342346224	0.999994883
positive regulation of extracellular matrix org	44638	0.342346224	0.999994883
positive regulation of interleukin-4 productio	44638	0.342346224	0.999994883
regulation of adaptive immune response (GO	44638	0.342346224	0.999994883
regulation of fatty acid metabolic process (G(	44638	0.342346224	0.999994883
regulation of mitochondrial outer membrane	44638	0.342346224	0.999994883
regulation of multicellular organism growth (	44638	0.342346224	0.999994883
release of cytochrome c from mitochondria (	44638	0.342346224	0.999994883
triglyceride biosynthetic process (GO:001943	44638	0.342346224	0.999994883
DNA damage response, signal transduction b	27303	0.342462558	0.999994883
proteolysis involved in cellular protein catabo	27303	0.342462558	0.999994883
cellular response to nutrient levels (GO:0031	24351	0.345104875	0.999994883
negative regulation of neuron projection dev	21398	0.347514897	0.999994883
receptor metabolic process (GO:0043112)	21398	0.347514897	0.999994883
endomembrane system organization (GO:00	25/199	0.347647062	0.999994883
lamellipodium assembly (GO:0030032)	44677	0.349157871	0.999994883
negative regulation of intrinsic apoptotic sign	44677	0.349157871	0.999994883
organelle fission (GO:0048285)	44677	0.349157871	0.999994883
positive regulation of protein insertion into n	44677	0.349157871	0.999994883
proteoglycan metabolic process (GO:000602	44677	0.349157871	0.999994883
regulation of monocyte chemotaxis (GO:009(	44677	0.349157871	0.999994883
regulation of myelination (GO:0031641)	44677	0.349157871	0.999994883
regulation of protein insertion into mitochon	44677	0.349157871	0.999994883
regulation of tumor necrosis factor productic	16/124	0.349499471	0.999994883
neuron migration (GO:0001764)	18445	0.349539838	0.999994883
phosphatidylinositol phosphate biosynthetic	15493	0.350913806	0.999994883
positive regulation of protein tyrosine kinase	15493	0.350913806	0.999994883
regulation of ubiquitin-dependent protein ca	15493	0.350913806	0.999994883
skeletal system morphogenesis (GO:0048705	15493	0.350913806	0.999994883
cellular response to amino acid stimulus (GO	12540	0.351136856	0.999994883
negative regulation of blood vessel endotheli	12540	0.351136856	0.999994883
positive regulation of telomerase activity (GC	12540	0.351136856	0.999994883
regulation of glucose metabolic process (GO:	12540	0.351136856	0.999994883
positive regulation of transport (GO:0051050	33573	0.351137263	0.999994883

Ras protein signal transduction (GO:0007265	18/142	0.36519424	0.999994883
response to reactive oxygen species (GO:000	21763	0.365611025	0.999994883
actin filament network formation (GO:00516	44603	0.365701215	0.999994883
axonal transport of mitochondrion (GO:0019	44603	0.365701215	0.999994883
camera-type eye morphogenesis (GO:00485	44603	0.365701215	0.999994883
carnitine shuttle (GO:0006853)	44603	0.365701215	0.999994883
cellular response to cholesterol (GO:0071397	44603	0.365701215	0.999994883
coenzyme A biosynthetic process (GO:00159	44603	0.365701215	0.999994883
copper ion transport (GO:0006825)	44603	0.365701215	0.999994883
detection of light stimulus involved in sensor	44603	0.365701215	0.999994883
detection of light stimulus involved in visual	44603	0.365701215	0.999994883
DNA damage response, signal transduction re	44603	0.365701215	0.999994883
embryonic eye morphogenesis (GO:0048048	44603	0.365701215	0.999994883
glycerol metabolic process (GO:0006071)	44603	0.365701215	0.999994883
inositol phosphate biosynthetic process (GO:	44603	0.365701215	0.999994883
mitochondrial transcription (GO:0006390)	44603	0.365701215	0.999994883
negative regulation of nuclear division (GO:0	44603	0.365701215	0.999994883
negative regulation of protein maturation (G	44603	0.365701215	0.999994883
negative regulation of response to cytokine s	44603	0.365701215	0.999994883
peptidyl-lysine monomethylation (GO:00180	44603	0.365701215	0.999994883
positive regulation by host of viral process (G	44603	0.365701215	0.999994883
positive regulation of DNA-dependent DNA r	44603	0.365701215	0.999994883
positive regulation of interleukin-13 producti	44603	0.365701215	0.999994883
positive regulation of myelination (GO:00316	44603	0.365701215	0.999994883
positive regulation of vacuole organization (G	44603	0.365701215	0.999994883
positive regulation of viral release from host	44603	0.365701215	0.999994883
positive regulation of voltage-gated potassiu	44603	0.365701215	0.999994883
proteasome assembly (GO:0043248)	44603	0.365701215	0.999994883
protein oxidation (GO:0018158)	44603	0.365701215	0.999994883
purine nucleoside bisphosphate biosynthetic	44603	0.365701215	0.999994883
pyrimidine nucleoside salvage (GO:0043097)	44603	0.365701215	0.999994883
pyrimidine-containing compound salvage (GO	44603	0.365701215	0.999994883
rDNA heterochromatin assembly (GO:00001	44603	0.365701215	0.999994883
regulation of amyloid precursor protein biosy	44603	0.365701215	0.999994883
regulation of cysteine-type endopeptidase ac	44603	0.365701215	0.999994883
regulation of dendritic cell apoptotic process	44603	0.365701215	0.999994883
regulation of microtubule-based movement (	44603	0.365701215	0.999994883
regulation of monocyte chemotactic protein-	44603	0.365701215	0.999994883
regulation of toll-like receptor 9 signaling pat	44603	0.365701215	0.999994883
response to hydroxyurea (GO:0072710)	44603	0.365701215	0.999994883
ribonucleoside bisphosphate biosynthetic pro	44603	0.365701215	0.999994883
somite development (GO:0061053)	44603	0.365701215	0.999994883
sphingomyelin metabolic process (GO:00066	44603	0.365701215	0.999994883
tetrahydrobiopterin metabolic process (GO:0	44603	0.365701215	0.999994883
tetrahydrofolate metabolic process (GO:004	44603	0.365701215	0.999994883
tryptophan catabolic process (GO:0006569)	44603	0.365701215	0.999994883
urate metabolic process (GO:0046415)	44603	0.365701215	0.999994883

V(D)J recombination (GO:0033151)	44603	0.365701215	0.999994883
positive regulation of protein phosphorylatio	45/371	0.371072844	0.999994883
heart looping (GO:0001947)	15858	0.372323175	0.999994883
positive regulation of neuron differentiation	15858	0.372323175	0.999994883
regulation of carbohydrate catabolic process	15858	0.372323175	0.999994883
protein import into nucleus (GO:0006606)	28034	0.374370827	0.999994883
regulation of T cell proliferation (GO:004212	28034	0.374370827	0.999994883
cellular component assembly (GO:0022607)	32/261	0.374488602	0.999994883
cellular response to amyloid-beta (GO:19046	12905	0.375004636	0.999994883
cellular response to hydrogen peroxide (GO:(	12905	0.375004636	0.999994883
negative regulation of T cell proliferation (GC	12905	0.375004636	0.999994883
positive regulation of reproductive process ((	12905	0.375004636	0.999994883
regulation of autophagosome assembly (GO:	12905	0.375004636	0.999994883
actin filament capping (GO:0051693)	44639	0.375273517	0.999994883
barbed-end actin filament capping (GO:0051(	44639	0.375273517	0.999994883
detection of mechanical stimulus (GO:00509	44639	0.375273517	0.999994883
leukotriene biosynthetic process (GO:001937	44639	0.375273517	0.999994883
negative regulation of amyloid precursor pro	44639	0.375273517	0.999994883
neuromuscular process (GO:0050905)	44639	0.375273517	0.999994883
positive regulation of cellular protein catabol	44639	0.375273517	0.999994883
positive regulation of monocyte chemotaxis (	44639	0.375273517	0.999994883
purine ribonucleoside bisphosphate metabol	44639	0.375273517	0.999994883
Rac protein signal transduction (GO:0016601	44639	0.375273517	0.999994883
regulation of autophagy of mitochondrion (G	44639	0.375273517	0.999994883
regulation of histone H3-K4 methylation (GO	44639	0.375273517	0.999994883
regulation of insulin-like growth factor recep	44639	0.375273517	0.999994883
regulation of lymphocyte proliferation (GO:0(	44639	0.375273517	0.999994883
regulation of mitochondrial membrane perm	44639	0.375273517	0.999994883
response to cholesterol (GO:0070723)	44639	0.375273517	0.999994883
vesicle transport along actin filament (GO:00	44639	0.375273517	0.999994883
L-alpha-amino acid transmembrane transpor	44678	0.376520997	0.999994883
mitotic chromosome condensation (GO:0007	44678	0.376520997	0.999994883
monovalent inorganic cation homeostasis (G	44678	0.376520997	0.999994883
positive regulation of nitric oxide biosyntheti	44678	0.376520997	0.999994883
release of sequestered calcium ion into cytos	44678	0.376520997	0.999994883
nitrogen compound transport (GO:0071705)	18/143	0.3768264	0.999994883
receptor-mediated endocytosis (GO:000689	18/143	0.3768264	0.999994883
regulation of cellular response to stress (GO:(	15/118	0.378941549	0.999994883
response to organic cyclic compound (GO:00	22129	0.383786313	0.999994883
amide biosynthetic process (GO:0043604)	19176	0.388717843	0.999994883
plasma membrane bounded cell projection m	19176	0.388717843	0.999994883
positive regulation of developmental growth	19176	0.388717843	0.999994883
regulation of telomere maintenance via telor	19176	0.388717843	0.999994883
positive regulation of cell growth (GO:00303(	13/102	0.389126932	0.999994883
cholesterol metabolic process (GO:0008203)	28399	0.390438113	0.999994883
negative regulation of developmental proces	28399	0.390438113	0.999994883
positive regulation of osteoblast differentiati	16224	0.393768454	0.999994883

negative regulation of cell death (GO:006054	34669	0.394606387	0.999994883
positive regulation of epithelial cell migratior	34669	0.394606387	0.999994883
regulation of kinase activity (GO:0043549)	34669	0.394606387	0.999994883
regulation of protein serine/threonine kinase	14/111	0.397316193	0.999994883
regulation of Wnt signaling pathway (GO:003	14/111	0.397316193	0.999994883
regulation of embryonic development (GO:0(	13271	0.398858534	0.999994883
retina homeostasis (GO:0001895)	13271	0.398858534	0.999994883
negative regulation of phosphorylation (GO:(	31717	0.400394769	0.999994883
positive regulation of proteasomal protein ca	31717	0.400394769	0.999994883
protein stabilization (GO:0050821)	22/179	0.401320679	0.999994883
protein lipidation (GO:0006497)	22494	0.402000126	0.999994883
regulation of DNA-templated transcription, ir	22494	0.402000126	0.999994883
regulation of endocytosis (GO:0030100)	22494	0.402000126	0.999994883
cellular response to organonitrogen compou	13/103	0.403088809	0.999994883
bile acid and bile salt transport (GO:0015721	44679	0.403770412	0.999994883
cristae formation (GO:0042407)	44679	0.403770412	0.999994883
cytosolic calcium ion transport (GO:0060401)	44679	0.403770412	0.999994883
glycerophospholipid catabolic process (GO:0(	44679	0.403770412	0.999994883
negative regulation of calcium ion transmem	44679	0.403770412	0.999994883
photoperiodism (GO:0009648)	44679	0.403770412	0.999994883
positive regulation of microtubule polymeriz	44679	0.403770412	0.999994883
positive regulation of nitric oxide metabolic p	44679	0.403770412	0.999994883
protein localization to Golgi apparatus (GO:0(	44679	0.403770412	0.999994883
regulation of DNA damage response, signal tr	44679	0.403770412	0.999994883
regulation of immunoglobulin production (G(	44679	0.403770412	0.999994883
regulation of postsynapse organization (GO:(	44679	0.403770412	0.999994883
regulation of reactive oxygen species biosynt	44679	0.403770412	0.999994883
RNA phosphodiester bond hydrolysis (GO:00(	44679	0.403770412	0.999994883
cellular response to nitrogen compound (GO:	44640	0.40784951	0.999994883
inositol phosphate-mediated signaling (GO:0(	44640	0.40784951	0.999994883
insulin secretion (GO:0030073)	44640	0.40784951	0.999994883
negative regulation of osteoclast differentiat	44640	0.40784951	0.999994883
negative regulation of telomere maintenance	44640	0.40784951	0.999994883
nucleobase-containing compound biosynthet	44640	0.40784951	0.999994883
positive regulation of dendrite morphogenes	44640	0.40784951	0.999994883
positive regulation of epithelial cell differenti	44640	0.40784951	0.999994883
positive regulation of natural killer cell media	44640	0.40784951	0.999994883
positive regulation of nitrogen compound me	44640	0.40784951	0.999994883
protein targeting to lysosome (GO:0006622)	44640	0.40784951	0.999994883
regulation of fibroblast growth factor recepto	44640	0.40784951	0.999994883
positive regulation of B cell activation (GO:0(	19541	0.408351479	0.999994883
actin crosslink formation (GO:0051764)	44604	0.408552428	0.999994883
axonal fasciculation (GO:0007413)	44604	0.408552428	0.999994883
C-terminal protein amino acid modification ((	44604	0.408552428	0.999994883
calcium ion-regulated exocytosis of neurotra	44604	0.408552428	0.999994883
cell cycle checkpoint signaling (GO:0000075)	44604	0.408552428	0.999994883
cellular response to fluid shear stress (GO:00	44604	0.408552428	0.999994883

cellular response to thyroid hormone stimulu	44604	0.408552428	0.999994883
cGMP metabolic process (GO:0046068)	44604	0.408552428	0.999994883
depurination (GO:0045007)	44604	0.408552428	0.999994883
eye photoreceptor cell differentiation (GO:0(	44604	0.408552428	0.999994883
ganglion development (GO:0061548)	44604	0.408552428	0.999994883
Golgi localization (GO:0051645)	44604	0.408552428	0.999994883
hemidesmosome assembly (GO:0031581)	44604	0.408552428	0.999994883
homocysteine metabolic process (GO:005066	44604	0.408552428	0.999994883
macrophage chemotaxis (GO:0048246)	44604	0.408552428	0.999994883
magnesium ion transport (GO:0015693)	44604	0.408552428	0.999994883
megakaryocyte differentiation (GO:0030219)	44604	0.408552428	0.999994883
microtubule anchoring at microtubule organi	44604	0.408552428	0.999994883
mitotic G1/S transition checkpoint signaling (	44604	0.408552428	0.999994883
mitotic nuclear membrane disassembly (GO:(	44604	0.408552428	0.999994883
morphogenesis of a polarized epithelium (GC	44604	0.408552428	0.999994883
negative regulation of amyloid fibril formatio	44604	0.408552428	0.999994883
negative regulation of calcineurin-mediated s	44604	0.408552428	0.999994883
negative regulation of calcineurin-NFAT signa	44604	0.408552428	0.999994883
negative regulation of cell division (GO:00517	44604	0.408552428	0.999994883
negative regulation of gene silencing by miRN	44604	0.408552428	0.999994883
negative regulation of oxidoreductase activit	44604	0.408552428	0.999994883
neurotransmitter uptake (GO:0001504)	44604	0.408552428	0.999994883
nucleoside salvage (GO:0043174)	44604	0.408552428	0.999994883
P-body assembly (GO:0033962)	44604	0.408552428	0.999994883
phosphate ion transmembrane transport (GC	44604	0.408552428	0.999994883
poly-N-acetyllactosamine biosynthetic proce	44604	0.408552428	0.999994883
positive regulation of fatty acid oxidation (GC	44604	0.408552428	0.999994883
positive regulation of myeloid leukocyte med	44604	0.408552428	0.999994883
positive regulation of neuroinflammatory res	44604	0.408552428	0.999994883
positive regulation of protein maturation (GC	44604	0.408552428	0.999994883
positive regulation of ubiquitin protein ligase	44604	0.408552428	0.999994883
protein auto-ADP-ribosylation (GO:0070213)	44604	0.408552428	0.999994883
protein localization to synapse (GO:0035418)	44604	0.408552428	0.999994883
pyrimidine nucleobase metabolic process (GC	44604	0.408552428	0.999994883
regulation of CD4-positive, alpha-beta T cell c	44604	0.408552428	0.999994883
regulation of cholesterol esterification (GO:0	44604	0.408552428	0.999994883
regulation of flagellated sperm motility (GO:1	44604	0.408552428	0.999994883
regulation of histone H3-K9 methylation (GO	44604	0.408552428	0.999994883
regulation of leukocyte cell-cell adhesion (GC	44604	0.408552428	0.999994883
regulation of nucleobase-containing compou	44604	0.408552428	0.999994883
regulation of response to oxidative stress (GC	44604	0.408552428	0.999994883
regulation of sensory perception (GO:005193	44604	0.408552428	0.999994883
regulation of vascular associated smooth mu	44604	0.408552428	0.999994883
sensory perception of taste (GO:0050909)	44604	0.408552428	0.999994883
serine family amino acid biosynthetic process	44604	0.408552428	0.999994883
smooth muscle cell differentiation (GO:0051	44604	0.408552428	0.999994883
thyroid hormone generation (GO:0006590)	44604	0.408552428	0.999994883

tricarboxylic acid metabolic process (GO:007	44604	0.408552428	0.999994883
tyrosine metabolic process (GO:0006570)	44604	0.408552428	0.999994883
apoptotic process (GO:0006915)	28/231	0.4105335	0.999994883
positive regulation of GTPase activity (GO:00	26/214	0.411102326	0.999994883
cellular response to insulin stimulus (GO:003	16/129	0.411611081	0.999994883
COPII-coated vesicle budding (GO:0090114)	25812	0.413119466	0.999994883
chromosome condensation (GO:0030261)	16589	0.415185517	0.999994883
negative regulation of T cell activation (GO:0	16589	0.415185517	0.999994883
protein deacetylation (GO:0006476)	16589	0.415185517	0.999994883
steroid metabolic process (GO:0008202)	13/104	0.417077767	0.999994883
anterograde axonal transport (GO:0008089)	13636	0.42261326	0.999994883
neural crest cell migration (GO:0001755)	13636	0.42261326	0.999994883
protein insertion into ER membrane (GO:004	13636	0.42261326	0.999994883
regulation of transport (GO:0051049)	13636	0.42261326	0.999994883
regulation of cyclin-dependent protein kinase	19906	0.427949765	0.999994883
regulation of megakaryocyte differentiation (	19906	0.427949765	0.999994883
striated muscle contraction (GO:0006941)	19906	0.427949765	0.999994883
negative regulation of neuron apoptotic proc	26177	0.430179414	0.999994883
regulation of G1/S transition of mitotic cell cy	26177	0.430179414	0.999994883
establishment of mitotic spindle localization	44680	0.430785809	0.999994883
homologous chromosome pairing at meiosis	44680	0.430785809	0.999994883
lamellipodium organization (GO:0097581)	44680	0.430785809	0.999994883
limb development (GO:0060173)	44680	0.430785809	0.999994883
lipid catabolic process (GO:0016042)	44680	0.430785809	0.999994883
negative regulation of interferon-gamma pro	44680	0.430785809	0.999994883
negative regulation of transferase activity (G	44680	0.430785809	0.999994883
positive regulation of viral genome replicatio	44680	0.430785809	0.999994883
regulation of double-strand break repair via r	44680	0.430785809	0.999994883
regulation of fatty acid biosynthetic process (	44680	0.430785809	0.999994883
regulation of response to biotic stimulus (GO	44680	0.430785809	0.999994883
metal ion transport (GO:0030001)	32448	0.431001811	0.999994883
negative regulation of tumor necrosis factor	16954	0.436513498	0.999994883
positive regulation of nucleocytoplasmic tran	16954	0.436513498	0.999994883
regulation of cellular protein localization (GO	16954	0.436513498	0.999994883
regulation of telomerase activity (GO:005197	16954	0.436513498	0.999994883
positive regulation of cellular component org	14/114	0.437665214	0.999994883
actin cytoskeleton reorganization (GO:00315	23224	0.438386794	0.999994883
glycosaminoglycan biosynthetic process (GO:	35765	0.43840844	0.999994883
regulation of fat cell differentiation (GO:0045	29495	0.438759483	0.999994883
actin filament-based transport (GO:0099515)	44641	0.439889272	0.999994883
aerobic respiration (GO:0009060)	44641	0.439889272	0.999994883
cellular response to inorganic substance (GO:	44641	0.439889272	0.999994883
cobalamin metabolic process (GO:0009235)	44641	0.439889272	0.999994883
linoleic acid metabolic process (GO:0043651)	44641	0.439889272	0.999994883
mitochondrial calcium ion transmembrane tr	44641	0.439889272	0.999994883
NAD biosynthetic process (GO:0009435)	44641	0.439889272	0.999994883
negative regulation of protein localization to	44641	0.439889272	0.999994883

positive regulation of T cell cytokine producti	44641	0.439889272	0.999994883
positive regulation of transcription regulatory	44641	0.439889272	0.999994883
protein localization to chromatin (GO:00711(	44641	0.439889272	0.999994883
purinergic nucleotide receptor signaling path	44641	0.439889272	0.999994883
regulation of cardiac muscle contraction by c	44641	0.439889272	0.999994883
regulation of cell-substrate junction assembly	44641	0.439889272	0.999994883
regulation of lipid catabolic process (GO:005(	44641	0.439889272	0.999994883
regulation of lipopolysaccharide-mediated sig	44641	0.439889272	0.999994883
regulation of lipoprotein lipase activity (GO:0	44641	0.439889272	0.999994883
regulation of mitochondrial translation (GO:0	44641	0.439889272	0.999994883
regulation of transcription by RNA polymeras	44641	0.439889272	0.999994883
zinc ion transport (GO:0006829)	44641	0.439889272	0.999994883
positive regulation of protein serine/threonir	13/106	0.4450661	0.999994883
actin-myosin filament sliding (GO:0033275)	14001	0.446189423	0.999994883
muscle filament sliding (GO:0030049)	14001	0.446189423	0.999994883
negative regulation of endothelial cell migrat	14001	0.446189423	0.999994883
positive regulation of production of molecula	14001	0.446189423	0.999994883
regulation of apoptotic signaling pathway (G(	14001	0.446189423	0.999994883
protein import (GO:0017038)	32813	0.446286388	0.999994883
cytoskeleton-dependent cytokinesis (GO:006	26543	0.447198382	0.999994883
extrinsic apoptotic signaling pathway (GO:00	26543	0.447198382	0.999994883
regulation of blood vessel endothelial cell mi	20271	0.447466498	0.999994883
chondroitin sulfate catabolic process (GO:00	44605	0.449931791	0.999994883
dermatan sulfate metabolic process (GO:003	44605	0.449931791	0.999994883
detection of calcium ion (GO:0005513)	44605	0.449931791	0.999994883
embryonic appendage morphogenesis (GO:0(	44605	0.449931791	0.999994883
establishment of protein localization to chro	44605	0.449931791	0.999994883
Golgi ribbon formation (GO:0090161)	44605	0.449931791	0.999994883
lipid oxidation (GO:0034440)	44605	0.449931791	0.999994883
mitochondrion transport along microtubule (	44605	0.449931791	0.999994883
negative regulation of adenylate cyclase activ	44605	0.449931791	0.999994883
negative regulation of alcohol biosynthetic pr	44605	0.449931791	0.999994883
negative regulation of CD4-positive, alpha-be	44605	0.449931791	0.999994883
negative regulation of cell morphogenesis inv	44605	0.449931791	0.999994883
negative regulation of chromatin organizatio	44605	0.449931791	0.999994883
negative regulation of chromatin silencing (G	44605	0.449931791	0.999994883
negative regulation of gene silencing (GO:00(	44605	0.449931791	0.999994883
negative regulation of histone methylation (G	44605	0.449931791	0.999994883
negative regulation of intrinsic apoptotic sign	44605	0.449931791	0.999994883
negative regulation of mononuclear cell migr	44605	0.449931791	0.999994883
negative regulation of substrate adhesion-de	44605	0.449931791	0.999994883
pentose-phosphate shunt (GO:0006098)	44605	0.449931791	0.999994883
poly-N-acetyllactosamine metabolic process	44605	0.449931791	0.999994883
polyamine metabolic process (GO:0006595)	44605	0.449931791	0.999994883
positive regulation of calcium ion-dependent	44605	0.449931791	0.999994883
positive regulation of calcium-mediated signa	44605	0.449931791	0.999994883
positive regulation of fatty acid biosynthetic p	44605	0.449931791	0.999994883

positive regulation of insulin receptor signalir	44605	0.449931791	0.999994883
positive regulation of lipid transport (GO:003	44605	0.449931791	0.999994883
positive regulation of protein localization to (	44605	0.449931791	0.999994883
positive regulation of reactive oxygen species	44605	0.449931791	0.999994883
positive regulation of sodium ion transport ((	44605	0.449931791	0.999994883
positive regulation of steroid metabolic proc	44605	0.449931791	0.999994883
pteridine-containing compound metabolic pr	44605	0.449931791	0.999994883
regulation of chemokine (C-X-C motif) ligand	44605	0.449931791	0.999994883
regulation of histone modification (GO:0031(	44605	0.449931791	0.999994883
regulation of lysosomal lumen pH (GO:00357	44605	0.449931791	0.999994883
regulation of short-term neuronal synaptic pl	44605	0.449931791	0.999994883
regulation of T cell differentiation in thymus (	44605	0.449931791	0.999994883
regulation of tube diameter (GO:0035296)	44605	0.449931791	0.999994883
response to iron ion (GO:0010039)	44605	0.449931791	0.999994883
response to thyroid hormone (GO:0097066)	44605	0.449931791	0.999994883
semaphorin-plexin signaling pathway involve	44605	0.449931791	0.999994883
spinal cord development (GO:0021510)	44605	0.449931791	0.999994883
transport along microtubule (GO:0010970)	44605	0.449931791	0.999994883
tRNA 5'-leader removal (GO:0001682)	44605	0.449931791	0.999994883
vascular process in circulatory system (GO:0(	44605	0.449931791	0.999994883
cellular response to molecule of bacterial ori	14/115	0.451112169	0.999994883
regulation of small GTPase mediated signal tr	17/141	0.454377405	0.999994883
positive regulation of phosphorylation (GO:0(	30/253	0.455184828	0.999994883
regulation of cellular ketone metabolic proce	23590	0.456484936	0.999994883
tRNA processing (GO:0008033)	23590	0.456484936	0.999994883
non-canonical Wnt signaling pathway (GO:00	15/124	0.456650371	0.999994883
activation of protein kinase C activity (GO:19	44566	0.456678815	0.999994883
ADP transport (GO:0015866)	44566	0.456678815	0.999994883
AMP biosynthetic process (GO:0006167)	44566	0.456678815	0.999994883
antigen processing and presentation of lipid a	44566	0.456678815	0.999994883
antigen processing and presentation, endoge	44566	0.456678815	0.999994883
antigen processing and presentation, exogen	44566	0.456678815	0.999994883
auditory receptor cell morphogenesis (GO:0(	44566	0.456678815	0.999994883
auditory receptor cell stereocilium organizati	44566	0.456678815	0.999994883
C-terminal protein deglutamylation (GO:003	44566	0.456678815	0.999994883
cell migration involved in gastrulation (GO:0(	44566	0.456678815	0.999994883
cell-cell adhesion mediated by integrin (GO:0	44566	0.456678815	0.999994883
cellular response to cGMP (GO:0071321)	44566	0.456678815	0.999994883
cellular response to erythropoietin (GO:0036	44566	0.456678815	0.999994883
cellular response to macrophage colony-stim	44566	0.456678815	0.999994883
cellular response to nutrient (GO:0031670)	44566	0.456678815	0.999994883
cellular response to testosterone stimulus (G	44566	0.456678815	0.999994883
cerebellar Purkinje cell differentiation (GO:0(	44566	0.456678815	0.999994883
cerebral cortex neuron differentiation (GO:0(	44566	0.456678815	0.999994883
chemokine (C-X-C motif) ligand 12 signaling p	44566	0.456678815	0.999994883
ciliary neurotrophic factor-mediated signaling	44566	0.456678815	0.999994883
CRD-mediated mRNA stabilization (GO:0070(	44566	0.456678815	0.999994883

cyclic-GMP-AMP transmembrane import acr	44566	0.456678815	0.999994883
deadenylation-independent decapping of nu	44566	0.456678815	0.999994883
determination of dorsal/ventral asymmetry (	44566	0.456678815	0.999994883
determination of left/right asymmetry in late	44566	0.456678815	0.999994883
DNA ligation involved in DNA repair (GO:005	44566	0.456678815	0.999994883
embryonic viscerocranium morphogenesis (G	44566	0.456678815	0.999994883
enamel mineralization (GO:0070166)	44566	0.456678815	0.999994883
endothelin receptor signaling pathway (GO:0	44566	0.456678815	0.999994883
establishment of monopolar cell polarity (GO	44566	0.456678815	0.999994883
fructose transmembrane transport (GO:0015	44566	0.456678815	0.999994883
gamma-aminobutyric acid metabolic process	44566	0.456678815	0.999994883
glomerular visceral epithelial cell migration ((	44566	0.456678815	0.999994883
glucose import across plasma membrane (GC	44566	0.456678815	0.999994883
glucose-6-phosphate transport (GO:0015760	44566	0.456678815	0.999994883
glutathione transport (GO:0034635)	44566	0.456678815	0.999994883
glycerol biosynthetic process (GO:0006114)	44566	0.456678815	0.999994883
glycerol ether metabolic process (GO:000666	44566	0.456678815	0.999994883
hematopoietic stem cell migration (GO:0035	44566	0.456678815	0.999994883
heparin metabolic process (GO:0030202)	44566	0.456678815	0.999994883
hexose phosphate transport (GO:0015712)	44566	0.456678815	0.999994883
histone citrullination (GO:0036414)	44566	0.456678815	0.999994883
histone H4-K20 methylation (GO:0034770)	44566	0.456678815	0.999994883
histone H4-K20 trimethylation (GO:0034773)	44566	0.456678815	0.999994883
homoserine metabolic process (GO:0009092	44566	0.456678815	0.999994883
intracellular sequestering of iron ion (GO:000	44566	0.456678815	0.999994883
isocitrate metabolic process (GO:0006102)	44566	0.456678815	0.999994883
L-aspartate transmembrane transport (GO:0(	44566	0.456678815	0.999994883
late endosome to Golgi transport (GO:00344	44566	0.456678815	0.999994883
late endosome to lysosome transport (GO:19	44566	0.456678815	0.999994883
long-chain fatty acid catabolic process (GO:0(	44566	0.456678815	0.999994883
mannose trimming involved in glycoprotein E	44566	0.456678815	0.999994883
mature conventional dendritic cell differentia	44566	0.456678815	0.999994883
medium-chain fatty acid catabolic process (G	44566	0.456678815	0.999994883
meiotic sister chromatid segregation (GO:004	44566	0.456678815	0.999994883
membrane raft distribution (GO:0031580)	44566	0.456678815	0.999994883
mesonephric duct development (GO:007217	44566	0.456678815	0.999994883
metanephric distal tubule development (GO:	44566	0.456678815	0.999994883
mRNA cleavage involved in gene silencing by	44566	0.456678815	0.999994883
negative regulation of anion transmembrane	44566	0.456678815	0.999994883
negative regulation of CD4-positive, alpha-be	44566	0.456678815	0.999994883
negative regulation of cell volume (GO:00457	44566	0.456678815	0.999994883
negative regulation of cellular respiration (GC	44566	0.456678815	0.999994883
negative regulation of ceramide biosynthetic	44566	0.456678815	0.999994883
negative regulation of CREB transcription fac	44566	0.456678815	0.999994883
negative regulation of gene silencing by RNA	44566	0.456678815	0.999994883
negative regulation of histone deacetylation	44566	0.456678815	0.999994883
negative regulation of hydrogen peroxide-inc	44566	0.456678815	0.999994883

negative regulation of interferon-alpha prod	44566	0.456678815	0.999994883
negative regulation of lipid transport (GO:00	44566	0.456678815	0.999994883
negative regulation of macrophage differenti	44566	0.456678815	0.999994883
negative regulation of mast cell activation in	44566	0.456678815	0.999994883
negative regulation of metallopeptidase activ	44566	0.456678815	0.999994883
negative regulation of oxidative stress-induce	44566	0.456678815	0.999994883
negative regulation of posttranscriptional ge	44566	0.456678815	0.999994883
negative regulation of protein acetylation (G	44566	0.456678815	0.999994883
negative regulation of response to food (GO:	44566	0.456678815	0.999994883
negative regulation of smooth muscle contra	44566	0.456678815	0.999994883
negative regulation of vascular endothelial ce	44566	0.456678815	0.999994883
nephric duct development (GO:0072176)	44566	0.456678815	0.999994883
nucleoside transport (GO:0015858)	44566	0.456678815	0.999994883
nucleoside triphosphate catabolic process (G	44566	0.456678815	0.999994883
oxaloacetate metabolic process (GO:000610	44566	0.456678815	0.999994883
oxaloacetate transport (GO:0015729)	44566	0.456678815	0.999994883
pentose catabolic process (GO:0019323)	44566	0.456678815	0.999994883
peptidyl-lysine oxidation (GO:0018057)	44566	0.456678815	0.999994883
PML body organization (GO:0030578)	44566	0.456678815	0.999994883
positive regulation by host of viral genome re	44566	0.456678815	0.999994883
positive regulation of anoikis (GO:2000210)	44566	0.456678815	0.999994883
positive regulation of attachment of spindle r	44566	0.456678815	0.999994883
positive regulation of axon extension involve	44566	0.456678815	0.999994883
positive regulation of bicellular tight junction	44566	0.456678815	0.999994883
positive regulation of cAMP-dependent prote	44566	0.456678815	0.999994883
positive regulation of fertilization (GO:19055	44566	0.456678815	0.999994883
positive regulation of fibroblast growth facto	44566	0.456678815	0.999994883
positive regulation of heat generation (GO:0(	44566	0.456678815	0.999994883
positive regulation of histone H3-K9 acetylati	44566	0.456678815	0.999994883
positive regulation of leukocyte tethering or r	44566	0.456678815	0.999994883
positive regulation of maintenance of mitotic	44566	0.456678815	0.999994883
positive regulation of maintenance of sister c	44566	0.456678815	0.999994883
positive regulation of mast cell activation inv	44566	0.456678815	0.999994883
positive regulation of mast cell chemotaxis (G	44566	0.456678815	0.999994883
positive regulation of mitochondrial depolari	44566	0.456678815	0.999994883
positive regulation of non-motile cilium asser	44566	0.456678815	0.999994883
positive regulation of peroxisome proliferato	44566	0.456678815	0.999994883
positive regulation of protein catabolic proce	44566	0.456678815	0.999994883
positive regulation of protein localization to c	44566	0.456678815	0.999994883
positive regulation of protein monoubiquitina	44566	0.456678815	0.999994883
positive regulation of the force of heart contr	44566	0.456678815	0.999994883
postsynaptic endocytosis (GO:0140239)	44566	0.456678815	0.999994883
postsynaptic neurotransmitter receptor inter	44566	0.456678815	0.999994883
protein C-linked glycosylation via 2'-alpha-ma	44566	0.456678815	0.999994883
protein C-linked glycosylation via tryptophan	44566	0.456678815	0.999994883
protein citrullination (GO:0018101)	44566	0.456678815	0.999994883
protein deglycosylation involved in glycoprot	44566	0.456678815	0.999994883

protein K69-linked ufmylation (GO:1990592)	44566	0.456678815	0.999994883
protein localization to axon (GO:0099612)	44566	0.456678815	0.999994883
protein localization to microtubule end (GO:1	44566	0.456678815	0.999994883
protein localization to microtubule plus-end (	44566	0.456678815	0.999994883
protein localization to site of double-strand b	44566	0.456678815	0.999994883
protein polyufmylation (GO:1990564)	44566	0.456678815	0.999994883
protein sialylation (GO:1990743)	44566	0.456678815	0.999994883
protein side chain deglutamylation (GO:0035	44566	0.456678815	0.999994883
pyrimidine deoxyribonucleotide biosynthetic	44566	0.456678815	0.999994883
pyrimidine nucleobase biosynthetic process (	44566	0.456678815	0.999994883
pyrimidine nucleoside transport (GO:001586	44566	0.456678815	0.999994883
pyrimidine nucleotide metabolic process (GO	44566	0.456678815	0.999994883
receptor-mediated virion attachment to host	44566	0.456678815	0.999994883
regulation of astrocyte activation (GO:00618	44566	0.456678815	0.999994883
regulation of caveolin-mediated endocytosis	44566	0.456678815	0.999994883
regulation of cellular response to osmotic str	44566	0.456678815	0.999994883
regulation of chaperone-mediated protein fo	44566	0.456678815	0.999994883
regulation of cytochrome-c oxidase activity ((	44566	0.456678815	0.999994883
regulation of germinal center formation (GO:	44566	0.456678815	0.999994883
regulation of glomerular mesangial cell prolif	44566	0.456678815	0.999994883
regulation of granulocyte colony-stimulating	44566	0.456678815	0.999994883
regulation of hippocampal neuron apoptotic	44566	0.456678815	0.999994883
regulation of histone H4-K16 acetylation (GO	44566	0.456678815	0.999994883
regulation of hydrogen peroxide biosynthetic	44566	0.456678815	0.999994883
regulation of inward rectifier potassium chan	44566	0.456678815	0.999994883
regulation of low-density lipoprotein particle	44566	0.456678815	0.999994883
regulation of maintenance of mitotic sister ch	44566	0.456678815	0.999994883
regulation of metaphase plate congression (G	44566	0.456678815	0.999994883
regulation of microglial cell mediated cytotox	44566	0.456678815	0.999994883
regulation of microvillus assembly (GO:00325	44566	0.456678815	0.999994883
regulation of mitophagy (GO:1901524)	44566	0.456678815	0.999994883
regulation of morphogenesis of a branching s	44566	0.456678815	0.999994883
regulation of myoblast proliferation (GO:200	44566	0.456678815	0.999994883
regulation of natural killer cell differentiation	44566	0.456678815	0.999994883
regulation of neutrophil activation (GO:1902	44566	0.456678815	0.999994883
regulation of phosphatidylinositol biosynthet	44566	0.456678815	0.999994883
regulation of phosphatidylinositol dephospho	44566	0.456678815	0.999994883
regulation of postsynaptic density organizatio	44566	0.456678815	0.999994883
regulation of protein monoubiquitination (GO	44566	0.456678815	0.999994883
regulation of respiratory burst involved in inf	44566	0.456678815	0.999994883
regulation of snRNA transcription by RNA pol	44566	0.456678815	0.999994883
regulation of sterol transport (GO:0032371)	44566	0.456678815	0.999994883
regulation of synaptic vesicle recycling (GO:1	44566	0.456678815	0.999994883
regulation of triglyceride metabolic process (	44566	0.456678815	0.999994883
regulation of type B pancreatic cell apoptotic	44566	0.456678815	0.999994883
renal tubule development (GO:0061326)	44566	0.456678815	0.999994883
rescue of stalled ribosome (GO:0072344)	44566	0.456678815	0.999994883

response to acetylcholine (GO:1905144)	44566	0.456678815	0.999994883
response to cGMP (GO:0070305)	44566	0.456678815	0.999994883
response to denervation involved in regulatic	44566	0.456678815	0.999994883
response to macrophage colony-stimulating f	44566	0.456678815	0.999994883
response to mitochondrial depolarisation (G(	44566	0.456678815	0.999994883
response to morphine (GO:0043278)	44566	0.456678815	0.999994883
response to prostaglandin (GO:0034694)	44566	0.456678815	0.999994883
ribose phosphate metabolic process (GO:001	44566	0.456678815	0.999994883
ribosome localization (GO:0033750)	44566	0.456678815	0.999994883
Schwann cell differentiation (GO:0014037)	44566	0.456678815	0.999994883
sensory perception of sour taste (GO:005091	44566	0.456678815	0.999994883
short-term memory (GO:0007614)	44566	0.456678815	0.999994883
sialic acid transport (GO:0015739)	44566	0.456678815	0.999994883
sulfide oxidation (GO:0019418)	44566	0.456678815	0.999994883
sulfide oxidation, using sulfide:quinone oxido	44566	0.456678815	0.999994883
tight junction organization (GO:0120193)	44566	0.456678815	0.999994883
Toll signaling pathway (GO:0008063)	44566	0.456678815	0.999994883
transsulfuration (GO:0019346)	44566	0.456678815	0.999994883
tricuspid valve morphogenesis (GO:0003186)	44566	0.456678815	0.999994883
trivalent inorganic anion homeostasis (GO:00	44566	0.456678815	0.999994883
trophoblast giant cell differentiation (GO:006	44566	0.456678815	0.999994883
tryptophan catabolic process to kynurenine (	44566	0.456678815	0.999994883
ubiquitin-dependent glycoprotein ERAD path	44566	0.456678815	0.999994883
uridine transport (GO:0015862)	44566	0.456678815	0.999994883
vascular endothelial growth factor receptor-2	44566	0.456678815	0.999994883
vesicle fusion with Golgi apparatus (GO:0048	44566	0.456678815	0.999994883
vesicle tethering to Golgi (GO:0099041)	44566	0.456678815	0.999994883
vitamin D3 metabolic process (GO:0070640)	44566	0.456678815	0.999994883
chondroitin sulfate metabolic process (GO:00	44681	0.457458652	0.999994883
establishment of spindle orientation (GO:005	44681	0.457458652	0.999994883
estrogen metabolic process (GO:0008210)	44681	0.457458652	0.999994883
ion homeostasis (GO:0050801)	44681	0.457458652	0.999994883
morphogenesis of an epithelium (GO:000200	44681	0.457458652	0.999994883
ncRNA catabolic process (GO:0034661)	44681	0.457458652	0.999994883
positive regulation of B cell proliferation (GO	44681	0.457458652	0.999994883
positive regulation of DNA recombination (G(	44681	0.457458652	0.999994883
regulation of T cell activation (GO:0050863)	17319	0.457695073	0.999994883
regulation of cytokine production (GO:00018	18/150	0.459169711	0.999994883
positive regulation of autophagy (GO:001050	33178	0.461528755	0.999994883
positive regulation of binding (GO:0051099)	33178	0.461528755	0.999994883
protein complex oligomerization (GO:005125	33178	0.461528755	0.999994883
cellular response to oxygen-containing comp	38/323	0.463046977	0.999994883
ubiquitin-dependent ERAD pathway (GO:003	26908	0.464146465	0.999994883
regulation of protein-containing complex ass	14/116	0.464532339	0.999994883
DNA damage response, signal transduction b	20637	0.466857819	0.999994883
positive regulation of establishment of prote	20637	0.466857819	0.999994883
regulation of ATP metabolic process (GO:190	20637	0.466857819	0.999994883

membrane protein proteolysis (GO:0033619)	14366	0.469513813	0.999994883
phospholipid dephosphorylation (GO:004683	14366	0.469513813	0.999994883
regulation of dendrite development (GO:005	14366	0.469513813	0.999994883
regulation of intracellular transport (GO:003	14366	0.469513813	0.999994883
regulation of protein tyrosine kinase activity	14366	0.469513813	0.999994883
regulation of receptor-mediated endocytosis	14366	0.469513813	0.999994883
ephrin receptor signaling pathway (GO:0048(	30225	0.470808832	0.999994883
regulation of gene expression, epigenetic (GC	30225	0.470808832	0.999994883
amino acid import (GO:0043090)	44642	0.471235573	0.999994883
cell projection assembly (GO:0030031)	44642	0.471235573	0.999994883
chaperone-mediated protein complex assem	44642	0.471235573	0.999994883
glutamate metabolic process (GO:0006536)	44642	0.471235573	0.999994883
limb morphogenesis (GO:0035108)	44642	0.471235573	0.999994883
lipid droplet organization (GO:0034389)	44642	0.471235573	0.999994883
membrane lipid metabolic process (GO:0006	44642	0.471235573	0.999994883
membrane protein intracellular domain prot	44642	0.471235573	0.999994883
metallo-sulfur cluster assembly (GO:0031163	44642	0.471235573	0.999994883
microglial cell activation (GO:0001774)	44642	0.471235573	0.999994883
negative regulation of lipid biosynthetic proc	44642	0.471235573	0.999994883
negative regulation of lymphocyte activation	44642	0.471235573	0.999994883
neuronal action potential (GO:0019228)	44642	0.471235573	0.999994883
osteoclast differentiation (GO:0030316)	44642	0.471235573	0.999994883
regulation of centrosome cycle (GO:0046605	44642	0.471235573	0.999994883
regulation of platelet activation (GO:001054	44642	0.471235573	0.999994883
tetrapyrrole metabolic process (GO:0033013	44642	0.471235573	0.999994883
zinc ion transmembrane transport (GO:0071	44642	0.471235573	0.999994883
cognition (GO:0050890)	17685	0.478676666	0.999994883
histone H4 acetylation (GO:0043967)	17685	0.478676666	0.999994883
negative regulation of mitotic cell cycle (GO:(	17685	0.478676666	0.999994883
negative regulation of tumor necrosis factor	17685	0.478676666	0.999994883
negative regulation of axon extension (GO:0(	11414	0.483692216	0.999994883
negative regulation of proteasomal ubiquitin	11414	0.483692216	0.999994883
protein acetylation (GO:0006473)	11414	0.483692216	0.999994883
protein palmitoylation (GO:0018345)	11414	0.483692216	0.999994883
regulation of protein ubiquitination (GO:003	13/109	0.486818653	0.999994883
activation of cysteine-type endopeptidase ac	44606	0.489612115	0.999994883
C4-dicarboxylate transport (GO:0015740)	44606	0.489612115	0.999994883
cellular copper ion homeostasis (GO:000687	44606	0.489612115	0.999994883
ceramide transport (GO:0035627)	44606	0.489612115	0.999994883
cGMP-mediated signaling (GO:0019934)	44606	0.489612115	0.999994883
intestinal absorption (GO:0050892)	44606	0.489612115	0.999994883
low-density lipoprotein particle remodeling (	44606	0.489612115	0.999994883
negative regulation of coagulation (GO:0050	44606	0.489612115	0.999994883
negative regulation of cyclase activity (GO:0(	44606	0.489612115	0.999994883
negative regulation of fibroblast growth fact	44606	0.489612115	0.999994883
negative regulation of translational initiation	44606	0.489612115	0.999994883
neurotransmitter biosynthetic process (GO:0	44606	0.489612115	0.999994883

nuclear membrane disassembly (GO:005108:	44606	0.489612115	0.999994883
positive regulation of alpha-beta T cell differe	44606	0.489612115	0.999994883
positive regulation of long-term synaptic pot	44606	0.489612115	0.999994883
positive regulation of mitochondrial translati	44606	0.489612115	0.999994883
positive regulation of superoxide anion gene	44606	0.489612115	0.999994883
positive regulation of transmembrane transp	44606	0.489612115	0.999994883
protein modification by small protein conjug	44606	0.489612115	0.999994883
regulation of chromatin organization (GO:19(	44606	0.489612115	0.999994883
regulation of fatty acid beta-oxidation (GO:0(	44606	0.489612115	0.999994883
regulation of intrinsic apoptotic signaling pat	44606	0.489612115	0.999994883
regulation of protein kinase C signaling (GO:(	44606	0.489612115	0.999994883
regulation of sensory perception of pain (GO:	44606	0.489612115	0.999994883
regulation of trophoblast cell migration (GO::	44606	0.489612115	0.999994883
renal absorption (GO:0070293)	44606	0.489612115	0.999994883
T-helper cell differentiation (GO:0042093)	44606	0.489612115	0.999994883
tRNA wobble uridine modification (GO:0002(	44606	0.489612115	0.999994883
negative regulation of mitotic cell cycle phas	33909	0.491802294	0.999994883
cellular component disassembly (GO:002241	24320	0.492316285	0.999994883
extracellular matrix disassembly (GO:002261	24320	0.492316285	0.999994883
negative regulation of G2/M transition of mit	24320	0.492316285	0.999994883
regulation of protein localization (GO:003288	24320	0.492316285	0.999994883
negative regulation of I-kappaB kinase/NF-ka	14732	0.49251957	0.999994883
positive regulation of double-strand break re	14732	0.49251957	0.999994883
regulation of sodium ion transmembrane tra	14732	0.49251957	0.999994883
epithelial cell differentiation (GO:0030855)	12/101	0.49640466	0.999994883
intracellular protein transport (GO:0006886)	39/336	0.497592756	0.999994883
cellular response to mechanical stimulus (GO	18050	0.499408614	0.999994883
negative regulation of catabolic process (GO:	18050	0.499408614	0.999994883
negative regulation of cell projection organiz	18050	0.499408614	0.999994883
positive regulation of reactive oxygen specie	18050	0.499408614	0.999994883
receptor internalization (GO:0031623)	18050	0.499408614	0.999994883
RNA catabolic process (GO:0006401)	18050	0.499408614	0.999994883
cilium-dependent cell motility (GO:0060285)	44643	0.501757184	0.999994883
glucose 6-phosphate metabolic process (GO:(	44643	0.501757184	0.999994883
negative regulation of phosphoprotein phosp	44643	0.501757184	0.999994883
negative regulation of smoothened signaling	44643	0.501757184	0.999994883
oligosaccharide biosynthetic process (GO:00(	44643	0.501757184	0.999994883
positive regulation of cholesterol efflux (GO:(	44643	0.501757184	0.999994883
positive regulation of epithelial cell apoptotic	44643	0.501757184	0.999994883
positive regulation of natural killer cell media	44643	0.501757184	0.999994883
regulation of B cell receptor signaling pathwa	44643	0.501757184	0.999994883
regulation of peptidase activity (GO:0052547	44643	0.501757184	0.999994883
triglyceride catabolic process (GO:0019433)	44643	0.501757184	0.999994883
chordate embryonic development (GO:0043(	21367	0.50510143	0.999994883
muscle organ development (GO:0007517)	21367	0.50510143	0.999994883
positive regulation of mitotic cell cycle phase	21367	0.50510143	0.999994883
regulation of calcium ion transport (GO:0051	21367	0.50510143	0.999994883

regulation of tumor necrosis factor-mediatec	21367	0.50510143	0.999994883
endodermal cell differentiation (GO:0035987	11780	0.50940142	0.999994883
gene silencing by miRNA (GO:0035195)	11780	0.50940142	0.999994883
metal ion export (GO:0070839)	11780	0.50940142	0.999994883
negative regulation of DNA biosynthetic proc	11780	0.50940142	0.999994883
regulation of cellular biosynthetic process (G	11780	0.50940142	0.999994883
regulation of chemotaxis (GO:0050920)	11780	0.50940142	0.999994883
establishment of protein localization to orgar	28004	0.514285484	0.999994883
regulation of cell division (GO:0051302)	28004	0.514285484	0.999994883
endosome organization (GO:0007032)	15097	0.515146251	0.999994883
epithelial cell migration (GO:0010631)	15097	0.515146251	0.999994883
response to growth factor (GO:0070848)	15097	0.515146251	0.999994883
proteasome-mediated ubiquitin-dependent p	37/321	0.517056767	0.999994883
cytoskeleton organization (GO:0007010)	14/120	0.517656761	0.999994883
acetyl-CoA biosynthetic process from pyruvat	44567	0.519094735	0.999994883
adiponectin-activated signaling pathway (GO	44567	0.519094735	0.999994883
alditol metabolic process (GO:0019400)	44567	0.519094735	0.999994883
amino-acid betaine transport (GO:0015838)	44567	0.519094735	0.999994883
aminophospholipid transport (GO:0015917)	44567	0.519094735	0.999994883
anterior/posterior axis specification, embryo	44567	0.519094735	0.999994883
aromatic amino acid transport (GO:0015801)	44567	0.519094735	0.999994883
aspartate metabolic process (GO:0006531)	44567	0.519094735	0.999994883
B cell chemotaxis (GO:0035754)	44567	0.519094735	0.999994883
cell junction disassembly (GO:0150146)	44567	0.519094735	0.999994883
cellular heat acclimation (GO:0070370)	44567	0.519094735	0.999994883
cellular response to bacterial lipopeptide (GC	44567	0.519094735	0.999994883
cellular response to cold (GO:0070417)	44567	0.519094735	0.999994883
cellular response to granulocyte macrophage	44567	0.519094735	0.999994883
cellular response to iron ion (GO:0071281)	44567	0.519094735	0.999994883
cellular response to magnesium ion (GO:007	44567	0.519094735	0.999994883
cellular triglyceride homeostasis (GO:003535	44567	0.519094735	0.999994883
choline catabolic process (GO:0042426)	44567	0.519094735	0.999994883
dehydroascorbic acid transport (GO:0070837	44567	0.519094735	0.999994883
dendrite extension (GO:0097484)	44567	0.519094735	0.999994883
dermatan sulfate proteoglycan metabolic pro	44567	0.519094735	0.999994883
detection of virus (GO:0009597)	44567	0.519094735	0.999994883
determination of liver left/right asymmetry ((	44567	0.519094735	0.999994883
double-strand break repair via classical nonh	44567	0.519094735	0.999994883
embryonic camera-type eye development (G	44567	0.519094735	0.999994883
embryonic camera-type eye morphogenesis (	44567	0.519094735	0.999994883
epithelial tube formation (GO:0072175)	44567	0.519094735	0.999994883
foam cell differentiation (GO:0090077)	44567	0.519094735	0.999994883
galactolipid biosynthetic process (GO:001937	44567	0.519094735	0.999994883
galactosylceramide biosynthetic process (GO	44567	0.519094735	0.999994883
gamma-aminobutyric acid transport (GO:001	44567	0.519094735	0.999994883
glomerulus vasculature development (GO:00	44567	0.519094735	0.999994883
glycerol-3-phosphate metabolic process (GO:	44567	0.519094735	0.999994883

glycolipid transport (GO:0046836)	44567	0.519094735	0.999994883
glycosylceramide catabolic process (GO:0046	44567	0.519094735	0.999994883
glycosylceramide metabolic process (GO:000	44567	0.519094735	0.999994883
growth hormone secretion (GO:0030252)	44567	0.519094735	0.999994883
guanine nucleotide transmembrane transpor	44567	0.519094735	0.999994883
heat acclimation (GO:0010286)	44567	0.519094735	0.999994883
heparan sulfate proteoglycan biosynthetic pr	44567	0.519094735	0.999994883
hexose import across plasma membrane (GO	44567	0.519094735	0.999994883
hydrogen sulfide metabolic process (GO:007(	44567	0.519094735	0.999994883
IMP biosynthetic process (GO:0006188)	44567	0.519094735	0.999994883
L-ornithine transmembrane transport (GO:19	44567	0.519094735	0.999994883
L-serine biosynthetic process (GO:0006564)	44567	0.519094735	0.999994883
leukocyte chemotaxis involved in inflammatc	44567	0.519094735	0.999994883
lipoxin metabolic process (GO:2001300)	44567	0.519094735	0.999994883
macromolecule biosynthetic process (GO:00(	44567	0.519094735	0.999994883
macrophage derived foam cell differentiatior	44567	0.519094735	0.999994883
magnesium ion homeostasis (GO:0010960)	44567	0.519094735	0.999994883
maintenance of DNA methylation (GO:00102	44567	0.519094735	0.999994883
maintenance of DNA repeat elements (GO:0(	44567	0.519094735	0.999994883
medium-chain fatty acid biosynthetic process	44567	0.519094735	0.999994883
meiotic DNA double-strand break formation (	44567	0.519094735	0.999994883
metaphase/anaphase transition of cell cycle (	44567	0.519094735	0.999994883
metaphase/anaphase transition of mitotic ce	44567	0.519094735	0.999994883
mitochondrial ribosome assembly (GO:00616	44567	0.519094735	0.999994883
mRNA 5'-splice site recognition (GO:0000395	44567	0.519094735	0.999994883
multinuclear osteoclast differentiation (GO:0	44567	0.519094735	0.999994883
N-terminal peptidyl-methionine acetylation (	44567	0.519094735	0.999994883
negative regulation of actin filament depolyn	44567	0.519094735	0.999994883
negative regulation of amino acid transport (	44567	0.519094735	0.999994883
negative regulation of anion transport (GO:19	44567	0.519094735	0.999994883
negative regulation of Arp2/3 complex-medi	44567	0.519094735	0.999994883
negative regulation of astrocyte differentiatic	44567	0.519094735	0.999994883
negative regulation of B cell receptor signalin	44567	0.519094735	0.999994883
negative regulation of chemokine-mediated s	44567	0.519094735	0.999994883
negative regulation of cytokinesis (GO:00324	44567	0.519094735	0.999994883
negative regulation of endoplasmic reticulum	44567	0.519094735	0.999994883
negative regulation of ERAD pathway (GO:19	44567	0.519094735	0.999994883
negative regulation of glial cell proliferation (	44567	0.519094735	0.999994883
negative regulation of glycogen biosynthetic	44567	0.519094735	0.999994883
negative regulation of lipoprotein lipase activ	44567	0.519094735	0.999994883
negative regulation of mast cell activation (G	44567	0.519094735	0.999994883
negative regulation of monocyte chemotaxis	44567	0.519094735	0.999994883
negative regulation of myeloid leukocyte me	44567	0.519094735	0.999994883
negative regulation of T cell differentiation in	44567	0.519094735	0.999994883
negative regulation of toll-like receptor 2 sigr	44567	0.519094735	0.999994883
negative regulation of trophoblast cell migrat	44567	0.519094735	0.999994883
nephric duct morphogenesis (GO:0072178)	44567	0.519094735	0.999994883

nuclear polyadenylation-dependent ncRNA c	44567	0.519094735	0.999994883
nuclear polyadenylation-dependent rRNA cat	44567	0.519094735	0.999994883
nuclear polyadenylation-dependent tRNA cat	44567	0.519094735	0.999994883
nucleotide transport (GO:0006862)	44567	0.519094735	0.999994883
pentose-phosphate shunt, non-oxidative bra	44567	0.519094735	0.999994883
peptidyl-diphthamide biosynthetic process fr	44567	0.519094735	0.999994883
peptidyl-diphthamide metabolic process (GO	44567	0.519094735	0.999994883
peroxisome proliferator activated receptor si	44567	0.519094735	0.999994883
photoreceptor cell outer segment organizatic	44567	0.519094735	0.999994883
polyphosphate metabolic process (GO:00067	44567	0.519094735	0.999994883
positive regulation of antigen processing and	44567	0.519094735	0.999994883
positive regulation of autophagy of mitochon	44567	0.519094735	0.999994883
positive regulation of centriole replication (G	44567	0.519094735	0.999994883
positive regulation of cholesterol storage (GC	44567	0.519094735	0.999994883
positive regulation of dendritic cell antigen p	44567	0.519094735	0.999994883
positive regulation of endoplasmic reticulum	44567	0.519094735	0.999994883
positive regulation of gluconeogenesis (GO:0	44567	0.519094735	0.999994883
positive regulation of gonad development (G	44567	0.519094735	0.999994883
positive regulation of histone phosphorylatio	44567	0.519094735	0.999994883
positive regulation of male gonad developme	44567	0.519094735	0.999994883
positive regulation of microglial cell migratio	44567	0.519094735	0.999994883
positive regulation of natural killer cell media	44567	0.519094735	0.999994883
positive regulation of natural killer cell media	44567	0.519094735	0.999994883
positive regulation of non-membrane spanni	44567	0.519094735	0.999994883
positive regulation of plasminogen activation	44567	0.519094735	0.999994883
positive regulation of receptor binding (GO:1	44567	0.519094735	0.999994883
positive regulation of tau-protein kinase activ	44567	0.519094735	0.999994883
positive regulation of Wnt signaling pathway,	44567	0.519094735	0.999994883
proline transport (GO:0015824)	44567	0.519094735	0.999994883
pronephros development (GO:0048793)	44567	0.519094735	0.999994883
protein localization to nuclear envelope (GO:	44567	0.519094735	0.999994883
protein localization to nucleolus (GO:190257	44567	0.519094735	0.999994883
protein sulfation (GO:0006477)	44567	0.519094735	0.999994883
protein ufmylation (GO:0071569)	44567	0.519094735	0.999994883
protein-DNA covalent cross-linking repair (GC	44567	0.519094735	0.999994883
proton-transporting V-type ATPase complex a	44567	0.519094735	0.999994883
pyrimidine nucleotide-sugar transmembrane	44567	0.519094735	0.999994883
regulation of adiponectin secretion (GO:007C	44567	0.519094735	0.999994883
regulation of cardiac muscle hypertrophy in r	44567	0.519094735	0.999994883
regulation of collagen fibril organization (GO:	44567	0.519094735	0.999994883
regulation of digestive system process (GO:0(	44567	0.519094735	0.999994883
regulation of excitatory synapse assembly (G	44567	0.519094735	0.999994883
regulation of glucagon secretion (GO:007009	44567	0.519094735	0.999994883
regulation of hyaluronan biosynthetic proces	44567	0.519094735	0.999994883
regulation of immunoglobulin mediated imm	44567	0.519094735	0.999994883
regulation of interleukin-1-mediated signalin	44567	0.519094735	0.999994883
regulation of keratinocyte apoptotic process	44567	0.519094735	0.999994883

regulation of mast cell chemotaxis (GO:0060	44567	0.519094735	0.999994883
regulation of mitotic sister chromatid segreg	44567	0.519094735	0.999994883
regulation of mitotic spindle checkpoint (GO:	44567	0.519094735	0.999994883
regulation of nitric oxide mediated signal tra	44567	0.519094735	0.999994883
regulation of non-motile cilium assembly (GC	44567	0.519094735	0.999994883
regulation of nuclease activity (GO:0032069)	44567	0.519094735	0.999994883
regulation of protein autoubiquitination (GO:	44567	0.519094735	0.999994883
regulation of resting membrane potential (G	44567	0.519094735	0.999994883
regulation of retrograde transport, endosom	44567	0.519094735	0.999994883
regulation of T-helper 17 cell lineage commit	44567	0.519094735	0.999994883
regulation of type 2 immune response (GO:0	44567	0.519094735	0.999994883
regulation of ventricular cardiac muscle cell r	44567	0.519094735	0.999994883
replication-born double-strand break repair v	44567	0.519094735	0.999994883
response to catecholamine (GO:0071869)	44567	0.519094735	0.999994883
response to DNA damage checkpoint signalin	44567	0.519094735	0.999994883
response to granulocyte macrophage colony-	44567	0.519094735	0.999994883
response to testosterone (GO:0033574)	44567	0.519094735	0.999994883
sialylation (GO:0097503)	44567	0.519094735	0.999994883
signal complex assembly (GO:0007172)	44567	0.519094735	0.999994883
snRNA modification (GO:0040031)	44567	0.519094735	0.999994883
spinal cord motor neuron differentiation (GO	44567	0.519094735	0.999994883
succinate transmembrane transport (GO:007	44567	0.519094735	0.999994883
T-tubule organization (GO:0033292)	44567	0.519094735	0.999994883
tripartite regional subdivision (GO:0007351)	44567	0.519094735	0.999994883
tRNA surveillance (GO:0106354)	44567	0.519094735	0.999994883
xenobiotic transport across blood-brain barri	44567	0.519094735	0.999994883
amino acid transport (GO:0006865)	18415	0.519845256	0.999994883
positive regulation of cell morphogenesis inv	18415	0.519845256	0.999994883
cardiac myofibril assembly (GO:0055003)	44607	0.527437763	0.999994883
cellular response to estrogen stimulus (GO:0	44607	0.527437763	0.999994883
contractile actin filament bundle assembly (G	44607	0.527437763	0.999994883
embryonic cranial skeleton morphogenesis (G	44607	0.527437763	0.999994883
endoplasmic reticulum tubular network orga	44607	0.527437763	0.999994883
establishment of apical/basal cell polarity (G	44607	0.527437763	0.999994883
eye photoreceptor cell development (GO:004	44607	0.527437763	0.999994883
glucuronate metabolic process (GO:0019585)	44607	0.527437763	0.999994883
histone H3 deacetylation (GO:0070932)	44607	0.527437763	0.999994883
histone mRNA catabolic process (GO:007104	44607	0.527437763	0.999994883
integrated stress response signaling (GO:014	44607	0.527437763	0.999994883
lipoxygenase pathway (GO:0019372)	44607	0.527437763	0.999994883
macrophage differentiation (GO:0030225)	44607	0.527437763	0.999994883
macrophage migration (GO:1905517)	44607	0.527437763	0.999994883
membrane raft organization (GO:0031579)	44607	0.527437763	0.999994883
mitotic intra-S DNA damage checkpoint signa	44607	0.527437763	0.999994883
myoblast differentiation (GO:0045445)	44607	0.527437763	0.999994883
negative regulation of blood pressure (GO:00	44607	0.527437763	0.999994883
negative regulation of cellular component m	44607	0.527437763	0.999994883

negative regulation of protein processing (GC	44607	0.527437763	0.999994883
nucleobase-containing small molecule catabc	44607	0.527437763	0.999994883
positive regulation of acute inflammatory res	44607	0.527437763	0.999994883
positive regulation of double-strand break re	44607	0.527437763	0.999994883
positive regulation of natural killer cell activa	44607	0.527437763	0.999994883
protein homotrimerization (GO:0070207)	44607	0.527437763	0.999994883
protein trimerization (GO:0070206)	44607	0.527437763	0.999994883
pyrimidine nucleoside metabolic process (GC	44607	0.527437763	0.999994883
regulation of aerobic respiration (GO:190371	44607	0.527437763	0.999994883
regulation of amyloid fibril formation (GO:19	44607	0.527437763	0.999994883
regulation of dephosphorylation (GO:003530	44607	0.527437763	0.999994883
regulation of integrin activation (GO:003362	44607	0.527437763	0.999994883
regulation of macrophage differentiation (GC	44607	0.527437763	0.999994883
regulation of phospholipase C activity (GO:19	44607	0.527437763	0.999994883
regulation of superoxide anion generation (G	44607	0.527437763	0.999994883
regulation of triglyceride biosynthetic proces	44607	0.527437763	0.999994883
steroid hormone mediated signaling pathwa	44607	0.527437763	0.999994883
stress fiber assembly (GO:0043149)	44607	0.527437763	0.999994883
superoxide anion generation (GO:0042554)	44607	0.527437763	0.999994883
tRNA 5'-end processing (GO:0099116)	44607	0.527437763	0.999994883
import into nucleus (GO:0051170)	28369	0.53067704	0.999994883
inorganic cation import across plasma memb	28369	0.53067704	0.999994883
positive regulation of endothelial cell prolifer	28369	0.53067704	0.999994883
axon extension (GO:0048675)	44644	0.531346959	0.999994883
carbohydrate biosynthetic process (GO:0016	44644	0.531346959	0.999994883
DNA packaging (GO:0006323)	44644	0.531346959	0.999994883
establishment of mitotic spindle orientation (	44644	0.531346959	0.999994883
iron-sulfur cluster assembly (GO:0016226)	44644	0.531346959	0.999994883
ncRNA 3'-end processing (GO:0043628)	44644	0.531346959	0.999994883
positive regulation of cellular response to tra	44644	0.531346959	0.999994883
positive regulation of neuron apoptotic proc	44644	0.531346959	0.999994883
positive regulation of transforming growth fa	44644	0.531346959	0.999994883
regulation of axon extension involved in axor	44644	0.531346959	0.999994883
regulation of cellular response to transformir	44644	0.531346959	0.999994883
regulation of vascular endothelial growth fac	44644	0.531346959	0.999994883
response to gamma radiation (GO:0010332)	44644	0.531346959	0.999994883
regulation of Ras protein signal transduction	31686	0.533639108	0.999994883
actin filament bundle assembly (GO:0051017	12145	0.534512503	0.999994883
exonucleolytic catabolism of deadenylated m	12145	0.534512503	0.999994883
negative regulation of JNK cascade (GO:0046	12145	0.534512503	0.999994883
negative regulation of smooth muscle cell pr	12145	0.534512503	0.999994883
positive regulation of cholesterol transport (C	12145	0.534512503	0.999994883
regulation of histone acetylation (GO:003506	12145	0.534512503	0.999994883
heterophilic cell-cell adhesion via plasma me	15462	0.537339813	0.999994883
mitochondrial gene expression (GO:0140053	15462	0.537339813	0.999994883
negative regulation of protein catabolic proc	15462	0.537339813	0.999994883
inositol lipid-mediated signaling (GO:004801	18780	0.539944985	0.999994883

mitotic metaphase plate congression (GO:00(	18780	0.539944985	0.999994883
negative regulation of transport (GO:005105:	18780	0.539944985	0.999994883
negative regulation of blood vessel morphog	28734	0.546868371	0.999994883
neuron projection morphogenesis (GO:0048{	16/140	0.547992272	0.999994883
protein targeting to membrane (GO:0006612	32051	0.54895625	0.999994883
regulation of JNK cascade (GO:0046328)	12/105	0.552884671	0.999994883
organelle disassembly (GO:1903008)	12510	0.558962574	0.999994883
phosphatidylinositol 3-kinase signaling (GO:0	12510	0.558962574	0.999994883
regulation of amyloid-beta formation (GO:19	12510	0.558962574	0.999994883
response to steroid hormone (GO:0048545)	12510	0.558962574	0.999994883
anion transport (GO:0006820)	15827	0.559052517	0.999994883
lipid modification (GO:0030258)	15827	0.559052517	0.999994883
positive regulation of axonogenesis (GO:005(	15827	0.559052517	0.999994883
positive regulation of leukocyte mediated cyt	15827	0.559052517	0.999994883
regulation of cell-substrate adhesion (GO:001	15827	0.559052517	0.999994883
regulation of cytokine production involved in	15827	0.559052517	0.999994883
regulation of purine nucleotide metabolic pr(	15827	0.559052517	0.999994883
substantia nigra development (GO:0021762)	15827	0.559052517	0.999994883
negative regulation of cellular biosynthetic pı	19146	0.559670254	0.999994883
regulation of intrinsic apoptotic signaling patl	19146	0.559670254	0.999994883
negative regulation of ion transport (GO:004:	44645	0.559919776	0.999994883
organophosphate ester transport (GO:00157	44645	0.559919776	0.999994883
phosphatidylinositol dephosphorylation (GO:	44645	0.559919776	0.999994883
positive regulation of release of cytochrome	44645	0.559919776	0.999994883
receptor catabolic process (GO:0032801)	44645	0.559919776	0.999994883
regulation of protein processing (GO:007061:	44645	0.559919776	0.999994883
regulation of proteolysis involved in cellular p	44645	0.559919776	0.999994883
regulation of ryanodine-sensitive calcium-rel(	44645	0.559919776	0.999994883
O-glycan processing (GO:0016266)	22463	0.560579382	0.999994883
pattern recognition receptor signaling pathw	22463	0.560579382	0.999994883
axon development (GO:0061564)	29099	0.562838079	0.999994883
positive regulation of proteasomal ubiquitin-	29099	0.562838079	0.999994883
positive regulation of ubiquitin-dependent pr	29099	0.562838079	0.999994883
regulation of cellular response to heat (GO:1!	29099	0.562838079	0.999994883
regulation of neuron differentiation (GO:004!	29099	0.562838079	0.999994883
B cell activation involved in immune respons(	44608	0.563311222	0.999994883
basement membrane organization (GO:0071	44608	0.563311222	0.999994883
cellular response to sterol (GO:0036315)	44608	0.563311222	0.999994883
dendritic spine morphogenesis (GO:0060997	44608	0.563311222	0.999994883
glycosphingolipid biosynthetic process (GO:0(	44608	0.563311222	0.999994883
histone H2A acetylation (GO:0043968)	44608	0.563311222	0.999994883
mesenchyme development (GO:0060485)	44608	0.563311222	0.999994883
motor neuron axon guidance (GO:0008045)	44608	0.563311222	0.999994883
negative regulation of cell-substrate junction	44608	0.563311222	0.999994883
negative regulation of DNA replication (GO:0(	44608	0.563311222	0.999994883
negative regulation of focal adhesion assemb	44608	0.563311222	0.999994883
negative regulation of histone modification ((	44608	0.563311222	0.999994883

negative regulation of lyase activity (GO:005	44608	0.563311222	0.999994883
neuron projection organization (GO:0106027	44608	0.563311222	0.999994883
oligodendrocyte development (GO:0014003)	44608	0.563311222	0.999994883
platelet-derived growth factor receptor signa	44608	0.563311222	0.999994883
positive regulation by host of viral transcripti	44608	0.563311222	0.999994883
positive regulation of isotype switching (GO:(	44608	0.563311222	0.999994883
positive regulation of leukocyte adhesion to v	44608	0.563311222	0.999994883
positive regulation of syncytium formation by	44608	0.563311222	0.999994883
regulation of amyloid-beta clearance (GO:19(	44608	0.563311222	0.999994883
regulation of chromatin silencing (GO:00319:	44608	0.563311222	0.999994883
regulation of defense response to virus (GO:(	44608	0.563311222	0.999994883
regulation of granulocyte macrophage colony	44608	0.563311222	0.999994883
regulation of interleukin-1 production (GO:0(	44608	0.563311222	0.999994883
regulation of interleukin-13 production (GO:(	44608	0.563311222	0.999994883
regulation of intrinsic apoptotic signaling pat	44608	0.563311222	0.999994883
regulation of isotype switching (GO:0045191)	44608	0.563311222	0.999994883
regulation of leukocyte activation (GO:00026	44608	0.563311222	0.999994883
regulation of mast cell degranulation (GO:004	44608	0.563311222	0.999994883
regulation of neurotransmitter transport (GO	44608	0.563311222	0.999994883
regulation of oxidative phosphorylation (GO:(	44608	0.563311222	0.999994883
regulation of Rac protein signal transduction	44608	0.563311222	0.999994883
retrograde axonal transport (GO:0008090)	44608	0.563311222	0.999994883
transepithelial transport (GO:0070633)	44608	0.563311222	0.999994883
positive regulation of cold-induced thermoge	35735	0.565354285	0.999994883
negative regulation of programmed cell death	43/381	0.573257518	0.999994883
acylglycerol acyl-chain remodeling (GO:0036:	44568	0.574343152	0.999994883
adenylate cyclase-activating dopamine recep	44568	0.574343152	0.999994883
angiotensin-activated signaling pathway (GO:	44568	0.574343152	0.999994883
arginine catabolic process (GO:0006527)	44568	0.574343152	0.999994883
aspartate transmembrane transport (GO:001	44568	0.574343152	0.999994883
atrioventricular valve formation (GO:000319(	44568	0.574343152	0.999994883
axon ensheathment in central nervous syster	44568	0.574343152	0.999994883
calcitonin family receptor signaling pathway (	44568	0.574343152	0.999994883
calcium ion export (GO:1901660)	44568	0.574343152	0.999994883
catecholamine catabolic process (GO:004242	44568	0.574343152	0.999994883
catecholamine uptake (GO:0090493)	44568	0.574343152	0.999994883
Cdc42 protein signal transduction (GO:00324	44568	0.574343152	0.999994883
cellular amino acid biosynthetic process (GO:	44568	0.574343152	0.999994883
cellular protein complex disassembly (GO:004	44568	0.574343152	0.999994883
cellular response to laminar fluid shear stress	44568	0.574343152	0.999994883
cellular response to monoamine stimulus (GO	44568	0.574343152	0.999994883
cellular response to platelet-derived growth f	44568	0.574343152	0.999994883
citrulline metabolic process (GO:0000052)	44568	0.574343152	0.999994883
collagen-activated tyrosine kinase receptor si	44568	0.574343152	0.999994883
coronary vasculature development (GO:0060	44568	0.574343152	0.999994883
creatine metabolic process (GO:0006600)	44568	0.574343152	0.999994883
cytochrome complex assembly (GO:0017004	44568	0.574343152	0.999994883

definitive hemopoiesis (GO:0060216)	44568	0.574343152	0.999994883
dendrite arborization (GO:0140059)	44568	0.574343152	0.999994883
dense core granule cytoskeletal transport (G	44568	0.574343152	0.999994883
desmosome organization (GO:0002934)	44568	0.574343152	0.999994883
determination of digestive tract left/right asy	44568	0.574343152	0.999994883
DNA ligation (GO:0006266)	44568	0.574343152	0.999994883
dolichyl diphosphate biosynthetic process (G	44568	0.574343152	0.999994883
dolichyl diphosphate metabolic process (GO:(	44568	0.574343152	0.999994883
dopamine transport (GO:0015872)	44568	0.574343152	0.999994883
endosome to lysosome transport via multive	44568	0.574343152	0.999994883
ethanol catabolic process (GO:0006068)	44568	0.574343152	0.999994883
excitatory chemical synaptic transmission (G	44568	0.574343152	0.999994883
glial cell migration (GO:0008347)	44568	0.574343152	0.999994883
glomerular visceral epithelial cell developme	44568	0.574343152	0.999994883
glutamine transport (GO:0006868)	44568	0.574343152	0.999994883
glycosylceramide biosynthetic process (GO:0(	44568	0.574343152	0.999994883
Golgi disassembly (GO:0090166)	44568	0.574343152	0.999994883
heart trabecula formation (GO:0060347)	44568	0.574343152	0.999994883
histone H3-K4 dimethylation (GO:0044648)	44568	0.574343152	0.999994883
histone H3-K9 methylation (GO:0051567)	44568	0.574343152	0.999994883
hyaluronan biosynthetic process (GO:003021	44568	0.574343152	0.999994883
hyperosmotic response (GO:0006972)	44568	0.574343152	0.999994883
hypotonic response (GO:0006971)	44568	0.574343152	0.999994883
insulin secretion involved in cellular response	44568	0.574343152	0.999994883
intermembrane lipid transfer (GO:0120009)	44568	0.574343152	0.999994883
iron coordination entity transport (GO:19016	44568	0.574343152	0.999994883
iron import into cell (GO:0033212)	44568	0.574343152	0.999994883
L-alanine transport (GO:0015808)	44568	0.574343152	0.999994883
lipoxin biosynthetic process (GO:2001301)	44568	0.574343152	0.999994883
long-term synaptic depression (GO:0060292)	44568	0.574343152	0.999994883
macropinocytosis (GO:0044351)	44568	0.574343152	0.999994883
maintenance of protein location in extracellu	44568	0.574343152	0.999994883
malate metabolic process (GO:0006108)	44568	0.574343152	0.999994883
membrane biogenesis (GO:0044091)	44568	0.574343152	0.999994883
metanephric nephron tubule development (G	44568	0.574343152	0.999994883
miRNA catabolic process (GO:0010587)	44568	0.574343152	0.999994883
mitochondrion-endoplasmic reticulum memb	44568	0.574343152	0.999994883
modulation by symbiont of host defense resp	44568	0.574343152	0.999994883
negative regulation by host of viral genome r	44568	0.574343152	0.999994883
negative regulation of acute inflammatory re	44568	0.574343152	0.999994883
negative regulation of DNA repair (GO:00457	44568	0.574343152	0.999994883
negative regulation of double-strand break re	44568	0.574343152	0.999994883
negative regulation of glycogen metabolic pr	44568	0.574343152	0.999994883
negative regulation of interferon-gamma-me	44568	0.574343152	0.999994883
negative regulation of meiotic nuclear divisio	44568	0.574343152	0.999994883
negative regulation of membrane protein ect	44568	0.574343152	0.999994883
negative regulation of mitochondrial outer m	44568	0.574343152	0.999994883

negative regulation of MyD88-independent t	44568	0.574343152	0.999994883
negative regulation of NLRP3 inflammasome	44568	0.574343152	0.999994883
negative regulation of p38MAPK cascade (GC	44568	0.574343152	0.999994883
negative regulation of protein kinase activity	44568	0.574343152	0.999994883
negative regulation of protein sumoylation (C	44568	0.574343152	0.999994883
negative regulation of response to interferon	44568	0.574343152	0.999994883
negative regulation of steroid metabolic proc	44568	0.574343152	0.999994883
negative regulation of stress-activated protei	44568	0.574343152	0.999994883
negative regulation of striated muscle tissue	44568	0.574343152	0.999994883
negative regulation of telomere capping (GO:	44568	0.574343152	0.999994883
nodal signaling pathway (GO:0038092)	44568	0.574343152	0.999994883
nuclear-transcribed mRNA catabolic process,	44568	0.574343152	0.999994883
nucleobase catabolic process (GO:0046113)	44568	0.574343152	0.999994883
pharyngeal arch artery morphogenesis (GO:0	44568	0.574343152	0.999994883
polyamine biosynthetic process (GO:000659(	44568	0.574343152	0.999994883
positive regulation by symbiont of host autop	44568	0.574343152	0.999994883
positive regulation of amyloid-beta clearance	44568	0.574343152	0.999994883
positive regulation of B cell receptor signalin	44568	0.574343152	0.999994883
positive regulation of blood circulation (GO:1	44568	0.574343152	0.999994883
positive regulation of chemokine (C-X-C moti	44568	0.574343152	0.999994883
positive regulation of cilium movement (GO:(	44568	0.574343152	0.999994883
positive regulation of cilium-dependent cell r	44568	0.574343152	0.999994883
positive regulation of ER-associated ubiquitin	44568	0.574343152	0.999994883
positive regulation of fibroblast apoptotic pro	44568	0.574343152	0.999994883
positive regulation of flagellated sperm motil	44568	0.574343152	0.999994883
positive regulation of gastrulation (GO:20005	44568	0.574343152	0.999994883
positive regulation of histone H4 acetylation	44568	0.574343152	0.999994883
positive regulation of icosanoid secretion (GC	44568	0.574343152	0.999994883
positive regulation of lamellipodium morpho	44568	0.574343152	0.999994883
positive regulation of mast cell activation (GC	44568	0.574343152	0.999994883
positive regulation of membrane depolarizati	44568	0.574343152	0.999994883
positive regulation of microtubule nucleation	44568	0.574343152	0.999994883
positive regulation of phospholipid biosynthe	44568	0.574343152	0.999994883
positive regulation of pinocytosis (GO:00485	44568	0.574343152	0.999994883
positive regulation of protein localization to c	44568	0.574343152	0.999994883
positive regulation of receptor catabolic proc	44568	0.574343152	0.999994883
positive regulation of RNA polymerase II tran	44568	0.574343152	0.999994883
positive regulation of trophoblast cell migrati	44568	0.574343152	0.999994883
positive regulation of vesicle fusion (GO:0031	44568	0.574343152	0.999994883
positive regulation of voltage-gated calcium c	44568	0.574343152	0.999994883
protein localization to cytoplasmic stress gra	44568	0.574343152	0.999994883
regulation of cardiac muscle cell membrane p	44568	0.574343152	0.999994883
regulation of cilium beat frequency (GO:0003	44568	0.574343152	0.999994883
regulation of entry of bacterium into host cel	44568	0.574343152	0.999994883
regulation of extracellular matrix assembly (G	44568	0.574343152	0.999994883
regulation of glial cell differentiation (GO:004	44568	0.574343152	0.999994883
regulation of histone deacetylase activity (GC	44568	0.574343152	0.999994883

regulation of ketone biosynthetic process (G(	44568	0.574343152	0.999994883
regulation of male gonad development (GO:2	44568	0.574343152	0.999994883
regulation of microglial cell migration (GO:19	44568	0.574343152	0.999994883
regulation of NAD(P)H oxidase activity (GO:0(	44568	0.574343152	0.999994883
regulation of natural killer cell mediated cyto	44568	0.574343152	0.999994883
regulation of non-membrane spanning protei	44568	0.574343152	0.999994883
regulation of phospholipid transport (GO:200	44568	0.574343152	0.999994883
regulation of potassium ion export across pla	44568	0.574343152	0.999994883
regulation of T cell mediated immune respon	44568	0.574343152	0.999994883
regulation of transforming growth factor beta	44568	0.574343152	0.999994883
regulation of transforming growth factor beta	44568	0.574343152	0.999994883
regulation of vesicle size (GO:0097494)	44568	0.574343152	0.999994883
response to alkaloid (GO:0043279)	44568	0.574343152	0.999994883
response to host defenses (GO:0052200)	44568	0.574343152	0.999994883
response to increased oxygen levels (GO:003	44568	0.574343152	0.999994883
response to lead ion (GO:0010288)	44568	0.574343152	0.999994883
retinal rod cell development (GO:0046548)	44568	0.574343152	0.999994883
ribosomal large subunit export from nucleus	44568	0.574343152	0.999994883
ribosomal small subunit export from nucleus	44568	0.574343152	0.999994883
rRNA-containing ribonucleoprotein complex e	44568	0.574343152	0.999994883
selenocysteine incorporation (GO:0001514)	44568	0.574343152	0.999994883
smooth muscle cell migration (GO:0014909)	44568	0.574343152	0.999994883
somatic recombination of immunoglobulin ge	44568	0.574343152	0.999994883
substrate-dependent cell migration, cell exte	44568	0.574343152	0.999994883
succinate transport (GO:0015744)	44568	0.574343152	0.999994883
synaptic vesicle budding from presynaptic en	44568	0.574343152	0.999994883
tachykinin receptor signaling pathway (GO:0(	44568	0.574343152	0.999994883
translational readthrough (GO:0006451)	44568	0.574343152	0.999994883
vitamin A metabolic process (GO:0006776)	44568	0.574343152	0.999994883
white fat cell differentiation (GO:0050872)	44568	0.574343152	0.999994883
phosphatidylinositol-mediated signaling (GO:	26146	0.578353792	0.999994883
negative regulation of cell cycle (GO:004578(	29465	0.578566343	0.999994883
positive regulation of cell adhesion (GO:0045	29465	0.578566343	0.999994883
positive regulation of macroautophagy (GO:0	19511	0.578987533	0.999994883
regulation of endothelial cell migration (GO:0	32782	0.578989006	0.999994883
response to calcium ion (GO:0051592)	12/107	0.580242559	0.999994883
embryonic organ morphogenesis (GO:00485(	16193	0.580242768	0.999994883
intracellular protein transmembrane transpo	16193	0.580242768	0.999994883
mRNA catabolic process (GO:0006402)	16193	0.580242768	0.999994883
positive regulation of protein modification pr	24/214	0.581731531	0.999994883
regulation of phosphorylation (GO:0042325)	14/125	0.581825163	0.999994883
blood vessel diameter maintenance (GO:009	12875	0.582699068	0.999994883
embryonic skeletal system development (GO	12875	0.582699068	0.999994883
muscle cell differentiation (GO:0042692)	12875	0.582699068	0.999994883
nuclear-transcribed mRNA catabolic process,	12875	0.582699068	0.999994883
positive regulation of lipid biosynthetic proce	12875	0.582699068	0.999994883
regulation of JUN kinase activity (GO:004350(	12875	0.582699068	0.999994883

regulation of lipid biosynthetic process (GO:0	12875	0.582699068	0.999994883
response to estrogen (GO:0043627)	12875	0.582699068	0.999994883
semaphorin-plexin signaling pathway (GO:00	12875	0.582699068	0.999994883
negative regulation of protein localization to	44646	0.587410441	0.999994883
negative regulation of signaling receptor acti	44646	0.587410441	0.999994883
phosphatidylethanolamine acyl-chain remod	44646	0.587410441	0.999994883
positive regulation of histone methylation (G	44646	0.587410441	0.999994883
positive regulation of ion transmembrane tra	44646	0.587410441	0.999994883
positive regulation of microtubule polymeriz	44646	0.587410441	0.999994883
regulation of actin filament bundle assembly	44646	0.587410441	0.999994883
regulation of biomineral tissue development	44646	0.587410441	0.999994883
regulation of glycogen biosynthetic process (	44646	0.587410441	0.999994883
regulation of telomere maintenance (GO:003	44646	0.587410441	0.999994883
snRNA processing (GO:0016180)	44646	0.587410441	0.999994883
TOR signaling (GO:0031929)	44646	0.587410441	0.999994883
positive regulation of stress-activated MAPK	36465	0.593565601	0.999994883
negative regulation of gene expression (GO:0	36/322	0.594998027	0.999994883
COPII vesicle coating (GO:0048208)	23193	0.595951349	0.999994883
positive regulation of viral process (GO:0048	23193	0.595951349	0.999994883
vesicle coating (GO:0006901)	23193	0.595951349	0.999994883
vesicle targeting, rough ER to cis-Golgi (GO:0	23193	0.595951349	0.999994883
cellular modified amino acid catabolic proces	44609	0.597181815	0.999994883
cellular response to fatty acid (GO:0071398)	44609	0.597181815	0.999994883
detection of visible light (GO:0009584)	44609	0.597181815	0.999994883
epithelial cell morphogenesis (GO:0003382)	44609	0.597181815	0.999994883
mitochondrial ATP synthesis coupled proton	44609	0.597181815	0.999994883
negative regulation of ATP metabolic process	44609	0.597181815	0.999994883
negative regulation of chemokine production	44609	0.597181815	0.999994883
negative regulation of execution phase of ap	44609	0.597181815	0.999994883
negative regulation of intrinsic apoptotic sign	44609	0.597181815	0.999994883
negative regulation of phagocytosis (GO:005	44609	0.597181815	0.999994883
phosphate ion transport (GO:0006817)	44609	0.597181815	0.999994883
positive regulation of dendrite extension (GO	44609	0.597181815	0.999994883
positive regulation of DNA replication (GO:0	44609	0.597181815	0.999994883
positive regulation of macrophage activation	44609	0.597181815	0.999994883
positive regulation of regulated secretory pat	44609	0.597181815	0.999994883
positive regulation of smooth muscle cell mig	44609	0.597181815	0.999994883
pyrimidine-containing compound catabolic pr	44609	0.597181815	0.999994883
regulation of Arp2/3 complex-mediated actin	44609	0.597181815	0.999994883
regulation of cardiac muscle contraction by r	44609	0.597181815	0.999994883
regulation of cellular respiration (GO:004345	44609	0.597181815	0.999994883
regulation of leukocyte migration (GO:00026	44609	0.597181815	0.999994883
regulation of metal ion transport (GO:00109	44609	0.597181815	0.999994883
regulation of NLRP3 inflammasome complex	44609	0.597181815	0.999994883
ribosomal small subunit assembly (GO:00000	44609	0.597181815	0.999994883
snRNA metabolic process (GO:0016073)	44609	0.597181815	0.999994883
synaptic vesicle membrane organization (GO	44609	0.597181815	0.999994883

inorganic anion transport (GO:0015698)	19876	0.597867242	0.999994883
regulation of focal adhesion assembly (GO:0(	19876	0.597867242	0.999994883
regulation of potassium ion transmembrane	19876	0.597867242	0.999994883
regulation of proteolysis (GO:0030162)	19876	0.597867242	0.999994883
regulation of GTPase activity (GO:0043087)	21/189	0.598483373	0.999994883
extracellular structure organization (GO:0043	24/216	0.600754674	0.999994883
positive regulation of chemotaxis (GO:00509	16558	0.600874911	0.999994883
regulation of insulin receptor signaling pathw	16558	0.600874911	0.999994883
zymogen activation (GO:0031638)	16558	0.600874911	0.999994883
axonal transport (GO:0098930)	13241	0.605679118	0.999994883
cyclic-nucleotide-mediated signaling (GO:001	13241	0.605679118	0.999994883
dendrite morphogenesis (GO:0048813)	13241	0.605679118	0.999994883
embryonic limb morphogenesis (GO:003032(	13241	0.605679118	0.999994883
endoderm formation (GO:0001706)	13241	0.605679118	0.999994883
regulation of microtubule-based process (GO	13241	0.605679118	0.999994883
regulation of osteoclast differentiation (GO:0	13241	0.605679118	0.999994883
regulation of actin cytoskeleton organization	33512	0.608111515	0.999994883
positive regulation of protein ubiquitination (	30195	0.609227174	0.999994883
external encapsulating structure organizatior	24/217	0.610134822	0.999994883
antigen processing and presentation of exoge	26877	0.61082226	0.999994883
insulin receptor signaling pathway (GO:0008	26877	0.61082226	0.999994883
positive regulation of JNK cascade (GO:00463	26877	0.61082226	0.999994883
protein secretion (GO:0009306)	23559	0.613078792	0.999994883
calcium-ion regulated exocytosis (GO:001715	44647	0.613771602	0.999994883
chondroitin sulfate proteoglycan biosynthetic	44647	0.613771602	0.999994883
entrainment of circadian clock by photoperio	44647	0.613771602	0.999994883
melanosome organization (GO:0032438)	44647	0.613771602	0.999994883
microtubule polymerization or depolymerizat	44647	0.613771602	0.999994883
peptide hormone secretion (GO:0030072)	44647	0.613771602	0.999994883
positive regulation of cellular component mo	44647	0.613771602	0.999994883
positive regulation of nuclear division (GO:00	44647	0.613771602	0.999994883
positive regulation of toll-like receptor signal	44647	0.613771602	0.999994883
protein export from nucleus (GO:0006611)	44647	0.613771602	0.999994883
regulation of toll-like receptor signaling path	44647	0.613771602	0.999994883
regulation of transcription regulatory region	44647	0.613771602	0.999994883
regulation of vasculature development (GO:1	44647	0.613771602	0.999994883
negative regulation of cysteine-type endopep	20241	0.616283647	0.999994883
protein targeting to mitochondrion (GO:0006	20241	0.616283647	0.999994883
regulation of cardiac conduction (GO:190377	20241	0.616283647	0.999994883
negative regulation of Wnt signaling pathway	21/191	0.618431328	0.999994883
negative regulation of apoptotic process (GO	54/485	0.618478677	0.999994883
establishment of protein localization to extra	16923	0.620918971	0.999994883
positive regulation of smooth muscle cell pro	16923	0.620918971	0.999994883
regulation of DNA metabolic process (GO:005	16923	0.620918971	0.999994883
regulation of endothelial cell proliferation (G	33878	0.622295557	0.999994883
ammonium transmembrane transport (GO:0(	44569	0.623246824	0.999994883
anterograde axonal protein transport (GO:00	44569	0.623246824	0.999994883

antigen processing and presentation of endo	44569	0.623246824	0.999994883
aromatic compound biosynthetic process (G	44569	0.623246824	0.999994883
autophagosome-lysosome fusion (GO:00619	44569	0.623246824	0.999994883
axo-dendritic protein transport (GO:0099640	44569	0.623246824	0.999994883
axon extension involved in axon guidance (G	44569	0.623246824	0.999994883
basic amino acid transport (GO:0015802)	44569	0.623246824	0.999994883
cell migration involved in heart development	44569	0.623246824	0.999994883
cellular response to angiotensin (GO:190438	44569	0.623246824	0.999994883
cellular response to interferon-alpha (GO:00	44569	0.623246824	0.999994883
cellular response to potassium ion (GO:0035	44569	0.623246824	0.999994883
cellular response to UV-B (GO:0071493)	44569	0.623246824	0.999994883
cysteine metabolic process (GO:0006534)	44569	0.623246824	0.999994883
cytoplasmic sequestering of NF-kappaB (GO:	44569	0.623246824	0.999994883
dopamine uptake (GO:0090494)	44569	0.623246824	0.999994883
dynamin family protein polymerization involv	44569	0.623246824	0.999994883
dynamin family protein polymerization involv	44569	0.623246824	0.999994883
establishment of Golgi localization (GO:0051	44569	0.623246824	0.999994883
excitatory synapse assembly (GO:1904861)	44569	0.623246824	0.999994883
fusion of virus membrane with host plasma n	44569	0.623246824	0.999994883
galactosylceramide metabolic process (GO:0	44569	0.623246824	0.999994883
histidine catabolic process (GO:0006548)	44569	0.623246824	0.999994883
histidine metabolic process (GO:0006547)	44569	0.623246824	0.999994883
histone H3-K4 demethylation (GO:0034720)	44569	0.623246824	0.999994883
histone H3-K4 monomethylation (GO:009769	44569	0.623246824	0.999994883
immunological synapse formation (GO:00017	44569	0.623246824	0.999994883
internal protein amino acid acetylation (GO:0	44569	0.623246824	0.999994883
kidney mesenchyme development (GO:0072	44569	0.623246824	0.999994883
mammary gland epithelial cell differentiation	44569	0.623246824	0.999994883
meiotic sister chromatid cohesion (GO:00511	44569	0.623246824	0.999994883
membrane fusion involved in viral entry into	44569	0.623246824	0.999994883
mitochondrial respiratory chain complex III a	44569	0.623246824	0.999994883
mitophagy (GO:0000423)	44569	0.623246824	0.999994883
monoamine transport (GO:0015844)	44569	0.623246824	0.999994883
negative regulation of alpha-beta T cell differ	44569	0.623246824	0.999994883
negative regulation of CD4-positive, alpha-be	44569	0.623246824	0.999994883
negative regulation of fatty acid oxidation (G	44569	0.623246824	0.999994883
negative regulation of microglial cell activatio	44569	0.623246824	0.999994883
negative regulation of mitochondrial membra	44569	0.623246824	0.999994883
negative regulation of muscle cell apoptotic p	44569	0.623246824	0.999994883
negative regulation of nitrogen compound m	44569	0.623246824	0.999994883
negative regulation of osteoblast proliferatio	44569	0.623246824	0.999994883
negative regulation of phospholipase activity	44569	0.623246824	0.999994883
negative regulation of potassium ion transme	44569	0.623246824	0.999994883
negative regulation of T-helper 17 cell differe	44569	0.623246824	0.999994883
neuron projection extension involved in neur	44569	0.623246824	0.999994883
neurotransmitter receptor diffusion trapping	44569	0.623246824	0.999994883
neurotransmitter reuptake (GO:0098810)	44569	0.623246824	0.999994883

osteoblast development (GO:0002076)	44569	0.623246824	0.999994883
peptidyl-tyrosine dephosphorylation involvec	44569	0.623246824	0.999994883
plasma membrane phospholipid scrambling (	44569	0.623246824	0.999994883
positive regulation of apoptotic cell clearance	44569	0.623246824	0.999994883
positive regulation of aspartic-type peptidase	44569	0.623246824	0.999994883
positive regulation of CD4-positive, alpha-bet	44569	0.623246824	0.999994883
positive regulation of defense response to ba	44569	0.623246824	0.999994883
positive regulation of dendritic cell chemotax	44569	0.623246824	0.999994883
positive regulation of dendritic cell cytokine p	44569	0.623246824	0.999994883
positive regulation of early endosome to late	44569	0.623246824	0.999994883
positive regulation of extracellular matrix dis	44569	0.623246824	0.999994883
positive regulation of glial cell migration (GO:	44569	0.623246824	0.999994883
positive regulation of lipoprotein lipase activi	44569	0.623246824	0.999994883
positive regulation of meiotic nuclear divisior	44569	0.623246824	0.999994883
positive regulation of monocyte chemotactic	44569	0.623246824	0.999994883
positive regulation of myotube differentiatio	44569	0.623246824	0.999994883
positive regulation of oligodendrocyte differe	44569	0.623246824	0.999994883
positive regulation of peptide secretion (GO:(	44569	0.623246824	0.999994883
positive regulation of ryanodine-sensitive cal	44569	0.623246824	0.999994883
positive regulation of steroid biosynthetic pr	44569	0.623246824	0.999994883
positive regulation of T-helper 2 cell cytokine	44569	0.623246824	0.999994883
positive regulation of vascular associated sm	44569	0.623246824	0.999994883
postsynaptic neurotransmitter receptor diffu	44569	0.623246824	0.999994883
protein deglycosylation (GO:0006517)	44569	0.623246824	0.999994883
protein localization to microtubule (GO:0035	44569	0.623246824	0.999994883
protein localization to microtubule cytoskele	44569	0.623246824	0.999994883
protein localization to presynapse (GO:19053	44569	0.623246824	0.999994883
protein retention in ER lumen (GO:0006621)	44569	0.623246824	0.999994883
regulation of actin filament length (GO:00308	44569	0.623246824	0.999994883
regulation of alpha-beta T cell differentiation	44569	0.623246824	0.999994883
regulation of alpha-beta T cell proliferation ((	44569	0.623246824	0.999994883
regulation of apoptotic cell clearance (GO:20	44569	0.623246824	0.999994883
regulation of ATPase-coupled calcium transm	44569	0.623246824	0.999994883
regulation of cardiac muscle cell action poter	44569	0.623246824	0.999994883
regulation of CD4-positive, alpha-beta T cell a	44569	0.623246824	0.999994883
regulation of Cdc42 protein signal transducti	44569	0.623246824	0.999994883
regulation of chemokine-mediated signaling p	44569	0.623246824	0.999994883
regulation of cytoplasmic translational elong	44569	0.623246824	0.999994883
regulation of dendritic cell chemotaxis (GO:2(	44569	0.623246824	0.999994883
regulation of dopamine receptor signaling pa	44569	0.623246824	0.999994883
regulation of endodeoxyribonuclease activity	44569	0.623246824	0.999994883
regulation of interleukin-18 production (GO:(	44569	0.623246824	0.999994883
regulation of intestinal cholesterol absorptio	44569	0.623246824	0.999994883
regulation of lymphocyte apoptotic process (	44569	0.623246824	0.999994883
regulation of meiotic nuclear division (GO:00	44569	0.623246824	0.999994883
regulation of metaphase/anaphase transitior	44569	0.623246824	0.999994883
regulation of microvillus organization (GO:00	44569	0.623246824	0.999994883

regulation of MyD88-independent toll-like re	44569	0.623246824	0.999994883
regulation of myeloid leukocyte differentiatic	44569	0.623246824	0.999994883
regulation of pattern recognition receptor sig	44569	0.623246824	0.999994883
regulation of phospholipase A2 activity (GO:0	44569	0.623246824	0.999994883
regulation of protein K63-linked ubiquitinatic	44569	0.623246824	0.999994883
regulation of protein localization to cell corte	44569	0.623246824	0.999994883
regulation of proton transport (GO:0010155)	44569	0.623246824	0.999994883
regulation of response to wounding (GO:190	44569	0.623246824	0.999994883
regulation of striated muscle tissue developn	44569	0.623246824	0.999994883
regulation of translational termination (GO:0	44569	0.623246824	0.999994883
regulation of vascular wound healing (GO:00	44569	0.623246824	0.999994883
regulation of wound healing, spreading of ep	44569	0.623246824	0.999994883
respiratory chain complex III assembly (GO:0	44569	0.623246824	0.999994883
response to potassium ion (GO:0035864)	44569	0.623246824	0.999994883
RNA secondary structure unwinding (GO:001	44569	0.623246824	0.999994883
rRNA base methylation (GO:0070475)	44569	0.623246824	0.999994883
self proteolysis (GO:0097264)	44569	0.623246824	0.999994883
sequestering of BMP from receptor via BMP	44569	0.623246824	0.999994883
snRNA transcription by RNA polymerase III (G	44569	0.623246824	0.999994883
spleen development (GO:0048536)	44569	0.623246824	0.999994883
SREBP signaling pathway (GO:0032933)	44569	0.623246824	0.999994883
sulfur amino acid biosynthetic process (GO:0	44569	0.623246824	0.999994883
synaptic vesicle budding (GO:0070142)	44569	0.623246824	0.999994883
T-helper cell lineage commitment (GO:00022	44569	0.623246824	0.999994883
TORC1 signaling (GO:0038202)	44569	0.623246824	0.999994883
U4 snRNA 3'-end processing (GO:0034475)	44569	0.623246824	0.999994883
vascular associated smooth muscle contracti	44569	0.623246824	0.999994883
wound healing, spreading of epidermal cells (	44569	0.623246824	0.999994883
positive regulation of plasma membrane bou	30560	0.624128015	0.999994883
regulation of defense response (GO:0031347	30560	0.624128015	0.999994883
regulation of osteoblast differentiation (GO:0	30560	0.624128015	0.999994883
regulation of stress fiber assembly (GO:0051	27242	0.626558887	0.999994883
lysosome localization (GO:0032418)	13606	0.627868903	0.999994883
ncRNA metabolic process (GO:0034660)	13606	0.627868903	0.999994883
negative regulation of endothelial cell prolife	13606	0.627868903	0.999994883
negative regulation of stress-activated MAPK	13606	0.627868903	0.999994883
phagocytosis, engulfment (GO:0006911)	13606	0.627868903	0.999994883
positive regulation of myeloid cell differentia	13606	0.627868903	0.999994883
carbohydrate derivative transport (GO:19012	44610	0.629036238	0.999994883
DNA conformation change (GO:0071103)	44610	0.629036238	0.999994883
embryonic axis specification (GO:0000578)	44610	0.629036238	0.999994883
glycoprotein catabolic process (GO:0006516)	44610	0.629036238	0.999994883
high-density lipoprotein particle remodeling (	44610	0.629036238	0.999994883
intermediate filament organization (GO:0045	44610	0.629036238	0.999994883
mitochondrial fusion (GO:0008053)	44610	0.629036238	0.999994883
negative regulation of double-strand break re	44610	0.629036238	0.999994883
negative regulation of fibroblast proliferation	44610	0.629036238	0.999994883

negative regulation of interleukin-8 productic	44610	0.629036238	0.999994883
negative regulation of lipid catabolic process	44610	0.629036238	0.999994883
negative regulation of Rho protein signal trar	44610	0.629036238	0.999994883
neuron maturation (GO:0042551)	44610	0.629036238	0.999994883
nitric oxide mediated signal transduction (GC	44610	0.629036238	0.999994883
positive chemotaxis (GO:0050918)	44610	0.629036238	0.999994883
positive regulation of amyloid-beta formatior	44610	0.629036238	0.999994883
positive regulation of cell migration involved	44610	0.629036238	0.999994883
positive regulation of excitatory postsynaptic	44610	0.629036238	0.999994883
positive regulation of glial cell differentiation	44610	0.629036238	0.999994883
positive regulation of macrophage derived fo	44610	0.629036238	0.999994883
positive regulation of nervous system proces	44610	0.629036238	0.999994883
positive regulation of stress-activated protein	44610	0.629036238	0.999994883
programmed necrotic cell death (GO:009730	44610	0.629036238	0.999994883
regulation of cellular protein catabolic proces	44610	0.629036238	0.999994883
regulation of chromosome segregation (GO:0	44610	0.629036238	0.999994883
regulation of dendrite extension (GO:190385	44610	0.629036238	0.999994883
regulation of membrane depolarization (GO:(	44610	0.629036238	0.999994883
regulation of oxidative stress-induced intrinsi	44610	0.629036238	0.999994883
regulation of protein-containing complex disa	44610	0.629036238	0.999994883
rRNA catabolic process (GO:0016075)	44610	0.629036238	0.999994883
ventricular cardiac muscle cell action potenti	44610	0.629036238	0.999994883
regulation of RNA metabolic process (GO:005	23924	0.629807128	0.999994883
tRNA modification (GO:0006400)	23924	0.629807128	0.999994883
extracellular matrix organization (GO:003019	33/300	0.631767688	0.999994883
negative regulation of metabolic process (GO	20607	0.634214733	0.999994883
calcium-mediated signaling (GO:0019722)	11/102	0.634236003	0.999994883
visual perception (GO:0007601)	34243	0.636211501	0.999994883
cellular response to acid chemical (GO:00712	44648	0.638971724	0.999994883
histone mRNA metabolic process (GO:00083	44648	0.638971724	0.999994883
keratan sulfate biosynthetic process (GO:001	44648	0.638971724	0.999994883
negative regulation of axonogenesis (GO:005	44648	0.638971724	0.999994883
negative regulation of phosphatase activity ((	44648	0.638971724	0.999994883
neutral amino acid transport (GO:0015804)	44648	0.638971724	0.999994883
positive regulation of protein import into nuc	44648	0.638971724	0.999994883
positive regulation of response to wounding (	44648	0.638971724	0.999994883
protein depolymerization (GO:0051261)	44648	0.638971724	0.999994883
protein localization to cell surface (GO:00343	44648	0.638971724	0.999994883
regulation of B cell activation (GO:0050864)	44648	0.638971724	0.999994883
regulation of calcium-mediated signaling (GO	44648	0.638971724	0.999994883
regulation of microtubule polymerization or (	44648	0.638971724	0.999994883
histone deacetylation (GO:0016575)	17288	0.640350373	0.999994883
negative regulation of cold-induced thermog	17288	0.640350373	0.999994883
regulation of cellular metabolic process (GO:(	17288	0.640350373	0.999994883
regulation of protein localization to nucleus (	17288	0.640350373	0.999994883
positive regulation of response to external st	15/139	0.641103139	0.999994883
integrin-mediated signaling pathway (GO:00(	27607	0.641943024	0.999994883

positive regulation of lymphocyte proliferatic	27607	0.641943024	0.999994883
regulation of transcription from RNA polyme	27607	0.641943024	0.999994883
cell-cell junction assembly (GO:0007043)	24289	0.646119589	0.999994883
positive regulation of T cell proliferation (GO:	24289	0.646119589	0.999994883
negative regulation of proteasomal protein c	13971	0.649242942	0.999994883
response to cAMP (GO:0051591)	13971	0.649242942	0.999994883
response to estradiol (GO:0032355)	13971	0.649242942	0.999994883
synaptic vesicle endocytosis (GO:0048488)	13971	0.649242942	0.999994883
icosanoid metabolic process (GO:0006690)	20972	0.651642057	0.999994883
actomyosin structure organization (GO:0031(	27973	0.656961547	0.999994883
ATP synthesis coupled proton transport (GO:(	44611	0.658890649	0.999994883
carbohydrate derivative catabolic process (G(	44611	0.658890649	0.999994883
cellular glucuronidation (GO:0052695)	44611	0.658890649	0.999994883
DNA alkylation (GO:0006305)	44611	0.658890649	0.999994883
DNA methylation or demethylation (GO:0044	44611	0.658890649	0.999994883
ethanol metabolic process (GO:0006067)	44611	0.658890649	0.999994883
excitatory postsynaptic potential (GO:00600	44611	0.658890649	0.999994883
histone H4-K16 acetylation (GO:0043984)	44611	0.658890649	0.999994883
negative regulation of cytokine production in	44611	0.658890649	0.999994883
peptidyl-lysine dimethylation (GO:0018027)	44611	0.658890649	0.999994883
positive regulation of cilium assembly (GO:0(	44611	0.658890649	0.999994883
positive regulation of focal adhesion assembl	44611	0.658890649	0.999994883
positive regulation of oxidoreductase activity	44611	0.658890649	0.999994883
postsynaptic membrane organization (GO:00	44611	0.658890649	0.999994883
pyroptosis (GO:0070269)	44611	0.658890649	0.999994883
regulation of leukocyte chemotaxis (GO:0002	44611	0.658890649	0.999994883
regulation of mitotic spindle assembly (GO:19	44611	0.658890649	0.999994883
regulation of oligodendrocyte differentiation	44611	0.658890649	0.999994883
regulation of T cell cytokine production (GO:(	44611	0.658890649	0.999994883
response to fatty acid (GO:0070542)	44611	0.658890649	0.999994883
synaptic transmission, cholinergic (GO:00072	44611	0.658890649	0.999994883
ureteric bud development (GO:0001657)	44611	0.658890649	0.999994883
myelination (GO:0042552)	17654	0.659149626	0.999994883
positive regulation of blood vessel endotheli	17654	0.659149626	0.999994883
regulation of mitochondrion organization (G(	17654	0.659149626	0.999994883
regulation of insulin secretion (GO:0050796)	11/104	0.660123788	0.999994883
vascular endothelial growth factor receptor s	24654	0.662001938	0.999994883
glial cell differentiation (GO:0010001)	44649	0.662993155	0.999994883
intrinsic apoptotic signaling pathway in respo	44649	0.662993155	0.999994883
MyD88-dependent toll-like receptor signaling	44649	0.662993155	0.999994883
negative regulation of mRNA catabolic proce	44649	0.662993155	0.999994883
negative regulation of wound healing (GO:00	44649	0.662993155	0.999994883
regulation of DNA biosynthetic process (GO:2	44649	0.662993155	0.999994883
regulation of gluconeogenesis (GO:0006111)	44649	0.662993155	0.999994883
positive regulation of cellular catabolic proce	15/141	0.663264699	0.999994883
actin-mediated cell contraction (GO:0070252	44570	0.666534103	0.999994883
adult heart development (GO:0007512)	44570	0.666534103	0.999994883

androgen biosynthetic process (GO:0006702)	44570	0.666534103	0.999994883
associative learning (GO:0008306)	44570	0.666534103	0.999994883
astral microtubule organization (GO:0030953	44570	0.666534103	0.999994883
basement membrane assembly (GO:0070831	44570	0.666534103	0.999994883
CD40 signaling pathway (GO:0023035)	44570	0.666534103	0.999994883
cellular response to nitric oxide (GO:0071732	44570	0.666534103	0.999994883
cellular response to reactive nitrogen species	44570	0.666534103	0.999994883
cellular response to sterol depletion (GO:007	44570	0.666534103	0.999994883
cholesterol catabolic process (GO:0006707)	44570	0.666534103	0.999994883
chylomicron remodeling (GO:0034371)	44570	0.666534103	0.999994883
collagen-activated signaling pathway (GO:00	44570	0.666534103	0.999994883
complement activation, classical pathway (G	44570	0.666534103	0.999994883
development of primary female sexual chara	44570	0.666534103	0.999994883
DNA topological change (GO:0006265)	44570	0.666534103	0.999994883
embryonic forelimb morphogenesis (GO:003	44570	0.666534103	0.999994883
endochondral ossification (GO:0001958)	44570	0.666534103	0.999994883
epithelial cilium movement involved in deter	44570	0.666534103	0.999994883
flavonoid glucuronidation (GO:0052696)	44570	0.666534103	0.999994883
fucose catabolic process (GO:0019317)	44570	0.666534103	0.999994883
glycerolipid biosynthetic process (GO:004501	44570	0.666534103	0.999994883
histone phosphorylation (GO:0016572)	44570	0.666534103	0.999994883
IMP metabolic process (GO:0046040)	44570	0.666534103	0.999994883
intestinal cholesterol absorption (GO:003029	44570	0.666534103	0.999994883
isoprenoid biosynthetic process (GO:000829	44570	0.666534103	0.999994883
L-fucose catabolic process (GO:0042355)	44570	0.666534103	0.999994883
L-fucose metabolic process (GO:0042354)	44570	0.666534103	0.999994883
mesodermal cell differentiation (GO:004833	44570	0.666534103	0.999994883
mitral valve morphogenesis (GO:0003183)	44570	0.666534103	0.999994883
negative regulation of alpha-beta T cell activa	44570	0.666534103	0.999994883
negative regulation of biomineralization (GO:	44570	0.666534103	0.999994883
negative regulation of exocytosis (GO:00459	44570	0.666534103	0.999994883
negative regulation of glycoprotein biosynthe	44570	0.666534103	0.999994883
negative regulation of leukocyte degranulatio	44570	0.666534103	0.999994883
negative regulation of leukocyte proliferatior	44570	0.666534103	0.999994883
negative regulation of lipase activity (GO:006	44570	0.666534103	0.999994883
negative regulation of lipid localization (GO:1	44570	0.666534103	0.999994883
negative regulation of membrane potential ((	44570	0.666534103	0.999994883
negative regulation of necroptotic process (G	44570	0.666534103	0.999994883
negative regulation of pathway-restricted SM	44570	0.666534103	0.999994883
negative regulation of protein-containing cor	44570	0.666534103	0.999994883
nuclear RNA surveillance (GO:0071027)	44570	0.666534103	0.999994883
organic acid catabolic process (GO:0016054)	44570	0.666534103	0.999994883
ornithine metabolic process (GO:0006591)	44570	0.666534103	0.999994883
phosphorylation of RNA polymerase II C-term	44570	0.666534103	0.999994883
positive regulation of ATP biosynthetic proce	44570	0.666534103	0.999994883
positive regulation of autophagosome assem	44570	0.666534103	0.999994883
positive regulation of B cell differentiation (G	44570	0.666534103	0.999994883

positive regulation of blood pressure (GO:00	44570	0.666534103	0.999994883
positive regulation of cholesterol esterificatic	44570	0.666534103	0.999994883
positive regulation of fatty acid beta-oxidatio	44570	0.666534103	0.999994883
positive regulation of mast cell degranulation	44570	0.666534103	0.999994883
positive regulation of memory T cell differen	44570	0.666534103	0.999994883
positive regulation of mitochondrial membra	44570	0.666534103	0.999994883
positive regulation of NLRP3 inflammasome (	44570	0.666534103	0.999994883
positive regulation of protein kinase A signali	44570	0.666534103	0.999994883
positive regulation of protein kinase C signali	44570	0.666534103	0.999994883
positive regulation of triglyceride lipase activ	44570	0.666534103	0.999994883
progesterone metabolic process (GO:004244	44570	0.666534103	0.999994883
quaternary ammonium group transport (GO:	44570	0.666534103	0.999994883
regulation of animal organ morphogenesis (G	44570	0.666534103	0.999994883
regulation of CD8-positive, alpha-beta T cell a	44570	0.666534103	0.999994883
regulation of complement activation, classica	44570	0.666534103	0.999994883
regulation of epidermis development (GO:00	44570	0.666534103	0.999994883
regulation of glucan biosynthetic process (GC	44570	0.666534103	0.999994883
regulation of lipid transport (GO:0032368)	44570	0.666534103	0.999994883
regulation of PERK-mediated unfolded protei	44570	0.666534103	0.999994883
regulation of peroxisome proliferator activat	44570	0.666534103	0.999994883
regulation of pinocytosis (GO:0048548)	44570	0.666534103	0.999994883
regulation of respiratory burst (GO:0060263)	44570	0.666534103	0.999994883
regulation of smooth muscle cell apoptotic p	44570	0.666534103	0.999994883
regulation of sterol biosynthetic process (GO	44570	0.666534103	0.999994883
regulation of tumor necrosis factor superfam	44570	0.666534103	0.999994883
regulation of vesicle fusion (GO:0031338)	44570	0.666534103	0.999994883
regulation of Wnt signaling pathway, planar c	44570	0.666534103	0.999994883
response to magnesium ion (GO:0032026)	44570	0.666534103	0.999994883
response to type I interferon (GO:0034340)	44570	0.666534103	0.999994883
response to vitamin D (GO:0033280)	44570	0.666534103	0.999994883
retinal rod cell differentiation (GO:0060221)	44570	0.666534103	0.999994883
semaphorin-plexin signaling pathway involve	44570	0.666534103	0.999994883
sensory organ morphogenesis (GO:0090596)	44570	0.666534103	0.999994883
somatic recombination of immunoglobulin ge	44570	0.666534103	0.999994883
sterol catabolic process (GO:0016127)	44570	0.666534103	0.999994883
sympathetic ganglion development (GO:0061	44570	0.666534103	0.999994883
T-helper 1 type immune response (GO:00420	44570	0.666534103	0.999994883
very-low-density lipoprotein particle remode	44570	0.666534103	0.999994883
glucose homeostasis (GO:0042593)	31656	0.66695454	0.999994883
regulation of neuron death (GO:1901214)	31656	0.66695454	0.999994883
positive regulation of epithelial cell proliferat	13/123	0.667181378	0.999994883
fat cell differentiation (GO:0045444)	21337	0.668550577	0.999994883
negative regulation of hydrolase activity (GO	21337	0.668550577	0.999994883
cellular response to ketone (GO:1901655)	14336	0.669783396	0.999994883
mitochondrial electron transport, NADH to u	14336	0.669783396	0.999994883
negative regulation of lymphocyte proliferati	14336	0.669783396	0.999994883
protein monoubiquitination (GO:0006513)	14336	0.669783396	0.999994883

regulation of cellular component biogenesis (	14336	0.669783396	0.999994883
regulation of ion transmembrane transporter	14336	0.669783396	0.999994883
regulation of nitric-oxide synthase activity (G	14336	0.669783396	0.999994883
vesicle cytoskeletal trafficking (GO:0099518)	14336	0.669783396	0.999994883
regulation of cell cycle (GO:0051726)	32/296	0.670008816	0.999994883
adherens junction organization (GO:0034332	18019	0.677301999	0.999994883
inner mitochondrial membrane organization	18019	0.677301999	0.999994883
regulation of cellular localization (GO:006034	18019	0.677301999	0.999994883
positive regulation of protein localization to r	25020	0.67744237	0.999994883
regulation of translational initiation (GO:000(	25020	0.67744237	0.999994883
negative regulation of angiogenesis (GO:001(	32021	0.680569717	0.999994883
actin filament organization (GO:0007015)	16/152	0.682559629	0.999994883
negative regulation of intracellular signal trar	21/198	0.68446785	0.999994883
negative regulation of DNA-binding transcrip	15/143	0.68466458	0.999994883
cell projection organization (GO:0030030)	44650	0.6858303	0.999994883
maintenance of blood-brain barrier (GO:0035	44650	0.6858303	0.999994883
negative regulation of cytoskeleton organizat	44650	0.6858303	0.999994883
negative regulation of interleukin-1 productic	44650	0.6858303	0.999994883
peptidyl-lysine trimethylation (GO:0018023)	44650	0.6858303	0.999994883
plasma membrane invagination (GO:009902	44650	0.6858303	0.999994883
positive regulation of protein import (GO:19(	44650	0.6858303	0.999994883
positive regulation of small GTPase mediated	44650	0.6858303	0.999994883
regulation of natural killer cell mediated cyto	44650	0.6858303	0.999994883
response to alcohol (GO:0097305)	44650	0.6858303	0.999994883
snRNA 3'-end processing (GO:0034472)	44650	0.6858303	0.999994883
antigen processing and presentation of exoge	28703	0.685858618	0.999994883
protein modification process (GO:0036211)	28703	0.685858618	0.999994883
early endosome to late endosome transport	44612	0.686784081	0.999994883
endoplasmic reticulum calcium ion homeosta	44612	0.686784081	0.999994883
epithelial cilium movement involved in extra(	44612	0.686784081	0.999994883
establishment of epithelial cell polarity (GO:(	44612	0.686784081	0.999994883
gastrulation (GO:0007369)	44612	0.686784081	0.999994883
glucose transmembrane transport (GO:19046	44612	0.686784081	0.999994883
granulocyte differentiation (GO:0030851)	44612	0.686784081	0.999994883
hepaticobiliary system development (GO:006	44612	0.686784081	0.999994883
negative regulation of axon extension involve	44612	0.686784081	0.999994883
negative regulation of cyclin-dependent prot	44612	0.686784081	0.999994883
oligodendrocyte differentiation (GO:004870	44612	0.686784081	0.999994883
organic cation transport (GO:0015695)	44612	0.686784081	0.999994883
positive regulation of activated T cell prolifer	44612	0.686784081	0.999994883
positive regulation of alpha-beta T cell activa	44612	0.686784081	0.999994883
positive regulation of hormone secretion (GC	44612	0.686784081	0.999994883
positive regulation of lymphocyte differentia	44612	0.686784081	0.999994883
positive regulation of peptidyl-lysine acetylat	44612	0.686784081	0.999994883
positive regulation of protein processing (GO	44612	0.686784081	0.999994883
regulation of acute inflammatory response ((	44612	0.686784081	0.999994883
regulation of smooth muscle cell migration ((	44612	0.686784081	0.999994883

xenobiotic transport (GO:0042908)	44612	0.686784081	0.999994883
negative regulation of cell-substrate adhesio	14702	0.689479358	0.999994883
positive regulation of intrinsic apoptotic signa	14702	0.689479358	0.999994883
positive regulation of wound healing (GO:00	14702	0.689479358	0.999994883
protein targeting (GO:0006605)	13/125	0.689888945	0.999994883
cellular response to calcium ion (GO:007127	25385	0.692431402	0.999994883
cellular response to decreased oxygen levels	25385	0.692431402	0.999994883
negative regulation of binding (GO:0051100)	32387	0.693840845	0.999994883
sensory perception of mechanical stimulus (G	32387	0.693840845	0.999994883
positive regulation of ion transport (GO:0043	18384	0.694797176	0.999994883
regulation of generation of precursor metabo	18384	0.694797176	0.999994883
cellular protein catabolic process (GO:00442	22068	0.700766989	0.999994883
positive regulation of defense response (GO:(	36069	0.701429418	0.999994883
regulation of peptidyl-serine phosphorylation	36069	0.701429418	0.999994883
adherens junction assembly (GO:0034333)	44571	0.704849758	0.999994883
alanine transport (GO:0032328)	44571	0.704849758	0.999994883
amino sugar metabolic process (GO:0006040	44571	0.704849758	0.999994883
arginine metabolic process (GO:0006525)	44571	0.704849758	0.999994883
cellular response to acetylcholine (GO:19051	44571	0.704849758	0.999994883
cellular response to interleukin-4 (GO:00713	44571	0.704849758	0.999994883
cellular response to purine-containing compo	44571	0.704849758	0.999994883
cGMP biosynthetic process (GO:0006182)	44571	0.704849758	0.999994883
chloride ion homeostasis (GO:0055064)	44571	0.704849758	0.999994883
chondroitin sulfate proteoglycan metabolic p	44571	0.704849758	0.999994883
chylomicron assembly (GO:0034378)	44571	0.704849758	0.999994883
complement activation, lectin pathway (GO:(	44571	0.704849758	0.999994883
dicarboxylic acid biosynthetic process (GO:00	44571	0.704849758	0.999994883
forelimb morphogenesis (GO:0035136)	44571	0.704849758	0.999994883
genetic imprinting (GO:0071514)	44571	0.704849758	0.999994883
hematopoietic stem cell differentiation (GO:(	44571	0.704849758	0.999994883
histone H3-K36 demethylation (GO:0070544)	44571	0.704849758	0.999994883
I-kappaB phosphorylation (GO:0007252)	44571	0.704849758	0.999994883
immunoglobulin mediated immune response	44571	0.704849758	0.999994883
indolalkylamine catabolic process (GO:00462	44571	0.704849758	0.999994883
inner ear receptor cell stereocilium organizat	44571	0.704849758	0.999994883
lactation (GO:0007595)	44571	0.704849758	0.999994883
leptin-mediated signaling pathway (GO:0033	44571	0.704849758	0.999994883
lipid phosphorylation (GO:0046834)	44571	0.704849758	0.999994883
lung epithelium development (GO:0060428)	44571	0.704849758	0.999994883
methylguanosine-cap decapping (GO:011015	44571	0.704849758	0.999994883
modification-dependent macromolecule cata	44571	0.704849758	0.999994883
modulation by symbiont of host process (GO	44571	0.704849758	0.999994883
monocyte activation (GO:0042117)	44571	0.704849758	0.999994883
monovalent inorganic anion homeostasis (GO	44571	0.704849758	0.999994883
muscle cell migration (GO:0014812)	44571	0.704849758	0.999994883
negative regulation of alpha-beta T cell prolif	44571	0.704849758	0.999994883
negative regulation of cellular protein catabo	44571	0.704849758	0.999994883

negative regulation of circadian rhythm (GO:(	44571	0.704849758	0.999994883
negative regulation of glycolytic process (GO:	44571	0.704849758	0.999994883
negative regulation of hormone secretion (G(	44571	0.704849758	0.999994883
negative regulation of humoral immune resp	44571	0.704849758	0.999994883
negative regulation of inclusion body assemb	44571	0.704849758	0.999994883
negative regulation of protein autophosphor	44571	0.704849758	0.999994883
negative regulation of purine nucleotide met	44571	0.704849758	0.999994883
negative regulation of sodium ion transmeml	44571	0.704849758	0.999994883
negative regulation of toll-like receptor 4 sigr	44571	0.704849758	0.999994883
negative regulation of transforming growth fa	44571	0.704849758	0.999994883
negative regulation of voltage-gated calcium	44571	0.704849758	0.999994883
neuron projection fasciculation (GO:0106030	44571	0.704849758	0.999994883
neuron remodeling (GO:0016322)	44571	0.704849758	0.999994883
nuclear mRNA surveillance (GO:0071028)	44571	0.704849758	0.999994883
nuclear-transcribed mRNA catabolic process,	44571	0.704849758	0.999994883
nucleoside metabolic process (GO:0009116)	44571	0.704849758	0.999994883
omega-hydroxylase P450 pathway (GO:0097	44571	0.704849758	0.999994883
phosphate ion homeostasis (GO:0055062)	44571	0.704849758	0.999994883
positive regulation by symbiont of entry into	44571	0.704849758	0.999994883
positive regulation of circadian rhythm (GO:0	44571	0.704849758	0.999994883
positive regulation of coagulation (GO:00508	44571	0.704849758	0.999994883
positive regulation of dendritic spine morpho	44571	0.704849758	0.999994883
positive regulation of hemostasis (GO:19000	44571	0.704849758	0.999994883
positive regulation of keratinocyte migration	44571	0.704849758	0.999994883
positive regulation of skeletal muscle tissue g	44571	0.704849758	0.999994883
positive regulation of transcription by RNA p(	44571	0.704849758	0.999994883
positive regulation of transcription of nucleol	44571	0.704849758	0.999994883
positive regulation of vascular endothelial gr(	44571	0.704849758	0.999994883
positive regulation of viral entry into host cel	44571	0.704849758	0.999994883
primary alcohol catabolic process (GO:00343	44571	0.704849758	0.999994883
primary miRNA processing (GO:0031053)	44571	0.704849758	0.999994883
protein insertion into ER membrane by stop-t	44571	0.704849758	0.999994883
protein prenylation (GO:0018342)	44571	0.704849758	0.999994883
receptor guanylyl cyclase signaling pathway (	44571	0.704849758	0.999994883
regulation of actin filament-based movemen	44571	0.704849758	0.999994883
regulation of bile acid biosynthetic process (G	44571	0.704849758	0.999994883
regulation of carbohydrate biosynthetic proc	44571	0.704849758	0.999994883
regulation of cell-cell adhesion mediated by i	44571	0.704849758	0.999994883
regulation of DNA methylation (GO:0044030)	44571	0.704849758	0.999994883
regulation of granulocyte differentiation (GO	44571	0.704849758	0.999994883
regulation of high voltage-gated calcium cha	44571	0.704849758	0.999994883
regulation of leukocyte tethering or rolling (G	44571	0.704849758	0.999994883
regulation of mast cell activation (GO:00330(	44571	0.704849758	0.999994883
regulation of memory T cell differentiation (G	44571	0.704849758	0.999994883
regulation of phospholipid metabolic process	44571	0.704849758	0.999994883
regulation of protein localization to centroso	44571	0.704849758	0.999994883
regulation of receptor binding (GO:1900120)	44571	0.704849758	0.999994883

regulation of store-operated calcium entry (G	44571	0.704849758	0.999994883
regulation of tau-protein kinase activity (GO:	44571	0.704849758	0.999994883
response to interleukin-4 (GO:0070670)	44571	0.704849758	0.999994883
response to laminar fluid shear stress (GO:00	44571	0.704849758	0.999994883
retinoic acid receptor signaling pathway (GO:	44571	0.704849758	0.999994883
sarcoplasmic reticulum calcium ion transport	44571	0.704849758	0.999994883
sequestering of actin monomers (GO:004298	44571	0.704849758	0.999994883
sulfur amino acid catabolic process (GO:0000	44571	0.704849758	0.999994883
collagen fibril organization (GO:0030199)	32752	0.706761666	0.999994883
positive regulation of inflammatory response	32752	0.706761666	0.999994883
carbohydrate homeostasis (GO:0033500)	25750	0.706961756	0.999994883
regulation of plasma membrane bounded cel	25750	0.706961756	0.999994883
positive regulation of gene expression (GO:0(	52/482	0.707302803	0.999994883
'de novo' posttranslational protein folding (G	44651	0.70748793	0.999994883
cellular response to cAMP (GO:0071320)	44651	0.70748793	0.999994883
negative regulation of DNA binding (GO:0043	44651	0.70748793	0.999994883
negative regulation of osteoblast differentiat	44651	0.70748793	0.999994883
positive regulation of protein targeting to mi	44651	0.70748793	0.999994883
positive regulation of ubiquitin-protein transl	44651	0.70748793	0.999994883
regulation of calcium ion-dependent exocyto	44651	0.70748793	0.999994883
regulation of cellular component size (GO:00	44651	0.70748793	0.999994883
regulation of developmental growth (GO:004	44651	0.70748793	0.999994883
triglyceride homeostasis (GO:0070328)	44651	0.70748793	0.999994883
JNK cascade (GO:0007254)	15067	0.708326162	0.999994883
nucleobase-containing compound catabolic p	15067	0.708326162	0.999994883
protein methylation (GO:0006479)	15067	0.708326162	0.999994883
regulation of mitochondrial membrane poter	15067	0.708326162	0.999994883
regulation of cellular amine metabolic proces	18749	0.71162892	0.999994883
regulation of epithelial cell migration (GO:00	18749	0.71162892	0.999994883
regulation of substrate adhesion-dependent	18749	0.71162892	0.999994883
autonomic nervous system development (GC	44613	0.71277298	0.999994883
cellular response to steroid hormone stimulu	44613	0.71277298	0.999994883
chondroitin sulfate biosynthetic process (GO:	44613	0.71277298	0.999994883
myotube differentiation (GO:0014902)	44613	0.71277298	0.999994883
negative regulation of ion transmembrane tr	44613	0.71277298	0.999994883
negative regulation of microtubule depolyme	44613	0.71277298	0.999994883
negative regulation of protein localization to	44613	0.71277298	0.999994883
negative regulation of reproductive process (	44613	0.71277298	0.999994883
negative regulation of response to wounding	44613	0.71277298	0.999994883
neuron apoptotic process (GO:0051402)	44613	0.71277298	0.999994883
positive regulation of antigen receptor-medi	44613	0.71277298	0.999994883
regulation of anoikis (GO:2000209)	44613	0.71277298	0.999994883
regulation of cardiac muscle cell proliferation	44613	0.71277298	0.999994883
regulation of ubiquitin protein ligase activity	44613	0.71277298	0.999994883
rRNA modification (GO:0000154)	44613	0.71277298	0.999994883
sensory perception of pain (GO:0019233)	44613	0.71277298	0.999994883
regulation of mRNA stability (GO:0043488)	15/146	0.715255493	0.999994883

cholesterol homeostasis (GO:0042632)	26115	0.721028238	0.999994883
Fc-gamma receptor signaling pathway involv	26115	0.721028238	0.999994883
histone acetylation (GO:0016573)	26115	0.721028238	0.999994883
cell-matrix adhesion (GO:0007160)	10/100	0.725348372	0.999994883
positive regulation of translation (GO:004572	10/100	0.725348372	0.999994883
regulation of transforming growth factor bet	10/100	0.725348372	0.999994883
ATP-dependent chromatin remodeling (GO:0	15432	0.726324705	0.999994883
ceramide biosynthetic process (GO:0046513)	15432	0.726324705	0.999994883
monocyte chemotaxis (GO:0002548)	15432	0.726324705	0.999994883
nucleic acid-templated transcription (GO:009	15432	0.726324705	0.999994883
regulation of nervous system development ((	15432	0.726324705	0.999994883
regulation of angiogenesis (GO:0045765)	21/203	0.727518884	0.999994883
activation of phospholipase C activity (GO:00	11749	0.727979614	0.999994883
cardiac muscle tissue morphogenesis (GO:00	11749	0.727979614	0.999994883
cellular response to topologically incorrect pr	11749	0.727979614	0.999994883
intra-Golgi vesicle-mediated transport (GO:0(	11749	0.727979614	0.999994883
mitochondrial membrane organization (GO:0	11749	0.727979614	0.999994883
modulation by host of symbiont process (GO	11749	0.727979614	0.999994883
negative regulation of cell-matrix adhesion ((	11749	0.727979614	0.999994883
negative regulation of developmental growth	11749	0.727979614	0.999994883
negative regulation of intracellular steroid ho	11749	0.727979614	0.999994883
peptidyl-proline modification (GO:0018208)	11749	0.727979614	0.999994883
positive regulation of lamellipodium organiza	11749	0.727979614	0.999994883
regulation of cell migration involved in sprou	11749	0.727979614	0.999994883
regulation of NMDA receptor activity (GO:20(	11749	0.727979614	0.999994883
response to amino acid (GO:0043200)	11749	0.727979614	0.999994883
positive regulation of cysteine-type endopep	22798	0.730804722	0.999994883
response to endoplasmic reticulum stress (G(	11/110	0.731220166	0.999994883
sensory perception of sound (GO:0007605)	33482	0.731533817	0.999994883
positive regulation of macromolecule biosynt	13/129	0.732452486	0.999994883
Fc-gamma receptor signaling pathway (GO:0(	26481	0.734627613	0.999994883
positive regulation of protein secretion (GO:(	26481	0.734627613	0.999994883
sterol homeostasis (GO:0055092)	26481	0.734627613	0.999994883
homologous chromosome segregation (GO:0	44614	0.736926691	0.999994883
natural killer cell mediated cytotoxicity (GO:(	44614	0.736926691	0.999994883
negative regulation of cyclin-dependent prot	44614	0.736926691	0.999994883
negative regulation of interleukin-2 productio	44614	0.736926691	0.999994883
negative regulation of myeloid cell differentia	44614	0.736926691	0.999994883
negative regulation of protein dephosphoryla	44614	0.736926691	0.999994883
organelle fusion (GO:0048284)	44614	0.736926691	0.999994883
phosphatidylserine acyl-chain remodeling (G(	44614	0.736926691	0.999994883
positive regulation of amyloid precursor prot	44614	0.736926691	0.999994883
positive regulation of DNA-templated transcr	44614	0.736926691	0.999994883
positive regulation of peptidase activity (GO:(	44614	0.736926691	0.999994883
positive regulation of signal transduction by p	44614	0.736926691	0.999994883
proteasomal ubiquitin-independent protein c	44614	0.736926691	0.999994883
protein localization to cell junction (GO:1902	44614	0.736926691	0.999994883

regulation of adenylate cyclase activity (GO:0	44614	0.736926691	0.999994883
regulation of endoplasmic reticulum stress-in	44614	0.736926691	0.999994883
regulation of lipid storage (GO:0010883)	44614	0.736926691	0.999994883
regulation of response to cytokine stimulus ((	44614	0.736926691	0.999994883
rRNA methylation (GO:0031167)	44614	0.736926691	0.999994883
ubiquitin-dependent protein catabolic proces	44614	0.736926691	0.999994883
cellular response to lipopolysaccharide (GO:0	12/120	0.736931566	0.999994883
protein dephosphorylation (GO:0006470)	14/139	0.73830548	0.999994883
alcohol catabolic process (GO:0046164)	44572	0.738764569	0.999994883
aminoglycan metabolic process (GO:0006022	44572	0.738764569	0.999994883
angiogenesis involved in wound healing (GO:(	44572	0.738764569	0.999994883
atrial septum morphogenesis (GO:0060413)	44572	0.738764569	0.999994883
B cell mediated immunity (GO:0019724)	44572	0.738764569	0.999994883
cardiac muscle cell membrane repolarization	44572	0.738764569	0.999994883
cell differentiation in spinal cord (GO:002151	44572	0.738764569	0.999994883
cell proliferation in forebrain (GO:0021846)	44572	0.738764569	0.999994883
cellular response to increased oxygen levels (	44572	0.738764569	0.999994883
chromatin-mediated maintenance of transcri	44572	0.738764569	0.999994883
enteric nervous system development (GO:00	44572	0.738764569	0.999994883
establishment of epithelial cell apical/basal p	44572	0.738764569	0.999994883
Golgi inheritance (GO:0048313)	44572	0.738764569	0.999994883
humoral immune response mediated by circu	44572	0.738764569	0.999994883
induction of positive chemotaxis (GO:005093	44572	0.738764569	0.999994883
inositol phosphate dephosphorylation (GO:0(	44572	0.738764569	0.999994883
insulin-like growth factor receptor signaling p	44572	0.738764569	0.999994883
intestinal lipid absorption (GO:0098856)	44572	0.738764569	0.999994883
isotype switching (GO:0045190)	44572	0.738764569	0.999994883
lipoprotein biosynthetic process (GO:004215	44572	0.738764569	0.999994883
metanephric mesenchyme development (GO	44572	0.738764569	0.999994883
miRNA mediated inhibition of translation (GC	44572	0.738764569	0.999994883
myotube cell development (GO:0014904)	44572	0.738764569	0.999994883
negative regulation of activated T cell prolife	44572	0.738764569	0.999994883
negative regulation of activin receptor signali	44572	0.738764569	0.999994883
negative regulation of cholesterol transport (	44572	0.738764569	0.999994883
negative regulation of defense response to vi	44572	0.738764569	0.999994883
negative regulation of interleukin-17 product	44572	0.738764569	0.999994883
negative regulation of lymphocyte migration	44572	0.738764569	0.999994883
negative regulation of oxidative stress-induce	44572	0.738764569	0.999994883
negative regulation of potassium ion transme	44572	0.738764569	0.999994883
negative regulation of programmed necrotic	44572	0.738764569	0.999994883
negative regulation of protein localization to	44572	0.738764569	0.999994883
negative regulation of sprouting angiogenesis	44572	0.738764569	0.999994883
negative regulation of T-helper cell differenti	44572	0.738764569	0.999994883
negative regulation of translation, ncRNA-me	44572	0.738764569	0.999994883
organophosphate catabolic process (GO:004(	44572	0.738764569	0.999994883
phosphorylated carbohydrate dephosphoryla	44572	0.738764569	0.999994883
positive regulation of actin nucleation (GO:0(	44572	0.738764569	0.999994883

positive regulation of alcohol biosynthetic pr	44572	0.738764569	0.999994883
positive regulation of cellular respiration (GO	44572	0.738764569	0.999994883
positive regulation of cytoplasmic transport (	44572	0.738764569	0.999994883
positive regulation of dendrite development	44572	0.738764569	0.999994883
positive regulation of DNA methylation-depe	44572	0.738764569	0.999994883
positive regulation of histone exchange (GO:1	44572	0.738764569	0.999994883
positive regulation of keratinocyte proliferati	44572	0.738764569	0.999994883
positive regulation of macrophage differentia	44572	0.738764569	0.999994883
positive regulation of non-canonical Wnt sign	44572	0.738764569	0.999994883
positive regulation of phospholipid transport	44572	0.738764569	0.999994883
positive regulation of transcription from RNA	44572	0.738764569	0.999994883
positive regulation of triglyceride biosyntheti	44572	0.738764569	0.999994883
protein kinase C signaling (GO:0070528)	44572	0.738764569	0.999994883
protein localization to phagophore assembly	44572	0.738764569	0.999994883
pyrimidine nucleoside catabolic process (GO:	44572	0.738764569	0.999994883
regulation of cardiac muscle cell apoptotic pr	44572	0.738764569	0.999994883
regulation of CD4-positive, alpha-beta T cell p	44572	0.738764569	0.999994883
regulation of coagulation (GO:0050818)	44572	0.738764569	0.999994883
regulation of gene expression by genetic imp	44572	0.738764569	0.999994883
regulation of histone exchange (GO:1900049	44572	0.738764569	0.999994883
regulation of inclusion body assembly (GO:0(	44572	0.738764569	0.999994883
regulation of lymphocyte migration (GO:200(	44572	0.738764569	0.999994883
regulation of mast cell activation involved in	44572	0.738764569	0.999994883
regulation of mitochondrial depolarization (G	44572	0.738764569	0.999994883
regulation of phospholipase activity (GO:001(	44572	0.738764569	0.999994883
regulation of stress-activated protein kinase s	44572	0.738764569	0.999994883
regulation of T cell apoptotic process (GO:00	44572	0.738764569	0.999994883
regulation of T cell mediated immunity (GO:0	44572	0.738764569	0.999994883
regulation of T-helper 2 cell cytokine product	44572	0.738764569	0.999994883
regulation of toll-like receptor 2 signaling pat	44572	0.738764569	0.999994883
response to sterol (GO:0036314)	44572	0.738764569	0.999994883
signal peptide processing (GO:0006465)	44572	0.738764569	0.999994883
skeletal muscle cell differentiation (GO:0035(	44572	0.738764569	0.999994883
synaptic vesicle transport (GO:0048489)	44572	0.738764569	0.999994883
tryptophan metabolic process (GO:0006568)	44572	0.738764569	0.999994883
vasoconstriction (GO:0042310)	44572	0.738764569	0.999994883
xenobiotic glucuronidation (GO:0052697)	44572	0.738764569	0.999994883
Fc-epsilon receptor signaling pathway (GO:0(	11/111	0.742059775	0.999994883
regulation of response to external stimulus ((	13/130	0.742479246	0.999994883
positive regulation of NIK/NF-kappaB signalin	19480	0.74329545	0.999994883
positive regulation of phospholipase C activit	15797	0.743480808	0.999994883
spermatid development (GO:0007286)	15797	0.743480808	0.999994883
tRNA aminoacylation for protein translation (	15797	0.743480808	0.999994883
proteasomal protein catabolic process (GO:0(	21/205	0.743692008	0.999994883
positive regulation of hydrolase activity (GO:(	15/149	0.743954795	0.999994883
amyloid fibril formation (GO:1990000)	23163	0.744999799	0.999994883
cellular protein-containing complex assembly	17/168	0.74609982	0.999994883

actin filament bundle organization (GO:0061	12114	0.747326302	0.999994883
muscle cell development (GO:0055001)	12114	0.747326302	0.999994883
negative chemotaxis (GO:0050919)	12114	0.747326302	0.999994883
positive regulation of cytokine production in	12114	0.747326302	0.999994883
regulation of neurotransmitter secretion (GO	12114	0.747326302	0.999994883
RNA stabilization (GO:0043489)	12114	0.747326302	0.999994883
signal transduction by p53 class mediator (G	12114	0.747326302	0.999994883
vasculogenesis (GO:0001570)	12114	0.747326302	0.999994883
positive regulation of cellular protein metabo	10/102	0.747975547	0.999994883
positive regulation of vasculature developme	10/102	0.747975547	0.999994883
positive regulation of signal transduction (GO	26/252	0.748887151	0.999994883
cellular protein metabolic process (GO:00442	44/417	0.749032073	0.999994883
protein autophosphorylation (GO:0046777)	16/159	0.749412109	0.999994883
glycoprotein biosynthetic process (GO:00091	30529	0.751129752	0.999994883
regulation of translation (GO:0006417)	18/178	0.751540981	0.999994883
Fc receptor signaling pathway (GO:0038093)	11/112	0.752603375	0.999994883
positive regulation of peptidyl-serine phosph	34213	0.754861129	0.999994883
regulation of heart contraction (GO:0008016	34213	0.754861129	0.999994883
positive regulation of leukocyte chemotaxis (	19845	0.758135045	0.999994883
regulation of cellular amino acid metabolic pı	19845	0.758135045	0.999994883
diterpenoid metabolic process (GO:0016101)	23529	0.758646784	0.999994883
regulation of transcription initiation from RN	23529	0.758646784	0.999994883
negative regulation of G protein-coupled rec	44615	0.759323757	0.999994883
negative regulation of GTPase activity (GO:0(	44615	0.759323757	0.999994883
positive regulation of histone acetylation (GO	44615	0.759323757	0.999994883
positive regulation of JUN kinase activity (GO	44615	0.759323757	0.999994883
positive regulation of transcription initiation	44615	0.759323757	0.999994883
regulation of calcium ion transmembrane tra	44615	0.759323757	0.999994883
regulation of release of sequestered calcium	44615	0.759323757	0.999994883
regulation of supramolecular fiber organizati	44615	0.759323757	0.999994883
vesicle transport along microtubule (GO:004	44615	0.759323757	0.999994883
homotypic cell-cell adhesion (GO:0034109)	16163	0.759804592	0.999994883
intracellular steroid hormone receptor signal	16163	0.759804592	0.999994883
positive regulation of cell-matrix adhesion (G	16163	0.759804592	0.999994883
positive regulation of stress fiber assembly (G	16163	0.759804592	0.999994883
Fc receptor mediated stimulatory signaling pa	27211	0.760421098	0.999994883
regulation of signal transduction (GO:000996	20/198	0.761874857	0.999994883
positive regulation of metabolic process (GO:	11/113	0.762849925	0.999994883
response to insulin (GO:0032868)	30895	0.762961931	0.999994883
regulation of cell growth (GO:0001558)	22/217	0.764265195	0.999994883
cell-substrate junction assembly (GO:000704	12479	0.765555026	0.999994883
central nervous system neuron differentiatio	12479	0.765555026	0.999994883
histone lysine methylation (GO:0034968)	12479	0.765555026	0.999994883
organic cyclic compound biosynthetic proces	12479	0.765555026	0.999994883
positive regulation of calcium ion transport in	12479	0.765555026	0.999994883
positive regulation of epidermal growth factc	12479	0.765555026	0.999994883
positive regulation of interleukin-12 producti	12479	0.765555026	0.999994883

positive regulation of pri-miRNA transcriptior	12479	0.765555026	0.999994883
positive regulation of release of sequestered	12479	0.765555026	0.999994883
protein insertion into membrane (GO:00512(	12479	0.765555026	0.999994883
regulation of activated T cell proliferation (G(	12479	0.765555026	0.999994883
tRNA methylation (GO:0030488)	12479	0.765555026	0.999994883
hemopoiesis (GO:0030097)	34578	0.765980109	0.999994883
negative regulation of cellular protein metab	34578	0.765980109	0.999994883
adipose tissue development (GO:0060612)	44573	0.768783811	0.999994883
angiotensin maturation (GO:0002003)	44573	0.768783811	0.999994883
ATP transport (GO:0015867)	44573	0.768783811	0.999994883
attachment of mitotic spindle microtubules t	44573	0.768783811	0.999994883
brain morphogenesis (GO:0048854)	44573	0.768783811	0.999994883
cell differentiation in hindbrain (GO:0021533	44573	0.768783811	0.999994883
cellular response to nitrogen levels (GO:0043	44573	0.768783811	0.999994883
cellular response to nitrogen starvation (GO:(	44573	0.768783811	0.999994883
dermatan sulfate biosynthetic process (GO:0(	44573	0.768783811	0.999994883
early endosome to Golgi transport (GO:0034(	44573	0.768783811	0.999994883
endoplasmic reticulum membrane organizati	44573	0.768783811	0.999994883
energy coupled proton transport, down elect	44573	0.768783811	0.999994883
epithelial cell-cell adhesion (GO:0090136)	44573	0.768783811	0.999994883
ethanol oxidation (GO:0006069)	44573	0.768783811	0.999994883
glomerular visceral epithelial cell differentiat	44573	0.768783811	0.999994883
inositol phosphate catabolic process (GO:007	44573	0.768783811	0.999994883
maintenance of protein localization in endop	44573	0.768783811	0.999994883
melanocyte differentiation (GO:0030318)	44573	0.768783811	0.999994883
mitochondrial electron transport, ubiquinol t	44573	0.768783811	0.999994883
mitochondrion distribution (GO:0048311)	44573	0.768783811	0.999994883
modulation by host of viral process (GO:0044	44573	0.768783811	0.999994883
motile cilium assembly (GO:0044458)	44573	0.768783811	0.999994883
negative regulation by host of viral process ((	44573	0.768783811	0.999994883
negative regulation of cardiac muscle hypert	44573	0.768783811	0.999994883
negative regulation of cellular response to va	44573	0.768783811	0.999994883
negative regulation of complement activatio	44573	0.768783811	0.999994883
negative regulation of fatty acid biosynthetic	44573	0.768783811	0.999994883
negative regulation of hemostasis (GO:19000	44573	0.768783811	0.999994883
negative regulation of production of miRNAs	44573	0.768783811	0.999994883
negative regulation of transcription elongatic	44573	0.768783811	0.999994883
nuclear body organization (GO:0030575)	44573	0.768783811	0.999994883
nucleoside catabolic process (GO:0009164)	44573	0.768783811	0.999994883
organic hydroxy compound catabolic process	44573	0.768783811	0.999994883
peptidyl-methionine modification (GO:00182	44573	0.768783811	0.999994883
phasic smooth muscle contraction (GO:0014(	44573	0.768783811	0.999994883
phospholipid efflux (GO:0033700)	44573	0.768783811	0.999994883
phospholipid homeostasis (GO:0055091)	44573	0.768783811	0.999994883
positive regulation of cellular senescence (GC	44573	0.768783811	0.999994883
positive regulation of endoplasmic reticulum	44573	0.768783811	0.999994883
positive regulation of metaphase/anaphase t	44573	0.768783811	0.999994883

positive regulation of mitotic metaphase/ana	44573	0.768783811	0.999994883
positive regulation of mitotic sister chromati	44573	0.768783811	0.999994883
positive regulation of protein depolymerizati	44573	0.768783811	0.999994883
purine nucleotide biosynthetic process (GO:0	44573	0.768783811	0.999994883
regulation of actin filament depolymerizatior	44573	0.768783811	0.999994883
regulation of alcohol biosynthetic process (G	44573	0.768783811	0.999994883
regulation of amyloid precursor protein catal	44573	0.768783811	0.999994883
regulation of angiotensin levels in blood (GO:	44573	0.768783811	0.999994883
regulation of axon regeneration (GO:004867	44573	0.768783811	0.999994883
regulation of feeding behavior (GO:0060259)	44573	0.768783811	0.999994883
regulation of glycogen metabolic process (GC	44573	0.768783811	0.999994883
regulation of hemopoiesis (GO:1903706)	44573	0.768783811	0.999994883
regulation of keratinocyte migration (GO:005	44573	0.768783811	0.999994883
regulation of muscle system process (GO:009	44573	0.768783811	0.999994883
regulation of natural killer cell activation (GO	44573	0.768783811	0.999994883
regulation of plasminogen activation (GO:001	44573	0.768783811	0.999994883
regulation of sequestering of calcium ion (GC	44573	0.768783811	0.999994883
regulation of sister chromatid cohesion (GO:(	44573	0.768783811	0.999994883
toll-like receptor 3 signaling pathway (GO:00	44573	0.768783811	0.999994883
regulation of cell-matrix adhesion (GO:00019	23894	0.771749106	0.999994883
protein sumoylation (GO:0016925)	20210	0.772320168	0.999994883
regulation of gene silencing by RNA (GO:006(	20210	0.772320168	0.999994883
regulation of posttranscriptional gene silenci	20210	0.772320168	0.999994883
activation of protein kinase activity (GO:0032	11/114	0.772799096	0.999994883
histone modification (GO:0016570)	11/114	0.772799096	0.999994883
negative regulation of cell motility (GO:2000	11/114	0.772799096	0.999994883
Wnt signaling pathway, planar cell polarity pa	31260	0.774386229	0.999994883
neural crest cell development (GO:0014032)	16528	0.775309906	0.999994883
positive regulation of response to biotic stim	16528	0.775309906	0.999994883
regulation of pri-miRNA transcription by RNA	16528	0.775309906	0.999994883
sensory perception of light stimulus (GO:005	34943	0.776736509	0.999994883
regulation of macromolecule metabolic proc	20/200	0.777018313	0.999994883
cellular response to lipid (GO:0071396)	22/219	0.778685245	0.999994883
cardiac muscle cell development (GO:005501	44616	0.78004889	0.999994883
heterochromatin assembly (GO:0031507)	44616	0.78004889	0.999994883
immune response-activating cell surface rece	44616	0.78004889	0.999994883
negative regulation of lipid metabolic proces	44616	0.78004889	0.999994883
negative regulation of protein depolymerizat	44616	0.78004889	0.999994883
negative regulation of synaptic transmission	44616	0.78004889	0.999994883
nucleotide-binding domain, leucine rich repe	44616	0.78004889	0.999994883
positive regulation of cell-substrate junction	44616	0.78004889	0.999994883
protein alpha-1,2-demannosylation (GO:003(	44616	0.78004889	0.999994883
regulation of monooxygenase activity (GO:00	44616	0.78004889	0.999994883
positive regulation of protein metabolic proc	11/115	0.782451235	0.999994883
acylglycerol catabolic process (GO:0046464)	12844	0.782697748	0.999994883
negative regulation of epithelial cell migratio	12844	0.782697748	0.999994883
negative regulation of neurogenesis (GO:005	12844	0.782697748	0.999994883

regulation of blood circulation (GO:1903522)	12844	0.782697748	0.999994883
regulation of ion transmembrane transport ((	12844	0.782697748	0.999994883
regulation of protein polymerization (GO:003	12844	0.782697748	0.999994883
negative regulation of cell migration (GO:003	14/144	0.783763263	0.999994883
cell morphogenesis involved in neuron differ(	27942	0.78435054	0.999994883
cellular response to hormone stimulus (GO:0	27942	0.78435054	0.999994883
positive regulation of growth (GO:0045927)	27942	0.78435054	0.999994883
regulation of interferon-gamma production (	31625	0.785404851	0.999994883
chemokine-mediated signaling pathway (GO:	20576	0.785859898	0.999994883
nuclear-transcribed mRNA catabolic process,	20576	0.785859898	0.999994883
peptidyl-tyrosine modification (GO:0018212)	20576	0.785859898	0.999994883
tight junction assembly (GO:0120192)	20576	0.785859898	0.999994883
interleukin-12-mediated signaling pathway ((	16893	0.790013784	0.999994883
regulation of B cell proliferation (GO:003088	16893	0.790013784	0.999994883
tumor necrosis factor-mediated signaling pat	11/116	0.791807327	0.999994883
positive regulation of cell motility (GO:20001	22/221	0.792501974	0.999994883
negative regulation of cell growth (GO:00303	12/126	0.794513459	0.999994883
negative regulation of growth (GO:0045926)	12/126	0.794513459	0.999994883
AMP metabolic process (GO:0046033)	44574	0.795354769	0.999994883
cellular biogenic amine metabolic process (G	44574	0.795354769	0.999994883
chromatin organization involved in regulatior	44574	0.795354769	0.999994883
embryonic hemopoiesis (GO:0035162)	44574	0.795354769	0.999994883
endochondral bone morphogenesis (GO:006(	44574	0.795354769	0.999994883
extracellular transport (GO:0006858)	44574	0.795354769	0.999994883
high-density lipoprotein particle assembly (G	44574	0.795354769	0.999994883
homeostasis of number of cells (GO:0048872	44574	0.795354769	0.999994883
inner dynein arm assembly (GO:0036159)	44574	0.795354769	0.999994883
kinetochore organization (GO:0051383)	44574	0.795354769	0.999994883
lymphocyte mediated immunity (GO:000244	44574	0.795354769	0.999994883
microtubule-based transport (GO:0099111)	44574	0.795354769	0.999994883
mitotic DNA integrity checkpoint signaling (G	44574	0.795354769	0.999994883
muscle tissue development (GO:0060537)	44574	0.795354769	0.999994883
negative regulation by host of viral transcript	44574	0.795354769	0.999994883
negative regulation of autophagosome assen	44574	0.795354769	0.999994883
negative regulation of endoplasmic reticulum	44574	0.795354769	0.999994883
negative regulation of epidermal growth fact	44574	0.795354769	0.999994883
negative regulation of gluconeogenesis (GO:(	44574	0.795354769	0.999994883
negative regulation of hippo signaling (GO:00	44574	0.795354769	0.999994883
negative regulation of locomotion (GO:0040(	44574	0.795354769	0.999994883
negative regulation of macromolecule biosyn	44574	0.795354769	0.999994883
negative regulation of potassium ion transpo	44574	0.795354769	0.999994883
negative regulation of reactive oxygen specie	44574	0.795354769	0.999994883
negative regulation of vascular endothelial gr	44574	0.795354769	0.999994883
plasma membrane repair (GO:0001778)	44574	0.795354769	0.999994883
positive regulation of CD4-positive, alpha-bet	44574	0.795354769	0.999994883
positive regulation of cell aging (GO:0090343	44574	0.795354769	0.999994883
positive regulation of cellular carbohydrate m	44574	0.795354769	0.999994883

positive regulation of ERAD pathway (GO:19(	44574	0.795354769	0.999994883
positive regulation of heterochromatin assen	44574	0.795354769	0.999994883
positive regulation of protein exit from endo	44574	0.795354769	0.999994883
positive regulation of purine nucleotide biosy	44574	0.795354769	0.999994883
positive regulation of transporter activity (GC	44574	0.795354769	0.999994883
protein neddylation (GO:0045116)	44574	0.795354769	0.999994883
purine ribonucleoside triphosphate metaboli	44574	0.795354769	0.999994883
purine-containing compound salvage (GO:00	44574	0.795354769	0.999994883
regulation of antigen receptor-mediated sign	44574	0.795354769	0.999994883
regulation of homotypic cell-cell adhesion (G	44574	0.795354769	0.999994883
regulation of nucleocytoplasmic transport (G	44574	0.795354769	0.999994883
regulation of oxidoreductase activity (GO:005	44574	0.795354769	0.999994883
regulation of platelet-derived growth factor r	44574	0.795354769	0.999994883
regulation of protein exit from endoplasmic r	44574	0.795354769	0.999994883
regulation of receptor signaling pathway via S	44574	0.795354769	0.999994883
regulation of retrograde protein transport, EI	44574	0.795354769	0.999994883
response to UV-B (GO:0010224)	44574	0.795354769	0.999994883
reticulophagy (GO:0061709)	44574	0.795354769	0.999994883
ribosomal subunit export from nucleus (GO:0	44574	0.795354769	0.999994883
sodium ion export across plasma membrane	44574	0.795354769	0.999994883
synaptic vesicle localization (GO:0097479)	44574	0.795354769	0.999994883
transcription preinitiation complex assembly	44574	0.795354769	0.999994883
triglyceride-rich lipoprotein particle remodeli	44574	0.795354769	0.999994883
positive regulation of NF-kappaB transcriptio	15/155	0.795487786	0.999994883
positive regulation of protein modification by	28307	0.795625258	0.999994883
ERAD pathway (GO:0036503)	31990	0.796021054	0.999994883
regulation of transcription from RNA polymer	31990	0.796021054	0.999994883
sodium ion transmembrane transport (GO:00	31990	0.796021054	0.999994883
regulation of gene silencing by miRNA (GO:0(	24624	0.796342528	0.999994883
calcium ion homeostasis (GO:0055074)	35674	0.797168732	0.999994883
arachidonic acid metabolic process (GO:0019	20941	0.798765442	0.999994883
cellular response to peptide (GO:1901653)	20941	0.798765442	0.999994883
negative regulation of cell cycle G2/M phase	20941	0.798765442	0.999994883
positive regulation of cell junction assembly (	20941	0.798765442	0.999994883
positive regulation of gene expression, epige	20941	0.798765442	0.999994883
positive regulation of interferon-gamma proc	20941	0.798765442	0.999994883
regulation of bone mineralization (GO:00305	20941	0.798765442	0.999994883
renal system development (GO:0072001)	20941	0.798765442	0.999994883
macrophage activation (GO:0042116)	13210	0.798790326	0.999994883
negative regulation of cellular protein localiz	13210	0.798790326	0.999994883
platelet aggregation (GO:0070527)	13210	0.798790326	0.999994883
positive regulation of bone mineralization (G	13210	0.798790326	0.999994883
positive regulation of mitotic nuclear division	13210	0.798790326	0.999994883
positive regulation of substrate adhesion-dep	13210	0.798790326	0.999994883
positive regulation of T cell mediated immun	13210	0.798790326	0.999994883
regulation of androgen receptor signaling pat	13210	0.798790326	0.999994883
regulation of cell cycle G1/S phase transition	13210	0.798790326	0.999994883

negative regulation of canonical Wnt signalin	16/165	0.798828989	0.999994883
acylglycerol homeostasis (GO:0055090)	44617	0.799190521	0.999994883
cAMP-mediated signaling (GO:0019933)	44617	0.799190521	0.999994883
chemical synaptic transmission, postsynaptic	44617	0.799190521	0.999994883
divalent inorganic cation homeostasis (GO:0(	44617	0.799190521	0.999994883
endosome transport via multivesicular body :	44617	0.799190521	0.999994883
negative regulation of actin filament polymer	44617	0.799190521	0.999994883
negative regulation of antigen receptor-medi	44617	0.799190521	0.999994883
negative regulation of cell junction assembly	44617	0.799190521	0.999994883
negative regulation of cellular carbohydrate r	44617	0.799190521	0.999994883
peptide catabolic process (GO:0043171)	44617	0.799190521	0.999994883
positive regulation of lipid metabolic process	44617	0.799190521	0.999994883
positive regulation of peptidyl-threonine pho	44617	0.799190521	0.999994883
protein quality control for misfolded or incon	44617	0.799190521	0.999994883
receptor signaling pathway via STAT (GO:009	44617	0.799190521	0.999994883
regulation of epidermal cell differentiation (G	44617	0.799190521	0.999994883
regulation of heterotypic cell-cell adhesion (G	44617	0.799190521	0.999994883
regulation of microtubule depolymerization (	44617	0.799190521	0.999994883
regulation of mitochondrial fission (GO:0090:	44617	0.799190521	0.999994883
regulation of rhodopsin mediated signaling p	44617	0.799190521	0.999994883
regulation of spindle assembly (GO:0090169)	44617	0.799190521	0.999994883
response to hexose (GO:0009746)	44617	0.799190521	0.999994883
ventricular cardiac muscle tissue developmer	44617	0.799190521	0.999994883
epithelial to mesenchymal transition (GO:00(	17258	0.803935941	0.999994883
positive regulation of neuron death (GO:190:	17258	0.803935941	0.999994883
positive regulation of pathway-restricted SM/	17258	0.803935941	0.999994883
regulation of establishment of planar polarity	32356	0.806239061	0.999994883
positive regulation of multicellular organisma	35/345	0.807262083	0.999994883
regulation of myeloid cell differentiation (GO	24990	0.807848979	0.999994883
autophagosome assembly (GO:0000045)	21306	0.811049845	0.999994883
nucleosome assembly (GO:0006334)	21306	0.811049845	0.999994883
regulation of pathway-restricted SMAD prote	21306	0.811049845	0.999994883
negative regulation of epithelial cell apoptoti	13575	0.813871603	0.999994883
regulation of erythrocyte differentiation (GO	13575	0.813871603	0.999994883
regulation of microtubule cytoskeleton orgar	13575	0.813871603	0.999994883
regulation of p38MAPK cascade (GO:190074	13575	0.813871603	0.999994883
regulation of cytosolic calcium ion concentra	14/148	0.815924078	0.999994883
regulation of cysteine-type endopeptidase ac	32721	0.816063975	0.999994883
second-messenger-mediated signaling (GO:0(	32721	0.816063975	0.999994883
mRNA-containing ribonucleoprotein complex	36404	0.816180339	0.999994883
negative regulation of NF-kappaB transcriptic	29037	0.81682355	0.999994883
chaperone cofactor-dependent protein refol	44618	0.81683883	0.999994883
clathrin-dependent endocytosis (GO:007258:	44618	0.81683883	0.999994883
glial cell development (GO:0021782)	44618	0.81683883	0.999994883
histone lysine demethylation (GO:0070076)	44618	0.81683883	0.999994883
histone methylation (GO:0016571)	44618	0.81683883	0.999994883
meiosis I (GO:0007127)	44618	0.81683883	0.999994883

membrane depolarization during action pote	44618	0.81683883	0.999994883
negative regulation of interleukin-1 beta pro	44618	0.81683883	0.999994883
negative regulation of protein transport (GO:	44618	0.81683883	0.999994883
positive regulation of filopodium assembly (G	44618	0.81683883	0.999994883
positive regulation of G1/S transition of mito	44618	0.81683883	0.999994883
positive regulation of interleukin-2 productio	44618	0.81683883	0.999994883
regulation of mitotic metaphase/anaphase tr	44618	0.81683883	0.999994883
regulation of regulatory T cell differentiation	44618	0.81683883	0.999994883
regulation of viral life cycle (GO:1903900)	44618	0.81683883	0.999994883
retinoic acid metabolic process (GO:0042573	44618	0.81683883	0.999994883
cellular response to interleukin-12 (GO:0071	17624	0.817098312	0.999994883
establishment of protein localization to mito	17624	0.817098312	0.999994883
negative regulation of MAP kinase activity (G	17624	0.817098312	0.999994883
regulation of interleukin-2 production (GO:0(	17624	0.817098312	0.999994883
regulation of protein metabolic process (GO:(	17624	0.817098312	0.999994883
positive regulation of MAP kinase activity (G(	25355	0.818841112	0.999994883
positive regulation of protein polymerization	25355	0.818841112	0.999994883
antigen processing and presentation of endo	44575	0.818873391	0.999994883
aorta development (GO:0035904)	44575	0.818873391	0.999994883
atrial septum development (GO:0003283)	44575	0.818873391	0.999994883
atrioventricular valve development (GO:0003	44575	0.818873391	0.999994883
bone morphogenesis (GO:0060349)	44575	0.818873391	0.999994883
carbohydrate transport (GO:0008643)	44575	0.818873391	0.999994883
heart process (GO:0003015)	44575	0.818873391	0.999994883
membrane repolarization during action pote	44575	0.818873391	0.999994883
microvillus organization (GO:0032528)	44575	0.818873391	0.999994883
myeloid dendritic cell activation (GO:000177	44575	0.818873391	0.999994883
N-terminal protein amino acid modification (	44575	0.818873391	0.999994883
NAD biosynthesis via nicotinamide riboside s	44575	0.818873391	0.999994883
negative regulation of cell migration involved	44575	0.818873391	0.999994883
negative regulation of DNA-templated transc	44575	0.818873391	0.999994883
negative regulation of smooth muscle cell mi	44575	0.818873391	0.999994883
neuromuscular process controlling balance (G	44575	0.818873391	0.999994883
nuclear migration (GO:0007097)	44575	0.818873391	0.999994883
ovarian follicle development (GO:0001541)	44575	0.818873391	0.999994883
polarized epithelial cell differentiation (GO:0(	44575	0.818873391	0.999994883
positive regulation of brown fat cell different	44575	0.818873391	0.999994883
positive regulation of glycogen biosynthetic p	44575	0.818873391	0.999994883
positive regulation of granulocyte macropha	44575	0.818873391	0.999994883
positive regulation of insulin secretion involv	44575	0.818873391	0.999994883
positive regulation of leukocyte degranulatio	44575	0.818873391	0.999994883
positive regulation of potassium ion transme	44575	0.818873391	0.999994883
positive regulation of T cell chemotaxis (GO:(	44575	0.818873391	0.999994883
positive regulation of T cell receptor signaling	44575	0.818873391	0.999994883
potassium ion export across plasma membra	44575	0.818873391	0.999994883
regulation of DNA methylation-dependent he	44575	0.818873391	0.999994883
regulation of histone deacetylation (GO:0031	44575	0.818873391	0.999994883

regulation of lamellipodium organization (GC	44575	0.818873391	0.999994883
regulation of lipase activity (GO:0060191)	44575	0.818873391	0.999994883
regulation of nitric-oxide synthase biosynthet	44575	0.818873391	0.999994883
regulation of transcription of nucleolar large	44575	0.818873391	0.999994883
relaxation of muscle (GO:0090075)	44575	0.818873391	0.999994883
response to chemokine (GO:1990868)	44575	0.818873391	0.999994883
secretion (GO:0046903)	44575	0.818873391	0.999994883
sequestering of extracellular ligand from rece	44575	0.818873391	0.999994883
smooth muscle contraction (GO:0006939)	44575	0.818873391	0.999994883
sodium-independent organic anion transport	44575	0.818873391	0.999994883
striated muscle cell development (GO:00550(	44575	0.818873391	0.999994883
substrate-dependent cell migration (GO:0006	44575	0.818873391	0.999994883
thymus development (GO:0048538)	44575	0.818873391	0.999994883
tRNA wobble base modification (GO:0002097	44575	0.818873391	0.999994883
vascular endothelial growth factor signaling p	44575	0.818873391	0.999994883
vasodilation (GO:0042311)	44575	0.818873391	0.999994883
phospholipid transport (GO:0015914)	21671	0.82272773	0.999994883
positive regulation of apoptotic signaling patl	21671	0.82272773	0.999994883
negative regulation of cellular response to gr	29403	0.826761805	0.999994883
positive regulation of canonical Wnt signaling	12/130	0.827495709	0.999994883
connective tissue development (GO:0061448	13940	0.827982606	0.999994883
negative regulation of ubiquitin-dependent p	13940	0.827982606	0.999994883
positive regulation of insulin secretion (GO:0(	13940	0.827982606	0.999994883
positive regulation of potassium ion transpor	13940	0.827982606	0.999994883
spliceosomal snRNP assembly (GO:0000387)	13940	0.827982606	0.999994883
tRNA aminoacylation (GO:0043039)	13940	0.827982606	0.999994883
aerobic electron transport chain (GO:001964	25720	0.829329785	0.999994883
establishment of protein localization to mem	25720	0.829329785	0.999994883
positive regulation of cell-substrate adhesion	25720	0.829329785	0.999994883
positive regulation of actin filament polymeri	17989	0.829524629	0.999994883
regulation of smooth muscle cell proliferatio	17989	0.829524629	0.999994883
response to unfolded protein (GO:0006986)	17989	0.829524629	0.999994883
camera-type eye development (GO:0043010)	44619	0.833084176	0.999994883
cellular response to cadmium ion (GO:00712	44619	0.833084176	0.999994883
cytoplasmic pattern recognition receptor sigr	44619	0.833084176	0.999994883
modulation of excitatory postsynaptic potent	44619	0.833084176	0.999994883
negative regulation of catalytic activity (GO:0	44619	0.833084176	0.999994883
negative regulation of endothelial cell apopto	44619	0.833084176	0.999994883
negative regulation of insulin receptor signali	44619	0.833084176	0.999994883
positive regulation of erythrocyte differentia	44619	0.833084176	0.999994883
positive regulation of striated muscle cell diff	44619	0.833084176	0.999994883
presynaptic endocytosis (GO:0140238)	44619	0.833084176	0.999994883
protein peptidyl-prolyl isomerization (GO:00(	44619	0.833084176	0.999994883
regulation of blood coagulation (GO:0030193	44619	0.833084176	0.999994883
regulation of cardiac muscle cell contraction	44619	0.833084176	0.999994883
homophilic cell adhesion via plasma membra	22037	0.833815052	0.999994883
Notch signaling pathway (GO:0007219)	22037	0.833815052	0.999994883

RNA methylation (GO:0001510)	22037	0.833815052	0.999994883
positive regulation of supramolecular fiber or	33451	0.834558824	0.999994883
toll-like receptor signaling pathway (GO:0002	33451	0.834558824	0.999994883
cellular response to hypoxia (GO:0071456)	12/131	0.835082904	0.999994883
cellular response to metal ion (GO:0071248)	12/131	0.835082904	0.999994883
mitochondrial ATP synthesis coupled electror	26085	0.839326835	0.999994883
nucleic acid metabolic process (GO:0090304)	26085	0.839326835	0.999994883
regulation of hematopoietic stem cell differe	26085	0.839326835	0.999994883
aflatoxin metabolic process (GO:0046222)	44576	0.839690177	0.999994883
androgen receptor signaling pathway (GO:00	44576	0.839690177	0.999994883
catecholamine metabolic process (GO:00065	44576	0.839690177	0.999994883
cellular response to arsenic-containing substa	44576	0.839690177	0.999994883
cellular sodium ion homeostasis (GO:000688	44576	0.839690177	0.999994883
clathrin coat assembly (GO:0048268)	44576	0.839690177	0.999994883
dermatan sulfate proteoglycan biosynthetic p	44576	0.839690177	0.999994883
endoderm development (GO:0007492)	44576	0.839690177	0.999994883
engulfment of apoptotic cell (GO:0043652)	44576	0.839690177	0.999994883
establishment of spindle localization (GO:005	44576	0.839690177	0.999994883
ganglioside biosynthetic process (GO:000157	44576	0.839690177	0.999994883
GTP metabolic process (GO:0046039)	44576	0.839690177	0.999994883
heterocycle biosynthetic process (GO:00181	44576	0.839690177	0.999994883
histone H4-K5 acetylation (GO:0043981)	44576	0.839690177	0.999994883
histone H4-K8 acetylation (GO:0043982)	44576	0.839690177	0.999994883
mammary gland epithelium development (G	44576	0.839690177	0.999994883
membrane repolarization during cardiac mus	44576	0.839690177	0.999994883
microvillus assembly (GO:0030033)	44576	0.839690177	0.999994883
mRNA methylation (GO:0080009)	44576	0.839690177	0.999994883
mycotoxin metabolic process (GO:0043385)	44576	0.839690177	0.999994883
myoblast fusion (GO:0007520)	44576	0.839690177	0.999994883
negative regulation of androgen receptor sig	44576	0.839690177	0.999994883
negative regulation of endoplasmic reticulum	44576	0.839690177	0.999994883
negative regulation of ubiquitin-protein trans	44576	0.839690177	0.999994883
nucleosome positioning (GO:0016584)	44576	0.839690177	0.999994883
organic heteropentacyclic compound metabo	44576	0.839690177	0.999994883
peptidyl-arginine modification (GO:0018195)	44576	0.839690177	0.999994883
peptidyl-tyrosine autophosphorylation (GO:0	44576	0.839690177	0.999994883
positive regulation of cell killing (GO:003134	44576	0.839690177	0.999994883
positive regulation of chromatin organization	44576	0.839690177	0.999994883
positive regulation of DNA damage response,	44576	0.839690177	0.999994883
positive regulation of endothelial cell chemot	44576	0.839690177	0.999994883
positive regulation of exosomal secretion (GO	44576	0.839690177	0.999994883
positive regulation of glycogen metabolic pro	44576	0.839690177	0.999994883
positive regulation of lyase activity (GO:0051	44576	0.839690177	0.999994883
positive regulation of pattern recognition rec	44576	0.839690177	0.999994883
positive regulation of response to cytokine st	44576	0.839690177	0.999994883
positive regulation of secretion (GO:0051047	44576	0.839690177	0.999994883
protein localization to cell-cell junction (GO:0	44576	0.839690177	0.999994883

regulation of endothelial cell chemotaxis (GO	44576	0.839690177	0.999994883
regulation of extracellular matrix disassembl	44576	0.839690177	0.999994883
regulation of non-canonical Wnt signaling pat	44576	0.839690177	0.999994883
regulation of secretion (GO:0051046)	44576	0.839690177	0.999994883
regulation of synaptic transmission, GABAerg	44576	0.839690177	0.999994883
regulation of T cell chemotaxis (GO:0010819)	44576	0.839690177	0.999994883
response to ethanol (GO:0045471)	44576	0.839690177	0.999994883
response to muscle stretch (GO:0035994)	44576	0.839690177	0.999994883
vitamin D metabolic process (GO:0042359)	44576	0.839690177	0.999994883
neuron projection development (GO:003117	16/171	0.840909207	0.999994883
protein-containing complex assembly (GO:00	26/267	0.841053416	0.999994883
endothelial cell migration (GO:0043542)	14305	0.841165848	0.999994883
negative regulation of protein secretion (GO:	14305	0.841165848	0.999994883
negative regulation of secretion by cell (GO:1	14305	0.841165848	0.999994883
protein acylation (GO:0043543)	14305	0.841165848	0.999994883
regulation of peptidyl-threonine phosphoryla	14305	0.841165848	0.999994883
regulation of protein targeting to mitochondı	14305	0.841165848	0.999994883
response to peptide (GO:1901652)	14305	0.841165848	0.999994883
regulation of complement activation (GO:003	18354	0.841240039	0.999994883
regulation of cytoskeleton organization (GO:(	10/112	0.841708529	0.999994883
potassium ion transport (GO:0006813)	11/122	0.841852347	0.999994883
regulation of mRNA catabolic process (GO:00	11/122	0.841852347	0.999994883
regulation of cell death (GO:0010941)	9/102	0.84211168	0.999994883
retinoid metabolic process (GO:0001523)	33817	0.843242611	0.999994883
positive regulation of ERK1 and ERK2 cascade	16/172	0.847228507	0.999994883
internal peptidyl-lysine acetylation (GO:0018	44620	0.848015872	0.999994883
leukocyte cell-cell adhesion (GO:0007159)	44620	0.848015872	0.999994883
negative regulation of cellular response to in:	44620	0.848015872	0.999994883
negative regulation of oxidative stress-induce	44620	0.848015872	0.999994883
nucleotide-binding oligomerization domain c	44620	0.848015872	0.999994883
positive regulation of cell communication (G(	44620	0.848015872	0.999994883
positive regulation of monooxygenase activit	44620	0.848015872	0.999994883
positive regulation of synapse assembly (GO:	44620	0.848015872	0.999994883
receptor clustering (GO:0043113)	44620	0.848015872	0.999994883
regulation of DNA-templated transcription, e	44620	0.848015872	0.999994883
regulation of multicellular organismal develo	44620	0.848015872	0.999994883
regulation of muscle contraction (GO:000693	44620	0.848015872	0.999994883
regulation of phosphatase activity (GO:0010(	44620	0.848015872	0.999994883
response to ketone (GO:1901654)	44620	0.848015872	0.999994883
T cell activation involved in immune response	44620	0.848015872	0.999994883
ventricular septum morphogenesis (GO:0060	44620	0.848015872	0.999994883
negative regulation of cytokine production (G	17/182	0.848824265	0.999994883
positive regulation of secretion by cell (GO:1(	26451	0.848844929	0.999994883
positive regulation of cell migration (GO:003(	26/269	0.851188714	0.999994883
blood circulation (GO:0008015)	18719	0.852270751	0.999994883
mesenchymal cell differentiation (GO:00487(	18719	0.852270751	0.999994883
negative regulation of protein ubiquitination	18719	0.852270751	0.999994883

positive regulation of actin filament bundle a	18719	0.852270751	0.999994883
regulation of axonogenesis (GO:0050770)	18719	0.852270751	0.999994883
sensory perception (GO:0007600)	18719	0.852270751	0.999994883
digestive tract development (GO:0048565)	14671	0.853464727	0.999994883
lymphocyte migration (GO:0072676)	14671	0.853464727	0.999994883
negative regulation of blood coagulation (GO	14671	0.853464727	0.999994883
positive regulation of cation channel activity	14671	0.853464727	0.999994883
positive regulation of ossification (GO:00457	14671	0.853464727	0.999994883
response to organonitrogen compound (GO:(	14671	0.853464727	0.999994883
synaptic vesicle exocytosis (GO:0016079)	14671	0.853464727	0.999994883
positive regulation of interleukin-1 productio	22767	0.854287101	0.999994883
cellular metal ion homeostasis (GO:0006875)	9/104	0.857742192	0.999994883
mRNA transport (GO:0051028)	9/104	0.857742192	0.999994883
positive regulation of macromolecule metab	38/384	0.857825322	0.999994883
regulation of actin filament polymerization ((	26816	0.857897431	0.999994883
regulation of actin filament-based process (G	26816	0.857897431	0.999994883
body fluid secretion (GO:0007589)	44577	0.858115396	0.999994883
cellular response to corticosteroid stimulus ((	44577	0.858115396	0.999994883
digestive tract morphogenesis (GO:0048546)	44577	0.858115396	0.999994883
eosinophil chemotaxis (GO:0048245)	44577	0.858115396	0.999994883
eosinophil migration (GO:0072677)	44577	0.858115396	0.999994883
filopodium assembly (GO:0046847)	44577	0.858115396	0.999994883
male meiosis I (GO:0007141)	44577	0.858115396	0.999994883
membrane repolarization (GO:0086009)	44577	0.858115396	0.999994883
mitotic sister chromatid cohesion (GO:00070	44577	0.858115396	0.999994883
mRNA cis splicing, via spliceosome (GO:0045	44577	0.858115396	0.999994883
N-terminal protein amino acid acetylation (G	44577	0.858115396	0.999994883
necroptotic process (GO:0070266)	44577	0.858115396	0.999994883
negative regulation of anoikis (GO:2000811)	44577	0.858115396	0.999994883
negative regulation of epithelial cell different	44577	0.858115396	0.999994883
negative regulation of macrophage activatior	44577	0.858115396	0.999994883
odontogenesis of dentin-containing tooth (G(	44577	0.858115396	0.999994883
positive regulation of alpha-beta T cell prolife	44577	0.858115396	0.999994883
positive regulation of double-strand break re	44577	0.858115396	0.999994883
positive regulation of endothelial cell apopto	44577	0.858115396	0.999994883
positive regulation of myeloid leukocyte cyto	44577	0.858115396	0.999994883
positive regulation of vasoconstriction (GO:0(	44577	0.858115396	0.999994883
regulation of activin receptor signaling pathw	44577	0.858115396	0.999994883
regulation of mitotic sister chromatid separat	44577	0.858115396	0.999994883
regulation of phosphate metabolic process ((	44577	0.858115396	0.999994883
regulation of rRNA processing (GO:2000232)	44577	0.858115396	0.999994883
sympathetic nervous system development (G	44577	0.858115396	0.999994883
interleukin-1-mediated signaling pathway (G(	34547	0.859521839	0.999994883
negative regulation of MAPK cascade (GO:00	34547	0.859521839	0.999994883
protein ubiquitination (GO:0016567)	53/525	0.86102452	0.999994883
actin filament polymerization (GO:0030041)	47150	0.861721227	0.999994883
aggrephagy (GO:0035973)	47150	0.861721227	0.999994883

positive regulation of extrinsic apoptotic sign	47150	0.861721227	0.999994883
positive regulation of leukocyte migration (G	47150	0.861721227	0.999994883
regulation of actin polymerization or depolyn	47150	0.861721227	0.999994883
regulation of ubiquitin-protein transferase ac	47150	0.861721227	0.999994883
response to cadmium ion (GO:0046686)	47150	0.861721227	0.999994883
anaphase-promoting complex-dependent cat	30864	0.862318465	0.999994883
regulation of release of sequestered calcium	19085	0.862643732	0.999994883
sprouting angiogenesis (GO:0002040)	19085	0.862643732	0.999994883
positive regulation of Ras protein signal trans	23132	0.863708401	0.999994883
acylglycerol metabolic process (GO:0006639)	15036	0.864923009	0.999994883
cortical cytoskeleton organization (GO:00308	15036	0.864923009	0.999994883
heart contraction (GO:0060047)	15036	0.864923009	0.999994883
negative regulation of cell-cell adhesion (GO:	15036	0.864923009	0.999994883
positive regulation of biomineral tissue devel	15036	0.864923009	0.999994883
positive regulation of cation transmembrane	15036	0.864923009	0.999994883
regulation of cell development (GO:0060284)	15036	0.864923009	0.999994883
regulation of filopodium assembly (GO:0051	15036	0.864923009	0.999994883
positive regulation of cellular metabolic proc	9/105	0.865080353	0.999994883
negative regulation of protein binding (GO:0(	27181	0.866498267	0.999994883
NIK/NF-kappaB signaling (GO:0038061)	27181	0.866498267	0.999994883
regulation of MAPK cascade (GO:0043408)	15/166	0.869917329	0.999994883
positive regulation of angiogenesis (GO:0045	10/116	0.87059241	0.999994883
protein localization to nucleus (GO:0034504)	9/106	0.872110204	0.999994883
regulation of phosphatidylinositol 3-kinase si	9/106	0.872110204	0.999994883
RNA export from nucleus (GO:0006405)	9/106	0.872110204	0.999994883
bicellular tight junction assembly (GO:00708	19450	0.872386427	0.999994883
cellular macromolecule catabolic process (GC	19450	0.872386427	0.999994883
negative regulation of cysteine-type endopep	19450	0.872386427	0.999994883
positive regulation of phagocytosis (GO:0050	19450	0.872386427	0.999994883
regulation of immune effector process (GO:0	19450	0.872386427	0.999994883
negative regulation of intrinsic apoptotic sign	23498	0.872611909	0.999994883
artery morphogenesis (GO:0048844)	10990	0.874284832	0.999994883
cardiac muscle cell action potential (GO:0086	10990	0.874284832	0.999994883
histone H3-K4 methylation (GO:0051568)	10990	0.874284832	0.999994883
multivesicular body assembly (GO:0036258)	10990	0.874284832	0.999994883
phosphatidylcholine acyl-chain remodeling (G	10990	0.874284832	0.999994883
positive regulation of phosphate metabolic p	10990	0.874284832	0.999994883
regulation of long-term synaptic potentiation	10990	0.874284832	0.999994883
regulation of macrophage activation (GO:004	10990	0.874284832	0.999994883
regulation of vasoconstriction (GO:0019229)	10990	0.874284832	0.999994883
termination of RNA polymerase I transcriptio	10990	0.874284832	0.999994883
cellular biogenic amine biosynthetic process	44578	0.874423701	0.999994883
establishment of protein localization to endo	44578	0.874423701	0.999994883
gliogenesis (GO:0042063)	44578	0.874423701	0.999994883
maturation of 5.8S rRNA (GO:0000460)	44578	0.874423701	0.999994883
membrane depolarization during cardiac mus	44578	0.874423701	0.999994883
mesonephric tubule development (GO:0072	44578	0.874423701	0.999994883

mitochondrial electron transport, cytochrom	44578	0.874423701	0.999994883
muscle tissue morphogenesis (GO:0060415)	44578	0.874423701	0.999994883
negative regulation of fatty acid metabolic pr	44578	0.874423701	0.999994883
negative regulation of peptidyl-threonine ph	44578	0.874423701	0.999994883
pharyngeal system development (GO:006003	44578	0.874423701	0.999994883
positive regulation of blood coagulation (GO:	44578	0.874423701	0.999994883
positive regulation of cardiac muscle tissue g	44578	0.874423701	0.999994883
positive regulation of cytokine production in	44578	0.874423701	0.999994883
positive regulation of positive chemotaxis (G	44578	0.874423701	0.999994883
positive regulation of stem cell differentiatio	44578	0.874423701	0.999994883
positive regulation of stem cell proliferation (	44578	0.874423701	0.999994883
protein autoprocessing (GO:0016540)	44578	0.874423701	0.999994883
regulation of cell killing (GO:0031341)	44578	0.874423701	0.999994883
regulation of Golgi organization (GO:190335	44578	0.874423701	0.999994883
regulation of osteoblast proliferation (GO:00	44578	0.874423701	0.999994883
regulation of steroid biosynthetic process (G	44578	0.874423701	0.999994883
ruffle organization (GO:0031529)	44578	0.874423701	0.999994883
stabilization of membrane potential (GO:003	44578	0.874423701	0.999994883
sulfation (GO:0051923)	44578	0.874423701	0.999994883
positive regulation of immune response (GO:	27546	0.874661807	0.999994883
regulation of hematopoietic progenitor cell d	27546	0.874661807	0.999994883
histone H3 acetylation (GO:0043966)	15401	0.875584392	0.999994883
positive regulation of epithelial to mesenchy	15401	0.875584392	0.999994883
negative regulation of nucleic acid-templatec	46/464	0.875822906	0.999994883
positive regulation of developmental process	16/177	0.875988534	0.999994883
positive regulation of cell projection organiza	10/117	0.877108608	0.999994883
negative regulation of cellular amide metabo	31594	0.877724152	0.999994883
mRNA export from nucleus (GO:0006406)	9/107	0.87883942	0.999994883
protein polyubiquitination (GO:0000209)	30/314	0.881129321	0.999994883
regulation of humoral immune response (GO	19815	0.881526516	0.999994883
nervous system development (GO:0007399)	44/447	0.881809712	0.999994883
chloride transport (GO:0006821)	27912	0.882402756	0.999994883
regulation of epithelial to mesenchymal trans	27912	0.882402756	0.999994883
RNA transport (GO:0050658)	27912	0.882402756	0.999994883
cellular glucose homeostasis (GO:0001678)	15766	0.885492135	0.999994883
myofibril assembly (GO:0030239)	15766	0.885492135	0.999994883
positive regulation of peptide hormone secre	15766	0.885492135	0.999994883
cardiac muscle cell action potential involved	11355	0.885788035	0.999994883
multivesicular body organization (GO:003625	11355	0.885788035	0.999994883
negative regulation of interleukin-6 productic	11355	0.885788035	0.999994883
negative regulation of response to biotic stim	11355	0.885788035	0.999994883
organelle transport along microtubule (GO:0(	11355	0.885788035	0.999994883
positive regulation of RNA splicing (GO:0033	11355	0.885788035	0.999994883
receptor signaling pathway via JAK-STAT (GO	11355	0.885788035	0.999994883
regulation of cellular pH (GO:0030641)	11355	0.885788035	0.999994883
regulation of potassium ion transport (GO:00	11355	0.885788035	0.999994883
alternative mRNA splicing, via spliceosome (G	44579	0.888858213	0.999994883

cell migration involved in sprouting angiogen	44579	0.888858213	0.999994883
cellular response to glucocorticoid stimulus ((	44579	0.888858213	0.999994883
cellular response to zinc ion (GO:0071294)	44579	0.888858213	0.999994883
embryonic digit morphogenesis (GO:004273:	44579	0.888858213	0.999994883
endothelial cell proliferation (GO:0001935)	44579	0.888858213	0.999994883
epithelial structure maintenance (GO:001066	44579	0.888858213	0.999994883
establishment of vesicle localization (GO:005	44579	0.888858213	0.999994883
leukocyte tethering or rolling (GO:0050901)	44579	0.888858213	0.999994883
long-chain fatty-acyl-CoA biosynthetic proces	44579	0.888858213	0.999994883
maintenance of gastrointestinal epithelium ((	44579	0.888858213	0.999994883
mitochondrial fission (GO:0000266)	44579	0.888858213	0.999994883
phosphatidylglycerol acyl-chain remodeling ((	44579	0.888858213	0.999994883
phosphatidylinositol acyl-chain remodeling ((	44579	0.888858213	0.999994883
positive regulation of cell adhesion mediated	44579	0.888858213	0.999994883
positive regulation of cell cycle phase transiti	44579	0.888858213	0.999994883
positive regulation of lymphocyte chemotaxis	44579	0.888858213	0.999994883
positive regulation of mRNA splicing, via splic	44579	0.888858213	0.999994883
positive regulation of response to endoplasm	44579	0.888858213	0.999994883
regulation of B cell differentiation (GO:00455	44579	0.888858213	0.999994883
regulation of brown fat cell differentiation (G	44579	0.888858213	0.999994883
regulation of cartilage development (GO:006	44579	0.888858213	0.999994883
regulation of catabolic process (GO:0009894)	44579	0.888858213	0.999994883
regulation of early endosome to late endosor	44579	0.888858213	0.999994883
regulation of production of miRNAs involved	44579	0.888858213	0.999994883
regulation of protein sumoylation (GO:00332	44579	0.888858213	0.999994883
regulation of transforming growth factor beta	44579	0.888858213	0.999994883
regulation of ventricular cardiac muscle cell r	44579	0.888858213	0.999994883
response to interferon-alpha (GO:0035455)	44579	0.888858213	0.999994883
rRNA transcription (GO:0009303)	44579	0.888858213	0.999994883
T cell migration (GO:0072678)	44579	0.888858213	0.999994883
tRNA metabolic process (GO:0006399)	44579	0.888858213	0.999994883
positive regulation of cell death (GO:001094	24228	0.888943751	0.999994883
positive regulation of phosphatidylinositol 3-	28277	0.889736049	0.999994883
negative regulation of protein modification b	20180	0.890091698	0.999994883
positive regulation of response to DNA dama	20180	0.890091698	0.999994883
brain development (GO:0007420)	13/150	0.891563782	0.999994883
metal ion homeostasis (GO:0055065)	16132	0.894688759	0.999994883
mRNA stabilization (GO:0048255)	16132	0.894688759	0.999994883
protein K63-linked ubiquitination (GO:00705	16132	0.894688759	0.999994883
regulation of endothelial cell apoptotic proce	16132	0.894688759	0.999994883
negative regulation of cell differentiation (GC	17/191	0.895912279	0.999994883
aortic valve morphogenesis (GO:0003180)	11720	0.896308565	0.999994883
B cell proliferation (GO:0042100)	11720	0.896308565	0.999994883
cellular response to glucose stimulus (GO:00	11720	0.896308565	0.999994883
hematopoietic progenitor cell differentiation	11720	0.896308565	0.999994883
liver development (GO:0001889)	11720	0.896308565	0.999994883
membrane depolarization (GO:0051899)	11720	0.896308565	0.999994883

negative regulation of chemotaxis (GO:00509	11720	0.896308565	0.999994883
positive regulation of glucose transmembran	11720	0.896308565	0.999994883
positive regulation of interleukin-10 producti	11720	0.896308565	0.999994883
protein K63-linked deubiquitination (GO:007(	11720	0.896308565	0.999994883
skeletal muscle organ development (GO:006(	11720	0.896308565	0.999994883
transcription initiation from RNA polymerase	11720	0.896308565	0.999994883
positive regulation of catabolic process (GO:(	24593	0.896411573	0.999994883
regulation of epidermal growth factor recept	24593	0.896411573	0.999994883
negative regulation of protein serine/threoni	28642	0.896676761	0.999994883
autophagosome organization (GO:1905037)	20546	0.898109507	0.999994883
mitochondrial transport (GO:0006839)	20546	0.898109507	0.999994883
positive regulation of interleukin-1 beta prod	20546	0.898109507	0.999994883
regulation of type I interferon production (G(	32690	0.898122727	0.999994883
activin receptor signaling pathway (GO:00325	44580	0.901634146	0.999994883
atrioventricular valve morphogenesis (GO:00	44580	0.901634146	0.999994883
branching involved in ureteric bud morphoge	44580	0.901634146	0.999994883
cardiac atrium morphogenesis (GO:0003209)	44580	0.901634146	0.999994883
cellular response to copper ion (GO:0071280	44580	0.901634146	0.999994883
dopamine metabolic process (GO:0042417)	44580	0.901634146	0.999994883
endoplasmic reticulum mannose trimming (G	44580	0.901634146	0.999994883
establishment or maintenance of apical/basa	44580	0.901634146	0.999994883
glycerolipid catabolic process (GO:0046503)	44580	0.901634146	0.999994883
heart trabecula morphogenesis (GO:0061384	44580	0.901634146	0.999994883
leukocyte adhesion to vascular endothelial ce	44580	0.901634146	0.999994883
long-term memory (GO:0007616)	44580	0.901634146	0.999994883
myeloid cell activation involved in immune re	44580	0.901634146	0.999994883
negative regulation of immune system proce	44580	0.901634146	0.999994883
negative regulation of oxidative stress-induce	44580	0.901634146	0.999994883
negative regulation of RNA metabolic proces	44580	0.901634146	0.999994883
negative regulation of T cell receptor signalin	44580	0.901634146	0.999994883
nuclear membrane organization (GO:007176	44580	0.901634146	0.999994883
positive regulation of establishment of protei	44580	0.901634146	0.999994883
positive regulation of G protein-coupled rece	44580	0.901634146	0.999994883
positive regulation of macrophage migration	44580	0.901634146	0.999994883
positive regulation of mitochondrial fission ((	44580	0.901634146	0.999994883
positive regulation of neutrophil chemotaxis	44580	0.901634146	0.999994883
protein import into mitochondrial matrix (GO	44580	0.901634146	0.999994883
regulation of bicellular tight junction assembl	44580	0.901634146	0.999994883
regulation of collagen biosynthetic process ((	44580	0.901634146	0.999994883
regulation of exosomal secretion (GO:190354	44580	0.901634146	0.999994883
regulation of glucose transmembrane transp	44580	0.901634146	0.999994883
regulation of synaptic vesicle exocytosis (GO:	44580	0.901634146	0.999994883
regulation of vascular endothelial growth fac	44580	0.901634146	0.999994883
striated muscle cell differentiation (GO:0051	44580	0.901634146	0.999994883
ureteric bud morphogenesis (GO:0060675)	44580	0.901634146	0.999994883
membrane organization (GO:0061024)	22/242	0.902467795	0.999994883
cellular divalent inorganic cation homeostasi	9/111	0.902910568	0.999994883

action potential (GO:0001508)	16497	0.903215795	0.999994883
sodium ion transport (GO:0006814)	33055	0.904247377	0.999994883
carboxylic acid transport (GO:0046942)	20911	0.905607151	0.999994883
protein K48-linked ubiquitination (GO:00709	20911	0.905607151	0.999994883
antigen processing and presentation of pepti	12086	0.905920293	0.999994883
regulation of sprouting angiogenesis (GO:190	12086	0.905920293	0.999994883
regulation of canonical Wnt signaling pathwa	23/253	0.906848156	0.999994883
neuron development (GO:0048666)	12/143	0.907326826	0.999994883
negative regulation of multicellular organism	19/214	0.908810691	0.999994883
negative regulation of extrinsic apoptotic sig	29373	0.909440941	0.999994883
heart development (GO:0007507)	14/164	0.909845886	0.999994883
negative regulation of cellular catabolic proc	25324	0.910049626	0.999994883
synapse assembly (GO:0007416)	25324	0.910049626	0.999994883
regulation of stem cell differentiation (GO:20	33420	0.910054741	0.999994883
cellular response to organic substance (GO:0(	10/123	0.910801539	0.999994883
erythrocyte differentiation (GO:0030218)	16862	0.911113584	0.999994883
positive regulation of organelle assembly (GC	16862	0.911113584	0.999994883
positive regulation of response to stimulus (G	16862	0.911113584	0.999994883
posttranscriptional regulation of gene expres	16862	0.911113584	0.999994883
vesicle organization (GO:0016050)	16862	0.911113584	0.999994883
eye development (GO:0001654)	21276	0.912611375	0.999994883
regulation of phagocytosis (GO:0050764)	21276	0.912611375	0.999994883
RNA modification (GO:0009451)	21276	0.912611375	0.999994883
adaptive immune response based on somatic	44581	0.912942	0.999994883
calcium-independent cell-cell adhesion via pl	44581	0.912942	0.999994883
cardiac epithelial to mesenchymal transition	44581	0.912942	0.999994883
cardiac ventricle development (GO:0003231)	44581	0.912942	0.999994883
cellular monovalent inorganic cation homeos	44581	0.912942	0.999994883
cellular response to misfolded protein (GO:0(	44581	0.912942	0.999994883
cortical actin cytoskeleton organization (GO:(	44581	0.912942	0.999994883
lipopolysaccharide-mediated signaling pathw	44581	0.912942	0.999994883
maintenance of protein location in nucleus ((	44581	0.912942	0.999994883
mesoderm formation (GO:0001707)	44581	0.912942	0.999994883
mitotic cytokinetic process (GO:1902410)	44581	0.912942	0.999994883
modulation by symbiont of entry into host (G	44581	0.912942	0.999994883
natural killer cell mediated immunity (GO:00(	44581	0.912942	0.999994883
negative regulation of dephosphorylation (G(	44581	0.912942	0.999994883
neuromuscular synaptic transmission (GO:00	44581	0.912942	0.999994883
positive regulation of embryonic developmer	44581	0.912942	0.999994883
positive regulation of epidermal cell differen	44581	0.912942	0.999994883
positive regulation of heart contraction (GO:(	44581	0.912942	0.999994883
post-transcriptional gene silencing by RNA (G	44581	0.912942	0.999994883
regulation of hippo signaling (GO:0035330)	44581	0.912942	0.999994883
regulation of lymphocyte differentiation (GO	44581	0.912942	0.999994883
regulation of protein kinase A signaling (GO:(	44581	0.912942	0.999994883
regulation of protein modification by small p	44581	0.912942	0.999994883
regulation of tissue remodeling (GO:0034103	44581	0.912942	0.999994883

negative regulation of transcription by RNA p	68/684	0.913478994	0.999994883
positive regulation of peptidyl-tyrosine phosp	11/134	0.913522682	0.999994883
autophagosome maturation (GO:0097352)	12451	0.914693091	0.999994883
B cell receptor signaling pathway (GO:00508	12451	0.914693091	0.999994883
cardiac muscle contraction (GO:0060048)	12451	0.914693091	0.999994883
cellular response to vascular endothelial grov	12451	0.914693091	0.999994883
epithelial tube morphogenesis (GO:0060562)	12451	0.914693091	0.999994883
protein destabilization (GO:0031648)	12451	0.914693091	0.999994883
regulation of cell adhesion mediated by integ	12451	0.914693091	0.999994883
regulation of lamellipodium assembly (GO:00	12451	0.914693091	0.999994883
regulation of myoblast differentiation (GO:00	12451	0.914693091	0.999994883
secondary alcohol biosynthetic process (GO:1	12451	0.914693091	0.999994883
synaptic vesicle recycling (GO:0036465)	12451	0.914693091	0.999994883
termination of RNA polymerase II transcriptio	12451	0.914693091	0.999994883
transcription by RNA polymerase I (GO:00063	12451	0.914693091	0.999994883
ventricular cardiac muscle tissue morphogen	12451	0.914693091	0.999994883
positive regulation of transmembrane recept	33786	0.915556901	0.999994883
T cell activation (GO:0042110)	33786	0.915556901	0.999994883
DNA-templated transcription, termination (G	25689	0.916258826	0.999994883
kidney development (GO:0001822)	25689	0.916258826	0.999994883
snRNA transcription by RNA polymerase II (G	25689	0.916258826	0.999994883
positive regulation of DNA-binding transcript	22/246	0.916827754	0.999994883
positive regulation of cell-cell adhesion (GO:0	17227	0.918421126	0.999994883
regulation of wound healing (GO:0061041)	17227	0.918421126	0.999994883
regulation of secretion by cell (GO:1903530)	21641	0.919148346	0.999994883
selective autophagy (GO:0061912)	21641	0.919148346	0.999994883
cell-cell junction organization (GO:0045216)	30103	0.920815695	0.999994883
regulation of G protein-coupled receptor sign	30103	0.920815695	0.999994883
response to metal ion (GO:0010038)	26054	0.922086988	0.999994883
snRNA transcription (GO:0009301)	26054	0.922086988	0.999994883
protein localization to plasma membrane (GO	11/136	0.922305213	0.999994883
cholesterol biosynthetic process (GO:000669	12816	0.922692778	0.999994883
lung development (GO:0030324)	12816	0.922692778	0.999994883
negative regulation of Ras protein signal tran	12816	0.922692778	0.999994883
peptidyl-tyrosine dephosphorylation (GO:003	12816	0.922692778	0.999994883
positive regulation of lymphocyte activation (	12816	0.922692778	0.999994883
regulation of mitotic spindle organization (GO	12816	0.922692778	0.999994883
regulation of postsynaptic membrane potent	12816	0.922692778	0.999994883
regulation of regulated secretory pathway (G	12816	0.922692778	0.999994883
regulation of T cell receptor signaling pathwa	12816	0.922692778	0.999994883
regulation of trans-synaptic signaling (GO:00	12816	0.922692778	0.999994883
actin nucleation (GO:0045010)	44582	0.922950408	0.999994883
anterior/posterior axis specification (GO:000	44582	0.922950408	0.999994883
beta-catenin destruction complex disassembl	44582	0.922950408	0.999994883
calcium-mediated signaling using intracellula	44582	0.922950408	0.999994883
cyclic purine nucleotide metabolic process (G	44582	0.922950408	0.999994883
endocardial cushion development (GO:0003	44582	0.922950408	0.999994883

epithelial cell development (GO:0002064)	44582	0.922950408	0.999994883
focal adhesion assembly (GO:0048041)	44582	0.922950408	0.999994883
histone ubiquitination (GO:0016574)	44582	0.922950408	0.999994883
innate immune response in mucosa (GO:000	44582	0.922950408	0.999994883
long-term synaptic potentiation (GO:006029	44582	0.922950408	0.999994883
mitotic spindle assembly checkpoint signaling	44582	0.922950408	0.999994883
mitotic spindle checkpoint signaling (GO:007	44582	0.922950408	0.999994883
natural killer cell activation involved in immu	44582	0.922950408	0.999994883
negative regulation of cell communication (G	44582	0.922950408	0.999994883
negative regulation of peptidyl-serine phospl	44582	0.922950408	0.999994883
nuclear-transcribed mRNA poly(A) tail shorte	44582	0.922950408	0.999994883
positive regulation of immune system proces	44582	0.922950408	0.999994883
positive regulation of transcription from RNA	44582	0.922950408	0.999994883
regulation of dendritic spine development (G	44582	0.922950408	0.999994883
regulation of fibroblast migration (GO:00107	44582	0.922950408	0.999994883
response to progesterone (GO:0032570)	44582	0.922950408	0.999994883
retinol metabolic process (GO:0042572)	44582	0.922950408	0.999994883
spindle assembly checkpoint signaling (GO:0(	44582	0.922950408	0.999994883
stress granule assembly (GO:0034063)	44582	0.922950408	0.999994883
central nervous system development (GO:00	24/268	0.923876124	0.999994883
positive regulation of cytosolic calcium ion cc	12/147	0.924604243	0.999994883
apical junction assembly (GO:0043297)	22007	0.92524356	0.999994883
cellular response to chemokine (GO:1990869	22007	0.92524356	0.999994883
ribonucleoprotein complex biogenesis (GO:0(	22007	0.92524356	0.999994883
regulation of interleukin-1 beta production ((	30468	0.926019075	0.999994883
cellular response to growth factor stimulus ((	13/158	0.926981833	0.999994883
negative regulation of epithelial cell prolifera	26420	0.927552795	0.999994883
activation of adenylate cyclase activity (GO:0	13181	0.929981126	0.999994883
aortic valve development (GO:0003176)	13181	0.929981126	0.999994883
cellular response to heat (GO:0034605)	13181	0.929981126	0.999994883
membrane fusion (GO:0061025)	13181	0.929981126	0.999994883
negative regulation of toll-like receptor signa	13181	0.929981126	0.999994883
regulation of defense response to virus by ho	13181	0.929981126	0.999994883
regulation of ossification (GO:0030278)	13181	0.929981126	0.999994883
mRNA metabolic process (GO:0016071)	34881	0.930351639	0.999994883
cellular response to peptide hormone stimul	8/106	0.930594758	0.999994883
cellular defense response (GO:0006968)	17958	0.93141406	0.999994883
response to glucose (GO:0009749)	17958	0.93141406	0.999994883
cellular response to nerve growth factor stim	44583	0.931808638	0.999994883
exogenous drug catabolic process (GO:00427	44583	0.931808638	0.999994883
female gonad development (GO:0008585)	44583	0.931808638	0.999994883
mRNA modification (GO:0016556)	44583	0.931808638	0.999994883
negative regulation of B cell activation (GO:0(	44583	0.931808638	0.999994883
negative regulation of biomineral tissue deve	44583	0.931808638	0.999994883
negative regulation of DNA recombination at	44583	0.931808638	0.999994883
negative regulation of mitotic metaphase/an	44583	0.931808638	0.999994883
negative regulation of phosphate metabolic p	44583	0.931808638	0.999994883

negative regulation of small molecule metab	44583	0.931808638	0.999994883
peptidyl-threonine dephosphorylation (GO:0	44583	0.931808638	0.999994883
positive regulation of dendritic spine develop	44583	0.931808638	0.999994883
positive regulation of granulocyte chemotaxi	44583	0.931808638	0.999994883
positive regulation of neutrophil migration (G	44583	0.931808638	0.999994883
positive regulation of translational initiation (	44583	0.931808638	0.999994883
regulation of cardiac muscle cell membrane r	44583	0.931808638	0.999994883
regulation of chromosome organization (GO:	44583	0.931808638	0.999994883
regulation of DNA recombination at telomere	44583	0.931808638	0.999994883
regulation of membrane protein ectodomain	44583	0.931808638	0.999994883
regulation of viral release from host cell (GO:	44583	0.931808638	0.999994883
regulation of voltage-gated calcium channel a	44583	0.931808638	0.999994883
regulation of cell migration (GO:0030334)	38/408	0.932360072	0.999994883
positive regulation of synaptic transmission (	26785	0.932674494	0.999994883
potassium ion transmembrane transport (GO	11/139	0.934051073	0.999994883
regulation of protein binding (GO:0043393)	9/118	0.935364734	0.999994883
I-kappaB kinase/NF-kappaB signaling (GO:00(	22737	0.936206891	0.999994883
stress-activated MAPK cascade (GO:0051403	22737	0.936206891	0.999994883
positive regulation of exocytosis (GO:004592	13547	0.936615926	0.999994883
positive regulation of signaling receptor activ	13547	0.936615926	0.999994883
regulation of intracellular pH (GO:0051453)	13547	0.936615926	0.999994883
skeletal muscle tissue development (GO:000	13547	0.936615926	0.999994883
actin polymerization or depolymerization (G(	18323	0.937169824	0.999994883
regulation of cellular component movement	18323	0.937169824	0.999994883
regulation of cytokine-mediated signaling pat	27150	0.937469855	0.999994883
regulation of MAP kinase activity (GO:00434(	35612	0.938905206	0.999994883
artery development (GO:0060840)	44584	0.939648819	0.999994883
blood vessel endothelial cell migration (GO:0	44584	0.939648819	0.999994883
drug catabolic process (GO:0042737)	44584	0.939648819	0.999994883
ear morphogenesis (GO:0042471)	44584	0.939648819	0.999994883
ERK1 and ERK2 cascade (GO:0070371)	44584	0.939648819	0.999994883
negative regulation of extrinsic apoptotic sigr	44584	0.939648819	0.999994883
negative regulation of signal transduction in a	44584	0.939648819	0.999994883
positive regulation of mRNA processing (GO:(	44584	0.939648819	0.999994883
positive regulation of transcription by RNA p(	44584	0.939648819	0.999994883
regulation of cysteine-type endopeptidase ac	44584	0.939648819	0.999994883
regulation of interferon-gamma-mediated sig	44584	0.939648819	0.999994883
regulation of mononuclear cell migration (GC	44584	0.939648819	0.999994883
regulation of necroptotic process (GO:00605	44584	0.939648819	0.999994883
regulation of neural precursor cell proliferati	44584	0.939648819	0.999994883
regulation of toll-like receptor 4 signaling pat	44584	0.939648819	0.999994883
respiratory chain complex IV assembly (GO:0	44584	0.939648819	0.999994883
response to copper ion (GO:0046688)	44584	0.939648819	0.999994883
response to nutrient levels (GO:0031667)	44584	0.939648819	0.999994883
negative regulation of peptidase activity (GO	23102	0.941122022	0.999994883
positive regulation of T cell activation (GO:00	27515	0.941956125	0.999994883
ubiquitin-dependent protein catabolic proces	32/354	0.942137449	0.999994883

positive regulation of fat cell differentiation (	18688	0.942475992	0.999994883
regulation of interleukin-12 production (GO:(	18688	0.942475992	0.999994883
modulation of chemical synaptic transmissio	8/109	0.942484327	0.999994883
negative regulation of innate immune respor	13912	0.94265108	0.999994883
positive regulation of signaling (GO:0023056)	13912	0.94265108	0.999994883
regulation of cell communication (GO:00106	13912	0.94265108	0.999994883
regulation of phosphoprotein phosphatase a	13912	0.94265108	0.999994883
sterol biosynthetic process (GO:0016126)	13912	0.94265108	0.999994883
ventricular septum development (GO:00032	13912	0.94265108	0.999994883
cation transport (GO:0006812)	14/174	0.945224587	0.999994883
positive regulation of Wnt signaling pathway	12/153	0.945353853	0.999994883
plasma membrane organization (GO:000700	23468	0.945689342	0.999994883
regulation of interleukin-6 production (GO:0	8/110	0.946027932	0.999994883
positive regulation of interleukin-6 productio	27881	0.946150006	0.999994883
regulation of BMP signaling pathway (GO:00	27881	0.946150006	0.999994883
regulation of RNA splicing (GO:0043484)	27881	0.946150006	0.999994883
organic anion transport (GO:0015711)	36342	0.946516335	0.999994883
amino acid import across plasma membrane	44585	0.946587905	0.999994883
dorsal/ventral pattern formation (GO:00099	44585	0.946587905	0.999994883
long-chain fatty-acyl-CoA metabolic process (	44585	0.946587905	0.999994883
lymphocyte activation involved in immune re	44585	0.946587905	0.999994883
mammary gland development (GO:0030879)	44585	0.946587905	0.999994883
negative regulation of neuron differentiation	44585	0.946587905	0.999994883
negative regulation of protein tyrosine kinas	44585	0.946587905	0.999994883
negative regulation of stress fiber assembly (	44585	0.946587905	0.999994883
neuromuscular junction development (GO:0(	44585	0.946587905	0.999994883
phospholipid catabolic process (GO:0009395)	44585	0.946587905	0.999994883
positive regulation of lamellipodium assembl	44585	0.946587905	0.999994883
positive regulation of p38MAPK cascade (GO	44585	0.946587905	0.999994883
positive regulation of phospholipase activity	44585	0.946587905	0.999994883
positive regulation of protein targeting to me	44585	0.946587905	0.999994883
positive regulation of transcription from RNA	44585	0.946587905	0.999994883
potassium ion homeostasis (GO:0055075)	44585	0.946587905	0.999994883
protein exit from endoplasmic reticulum (GO	44585	0.946587905	0.999994883
purine nucleotide metabolic process (GO:00(	44585	0.946587905	0.999994883
regulation of cell size (GO:0008361)	44585	0.946587905	0.999994883
regulation of cytokine production involved in	44585	0.946587905	0.999994883
regulation of keratinocyte proliferation (GO:(	44585	0.946587905	0.999994883
wound healing, spreading of cells (GO:00443	44585	0.946587905	0.999994883
cartilage development (GO:0051216)	19054	0.947363657	0.999994883
myeloid cell differentiation (GO:0030099)	19054	0.947363657	0.999994883
negative regulation of BMP signaling pathwa	19054	0.947363657	0.999994883
regulation of exocytosis (GO:0017157)	19054	0.947363657	0.999994883
positive regulation of neuron projection deve	32295	0.947763444	0.999994883
odontogenesis (GO:0042476)	14277	0.948136739	0.999994883
regulation of T cell differentiation (GO:00455	14277	0.948136739	0.999994883
regulation of cell motility (GO:2000145)	10/133	0.949620051	0.999994883

RNA metabolic process (GO:0016070)	10/133	0.949620051	0.999994883
BMP signaling pathway (GO:0030509)	23833	0.949930123	0.999994883
inorganic anion transmembrane transport (G	23833	0.949930123	0.999994883
positive regulation of type I interferon produ	28246	0.950067624	0.999994883
heart morphogenesis (GO:0003007)	19419	0.951862267	0.999994883
positive regulation of chemokine production	19419	0.951862267	0.999994883
cellular response to hexose stimulus (GO:007	44586	0.952729422	0.999994883
detection of chemical stimulus involved in se	44586	0.952729422	0.999994883
negative regulation of signaling (GO:0023057	44586	0.952729422	0.999994883
positive regulation of DNA-templated transcr	44586	0.952729422	0.999994883
positive regulation of T cell migration (GO:20	44586	0.952729422	0.999994883
regulation of AMPA receptor activity (GO:200	44586	0.952729422	0.999994883
regulation of cardiac muscle cell action poter	44586	0.952729422	0.999994883
regulation of dopamine secretion (GO:00140	44586	0.952729422	0.999994883
regulation of interferon-alpha production (G(	44586	0.952729422	0.999994883
regulation of myotube differentiation (GO:00	44586	0.952729422	0.999994883
regulation of neutrophil chemotaxis (GO:009	44586	0.952729422	0.999994883
response to dsRNA (GO:0043331)	44586	0.952729422	0.999994883
ribosomal large subunit assembly (GO:00000	44586	0.952729422	0.999994883
RNA splicing, via transesterification reactions	44586	0.952729422	0.999994883
sodium ion homeostasis (GO:0055078)	44586	0.952729422	0.999994883
autophagy of mitochondrion (GO:0000422)	14642	0.953119447	0.999994883
negative regulation of ERBB signaling pathwa	14642	0.953119447	0.999994883
negative regulation of protein kinase B signal	14642	0.953119447	0.999994883
ribosomal small subunit biogenesis (GO:0042	14642	0.953119447	0.999994883
stem cell differentiation (GO:0048863)	14642	0.953119447	0.999994883
protein modification by small protein conjug	37/409	0.95336988	0.999994883
regulation of cell differentiation (GO:004559	12/156	0.953724811	0.999994883
embryonic organ development (GO:0048568	24198	0.953864707	0.999994883
negative regulation of cellular macromolecul	51/547	0.956275053	0.999994883
cell junction assembly (GO:0034329)	7/102	0.956352056	0.999994883
regulation of protein catabolic process (GO:0	7/102	0.956352056	0.999994883
regulation of viral genome replication (GO:00	24563	0.957512505	0.999994883
regulation of protein dephosphorylation (GO	15008	0.957642312	0.999994883
regulation of viral transcription (GO:0046782	15008	0.957642312	0.999994883
visual system development (GO:0150063)	15008	0.957642312	0.999994883
cellular calcium ion homeostasis (GO:000687	10/136	0.957910554	0.999994883
endothelial cell development (GO:0001885)	44587	0.958165006	0.999994883
metanephros development (GO:0001656)	44587	0.958165006	0.999994883
mRNA polyadenylation (GO:0006378)	44587	0.958165006	0.999994883
negative regulation of cell development (GO:	44587	0.958165006	0.999994883
negative regulation of macroautophagy (GO:	44587	0.958165006	0.999994883
negative regulation of proteolysis involved in	44587	0.958165006	0.999994883
negative regulation of transposition (GO:001	44587	0.958165006	0.999994883
positive regulation of glucose import (GO:00	44587	0.958165006	0.999994883
positive regulation of T cell mediated cytotox	44587	0.958165006	0.999994883
positive regulation of viral transcription (GO:	44587	0.958165006	0.999994883

regulation of chondrocyte differentiation (GC	44587	0.958165006	0.999994883
regulation of potassium ion transmembrane	44587	0.958165006	0.999994883
RNA polyadenylation (GO:0043631)	44587	0.958165006	0.999994883
transcription, DNA-templated (GO:0006351)	18/221	0.958174272	0.999994883
response to lipid (GO:0033993)	8/114	0.95834163	0.999994883
negative regulation of transcription, DNA-ten	93/948	0.95859877	0.999994883
regulation of NIK/NF-kappaB signaling (GO:19	29342	0.960315239	0.999994883
regulation of organelle organization (GO:003	29342	0.960315239	0.999994883
circulatory system development (GO:007235	9/126	0.960508097	0.999994883
regulation of peptidyl-tyrosine phosphorylati	33756	0.960821083	0.999994883
canonical Wnt signaling pathway (GO:006007	24929	0.960891995	0.999994883
negative regulation of transforming growth fa	24929	0.960891995	0.999994883
response to lipopolysaccharide (GO:0032496	12/159	0.960947233	0.999994883
cellular response to lectin (GO:1990858)	8/115	0.960996825	0.999994883
stimulatory C-type lectin receptor signaling p	8/115	0.960996825	0.999994883
potassium ion import across plasma membra	15373	0.961745179	0.999994883
regulation of chemokine production (GO:003	15373	0.961745179	0.999994883
regulation of extrinsic apoptotic signaling pat	15373	0.961745179	0.999994883
acute inflammatory response (GO:0002526)	44588	0.962975769	0.999994883
cellular response to unfolded protein (GO:00	44588	0.962975769	0.999994883
cellular senescence (GO:0090398)	44588	0.962975769	0.999994883
negative regulation of actin filament bundle a	44588	0.962975769	0.999994883
positive regulation of calcium ion transmemb	44588	0.962975769	0.999994883
regulation of epidermal growth factor-activat	44588	0.962975769	0.999994883
regulation of transcription elongation from R	44588	0.962975769	0.999994883
response to glucocorticoid (GO:0051384)	44588	0.962975769	0.999994883
stress-activated protein kinase signaling casca	44588	0.962975769	0.999994883
regulation of interleukin-8 production (GO:00	29707	0.963277109	0.999994883
blood vessel morphogenesis (GO:0048514)	20515	0.963294003	0.999994883
Rho protein signal transduction (GO:0007266	20515	0.963294003	0.999994883
sensory organ development (GO:0007423)	20515	0.963294003	0.999994883
cell chemotaxis (GO:0060326)	25294	0.964020737	0.999994883
peptidyl-tyrosine phosphorylation (GO:00181	25294	0.964020737	0.999994883
regulation of cellular component organizatio	10/139	0.964964818	0.999994883
positive regulation of protein kinase B signali	12/161	0.96518894	0.999994883
plasma membrane bounded cell projection o	9/128	0.965233856	0.999994883
natural killer cell activation (GO:0030101)	15738	0.965464812	0.999994883
negative regulation of type I interferon produ	15738	0.965464812	0.999994883
positive regulation of T cell differentiation (G	15738	0.965464812	0.999994883
regulation of cell-cell adhesion (GO:0022407)	15738	0.965464812	0.999994883
signal release from synapse (GO:0099643)	15738	0.965464812	0.999994883
nucleosome organization (GO:0034728)	34486	0.966166888	0.999994883
negative regulation of signal transduction (GC	22/267	0.966559059	0.999994883
cellular response to light stimulus (GO:00714	25659	0.966915379	0.999994883
neutrophil chemotaxis (GO:0030593)	25659	0.966915379	0.999994883
wound healing (GO:0042060)	25659	0.966915379	0.999994883
protein localization to cell periphery (GO:199	10/140	0.967068962	0.999994883

cellular zinc ion homeostasis (GO:0006882)	44589	0.967233504	0.999994883
mucosal immune response (GO:0002385)	44589	0.967233504	0.999994883
positive regulation of defense response to vi	44589	0.967233504	0.999994883
regulation of extrinsic apoptotic signaling pat	44589	0.967233504	0.999994883
regulation of insulin secretion involved in cell	44589	0.967233504	0.999994883
regulation of protein transport (GO:0051223)	44589	0.967233504	0.999994883
sarcomere organization (GO:0045214)	44589	0.967233504	0.999994883
negative regulation of cell population prolife	33/379	0.967499887	0.999994883
negative regulation of cellular process (GO:0	52/566	0.967646602	0.999994883
protein localization to membrane (GO:00726	15/195	0.968443004	0.999994883
positive regulation of cell differentiation (GO	21/258	0.968554753	0.999994883
antibacterial humoral response (GO:0019731	16103	0.968835072	0.999994883
cardiac ventricle morphogenesis (GO:000320	16103	0.968835072	0.999994883
lymphocyte chemotaxis (GO:0048247)	16103	0.968835072	0.999994883
neurogenesis (GO:0022008)	16103	0.968835072	0.999994883
neurotransmitter secretion (GO:0007269)	16103	0.968835072	0.999994883
positive regulation of biosynthetic process (G	16103	0.968835072	0.999994883
regulation of inflammatory response (GO:005	16/206	0.969060041	0.999994883
positive regulation of protein binding (GO:00	21245	0.969438097	0.999994883
regulation of neurotransmitter receptor activ	21245	0.969438097	0.999994883
regulation of primary metabolic process (GO:	9/130	0.969443926	0.999994883
cellular response to BMP stimulus (GO:00717	26024	0.969591681	0.999994883
regulation of endopeptidase activity (GO:005	26024	0.969591681	0.999994883
innate immune response activating cell surfa	8/119	0.97015798	0.999994883
nuclear export (GO:0051168)	30803	0.970984201	0.999994883
establishment of endothelial barrier (GO:006	44590	0.971001763	0.999994883
negative regulation of epithelial to mesenchy	44590	0.971001763	0.999994883
regulation of protein targeting to membrane	44590	0.971001763	0.999994883
regulation of T cell mediated cytotoxicity (GC	44590	0.971001763	0.999994883
response to zinc ion (GO:0010043)	44590	0.971001763	0.999994883
negative regulation of transmembrane recep	7/108	0.971287561	0.999994883
positive regulation of nervous system develo	16469	0.971887105	0.999994883
positive regulation of RNA metabolic process	16469	0.971887105	0.999994883
regulation of DNA repair (GO:0006282)	16469	0.971887105	0.999994883
positive regulation of neurogenesis (GO:0050	26390	0.972064538	0.999994883
macroautophagy (GO:0016236)	8/120	0.972119061	0.999994883
negative regulation of autophagy (GO:00105(	21610	0.972132168	0.999994883
protein polymerization (GO:0051258)	21610	0.972132168	0.999994883
negative regulation of defense response (GO	31168	0.973200076	0.999994883
positive regulation of protein catabolic proce	31168	0.973200076	0.999994883
transmembrane receptor protein tyrosine kir	35/404	0.973339511	0.999994883
MAPK cascade (GO:0000165)	25/303	0.973616668	0.999994883
extrinsic apoptotic signaling pathway via dea	44591	0.974336793	0.999994883
heterotypic cell-cell adhesion (GO:0034113)	44591	0.974336793	0.999994883
mRNA splice site selection (GO:0006376)	44591	0.974336793	0.999994883
negative regulation of Notch signaling pathw	44591	0.974336793	0.999994883
positive regulation of endopeptidase activity	44591	0.974336793	0.999994883

regulation of catecholamine secretion (GO:0(	44591	0.974336793	0.999994883
regulation of striated muscle contraction (GC	44591	0.974336793	0.999994883
respiratory tube development (GO:0030323)	44591	0.974336793	0.999994883
synaptic vesicle cycle (GO:0099504)	44591	0.974336793	0.999994883
TRIF-dependent toll-like receptor signaling pa	44591	0.974336793	0.999994883
zinc ion homeostasis (GO:0055069)	44591	0.974336793	0.999994883
granulocyte chemotaxis (GO:0071621)	26755	0.974347999	0.999994883
negative regulation of cell adhesion (GO:000	26755	0.974347999	0.999994883
regulation of Rho protein signal transduction	26755	0.974347999	0.999994883
regulation of synaptic transmission, glutamat	16834	0.974649511	0.999994883
transmembrane receptor protein serine/thre	9/133	0.974897276	0.999994883
positive regulation of interleukin-8 productio	22341	0.976859164	0.999994883
epidermal growth factor receptor signaling p	17199	0.977148524	0.999994883
regulation of synapse assembly (GO:0051963	17199	0.977148524	0.999994883
MyD88-independent toll-like receptor signali	44592	0.977288382	0.999994883
peptide cross-linking (GO:0018149)	44592	0.977288382	0.999994883
phospholipid translocation (GO:0045332)	44592	0.977288382	0.999994883
renal water homeostasis (GO:0003091)	44592	0.977288382	0.999994883
response to retinoic acid (GO:0032526)	22706	0.978926207	0.999994883
retrograde transport, endosome to Golgi (GC	32264	0.978938743	0.999994883
regulation of I-kappaB kinase/NF-kappaB sigr	17/224	0.97906799	0.999994883
nucleus organization (GO:0006997)	17564	0.979408174	0.999994883
regulation of interleukin-10 production (GO:(	17564	0.979408174	0.999994883
cell-cell adhesion via plasma-membrane adhe	12/170	0.979610356	0.999994883
axon guidance (GO:0007411)	15/203	0.979695521	0.999994883
7-methylguanosine mRNA capping (GO:0006	11689	0.9799006	0.999994883
7-methylguanosine RNA capping (GO:000945	11689	0.9799006	0.999994883
chondrocyte differentiation (GO:0002062)	11689	0.9799006	0.999994883
ERBB2 signaling pathway (GO:0038128)	11689	0.9799006	0.999994883
establishment or maintenance of epithelial c	11689	0.9799006	0.999994883
positive regulation of immune effector proce	11689	0.9799006	0.999994883
regulation of cellular amide metabolic proces	11689	0.9799006	0.999994883
regulation of cellular protein metabolic proce	17930	0.981450452	0.999994883
neutrophil migration (GO:1990266)	28216	0.981841037	0.999994883
positive regulation of histone modification (G	12055	0.98221245	0.999994883
regulation of interleukin-17 production (GO:(	12055	0.98221245	0.999994883
regulation of ERK1 and ERK2 cascade (GO:00	18/238	0.982450477	0.999994883
chloride transmembrane transport (GO:1902	18295	0.983295453	0.999994883
negative regulation of ERK1 and ERK2 cascad	18295	0.983295453	0.999994883
ribosome assembly (GO:0042255)	18295	0.983295453	0.999994883
antigen receptor-mediated signaling pathwa	13/185	0.983892587	0.999994883
cytosolic transport (GO:0016482)	7/116	0.983955815	0.999994883
axonogenesis (GO:0007409)	18/240	0.984238888	0.999994883
female gamete generation (GO:0007292)	12420	0.984258458	0.999994883
negative regulation of extrinsic apoptotic sigr	12420	0.984258458	0.999994883
regulation of keratinocyte differentiation (GC	12420	0.984258458	0.999994883
striated muscle tissue development (GO:001	12420	0.984258458	0.999994883

positive regulation of cytokine production (G	27/335	0.984341319	0.999994883
regulation of cellular macromolecule biosynt	40/468	0.984627408	0.999994883
regulation of ion transport (GO:0043269)	28946	0.984759493	0.999994883
regulation of lipid metabolic process (GO:001	33725	0.984815109	0.999994883
Wnt signaling pathway (GO:0016055)	33725	0.984815109	0.999994883
ERBB signaling pathway (GO:0038127)	24167	0.985562805	0.999994883
positive regulation of MAPK cascade (GO:004	21/274	0.985761293	0.999994883
regulation of epithelial cell proliferation (GO:	34090	0.986021435	0.999994883
cellular response to virus (GO:0098586)	12785	0.98606918	0.999994883
positive regulation of cell cycle G1/S phase tr	12785	0.98606918	0.999994883
respiratory system development (GO:006054	12785	0.98606918	0.999994883
response to exogenous dsRNA (GO:0043330)	12785	0.98606918	0.999994883
endocytic recycling (GO:0032456)	19025	0.986465419	0.999994883
response to peptide hormone (GO:0043434)	19025	0.986465419	0.999994883
calcium-dependent cell-cell adhesion via plas	13150	0.987671664	0.999994883
membrane assembly (GO:0071709)	13150	0.987671664	0.999994883
mitochondrion disassembly (GO:0061726)	13150	0.987671664	0.999994883
positive regulation of cytokine-mediated sign	13150	0.987671664	0.999994883
positive regulation of innate immune respons	13150	0.987671664	0.999994883
positive regulation of interferon-beta produc	13150	0.987671664	0.999994883
positive regulation of myeloid leukocyte diffe	13150	0.987671664	0.999994883
regulation of cardiac muscle contraction (GO	13150	0.987671664	0.999994883
interferon-gamma-mediated signaling pathw	24898	0.988076961	0.999994883
regulation of immune response (GO:005077(	12/179	0.98837376	0.999994883
DNA-templated transcription, initiation (GO:(	11/168	0.988699026	0.999994883
generation of neurons (GO:0048699)	14/202	0.988700136	0.999994883
regulation of cell adhesion (GO:0030155)	8/133	0.988874125	0.999994883
regulation of alternative mRNA splicing, via s	19756	0.98904631	0.999994883
glutamate receptor signaling pathway (GO:0(	13516	0.989089848	0.999994883
regulation of glucose import (GO:0046324)	13516	0.989089848	0.999994883
regulation of vesicle-mediated transport (GO	35186	0.989119927	0.999994883
DNA-templated transcription, elongation (GC	25263	0.989170407	0.999994883
RNA 3'-end processing (GO:0031123)	25263	0.989170407	0.999994883
translation (GO:0006412)	15/214	0.989266409	0.999994883
epidermis development (GO:0008544)	30407	0.989313954	0.999994883
skeletal system development (GO:0001501)	10/158	0.989850588	0.999994883
T cell receptor signaling pathway (GO:00508	10/158	0.989850588	0.999994883
lymphocyte proliferation (GO:0046651)	13881	0.990344919	0.999994883
mRNA destabilization (GO:0061157)	13881	0.990344919	0.999994883
cellular response to tumor necrosis factor (G	13/194	0.990770104	0.999994883
RNA splicing (GO:0008380)	35916	0.990810574	0.999994883
B cell activation (GO:0042113)	31138	0.991071414	0.999994883
gland development (GO:0048732)	25993	0.991074592	0.999994883
protein-containing complex disassembly (GO	20486	0.991144484	0.999994883
regulation of viral entry into host cell (GO:00	14246	0.991455631	0.999994883
regulation of protein kinase B signaling (GO:(	14/207	0.991687302	0.999994883
positive regulation of proteolysis (GO:00458(	20852	0.992040669	0.999994883

bone development (GO:0060348)	14611	0.992438581	0.999994883
synapse organization (GO:0050808)	7/126	0.992504685	0.999994883
chromatin assembly (GO:0031497)	26724	0.992653356	0.999994883
neurotransmitter transport (GO:0006836)	26724	0.992653356	0.999994883
cellular response to transforming growth fact	6/114	0.992877136	0.999994883
keratinocyte differentiation (GO:0030216)	14977	0.99330846	0.999994883
transcription initiation from RNA polymerase	8/140	0.993380157	0.999994883
protein deubiquitination (GO:0016579)	19/267	0.993559163	0.999994883
positive regulation of tyrosine phosphorylatic	21582	0.993574727	0.999994883
regulation of cation channel activity (GO:200	32599	0.993791909	0.999994883
transforming growth factor beta receptor sig	32599	0.993791909	0.999994883
modification-dependent protein catabolic pr	13/201	0.994109749	0.999994883
negative regulation of translation (GO:00171	32964	0.994335601	0.999994883
positive regulation of cellular process (GO:00	53/625	0.994557638	0.999994883
cellular response to interleukin-1 (GO:00713	9/155	0.994614247	0.999994883
RNA processing (GO:0006396)	11/179	0.994621092	0.999994883
cellular response to retinoic acid (GO:007130	15707	0.994759513	0.999994883
development of primary male sexual charact	15707	0.994759513	0.999994883
adenylate cyclase-activating G protein-couple	6/118	0.9948733	0.999994883
branching morphogenesis of an epithelial tub	16072	0.995362381	0.999994883
detection of chemical stimulus involved in se	16072	0.995362381	0.999994883
negative regulation of epidermal growth fact	16072	0.995362381	0.999994883
anterior/posterior pattern specification (GO:(	23043	0.995823905	0.999994883
negative regulation of endopeptidase activity	23043	0.995823905	0.999994883
neuropeptide signaling pathway (GO:000721	23043	0.995823905	0.999994883
positive regulation of Notch signaling pathwa	16438	0.995895883	0.999994883
regulation of receptor signaling pathway via J	16438	0.995895883	0.999994883
mRNA 3'-end processing (GO:0031124)	28915	0.995931706	0.999994883
positive regulation of I-kappaB kinase/NF-kap	10/171	0.995935294	0.999994883
antimicrobial humoral immune response me	23408	0.996252271	0.999994883
regulation of innate immune response (GO:0(	23408	0.996252271	0.999994883
ribonucleoprotein complex assembly (GO:00	7/136	0.996610577	0.999994883
regulation of nucleic acid-templated transcri	33/430	0.996628829	0.999994883
G protein-coupled receptor signaling pathwa	23774	0.99663734	0.999994883
neuron differentiation (GO:0030182)	10/174	0.996731365	0.999994883
peptide biosynthetic process (GO:0043043)	9/162	0.996802492	0.999994883
response to cytokine (GO:0034097)	8/150	0.99692811	0.999994883
negative regulation of inflammatory respons	13/212	0.997166851	0.999994883
regulation of gene expression (GO:0010468)	97/1079	0.99719636	0.999994883
regulation of Notch signaling pathway (GO:0(	30376	0.99727106	0.999994883
transcription elongation from RNA polymera	24504	0.997294327	0.999994883
ncRNA processing (GO:0034470)	12/201	0.997333807	0.999994883
regulation of interferon-beta production (GO	17899	0.997482666	0.999994883
enzyme linked receptor protein signaling pat	7/140	0.997552346	0.999994883
negative regulation of immune response (GO	10/178	0.997564656	0.999994883
regulation of tyrosine phosphorylation of STA	24869	0.997573623	0.999994883
positive regulation of nucleic acid-templated	40/511	0.997629106	0.999994883

chromatin organization (GO:0006325)	7/142	0.997923311	0.999994883
response to interleukin-1 (GO:0070555)	31472	0.997982303	0.999994883
protein modification by small protein remova	18/276	0.998075677	0.999994883
gene expression (GO:0010467)	25/356	0.998233756	0.999994883
chromatin remodeling (GO:0006338)	4/103	0.998322905	0.999994883
negative regulation of response to external s	5/118	0.998415162	0.999994883
cardiac muscle tissue development (GO:0048	19360	0.998455675	0.999994883
epidermal cell differentiation (GO:0009913)	19360	0.998455675	0.999994883
defense response to Gram-negative bacteriu	26696	0.998596037	0.999994883
response to molecule of bacterial origin (GO:	26696	0.998596037	0.999994883
regulation of mRNA splicing, via spliceosome	32933	0.998655005	0.999994883
fibroblast growth factor receptor signaling pa	27426	0.998873077	0.999994883
negative regulation of inflammatory respons	6/136	0.998896502	0.999994883
cellular response to fibroblast growth factor	33664	0.998903128	0.999994883
regulation of inflammatory response to antig	6/137	0.998989115	0.999994883
ribosomal large subunit biogenesis (GO:0042	20821	0.999052248	0.999994883
inflammatory response (GO:0006954)	13/230	0.999195023	0.999994883
anterograde trans-synaptic signaling (GO:009	14/244	0.999292744	0.999994883
skin development (GO:0043588)	29252	0.999350742	0.999994883
B cell differentiation (GO:0030183)	22282	0.999417973	0.999994883
regulation of neurogenesis (GO:0050767)	22647	0.999484683	0.999994883
transcription by RNA polymerase II (GO:0006	20/320	0.99948746	0.999994883
positive regulation of intracellular signal tran	40/546	0.999573969	0.999994883
positive regulation of transcription, DNA-tem	102/1183	0.999581772	0.999994883
positive regulation of cell population prolifer	33/474	0.999661461	0.999994883
ribosome biogenesis (GO:0042254)	9/192	0.999699699	0.999994883
cellular response to interferon-gamma (GO:0	4/121	0.999706942	0.999994883
defense response to symbiont (GO:0140546)	4/124	0.99978167	0.999994883
defense response to Gram-positive bacterium	25569	0.999804582	0.999994883
response to tumor necrosis factor (GO:00346	3/110	0.999828654	0.999994883
cell junction organization (GO:0034330)	26299	0.999846357	0.999994883
cotranslational protein targeting to membrar	34366	0.99986186	0.999994883
nuclear-transcribed mRNA catabolic process,	3/113	0.999874282	0.999994883
defense response to virus (GO:0051607)	4/133	0.999909474	0.999994883
positive regulation of transcription by RNA p	71/908	0.999913318	0.999994883
RNA splicing, via transesterification reactions	12/251	0.999934141	0.999994883
response to interferon-gamma (GO:0034341	29221	0.99994034	0.999994883
phospholipase C-activating G protein-couple	29587	0.999946846	0.999994883
chemical synaptic transmission (GO:0007268	16/306	0.999948915	0.999994883
nuclear-transcribed mRNA catabolic process	6/171	0.999951317	0.999994883
rRNA processing (GO:0006364)	6/173	0.999959017	0.999994883
lymphocyte differentiation (GO:0030098)	30682	0.999962191	0.999994883
mRNA splicing, via spliceosome (GO:0000398	13/274	0.999967501	0.999994883
defense response to bacterium (GO:0042742	6/176	0.999968172	0.999994883
regulation of cell population proliferation (G	55/764	0.999970926	0.999994883
rRNA metabolic process (GO:0016072)	5/162	0.999972237	0.999994883
adenylate cyclase-modulating G protein-coup	5/165	0.99997834	0.999994883

SRP-dependent cotranslational protein targe	32874	0.999980142	0.999994883
mRNA processing (GO:0006397)	14/300	0.999985225	0.999994883
regulation of transcription, DNA-templated ((	197/2244	0.999987354	0.999994883
cytokine-mediated signaling pathway (GO:00	40/621	0.999987896	0.999994883
sensory perception of chemical stimulus (GO	36161	0.99999112	0.999994883
regulation of transcription by RNA polymeras	188/2206	0.999991194	0.999994883
protein targeting to ER (GO:0045047)	1/103	0.999993207	0.999994883
cellular response to cytokine stimulus (GO:0(	22/482	0.999994384	0.999994883
innate immune response (GO:0045087)	11/302	0.999994883	0.999994883

ıalysis of significant highly-correlated RNA-seq-based modules (blue; Significan

Old P-value	Old Adjusted P-value	Odds Ratio	Combined Score	Genes	KEGG
0	0	8.766291231	334.2498805	ABCD4;AC/	.
0	0	3.030701457	102.7281621	DYNC2I2;D	.
0	0	3.102052021	105.0470961	DCLRE1B;N	.
0	0	9.829000843	315.4306841	ABCD4;GCI	.
0	0	7.508259912	194.7044649	DCLRE1B;D	.
0	0	2.762084955	68.97822484	DCLRE1B;F	.
0	0	2.930632598	69.56983626	DYNC2I2;D	.
0	0	5.031856796	112.3160904	FEN1;BLM;	.
0	0	4.402576937	97.93436231	BLM;FEN1;	.
0	0	6.130258997	134.8251673	ABCD4;AC/	.
0	0	3.139760684	63.54303684	DCLRE1B;D	.
0	0	7.76592007	155.3099935	DYNC2I2;D	.
0	0	2.490731728	49.56501048	DYNC2I2;D	.
0	0	2.252634334	42.93274461	FEN1;MCM	.
0	0	6.040421793	108.0650671	RFC5;MBD	.
0	0	3.408515694	58.40615456	CPM;SLC4(	.
0	0	7.325657895	121.9945554	RFC5;MBD	.
0	0	3.590919887	56.79325056	CETN2;CEP	.
0	0	61.86806466	942.5012295	MCEE;MM	.
0	0	3.131589505	43.60912426	BLM;FEN1;	.
0	0	3.42374374	45.30117331	CETN2;CEP	.
0	0	106218	1379839.372	TCTN2;TCT	.
0	0	5.391990546	69.66830602	RFC5;RFC3	.
0	0	5.391990546	69.66830602	GEN1;ZRAI	.
0	0	9.460192476	120.9822326	ACAD8;MC	.
0	0	9.460192476	120.9822326	ACAD8;MC	.
0	0	1.844512163	23.54100156	DYNC2I2;D	.
0	0	2.673324315	31.89960031	PSMD10;P	.
0	0	2.704443805	31.94972107	ABCD3;AA	.
0	0	11.6020542	134.852937	ACOT8;AM	.
0	0	2.198995402	25.36660553	CCNJ;CETN	.
0	0	2.82479266	31.58693124	CETN2;OG	.
0	0	6.19273523	68.04639586	DCTD;RRM	.
0	0	2.985847779	32.53659264	GCDH;ECH	.
0	0	88515	958135.3914	DCXR;AKR1	.
0	0	88515	958135.3914	DCXR;AKR1	.
0	0	88515	958135.3914	DCXR;AKR1	.
0	0	12.37081695	132.354171	MBD4;NEIl	.
0	0	18.0349345	192.7178479	GCDH;ACA	.
0	0	18.0349345	192.7178479	ABCA2;CN	.
0	0	18.0349345	192.7178479	BLM;RTEL1	.
0	0	4.713858577	48.9154733	RFC5;RFC3	.
0	0	3.874780702	40.18170499	BLM;RTEL1	.
0	0	4.149320771	41.10721676	GEN1;ZRAI	.

0	0	23.17896115	228.6584902	MBD4;NEIL
0	0	23.17896115	228.6584902	MCEE;MM
0	0	2.297803992	22.22597777	PSMD10;C
0	0	2.331227915	22.53302032	AASDH;GL(
0	0	4.574371119	43.46457186	INVS;TTC2(
0	0	8.835299257	82.18892731	CIDEA;PLIN
0	0	2.960600735	27.53146857	ABCD4;MC
0	0	6.959659091	63.60064248	UGDH;GNF
0	0	4.014600672	36.40587783	GALT;PMM
0	0	3.37705803	30.52454462	DCLRE1B;B
0	0	3.067795215	27.36668567	MCFD2;AL(
0	0	2.329466255	20.7793054	CETN2;CEP
0	0	15.45176779	137.0445756	MCCC2;BTI
0	0	15.45176779	137.0445756	RFC5;RFC3
0	0	15.45176779	137.0445756	RFC5;RFC3
0	0	2.306271209	20.23670839	CETN2;CEP
0	0	2.034841072	17.64110258	PSMD10;C
0	0	3.737308744	31.73189383	GSTM1;GS
0	0	4.727690289	39.9285104	MSH6;RNA
0	0	2.818381443	23.66132371	RFC5;FEN1
0	0	9.015938865	75.19271222	DYNC2I2;D
0	0	6.871122761	56.24276599	SLC25A1;G
0	0	11.5881711	93.34879843	IMPACT;SE
0	0	2.066379089	16.1268278	AHCTF1;IN
0	0	6.183660987	47.63533242	DCLRE1B;G
0	0	2.049731449	15.75156483	ACHE;SLC2
0	0	2.862023265	21.42428965	ACOT8;OSI
0	0	4.051618548	30.20755397	ABCD4;SLC
0	0	2.240510788	16.67889493	HACD1;PPI
0	0	2.12941695	15.40363634	POGLUT1;I
0	0	30.88006978	220.6577689	SLC27A1;F
0	0	12.87085515	91.37562389	SLC46A1;A
0	0	12.87085515	91.37562389	ABHD10;FU
0	0	12.87085515	91.37562389	GSTZ1;PDP
0	0	12.87085515	91.37562389	GSTZ1;PDP
0	0	12.87085515	91.37562389	BLM;WRN;
0	0	4.638461538	32.57830159	RFC5;RFC3
0	0	4.069684487	28.13120301	DDB1;PARI
0	0	3.438074398	23.68130847	GEN1;RAD
0	0	3.438074398	23.68130847	CENPX;CEN
0	0	5.152468327	35.33122501	SLC27A1;F
0	0	7.724574422	52.36032864	ACOT8;GN
0	0	7.724574422	52.36032864	TMLHE;AC
0	0	3.865981635	25.57099115	BBS1;TTC8
0	0	2.488920579	16.23470003	NCAPG2;SI
0	0	4.755855765	30.83144038	RFC5;RFC3
0	0	4.755855765	30.83144038	ABCD4;ARV

0	0	4.755855765	30.83144038	DDB1;PARI.
0	0	4.755855765	30.83144038	DDB1;PARI.
0	0	9.652595986	61.66004937	GSTZ1;QDI.
0	0	9.652595986	61.66004937	SLC27A1;G.
0	0	4.092297408	26.04842477	MBD4;NEIl.
0	0	3.402589676	21.6085644	GGA2;BBS.
0	0	5.408340611	34.22668937	DDB1;PCG.
0	0	6.620689655	41.45357753	UGDH;SLC.
0	0	6.620689655	41.45357753	DDB1;POL.
0	0	3.093741794	19.10382545	ZRANB3;M.
0	0	15.43916267	94.8400082	PIGS;PIGU;.
0	0	15.43916267	94.8400082	GNPDA1;N.
0	0	15.43916267	94.8400082	PPARG;TRE.
0	0	15.43916267	94.8400082	CCDC88A;C.
0	0	15.43916267	94.8400082	RTEL1;SLX4.
0	0	4.415902141	27.09564167	GSTZ1;GST.
0	0	4.415902141	27.09564167	GSTZ1;GST.
0	0	4.415902141	27.09564167	DDB1;PARI.
0	0	4.415902141	27.09564167	DPY19L1;B.
0	0	3.27153577	19.97526797	MAP10;SP.
0	0	3.514131256	21.31196412	BRIP1;CHE.
0	0	2.873204904	17.40331214	BBS2;BBS1.
0	0	2.298761249	13.91320524	CPM;GSTM.
0	0	4.916395395	29.20110325	GINS1;POL.
0	0	4.916395395	29.20110325	B4GAT1;PC.
0	0	1.975574378	11.73240909	AHCTF1;IN.
0	0	3.15018956	18.49749486	PRIM2;POI.
0	0	3.15018956	18.49749486	ZNHIT1;CE.
0	0	3.36115283	19.53041137	ABCD4;HA.
0	0	5.79277608	33.61650193	HADHB;HA.
0	0	5.79277608	33.61650193	ADK;GMPS.
0	0	7.721640489	44.73823294	IMPACT;PK.
0	0	7.721640489	44.73823294	TREM2;AD.
0	0	7.721640489	44.73823294	GINS1;POL.
0	0	7.721640489	44.73823294	GNPDA1;N.
0	0	7.721640489	44.73823294	ABCA2;NE.
0	0	7.721640489	44.73823294	GCSH;SHM.
0	0	2.900054705	16.66474255	MAP10;SP.
0	0	2.717588867	15.39737332	SLC27A1;P.
0	0	4.506441048	25.16072905	ABCD4;SLC.
0	0	4.506441048	25.16072905	PLK4;STIL;A.
0	0	3.220922606	17.93784181	LATS1;SGO.
0	0	1.936949824	10.74439538	VKORC1L1.
0	0	3.477862762	19.19256413	SLC46A1;S.
0	0	3.477862762	19.19256413	PRDX2;PRI.
0	0	3.863477501	21.29767177	AGBL5;VKC.
0	0	2.028351648	11.14377041	RALBP1;DN.

0	0	2.518513991	13.71195407	SLC46A1;A
0	0	2.417698291	13.12582177	LRSAM1;N
0	0	5.1488433	27.77104776	GEN1;RAD
0	0	5.1488433	27.77104776	IMPACT;PK
0	0	5.1488433	27.77104776	COQ3;AIFM
0	0	10.29219363	55.48409681	GNPDA1;N
0	0	10.29219363	55.48409681	SLC27A1;T
0	0	10.29219363	55.48409681	DNMT1;PD
0	0	10.29219363	55.48409681	GSTM1;GS
0	0	2.032529657	10.82144122	MAP10;GE
0	0	2.57793345	13.66706323	ARSA;ABCA
0	0	6.434336824	34.01512639	BLM;WRN;
0	0	6.434336824	34.01512639	ACSS3;BDH
0	0	6.434336824	34.01512639	BLM;WRN;
0	0	6.434336824	34.01512639	BLM;WRN;
0	0	6.434336824	34.01512639	GNPDA1;N
0	0	2.461135667	12.98862647	HACD1;PPI
0	0	3.312062937	17.44624021	CENPX;CEN
0	0	3.312062937	17.44624021	CENPX;CEN
0	0	4.159556601	21.86072029	MBD4;NEIL
0	0	4.159556601	21.86072029	GGCT;SLC2
0	0	2.651028446	13.68915659	DCLRE1B;B
0	0	1.831063608	9.32656466	SLC48A1;C
0	0	1.639787611	8.33465671	GPI;GDE1;I
0	0	2.743092597	13.8054988	RFC5;RFC3
0	0	3.161335823	15.90159424	PLA2G15;S
0	0	3.161335823	15.90159424	ACBD6;ACO
0	0	3.161335823	15.90159424	ACBD6;ACO
0	0	4.633697076	23.28274267	BLM;WRN;
0	0	4.633697076	23.28274267	NXT1;XPO1
0	0	4.633697076	23.28274267	ENTPD5;AH
0	0	2.577242888	12.84490258	BLM;WRN;
0	0	2.577242888	12.84490258	SLC27A1;P
0	0	3.433813893	17.05888329	ZRANB3;BL
0	0	3.433813893	17.05888329	DDB1;PARI
0	0	2.862556479	14.06016668	ATP6V1A;D
0	0	5.514834206	26.72442848	GNPDA1;N
0	0	5.514834206	26.72442848	GCSH;SHM
0	0	5.514834206	26.72442848	GMPS;ADS
0	0	2.657220582	12.87286238	RFC5;POLA
0	0	1.448648555	6.962778846	LRSAM1;TH
0	0	3.023715415	14.52919797	CENPX;CEN
0	0	7.718709115	36.99326563	PLA2G15;G
0	0	7.718709115	36.99326563	DDT;STAP1
0	0	7.718709115	36.99326563	WNK1;WN
0	0	7.718709115	36.99326563	DNMT1;NH
0	0	7.718709115	36.99326563	CHRNB1;PI

0	0	2.133970279	10.07650335	HACD1;PPI.
0	0	3.252902899	15.35553848	CYP27A1;A.
0	0	2.760166157	13.00745834	PCGF6;CBX.
0	0	4.212213801	19.75555457	ALG8;ALG9.
0	0	3.604541485	16.84200888	RFC5;RFC3.
0	0	1.255181003	5.831780606	PGAP1;LRR.
0	0	2.897563374	13.30485296	CYP27A1;A.
0	0	1.910896404	8.753717265	VKORC1L1.
0	0	2.664837236	12.05125314	BRIP1;CHE.
0	0	3.090083006	13.86807003	SLC27A1;SI.
0	0	3.090083006	13.86807003	ALG8;RRM.
0	0	4.825207243	21.51303002	ALG8;ALG9.
0	0	4.825207243	21.51303002	GNPDA1;N.
0	0	3.379066594	14.90790808	DCTD;AK1;.
0	0	3.379066594	14.90790808	DDB1;PARI.
0	0	3.860977739	16.93050125	IMPACT;PK.
0	0	3.860977739	16.93050125	BCAS3;KAN.
0	0	3.860977739	16.93050125	MORN4;RT.
0	0	11.57432432	50.58341126	TMLHE;AC.
0	0	11.57432432	50.58341126	TMLHE;AC.
0	0	11.57432432	50.58341126	POLA1;PRI.
0	0	11.57432432	50.58341126	RAD51;FAN.
0	0	11.57432432	50.58341126	GSTZ1;QDP.
0	0	11.57432432	50.58341126	NAAA;GDE.
0	0	11.57432432	50.58341126	OXCT1;FITI.
0	0	11.57432432	50.58341126	SLC46A1;A.
0	0	11.57432432	50.58341126	GSTZ1;QDP.
0	0	11.57432432	50.58341126	MCCC2;IVD.
0	0	11.57432432	50.58341126	NAAA;GDE.
0	0	11.57432432	50.58341126	DDT;STAP1.
0	0	11.57432432	50.58341126	LGALS3;LG.
0	0	11.57432432	50.58341126	RAD51;XRC.
0	0	11.57432432	50.58341126	CCDC88A;E.
0	0	11.57432432	50.58341126	GRN;ALOX.
0	0	1.397359381	6.093824225	DGKA;TSSK.
0	0	1.826059912	7.922018374	TSPYL2;WV.
0	0	2.318993435	10.03749921	CASP9;ACE.
0	0	6.174618404	26.54698737	ERI1;ERI2;E.
0	0	6.174618404	26.54698737	ERI1;ERI2;E.
0	0	6.174618404	26.54698737	ALDH3A2;F.
0	0	6.174618404	26.54698737	GALE;GALT.
0	0	6.174618404	26.54698737	ACSS3;BDH.
0	0	6.174618404	26.54698737	CYB5A;CYB.
0	0	6.174618404	26.54698737	ABHD4;NA.
0	0	6.174618404	26.54698737	AK1;CMPK.
0	0	6.174618404	26.54698737	AK1;CMPK.
0	0	6.174618404	26.54698737	AK1;CMPK.

0	0	6.174618404	26.54698737	CIDEA;PLIN.
0	0	1.962634197	8.400843867	MAP10;PLI.
0	0	2.942769768	12.56200937	BDH2;HEPI.
0	0	1.745317916	7.339255534	CD63;SPAR.
0	0	2.674371302	11.22339043	TCHP;CDK1.
0	0	2.492630154	10.38576042	PCGF6;CBX.
0	0	2.361439195	9.831979829	SMPD3;NE.
0	0	4.288830716	17.64567295	NCEH1;DH.
0	0	4.288830716	17.64567295	AK1;CMPK.
0	0	4.288830716	17.64567295	AK1;CMPK.
0	0	4.288830716	17.64567295	AGO4;TUT.
0	0	4.288830716	17.64567295	RNF128;GL.
0	0	4.288830716	17.64567295	COQ3;PDS.
0	0	4.288830716	17.64567295	NDUFA5;E.
0	0	3.563777994	14.63169486	ACER2;ABC.
0	0	3.563777994	14.63169486	DCLRE1B;D.
0	0	2.808848644	11.40956683	GGA2;BBS2.
0	0	1.999720451	8.088160835	RFC5;RFC3.
0	0	2.575174825	10.33544	DCLRE1B;R.
0	0	1.933252959	7.714156656	PIGQ;GDE1.
0	0	2.042165638	8.146450568	SLC25A1;S.
0	0	1.580439851	6.286567717	PI4K2B;MT.
0	0	3.003275109	11.83993386	ABCD4;AC.
0	0	2.093503722	8.245993463	ATP6V1A;S.
0	0	2.093503722	8.245993463	RFC5;RFC3.
0	0	1.569671789	6.130713085	PSMD10;C.
0	0	5.145224597	19.97672504	DIP2A;MLY.
0	0	5.145224597	19.97672504	NEU3;GM2.
0	0	5.145224597	19.97672504	SLC27A1;C.
0	0	5.145224597	19.97672504	SGPL1;FUC.
0	0	5.145224597	19.97672504	PRDX2;PRD.
0	0	5.145224597	19.97672504	ERI1;ERI2;E.
0	0	5.145224597	19.97672504	MFAP4;FEI.
0	0	2.686572834	10.38811898	ACER2;PM.
0	0	2.686572834	10.38811898	RBL1;NEK4.
0	0	2.686572834	10.38811898	STAR;SRD5.
0	0	3.309035356	12.73587535	SLC46A1;M.
0	0	3.309035356	12.73587535	CCDC57;TU.
0	0	2.483063811	9.532734934	ACBD6;MC.
0	0	2.483063811	9.532734934	CENPX;CEN.
0	0	2.483063811	9.532734934	DNMT1;PD.
0	0	1.318728005	5.057568996	TSSK1B;AA.
0	0	3.859729494	14.69088408	OXSM;ACA.
0	0	3.859729494	14.69088408	KIAA0586;.
0	0	3.859729494	14.69088408	COQ3;PDS.
0	0	1.770629489	6.723173808	GALNT12;C.
0	0	1.738340908	6.577449925	ABCA2;SLC.

0	0	7.715780296	29.05719477	ABHD10;EI
0	0	7.715780296	29.05719477	XRCC5;NU(
0	0	7.715780296	29.05719477	QDPR;KYA
0	0	7.715780296	29.05719477	GALE;GALT
0	0	7.715780296	29.05719477	GMDS;PMI
0	0	7.715780296	29.05719477	FUCA1;FU(
0	0	7.715780296	29.05719477	FUCA1;FU(
0	0	7.715780296	29.05719477	RPS6KA5;N
0	0	7.715780296	29.05719477	ILVBL;ACAI
0	0	7.715780296	29.05719477	KANK1;ABI
0	0	7.715780296	29.05719477	SHMT2;GN
0	0	7.715780296	29.05719477	ETAA1;RFV
0	0	7.715780296	29.05719477	MMP3;NO
0	0	7.715780296	29.05719477	ATP2B4;TX
0	0	2.845047116	10.61262524	NEU3;ABC/
0	0	2.17941988	8.105554763	ATP6V1A;T
0	0	1.901050272	7.035325442	ABCA2;GDI
0	0	2.574486675	9.479084988	PIGS;PIGU;
0	0	3.088258402	11.15434898	PRDX2;PRI
0	0	3.088258402	11.15434898	MSR1;ARV
0	0	3.088258402	11.15434898	GRN;DMXL
0	0	1.870282152	6.718789642	TMEM161/
0	0	1.870282152	6.718789642	ACBD6;AC(
0	0	2.124814086	7.611171503	STX12;MSF
0	0	2.124814086	7.611171503	CASP9;MSI
0	0	1.970021634	7.027887488	ABCA2;ABI
0	0	2.207258417	7.817502965	TTC26;SPA
0	0	2.702641921	9.544013436	PLA2G15;A
0	0	2.702641921	9.544013436	TCHP;KANI
0	0	2.702641921	9.544013436	ABCD4;ALI
0	0	3.508646676	12.38009998	ACER2;NEU
0	0	3.508646676	12.38009998	SLCO2B1;B
0	0	3.508646676	12.38009998	RTEL1;RAD
0	0	3.508646676	12.38009998	SLCO2B1;B
0	0	3.508646676	12.38009998	GMPS;ADS
0	0	3.508646676	12.38009998	SCARB2;PI
0	0	3.508646676	12.38009998	SMPD3;SPI
0	0	3.508646676	12.38009998	BCAS3;KAN
0	0	3.508646676	12.38009998	ACADVL;FA
0	0	3.508646676	12.38009998	SLX4;CENP
0	0	4.409943306	15.54132076	PPP1R3C;G
0	0	4.409943306	15.54132076	PRDX2;PRI
0	0	4.409943306	15.54132076	ABCA2;CN
0	0	4.409943306	15.54132076	CCNF;TRIM
0	0	4.409943306	15.54132076	ORC3;DON
0	0	4.409943306	15.54132076	SMPD3;SPI
0	0	4.409943306	15.54132076	SMPD3;SPI

0	0	4.409943306	15.54132076	RAD50;RAI.
0	0	1.537016025	5.416426455	POGLUT1;(.
0	0	2.015831034	7.067697383	ATP6V1A;S .
0	0	1.932027145	6.668080453	ABHD4;ABI .
0	0	2.072871989	7.151515532	CLIP3;LGAI .
0	0	2.072871989	7.151515532	TRPM2;SH .
0	0	2.145824224	7.298727063	RFC5;RFC3 .
0	0	2.895078568	9.82183541	SLC25A1;G .
0	0	2.242386646	7.541781176	SLC25A1;G .
0	0	2.242386646	7.541781176	PIGU;SCCP .
0	0	2.242386646	7.541781176	GALNS;TST .
0	0	2.573799127	8.60849937	CDK4;PDGI .
0	0	2.573799127	8.60849937	SCARB2;RN .
0	0	2.573799127	8.60849937	ACADVL;AI .
0	0	2.376180395	7.939274771	TWIST1;PP .
0	0	5.786508282	19.06363776	HADHB;HA .
0	0	5.786508282	19.06363776	NEU3;GM2 .
0	0	5.786508282	19.06363776	SLC48A1;A .
0	0	5.786508282	19.06363776	GPI;VWF;H .
0	0	5.786508282	19.06363776	AHI1;CITED .
0	0	5.786508282	19.06363776	MCCC2;IVD .
0	0	5.786508282	19.06363776	AGO4;DICE .
0	0	5.786508282	19.06363776	TRIM37;CD .
0	0	5.786508282	19.06363776	MDFIC;RAE .
0	0	5.786508282	19.06363776	MDFIC;RAE .
0	0	5.786508282	19.06363776	KANK1;ABI .
0	0	5.786508282	19.06363776	SHMT2;GN .
0	0	5.786508282	19.06363776	CD63;LOXL .
0	0	5.786508282	19.06363776	WNK1;WN .
0	0	5.786508282	19.06363776	ARL3;WDR .
0	0	5.786508282	19.06363776	MAPKBP1; .
0	0	5.786508282	19.06363776	DENND1A; .
0	0	5.786508282	19.06363776	NFATC3;PD .
0	0	5.786508282	19.06363776	ABCD4;AB(.
0	0	1.78365806	5.858946981	STX8;ATP2 .
0	0	3.216077661	10.53817717	ACER2;QDI .
0	0	3.216077661	10.53817717	POLA1;RFC .
0	0	3.216077661	10.53817717	DDB1;KDM .
0	0	3.216077661	10.53817717	SLC46A1;C .
0	0	3.216077661	10.53817717	RBL1;AKT3 .
0	0	3.216077661	10.53817717	PARP1;PRK .
0	0	1.931619256	6.312669327	HIPK4;SBK1 .
0	0	3.858482338	12.39259088	GALNS;GLE .
0	0	3.858482338	12.39259088	GCDH;HYK .
0	0	3.858482338	12.39259088	GCDH;HYK .
0	0	3.858482338	12.39259088	MGME1;PA .
0	0	3.858482338	12.39259088	TCHP;CDK1 .

0	0	3.858482338	12.39259088	DDT;STAP1.
0	0	3.858482338	12.39259088	CLIP3;TBCI.
0	0	3.858482338	12.39259088	GGCT;BDH.
0	0	3.858482338	12.39259088	SCIN;PICK1.
0	0	3.858482338	12.39259088	SPHK2;NA/.
0	0	1.803197547	5.777801599	ATP6V1A;N.
0	0	1.976235529	6.324913072	NDST1;UGI.
0	0	2.724625773	8.689337957	CCDC88A;T.
0	0	2.724625773	8.689337957	CEMIP2;AE.
0	0	2.724625773	8.689337957	RAD51B;A.
0	0	2.724625773	8.689337957	ABHD10;PI.
0	0	1.365035929	4.348183673	CPM;CUL7.
0	0	2.28804427	7.28489116	LIPT1;MINI.
0	0	2.28804427	7.28489116	SESN3;RRA.
0	0	2.28804427	7.28489116	TTC26;STIL.
0	0	2.456669313	7.785474442	ALDH3A2;/.
0	0	1.773536402	5.506398198	ATP6V1A;N.
0	0	2.106246027	6.489405161	NDUFA5;C.
0	0	2.106246027	6.489405161	RTEL1;SLF1.
0	0	2.968519264	9.046484812	BACE1;ACH.
0	0	2.968519264	9.046484812	EPS8;TRPM.
0	0	2.968519264	9.046484812	CEMIP2;HE.
0	0	2.968519264	9.046484812	ODAD1;OD.
0	0	2.968519264	9.046484812	PARP1;PRK.
0	0	2.968519264	9.046484812	GSTM1;GS.
0	0	2.968519264	9.046484812	RTEL1;SLX4.
0	0	1.85414442	5.647286493	SLC25A1;G.
0	0	2.206203582	6.694823854	P2RX7;WN.
0	0	1.980424473	5.967749127	CYP27A1;A.
0	0	2.349724701	7.058185561	GSTZ1;KYA.
0	0	2.349724701	7.058185561	CCDC57;TU.
0	0	2.349724701	7.058185561	CD63;KCNI.
0	0	2.573112178	7.719447843	PARP1;PRK.
0	0	2.573112178	7.719447843	EPS8;KANK.
0	0	1.888188976	5.605606908	GALNS;CEN.
0	0	3.429568251	10.07147516	ACOT8;HSI.
0	0	3.429568251	10.07147516	NASP;HAT1.
0	0	3.429568251	10.07147516	CNTNAP1;I.
0	0	3.429568251	10.07147516	RBL1;AKT3.
0	0	3.429568251	10.07147516	ZRANB3;BI.
0	0	3.429568251	10.07147516	MDFIC;RAE.
0	0	3.429568251	10.07147516	CIB1;IGF1;I.
0	0	3.429568251	10.07147516	CIB1;IGF1;I.
0	0	3.429568251	10.07147516	LGALS3;SP.
0	0	3.429568251	10.07147516	NEK4;MIF;.
0	0	1.679876539	4.892398903	NEK7;HAU.
0	0	4.628945074	13.47968695	PON2;PDX.

0	0	4.628945074	13.47968695	ATP2B4;SIF.
0	0	4.628945074	13.47968695	HGF;SIRT2;.
0	0	4.628945074	13.47968695	CHEK2;CHE.
0	0	4.628945074	13.47968695	MFAP4;TN .
0	0	4.628945074	13.47968695	PEX6;HACL.
0	0	4.628945074	13.47968695	SORD;AKR.
0	0	4.628945074	13.47968695	PCGF6;TRI.
0	0	4.628945074	13.47968695	SLC27A1;C .
0	0	4.628945074	13.47968695	MSRA;MTH.
0	0	4.628945074	13.47968695	MGME1;P(.
0	0	4.628945074	13.47968695	PRKCA;TRE.
0	0	4.628945074	13.47968695	HDAC6;SIR .
0	0	4.628945074	13.47968695	CHPT1;PLA.
0	0	4.628945074	13.47968695	SMC6;RAD .
0	0	4.628945074	13.47968695	LGALS3;LG .
0	0	4.628945074	13.47968695	APOA4;ABI.
0	0	4.628945074	13.47968695	ORC3;MCM.
0	0	4.628945074	13.47968695	MTRES1;SH.
0	0	4.628945074	13.47968695	WNK1;WN .
0	0	4.628945074	13.47968695	ZRANB3;BL.
0	0	4.628945074	13.47968695	ATP2B4;SIF.
0	0	4.628945074	13.47968695	HGF;SIRT2;.
0	0	4.628945074	13.47968695	MSH6;PMS.
0	0	2.13000708	6.161332813	P2RX7;LGA.
0	0	2.13000708	6.161332813	TRPM2;BC.
0	0	2.13000708	6.161332813	MOB1B;IM.
0	0	1.562452132	4.48559876	B4GALT2;S.
0	0	2.25169214	6.412892949	GSTM1;GS.
0	0	2.25169214	6.412892949	SLC27A1;SI.
0	0	1.782629187	5.059104994	TOM1L2;P(.
0	0	2.756326353	7.822104824	GCDH;HYK .
0	0	2.756326353	7.822104824	MSRA;MTH.
0	0	2.756326353	7.822104824	SPR;SPHK2.
0	0	2.756326353	7.822104824	BLM;RAD5 .
0	0	2.756326353	7.822104824	SLC46A1;M.
0	0	2.756326353	7.822104824	NDST1;UGI.
0	0	2.756326353	7.822104824	BCAS3;CDK.
0	0	2.756326353	7.822104824	CBR1;PTGE.
0	0	1.424891559	4.035642654	CD63;SPAF.
0	0	1.731573465	4.895000022	SHMT2;PKI.
0	0	1.6557844	4.678371218	GOLPH3L;C.
0	0	2.437547382	6.883169992	LGALS3;SPI.
0	0	1.985664336	5.605922437	TRPM2;SLC.
0	0	1.985664336	5.605922437	SLC25A1;G.
0	0	1.985664336	5.605922437	MAP10;RA .
0	0	1.985664336	5.605922437	CD63;AHI1.
0	0	1.482003078	4.175524405	PSMD10;P.

0	0	1.883605106	5.235860238	ABCA2;CCI
0	0	2.058890345	5.677803566	EPM2A;SE
0	0	1.515668191	4.163441468	CBR1;STIL;
0	0	1.748895586	4.790646768	SCARB2;AC
0	0	2.161502183	5.838236853	ODAD1;DN
0	0	2.161502183	5.838236853	PKIB;RTEL1
0	0	2.161502183	5.838236853	GEN1;STIL;
0	0	2.161502183	5.838236853	BCAS3;RIP
0	0	2.161502183	5.838236853	NPAT;KLF1
0	0	3.086436982	8.309617421	TRPM2;AT
0	0	3.086436982	8.309617421	ACOT8;QP
0	0	3.086436982	8.309617421	C1QTNF1;F
0	0	3.086436982	8.309617421	SESN3;BM
0	0	3.086436982	8.309617421	NDC1;AHC
0	0	3.086436982	8.309617421	WNK1;WN
0	0	3.086436982	8.309617421	NFU1;MAG
0	0	3.086436982	8.309617421	PKIB;MST1
0	0	3.086436982	8.309617421	POGLUT1;T
0	0	3.086436982	8.309617421	BLM;XRCC
0	0	1.4108376	3.793434535	ATP23;ATP
0	0	1.281834604	3.43919183	LRR1;DSCC
0	0	1.838653258	4.908615295	ODAD1;DN
0	0	2.315539066	6.157727863	TRPM2;PD
0	0	2.315539066	6.157727863	STN1;SLX4
0	0	1.6096078	4.27944298	MCUR1;MC
0	0	1.638713017	4.340817645	ABCD3;SRI
0	0	2.572425829	6.805524457	ABCA2;NEI
0	0	2.572425829	6.805524457	ITGB3;TRE
0	0	2.572425829	6.805524457	RAD51B;CI
0	0	2.572425829	6.805524457	AGO4;ZC3I
0	0	2.572425829	6.805524457	GMPS;ADS
0	0	2.572425829	6.805524457	CUL7;PDXF
0	0	2.572425829	6.805524457	ABCA2;MN
0	0	1.716411379	4.537726753	PSMD10;C
0	0	1.23236973	3.25343448	GPI;GHDC;
0	0	1.992361786	5.238555063	BCAS3;RIP
0	0	1.427297032	3.708564515	SLC27A1;C
0	0	3.857236269	10.00372234	BACE1;APH
0	0	3.857236269	10.00372234	RTN4RL2;F
0	0	3.857236269	10.00372234	HSD17B14
0	0	3.857236269	10.00372234	PFKL;ALDO
0	0	3.857236269	10.00372234	GSTM1;AL
0	0	3.857236269	10.00372234	GSTM1;AL
0	0	3.857236269	10.00372234	P2RX7;UBA
0	0	3.857236269	10.00372234	C1QTNF1;C
0	0	3.857236269	10.00372234	NFATC3;PI
0	0	3.857236269	10.00372234	PEX6;HACL

0	0	3.857236269	10.00372234	MED25;ZN
0	0	3.857236269	10.00372234	DAG1;EMI
0	0	3.857236269	10.00372234	MCUR1;AT
0	0	3.857236269	10.00372234	ANKRD39;I
0	0	3.857236269	10.00372234	SHMT2;GM
0	0	3.857236269	10.00372234	RINT1;PGA
0	0	3.857236269	10.00372234	GAS6;IER3I
0	0	3.857236269	10.00372234	MST1;BRC/
0	0	3.857236269	10.00372234	GPC1;KLHL
0	0	3.857236269	10.00372234	CLU;HDAC(
0	0	3.857236269	10.00372234	AGO4;DICE
0	0	1.878118503	4.859170713	OAT;MTHF
0	0	1.878118503	4.859170713	MED25;CD
0	0	1.795792192	4.604279865	TSPYL2;CCI
0	0	2.078249916	5.324755552	B4GALT2;G
0	0	2.078249916	5.324755552	P2RX7;ATL
0	0	1.483119164	3.736904105	SLF1;TFRC;
0	0	1.220322447	3.063721958	GPI;GHDC;
0	0	1.929991263	4.83868503	NXT1;XPO1
0	0	1.929991263	4.83868503	MSH6;BCA
0	0	1.929991263	4.83868503	CLIP3;TBCI
0	0	2.205150589	5.525014325	PLA2G15;A
0	0	1.458141712	3.618946297	PI4K2B;MT
0	0	1.828590817	4.529050825	TFAP4;E2F
0	0	2.805693217	6.940605635	DIP2A;MLY
0	0	2.805693217	6.940605635	STAR;FDX1
0	0	2.805693217	6.940605635	TRPM2;ATI
0	0	2.805693217	6.940605635	P2RX7;P2R
0	0	2.805693217	6.940605635	NDUFA5;E
0	0	2.805693217	6.940605635	ALOX5;MG
0	0	2.805693217	6.940605635	CYB5R3;M
0	0	2.805693217	6.940605635	XRCC5;PO1
0	0	2.805693217	6.940605635	NEU3;DAB
0	0	2.805693217	6.940605635	TNFSF18;C
0	0	2.411512871	5.953050704	SRD5A1;SP
0	0	2.411512871	5.953050704	UGDH;GPC
0	0	2.411512871	5.953050704	MSR1;CIDE
0	0	2.411512871	5.953050704	DNMT1;PD
0	0	2.411512871	5.953050704	ABCA2;AC/
0	0	1.526036339	3.733480009	LIPT1;CPM
0	0	2.001164483	4.864514415	DNAI4;TTC
0	0	2.001164483	4.864514415	PSMD10;V
0	0	2.001164483	4.864514415	STIL;KDM2
0	0	2.001164483	4.864514415	SLF1;MRNI
0	0	1.364343094	3.300483821	SLC27A1;SI
0	0	1.211436862	2.92759495	GPI;GHDC;
0	0	1.492499003	3.582710139	RARS2;FAS

0	0	1.399760386	3.351387104	H2AZ1;BLM
0	0	1.87140077	4.473944619	GPI;NEU3;
0	0	1.87140077	4.473944619	SLC27A1;A
0	0	1.87140077	4.473944619	LRSAM1;SL
0	0	1.781603012	4.2242183	PRKCG;SLF
0	0	1.781603012	4.2242183	CLIP3;DAB
0	0	1.665482991	3.941972535	DCLRE1B;D
0	0	1.665482991	3.941972535	WWTR1;UI
0	0	1.715784871	4.056949439	PLA2G15;A
0	0	2.104797429	4.970478527	PPP1R3C;G
0	0	2.104797429	4.970478527	PIGU;PGAF
0	0	2.104797429	4.970478527	LRSAM1;M
0	0	2.104797429	4.970478527	ACTN3;ATF
0	0	2.104797429	4.970478527	NTNG2;SH
0	0	2.104797429	4.970478527	NTNG2;CC
0	0	2.104797429	4.970478527	CRCP;ICE2;
0	0	1.260955763	2.97180249	FEN1;BLM;
0	0	1.475645575	3.442665381	NDC1;LIPT
0	0	3.306015693	7.680184205	QDPR;KYA
0	0	3.306015693	7.680184205	MCUR1;MC
0	0	3.306015693	7.680184205	SESN3;SES
0	0	3.306015693	7.680184205	NASP;HAT
0	0	3.306015693	7.680184205	NASP;HAT
0	0	3.306015693	7.680184205	DHRS7B;CH
0	0	3.306015693	7.680184205	ARL6IP5;SL
0	0	3.306015693	7.680184205	UNC119;PF
0	0	3.306015693	7.680184205	IMPACT;CI
0	0	3.306015693	7.680184205	RTN4RL2;F
0	0	3.306015693	7.680184205	NDC1;AHC
0	0	3.306015693	7.680184205	YBX1;CKAP
0	0	3.306015693	7.680184205	PLA2G15;P
0	0	3.306015693	7.680184205	CARMIL1;P
0	0	3.306015693	7.680184205	DROSHA;D
0	0	3.306015693	7.680184205	RACGAP1;I
0	0	3.306015693	7.680184205	ETAA1;RFV
0	0	3.306015693	7.680184205	CDH3;CLO
0	0	3.306015693	7.680184205	CNPY2;TRE
0	0	3.306015693	7.680184205	MST1;MTL
0	0	3.306015693	7.680184205	RANGRF;CI
0	0	3.306015693	7.680184205	THRA;HMG
0	0	3.306015693	7.680184205	SESN3;SES
0	0	3.306015693	7.680184205	DCLRE1B;D
0	0	3.306015693	7.680184205	SLC25A15;
0	0	1.568704849	3.622273983	ACHE;SLC2
0	0	1.489095356	3.433488801	ZRANB3;FE
0	0	2.269530849	5.231970002	FECH;COX1
0	0	2.269530849	5.231970002	SHTN1;GO

0	0	2.269530849	5.231970002	DDT;MST1 .
0	0	2.269530849	5.231970002	SCARB2;NF .
0	0	1.597675998	3.661754274	CYP27A1;A .
0	0	1.816256778	4.140636142	TRPM2;ATI .
0	0	1.816256778	4.140636142	ODAD3;STI .
0	0	1.816256778	4.140636142	DNAJB2;M .
0	0	2.571740078	5.856306561	DFFA;DNA' .
0	0	2.571740078	5.856306561	GSTZ1;QDF .
0	0	2.571740078	5.856306561	GNPDA1;N .
0	0	2.571740078	5.856306561	C1QTNF1;F .
0	0	2.571740078	5.856306561	PSMD10;H .
0	0	2.571740078	5.856306561	STIL;ALDH1 .
0	0	2.571740078	5.856306561	CYB5R3;M' .
0	0	2.571740078	5.856306561	RRAGB;RRA .
0	0	2.571740078	5.856306561	ACER2;SGF .
0	0	5.1416122	11.63167952	TRIM37;HD .
0	0	5.1416122	11.63167952	GPAM;ACP .
0	0	5.1416122	11.63167952	TNFSF4;HM .
0	0	5.1416122	11.63167952	AKR1B1;SL .
0	0	5.1416122	11.63167952	GAS6;FOLR .
0	0	5.1416122	11.63167952	PLK4;CCDC .
0	0	5.1416122	11.63167952	PLK4;CCDC .
0	0	5.1416122	11.63167952	RRM1;RRM .
0	0	5.1416122	11.63167952	SLX4;SLX1A .
0	0	5.1416122	11.63167952	GLRX2;DCT .
0	0	5.1416122	11.63167952	SLX4;SLX1A .
0	0	5.1416122	11.63167952	SLC46A1;SI .
0	0	5.1416122	11.63167952	POT1;BRCA .
0	0	5.1416122	11.63167952	CRTAM;CC .
0	0	5.1416122	11.63167952	SLC27A1;SI .
0	0	5.1416122	11.63167952	PRKCA;VRK .
0	0	5.1416122	11.63167952	ADI1;MRI1 .
0	0	5.1416122	11.63167952	AHI1;CITED .
0	0	5.1416122	11.63167952	MSH6;MSH .
0	0	5.1416122	11.63167952	MGME1;PA .
0	0	5.1416122	11.63167952	VGLL4;TP7 .
0	0	5.1416122	11.63167952	SCAP;SOD1 .
0	0	5.1416122	11.63167952	SCAP;SOD1 .
0	0	5.1416122	11.63167952	PARK7;MM .
0	0	5.1416122	11.63167952	MMP3;HDA .
0	0	5.1416122	11.63167952	LAG3;TNFS .
0	0	5.1416122	11.63167952	DNMT1;IGI .
0	0	5.1416122	11.63167952	ABCA2;ORI .
0	0	5.1416122	11.63167952	SCAP;SOD1 .
0	0	5.1416122	11.63167952	KIF3A;KIFA .
0	0	5.1416122	11.63167952	DAG1;CLA' .
0	0	5.1416122	11.63167952	CCL19;IGF1 .

0	0	5.1416122	11.63167952	CNPY2;PPA
0	0	5.1416122	11.63167952	HMGB1;RT
0	0	5.1416122	11.63167952	IMPACT;EI
0	0	5.1416122	11.63167952	PDCD4;PP/
0	0	5.1416122	11.63167952	GCSH;LIPT
0	0	5.1416122	11.63167952	IMMP1L;IN
0	0	5.1416122	11.63167952	CMPK1;DH
0	0	5.1416122	11.63167952	APLP1;PRK
0	0	5.1416122	11.63167952	CARMIL1;C
0	0	5.1416122	11.63167952	DAG1;CLA
0	0	5.1416122	11.63167952	CD63;ATP2
0	0	5.1416122	11.63167952	APOA4;PR/
0	0	5.1416122	11.63167952	ABCA2;AR\
0	0	5.1416122	11.63167952	TST;MRPL1
0	0	5.1416122	11.63167952	TST;MRPL1
0	0	5.1416122	11.63167952	SUCLG2;AC
0	0	5.1416122	11.63167952	CRCP;POLF
0	0	1.522878841	3.433767493	KLF11;CAM
0	0	1.404798978	3.145132959	PI4K2B;BC/
0	0	1.433564188	3.202836877	MCUR1;M(
0	0	2.01317063	4.482312981	ODAD3;STI
0	0	2.01317063	4.482312981	ZC3H7B;AC
0	0	2.01317063	4.482312981	HPF1;PARF
0	0	2.01317063	4.482312981	SYNGR1;DI
0	0	1.570507733	3.472423557	EPM2A;TB(
0	0	1.862942328	4.077981281	ZRANB3;M
0	0	1.862942328	4.077981281	WWTR1;AI
0	0	1.862942328	4.077981281	CD63;AHI1
0	0	1.862942328	4.077981281	ATP6V1A;T
0	0	1.862942328	4.077981281	TFRC;HEPH
0	0	1.501642576	3.277475697	ABCA2;SLC
0	0	1.642586683	3.580840789	TOM1L2;C
0	0	1.694503667	3.681491249	CYP27A1;A
0	0	2.143324607	4.617366025	PLA2G15;G
0	0	2.143324607	4.617366025	PLA2G15;G
0	0	2.143324607	4.617366025	SLC45A3;P
0	0	2.143324607	4.617366025	ZWILCH;IN
0	0	2.143324607	4.617366025	MMP3;SIR
0	0	2.143324607	4.617366025	RAD50;RAI
0	0	2.143324607	4.617366025	CD63;AHI1
0	0	2.143324607	4.617366025	ABCA2;AC/
0	0	2.143324607	4.617366025	PKIB;RTEL1
0	0	1.303679239	2.757895637	ANP32A;M
0	0	1.572688831	3.320220143	SH3RF3;LR
0	0	1.436905478	3.028811626	GSKIP;ATP
0	0	1.225600718	2.576241043	CD63;STX1
0	0	1.929179398	4.050851137	MCFD2;FU

0	0	2.373779731	4.983735379	BACE1;APH
0	0	2.373779731	4.983735379	SLC45A3;SI
0	0	2.373779731	4.983735379	PDCD4;PPA
0	0	2.373779731	4.983735379	PSMD10;PI
0	0	2.373779731	4.983735379	PKIB;RTEL1
0	0	2.373779731	4.983735379	TMEM120I
0	0	2.373779731	4.983735379	SFRP4;TWS
0	0	2.373779731	4.983735379	AGO4;DRO
0	0	1.608275033	3.366085502	NDUFA11;I
0	0	1.608275033	3.366085502	NDUFA11;I
0	0	1.608275033	3.366085502	MLLT11;RA
0	0	2.892600262	6.04628545	PPP3CA;PP
0	0	2.892600262	6.04628545	MMP3;MM
0	0	2.892600262	6.04628545	CBR1;PTGE
0	0	2.892600262	6.04628545	GGCT;MGS
0	0	2.892600262	6.04628545	PLA2G15;D
0	0	2.892600262	6.04628545	HGF;MST1
0	0	2.892600262	6.04628545	ABHD10;PI
0	0	2.892600262	6.04628545	UNC119;PI
0	0	2.892600262	6.04628545	IMMP1L;IM
0	0	2.892600262	6.04628545	NUBPL;MY
0	0	2.892600262	6.04628545	PDE1B;PIR
0	0	2.892600262	6.04628545	P2RX7;UBA
0	0	2.892600262	6.04628545	C1QTNF1;C
0	0	2.892600262	6.04628545	CRTAP;P4H
0	0	2.892600262	6.04628545	PLEKHM1;S
0	0	2.892600262	6.04628545	PRKD3;PIC
0	0	2.892600262	6.04628545	TTLL4;CEP4
0	0	2.892600262	6.04628545	SPHK2;ALC
0	0	2.892600262	6.04628545	SPHK2;CHE
0	0	2.892600262	6.04628545	KANK1;ARI
0	0	2.892600262	6.04628545	RBL2;RBL1
0	0	2.892600262	6.04628545	SYNGR1;DI
0	0	2.892600262	6.04628545	CDH3;GIPC
0	0	2.892600262	6.04628545	VAT1;TFRC
0	0	2.892600262	6.04628545	PDK4;PDK2
0	0	2.892600262	6.04628545	GNG2;TNF
0	0	1.498209478	3.122341108	CARMIL1;L
0	0	1.654064685	3.439725529	STK36;SUF
0	0	1.800742358	3.741155342	GPAM;SPH
0	0	1.800742358	3.741155342	LATS1;GPA
0	0	1.800742358	3.741155342	NDC1;XPO
0	0	1.336157015	2.772175453	PRKCG;HIP
0	0	2.030403233	4.089972462	DFFA;ACVR
0	0	2.030403233	4.089972462	STAR;FDX1
0	0	2.030403233	4.089972462	GNG2;APLI
0	0	2.030403233	4.089972462	NTNG2;MP

0	0	2.030403233	4.089972462	DDB1;KDM
0	0	2.030403233	4.089972462	FECH;COX1
0	0	2.030403233	4.089972462	P2RX7;ENT
0	0	2.030403233	4.089972462	MSRA;MTH
0	0	1.476093283	2.972184204	ABCA2;SPH
0	0	1.430032136	2.876627689	ATP6V1A;S
0	0	1.575363858	3.165294283	MDC1;RIN
0	0	1.615506586	3.215445818	CLIP3;LGAI
0	0	1.851907464	3.668114971	CCDC88A;F
0	0	1.851907464	3.668114971	IDUA;GLB1
0	0	1.851907464	3.668114971	PSMD10;R
0	0	1.851907464	3.668114971	MCFD2;FU
0	0	1.851907464	3.668114971	UGDH;CHS
0	0	1.851907464	3.668114971	LATS1;SFRI
0	0	1.851907464	3.668114971	STIL;MTHF
0	0	1.441331581	2.851206773	FBXW4;PSI
0	0	1.742555289	3.436179506	SHTN1;GO
0	0	1.381975993	2.710624215	EPM2A;AT
0	0	1.516349519	2.964834181	HIPK4;SBK
0	0	1.454618138	2.829507992	PSMD10;B
0	0	2.204099433	4.272053809	GIPC1;ARL
0	0	2.204099433	4.272053809	BLM;RAD5
0	0	2.204099433	4.272053809	BBS2;MYO
0	0	2.204099433	4.272053809	KIF18A;KIF
0	0	2.204099433	4.272053809	GSTP1;PEL
0	0	2.204099433	4.272053809	RRM1;MTH
0	0	2.204099433	4.272053809	BBS2;MYO
0	0	2.204099433	4.272053809	SLC45A3;A
0	0	2.204099433	4.272053809	NEDD1;STI
0	0	2.204099433	4.272053809	C1QTNF1;C
0	0	2.204099433	4.272053809	AKT3;PPAR
0	0	2.204099433	4.272053809	SLC9A9;SL
0	0	3.855991285	7.456679646	SLC26A1;P
0	0	3.855991285	7.456679646	CASP9;BOK
0	0	3.855991285	7.456679646	SLC22A5;SI
0	0	3.855991285	7.456679646	AKR1B1;RC
0	0	3.855991285	7.456679646	DHRS7B;PE
0	0	3.855991285	7.456679646	STARD5;CD
0	0	3.855991285	7.456679646	CRTAM;CC
0	0	3.855991285	7.456679646	UGDH;ME
0	0	3.855991285	7.456679646	DHRS7B;PE
0	0	3.855991285	7.456679646	DUOX2;SO
0	0	3.855991285	7.456679646	TRIM37;HD
0	0	3.855991285	7.456679646	HPS4;RAB3
0	0	3.855991285	7.456679646	ATP23;TMI
0	0	3.855991285	7.456679646	POLA1;GIN
0	0	3.855991285	7.456679646	VGLL4;TP7

0	0	3.855991285	7.456679646	E2F1;TREM
0	0	3.855991285	7.456679646	CLOCK;ARN
0	0	3.855991285	7.456679646	DNMT1;DN
0	0	3.855991285	7.456679646	RACGAP1;I
0	0	3.855991285	7.456679646	POLA1;GIN
0	0	3.855991285	7.456679646	KIF3A;KIFA
0	0	3.855991285	7.456679646	SCAP;LDLR
0	0	3.855991285	7.456679646	P2RX7;WN
0	0	3.855991285	7.456679646	TREM2;LDI
0	0	3.855991285	7.456679646	STAP1;TRE
0	0	3.855991285	7.456679646	CDC7;DBF4
0	0	3.855991285	7.456679646	CD86;TNFS
0	0	3.855991285	7.456679646	UBE2D4;UI
0	0	3.855991285	7.456679646	UBE2D4;UI
0	0	3.855991285	7.456679646	BBIP1;SPA
0	0	3.855991285	7.456679646	MSRA;MSF
0	0	3.855991285	7.456679646	QDPR;SPR
0	0	3.855991285	7.456679646	SLC26A1;P
0	0	3.855991285	7.456679646	ATL3;LNPK
0	0	3.855991285	7.456679646	PDGFB;GA
0	0	3.855991285	7.456679646	LGALS3;HA
0	0	3.855991285	7.456679646	STARD5;CD
0	0	3.855991285	7.456679646	GSTZ1;FAH
0	0	3.855991285	7.456679646	ALDH6A1;I
0	0	1.211685475	2.337400014	GRN;ITSN1
0	0	1.388234019	2.672203573	BCAS3;RAL
0	0	1.422286004	2.722117737	NDUFA11;I
0	0	1.578701128	3.007182092	TSPYL2;AC
0	0	1.349595505	2.547740147	BLM;ATL3;
0	0	2.571054926	4.852948904	PPP3CA;PP
0	0	2.571054926	4.852948904	CDC7;MCM
0	0	2.571054926	4.852948904	EPS8;SPAS
0	0	2.571054926	4.852948904	P2RX3;PKD
0	0	2.571054926	4.852948904	ARL6IP5;G
0	0	2.571054926	4.852948904	DAG1;GCC
0	0	2.571054926	4.852948904	GSTP1;DUS
0	0	2.571054926	4.852948904	CCL19;GAS
0	0	2.571054926	4.852948904	DLG4;WDR
0	0	2.571054926	4.852948904	GSTO1;CLI
0	0	2.571054926	4.852948904	GSTO1;CLI
0	0	2.571054926	4.852948904	FUT8;GALT
0	0	2.571054926	4.852948904	CARMIL1;C
0	0	2.571054926	4.852948904	WNK1;WN
0	0	2.571054926	4.852948904	PEX6;PEX1
0	0	2.571054926	4.852948904	ZWILCH;ZW
0	0	2.571054926	4.852948904	DCTD;THTI
0	0	2.571054926	4.852948904	MED25;ZN

0	0	2.571054926	4.852948904	LGALS3;LG .
0	0	2.571054926	4.852948904	BLM;GMNI .
0	0	2.571054926	4.852948904	LANCL1;MI .
0	0	2.571054926	4.852948904	APOA4;ABI .
0	0	2.571054926	4.852948904	CHEK2;CHE .
0	0	1.624703962	3.062744905	RTEL1;MRI .
0	0	1.928773997	3.634690646	TPST1;SLC2 .
0	0	1.928773997	3.634690646	ALDH3A2;(.
0	0	1.928773997	3.634690646	ABCA2;ARV .
0	0	1.433756567	2.693899442	ACOT8;GST .
0	0	1.333973182	2.499260521	MYBPC3;C .
0	0	1.688004913	3.15946878	ABCA2;EDI .
0	0	1.688004913	3.15946878	PPIP5K1;G .
0	0	1.780579525	3.327471093	CLIP3;TBCI .
0	0	1.780579525	3.327471093	PRDX2;PRI .
0	0	1.372731258	2.562931086	CPM;ATP2 .
0	0	1.372731258	2.562931086	PLK4;CUL7 .
0	0	1.513413411	2.801520373	RBL1;UBAS .
0	0	1.513413411	2.801520373	MSH6;ZRA .
0	0	1.543531469	2.813611189	MAP10;CLI .
0	0	1.543531469	2.813611189	PRKCG;USI .
0	0	1.263245349	2.301171953	DCTN5;MC .
0	0	1.463895677	2.649614716	ACHE;BCAS .
0	0	1.123026681	2.02115481	TFRC;CITEI .
0	0	1.582955271	2.845289397	MINPP1;PI .
0	0	2.057043175	3.684896299	BBS2;MYO .
0	0	2.057043175	3.684896299	BRAT1;ATI .
0	0	2.057043175	3.684896299	FUT8;MGA .
0	0	2.057043175	3.684896299	LATS1;MDI .
0	0	2.057043175	3.684896299	NUP35;CBI .
0	0	2.057043175	3.684896299	NDC1;P2RX .
0	0	2.057043175	3.684896299	SLC27A1;A .
0	0	2.057043175	3.684896299	MMP3;TRE .
0	0	2.057043175	3.684896299	P2RX7;P2R .
0	0	1.323738482	2.360161451	POGLUT1;S .
0	0	1.636760619	2.907920263	LIPT1;CYB5 .
0	0	1.362427179	2.413574276	SLC27A1;SI .
0	0	1.836823735	3.23954525	ACER2;RAI .
0	0	1.836823735	3.23954525	LATS1;MOI .
0	0	1.836823735	3.23954525	MTHFD1;S .
0	0	1.714535137	3.023366414	ITGB3;TREI .
0	0	1.714535137	3.023366414	GGCT;AIFM .
0	0	1.714535137	3.023366414	GRN;ACP4; .
0	0	1.714535137	3.023366414	RINT1;BLM .
0	0	1.714535137	3.023366414	ACHE;SLC2 .
0	0	1.714535137	3.023366414	P2RX7;ACT .
0	0	1.714535137	3.023366414	ALDH3A2;I .

0	0	1.714535137	3.023366414	ABCA2;EEF
0	0	1.509890924	2.633539569	FUT8;MGA
0	0	1.543294015	2.6448335	GRAMD1B
0	0	1.543294015	2.6448335	MINPP1;PF
0	0	1.543294015	2.6448335	NTNG2;PA
0	0	1.403381739	2.404819077	PSMD10;LC
0	0	2.313818657	3.955350344	NUBPL;MY
0	0	2.313818657	3.955350344	PICK1;TREI
0	0	2.313818657	3.955350344	LATS1;SUF
0	0	2.313818657	3.955350344	HACD1;HA
0	0	2.313818657	3.955350344	PPP1R3C;G
0	0	2.313818657	3.955350344	SLC27A1;SI
0	0	2.313818657	3.955350344	PPP1R3C;G
0	0	2.313818657	3.955350344	ARV1;STAR
0	0	2.313818657	3.955350344	FER1L5;GR
0	0	2.313818657	3.955350344	HGF;PARK7
0	0	2.313818657	3.955350344	ABCA5;ITG
0	0	2.313818657	3.955350344	SHTN1;SEM
0	0	2.313818657	3.955350344	DIP2A;RAP
0	0	2.313818657	3.955350344	EPS8;PLEKI
0	0	2.313818657	3.955350344	AKT3;HMG
0	0	2.313818657	3.955350344	KRT10;PKD
0	0	2.313818657	3.955350344	ALMS1;ASA
0	0	2.313818657	3.955350344	GEN1;XRCC
0	0	2.313818657	3.955350344	PARK7;RAF
0	0	2.313818657	3.955350344	MMP3;TXN
0	0	2.313818657	3.955350344	ACER2;ABC
0	0	2.313818657	3.955350344	ACER2;ABC
0	0	2.313818657	3.955350344	HACD1;HA
0	0	1.267895686	2.164552047	RFC5;BLM;
0	0	1.456138469	2.482219808	LATS1;NAS
0	0	1.456138469	2.482219808	RTEL1;WRI
0	0	1.374601156	2.32573708	GPI;BCAS3
0	0	1.588530696	2.678837249	SLC25A1;G
0	0	1.588530696	2.678837249	RRAGB;RRA
0	0	1.588530696	2.678837249	PSMD10;M
0	0	1.414938758	2.369488523	HACD1;ABC
0	0	1.414938758	2.369488523	FARP2;PAR
0	0	3.084618736	5.161868477	PDXP;HOG
0	0	3.084618736	5.161868477	CROT;CPT1
0	0	3.084618736	5.161868477	STX17;ATG
0	0	3.084618736	5.161868477	P2RX7;PMI
0	0	3.084618736	5.161868477	CAB39;SLC
0	0	3.084618736	5.161868477	PM20D1;T
0	0	3.084618736	5.161868477	ALOX5;PDC
0	0	3.084618736	5.161868477	GNG2;TNF
0	0	3.084618736	5.161868477	ABCC5;SLC

0	0	3.084618736	5.161868477	FLAD1;ACP
0	0	3.084618736	5.161868477	BLM;WRN
0	0	3.084618736	5.161868477	MYO1E;FO
0	0	3.084618736	5.161868477	GALE;GALT
0	0	3.084618736	5.161868477	ALOX5;PD(
0	0	3.084618736	5.161868477	ADI1;MRI1
0	0	3.084618736	5.161868477	SPAST;COR
0	0	3.084618736	5.161868477	MGME1;P/
0	0	3.084618736	5.161868477	CCL19;GAS
0	0	3.084618736	5.161868477	ABCA2;ITG
0	0	3.084618736	5.161868477	QPRT;NMN
0	0	3.084618736	5.161868477	APH1B;PSE
0	0	3.084618736	5.161868477	DCXR;XYLB
0	0	3.084618736	5.161868477	CD209;AB(
0	0	3.084618736	5.161868477	AGTPBP1;/
0	0	3.084618736	5.161868477	MSH6;POT
0	0	3.084618736	5.161868477	PRKCA;SAS
0	0	3.084618736	5.161868477	TOMM7;H
0	0	3.084618736	5.161868477	GEN1;XRC(
0	0	3.084618736	5.161868477	MMP3;SOI
0	0	3.084618736	5.161868477	GEN1;XRC(
0	0	3.084618736	5.161868477	GSTO1;ATF
0	0	3.084618736	5.161868477	DCLRE1B;D
0	0	3.084618736	5.161868477	ATP23;TMI
0	0	3.084618736	5.161868477	CMPK1;DH
0	0	3.084618736	5.161868477	TPK1;DHOI
0	0	3.084618736	5.161868477	DDB1;HAC
0	0	3.084618736	5.161868477	E2F1;TREM
0	0	3.084618736	5.161868477	PRKCA;TRE
0	0	3.084618736	5.161868477	CLOCK;ARN
0	0	3.084618736	5.161868477	SVBP;TIMP
0	0	3.084618736	5.161868477	PPP2CB;G/
0	0	3.084618736	5.161868477	STPG1;CAM
0	0	3.084618736	5.161868477	TREM2;PA
0	0	3.084618736	5.161868477	TNFSF4;CC
0	0	3.084618736	5.161868477	FLAD1;ACP
0	0	3.084618736	5.161868477	SFXN3;SFX
0	0	3.084618736	5.161868477	THTPA;TPK
0	0	1.653208206	2.751122903	PLA2G15;S
0	0	1.653208206	2.751122903	PPP3CC;YV
0	0	1.653208206	2.751122903	NDC1;XPO
0	0	1.653208206	2.751122903	NDC1;XPO
0	0	1.928368949	3.195652057	PPP1R3C;G
0	0	1.928368949	3.195652057	AGTPBP1;(
0	0	1.928368949	3.195652057	TUT4;DRO
0	0	1.928368949	3.195652057	PSMD10;P
0	0	1.928368949	3.195652057	CCDC78;M

0	0	1.183955933	1.961752412	ITSN1;PSEI.
0	0	1.753232588	2.89493516	DLG4;PICK .
0	0	1.753232588	2.89493516	GSTO1;GN .
0	0	1.753232588	2.89493516	CLIP3;KANI.
0	0	1.753232588	2.89493516	SETD4;SUV.
0	0	1.753232588	2.89493516	CCDC57;PF.
0	0	1.429091969	2.337300128	PSMD10;P.
0	0	1.429091969	2.337300128	DDB1;LRSA.
0	0	1.429091969	2.337300128	TCHP;CCD(.
0	0	1.505567454	2.459837255	NDST1;UGI.
0	0	1.505567454	2.459837255	NEU3;FUTE.
0	0	1.505567454	2.459837255	TRPM2;IM .
0	0	1.391664157	2.241206816	CLIP3;KANI.
0	0	1.391664157	2.241206816	BLM;MRNI .
0	0	1.446814904	2.309680641	SLC27A1;S.
0	0	1.140400371	1.802081357	ABCD4;PI4 .
0	0	1.596110718	2.506776691	ATP6V1A;D.
0	0	1.596110718	2.506776691	RBL2;RBL1 .
0	0	1.596110718	2.506776691	CD86;SASH.
0	0	1.596110718	2.506776691	CD19;PDGI.
0	0	1.403028978	2.201291152	CYP27A1;A.
0	0	1.317767593	2.062706948	MRPS22;M.
0	0	1.300899073	2.025078354	EEFSEC;MF.
0	0	2.103352619	3.264146795	PHYH;IDH1.
0	0	2.103352619	3.264146795	BACE1;APH.
0	0	2.103352619	3.264146795	CD9;PPARC.
0	0	2.103352619	3.264146795	CROT;PPCD.
0	0	2.103352619	3.264146795	SCAP;SEC2 .
0	0	2.103352619	3.264146795	PARP2;HLC .
0	0	2.103352619	3.264146795	PSMD10;SI.
0	0	2.103352619	3.264146795	PSMD10;T.
0	0	2.103352619	3.264146795	GRN;TREM.
0	0	2.103352619	3.264146795	NFATC3;PD.
0	0	2.103352619	3.264146795	LAG3;TNFS.
0	0	2.103352619	3.264146795	ENTPD5;EN.
0	0	2.103352619	3.264146795	PPP2CB;PP.
0	0	2.103352619	3.264146795	GKAP1;ECH.
0	0	2.103352619	3.264146795	DDB1;SLC4.
0	0	2.103352619	3.264146795	ABCA2;IGF .
0	0	2.103352619	3.264146795	DAB2;RBPI.
0	0	2.103352619	3.264146795	CD86;TNFS.
0	0	2.103352619	3.264146795	CD86;DENI.
0	0	2.103352619	3.264146795	ZWILCH;ZW.
0	0	2.103352619	3.264146795	PUDP;TK1; .
0	0	2.103352619	3.264146795	NTNG2;TRI.
0	0	2.103352619	3.264146795	CD63;LOXL.
0	0	2.103352619	3.264146795	WFS1;ALO.

0	0	2.103352619	3.264146795	MMP3;MM.
0	0	2.103352619	3.264146795	SPP1;HSD1.
0	0	2.103352619	3.264146795	SLC26A1;R.
0	0	1.28649715	1.994307691	PI4K2B;MT.
0	0	1.369140349	2.12012538	ALDH3A2;S.
0	0	1.676910236	2.593087301	MCUR1;MC.
0	0	1.676910236	2.593087301	ARL6IP5;SL.
0	0	1.676910236	2.593087301	ATP6V1A;A.
0	0	1.676910236	2.593087301	CD19;PDGI.
0	0	1.676910236	2.593087301	ATP2B4;RA.
0	0	1.676910236	2.593087301	SLC27A1;SI.
0	0	1.814832867	2.784461865	TRPM2;ATI.
0	0	1.814832867	2.784461865	H2AZ1;FAM.
0	0	1.814832867	2.784461865	CASP9;CAS.
0	0	1.814832867	2.784461865	RPS27L;CD.
0	0	1.814832867	2.784461865	BBS2;MYO.
0	0	1.814832867	2.784461865	P2RX7;ENT.
0	0	1.814832867	2.784461865	P2RX7;ENT.
0	0	1.814832867	2.784461865	STK36;ARM.
0	0	1.342136809	2.05768045	CASP9;ACE.
0	0	1.342136809	2.05768045	WWTR1;IM.
0	0	1.342136809	2.05768045	CD86;SETD.
0	0	1.320115909	2.008655202	MRPS22;M.
0	0	1.50010917	2.278949349	IMPACT;TE.
0	0	1.50010917	2.278949349	CSTB;CDK5.
0	0	1.22820139	1.839321896	PPM1L;PD.
0	0	1.347331584	2.005798351	GLP1R;TFR.
0	0	1.435378504	2.130869077	NDC1;AHC.
0	0	1.435378504	2.130869077	NDC1;AHC.
0	0	1.542819729	2.286950866	RPS27L;TM.
0	0	1.542819729	2.286950866	PKIB;RTEL1.
0	0	1.542819729	2.286950866	MDFIC;RAE.
0	0	1.542819729	2.286950866	PPP3CA;GM.
0	0	1.286246167	1.880625622	DCTN5;LAC.
0	0	2.57037037	3.755166937	MTHFD1;P.
0	0	2.57037037	3.755166937	KYAT1;ACA.
0	0	2.57037037	3.755166937	DPY30;SIR.
0	0	2.57037037	3.755166937	PICK1;TREI.
0	0	2.57037037	3.755166937	WFS1;ATG.
0	0	2.57037037	3.755166937	HYI;HOGA1.
0	0	2.57037037	3.755166937	NDST1;HS2.
0	0	2.57037037	3.755166937	PHYH;PDS5.
0	0	2.57037037	3.755166937	ABHD10;PI.
0	0	2.57037037	3.755166937	PARP1;ST3.
0	0	2.57037037	3.755166937	MAP10;RA.
0	0	2.57037037	3.755166937	MAP10;RA.
0	0	2.57037037	3.755166937	PLK4;CCDC.

0	0	2.57037037	3.755166937	PICK1;ARPI.
0	0	2.57037037	3.755166937	BBS2;NENF.
0	0	2.57037037	3.755166937	PKIB;PKIG .
0	0	2.57037037	3.755166937	VAT1;TFRC.
0	0	2.57037037	3.755166937	TOM1L2;CI.
0	0	2.57037037	3.755166937	ATP2B4;GL.
0	0	2.57037037	3.755166937	KDM2B;SIF.
0	0	2.57037037	3.755166937	PARK7;TXN.
0	0	2.57037037	3.755166937	PLOD3;PLC.
0	0	2.57037037	3.755166937	P4HA2;P4H.
0	0	2.57037037	3.755166937	SASH3;EIF2.
0	0	2.57037037	3.755166937	SIRT2;BOK .
0	0	2.57037037	3.755166937	CDH3;IGF1.
0	0	2.57037037	3.755166937	CDH3;GIPC.
0	0	2.57037037	3.755166937	STAP1;TRE.
0	0	2.57037037	3.755166937	DLG4;MAP.
0	0	2.57037037	3.755166937	CDH3;GIPC.
0	0	2.57037037	3.755166937	AGBL5;AGT.
0	0	2.57037037	3.755166937	ABHD10;PI.
0	0	2.57037037	3.755166937	ALDH6A1;I.
0	0	2.57037037	3.755166937	ADTRP;IER.
0	0	2.57037037	3.755166937	LANCL1;TR.
0	0	2.57037037	3.755166937	HPF1;XRCC.
0	0	2.57037037	3.755166937	ABCA2;FKT.
0	0	2.57037037	3.755166937	CD86;TNFS.
0	0	2.57037037	3.755166937	XRCC1;APC.
0	0	2.57037037	3.755166937	MTIF2;MRI.
0	0	2.57037037	3.755166937	TDP1;ERCC.
0	0	2.57037037	3.755166937	PPP3CA;LA.
0	0	2.57037037	3.755166937	HDAC6;SRI.
0	0	2.57037037	3.755166937	PLA2R1;AR.
0	0	2.57037037	3.755166937	CADM1;CR.
0	0	2.57037037	3.755166937	TBCEL;TBC.
0	0	2.57037037	3.755166937	CBR1;VKOI.
0	0	1.272163419	1.854730162	PARP1;CET.
0	0	1.60694808	2.327652553	GPI;PFKL;A.
0	0	1.60694808	2.327652553	GPR137;TC.
0	0	1.60694808	2.327652553	ANAPC13;C.
0	0	1.60694808	2.327652553	RTEL1;RAD.
0	0	1.136049002	1.638216679	MAP10;TN.
0	0	1.459483064	2.104274245	GNG2;KCN.
0	0	1.459483064	2.104274245	CDK5;MMI.
0	0	1.713911906	2.436248367	CAB39;WN.
0	0	1.713911906	2.436248367	ERI1;ERI2;I.
0	0	1.713911906	2.436248367	MCUR1;MC.
0	0	1.713911906	2.436248367	GSTO1;ATF.
0	0	1.713911906	2.436248367	TWIST1;AP.

0	0	1.713911906	2.436248367	ALDH3A2;A
0	0	1.713911906	2.436248367	DFFA;CIDE
0	0	1.402676834	1.984563113	SGPL1;PKN
0	0	1.402676834	1.984563113	PRKCG;CD8
0	0	1.402676834	1.984563113	IMPACT;TH
0	0	1.927964255	2.721575231	AGL;PHKB;
0	0	1.927964255	2.721575231	NAGK;PGM
0	0	1.927964255	2.721575231	AGL;PHKB;
0	0	1.927964255	2.721575231	STAR;NPC2
0	0	1.927964255	2.721575231	FASTKD1;M
0	0	1.927964255	2.721575231	NUCKS1;EI
0	0	1.927964255	2.721575231	CD84;GRN;
0	0	1.927964255	2.721575231	SLC27A1;P
0	0	1.927964255	2.721575231	AHI1;ARL3
0	0	1.927964255	2.721575231	CUL7;PPAR
0	0	1.927964255	2.721575231	FEN1;RTEL
0	0	1.927964255	2.721575231	DNMT1;AU
0	0	1.927964255	2.721575231	GAS6;GTSE
0	0	1.927964255	2.721575231	PRXL2B;MI
0	0	1.927964255	2.721575231	ASPH;PLOD
0	0	1.927964255	2.721575231	CD19;CRTA
0	0	1.927964255	2.721575231	GRN;STAP1
0	0	1.927964255	2.721575231	NTNG2;DLG
0	0	1.927964255	2.721575231	POP7;LACT
0	0	1.927964255	2.721575231	SYCE2;STAG
0	0	1.927964255	2.721575231	SYCE2;STAG
0	0	1.927964255	2.721575231	TSEN15;FA
0	0	1.492966869	2.088754061	OAT;ALDH9
0	0	1.492966869	2.088754061	RBL2;RBL1
0	0	1.492966869	2.088754061	ATP6V1A;A
0	0	1.206013944	1.659695057	BCAS3;RIPG
0	0	1.112337759	1.528020063	PHF20;ITSN
0	0	1.285995624	1.76149353	ABCA2;SLC
0	0	1.420995174	1.944246136	SLC38A7;SI
0	0	1.420995174	1.944246136	BLM;RAD5
0	0	1.420995174	1.944246136	RINT1;BLM
0	0	1.269768782	1.735052116	SLF1;TFRC;
0	0	1.234756686	1.685999578	CHRNB1;SI
0	0	1.256190855	1.714498648	DCTN5;LAG
0	0	1.542582897	2.093402779	SLC25A1;G
0	0	1.542582897	2.093402779	GSTM1;GST
0	0	1.542582897	2.093402779	DNMT1;EE
0	0	1.542582897	2.093402779	CD19;PDGI
0	0	1.542582897	2.093402779	STIL;MTHF
0	0	1.542582897	2.093402779	MMP14;CD
0	0	1.542582897	2.093402779	RTEL1;RAD
0	0	1.214729532	1.610029264	GLP1R;ACH

0	0	1.285870516	1.69934976	SETD4;FZD
0	0	1.285870516	1.69934976	ODAD3;TB
0	0	1.446229812	1.909699015	GRN;ACP4
0	0	1.446229812	1.909699015	NDC1;XPO
0	0	1.241681393	1.636952763	ATP2B4;CI
0	0	1.623614203	2.13939009	DFFA;DNA
0	0	1.623614203	2.13939009	DNMT1;DN
0	0	1.623614203	2.13939009	BACE1;SPP
0	0	1.623614203	2.13939009	MDFIC;RAE
0	0	1.623614203	2.13939009	CLIP3;ZDHI
0	0	1.623614203	2.13939009	CLIP3;ZDHI
0	0	1.623614203	2.13939009	METTL22;E
0	0	1.623614203	2.13939009	CD86;TNFS
0	0	1.623614203	2.13939009	PARK7;GAS
0	0	1.623614203	2.13939009	WWTR1;DA
0	0	1.18303978	1.545184109	ATP6V1A;F
0	0	1.192102615	1.543576922	BBS2;BBS1
0	0	1.13063198	1.454564957	ATP6V1A;S
0	0	1.779558715	2.288838859	AGL;PHKB;
0	0	1.779558715	2.288838859	TRPM2;HM
0	0	1.779558715	2.288838859	LGALS3;GR
0	0	1.779558715	2.288838859	CYP27A1;P
0	0	1.779558715	2.288838859	TFRC;SHLD
0	0	1.779558715	2.288838859	SLC45A3;P
0	0	1.779558715	2.288838859	NEDD1;STI
0	0	1.779558715	2.288838859	PARP1;SPH
0	0	1.779558715	2.288838859	MSR1;TREI
0	0	1.779558715	2.288838859	MVB12A;W
0	0	1.779558715	2.288838859	P2RX7;RFC
0	0	1.779558715	2.288838859	TSEN15;FA
0	0	1.779558715	2.288838859	MTHFD1;S
0	0	1.779558715	2.288838859	CADM1;CR
0	0	1.341538929	1.723332762	NDC1;AHC
0	0	1.341538929	1.723332762	ACOT8;GST
0	0	2.203050109	2.8285501	MTHFD1;IL
0	0	2.203050109	2.8285501	ACP5;TPP1
0	0	2.203050109	2.8285501	TEKT3;GAS
0	0	2.203050109	2.8285501	CD63;RAB3
0	0	2.203050109	2.8285501	CD63;RAB3
0	0	2.203050109	2.8285501	MYO1E;XP
0	0	2.203050109	2.8285501	GNPDA1;G
0	0	2.203050109	2.8285501	PPIP5K1;IN
0	0	2.203050109	2.8285501	AFMID;KYA
0	0	2.203050109	2.8285501	APOA4;CTS
0	0	2.203050109	2.8285501	GRN;PPT1
0	0	2.203050109	2.8285501	ATP2B4;GL
0	0	2.203050109	2.8285501	ATP2B4;GL

0	0	2.203050109	2.8285501	KCNIP2;PIC
0	0	2.203050109	2.8285501	APH1B;PSE
0	0	2.203050109	2.8285501	ENTPD5;EN
0	0	2.203050109	2.8285501	NEU3;MAN
0	0	2.203050109	2.8285501	HSD17B14
0	0	2.203050109	2.8285501	TMX3;PAR
0	0	2.203050109	2.8285501	CNTNAP1;S
0	0	2.203050109	2.8285501	ACOT8;PEX
0	0	2.203050109	2.8285501	PARK7;SLC
0	0	2.203050109	2.8285501	XRCC1;GCL
0	0	2.203050109	2.8285501	SCIN;PITHD
0	0	2.203050109	2.8285501	STAP1;TRE
0	0	2.203050109	2.8285501	PDCD4;PPA
0	0	2.203050109	2.8285501	UGDH;SPA
0	0	2.203050109	2.8285501	AIFM2;ALC
0	0	2.203050109	2.8285501	CCL19;CD6
0	0	2.203050109	2.8285501	USP14;UBC
0	0	2.203050109	2.8285501	INTS13;LHI
0	0	2.203050109	2.8285501	MSH6;POT
0	0	2.203050109	2.8285501	CHEK1;CEP
0	0	2.203050109	2.8285501	CDC7;DBF4
0	0	2.203050109	2.8285501	IMPACT;W
0	0	2.203050109	2.8285501	HLCS;SPP1
0	0	2.203050109	2.8285501	CNTNAP1;S
0	0	2.203050109	2.8285501	TREM2;C1(
0	0	2.203050109	2.8285501	MTHFD1;S
0	0	2.203050109	2.8285501	DECR2;FAD
0	0	1.131420757	1.446330212	TFRC;ITGB3
0	0	1.227501692	1.562856847	NCAPG2;KI
0	0	1.227501692	1.562856847	PSMD10;ZI
0	0	1.483168882	1.886000893	DYNC2I1;H
0	0	1.483168882	1.886000893	PDGFB;TW
0	0	1.483168882	1.886000893	LGALS3;HM
0	0	1.483168882	1.886000893	OSBPL7;MA
0	0	1.483168882	1.886000893	MSR1;ABC
0	0	1.402325305	1.747636698	CDC23;ZW
0	0	1.198588594	1.485598479	BEX3;CASP
0	0	1.349792576	1.662647836	AHI1;STIL;E
0	0	1.349792576	1.662647836	AHI1;STIL;E
0	0	1.213640636	1.492050822	DCTN5;LAC
0	0	1.1692019	1.435775274	WWTR1;GS
0	0	1.223105591	1.498604331	PSMD10;AT
0	0	1.312921186	1.606707091	RNF113A;C
0	0	1.312921186	1.606707091	GPI;PFKL;G
0	0	1.312921186	1.606707091	FABP3;FAB
0	0	1.542346271	1.884808131	GPI;PFKL;A
0	0	1.542346271	1.884808131	STX12;ABC

0	0	1.542346271	1.884808131	TRPM2;TRI.
0	0	1.542346271	1.884808131	GPI;PFKL;A.
0	0	1.542346271	1.884808131	ALOX5;DPE.
0	0	1.542346271	1.884808131	DDB1;LGAI.
0	0	1.542346271	1.884808131	IGF1;ADTR.
0	0	1.542346271	1.884808131	FITM2;MLY.
0	0	1.285620629	1.568292159	TRPM2;IM.
0	0	1.264596042	1.541243942	WWTR1;C(.
0	0	1.264596042	1.541243942	NDC1;P2R).
0	0	1.141631594	1.373010165	DNMT1;CI".
0	0	1.19306631	1.423493739	NDC1;WDF.
0	0	1.428155905	1.701824406	OGG1;SHLI.
0	0	1.428155905	1.701824406	AIFM1;PEX.
0	0	1.428155905	1.701824406	NTNG2;SP/.
0	0	1.428155905	1.701824406	CUL7;RAP2.
0	0	1.428155905	1.701824406	CUX2;CDK5.
0	0	1.428155905	1.701824406	LATS1;GPA.
0	0	1.428155905	1.701824406	PRIM2;POI.
0	0	1.361003415	1.600702688	RALBP1;ST.
0	0	1.361003415	1.600702688	DDAH2;AT.
0	0	1.652353967	1.939042542	WRN;XRCC.
0	0	1.652353967	1.939042542	SLC31A1;C.
0	0	1.652353967	1.939042542	IGF1;CLU;F.
0	0	1.652353967	1.939042542	PIGQ;PIGF;.
0	0	1.652353967	1.939042542	ZWILCH;ZW.
0	0	1.652353967	1.939042542	ABCC5;SLC.
0	0	1.652353967	1.939042542	ABCA2;SCA.
0	0	1.652353967	1.939042542	P2RX7;TRP.
0	0	1.652353967	1.939042542	ABCA5;AP(.
0	0	1.652353967	1.939042542	UBL4A;GET.
0	0	1.316796251	1.538714482	GUCY2C;SL.
0	0	1.244128807	1.452909207	NTNG2;PA.
0	0	1.262174189	1.471335242	LGALS3;W\.
0	0	1.927559913	2.186157776	COMT;ALD.
0	0	1.927559913	2.186157776	BLM;SPIDR.
0	0	1.927559913	2.186157776	ATP6V1A;F.
0	0	1.927559913	2.186157776	GNG2;TNF.
0	0	1.927559913	2.186157776	PRDX2;ABI.
0	0	1.927559913	2.186157776	TFAP4;RPS.
0	0	1.927559913	2.186157776	PFKL;PFKM.
0	0	1.927559913	2.186157776	SMARCAD1.
0	0	1.927559913	2.186157776	ABCC5;SLC.
0	0	1.927559913	2.186157776	SHMT2;SEI.
0	0	1.927559913	2.186157776	BSCL2;FITM.
0	0	1.927559913	2.186157776	KIF3A;CEP1.
0	0	1.927559913	2.186157776	CLU;SOD1 .
0	0	1.927559913	2.186157776	ACER2;WN.

0	0	1.927559913	2.186157776	PPARG;TRE.
0	0	1.927559913	2.186157776	EMILIN1;A.
0	0	1.927559913	2.186157776	WNK1;MA.
0	0	1.927559913	2.186157776	EMILIN1;A.
0	0	1.927559913	2.186157776	TWIST1;TR.
0	0	1.927559913	2.186157776	POT1;CERS.
0	0	1.927559913	2.186157776	TTLL4;FKBI.
0	0	1.927559913	2.186157776	SFRP4;KRT.
0	0	1.927559913	2.186157776	POGLUT1;I.
0	0	1.927559913	2.186157776	PARP1;PAI.
0	0	1.927559913	2.186157776	RAP2A;RAI.
0	0	1.927559913	2.186157776	EMILIN1;TI.
0	0	1.927559913	2.186157776	WNK1;MA.
0	0	1.927559913	2.186157776	CFAP206;D.
0	0	1.927559913	2.186157776	TEK;BOK .
0	0	1.927559913	2.186157776	RPS6KA5;T.
0	0	1.927559913	2.186157776	PARK7;TXN.
0	0	1.927559913	2.186157776	LATS1;SOD.
0	0	1.927559913	2.186157776	DIP2A;PAR.
0	0	1.927559913	2.186157776	STAP1;TRE.
0	0	1.927559913	2.186157776	CLOCK;ARN.
0	0	1.927559913	2.186157776	MYO1E;XP.
0	0	1.927559913	2.186157776	STXBP6;VA.
0	0	1.468818142	1.665324187	NDST1;B4C.
0	0	1.468818142	1.665324187	ACADVL;CC.
0	0	1.468818142	1.665324187	VKORC1L1.
0	0	1.468818142	1.665324187	GPI;PFKL;A.
0	0	1.468818142	1.665324187	FUT8;STIL;.
0	0	1.468818142	1.665324187	SCAMP5;LC.
0	0	1.468818142	1.665324187	WFS1;ALO.
0	0	1.468818142	1.665324187	TRPM2;ITP.
0	0	1.468818142	1.665324187	PLA2G15;S.
0	0	1.468818142	1.665324187	NEU3;CCDC.
0	0	1.202148399	1.359965733	MRPL30;M.
0	0	1.202148399	1.359965733	AP1G2;OSB.
0	0	1.224311325	1.369733016	SCARB2;VA.
0	0	1.377072426	1.537828626	IMPACT;AC.
0	0	1.377072426	1.537828626	PKIB;XRCC.
0	0	1.377072426	1.537828626	ABCA2;RAI.
0	0	1.168831169	1.302683306	EPHA10;XP.
0	0	1.239565122	1.380572543	RBL2;PIDD.
0	0	1.259189914	1.397775093	MSH6;ZRA.
0	0	1.259189914	1.397775093	CBR1;SPHK.
0	0	1.322042776	1.46727324	CASP9;ETA.
0	0	1.285371179	1.424662717	CUL7;SPAS.
0	0	1.285371179	1.424662717	RAP2A;GST.
0	0	1.107812964	1.216588891	ATP6V1A;N.

0	0	1.179736273	1.294019585	PRKCG;GRI.
0	0	1.179736273	1.294019585	PRKCG;GRI.
0	0	1.186668911	1.291346434	WWTR1;UI.
0	0	1.136268044	1.23051459	RFC5;RFC3.
0	0	1.194977388	1.290275544	PLK4;P2RX.
0	0	1.125082381	1.206243357	SCARB2;NT.
0	0	1.542109852	1.653037983	ABCC5;SLC.
0	0	1.542109852	1.653037983	CITED2;IFT.
0	0	1.542109852	1.653037983	TADA3;TRI.
0	0	1.542109852	1.653037983	GSTP1;EMI.
0	0	1.542109852	1.653037983	CAB39;COI.
0	0	1.542109852	1.653037983	GPNMB;W.
0	0	1.542109852	1.653037983	PSMD10;T'.
0	0	1.542109852	1.653037983	RPS6KA5;L.
0	0	1.542109852	1.653037983	EMILIN1;IE.
0	0	1.542109852	1.653037983	CD86;TNFS.
0	0	1.542109852	1.653037983	SASH3;TNF.
0	0	1.542109852	1.653037983	FABP3;PDK.
0	0	1.542109852	1.653037983	ZNF205;TM.
0	0	1.542109852	1.653037983	BBS2;IGF1;.
0	0	1.542109852	1.653037983	GGCT;CLU;.
0	0	1.542109852	1.653037983	GPAM;MO.
0	0	1.205113139	1.291390739	RBL2;ACER.
0	0	1.205113139	1.291390739	DDB1;PSM.
0	0	1.217749356	1.295571969	RIPOR1;WI.
0	0	1.233936217	1.304206104	KANK1;RUI.
0	0	1.233936217	1.304206104	CALCRL;TFI.
0	0	1.108509896	1.171215534	PI4K2B;CU.
0	0	1.401974388	1.475201062	CARMIL1;C.
0	0	1.401974388	1.475201062	TMEM161.
0	0	1.401974388	1.475201062	ACOT8;PEX.
0	0	1.401974388	1.475201062	PPP3CC;YV.
0	0	1.401974388	1.475201062	CHST10;CH.
0	0	1.401974388	1.475201062	HMGB1;PL.
0	0	1.401974388	1.475201062	TENM4;KIF.
0	0	1.401974388	1.475201062	PPP3CC;YV.
0	0	1.142773637	1.20134448	SETD4;FZD.
0	0	1.255407738	1.319606452	AUTS2;CDH.
0	0	1.285246617	1.34592909	PI4K2B;TTC.
0	0	1.285246617	1.34592909	DLG4;PDGI.
0	0	1.285246617	1.34592909	LATS1;XPO.
0	0	1.285246617	1.34592909	DYNC2I1;W.
0	0	1.329511946	1.391439588	SESN3;RRA.
0	0	1.329511946	1.391439588	ATP2B4;PP.
0	0	1.329511946	1.391439588	PKIB;XRCC.
0	0	1.329511946	1.391439588	SLC45A3;P.
0	0	1.171581309	1.226151305	CLIP3;DAB.

0	0	1.119697377	1.127900172	FARP2;RIP(.
0	0	1.20967286	1.217155032	ERCC6L2;G .
0	0	1.71328976	1.723464355	FHOD3;CA .
0	0	1.71328976	1.723464355	SPAST;MG .
0	0	1.71328976	1.723464355	KDM2B;IFT .
0	0	1.71328976	1.723464355	SLC25A20; .
0	0	1.71328976	1.723464355	GRAMD1B .
0	0	1.71328976	1.723464355	PPCDC;AC .
0	0	1.71328976	1.723464355	SLC31A1;A .
0	0	1.71328976	1.723464355	CEP250;CA .
0	0	1.71328976	1.723464355	CEP250;CA .
0	0	1.71328976	1.723464355	TFAP4;RPS .
0	0	1.71328976	1.723464355	KDM2B;MI .
0	0	1.71328976	1.723464355	COQ3;PDX .
0	0	1.71328976	1.723464355	PPIP5K1;IP .
0	0	1.71328976	1.723464355	MTERF2;TE .
0	0	1.71328976	1.723464355	TOM1L2;C .
0	0	1.71328976	1.723464355	ACP4;GAS1 .
0	0	1.71328976	1.723464355	MAP2K5;T .
0	0	1.71328976	1.723464355	SETD4;ME .
0	0	1.71328976	1.723464355	NUCKS1;ZN .
0	0	1.71328976	1.723464355	CDC7;DBF4 .
0	0	1.71328976	1.723464355	SPHK2;TNF .
0	0	1.71328976	1.723464355	TENM4;DI(.
0	0	1.71328976	1.723464355	GRN;LRSAM .
0	0	1.71328976	1.723464355	DDB1;ZNF5 .
0	0	1.71328976	1.723464355	KCNIP2;TR .
0	0	1.71328976	1.723464355	PSMD10;P .
0	0	1.71328976	1.723464355	TMX3;LOX .
0	0	1.71328976	1.723464355	PPCDC;AC .
0	0	1.71328976	1.723464355	PUDP;TK1 .
0	0	1.71328976	1.723464355	PUDP;TK1 .
0	0	1.71328976	1.723464355	SUV39H1;S .
0	0	1.71328976	1.723464355	ABCA2;NE(.
0	0	1.71328976	1.723464355	PARK7;MM .
0	0	1.71328976	1.723464355	CCL19;GAS .
0	0	1.71328976	1.723464355	DRC1;HDA(.
0	0	1.71328976	1.723464355	GSTP1;TW .
0	0	1.71328976	1.723464355	HMGB1;RT .
0	0	1.71328976	1.723464355	BLM;SPIDR .
0	0	1.71328976	1.723464355	PPCDC;AC .
0	0	1.71328976	1.723464355	MTHFD1;L(.
0	0	1.71328976	1.723464355	SMPD3;AB .
0	0	1.71328976	1.723464355	QDPR;SPR .
0	0	1.71328976	1.723464355	MTHFD1;S .
0	0	1.71328976	1.723464355	AFMID;KY .
0	0	1.71328976	1.723464355	CARMIL1;A .

0	0	1.71328976	1.723464355	LIG1;HMGI.
0	0	1.06512684	1.055920833	TFRC;CAB3.
0	0	1.25043944	1.235425479	AHI1;STIL;I.
0	0	1.25043944	1.235425479	IMPACT;BF.
0	0	1.25043944	1.235425479	SCARB2;NI.
0	0	1.168462058	1.148023852	IPO11;NXT.
0	0	1.168462058	1.148023852	CD86;TNFS.
0	0	1.078049298	1.058853457	TTC26;LAM.
0	0	1.285122164	1.260469524	CDK5;TREM.
0	0	1.285122164	1.260469524	TRPM2;IM.
0	0	1.285122164	1.260469524	CD86;GPNI.
0	0	1.285122164	1.260469524	SYDE1;ANK.
0	0	1.285122164	1.260469524	LRSAM1;N.
0	0	1.445646251	1.416878094	EPS8;SCIN;.
0	0	1.445646251	1.416878094	EPS8;SCIN;.
0	0	1.445646251	1.416878094	PKD1L2;PK.
0	0	1.445646251	1.416878094	ALOX5;MG.
0	0	1.445646251	1.416878094	IGF1;CLU;F.
0	0	1.445646251	1.416878094	AGTPBP1;L.
0	0	1.445646251	1.416878094	ABCA2;RNI.
0	0	1.445646251	1.416878094	HMGB1;PL.
0	0	1.445646251	1.416878094	TPST1;ABH.
0	0	1.445646251	1.416878094	FARP2;EPS.
0	0	1.445646251	1.416878094	FZD5;PARK.
0	0	1.445646251	1.416878094	DNMT1;AL.
0	0	1.445646251	1.416878094	CDH3;IGFB.
0	0	1.445646251	1.416878094	TNFSF18;L.
0	0	1.445646251	1.416878094	CAMK2A;A.
0	0	1.445646251	1.416878094	ABCA2;GR.
0	0	1.445646251	1.416878094	MYO1E;MY.
0	0	1.340943135	1.3098084	ARL6IP5;SL.
0	0	1.340943135	1.3098084	NCAPG2;N.
0	0	1.340943135	1.3098084	PDK4;SLC1.
0	0	1.340943135	1.3098084	DDAH2;CD.
0	0	1.340943135	1.3098084	TRPM2;ITP.
0	0	1.110676613	1.083987804	SCARB2;SL.
0	0	1.110676613	1.083987804	SCARB2;M.
0	0	1.123184398	1.089908161	NDC1;NEK.
0	0	1.186342709	1.136124059	TRPM2;AB.
0	0	1.199475983	1.133386702	PM20D1;S.
0	0	1.199475983	1.133386702	SHTN1;CN.
0	0	1.199475983	1.133386702	CPNE9;SHT.
0	0	1.199475983	1.133386702	PKIB;STN1;.
0	0	1.126458608	1.063207603	CPNE9;PSM.
0	0	1.150957064	1.082458781	CYP27A1;A.
0	0	1.150957064	1.082458781	VAT1;KANI.
0	0	1.217464219	1.134667185	WWTR1;ZH.

0	0	1.128526445	1.049378936	DUS2;PM2 .
0	0	1.128526445	1.049378936	GPI;BCAS3 .
0	0	1.128526445	1.049378936	TSPYL2;RB .
0	0	1.113040808	1.027362109	SLC27A1;B .
0	0	1.113040808	1.027362109	RNF43;KA .
0	0	1.243596239	1.143049588	POGLUT1;I .
0	0	1.243596239	1.143049588	CDH3;PRD .
0	0	1.130988626	1.035198748	WWTR1;IN .
0	0	1.130988626	1.035198748	PSMD10;D .
0	0	1.080736334	0.986706298	STX12;CRT .
0	0	1.163892942	1.060658986	PIGU;PIGQ .
0	0	1.163892942	1.060658986	CDK8;MED .
0	0	1.163892942	1.060658986	SCAMP5;C .
0	0	1.113879159	1.012068791	PDXP;TRPV .
0	0	1.284997819	1.165375894	STARD5;SL .
0	0	1.284997819	1.165375894	DMAC2L;A .
0	0	1.284997819	1.165375894	MCUR1;M .
0	0	1.284997819	1.165375894	PLA2G15;G .
0	0	1.284997819	1.165375894	GSTO1;GN .
0	0	1.284997819	1.165375894	FBXL8;CRT .
0	0	1.284997819	1.165375894	TOGARAM .
0	0	1.284997819	1.165375894	DDAH2;CD .
0	0	1.284997819	1.165375894	RIPOR1;GC .
0	0	1.284997819	1.165375894	PSMD10;T .
0	0	1.284997819	1.165375894	CD86;SASH .
0	0	1.284997819	1.165375894	CDK5;ABI3 .
0	0	1.284997819	1.165375894	SPHK2;ALC .
0	0	1.284997819	1.165375894	POP7;LACT .
0	0	1.360531309	1.220202057	BLM;ATP2I .
0	0	1.360531309	1.220202057	PPP3CA;PP .
0	0	1.360531309	1.220202057	PARK7;CAM .
0	0	1.360531309	1.220202057	GPR137;TC .
0	0	1.360531309	1.220202057	STN1;TEN1 .
0	0	1.360531309	1.220202057	POLD2;ADI .
0	0	1.360531309	1.220202057	CUL7;CUX2 .
0	0	1.360531309	1.220202057	AHI1;SFRP4 .
0	0	1.360531309	1.220202057	CADM1;CR .
0	0	1.360531309	1.220202057	WFS1;PDG .
0	0	1.360531309	1.220202057	SCARB2;GC .
0	0	1.360531309	1.220202057	DSTYK;GPC .
0	0	1.173333966	1.050869588	VAV3;SASH .
0	0	1.541873638	1.380185107	EPS8;BAIAI .
0	0	1.541873638	1.380185107	MEGF8;RTI .
0	0	1.541873638	1.380185107	AGTPBP1;T .
0	0	1.541873638	1.380185107	SYT2;DOC2 .
0	0	1.541873638	1.380185107	ZWILCH;ZW .
0	0	1.541873638	1.380185107	PKD2;MAP .

0	0	1.541873638	1.380185107	THRB;CTSB.
0	0	1.541873638	1.380185107	GUCY2C;PI.
0	0	1.541873638	1.380185107	OGG1;POT.
0	0	1.541873638	1.380185107	AGTPBP1;C.
0	0	1.541873638	1.380185107	TUBB3;SEM.
0	0	1.541873638	1.380185107	RIPOR1;TB.
0	0	1.541873638	1.380185107	LAMA3;LAI.
0	0	1.541873638	1.380185107	TST;MMUT.
0	0	1.541873638	1.380185107	LGALS3;ED.
0	0	1.541873638	1.380185107	NIPA1;SLC4.
0	0	1.541873638	1.380185107	UBA5;ZFPM.
0	0	1.541873638	1.380185107	KIF3A;CEP1.
0	0	1.541873638	1.380185107	RFWD3;RP.
0	0	1.541873638	1.380185107	PRKCA;VRK.
0	0	1.541873638	1.380185107	AHI1;LAMA.
0	0	1.541873638	1.380185107	TREM2;CLI.
0	0	1.541873638	1.380185107	ACTN3;ATP.
0	0	1.541873638	1.380185107	ACTN3;ATP.
0	0	1.541873638	1.380185107	BLM;ZFYVE.
0	0	1.541873638	1.380185107	PPARG;ESR.
0	0	1.541873638	1.380185107	ETFBKMT;H.
0	0	1.541873638	1.380185107	SLC1A3;SLC.
0	0	1.541873638	1.380185107	PUDP;TK1 .
0	0	1.541873638	1.380185107	LSM4;LSM1.
0	0	1.541873638	1.380185107	SLC37A4;SI.
0	0	1.541873638	1.380185107	B4GAT1;B3.
0	0	1.541873638	1.380185107	TWIST1;MI.
0	0	1.541873638	1.380185107	STAP1;TICA.
0	0	1.541873638	1.380185107	STAP1;TRE.
0	0	1.541873638	1.380185107	TFR2;NKD2.
0	0	1.541873638	1.380185107	GORASP1;C.
0	0	1.541873638	1.380185107	PARP1;PAR.
0	0	1.541873638	1.380185107	DLG4;ZDHH.
0	0	1.541873638	1.380185107	ALDH6A1;D.
0	0	1.541873638	1.380185107	TNFSF4;HM.
0	0	1.541873638	1.380185107	ABCA2;APC.
0	0	1.541873638	1.380185107	TACR2;CFA.
0	0	1.541873638	1.380185107	DNMT1;DM.
0	0	1.541873638	1.380185107	WNK1;ADT.
0	0	1.541873638	1.380185107	PCBP3;IGF.
0	0	1.541873638	1.380185107	AIFM2;ALC.
0	0	1.541873638	1.380185107	ZFHX2;SCN.
0	0	1.541873638	1.380185107	PDGFB;PRK.
0	0	1.541873638	1.380185107	PKD2L1;CD.
0	0	1.541873638	1.380185107	MTHFD1;S .
0	0	1.541873638	1.380185107	EDNRB;TM.
0	0	1.541873638	1.380185107	CTSK;DUOX.

0	0	1.541873638	1.380185107	IDH1;ACO1.
0	0	1.541873638	1.380185107	GSTZ1;FAH.
0	0	1.06381362	0.947110867	MAGEH1;P.
0	0	1.066617012	0.948129863	CCDC125;A.
0	0	1.091898057	0.969252087	ATP6V1A;S.
0	0	1.137639	1.005693882	MCFD2;TR.
0	0	1.186180036	1.042687636	AIFM1;NCA.
0	0	1.186180036	1.042687636	CD86;LGAL.
0	0	1.186180036	1.042687636	BRMS1L;M.
0	0	1.101576182	0.963309184	SRD5A1;HS.
0	0	1.204665685	1.037575901	SPAST;KIF3.
0	0	1.204665685	1.037575901	SEMA3A;SI.
0	0	1.204665685	1.037575901	UBL4A;ALD.
0	0	1.204665685	1.037575901	CDK5;REEP.
0	0	1.148304376	0.974622721	CCNB3;BLM.
0	0	1.148304376	0.974622721	SCIN;AGO4.
0	0	1.148304376	0.974622721	MYBPC3;C.
0	0	1.11922654	0.94412681	PRKCG;GRI.
0	0	1.11922654	0.94412681	LSM10;RBL.
0	0	1.233528129	1.038808652	ZW10;SPDI.
0	0	1.233528129	1.038808652	SYCE2;STA.
0	0	1.233528129	1.038808652	CARMIL1;C.
0	0	1.233528129	1.038808652	IQCE;IFT12.
0	0	1.233528129	1.038808652	PPT1;HSD1.
0	0	1.233528129	1.038808652	TNFSF4;HM.
0	0	1.233528129	1.038808652	NPRL2;PO1.
0	0	1.233528129	1.038808652	DDB1;PPIH.
0	0	1.233528129	1.038808652	MRNIP;SHI.
0	0	1.233528129	1.038808652	ACADVL;SL.
0	0	1.233528129	1.038808652	ELMOD2;T.
0	0	1.101487314	0.927059073	TRPM2;CA.
0	0	1.156460061	0.958631354	GSTP1;CID.
0	0	1.156460061	0.958631354	PIK3R2;EF(.
0	0	1.156460061	0.958631354	ABCA2;PAF.
0	0	1.156460061	0.958631354	PKIB;XRCC.
0	0	1.079465615	0.891963532	SLF1;TFRC;.
0	0	1.121442472	0.924801648	FARP2;SYD.
0	0	1.088510748	0.897590633	B4GALT2;M.
0	0	1.101442938	0.907372977	WWTR1;AI.
0	0	1.284873583	1.055179608	MYO1E;MY.
0	0	1.284873583	1.055179608	SDHB;SLC2.
0	0	1.284873583	1.055179608	BLM;MMP.
0	0	1.284873583	1.055179608	ABCD4;MM.
0	0	1.284873583	1.055179608	GSTP1;ALC.
0	0	1.284873583	1.055179608	MCUR1;MC.
0	0	1.284873583	1.055179608	NAXE;QPR.
0	0	1.284873583	1.055179608	DAB2;ABI3.

0	0	1.284873583	1.055179608	DENND1B; .
0	0	1.284873583	1.055179608	TWIST1;IGI .
0	0	1.284873583	1.055179608	MRNIP;MC .
0	0	1.284873583	1.055179608	P2RX7;ENT .
0	0	1.284873583	1.055179608	GSTO1;CLI(.
0	0	1.284873583	1.055179608	CLASP1;CC .
0	0	1.284873583	1.055179608	BSCL2;CIDE .
0	0	1.284873583	1.055179608	PRKCA;CD3 .
0	0	1.284873583	1.055179608	APOA4;AN .
0	0	1.284873583	1.055179608	FASTKD2;S .
0	0	1.284873583	1.055179608	ICE2;POLR3 .
0	0	1.284873583	1.055179608	TRPM2;SLC .
0	0	1.077763968	0.872484926	PSMD10;SI .
0	0	1.168094558	0.942665978	MYBPC3;M .
0	0	1.168094558	0.942665978	MYBPC3;M .
0	0	1.168094558	0.942665978	SVBP;ATP2 .
0	0	1.168094558	0.942665978	CD86;SASH .
0	0	1.168094558	0.942665978	PTPMT1;M .
0	0	1.087303991	0.877230778	ALDH3A2;I .
0	0	1.101398601	0.886353802	CUL7;SPAS .
0	0	1.101398601	0.886353802	CASP9;MLI .
0	0	1.124317686	0.904124125	AKT3;PDGI .
0	0	1.401624084	1.119420086	IDUA;HEXA .
0	0	1.401624084	1.119420086	IDUA;CHST .
0	0	1.401624084	1.119420086	KCNIP2;KC .
0	0	1.401624084	1.119420086	FBXW4;ME .
0	0	1.401624084	1.119420086	POT1;BRCA .
0	0	1.401624084	1.119420086	GCC2;VAM .
0	0	1.401624084	1.119420086	ALOX5;PLA .
0	0	1.401624084	1.119420086	SPAST;MGA .
0	0	1.401624084	1.119420086	EDNRB;PAI .
0	0	1.401624084	1.119420086	SCAP;SOD1 .
0	0	1.401624084	1.119420086	TWSG1;HN .
0	0	1.401624084	1.119420086	KANK1;COI .
0	0	1.401624084	1.119420086	H1-10;ASF1 .
0	0	1.401624084	1.119420086	H1-10;ASF1 .
0	0	1.401624084	1.119420086	H1-10;ASF1 .
0	0	1.401624084	1.119420086	DNMT1;DN .
0	0	1.401624084	1.119420086	MIF;TAF9B .
0	0	1.401624084	1.119420086	ADTRP;NBI .
0	0	1.401624084	1.119420086	KANK1;COI .
0	0	1.401624084	1.119420086	SHPK;PGD .
0	0	1.401624084	1.119420086	B4GAT1;B3 .
0	0	1.401624084	1.119420086	HDAC6;SRI .
0	0	1.401624084	1.119420086	SCAMP5;D .
0	0	1.401624084	1.119420086	P2RX3;TRE .
0	0	1.401624084	1.119420086	SLC45A3;A .

0	0	1.401624084	1.119420086	GKAP1;SN	.
0	0	1.401624084	1.119420086	SPP1;PRAP	.
0	0	1.401624084	1.119420086	RANGRF;G	.
0	0	1.401624084	1.119420086	ZNF205;CD	.
0	0	1.401624084	1.119420086	WNK3;GPD	.
0	0	1.401624084	1.119420086	APOA4;LDI	.
0	0	1.401624084	1.119420086	QDPR;SPR	.
0	0	1.401624084	1.119420086	HMGB1;M	.
0	0	1.401624084	1.119420086	HPF1;PARK	.
0	0	1.401624084	1.119420086	GRN;PPT1	.
0	0	1.401624084	1.119420086	SYNGR1;SY	.
0	0	1.401624084	1.119420086	FOXJ1;SOD	.
0	0	1.401624084	1.119420086	SCPEP1;GC	.
0	0	1.401624084	1.119420086	TFR2;ACO1	.
0	0	1.401624084	1.119420086	THRB;CTSB	.
0	0	1.401624084	1.119420086	SEMA3A;P	.
0	0	1.401624084	1.119420086	LOXL3;PKD	.
0	0	1.401624084	1.119420086	CLIP3;COP	.
0	0	1.401624084	1.119420086	POP7;POP4	.
0	0	1.401624084	1.119420086	SCPEP1;GC	.
0	0	1.068717121	0.850740786	CD86;FZD5	.
0	0	1.057028155	0.833812494	VAV3;RALB	.
0	0	1.037304591	0.81641237	TFRC;EPHA	.
0	0	1.101354303	0.86368158	PSMD10;P	.
0	0	1.101354303	0.86368158	DTWD1;PC	.
0	0	1.060995907	0.831648096	PSMD10;F	.
0	0	1.927155923	1.510456531	CD86	.
0	0	1.927155923	1.510456531	SLC25A4	.
0	0	1.927155923	1.510456531	ADSS1	.
0	0	1.927155923	1.510456531	CD1B	.
0	0	1.927155923	1.510456531	CD1B	.
0	0	1.927155923	1.510456531	CD1B	.
0	0	1.927155923	1.510456531	SOD1	.
0	0	1.927155923	1.510456531	SOD1	.
0	0	1.927155923	1.510456531	AGTPBP1	.
0	0	1.927155923	1.510456531	MEGF8	.
0	0	1.927155923	1.510456531	PLPP3	.
0	0	1.927155923	1.510456531	HCN2	.
0	0	1.927155923	1.510456531	RHEX	.
0	0	1.927155923	1.510456531	PDE1B	.
0	0	1.927155923	1.510456531	PDK2	.
0	0	1.927155923	1.510456531	SPP1	.
0	0	1.927155923	1.510456531	AGTPBP1	.
0	0	1.927155923	1.510456531	CHD5	.
0	0	1.927155923	1.510456531	TREM2	.
0	0	1.927155923	1.510456531	CNTFR	.
0	0	1.927155923	1.510456531	YBX1	.

0	0	1.927155923	1.510456531	SLC19A1	.
0	0	1.927155923	1.510456531	PNRC2	.
0	0	1.927155923	1.510456531	NBL1	.
0	0	1.927155923	1.510456531	CITED2	.
0	0	1.927155923	1.510456531	XRCC1	.
0	0	1.927155923	1.510456531	MTHFD1	.
0	0	1.927155923	1.510456531	FAM20C	.
0	0	1.927155923	1.510456531	EDNRB	.
0	0	1.927155923	1.510456531	FOXJ1	.
0	0	1.927155923	1.510456531	SLC2A8	.
0	0	1.927155923	1.510456531	ALDH5A1	.
0	0	1.927155923	1.510456531	KANK1	.
0	0	1.927155923	1.510456531	SLC5A2	.
0	0	1.927155923	1.510456531	SLC37A4	.
0	0	1.927155923	1.510456531	ABCC5	.
0	0	1.927155923	1.510456531	PDXP	.
0	0	1.927155923	1.510456531	NCEH1	.
0	0	1.927155923	1.510456531	GAS6	.
0	0	1.927155923	1.510456531	IDUA	.
0	0	1.927155923	1.510456531	SLC37A4	.
0	0	1.927155923	1.510456531	PADI6	.
0	0	1.927155923	1.510456531	SETD4	.
0	0	1.927155923	1.510456531	SETD4	.
0	0	1.927155923	1.510456531	TST	.
0	0	1.927155923	1.510456531	FTL	.
0	0	1.927155923	1.510456531	IDH1	.
0	0	1.927155923	1.510456531	SLC1A3	.
0	0	1.927155923	1.510456531	GCC2	.
0	0	1.927155923	1.510456531	PLEKHM1	.
0	0	1.927155923	1.510456531	ADTRP	.
0	0	1.927155923	1.510456531	EDEM2	.
0	0	1.927155923	1.510456531	CCL19	.
0	0	1.927155923	1.510456531	ACADM	.
0	0	1.927155923	1.510456531	SGO2	.
0	0	1.927155923	1.510456531	NAXE	.
0	0	1.927155923	1.510456531	PKD2	.
0	0	1.927155923	1.510456531	PKD2	.
0	0	1.927155923	1.510456531	AGO4	.
0	0	1.927155923	1.510456531	ARL6IP5	.
0	0	1.927155923	1.510456531	HMGB1	.
0	0	1.927155923	1.510456531	P2RX7	.
0	0	1.927155923	1.510456531	ACTN3	.
0	0	1.927155923	1.510456531	ORMDL1	.
0	0	1.927155923	1.510456531	EIF2AK4	.
0	0	1.927155923	1.510456531	PPARG	.
0	0	1.927155923	1.510456531	SPHK2	.
0	0	1.927155923	1.510456531	PARK7	.

0	0	1.927155923	1.510456531	HAVCR2	.
0	0	1.927155923	1.510456531	ITGB3	.
0	0	1.927155923	1.510456531	C1QC	.
0	0	1.927155923	1.510456531	CD84	.
0	0	1.927155923	1.510456531	TIMP2	.
0	0	1.927155923	1.510456531	PARK7	.
0	0	1.927155923	1.510456531	PPARG	.
0	0	1.927155923	1.510456531	PARK7	.
0	0	1.927155923	1.510456531	NENF	.
0	0	1.927155923	1.510456531	SOD1	.
0	0	1.927155923	1.510456531	PPARG	.
0	0	1.927155923	1.510456531	PKD2	.
0	0	1.927155923	1.510456531	SLC29A1	.
0	0	1.927155923	1.510456531	DCTPP1	.
0	0	1.927155923	1.510456531	MDH1	.
0	0	1.927155923	1.510456531	SLC25A14	.
0	0	1.927155923	1.510456531	XYLB	.
0	0	1.927155923	1.510456531	LOXL3	.
0	0	1.927155923	1.510456531	HABP4	.
0	0	1.927155923	1.510456531	NUCKS1	.
0	0	1.927155923	1.510456531	TLE5	.
0	0	1.927155923	1.510456531	SIRT2	.
0	0	1.927155923	1.510456531	MEGF8	.
0	0	1.927155923	1.510456531	NPHP4	.
0	0	1.927155923	1.510456531	ATP2B4	.
0	0	1.927155923	1.510456531	LHFPL2	.
0	0	1.927155923	1.510456531	DSTYK	.
0	0	1.927155923	1.510456531	SLC27A1	.
0	0	1.927155923	1.510456531	SPHK2	.
0	0	1.927155923	1.510456531	ST3GAL4	.
0	0	1.927155923	1.510456531	SLF1	.
0	0	1.927155923	1.510456531	SLF1	.
0	0	1.927155923	1.510456531	SPHK2	.
0	0	1.927155923	1.510456531	VEGFB	.
0	0	1.927155923	1.510456531	MLLT11	.
0	0	1.927155923	1.510456531	SEPTIN9	.
0	0	1.927155923	1.510456531	CITED2	.
0	0	1.927155923	1.510456531	RNF128	.
0	0	1.927155923	1.510456531	EPB41	.
0	0	1.927155923	1.510456531	FANCM	.
0	0	1.927155923	1.510456531	SLC9A1	.
0	0	1.927155923	1.510456531	DNM1	.
0	0	1.927155923	1.510456531	DNM1	.
0	0	1.927155923	1.510456531	DPY19L1	.
0	0	1.927155923	1.510456531	DPY19L1	.
0	0	1.927155923	1.510456531	PADI6	.
0	0	1.927155923	1.510456531	EDEM2	.

0	0	1.927155923	1.510456531	UBA5	.
0	0	1.927155923	1.510456531	CNTNAP1	.
0	0	1.927155923	1.510456531	MAPRE3	.
0	0	1.927155923	1.510456531	MAPRE3	.
0	0	1.927155923	1.510456531	SLF1	.
0	0	1.927155923	1.510456531	UBA5	.
0	0	1.927155923	1.510456531	ST3GAL4	.
0	0	1.927155923	1.510456531	AGTPBP1	.
0	0	1.927155923	1.510456531	DCTD	.
0	0	1.927155923	1.510456531	DHODH	.
0	0	1.927155923	1.510456531	SLC29A1	.
0	0	1.927155923	1.510456531	DCTD	.
0	0	1.927155923	1.510456531	GAS6	.
0	0	1.927155923	1.510456531	TREM2	.
0	0	1.927155923	1.510456531	UNC119	.
0	0	1.927155923	1.510456531	SLC25A23	.
0	0	1.927155923	1.510456531	DNAJB2	.
0	0	1.927155923	1.510456531	SPHK2	.
0	0	1.927155923	1.510456531	FOXJ1	.
0	0	1.927155923	1.510456531	PDGFB	.
0	0	1.927155923	1.510456531	HAVCR2	.
0	0	1.927155923	1.510456531	TREM2	.
0	0	1.927155923	1.510456531	AUTS2	.
0	0	1.927155923	1.510456531	ZNF205	.
0	0	1.927155923	1.510456531	TREM2	.
0	0	1.927155923	1.510456531	ABCA2	.
0	0	1.927155923	1.510456531	SLF1	.
0	0	1.927155923	1.510456531	TTL	.
0	0	1.927155923	1.510456531	STAP1	.
0	0	1.927155923	1.510456531	PLD1	.
0	0	1.927155923	1.510456531	SLC25A4	.
0	0	1.927155923	1.510456531	RTN4	.
0	0	1.927155923	1.510456531	KLHL41	.
0	0	1.927155923	1.510456531	GAS6	.
0	0	1.927155923	1.510456531	GRN	.
0	0	1.927155923	1.510456531	PDGFB	.
0	0	1.927155923	1.510456531	MTMR1	.
0	0	1.927155923	1.510456531	ABI3	.
0	0	1.927155923	1.510456531	FANCM	.
0	0	1.927155923	1.510456531	GRN	.
0	0	1.927155923	1.510456531	CC2D1A	.
0	0	1.927155923	1.510456531	APOA4	.
0	0	1.927155923	1.510456531	CDK5	.
0	0	1.927155923	1.510456531	FITM2	.
0	0	1.927155923	1.510456531	WFS1	.
0	0	1.927155923	1.510456531	PKD2	.
0	0	1.927155923	1.510456531	MTRES1	.

0	0	1.927155923	1.510456531	ATP2B4	.
0	0	1.927155923	1.510456531	HCN2	.
0	0	1.927155923	1.510456531	ACTN3	.
0	0	1.927155923	1.510456531	PDE1B	.
0	0	1.927155923	1.510456531	ATG14	.
0	0	1.927155923	1.510456531	PRKCG	.
0	0	1.927155923	1.510456531	CCL19	.
0	0	1.927155923	1.510456531	NUDT14	.
0	0	1.927155923	1.510456531	XPO1	.
0	0	1.927155923	1.510456531	GPC1	.
0	0	1.927155923	1.510456531	PKD2L1	.
0	0	1.927155923	1.510456531	CUX2	.
0	0	1.927155923	1.510456531	SLC17A5	.
0	0	1.927155923	1.510456531	ETHE1	.
0	0	1.927155923	1.510456531	ETHE1	.
0	0	1.927155923	1.510456531	CLDN12	.
0	0	1.927155923	1.510456531	PELI3	.
0	0	1.927155923	1.510456531	TST	.
0	0	1.927155923	1.510456531	ZFPM1	.
0	0	1.927155923	1.510456531	SFRP4	.
0	0	1.927155923	1.510456531	PLK4	.
0	0	1.927155923	1.510456531	AFMID	.
0	0	1.927155923	1.510456531	EDEM2	.
0	0	1.927155923	1.510456531	SLC29A1	.
0	0	1.927155923	1.510456531	CLEC14A	.
0	0	1.927155923	1.510456531	BET1	.
0	0	1.927155923	1.510456531	WDR11	.
0	0	1.927155923	1.510456531	CYP27A1	.
0	0	1.186017646	0.927547368	UGDH;CHP	.
0	0	1.186017646	0.927547368	ZW10;SPDI	.
0	0	1.186017646	0.927547368	HSD17B14	.
0	0	1.186017646	0.927547368	WNK1;WN	.
0	0	1.186017646	0.927547368	AHI1;KDM1	.
0	0	1.186017646	0.927547368	TUT4;EXOS	.
0	0	1.186017646	0.927547368	SASH3;VAV	.
0	0	1.186017646	0.927547368	MRNIP;TFF	.
0	0	1.128189841	0.881739136	TNFSF18;L(	.
0	0	1.051358251	0.818309341	CADM1;CR	.
0	0	1.073479739	0.830026256	EPM2A;SC(	.
0	0	1.073479739	0.830026256	MED25;ZN	.
0	0	1.073479739	0.830026256	UGDH;TMI	.
0	0	1.028065516	0.791535159	CD86;GSTF	.
0	0	1.084127786	0.832127832	DNAJB2;FC	.
0	0	1.058179382	0.811331636	FARP2;SLF1	.
0	0	1.101310044	0.838901476	RBL2;PIDD	.
0	0	1.101310044	0.838901476	PPP3CC;YV	.
0	0	1.101310044	0.838901476	NDC1;SPHI	.

0	0	1.133674674	0.857123308	BACE1;APH
0	0	1.133674674	0.857123308	MTMR1;M
0	0	1.133674674	0.857123308	RAP2A;RTN
0	0	1.133674674	0.857123308	MYBPC3;R
0	0	1.133674674	0.857123308	DLG4;PDGI
0	0	1.133674674	0.857123308	PPT1;CCL1
0	0	1.070725842	0.806581144	VAV3;APH
0	0	1.070725842	0.806581144	DNMT1;TA
0	0	1.217179828	0.915802641	SFXN3;SLC
0	0	1.217179828	0.915802641	SCIN;PARV
0	0	1.217179828	0.915802641	BBS12;NDU
0	0	1.217179828	0.915802641	OAT;ALDH
0	0	1.217179828	0.915802641	FBXW4;IQC
0	0	1.217179828	0.915802641	BSCL2;CIDE
0	0	1.217179828	0.915802641	ARV1;SPHK
0	0	1.217179828	0.915802641	APH1B;SPF
0	0	1.217179828	0.915802641	NFU1;NUB
0	0	1.217179828	0.915802641	GRN;TREM
0	0	1.217179828	0.915802641	ABCA2;ACA
0	0	1.217179828	0.915802641	LGALS3;GP
0	0	1.217179828	0.915802641	SCN11A;KC
0	0	1.217179828	0.915802641	FARP2;GLC
0	0	1.217179828	0.915802641	GEN1;CEP1
0	0	1.217179828	0.915802641	C1QTNF1;F
0	0	1.217179828	0.915802641	ABCD4;MM
0	0	1.217179828	0.915802641	TRPM2;SLC
0	0	1.101265823	0.81133549	TTC8;CUX2
0	0	1.101265823	0.81133549	PHF20;HAT
0	0	1.101265823	0.81133549	TOM1L2;B
0	0	1.101265823	0.81133549	GSTP1;CID
0	0	1.142026457	0.829461229	SEMA3A;SI
0	0	1.142026457	0.829461229	USP14;GIP
0	0	1.142026457	0.829461229	DSCC1;HAT
0	0	1.142026457	0.829461229	CLIP3;ZDHI
0	0	1.043905976	0.751469915	PRKCG;PSM
0	0	1.284749455	0.917493292	ASPH;LGM
0	0	1.284749455	0.917493292	SLC25A12;
0	0	1.284749455	0.917493292	SLC31A1;A
0	0	1.284749455	0.917493292	ABCA2;PLE
0	0	1.284749455	0.917493292	CD36;PDES
0	0	1.284749455	0.917493292	SLC46A1;C
0	0	1.284749455	0.917493292	MPO;PLA2
0	0	1.284749455	0.917493292	PROCR;ADT
0	0	1.284749455	0.917493292	EDNRB;PAI
0	0	1.284749455	0.917493292	GPC1;APLN
0	0	1.284749455	0.917493292	EIF2AK4;PA
0	0	1.284749455	0.917493292	ACHE;ALDH

0	0	1.284749455	0.917493292	PRKCA;VRK
0	0	1.284749455	0.917493292	TNFSF4;NK
0	0	1.284749455	0.917493292	EIF2AK4;LG
0	0	1.284749455	0.917493292	FASTKD2;R
0	0	1.284749455	0.917493292	GSTP1;SOD
0	0	1.284749455	0.917493292	CLIP3;P2RX
0	0	1.284749455	0.917493292	UBA5;ATG
0	0	1.284749455	0.917493292	HPF1;MET
0	0	1.284749455	0.917493292	TWIST1;TY
0	0	1.284749455	0.917493292	MIF;TAF9B
0	0	1.284749455	0.917493292	SPHK2;GPD
0	0	1.284749455	0.917493292	ZFHX2;SCN
0	0	1.284749455	0.917493292	SYDE1;ACV
0	0	1.284749455	0.917493292	WNK4;MAG
0	0	1.284749455	0.917493292	HMGB1;ZF
0	0	1.284749455	0.917493292	ELP1;ELP4
0	0	1.046855254	0.74293065	RBL2;PSMD
0	0	1.063256052	0.753459297	MMP14;CT
0	0	1.063256052	0.753459297	MMP14;CT
0	0	1.063256052	0.753459297	PSMD10;P
0	0	1.063256052	0.753459297	PARP1;MM
0	0	1.10122164	0.779908383	MAPKBP1;
0	0	1.10122164	0.779908383	SLF1;MRNI
0	0	1.10122164	0.779908383	WNK1;WN
0	0	1.039352888	0.727925178	LATS1;LGA
0	0	1.012239311	0.706516007	STX12;IPO
0	0	1.075594084	0.746817942	CASP8AP2;
0	0	1.075594084	0.746817942	PRKCG;BSG
0	0	1.075594084	0.746817942	KANK1;GO
0	0	1.075594084	0.746817942	CBR1;DCXR
0	0	1.075594084	0.746817942	CALCRL;TF
0	0	1.075594084	0.746817942	RNASEH2C
0	0	1.156255449	0.79739882	TEKT3;DRC
0	0	1.156255449	0.79739882	GPI;SHPK;F
0	0	1.156255449	0.79739882	LGALS3;TIF
0	0	1.156255449	0.79739882	SUFU;IFT1
0	0	1.156255449	0.79739882	FUT8;B3GA
0	0	1.156255449	0.79739882	EEPD1;TRE
0	0	1.156255449	0.79739882	SFRP4;PDC
0	0	1.156255449	0.79739882	CADM1;CR
0	0	1.156255449	0.79739882	CD19;LPXN
0	0	1.156255449	0.79739882	CSTB;SVBP
0	0	1.156255449	0.79739882	FABP3;FAB
0	0	1.058001541	0.722610839	FUT8;STIL;
0	0	1.058001541	0.722610839	SMTN;MEF
0	0	1.058001541	0.722610839	LSM10;RAI
0	0	1.058001541	0.722610839	CD84;EPB4

0	0	1.058001541	0.722610839	CLIP3;SPPL	.
0	0	1.101177497	0.742765066	MMP14;IT	.
0	0	1.101177497	0.742765066	ZC3H7B;AC	.
0	0	1.101177497	0.742765066	KCNIP2;SL	.
0	0	1.101177497	0.742765066	STN1;TEN1	.
0	0	1.101177497	0.742765066	PDK4;CTNS	.
0	0	1.101177497	0.742765066	USP14;PDC	.
0	0	1.035408621	0.688522662	IPO11;LRSA	.
0	0	1.035408621	0.688522662	PLK4;KLHL	.
0	0	1.070571553	0.71011486	PI4K2B;ALS	.
0	0	1.070571553	0.71011486	KANK1;PKN	.
0	0	1.070571553	0.71011486	ACVR1C;PI	.
0	0	1.004149009	0.662339308	PSMD10;U	.
0	0	1.018016678	0.670305833	CNTNAP1;I	.
0	0	1.541637631	1.010803816	DLD	.
0	0	1.541637631	1.010803816	SLC27A1	.
0	0	1.541637631	1.010803816	COQ3	.
0	0	1.541637631	1.010803816	SLC22A5	.
0	0	1.541637631	1.010803816	SCARB2	.
0	0	1.541637631	1.010803816	FZD5	.
0	0	1.541637631	1.010803816	SLC36A4	.
0	0	1.541637631	1.010803816	ASPA	.
0	0	1.541637631	1.010803816	GAS6	.
0	0	1.541637631	1.010803816	C1QC	.
0	0	1.541637631	1.010803816	RBBP7	.
0	0	1.541637631	1.010803816	CD36	.
0	0	1.541637631	1.010803816	EIF2AK4	.
0	0	1.541637631	1.010803816	PDE1B	.
0	0	1.541637631	1.010803816	TFR2	.
0	0	1.541637631	1.010803816	SLC41A1	.
0	0	1.541637631	1.010803816	FITM2	.
0	0	1.541637631	1.010803816	ALDH7A1	.
0	0	1.541637631	1.010803816	SLC2A8	.
0	0	1.541637631	1.010803816	AUTS2	.
0	0	1.541637631	1.010803816	CHST14	.
0	0	1.541637631	1.010803816	SERINC5	.
0	0	1.541637631	1.010803816	PKD2	.
0	0	1.541637631	1.010803816	ERCC8	.
0	0	1.541637631	1.010803816	KDM2B	.
0	0	1.541637631	1.010803816	KDM2B	.
0	0	1.541637631	1.010803816	CEP290	.
0	0	1.541637631	1.010803816	PPARG	.
0	0	1.541637631	1.010803816	B3GALT2	.
0	0	1.541637631	1.010803816	B3GALT2	.
0	0	1.541637631	1.010803816	SLC6A12	.
0	0	1.541637631	1.010803816	TEK	.
0	0	1.541637631	1.010803816	GPAM	.

0	0	1.541637631	1.010803816	NPC2	.
0	0	1.541637631	1.010803816	GLA	.
0	0	1.541637631	1.010803816	GLA	.
0	0	1.541637631	1.010803816	LTBP4	.
0	0	1.541637631	1.010803816	SLC19A1	.
0	0	1.541637631	1.010803816	RBBP7	.
0	0	1.541637631	1.010803816	HS2ST1	.
0	0	1.541637631	1.010803816	SLC5A2	.
0	0	1.541637631	1.010803816	ETHE1	.
0	0	1.541637631	1.010803816	PFAS	.
0	0	1.541637631	1.010803816	SLC25A15	.
0	0	1.541637631	1.010803816	SERINC5	.
0	0	1.541637631	1.010803816	ALOX5	.
0	0	1.541637631	1.010803816	ALOX5	.
0	0	1.541637631	1.010803816	COL5A1	.
0	0	1.541637631	1.010803816	PPARG	.
0	0	1.541637631	1.010803816	SLC41A1	.
0	0	1.541637631	1.010803816	DNMT1	.
0	0	1.541637631	1.010803816	MSH6	.
0	0	1.541637631	1.010803816	OXSM	.
0	0	1.541637631	1.010803816	ANKRD31	.
0	0	1.541637631	1.010803816	CDC23	.
0	0	1.541637631	1.010803816	CDC23	.
0	0	1.541637631	1.010803816	FASTKD2	.
0	0	1.541637631	1.010803816	PSIP1	.
0	0	1.541637631	1.010803816	TCTA	.
0	0	1.541637631	1.010803816	NAA16	.
0	0	1.541637631	1.010803816	SCIN	.
0	0	1.541637631	1.010803816	ARL6IP5	.
0	0	1.541637631	1.010803816	SFRP4	.
0	0	1.541637631	1.010803816	PICK1	.
0	0	1.541637631	1.010803816	TREM2	.
0	0	1.541637631	1.010803816	LPXN	.
0	0	1.541637631	1.010803816	RNF113A	.
0	0	1.541637631	1.010803816	ZFYVE19	.
0	0	1.541637631	1.010803816	ATP2A1	.
0	0	1.541637631	1.010803816	USP14	.
0	0	1.541637631	1.010803816	DICER1	.
0	0	1.541637631	1.010803816	PASK	.
0	0	1.541637631	1.010803816	ANGPTL4	.
0	0	1.541637631	1.010803816	CD84	.
0	0	1.541637631	1.010803816	NBL1	.
0	0	1.541637631	1.010803816	CD84	.
0	0	1.541637631	1.010803816	FOXJ1	.
0	0	1.541637631	1.010803816	TREM2	.
0	0	1.541637631	1.010803816	ACVR1C	.
0	0	1.541637631	1.010803816	AHI1	.

0	0	1.541637631	1.010803816	EXOSC9	.
0	0	1.541637631	1.010803816	EXOSC9	.
0	0	1.541637631	1.010803816	EXOSC9	.
0	0	1.541637631	1.010803816	ABCC5	.
0	0	1.541637631	1.010803816	SHPK	.
0	0	1.541637631	1.010803816	DPH6	.
0	0	1.541637631	1.010803816	DPH6	.
0	0	1.541637631	1.010803816	PPARG	.
0	0	1.541637631	1.010803816	AHI1	.
0	0	1.541637631	1.010803816	MINPP1	.
0	0	1.541637631	1.010803816	CCL19	.
0	0	1.541637631	1.010803816	TOMM7	.
0	0	1.541637631	1.010803816	PLK4	.
0	0	1.541637631	1.010803816	MSR1	.
0	0	1.541637631	1.010803816	CCL19	.
0	0	1.541637631	1.010803816	BOK	.
0	0	1.541637631	1.010803816	DDB1	.
0	0	1.541637631	1.010803816	CITED2	.
0	0	1.541637631	1.010803816	RPS6KA5	.
0	0	1.541637631	1.010803816	CITED2	.
0	0	1.541637631	1.010803816	TREM2	.
0	0	1.541637631	1.010803816	CRTAM	.
0	0	1.541637631	1.010803816	CRTAM	.
0	0	1.541637631	1.010803816	STAP1	.
0	0	1.541637631	1.010803816	PLGRKT	.
0	0	1.541637631	1.010803816	MMP9	.
0	0	1.541637631	1.010803816	CLU	.
0	0	1.541637631	1.010803816	DAB2	.
0	0	1.541637631	1.010803816	SLC36A4	.
0	0	1.541637631	1.010803816	CEP290	.
0	0	1.541637631	1.010803816	INTS13	.
0	0	1.541637631	1.010803816	WRN	.
0	0	1.541637631	1.010803816	TPST1	.
0	0	1.541637631	1.010803816	UBA5	.
0	0	1.541637631	1.010803816	TRAIP	.
0	0	1.541637631	1.010803816	VMA21	.
0	0	1.541637631	1.010803816	SLC35A1	.
0	0	1.541637631	1.010803816	RAB11FIP5	.
0	0	1.541637631	1.010803816	ATP2B4	.
0	0	1.541637631	1.010803816	EMILIN1	.
0	0	1.541637631	1.010803816	EPB41	.
0	0	1.541637631	1.010803816	ABI3	.
0	0	1.541637631	1.010803816	PASK	.
0	0	1.541637631	1.010803816	PDGFB	.
0	0	1.541637631	1.010803816	TNFSF4	.
0	0	1.541637631	1.010803816	VRK2	.
0	0	1.541637631	1.010803816	SFRP4	.

0	0	1.541637631	1.010803816	VEGFB	.
0	0	1.541637631	1.010803816	CDK5RAP2	.
0	0	1.541637631	1.010803816	CDK5RAP2	.
0	0	1.541637631	1.010803816	ATP2B4	.
0	0	1.541637631	1.010803816	SEPTIN9	.
0	0	1.541637631	1.010803816	NEIL1	.
0	0	1.541637631	1.010803816	SASH1	.
0	0	1.541637631	1.010803816	TREM2	.
0	0	1.541637631	1.010803816	ARFIP1	.
0	0	1.541637631	1.010803816	LOXL3	.
0	0	1.541637631	1.010803816	TNFSF4	.
0	0	1.541637631	1.010803816	GPD1L	.
0	0	1.541637631	1.010803816	XRCC1	.
0	0	1.541637631	1.010803816	GNG2	.
0	0	1.541637631	1.010803816	SLX4	.
0	0	1.541637631	1.010803816	PDE1B	.
0	0	1.541637631	1.010803816	SPP1	.
0	0	1.541637631	1.010803816	ST3GAL4	.
0	0	1.541637631	1.010803816	MAPK8IP2	.
0	0	1.541637631	1.010803816	METTL4	.
0	0	1.541637631	1.010803816	ZC4H2	.
0	0	1.541637631	1.010803816	SLC25A14	.
0	0	1.541637631	1.010803816	FER1L5	.
0	0	1.541637631	1.010803816	FZD5	.
0	0	1.541637631	1.010803816	EXOSC9	.
0	0	1.541637631	1.010803816	ABCG2	.
0	0	1.051089242	0.68764791	SLC38A7;SI	.
0	0	1.051089242	0.68764791	CARMIL1;C	.
0	0	1.185855539	0.758620729	FHOD3;OB	.
0	0	1.185855539	0.758620729	BCAS3;SFR	.
0	0	1.185855539	0.758620729	FAM171A1	.
0	0	1.185855539	0.758620729	MTHFD1;T	.
0	0	1.185855539	0.758620729	RTN4;LNPK	.
0	0	1.185855539	0.758620729	RAP2A;FO)	.
0	0	1.185855539	0.758620729	RPGRIP1L;(	.
0	0	1.185855539	0.758620729	ABHD10;U	.
0	0	1.185855539	0.758620729	SMARCAD1	.
0	0	1.185855539	0.758620729	ERI1;TUT4	.
0	0	1.185855539	0.758620729	IMPACT;EI	.
0	0	1.185855539	0.758620729	PON2;ALO1	.
0	0	1.185855539	0.758620729	PARP1;MM	.
0	0	1.185855539	0.758620729	LGALS3;ED	.
0	0	1.185855539	0.758620729	NAXE;PPT1	.
0	0	1.185855539	0.758620729	MDC1;CHE	.
0	0	1.185855539	0.758620729	IGF1;HINFI	.
0	0	1.185855539	0.758620729	SCPEP1;AP	.
0	0	1.185855539	0.758620729	CCDC125;C	.

0	0	1.185855539	0.758620729	ACP4;GAS1.
0	0	1.185855539	0.758620729	ENTPD5;EN.
0	0	1.185855539	0.758620729	CREB3L3;P.
0	0	1.185855539	0.758620729	MRNIP;PAI.
0	0	1.185855539	0.758620729	TICAM1;GA.
0	0	1.185855539	0.758620729	P2RX3;MIF.
0	0	1.185855539	0.758620729	P2RX3;MIF.
0	0	1.185855539	0.758620729	NT5M;DHC.
0	0	1.185855539	0.758620729	ACTN3;SHN.
0	0	1.185855539	0.758620729	TREM2;CLU.
0	0	1.185855539	0.758620729	MTMR1;PF.
0	0	1.185855539	0.758620729	FARP2;KIF1.
0	0	1.185855539	0.758620729	PRKCA;C1C.
0	0	1.185855539	0.758620729	ESR1;RASG.
0	0	1.185855539	0.758620729	GSTP1;SOD.
0	0	1.185855539	0.758620729	SLC27A1;FI.
0	0	1.185855539	0.758620729	ESR1;PLPP.
0	0	1.185855539	0.758620729	FAM171A1.
0	0	1.185855539	0.758620729	NOXA1;DU.
0	0	1.185855539	0.758620729	POP7;POP4.
0	0	1.020124177	0.646352366	IPO11;NXT.
0	0	1.020124177	0.646352366	TRPM2;SLC.
0	0	1.020124177	0.646352366	ITGB3;TNF.
0	0	1.101133391	0.696290759	AUTS2;CDK.
0	0	1.101133391	0.696290759	FUT8;B3GA.
0	0	1.101133391	0.696290759	AIFM1;HAT.
0	0	1.101133391	0.696290759	ZW10;SPDL.
0	0	1.101133391	0.696290759	NFU1;NUB.
0	0	1.101133391	0.696290759	INTS14;ERI.
0	0	1.101133391	0.696290759	DAB2;CITE.
0	0	1.101133391	0.696290759	BACE1;GRN.
0	0	1.101133391	0.696290759	DAB2;CITE.
0	0	1.101133391	0.696290759	SEMA3A;SI.
0	0	1.101133391	0.696290759	LATS1;LTBI.
0	0	1.101133391	0.696290759	TMEM204;.
0	0	1.101133391	0.696290759	WRN;XRCC.
0	0	1.014141716	0.636916996	EPS8;KANK.
0	0	1.063145706	0.665954638	EPS8;CALD.
0	0	1.063145706	0.665954638	EXOSC9;LS.
0	0	1.063145706	0.665954638	GSTP1;DUS.
0	0	1.063145706	0.665954638	PDCD4;PPA.
0	0	1.063145706	0.665954638	EEPD1;ABC.
0	0	1.063145706	0.665954638	RPS6KA5;C.
0	0	1.041578227	0.646949844	TENM4;CA.
0	0	1.041578227	0.646949844	RARS2;LAR.
0	0	1.041578227	0.646949844	PRKCG;TIM.
0	0	1.027673505	0.633342874	PLCL1;PIK3.

0	0	1.027673505	0.633342874	KIF18A;CD
0	0	1.027673505	0.633342874	SCAMP5;L
0	0	1.005282761	0.60673554	SPARC;NA
0	0	0.994413882	0.598134077	NTNG2;CN
0	0	1.000914258	0.600284844	ALDH3A2;A
0	0	0.994423661	0.58930128	SH3RF3;M
0	0	1.027649368	0.597755643	UBA5;MTI
0	0	1.027649368	0.597755643	PIK3R2;IGF
0	0	1.027649368	0.597755643	ABCA2;IGF
0	0	1.027649368	0.597755643	ABCA2;CA
0	0	1.014110866	0.589717499	SLCO2B1;S
0	0	1.014110866	0.589717499	DGKA;ALO
0	0	1.014110866	0.589717499	SHTN1;GO
0	0	1.014110866	0.589717499	CADM1;CR
0	0	1.014110866	0.589717499	PDGFB;TB
0	0	1.014110866	0.589717499	ALOX5;PD
0	0	1.014110866	0.589717499	NDC1;NUP
0	0	1.014110866	0.589717499	YWHAQ;GI
0	0	1.005275843	0.58346964	ABCA2;AC
0	0	1.005275843	0.58346964	PTPMT1;SE
0	0	1.05102243	0.609552821	WNK1;WN
0	0	1.05102243	0.609552821	OSBPL5;NF
0	0	1.05102243	0.609552821	MTMR1;M
0	0	1.05102243	0.609552821	MLLT11;FA
0	0	1.05102243	0.609552821	RNF43;MV
0	0	1.05102243	0.609552821	ACP4;GAS1
0	0	1.05102243	0.609552821	LATS1;USP
0	0	1.05102243	0.609552821	GSTO1;PKD
0	0	0.999053857	0.578236806	GALNT12;C
0	0	0.999053857	0.578236806	CTSK;HMG
0	0	0.990865385	0.569513054	SHTN1;NTI
0	0	0.990865385	0.569513054	PSMD10;D
0	0	0.990865385	0.569513054	PSMD10;D
0	0	0.990865385	0.569513054	NDC1;RPA3
0	0	0.990865385	0.569513054	IMPACT;BF
0	0	1.101089325	0.631940501	MSH6;CD1
0	0	1.101089325	0.631940501	NTNG2;NID
0	0	1.101089325	0.631940501	GRAMD1B
0	0	1.101089325	0.631940501	DLG4;DIP2
0	0	1.101089325	0.631940501	ST3GAL5;L
0	0	1.101089325	0.631940501	SPHK2;MSI
0	0	1.101089325	0.631940501	CRELD1;PK
0	0	1.101089325	0.631940501	SEMA3A;C
0	0	1.101089325	0.631940501	BCAS3;COF
0	0	1.101089325	0.631940501	TSPYL2;GM
0	0	1.101089325	0.631940501	BCAS3;COF
0	0	1.101089325	0.631940501	SPHK2;TW

0	0	1.101089325	0.631940501	EDNRB;PAI.
0	0	1.101089325	0.631940501	PICK1;LGM.
0	0	1.101089325	0.631940501	CNTNAP1;I.
0	0	1.101089325	0.631940501	PDGFD;PD.
0	0	1.101089325	0.631940501	TFAP4;NU.
0	0	1.101089325	0.631940501	TFRC;SHLD.
0	0	1.101089325	0.631940501	ALOX5;ST3.
0	0	1.101089325	0.631940501	TREM2;RA.
0	0	1.101089325	0.631940501	TREM2;CL.
0	0	1.101089325	0.631940501	H1-10;ASF.
0	0	1.101089325	0.631940501	ELMOD2;Z.
0	0	1.101089325	0.631940501	CD84;RAS.
0	0	1.101089325	0.631940501	HMGB1;GA.
0	0	1.101089325	0.631940501	SPHK2;TNF.
0	0	1.101089325	0.631940501	TMEM161.
0	0	1.101089325	0.631940501	TFRC;SHLD.
0	0	1.101089325	0.631940501	SHPK;MIF .
0	0	1.101089325	0.631940501	CD84;SPH.
0	0	1.101089325	0.631940501	CAMK2A;K.
0	0	1.101089325	0.631940501	ACTN3;SH.
0	0	1.101089325	0.631940501	AUTS2;ALS.
0	0	1.101089325	0.631940501	MGARP;SC.
0	0	1.101089325	0.631940501	SLC1A3;AB.
0	0	0.985711815	0.562154101	BSCL2;ACH.
0	0	0.98010506	0.545350294	PSMD10;TI.
0	0	1.284625436	0.712361076	PNPLA2 .
0	0	1.284625436	0.712361076	GNG2 .
0	0	1.284625436	0.712361076	CAMK2A .
0	0	1.284625436	0.712361076	OAT .
0	0	1.284625436	0.712361076	SLC25A12 .
0	0	1.284625436	0.712361076	ZFPM1 .
0	0	1.284625436	0.712361076	CNTNAP1 .
0	0	1.284625436	0.712361076	CALCRL .
0	0	1.284625436	0.712361076	ATP2B4 .
0	0	1.284625436	0.712361076	COMT .
0	0	1.284625436	0.712361076	MAPK15 .
0	0	1.284625436	0.712361076	SHTN1 .
0	0	1.284625436	0.712361076	ILVBL .
0	0	1.284625436	0.712361076	APEH .
0	0	1.284625436	0.712361076	MAP2K5 .
0	0	1.284625436	0.712361076	GNG2 .
0	0	1.284625436	0.712361076	MTSS2 .
0	0	1.284625436	0.712361076	DDAH2 .
0	0	1.284625436	0.712361076	UBASH3B .
0	0	1.284625436	0.712361076	APLN .
0	0	1.284625436	0.712361076	GATM .
0	0	1.284625436	0.712361076	COX15 .

0	0	1.284625436	0.712361076	TEK	.
0	0	1.284625436	0.712361076	SEMA3A	.
0	0	1.284625436	0.712361076	TANC2	.
0	0	1.284625436	0.712361076	PRKCA	.
0	0	1.284625436	0.712361076	MEGF8	.
0	0	1.284625436	0.712361076	LIG1	.
0	0	1.284625436	0.712361076	DOLPP1	.
0	0	1.284625436	0.712361076	DOLPP1	.
0	0	1.284625436	0.712361076	MAPK15	.
0	0	1.284625436	0.712361076	MVB12A	.
0	0	1.284625436	0.712361076	SULT1C4	.
0	0	1.284625436	0.712361076	GRIN2C	.
0	0	1.284625436	0.712361076	CD9	.
0	0	1.284625436	0.712361076	MYO1E	.
0	0	1.284625436	0.712361076	SLC38A6	.
0	0	1.284625436	0.712361076	B3GALT2	.
0	0	1.284625436	0.712361076	VRK1	.
0	0	1.284625436	0.712361076	TEK	.
0	0	1.284625436	0.712361076	SETD4	.
0	0	1.284625436	0.712361076	SUV39H1	.
0	0	1.284625436	0.712361076	ABCC5	.
0	0	1.284625436	0.712361076	RCSD1	.
0	0	1.284625436	0.712361076	CAB39	.
0	0	1.284625436	0.712361076	RAB11FIP5	.
0	0	1.284625436	0.712361076	PLEKHA8	.
0	0	1.284625436	0.712361076	SLC48A1	.
0	0	1.284625436	0.712361076	TFR2	.
0	0	1.284625436	0.712361076	SLC36A4	.
0	0	1.284625436	0.712361076	ALOX5	.
0	0	1.284625436	0.712361076	PICK1	.
0	0	1.284625436	0.712361076	CARMIL1	.
0	0	1.284625436	0.712361076	NBL1	.
0	0	1.284625436	0.712361076	MDH1	.
0	0	1.284625436	0.712361076	CLIP3	.
0	0	1.284625436	0.712361076	PKD2	.
0	0	1.284625436	0.712361076	TUT4	.
0	0	1.284625436	0.712361076	PSEN2	.
0	0	1.284625436	0.712361076	MRC1	.
0	0	1.284625436	0.712361076	EIF2AK4	.
0	0	1.284625436	0.712361076	GSTP1	.
0	0	1.284625436	0.712361076	TWIST1	.
0	0	1.284625436	0.712361076	NUDT16L1	.
0	0	1.284625436	0.712361076	PASK	.
0	0	1.284625436	0.712361076	PPARG	.
0	0	1.284625436	0.712361076	RAD1	.
0	0	1.284625436	0.712361076	TIMP2	.
0	0	1.284625436	0.712361076	TMEM14A	.

0	0	1.284625436	0.712361076	TICAM1	.
0	0	1.284625436	0.712361076	TREM2	.
0	0	1.284625436	0.712361076	TREM2	.
0	0	1.284625436	0.712361076	CORO1C	.
0	0	1.284625436	0.712361076	PARK7	.
0	0	1.284625436	0.712361076	PPARG	.
0	0	1.284625436	0.712361076	ABCA2	.
0	0	1.284625436	0.712361076	GSTP1	.
0	0	1.284625436	0.712361076	SIRT2	.
0	0	1.284625436	0.712361076	RAD50	.
0	0	1.284625436	0.712361076	ACVR1C	.
0	0	1.284625436	0.712361076	PNRC2	.
0	0	1.284625436	0.712361076	DPYSL2	.
0	0	1.284625436	0.712361076	FOLR1	.
0	0	1.284625436	0.712361076	SRM	.
0	0	1.284625436	0.712361076	EIF2AK4	.
0	0	1.284625436	0.712361076	TREM2	.
0	0	1.284625436	0.712361076	STAP1	.
0	0	1.284625436	0.712361076	APLN	.
0	0	1.284625436	0.712361076	HMGB1	.
0	0	1.284625436	0.712361076	TACR2	.
0	0	1.284625436	0.712361076	TACR2	.
0	0	1.284625436	0.712361076	UBQLN2	.
0	0	1.284625436	0.712361076	PRDM11	.
0	0	1.284625436	0.712361076	TACR2	.
0	0	1.284625436	0.712361076	TENM4	.
0	0	1.284625436	0.712361076	AUTS2	.
0	0	1.284625436	0.712361076	PLA2R1	.
0	0	1.284625436	0.712361076	CORO1C	.
0	0	1.284625436	0.712361076	SPHK2	.
0	0	1.284625436	0.712361076	MLLT11	.
0	0	1.284625436	0.712361076	CKAP5	.
0	0	1.284625436	0.712361076	FABP3	.
0	0	1.284625436	0.712361076	PPT1	.
0	0	1.284625436	0.712361076	CEP250	.
0	0	1.284625436	0.712361076	ABCA2	.
0	0	1.284625436	0.712361076	ESR1	.
0	0	1.284625436	0.712361076	SYDE1	.
0	0	1.284625436	0.712361076	DOC2B	.
0	0	1.284625436	0.712361076	NIPSNAP2	.
0	0	1.284625436	0.712361076	YBX1	.
0	0	1.284625436	0.712361076	SLC9A1	.
0	0	1.284625436	0.712361076	CFAP206	.
0	0	1.284625436	0.712361076	FUCA2	.
0	0	1.284625436	0.712361076	EMILIN1	.
0	0	1.284625436	0.712361076	SLC45A3	.
0	0	1.284625436	0.712361076	SPHK2	.

0	0	1.284625436	0.712361076	SIRT5	.
0	0	1.284625436	0.712361076	CITED2	.
0	0	1.284625436	0.712361076	TREM2	.
0	0	1.284625436	0.712361076	PARK7	.
0	0	1.284625436	0.712361076	CRTAM	.
0	0	1.284625436	0.712361076	STAP1	.
0	0	1.284625436	0.712361076	PRAP1	.
0	0	1.284625436	0.712361076	KCNIP2	.
0	0	1.284625436	0.712361076	HMGB1	.
0	0	1.284625436	0.712361076	ITGB8	.
0	0	1.284625436	0.712361076	CDH3	.
0	0	1.284625436	0.712361076	ALS2	.
0	0	1.284625436	0.712361076	TRPV1	.
0	0	1.284625436	0.712361076	MRC1	.
0	0	1.284625436	0.712361076	ATP6V1A	.
0	0	1.284625436	0.712361076	PPP2CB	.
0	0	1.284625436	0.712361076	RPGRIP1L	.
0	0	1.284625436	0.712361076	XPO1	.
0	0	1.284625436	0.712361076	XPO1	.
0	0	1.284625436	0.712361076	XPO1	.
0	0	1.284625436	0.712361076	EEFSEC	.
0	0	1.284625436	0.712361076	ITGB3	.
0	0	1.284625436	0.712361076	MSH6	.
0	0	1.284625436	0.712361076	SHTN1	.
0	0	1.284625436	0.712361076	SLC25A14	.
0	0	1.284625436	0.712361076	DNM1	.
0	0	1.284625436	0.712361076	TACR2	.
0	0	1.284625436	0.712361076	EEFSEC	.
0	0	1.284625436	0.712361076	ALDH1A2	.
0	0	1.284625436	0.712361076	PPARG	.
0	0	0.978593272	0.535847829	PLCL1;PIK3	.
0	0	0.976854132	0.534536591	TSPYL2;LA	.
0	0	0.976854132	0.534536591	TNFSF18;P	.
0	0	0.983831273	0.53763854	EPM2A;LR	.
0	0	0.97546396	0.533063535	GPI;BCAS3	.
0	0	0.973377865	0.529818389	CPNE9;TRF	.
0	0	0.988052088	0.537805345	DYNC2I1;M	.
0	0	0.988052088	0.537805345	AIFM1;PEX	.
0	0	0.988052088	0.537805345	AGO4;TUT	.
0	0	0.973237317	0.527247642	RALBP1;TF	.
0	0	0.971883842	0.526357985	NDC1;GLM	.
0	0	0.994443116	0.537083219	SCPEP1;ED	.
0	0	0.994443116	0.537083219	DYNC2I1;H	.
0	0	0.994443116	0.537083219	CHRNB1;TI	.
0	0	0.994443116	0.537083219	EXOSC9;LS	.
0	0	0.994443116	0.537083219	SLC27A1;F	.
0	0	0.994443116	0.537083219	GSTP1;DU	.

0	0	0.994443116	0.537083219	STAR;PDK4 .
0	0	0.994443116	0.537083219	BCAS3;SFR .
0	0	0.994443116	0.537083219	FARP2;SEM .
0	0	1.005268944	0.534834729	DAB2;ABI3 .
0	0	1.005268944	0.534834729	CNRIP1;CB .
0	0	1.005268944	0.534834729	PLA2G12A .
0	0	1.005268944	0.534834729	DNMT1;AL .
0	0	1.005268944	0.534834729	WNK1;WN .
0	0	1.005268944	0.534834729	TOGARAM .
0	0	1.005268944	0.534834729	ALMS1;AS .
0	0	1.005268944	0.534834729	ANKH;TWI .
0	0	1.005268944	0.534834729	PPP1R3C;I .
0	0	1.005268944	0.534834729	RTEL1;RAD .
0	0	1.005268944	0.534834729	INTS14;INT .
0	0	1.005268944	0.534834729	CCDC88A;M .
0	0	0.963199913	0.502412336	SH3RF3;M .
0	0	0.969637174	0.503432895	DNMT1;CI .
0	0	0.963264192	0.498581929	MCFD2;TR .
0	0	0.963264192	0.498581929	DDB1;MDF .
0	0	0.963264192	0.498581929	MCFD2;TR .
0	0	0.963264192	0.498581929	MCFD2;TR .
0	0	1.027625272	0.529775422	HOGA1;GG .
0	0	1.027625272	0.529775422	PDK4;AKR1 .
0	0	1.027625272	0.529775422	CEP250;CA .
0	0	1.027625272	0.529775422	RILPL1;CCD .
0	0	1.027625272	0.529775422	DMAC2L;A .
0	0	1.027625272	0.529775422	ACTN3;PAF .
0	0	1.027625272	0.529775422	GSTP1;MA .
0	0	1.027625272	0.529775422	DFFA;CIDE .
0	0	1.027625272	0.529775422	MIF;TAF9B .
0	0	1.027625272	0.529775422	FER1L5;HM .
0	0	1.027625272	0.529775422	SLC37A4;SI .
0	0	1.027625272	0.529775422	CPNE9;SYT .
0	0	1.027625272	0.529775422	STN1;ATAD .
0	0	1.027625272	0.529775422	STAP1;TRE .
0	0	1.027625272	0.529775422	SCAMP5;D .
0	0	1.027625272	0.529775422	PDGFB;IGF .
0	0	1.027625272	0.529775422	DPYSL2;NT .
0	0	1.027625272	0.529775422	PICK1;ARFI .
0	0	1.027625272	0.529775422	GSTO1;CLI .
0	0	1.027625272	0.529775422	ACTN3;SHM .
0	0	1.027625272	0.529775422	TNFSF18;A .
0	0	1.027625272	0.529775422	EPB41;CAM .
0	0	1.027625272	0.529775422	TREM2;CD .
0	0	1.027625272	0.529775422	XRCC5;RPS .
0	0	1.027625272	0.529775422	INTS3;INTS .
0	0	1.027625272	0.529775422	SYNGR1;SY .

0	0	0.963280227	0.495498396	SLC26A1;R	.
0	0	0.963280227	0.495498396	BCAS3;TEK	.
0	0	0.963280227	0.495498396	CD63;GNG	.
0	0	0.963280227	0.495498396	CSTB;ASPH	.
0	0	0.963038225	0.494381967	VAV3;BCA	.
0	0	0.962989441	0.490709205	SPARC;ITG	.
0	0	0.963296248	0.490672766	PDGFB;TRE	.
0	0	0.963296248	0.490672766	KANK1;GK	.
0	0	0.963296248	0.490672766	MMP14;A	.
0	0	0.963312255	0.483009524	SPAST;KIF	.
0	0	0.963312255	0.483009524	GLP1R;CD	.
0	0	0.963312255	0.483009524	DLG4;TME	.
0	0	0.963312255	0.483009524	FBXW4;TW	.
0	0	0.963312255	0.483009524	MMP14;IT	.
0	0	0.963312255	0.483009524	MAP10;HD	.
0	0	0.963312255	0.483009524	UBASH3B;(	.
0	0	0.951270466	0.473159077	EPS8;TRPM	.
0	0	0.949983236	0.470777542	PSMD10;F	.
0	0	0.95794515	0.473297063	SPARC;ITG	.
0	0	0.948375172	0.467500842	PSMD10;P	.
0	0	0.948375172	0.467500842	ATP6V1A;F	.
0	0	0.948375172	0.467500842	SH3RF3;M	.
0	0	0.946311193	0.462993934	ARL4D;NE(	.
0	0	0.963328248	0.470231733	SCIN;SYT2;	.
0	0	0.963328248	0.470231733	UGDH;CHP	.
0	0	0.963328248	0.470231733	FBXL8;CRT	.
0	0	0.963328248	0.470231733	PMEL;HPS	.
0	0	0.963328248	0.470231733	KIF18A;KIF	.
0	0	0.963328248	0.470231733	LTBP4;PAR	.
0	0	0.963328248	0.470231733	TWIST1;CC	.
0	0	0.963328248	0.470231733	PDGFB;IGF	.
0	0	0.963328248	0.470231733	HMGB1;TL	.
0	0	0.963328248	0.470231733	XPO1;STRA	.
0	0	0.963328248	0.470231733	TREM2;CD	.
0	0	0.963328248	0.470231733	TWIST1;PA	.
0	0	0.963328248	0.470231733	GPNMB;VA	.
0	0	0.943567999	0.456732161	BEX3;HGF;	.
0	0	0.943567999	0.456732161	IMMP1L;IM	.
0	0	0.943567999	0.456732161	ASPH;TME	.
0	0	0.951599814	0.457309488	PSMD10;IM	.
0	0	0.964783451	0.463571273	TFRC;CITED	.
0	0	0.93974801	0.447841318	ARL4D;NE(	.
0	0	0.93974801	0.447841318	DNMT1;PD	.
0	0	0.93974801	0.447841318	KDM1B;XR	.
0	0	0.939616283	0.445697707	SPARC;ITG	.
0	0	1.101045296	0.520588146	SLC12A6	.
0	0	1.101045296	0.520588146	MAPK8IP3	.

0	0	1.101045296	0.520588146	ABCB9	.
0	0	1.101045296	0.520588146	TPK1	.
0	0	1.101045296	0.520588146	PLEKHM1	.
0	0	1.101045296	0.520588146	MAPK8IP3	.
0	0	1.101045296	0.520588146	SEMA3A	.
0	0	1.101045296	0.520588146	SLC3A1	.
0	0	1.101045296	0.520588146	FOLR1	.
0	0	1.101045296	0.520588146	CAMK2A	.
0	0	1.101045296	0.520588146	GAS6	.
0	0	1.101045296	0.520588146	DLG4	.
0	0	1.101045296	0.520588146	MFAP4	.
0	0	1.101045296	0.520588146	TST	.
0	0	1.101045296	0.520588146	PSMD10	.
0	0	1.101045296	0.520588146	MAPK15	.
0	0	1.101045296	0.520588146	DNM1	.
0	0	1.101045296	0.520588146	DNM1	.
0	0	1.101045296	0.520588146	RIPOR1	.
0	0	1.101045296	0.520588146	PLXNB2	.
0	0	1.101045296	0.520588146	GAS6	.
0	0	1.101045296	0.520588146	B3GALT2	.
0	0	1.101045296	0.520588146	CARNS1	.
0	0	1.101045296	0.520588146	CARNS1	.
0	0	1.101045296	0.520588146	KDM1B	.
0	0	1.101045296	0.520588146	SETD4	.
0	0	1.101045296	0.520588146	CCL19	.
0	0	1.101045296	0.520588146	HAT1	.
0	0	1.101045296	0.520588146	PKD2	.
0	0	1.101045296	0.520588146	LATS1	.
0	0	1.101045296	0.520588146	SGO2	.
0	0	1.101045296	0.520588146	GAS6	.
0	0	1.101045296	0.520588146	UQCC3	.
0	0	1.101045296	0.520588146	ATG14	.
0	0	1.101045296	0.520588146	PICK1	.
0	0	1.101045296	0.520588146	HMGB1	.
0	0	1.101045296	0.520588146	TWSG1	.
0	0	1.101045296	0.520588146	ACADVL	.
0	0	1.101045296	0.520588146	GRN	.
0	0	1.101045296	0.520588146	ARL6IP5	.
0	0	1.101045296	0.520588146	IGF1	.
0	0	1.101045296	0.520588146	ABCA2	.
0	0	1.101045296	0.520588146	ATRAID	.
0	0	1.101045296	0.520588146	PLA2R1	.
0	0	1.101045296	0.520588146	CAB39	.
0	0	1.101045296	0.520588146	LOXL3	.
0	0	1.101045296	0.520588146	SEMA3A	.
0	0	1.101045296	0.520588146	DLG4	.
0	0	1.101045296	0.520588146	SLC29A1	.

0	0	1.101045296	0.520588146	ACHE	.
0	0	1.101045296	0.520588146	ACP4	.
0	0	1.101045296	0.520588146	P2RX7	.
0	0	1.101045296	0.520588146	TREM2	.
0	0	1.101045296	0.520588146	GRN	.
0	0	1.101045296	0.520588146	TNFSF4	.
0	0	1.101045296	0.520588146	GRN	.
0	0	1.101045296	0.520588146	GAS6	.
0	0	1.101045296	0.520588146	TICAM1	.
0	0	1.101045296	0.520588146	DAB2	.
0	0	1.101045296	0.520588146	CLASP1	.
0	0	1.101045296	0.520588146	TREM2	.
0	0	1.101045296	0.520588146	APOA4	.
0	0	1.101045296	0.520588146	SIRT2	.
0	0	1.101045296	0.520588146	TWIST1	.
0	0	1.101045296	0.520588146	MMP14	.
0	0	1.101045296	0.520588146	TENM4	.
0	0	1.101045296	0.520588146	TFR2	.
0	0	1.101045296	0.520588146	GSTO1	.
0	0	1.101045296	0.520588146	STAR	.
0	0	1.101045296	0.520588146	DENND1B	.
0	0	1.101045296	0.520588146	PDGFB	.
0	0	1.101045296	0.520588146	DLG4	.
0	0	1.101045296	0.520588146	PARK7	.
0	0	1.101045296	0.520588146	KIF20B	.
0	0	1.101045296	0.520588146	KIF20B	.
0	0	1.101045296	0.520588146	MAPK8IP3	.
0	0	1.101045296	0.520588146	KDELR3	.
0	0	1.101045296	0.520588146	EPS8	.
0	0	1.101045296	0.520588146	NKAP	.
0	0	1.101045296	0.520588146	TNFSF4	.
0	0	1.101045296	0.520588146	HMGB1	.
0	0	1.101045296	0.520588146	ATP2A1	.
0	0	1.101045296	0.520588146	RANGRF	.
0	0	1.101045296	0.520588146	TWSG1	.
0	0	1.101045296	0.520588146	RALBP1	.
0	0	1.101045296	0.520588146	RNF113A	.
0	0	1.101045296	0.520588146	DPH6	.
0	0	1.101045296	0.520588146	GAS6	.
0	0	1.101045296	0.520588146	PALM	.
0	0	1.101045296	0.520588146	HMGB1	.
0	0	1.101045296	0.520588146	CD84	.
0	0	1.101045296	0.520588146	APOA4	.
0	0	1.101045296	0.520588146	LGALS3	.
0	0	1.101045296	0.520588146	SIRT2	.
0	0	1.101045296	0.520588146	CDC23	.
0	0	1.101045296	0.520588146	PLD1	.

0	0	1.101045296	0.520588146	TICAM1	.
0	0	1.101045296	0.520588146	UBASH3B	.
0	0	1.101045296	0.520588146	CD36	.
0	0	1.101045296	0.520588146	PLA2R1	.
0	0	1.101045296	0.520588146	SASH1	.
0	0	1.101045296	0.520588146	EPB41	.
0	0	1.101045296	0.520588146	SPHK2	.
0	0	1.101045296	0.520588146	ALOX5	.
0	0	1.101045296	0.520588146	SIRT2	.
0	0	1.101045296	0.520588146	GLE1	.
0	0	1.101045296	0.520588146	ALOX5	.
0	0	1.101045296	0.520588146	CLASP1	.
0	0	1.101045296	0.520588146	UQCC3	.
0	0	1.101045296	0.520588146	DLG4	.
0	0	1.101045296	0.520588146	AGO4	.
0	0	1.101045296	0.520588146	METTL15	.
0	0	1.101045296	0.520588146	LGMN	.
0	0	1.101045296	0.520588146	NBL1	.
0	0	1.101045296	0.520588146	ICE2	.
0	0	1.101045296	0.520588146	CITED2	.
0	0	1.101045296	0.520588146	SCAP	.
0	0	1.101045296	0.520588146	MTHFD1	.
0	0	1.101045296	0.520588146	DNM1	.
0	0	1.101045296	0.520588146	ZFPM1	.
0	0	1.101045296	0.520588146	NPRL3	.
0	0	1.101045296	0.520588146	EXOSC9	.
0	0	1.101045296	0.520588146	EDNRB	.
0	0	1.101045296	0.520588146	COL5A1	.
0	0	0.937092468	0.441745183	EPS8;P2RX	.
0	0	0.937092468	0.441745183	PSMA6;GR	.
0	0	0.937092468	0.441745183	WWTR1;ZH	.
0	0	0.933952897	0.436634668	CARMIL1;C	.
0	0	0.934068112	0.434737613	PLEKHM1;T	.
0	0	0.934068112	0.434737613	TUT4;DRO	.
0	0	0.934068112	0.434737613	SPARC;ALC	.
0	0	0.934068112	0.434737613	GSTP1;DU	.
0	0	0.934068112	0.434737613	MSR1;CD3	.
0	0	0.934068112	0.434737613	FAM210B;I	.
0	0	0.963344227	0.446574026	NPC2;SLC2	.
0	0	0.963344227	0.446574026	HAT1;HMG	.
0	0	0.963344227	0.446574026	STIL;FZD5	.
0	0	0.963344227	0.446574026	EDEM2;ST	.
0	0	0.963344227	0.446574026	ABCA5;AP(	.
0	0	0.963344227	0.446574026	KLHL24;MT	.
0	0	0.963344227	0.446574026	MIGA2;MI(	.
0	0	0.963344227	0.446574026	SHLD2;MA	.
0	0	0.963344227	0.446574026	MED25;GS	.

0	0	0.963344227	0.446574026	MAPKBP1; .
0	0	0.963344227	0.446574026	BSCL2;CIDE .
0	0	0.963344227	0.446574026	KANK1;CCI .
0	0	0.963344227	0.446574026	FARP2;PICI .
0	0	0.963344227	0.446574026	DDAH2;CD .
0	0	0.963344227	0.446574026	LGALS3;GP .
0	0	0.963344227	0.446574026	ABCA2;CLL .
0	0	0.963344227	0.446574026	AKT3;CIB1 .
0	0	0.963344227	0.446574026	CUX2;DLG4 .
0	0	0.963344227	0.446574026	TENM4;DIC .
0	0	0.963344227	0.446574026	MSR1;CD3 .
0	0	0.963344227	0.446574026	TENM4;DIC .
0	0	0.963344227	0.446574026	SEMA4C;AI .
0	0	0.963344227	0.446574026	ALKBH7;TIC .
0	0	0.963344227	0.446574026	ATRAID;VG .
0	0	0.963344227	0.446574026	SMC6;RAD .
0	0	0.963344227	0.446574026	CPNE9;SYT .
0	0	0.963344227	0.446574026	RANGRF;G .
0	0	0.963344227	0.446574026	TREM2;SO .
0	0	0.963344227	0.446574026	GLE1;HDAC .
0	0	0.963344227	0.446574026	EXOSC9;DI .
0	0	0.963344227	0.446574026	GPD1L;SNT .
0	0	0.92994278	0.429951282	MBNL2;PC .
0	0	0.92994278	0.429951282	DUS2;DTW .
0	0	0.951860087	0.437126072	SPARC;ITG .
0	0	0.92464426	0.421053117	ACTN3;GST .
0	0	0.931287435	0.424046972	P2RX7;TRP .
0	0	0.928242924	0.419773934	BBS2;OAT; .
0	0	0.924742807	0.414187749	RRAGB;RRA .
0	0	0.924742807	0.414187749	LSM10;ERI .
0	0	0.924742807	0.414187749	B4GALT2;B .
0	0	0.924742807	0.414187749	RUFY3;KIA .
0	0	0.924742807	0.414187749	PPP1R26;T .
0	0	0.924742807	0.414187749	SLC38A6;C .
0	0	0.924742807	0.414187749	PIK3R2;EFC .
0	0	0.924742807	0.414187749	KANK1;GRI .
0	0	0.924742807	0.414187749	KIF18A;KIF .
0	0	0.924742807	0.414187749	GGA2;PIGL .
0	0	0.924742807	0.414187749	CD19;TNFS .
0	0	0.924742807	0.414187749	P2RX3;RGN .
0	0	0.924742807	0.414187749	MAPRE3;C .
0	0	0.917321117	0.408886526	BRMS1L;SN .
0	0	0.917321117	0.408886526	ACTN3;PLC .
0	0	0.917321117	0.408886526	ABCA2;NPC .
0	0	0.917321117	0.408886526	LATS1;WW .
0	0	0.931854485	0.414269825	SETD4;LRS .
0	0	0.919961138	0.407778042	DAB2;ITGB .

0	0	0.919961138	0.407778042	CD86;VAV	.
0	0	0.919961138	0.407778042	PSMD10;P	.
0	0	0.914129228	0.399264836	CNTNAP1;(	.
0	0	0.914129228	0.399264836	CD86;TFRC	.
0	0	0.906544214	0.391580232	PRKCG;GIP	.
0	0	0.906544214	0.391580232	PKD2;DUO	.
0	0	0.906544214	0.391580232	H2AZ1;FAM	.
0	0	0.906544214	0.391580232	SYT2;CDK5	.
0	0	0.906462629	0.388201559	PON2;ALO	.
0	0	0.906380901	0.380797617	FHOD3;FAI	.
0	0	0.906625657	0.378242132	DMAC2L;A	.
0	0	0.906625657	0.378242132	FUCA1;STT	.
0	0	0.906625657	0.378242132	ABHD10;U	.
0	0	0.906625657	0.378242132	DNMT1;DM	.
0	0	0.906625657	0.378242132	DNMT1;DM	.
0	0	0.906625657	0.378242132	ACSS1;SUL	.
0	0	0.906625657	0.378242132	GRIN2C;MA	.
0	0	0.906625657	0.378242132	PHF20;MSI	.
0	0	0.906625657	0.378242132	PDCD4;TRE	.
0	0	0.906625657	0.378242132	SETD4;SUV	.
0	0	0.906625657	0.378242132	CCDC88A;S	.
0	0	0.906625657	0.378242132	TEK;LIMS1	.
0	0	0.906625657	0.378242132	PARK7;SIR	.
0	0	0.906625657	0.378242132	CHRNB1;D	.
0	0	0.906625657	0.378242132	GSDMB;TR	.
0	0	0.906625657	0.378242132	MST1;MTL	.
0	0	0.906625657	0.378242132	CEP97;CCS	.
0	0	0.906625657	0.378242132	SLC45A3;T	.
0	0	0.906625657	0.378242132	FZD5;TNFS	.
0	0	0.906625657	0.378242132	PDK4;CD36	.
0	0	0.906625657	0.378242132	ACHE;CHRI	.
0	0	0.906625657	0.378242132	FOXJ1;PKD	.
0	0	0.895937335	0.37343091	CNTNAP1;(	.
0	0	0.895937335	0.37343091	AKT3;PDGF	.
0	0	0.895937335	0.37343091	INF2;FZD5;	.
0	0	0.911156267	0.378428622	GLP1R;ALC	.
0	0	0.898842795	0.370760784	VAV3;ITGB	.
0	0	0.889125478	0.365422225	CDK5;GPC1	.
0	0	0.889125478	0.365422225	AIFM1;DNA	.
0	0	0.889125478	0.365422225	CD36;TAB1	.
0	0	0.889125478	0.365422225	E2F1;CIRBP	.
0	0	0.889125478	0.365422225	ALOX5;ADT	.
0	0	0.889125478	0.365422225	HGF;PDGFI	.
0	0	0.889125478	0.365422225	DDB1;MST	.
0	0	0.916958808	0.376485978	ENTPD5;NI	.
0	0	0.963360192	0.390800524	CCDC88C	.
0	0	0.963360192	0.390800524	MYH7	.

0	0	0.963360192	0.390800524	SRD5A1	.
0	0	0.963360192	0.390800524	LGMN	.
0	0	0.963360192	0.390800524	CLASP1	.
0	0	0.963360192	0.390800524	NTNG2	.
0	0	0.963360192	0.390800524	CD86	.
0	0	0.963360192	0.390800524	MMP3	.
0	0	0.963360192	0.390800524	MMP3	.
0	0	0.963360192	0.390800524	SCAP	.
0	0	0.963360192	0.390800524	CYP27A1	.
0	0	0.963360192	0.390800524	APOA4	.
0	0	0.963360192	0.390800524	UBASH3B	.
0	0	0.963360192	0.390800524	C1QC	.
0	0	0.963360192	0.390800524	LHFPL2	.
0	0	0.963360192	0.390800524	HMGB1	.
0	0	0.963360192	0.390800524	ZNF358	.
0	0	0.963360192	0.390800524	INPPL1	.
0	0	0.963360192	0.390800524	ODAD4	.
0	0	0.963360192	0.390800524	UGT1A6	.
0	0	0.963360192	0.390800524	FUT8	.
0	0	0.963360192	0.390800524	HDHD5	.
0	0	0.963360192	0.390800524	RPS6KA5	.
0	0	0.963360192	0.390800524	ADSS1	.
0	0	0.963360192	0.390800524	CD36	.
0	0	0.963360192	0.390800524	PDSS2	.
0	0	0.963360192	0.390800524	FUT8	.
0	0	0.963360192	0.390800524	FUT8	.
0	0	0.963360192	0.390800524	ITGB3	.
0	0	0.963360192	0.390800524	ZFPM1	.
0	0	0.963360192	0.390800524	TWSG1	.
0	0	0.963360192	0.390800524	GAS6	.
0	0	0.963360192	0.390800524	STXBP6	.
0	0	0.963360192	0.390800524	ACOT8	.
0	0	0.963360192	0.390800524	CD84	.
0	0	0.963360192	0.390800524	GSTP1	.
0	0	0.963360192	0.390800524	ANGPTL4	.
0	0	0.963360192	0.390800524	ITGB3	.
0	0	0.963360192	0.390800524	ARL6IP5	.
0	0	0.963360192	0.390800524	SLC25A4	.
0	0	0.963360192	0.390800524	EMILIN1	.
0	0	0.963360192	0.390800524	HDAC6	.
0	0	0.963360192	0.390800524	EXOSC9	.
0	0	0.963360192	0.390800524	TST	.
0	0	0.963360192	0.390800524	ASL	.
0	0	0.963360192	0.390800524	GTF2H5	.
0	0	0.963360192	0.390800524	TREM2	.
0	0	0.963360192	0.390800524	LRSAM1	.
0	0	0.963360192	0.390800524	MMP14	.

0	0	0.963360192	0.390800524	GLP1R	.
0	0	0.963360192	0.390800524	APOA4	.
0	0	0.963360192	0.390800524	TWIST1	.
0	0	0.963360192	0.390800524	SPHK2	.
0	0	0.963360192	0.390800524	TNFSF4	.
0	0	0.963360192	0.390800524	STPG1	.
0	0	0.963360192	0.390800524	CD36	.
0	0	0.963360192	0.390800524	MIF	.
0	0	0.963360192	0.390800524	SPHK2	.
0	0	0.963360192	0.390800524	APOA4	.
0	0	0.963360192	0.390800524	AKR1C4	.
0	0	0.963360192	0.390800524	SLC22A5	.
0	0	0.963360192	0.390800524	CITED2	.
0	0	0.963360192	0.390800524	CRTAM	.
0	0	0.963360192	0.390800524	TREM2	.
0	0	0.963360192	0.390800524	KRT10	.
0	0	0.963360192	0.390800524	PPP1R3C	.
0	0	0.963360192	0.390800524	ITGB3	.
0	0	0.963360192	0.390800524	BOK	.
0	0	0.963360192	0.390800524	CITED2	.
0	0	0.963360192	0.390800524	PPT1	.
0	0	0.963360192	0.390800524	NOXA1	.
0	0	0.963360192	0.390800524	IGF1	.
0	0	0.963360192	0.390800524	ABCA2	.
0	0	0.963360192	0.390800524	PARK7	.
0	0	0.963360192	0.390800524	DOC2B	.
0	0	0.963360192	0.390800524	DAB2	.
0	0	0.963360192	0.390800524	SLC41A1	.
0	0	0.963360192	0.390800524	SHMT2	.
0	0	0.963360192	0.390800524	SPP1	.
0	0	0.963360192	0.390800524	RPGRIP1L	.
0	0	0.963360192	0.390800524	PLXNB2	.
0	0	0.963360192	0.390800524	COL5A1	.
0	0	0.963360192	0.390800524	MSH6	.
0	0	0.963360192	0.390800524	CYP27A1	.
0	0	0.963360192	0.390800524	SEMA3A	.
0	0	0.963360192	0.390800524	HMGB1	.
0	0	0.963360192	0.390800524	APOA4	.
0	0	0.900429116	0.364703858	WFS1;ALO	.
0	0	0.900429116	0.364703858	PM20D1;G	.
0	0	0.910320809	0.368400768	GRN;TNFSI	.
0	0	0.888980291	0.357941894	BSCL2;CLIP	.
0	0	0.888980291	0.357941894	PPP1R26;B	.
0	0	0.880593109	0.352942518	GNG2;SPH	.
0	0	0.880593109	0.352942518	NDUFA11;I	.
0	0	0.880593109	0.352942518	CD86;GPNI	.
0	0	0.880593109	0.352942518	UBE3D;FAI	.

0	0	0.880593109	0.352942518	LATS1;CCL
0	0	0.880593109	0.352942518	SPHK2;WN
0	0	0.880593109	0.352942518	SPR;DDAH
0	0	0.880593109	0.352942518	MYO1E;MY
0	0	0.93325306	0.373734635	INTS13;TP
0	0	0.875525543	0.341138041	CDH3;CAD
0	0	0.875525543	0.341138041	DMAC2L;A
0	0	0.875525543	0.341138041	KIAA1614;I
0	0	0.884057556	0.344279235	WWTR1;TF
0	0	0.884057556	0.344279235	GLE1;IMPA
0	0	0.888834723	0.342045833	SPARC;NA
0	0	0.906052557	0.346026353	FHOD3;CA
0	0	0.913601025	0.346358577	EPM2A;PS
0	0	0.902528621	0.34190151	PSMD10;W
0	0	0.856146469	0.322874287	SCIN;PARV
0	0	0.856146469	0.322874287	CLDN12;W
0	0	0.856146469	0.322874287	KANK1;ARI
0	0	0.856146469	0.322874287	GSTP1;IGF
0	0	0.856146469	0.322874287	SETD4;SUV
0	0	0.856146469	0.322874287	MSR1;CD3
0	0	0.856146469	0.322874287	PIK3R2;EF(
0	0	0.856146469	0.322874287	LRRC59;IGI
0	0	0.856146469	0.322874287	CADM1;CR
0	0	0.856146469	0.322874287	ABCA2;CCL
0	0	0.856146469	0.322874287	INTS14;EX(
0	0	0.880384447	0.331978685	PSMD10;P
0	0	0.880384447	0.331978685	UBL4A;LIP
0	0	0.85620915	0.321708026	STX8;RILP
0	0	0.85620915	0.321708026	WFS1;ATP
0	0	0.85620915	0.321708026	ODAD4;SP
0	0	0.85620915	0.321708026	RAP2A;CLA
0	0	0.85620915	0.321708026	UGDH;ME(
0	0	0.85620915	0.321708026	PPBP;SLC2
0	0	0.85620915	0.321708026	CDK4;E2F1
0	0	0.85620915	0.321708026	CITED2;PKI
0	0	0.85620915	0.321708026	SEMA3A;SI
0	0	0.85620915	0.321708026	LATS1;TFA
0	0	0.85620915	0.321708026	CDK5;EIF2I
0	0	0.85620915	0.321708026	RALBP1;SL
0	0	0.85620915	0.321708026	HMGB1;IG
0	0	0.85620915	0.321708026	TNFSF4;NK
0	0	0.85620915	0.321708026	TFR2;SPP1
0	0	0.85620915	0.321708026	MMP14;GA
0	0	0.85620915	0.321708026	RPS6KA5;D
0	0	0.85620915	0.321708026	PLGRKT;NK
0	0	0.85620915	0.321708026	CREB3L3;G
0	0	0.85620915	0.321708026	PDGFB;IGF

0	0	0.85620915	0.321708026	ABCC5;ABC	.
0	0	0.856083733	0.318307786	ACER2;KAN	.
0	0	0.856083733	0.318307786	SEPTIN4;ST	.
0	0	0.856083733	0.318307786	KANK1;ST3	.
0	0	0.893963441	0.33186126	HPS4;ZDHH	.
0	0	0.86974926	0.319672953	CPNE9;TRF	.
0	0	0.86974926	0.319672953	TBL2;FAM1	.
0	0	0.877533859	0.320749747	DNAJB2;DA	.
0	0	0.877533859	0.320749747	WFS1;COL1	.
0	0	0.856020942	0.31170745	P2RX7;WFS	.
0	0	0.856020942	0.31170745	NDC1;NUP	.
0	0	0.855958097	0.304361448	PSMA6;CTS	.
0	0	0.875253409	0.310395492	SETD4;LRS1	.
0	0	0.875253409	0.310395492	LATS1;TFR(	.
0	0	0.856271777	0.2994987	TBCD	.
0	0	0.856271777	0.2994987	SLC36A4	.
0	0	0.856271777	0.2994987	GNE	.
0	0	0.856271777	0.2994987	DDAH2	.
0	0	0.856271777	0.2994987	ATP2B4	.
0	0	0.856271777	0.2994987	SHPK	.
0	0	0.856271777	0.2994987	TRPM2	.
0	0	0.856271777	0.2994987	GUCY2C	.
0	0	0.856271777	0.2994987	SLC12A6	.
0	0	0.856271777	0.2994987	XYLT2	.
0	0	0.856271777	0.2994987	APOA4	.
0	0	0.856271777	0.2994987	MFAP4	.
0	0	0.856271777	0.2994987	MTHFD1	.
0	0	0.856271777	0.2994987	ZNF358	.
0	0	0.856271777	0.2994987	KDM1B	.
0	0	0.856271777	0.2994987	HOXB4	.
0	0	0.856271777	0.2994987	KDM2B	.
0	0	0.856271777	0.2994987	PRDX4	.
0	0	0.856271777	0.2994987	CD19	.
0	0	0.856271777	0.2994987	KYAT1	.
0	0	0.856271777	0.2994987	SOD1	.
0	0	0.856271777	0.2994987	APLN	.
0	0	0.856271777	0.2994987	BBS2	.
0	0	0.856271777	0.2994987	DGKA	.
0	0	0.856271777	0.2994987	FOXJ1	.
0	0	0.856271777	0.2994987	PNRC2	.
0	0	0.856271777	0.2994987	TUT4	.
0	0	0.856271777	0.2994987	MRC1	.
0	0	0.856271777	0.2994987	FER1L5	.
0	0	0.856271777	0.2994987	SLC12A6	.
0	0	0.856271777	0.2994987	ITGB3	.
0	0	0.856271777	0.2994987	TWSG1	.
0	0	0.856271777	0.2994987	ATRAID	.

0	0	0.856271777	0.2994987	SUV39H1	.
0	0	0.856271777	0.2994987	ACTN3	.
0	0	0.856271777	0.2994987	RAB11FIP5	.
0	0	0.856271777	0.2994987	FOXJ1	.
0	0	0.856271777	0.2994987	DNAJB2	.
0	0	0.856271777	0.2994987	IMPACT	.
0	0	0.856271777	0.2994987	ACTN3	.
0	0	0.856271777	0.2994987	COMMD1	.
0	0	0.856271777	0.2994987	TREM2	.
0	0	0.856271777	0.2994987	CDH3	.
0	0	0.856271777	0.2994987	GNB5	.
0	0	0.856271777	0.2994987	RTN4	.
0	0	0.856271777	0.2994987	FARP2	.
0	0	0.856271777	0.2994987	EXOSC9	.
0	0	0.856271777	0.2994987	EXOSC9	.
0	0	0.856271777	0.2994987	NME4	.
0	0	0.856271777	0.2994987	CYP2U1	.
0	0	0.856271777	0.2994987	SFRP4	.
0	0	0.856271777	0.2994987	LGALS1	.
0	0	0.856271777	0.2994987	ARNTL	.
0	0	0.856271777	0.2994987	ST3GAL4	.
0	0	0.856271777	0.2994987	CUX2	.
0	0	0.856271777	0.2994987	ST3GAL4	.
0	0	0.856271777	0.2994987	MMP9	.
0	0	0.856271777	0.2994987	ACTN3	.
0	0	0.856271777	0.2994987	ICE2	.
0	0	0.856271777	0.2994987	PWP1	.
0	0	0.856271777	0.2994987	ITGB3	.
0	0	0.856271777	0.2994987	LGALS1	.
0	0	0.856271777	0.2994987	SULT1C4	.
0	0	0.856271777	0.2994987	DROSHA	.
0	0	0.856271777	0.2994987	EMC9	.
0	0	0.856271777	0.2994987	FNTB	.
0	0	0.856271777	0.2994987	GUCY2C	.
0	0	0.856271777	0.2994987	MYBPC3	.
0	0	0.856271777	0.2994987	STAR	.
0	0	0.856271777	0.2994987	PDK2	.
0	0	0.856271777	0.2994987	WNK1	.
0	0	0.856271777	0.2994987	KDM1B	.
0	0	0.856271777	0.2994987	C1QC	.
0	0	0.856271777	0.2994987	NIPSNAP2	.
0	0	0.856271777	0.2994987	ST3GAL4	.
0	0	0.856271777	0.2994987	CD84	.
0	0	0.856271777	0.2994987	TNFSF4	.
0	0	0.856271777	0.2994987	MTMR1	.
0	0	0.856271777	0.2994987	CEP250	.
0	0	0.856271777	0.2994987	MMP9	.

0	0	0.856271777	0.2994987	CD84	.
0	0	0.856271777	0.2994987	CLU	.
0	0	0.856271777	0.2994987	SHPK	.
0	0	0.856271777	0.2994987	MAP2K5	.
0	0	0.856271777	0.2994987	PPARG	.
0	0	0.856271777	0.2994987	ATP2A1	.
0	0	0.856271777	0.2994987	SCIN	.
0	0	0.856271777	0.2994987	TST	.
0	0	0.866515516	0.300734414	CRTAP;COI	.
0	0	0.866515516	0.300734414	SETD4;GRI	.
0	0	0.855895197	0.296806231	WFS1;ALO	.
0	0	0.855895197	0.296806231	TRPM2;OD	.
0	0	0.930435593	0.322206508	TFRC;CITE	.
0	0	0.825523104	0.285659648	DNAJB4;EI	.
0	0	0.825523104	0.285659648	PKD2;HCN	.
0	0	0.825523104	0.285659648	TFAP4;E2F	.
0	0	0.825523104	0.285659648	SUFU;TWI	.
0	0	0.825523104	0.285659648	FZD5;HPS4	.
0	0	0.825523104	0.285659648	GORASP1;I	.
0	0	0.825523104	0.285659648	SCAMP5;S	.
0	0	0.825523104	0.285659648	EPS8;VAV3	.
0	0	0.825523104	0.285659648	LATS1;IGF1	.
0	0	0.825523104	0.285659648	FITM2;APC	.
0	0	0.832899188	0.287225794	MAP4K2;T	.
0	0	0.832899188	0.287225794	RNASEH2C	.
0	0	0.832899188	0.287225794	METTL22;E	.
0	0	0.832899188	0.287225794	PPA2;ARL6	.
0	0	0.837364368	0.284870256	PSMD10;P	.
0	0	0.837364368	0.284870256	HDAC6;RTI	.
0	0	0.837364368	0.284870256	KANK1;CAI	.
0	0	0.811099645	0.274632103	EDNRB;SEI	.
0	0	0.811099645	0.274632103	ADTRP;MG	.
0	0	0.811099645	0.274632103	UGDH;CHP	.
0	0	0.811099645	0.274632103	IGF1;PLD3	.
0	0	0.811099645	0.274632103	CAB39;MI	.
0	0	0.811099645	0.274632103	CIB1;CLASI	.
0	0	0.811099645	0.274632103	DAB2;ABI3	.
0	0	0.811099645	0.274632103	ACVR1C;IG	.
0	0	0.811099645	0.274632103	ALOX5;SIG	.
0	0	0.811099645	0.274632103	CDK5;FAM	.
0	0	0.811099645	0.274632103	STAP1;KCI	.
0	0	0.811099645	0.274632103	PDK4;TLE5	.
0	0	0.811099645	0.274632103	VGLL4;TP7	.
0	0	0.811099645	0.274632103	GORASP1;(	.
0	0	0.811099645	0.274632103	METTL5;TI	.
0	0	0.811099645	0.274632103	P2RX7;NIP	.
0	0	0.881709495	0.295474489	PSMD10;A	.

0	0	0.842474072	0.275553873	GRAMD1B
0	0	0.842474072	0.275553873	VAV3;NCKI
0	0	0.842474072	0.275553873	PHF20;HAT
0	0	0.855706165	0.274770011	CD63;ACTN
0	0	0.855706165	0.274770011	FASTKD2;R
0	0	0.855706165	0.274770011	LATS1;DAB
0	0	0.810934882	0.259303006	ZNHIT1;NA
0	0	0.810934882	0.259303006	ST3GAL5;C
0	0	0.810934882	0.259303006	LGALS3;PD
0	0	0.810934882	0.259303006	THRB;TAF1
0	0	0.810934882	0.259303006	TENM4;KIF
0	0	0.888248614	0.282565495	GRN;SPAR(
0	0	0.797011695	0.253037053	CD86;LPAR
0	0	0.797011695	0.253037053	MYBPC3;ZI
0	0	0.797011695	0.253037053	TM7SF3;HI
0	0	0.797011695	0.253037053	COG2;COP
0	0	0.797011695	0.253037053	APOOL;MT
0	0	0.797011695	0.253037053	TFAP4;NAF
0	0	0.797011695	0.253037053	ACER2;BCA
0	0	0.797011695	0.253037053	BBS2;KIAA(
0	0	0.797011695	0.253037053	DAB2;CLO(
0	0	0.797011695	0.253037053	FKBP7;PPIF
0	0	0.797011695	0.253037053	CARMIL1;A
0	0	0.797011695	0.253037053	AKT3;CIB1;
0	0	0.797011695	0.253037053	DLG4;CAM
0	0	0.797011695	0.253037053	RRAGB;RRA
0	0	0.825294631	0.258819818	ACVR1C;AS
0	0	0.855643045	0.26785108	SCAMP5;CI
0	0	0.84528505	0.264246107	WFS1;COL1
0	0	0.862940848	0.268682506	STN1;ATAD
0	0	0.829465905	0.255800283	VAV3;NCKI
0	0	0.829465905	0.255800283	ACHE;GOLI
0	0	0.829465905	0.255800283	GRAMD1B
0	0	0.770501089	0.235208449	SGO2;ANK
0	0	0.770501089	0.235208449	TUBB;KLRF
0	0	0.770501089	0.235208449	LATS1;TFAI
0	0	0.770501089	0.235208449	VSIG4;HAV
0	0	0.770501089	0.235208449	MEIS1;CIB1
0	0	0.770501089	0.235208449	TIPRL;STYX
0	0	0.770501089	0.235208449	MIGA2;MI(
0	0	0.770501089	0.235208449	PLA2G12A
0	0	0.770501089	0.235208449	ABCA2;CLU
0	0	0.770501089	0.235208449	MED24;TW
0	0	0.770501089	0.235208449	GRN;APH1
0	0	0.770501089	0.235208449	CHD5;PLA2
0	0	0.770501089	0.235208449	PSMA6;PSI
0	0	0.770501089	0.235208449	DLG4;KIF3A

0	0	0.770501089	0.235208449	EDNRB;PAI	.
0	0	0.770501089	0.235208449	PARK7;BOI	.
0	0	0.770501089	0.235208449	ITGB3;ALKI	.
0	0	0.770501089	0.235208449	MAP2K5;TI	.
0	0	0.770501089	0.235208449	METTL5;M	.
0	0	0.770501089	0.235208449	MVB12A;V	.
0	0	0.855579869	0.261174521	CD86;IL36A	.
0	0	0.862346036	0.261633727	PPM1L;PDI	.
0	0	0.770601045	0.233319494	CYP27A1	.
0	0	0.770601045	0.233319494	XYLT2	.
0	0	0.770601045	0.233319494	ITGB3	.
0	0	0.770601045	0.233319494	ZFPM1	.
0	0	0.770601045	0.233319494	CD19	.
0	0	0.770601045	0.233319494	KCNIP2	.
0	0	0.770601045	0.233319494	ZC4H2	.
0	0	0.770601045	0.233319494	KIF14	.
0	0	0.770601045	0.233319494	ATP6V1A	.
0	0	0.770601045	0.233319494	CHEK1	.
0	0	0.770601045	0.233319494	EDNRB	.
0	0	0.770601045	0.233319494	RAP2A	.
0	0	0.770601045	0.233319494	VRK1	.
0	0	0.770601045	0.233319494	C1QC	.
0	0	0.770601045	0.233319494	VEGFB	.
0	0	0.770601045	0.233319494	IMPA2	.
0	0	0.770601045	0.233319494	IGF1	.
0	0	0.770601045	0.233319494	CD36	.
0	0	0.770601045	0.233319494	MSH6	.
0	0	0.770601045	0.233319494	ATG10	.
0	0	0.770601045	0.233319494	PKD2	.
0	0	0.770601045	0.233319494	AGO4	.
0	0	0.770601045	0.233319494	IGF1	.
0	0	0.770601045	0.233319494	CRTAM	.
0	0	0.770601045	0.233319494	FSTL3	.
0	0	0.770601045	0.233319494	ABCA2	.
0	0	0.770601045	0.233319494	TARBP2	.
0	0	0.770601045	0.233319494	TNFSF4	.
0	0	0.770601045	0.233319494	ADTRP	.
0	0	0.770601045	0.233319494	PARK7	.
0	0	0.770601045	0.233319494	CAB39	.
0	0	0.770601045	0.233319494	SLC25A4	.
0	0	0.770601045	0.233319494	COMMD1	.
0	0	0.770601045	0.233319494	ALOX5	.
0	0	0.770601045	0.233319494	TNFSF4	.
0	0	0.770601045	0.233319494	AGO4	.
0	0	0.770601045	0.233319494	PDXP	.
0	0	0.770601045	0.233319494	IMPA2	.
0	0	0.770601045	0.233319494	SCIN	.

0	0	0.770601045	0.233319494	SCAP	.
0	0	0.770601045	0.233319494	PARK7	.
0	0	0.770601045	0.233319494	DAB2	.
0	0	0.770601045	0.233319494	ZDHHC15	.
0	0	0.770601045	0.233319494	DNMT1	.
0	0	0.770601045	0.233319494	POT1	.
0	0	0.770601045	0.233319494	CDH3	.
0	0	0.770601045	0.233319494	PRKCA	.
0	0	0.770601045	0.233319494	DAB2	.
0	0	0.770601045	0.233319494	PRAP1	.
0	0	0.770601045	0.233319494	CREB3L3	.
0	0	0.770601045	0.233319494	SLC27A1	.
0	0	0.770601045	0.233319494	PDGFB	.
0	0	0.770601045	0.233319494	STX17	.
0	0	0.770601045	0.233319494	NT5M	.
0	0	0.770601045	0.233319494	CAMK2A	.
0	0	0.770601045	0.233319494	TWSG1	.
0	0	0.770601045	0.233319494	PROCR	.
0	0	0.770601045	0.233319494	KDM1B	.
0	0	0.770601045	0.233319494	POT1	.
0	0	0.770601045	0.233319494	DNAJB2	.
0	0	0.770601045	0.233319494	ADTRP	.
0	0	0.770601045	0.233319494	SPHK2	.
0	0	0.770601045	0.233319494	MLLT11	.
0	0	0.770601045	0.233319494	RASGRP1	.
0	0	0.770601045	0.233319494	GSTP1	.
0	0	0.770601045	0.233319494	LGALS3	.
0	0	0.770601045	0.233319494	HMGB1	.
0	0	0.770601045	0.233319494	DENND1B	.
0	0	0.770601045	0.233319494	TREM2	.
0	0	0.770601045	0.233319494	ABCA2	.
0	0	0.770601045	0.233319494	SEC11C	.
0	0	0.770601045	0.233319494	KLHL41	.
0	0	0.770601045	0.233319494	CDK5	.
0	0	0.770601045	0.233319494	KYAT1	.
0	0	0.770601045	0.233319494	EDNRB	.
0	0	0.770601045	0.233319494	UGT1A6	.
0	0	0.847038495	0.252693165	PSMD10;V	.
0	0	0.855516637	0.254738942	USP14;GRI	.
0	0	0.80238329	0.238036366	CD86;PDCI	.
0	0	0.790096951	0.234194476	CD86;LPAR	.
0	0	0.790096951	0.234194476	ZMYND15;	.
0	0	0.790096951	0.234194476	RARS2;LAR	.
0	0	0.878493448	0.260146769	PSMD10;U	.
0	0	0.86182257	0.254905576	BCAS3;RAL	.
0	0	0.810769832	0.238667394	BACE1;GGA	.
0	0	0.866689904	0.253849903	DNAI4;NDC	.

0	0	0.770401046	0.224381903	EPS8;CALD
0	0	0.770401046	0.224381903	CHRNB1;FE
0	0	0.770401046	0.224381903	ITGB3;SEM
0	0	0.770401046	0.224381903	FZD5;SPHK
0	0	0.770401046	0.224381903	PREPL;CAM
0	0	0.770401046	0.224381903	E2F1;CIRBP
0	0	0.770401046	0.224381903	ACER2;PDK
0	0	0.770401046	0.224381903	CUL7;GLM
0	0	0.837008802	0.243054795	ASPH;ATG1
0	0	0.837008802	0.243054795	GRN;TNFSF
0	0	0.885349326	0.256013784	CD63;KANI
0	0	0.907363313	0.26220393	LIPT1;ATP2
0	0	0.861356968	0.248472402	CAMK2A;A
0	0	0.821459152	0.235082609	B3GALT2;M
0	0	0.865988372	0.24735186	KLHL25;SH
0	0	0.838604333	0.238345537	PSMD10;V
0	0	0.825065559	0.232026159	LATS1;TFR(
0	0	0.825065559	0.232026159	ASPH;TME
0	0	0.7859636	0.217628408	VEGFB;HM
0	0	0.7859636	0.217628408	PSMD10;P
0	0	0.796745887	0.220076336	ALDH3A2;(
0	0	0.796745887	0.220076336	CDK8;MED
0	0	0.733769063	0.202026461	APLP1;RPG
0	0	0.733769063	0.202026461	BCAS3;WN
0	0	0.733769063	0.202026461	RPS6KA5;S
0	0	0.733769063	0.202026461	DUSP19;SA
0	0	0.733769063	0.202026461	MED24;ESI
0	0	0.733769063	0.202026461	UBASH3B;I
0	0	0.733769063	0.202026461	GSTO1;CLI(
0	0	0.733769063	0.202026461	MAPRE3;P
0	0	0.733769063	0.202026461	KIF3A;KIFA
0	0	0.770300916	0.211597036	UBASH3B;I
0	0	0.770300916	0.211597036	TADA3;TRI
0	0	0.770300916	0.211597036	CIB1;CD36
0	0	0.770300916	0.211597036	CARMIL1;C
0	0	0.804614482	0.220370166	VAV3;NCKI
0	0	0.86477871	0.235196431	TSPYL2;WV
0	0	0.830335546	0.224766816	BSCL2;ACH
0	0	0.810604493	0.219306729	SLC27A1;P
0	0	0.86824683	0.233419857	TSPYL2;PSI
0	0	0.745507214	0.199165372	ACTN3;LAM
0	0	0.745507214	0.199165372	AGTPBP1;Z
0	0	0.745507214	0.199165372	SUV39H1;D
0	0	0.745507214	0.199165372	STAR;SRD5
0	0	0.745507214	0.199165372	P2RX7;P2R
0	0	0.745507214	0.199165372	NEU3;CCD(
0	0	0.745507214	0.199165372	TNFSF4;HM

0	0	0.745507214	0.199165372	PDGFB;PP/	.
0	0	0.745507214	0.199165372	GSTO1;CD1	.
0	0	0.745507214	0.199165372	ALDH3A2;(	.
0	0	0.745507214	0.199165372	CRTAM;HN	.
0	0	0.745507214	0.199165372	THUMPD2	.
0	0	0.815312629	0.217361594	MEIS1;MEI	.
0	0	0.815312629	0.217361594	CSTB;EDNF	.
0	0	0.70050681	0.184195098	DYRK1B	.
0	0	0.70050681	0.184195098	CPA3	.
0	0	0.70050681	0.184195098	SLC25A4	.
0	0	0.70050681	0.184195098	RMDN1	.
0	0	0.70050681	0.184195098	BBS2	.
0	0	0.70050681	0.184195098	AGTPBP1	.
0	0	0.70050681	0.184195098	NPRL2	.
0	0	0.70050681	0.184195098	NPRL2	.
0	0	0.70050681	0.184195098	CHST14	.
0	0	0.70050681	0.184195098	STX10	.
0	0	0.70050681	0.184195098	RTN4	.
0	0	0.70050681	0.184195098	ATP5PO	.
0	0	0.70050681	0.184195098	ITGB5	.
0	0	0.70050681	0.184195098	ACSS1	.
0	0	0.70050681	0.184195098	MYO1E	.
0	0	0.70050681	0.184195098	IMPA2	.
0	0	0.70050681	0.184195098	KDELR3	.
0	0	0.70050681	0.184195098	SLC24A5	.
0	0	0.70050681	0.184195098	UQCC3	.
0	0	0.70050681	0.184195098	MTM1	.
0	0	0.70050681	0.184195098	ZNF502	.
0	0	0.70050681	0.184195098	BBS5	.
0	0	0.70050681	0.184195098	EIF2AK4	.
0	0	0.70050681	0.184195098	ATP2B4	.
0	0	0.70050681	0.184195098	ATP2B4	.
0	0	0.70050681	0.184195098	VSIG4	.
0	0	0.70050681	0.184195098	ACADVL	.
0	0	0.70050681	0.184195098	ADTRP	.
0	0	0.70050681	0.184195098	ESR1	.
0	0	0.70050681	0.184195098	RECQL5	.
0	0	0.70050681	0.184195098	HABP4	.
0	0	0.70050681	0.184195098	NT5M	.
0	0	0.70050681	0.184195098	PDXP	.
0	0	0.70050681	0.184195098	NAA16	.
0	0	0.70050681	0.184195098	EDNRB	.
0	0	0.70050681	0.184195098	APOA4	.
0	0	0.70050681	0.184195098	FABP3	.
0	0	0.70050681	0.184195098	ABI3	.
0	0	0.70050681	0.184195098	BOK	.
0	0	0.70050681	0.184195098	CDC23	.

0	0	0.70050681	0.184195098	CDC23	.
0	0	0.70050681	0.184195098	CDC23	.
0	0	0.70050681	0.184195098	PDXP	.
0	0	0.70050681	0.184195098	MTHFD1	.
0	0	0.70050681	0.184195098	PDXP	.
0	0	0.70050681	0.184195098	ABCA2	.
0	0	0.70050681	0.184195098	ABCA2	.
0	0	0.70050681	0.184195098	CPA3	.
0	0	0.70050681	0.184195098	GRN	.
0	0	0.70050681	0.184195098	EIF2AK4	.
0	0	0.70050681	0.184195098	PPP1R3C	.
0	0	0.70050681	0.184195098	LGALS3	.
0	0	0.70050681	0.184195098	MMP9	.
0	0	0.70050681	0.184195098	MYL9	.
0	0	0.70050681	0.184195098	TICAM1	.
0	0	0.70050681	0.184195098	PLGRKT	.
0	0	0.70050681	0.184195098	UBASH3B	.
0	0	0.70050681	0.184195098	FEN1	.
0	0	0.70050681	0.184195098	TICAM1	.
0	0	0.783197331	0.202923118	ACER2;CIB	.
0	0	0.770200698	0.198986041	NDC1;NUP	.
0	0	0.770200698	0.198986041	NDC1;NUP	.
0	0	0.770200698	0.198986041	NDC1;NUP	.
0	0	0.822227319	0.211917717	CD86;CCD(	.
0	0	0.822227319	0.211917717	RPS6KA5;P	.
0	0	0.822227319	0.211917717	KANK1;RAI	.
0	0	0.800031773	0.204555744	PSMD10;V	.
0	0	0.751470541	0.19124358	SEMA3A;SI	.
0	0	0.751470541	0.19124358	GRN;POLR	.
0	0	0.751470541	0.19124358	PDGFB;NF/	.
0	0	0.80578651	0.203585265	BBS2;OAT;	.
0	0	0.855072464	0.215727394	SCARB2;M	.
0	0	0.859333966	0.214960986	CD86;H2A	.
0	0	0.700376312	0.173972553	FHOD3;OB	.
0	0	0.700376312	0.173972553	SUV39H1;S	.
0	0	0.700376312	0.173972553	CD19;SPG2	.
0	0	0.700376312	0.173972553	BSCL2;CIDE	.
0	0	0.700376312	0.173972553	CIB1;CLASF	.
0	0	0.700376312	0.173972553	ACHE;PICK	.
0	0	0.700376312	0.173972553	TAB1;MAP	.
0	0	0.700376312	0.173972553	TEK;LIMS1	.
0	0	0.700376312	0.173972553	EDEM2;MA	.
0	0	0.700376312	0.173972553	SPR;DDAH	.
0	0	0.814275019	0.199760942	CD86;DDB	.
0	0	0.722169246	0.176937731	FABP3;FAB	.
0	0	0.722169246	0.176937731	SVBP;VASH	.
0	0	0.722169246	0.176937731	GORASP1;I	.

0	0	0.722169246	0.176937731	KCNIP2;AD	.
0	0	0.722169246	0.176937731	P2RX7;WN	.
0	0	0.722169246	0.176937731	LATS1;ARH	.
0	0	0.828943024	0.201970529	KANK1;CIT	.
0	0	0.781203721	0.189753791	SHTN1;NTI	.
0	0	0.781203721	0.189753791	BCAS3;THF	.
0	0	0.781203721	0.189753791	PSMD10;M	.
0	0	0.789730148	0.190764024	FZD5;TNFS	.
0	0	0.755055949	0.181950928	WNK1;CIB1	.
0	0	0.755055949	0.181950928	TUT4;EXOS	.
0	0	0.755055949	0.181950928	TPST1;ABI3	.
0	0	0.755055949	0.181950928	CLDN12;TE	.
0	0	0.733536851	0.17289822	GSTO1;PDC	.
0	0	0.733536851	0.17289822	SASH3;VAV	.
0	0	0.806474191	0.188261069	PSMD10;TI	.
0	0	0.850600254	0.197815836	CARMIL1;C	.
0	0	0.810272947	0.186383321	TSPYL2;TCI	.
0	0	0.810272947	0.186383321	TSPYL2;TCI	.
0	0	0.642094948	0.147018562	ADSS1	.
0	0	0.642094948	0.147018562	SRM	.
0	0	0.642094948	0.147018562	CHEK1	.
0	0	0.642094948	0.147018562	ZFPM1	.
0	0	0.642094948	0.147018562	INPPL1	.
0	0	0.642094948	0.147018562	SPA17	.
0	0	0.642094948	0.147018562	APOA4	.
0	0	0.642094948	0.147018562	NAPEPLD	.
0	0	0.642094948	0.147018562	DNAAF5	.
0	0	0.642094948	0.147018562	CENPH	.
0	0	0.642094948	0.147018562	MYO1G	.
0	0	0.642094948	0.147018562	SPA17	.
0	0	0.642094948	0.147018562	CHEK2	.
0	0	0.642094948	0.147018562	POGLUT1	.
0	0	0.642094948	0.147018562	TFAP4	.
0	0	0.642094948	0.147018562	MTM1	.
0	0	0.642094948	0.147018562	WFS1	.
0	0	0.642094948	0.147018562	CBLB	.
0	0	0.642094948	0.147018562	MST1	.
0	0	0.642094948	0.147018562	VGLL4	.
0	0	0.642094948	0.147018562	CCDC125	.
0	0	0.642094948	0.147018562	GSTP1	.
0	0	0.642094948	0.147018562	CAB39	.
0	0	0.642094948	0.147018562	PARK7	.
0	0	0.642094948	0.147018562	EMILIN1	.
0	0	0.642094948	0.147018562	FER1L5	.
0	0	0.642094948	0.147018562	TNFSF4	.
0	0	0.642094948	0.147018562	ABI3	.
0	0	0.642094948	0.147018562	SLC45A3	.

0	0	0.642094948	0.147018562	UBQLN2	.
0	0	0.642094948	0.147018562	DNMT1	.
0	0	0.642094948	0.147018562	EDEM2	.
0	0	0.642094948	0.147018562	TREM2	.
0	0	0.642094948	0.147018562	WNK3	.
0	0	0.642094948	0.147018562	UBE2F	.
0	0	0.642094948	0.147018562	RAB23	.
0	0	0.642094948	0.147018562	ADK	.
0	0	0.642094948	0.147018562	CD19	.
0	0	0.642094948	0.147018562	PRKCA	.
0	0	0.642094948	0.147018562	AAAS	.
0	0	0.642094948	0.147018562	HDAC6	.
0	0	0.642094948	0.147018562	CBLB	.
0	0	0.642094948	0.147018562	GCC2	.
0	0	0.642094948	0.147018562	PIGU	.
0	0	0.642094948	0.147018562	EDEM2	.
0	0	0.642094948	0.147018562	MFAP4	.
0	0	0.642094948	0.147018562	UBA5	.
0	0	0.642094948	0.147018562	XPO1	.
0	0	0.642094948	0.147018562	SLC9A1	.
0	0	0.642094948	0.147018562	CDK5	.
0	0	0.642094948	0.147018562	TAF1B	.
0	0	0.642094948	0.147018562	APOA4	.
0	0	0.824605609	0.188669586	TNFSF18;E	.
0	0	0.77	0.176042779	PSMD10;F	.
0	0	0.779689323	0.177870248	DNAJB2;FC	.
0	0	0.779689323	0.177870248	PSMD10;P	.
0	0	0.779689323	0.177870248	SCN11A;SL	.
0	0	0.757432863	0.172487061	NDC1;NUP	.
0	0	0.787383781	0.178491174	CALCB;WF	.
0	0	0.74049369	0.166380003	CBR1;CYP2	.
0	0	0.74049369	0.166380003	CDK5;TREM	.
0	0	0.74049369	0.166380003	PSMD10;P	.
0	0	0.74049369	0.166380003	CUX2;CLST	.
0	0	0.74049369	0.166380003	TAF1B;SPH	.
0	0	0.74049369	0.166380003	FZD5;TNFS	.
0	0	0.74049369	0.166380003	P2RX7;ANK	.
0	0	0.74049369	0.166380003	WFS1;ARL3	.
0	0	0.7002457	0.15731495	FER1L5;TRI	.
0	0	0.7002457	0.15731495	LATS1;COM	.
0	0	0.7002457	0.15731495	UBASH3B;I	.
0	0	0.7002457	0.15731495	P2RX7;ALC	.
0	0	0.7002457	0.15731495	CDC23;PDC	.
0	0	0.7002457	0.15731495	CARMIL1;C	.
0	0	0.7002457	0.15731495	FZD5;TNFS	.
0	0	0.7002457	0.15731495	DAB2;PARI	.
0	0	0.7002457	0.15731495	KIF14;E2F1	.

0	0	0.826388991	0.185613899	PSMD10;IN
0	0	0.669887279	0.150159194	APOA4;AN
0	0	0.669887279	0.150159194	GLP1R;RAF
0	0	0.669887279	0.150159194	GRIN2C;M/
0	0	0.669887279	0.150159194	WFS1;TMT
0	0	0.669887279	0.150159194	MVB12A;R
0	0	0.669887279	0.150159194	KANK1;SCI
0	0	0.669887279	0.150159194	LGALS3;LP1
0	0	0.669887279	0.150159194	BCAS3;COF
0	0	0.669887279	0.150159194	ACTN3;MS
0	0	0.669887279	0.150159194	TPP1;LTA4
0	0	0.669887279	0.150159194	APOA4;PP/
0	0	0.669887279	0.150159194	CAB39;WN
0	0	0.669887279	0.150159194	ZER1;HDA(
0	0	0.669887279	0.150159194	PKD2;SOCS
0	0	0.669887279	0.150159194	SFRP4;CTSI
0	0	0.669887279	0.150159194	WNK1;MA
0	0	0.669887279	0.150159194	CIB1;CLASF
0	0	0.669887279	0.150159194	RALBP1;IN
0	0	0.669887279	0.150159194	FNTB;PPEF
0	0	0.669887279	0.150159194	CEP97;CCS
0	0	0.669887279	0.150159194	PFKL;EIF2B
0	0	0.669887279	0.150159194	MYBPC3;M
0	0	0.716437286	0.156352185	CUL7;HGF;
0	0	0.716437286	0.156352185	BACE1;GRI
0	0	0.716437286	0.156352185	DAB2;TWS
0	0	0.769899519	0.165817093	PSMD10;V
0	0	0.868136961	0.185874114	ACHE;SLC2
0	0	0.745173963	0.159005329	LGALS3;MI
0	0	0.726480951	0.15214383	STX12;STX
0	0	0.726480951	0.15214383	NASP;HAT1
0	0	0.726480951	0.15214383	TWSG1;DA
0	0	0.679611775	0.139967854	WFS1;TEK;
0	0	0.679611775	0.139967854	FAM210B;I
0	0	0.679611775	0.139967854	MAPRE3;C
0	0	0.679611775	0.139967854	TREM2;RA
0	0	0.804015403	0.163564045	GLP1R;CAL
0	0	0.760351439	0.154550954	BEX3;ACVR
0	0	0.760351439	0.154550954	EDNRB;DD
0	0	0.769798951	0.15636152	GLE1;NDC1
0	0	0.748526201	0.151450939	PSMD10;A
0	0	0.641938998	0.129872909	DNAJB4;DN
0	0	0.641938998	0.129872909	FCHO1;ITSI
0	0	0.641938998	0.129872909	PICK1;EIF2
0	0	0.641938998	0.129872909	KDM2B;KD
0	0	0.641938998	0.129872909	SUV39H1;S
0	0	0.641938998	0.129872909	SGO2;SYCF

0	0	0.641938998	0.129872909	SCN11A;H(	.
0	0	0.641938998	0.129872909	GSTP1;IGF:	.
0	0	0.641938998	0.129872909	ADTRP;SER	.
0	0	0.641938998	0.129872909	BCAS3;PAL	.
0	0	0.641938998	0.129872909	LSM10;CDI	.
0	0	0.641938998	0.129872909	CD86;GLM	.
0	0	0.641938998	0.129872909	CDC23;CDI	.
0	0	0.641938998	0.129872909	LAG3;TNFS	.
0	0	0.641938998	0.129872909	CD209;KPN	.
0	0	0.641938998	0.129872909	SCPEP1;AL	.
0	0	0.700114974	0.141420326	GSTO1;PD(	.
0	0	0.700114974	0.141420326	AIFM1;TOM	.
0	0	0.700114974	0.141420326	UCHL1;GST	.
0	0	0.700114974	0.141420326	CD86;GLM	.
0	0	0.700114974	0.141420326	WFS1;CHEI	.
0	0	0.733304234	0.146562009	DIRAS1;PD	.
0	0	0.733304234	0.146562009	CARMIL1;C	.
0	0	0.592669526	0.11843066	ABCB9	.
0	0	0.592669526	0.11843066	PKD2	.
0	0	0.592669526	0.11843066	ZFPM1	.
0	0	0.592669526	0.11843066	ZFPM1	.
0	0	0.592669526	0.11843066	SFRP4	.
0	0	0.592669526	0.11843066	SLC50A1	.
0	0	0.592669526	0.11843066	SOD1	.
0	0	0.592669526	0.11843066	KCNIP2	.
0	0	0.592669526	0.11843066	RAP2A	.
0	0	0.592669526	0.11843066	HMGB1	.
0	0	0.592669526	0.11843066	NAA16	.
0	0	0.592669526	0.11843066	NAXE	.
0	0	0.592669526	0.11843066	MAP2K5	.
0	0	0.592669526	0.11843066	RECQL5	.
0	0	0.592669526	0.11843066	PRKG1	.
0	0	0.592669526	0.11843066	TPP1	.
0	0	0.592669526	0.11843066	TMEM201	.
0	0	0.592669526	0.11843066	SOD1	.
0	0	0.592669526	0.11843066	RAP2A	.
0	0	0.592669526	0.11843066	NAPEPLD	.
0	0	0.592669526	0.11843066	IGF1	.
0	0	0.592669526	0.11843066	RASGRP1	.
0	0	0.592669526	0.11843066	PLA2G6	.
0	0	0.592669526	0.11843066	SPHK2	.
0	0	0.592669526	0.11843066	KCNIP2	.
0	0	0.592669526	0.11843066	WNK1	.
0	0	0.592669526	0.11843066	KCNN4	.
0	0	0.592669526	0.11843066	KCNIP2	.
0	0	0.592669526	0.11843066	DNMT1	.
0	0	0.592669526	0.11843066	SPHK2	.

0	0	0.592669526	0.11843066	CARMIL1	.
0	0	0.592669526	0.11843066	LMF1	.
0	0	0.592669526	0.11843066	GSTP1	.
0	0	0.592669526	0.11843066	PWP1	.
0	0	0.592669526	0.11843066	ATP2A1	.
0	0	0.592669526	0.11843066	WNK1	.
0	0	0.592669526	0.11843066	TPD52	.
0	0	0.592669526	0.11843066	NBL1	.
0	0	0.592669526	0.11843066	SMTN	.
0	0	0.592669526	0.11843066	SLCO2B1	.
0	0	0.592669526	0.11843066	KLHL41	.
0	0	0.592669526	0.11843066	SHTN1	.
0	0	0.592669526	0.11843066	SOD1	.
0	0	0.592669526	0.11843066	ELP4	.
0	0	0.592669526	0.11843066	VEGFB	.
0	0	0.592669526	0.11843066	SOD1	.
0	0	0.712987202	0.139125163	SCARB2;OS	.
0	0	0.712987202	0.139125163	WWOX;TN	.
0	0	0.738230544	0.140439981	GPC1;ATP2	.
0	0	0.782628046	0.148191683	PSMD10;SI	.
0	0	0.660156931	0.12461329	COL11A2;I	.
0	0	0.660156931	0.12461329	GIPC1;PAR	.
0	0	0.660156931	0.12461329	DOC2B;PLA	.
0	0	0.660156931	0.12461329	GNG2;KCN	.
0	0	0.660156931	0.12461329	GEMIN2;G	.
0	0	0.660156931	0.12461329	RARS2;LAR	.
0	0	0.721805434	0.135076786	NDUFA11;I	.
0	0	0.721805434	0.135076786	GORASP1;Z	.
0	0	0.721805434	0.135076786	CARMIL1;P	.
0	0	0.684518099	0.127938129	CARMIL1;S	.
0	0	0.684518099	0.127938129	XRCC5;PDC	.
0	0	0.684518099	0.127938129	DNAJB2;DI	.
0	0	0.61622658	0.112535661	IFT122;CEP	.
0	0	0.61622658	0.112535661	MMP9;MT	.
0	0	0.61622658	0.112535661	TAB1;MAP	.
0	0	0.61622658	0.112535661	CUX2;DLG4	.
0	0	0.61622658	0.112535661	CAMK2A;H	.
0	0	0.61622658	0.112535661	TEK;GAS6	.
0	0	0.61622658	0.112535661	KANK1;SLC	.
0	0	0.61622658	0.112535661	FAM210B;I	.
0	0	0.61622658	0.112535661	MMP14;IG	.
0	0	0.61622658	0.112535661	SYT2;CDK5	.
0	0	0.61622658	0.112535661	PPIH;PPIL3	.
0	0	0.61622658	0.112535661	ST3GAL4;A	.
0	0	0.61622658	0.112535661	RANGRF;A	.
0	0	0.699984135	0.12721768	CD84;CADI	.
0	0	0.699984135	0.12721768	APH1B;GM	.

0	0	0.699984135	0.12721768	THUMPD2	.
0	0	0.741945502	0.134182364	CARMIL1;C	.
0	0	0.741945502	0.134182364	CTSK;HMG	.
0	0	0.776007208	0.139855335	PSMD10;P	.
0	0	0.776007208	0.139855335	CPNE9;TRF	.
0	0	0.710660444	0.124475798	NDUFA11;I	.
0	0	0.710660444	0.124475798	FEN1;WRN	.
0	0	0.710660444	0.124475798	PSMD10;P	.
0	0	0.550304878	0.09615053	MGST2	.
0	0	0.550304878	0.09615053	PLPP1	.
0	0	0.550304878	0.09615053	COMT	.
0	0	0.550304878	0.09615053	GSTO1	.
0	0	0.550304878	0.09615053	SLC9A1	.
0	0	0.550304878	0.09615053	FCHO1	.
0	0	0.550304878	0.09615053	CHST14	.
0	0	0.550304878	0.09615053	LAMC1	.
0	0	0.550304878	0.09615053	RHOBTB2	.
0	0	0.550304878	0.09615053	CLASP1	.
0	0	0.550304878	0.09615053	ST3GAL5	.
0	0	0.550304878	0.09615053	RAB23	.
0	0	0.550304878	0.09615053	ALOX5	.
0	0	0.550304878	0.09615053	PHF20	.
0	0	0.550304878	0.09615053	PHF20	.
0	0	0.550304878	0.09615053	LATS1	.
0	0	0.550304878	0.09615053	KCNIP2	.
0	0	0.550304878	0.09615053	RAP2A	.
0	0	0.550304878	0.09615053	METTL8	.
0	0	0.550304878	0.09615053	MGST2	.
0	0	0.550304878	0.09615053	CD9	.
0	0	0.550304878	0.09615053	DAB2	.
0	0	0.550304878	0.09615053	PARK7	.
0	0	0.550304878	0.09615053	PARK7	.
0	0	0.550304878	0.09615053	H1-10	.
0	0	0.550304878	0.09615053	MGST2	.
0	0	0.550304878	0.09615053	PARK7	.
0	0	0.550304878	0.09615053	AATK	.
0	0	0.550304878	0.09615053	NOXA1	.
0	0	0.550304878	0.09615053	POT1	.
0	0	0.550304878	0.09615053	PLA2R1	.
0	0	0.550304878	0.09615053	LGMN	.
0	0	0.550304878	0.09615053	SMPD3	.
0	0	0.550304878	0.09615053	IGF1	.
0	0	0.550304878	0.09615053	PARK7	.
0	0	0.550304878	0.09615053	TLR5	.
0	0	0.550304878	0.09615053	GAS6	.
0	0	0.550304878	0.09615053	SCIN	.
0	0	0.550304878	0.09615053	MPP7	.

0	0	0.550304878	0.09615053	LGMN	.
0	0	0.550304878	0.09615053	CLASP1	.
0	0	0.550304878	0.09615053	SFRP4	.
0	0	0.550304878	0.09615053	SCIN	.
0	0	0.550304878	0.09615053	USP46	.
0	0	0.550304878	0.09615053	WNK1	.
0	0	0.550304878	0.09615053	SOD1	.
0	0	0.550304878	0.09615053	SLC9A1	.
0	0	0.550304878	0.09615053	LGMN	.
0	0	0.794128212	0.137599853	CNTNAP1;I	.
0	0	0.829532021	0.143592081	BLM;MCFD	.
0	0	0.641782912	0.111006902	TNFSF12;G	.
0	0	0.641782912	0.111006902	ADTRP;SER	.
0	0	0.641782912	0.111006902	STXBP6;AD	.
0	0	0.641782912	0.111006902	ZDHHC6;CI	.
0	0	0.641782912	0.111006902	CAB39;WN	.
0	0	0.641782912	0.111006902	FZD5;HPS4	.
0	0	0.641782912	0.111006902	MMP3;EIF	.
0	0	0.669599348	0.115759156	PROS1;CD	.
0	0	0.754520435	0.130020086	P2RX7;SYD	.
0	0	0.762620889	0.131285674	KCNIP2;SL	.
0	0	0.762620889	0.131285674	PSMD10;P	.
0	0	0.744839838	0.127995242	ACER2;DU	.
0	0	0.73307121	0.124989058	SCPEP1;RE	.
0	0	0.788992682	0.130803023	PDGFB;CIB	.
0	0	0.59249204	0.097675824	PHF20;MSI	.
0	0	0.59249204	0.097675824	CD209;AP(	.
0	0	0.59249204	0.097675824	KANK1;SLC	.
0	0	0.59249204	0.097675824	PARK7;TXN	.
0	0	0.59249204	0.097675824	TAB1;MAP	.
0	0	0.59249204	0.097675824	DLG4;CLST	.
0	0	0.59249204	0.097675824	CDH3;PARI	.
0	0	0.59249204	0.097675824	CUX2;CLST	.
0	0	0.59249204	0.097675824	DLG4;PICK	.
0	0	0.59249204	0.097675824	TCEA2;HM	.
0	0	0.59249204	0.097675824	RACGAP1;(	.
0	0	0.59249204	0.097675824	MYBPC3;M	.
0	0	0.59249204	0.097675824	PPP1R26;T	.
0	0	0.59249204	0.097675824	CATSPERD	.
0	0	0.59249204	0.097675824	TNFSF18;E	.
0	0	0.59249204	0.097675824	CITED2;ZFP	.
0	0	0.792519936	0.129896478	MAPKBP1;	.
0	0	0.69985318	0.114691072	ACHE;GOLI	.
0	0	0.822610369	0.13254015	GRN;RIPOP	.
0	0	0.655315437	0.104752841	SCPEP1;CY	.
0	0	0.655315437	0.104752841	CUL7;HGF;	.
0	0	0.655315437	0.104752841	PRKCG;NXI	.

0	0	0.655315437	0.104752841	CARMIL1;C	.
0	0	0.655315437	0.104752841	RUFY3;CHI	.
0	0	0.655315437	0.104752841	P2RX7;TTC	.
0	0	0.624402083	0.098937175	EDNRB;BBS	.
0	0	0.624402083	0.098937175	CRTAM;CC	.
0	0	0.624402083	0.098937175	C1QTNF1;F	.
0	0	0.624402083	0.098937175	GSTO1;KCI	.
0	0	0.624402083	0.098937175	P2RX7;ALC	.
0	0	0.624402083	0.098937175	TRPM2;HL(	.
0	0	0.624402083	0.098937175	SYT2;CDK5	.
0	0	0.675346744	0.106358979	P2RX7;FZD	.
0	0	0.729076187	0.11187798	CALCB;RGI	.
0	0	0.729076187	0.11187798	GLE1;NDC1	.
0	0	0.843851313	0.129408639	CD63;DNM	.
0	0	0.689368522	0.105660017	LATS1;KAN	.
0	0	0.689368522	0.105660017	CCDC88A;A	.
0	0	0.51358885	0.078587668	APLN	.
0	0	0.51358885	0.078587668	SSTR2	.
0	0	0.51358885	0.078587668	BBS7	.
0	0	0.51358885	0.078587668	LGALS3	.
0	0	0.51358885	0.078587668	LGALS3	.
0	0	0.51358885	0.078587668	FGD1	.
0	0	0.51358885	0.078587668	SYCP3	.
0	0	0.51358885	0.078587668	KCNIP2	.
0	0	0.51358885	0.078587668	DSCC1	.
0	0	0.51358885	0.078587668	PSIP1	.
0	0	0.51358885	0.078587668	NAA16	.
0	0	0.51358885	0.078587668	TICAM1	.
0	0	0.51358885	0.078587668	PDK4	.
0	0	0.51358885	0.078587668	MMP9	.
0	0	0.51358885	0.078587668	GRN	.
0	0	0.51358885	0.078587668	EDA	.
0	0	0.51358885	0.078587668	TNFSF4	.
0	0	0.51358885	0.078587668	SHLD2	.
0	0	0.51358885	0.078587668	PDCD4	.
0	0	0.51358885	0.078587668	TICAM1	.
0	0	0.51358885	0.078587668	SMTNL2	.
0	0	0.51358885	0.078587668	FSTL3	.
0	0	0.51358885	0.078587668	CDC23	.
0	0	0.51358885	0.078587668	SIRT2	.
0	0	0.51358885	0.078587668	METTL18	.
0	0	0.51358885	0.078587668	SEMA3A	.
0	0	0.715941764	0.108378581	PSMD10;P	.
0	0	0.715941764	0.108378581	PSMD10;P	.
0	0	0.862226767	0.129016971	LRSAM1;U	.
0	0	0.570515614	0.08490611	MSRB2;WA	.
0	0	0.570515614	0.08490611	PARK7;HDA	.

0	0	0.570515614	0.08490611	WWOX;TN	.
0	0	0.570515614	0.08490611	TNFSF18;L	.
0	0	0.570515614	0.08490611	LATS1;ARH	.
0	0	0.570515614	0.08490611	PARK7;BM	.
0	0	0.570515614	0.08490611	MMP9;MT	.
0	0	0.699722112	0.103650275	PSMD10;P	.
0	0	0.64162669	0.094802588	UBASH3B;(	.
0	0	0.64162669	0.094802588	NAXE;VEGI	.
0	0	0.663665222	0.097240272	LRRC59;AL	.
0	0	0.607936035	0.088220505	DGKA;LMF	.
0	0	0.607936035	0.088220505	FHOD3;RN	.
0	0	0.607936035	0.088220505	MYBPC3;S(	.
0	0	0.607936035	0.088220505	WNK1;ADT	.
0	0	0.607936035	0.088220505	P2RX7;ALC	.
0	0	0.607936035	0.088220505	GNG2;KCN	.
0	0	0.607936035	0.088220505	GRN;CLOC	.
0	0	0.607936035	0.088220505	TRPM2;BC	.
0	0	0.721440669	0.104560476	SFRP4;AHI	.
0	0	0.679192236	0.097324967	DNAJB2;D/	.
0	0	0.679192236	0.097324967	PSMD10;P	.
0	0	0.764056161	0.106476648	PSMD10;G	.
0	0	0.725882964	0.100593855	GRN;TNFSI	.
0	0	0.713962584	0.09769827	IPO11;INT	.
0	0	0.713962584	0.09769827	ENTPD5;H(	.
0	0	0.713962584	0.09769827	GLE1;NDC1	.
0	0	0.628496667	0.085804127	TBCD;PARI	.
0	0	0.628496667	0.085804127	RNASEH2C	.
0	0	0.628496667	0.085804127	BEX3;HGF;	.
0	0	0.628496667	0.085804127	STAP1;TRE	.
0	0	0.628496667	0.085804127	PROS1;CD1	.
0	0	0.652379685	0.088896107	TMEM161/	.
0	0	0.550108932	0.073906619	PKD2;FOLR	.
0	0	0.550108932	0.073906619	KCNIP2;HC	.
0	0	0.550108932	0.073906619	SETD4;DPY	.
0	0	0.550108932	0.073906619	MVB12A;V	.
0	0	0.550108932	0.073906619	PLA2G12A	.
0	0	0.550108932	0.073906619	GLMN;MIF	.
0	0	0.550108932	0.073906619	EIF2AK4;LC	.
0	0	0.550108932	0.073906619	SHPK;MIF	.
0	0	0.550108932	0.073906619	KCNMB4;S	.
0	0	0.550108932	0.073906619	TAF1B;GTF	.
0	0	0.481462326	0.064607544	SRM	.
0	0	0.481462326	0.064607544	SRP14	.
0	0	0.481462326	0.064607544	CD9	.
0	0	0.481462326	0.064607544	MPHOSPH(	.
0	0	0.481462326	0.064607544	HCN2	.
0	0	0.481462326	0.064607544	PKD2	.

0	0	0.481462326	0.064607544	COX15	.
0	0	0.481462326	0.064607544	ZFPM1	.
0	0	0.481462326	0.064607544	ACADVL	.
0	0	0.481462326	0.064607544	SIRT2	.
0	0	0.481462326	0.064607544	FOLR1	.
0	0	0.481462326	0.064607544	ST3GAL4	.
0	0	0.481462326	0.064607544	IGF1	.
0	0	0.481462326	0.064607544	TICAM1	.
0	0	0.481462326	0.064607544	VEGFB	.
0	0	0.481462326	0.064607544	HOXB4	.
0	0	0.481462326	0.064607544	CCNE1	.
0	0	0.481462326	0.064607544	PIDD1	.
0	0	0.481462326	0.064607544	NOXA1	.
0	0	0.481462326	0.064607544	MYO5A	.
0	0	0.481462326	0.064607544	ATRAID	.
0	0	0.481462326	0.064607544	STAR	.
0	0	0.481462326	0.064607544	CARMIL1	.
0	0	0.481462326	0.064607544	KCNN4	.
0	0	0.481462326	0.064607544	SULT1C4	.
0	0	0.669310914	0.089632761	SASH3;GRI	.
0	0	0.669310914	0.089632761	PSMD10;P	.
0	0	0.592314399	0.078697106	TADA3;MB	.
0	0	0.592314399	0.078697106	WWTR1;D/	.
0	0	0.845036443	0.11204454	ZMYND15;	.
0	0	0.764271963	0.101191348	RALBP1;TF	.
0	0	0.719058147	0.094286107	SCARB2;CA	.
0	0	0.681930242	0.088939328	ORMDL1;IC	.
0	0	0.706637113	0.091264362	GLE1;NDC1	.
0	0	0.811660878	0.102716394	ANKRD39;I	.
0	0	0.615891845	0.077664083	PROS1;CD1	.
0	0	0.838363847	0.10544856	CNTFR;ACH	.
0	0	0.659711916	0.082534373	SLC26A1;P	.
0	0	0.659711916	0.082534373	WWTR1;D/	.
0	0	0.659711916	0.082534373	TST;UPF3B	.
0	0	0.577473845	0.070227578	NUCKS1;PI	.
0	0	0.577473845	0.070227578	FHOD3;OB	.
0	0	0.577473845	0.070227578	TFR2;DOC2	.
0	0	0.531109609	0.064411696	GPD1L;SNT	.
0	0	0.531109609	0.064411696	MVB12A;V	.
0	0	0.531109609	0.064411696	FOXJ1;GAS	.
0	0	0.531109609	0.064411696	MAPKBP1;	.
0	0	0.531109609	0.064411696	TMEM201;	.
0	0	0.531109609	0.064411696	HABP4;CIR	.
0	0	0.531109609	0.064411696	PKD2;SOCS	.
0	0	0.531109609	0.064411696	SLC9A9;SL(	.
0	0	0.531109609	0.064411696	CD63;KCNI	.
0	0	0.453115392	0.053384944	RSRC1	.

0	0	0.453115392	0.053384944	ADTRP	.
0	0	0.453115392	0.053384944	SSTR2	.
0	0	0.453115392	0.053384944	MT1E	.
0	0	0.453115392	0.053384944	TWIST1	.
0	0	0.453115392	0.053384944	TEK	.
0	0	0.453115392	0.053384944	CRACD	.
0	0	0.453115392	0.053384944	CDK5	.
0	0	0.453115392	0.053384944	PODXL2	.
0	0	0.453115392	0.053384944	HACD1	.
0	0	0.453115392	0.053384944	CRACD	.
0	0	0.453115392	0.053384944	DNM1	.
0	0	0.453115392	0.053384944	PLA2G12A	.
0	0	0.453115392	0.053384944	PLA2G12A	.
0	0	0.453115392	0.053384944	CIB1	.
0	0	0.453115392	0.053384944	ATAD5	.
0	0	0.453115392	0.053384944	WNK1	.
0	0	0.453115392	0.053384944	CIRBP	.
0	0	0.453115392	0.053384944	BOK	.
0	0	0.453115392	0.053384944	MMP14	.
0	0	0.453115392	0.053384944	NAPEPLD	.
0	0	0.453115392	0.053384944	SCIN	.
0	0	0.453115392	0.053384944	CHEK2	.
0	0	0.453115392	0.053384944	DAB2	.
0	0	0.453115392	0.053384944	ESR1	.
0	0	0.453115392	0.053384944	PARK7	.
0	0	0.453115392	0.053384944	ITGB8	.
0	0	0.453115392	0.053384944	SNTA1	.
0	0	0.453115392	0.053384944	GAS6	.
0	0	0.453115392	0.053384944	TAF1B	.
0	0	0.453115392	0.053384944	MYO1G	.
0	0	0.453115392	0.053384944	POP7	.
0	0	0.630918662	0.074272576	ACER2;MM	.
0	0	0.650383313	0.075984565	HGF;PDGFI	.
0	0	0.603781329	0.070298737	PRKCG;NXI	.
0	0	0.603781329	0.070298737	NSMCE4A;	.
0	0	0.729792783	0.083764375	BBS2;ZFHX	.
0	0	0.56335722	0.06269004	WFS1;TMT	.
0	0	0.56335722	0.06269004	E2F1;CIRBI	.
0	0	0.56335722	0.06269004	UBE2D4;PI	.
0	0	0.56335722	0.06269004	PDCD4;TEI	.
0	0	0.751141863	0.082560086	WWTR1;AI	.
0	0	0.513376906	0.056199649	TWIST1;EM	.
0	0	0.513376906	0.056199649	CD19;RASC	.
0	0	0.513376906	0.056199649	GAS6;RAB1	.
0	0	0.513376906	0.056199649	HOXB4;FST	.
0	0	0.513376906	0.056199649	CITED2;PKI	.
0	0	0.513376906	0.056199649	P2RX7;SCN	.

0	0	0.513376906	0.056199649	SEMA3A;SI	.
0	0	0.513376906	0.056199649	CLIP3;IGF1	.
0	0	0.513376906	0.056199649	TNFSF4;HM	.
0	0	0.513376906	0.056199649	SHMT2;OT	.
0	0	0.513376906	0.056199649	MYH14;LA	.
0	0	0.513376906	0.056199649	TAF1B;GTF	.
0	0	0.620707369	0.067877843	DDB1;ACTI	.
0	0	0.620707369	0.067877843	NEU3;CCD	.
0	0	0.641313837	0.069941583	LATS1;PKIE	.
0	0	0.592136603	0.063632937	STX12;RAB	.
0	0	0.592136603	0.063632937	TOMM7;M	.
0	0	0.592136603	0.063632937	P2RX7;FZD	.
0	0	0.656869741	0.070579703	POLA1;CR(	.
0	0	0.427918118	0.0443094	ACVR1C	.
0	0	0.427918118	0.0443094	ZFPM1	.
0	0	0.427918118	0.0443094	PKD2	.
0	0	0.427918118	0.0443094	ZFPM1	.
0	0	0.427918118	0.0443094	MT1E	.
0	0	0.427918118	0.0443094	COMT	.
0	0	0.427918118	0.0443094	EDEM2	.
0	0	0.427918118	0.0443094	FOXJ1	.
0	0	0.427918118	0.0443094	GDE1	.
0	0	0.427918118	0.0443094	TEK	.
0	0	0.427918118	0.0443094	PODXL2	.
0	0	0.427918118	0.0443094	EIF2AK4	.
0	0	0.427918118	0.0443094	FER1L5	.
0	0	0.427918118	0.0443094	ADTRP	.
0	0	0.427918118	0.0443094	PARK7	.
0	0	0.427918118	0.0443094	ESR1	.
0	0	0.427918118	0.0443094	LGALS3	.
0	0	0.427918118	0.0443094	SPAST	.
0	0	0.427918118	0.0443094	TREM2	.
0	0	0.427918118	0.0443094	PRKCA	.
0	0	0.427918118	0.0443094	TREM2	.
0	0	0.427918118	0.0443094	RALBP1	.
0	0	0.427918118	0.0443094	CCL19	.
0	0	0.427918118	0.0443094	DNAJC15	.
0	0	0.427918118	0.0443094	NPHP4	.
0	0	0.427918118	0.0443094	EMILIN1	.
0	0	0.427918118	0.0443094	SMPD3	.
0	0	0.427918118	0.0443094	CLIP3	.
0	0	0.427918118	0.0443094	PREPL	.
0	0	0.427918118	0.0443094	CD63	.
0	0	0.427918118	0.0443094	PLD3	.
0	0	0.427918118	0.0443094	PKD2	.
0	0	0.768483516	0.078863526	SCARB2;CH	.
0	0	0.678771596	0.069324144	CALCB;RGM	.

0	0	0.549912816	0.055977703	SCN11A;KC	.
0	0	0.648918819	0.065315177	SCN11A;SL	.
0	0	0.5809313	0.05759915	SLC17A5;SI	.
0	0	0.5809313	0.05759915	UBE2D4;UI	.
0	0	0.496788249	0.049084643	ABCB9;SEC	.
0	0	0.496788249	0.049084643	CEMIP2;AL	.
0	0	0.768381706	0.07513256	INVS;PSMI	.
0	0	0.704441512	0.068508738	UGDH;CDK	.
0	0	0.748862025	0.071605039	BBS2;GRN;	.
0	0	0.623910248	0.059224817	LGALS3;GS	.
0	0	0.71759965	0.067798851	MYBPC3;CI	.
0	0	0.601242092	0.056670763	HGF;TIMP2	.
0	0	0.601242092	0.056670763	ACHE;FZD5	.
0	0	0.641157205	0.060429404	PSMD10;P	.
0	0	0.680645898	0.06359292	ACVR1C;AF	.
0	0	0.537093733	0.049996825	UBA5;CDIN	.
0	0	0.537093733	0.049996825	PLK4;CCDC	.
0	0	0.537093733	0.049996825	NSMCE4A;	.
0	0	0.537093733	0.049996825	ZC3H7B;AT	.
0	0	0.537093733	0.049996825	PI4K2B;ALS	.
0	0	0.570141009	0.052136628	MEIS1;COL	.
0	0	0.570141009	0.052136628	FER1L5;TRI	.
0	0	0.570141009	0.052136628	DTWD1;TY	.
0	0	0.405373189	0.036922577	MYO1G	.
0	0	0.405373189	0.036922577	CLDN12	.
0	0	0.405373189	0.036922577	PDCD4	.
0	0	0.405373189	0.036922577	TMEM65	.
0	0	0.405373189	0.036922577	SLC9A1	.
0	0	0.405373189	0.036922577	DNAJC18	.
0	0	0.405373189	0.036922577	FHOD3	.
0	0	0.405373189	0.036922577	TICAM1	.
0	0	0.405373189	0.036922577	PARK7	.
0	0	0.405373189	0.036922577	ITGB3	.
0	0	0.405373189	0.036922577	CNTROB	.
0	0	0.405373189	0.036922577	FUCA2	.
0	0	0.405373189	0.036922577	TUBB	.
0	0	0.405373189	0.036922577	PPP1R26	.
0	0	0.405373189	0.036922577	CHRNB1	.
0	0	0.405373189	0.036922577	TENM4	.
0	0	0.405373189	0.036922577	SFRP4	.
0	0	0.405373189	0.036922577	APLN	.
0	0	0.405373189	0.036922577	AGO4	.
0	0	0.405373189	0.036922577	VGLL4	.
0	0	0.405373189	0.036922577	CRTAM	.
0	0	0.405373189	0.036922577	MIF	.
0	0	0.405373189	0.036922577	DNAJB2	.
0	0	0.405373189	0.036922577	GPNMB	.

0	0	0.846221298	0.07657871	ZNF174;TH	.
0	0	0.687749397	0.06220492	TNFSF18;D	.
0	0	0.481236383	0.042910255	STX17;ATG	.
0	0	0.481236383	0.042910255	VAV3;CD19	.
0	0	0.481236383	0.042910255	MYBPC3;M	.
0	0	0.481236383	0.042910255	VEGFB;GAS	.
0	0	0.481236383	0.042910255	PKD2;MEG	.
0	0	0.481236383	0.042910255	CCDC88C;I	.
0	0	0.481236383	0.042910255	ACER2;CIB	.
0	0	0.481236383	0.042910255	AUTS2;ABI	.
0	0	0.481236383	0.042910255	TRIP4;KLHI	.
0	0	0.481236383	0.042910255	ARV1;APOA	.
0	0	0.481236383	0.042910255	SYT2;CDK5	.
0	0	0.481236383	0.042910255	LSM10;TTF	.
0	0	0.481236383	0.042910255	TAF1B;GTF	.
0	0	0.481236383	0.042910255	MYBPC3;M	.
0	0	0.633578217	0.055896021	TWSG1;DA	.
0	0	0.633578217	0.055896021	PPP3CA;TM	.
0	0	0.591958652	0.051770569	LSM10;TAF	.
0	0	0.591958652	0.051770569	WFS1;ARL3	.
0	0	0.591958652	0.051770569	INTS13;INT	.
0	0	0.754587912	0.06552514	TNFSF18;E	.
0	0	0.524857335	0.044664966	CITED2;PLF	.
0	0	0.524857335	0.044664966	KANK1;ALC	.
0	0	0.559743092	0.04719068	CAMK2A;K	.
0	0	0.559743092	0.04719068	UBA5;PARI	.
0	0	0.607422638	0.050109559	CDH3;CAD	.
0	0	0.607422638	0.050109559	FNTB;CAM	.
0	0	0.582956529	0.047286934	PPP3CA;PP	.
0	0	0.582956529	0.047286934	INTS13;INT	.
0	0	0.676668416	0.054728317	CCDC88A;F	.
0	0	0.466627055	0.037544324	ARV1;APOA	.
0	0	0.466627055	0.037544324	LOXL3;FOX	.
0	0	0.466627055	0.037544324	KANK1;CCI	.
0	0	0.466627055	0.037544324	UBASH3B;A	.
0	0	0.466627055	0.037544324	TNFSF4;TIC	.
0	0	0.466627055	0.037544324	CEP97;CCS	.
0	0	0.466627055	0.037544324	GRIN2C;MA	.
0	0	0.466627055	0.037544324	PREPL;SYT7	.
0	0	0.466627055	0.037544324	LGALS3;KC	.
0	0	0.466627055	0.037544324	IQSEC2;FAI	.
0	0	0.385082753	0.030875848	SCIN	.
0	0	0.385082753	0.030875848	FZD5	.
0	0	0.385082753	0.030875848	FZD5	.
0	0	0.385082753	0.030875848	TRPM2	.
0	0	0.385082753	0.030875848	GUCY2C	.
0	0	0.385082753	0.030875848	CRELD1	.

0	0	0.385082753	0.030875848	RILPL1	.
0	0	0.385082753	0.030875848	ACTN3	.
0	0	0.385082753	0.030875848	PHC1	.
0	0	0.385082753	0.030875848	APOA4	.
0	0	0.385082753	0.030875848	GRIN2C	.
0	0	0.385082753	0.030875848	ZW10	.
0	0	0.385082753	0.030875848	ZW10	.
0	0	0.385082753	0.030875848	KLRF2	.
0	0	0.385082753	0.030875848	UBASH3B	.
0	0	0.385082753	0.030875848	GPD1L	.
0	0	0.385082753	0.030875848	TUT4	.
0	0	0.385082753	0.030875848	TNFSF18	.
0	0	0.385082753	0.030875848	RUNX2	.
0	0	0.385082753	0.030875848	TANC2	.
0	0	0.385082753	0.030875848	CORO1C	.
0	0	0.385082753	0.030875848	CATSPERD	.
0	0	0.385082753	0.030875848	RETSAT	.
0	0	0.385082753	0.030875848	ZW10	.
0	0	0.385082753	0.030875848	CIRBP	.
0	0	0.755511962	0.059819383	ZFHX2;GST	.
0	0	0.683413567	0.053572433	GLP1R;P2R	.
0	0	0.549716529	0.042712022	TBCD;PARI	.
0	0	0.549716529	0.042712022	WNK1;CCL	.
0	0	0.549716529	0.042712022	XPO1;HEA	.
0	0	0.59950002	0.046077838	P2RX7;FZD	.
0	0	0.689214325	0.052257134	WWOX;HG	.
0	0	0.574223125	0.043184774	SPARC;MA	.
0	0	0.452877099	0.032874796	GLP1R;ADC	.
0	0	0.452877099	0.032874796	TWIST1;EM	.
0	0	0.452877099	0.032874796	RBBP7;TRP	.
0	0	0.452877099	0.032874796	FER1L5;DN	.
0	0	0.452877099	0.032874796	TREM2;TIC	.
0	0	0.452877099	0.032874796	EIF2AK4;TA	.
0	0	0.452877099	0.032874796	ANKH;TWI	.
0	0	0.611874752	0.044172864	LSM10;PCE	.
0	0	0.627847469	0.04516193	PARP1;TBC	.
0	0	0.501980592	0.0356664	RAB23;CD5	.
0	0	0.501980592	0.0356664	PFKL;EIF2B	.
0	0	0.366724739	0.025900965	CIB1	.
0	0	0.366724739	0.025900965	CYP2U1	.
0	0	0.366724739	0.025900965	SOD1	.
0	0	0.366724739	0.025900965	METTL8	.
0	0	0.366724739	0.025900965	FOXJ1	.
0	0	0.366724739	0.025900965	GAS6	.
0	0	0.366724739	0.025900965	POT1	.
0	0	0.366724739	0.025900965	ZW10	.
0	0	0.366724739	0.025900965	STAP1	.

0	0	0.366724739	0.025900965	MST1	.
0	0	0.366724739	0.025900965	PPP2CB	.
0	0	0.366724739	0.025900965	CUX2	.
0	0	0.366724739	0.025900965	CCL19	.
0	0	0.366724739	0.025900965	CCL19	.
0	0	0.366724739	0.025900965	HABP4	.
0	0	0.366724739	0.025900965	SNTA1	.
0	0	0.366724739	0.025900965	XRCC5	.
0	0	0.366724739	0.025900965	POT1	.
0	0	0.366724739	0.025900965	TIMP2	.
0	0	0.366724739	0.025900965	DDB1	.
0	0	0.366724739	0.025900965	GNB5	.
0	0	0.78802388	0.055190195	KANK1;GRI	.
0	0	0.565746587	0.039431982	DLG4;CLST	.
0	0	0.660696222	0.045075445	KCNIP2;SL(	.
0	0	0.634928145	0.042425096	DNAJB2;DA	.
0	0	0.530700633	0.034983143	IRAK1BP1;I	.
0	0	0.530700633	0.034983143	MAP4K2;T/	.
0	0	0.439912854	0.028806364	SMPD3;CL/	.
0	0	0.439912854	0.028806364	PARK7;HD/	.
0	0	0.439912854	0.028806364	SLC9A9;SL(	.
0	0	0.439912854	0.028806364	MYH14;KLI	.
0	0	0.491272329	0.03187904	SCIN;MSRE	.
0	0	0.491272329	0.03187904	ARHGAP18	.
0	0	0.557515745	0.035999169	CLIP3;SPPL	.
0	0	0.598209607	0.037711586	UCHL1;PD(	.
0	0	0.350035635	0.021789393	PKD2	.
0	0	0.350035635	0.021789393	ADTRP	.
0	0	0.350035635	0.021789393	CYP2U1	.
0	0	0.350035635	0.021789393	TWIST1	.
0	0	0.350035635	0.021789393	IGF1	.
0	0	0.350035635	0.021789393	MAP2K5	.
0	0	0.350035635	0.021789393	MAP2K5	.
0	0	0.350035635	0.021789393	CIRBP	.
0	0	0.350035635	0.021789393	PWP1	.
0	0	0.350035635	0.021789393	BEX3	.
0	0	0.350035635	0.021789393	PPARG	.
0	0	0.350035635	0.021789393	LGALS3	.
0	0	0.350035635	0.021789393	SLC25A4	.
0	0	0.350035635	0.021789393	KDM2B	.
0	0	0.350035635	0.021789393	TREM2	.
0	0	0.350035635	0.021789393	COX15	.
0	0	0.350035635	0.021789393	MT1E	.
0	0	0.350035635	0.021789393	CD68	.
0	0	0.52167614	0.0316566	CSTB;TIMP	.
0	0	0.54952007	0.032859422	CD86;TFRC	.
0	0	0.762606776	0.045454493	PSMD10;U	.

0	0	0.481010244	0.028497372	NAPEPLD;F	.
0	0	0.481010244	0.028497372	TNFSF4;HM	.
0	0	0.609094723	0.036080329	USP46;IQS	.
0	0	0.427668845	0.025257727	GRN;VSIG4	.
0	0	0.427668845	0.025257727	DLG4;CLST	.
0	0	0.427668845	0.025257727	TSPYL2;GLI	.
0	0	0.427668845	0.025257727	TIPRL;STYX	.
0	0	0.427668845	0.025257727	ARV1;APOA	.
0	0	0.427668845	0.025257727	CITED2;ZFP	.
0	0	0.672366404	0.03787623	CHRNB1;KC	.
0	0	0.654108664	0.036758273	PSMD10;SI	.
0	0	0.512952464	0.028643858	P2RX7;ARV	.
0	0	0.603088942	0.033461295	SETD4;SPH	.
0	0	0.541749625	0.029988092	SETD4;SPH	.
0	0	0.541749625	0.029988092	SFRP4;TWS	.
0	0	0.541749625	0.029988092	MBNL2;FAS	.
0	0	0.585138599	0.032163343	SLC35A1;SI	.
0	0	0.334797758	0.018377531	SLC1A3	.
0	0	0.334797758	0.018377531	NBL1	.
0	0	0.334797758	0.018377531	HACD1	.
0	0	0.334797758	0.018377531	EIF2AK4	.
0	0	0.334797758	0.018377531	APLN	.
0	0	0.334797758	0.018377531	EIF2AK4	.
0	0	0.334797758	0.018377531	CBLB	.
0	0	0.334797758	0.018377531	CLASP1	.
0	0	0.334797758	0.018377531	ZC4H2	.
0	0	0.334797758	0.018377531	GDE1	.
0	0	0.334797758	0.018377531	AUTS2	.
0	0	0.334797758	0.018377531	SASH1	.
0	0	0.334797758	0.018377531	ESR1	.
0	0	0.334797758	0.018377531	CIB1	.
0	0	0.334797758	0.018377531	CREB3L3	.
0	0	0.334797758	0.018377531	SLC12A6	.
0	0	0.334797758	0.018377531	RANGRF	.
0	0	0.334797758	0.018377531	MTHFD1	.
0	0	0.334797758	0.018377531	VAV3	.
0	0	0.334797758	0.018377531	SPHK2	.
0	0	0.334797758	0.018377531	CDH3	.
0	0	0.334797758	0.018377531	COL5A1	.
0	0	0.47116702	0.025477061	COL11A2;I	.
0	0	0.47116702	0.025477061	UBA5;CDIN	.
0	0	0.47116702	0.025477061	PPARG;NBI	.
0	0	0.47116702	0.025477061	STXBP6;SEI	.
0	0	0.562785449	0.03019363	SCARB2;CL	.
0	0	0.416086675	0.02215934	EDA;ACP4	.
0	0	0.416086675	0.02215934	CRTAM;SO	.
0	0	0.624953342	0.032305913	TBCCD1;AE	.

0	0	0.624953342	0.032305913	RNASEH2C	.
0	0	0.50451481	0.025915338	PDCD4;GD	.
0	0	0.50451481	0.025915338	SLC1A3;SL(	.
0	0	0.534195026	0.027362598	CRCP;POLF	.
0	0	0.461717524	0.022778803	MYBPC3;M	.
0	0	0.461717524	0.022778803	TNFSF4;TW	.
0	0	0.320829704	0.015535966	GAS6	.
0	0	0.320829704	0.015535966	PKD2L1	.
0	0	0.320829704	0.015535966	UBASH3B	.
0	0	0.320829704	0.015535966	HMGN1	.
0	0	0.320829704	0.015535966	WNK1	.
0	0	0.320829704	0.015535966	MAPK8IP2	.
0	0	0.320829704	0.015535966	RANGRF	.
0	0	0.320829704	0.015535966	SYT2	.
0	0	0.320829704	0.015535966	HAVCR2	.
0	0	0.320829704	0.015535966	MMP14	.
0	0	0.320829704	0.015535966	CCL19	.
0	0	0.320829704	0.015535966	TICAM1	.
0	0	0.320829704	0.015535966	FASTKD2	.
0	0	0.320829704	0.015535966	GEMIN2	.
0	0	0.320829704	0.015535966	SLC9A1	.
0	0	0.405114092	0.019451572	CTSK;ATG1	.
0	0	0.405114092	0.019451572	ACP4;LGM	.
0	0	0.405114092	0.019451572	DAG1;CIB1	.
0	0	0.405114092	0.019451572	RPS27L;ME	.
0	0	0.405114092	0.019451572	HOXB4;ME	.
0	0	0.762735512	0.036422397	CUL7;MAR	.
0	0	0.640371991	0.030340894	LGALS3;SC	.
0	0	0.496349338	0.023444284	STIL;IFT122	.
0	0	0.787741828	0.035219697	ZMYND15;	.
0	0	0.566564008	0.025285284	ACHE;FZD5	.
0	0	0.566564008	0.025285284	PRKCG;DDI	.
0	0	0.488443088	0.021206489	DDB1;PPIH	.
0	0	0.394704206	0.017083169	PPP1R16A;	.
0	0	0.394704206	0.017083169	MDFIC;TAF	.
0	0	0.394704206	0.017083169	MEIS1;PBX	.
0	0	0.609969392	0.026229216	CALCB;WF5	.
0	0	0.307979094	0.013161571	RAPGEF3	.
0	0	0.307979094	0.013161571	PKD2	.
0	0	0.307979094	0.013161571	GRSF1	.
0	0	0.307979094	0.013161571	IGF1	.
0	0	0.307979094	0.013161571	MTM1	.
0	0	0.307979094	0.013161571	PRKCG	.
0	0	0.307979094	0.013161571	TUT4	.
0	0	0.307979094	0.013161571	IGF1	.
0	0	0.307979094	0.013161571	CD1B	.
0	0	0.307979094	0.013161571	MDFIC	.

0	0	0.307979094	0.013161571	SCIN	.
0	0	0.307979094	0.013161571	CAB39	.
0	0	0.307979094	0.013161571	GRSF1	.
0	0	0.680879394	0.029090985	CRCP;THRE	.
0	0	0.580198983	0.024688022	ACER2;ABC	.
0	0	0.831483427	0.035157343	ZMYND15;	.
0	0	0.512739965	0.020762725	CD86;PDCI	.
0	0	0.512739965	0.020762725	SCARB2;SY	.
0	0	0.591245293	0.023822968	MTHFD1;C	.
0	0	0.53648757	0.021441834	ITGB3;HGF	.
0	0	0.480783908	0.019180039	SFRP4;CDH	.
0	0	0.480783908	0.019180039	WFIKKN1;C	.
0	0	0.627195999	0.024984842	CD86;IL36A	.
0	0	0.574743899	0.022865711	PSMD10;P	.
0	0	0.574743899	0.022865711	PSMD10;P	.
0	0	0.384814815	0.01500999	SLC12A6;H	.
0	0	0.384814815	0.01500999	TNFSF4;TR	.
0	0	0.384814815	0.01500999	LGALS3;MA	.
0	0	0.296116993	0.011171615	TNFSF4	.
0	0	0.296116993	0.011171615	TM7SF3	.
0	0	0.296116993	0.011171615	SMC6	.
0	0	0.296116993	0.011171615	CLASP1	.
0	0	0.296116993	0.011171615	CD19	.
0	0	0.296116993	0.011171615	CBLB	.
0	0	0.296116993	0.011171615	RECQL5	.
0	0	0.296116993	0.011171615	SSTR2	.
0	0	0.296116993	0.011171615	CCDC88C	.
0	0	0.505964683	0.01893024	MAPKBP1;	.
0	0	0.435508546	0.016286545	CUL7;GLM	.
0	0	0.435508546	0.016286545	EPS8;SHTN	.
0	0	0.435508546	0.016286545	AHI1;MEIS	.
0	0	0.473360395	0.017345096	HGF;CCR9;	.
0	0	0.473360395	0.017345096	ABI3;PDGF	.
0	0	0.595682371	0.021244199	LATS1;TFR(	.
0	0	0.618706769	0.02192165	CD86;HGF;	.
0	0	0.581242287	0.020567182	ARMC2;CA	.
0	0	0.375407833	0.013193942	PRDX1;RAS	.
0	0	0.375407833	0.013193942	NLRX1;HAV	.
0	0	0.375407833	0.013193942	TNFSF4;NK	.
0	0	0.375407833	0.013193942	CITED2;FST	.
0	0	0.375407833	0.013193942	CDK5;NAA	.
0	0	0.524235149	0.018043491	ZNHIT1;NA	.
0	0	0.689080063	0.023437595	KANK1;WV	.
0	0	0.466161836	0.015683687	CASP9;TMI	.
0	0	0.466161836	0.015683687	LGALS3;CC	.
0	0	0.466161836	0.015683687	PPP3CA;FE	.
0	0	0.591066564	0.019792142	RAP2A;ARI	.

0	0	0.285133566	0.009499322	MT1E	.
0	0	0.285133566	0.009499322	APOA4	.
0	0	0.285133566	0.009499322	EIF2AK4	.
0	0	0.285133566	0.009499322	MAP2K5	.
0	0	0.285133566	0.009499322	PLA2G6	.
0	0	0.285133566	0.009499322	ARFIP1	.
0	0	0.285133566	0.009499322	FHOD3	.
0	0	0.73119983	0.024158821	MAGED1;G	.
0	0	0.774594646	0.025475131	GMNN;CHI	.
0	0	0.639899211	0.020518783	NDC1;ARL3	.
0	0	0.679973749	0.021725341	MSR1;WW	.
0	0	0.366448802	0.011602094	PLA2G6;W	.
0	0	0.366448802	0.011602094	MYBPC3;M	.
0	0	0.366448802	0.011602094	CCL19;GAS	.
0	0	0.366448802	0.011602094	BTBD2;CDI	.
0	0	0.366448802	0.011602094	CDK5;NAA	.
0	0	0.366448802	0.011602094	APOA4;CD	.
0	0	0.646549297	0.020320209	SETD4;GRM	.
0	0	0.419624316	0.013024575	PPP2CB;EP	.
0	0	0.419624316	0.013024575	DLG4;CAM	.
0	0	0.571569959	0.017737327	PSMD10;P	.
0	0	0.459178161	0.014179533	PDCD4;GD	.
0	0	0.459178161	0.014179533	APH1B;TIM	.
0	0	0.553906462	0.016781347	PSMD10;P	.
0	0	0.486667992	0.014329979	XPO1;STRA	.
0	0	0.274934669	0.008090501	RAPGEF3	.
0	0	0.274934669	0.008090501	VASN	.
0	0	0.274934669	0.008090501	CIB1	.
0	0	0.274934669	0.008090501	CD1B	.
0	0	0.274934669	0.008090501	MT1E	.
0	0	0.53272515	0.015519725	WFIKKN1;C	.
0	0	0.35790647	0.010205928	CUX2;CLST	.
0	0	0.35790647	0.010205928	HABP4;GR	.
0	0	0.35790647	0.010205928	TMEM161	.
0	0	0.452399887	0.012817882	CUL7;CUX2	.
0	0	0.548929664	0.015522079	STX17;MTM	.
0	0	0.412107672	0.011647609	HGF;TREM	.
0	0	0.412107672	0.011647609	MSRB2;CK	.
0	0	0.480557373	0.013054624	MAPKBP1;	.
0	0	0.480557373	0.013054624	DDB1;TNF	.
0	0	0.726855147	0.019641317	ATP6V1A;E	.
0	0	0.689699121	0.018440911	PSMD10;C	.
0	0	0.265439145	0.006900954	CASP8AP2	.
0	0	0.265439145	0.006900954	ITGB3	.
0	0	0.265439145	0.006900954	PSIP1	.
0	0	0.265439145	0.006900954	MMP14	.
0	0	0.265439145	0.006900954	APH1B	.

0	0	0.265439145	0.006900954	SYT2	.
0	0	0.265439145	0.006900954	MYBPC3	.
0	0	0.265439145	0.006900954	LOXL3	.
0	0	0.265439145	0.006900954	CDK5	.
0	0	0.265439145	0.006900954	TICAM1	.
0	0	0.265439145	0.006900954	MT1E	.
0	0	0.445818085	0.011585363	LGALS3;CC	.
0	0	0.445818085	0.011585363	ACER2;TBC	.
0	0	0.445818085	0.011585363	EPS8;KANK	.
0	0	0.349752426	0.008980715	CDK5;MAP	.
0	0	0.557646487	0.014177142	TWSG1;AC	.
0	0	0.397851968	0.009314824	HMGB1;PA	.
0	0	0.341960784	0.007904977	RPS6KA5;R	.
0	0	0.341960784	0.007904977	CUX2;CLST	.
0	0	0.256576655	0.005894464	TICAM1	.
0	0	0.256576655	0.005894464	KRT10	.
0	0	0.256576655	0.005894464	P2RX7	.
0	0	0.256576655	0.005894464	WFS1	.
0	0	0.391086549	0.008329758	ACER2;TM	.
0	0	0.46310898	0.009857835	PREPL;HEA	.
0	0	0.63020595	0.013331497	MAPKBP1;	.
0	0	0.334507909	0.006960037	NDC1;NUP	.
0	0	0.334507909	0.006960037	TNFSF4;HN	.
0	0	0.583164834	0.012013419	CD84;CDH	.
0	0	0.612389748	0.012562225	EPHA10;SE	.
0	0	0.248285939	0.005041233	GTF2H5	.
0	0	0.248285939	0.005041233	GTF2H5	.
0	0	0.248285939	0.005041233	RUNX2	.
0	0	0.248285939	0.005041233	PRKCA	.
0	0	0.248285939	0.005041233	RAP2A	.
0	0	0.248285939	0.005041233	TNFSF4	.
0	0	0.248285939	0.005041233	METTL18	.
0	0	0.327372178	0.006129634	EDNRB;ME	.
0	0	0.421294111	0.007720577	LGALS3;CC	.
0	0	0.240513393	0.00431665	RPS6KA5	.
0	0	0.240513393	0.00431665	TNFSF4	.
0	0	0.62765567	0.011112858	GSTP1;PDC	.
0	0	0.320533769	0.005399597	SLC1A3;SL	.
0	0	0.320533769	0.005399597	GSTP1;EMI	.
0	0	0.320533769	0.005399597	RPS27L;MF	.
0	0	0.580130228	0.009420472	PSMD10;V	.
0	0	0.493401707	0.007980421	PREPL;HEA	.
0	0	0.62192996	0.009880377	NTNG2;EPI	.
0	0	0.23321191	0.003700317	MCM8	.
0	0	0.23321191	0.003700317	PARK7	.
0	0	0.23321191	0.003700317	CTSK	.
0	0	0.23321191	0.003700317	MYH14	.

0	0	0.671756107	0.01060204	SETD4;CD8	.
0	0	0.715323873	0.01108178	ZNF395;M/	.
0	0	0.410013083	0.006296914	P2RX7;SYT	.
0	0	0.441716315	0.006758861	ZFP69;GPA	.
0	0	0.441716315	0.006758861	SFRP4;FZD	.
0	0	0.366172624	0.005325038	RPS6KA5;R	.
0	0	0.636387949	0.009126472	DIRAS1;SEI	.
0	0	0.436672021	0.006147113	GRN;MAGI	.
0	0	0.226339926	0.003175269	CCL19	.
0	0	0.226339926	0.003175269	LSM10	.
0	0	0.226339926	0.003175269	LOXL3	.
0	0	0.226339926	0.003175269	TICAM1	.
0	0	0.30767756	0.004192725	DENND1B;	.
0	0	0.30767756	0.004192725	SLC27A1;E	.
0	0	0.219860627	0.002727362	CDH24	.
0	0	0.219860627	0.002727362	SPAST	.
0	0	0.219860627	0.002727362	CTSK	.
0	0	0.219860627	0.002727362	GAS6	.
0	0	0.219860627	0.002727362	POLR3G	.
0	0	0.219860627	0.002727362	POLR3G	.
0	0	0.219860627	0.002727362	PRKCA	.
0	0	0.219860627	0.002727362	SLC9A1	.
0	0	0.354865536	0.004256501	CAMK2A;F	.
0	0	0.551453766	0.006448895	TREML1;DI	.
0	0	0.53776797	0.006111902	WWTR1;CI	.
0	0	0.571313408	0.006492516	DTNB;FZD5	.
0	0	0.491477501	0.005498763	TNFSF18;P	.
0	0	0.29581029	0.003258091	MBNL2;RB	.
0	0	0.213741289	0.002344764	GRIN2C	.
0	0	0.213741289	0.002344764	IGF1	.
0	0	0.422204323	0.004618786	RINT1;RUF	.
0	0	0.34946897	0.003805249	TCEA2;ELP	.
0	0	0.34946897	0.003805249	TUT4;UPF3	.
0	0	0.578175716	0.006239448	RARS2;EEF	.
0	0	0.389164601	0.00418101	ALDH3A2;I	.
0	0	0.518648294	0.00529087	WWOX;MI	.
0	0	0.518648294	0.00529087	PSMD10;D	.
0	0	0.207952726	0.002017556	RASGRP1	.
0	0	0.207952726	0.002017556	TUT4	.
0	0	0.551000958	0.005109297	TNFSF18;P	.
0	0	0.413077746	0.003813496	RNF113A;F	.
0	0	0.379512526	0.003403728	CD86;FCRL	.
0	0	0.339152008	0.00304066	CITED2;PKI	.
0	0	0.284822077	0.002533481	STX17;FZD	.
0	0	0.202468825	0.001737401	LGALS1	.
0	0	0.556353675	0.004644129	CD86;HGF;	.
0	0	0.279627649	0.002234554	ASPH;NKD2	.

0	0	0.197266148	0.00149728	SFRP4	.
0	0	0.451682507	0.003398254	ACHE;FZD5	.
0	0	0.329424586	0.002429099	H1-10;H2B	.
0	0	0.329424586	0.002429099	NAAA;SLC1	.
0	0	0.426669577	0.003049985	WWOX;TW	.
0	0	0.192323606	0.001291266	KRT10	.
0	0	0.465228961	0.003089982	WWTR1;TH	.
0	0	0.587040485	0.003793261	PSMD10;U	.
0	0	0.269785575	0.001739039	TNFSF18;IC	.
0	0	0.361571022	0.002251662	DLG4;CAM	.
0	0	0.361571022	0.002251662	TWSG1;ITG	.
0	0	0.530273037	0.003132676	FBXW4;RN	.
0	0	0.357346423	0.002029907	IGF2BP3;YI	.
0	0	0.707358706	0.003860216	CD86;TENM	.
0	0	0.473024835	0.00255448	PSMD10;P	.
0	0	0.502241907	0.002708805	RBPMS;FAS	.
0	0	0.183144599	9.62E-04	BRINP1	.
0	0	0.183144599	9.62E-04	LHFPL2	.
0	0	0.411337844	0.00211423	GLP1R;CAL	.
0	0	0.178875294	8.31E-04	PKD2	.
0	0	0.178875294	8.31E-04	PKD2L1	.
0	0	0.178875294	8.31E-04	CBLB	.
0	0	0.252037573	0.001054737	HOXB4;HO	.
0	0	0.252037573	0.001054737	TIMP2;SER	.
0	0	0.252037573	0.001054737	SSTR2;HCR	.
0	0	0.174800048	7.19E-04	POGLUT1	.
0	0	0.174800048	7.19E-04	PIGU	.
0	0	0.303314138	0.001236488	UPF3B;MA	.
0	0	0.476416798	0.00194044	LGALS1;GC	.
0	0	0.247958395	9.31E-04	PPBP;CXCL	.
0	0	0.247958395	9.31E-04	POLR3G;TF	.
0	0	0.4164314	0.00141386	XRCC5;GEM	.
0	0	0.635394879	0.002145644	ZNF395;MA	.
0	0	0.244008715	8.22E-04	CALCRL;SST	.
0	0	0.467621871	0.001530989	UGDH;DTN	.
0	0	0.451203209	0.001445037	MRPL42;M	.
0	0	0.432220233	0.001329776	SHMT2;ALI	.
0	0	0.500646842	0.00142042	GLP1R;GRM	.
0	0	0.75075773	0.002107811	TFRC;PARK	.
0	0	0.288083043	7.87E-04	MMP14;PC	.
0	0	0.23647394	6.41E-04	ELP4;GTF2	.
0	0	0.486652079	0.001299241	POP7;HELC	.
0	0	0.160197082	4.04E-04	POLR3G	.
0	0	0.403815215	9.90E-04	GUCY2C;AI	.
0	0	0.456383909	0.001112807	GLP1R;MA	.
0	0	0.232877798	5.66E-04	TNFSF18;IC	.
0	0	0.648400306	0.001539114	CD86;BLM	.

0	0	0.397787482	8.27E-04	SUV39H1;(	.
0	0	0.277623134	5.61E-04	PRKCA;CCL	.
0	0	0.534046961	0.001028669	PSMD10;U	.
0	0	0.577502021	0.001020912	NXT1;THRE	.
0	0	0.310193078	5.21E-04	GATAD1;SI	.
0	0	0.339580534	5.39E-04	MAPKBP1;	.
0	0	0.147840726	2.28E-04	ZFPM1	.
0	0	0.147840726	2.28E-04	KRT10	.
0	0	0.216416582	3.04E-04	DROSHA;TI	.
0	0	0.216416582	3.04E-04	FZD5;SIRT2	.
0	0	0.264798725	3.56E-04	MBNL2;CIF	.
0	0	0.210463485	2.37E-04	FRS3;FGFR	.
0	0	0.35402075	3.91E-04	GLP1R;CAL	.
0	0	0.258818804	2.84E-04	DSTYK;FRS	.
0	0	0.35129831	3.55E-04	GLP1R;CAL	.
0	0	0.137249564	1.30E-04	HEATR3	.
0	0	0.458646404	3.69E-04	NFATC3;LC	.
0	0	0.465866804	3.30E-04	CHRNB1;K(	.
0	0	0.196916373	1.28E-04	COL5A1;KF	.
0	0	0.128070557	7.46E-05	TPD52	.
0	0	0.1259639	6.49E-05	ARNTL	.
0	0	0.509530083	2.61E-04	WWTR1;IN	.
0	0	0.602324608	2.57E-04	CD86;TFRC	.
0	0	0.714534547	2.99E-04	CD86;CRTC	.
0	0	0.570545179	1.93E-04	CD86;GRN	.
0	0	0.376590622	1.13E-04	HELQ;XPO1	.
0	0	0.26220269	7.69E-05	CAMK2A;C	.
0	0	0.255604012	5.58E-05	AGBL5;NDI	.
0	0	0.111308893	2.18E-05	DROSHA	.
0	0	0.215059195	3.69E-05	CIB1;CCL19	.
0	0	0.108161162	1.66E-05	LIMS1	.
0	0	0.166818225	2.30E-05	SRP14;SIL1	.
0	0	0.209158279	2.63E-05	UPF3B;MA	.
0	0	0.237649469	2.15E-05	AGBL5;NDI	.
0	0	0.642717058	5.57E-05	THRB;THRA	.
0	0	0.383743351	2.53E-05	RNF113A;F	.
0	0	0.097164028	5.80E-06	CCL19	.
0	0	0.095944033	5.10E-06	ESR1	.
0	0	0.421182482	2.15E-05	CHRNB1;K(	.
0	0	0.278369906	1.36E-05	ERI1;TUT4;	.
0	0	0.27500477	1.13E-05	HELQ;ERI1	.
0	0	0.092460434	3.50E-06	TPD52	.
0	0	0.380367172	1.24E-05	GEMIN2;U	.
0	0	0.270105528	8.60E-06	GSDMB;DF	.
0	0	0.587998827	1.71E-05	SETD4;CD8	.
0	0	0.243800091	6.77E-06	HELQ;POP4	.
0	0	0.239187936	5.18E-06	GLP1R;CAL	.

0	0	0.086197784	1.71E-06	SRP14	.
0	0	0.373447402	5.52E-06	GEMIN2;U	.
0	0	0.717480168	9.07E-06	ZNF174;SP	.
0	0	0.522284085	6.32E-06	CD86;PSM	.
0	0	0.078241663	6.95E-07	CD36	.
0	0	0.69285863	6.10E-06	ZNF572;ZN	.
0	0	0.075156282	5.11E-07	SRP14	.
0	0	0.362490205	2.04E-06	CD86;CNTF	.
0	0	0.287920196	1.47E-06	TREML1;M	.

t terms were highlighted)

Term	Overlap	P-value	Adjusted P-value	Old P-value
Valine, leucine and isoleucine degradation	26/48	6.92E-13	2.16E-10	0
Fanconi anemia pathway	26/54	2.37E-11	3.70E-09	0
Lysosome	40/128	1.66E-09	1.73E-07	0
Glyoxylate and dicarboxylate metabolism	17/30	2.72E-09	2.13E-07	0
Propanoate metabolism	18/34	4.05E-09	2.53E-07	0
Fatty acid degradation	19/43	6.70E-08	3.49E-06	0
Amino sugar and nucleotide sugar metabolis	20/48	1.01E-07	4.48E-06	0
DNA replication	16/36	6.65E-07	2.59E-05	0
Base excision repair	15/33	1.04E-06	3.62E-05	0
Peroxisome	25/82	3.01E-06	9.39E-05	0
Nucleotide excision repair	16/47	3.97E-05	0.001127243	0
Fatty acid elongation	44892	1.01E-04	0.00260755	0
Mismatch repair	44857	1.09E-04	0.00260755	0
Fructose and mannose metabolism	12389	1.78E-04	0.003974324	0
Homologous recombination	13/41	4.60E-04	0.009575222	0
Lysine degradation	17/63	5.61E-04	0.01094032	0
Tryptophan metabolism	13/42	5.97E-04	0.010962981	0
Butanoate metabolism	44862	7.26E-04	0.012587952	0
Riboflavin metabolism	44689	8.26E-04	0.013556934	0
N-Glycan biosynthesis	14/50	0.001134877	0.017704074	0
beta-Alanine metabolism	44864	0.001340974	0.01992304	0
Galactose metabolism	44865	0.001778132	0.025217139	0
Other glycan degradation	44760	0.002633253	0.035720655	0
p53 signaling pathway	17/73	0.003220685	0.0418689	0
Various types of N-glycan biosynthesis	14550	0.003523814	0.043977194	0
Glutathione metabolism	14/57	0.004320163	0.051841956	0
Thiamine metabolism	44727	0.004545362	0.052524184	0
Glycosylphosphatidylinositol (GPI)-anchor bio	44799	0.006957664	0.077528261	0
Porphyrin and chlorophyll metabolism	16011	0.007871679	0.084688407	0
Glycerolipid metabolism	14/61	0.008169261	0.084960313	0
Biosynthesis of unsaturated fatty acids	44800	0.008910146	0.08956441	0
Primary bile acid biosynthesis	44729	0.009186093	0.08956441	0
Mannose type O-glycan biosynthesis	44765	0.012132809	0.113889055	0
Pentose and glucuronate interconversions	12663	0.012410987	0.113889055	0
Nicotinate and nicotinamide metabolism	13028	0.015045952	0.134123914	0
Pyruvate metabolism	17472	0.015552186	0.134785609	0
Glycosaminoglycan degradation	44731	0.016478981	0.138957897	0
Ascorbate and aldarate metabolism	44803	0.017214411	0.141339372	0
Sphingolipid metabolism	18203	0.021034866	0.165212598	0
Purine metabolism	23/129	0.021181102	0.165212598	0
Pyrimidine metabolism	20790	0.023257035	0.176980366	0
Ubiquinone and other terpenoid-quinone bio	44662	0.029476725	0.218969954	0
Glycolysis / Gluconeogenesis	13/67	0.039559098	0.287033452	0
PPAR signaling pathway	14/74	0.040591451	0.287830292	0

Phosphatidylinositol signaling system	17/97	0.049552492	0.329236307	0
Citrate cycle (TCA cycle)	44772	0.049596495	0.329236307	0
Pentose phosphate pathway	44772	0.049596495	0.329236307	0
Non-homologous end-joining	44664	0.053042607	0.33857292	0
Glycerophospholipid metabolism	17/98	0.053797698	0.33857292	0
Arginine and proline metabolism	18537	0.05534365	0.33857292	0
Cholesterol metabolism	18537	0.05534365	0.33857292	0
Drug metabolism	18/108	0.066817989	0.400907933	0
Folate biosynthesis	44738	0.069996755	0.410871417	0
Inositol phosphate metabolism	13/73	0.071112361	0.410871417	0
Cell cycle	20/124	0.073420554	0.416494781	0
Gap junction	15/88	0.075875669	0.417619971	0
Dopaminergic synapse	21/132	0.076295956	0.417619971	0
Long-term potentiation	24807	0.077976356	0.419459017	0
Other types of O-glycan biosynthesis	17411	0.084011767	0.435764972	0
Glioma	13/75	0.084490336	0.435764972	0
Arachidonic acid metabolism	22586	0.085574976	0.435764972	0
Fc gamma R-mediated phagocytosis	16/97	0.086594321	0.435764972	0
Sulfur metabolism	44630	0.097970027	0.471441337	0
Synthesis and degradation of ketone bodies	44630	0.097970027	0.471441337	0
Histidine metabolism	44703	0.099727975	0.471441337	0
Terpenoid backbone biosynthesis	44703	0.099727975	0.471441337	0
Phagosome	23/152	0.101922979	0.474165193	0
Ether lipid metabolism	18142	0.103343696	0.474165193	0
Fat digestion and absorption	15919	0.113720564	0.507580744	0
Cysteine and methionine metabolism	18507	0.113880295	0.507580744	0
Selenocompound metabolism	44668	0.122518455	0.538390955	0
ECM-receptor interaction	14/88	0.129464968	0.561014861	0
Vitamin B6 metabolism	44598	0.144599043	0.612789909	0
Mineral absorption	22190	0.145341196	0.612789909	0
Glycosaminoglycan biosynthesis	19603	0.148845604	0.619197714	0
Thyroid hormone signaling pathway	18/121	0.151407477	0.621567538	0
Calcium signaling pathway	33/240	0.157191084	0.636930106	0
Glycine, serine and threonine metabolism	14793	0.169207185	0.676828738	0
Cellular senescence	22/156	0.18137285	0.716307967	0
One carbon pool by folate	44671	0.190676166	0.743637047	0
GnRH secretion	23651	0.194852164	0.750541667	0
AMPK signaling pathway	17/120	0.213220912	0.811279567	0
Circadian entrainment	14/97	0.220261004	0.827969074	0
Oocyte meiosis	18/129	0.223719734	0.830959014	0
Starch and sucrose metabolism	13302	0.227110428	0.83109689	0
Hypertrophic cardiomyopathy	13/90	0.230331798	0.83109689	0
Aldosterone synthesis and secretion	14/98	0.231748171	0.83109689	0
Alanine, aspartate and glutamate metabolism	13667	0.24682824	0.875118306	0
ABC transporters	16619	0.254557502	0.882466006	0
Glycosphingolipid biosynthesis	16619	0.254557502	0.882466006	0
Protein export	44674	0.267758063	0.918027645	0

Apoptosis	19/142	0.273942893	0.929023723	0
Sphingolipid signaling pathway	16/119	0.289541528	0.971365125	0
Vitamin digestion and absorption	44675	0.294628646	0.977916358	0
Dilated cardiomyopathy	13/96	0.30694585	0.999994944	0
mTOR signaling pathway	20/154	0.313805307	0.999994944	0
Cholinergic synapse	15/113	0.315606229	0.999994944	0
Inflammatory mediator regulation of TRP cha	13/98	0.333913963	0.999994944	0
Fatty acid biosynthesis	44638	0.342346224	0.999994944	0
Glucagon signaling pathway	14/107	0.344089645	0.999994944	0
Thyroid hormone synthesis	27668	0.358369518	0.999994944	0
Adrenergic signaling in cardiomyocytes	19/150	0.360942311	0.999994944	0
VEGF signaling pathway	21763	0.365611025	0.999994944	0
Rap1 signaling pathway	26/210	0.37247049	0.999994944	0
Pancreatic cancer	28034	0.374370827	0.999994944	0
Diabetic cardiomyopathy	25/203	0.386640679	0.999994944	0
Arrhythmogenic right ventricular cardiomyop	28399	0.390438113	0.999994944	0
Amphetamine addiction	25447	0.396049571	0.999994944	0
Insulin secretion	31717	0.400394769	0.999994944	0
Autophagy	17/137	0.405791629	0.999994944	0
Proteoglycans in cancer	25/205	0.406394417	0.999994944	0
Endocrine and other factor-regulated calcium	19541	0.408351479	0.999994944	0
Glutamatergic synapse	14/114	0.437665214	0.999994944	0
Prostate cancer	35765	0.43840844	0.999994944	0
Ubiquitin mediated proteolysis	17/140	0.442230217	0.999994944	0
Melanoma	26543	0.447198382	0.999994944	0
Non-small cell lung cancer	26543	0.447198382	0.999994944	0
Focal adhesion	24/201	0.452206231	0.999994944	0
Choline metabolism in cancer	36130	0.452989061	0.999994944	0
cGMP-PKG signaling pathway	20/167	0.456728158	0.999994944	0
HIF-1 signaling pathway	13/109	0.486818653	0.999994944	0
Salivary secretion	34274	0.506793151	0.999994944	0
Amyotrophic lateral sclerosis	42/364	0.512002435	0.999994944	0
Gastric acid secretion	28004	0.514285484	0.999994944	0
Ferroptosis	15097	0.515146251	0.999994944	0
Phosphonate and phosphinate metabolism	44567	0.519094735	0.999994944	0
Vibrio cholerae infection	18415	0.519845256	0.999994944	0
SNARE interactions in vesicular transport	12145	0.534512503	0.999994944	0
Phospholipase D signaling pathway	17/148	0.538300278	0.999994944	0
Long-term depression	22098	0.542381771	0.999994944	0
Renin secretion	25416	0.544682261	0.999994944	0
alpha-Linolenic acid metabolism	44645	0.559919776	0.999994944	0
Vascular smooth muscle contraction	15/133	0.570552944	0.999994944	0
Ras signaling pathway	26/232	0.584067526	0.999994944	0
Insulin resistance	12/108	0.593653642	0.999994944	0
B cell receptor signaling pathway	29830	0.594034926	0.999994944	0
Tyrosine metabolism	13241	0.605679118	0.999994944	0
Collecting duct acid secretion	44647	0.613771602	0.999994944	0

Regulation of lipolysis in adipocytes	20241	0.616283647	0.999994944	0
Small cell lung cancer	33878	0.622295557	0.999994944	0
Sulfur relay system	44569	0.623246824	0.999994944	0
African trypanosomiasis	13606	0.627868903	0.999994944	0
Aldosterone-regulated sodium reabsorption	13606	0.627868903	0.999994944	0
Hedgehog signaling pathway	20607	0.634214733	0.999994944	0
Pancreatic secretion	11/102	0.634236003	0.999994944	0
GnRH signaling pathway	34243	0.636211501	0.999994944	0
Rheumatoid arthritis	34243	0.636211501	0.999994944	0
Carbohydrate digestion and absorption	17288	0.640350373	0.999994944	0
Fluid shear stress and atherosclerosis	15/139	0.641103139	0.999994944	0
Human immunodeficiency virus 1 infection	23/212	0.646873411	0.999994944	0
Metabolism of xenobiotics by cytochrome P4	27973	0.656961547	0.999994944	0
Serotonergic synapse	12/113	0.657589821	0.999994944	0
Fc epsilon RI signaling pathway	25020	0.67744237	0.999994944	0
RNA degradation	29068	0.699720075	0.999994944	0
Viral myocarditis	22068	0.700766989	0.999994944	0
Oxytocin signaling pathway	16/154	0.702638919	0.999994944	0
GABAergic synapse	32752	0.706761666	0.999994944	0
PD-L1 expression and PD-1 checkpoint pathw	32752	0.706761666	0.999994944	0
Central carbon metabolism in cancer	25750	0.706961756	0.999994944	0
RNA polymerase	44651	0.70748793	0.999994944	0
Bladder cancer	15067	0.708326162	0.999994944	0
Ovarian steroidogenesis	18749	0.71162892	0.999994944	0
Pantothenate and CoA biosynthesis	44613	0.71277298	0.999994944	0
Apelin signaling pathway	14/137	0.718495747	0.999994944	0
Kaposi sarcoma-associated herpesvirus infec	20/193	0.721154727	0.999994944	0
Progesterone-mediated oocyte maturation	10/100	0.725348372	0.999994944	0
Neurotrophin signaling pathway	12/119	0.72638358	0.999994944	0
Arginine biosynthesis	44614	0.736926691	0.999994944	0
Huntington disease	32/306	0.740697886	0.999994944	0
Hepatocellular carcinoma	17/168	0.74609982	0.999994944	0
PI3K-Akt signaling pathway	37/354	0.754399343	0.999994944	0
Renin-angiotensin system	44615	0.759323757	0.999994944	0
Prion disease	28/273	0.765968774	0.999994944	0
C-type lectin receptor signaling pathway	10/104	0.769297369	0.999994944	0
T cell receptor signaling pathway	10/104	0.769297369	0.999994944	0
Oxidative phosphorylation	13/133	0.771054668	0.999994944	0
Cortisol synthesis and secretion	23894	0.771749106	0.999994944	0
Hepatitis B	16/162	0.775045454	0.999994944	0
Spinocerebellar ataxia	14/143	0.775139996	0.999994944	0
Axon guidance	18/182	0.783455481	0.999994944	0
Parkinson disease	25/249	0.791455961	0.999994944	0
Salmonella infection	25/249	0.791455961	0.999994944	0
Osteoclast differentiation	12/127	0.803159403	0.999994944	0
Synaptic vesicle cycle	28672	0.806447306	0.999994944	0
Pathways of neurodegeneration	49/475	0.810007311	0.999994944	0

Thyroid cancer	13575	0.813871603	0.999994944	0
Lipid and atherosclerosis	21/215	0.815177369	0.999994944	0
Retrograde endocannabinoid signaling	14/148	0.815924078	0.999994944	0
Growth hormone synthesis, secretion and ac	11/119	0.818117885	0.999994944	0
Relaxin signaling pathway	12/129	0.819648045	0.999994944	0
Pathogenic Escherichia coli infection	19/197	0.822026746	0.999994944	0
Primary immunodeficiency	13940	0.827982606	0.999994944	0
Cocaine addiction	17989	0.829524629	0.999994944	0
Melanogenesis	9/101	0.833805563	0.999994944	0
MAPK signaling pathway	29/294	0.833894805	0.999994944	0
Protein processing in endoplasmic reticulum	16/171	0.840909207	0.999994944	0
TNF signaling pathway	10/112	0.841708529	0.999994944	0
Longevity regulating pathway	9/102	0.84211168	0.999994944	0
Steroid hormone biosynthesis	22402	0.844328862	0.999994944	0
Toll-like receptor signaling pathway	9/104	0.857742192	0.999994944	0
Endocytosis	24/252	0.861636406	0.999994944	0
Linoleic acid metabolism	47150	0.861721227	0.999994944	0
Wnt signaling pathway	15/166	0.869917329	0.999994944	0
ErbB signaling pathway	31229	0.870209805	0.999994944	0
RNA transport	17/186	0.871455367	0.999994944	0
Phenylalanine metabolism	44578	0.874423701	0.999994944	0
Circadian rhythm	11355	0.885788035	0.999994944	0
Tuberculosis	16/180	0.891080991	0.999994944	0
Hematopoietic cell lineage	36373	0.894283507	0.999994944	0
Acute myeloid leukemia	24593	0.896411573	0.999994944	0
Alzheimer disease	35/369	0.905685091	0.999994944	0
Human papillomavirus infection	31/331	0.907264923	0.999994944	0
Morphine addiction	33420	0.910054741	0.999994944	0
Proteasome	16862	0.911113584	0.999994944	0
Amoebiasis	8/102	0.911451747	0.999994944	0
Endometrial cancer	21276	0.912611375	0.999994944	0
Human cytomegalovirus infection	20/225	0.912764167	0.999994944	0
Steroid biosynthesis	44581	0.912942	0.999994944	0
cAMP signaling pathway	19/216	0.916248934	0.999994944	0
Prolactin signaling pathway	25689	0.916258826	0.999994944	0
Estrogen signaling pathway	11/137	0.926404553	0.999994944	0
Yersinia infection	11/137	0.926404553	0.999994944	0
Neutrophil extracellular trap formation	16/189	0.927664715	0.999994944	0
Mucin type O-glycan biosynthesis	13181	0.929981126	0.999994944	0
Parathyroid hormone synthesis, secretion an	8/106	0.930594758	0.999994944	0
Complement and coagulation cascades	31199	0.935529922	0.999994944	0
Proximal tubule bicarbonate reclamation	44584	0.939648819	0.999994944	0
mRNA surveillance pathway	35977	0.942823118	0.999994944	0
Cardiac muscle contraction	31929	0.943938816	0.999994944	0
Chronic myeloid leukemia	27881	0.946150006	0.999994944	0
AGE-RAGE signaling pathway in diabetic com	7/100	0.949995427	0.999994944	0
Bacterial invasion of epithelial cells	28246	0.950067624	0.999994944	0

Cushing syndrome	12/155	0.951068804	0.999994944	0
Regulation of actin cytoskeleton	18/218	0.951674125	0.999994944	0
Aminoacyl-tRNA biosynthesis	24198	0.953864707	0.999994944	0
Platelet activation	9/124	0.955214844	0.999994944	0
Chagas disease	7/102	0.956352056	0.999994944	0
Protein digestion and absorption	7/103	0.95924923	0.999994944	0
Thermogenesis	19/232	0.959477141	0.999994944	0
Pathways in cancer	49/531	0.960747426	0.999994944	0
Mitophagy	24929	0.960891995	0.999994944	0
NF-kappa B signaling pathway	7/104	0.961971541	0.999994944	0
Renal cell carcinoma	25294	0.964020737	0.999994944	0
Type I diabetes mellitus	15738	0.965464812	0.999994944	0
Epithelial cell signaling in Helicobacter pylori	25659	0.966915379	0.999994944	0
Phototransduction	44589	0.967233504	0.999994944	0
Vasopressin-regulated water reabsorption	16103	0.968835072	0.999994944	0
Hippo signaling pathway	12/163	0.969014796	0.999994944	0
Adherens junction	26024	0.969591681	0.999994944	0
Chemical carcinogenesis	19/239	0.971203954	0.999994944	0
Alcoholism	14/186	0.971274325	0.999994944	0
Ribosome biogenesis in eukaryotes	7/108	0.971287561	0.999994944	0
Basal transcription factors	16469	0.971887105	0.999994944	0
Notch signaling pathway	21610	0.972132168	0.999994944	0
Colorectal cancer	31533	0.97525776	0.999994944	0
Taste transduction	31533	0.97525776	0.999994944	0
Tight junction	12/169	0.978332131	0.999994944	0
Toxoplasmosis	7/112	0.978468124	0.999994944	0
Intestinal immune network for IgA productio	17564	0.979408174	0.999994944	0
Transcriptional misregulation in cancer	14/192	0.979567595	0.999994944	0
Necroptosis	11/159	0.979825447	0.999994944	0
Pertussis	27851	0.980190488	0.999994944	0
Basal cell carcinoma	23071	0.980816395	0.999994944	0
Cytosolic DNA-sensing pathway	23071	0.980816395	0.999994944	0
Leukocyte transendothelial migration	7/114	0.981398994	0.999994944	0
Influenza A	12/172	0.98196292	0.999994944	0
Bile secretion	32994	0.982102214	0.999994944	0
Measles	9/139	0.983229918	0.999994944	0
Malaria	18295	0.983295453	0.999994944	0
Human T-cell leukemia virus 1 infection	16/219	0.984794393	0.999994944	0
Signaling pathways regulating pluripotency o	9/143	0.987275765	0.999994944	0
Retinol metabolism	24898	0.988076961	0.999994944	0
Hepatitis C	10/157	0.989133435	0.999994944	0
Adipocytokine signaling pathway	25263	0.989170407	0.999994944	0
Chemokine signaling pathway	13/192	0.989532758	0.999994944	0
Allograft rejection	13881	0.990344919	0.999994944	0
Breast cancer	9/147	0.990397692	0.999994944	0
Insulin signaling pathway	8/137	0.991714272	0.999994944	0
Legionellosis	20852	0.992040669	0.999994944	0

Viral protein interaction with cytokine and cy	5/100	0.992249317	0.999994944	0
Nicotine addiction	14611	0.992438581	0.999994944	0
Herpes simplex virus 1 infection	41/498	0.993249376	0.999994944	0
Graft-versus-host disease	15342	0.994078268	0.999994944	0
Epstein-Barr virus infection	13/202	0.994481831	0.999994944	0
Viral carcinogenesis	13/203	0.994831776	0.999994944	0
FoxO signaling pathway	7/131	0.99494062	0.999994944	0
Natural killer cell mediated cytotoxicity	7/131	0.99494062	0.999994944	0
Th1 and Th2 cell differentiation	33695	0.99528862	0.999994944	0
NOD-like receptor signaling pathway	11/181	0.995317772	0.999994944	0
Antigen processing and presentation	28550	0.99550746	0.999994944	0
IL-17 signaling pathway	34425	0.996085905	0.999994944	0
TGF-beta signaling pathway	34425	0.996085905	0.999994944	0
Type II diabetes mellitus	16803	0.996368	0.999994944	0
Shigellosis	16/246	0.996995576	0.999994944	0
Non-alcoholic fatty liver disease	8/155	0.997929032	0.999994944	0
Autoimmune thyroid disease	19360	0.998455675	0.999994944	0
Cell adhesion molecules	7/148	0.998739156	0.999994944	0
Systemic lupus erythematosus	6/135	0.998795662	0.999994944	0
Gastric cancer	7/149	0.998840718	0.999994944	0
Th17 cell differentiation	4/107	0.998856341	0.999994944	0
MicroRNAs in cancer	20/310	0.999036019	0.999994944	0
Leishmaniasis	28157	0.999095872	0.999994944	0
Staphylococcus aureus infection	34759	0.999193212	0.999994944	0
Ribosome	7/158	0.99946055	0.999994944	0
Inflammatory bowel disease	23743	0.999642145	0.999994944	0
Spliceosome	6/150	0.999681833	0.999994944	0
RIG-I-like receptor signaling pathway	25569	0.999804582	0.999994944	0
JAK-STAT signaling pathway	6/162	0.999892002	0.999994944	0
Neuroactive ligand-receptor interaction	18/341	0.999972834	0.999994944	0
Cytokine-cytokine receptor interaction	14/295	0.999980359	0.999994944	0
Olfactory transduction	5/440	0.999994547	0.999994944	0
Coronavirus disease	7/232	0.999994944	0.999994944	0

Old Adjusted P-value	Odds Ratio	Combined Score	Genes
0	9.201112846	257.6291864	ECHS1;ACAT1;MCEE;OXCT1;DBT;ACADM;MMUT;ACAA1
0	7.226992514	176.8105473	BLM;FAAP24;BRCA2;BRIP1;SLX4;REV3L;POLI;PMS2;FAAI
0	3.547549039	71.71247101	SCARB2;CD63;IDUA;HEXA;ABCB9;LIPA;GNS;MFSD8;GGA
0	10.14608637	200.0902188	MDH1;SHMT2;AMT;HOGA1;ACAT1;GCSH;CS;MCEE;PCC/
0	8.73096753	168.7272644	ACSS3;ECHS1;BCKDHB;ACAT1;HADHA;MCEE;ALDH6A1;F
0	6.14393108	101.4851526	GCDH;ACADVL;ECHS1;ECI1;ECI2;ACADSB;CPT1B;ACAT1;
0	5.544576197	89.33843535	GPI;GALT;PMM1;HEXA;MPI;NPL;UGDH;GALE;CYB5R3;GI
0	6.201841298	88.21511081	RFC5;PRIM2;RNASEH2C;FEN1;RFC3;RNASEH2A;RFC4;LIG
0	6.458150745	88.94471681	MBD4;FEN1;LIG1;PARP1;PARP2;OGG1;APEX2;XRCC1;HM
0	3.406458488	43.30805616	ABCD4;ABCD3;ECI2;HSD17B4;CROT;PEX26;PRDX1;NUDT
0	3.998698929	40.5191681	RFC5;RFC3;RFC4;LIG1;RFC2;CETN2;XPA;RPA1;XPC;GTF2I
0	5.319253062	48.95573546	HADHB;HADHA;HACD1;ECHS1;MECR;ACOT2;PPT1;HACD
0	5.950018499	54.30818806	RFC5;MSH6;RFC3;RFC4;LIG1;RFC2;RPA3;POLD2;RPA1;PI
0	4.421881838	38.16900508	PFKL;GMDS;PMM1;FCSK;ENOSF1;FPGT;MPI;GMPPA;SO
0	3.592929072	27.60637658	BLM;XRCC3;RPA1;BRCA2;PALB2;RAD54B;RAD51B;BRIP1
0	2.862023265	21.42428965	GCDH;ECHS1;SUV39H1;PLOD3;PLOD2;ACAT1;ALDH3A2;
0	3.468838698	25.74926197	GCDH;ECHS1;ACAT1;ALDH3A2;HADHA;EHHADH;AFMID;
0	4.296020988	31.05012112	HADHA;ECHS1;ALDH5A1;BDH2;OXCT1;EHHADH;L2HGDH
0	12.87085515	91.37562389	FLAD1;ACP5;BLVRB;ACP2;ACP1
0	3.009417433	20.40755607	B4GALT2;ALG8;ALG9;ALG6;ALG14;ALG13;MOGS;ALG10;
0	3.865981635	25.57099115	ALDH3A2;HADHA;ALDH6A1;ECHS1;EHHADH;CARNS1;M
0	3.681679056	23.31309911	B4GALT2;GALE;PFKL;GALT;GLB1;AKR1B1;GALM;GLA;PFI
0	4.916395395	29.20110325	NEU3;GLB1;FUCA1;FUCA2;HEXA;HEXD;MAN2C1
0	2.349616228	13.482477	IGF1;DDB2;CASP9;PIDD1;TP53I3;SESN3;RRM2B;AIFM2;(
0	3.037510936	17.15650406	B4GALT2;FUT8;ALG9;MGAT4A;HEXA;MGAT4B;HEXD;MA
0	2.518513991	13.71195407	RRM1;GSTM1;GSTO1;GSTP1;IDH1;GSR;GPX7;MGST2;PG
0	5.1488433	27.77104776	THTPA;TPK1;AK1;AK7;ACP1;AK8
0	3.433813893	17.05888329	PIGS;PIGU;PGAP1;PIGQ;PIGK;MPPE1;PIGF;PIGY
0	2.657220582	12.87286238	FECH;HEPH;COX15;UROS;HMBS;BLVRB;GUSB;CP;HMOX
0	2.303650479	11.07451596	DGKA;MOGAT1;AKR1A1;AKR1B1;AGPAT4;ALDH3A2;GPA
0	3.252902899	15.35553848	HACD1;ACOT2;HSD17B4;HACD3;ACAA1;FADS1;ACOT4;H
0	4.212213801	19.75555457	CYP27A1;ACOT8;AMACR;HSD17B4;AKR1C4;SLC27A5
0	3.379066594	14.90790808	B4GALT2;B4GAT1;POMT1;CHST10;LARGE1;POMGNT1;F
0	2.781503497	12.20850053	UGDH;DCXR;AKR1A1;SORD;AKR1B1;CRYL1;GUSB;XYLB;U
0	2.674371302	11.22339043	NADK2;NNT;NMRK1;QPRT;SIRT5;NT5M;NMNAT2;SIRT2;
0	2.361439195	9.831979829	ALDH3A2;MDH1;GLO1;AKR1A1;ACYP2;ACYP1;ACSS1;AL
0	3.563777994	14.63169486	GALNS;IDUA;GLB1;HEXA;GUSB;GNS
0	2.808848644	11.40956683	ALDH3A2;UGDH;AKR1A1;RGN;GUSB;ALDH7A1;UGT1A6;
0	2.236899664	8.637953384	SMPD3;ACER2;ARSA;NEU3;SGPL1;SPHK2;GLB1;PLPP3;G
0	1.67907519	6.472240288	GUCY2C;RRM1;PDE1B;ENTPD5;AK1;GMPS;ADK;ENTPD8
0	2.107698428	7.927364889	DCTD;RRM1;RRM2B;NME7;ENTPD5;CMPK1;ENTPD8;NM
0	4.409943306	15.54132076	COQ3;VKORC1L1;GGCX;COQ6
0	1.860259778	6.008563899	GPI;AKR1A1;ALDH3A2;MINPP1;PFKL;GALM;ALDOA;ACS
0	1.803197547	5.777801599	SLC27A1;CPT1B;CYP27A1;FABP3;FABP5;EHHADH;PLIN2;

0	1.642494518	4.935240594	PRKCG;PI4K2B;MTMR1;DGKA;MTMR14;INPPL1;PRKCA;I
0	2.349724701	7.058185561	CS;MDH1;IDH1;SUCLG2;ACO1;SDHB;DLD
0	2.349724701	7.058185561	GPI;PFKL;RGN;PGD;ALDOA;PFKM;PGM1
0	3.429568251	10.07147516	FEN1;RAD50;XRCC5;POLL
0	1.622124756	4.740699496	ACHE;PLA2G12A;PNPLA7;DGKA;PLA2G6;PLD1;PLD3;AGI
0	1.930804547	5.58812167	ALDH3A2;GATM;OAT;P4HA2;CARNS1;HOGA1;L3HYPDH
0	1.930804547	5.58812167	CYP27A1;NCEH1;OSBPL5;STAR;NPC2;APOA4;CD36;ANG
0	1.545677929	4.182268971	RRM1;GSTM1;GSTO1;GSTP1;GMPS;MGST2;NME4;FMO
0	2.315539066	6.157727863	QDPR;CBR1;SPR;AKR1B1;GGH;PCBD1
0	1.673664623	4.424322572	PI4K2B;MTMR1;MTMR14;INPPL1;MTM1;FIG4;MINPP1;
0	1.486351812	3.881684083	ANAPC13;CDC7;SMC3;PKMYT1;ANAPC10;CDC14B;CDC2
0	1.587468335	4.093539839	PRKCG;TUBB;PDGFB;PRKCA;ITPR3;TUBB4A;TUBA1C;TUE
0	1.46230941	3.762720019	PRKCG;CAMK2A;PRKCA;ITPR3;PPP2R5D;CALML4;COMT
0	1.685108415	4.299300731	PRKCG;PPP3CA;PPP3CC;RPS6KA2;CAMK2A;PRKCA;ITPR3
0	1.828590817	4.529050825	B4GALT2;GALNT12;GALNT6;POGLUT1;POFUT1;POMT1;
0	1.619491837	4.001955611	PRKCG;CAMK2A;PDGFB;PRKCA;PIK3R2;CALML4;IGF1;DI
0	1.698888889	4.176484526	CBR1;PLA2G12A;CYP2U1;PTGES2;ALOX5;PRXL2B;GPX7;
0	1.526036339	3.733480009	PRKCG;VAV3;SPHK2;INPPL1;ASAP3;PRKCA;PIK3R2;PLA2
0	3.306015693	7.680184205	TST;ETHE1;PAPSS2
0	3.306015693	7.680184205	BDH2;OXCT1;ACAT1
0	2.269530849	5.231970002	ALDH3A2;CARNS1;ALDH7A1;ASPA;ALDH9A1
0	2.269530849	5.231970002	FNTB;PDSS2;ACAT1;ZMPSTE24;PCYOX1
0	1.377901863	3.146491067	ATP6V1A;MSR1;STX12;TFRC;ITGB5;ITGB3;TUBB;MPO;TU
0	1.736964598	3.942379849	PLA2G12A;PEDS1;CHPT1;PLPP3;PLA2G6;PLD1;PLA2G7;P
0	1.764263871	3.835529122	SLC27A1;PLA2G12A;APOA4;CD36;PLPP3;PLPP1;ACAT1;S
0	1.694503667	3.681491249	DNMT1;TST;MDH1;ADI1;DNMT3B;MRI1;KYAT1;GCLM;S
0	2.373779731	4.983735379	TXNRD3;TXNRD1;KYAT1;PAPSS2
0	1.460891904	2.986566988	TNXB;ITGB5;VWF;ITGB3;LAMA3;LAMC1;HMMR;SV2C;IT
0	3.855991285	7.456679646	PHOSPHO2;PDXP
0	1.54376913	2.977423094	SLC46A1;HEPH;SLC31A1;SLC40A1;ATP2B4;ATP2B2;HMC
0	1.578701128	3.007182092	B4GALT2;NDST1;FUT8;EXTL1;CHPF;XYLT2;CHST14;EXTL3
0	1.349595505	2.547740147	PRKCG;THRB;THRA;ITGB3;PRKCA;PIK3R2;ATP2A1;ESR1;S
0	1.23198648	2.279536107	PDE1B;CAMK2A;PDGFB;ITPR3;ATP2A1;CALML4;CACNA1
0	1.636760619	2.907920263	GCSH;GATM;SHMT2;AMT;ALDH7A1;DLD;GCAT
0	1.267895686	2.164552047	HIPK4;NFATC3;ITPR3;PIK3R2;CALML4;LIN9;CCNB3;RBL2
0	1.928368949	3.195652057	MTFMT;MTHFD1;SHMT2;AMT
0	1.429091969	2.337300128	PRKCG;AKT3;SPP1;PRKCA;ITPR3;PIK3R2;CACNA1F;KCNN
0	1.274058934	1.968964446	CAB39;CAB39L;STRADA;PIK3R2;PPP2R5D;IGF1;CPT1B;PI
0	1.301816992	1.969573676	PRKCG;CAMK2A;PRKCA;ITPR3;CALML4;GRIN2C;GNG3;R
0	1.251758121	1.874334037	ANAPC13;CAMK2A;ITPR3;PPP2R5D;CALML4;IGF1;SMC3
0	1.542819729	2.286950866	GPI;AMY2B;GBE1;AGL;PYGL;PGM1
0	1.302897628	1.912959131	MYBPC3;ITGB5;ITGB3;TPM2;ATP2A1;IGF1;CACNA1F;SG
0	1.286246167	1.880625622	PRKCG;CAMK2A;ATP2B4;PRKCA;ITPR3;ATP2B2;CALML4
0	1.492966869	2.088754061	ALDH5A1;GPT;ASL;ADSS1;RIMKLA;ASPA
0	1.420995174	1.944246136	ABCD4;ABCA2;ABCD3;ABCA5;ABCC5;ABCB9;ABCG2
0	1.420995174	1.944246136	B4GALT2;GLB1;B3GALT2;HEXA;ST3GAL4;ST3GAL5;GLA
0	1.623614203	2.13939009	IMMP1L;IMMP2L;SRP14;SEC11C

0	1.192102615	1.543576922	DFFA;PARP1;PARP2;ITPR3;PIK3R2;SEPTIN4;CASP9;PIDD
0	1.198588594	1.485598479	PRKCG;SPHK2;PRKCA;PIK3R2;PPP2R5D;PLD1;ACER2;PPF
0	1.542346271	1.884808131	SLC46A1;BTD;APOA4;SLC19A1
0	1.208300804	1.427104665	MYBPC3;ITGB5;ITGB3;TPM2;ATP2A1;IGF1;CACNA1F;SG
0	1.151620029	1.334707492	PRKCG;ATP6V1A;FZD5;CAB39;CAB39L;STRADA;NPRL2;N
0	1.180825091	1.361798291	PRKCG;ACHE;CAMK2A;PRKCA;ITPR3;PIK3R2;CACNA1F;G
0	1.179736273	1.294019585	PRKCG;CAMK2A;TRPV2;PRKCA;ITPR3;PIK3R2;CALML4;IC
0	1.542109852	1.653037983	MECR;OXSM;HSD17B8
0	1.161177285	1.238805539	CAMK2A;ITPR3;PHKB;CALML4;PYGL;CPT1B;PPP3CA;PFK
0	1.186505667	1.217581024	PRKCG;CREB3L3;GSR;GPX7;PRKCA;ITPR3;TTF2;PLCB2;DU
0	1.118793102	1.14009172	TPM2;CAMK2A;ATP2B4;PRKCA;ATP2A1;PPP2R5D;ATP2I
0	1.20967286	1.217155032	CASP9;PRKCG;PPP3CA;PPP3CC;SPHK2;AKT3;PRKCA;PIK3
0	1.090053223	1.076533801	ITGB3;PDGFB;LPAR2;PARD6G;PIK3R2;CALML4;SIPA1L2;I
0	1.168462058	1.148023852	CASP9;RALBP1;RAD51;CDK4;AKT3;E2F1;PIK3R2;BRCA2;I
0	1.083352291	1.0294658	NDUFA11;CAMK2A;NDUFA4L2;PIK3R2;ATP2A1;MPC1;A
0	1.150957064	1.082458781	ITGB5;SGCA;ACTN3;SGCB;ITGB3;ITGA10;DAG1;ITGB8;AT
0	1.15666521	1.071321704	PRKCG;PPP3CA;PPP3CC;CREB3L3;CAMK2A;PRKCA;CALM
0	1.130988626	1.035198748	GLP1R;PRKCG;CREB3L3;CAMK2A;KCNMB4;PRKCA;ITPR3
0	1.092510965	0.985352551	STX17;MTMR14;ATG10;PIK3R2;EIF2AK4;HMGB1;ATG14
0	1.071192782	0.964535317	CD63;ITGB5;ITGB3;CAMK2A;TWIST1;PIK3R2;ITPR3;SLC9
0	1.173333966	1.050869588	PRKCG;ATP2B4;PRKCA;ATP2B2;PLCB2;ESR1;DNM1
0	1.079465615	0.891963532	PRKCG;SLC1A3;PRKCA;ITPR3;PLD1;GRIN2C;PPP3CA;GNC
0	1.088510748	0.897590633	CASP9;CREB3L3;CCNE1;PDGFD;GSTP1;AKT3;MMP3;PDG
0	1.065682499	0.869516653	UBE2F;ANAPC13;CUL7;UBE2D4;FANCL;WWP1;CBLB;ANA
0	1.101398601	0.886353802	CDK4;HGF;PDGFD;AKT3;PDGFB;E2F1;PIK3R2;IGF1;DDB2
0	1.101398601	0.886353802	CASP9;PRKCG;CDK4;HGF;AKT3;E2F1;PRKCA;PIK3R2;DDE
0	1.045493524	0.82972137	PRKCG;VAV3;TNXB;ITGB5;VWF;HGF;ITGB3;LAMA3;PDGI
0	1.075792581	0.851906485	PRKCG;SLC22A5;DGKA;PDGFD;AKT3;PDGFB;PRKCA;PIK3
0	1.04899931	0.822066043	MEF2B;NFATC3;ATP2B4;ITPR3;ATP2A1;ATP2B2;CALML4
0	1.043905976	0.751469915	PRKCG;TFRC;CAMK2A;PRKCA;PIK3R2;IGF1;PFKL;AKT3;TE
0	1.034030045	0.702780945	PRKCG;AMY2B;ATP2B4;PRKCA;ITPR3;ATP2B2;CALML4;K
0	1.005360069	0.673014067	DCTN5;NXT1;NDUFA11;NDUFA4L2;ITPR3;DNAH9;HDAC
0	1.035408621	0.688522662	PRKCG;CAMK2A;PRKCA;ITPR3;CALML4;SSTR2;PLCB2;CA
0	1.070571553	0.71011486	TFRC;SLC40A1;GCLM;CP;FTL
0	1.541637631	1.010803816	CHPT1
0	1.051089242	0.68764791	ATP6V1A;ATP6V1H;PRKCA;KDELR3;ATP6V0E2;ATP6V0A
0	1.063145706	0.665954638	STX17;STX8;VAMP4;BET1
0	1.000147315	0.619429975	SPHK2;DGKA;PDGFB;LPAR2;PRKCA;PIK3R2;PLD1;DNM1;
0	1.017961605	0.622773794	PRKCG;PPP2CB;PRKCA;ITPR3;IGF1;PLCB2;PRKG1
0	1.010792887	0.614109909	PPP3CA;PPP3CC;PDE1B;ITPR3;CALML4;CACNA1F;PLCB2
0	1.05102243	0.609552821	PLA2G12A;PLA2G6;ACAA1
0	0.979571146	0.549685675	PRKCG;PLA2G12A;CALCB;CALCRL;PRKCA;ITPR3;CALML4
0	0.972417095	0.522906281	PDGFB;PIK3R2;CALML4;PLA2G6;PLD1;EFNA4;RASGRP1;
0	0.963183807	0.502261081	SLC27A1;CREB3L3;PPP1R3C;TBC1D4;RPS6KA2;AKT3;PIK
0	0.96323208	0.5016678	VAV3;PPP3CA;PPP3CC;CD19;AKT3;INPPL1;NFATC3;PIK3
0	0.963312255	0.483009524	GSTZ1;MIF;COMT;FAH
0	0.963328248	0.470231733	ATP6V1A;ATP6V0E2;ATP6V0A1

0	0.943567999	0.456732161	AKT3;PIK3R2;ABHD5;PRKG1;PTGS1;PNPLA2
0	0.939616283	0.445697707	CASP9;CCNE1;CDK4;AKT3;LAMA3;CKS2;E2F1;PIK3R2;LA
0	1.101045296	0.520588146	TST
0	0.934068112	0.434737613	PRKCG;PRKCA;PLCB2;THOP1
0	0.934068112	0.434737613	PRKCG;PIK3R2;PRKCA;IGF1
0	0.92464426	0.421053117	KIF3A;SUFU;IQCE;GAS1;EFCAB7;MEGF8
0	0.931287435	0.424046972	CPA3;PRKCG;PLA2G12A;AMY2B;ATP2B4;PRKCA;ITPR3;A
0	0.928242924	0.419773934	MMP14;CAMK2A;PRKCA;ITPR3;CALML4;CACNA1F;PLD1
0	0.928242924	0.419773934	CD86;ATP6V1A;CTSK;MMP3;ACP5;ATP6V1H;TEK;ATP6V
0	0.917321117	0.408886526	AMY2B;AKT3;PIK3R2;SLC37A4;PLCB2
0	0.931854485	0.414269825	GSTM1;GSTO1;ITGB3;GSTP1;PDGFB;MGST2;PIK3R2;CAL
0	0.9372618	0.408275607	PRKCG;AP1B1;NFATC3;PRKCA;PIK3R2;ITPR3;CALML4;DD
0	0.906380901	0.380797617	CBR1;GSTM1;GSTA4;GSTO1;GSTP1;MGST2;CBR3;UGT1A
0	0.915241459	0.383645345	PRKCG;GNG3;GNG2;ALOX5;GNB4;PRKCA;ITPR3;GNB5;C
0	0.884057556	0.344279235	VAV3;ALOX5;AKT3;PRKCA;PIK3R2;LAT;MAP2K6
0	0.867935441	0.309917975	PFKL;EXOSC9;DIS3L;LSM5;LSM4;PFKM;LSM3;MPHOSPH
0	0.855958097	0.304361448	CD86;CASP9;SGCA;SGCB;DAG1;MYH7
0	0.892819702	0.315086918	PRKCG;CAMK2A;NFATC3;PRKCA;ITPR3;CALML4;CACNA1
0	0.866515516	0.300734414	PRKCG;GNG3;GNG2;PLCL1;GNB4;SLC6A12;PRKCA;GNB5
0	0.866515516	0.300734414	PPP3CA;PPP3CC;AKT3;NFATC3;PIK3R2;TICAM1;RASGRP
0	0.855895197	0.296806231	PFKL;IDH1;AKT3;PIK3R2;PFKM;PDK1;SIRT3
0	0.825523104	0.285659648	POLR3GL;POLR3G;POLR3H
0	0.832899188	0.287225794	RPS6KA5;CDK4;E2F1;MMP9
0	0.837364368	0.284870256	STAR;ALOX5;ACOT2;IGF1;ACOT4
0	0.811099645	0.274632103	ALDH3A2;PPCDC
0	0.876467635	0.28975625	MEF2B;SPHK2;ITPR3;CALML4;SLC9A1;APLN;GNG3;MRA
0	0.890026173	0.290950948	CD86;PDGFB;NFATC3;PIK3R2;ITPR3;CALML4;ATG14;TIC
0	0.855706165	0.274770011	CCNB3;ANAPC13;CDC23;RPS6KA2;AKT3;PIK3R2;IGF1;PK
0	0.863625023	0.276081106	BEX3;RPS6KA5;MAGED1;RPS6KA2;AKT3;CAMK2A;PSEN2
0	0.770501089	0.235208449	GPT;ASL
0	0.898677108	0.269749121	DCTN5;NDUFA11;NDUFA4L2;SLC1A3;DNAH9;CASP9;TUI
0	0.866689904	0.253849903	PRKCG;GSTM1;FZD5;TXNRD3;GSTO1;HGF;GSTP1;TXNRD
0	0.897911839	0.253061563	TNXB;ITGB5;PKN3;ITGB3;LAMA3;PDGFB;LPAR2;PIK3R2;
0	0.733769063	0.202026461	CPA3;THOP1
0	0.879330101	0.234441605	NDUFA11;NDUFA4L2;PIK3R2;ITPR3;LAMC1;CACNA1F;CA
0	0.819107071	0.21483351	PPP3CA;PPP3CC;MRAS;CD209;AKT3;NFATC3;CBLB;ITPR3
0	0.819107071	0.21483351	VAV3;PPP3CA;PPP3CC;CDK4;AKT3;NFATC3;CBLB;PIK3R2
0	0.833986427	0.216833137	ATP6V1A;NDUFA11;NDUFA5;COX15;NDUFA4L2;NDUFC1
0	0.783197331	0.202923118	NCEH1;CREB3L3;STAR;ITPR3;CACNA1F;PLCB2
0	0.84351372	0.214955639	PRKCG;NFATC3;PRKCA;PIK3R2;TICAM1;MMP9;DDB2;CA
0	0.835416476	0.212790289	PRKCG;BEAN1;PRKCA;ITPR3;PIK3R2;ATP2A1;ATG14;GRI
0	0.844674065	0.206135137	NTNG2;SEMA3A;CAMK2A;SEMA4C;NFATC3;PARD6G;PR
0	0.858618508	0.200814591	NDUFA11;CAMK2A;NDUFA4L2;ITPR3;CALML4;TXN;PARI
0	0.858618508	0.200814591	DCTN5;CSE1L;GCC2;TXN;ACTR3B;STX10;TUBA1C;TUBA1
0	0.803181429	0.176059036	PPP3CA;PPP3CC;ITGB3;CTSK;AKT3;ACP5;PIK3R2;TREM2
0	0.759111876	0.163297657	ATP6V1A;SLC6A12;SLC1A3;ATP6V1H;ATP6V0E2;DNM1;A
0	0.884012706	0.18627209	NDUFA11;ATP2A1;PARK7;CALML4;CASP9;TUBA1C;PPP3

0	0.679611775	0.139967854	CCDC6;PPARG;DDB2
0	0.832734676	0.170168964	VAV3;MMP3;CAMK2A;NFATC3;MIB2;PRKCA;PIK3R2;AP(
0	0.804015403	0.163564045	PRKCG;NDUFA11;NDUFA5;NDUFA4L2;PRKCA;ITPR3;NDU
0	0.783938466	0.157374737	PRKCG;CREB3L3;AKT3;PRKCA;ITPR3;PIK3R2;IGF1;CACNA
0	0.78936206	0.156988519	GNG3;EDNRB;GNG2;CREB3L3;AKT3;GNB4;VEGFB;PRKCA
0	0.821179134	0.160936613	TUBB;LPAR2;MYO5A;BAIAP2;ACTR3B;TUBB4A;CASP9;TU
0	0.660156931	0.12461329	CD19;RFXAP;UNG
0	0.684518099	0.127938129	CREB3L3;CDK5;DLG4;GRIN2C
0	0.752978679	0.136857672	PRKCG;EDNRB;CREB3L3;FZD5;CAMK2A;PRKCA;CALML4;
0	0.841406276	0.152839782	PDGFB;CACNA1F;EFNA4;RASGRP1;RASGRP3;PPP3CA;RP
0	0.794128212	0.137599853	UBE2D4;WFS1;EDEM2;SSR3;MOGS;EIF2AK4;DNAJB2;DN
0	0.754520435	0.130020086	MMP14;RPS6KA5;CREB3L3;AKT3;MMP3;PIK3R2;TAB1;N
0	0.744839838	0.127995242	CREB3L3;SESN3;SESN1;AKT3;CAT;PIK3R2;PPARG;IGF1;S(
0	0.687445462	0.116324856	SRD5A1;AKR1C4;COMT;HSD17B8;UGT1A6
0	0.729076187	0.11187798	CD86;CTSK;AKT3;SPP1;PIK3R2;TAB1;TICAM1;TLR5;MAP
0	0.809271308	0.120518221	TFRC;IQSEC2;ARAP2;ASAP3;AGAP1;WWP1;VPS37D;PAR
0	0.570515614	0.08490611	PLA2G12A;PLA2G6
0	0.764056161	0.106476648	PRKCG;INVS;RNF43;FZD5;CAMK2A;NFATC3;PRKCA;NKD
0	0.690712126	0.09602345	PRKCG;AKT3;CAMK2A;CBLB;PRKCA;PIK3R2;CAMK2G
0	0.773585591	0.106438128	NDC1;POP7;NXT1;GEMIN2;POP4;ELAC1;UPF3B;AAAS;M
0	0.481462326	0.064607544	MIF
0	0.531109609	0.064411696	CLOCK;ARNTL
0	0.750163065	0.086508772	SPHK2;CAMK2A;CALML4;CASP9;PPP3CA;PPP3CC;CD209
0	0.676412273	0.075577189	TFRC;IL11RA;CD19;ITGB3;CD9;CD36;FCGR1A;CD1B
0	0.620707369	0.067877843	AKT3;PIK3R2;PIM2;FCGR1A;MPO
0	0.804644028	0.079710946	NDUFA11;NDUFA4L2;PSEN2;PIK3R2;ITPR3;ATP2A1;CALI
0	0.793605472	0.077234307	ATP6V1A;TNXB;ITGB5;ITGB3;LAMA3;PARD6G;PIK3R2;LA
0	0.641157205	0.060429404	PRKCG;GNG3;GNG2;PDE1B;GNB4;PRKCA;GNB5
0	0.537093733	0.049996825	PSMA6;PSMB5;PSMD1
0	0.654713105	0.060702789	PRKCG;PRDX1;LAMA3;PRKCA;PIK3R2;LAMC1;CD1B;PLCI
0	0.570141009	0.052136628	CASP9;AKT3;PIK3R2;DDB2
0	0.749724177	0.068433126	PRKCG;ITGB3;NFATC3;PRKCA;PIK3R2;ITPR3;CALML4;CA
0	0.405373189	0.036922577	LIPA
0	0.741174688	0.064828467	VAV3;GLP1R;CAMK2A;ATP2B4;PIK3R2;ATP2A1;ATP2B2;
0	0.591958652	0.051770569	GALT;AKT3;PIK3R2;SOCS6;ESR1
0	0.671259843	0.05131396	CREB3L3;AKT3;ITPR3;PIK3R2;CALML4;KRT10;ESR1;CTSD
0	0.671259843	0.05131396	VAV3;RPS6KA2;AKT3;NFATC3;PIK3R2;TAB1;TICAM1;BAI
0	0.710772326	0.053368276	PRKCG;H2AZ1;H2AZ2;VWF;ITGB3;PRKCA;PIK3R2;HMGB
0	0.452877099	0.032874796	GALNT12;GALNT6
0	0.627847469	0.04516193	PRKCG;MMP14;CREB3L3;PRKCA;ITPR3;PLD1;PLCB2;RUN
0	0.584256502	0.038936109	PROCR;VWF;PROS1;VSIG4;CLU;C1QC
0	0.350035635	0.021789393	MDH1
0	0.591602284	0.034831524	GLE1;PPP2CB;NXT1;PPP2R2C;UPF3B;PPP2R5D;MAGOHB
0	0.56976575	0.032872024	ASPH;TPM2;ATP2A1;CACNA1F;MYH7;SLC9A1
0	0.541749625	0.029988092	CDK4;AKT3;E2F1;PIK3R2;DDB2
0	0.578813917	0.029692059	CDK4;AKT3;VEGFB;PRKCA;PIK3R2;PLCB2;PLCD1
0	0.534195026	0.027362598	ARHGAP10;PIK3R2;SEPTIN9;ACTR3B;DNM1

0	0.644886842	0.032353244	NCEH1;CREB3L3;FZD5;STAR;CCNE1;CDK4;CAMK2A;E2F1
0	0.691211057	0.034237487	VAV3;ITGB5;ITGB3;PDGFB;LPAR2;PIK3R2;BAIAP2;ACTR3
0	0.496349338	0.023444284	RARS2;LARS2;MTFMT;CARS2
0	0.60159623	0.027564536	VWF;ITGB3;AKT3;ITPR3;PIK3R2;RASGRP1;PLCB2;PRKG1
0	0.566564008	0.025285284	PPP2CB;PPP2R2C;AKT3;PIK3R2;TICAM1;PLCB2;C1QC
0	0.560630459	0.023324667	CPA3;COL5A1;COL14A1;COL11A2;SLC3A1;KCNN4;SLC36
0	0.684873066	0.028330999	NDUFA11;NDUFA5;COX15;NDUFA4L2;NDUFC1;CPT1B;S
0	0.778773386	0.03118499	CALML4;LAMC1;BRCA2;CASP9;EDNRB;RPS6KA5;SUFU;A
0	0.480783908	0.019180039	MRAS;CITED2;E2F1;TOMM7
0	0.55481925	0.021510571	PIDD1;EDA;PARP1;TAB1;CCL19;TICAM1;LAT
0	0.473360395	0.017345096	HGF;AKT3;PDGFB;PIK3R2
0	0.375407833	0.013193942	CD86;ICA1
0	0.466161836	0.015683687	ATP6V1A;ATP6V1H;ATP6V0E2;ATP6V0A1
0	0.285133566	0.009499322	CALML4
0	0.366448802	0.011602094	DCTN5;CREB3L3
0	0.610442419	0.019213918	MOB1B;LATS1;WWTR1;PPP2CB;FZD5;YWHAQ;PPP2R2C
0	0.459178161	0.014179533	FARP2;BAIAP2;ACP1;NECTIN3
0	0.662816266	0.019366687	PRKCG;CBR1;GSTM1;GSTO1;GSTP1;MGST2;EPHX3;PRKC
0	0.625029286	0.018217311	H2AZ1;H2AZ2;CALML4;GRIN2C;H2BC18;HDAC6;GNG3;G
0	0.53272515	0.015519725	POP7;NXT1;XPO1;POP4;DROSHA;AK6;REXO5
0	0.35790647	0.010205928	TAF9B;GTF2H5
0	0.412107672	0.011647609	APH1B;PSEN2;CIR1
0	0.474597634	0.01189032	CASP9;MSH6;AKT3;PIK3R2;DDB2
0	0.474597634	0.01189032	P2RX3;PDE1B;PKD2L1;ITPR3;PLCB2
0	0.58691271	0.012856948	TUBA1C;PPP2CB;TUBA1B;TUBA1A;PPP2R2C;CDK4;MYH
0	0.51231441	0.011151583	CASP9;ALOX5;AKT3;LAMA3;TAB1;LAMC1;MAP2K6
0	0.334507909	0.006960037	CD86;CCR9
0	0.603754177	0.012463922	CD86;SLC45A3;MMP3;IGF1;BMI1;MPO;MMP9;RUNX2;D
0	0.570762692	0.011632622	H2AZ1;H2AZ2;AIFM1;PARP1;CAMK2A;HMGB1;PYGL;TIC
0	0.427169647	0.00854696	CALML4;TICAM1;CXCL5;C1QC
0	0.384546643	0.007448668	FZD5;SUFU;DDB2
0	0.384546643	0.007448668	POLR3GL;POLR3G;POLR3H
0	0.502681304	0.009438435	PRKCG;VAV3;PRKCA;PIK3R2;MYL9;MMP9;RAPGEF3
0	0.575809628	0.010480732	CASP9;NLRX1;NXT1;XPO1;CDK4;AKT3;PRKCA;PIK3R2;KP
0	0.452160969	0.008165977	NCEH1;SLC27A5;ABCG2;SLC9A1;UGT1A6
0	0.531727407	0.008992729	CASP9;CCNE1;CD209;CDK4;AKT3;CBLB;PIK3R2;EIF2AK4;
0	0.320533769	0.005399597	HGF;CD36
0	0.60469546	0.009265384	CRTC1;NFATC3;PIK3R2;ANAPC10;PPP3CA;CDC23;PPP3C
0	0.515737527	0.006604474	PCGF6;MEIS1;ACVR1C;FZD5;AKT3;SMARCAD1;PIK3R2;IC
0	0.354865536	0.004256501	RETSAT;ALDH1A2;UGT1A6
0	0.522206259	0.005705645	CASP9;PPP2CB;YWHAQ;PPP2R2C;CDK4;AKT3;E2F1;PIK3
0	0.34946897	0.003805249	AKT3;CD36;CPT1B
0	0.557220988	0.005863307	VAV3;PIK3R2;PPBP;CXCL5;GNG3;GNG2;AKT3;GNB4;CCR
0	0.207952726	0.002017556	CD86
0	0.500674597	0.004830862	FZD5;CDK4;AKT3;E2F1;PIK3R2;IGF1;BRCA2;ESR1;DDB2
0	0.476129517	0.003961514	PPP1R3C;AKT3;INPPL1;CBLB;PIK3R2;PHKB;CALML4;PYG
0	0.279627649	0.002234554	CASP9;TLR5

0	0.404335446	0.003146084	CCR9;PPBP;CCL19;CCR4;CXCL5
0	0.197266148	0.00149728	GRIN2C
0	0.685830734	0.004645483	ZNF275;ZNF570;ITGB3;PIK3R2;ZNF3;ZNF25;CASP9;AKT3
0	0.187622164	0.001114351	CD86
0	0.527437245	0.002918548	ENTPD8;PIK3R2;DDB2;CASP9;CCNE1;CDK4;CD19;AKT3;E
0	0.524631302	0.002718443	PIK3R2;H2BC18;HDAC6;DDB1;RBL2;SCIN;RBL1;CREB3L3
0	0.433346246	0.002198028	CCNB3;PLK4;RBL2;AKT3;CAT;PIK3R2;IGF1
0	0.433346246	0.002198028	PRKCG;VAV3;PPP3CA;PPP3CC;PRKCA;PIK3R2;LAT
0	0.349185267	0.001649032	PPP3CA;PPP3CC;NFATC3;LAT
0	0.496276568	0.002329137	P2RX7;TRPM2;NLRX1;NEK7;TRPV2;ITPR3;TXN;TAB1;TIC/
0	0.307375763	0.001384009	RFXAP;CTSB;LGMN
0	0.341386829	0.001338842	MMP3;MMP9;MAPK15;CXCL5
0	0.341386829	0.001338842	PPP2CB;RBL1;ACVR1C;NBL1
0	0.170905923	6.22E-04	PIK3R2
0	0.532886034	0.001603425	UBE2D4;GLMN;PIK3R2;ITPR3;ATG14;SEPTIN9;ACTR3B;R
0	0.417399988	8.65E-04	NDUFA11;NDUFA5;AKT3;NDUFA4L2;PIK3R2;NDUFC1;PF
0	0.147840726	2.28E-04	CD86
0	0.38073028	4.80E-04	CD86;NTNG2;CNTNAP1;CDH3;CADM1;ITGB8;NECTIN3
0	0.356785399	4.30E-04	CD86;H2AZ1;H2AZ2;FCGR1A;H2BC18;C1QC
0	0.378027554	4.38E-04	FZD5;CCNE1;HGF;AKT3;E2F1;PIK3R2;DDB2
0	0.298078999	3.41E-04	PPP3CA;PPP3CC;NFATC3;LAT
0	0.527402965	5.09E-04	PRKCG;DNMT1;SLC45A3;TNXB;ITGB3;PDGFB;PRKCA;PIK
0	0.204827887	1.85E-04	TAB1;FCGR1A
0	0.250336416	2.02E-04	KRT10;FCGR1A;C1QC
0	0.355313919	1.92E-04	MRPL30;MRPL18;MRPL19;MRPS21;RPS27L;MRPL10;MF
0	0.120038926	4.30E-05	TLR5
0	0.319347447	1.02E-04	PRPF40B;PPIH;LSM5;MAGOHB;LSM4;LSM3
0	0.111308893	2.18E-05	NLRX1
0	0.294580801	3.18E-05	CNTFR;IL11RA;AKT3;PDGFB;PIK3R2;SOCS6
0	0.424986789	1.15E-05	GLP1R;CHRNB1;CALCB;CALCRL;THRB;THRA;TACR2;LPAR
0	0.380201489	7.47E-06	TNFSF18;CNTFR;EDA;IL11RA;TNFSF12;GDF1;PPBP;CXCL5
0	0.086598062	4.72E-07	PDE1B;CAMK2A;CALML4;CAMK2G;PRKG1
0	0.237449782	1.20E-06	PRKCG;VWF;MMP3;RPS27L;PRKCA;PIK3R2;C1QC

.;HADH;ACADS;ACAD8;MCCC2;BCKDHB;MCCC1;ACADSB;ALDH3A2;HADHB;HADHA;ALDH6A1;PCCA;EHHADH;IVD;
P100;FANCI;CENPX;FANCM;POLN;RMI1;FANCL;RPA1;FANCC;FANCE;PALB2;RAD51;RPA3;UBE2T;SLX1A;FAN1;TEL
\2;LAPTM4A;CTSO;AP1G2;GM2A;CTSK;SLC17A5;AP1S1;ATP6V1H;ACP5;ACP2;GUSB;CTSD;ATP6V0A1;CTSB;ARSA;

Γ19;HACL1;MLYCD;ACAA1;DECR2;ACOT8;PHYH;IDH1;ECH1;PEX1;SOD1;AMACR;EHHADH;PEX6;CAT;PXMP2;PEX1

;ARNTL;PPP3CA;PPP2CB;GNG3;PPP3CC;GNG2;CREB3L3;PPP2R2C;AKT3;GNB4;GNB5;CLOCK;PLCB2;CAMK2G

JBB4A;TUBA1C;TUBB6;TUBA1B;TUBA1A;TUBB3;CD209;MRC1;ATP6V1H;CD36;PLA2R1;ATP6V0E2;FCGR1A;RILP;A

LF;PPP3CA;EDNRB;PPP3CC;PDGFD;CAMK2G;PRKCG;MCOLN3;SPHK2;HGF;MST1;TACR2;VEGFB;ATP2B4;PRKCA;PH

;PPP3CA;RAD50;PPP3CC;MRAS;RBL1;CCNE1;CDK4;CHEK2;AKT3;CHEK1;E2F1;RAD1;SLC25A4;MAP2K6

B2;CALML4;CACNA1F;SLC9A1;PPP2CB;RPS6KA5;CREB3L3;PPP2R2C;AKT3;PLCB2;CAMK2G;RAPGEF3;MYH7

EFNA4;RASGRP3;PDGFD;AKT3;MAP2K6;PRKCG;VAV3;FARP2;HGF;VEGFB;PRKCA;IGF1;MRAS;LPAR5;PRKD3;TEK;P

KT3;PDK4;CD36;CTSD;CAMK2G;PDK2;PRKCG;PARP1;NDUFA5;GSR;PRKCA;NDUFC1;CPT1B;SDHB;MMP9;TBC1D4;

A1;GPC1;AKT3;DROSHA;FLNB;CAMK2G;PRKCG;VAV3;FZD5;HGF;PRKCA;IGF1;NUDT16L1;ESR1;MMP9;MRAS;TFAI

FB;VEGFB;PRKCA;PIK3R2;IGF1;PARVB;LAMC1;PARVG;PDGFD;ITGA10;AKT3;CHAD;SPP1;ITGB8;FLNB;MYL9

1;CACNA1F;PPP3CA;EDNRB;PPP3CC;CREB3L3;ADORA3;AKT3;KCNMB4;MYL9;PLCB2;SLC25A4;PRKG1;MYH7

6;GLE1;CASP9;PPP3CA;TUBA1C;TUBA1B;TUBB6;ACTR1B;PPP3CC;TUBA1A;PSMB5;TUBB3;PSMD1;ANXA7;NUP43;

RASGRP3;GNG3;GNG2;PDGFD;AKT3;PRKCG;RALBP1;PLA2G12A;HGF;VEGFB;PRKCA;IGF1;MRAS;GNB4;GNB5;TEK;

DB1;CCNB3;CASP9;PPP3CA;GNG3;PPP3CC;GNG2;AP1G2;AKT3;CHEK1;GNB4;AP1S1;GNB5;TAB1;MAP2K6;CUL4B

BA1C;TUBA1B;TUBB6;ACTR1B;TUBA1A;PSMB5;CREB3L3;TUBB3;PSMD1;IFT57;DNAH12;NDUFA5;TUBB;GPX7;NDU

LAMC1;EFNA4;CASP9;PPP2CB;GNG3;GNG2;CREB3L3;YWHAQ;CD19;PDGFD;AKT3;CHAD;SPP1;ITGB8;VWF;HGF;VI

ASP9;PPP3CA;TUBA1C;TUBA1B;TUBB6;PPP3CC;TUBA1A;PSMB5;CREB3L3;TUBB3;PSMD1;NDUFA5;TUBB;NDUFC1

K7;CASP9;TUBA1C;TUBA1B;UCHL1;TUBB6;TUBA1A;PSMB5;TUBB3;PSMD1;CAMK2G;NDUFA5;TUBB;NDUFC1;TUB
.B;TUBB6;ACTR1B;TUBA1A;TUBB3;AKT3;FLNB;RILP;MAP2K6;TUBB;DYNLT3;TUBB4A;EXOC4;PLEKHM1;DYNLRB2;T

CA;TUBA1B;TUBB6;UCHL1;TUBA1A;ACTR1B;PPP3CC;TUBB3;PSMD1;IFT57;PRKCG;TUBB;GPX7;PRKCA;NDUFC1;A

OA4;CALML4;TICAM1;MMP9;CASP9;PPP3CA;PPP3CC;AKT3;PPARG;CD36;TAB1;PLCB2;CAMK2G;MAP2K6

'S6KA5;PPP3CC;RPS6KA2;PDGFD;AKT3;FLNB;MAP4K3;MAP2K5;MAP2K6;PRKCG;MAP4K2;HGF;NFATC3;VEGFB;PF

:D6G;CBLB;PLD1;ACTR3B;DNM1;DAB2;RUFY2;MVB12A;VPS45;LDLRAP1;FOLR2;FOLR1;SNX5;ARF5;SPG21;RAB11F

ML4;CACNA1F;RTN4;CASP9;PPP3CA;TUBA1C;TUBA1B;TUBB6;APH1B;PPP3CC;TUBA1A;PSMB5;TUBB3;AKT3;PSMI
AMC1;PPP2CB;CREB3L3;AKT3;CHAD;SPP1;E2F1;ATP6V1H;ITGB8;ATP6V0E2;ATP6V0A1;FZD5;VWF;PPP2R5D;TUBC

DHB;CREB3L3;NDUFAF7;RPS6KA2;NDUFAF4;NDUFAF2;ATP5PO;DPF3;PPARG;NDUFAF1;SLC25A20;PRKG1;PNPLA
KT3;PIM2;PRKCG;RALBP1;GSTO1;HGF;PRKCA;MMP9;DDB2;MSH6;CCNE1;CKS2;PPARG;PLCB2;GSTP1;CAMK2A;L

;ZNF527;ZNF404;ZNF624;ZNF205;ZNF568;ZNF689;ZNF667;ZNF248;ZNF786;EIF2B1;ZNF684;ZNF420;ZNF19;ZNF3

ABCA2;FUCA1;FUCA2;AP1B1;CTNS;MCOLN1;PLA2G15;GALNS;NPC2;GLB1;PPT1;TPP1;DNASE2;CD68;GLA;LGMN

;MAP2K6;UBQLN2;NDC1;DNAH12;NDUFA5;TUBB;GPX7;NDUFC1;ATG14;GRIN2C;TUBB4A;SDHB;SOD1;FIG4;PSMA

TG14;SDHB;PSMA6;ALS2;CAT;PLCB2;SLC25A4;DCTN5;CAMK2A;NDUFA4L2;PSEN2;ITPR3;DNAH9;CACNA1F;PSMB

D1;FZD5;NDUFA5;TUBB;NDUFC1;ATG14;GRIN2C;TUBB4A;SDHB;BACE1;PSMA6;CDK5;ATP5PO;PLCB2;SLC25A4

AMA3;PDGFB;LPAR2;MGST2;PIK3R2;PLD1;RASGRP1;RASGRP3;GNG3;GNG2;E2F1;CAMK2G;GSTM1;FZD5;TXNRD3

83;ZNF283;ZNF140;ZNF382;ZFP1;ZNF181;ZNF180;ZNF10;EIF2AK4;TICAM1;ZFP69;ZNF713;TAB1;ZNF599;ZNF555;

5;CAMK2G;MAP2K6;DNAH12;FZD5;NDUFA5;GRIN2C;TUBB4A;SOD1;FIG4;CDK5;DLG4;ATP5PO;DNAL1

Supplementary File S6: Comprehensive details of the results of functional enrichment analysis

BP	Term	Overlap	P-value	Adjusted P-value
	response to unfolded protein (GO:0006986)	13/49	9.86E-25	5.19E-22
	regulation of cellular response to heat (GO:1900034)	29160	1.22E-17	3.21E-15
	regulation of cellular response to stress (GO:008013	11/118	1.22E-15	2.14E-13
	chaperone-mediated protein complex assembly (GO	44764	2.51E-14	3.30E-12
	'de novo' posttranslational protein folding (GO:0051	44773	3.82E-13	4.02E-11
	chaperone cofactor-dependent protein refolding (GC	44738	1.77E-11	1.55E-09
	protein stabilization (GO:0050821)	9/179	1.63E-10	1.22E-08
	cellular protein-containing complex assembly (GO:0(	8/168	2.87E-09	1.85E-07
	cellular response to unfolded protein (GO:0034620)	44708	3.17E-09	1.85E-07
	positive regulation of DNA biosynthetic process (GO:	22433	4.03E-09	2.12E-07
	cellular response to heat (GO:0034605)	13271	1.46E-08	6.98E-07
	cellular response to topologically incorrect protein ((	11780	7.00E-07	3.07E-05
	positive regulation of telomerase activity (GO:00519	12510	9.00E-07	3.64E-05
	positive regulation of establishment of protein locali	44630	1.18E-06	3.88E-05
	negative regulation of inclusion body assembly (GO:(	44630	1.18E-06	3.88E-05
	negative regulation of transcription from RNA polym	44630	1.18E-06	3.88E-05
	regulation of establishment of protein localization to	44631	1.62E-06	4.26E-05
	regulation of inclusion body assembly (GO:0090083)	44631	1.62E-06	4.26E-05
	positive regulation of protein localization to Cajal bo	44631	1.62E-06	4.26E-05
	regulation of protein localization to Cajal body (GO:1	44631	1.62E-06	4.26E-05
	positive regulation of protein localization to chromo	44632	2.16E-06	5.40E-05
	regulation of telomerase activity (GO:0051972)	16893	3.11E-06	7.43E-05
	positive regulation of telomerase RNA localization to	44635	4.44E-06	1.01E-04
	regulation of telomerase RNA localization to Cajal bo	44638	7.92E-06	1.74E-04
	positive regulation of establishment of protein locali	44639	9.39E-06	1.98E-04
	regulation of protein modification by small protein c	44640	1.10E-05	2.23E-04
	positive regulation of protein localization to nucleus	24929	1.50E-05	2.92E-04
	negative regulation of cellular component organizati	29312	2.85E-05	5.36E-04
	telomere maintenance via telomerase (GO:0007004	44649	3.49E-05	6.33E-04
	RNA-dependent DNA biosynthetic process (GO:0006	44650	3.87E-05	6.74E-04
	regulation of transcription from RNA polymerase II p	31868	3.97E-05	6.74E-04
	positive regulation of telomere maintenance via telo	12114	5.18E-05	8.51E-04
	telomere maintenance via telomere lengthening (GC	13210	6.74E-05	0.001043033
	positive regulation of telomere maintenance via telo	13210	6.74E-05	0.001043033
	positive regulation of tau-protein kinase activity (GO	44598	7.06E-05	0.001060326
	regulation of protein ubiquitination (GO:0031396)	4/109	9.58E-05	0.001399663
	regulation of telomere maintenance via telomerase	19054	2.04E-04	0.002894727
	regulation of tau-protein kinase activity (GO:190294	44602	2.10E-04	0.002913512
	protein targeting to mitochondrion (GO:0006626)	20149	2.41E-04	0.003245155
	positive regulation of transferase activity (GO:00513	4/148	3.11E-04	0.004083144
	central nervous system neuron axonogenesis (GO:0(	44605	3.63E-04	0.004660981
	central nervous system neuron development (GO:00	44607	4.88E-04	0.006107907
	neutrophil degranulation (GO:0043312)	6/481	6.10E-04	0.007460259
	neutrophil activation involved in immune response (	6/485	6.37E-04	0.007522086

positive regulation of type I interferon production (G	28185	6.49E-04	0.007522086
neutrophil mediated immunity (GO:0002446)	6/488	6.58E-04	0.007522086
negative regulation of extrinsic apoptotic signaling p	29281	7.25E-04	0.008116063
positive regulation of interferon-alpha production (G	44612	8.76E-04	0.009603518
axon extension (GO:0048675)	44616	0.001265945	0.013317744
protein insertion into mitochondrial membrane (GO:	44616	0.001265945	0.013317744
regulation of peptidyl-serine phosphorylation (GO:0(	35855	0.00130603	0.013470036
regulation of interferon-alpha production (GO:0032(	44617	0.001374107	0.013899624
negative regulation of programmed cell death (GO:0	5/381	0.001441319	0.014304414
protein peptidyl-prolyl isomerization (GO:0000413)	44619	0.001603223	0.01533264
positive regulation of nitric oxide biosynthetic proce	44619	0.001603223	0.01533264
regulation of protein transport (GO:0051223)	44620	0.001724139	0.015910479
positive regulation of nitric oxide metabolic process	44620	0.001724139	0.015910479
peptidyl-proline modification (GO:0018208)	11720	0.002249771	0.020403091
neuron projection extension (GO:1990138)	12086	0.002391579	0.021321531
negative regulation of extrinsic apoptotic signaling p	12451	0.002537511	0.022245509
positive regulation of interferon-beta production (G(	13181	0.002841674	0.024503619
ribonucleoprotein complex assembly (GO:0022618)	3/136	0.003322434	0.027789512
regulation of cellular component biogenesis (GO:004	14277	0.003328402	0.027789512
regulation of nitric oxide biosynthetic process (GO:0(	14642	0.003498701	0.028754952
positive regulation of ATPase activity (GO:0032781)	15373	0.003851281	0.030235427
regulation of chemokine production (GO:0032642)	15373	0.003851281	0.030235427
regulation of extrinsic apoptotic signaling pathway vi	15373	0.003851281	0.030235427
regulation of mRNA stability (GO:0043488)	3/146	0.004054528	0.031362967
positive regulation of intracellular protein transport	3/148	0.004211774	0.032107144
regulation of cellular protein localization (GO:19038:	16834	0.004603868	0.034594778
negative regulation of cell projection organization (G	17930	0.00520926	0.037535217
regulation of cellular localization (GO:0060341)	17930	0.00520926	0.037535217
regulation of interferon-beta production (GO:00326-	17930	0.00520926	0.037535217
regulation of apoptotic process (GO:0042981)	6/742	0.005423111	0.038548062
negative regulation of protein ubiquitination (GO:00	18660	0.005632097	0.039499775
positive regulation of chemokine production (GO:00	19391	0.006070169	0.042011956
positive regulation of cytokine production (GO:0001	4/335	0.006194253	0.04231399
negative regulation of protein modification by small	20121	0.006523338	0.043990717
positive regulation of interferon-gamma production	20852	0.006991471	0.046550809
negative regulation of neuron projection developme	21217	0.007231107	0.047544529
positive regulation of interleukin-8 production (GO:0	22313	0.007972092	0.051769387
negative regulation of intrinsic apoptotic signaling pa	23408	0.008745845	0.055425474
protein catabolic process (GO:0030163)	23408	0.008745845	0.055425474
ERBB signaling pathway (GO:0038127)	24139	0.009279665	0.057424752
regulation of protein localization (GO:0032880)	24139	0.009279665	0.057424752
vascular endothelial growth factor receptor signaling	24504	0.009551922	0.058422222
cellular response to decreased oxygen levels (GO:00	25235	0.010107048	0.058858465
positive regulation of protein polymerization (GO:00	25235	0.010107048	0.058858465
Fc-gamma receptor signaling pathway involved in ph	25965	0.010676216	0.058858465
positive regulation of cellular protein localization (G(	25965	0.010676216	0.058858465
aggresome assembly (GO:0070842)	44566	0.010952688	0.058858465

fructose 2,6-bisphosphate metabolic process (GO:00	44566	0.010952688	0.058858465
RNA localization to Cajal body (GO:0090670)	44566	0.010952688	0.058858465
positive regulation of MHC class I biosynthetic proce	44566	0.010952688	0.058858465
scaRNA localization to Cajal body (GO:0090666)	44566	0.010952688	0.058858465
positive regulation of nucleotide-binding oligomeriza	44566	0.010952688	0.058858465
regulation of protein import (GO:1904589)	44566	0.010952688	0.058858465
Fc-gamma receptor signaling pathway (GO:0038094)	26330	0.010966026	0.058858465
Fc receptor mediated stimulatory signaling pathway	27061	0.011556016	0.059533789
positive regulation of T cell activation (GO:0050870)	27426	0.011856166	0.059533789
regulation of RNA splicing (GO:0043484)	27791	0.01215973	0.059533789
positive regulation of interleukin-6 production (GO:0	27791	0.01215973	0.059533789
negative regulation of establishment of protein local	44567	0.013129125	0.059533789
axo-dendritic transport (GO:0008088)	44567	0.013129125	0.059533789
heat acclimation (GO:0010286)	44567	0.013129125	0.059533789
positive regulation of immune response to tumor ce	44567	0.013129125	0.059533789
inclusion body assembly (GO:0070841)	44567	0.013129125	0.059533789
cellular heat acclimation (GO:0070370)	44567	0.013129125	0.059533789
signal complex assembly (GO:0007172)	44567	0.013129125	0.059533789
regulation of glutamate receptor signaling pathway (	44567	0.013129125	0.059533789
centromeric sister chromatid cohesion (GO:0070601	44567	0.013129125	0.059533789
medium-chain fatty acid biosynthetic process (GO:0(	44567	0.013129125	0.059533789
positive regulation of T cell mediated immune respo	44567	0.013129125	0.059533789
regulation of microtubule motor activity (GO:200057	44567	0.013129125	0.059533789
regulation of NK T cell activation (GO:0051133)	44567	0.013129125	0.059533789
regulation of nucleotide-binding oligomerization dor	44567	0.013129125	0.059533789
activation of cysteine-type endopeptidase activity in	29618	0.013728223	0.061195301
regulation of interleukin-8 production (GO:0032677)	29618	0.013728223	0.061195301
negative regulation of axon regeneration (GO:00486	44568	0.015300881	0.064204334
regulation of T cell mediated immune response to tu	44568	0.015300881	0.064204334
regulation of transforming growth factor beta activa	44568	0.015300881	0.064204334
negative regulation of mitochondrial outer membrar	44568	0.015300881	0.064204334
positive regulation of microtubule nucleation (GO:0(	44568	0.015300881	0.064204334
positive regulation of NK T cell activation (GO:00511	44568	0.015300881	0.064204334
regulation of MHC class I biosynthetic process (GO:0	44568	0.015300881	0.064204334
regulation of interferon-gamma production (GO:003	31444	0.015379745	0.064204334
protein import (GO:0017038)	32540	0.016409712	0.067068711
toll-like receptor signaling pathway (GO:0002224)	33270	0.017112375	0.067068711
regulation of transcription from RNA polymerase II p	44569	0.017467967	0.067068711
negative regulation of glucose import (GO:0046325)	44569	0.017467967	0.067068711
negative regulation of muscle cell apoptotic process	44569	0.017467967	0.067068711
negative regulation of neuron projection regeneratic	44569	0.017467967	0.067068711
negative regulation of nitrogen compound metaboli	44569	0.017467967	0.067068711
regulation of establishment of protein localization to	44569	0.017467967	0.067068711
negative regulation of striated muscle cell apoptotic	44569	0.017467967	0.067068711
peptidyl-proline hydroxylation to 4-hydroxy-L-prolin	44569	0.017467967	0.067068711
T cell activation (GO:0042110)	33635	0.017468467	0.067068711
positive regulation of peptidyl-serine phosphorylatio	34001	0.017827712	0.067952004

negative regulation of cell death (GO:0060548)	34366	0.018190096	0.068834465
protein maturation (GO:0051604)	35462	0.019295932	0.072206901
positive regulation of blood vessel endothelial cell pr	44570	0.019630393	0.072206901
fructose 1,6-bisphosphate metabolic process (GO:00	44570	0.019630393	0.072206901
positive regulation of tumor necrosis factor-mediate	44570	0.019630393	0.072206901
regulation of transforming growth factor beta recept	2/100	0.020429484	0.073939204
positive regulation of protein localization to membra	2/101	0.020813425	0.073939204
regulation of proteasomal ubiquitin-dependent proti	2/102	0.021200387	0.073939204
negative regulation of apoptotic process (GO:00430(	4/485	0.021589286	0.073939204
negative regulation of establishment of protein local	44571	0.021788169	0.073939204
negative regulation of glycolytic process (GO:004582	44571	0.021788169	0.073939204
negative regulation of leukocyte migration (GO:0002	44571	0.021788169	0.073939204
I-kappaB phosphorylation (GO:0007252)	44571	0.021788169	0.073939204
negative regulation of purine nucleotide metabolic p	44571	0.021788169	0.073939204
regulation of glycoprotein biosynthetic process (GO:(	44571	0.021788169	0.073939204
negative regulation of transforming growth factor be	44571	0.021788169	0.073939204
regulation of microtubule nucleation (GO:0010968)	44571	0.021788169	0.073939204
purine nucleoside bisphosphate biosynthetic process	44572	0.023941303	0.076787349
regulation of amyloid precursor protein biosynthetic	44572	0.023941303	0.076787349
ribonucleoside bisphosphate biosynthetic process (G	44572	0.023941303	0.076787349
isotype switching (GO:0045190)	44572	0.023941303	0.076787349
cellular response to UV-A (GO:0071492)	44572	0.023941303	0.076787349
coenzyme A biosynthetic process (GO:0015937)	44572	0.023941303	0.076787349
tetrahydrobiopterin metabolic process (GO:0046146	44572	0.023941303	0.076787349
cyclooxygenase pathway (GO:0019371)	44572	0.023941303	0.076787349
peptidyl-proline hydroxylation (GO:0019511)	44572	0.023941303	0.076787349
regulation of interleukin-6 production (GO:0032675)	2/110	0.024403106	0.077794143
positive regulation of programmed cell death (GO:0(	3/286	0.024899212	0.078897504
regulation of axon regeneration (GO:0048679)	44573	0.026089806	0.080724928
negative regulation of glucose transmembrane trans	44573	0.026089806	0.080724928
negative regulation of JUN kinase activity (GO:00435	44573	0.026089806	0.080724928
negative regulation of receptor internalization (GO:(	44573	0.026089806	0.080724928
regulation of protein-containing complex assembly ((	2/116	0.026927016	0.08282813
positive regulation of cysteine-type endopeptidase a	2/119	0.02822707	0.083903499
pteridine-containing compound metabolic process ((	44574	0.028233687	0.083903499
positive regulation of protein localization to cell surf	44574	0.028233687	0.083903499
toll-like receptor 9 signaling pathway (GO:0034162)	44574	0.028233687	0.083903499
transport along microtubule (GO:0010970)	44574	0.028233687	0.083903499
protein localization to mitochondrion (GO:0070585)	44574	0.028233687	0.083903499
regulation of mRNA catabolic process (GO:0061013)	2/122	0.029552027	0.087327899
regulation of response to interferon-gamma (GO:00(	44575	0.030372956	0.087781181
response to UV-A (GO:0070141)	44575	0.030372956	0.087781181
coenzyme A metabolic process (GO:0015936)	44575	0.030372956	0.087781181
N-terminal protein amino acid modification (GO:003	44575	0.030372956	0.087781181
positive regulation of apoptotic process (GO:004306	3/310	0.030607019	0.087974273
cellular response to oxidative stress (GO:0034599)	2/125	0.030901518	0.088338034
negative regulation of cell growth (GO:0030308)	2/126	0.031356737	0.089154831

positive regulation of intracellular signal transductio	4/546	0.031547321	0.089214466
negative regulation of endoplasmic reticulum stress-	44576	0.032507623	0.089523611
regulation of establishment of protein localization (G	44576	0.032507623	0.089523611
positive regulation of protein export from nucleus (G	44576	0.032507623	0.089523611
medium-chain fatty acid metabolic process (GO:005	44576	0.032507623	0.089523611
prostanoid biosynthetic process (GO:0046457)	44576	0.032507623	0.089523611
cellular response to hypoxia (GO:0071456)	2/131	0.033672647	0.092017317
regulation of blood vessel endothelial cell proliferati	44577	0.034637697	0.092017317
heme catabolic process (GO:0042167)	44577	0.034637697	0.092017317
mitotic sister chromatid cohesion (GO:0007064)	44577	0.034637697	0.092017317
regulation of phosphate metabolic process (GO:001	44577	0.034637697	0.092017317
N-terminal protein amino acid acetylation (GO:0006	44577	0.034637697	0.092017317
porphyrin-containing compound catabolic process (G	44577	0.034637697	0.092017317
negative regulation of ATP metabolic process (GO:19	44578	0.036763188	0.096206155
positive regulation of macrophage activation (GO:00	44578	0.036763188	0.096206155
regulation of leukocyte migration (GO:0002685)	44578	0.036763188	0.096206155
regulation of cellular component organization (GO:0	2/139	0.037512918	0.097682153
positive regulation of cell migration involved in spro	44579	0.038884106	0.098611473
regulation of cellular protein catabolic process (GO:1	44579	0.038884106	0.098611473
positive regulation of phosphoprotein phosphatase a	44579	0.038884106	0.098611473
regulation of mitochondrial outer membrane perme	44579	0.038884106	0.098611473
endothelial cell proliferation (GO:0001935)	44579	0.038884106	0.098611473
protein localization to organelle (GO:0033365)	2/142	0.038994651	0.098611473
receptor-mediated endocytosis (GO:0006898)	2/143	0.039493505	0.099383603
establishment or maintenance of apical/basal cell pc	44580	0.04100046	0.099383603
positive regulation of cellular protein catabolic proce	44580	0.04100046	0.099383603
negative regulation of immune system process (GO:(	44580	0.04100046	0.099383603
positive regulation of G protein-coupled receptor sig	44580	0.04100046	0.099383603
positive regulation of leukocyte activation (GO:0002	44580	0.04100046	0.099383603
regulation of mitotic spindle assembly (GO:1901673)	44580	0.04100046	0.099383603
diol metabolic process (GO:0034311)	44580	0.04100046	0.099383603
prostaglandin biosynthetic process (GO:0001516)	44580	0.04100046	0.099383603
positive regulation of hydrolase activity (GO:005134	2/149	0.04253765	0.102148867
positive regulation of alpha-beta T cell activation (G	44581	0.043112259	0.102148867
protein targeting to lysosome (GO:0006622)	44581	0.043112259	0.102148867
positive regulation of cyclin-dependent protein kinas	44581	0.043112259	0.102148867
regulation of programmed necrotic cell death (GO:0(	44581	0.043112259	0.102148867
positive regulation of protein kinase activity (GO:004	2/154	0.045139873	0.104781782
purinergic nucleotide receptor signaling pathway (G	44582	0.045219514	0.104781782
negative regulation of peptidyl-serine phosphorylati	44582	0.045219514	0.104781782
negative regulation of response to wounding (GO:19	44582	0.045219514	0.104781782
positive regulation of phosphatase activity (GO:0010	44582	0.045219514	0.104781782
regulation of endoplasmic reticulum stress-induced i	44583	0.047322234	0.108696485
lipid droplet organization (GO:0034389)	44583	0.047322234	0.108696485
positive regulation of protein kinase B signaling (GO:	2/161	0.048879819	0.110148919
regulation of supramolecular fiber organization (GO:	44584	0.049420428	0.110148919
negative regulation of extrinsic apoptotic signaling p	44584	0.049420428	0.110148919

negative regulation of signal transduction in absence	44584	0.049420428	0.110148919
regulation of interferon-gamma-mediated signaling p	44584	0.049420428	0.110148919
regulation of necroptotic process (GO:0060544)	44584	0.049420428	0.110148919
regulation of protein export from nucleus (GO:0046	44584	0.049420428	0.110148919
negative regulation of cell population proliferation (	3/379	0.050517174	0.111507899
regulation of neuron projection development (GO:0(	2/165	0.051066235	0.111507899
positive regulation of cellular response to transformi	44585	0.051514105	0.111507899
long-chain fatty-acyl-CoA metabolic process (GO:003	44585	0.051514105	0.111507899
positive regulation of protein targeting to membran	44585	0.051514105	0.111507899
positive regulation of transforming growth factor be	44585	0.051514105	0.111507899
regulation of monooxygenase activity (GO:0032768)	44585	0.051514105	0.111507899
negative regulation of cellular carbohydrate metabo	44586	0.053603276	0.114615136
regulation of spindle assembly (GO:0090169)	44586	0.053603276	0.114615136
negative regulation of response to endoplasmic retic	44586	0.053603276	0.114615136
negative regulation of proteolysis involved in cellula	44587	0.05568795	0.118590534
regulation of vasculature development (GO:1901342	44588	0.057768136	0.121544159
positive regulation of erythrocyte differentiation (GC	44588	0.057768136	0.121544159
regulation of epidermal growth factor-activated rece	44588	0.057768136	0.121544159
positive regulation of cellular biosynthetic process (G	2/180	0.059570098	0.122007217
negative regulation of axonogenesis (GO:0050771)	44589	0.059843844	0.122007217
positive regulation of defense response to virus by h	44589	0.059843844	0.122007217
positive regulation of microtubule polymerization (G	44589	0.059843844	0.122007217
internal peptidyl-lysine acetylation (GO:0018393)	44589	0.059843844	0.122007217
regulation of extrinsic apoptotic signaling pathway ir	44589	0.059843844	0.122007217
positive regulation of protein import into nucleus (G	44589	0.059843844	0.122007217
regulation of microtubule polymerization or depolyn	44589	0.059843844	0.122007217
regulation of protein targeting to membrane (GO:00	44590	0.061915083	0.122677034
negative regulation of mRNA catabolic process (GO:1	44590	0.061915083	0.122677034
transition metal ion homeostasis (GO:0055076)	44590	0.061915083	0.122677034
positive regulation of viral genome replication (GO:0	44590	0.061915083	0.122677034
MyD88-dependent toll-like receptor signaling pathw	44590	0.061915083	0.122677034
negative regulation of transcription by RNA polymer	4/684	0.062738066	0.122677034
extrinsic apoptotic signaling pathway via death dom	44591	0.063981862	0.122677034
negative regulation of cytoskeleton organization (GC	44591	0.063981862	0.122677034
regulation of type I interferon-mediated signaling pa	44591	0.063981862	0.122677034
positive regulation of phosphate metabolic process (	44591	0.063981862	0.122677034
long-chain fatty acid biosynthetic process (GO:00427	44591	0.063981862	0.122677034
positive regulation of protein import (GO:1904591)	44591	0.063981862	0.122677034
regulation of macrophage activation (GO:0043030)	44591	0.063981862	0.122677034
regulation of protein localization to membrane (GO:	44591	0.063981862	0.122677034
negative regulation of axon extension (GO:0030517)	44592	0.066044191	0.122677034
purine nucleoside bisphosphate metabolic process (G	44592	0.066044191	0.122677034
positive regulation of leukocyte cell-cell adhesion (G	44592	0.066044191	0.122677034
ribonucleoside bisphosphate metabolic process (GO:	44592	0.066044191	0.122677034
negative regulation of proteasomal ubiquitin-depen	44592	0.066044191	0.122677034
positive regulation of protein targeting to mitochon	44592	0.066044191	0.122677034
positive regulation of Rho protein signal transductio	44592	0.066044191	0.122677034

positive regulation of RNA splicing (GO:0033120)	44592	0.066044191	0.122677034
prostaglandin metabolic process (GO:0006693)	44592	0.066044191	0.122677034
protein acetylation (GO:0006473)	44592	0.066044191	0.122677034
regulation of programmed cell death (GO:0043067)	2/194	0.067915793	0.122677034
ERBB2 signaling pathway (GO:0038128)	11689	0.068102079	0.122677034
protein transmembrane import into intracellular org	11689	0.068102079	0.122677034
establishment or maintenance of epithelial cell apica	11689	0.068102079	0.122677034
negative regulation of developmental growth (GO:0(	11689	0.068102079	0.122677034
B cell proliferation (GO:0042100)	11689	0.068102079	0.122677034
regulation of cell migration involved in sprouting ang	11689	0.068102079	0.122677034
regulation of cellular amide metabolic process (GO:0	11689	0.068102079	0.122677034
negative regulation of microtubule polymerization o	11689	0.068102079	0.122677034
positive regulation of interleukin-10 production (GO:	11689	0.068102079	0.122677034
apoptotic mitochondrial changes (GO:0008637)	12055	0.070155536	0.124248526
negative regulation of JNK cascade (GO:0046329)	12055	0.070155536	0.124248526
RNA stabilization (GO:0043489)	12055	0.070155536	0.124248526
negative regulation of smooth muscle cell proliferati	12055	0.070155536	0.124248526
regulation of protein localization to cell surface (GO:	12055	0.070155536	0.124248526
negative regulation of mitochondrion organization ((	12420	0.072204571	0.126178087
positive regulation of interleukin-12 production (GO:	12420	0.072204571	0.126178087
positive regulation of protein dephosphorylation (G(	12420	0.072204571	0.126178087
protein insertion into membrane (GO:0051205)	12420	0.072204571	0.126178087
negative regulation of epithelial cell migration (GO:0	12785	0.074249193	0.126802193
negative regulation of neurogenesis (GO:0050768)	12785	0.074249193	0.126802193
positive regulation of lymphocyte activation (GO:005	12785	0.074249193	0.126802193
cellular response to virus (GO:0098586)	12785	0.074249193	0.126802193
regulation of JUN kinase activity (GO:0043506)	12785	0.074249193	0.126802193
regulation of mitotic spindle organization (GO:00602	12785	0.074249193	0.126802193
regulation of protein polymerization (GO:0032271)	12785	0.074249193	0.126802193
regulation of protein kinase B signaling (GO:005189(	2/207	0.075991802	0.127796911
negative regulation of cellular protein localization (G	13150	0.076289411	0.127796911
positive regulation of cytokine-mediated signaling pa	13150	0.076289411	0.127796911
regulation of defense response to virus by host (GO:	13150	0.076289411	0.127796911
positive regulation of T cell mediated immunity (GO:	13150	0.076289411	0.127796911
regulation of protein import into nucleus (GO:00423	13150	0.076289411	0.127796911
acyl-CoA metabolic process (GO:0006637)	13516	0.078325235	0.128747105
regulation of transport (GO:0051049)	13516	0.078325235	0.128747105
regulation of erythrocyte differentiation (GO:004564	13516	0.078325235	0.128747105
positive regulation of myeloid cell differentiation (G(	13516	0.078325235	0.128747105
regulation of glucose import (GO:0046324)	13516	0.078325235	0.128747105
protein insertion into ER membrane (GO:0045048)	13516	0.078325235	0.128747105
negative regulation of endothelial cell migration (GO	13881	0.080356674	0.129655247
regulation of axon extension (GO:0030516)	13881	0.080356674	0.129655247
negative regulation of proteasomal protein catabolic	13881	0.080356674	0.129655247
negative regulation of ubiquitin-dependent protein c	13881	0.080356674	0.129655247
lymphocyte proliferation (GO:0046651)	13881	0.080356674	0.129655247
regulation of phosphoprotein phosphatase activity ((	13881	0.080356674	0.129655247

regulation of protein targeting to mitochondrion (GC	14246	0.082383737	0.131713816
regulation of protein tyrosine kinase activity (GO:00(	14246	0.082383737	0.131713816
regulation of nitric-oxide synthase activity (GO:0050	14246	0.082383737	0.131713816
cellular response to cytokine stimulus (GO:0071345)	3/482	0.08927868	0.142304805
signal release from synapse (GO:0099643)	15707	0.090448414	0.143733733
intracellular protein transmembrane transport (GO:(	16072	0.092453735	0.145166164
neurotransmitter secretion (GO:0007269)	16072	0.092453735	0.145166164
mRNA catabolic process (GO:0006402)	16072	0.092453735	0.145166164
mRNA stabilization (GO:0048255)	16072	0.092453735	0.145166164
regulation of DNA repair (GO:0006282)	16438	0.094454736	0.14699169
positive regulation of RNA metabolic process (GO:00	16438	0.094454736	0.14699169
microtubule bundle formation (GO:0001578)	16438	0.094454736	0.14699169
establishment of protein localization to extracellular	16803	0.096451425	0.148778444
positive regulation of nucleocytoplasmic transport ((	16803	0.096451425	0.148778444
positive regulation of smooth muscle cell proliferatic	16803	0.096451425	0.148778444
axonogenesis (GO:0007409)	2/240	0.097747909	0.150077218
epidermal growth factor receptor signaling pathway	17168	0.098443811	0.150077218
regulation of T cell activation (GO:0050863)	17168	0.098443811	0.150077218
telomere organization (GO:0032200)	17168	0.098443811	0.150077218
establishment of protein localization to mitochondri	17533	0.100431903	0.150077218
positive regulation of blood vessel endothelial cell m	17533	0.100431903	0.150077218
purine ribonucleotide biosynthetic process (GO:000(	17533	0.100431903	0.150077218
positive regulation of DNA repair (GO:0045739)	17533	0.100431903	0.150077218
negative regulation of MAP kinase activity (GO:0043	17533	0.100431903	0.150077218
regulation of interleukin-10 production (GO:003265:	17533	0.100431903	0.150077218
regulation of protein metabolic process (GO:005124	17533	0.100431903	0.150077218
negative regulation of catabolic process (GO:000989	17899	0.10241571	0.150476714
regulation of smooth muscle cell proliferation (GO:0	17899	0.10241571	0.150476714
response to hydrogen peroxide (GO:0042542)	17899	0.10241571	0.150476714
RNA catabolic process (GO:0006401)	17899	0.10241571	0.150476714
cellular response to mechanical stimulus (GO:00712(	17899	0.10241571	0.150476714
positive regulation of actin filament polymerization (	17899	0.10241571	0.150476714
regulation of generation of precursor metabolites ar	18264	0.104395242	0.152957932
regulation of axonogenesis (GO:0050770)	18629	0.106370508	0.154988607
regulation of interleukin-12 production (GO:003265!	18629	0.106370508	0.154988607
positive regulation of phosphorylation (GO:0042327	2/253	0.106756192	0.155120875
negative regulation of protein metabolic process (GC	18994	0.108341516	0.156990736
positive regulation of macroautophagy (GO:001623(	19360	0.110308275	0.158964801
positive regulation of NIK/NF-kappaB signaling (GO:1	19360	0.110308275	0.158964801
regulation of cyclin-dependent protein kinase activit	19725	0.112270794	0.160911274
regulation of proteasomal protein catabolic process	19725	0.112270794	0.160911274
positive regulation of response to DNA damage stim	20090	0.114229082	0.163273091
protein-containing complex disassembly (GO:00329(	20455	0.116183149	0.164280474
positive regulation of establishment of protein locali	20455	0.116183149	0.164280474
telomere maintenance (GO:0000723)	20455	0.116183149	0.164280474
mitochondrial transport (GO:0006839)	20455	0.116183149	0.164280474
arachidonic acid metabolic process (GO:0019369)	20821	0.118133003	0.166589703

regulation of tumor necrosis factor-mediated signali	21186	0.120078652	0.168430323
cellular iron ion homeostasis (GO:0006879)	21186	0.120078652	0.168430323
response to reactive oxygen species (GO:0000302)	21551	0.122020106	0.17069834
iron ion homeostasis (GO:0055072)	22282	0.125890464	0.17518091
pattern recognition receptor signaling pathway (GO:	22282	0.125890464	0.17518091
I-kappaB kinase/NF-kappaB signaling (GO:0007249)	22647	0.127819385	0.177395769
positive regulation of DNA metabolic process (GO:0(	23012	0.129744146	0.178652935
positive regulation of Ras protein signal transductior	23012	0.129744146	0.178652935
positive regulation of viral process (GO:0048524)	23012	0.129744146	0.178652935
protein secretion (GO:0009306)	23377	0.131664756	0.180353286
regulation of innate immune response (GO:0045088	23377	0.131664756	0.180353286
regulation of RNA metabolic process (GO:0051252)	23743	0.133581224	0.182503178
cellular response to nutrient levels (GO:0031669)	24108	0.135493557	0.184159202
positive regulation of T cell proliferation (GO:00421(	24108	0.135493557	0.184159202
regulation of viral genome replication (GO:0045069)	24473	0.137401765	0.186271466
regulation of translational initiation (GO:0006446)	24838	0.139305857	0.18788431
negative regulation of transforming growth factor be	24838	0.139305857	0.18788431
positive regulation of protein transport (GO:005122	25204	0.141205842	0.189959777
wound healing (GO:0042060)	25569	0.143101727	0.192019154
fatty acid biosynthetic process (GO:0006633)	25934	0.144993521	0.193079981
histone acetylation (GO:0016573)	25934	0.144993521	0.193079981
regulation of glycolytic process (GO:0006110)	25934	0.144993521	0.193079981
extrinsic apoptotic signaling pathway (GO:0097191)	26299	0.146881234	0.193632905
negative regulation of supramolecular fiber organiza	26299	0.146881234	0.193632905
positive regulation of protein secretion (GO:005071	26299	0.146881234	0.193632905
positive regulation of secretion by cell (GO:190353	26299	0.146881234	0.193632905
regulation of Rho protein signal transduction (GO:00	26665	0.148764874	0.194169538
regulation of actin filament polymerization (GO:003(	26665	0.148764874	0.194169538
neurotransmitter transport (GO:0006836)	26665	0.148764874	0.194169538
endoplasmic reticulum organization (GO:0007029)	26665	0.148764874	0.194169538
regulation of cytokine-mediated signaling pathway (	27030	0.150644449	0.196136089
positive regulation of lymphocyte proliferation (GO:(	27395	0.152519968	0.198087662
regulation of T cell proliferation (GO:0042129)	27760	0.154391439	0.200024377
cytokine-mediated signaling pathway (GO:0019221)	3/621	0.155794096	0.200468699
purine ribonucleotide metabolic process (GO:00091	28126	0.156258871	0.200468699
positive regulation of endothelial cell proliferation (	28126	0.156258871	0.200468699
cellular response to UV (GO:0034644)	28126	0.156258871	0.200468699
negative regulation of apoptotic signaling pathway (	28491	0.158122273	0.202365732
positive regulation of proteasomal ubiquitin-depend	28856	0.159981653	0.203753873
positive regulation of ubiquitin-dependent protein c	28856	0.159981653	0.203753873
regulation of NIK/NF-kappaB signaling (GO:1901222)	29221	0.16183702	0.205619015
positive regulation of cytoskeleton organization (GO	29952	0.165535746	0.209307217
ephrin receptor signaling pathway (GO:0048013)	29952	0.165535746	0.209307217
B cell activation (GO:0042113)	31048	0.171053944	0.214735978
regulation of cell cycle G2/M phase transition (GO:1	31048	0.171053944	0.214735978
positive regulation of protein catabolic process (GO:	31048	0.171053944	0.214735978
negative regulation of phosphorylation (GO:004232	31413	0.172885407	0.216004095

positive regulation of proteasomal protein catabolic	31413	0.172885407	0.216004095
positive regulation of inflammatory response (GO:0(	32509	0.1783561	0.220741902
regulation of endothelial cell migration (GO:001059	32509	0.1783561	0.220741902
collagen fibril organization (GO:0030199)	32509	0.1783561	0.220741902
post-Golgi vesicle-mediated transport (GO:0006892)	32509	0.1783561	0.220741902
supramolecular fiber organization (GO:0097435)	2/351	0.18041891	0.222770767
positive regulation of supramolecular fiber organizat	33239	0.181983566	0.224176477
positive regulation of transmembrane receptor prot	33604	0.183791425	0.225874508
ciliary basal body-plasma membrane docking (GO:00	34700	0.189191607	0.231429733
mRNA metabolic process (GO:0016071)	34700	0.189191607	0.231429733
cellular transition metal ion homeostasis (GO:00469	35065	0.190983896	0.233080115
positive regulation of defense response (GO:003134	35796	0.194556867	0.236891
positive regulation of protein phosphorylation (GO:0	2/371	0.196323949	0.238490525
cellular response to chemical stress (GO:0062197)	1/101	0.199887426	0.242172088
positive regulation of cellular protein metabolic proc	1/102	0.201656605	0.242172088
regulation of cell death (GO:0010941)	1/102	0.201656605	0.242172088
positive regulation of vasculature development (GO:	1/102	0.201656605	0.242172088
mitotic sister chromatid segregation (GO:0000070)	1/102	0.201656605	0.242172088
positive regulation of macromolecule metabolic pro	2/384	0.206760787	0.247736159
negative regulation of transmembrane receptor prot	1/108	0.212191676	0.253665504
response to endoplasmic reticulum stress (GO:0034	1/110	0.215673081	0.257242722
protein-containing complex subunit organization (GO	1/112	0.219139449	0.26078586
histone modification (GO:0016570)	1/114	0.222590844	0.26351637
positive regulation of kinase activity (GO:0033674)	1/114	0.222590844	0.26351637
transmembrane receptor protein tyrosine kinase sig	2/404	0.222936853	0.26351637
cellular amide metabolic process (GO:0043603)	1/115	0.224310946	0.264546093
positive regulation of angiogenesis (GO:0045766)	1/116	0.226027329	0.265973993
negative regulation of response to external stimulus	1/118	0.229448966	0.268797676
positive regulation of protein-containing complex as	1/118	0.229448966	0.268797676
regulation of anatomical structure morphogenesis (0	1/123	0.237938516	0.278123688
fatty acid metabolic process (GO:0006631)	1/124	0.239625424	0.278856134
defense response to symbiont (GO:0140546)	1/124	0.239625424	0.278856134
regulation of phosphorylation (GO:0042325)	1/125	0.241308681	0.2795779
regulation of protein secretion (GO:0050708)	1/125	0.241308681	0.2795779
negative regulation of growth (GO:0045926)	1/126	0.242988297	0.280289133
circulatory system development (GO:0072359)	1/126	0.242988297	0.280289133
positive regulation of macromolecule biosynthetic p	1/129	0.248005372	0.285450384
G2/M transition of mitotic cell cycle (GO:0000086)	1/130	0.249670498	0.28673948
cell cycle G2/M phase transition (GO:0044839)	1/131	0.25133202	0.287392701
cellular response to metal ion (GO:0071248)	1/131	0.25133202	0.287392701
defense response to virus (GO:0051607)	1/133	0.254644285	0.290548577
positive regulation of response to external stimulus (	1/139	0.264495386	0.30113544
positive regulation of cellular catabolic process (GO:(	1/141	0.267750723	0.304183326
monocarboxylic acid metabolic process (GO:003278	1/143	0.270991977	0.307202112
negative regulation of cell migration (GO:0030336)	1/144	0.272607342	0.308368736
regulation of G2/M transition of mitotic cell cycle (G	1/149	0.280631842	0.316764698
negative regulation of protein phosphorylation (GO:(	1/152	0.285404947	0.321462531

positive regulation of gene expression (GO:0010628)	2/482	0.286716992	0.322250294
positive regulation of NF-kappaB transcription factor	1/155	0.290147096	0.325410176
regulation of cell differentiation (GO:0045595)	1/156	0.291720968	0.326479211
cellular response to starvation (GO:0009267)	1/158	0.294858487	0.329289945
heart development (GO:0007507)	1/164	0.304189769	0.338991141
positive regulation of I-kappaB kinase/NF-kappaB sig	1/171	0.314923805	0.35021125
positive regulation of ERK1 and ERK2 cascade (GO:0(	1/172	0.316443967	0.351159339
mitochondrion organization (GO:0007005)	1/175	0.320984703	0.355448324
positive regulation of developmental process (GO:0(	1/177	0.32399547	0.358028607
regulation of mitotic cell cycle phase transition (GO::	1/188	0.340322933	0.375282731
regulation of GTPase activity (GO:0043087)	1/189	0.341787991	0.376109798
negative regulation of transcription, DNA-templated	3/948	0.347007258	0.381055987
negative regulation of macromolecule metabolic pro	1/194	0.349065721	0.382517852
regulation of signal transduction (GO:0009966)	1/198	0.354831229	0.387385459
negative regulation of cellular process (GO:0048523)	2/566	0.354980592	0.387385459
regulation of angiogenesis (GO:0045765)	1/203	0.361967969	0.394192861
regulation of inflammatory response (GO:0050727)	1/206	0.366212919	0.397991727
mitotic cell cycle phase transition (GO:0044772)	1/209	0.370430265	0.401744988
phosphate-containing compound metabolic process	1/212	0.37462018	0.405453117
positive regulation of GTPase activity (GO:0043547)	1/214	0.377398305	0.406785878
positive regulation of protein modification process (	1/214	0.377398305	0.406785878
regulation of cell growth (GO:0001558)	1/217	0.381542891	0.41041219
regulation of I-kappaB kinase/NF-kappaB signaling (G	1/224	0.391109017	0.419843558
apoptotic process (GO:0006915)	1/231	0.400530489	0.429081542
regulation of ERK1 and ERK2 cascade (GO:0070372)	1/238	0.409809443	0.438129608
membrane organization (GO:0061024)	1/242	0.415048527	0.44283068
positive regulation of DNA-binding transcription fact	1/246	0.420242152	0.447464316
regulation of gene expression (GO:0010468)	3/1079	0.426222628	0.452477547
RNA splicing, via transesterification reactions with bu	1/251	0.426670843	0.452477547
positive regulation of signal transduction (GO:00099	1/252	0.427948195	0.452919015
positive regulation of cell differentiation (GO:00455	1/258	0.435554108	0.460043094
cellular component assembly (GO:0022607)	1/261	0.439319914	0.46309073
regulation of protein phosphorylation (GO:0001932)	1/266	0.445541762	0.468709934
protein-containing complex assembly (GO:0065003)	1/267	0.44677801	0.469072322
positive regulation of MAPK cascade (GO:0043410)	1/274	0.455356635	0.476178112
mRNA splicing, via spliceosome (GO:0000398)	1/274	0.455356635	0.476178112
DNA metabolic process (GO:0006259)	1/277	0.458993265	0.479028685
regulation of cell cycle (GO:0051726)	1/296	0.481480306	0.501502259
extracellular matrix organization (GO:0030198)	1/300	0.486096675	0.504313316
mRNA processing (GO:0006397)	1/300	0.486096675	0.504313316
MAPK cascade (GO:0000165)	1/303	0.489532569	0.506878212
chemical synaptic transmission (GO:0007268)	1/306	0.49294601	0.509409826
cilium assembly (GO:0060271)	1/314	0.501939835	0.517686967
regulation of cell population proliferation (GO:00421	2/764	0.505144013	0.519972116
negative regulation of gene expression (GO:0010629	1/322	0.510777694	0.524744272
intracellular protein transport (GO:0006886)	1/336	0.525876582	0.539202889
cellular response to DNA damage stimulus (GO:0006	1/350	0.540519741	0.553138879

gene expression (GO:0010467)	1/356	0.546659218	0.558335434
protein transport (GO:0015031)	1/369	0.55968767	0.57053433
organelle organization (GO:0006996)	1/420	0.60735684	0.617929783
negative regulation of nucleic acid-templated transc	1/464	0.644400569	0.654352702
positive regulation of cell population proliferation (G	1/474	0.652330658	0.661128952
protein phosphorylation (GO:0006468)	1/496	0.669173374	0.676894605
negative regulation of cellular macromolecule biosyr	1/547	0.705209896	0.711977745
regulation of transcription by RNA polymerase II (GO	111856	0.730120497	0.73571529
positive regulation of cellular process (GO:0048522)	1/625	0.75302464	0.757344093
positive regulation of transcription by RNA polymera	1/908	0.870827861	0.874151631
positive regulation of transcription, DNA-templated (	1/1183	0.931826799	0.933601707
regulation of transcription, DNA-templated (GO:000	125676	0.965235434	0.965235434

of significant highly-correlated RNA-seq-based modules (cyan; Significant terms

Old P-value	Old Adjusted P-value	Odds Ratio	Combined Score	Genes	KEGG
0	0	232.0430108	12826.38247	HSPA8;HSF	.
0	0	97.49019608	3796.68677	DNAJB1;HS	.
0	0	61.83489097	2123.476966	DNAJB1;HS	.
0	0	251.5081081	7875.910109	CCT2;HSP9	.
0	0	157.1216216	4492.683105	DNAJB1;CC	.
0	0	157.3894737	3896.518354	DNAJB1;HS	.
0	0	29.92840336	674.5029385	CCT6A;CCT	.
0	0	27.49444444	540.761169	CCT2;HSP9	.
0	0	116.1655012	2273.188255	HSPA8;HSF	.
0	0	57.13205742	1104.284182	CCT6A;CCT	.
0	0	82.40281224	1486.713974	HSP90AA1	.
0	0	71.17142857	1008.626002	HSPA8;HSF	.
0	0	66.42	924.6065911	CCT2;HSP9	.
0	0	208.5261324	2846.511229	CCT6A;CCT	.
0	0	208.5261324	2846.511229	DNAJB1;DN	.
0	0	208.5261324	2846.511229	DNAJB1;BA	.
0	0	182.4512195	2432.750116	CCT6A;CCT	.
0	0	182.4512195	2432.750116	DNAJB1;DN	.
0	0	182.4512195	2432.750116	CCT6A;CCT	.
0	0	182.4512195	2432.750116	CCT6A;CCT	.
0	0	162.1707317	2115.931394	CCT6A;CCT	.
0	0	47.41428571	601.2932166	CCT2;HSP9	.
0	0	121.6097561	1498.89976	CCT6A;CCT	.
0	0	97.27317073	1142.568606	CCT6A;CCT	.
0	0	91.18902439	1055.573524	CCT6A;CCT	.
0	0	85.82065997	979.6154458	HSP90AA1	.
0	0	31.08125	345.29123	CCT6A;CCT	.
0	0	26.15789474	273.7355882	DNAJB1;HS	.
0	0	56.08818011	575.6726347	HSP90AA1	.
0	0	54.00813008	548.7162099	HSP90AA1	.
0	0	23.94337349	242.6467116	DNAJB1;BA	.
0	0	48.6	479.6311896	CCT6A;CCT	.
0	0	44.1751663	424.2831635	HSP90AA1	.
0	0	44.1751663	424.2831635	CCT6A;CCT	.
0	0	237.5238095	2270.521513	HSP90AA1	.
0	0	18.90571429	174.9403644	DNAJA1;HS	.
0	0	29.72672972	252.6548409	CCT6A;CCT	.
0	0	118.7380952	1005.249888	HSP90AA1	.
0	0	28.00750469	233.3678171	HSP90AA1	.
0	0	13.75833333	111.1303205	CCT2;HSP9	.
0	0	86.34199134	683.850896	HSP90AA1	.
0	0	73.05128205	557.0746629	HSP90AA1	.
0	0	6.47567867	47.93469728	HSPA8;CCT	.
0	0	6.420283485	47.24594968	HSPA8;CCT	.

0	0	19.65919578	144.3108152	HSP90AA1	.
0	0	6.379340467	46.7386946	HSPA8;CCT	.
0	0	18.89040228	136.5599222	PEA15;HM	.
0	0	52.74603175	371.3176123	TLR7;HSPD	.
0	0	43.14718615	287.8752745	HSP90AA1	.
0	0	43.14718615	287.8752745	HSP90AA1	.
0	0	15.29730424	101.5857752	HSP90AA1	.
0	0	41.26915114	271.9616824	TLR7;HSPD	.
0	0	6.676213857	43.67710248	DNAJA1;TI	.
0	0	37.96380952	244.3251845	FKBP4;PPII	.
0	0	37.96380952	244.3251845	HSP90AA1	.
0	0	36.5018315	232.2621485	DNAJA1;HS	.
0	0	36.5018315	232.2621485	HSP90AA1	.
0	0	31.62857143	192.8370933	FKBP4;PPII	.
0	0	30.60675883	184.7363254	HSP90AA1	.
0	0	29.64880952	177.1982383	PEA15;HM	.
0	0	27.90196078	163.5992917	HSP90AA1	.
0	0	10.90573996	62.23968484	HSP90AA1	.
0	0	25.63577864	146.258861	HSPA8;HSF	.
0	0	24.95989975	141.1573039	HSP90AA1	.
0	0	23.70952381	131.8095305	DNAJB1;AH	.
0	0	23.70952381	131.8095305	HMOX1;TL	.
0	0	23.70952381	131.8095305	PEA15;HM	.
0	0	10.13798397	55.83921465	HSPA8;TEN	.
0	0	9.997140454	54.6830729	HSPA1L;M	.
0	0	21.54978355	115.9563361	HSP90AA1	.
0	0	20.17122594	106.046538	RTN4R;FKB	.
0	0	20.17122594	106.046538	HSP90AA1	.
0	0	20.17122594	106.046538	HSP90AA1	.
0	0	4.123283753	21.51152412	DNAJA1;HS	.
0	0	19.34596696	100.1980519	DNAJA1;HS	.
0	0	18.58543417	94.86691228	HMOX1;TL	.
0	0	5.929003021	30.14384166	HMOX1;TL	.
0	0	17.88230009	89.99033326	DNAJA1;HS	.
0	0	17.23030303	85.51510117	TLR7;HSPD	.
0	0	16.92176871	83.41354267	RTN4R;FKB	.
0	0	16.05891848	77.59361647	TLR7;HSPA	.
0	0	15.27956989	72.41257982	DNAJA1;HS	.
0	0	15.27956989	72.41257982	HSPA8;HSF	.
0	0	14.80059524	69.26574678	HSP90AA1	.
0	0	14.80059524	69.26574678	HSP90AA1	.
0	0	14.57216117	67.77530918	HSP90AA1	.
0	0	14.13574982	64.94701728	TIGAR;HM	.
0	0	14.13574982	64.94701728	HSP90AA1	.
0	0	13.72463768	62.3062428	HSP90AA1	.
0	0	13.72463768	62.3062428	NECAB2;HS	.
0	0	116	523.6437583	BAG3	.

0	0	116	523.6437583	TIGAR	.
0	0	116	523.6437583	CCT2	.
0	0	116	523.6437583	HSPH1	.
0	0	116	523.6437583	CCT2	.
0	0	116	523.6437583	HSPA1A	.
0	0	116	523.6437583	HSPA8	.
0	0	13.52789116	61.05074177	HSP90AA1	.
0	0	13.15079365	58.65976046	HSP90AA1	.
0	0	12.96999348	57.52071791	NCK2;HSPI	.
0	0	12.79407979	56.41710205	RBM38;HS	.
0	0	12.79407979	56.41710205	TLR7;HSPD	.
0	0	92.79534884	402.0750334	DNAJA1	.
0	0	92.79534884	402.0750334	HSPA8	.
0	0	92.79534884	402.0750334	HSPA1A	.
0	0	92.79534884	402.0750334	HSPD1	.
0	0	92.79534884	402.0750334	BAG3	.
0	0	92.79534884	402.0750334	HSPA1A	.
0	0	92.79534884	402.0750334	NCK2	.
0	0	92.79534884	402.0750334	NECAB2	.
0	0	92.79534884	402.0750334	NAA50	.
0	0	92.79534884	402.0750334	ACOT7	.
0	0	92.79534884	402.0750334	HSPD1	.
0	0	92.79534884	402.0750334	MTCL1	.
0	0	92.79534884	402.0750334	HSPH1	.
0	0	92.79534884	402.0750334	HSPA1A	.
0	0	11.98131404	51.3794865	HSPE1;HSP	.
0	0	11.98131404	51.3794865	TLR7;HSPA	.
0	0	77.3255814	323.208935	RTN4R	.
0	0	77.3255814	323.208935	HSPD1	.
0	0	77.3255814	323.208935	HSP90AB1	.
0	0	77.3255814	323.208935	HSPA1A	.
0	0	77.3255814	323.208935	HSPA1A	.
0	0	77.3255814	323.208935	HSPH1	.
0	0	77.3255814	323.208935	HSPH1	.
0	0	11.26530612	47.02931709	TLR7;HSPD	.
0	0	10.87520525	44.69580966	HSP90AA1	.
0	0	10.62974853	43.24132174	TLR7;HSPD	.
0	0	66.27574751	268.2435667	HMOX1	.
0	0	66.27574751	268.2435667	PEA15	.
0	0	66.27574751	268.2435667	BAG3	.
0	0	66.27574751	268.2435667	RTN4R	.
0	0	66.27574751	268.2435667	HSP90AB1	.
0	0	66.27574751	268.2435667	DNAJA1	.
0	0	66.27574751	268.2435667	BAG3	.
0	0	66.27574751	268.2435667	P4HA1	.
0	0	10.51111111	42.54222889	NCK2;HSPI	.
0	0	10.39508111	41.86100377	HSP90AA1	.

0	0	10.2815735	41.19701054	TIGAR;HSP	.
0	0	9.955388471	39.30248946	NAA50;HSI	.
0	0	57.98837209	227.9335161	HMOX1	.
0	0	57.98837209	227.9335161	TIGAR	.
0	0	57.98837209	227.9335161	HSPA1A	.
0	0	9.649173955	37.54277574	HSP90AB1	.
0	0	9.551226551	36.98384948	NECAB2;M	.
0	0	9.455238095	36.43799007	HSP90AB1	.
0	0	4.048856549	15.52962456	DNAJA1;BA	.
0	0	51.54263566	197.222132	DNAJA1	.
0	0	51.54263566	197.222132	TIGAR	.
0	0	51.54263566	197.222132	HMOX1	.
0	0	51.54263566	197.222132	TLR7	.
0	0	51.54263566	197.222132	TIGAR	.
0	0	51.54263566	197.222132	NECAB2	.
0	0	51.54263566	197.222132	HSP90AB1	.
0	0	51.54263566	197.222132	HSPA1A	.
0	0	46.38604651	173.119691	ACOT7	.
0	0	46.38604651	173.119691	NECAB2	.
0	0	46.38604651	173.119691	ACOT7	.
0	0	46.38604651	173.119691	HSPD1	.
0	0	46.38604651	173.119691	PPID	.
0	0	46.38604651	173.119691	ACOT7	.
0	0	46.38604651	173.119691	HSP90AA1	.
0	0	46.38604651	173.119691	PTGES3	.
0	0	46.38604651	173.119691	P4HA1	.
0	0	8.751322751	32.49405409	TLR7;HSPD	.
0	0	5.086529346	18.78414146	DNAJA1;PF	.
0	0	42.16701903	153.7498329	RTN4R	.
0	0	42.16701903	153.7498329	PEA15	.
0	0	42.16701903	153.7498329	DNAJA1	.
0	0	42.16701903	153.7498329	NECAB2	.
0	0	8.288220551	29.95881083	HSPA8;HSF	.
0	0	8.074481074	28.80549994	HSPE1;HSP	.
0	0	38.65116279	137.8779524	HSP90AA1	.
0	0	38.65116279	137.8779524	HSP90AB1	.
0	0	38.65116279	137.8779524	TLR7	.
0	0	38.65116279	137.8779524	BAG3	.
0	0	38.65116279	137.8779524	DNAJA1	.
0	0	7.871428571	27.72004607	HSPA8;HSF	.
0	0	35.67620751	124.6598994	HSP90AB1	.
0	0	35.67620751	124.6598994	PPID	.
0	0	35.67620751	124.6598994	ACOT7	.
0	0	35.67620751	124.6598994	NAA50	.
0	0	4.68316517	16.32797674	DNAJA1;PF	.
0	0	7.678281069	26.69699919	HMOX1;HS	.
0	0	7.615975422	26.36899078	RTN4R;HSF	.

0	0	3.581918819	12.38006646	HSP90AA1	.
0	0	33.12624585	113.4998155	HSPA1A	.
0	0	33.12624585	113.4998155	DNAJA1	.
0	0	33.12624585	113.4998155	BAG3	.
0	0	33.12624585	113.4998155	ACOT7	.
0	0	33.12624585	113.4998155	PTGES3	.
0	0	7.318936877	24.81902311	TIGAR;HM	.
0	0	30.91627907	103.965655	HMOX1	.
0	0	30.91627907	103.965655	HMOX1	.
0	0	30.91627907	103.965655	NAA50	.
0	0	30.91627907	103.965655	TIGAR	.
0	0	30.91627907	103.965655	NAA50	.
0	0	30.91627907	103.965655	HMOX1	.
0	0	28.98255814	95.73687424	TIGAR	.
0	0	28.98255814	95.73687424	HSPD1	.
0	0	28.98255814	95.73687424	HMOX1	.
0	0	6.888773027	22.61632351	HSPA8;HSF	.
0	0	27.27633379	88.57088447	HMOX1	.
0	0	27.27633379	88.57088447	HSP90AA1	.
0	0	27.27633379	88.57088447	HSP90AB1	.
0	0	27.27633379	88.57088447	HSPA1A	.
0	0	27.27633379	88.57088447	HMOX1	.
0	0	6.740136054	21.86723097	DNAJA1;HI	.
0	0	6.691995947	21.62598154	HSP90AA1	.
0	0	25.75968992	82.28088014	MTCL1	.
0	0	25.75968992	82.28088014	HSP90AA1	.
0	0	25.75968992	82.28088014	HMOX1	.
0	0	25.75968992	82.28088014	NECAB2	.
0	0	25.75968992	82.28088014	HSPD1	.
0	0	25.75968992	82.28088014	HSPA1A	.
0	0	25.75968992	82.28088014	HSP90AA1	.
0	0	25.75968992	82.28088014	PTGES3	.
0	0	6.416909621	20.26053037	RTN4R;MT	.
0	0	24.40269278	76.72079425	HSPH1	.
0	0	24.40269278	76.72079425	HSPA8	.
0	0	24.40269278	76.72079425	HSP90AB1	.
0	0	24.40269278	76.72079425	HSP90AA1	.
0	0	6.204260652	19.22073326	HSP90AA1	.
0	0	23.18139535	71.77485187	HSP90AB1	.
0	0	23.18139535	71.77485187	NCK2	.
0	0	23.18139535	71.77485187	RTN4R	.
0	0	23.18139535	71.77485187	HSP90AB1	.
0	0	22.07641196	67.35016648	HSPA1A	.
0	0	22.07641196	67.35016648	PPID	.
0	0	5.929020665	17.89610065	HSP90AA1	.
0	0	21.07188161	63.37139604	HSPA8	.
0	0	21.07188161	63.37139604	HSPA1A	.

0	0	21.07188161	63.37139604	HSPA1A	.
0	0	21.07188161	63.37139604	HSP90AB1	.
0	0	21.07188161	63.37139604	HSP90AA1	.
0	0	21.07188161	63.37139604	BAG3	.
0	0	3.810326933	11.37550978	NCK2;HMC	.
0	0	5.78235466	17.20037584	RTN4R;FKB	.
0	0	20.15470172	59.77682212	HSP90AB1	.
0	0	20.15470172	59.77682212	ACOT7	.
0	0	20.15470172	59.77682212	MTCL1	.
0	0	20.15470172	59.77682212	HSP90AB1	.
0	0	20.15470172	59.77682212	HSP90AA1	.
0	0	19.31395349	56.51543007	TIGAR	.
0	0	19.31395349	56.51543007	HSPA1A	.
0	0	19.31395349	56.51543007	HSPA1A	.
0	0	18.54046512	53.54470544	HSP90AB1	.
0	0	17.82647585	50.82895022	HMOX1	.
0	0	17.82647585	50.82895022	HSPA1A	.
0	0	17.82647585	50.82895022	NCK2	.
0	0	5.291064741	14.9239854	HSP90AA1	.
0	0	17.16537468	48.3379819	RTN4R	.
0	0	17.16537468	48.3379819	HSP90AA1	.
0	0	17.16537468	48.3379819	HSPA1A	.
0	0	17.16537468	48.3379819	NAA50	.
0	0	17.16537468	48.3379819	HSPA1A	.
0	0	17.16537468	48.3379819	BAG3	.
0	0	17.16537468	48.3379819	FKBP4	.
0	0	16.55149502	46.04611786	MTCL1	.
0	0	16.55149502	46.04611786	TENT5C	.
0	0	16.55149502	46.04611786	HMOX1	.
0	0	16.55149502	46.04611786	PPID	.
0	0	16.55149502	46.04611786	HSPD1	.
0	0	2.834705882	7.848696527	DNAJB1;BA	.
0	0	15.97995188	43.93137486	BAG3	.
0	0	15.97995188	43.93137486	FKBP4	.
0	0	15.97995188	43.93137486	HSP90AB1	.
0	0	15.97995188	43.93137486	PTGES3	.
0	0	15.97995188	43.93137486	ACOT7	.
0	0	15.97995188	43.93137486	BAG3	.
0	0	15.97995188	43.93137486	HSPD1	.
0	0	15.97995188	43.93137486	NECAB2	.
0	0	15.44651163	41.97483259	RTN4R	.
0	0	15.44651163	41.97483259	ACOT7	.
0	0	15.44651163	41.97483259	HSPD1	.
0	0	15.44651163	41.97483259	ACOT7	.
0	0	15.44651163	41.97483259	HSP90AB1	.
0	0	15.44651163	41.97483259	HSPA1L	.
0	0	15.44651163	41.97483259	RTN4R	.

0	0	15.44651163	41.97483259	HSPA1A	.
0	0	15.44651163	41.97483259	PTGES3	.
0	0	15.44651163	41.97483259	NAA50	.
0	0	4.901785714	13.18328741	HSP90AA1	.
0	0	14.94748687	40.16012344	HSP90AA1	.
0	0	14.94748687	40.16012344	HSPD1	.
0	0	14.94748687	40.16012344	MTCL1	.
0	0	14.94748687	40.16012344	RTN4R	.
0	0	14.94748687	40.16012344	HSPD1	.
0	0	14.94748687	40.16012344	HMOX1	.
0	0	14.94748687	40.16012344	TIGAR	.
0	0	14.94748687	40.16012344	FKBP4	.
0	0	14.94748687	40.16012344	HSPD1	.
0	0	14.47965116	38.47302036	HSPD1	.
0	0	14.47965116	38.47302036	DNAJA1	.
0	0	14.47965116	38.47302036	TENT5C	.
0	0	14.47965116	38.47302036	HMOX1	.
0	0	14.47965116	38.47302036	HSP90AB1	.
0	0	14.04016913	36.90110156	HSPA1A	.
0	0	14.04016913	36.90110156	HSPD1	.
0	0	14.04016913	36.90110156	HSP90AB1	.
0	0	14.04016913	36.90110156	HMOX1	.
0	0	13.62653899	35.43347596	DNAJA4	.
0	0	13.62653899	35.43347596	RTN4R	.
0	0	13.62653899	35.43347596	HSPD1	.
0	0	13.62653899	35.43347596	HSP90AA1	.
0	0	13.62653899	35.43347596	DNAJA1	.
0	0	13.62653899	35.43347596	HSPA1A	.
0	0	13.62653899	35.43347596	HSP90AA1	.
0	0	4.587921022	11.82366806	HSP90AA1	.
0	0	13.23654485	34.06055692	DNAJA1	.
0	0	13.23654485	34.06055692	HSPA1A	.
0	0	13.23654485	34.06055692	HSP90AA1	.
0	0	13.23654485	34.06055692	HSPD1	.
0	0	13.23654485	34.06055692	BAG3	.
0	0	12.86821705	32.7738747	ACOT7	.
0	0	12.86821705	32.7738747	DNAJA1	.
0	0	12.86821705	32.7738747	HSPA1A	.
0	0	12.86821705	32.7738747	HSPA1A	.
0	0	12.86821705	32.7738747	PEA15	.
0	0	12.86821705	32.7738747	HMOX1	.
0	0	12.51979887	31.56592015	DNAJA4	.
0	0	12.51979887	31.56592015	RTN4R	.
0	0	12.51979887	31.56592015	HSP90AB1	.
0	0	12.51979887	31.56592015	HSP90AB1	.
0	0	12.51979887	31.56592015	HSPD1	.
0	0	12.51979887	31.56592015	HSP90AB1	.

0	0	12.18971848	30.43001378	HSPA1L	.
0	0	12.18971848	30.43001378	NCK2	.
0	0	12.18971848	30.43001378	HSP90AA1	.
0	0	2.975253322	7.1881899	HSPA8;HSF	.
0	0	11.02657807	26.49659809	HSPA8	.
0	0	10.76960519	25.64293525	HSPD1	.
0	0	10.76960519	25.64293525	HSPA8	.
0	0	10.76960519	25.64293525	HSPA1A	.
0	0	10.76960519	25.64293525	TENT5C	.
0	0	10.5243129	24.83353227	TIGAR	.
0	0	10.5243129	24.83353227	HSPA1A	.
0	0	10.5243129	24.83353227	MTCL1	.
0	0	10.28992248	24.06520397	PDIA4	.
0	0	10.28992248	24.06520397	BAG3	.
0	0	10.28992248	24.06520397	HMOX1	.
0	0	3.945178071	9.173972981	HSP90AA1	.
0	0	10.06572295	23.33505696	NCK2	.
0	0	10.06572295	23.33505696	HSPD1	.
0	0	10.06572295	23.33505696	PTGES3	.
0	0	9.85106383	22.64045732	HSPD1	.
0	0	9.85106383	22.64045732	HMOX1	.
0	0	9.85106383	22.64045732	ACOT7	.
0	0	9.85106383	22.64045732	TIGAR	.
0	0	9.85106383	22.64045732	DNAJA1	.
0	0	9.85106383	22.64045732	HSPD1	.
0	0	9.85106383	22.64045732	HSP90AB1	.
0	0	9.645348837	21.97900258	TIGAR	.
0	0	9.645348837	21.97900258	HMOX1	.
0	0	9.645348837	21.97900258	HMOX1	.
0	0	9.645348837	21.97900258	HSPA1A	.
0	0	9.645348837	21.97900258	TLR7	.
0	0	9.645348837	21.97900258	NCK2	.
0	0	9.448030375	21.34849709	TIGAR	.
0	0	9.258604651	20.74693057	RTN4R	.
0	0	9.258604651	20.74693057	HSPD1	.
0	0	3.738379814	8.363531826	HSP90AA1	.
0	0	9.076607387	20.17245912	HSP90AB1	.
0	0	8.901610018	19.62338864	BAG3	.
0	0	8.901610018	19.62338864	TLR7	.
0	0	8.733216323	19.09816008	HSP90AB1	.
0	0	8.733216323	19.09816008	HSP90AB1	.
0	0	8.571059432	18.59533643	TIGAR	.
0	0	8.414799154	18.11359115	HSPA8	.
0	0	8.414799154	18.11359115	HSPA1L	.
0	0	8.414799154	18.11359115	PTGES3	.
0	0	8.414799154	18.11359115	HSP90AA1	.
0	0	8.264119601	17.6516979	PTGES3	.

0	0	8.11872705	17.20852138	HSPA1A	.
0	0	8.11872705	17.20852138	HMOX1	.
0	0	7.978348035	16.78300913	HMOX1	.
0	0	7.711627907	15.98113875	HMOX1	.
0	0	7.711627907	15.98113875	TLR7	.
0	0	7.584826535	15.60302779	TLR7	.
0	0	7.462115529	15.23906422	TIGAR	.
0	0	7.462115529	15.23906422	RTN4R	.
0	0	7.462115529	15.23906422	PPID	.
0	0	7.343300111	14.88851389	PDIA4	.
0	0	7.343300111	14.88851389	HSP90AB1	.
0	0	7.228197674	14.55069131	RBM38	.
0	0	7.116636852	14.2249557	HSPA8	.
0	0	7.116636852	14.2249557	NCK2	.
0	0	7.00845666	13.91070752	PPID	.
0	0	6.903505727	13.60738519	NCK2	.
0	0	6.903505727	13.60738519	HSPA1A	.
0	0	6.801641587	13.31446223	PPID	.
0	0	6.70273003	13.03144454	HMOX1	.
0	0	6.606644518	12.75786804	ACOT7	.
0	0	6.606644518	12.75786804	NAA50	.
0	0	6.606644518	12.75786804	TIGAR	.
0	0	6.51326564	12.4932964	BAG3	.
0	0	6.51326564	12.4932964	HSPA8	.
0	0	6.51326564	12.4932964	PPID	.
0	0	6.51326564	12.4932964	PPID	.
0	0	6.42248062	12.23731909	RTN4R	.
0	0	6.42248062	12.23731909	NCK2	.
0	0	6.42248062	12.23731909	HSPA8	.
0	0	6.42248062	12.23731909	HMOX1	.
0	0	6.334182861	11.98954947	HSP90AB1	.
0	0	6.248271527	11.74962315	NCK2	.
0	0	6.164651163	11.51719639	NCK2	.
0	0	2.289604547	4.256878653	HSPA8;HSF	.
0	0	6.083231334	11.29194472	ACOT7	.
0	0	6.083231334	11.29194472	HMOX1	.
0	0	6.083231334	11.29194472	PPID	.
0	0	6.003926306	11.07356161	HSPA1A	.
0	0	5.926654741	10.86175725	HSPA1A	.
0	0	5.926654741	10.86175725	HSPA1A	.
0	0	5.851339417	10.65625749	TLR7	.
0	0	5.706287683	10.26314712	NCK2	.
0	0	5.706287683	10.26314712	NCK2	.
0	0	5.50166113	9.714702878	HSPD1	.
0	0	5.50166113	9.714702878	HSP90AA1	.
0	0	5.50166113	9.714702878	HSP90AA1	.
0	0	5.436662107	9.542028607	TIGAR	.

0	0	5.436662107	9.542028607	HSPA1A	.
0	0	5.250528541	9.051770323	TLR7	.
0	0	5.250528541	9.051770323	DNAJA4	.
0	0	5.250528541	9.051770323	P4HA1	.
0	0	5.250528541	9.051770323	HSPA8	.
0	0	2.675262655	4.581317344	HSP90AB1	.
0	0	5.133333333	8.746372989	NCK2	.
0	0	5.076667519	8.599639846	HSP90AB1	.
0	0	4.913904008	8.181625526	HSP90AA1	.
0	0	4.913904008	8.181625526	HSPA1A	.
0	0	4.861933905	8.049253281	HMOX1	.
0	0	4.761208343	7.794244625	TLR7	.
0	0	2.527680991	4.115037311	HSP90AA1	.
0	0	4.617674419	7.434460164	HSPA1A	.
0	0	4.571724614	7.320195173	HSP90AA1	.
0	0	4.571724614	7.320195173	HSPA1A	.
0	0	4.571724614	7.320195173	HMOX1	.
0	0	4.571724614	7.320195173	NAA50	.
0	0	2.44003989	3.845973242	DNAJA4;HS	.
0	0	4.31406216	6.687940779	HSPA1A	.
0	0	4.234478344	6.495653924	PDIA4	.
0	0	4.157762414	6.311678756	PPID	.
0	0	4.083762091	6.135525737	NAA50	.
0	0	4.083762091	6.135525737	TIGAR	.
0	0	2.316275764	3.476421207	HSP90AA1	.
0	0	4.047735618	6.050239634	ACOT7	.
0	0	4.012335693	5.966741857	HMOX1	.
0	0	3.943351222	5.804907341	RTN4R	.
0	0	3.943351222	5.804907341	HSP90AA1	.
0	0	3.78078536	5.428236017	HMOX1	.
0	0	3.749858196	5.357341072	ACOT7	.
0	0	3.749858196	5.357341072	TLR7	.
0	0	3.719429857	5.287832827	PTGES3	.
0	0	3.719429857	5.287832827	PPID	.
0	0	3.689488372	5.219674142	HSPA1A	.
0	0	3.689488372	5.219674142	CACYBP	.
0	0	3.60247093	5.022942769	HSPH1	.
0	0	3.574364521	4.959835532	HSP90AA1	.
0	0	3.546690519	4.897910178	HSP90AA1	.
0	0	3.546690519	4.897910178	TIGAR	.
0	0	3.492600423	4.777485049	TLR7	.
0	0	3.339737108	4.441621488	TLR7	.
0	0	3.291694352	4.33746193	HSP90AA1	.
0	0	3.245004913	4.236892789	ACOT7	.
0	0	3.222149943	4.187901829	HMOX1	.
0	0	3.112507857	3.955099958	HSP90AA1	.
0	0	3.050207916	3.824491729	NCK2	.

0	0	1.932142857	2.413748091	DNAJA4;HS	.
0	0	2.990335246	3.700142917	HSPA1A	.
0	0	2.970892723	3.66001364	HSP90AB1	.
0	0	2.932750704	3.581650372	HSPA8	.
0	0	2.823940648	3.360781739	CACYBP	.
0	0	2.706703146	3.127391289	HMOX1	.
0	0	2.690738474	3.095988151	NECAB2	.
0	0	2.643945469	3.004478662	HSPD1	.
0	0	2.613636364	2.945635473	HSP90AB1	.
0	0	2.458525059	2.649946583	HSP90AA1	.
0	0	2.445324097	2.62521349	RTN4R	.
0	0	1.472009292	1.55798874	DNAJB1;HS	.
0	0	2.38137125	2.506381484	HSP90AB1	.
0	0	2.332546335	2.416781612	NCK2	.
0	0	1.637284701	1.695722933	NCK2;HSPA	.
0	0	2.2742344	2.311075981	HMOX1	.
0	0	2.240612592	2.250785797	TLR7	.
0	0	2.207960644	2.192703795	HSP90AA1	.
0	0	2.176237187	2.13672242	TIGAR	.
0	0	2.155584671	2.100518402	RTN4R	.
0	0	2.155584671	2.100518402	HSP90AA1	.
0	0	2.125322997	2.047816732	HSPA1A	.
0	0	2.057878819	1.93187272	HMOX1	.
0	0	1.994539939	1.82493501	HSPD1	.
0	0	1.934942596	1.726090697	NECAB2	.
0	0	1.902441378	1.672930531	HSPA8	.
0	0	1.871001424	1.622016378	HSPA1A	.
0	0	1.283887932	1.094891243	RBM38;DN	.
0	0	1.833116279	1.561342902	HSPA8	.
0	0	1.825720374	1.549585883	NECAB2	.
0	0	1.782553615	1.481544922	HSP90AB1	.
0	0	1.761717352	1.449060791	PPID	.
0	0	1.728038613	1.397057518	HSP90AA1	.
0	0	1.7214548	1.386964822	PPID	.
0	0	1.67671863	1.319031544	NECAB2	.
0	0	1.67671863	1.319031544	HSPA8	.
0	0	1.658240647	1.291304729	PTGES3	.
0	0	1.549940875	1.132836209	HSP90AB1	.
0	0	1.528894765	1.102864807	P4HA1	.
0	0	1.528894765	1.102864807	HSPA8	.
0	0	1.513476051	1.081082426	PEA15	.
0	0	1.498360656	1.059873836	HSPA8	.
0	0	1.4594695	1.005975865	HSP90AA1	.
0	0	1.199475066	0.819135574	NCK2;HSPA	.
0	0	1.422516844	0.955676438	HSPA1A	.
0	0	1.362096494	0.875404064	BAG3	.
0	0	1.306523622	0.803804844	TIGAR	.

0	0	1.284048477	0.775474977	HSPD1	.
0	0	1.237866532	0.718428501	PDIA4	.
0	0	1.084364767	0.540706331	PPID	.
0	0	0.979104927	0.430252723	HSPA8	.
0	0	0.957913368	0.409224137	HMOX1	.
0	0	0.914305849	0.367287721	TLR7	.
0	0	0.826731408	0.288744043	HSPA8	.
0	0	0.80626703	0.253607823	DNAJB1;N(	.
0	0	0.720483005	0.204370285	HSP90AB1	.
0	0	0.488423374	0.067554304	NCK2	.
0	0	0.369377877	0.026081151	NCK2	.
0	0	0.376237203	0.013312489	HSPA8;HSF	.

s were highlighted)

Term	Overlap	P-value	Adjusted P-value	Old P-value
Protein processing in endoplasmic reticulum	10/171	3.09E-12	1.67E-10	0
Antigen processing and presentation	28642	1.81E-08	4.90E-07	0
Lipid and atherosclerosis	7/215	4.11E-07	7.12E-06	0
Estrogen signaling pathway	6/137	5.27E-07	7.12E-06	0
Legionellosis	20911	7.39E-06	7.98E-05	0
Measles	4/139	2.44E-04	0.002199886	0
Longevity regulating pathway	3/102	0.001465377	0.011304339	0
Toxoplasmosis	3/112	0.001915685	0.012930875	0
Prion disease	4/273	0.003001999	0.018011991	0
Fluid shear stress and atherosclerosis	3/139	0.003532696	0.019076561	0
Spliceosome	3/150	0.00437269	0.021465934	0
Necroptosis	3/159	0.005142913	0.023143109	0
Chemical carcinogenesis	3/239	0.015567685	0.06466577	0
Endocytosis	3/252	0.01790492	0.064893655	0
IL-17 signaling pathway	34366	0.018190096	0.064893655	0
Prostate cancer	35462	0.019295932	0.064893655	0
Progesterone-mediated oocyte maturation	2/100	0.020429484	0.064893655	0
Th17 cell differentiation	2/107	0.023180005	0.069540014	0
MAPK signaling pathway	3/294	0.026731012	0.075972351	0
Influenza A	2/172	0.054976005	0.141230001	0
Biosynthesis of unsaturated fatty acids	44588	0.057768136	0.141230001	0
Fatty acid elongation	44588	0.057768136	0.141230001	0
NOD-like receptor signaling pathway	2/181	0.060153519	0.141230001	0
Fructose and mannose metabolism	12055	0.070155536	0.157849957	0
Ferroptosis	14977	0.086424772	0.180896828	0
Type I diabetes mellitus	15707	0.090448414	0.180896828	0
Porphyrin and chlorophyll metabolism	15707	0.090448414	0.180896828	0
Salmonella infection	2/249	0.103960387	0.187911436	0
Arginine and proline metabolism	18264	0.104395242	0.187911436	0
Vibrio cholerae infection	18264	0.104395242	0.187911436	0
Pathways in cancer	3/531	0.111084024	0.193501203	0
Mineral absorption	21916	0.123957374	0.206002577	0
Arachidonic acid metabolism	22282	0.125890464	0.206002577	0
Central carbon metabolism in cancer	25569	0.143101727	0.227279213	0
Thyroid hormone synthesis	27395	0.152519968	0.235316522	0
RNA degradation	28856	0.159981653	0.23997248	0
ErbB signaling pathway	31048	0.171053944	0.249646297	0
PI3K-Akt signaling pathway	2/354	0.18279147	0.259756299	0
T cell receptor signaling pathway	1/104	0.205183503	0.276997729	0
Toll-like receptor signaling pathway	1/104	0.205183503	0.276997729	0
HIF-1 signaling pathway	1/109	0.213934262	0.281767077	0
Cellular senescence	1/156	0.291720968	0.374248274	0
Wnt signaling pathway	1/166	0.307273296	0.374248274	0
Hepatocellular carcinoma	1/168	0.310343467	0.374248274	0

Tight junction	1/169	0.311873561	0.374248274	0
Tuberculosis	1/180	0.328487172	0.380832613	0
Axon guidance	1/182	0.331465423	0.380832613	0
Neutrophil extracellular trap formation	1/189	0.341787991	0.38451149	0
Pathogenic Escherichia coli infection	1/197	0.353394548	0.389455216	0
Coronavirus disease	1/232	0.40186473	0.434013908	0
Shigellosis	1/246	0.420242152	0.444962279	0
MicroRNAs in cancer	1/310	0.497462585	0.516595761	0
Alzheimer disease	1/369	0.55968767	0.570247814	0
Pathways of neurodegeneration	1/475	0.653114095	0.653114095	0

Old Adjusted P-value	Odds Ratio	Combined Score	Genes
0	36.16185605	958.3708381	DNAJA1;DNAJB1;HSPA8;HSP90AA1;HSP90AB1;HSPH1;H
0	43.60526316	777.2496125	HSPA8;HSP90AA1;HSP90AB1;HSPA1L;HSPA4;HSPA1A
0	17.96205821	264.1123097	HSPA8;HSP90AA1;HSP90AB1;HSPA1L;HSPA4;HSPD1;HSI
0	23.89513861	345.4104961	HSPA8;HSP90AA1;HSP90AB1;HSPA1L;FKBP4;HSPA1A
0	37.55283019	443.6960181	HSPA8;HSPA1L;HSPD1;HSPA1A
0	14.68222222	122.1057896	HSPA8;HSPA1L;TLR7;HSPA1A
0	14.67627494	95.77212406	HSPA8;HSPA1L;HSPA1A
0	13.32311479	83.37178811	HSPA8;HSPA1L;HSPA1A
0	7.318587361	42.50984668	STIP1;HSPA8;HSPA1L;HSPA1A
0	10.66355811	60.20318423	HSP90AA1;HSP90AB1;HMOX1
0	9.860129418	53.5639389	HSPA8;HSPA1L;HSPA1A
0	9.287054409	48.94403594	HSP90AA1;HSP90AB1;PPID
0	6.114096734	25.4502821	HSP90AA1;HSP90AB1;PTGES3
0	5.791066706	23.29560684	HSPA8;HSPA1L;HSPA1A
0	10.2815735	41.19701054	HSP90AA1;HSP90AB1
0	9.955388471	39.30248946	HSP90AA1;HSP90AB1
0	9.649173955	37.54277574	HSP90AA1;HSP90AB1
0	9.002721088	33.89043064	HSP90AA1;HSP90AB1
0	4.944681921	17.90929615	HSPA8;HSPA1L;HSPA1A
0	5.542296919	16.07741891	DNAJB1;TLR7
0	17.82647585	50.82895022	ACOT7
0	17.82647585	50.82895022	ACOT7
0	5.261239691	14.78858366	HSP90AA1;HSP90AB1
0	14.47965116	38.47302036	TIGAR
0	11.57906977	28.35113154	HMOX1
0	11.02657807	26.49659809	HSPD1
0	11.02657807	26.49659809	HMOX1
0	3.799691537	8.601534035	HSP90AA1;HSP90AB1
0	9.448030375	21.34849709	P4HA1
0	9.448030375	21.34849709	PDIA4
0	2.692350333	5.916354752	HSP90AA1;HSP90AB1;HMOX1
0	7.842727631	16.37418424	HMOX1
0	7.711627907	15.98113875	PTGES3
0	6.70273003	13.03144454	TIGAR
0	6.248271527	11.74962315	PDIA4
0	5.926654741	10.86175725	HSPD1
0	5.50166113	9.714702878	NCK2
0	2.652056277	4.50692906	HSP90AA1;HSP90AB1
0	4.482501693	7.099612841	NCK2
0	4.482501693	7.099612841	TLR7
0	4.273901809	6.590726271	HMOX1
0	2.970892723	3.66001364	PPID
0	2.789429175	3.291575837	CACYBP
0	2.755744325	3.2244293	HMOX1

0	2.739202658	3.191602316	HSPA4
0	2.56944264	2.860451269	HSPD1
0	2.540794038	2.805625525	NCK2
0	2.445324097	2.62521349	TLR7
0	2.344565733	2.438747281	NCK2
0	1.985804893	1.810338655	TLR7
0	1.871001424	1.622016378	PPID
0	1.478663355	1.032454406	HMOX1
0	1.237866532	0.718428501	PPID
0	0.955843391	0.407192573	PPID

SPA1L;HSPA4L;PDIA4;HSPA1A

Supplementary File S6: Comprehensive details of the results of functional enrichment analysis

BP	Term	Overlap	P-value
	positive regulation of transcription, DNA-templated (GO:0045893)	68/1183	2.89E-14
	positive regulation of transcription by RNA polymerase II (GO:0045944)	54/908	4.93E-12
	regulation of transcription by RNA polymerase II (GO:0006357)	95/2206	5.01E-12
	regulation of transcription, DNA-templated (GO:0006355)	93/2244	7.43E-11
	histone H3-K4 monomethylation (GO:0097692)	44720	2.24E-09
	histone H3-K4 methylation (GO:0051568)	44834	7.06E-09
	histone H3-K4 dimethylation (GO:0044648)	44688	8.09E-08
	negative regulation of transcription, DNA-templated (GO:0045892)	46/948	1.16E-07
	regulation of myeloid cell differentiation (GO:0045637)	25143	1.61E-07
	histone H3-K4 trimethylation (GO:0080182)	44726	2.15E-07
	positive regulation of nucleic acid-templated transcription (GO:1903508	30/511	4.56E-07
	negative regulation of transcription by RNA polymerase II (GO:0000122)	35/684	1.26E-06
	regulation of megakaryocyte differentiation (GO:0045652)	19968	1.68E-06
	peptidyl-lysine trimethylation (GO:0018023)	44772	2.30E-06
	regulation of cellular macromolecule biosynthetic process (GO:2000112	27/468	2.41E-06
	regulation of nucleic acid-templated transcription (GO:1903506)	25/430	4.98E-06
	peptidyl-lysine dimethylation (GO:0018027)	44700	3.64E-05
	regulation of intracellular signal transduction (GO:1902531)	23/437	5.65E-05
	histone lysine methylation (GO:0034968)	12571	6.76E-05
	regulation of gene expression (GO:0010468)	42/1079	9.07E-05
	cardiac cell development (GO:0055006)	44664	1.18E-04
	epiboly involved in wound healing (GO:0090505)	44667	2.86E-04
	phosphorylation (GO:0016310)	20/400	3.33E-04
	posttranscriptional regulation of gene expression (GO:0010608)	16954	3.81E-04
	skeletal myofibril assembly (GO:0014866)	44628	4.76E-04
	tRNA transcription (GO:0009304)	44628	4.76E-04
	regulation of cellular component organization (GO:0051128)	10/139	7.20E-04
	negative regulation of nucleic acid-templated transcription (GO:190350	21/464	8.74E-04
	regulation of androgen receptor signaling pathway (GO:0060765)	13271	8.79E-04
	regulation of p38MAPK cascade (GO:1900744)	13636	9.99E-04
	monocarboxylic acid transport (GO:0015718)	20972	0.001215459
	regulation of transforming growth factor beta receptor signaling pathwa	8/100	0.001223062
	regulation of autophagy (GO:0010506)	13/231	0.001257346
	transcription by RNA polymerase II (GO:0006366)	16/320	0.001280045
	negative regulation of homotypic cell-cell adhesion (GO:0034111)	44631	0.001338196
	negative regulation of cellular macromolecule biosynthetic process (GO:	23/547	0.00135002
	cardiac muscle cell differentiation (GO:0055007)	44675	0.001459879
	wound healing, spreading of cells (GO:0044319)	44675	0.001459879
	positive regulation of p38MAPK cascade (GO:1900745)	44675	0.001459879
	regulation of alcohol biosynthetic process (GO:1902930)	44632	0.001756589
	negative regulation of gene silencing by miRNA (GO:0060965)	44632	0.001756589
	regulation of neurogenesis (GO:0050767)	22798	0.001886051
	protein phosphorylation (GO:0006468)	21/496	0.001982124
	regulation of actomyosin structure organization (GO:0110020)	44633	0.002248187

microtubule bundle formation (GO:0001578)	16558	0.002441803
transforming growth factor beta receptor signaling pathway (GO:00071	32690	0.002692384
negative regulation of TORC1 signaling (GO:1904262)	44634	0.002817046
DNA-templated transcription, initiation (GO:0006352)	10/168	0.002976937
regulation of lipid metabolic process (GO:0019216)	33786	0.00324526
regulation of mitochondrion organization (GO:0010821)	17654	0.003251202
histone H4 acetylation (GO:0043967)	17654	0.003251202
negative regulation of androgen receptor signaling pathway (GO:00607	44635	0.003466868
negative regulation of leukocyte mediated cytotoxicity (GO:0001911)	44635	0.003466868
hemopoiesis (GO:0030097)	34516	0.003659324
histone acetylation (GO:0016573)	26085	0.003753662
regulation of growth rate (GO:0040009)	44597	0.004218591
regulation of homophilic cell adhesion (GO:1903385)	44597	0.004218591
regulation of microglial cell mediated cytotoxicity (GO:1904149)	44597	0.004218591
Roundabout signaling pathway (GO:0035385)	44597	0.004218591
insulin metabolic process (GO:1901142)	44597	0.004218591
transcription initiation from RNA polymerase III promoter (GO:0006384)	44597	0.004218591
regulation of cell migration involved in sprouting angiogenesis (GO:0090	11780	0.004329303
negative regulation of intracellular steroid hormone receptor signaling p	11780	0.004329303
regulation of histone acetylation (GO:0035065)	12145	0.004846067
pulmonary valve morphogenesis (GO:0003184)	44637	0.00502254
cell-substrate junction assembly (GO:0007044)	12510	0.005402665
negative regulation of blood vessel endothelial cell migration (GO:00435	12510	0.005402665
regulation of signal transduction by p53 class mediator (GO:1901796)	9/156	0.005790318
pulmonary valve development (GO:0003177)	44638	0.005934169
regulation of production of miRNAs involved in gene silencing by miRNA	44638	0.005934169
rRNA transcription (GO:0009303)	44638	0.005934169
regulation of TORC1 signaling (GO:1903432)	12875	0.006000408
5S class rRNA transcription by RNA polymerase III (GO:0042791)	44598	0.006240179
skeletal muscle thin filament assembly (GO:0030240)	44598	0.006240179
megakaryocyte development (GO:0035855)	44598	0.006240179
mRNA 3'-splice site recognition (GO:0000389)	44598	0.006240179
negative regulation of chemokine-mediated signaling pathway (GO:007	44598	0.006240179
negative regulation of glial cell proliferation (GO:0060253)	44598	0.006240179
negative regulation of myeloid leukocyte mediated immunity (GO:00028	44598	0.006240179
DNA damage response, signal transduction by p53 class mediator resulti	20576	0.006328838
protein autophosphorylation (GO:0046777)	9/159	0.006538724
platelet aggregation (GO:0070527)	13241	0.006640567
atrioventricular valve morphogenesis (GO:0003181)	44639	0.006938351
regulation of autophagy of mitochondrion (GO:1903146)	44639	0.006938351
transmembrane receptor protein serine/threonine kinase signaling path	8/133	0.007105802
transcription, DNA-templated (GO:0006351)	11/221	0.007246495
regulation of erythrocyte differentiation (GO:0045646)	13606	0.007324371
regulation of intracellular steroid hormone receptor signaling pathway (	13606	0.007324371
fat cell differentiation (GO:0045444)	21306	0.007338286
negative regulation of transmembrane receptor protein serine/threonin	7/108	0.007777527
early endosome to late endosome transport (GO:0045022)	44640	0.008037249

granulocyte differentiation (GO:0030851)	44640	0.008037249
post-transcriptional gene silencing by RNA (GO:0035194)	44640	0.008037249
negative regulation of TOR signaling (GO:0032007)	13971	0.008053004
negative regulation of macromolecule metabolic process (GO:0010605)	10/194	0.008093809
ubiquitin-dependent protein catabolic process (GO:0006511)	15/354	0.008230538
negative regulation of gene expression (GO:0010629)	14/322	0.00848245
definitive hemopoiesis (GO:0060216)	44599	0.008615372
delamination (GO:0060232)	44599	0.008615372
regulation of transcription from RNA polymerase II promoter involved in	44599	0.008615372
tRNA transcription by RNA polymerase III (GO:0042797)	44599	0.008615372
negative regulation of protein kinase activity by regulation of protein ph	44599	0.008615372
protein monoubiquitination (GO:0006513)	14336	0.008827605
protein acylation (GO:0043543)	14336	0.008827605
regulation of Ras protein signal transduction (GO:0046578)	31564	0.009490685
transcription initiation from RNA polymerase II promoter (GO:0006367)	8/140	0.009552801
cellular response to transforming growth factor beta stimulus (GO:0071	7/114	0.010323284
negative regulation of cell-cell adhesion (GO:0022408)	15067	0.01051904
regulation of response to cytokine stimulus (GO:0060759)	44642	0.010526544
regulation of transcription initiation from RNA polymerase II promoter (	23498	0.011030261
mRNA processing (GO:0006397)	13/300	0.011254259
cytosolic transport (GO:0016482)	7/116	0.011292965
regulation of chemokine-mediated signaling pathway (GO:0070099)	44600	0.011328497
cardiac muscle hypertrophy (GO:0003300)	44600	0.011328497
regulation of pattern recognition receptor signaling pathway (GO:00622	44600	0.011328497
SREBP signaling pathway (GO:0032933)	44600	0.011328497
peptidyl-serine autophosphorylation (GO:0036289)	44600	0.011328497
positive regulation of chromosome segregation (GO:0051984)	44600	0.011328497
positive regulation of muscle contraction (GO:0045933)	44600	0.011328497
histone H3 acetylation (GO:0043966)	15432	0.011437919
positive regulation of autophagy (GO:0010508)	33025	0.011726524
mitotic G1 DNA damage checkpoint signaling (GO:0031571)	23863	0.011749087
glycerophospholipid biosynthetic process (GO:0046474)	9/177	0.012696617
positive regulation of developmental process (GO:0051094)	9/177	0.012696617
cardiac muscle cell development (GO:0055013)	44644	0.013414304
phospholipid catabolic process (GO:0009395)	44644	0.013414304
homotypic cell-cell adhesion (GO:0034109)	16163	0.013426748
negative regulation of transforming growth factor beta receptor signalin	24959	0.014094996
adult heart development (GO:0007512)	44601	0.014364383
bone cell development (GO:0098751)	44601	0.014364383
cellular response to sterol depletion (GO:0071501)	44601	0.014364383
regulation of mammary gland epithelial cell proliferation (GO:0033599)	44601	0.014364383
epithelial cell apoptotic process (GO:1904019)	44601	0.014364383
regulation of sterol biosynthetic process (GO:0106118)	44601	0.014364383
skeletal muscle fiber development (GO:0048741)	44601	0.014364383
mitral valve morphogenesis (GO:0003183)	44601	0.014364383
negative regulation of leukocyte degranulation (GO:0043301)	44601	0.014364383
negative regulation of platelet aggregation (GO:0090331)	44601	0.014364383

positive regulation of smooth muscle contraction (GO:0045987)	44601	0.014364383
positive regulation of synapse maturation (GO:0090129)	44601	0.014364383
regulation of pri-miRNA transcription by RNA polymerase II (GO:190289	16528	0.014498453
cellular response to hexose stimulus (GO:0071331)	44645	0.015010427
cellular response to organic substance (GO:0071310)	7/123	0.015208016
regulation of cellular protein localization (GO:1903827)	16893	0.01562277
organelle organization (GO:0006996)	16/420	0.016568861
myeloid leukocyte differentiation (GO:0002573)	26054	0.01673666
negative regulation of cold-induced thermogenesis (GO:0120163)	17258	0.016800453
phosphatidylinositol biosynthetic process (GO:0006661)	7/126	0.01715037
peptidyl-serine phosphorylation (GO:0018105)	8/156	0.017432491
RNA splicing, via transesterification reactions with bulged adenosine as r	11/251	0.017484895
positive regulation of neurogenesis (GO:0050769)	26420	0.017685366
adherens junction assembly (GO:0034333)	44602	0.017708343
regulation of granulocyte differentiation (GO:0030852)	44602	0.017708343
regulation of peptidyl-lysine acetylation (GO:2000756)	44602	0.017708343
response to laminar fluid shear stress (GO:0034616)	44602	0.017708343
negative regulation of cell-cell adhesion mediated by cadherin (GO:2000	44602	0.017708343
positive regulation of T cell apoptotic process (GO:0070234)	44602	0.017708343
positive regulation of stress-activated MAPK cascade (GO:0032874)	36312	0.018065326
cellular senescence (GO:0090398)	44647	0.018510965
positive regulation of BMP signaling pathway (GO:0030513)	44647	0.018510965
regulation of cellular localization (GO:0060341)	17989	0.019318681
DNA damage response, signal transduction by p53 class mediator (GO:0(	27150	0.019687902
bile acid and bile salt transport (GO:0015721)	44648	0.020416323
regulation of postsynapse organization (GO:0099175)	44648	0.020416323
transcription by RNA polymerase III (GO:0006383)	44648	0.020416323
protein localization to lysosome (GO:0061462)	44648	0.020416323
regulation of hematopoietic progenitor cell differentiation (GO:1901532	27515	0.020742635
cell proliferation in forebrain (GO:0021846)	44603	0.021346163
regulation of histone H3-K9 acetylation (GO:2000615)	44603	0.021346163
erythrocyte development (GO:0048821)	44603	0.021346163
regulation of synapse maturation (GO:0090128)	44603	0.021346163
Golgi to lysosome transport (GO:0090160)	44603	0.021346163
miRNA mediated inhibition of translation (GO:0035278)	44603	0.021346163
myotube cell development (GO:0014904)	44603	0.021346163
negative regulation of translation, ncRNA-mediated (GO:0040033)	44603	0.021346163
Notch signaling involved in heart development (GO:0061314)	44603	0.021346163
positive regulation of neuroblast proliferation (GO:0002052)	44603	0.021346163
regulation of BMP signaling pathway (GO:0030510)	27881	0.021833584
regulation of epithelial cell migration (GO:0010632)	18719	0.022058168
beta-catenin-TCF complex assembly (GO:1904837)	44649	0.022425404
negative regulation of BMP signaling pathway (GO:0030514)	19085	0.02351224
negative regulation of intracellular signal transduction (GO:1902532)	9/198	0.024411636
phosphatidylcholine acyl-chain remodeling (GO:0036151)	44650	0.024538249
cardiac muscle tissue development (GO:0048738)	19450	0.025023157
IRE1-mediated unfolded protein response (GO:0036498)	19450	0.025023157

positive regulation of macroautophagy (GO:0016239)	19450	0.025023157
actin crosslink formation (GO:0051764)	44604	0.025264088
regulation of hemopoiesis (GO:1903706)	44604	0.025264088
Golgi localization (GO:0051645)	44604	0.025264088
hemidesmosome assembly (GO:0031581)	44604	0.025264088
megakaryocyte differentiation (GO:0030219)	44604	0.025264088
negative regulation of production of miRNAs involved in gene silencing b	44604	0.025264088
negative regulation of NF-kappaB transcription factor activity (GO:0032(	28976	0.025327699
regulation of cell migration (GO:0030334)	15/408	0.026317251
regulation of organelle organization (GO:0033043)	29342	0.02656739
negative regulation of cellular response to growth factor stimulus (GO:0	29342	0.02656739
inorganic anion transport (GO:0015698)	19815	0.026591328
negative regulation of osteoblast differentiation (GO:0045668)	44651	0.026754742
protein acetylation (GO:0006473)	44651	0.026754742
negative regulation of cytokine-mediated signaling pathway (GO:000196	20180	0.028217114
aortic valve morphogenesis (GO:0003180)	11749	0.029074619
regulation of intracellular estrogen receptor signaling pathway (GO:003	11749	0.029074619
protein ubiquitination (GO:0016567)	18/525	0.029440699
regulation of oxidoreductase activity (GO:0051341)	44605	0.029448807
embryonic hemopoiesis (GO:0035162)	44605	0.029448807
regulation of receptor signaling pathway via STAT (GO:1904892)	44605	0.029448807
homeostasis of number of cells (GO:0048872)	44605	0.029448807
negative regulation of epidermal growth factor-activated receptor activi	44605	0.029448807
negative regulation of myotube differentiation (GO:0010832)	44605	0.029448807
positive regulation of transporter activity (GO:0032411)	44605	0.029448807
regulation of small GTPase mediated signal transduction (GO:0051056)	7/141	0.029523504
positive regulation of cellular catabolic process (GO:0031331)	7/141	0.029523504
proteasomal protein catabolic process (GO:0010498)	9/205	0.029630651
Rho protein signal transduction (GO:0007266)	20546	0.029900831
sensory organ development (GO:0007423)	20546	0.029900831
negative regulation of metabolic process (GO:0009892)	20546	0.029900831
regulation of Notch signaling pathway (GO:0008593)	30437	0.030516058
chromatin organization (GO:0006325)	7/142	0.030517428
mRNA splicing, via spliceosome (GO:0000398)	11/274	0.030737283
regulation of macroautophagy (GO:0016241)	6/112	0.030849913
phosphatidylinositol metabolic process (GO:0046488)	6/112	0.030849913
muscle cell development (GO:0055001)	12114	0.031497479
activation of protein kinase activity (GO:0032147)	6/114	0.033232568
histone modification (GO:0016570)	6/114	0.033232568
protein localization to vacuole (GO:0072665)	44606	0.033887443
atrioventricular valve development (GO:0003171)	44606	0.033887443
regulation of chromatin organization (GO:1902275)	44606	0.033887443
smooth muscle contraction (GO:0006939)	44606	0.033887443
monoacylglycerol metabolic process (GO:0046462)	44606	0.033887443
ncRNA transcription (GO:0098781)	44606	0.033887443
negative regulation of cell migration involved in sprouting angiogenesis	44606	0.033887443
negative regulation of DNA-templated transcription, elongation (GO:003	44606	0.033887443

negative regulation of pri-miRNA transcription by RNA polymerase II (GC	44606	0.033887443
cellular response to vascular endothelial growth factor stimulus (GO:003	12479	0.034022788
positive regulation of pri-miRNA transcription by RNA polymerase II (GO	12479	0.034022788
positive regulation of DNA-binding transcription factor activity (GO:0051	10/246	0.035638117
Notch signaling pathway (GO:0007219)	22007	0.037219662
negative regulation of multicellular organismal process (GO:0051241)	9/214	0.037426228
regulation of extracellular matrix organization (GO:1903053)	44607	0.038567541
clathrin coat assembly (GO:0048268)	44607	0.038567541
positive regulation of membrane protein ectodomain proteolysis (GO:0(	44607	0.038567541
B cell differentiation (GO:0030183)	22372	0.039196136
regulation of DNA-templated transcription, initiation (GO:2000142)	22372	0.039196136
regulation of endocytosis (GO:0030100)	22372	0.039196136
brain development (GO:0007420)	7/150	0.039284598
aortic valve development (GO:0003176)	13210	0.039378014
intrinsic apoptotic signaling pathway by p53 class mediator (GO:007233	13210	0.039378014
positive regulation of innate immune response (GO:0045089)	13210	0.039378014
negative regulation of protein kinase activity (GO:0006469)	32994	0.041102734
actin filament organization (GO:0007015)	7/152	0.041708722
regulation of stem cell differentiation (GO:2000736)	33359	0.042775056
positive regulation of transport (GO:0051050)	33359	0.042775056
positive regulation of viral process (GO:0048524)	23102	0.043325673
regulation of activin receptor signaling pathway (GO:0032925)	44608	0.043477053
transepithelial transport (GO:0070633)	44608	0.043477053
negative regulation of natural killer cell mediated cytotoxicity (GO:0045	44608	0.043477053
negative regulation of platelet activation (GO:0010544)	44608	0.043477053
positive regulation of transmembrane receptor protein serine/threonine	33725	0.044487804
negative regulation of endothelial cell migration (GO:0010596)	13940	0.045133709
positive regulation of cell development (GO:0010720)	13940	0.045133709
regulation of intracellular transport (GO:0032386)	14305	0.048159221
regulation of peptidyl-threonine phosphorylation (GO:0010799)	14305	0.048159221
regulation of protein targeting to mitochondrion (GO:1903214)	14305	0.048159221
regulation of receptor-mediated endocytosis (GO:0048259)	14305	0.048159221
replication fork processing (GO:0031297)	14305	0.048159221
positive regulation of intracellular transport (GO:0032388)	14305	0.048159221
regulation of cholesterol biosynthetic process (GO:0045540)	44609	0.04860433
cell surface receptor signaling pathway involved in heart development (	44609	0.04860433
regulation of Golgi organization (GO:1903358)	44609	0.04860433
regulation of neuroblast proliferation (GO:1902692)	44609	0.04860433
stabilization of membrane potential (GO:0030322)	44609	0.04860433
vasculature development (GO:0001944)	44609	0.04860433
muscle tissue morphogenesis (GO:0060415)	44609	0.04860433
negative regulation of fatty acid metabolic process (GO:0045922)	44609	0.04860433
positive regulation of telomere capping (GO:1904355)	44609	0.04860433
positive regulation of transcription of Notch receptor target (GO:000722	44609	0.04860433
regulation of cell cycle (GO:0051726)	11/296	0.048987959
cellular response to starvation (GO:0009267)	7/158	0.049555482
mRNA metabolic process (GO:0016071)	34820	0.049869504

cellular response to nutrient levels (GO:0031669)	24198	0.049960898
protein modification by small protein conjugation (GO:0032446)	14/409	0.05123276
organic hydroxy compound transport (GO:0015850)	14671	0.051281654
regulation of epidermal growth factor receptor signaling pathway (GO:0	24563	0.05228979
regulation of early endosome to late endosome transport (GO:2000641)	44610	0.053938108
regulation of platelet aggregation (GO:0090330)	44610	0.053938108
endothelial cell proliferation (GO:0001935)	44610	0.053938108
G protein-coupled acetylcholine receptor signaling pathway (GO:000721	44610	0.053938108
interleukin-6-mediated signaling pathway (GO:0070102)	44610	0.053938108
negative regulation of Rho protein signal transduction (GO:0035024)	44610	0.053938108
phosphatidylglycerol acyl-chain remodeling (GO:0036148)	44610	0.053938108
positive regulation of cell migration involved in sprouting angiogenesis (	44610	0.053938108
regulation of cell development (GO:0060284)	15036	0.054499759
response to growth factor (GO:0070848)	15036	0.054499759
JNK cascade (GO:0007254)	15036	0.054499759
apoptotic process (GO:0006915)	9/231	0.055744052
regulation of primary metabolic process (GO:0080090)	6/130	0.056584563
positive regulation of MAP kinase activity (GO:0043406)	25294	0.0571222
central nervous system development (GO:0007417)	10/268	0.057425365
phosphatidylinositol phosphate biosynthetic process (GO:0046854)	15401	0.057812212
positive regulation of epithelial to mesenchymal transition (GO:0010718	15401	0.057812212
positive regulation of cell migration (GO:0030335)	10/269	0.058585226
activin receptor signaling pathway (GO:0032924)	44611	0.059467499
regulation of cell-cell adhesion mediated by cadherin (GO:2000047)	44611	0.059467499
cardiac atrium morphogenesis (GO:0003209)	44611	0.059467499
regulation of epithelial cell differentiation (GO:0030856)	44611	0.059467499
regulation of histone H3-K4 methylation (GO:0051569)	44611	0.059467499
glycerolipid catabolic process (GO:0046503)	44611	0.059467499
histone H4-K16 acetylation (GO:0043984)	44611	0.059467499
striated muscle cell differentiation (GO:0051146)	44611	0.059467499
negative regulation of nervous system development (GO:0051961)	44611	0.059467499
negative regulation of RNA metabolic process (GO:0051253)	44611	0.059467499
negative regulation of striated muscle cell differentiation (GO:0051154)	44611	0.059467499
positive regulation of cell-substrate adhesion (GO:0010811)	25659	0.059625222
organic acid transport (GO:0015849)	5/100	0.059653091
regulation of cell-cell adhesion (GO:0022407)	15766	0.061217617
regulation of cell-substrate adhesion (GO:0010810)	15766	0.061217617
cellular glucose homeostasis (GO:0001678)	15766	0.061217617
cellular response to glucose starvation (GO:0042149)	15766	0.061217617
DNA-dependent DNA replication maintenance of fidelity (GO:0045005)	15766	0.061217617
regulation of cell motility (GO:2000145)	6/133	0.061835376
regulation of hematopoietic stem cell differentiation (GO:1902036)	26024	0.062185736
regulation of TOR signaling (GO:0032006)	26024	0.062185736
regulation of protein catabolic process (GO:0042176)	5/102	0.063851276
positive regulation of vasculature development (GO:1904018)	5/102	0.063851276
mRNA catabolic process (GO:0006402)	16132	0.064714514
negative regulation of epidermal growth factor receptor signaling pathw	16132	0.064714514

positive regulation of receptor-mediated endocytosis (GO:0048260)	16132	0.064714514
positive regulation of protein secretion (GO:0050714)	26390	0.064803407
regulation of smooth muscle contraction (GO:0006940)	44612	0.065181979
regulation of tissue remodeling (GO:0034103)	44612	0.065181979
skeletal muscle contraction (GO:0003009)	44612	0.065181979
myeloid cell development (GO:0061515)	44612	0.065181979
positive regulation of G2/M transition of mitotic cell cycle (GO:0010971)	44612	0.065181979
positive regulation of protein processing (GO:0010954)	44612	0.065181979
protein localization to plasma membrane (GO:0072659)	6/136	0.067365235
regulation of Rho protein signal transduction (GO:0035023)	26755	0.06747787
mRNA transport (GO:0051028)	5/104	0.068211438
regulation of receptor signaling pathway via JAK-STAT (GO:0046425)	16497	0.068301379
positive regulation of nervous system development (GO:0051962)	16497	0.068301379
positive regulation of RNA metabolic process (GO:0051254)	16497	0.068301379
protein deacetylation (GO:0006476)	16497	0.068301379
regulation of cytokine-mediated signaling pathway (GO:0001959)	27120	0.070208728
regulation of JNK cascade (GO:0046328)	5/105	0.070452
beta-catenin destruction complex disassembly (GO:1904886)	44613	0.071071377
regulation of cardiac muscle cell proliferation (GO:0060043)	44613	0.071071377
regulation of cholesterol metabolic process (GO:0090181)	44613	0.071071377
cellular response to estradiol stimulus (GO:0071392)	44613	0.071071377
focal adhesion assembly (GO:0048041)	44613	0.071071377
intrinsic apoptotic signaling pathway in response to DNA damage by p53	44613	0.071071377
negative regulation of peptidyl-serine phosphorylation (GO:0033137)	44613	0.071071377
neuron apoptotic process (GO:0051402)	44613	0.071071377
positive regulation of transcription from RNA polymerase II promoter in	44613	0.071071377
positive regulation of vascular associated smooth muscle cell proliferati	44613	0.071071377
response to amino acid starvation (GO:1990928)	27485	0.072995553
integrin-mediated signaling pathway (GO:0007229)	27485	0.072995553
protein localization to cell periphery (GO:1990778)	6/140	0.075171897
regulation of DNA binding (GO:0051101)	17227	0.075738651
histone deacetylation (GO:0016575)	17227	0.075738651
chloride transport (GO:0006821)	27851	0.075837886
regulation of centrosome cycle (GO:0046605)	44614	0.077125868
regulation of membrane protein ectodomain proteolysis (GO:0051043)	44614	0.077125868
regulation of voltage-gated calcium channel activity (GO:1901385)	44614	0.077125868
negative regulation of small molecule metabolic process (GO:0062014)	44614	0.077125868
peptidyl-threonine dephosphorylation (GO:0035970)	44614	0.077125868
positive regulation of DNA-templated transcription, initiation (GO:20001	44614	0.077125868
positive regulation of neural precursor cell proliferation (GO:2000179)	44614	0.077125868
proteasome-mediated ubiquitin-dependent protein catabolic process (G	11/321	0.077324951
phosphate-containing compound metabolic process (GO:0006796)	8/212	0.0794311
positive regulation of blood vessel endothelial cell migration (GO:00435	17593	0.07958575
positive regulation of endocytosis (GO:0045807)	17593	0.07958575
regulation of protein ubiquitination (GO:0031396)	5/109	0.079814136
lipid transport (GO:0006869)	5/109	0.079814136
negative regulation of DNA-binding transcription factor activity (GO:004	6/143	0.081350494

response to endoplasmic reticulum stress (GO:0034976)	5/110	0.082253773
blood vessel endothelial cell migration (GO:0043534)	44615	0.083335957
regulation of peptidase activity (GO:0052547)	44615	0.083335957
regulation of telomere capping (GO:1904353)	44615	0.083335957
negative regulation of phosphoprotein phosphatase activity (GO:00325	44615	0.083335957
positive regulation of cell cycle G2/M phase transition (GO:1902751)	44615	0.083335957
positive regulation of JUN kinase activity (GO:0043507)	44615	0.083335957
positive regulation of transcription initiation from RNA polymerase II pr	44615	0.083335957
protein deacylation (GO:0035601)	44615	0.083335957
adherens junction organization (GO:0034332)	17958	0.083516215
protein stabilization (GO:0050821)	7/179	0.084006667
regulation of cellular component movement (GO:0051270)	18323	0.087528286
neuron migration (GO:0001764)	18323	0.087528286
positive regulation of cell morphogenesis involved in differentiation (GO	18323	0.087528286
regulation of NIK/NF-kappaB signaling (GO:1901222)	29312	0.087752191
canonical glycolysis (GO:0061621)	44616	0.089692478
glucose catabolic process to pyruvate (GO:0061718)	44616	0.089692478
negative regulation of lipid metabolic process (GO:0045833)	44616	0.089692478
negative regulation of ossification (GO:0030279)	44616	0.089692478
negative regulation of protein tyrosine kinase activity (GO:0061099)	44616	0.089692478
positive regulation of cellular response to transforming growth factor be	44616	0.089692478
positive regulation of neuron apoptotic process (GO:0043525)	44616	0.089692478
positive regulation of phospholipase activity (GO:0010518)	44616	0.089692478
positive regulation of transcription from RNA polymerase II promoter in	44616	0.089692478
positive regulation of transforming growth factor beta receptor signaling	44616	0.089692478
nervous system development (GO:0007399)	14/447	0.090361754
phospholipase C-activating G protein-coupled receptor signaling pathwa	29677	0.090864247
regulation of substrate adhesion-dependent cell spreading (GO:190002	18688	0.091620171
positive regulation of fat cell differentiation (GO:0045600)	18688	0.091620171
response to lipid (GO:0033993)	5/114	0.092402357
positive regulation of cellular component organization (GO:0051130)	5/114	0.092402357
regulation of gene expression, epigenetic (GO:0040029)	30042	0.094028505
positive regulation of cell differentiation (GO:0045597)	9/258	0.09520065
positive regulation of cell motility (GO:2000147)	8/221	0.095259512
myeloid cell differentiation (GO:0030099)	19054	0.095790048
positive regulation of protein localization to cell periphery (GO:1904377	19054	0.095790048
regulation of epidermal cell differentiation (GO:0045604)	44617	0.096186575
regulation of myotube differentiation (GO:0010830)	44617	0.096186575
regulation of protein processing (GO:0070613)	44617	0.096186575
glycolytic process through glucose-6-phosphate (GO:0061620)	44617	0.096186575
negative regulation of cellular carbohydrate metabolic process (GO:001	44617	0.096186575
peptide catabolic process (GO:0043171)	44617	0.096186575
phosphatidylglycerol metabolic process (GO:0046471)	44617	0.096186575
positive regulation of DNA-templated transcription, elongation (GO:003	44617	0.096186575
positive regulation of ERBB signaling pathway (GO:1901186)	44617	0.096186575
positive regulation of peptidyl-threonine phosphorylation (GO:0010800)	44617	0.096186575
regulation of osteoblast differentiation (GO:0045667)	30407	0.097244327

positive regulation of angiogenesis (GO:0045766)	5/116	0.097707135
positive regulation of NIK/NF-kappaB signaling (GO:1901224)	19419	0.100036064
positive regulation of cell projection organization (GO:0031346)	5/117	0.100416163
lymphocyte differentiation (GO:0030098)	30773	0.100511056
protein localization to site of double-strand break (GO:1990166)	44566	0.100690974
protein retention in Golgi apparatus (GO:0045053)	44566	0.100690974
regulation of adherens junction organization (GO:1903391)	44566	0.100690974
regulation of antifungal innate immune response (GO:1905034)	44566	0.100690974
beta-catenin destruction complex assembly (GO:1904885)	44566	0.100690974
cardiac endothelial cell differentiation (GO:0003348)	44566	0.100690974
cardiac muscle cell myoblast differentiation (GO:0060379)	44566	0.100690974
regulation of chromosome separation (GO:1905818)	44566	0.100690974
regulation of cysteine-type endopeptidase activity involved in execution	44566	0.100690974
regulation of glial cell migration (GO:1903975)	44566	0.100690974
regulation of hippocampal neuron apoptotic process (GO:0110089)	44566	0.100690974
regulation of low-density lipoprotein particle receptor catabolic process	44566	0.100690974
coronary artery morphogenesis (GO:0060982)	44566	0.100690974
regulation of metaphase plate congression (GO:0090235)	44566	0.100690974
regulation of miRNA catabolic process (GO:2000625)	44566	0.100690974
regulation of mitophagy (GO:1901524)	44566	0.100690974
regulation of myoblast proliferation (GO:2000291)	44566	0.100690974
regulation of neutrophil degranulation (GO:0043313)	44566	0.100690974
regulation of nucleotide-binding oligomerization domain containing sign	44566	0.100690974
dorsal/ventral axis specification (GO:0009950)	44566	0.100690974
regulation of plasma membrane organization (GO:1903729)	44566	0.100690974
regulation of platelet-derived growth factor receptor-beta signaling patl	44566	0.100690974
endocardial cell differentiation (GO:0060956)	44566	0.100690974
endodermal cell fate specification (GO:0001714)	44566	0.100690974
endothelial cell apoptotic process (GO:0072577)	44566	0.100690974
ethanolamine-containing compound metabolic process (GO:0042439)	44566	0.100690974
extracellular exosome biogenesis (GO:0097734)	44566	0.100690974
regulation of triglyceride metabolic process (GO:0090207)	44566	0.100690974
glutathione transport (GO:0034635)	44566	0.100690974
rescue of stalled ribosome (GO:0072344)	44566	0.100690974
response to fructose (GO:0009750)	44566	0.100690974
retina vasculature development in camera-type eye (GO:0061298)	44566	0.100690974
toll-like receptor 2 signaling pathway (GO:0034134)	44566	0.100690974
mRNA cleavage (GO:0006379)	44566	0.100690974
mRNA cleavage involved in gene silencing by miRNA (GO:0035279)	44566	0.100690974
N-acylethanolamine metabolic process (GO:0070291)	44566	0.100690974
negative regulation of anion transmembrane transport (GO:1903960)	44566	0.100690974
negative regulation of CD4-positive, alpha-beta T cell differentiation (GC	44566	0.100690974
negative regulation of ceramide biosynthetic process (GO:1900060)	44566	0.100690974
negative regulation of gene silencing by RNA (GO:0060967)	44566	0.100690974
negative regulation of histone H4 acetylation (GO:0090241)	44566	0.100690974
negative regulation of posttranscriptional gene silencing (GO:0060149)	44566	0.100690974
negative regulation of protein acetylation (GO:1901984)	44566	0.100690974

negative regulation of sphingolipid biosynthetic process (GO:0090155)	44566	0.100690974
negative regulation of transcription by RNA polymerase I (GO:0016479)	44566	0.100690974
negative regulation of transforming growth factor beta1 production (GO	44566	0.100690974
non-canonical Wnt signaling pathway via MAPK cascade (GO:0038030)	44566	0.100690974
peripheral nervous system neuron differentiation (GO:0048934)	44566	0.100690974
positive regulation of AMPA receptor activity (GO:2000969)	44566	0.100690974
positive regulation of attachment of spindle microtubules to kinetochor	44566	0.100690974
positive regulation of CD8-positive, alpha-beta T cell differentiation (GO	44566	0.100690974
positive regulation of mononuclear cell proliferation (GO:0032946)	44566	0.100690974
positive regulation of neutrophil extravasation (GO:2000391)	44566	0.100690974
positive regulation of nucleotide-binding oligomerization domain contai	44566	0.100690974
positive regulation of protein localization to cell cortex (GO:1904778)	44566	0.100690974
positive regulation of toll-like receptor 9 signaling pathway (GO:003416	44566	0.100690974
positive regulation of transcription from RNA polymerase II promoter in	44566	0.100690974
positive regulation of transcription from RNA polymerase II promoter in	44566	0.100690974
protein localization to microtubule end (GO:1905725)	44566	0.100690974
protein localization to microtubule plus-end (GO:1904825)	44566	0.100690974
regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043122)	8/224	0.100908179
negative regulation of protein phosphorylation (GO:0001933)	6/152	0.101524864
regulation of actin filament bundle assembly (GO:0032231)	44618	0.102809702
chaperone cofactor-dependent protein refolding (GO:0051085)	44618	0.102809702
clathrin-dependent endocytosis (GO:0072583)	44618	0.102809702
regulation of regulatory T cell differentiation (GO:0045589)	44618	0.102809702
regulation of synapse organization (GO:0050807)	44618	0.102809702
TOR signaling (GO:0031929)	44618	0.102809702
negative regulation of cell development (GO:0010721)	44618	0.102809702
negative regulation of protein transport (GO:0051224)	44618	0.102809702
negative regulation of signaling receptor activity (GO:2000272)	44618	0.102809702
positive regulation of microtubule polymerization or depolymerization (	44618	0.102809702
positive regulation of viral transcription (GO:0050434)	44618	0.102809702
B cell activation (GO:0042113)	31138	0.103828013
positive regulation of protein catabolic process (GO:0045732)	31138	0.103828013
dephosphorylation (GO:0016311)	6/153	0.103915415
regulation of focal adhesion assembly (GO:0051893)	19784	0.104356346
negative regulation of cellular amide metabolic process (GO:0034249)	31503	0.1071945
cytoskeleton organization (GO:0007010)	5/120	0.108766045
positive regulation of NF-kappaB transcription factor activity (GO:00510	6/155	0.108783968
regulation of cell junction assembly (GO:1901888)	44619	0.109553606
cellular lipid catabolic process (GO:0044242)	44619	0.109553606
regulation of epidermal growth factor-activated receptor activity (GO:0(	44619	0.109553606
regulation of transcription elongation from RNA polymerase II promoter	44619	0.109553606
regulation of transcription regulatory region DNA binding (GO:2000677)	44619	0.109553606
negative regulation of catalytic activity (GO:0043086)	44619	0.109553606
positive regulation of erythrocyte differentiation (GO:0045648)	44619	0.109553606
protein-containing complex assembly (GO:0065003)	9/267	0.11124005
protein deubiquitination (GO:0016579)	9/267	0.11124005
regulation of DNA-templated transcription, elongation (GO:0032784)	44620	0.116410326

cellular response to interleukin-6 (GO:0071354)	44620	0.116410326
regulation of protein transport (GO:0051223)	44620	0.116410326
regulation of small molecule metabolic process (GO:0062012)	44620	0.116410326
glycerophospholipid catabolic process (GO:0046475)	44620	0.116410326
internal peptidyl-lysine acetylation (GO:0018393)	44620	0.116410326
ventricular septum morphogenesis (GO:0060412)	44620	0.116410326
positive regulation of cell communication (GO:0010647)	44620	0.116410326
positive regulation of microtubule polymerization (GO:0031116)	44620	0.116410326
protein localization to cell surface (GO:0034394)	44620	0.116410326
protein localization to Golgi apparatus (GO:0034067)	44620	0.116410326
regulation of anatomical structure morphogenesis (GO:0022603)	5/123	0.117442959
protein localization to membrane (GO:0072657)	7/195	0.117563893
carboxylic acid transport (GO:0046942)	20880	0.117743737
icosanoid metabolic process (GO:0006690)	20880	0.117743737
protein localization to perinuclear region of cytoplasm (GO:1905719)	44567	0.119581156
protein-DNA complex subunit organization (GO:0071824)	44567	0.119581156
regulation of adipose tissue development (GO:1904177)	44567	0.119581156
regulation of blood vessel remodeling (GO:0060312)	44567	0.119581156
cell junction disassembly (GO:0150146)	44567	0.119581156
regulation of hepatocyte proliferation (GO:2000345)	44567	0.119581156
regulation of mast cell chemotaxis (GO:0060753)	44567	0.119581156
regulation of neutrophil extravasation (GO:2000389)	44567	0.119581156
regulation of nucleotide-binding oligomerization domain containing 2 si	44567	0.119581156
double-strand break repair via classical nonhomologous end joining (GO	44567	0.119581156
regulation of pro-B cell differentiation (GO:2000973)	44567	0.119581156
regulation of protein targeting (GO:1903533)	44567	0.119581156
regulation of sarcomere organization (GO:0060297)	44567	0.119581156
foam cell differentiation (GO:0090077)	44567	0.119581156
regulation of thymocyte apoptotic process (GO:0070243)	44567	0.119581156
glomerular epithelial cell differentiation (GO:0072311)	44567	0.119581156
renal filtration cell differentiation (GO:0061318)	44567	0.119581156
response to manganese ion (GO:0010042)	44567	0.119581156
histone H3-K36 methylation (GO:0010452)	44567	0.119581156
intracellular pH elevation (GO:0051454)	44567	0.119581156
striated muscle hypertrophy (GO:0014897)	44567	0.119581156
macrophage derived foam cell differentiation (GO:0010742)	44567	0.119581156
taurine metabolic process (GO:0019530)	44567	0.119581156
TORC2 signaling (GO:0038203)	44567	0.119581156
mitochondrial protein catabolic process (GO:0035694)	44567	0.119581156
mitochondrial ribosome assembly (GO:0061668)	44567	0.119581156
vacuole organization (GO:0007033)	44567	0.119581156
venous blood vessel morphogenesis (GO:0048845)	44567	0.119581156
xenobiotic transport across blood-brain barrier (GO:1990962)	44567	0.119581156
N-acetylneuraminate catabolic process (GO:0019262)	44567	0.119581156
negative regulation of amino acid transport (GO:0051956)	44567	0.119581156
negative regulation of erythrocyte differentiation (GO:0045647)	44567	0.119581156
negative regulation of glucocorticoid receptor signaling pathway (GO:20	44567	0.119581156

negative regulation of SMAD protein signal transduction (GO:0060392)	44567	0.119581156
peptidyl-diphthamide biosynthetic process from peptidyl-histidine (GO:(	44567	0.119581156
peptidyl-diphthamide metabolic process (GO:0017182)	44567	0.119581156
peripheral nervous system neuron development (GO:0048935)	44567	0.119581156
peroxisome proliferator activated receptor signaling pathway (GO:0035	44567	0.119581156
positive regulation of activin receptor signaling pathway (GO:0032927)	44567	0.119581156
positive regulation of autophagosome maturation (GO:1901098)	44567	0.119581156
positive regulation of autophagy of mitochondrion in response to mitocl	44567	0.119581156
positive regulation of cholesterol storage (GO:0010886)	44567	0.119581156
positive regulation of gonad development (GO:1905941)	44567	0.119581156
positive regulation of granulocyte differentiation (GO:0030854)	44567	0.119581156
positive regulation of I-kappaB phosphorylation (GO:1903721)	44567	0.119581156
positive regulation of male gonad development (GO:2000020)	44567	0.119581156
positive regulation of T cell differentiation in thymus (GO:0033089)	44567	0.119581156
positive regulation of toll-like receptor 7 signaling pathway (GO:003415	44567	0.119581156
eye development (GO:0001654)	21245	0.122341957
regulation of tumor necrosis factor-mediated signaling pathway (GO:00	21245	0.122341957
membrane lipid biosynthetic process (GO:0046467)	21245	0.122341957
aggrephagy (GO:0035973)	47150	0.123372177
regulation of actin polymerization or depolymerization (GO:0008064)	47150	0.123372177
regulation of double-strand break repair via nonhomologous end joining	47150	0.123372177
regulation of gluconeogenesis (GO:0006111)	47150	0.123372177
intrinsic apoptotic signaling pathway in response to endoplasmic reticul	47150	0.123372177
negative regulation of mRNA catabolic process (GO:1902373)	47150	0.123372177
negative regulation of myeloid leukocyte differentiation (GO:0002762)	47150	0.123372177
positive regulation of viral genome replication (GO:0045070)	47150	0.123372177
circulatory system development (GO:0072359)	5/126	0.126436915
negative regulation of growth (GO:0045926)	5/126	0.126436915
endomembrane system organization (GO:0010256)	7/199	0.126903373
selective autophagy (GO:0061912)	21610	0.127004814
Wnt signaling pathway (GO:0016055)	33695	0.12839221
protein modification by small protein removal (GO:0070646)	9/276	0.128690907
Golgi to plasma membrane protein transport (GO:0043001)	10990	0.130431747
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8	10990	0.130431747
mRNA splice site selection (GO:0006376)	10990	0.130431747
negative regulation of interleukin-1 production (GO:0032692)	10990	0.130431747
negative regulation of Notch signaling pathway (GO:0045746)	10990	0.130431747
positive regulation of small GTPase mediated signal transduction (GO:0(	10990	0.130431747
RNA methylation (GO:0001510)	21976	0.131730351
peptidyl-threonine phosphorylation (GO:0018107)	21976	0.131730351
heart development (GO:0007507)	6/164	0.132095377
cellular protein modification process (GO:0006464)	27/1025	0.13407982
regulation of neuron projection development (GO:0010975)	6/165	0.134822719
negative regulation of response to stimulus (GO:0048585)	22341	0.136516605
'de novo' posttranslational protein folding (GO:0051084)	11355	0.13758189
regulation of cellular component size (GO:0032535)	11355	0.13758189
negative regulation of peptidyl-tyrosine phosphorylation (GO:0050732)	11355	0.13758189

positive regulation of protein targeting to mitochondrion (GO:1903955)	11355	0.13758189
positive regulation of RNA splicing (GO:0033120)	11355	0.13758189
acylglycerol acyl-chain remodeling (GO:0036155)	44568	0.138075472
amino sugar catabolic process (GO:0046348)	44568	0.138075472
regulation of aldosterone biosynthetic process (GO:0032347)	44568	0.138075472
regulation of atrial cardiac muscle cell membrane repolarization (GO:00	44568	0.138075472
atrioventricular valve formation (GO:0003190)	44568	0.138075472
regulation of CD8-positive, alpha-beta T cell differentiation (GO:004337	44568	0.138075472
cation homeostasis (GO:0055080)	44568	0.138075472
Cdc42 protein signal transduction (GO:0032488)	44568	0.138075472
cellular cation homeostasis (GO:0030003)	44568	0.138075472
cellular ion homeostasis (GO:0006873)	44568	0.138075472
regulation of extracellular matrix assembly (GO:1901201)	44568	0.138075472
cellular response to gonadotropin stimulus (GO:0071371)	44568	0.138075472
cellular response to laminar fluid shear stress (GO:0071499)	44568	0.138075472
regulation of glucocorticoid receptor signaling pathway (GO:2000322)	44568	0.138075472
regulation of I-kappaB phosphorylation (GO:1903719)	44568	0.138075472
regulation of ketone biosynthetic process (GO:0010566)	44568	0.138075472
regulation of lysosomal protein catabolic process (GO:1905165)	44568	0.138075472
regulation of male gonad development (GO:2000018)	44568	0.138075472
regulation of microglial cell migration (GO:1904139)	44568	0.138075472
regulation of microtubule binding (GO:1904526)	44568	0.138075472
detection of muscle stretch (GO:0035995)	44568	0.138075472
regulation of natural killer cell mediated cytotoxicity directed against tu	44568	0.138075472
regulation of Rab protein signal transduction (GO:0032483)	44568	0.138075472
regulation of smooth muscle cell differentiation (GO:0051150)	44568	0.138075472
regulation of striated muscle cell differentiation (GO:0051153)	44568	0.138075472
G protein-coupled receptor internalization (GO:0002031)	44568	0.138075472
regulation of toll-like receptor 7 signaling pathway (GO:0034155)	44568	0.138075472
regulation of transforming growth factor beta activation (GO:1901388)	44568	0.138075472
regulation of transforming growth factor beta1 production (GO:003290	44568	0.138075472
regulation of tubulin deacetylation (GO:0090043)	44568	0.138075472
regulation of vascular associated smooth muscle cell differentiation (GO	44568	0.138075472
regulation of vesicle size (GO:0097494)	44568	0.138075472
histone H3-K14 acetylation (GO:0044154)	44568	0.138075472
late nucleophagy (GO:0044805)	44568	0.138075472
somatic recombination of immunoglobulin gene segments (GO:001644	44568	0.138075472
leukotriene transport (GO:0071716)	44568	0.138075472
lymphoid progenitor cell differentiation (GO:0002320)	44568	0.138075472
lysosomal microautophagy (GO:0016237)	44568	0.138075472
marginal zone B cell differentiation (GO:0002315)	44568	0.138075472
TRAIL-activated apoptotic signaling pathway (GO:0036462)	44568	0.138075472
miRNA loading onto RISC involved in gene silencing by miRNA (GO:0035	44568	0.138075472
vascular associated smooth muscle cell development (GO:0097084)	44568	0.138075472
mitral valve development (GO:0003174)	44568	0.138075472
monoacylglycerol biosynthetic process (GO:0006640)	44568	0.138075472
monoacylglycerol catabolic process (GO:0052651)	44568	0.138075472

negative regulation of mitochondrial outer membrane permeabilization	44568	0.138075472
negative regulation of oligodendrocyte differentiation (GO:0048715)	44568	0.138075472
nose development (GO:0043584)	44568	0.138075472
pericardium morphogenesis (GO:0003344)	44568	0.138075472
phospholipase C-activating dopamine receptor signaling pathway (GO:0(	44568	0.138075472
piecemeal microautophagy of the nucleus (GO:0034727)	44568	0.138075472
platelet dense granule organization (GO:0060155)	44568	0.138075472
positive regulation of cardiac epithelial to mesenchymal transition (GO:(	44568	0.138075472
positive regulation of integrin-mediated signaling pathway (GO:200104(	44568	0.138075472
positive regulation of interleukin-23 production (GO:0032747)	44568	0.138075472
positive regulation of intracellular estrogen receptor signaling pathway (	44568	0.138075472
positive regulation of lamellipodium morphogenesis (GO:2000394)	44568	0.138075472
positive regulation of lymphocyte apoptotic process (GO:0070230)	44568	0.138075472
positive regulation of miRNA metabolic process (GO:2000630)	44568	0.138075472
positive regulation of mitophagy in response to mitochondrial depolariz	44568	0.138075472
positive regulation of protein localization to centrosome (GO:1904781)	44568	0.138075472
positive regulation of synaptic plasticity (GO:0031915)	44568	0.138075472
positive regulation of voltage-gated calcium channel activity (GO:19013(	44568	0.138075472
protein localization to endoplasmic reticulum exit site (GO:0070973)	44568	0.138075472
membrane organization (GO:0061024)	8/242	0.138595637
Golgi organization (GO:0007030)	5/130	0.138903161
response to retinoic acid (GO:0032526)	22706	0.141361614
stress-activated MAPK cascade (GO:0051403)	22706	0.141361614
negative regulation of kinase activity (GO:0033673)	22706	0.141361614
regulation of vesicle-mediated transport (GO:0060627)	35156	0.143417678
regulation of cell morphogenesis (GO:0022604)	11720	0.144815712
regulation of cellular amide metabolic process (GO:0034248)	11720	0.144815712
regulation of chemotaxis (GO:0050920)	11720	0.144815712
cardiac muscle tissue morphogenesis (GO:0055008)	11720	0.144815712
regulation of dendritic spine morphogenesis (GO:0061001)	11720	0.144815712
cellular response to glucose stimulus (GO:0071333)	11720	0.144815712
chondrocyte differentiation (GO:0002062)	11720	0.144815712
gene silencing by miRNA (GO:0035195)	11720	0.144815712
RNA biosynthetic process (GO:0032774)	11720	0.144815712
modulation by host of symbiont process (GO:0051851)	11720	0.144815712
positive regulation of receptor signaling pathway via STAT (GO:190489(	11720	0.144815712
positive regulation of telomere maintenance (GO:0032206)	11720	0.144815712
peptidyl-serine modification (GO:0018209)	6/169	0.145994625
actin cytoskeleton reorganization (GO:0031532)	23071	0.146263414
organonitrogen compound catabolic process (GO:1901565)	23071	0.146263414
positive regulation of Ras protein signal transduction (GO:0046579)	23071	0.146263414
positive regulation of programmed cell death (GO:0043068)	9/286	0.149676464
positive regulation of defense response (GO:0031349)	35886	0.151178649
regulation of cilium assembly (GO:1902017)	23437	0.151220041
regulation of innate immune response (GO:0045088)	23437	0.151220041
positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:004312(	6/171	0.151734195
regulation of cholesterol efflux (GO:0010874)	12086	0.15212657

regulation of sprouting angiogenesis (GO:1903670)	12086	0.15212657
lytic vacuole organization (GO:0080171)	12086	0.15212657
negative regulation of JNK cascade (GO:0046329)	12086	0.15212657
positive regulation of telomere maintenance via telomerase (GO:00322:	12086	0.15212657
mRNA-containing ribonucleoprotein complex export from nucleus (GO:(	36251	0.155118175
adenosine to inosine editing (GO:0006382)	44569	0.156182198
amine metabolic process (GO:0009308)	44569	0.156182198
antigen processing and presentation of exogenous peptide antigen via M	44569	0.156182198
regulation of actin filament length (GO:0030832)	44569	0.156182198
autophagosome-lysosome fusion (GO:0061909)	44569	0.156182198
axon extension involved in axon guidance (GO:0048846)	44569	0.156182198
basic amino acid transport (GO:0015802)	44569	0.156182198
brown fat cell differentiation (GO:0050873)	44569	0.156182198
cardiac atrium development (GO:0003230)	44569	0.156182198
regulation of chaperone-mediated autophagy (GO:1904714)	44569	0.156182198
cell migration involved in heart development (GO:0060973)	44569	0.156182198
regulation of cytoplasmic translational elongation (GO:1900247)	44569	0.156182198
regulation of establishment of protein localization to mitochondrion (GC	44569	0.156182198
regulation of extracellular matrix constituent secretion (GO:0003330)	44569	0.156182198
regulation of Golgi to plasma membrane protein transport (GO:0042996	44569	0.156182198
cellular response to UV-B (GO:0071493)	44569	0.156182198
chromatin silencing at telomere (GO:0006348)	44569	0.156182198
coronary vasculature morphogenesis (GO:0060977)	44569	0.156182198
regulation of nitric oxide metabolic process (GO:0080164)	44569	0.156182198
regulation of osteoclast development (GO:2001204)	44569	0.156182198
elastic fiber assembly (GO:0048251)	44569	0.156182198
regulation of protein ADP-ribosylation (GO:0010835)	44569	0.156182198
endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA a	44569	0.156182198
regulation of protein localization to cell cortex (GO:1904776)	44569	0.156182198
regulation of protein localization to chromatin (GO:1905634)	44569	0.156182198
entry of bacterium into host cell (GO:0035635)	44569	0.156182198
establishment of Golgi localization (GO:0051683)	44569	0.156182198
regulation of response to wounding (GO:1903034)	44569	0.156182198
regulation of stem cell division (GO:2000035)	44569	0.156182198
regulation of wound healing, spreading of epidermal cells (GO:1903689)	44569	0.156182198
histone H3-K4 demethylation (GO:0034720)	44569	0.156182198
RNA secondary structure unwinding (GO:0010501)	44569	0.156182198
integrin activation (GO:0033622)	44569	0.156182198
internal protein amino acid acetylation (GO:0006475)	44569	0.156182198
self proteolysis (GO:0097264)	44569	0.156182198
somatic hypermutation of immunoglobulin genes (GO:0016446)	44569	0.156182198
lymphatic endothelial cell differentiation (GO:0060836)	44569	0.156182198
macromolecule depalmitoylation (GO:0098734)	44569	0.156182198
macromolecule modification (GO:0043412)	44569	0.156182198
mammary gland epithelial cell differentiation (GO:0060644)	44569	0.156182198
TORC1 signaling (GO:0038202)	44569	0.156182198
vascular associated smooth muscle contraction (GO:0014829)	44569	0.156182198

venous blood vessel development (GO:0060841)	44569	0.156182198
ventricular trabecula myocardium morphogenesis (GO:0003222)	44569	0.156182198
negative regulation of alpha-beta T cell differentiation (GO:0046639)	44569	0.156182198
negative regulation of amyloid-beta clearance (GO:1900222)	44569	0.156182198
negative regulation of mitochondrial fusion (GO:0010637)	44569	0.156182198
negative regulation of mRNA polyadenylation (GO:1900364)	44569	0.156182198
negative regulation of muscle hypertrophy (GO:0014741)	44569	0.156182198
negative regulation of T cell mediated cytotoxicity (GO:0001915)	44569	0.156182198
negative regulation of vascular associated smooth muscle cell differenti	44569	0.156182198
neuron projection extension involved in neuron projection guidance (GC	44569	0.156182198
phosphatidylinositol-3-phosphate biosynthetic process (GO:0036092)	44569	0.156182198
positive regulation of astrocyte differentiation (GO:0048711)	44569	0.156182198
positive regulation of early endosome to late endosome transport (GO:2	44569	0.156182198
positive regulation of intracellular steroid hormone receptor signaling pa	44569	0.156182198
positive regulation of neuron projection arborization (GO:0150012)	44569	0.156182198
protein deglycosylation (GO:0006517)	44569	0.156182198
protein depalmitoylation (GO:0002084)	44569	0.156182198
BMP signaling pathway (GO:0030509)	23802	0.156229537
regulation of cellular catabolic process (GO:0031329)	23802	0.156229537
axoneme assembly (GO:0035082)	12451	0.15950806
regulation of glucose metabolic process (GO:0010906)	12451	0.15950806
regulation of keratinocyte differentiation (GO:0045616)	12451	0.15950806
negative regulation of mitochondrion organization (GO:0010823)	12451	0.15950806
neural tube closure (GO:0001843)	12451	0.15950806
positive regulation of epidermal growth factor receptor signaling pathw	12451	0.15950806
positive regulation of telomerase activity (GO:0051973)	12451	0.15950806
protein destabilization (GO:0031648)	12451	0.15950806
cell-cell junction assembly (GO:0007043)	24167	0.16128995
positive regulation of signal transduction (GO:0009967)	8/252	0.162200053
regulation of canonical Wnt signaling pathway (GO:0060828)	8/253	0.164658459
peptidyl-threonine modification (GO:0018210)	24532	0.166399335
regulation of JUN kinase activity (GO:0043506)	12816	0.166954013
regulation of muscle cell differentiation (GO:0051147)	12816	0.166954013
regulation of regulated secretory pathway (GO:1903305)	12816	0.166954013
regulation of trans-synaptic signaling (GO:0099177)	12816	0.166954013
response to estrogen (GO:0043627)	12816	0.166954013
negative regulation of neurogenesis (GO:0050768)	12816	0.166954013
negative regulation of Ras protein signal transduction (GO:0046580)	12816	0.166954013
intrinsic apoptotic signaling pathway (GO:0097193)	4/102	0.167162314
positive regulation of response to external stimulus (GO:0032103)	5/139	0.168794488
protein dephosphorylation (GO:0006470)	5/139	0.168794488
cellular response to organonitrogen compound (GO:0071417)	4/103	0.17124923
chromatin remodeling (GO:0006338)	4/103	0.17124923
canonical Wnt signaling pathway (GO:0060070)	24898	0.171555753
regulation of translation (GO:0006417)	6/178	0.172588445
regulation of cell growth (GO:0001558)	7/217	0.173260187
acid secretion (GO:0046717)	44570	0.173909438

anoikis (GO:0043276)	44570	0.173909438
regulation of actin filament organization (GO:0110053)	44570	0.173909438
astral microtubule organization (GO:0030953)	44570	0.173909438
ATF6-mediated unfolded protein response (GO:0036500)	44570	0.173909438
regulation of cell adhesion molecule production (GO:0060353)	44570	0.173909438
regulation of cellular extravasation (GO:0002691)	44570	0.173909438
regulation of DNA-templated transcription in response to stress (GO:00	44570	0.173909438
regulation of endothelial cell differentiation (GO:0045601)	44570	0.173909438
regulation of epidermis development (GO:0045682)	44570	0.173909438
cellular response to interleukin-17 (GO:0097398)	44570	0.173909438
regulation of glial cell proliferation (GO:0060251)	44570	0.173909438
regulation of histone H4 acetylation (GO:0090239)	44570	0.173909438
regulation of interleukin-23 production (GO:0032667)	44570	0.173909438
regulation of leukocyte degranulation (GO:0043300)	44570	0.173909438
regulation of peroxisome proliferator activated receptor signaling pathw	44570	0.173909438
regulation of protein deacetylation (GO:0090311)	44570	0.173909438
endosome to melanosome transport (GO:0035646)	44570	0.173909438
endosome to pigment granule transport (GO:0043485)	44570	0.173909438
epithelial to mesenchymal transition involved in endocardial cushion for	44570	0.173909438
regulation of RNA polymerase II regulatory region sequence-specific DN	44570	0.173909438
fructose 1,6-bisphosphate metabolic process (GO:0030388)	44570	0.173909438
regulation of tumor necrosis factor superfamily cytokine production (GC	44570	0.173909438
glucosamine-containing compound catabolic process (GO:1901072)	44570	0.173909438
regulation of vesicle fusion (GO:0031338)	44570	0.173909438
icosanoid transport (GO:0071715)	44570	0.173909438
interleukin-17-mediated signaling pathway (GO:0097400)	44570	0.173909438
Schwann cell development (GO:0014044)	44570	0.173909438
sensory organ morphogenesis (GO:0090596)	44570	0.173909438
small RNA loading onto RISC (GO:0070922)	44570	0.173909438
synapse pruning (GO:0098883)	44570	0.173909438
negative regulation of biomineralization (GO:0110150)	44570	0.173909438
negative regulation of glial cell differentiation (GO:0045686)	44570	0.173909438
negative regulation of mRNA 3'-end processing (GO:0031441)	44570	0.173909438
negative regulation of pathway-restricted SMAD protein phosphorylatio	44570	0.173909438
negative regulation of smooth muscle cell differentiation (GO:0051151)	44570	0.173909438
nucleotide phosphorylation (GO:0046939)	44570	0.173909438
pericardium development (GO:0060039)	44570	0.173909438
peripheral nervous system axon ensheathment (GO:0032292)	44570	0.173909438
positive regulation of autophagy of mitochondrion (GO:1903599)	44570	0.173909438
positive regulation of CD8-positive, alpha-beta T cell activation (GO:200	44570	0.173909438
regulation of microtubule-based process (GO:0032886)	13181	0.174458486
regulation of ossification (GO:0030278)	13181	0.174458486
regulation of receptor internalization (GO:0002090)	13181	0.174458486
mitochondrion disassembly (GO:0061726)	13181	0.174458486
Wnt signaling pathway, calcium modulating pathway (GO:0007223)	13181	0.174458486
positive regulation of substrate adhesion-dependent cell spreading (GO:	13181	0.174458486
positive regulation of telomere maintenance via telomere lengthening ((	13181	0.174458486

cell chemotaxis (GO:0060326)	25263	0.17675728
Ras protein signal transduction (GO:0007265)	5/142	0.179278668
regulation of plasma membrane bounded cell projection assembly (GO:(	25628	0.182002
wound healing (GO:0042060)	25628	0.182002
regulation of actin cytoskeleton reorganization (GO:2000249)	13547	0.182015758
regulation of microtubule cytoskeleton organization (GO:0070507)	13547	0.182015758
regulation of vascular associated smooth muscle cell proliferation (GO:1	13547	0.182015758
skeletal muscle tissue development (GO:0007519)	13547	0.182015758
lysosome localization (GO:0032418)	13547	0.182015758
negative regulation of stress-activated MAPK cascade (GO:0032873)	13547	0.182015758
positive regulation of exocytosis (GO:0045921)	13547	0.182015758
positive regulation of myeloid cell differentiation (GO:0045639)	13547	0.182015758
nitrogen compound transport (GO:0071705)	5/143	0.18282679
RNA export from nucleus (GO:0006405)	4/106	0.183713912
cellular response to BMP stimulus (GO:0071773)	25993	0.187288013
regulation of glycolytic process (GO:0006110)	25993	0.187288013
mRNA export from nucleus (GO:0006406)	4/107	0.187933738
actin-myosin filament sliding (GO:0033275)	13912	0.189620318
connective tissue development (GO:0061448)	13912	0.189620318
regulation of phosphoprotein phosphatase activity (GO:0043666)	13912	0.189620318
response to estradiol (GO:0032355)	13912	0.189620318
lysosome organization (GO:0007040)	13912	0.189620318
synaptic vesicle endocytosis (GO:0048488)	13912	0.189620318
ventricular septum development (GO:0003281)	13912	0.189620318
muscle filament sliding (GO:0030049)	13912	0.189620318
positive regulation of insulin secretion (GO:0032024)	13912	0.189620318
positive regulation of signaling (GO:0023056)	13912	0.189620318
receptor recycling (GO:0001881)	44571	0.191265125
regulation of attachment of spindle microtubules to kinetochore (GO:00	44571	0.191265125
regulation of axon guidance (GO:1902667)	44571	0.191265125
regulation of carbohydrate biosynthetic process (GO:0043255)	44571	0.191265125
regulation of cell-cell adhesion mediated by integrin (GO:0033632)	44571	0.191265125
regulation of DNA methylation (GO:0044030)	44571	0.191265125
regulation of endoplasmic reticulum unfolded protein response (GO:190	44571	0.191265125
regulation of hair cycle (GO:0042634)	44571	0.191265125
cellular response to purine-containing compound (GO:0071415)	44571	0.191265125
regulation of long-term synaptic depression (GO:1900452)	44571	0.191265125
regulation of macrophage migration (GO:1905521)	44571	0.191265125
defense response to tumor cell (GO:0002357)	44571	0.191265125
dicarboxylic acid biosynthetic process (GO:0043650)	44571	0.191265125
dosage compensation (GO:0007549)	44571	0.191265125
endodermal cell fate commitment (GO:0001711)	44571	0.191265125
regulation of protein localization to centrosome (GO:1904779)	44571	0.191265125
regulation of receptor binding (GO:1900120)	44571	0.191265125
fructose 6-phosphate metabolic process (GO:0006002)	44571	0.191265125
removal of superoxide radicals (GO:0019430)	44571	0.191265125
retinoic acid receptor signaling pathway (GO:0048384)	44571	0.191265125

secretory granule organization (GO:0033363)	44571	0.191265125
ionotropic glutamate receptor signaling pathway (GO:0035235)	44571	0.191265125
iron ion transmembrane transport (GO:0034755)	44571	0.191265125
microtubule anchoring at centrosome (GO:0034454)	44571	0.191265125
morphogenesis of an epithelial sheet (GO:0002011)	44571	0.191265125
N-acetylneuraminate metabolic process (GO:0006054)	44571	0.191265125
negative regulation of cAMP-mediated signaling (GO:0043951)	44571	0.191265125
negative regulation of cellular protein catabolic process (GO:1903363)	44571	0.191265125
negative regulation of establishment of protein localization (GO:190495	44571	0.191265125
negative regulation of extracellular matrix organization (GO:1903054)	44571	0.191265125
negative regulation of glycolytic process (GO:0045820)	44571	0.191265125
negative regulation of inclusion body assembly (GO:0090084)	44571	0.191265125
negative regulation of interferon-beta production (GO:0032688)	44571	0.191265125
negative regulation of lipopolysaccharide-mediated signaling pathway (G	44571	0.191265125
negative regulation of peptidyl-lysine acetylation (GO:2000757)	44571	0.191265125
negative regulation of purine nucleotide metabolic process (GO:190054	44571	0.191265125
negative regulation of receptor binding (GO:1900121)	44571	0.191265125
negative regulation of transforming growth factor beta production (GO:1	44571	0.191265125
negative regulation of tyrosine phosphorylation of STAT protein (GO:004	44571	0.191265125
negative regulation of vascular endothelial growth factor signaling pathv	44571	0.191265125
neuron projection fasciculation (GO:0106030)	44571	0.191265125
neuron remodeling (GO:0016322)	44571	0.191265125
peptidyl-lysine acetylation (GO:0018394)	44571	0.191265125
positive regulation of cell activation (GO:0050867)	44571	0.191265125
positive regulation of vasculogenesis (GO:2001214)	44571	0.191265125
protein localization to endosome (GO:0036010)	44571	0.191265125
cell morphogenesis involved in differentiation (GO:0000904)	26359	0.192613432
positive regulation of secretion by cell (GO:1903532)	26359	0.192613432
modulation of chemical synaptic transmission (GO:0050804)	4/109	0.196465277
regulation of cellular component biogenesis (GO:0044087)	14277	0.197266866
cellular response to ketone (GO:1901655)	14277	0.197266866
regulation of T cell differentiation (GO:0045580)	14277	0.197266866
negative regulation of cellular metabolic process (GO:0031324)	14277	0.197266866
positive regulation of cytosolic calcium ion concentration (GO:0007204)	5/147	0.197272077
endoplasmic reticulum organization (GO:0007029)	26724	0.197976386
positive regulation of JNK cascade (GO:0046330)	26724	0.197976386
cellular response to amino acid starvation (GO:0034198)	27089	0.20337502
regulation of stress fiber assembly (GO:0051492)	27089	0.20337502
negative regulation of protein binding (GO:0032091)	27089	0.20337502
cilium organization (GO:0044782)	7/228	0.204719213
autophagy of mitochondrion (GO:0000422)	14642	0.204950301
bone development (GO:0060348)	14642	0.204950301
regulation of microtubule polymerization (GO:0031113)	14642	0.204950301
negative regulation of cell-substrate adhesion (GO:0010812)	14642	0.204950301
negative regulation of ERBB signaling pathway (GO:1901185)	14642	0.204950301
negative regulation of I-kappaB kinase/NF-kappaB signaling (GO:004312	14642	0.204950301
negative regulation of protein kinase B signaling (GO:0051898)	14642	0.204950301

nucleocytoplasmic transport (GO:0006913)	14642	0.204950301
positive regulation of cation channel activity (GO:2001259)	14642	0.204950301
positive regulation of double-strand break repair (GO:2000781)	14642	0.204950301
regulation of Wnt signaling pathway (GO:0030111)	4/111	0.205113183
positive regulation of apoptotic process (GO:0043065)	9/310	0.206301101
actin filament network formation (GO:0051639)	44572	0.208257029
purine nucleoside bisphosphate biosynthetic process (GO:0034033)	44572	0.208257029
angiogenesis involved in wound healing (GO:0060055)	44572	0.208257029
atrial septum morphogenesis (GO:0060413)	44572	0.208257029
calcineurin-NFAT signaling cascade (GO:0033173)	44572	0.208257029
camera-type eye morphogenesis (GO:0048593)	44572	0.208257029
regulation of cytoplasmic transport (GO:1903649)	44572	0.208257029
cellular response to superoxide (GO:0071451)	44572	0.208257029
regulation of inclusion body assembly (GO:0090083)	44572	0.208257029
regulation of lamellipodium morphogenesis (GO:2000392)	44572	0.208257029
regulation of lipid kinase activity (GO:0043550)	44572	0.208257029
coenzyme A biosynthetic process (GO:0015937)	44572	0.208257029
regulation of long-term neuronal synaptic plasticity (GO:0048169)	44572	0.208257029
complement receptor mediated signaling pathway (GO:0002430)	44572	0.208257029
regulation of mast cell activation involved in immune response (GO:003	44572	0.208257029
regulation of mitochondrial fusion (GO:0010635)	44572	0.208257029
desensitization of G protein-coupled receptor signaling pathway (GO:00	44572	0.208257029
regulation of myeloid leukocyte mediated immunity (GO:0002886)	44572	0.208257029
regulation of stress-activated protein kinase signaling cascade (GO:0070	44572	0.208257029
regulation of T cell apoptotic process (GO:0070232)	44572	0.208257029
regulation of T cell mediated immunity (GO:0002709)	44572	0.208257029
regulation of toll-like receptor 9 signaling pathway (GO:0034163)	44572	0.208257029
glutamine family amino acid biosynthetic process (GO:0009084)	44572	0.208257029
hematopoietic stem cell proliferation (GO:0071425)	44572	0.208257029
ribonucleoside bisphosphate biosynthetic process (GO:0034030)	44572	0.208257029
signal peptide processing (GO:0006465)	44572	0.208257029
lipoprotein catabolic process (GO:0042159)	44572	0.208257029
UDP-N-acetylglucosamine biosynthetic process (GO:0006048)	44572	0.208257029
mitochondrial transcription (GO:0006390)	44572	0.208257029
V(D)J recombination (GO:0033151)	44572	0.208257029
vasoconstriction (GO:0042310)	44572	0.208257029
monocyte differentiation (GO:0030224)	44572	0.208257029
negative regulation of activin receptor signaling pathway (GO:0032926)	44572	0.208257029
negative regulation of cholesterol transport (GO:0032375)	44572	0.208257029
negative regulation of natural killer cell mediated immunity (GO:000271	44572	0.208257029
negative regulation of receptor signaling pathway via STAT (GO:190489	44572	0.208257029
negative regulation of response to cytokine stimulus (GO:0060761)	44572	0.208257029
negative regulation of sprouting angiogenesis (GO:1903671)	44572	0.208257029
organophosphate catabolic process (GO:0046434)	44572	0.208257029
positive regulation of bone resorption (GO:0045780)	44572	0.208257029
positive regulation of cellular extravasation (GO:0002693)	44572	0.208257029
positive regulation of cytoplasmic transport (GO:1903651)	44572	0.208257029

positive regulation of keratinocyte proliferation (GO:0010838)	44572	0.208257029
positive regulation of production of miRNAs involved in gene silencing b	44572	0.208257029
positive regulation of transcription elongation from RNA polymerase II p	44572	0.208257029
positive regulation of transcription from RNA polymerase II promoter in	44572	0.208257029
positive regulation of triglyceride biosynthetic process (GO:0010867)	44572	0.208257029
cellular response to organic cyclic compound (GO:0071407)	5/150	0.208356287
response to cytokine (GO:0034097)	5/150	0.208356287
regulation of protein dephosphorylation (GO:0035304)	15008	0.212665715
endosome organization (GO:0007032)	15008	0.212665715
regulation of viral transcription (GO:0046782)	15008	0.212665715
visual system development (GO:0150063)	15008	0.212665715
actomyosin structure organization (GO:0031032)	27820	0.214272005
regulation of cell division (GO:0051302)	27820	0.214272005
regulation of epithelial to mesenchymal transition (GO:0010717)	27820	0.214272005
cellular response to hormone stimulus (GO:0032870)	27820	0.214272005
regulation of RNA splicing (GO:0043484)	27820	0.214272005
phospholipid metabolic process (GO:0006644)	27820	0.214272005
positive regulation of growth (GO:0045927)	27820	0.214272005
regulation of apoptotic process (GO:0042981)	19/742	0.21823372
negative regulation of cell motility (GO:2000146)	4/114	0.218287083
positive regulation of Wnt signaling pathway (GO:0030177)	5/153	0.219638475
negative regulation of developmental process (GO:0051093)	28185	0.219766739
phosphatidylcholine metabolic process (GO:0046470)	28185	0.219766739
positive regulation of protein modification by small protein conjugation	28185	0.219766739
regulation of nervous system development (GO:0051960)	15373	0.220408392
skeletal system morphogenesis (GO:0048705)	15373	0.220408392
mitochondrial gene expression (GO:0140053)	15373	0.220408392
positive regulation of protein kinase activity (GO:0045860)	5/154	0.223440599
adipose tissue development (GO:0060612)	44573	0.224892758
amino sugar biosynthetic process (GO:0046349)	44573	0.224892758
regulation of astrocyte differentiation (GO:0048710)	44573	0.224892758
axonal fasciculation (GO:0007413)	44573	0.224892758
regulation of CD4-positive, alpha-beta T cell differentiation (GO:004337(	44573	0.224892758
calcineurin-mediated signaling (GO:0097720)	44573	0.224892758
carboxylic acid catabolic process (GO:0046395)	44573	0.224892758
cardiocyte differentiation (GO:0035051)	44573	0.224892758
cellular response to fluid shear stress (GO:0071498)	44573	0.224892758
cellular response to thyroid hormone stimulus (GO:0097067)	44573	0.224892758
dosage compensation by inactivation of X chromosome (GO:0009048)	44573	0.224892758
early endosome to Golgi transport (GO:0034498)	44573	0.224892758
regulation of plasminogen activation (GO:0010755)	44573	0.224892758
glomerular visceral epithelial cell differentiation (GO:0072112)	44573	0.224892758
glutamine metabolic process (GO:0006541)	44573	0.224892758
smooth muscle cell differentiation (GO:0051145)	44573	0.224892758
sphingoid metabolic process (GO:0046519)	44573	0.224892758
microtubule anchoring at microtubule organizing center (GO:0072393)	44573	0.224892758
very-low-density lipoprotein particle assembly (GO:0034379)	44573	0.224892758

negative regulation of cardiac muscle hypertrophy (GO:0010614)	44573	0.224892758
negative regulation of cellular response to vascular endothelial growth f	44573	0.224892758
negative regulation of fatty acid biosynthetic process (GO:0045717)	44573	0.224892758
negative regulation of histone acetylation (GO:0035067)	44573	0.224892758
negative regulation of leukocyte chemotaxis (GO:0002689)	44573	0.224892758
negative regulation of receptor internalization (GO:0002091)	44573	0.224892758
negative regulation of transcription elongation from RNA polymerase II	44573	0.224892758
negative regulation of vascular permeability (GO:0043116)	44573	0.224892758
polyol transport (GO:0015791)	44573	0.224892758
positive regulation of endoplasmic reticulum unfolded protein response	44573	0.224892758
positive regulation of myeloid leukocyte mediated immunity (GO:00028	44573	0.224892758
positive regulation of protein maturation (GO:1903319)	44573	0.224892758
regulation of carbohydrate catabolic process (GO:0043470)	15738	0.228173797
regulation of cytokine production involved in inflammatory response (G	15738	0.228173797
regulation of purine nucleotide metabolic process (GO:1900542)	15738	0.228173797
heart looping (GO:0001947)	15738	0.228173797
signal release from synapse (GO:0099643)	15738	0.228173797
positive regulation of phospholipase C activity (GO:0010863)	15738	0.228173797
regulation of cell differentiation (GO:0045595)	5/156	0.231103577
neurotransmitter secretion (GO:0007269)	16103	0.235957573
positive regulation of mRNA catabolic process (GO:0061014)	16103	0.235957573
positive regulation of stress fiber assembly (GO:0051496)	16103	0.235957573
regulation of fat cell differentiation (GO:0045598)	29281	0.236414649
positive regulation of cell adhesion (GO:0045785)	29281	0.236414649
cellular response to growth factor stimulus (GO:0071363)	5/158	0.238841106
cellular response to oxygen-containing compound (GO:1901701)	9/323	0.240162475
positive regulation of cysteine-type endopeptidase activity involved in a	4/119	0.240721007
antifungal innate immune response (GO:0061760)	44574	0.241179759
regulation of antigen receptor-mediated signaling pathway (GO:005085	44574	0.241179759
regulation of autophagosome maturation (GO:1901096)	44574	0.241179759
regulation of histone modification (GO:0031056)	44574	0.241179759
regulation of homotypic cell-cell adhesion (GO:0034110)	44574	0.241179759
central nervous system projection neuron axonogenesis (GO:0021952)	44574	0.241179759
chromatin organization involved in regulation of transcription (GO:0034	44574	0.241179759
regulation of leukocyte adhesion to vascular endothelial cell (GO:19049	44574	0.241179759
cytoplasmic sequestering of protein (GO:0051220)	44574	0.241179759
embryonic appendage morphogenesis (GO:0035113)	44574	0.241179759
regulation of platelet-derived growth factor receptor signaling pathway	44574	0.241179759
endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S	44574	0.241179759
regulation of protein exit from endoplasmic reticulum (GO:0070861)	44574	0.241179759
entry into host (GO:0044409)	44574	0.241179759
regulation of T cell differentiation in thymus (GO:0033081)	44574	0.241179759
response to muramyl dipeptide (GO:0032495)	44574	0.241179759
response to thyroid hormone (GO:0097066)	44574	0.241179759
response to UV-B (GO:0010224)	44574	0.241179759
reticulophagy (GO:0061709)	44574	0.241179759
sphingoid biosynthetic process (GO:0046520)	44574	0.241179759

sphingosine biosynthetic process (GO:0046512)	44574	0.241179759
macrophage activation involved in immune response (GO:0002281)	44574	0.241179759
mature B cell differentiation involved in immune response (GO:0002313	44574	0.241179759
toll-like receptor 9 signaling pathway (GO:0034162)	44574	0.241179759
transport along microtubule (GO:0010970)	44574	0.241179759
UDP-N-acetylglucosamine metabolic process (GO:0006047)	44574	0.241179759
myelination in peripheral nervous system (GO:0022011)	44574	0.241179759
negative regulation of autophagosome assembly (GO:1902902)	44574	0.241179759
negative regulation of CD4-positive, alpha-beta T cell activation (GO:200	44574	0.241179759
negative regulation of cell morphogenesis involved in differentiation (G(	44574	0.241179759
negative regulation of cellular senescence (GO:2000773)	44574	0.241179759
negative regulation of endoplasmic reticulum unfolded protein response	44574	0.241179759
negative regulation of gluconeogenesis (GO:0045721)	44574	0.241179759
negative regulation of intrinsic apoptotic signaling pathway in response	44574	0.241179759
negative regulation of locomotion (GO:0040013)	44574	0.241179759
negative regulation of myoblast differentiation (GO:0045662)	44574	0.241179759
negative regulation of stem cell differentiation (GO:2000737)	44574	0.241179759
negative regulation of substrate adhesion-dependent cell spreading (GO	44574	0.241179759
negative regulation of vascular endothelial growth factor receptor signa	44574	0.241179759
plasma membrane repair (GO:0001778)	44574	0.241179759
positive regulation of calcineurin-mediated signaling (GO:0106058)	44574	0.241179759
positive regulation of calcineurin-NFAT signaling cascade (GO:0070886)	44574	0.241179759
positive regulation of neuron migration (GO:2001224)	44574	0.241179759
positive regulation of nuclear-transcribed mRNA poly(A) tail shortening (	44574	0.241179759
positive regulation of protein exit from endoplasmic reticulum (GO:007(	44574	0.241179759
activation of cysteine-type endopeptidase activity involved in apoptotic	29646	0.242012741
negative regulation of protein modification process (GO:0031400)	29646	0.242012741
positive regulation of Notch signaling pathway (GO:0045747)	16469	0.243755537
positive regulation of response to biotic stimulus (GO:0002833)	16469	0.243755537
regulation of macromolecule metabolic process (GO:0060255)	6/200	0.244774101
ephrin receptor signaling pathway (GO:0048013)	30011	0.247632396
positive regulation of protein ubiquitination (GO:0031398)	30011	0.247632396
modification-dependent protein catabolic process (GO:0019941)	6/201	0.248252998
regulation of fibroblast proliferation (GO:0048145)	16834	0.251563669
regulation of telomerase activity (GO:0051972)	16834	0.251563669
spliceosomal complex assembly (GO:0000245)	16834	0.251563669
vesicle organization (GO:0016050)	16834	0.251563669
positive regulation of organelle assembly (GO:1902117)	16834	0.251563669
positive regulation of smooth muscle cell proliferation (GO:0048661)	16834	0.251563669
generation of neurons (GO:0048699)	6/202	0.251746043
regulation of defense response (GO:0031347)	30376	0.253271949
peptide metabolic process (GO:0006518)	30376	0.253271949
regulation of angiogenesis (GO:0045765)	6/203	0.255252846
quinone biosynthetic process (GO:1901663)	44575	0.257125326
antiviral innate immune response (GO:0140374)	44575	0.257125326
atrial septum development (GO:0003283)	44575	0.257125326
bone morphogenesis (GO:0060349)	44575	0.257125326

carbohydrate transport (GO:0008643)	44575	0.257125326
cardiac left ventricle morphogenesis (GO:0003214)	44575	0.257125326
cellular copper ion homeostasis (GO:0006878)	44575	0.257125326
cellular response to low-density lipoprotein particle stimulus (GO:00714	44575	0.257125326
regulation of histone methylation (GO:0031060)	44575	0.257125326
regulation of integrin-mediated signaling pathway (GO:2001044)	44575	0.257125326
regulation of intrinsic apoptotic signaling pathway in response to DNA d	44575	0.257125326
regulation of lamellipodium organization (GO:1902743)	44575	0.257125326
regulation of lipase activity (GO:0060191)	44575	0.257125326
coenzyme A metabolic process (GO:0015936)	44575	0.257125326
covalent chromatin modification (GO:0016569)	44575	0.257125326
endothelial cell differentiation (GO:0045446)	44575	0.257125326
regulation of retinoic acid receptor signaling pathway (GO:0048385)	44575	0.257125326
regulation of vasculogenesis (GO:2001212)	44575	0.257125326
response to chemokine (GO:1990868)	44575	0.257125326
intestinal absorption (GO:0050892)	44575	0.257125326
secondary palate development (GO:0062009)	44575	0.257125326
sodium-independent organic anion transport (GO:0043252)	44575	0.257125326
substrate-dependent cell migration (GO:0006929)	44575	0.257125326
sulfate transport (GO:0008272)	44575	0.257125326
mRNA cleavage involved in mRNA processing (GO:0098787)	44575	0.257125326
NAD biosynthesis via nicotinamide riboside salvage pathway (GO:00343	44575	0.257125326
negative regulation of interleukin-12 production (GO:0032695)	44575	0.257125326
negative regulation of mRNA splicing, via spliceosome (GO:0048025)	44575	0.257125326
negative regulation of T cell mediated immunity (GO:0002710)	44575	0.257125326
negative regulation of translational initiation (GO:0045947)	44575	0.257125326
nuclear migration (GO:0007097)	44575	0.257125326
peptidyl-serine dephosphorylation (GO:0070262)	44575	0.257125326
positive regulation of alpha-beta T cell differentiation (GO:0046638)	44575	0.257125326
positive regulation of brown fat cell differentiation (GO:0090336)	44575	0.257125326
positive regulation of cardiac muscle cell proliferation (GO:0060045)	44575	0.257125326
positive regulation of insulin secretion involved in cellular response to gl	44575	0.257125326
positive regulation of macrophage chemotaxis (GO:0010759)	44575	0.257125326
positive regulation of protein-containing complex disassembly (GO:0043	44575	0.257125326
positive regulation of transmembrane transport (GO:0034764)	44575	0.257125326
pre-miRNA processing (GO:0031054)	44575	0.257125326
protein localization to kinetochore (GO:0034501)	44575	0.257125326
response to insulin (GO:0032868)	30742	0.25892976
spindle assembly (GO:0051225)	30742	0.25892976
regulation of cellular metabolic process (GO:0031323)	17199	0.259378115
determination of heart left/right asymmetry (GO:0061371)	17199	0.259378115
embryonic heart tube morphogenesis (GO:0003143)	17199	0.259378115
epidermal growth factor receptor signaling pathway (GO:0007173)	17199	0.259378115
epithelial to mesenchymal transition (GO:0001837)	17199	0.259378115
positive regulation of neuron death (GO:1901216)	17199	0.259378115
non-canonical Wnt signaling pathway (GO:0035567)	4/124	0.263653062
regulation of inflammatory response (GO:0050727)	6/206	0.265851906

base-excision repair (GO:0006284)	17564	0.267195175
cognition (GO:0050890)	17564	0.267195175
substrate adhesion-dependent cell spreading (GO:0034446)	17564	0.267195175
phosphatidic acid biosynthetic process (GO:0006654)	17564	0.267195175
negative regulation of phosphorylation (GO:0042326)	31472	0.270293722
anterograde synaptic vesicle transport (GO:0048490)	44576	0.272736599
cardiac myofibril assembly (GO:0055003)	44576	0.272736599
regulation of clathrin-dependent endocytosis (GO:2000369)	44576	0.272736599
regulation of cytoplasmic translation (GO:2000765)	44576	0.272736599
regulation of endothelial cell chemotaxis (GO:2001026)	44576	0.272736599
cellular response to ATP (GO:0071318)	44576	0.272736599
contractile actin filament bundle assembly (GO:0030038)	44576	0.272736599
regulation of microglial cell activation (GO:1903978)	44576	0.272736599
regulation of neuron projection arborization (GO:0150011)	44576	0.272736599
regulation of nuclear-transcribed mRNA catabolic process, deadenylatio	44576	0.272736599
regulation of nuclear-transcribed mRNA poly(A) tail shortening (GO:006(	44576	0.272736599
regulation of phospholipase C activity (GO:1900274)	44576	0.272736599
electron transport chain (GO:0022900)	44576	0.272736599
regulation of triglyceride biosynthetic process (GO:0010866)	44576	0.272736599
response to muscle stretch (GO:0035994)	44576	0.272736599
histone H3 deacetylation (GO:0070932)	44576	0.272736599
histone H4-K5 acetylation (GO:0043981)	44576	0.272736599
histone H4-K8 acetylation (GO:0043982)	44576	0.272736599
stress fiber assembly (GO:0043149)	44576	0.272736599
synaptic vesicle transport along microtubule (GO:0099517)	44576	0.272736599
mammary gland epithelium development (GO:0061180)	44576	0.272736599
ubiquinone biosynthetic process (GO:0006744)	44576	0.272736599
ubiquinone metabolic process (GO:0006743)	44576	0.272736599
mitochondrial RNA metabolic process (GO:0000959)	44576	0.272736599
mitotic intra-S DNA damage checkpoint signaling (GO:0031573)	44576	0.272736599
mRNA methylation (GO:0080009)	44576	0.272736599
negative regulation of cellular component movement (GO:0051271)	44576	0.272736599
negative regulation of mRNA processing (GO:0050686)	44576	0.272736599
phosphatidylethanolamine biosynthetic process (GO:0006646)	44576	0.272736599
placenta development (GO:0001890)	44576	0.272736599
positive regulation of acute inflammatory response (GO:0002675)	44576	0.272736599
positive regulation of DNA damage response, signal transduction by p53	44576	0.272736599
positive regulation of double-strand break repair via homologous recom	44576	0.272736599
positive regulation of exosomal secretion (GO:1903543)	44576	0.272736599
positive regulation of histone H3-K4 methylation (GO:0051571)	44576	0.272736599
positive regulation of keratinocyte differentiation (GO:0045618)	44576	0.272736599
positive regulation of nuclear-transcribed mRNA catabolic process, dead	44576	0.272736599
positive regulation of pattern recognition receptor signaling pathway (G	44576	0.272736599
receptor internalization (GO:0031623)	17930	0.275011301
regulation of cellular protein metabolic process (GO:0032268)	17930	0.275011301
cellular response to mechanical stimulus (GO:0071260)	17930	0.275011301
regulation of stress-activated MAPK cascade (GO:0032872)	17930	0.275011301

response to glucose (GO:0009749)	17930	0.275011301
RNA catabolic process (GO:0006401)	17930	0.275011301
negative regulation of catabolic process (GO:0009895)	17930	0.275011301
retrograde transport, endosome to Golgi (GO:0042147)	32203	0.281711668
positive regulation of neuron projection development (GO:0010976)	32203	0.281711668
plasma membrane bounded cell projection organization (GO:0120036)	4/128	0.282282351
regulation of generation of precursor metabolites and energy (GO:0043	18295	0.282823094
ribosome assembly (GO:0042255)	18295	0.282823094
phosphatidic acid metabolic process (GO:0046473)	18295	0.282823094
cellular response to insulin stimulus (GO:0032869)	4/129	0.2869718
muscle contraction (GO:0006936)	4/129	0.2869718
second-messenger-mediated signaling (GO:0019932)	32568	0.287437055
positive regulation of inflammatory response (GO:0050729)	32568	0.287437055
activation of NF-kappaB-inducing kinase activity (GO:0007250)	44577	0.28802057
regulation of amyloid-beta clearance (GO:1900221)	44577	0.28802057
autophagy of nucleus (GO:0044804)	44577	0.28802057
regulation of cellular carbohydrate metabolic process (GO:0010675)	44577	0.28802057
regulation of ceramide biosynthetic process (GO:2000303)	44577	0.28802057
regulation of cholesterol storage (GO:0010885)	44577	0.28802057
regulation of ERBB signaling pathway (GO:1901184)	44577	0.28802057
regulation of interleukin-1 production (GO:0032652)	44577	0.28802057
regulation of isotype switching (GO:0045191)	44577	0.28802057
regulation of mast cell degranulation (GO:0043304)	44577	0.28802057
dendritic spine morphogenesis (GO:0060997)	44577	0.28802057
regulation of neurotransmitter transport (GO:0051588)	44577	0.28802057
regulation of Rac protein signal transduction (GO:0035020)	44577	0.28802057
glutamine family amino acid catabolic process (GO:0009065)	44577	0.28802057
resolution of meiotic recombination intermediates (GO:0000712)	44577	0.28802057
heme catabolic process (GO:0042167)	44577	0.28802057
histone H2A acetylation (GO:0043968)	44577	0.28802057
RNA splicing, via endonucleolytic cleavage and ligation (GO:0000394)	44577	0.28802057
sphingolipid catabolic process (GO:0030149)	44577	0.28802057
mitotic sister chromatid cohesion (GO:0007064)	44577	0.28802057
mRNA cis splicing, via spliceosome (GO:0045292)	44577	0.28802057
N-acetylglucosamine metabolic process (GO:0006044)	44577	0.28802057
N-terminal protein amino acid acetylation (GO:0006474)	44577	0.28802057
negative regulation of anoikis (GO:2000811)	44577	0.28802057
negative regulation of cell-substrate junction organization (GO:0150118	44577	0.28802057
negative regulation of focal adhesion assembly (GO:0051895)	44577	0.28802057
negative regulation of receptor signaling pathway via JAK-STAT (GO:004	44577	0.28802057
negative regulation of type I interferon-mediated signaling pathway (GO	44577	0.28802057
neuron cell-cell adhesion (GO:0007158)	44577	0.28802057
nuclear transport (GO:0051169)	44577	0.28802057
odontogenesis of dentin-containing tooth (GO:0042475)	44577	0.28802057
oogenesis (GO:0048477)	44577	0.28802057
platelet-derived growth factor receptor signaling pathway (GO:0048008	44577	0.28802057
porphyrin-containing compound catabolic process (GO:0006787)	44577	0.28802057

positive regulation by host of viral transcription (GO:0043923)	44577	0.28802057
positive regulation of collagen biosynthetic process (GO:0032967)	44577	0.28802057
positive regulation of double-strand break repair via nonhomologous en	44577	0.28802057
positive regulation of leukocyte adhesion to vascular endothelial cell (G	44577	0.28802057
protein localization to endoplasmic reticulum (GO:0070972)	44577	0.28802057
protein localization to microtubule organizing center (GO:1905508)	44577	0.28802057
inositol lipid-mediated signaling (GO:0048017)	18660	0.290627294
intrinsic apoptotic signaling pathway in response to DNA damage (GO:0	18660	0.290627294
mesenchymal cell differentiation (GO:0048762)	18660	0.290627294
negative regulation of protein ubiquitination (GO:0031397)	18660	0.290627294
positive regulation of actin filament bundle assembly (GO:0032233)	18660	0.290627294
neuron projection development (GO:0031175)	5/171	0.290641119
positive regulation of canonical Wnt signaling pathway (GO:0090263)	4/130	0.291672392
regulation of mRNA splicing, via spliceosome (GO:0048024)	32933	0.293171396
negative regulation of translation (GO:0017148)	32933	0.293171396
positive regulation of ERK1 and ERK2 cascade (GO:0070374)	5/172	0.294712967
cartilage development (GO:0051216)	19025	0.298420784
regulation of telomere maintenance via telomerase (GO:0032210)	19025	0.298420784
signal transduction in response to DNA damage (GO:0042770)	19025	0.298420784
negative regulation of cellular biosynthetic process (GO:0031327)	19025	0.298420784
negative regulation of protein-containing complex assembly (GO:00313	19025	0.298420784
positive regulation of protein localization to plasma membrane (GO:190	19025	0.298420784
adenylate cyclase-activating adrenergic receptor signaling pathway (GO:	44578	0.302984086
copper ion homeostasis (GO:0055070)	44578	0.302984086
diol biosynthetic process (GO:0034312)	44578	0.302984086
establishment of protein localization to endoplasmic reticulum (GO:007	44578	0.302984086
regulation of stem cell proliferation (GO:0072091)	44578	0.302984086
response to purine-containing compound (GO:0014074)	44578	0.302984086
RNA interference (GO:0016246)	44578	0.302984086
mesenchyme morphogenesis (GO:0072132)	44578	0.302984086
negative regulation of amyloid-beta formation (GO:1902430)	44578	0.302984086
negative regulation of ATP metabolic process (GO:1903579)	44578	0.302984086
negative regulation of cell aging (GO:0090344)	44578	0.302984086
negative regulation of execution phase of apoptosis (GO:1900118)	44578	0.302984086
negative regulation of intrinsic apoptotic signaling pathway by p53 class	44578	0.302984086
negative regulation of peptidyl-threonine phosphorylation (GO:0010801	44578	0.302984086
positive regulation of cardiac muscle tissue growth (GO:0055023)	44578	0.302984086
positive regulation of collagen metabolic process (GO:0010714)	44578	0.302984086
positive regulation of cytokine production involved in inflammatory resp	44578	0.302984086
positive regulation of regulated secretory pathway (GO:1903307)	44578	0.302984086
regulation of peptidyl-tyrosine phosphorylation (GO:0050730)	33664	0.304661132
heart morphogenesis (GO:0003007)	19391	0.306200577
cellular component assembly (GO:0022607)	7/261	0.309539967
neutrophil degranulation (GO:0043312)	12/481	0.312349587
cellular response to lipid (GO:0071396)	6/219	0.312914411
regulation of alternative mRNA splicing, via spliceosome (GO:0000381)	19756	0.313963816
regulation of cyclin-dependent protein kinase activity (GO:1904029)	19756	0.313963816

cytoplasmic microtubule organization (GO:0031122)	19756	0.313963816
regulation of potassium ion transmembrane transport (GO:1901379)	19756	0.313963816
striated muscle contraction (GO:0006941)	19756	0.313963816
unsaturated fatty acid metabolic process (GO:0033559)	19756	0.313963816
positive regulation of gene expression (GO:0010628)	12/482	0.314811485
cellular response to DNA damage stimulus (GO:0006974)	9/350	0.31578079
interleukin-1-mediated signaling pathway (GO:0070498)	34394	0.316169527
positive regulation of epithelial cell migration (GO:0010634)	34394	0.316169527
regulation of brown fat cell differentiation (GO:0090335)	44579	0.31763385
base conversion or substitution editing (GO:0016553)	44579	0.31763385
regulation of catabolic process (GO:0009894)	44579	0.31763385
carbohydrate derivative transport (GO:1901264)	44579	0.31763385
regulation of chromosome segregation (GO:0051983)	44579	0.31763385
cell migration involved in sprouting angiogenesis (GO:0002042)	44579	0.31763385
regulation of fatty acid metabolic process (GO:0019217)	44579	0.31763385
cellular response to zinc ion (GO:0071294)	44579	0.31763385
regulation of mitochondrial outer membrane permeabilization involved	44579	0.31763385
regulation of mRNA polyadenylation (GO:1900363)	44579	0.31763385
DNA conformation change (GO:0071103)	44579	0.31763385
embryonic axis specification (GO:0000578)	44579	0.31763385
regulation of spindle organization (GO:0090224)	44579	0.31763385
fluid transport (GO:0042044)	44579	0.31763385
regulation of transcription by RNA polymerase I (GO:0006356)	44579	0.31763385
regulation of transforming growth factor beta production (GO:0071634)	44579	0.31763385
RNA destabilization (GO:0050779)	44579	0.31763385
leukocyte tethering or rolling (GO:0050901)	44579	0.31763385
melanosome transport (GO:0032402)	44579	0.31763385
triglyceride biosynthetic process (GO:0019432)	44579	0.31763385
negative regulation of biosynthetic process (GO:0009890)	44579	0.31763385
negative regulation of cation transmembrane transport (GO:1904063)	44579	0.31763385
negative regulation of fibroblast proliferation (GO:0048147)	44579	0.31763385
negative regulation of interleukin-8 production (GO:0032717)	44579	0.31763385
negative regulation of signal transduction by p53 class mediator (GO:19(	44579	0.31763385
negative regulation of tumor necrosis factor-mediated signaling pathwa	44579	0.31763385
neuron maturation (GO:0042551)	44579	0.31763385
phosphatidylinositol acyl-chain remodeling (GO:0036149)	44579	0.31763385
pigment granule transport (GO:0051904)	44579	0.31763385
positive regulation of CREB transcription factor activity (GO:0032793)	44579	0.31763385
positive regulation of extracellular matrix organization (GO:1903055)	44579	0.31763385
positive regulation of glial cell differentiation (GO:0045687)	44579	0.31763385
positive regulation of response to endoplasmic reticulum stress (GO:190	44579	0.31763385
protein localization to centrosome (GO:0071539)	44579	0.31763385
negative regulation of immune response (GO:0050777)	5/178	0.319328722
regulation of blood vessel endothelial cell migration (GO:0043535)	20121	0.32170777
negative regulation of cysteine-type endopeptidase activity involved in a	20121	0.32170777
negative regulation of protein modification by small protein conjugation	20121	0.32170777
neutrophil activation involved in immune response (GO:0002283)	12/485	0.322225719

regulated exocytosis (GO:0045055)	5/180	0.327591457
protein-containing complex disassembly (GO:0032984)	20486	0.329429831
regulation of ATP metabolic process (GO:1903578)	20486	0.329429831
autophagosome organization (GO:1905037)	20486	0.329429831
positive regulation of establishment of protein localization to mitochonc	20486	0.329429831
neutrophil mediated immunity (GO:0002446)	12/488	0.32968039
negative regulation of signal transduction (GO:0009968)	7/267	0.3297302
pyroptosis (GO:0070269)	44580	0.331976424
regulation of bicellular tight junction assembly (GO:2000810)	44580	0.331976424
regulation of collagen biosynthetic process (GO:0032965)	44580	0.331976424
regulation of exosomal secretion (GO:1903541)	44580	0.331976424
regulation of lymphocyte proliferation (GO:0050670)	44580	0.331976424
detection of mechanical stimulus (GO:0050982)	44580	0.331976424
regulation of neuroinflammatory response (GO:0150077)	44580	0.331976424
diol metabolic process (GO:0034311)	44580	0.331976424
DNA double-strand break processing (GO:0000729)	44580	0.331976424
regulation of oligodendrocyte differentiation (GO:0048713)	44580	0.331976424
regulation of peptidyl-serine phosphorylation of STAT protein (GO:0033	44580	0.331976424
endocardial cushion morphogenesis (GO:0003203)	44580	0.331976424
establishment of melanosome localization (GO:0032401)	44580	0.331976424
establishment or maintenance of apical/basal cell polarity (GO:0035088	44580	0.331976424
excitatory postsynaptic potential (GO:0060079)	44580	0.331976424
regulation of stem cell population maintenance (GO:2000036)	44580	0.331976424
regulation of synaptic vesicle exocytosis (GO:2000300)	44580	0.331976424
regulation of vascular endothelial growth factor signaling pathway (GO:1	44580	0.331976424
response to ATP (GO:0033198)	44580	0.331976424
heart trabecula morphogenesis (GO:0061384)	44580	0.331976424
response to fatty acid (GO:0070542)	44580	0.331976424
leukocyte adhesion to vascular endothelial cell (GO:0061756)	44580	0.331976424
sphingosine metabolic process (GO:0006670)	44580	0.331976424
long-term memory (GO:0007616)	44580	0.331976424
mesenchymal cell development (GO:0014031)	44580	0.331976424
mitochondrion localization (GO:0051646)	44580	0.331976424
N-glycan processing (GO:0006491)	44580	0.331976424
negative regulation of amyloid precursor protein catabolic process (GO::	44580	0.331976424
negative regulation of immune system process (GO:0002683)	44580	0.331976424
negative regulation of RNA splicing (GO:0033119)	44580	0.331976424
negative regulation of T cell receptor signaling pathway (GO:0050860)	44580	0.331976424
nucleotide-sugar biosynthetic process (GO:0009226)	44580	0.331976424
positive regulation of cilium assembly (GO:0045724)	44580	0.331976424
positive regulation of focal adhesion assembly (GO:0051894)	44580	0.331976424
positive regulation of macrophage migration (GO:1905523)	44580	0.331976424
positive regulation of oxidoreductase activity (GO:0051353)	44580	0.331976424
positive regulation of triglyceride metabolic process (GO:0090208)	44580	0.331976424
protein maturation (GO:0051604)	35490	0.333443353
calcium ion homeostasis (GO:0055074)	35490	0.333443353
regulation of MAP kinase activity (GO:0043405)	35490	0.333443353

positive regulation of cold-induced thermogenesis (GO:0120162)	35490	0.333443353
arachidonic acid metabolic process (GO:0019369)	20852	0.337127506
positive regulation of proteolysis (GO:0045862)	20852	0.337127506
regulation of neuron apoptotic process (GO:0043523)	35855	0.339199079
receptor metabolic process (GO:0043112)	21217	0.344798418
RNA modification (GO:0009451)	21217	0.344798418
positive regulation of mitotic cell cycle phase transition (GO:1901992)	21217	0.344798418
response to UV (GO:0009411)	36220	0.344951606
protein targeting to lysosome (GO:0006622)	44581	0.346018236
adrenergic receptor signaling pathway (GO:0071875)	44581	0.346018236
regulation of acute inflammatory response (GO:0002673)	44581	0.346018236
cardiac epithelial to mesenchymal transition (GO:0060317)	44581	0.346018236
cardiac ventricle development (GO:0003231)	44581	0.346018236
regulation of granulocyte chemotaxis (GO:0071622)	44581	0.346018236
cortical actin cytoskeleton organization (GO:0030866)	44581	0.346018236
eye morphogenesis (GO:0048592)	44581	0.346018236
inositol phosphate-mediated signaling (GO:0048016)	44581	0.346018236
lipopolysaccharide-mediated signaling pathway (GO:0031663)	44581	0.346018236
toll-like receptor 4 signaling pathway (GO:0034142)	44581	0.346018236
xenobiotic transport (GO:0042908)	44581	0.346018236
negative regulation of osteoclast differentiation (GO:0045671)	44581	0.346018236
positive regulation of dendrite morphogenesis (GO:0050775)	44581	0.346018236
positive regulation of embryonic development (GO:0040019)	44581	0.346018236
positive regulation of epidermal cell differentiation (GO:0045606)	44581	0.346018236
production of small RNA involved in gene silencing by RNA (GO:0070918	44581	0.346018236
protein localization to organelle (GO:0033365)	4/142	0.348650499
cell-matrix adhesion (GO:0007160)	3/100	0.35069972
negative regulation of autophagy (GO:0010507)	21582	0.352440297
phospholipid transport (GO:0015914)	21582	0.352440297
neuron development (GO:0048666)	4/143	0.353422403
positive regulation of MAPK cascade (GO:0043410)	7/274	0.353523941
cellular response to chemical stress (GO:0062197)	3/101	0.356442234
epithelial cell differentiation (GO:0030855)	3/101	0.356442234
negative regulation of cell migration (GO:0030336)	4/144	0.35819445
acetylcholine receptor signaling pathway (GO:0095500)	44582	0.359765578
anterior/posterior axis specification (GO:0009948)	44582	0.359765578
regulation of anoikis (GO:2000209)	44582	0.359765578
regulation of cell-substrate junction assembly (GO:0090109)	44582	0.359765578
regulation of dendritic spine development (GO:0060998)	44582	0.359765578
regulation of fibroblast migration (GO:0010762)	44582	0.359765578
cobalamin metabolic process (GO:0009235)	44582	0.359765578
regulation of lipopolysaccharide-mediated signaling pathway (GO:00316	44582	0.359765578
regulation of lipoprotein lipase activity (GO:0051004)	44582	0.359765578
endocardial cushion development (GO:0003197)	44582	0.359765578
histone ubiquitination (GO:0016574)	44582	0.359765578
long-term synaptic potentiation (GO:0060291)	44582	0.359765578
melanosome localization (GO:0032400)	44582	0.359765578

myotube differentiation (GO:0014902)	44582	0.359765578
NAD biosynthetic process (GO:0009435)	44582	0.359765578
negative regulation of protein localization to plasma membrane (GO:19(	44582	0.359765578
nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)	44582	0.359765578
poly(A)+ mRNA export from nucleus (GO:0016973)	44582	0.359765578
positive regulation of lipid storage (GO:0010884)	44582	0.359765578
positive regulation of transcription regulatory region DNA binding (GO:2	44582	0.359765578
positive regulation of intracellular signal transduction (GO:1902533)	13/546	0.361669558
calcium-mediated signaling (GO:0019722)	3/102	0.362177988
response to light stimulus (GO:0009416)	22313	0.367628419
positive regulation of DNA biosynthetic process (GO:2000573)	22313	0.367628419
regulation of cardiac muscle cell membrane repolarization (GO:0099623	44583	0.373224609
regulation of macrophage chemotaxis (GO:0010758)	44583	0.373224609
fatty-acyl-CoA metabolic process (GO:0035337)	44583	0.373224609
glutamate metabolic process (GO:0006536)	44583	0.373224609
limb morphogenesis (GO:0035108)	44583	0.373224609
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8	44583	0.373224609
tetrapyrrole metabolic process (GO:0033013)	44583	0.373224609
membrane lipid metabolic process (GO:0006643)	44583	0.373224609
metallo-sulfur cluster assembly (GO:0031163)	44583	0.373224609
microglial cell activation (GO:0001774)	44583	0.373224609
ubiquitin-dependent protein catabolic process via the multivesicular boc	44583	0.373224609
mRNA modification (GO:0016556)	44583	0.373224609
negative regulation of biomineral tissue development (GO:0070168)	44583	0.373224609
negative regulation of lipid biosynthetic process (GO:0051055)	44583	0.373224609
negative regulation of myeloid cell differentiation (GO:0045638)	44583	0.373224609
negative regulation of protein dephosphorylation (GO:0035308)	44583	0.373224609
phosphatidylserine acyl-chain remodeling (GO:0036150)	44583	0.373224609
positive regulation of calcium ion transmembrane transporter activity (C	44583	0.373224609
positive regulation of dendritic spine development (GO:0060999)	44583	0.373224609
positive regulation of neutrophil migration (GO:1902624)	44583	0.373224609
positive regulation of translational initiation (GO:0045948)	44583	0.373224609
negative regulation of cell differentiation (GO:0045596)	5/191	0.373315611
cellular metal ion homeostasis (GO:0006875)	3/104	0.373624713
double-strand break repair via nonhomologous end joining (GO:000630:	22678	0.375170644
regulation of cytosolic calcium ion concentration (GO:0051480)	4/148	0.377269912
positive regulation of intracellular protein transport (GO:0090316)	4/148	0.377269912
activation of GTPase activity (GO:0090630)	3/105	0.379333499
nucleotide-excision repair (GO:0006289)	3/105	0.379333499
amyloid fibril formation (GO:1990000)	23043	0.382675797
anterior/posterior pattern specification (GO:0009952)	23043	0.382675797
regulation of ERK1 and ERK2 cascade (GO:0070372)	6/238	0.383650316
regulation of cell cycle process (GO:0010564)	3/106	0.385031156
cellular response to peptide hormone stimulus (GO:0071375)	3/106	0.385031156
chromosome organization (GO:0051276)	3/106	0.385031156
regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)	3/106	0.385031156
small GTPase mediated signal transduction (GO:0007264)	3/106	0.385031156

positive regulation of protein serine/threonine kinase activity (GO:0071	3/106	0.385031156
acylglycerol biosynthetic process (GO:0046463)	44584	0.386401364
artery development (GO:0060840)	44584	0.386401364
regulation of B cell receptor signaling pathway (GO:0050855)	44584	0.386401364
cytoskeleton-dependent intracellular transport (GO:0030705)	44584	0.386401364
regulation of mononuclear cell migration (GO:0071675)	44584	0.386401364
diacylglycerol metabolic process (GO:0046339)	44584	0.386401364
ERK1 and ERK2 cascade (GO:0070371)	44584	0.386401364
regulation of SMAD protein signal transduction (GO:0060390)	44584	0.386401364
regulation of supramolecular fiber organization (GO:1902903)	44584	0.386401364
membrane protein ectodomain proteolysis (GO:0006509)	44584	0.386401364
negative regulation of G protein-coupled receptor signaling pathway (GO	44584	0.386401364
negative regulation of GTPase activity (GO:0034260)	44584	0.386401364
negative regulation of smoothened signaling pathway (GO:0045879)	44584	0.386401364
positive regulation of cholesterol efflux (GO:0010875)	44584	0.386401364
positive regulation of interleukin-17 production (GO:0032740)	44584	0.386401364
positive regulation of receptor internalization (GO:0002092)	44584	0.386401364
axon extension (GO:0048675)	44585	0.399301747
regulation of cardiac muscle hypertrophy (GO:0010611)	44585	0.399301747
regulation of cellular response to transforming growth factor beta stimu	44585	0.399301747
regulation of keratinocyte proliferation (GO:0010837)	44585	0.399301747
defense response to fungus (GO:0050832)	44585	0.399301747
DNA packaging (GO:0006323)	44585	0.399301747
establishment of mitotic spindle orientation (GO:0000132)	44585	0.399301747
extracellular matrix assembly (GO:0085029)	44585	0.399301747
regulation of vascular endothelial growth factor receptor signaling pathv	44585	0.399301747
immune response-activating cell surface receptor signaling pathway (GO	44585	0.399301747
iron-sulfur cluster assembly (GO:0016226)	44585	0.399301747
leukotriene metabolic process (GO:0006691)	44585	0.399301747
lipid translocation (GO:0034204)	44585	0.399301747
long-chain fatty-acyl-CoA metabolic process (GO:0035336)	44585	0.399301747
negative regulation of NIK/NF-kappaB signaling (GO:1901223)	44585	0.399301747
negative regulation of stress fiber assembly (GO:0051497)	44585	0.399301747
nucleotide-binding domain, leucine rich repeat containing receptor signa	44585	0.399301747
peptidyl-glutamic acid modification (GO:0018200)	44585	0.399301747
positive regulation of cell-substrate junction organization (GO:0150117)	44585	0.399301747
protein exit from endoplasmic reticulum (GO:0032527)	44585	0.399301747
negative regulation of cell population proliferation (GO:0008285)	9/379	0.401573828
regulation of signal transduction (GO:0009966)	5/198	0.402452643
cellular component disassembly (GO:0022411)	24139	0.404951588
embryonic organ development (GO:0048568)	24139	0.404951588
regulation of protein localization (GO:0032880)	24139	0.404951588
ERBB signaling pathway (GO:0038127)	24139	0.404951588
extracellular matrix disassembly (GO:0022617)	24139	0.404951588
positive regulation of cell cycle (GO:0045787)	24139	0.404951588
regulation of protein kinase activity (GO:0045859)	3/110	0.40769036
response to tumor necrosis factor (GO:0034612)	3/110	0.40769036

cellular response to interleukin-1 (GO:0071347)	4/155	0.410499199
regulation of AMPA receptor activity (GO:2000311)	44586	0.411931543
regulation of cAMP-mediated signaling (GO:0043949)	44586	0.411931543
cardiac conduction system development (GO:0003161)	44586	0.411931543
chemical synaptic transmission, postsynaptic (GO:0099565)	44586	0.411931543
divalent inorganic cation homeostasis (GO:0072507)	44586	0.411931543
regulation of spindle assembly (GO:0090169)	44586	0.411931543
negative regulation of antigen receptor-mediated signaling pathway (GC	44586	0.411931543
negative regulation of cell junction assembly (GO:1901889)	44586	0.411931543
negative regulation of sequestering of calcium ion (GO:0051283)	44586	0.411931543
organophosphate ester transport (GO:0015748)	44586	0.411931543
outflow tract septum morphogenesis (GO:0003148)	44586	0.411931543
regulation of viral genome replication (GO:0045069)	24504	0.412291656
transcription elongation from RNA polymerase II promoter (GO:000636	24504	0.412291656
positive regulation of catabolic process (GO:0009896)	24504	0.412291656
cellular divalent inorganic cation homeostasis (GO:0072503)	3/111	0.413317502
regulation of protein serine/threonine kinase activity (GO:0071900)	3/111	0.413317502
protein-containing complex subunit organization (GO:0043933)	3/112	0.418927749
axon guidance (GO:0007411)	5/203	0.423177872
regulation of biomineral tissue development (GO:0070167)	44587	0.424296413
cellular response to drug (GO:0035690)	44587	0.424296413
histone lysine demethylation (GO:0070076)	44587	0.424296413
histone methylation (GO:0016571)	44587	0.424296413
RNA polyadenylation (GO:0043631)	44587	0.424296413
mononuclear cell differentiation (GO:1903131)	44587	0.424296413
mRNA polyadenylation (GO:0006378)	44587	0.424296413
negative regulation of interleukin-1 beta production (GO:0032691)	44587	0.424296413
negative regulation of intrinsic apoptotic signaling pathway in response	44587	0.424296413
negative regulation of macroautophagy (GO:0016242)	44587	0.424296413
negative regulation of receptor-mediated endocytosis (GO:0048261)	44587	0.424296413
phosphatidylethanolamine acyl-chain remodeling (GO:0036152)	44587	0.424296413
positive regulation of filopodium assembly (GO:0051491)	44587	0.424296413
positive regulation of glucose import (GO:0046326)	44587	0.424296413
positive regulation of histone methylation (GO:0031062)	44587	0.424296413
positive regulation of interleukin-2 production (GO:0032743)	44587	0.424296413
positive regulation of metabolic process (GO:0009893)	3/113	0.424520229
skeletal system development (GO:0001501)	4/158	0.424636408
organonitrogen compound biosynthetic process (GO:1901566)	4/158	0.424636408
cellular response to decreased oxygen levels (GO:0036294)	25235	0.426835317
DNA-templated transcription, elongation (GO:0006354)	25235	0.426835317
RNA 3'-end processing (GO:0031123)	25235	0.426835317
positive regulation of protein polymerization (GO:0032273)	25235	0.426835317
positive regulation of protein transport (GO:0051222)	25235	0.426835317
response to lipopolysaccharide (GO:0032496)	4/159	0.4293306
cellular response to molecule of bacterial origin (GO:0071219)	3/115	0.435648528
DNA repair (GO:0006281)	7/298	0.435781185
protein peptidyl-prolyl isomerization (GO:0000413)	44588	0.436401902

camera-type eye development (GO:0043010)	44588	0.436401902
cellular response to unfolded protein (GO:0034620)	44588	0.436401902
cytoplasmic pattern recognition receptor signaling pathway (GO:000275	44588	0.436401902
dendritic spine organization (GO:0097061)	44588	0.436401902
entrainment of circadian clock by photoperiod (GO:0043153)	44588	0.436401902
regulation of toll-like receptor signaling pathway (GO:0034121)	44588	0.436401902
release of sequestered calcium ion into cytosol (GO:0051209)	44588	0.436401902
response to glucocorticoid (GO:0051384)	44588	0.436401902
stress-activated protein kinase signaling cascade (GO:0031098)	44588	0.436401902
melanosome organization (GO:0032438)	44588	0.436401902
monocarboxylic acid catabolic process (GO:0072329)	44588	0.436401902
negative regulation of actin filament bundle assembly (GO:0032232)	44588	0.436401902
negative regulation of endothelial cell apoptotic process (GO:2000352)	44588	0.436401902
positive regulation of cellular component movement (GO:0051272)	44588	0.436401902
positive regulation of gene silencing by miRNA (GO:2000637)	44588	0.436401902
positive regulation of mitotic cell cycle (GO:0045931)	44588	0.436401902
positive regulation of muscle cell differentiation (GO:0051149)	44588	0.436401902
positive regulation of toll-like receptor signaling pathway (GO:0034123)	44588	0.436401902
presynaptic endocytosis (GO:0140238)	44588	0.436401902
positive regulation of multicellular organismal process (GO:0051240)	8/345	0.438411625
regulation of cell population proliferation (GO:0042127)	17/764	0.438477266
regulation of protein kinase B signaling (GO:0051896)	5/207	0.4396651
negative regulation of apoptotic process (GO:0043066)	11/485	0.44058249
regulation of endopeptidase activity (GO:0052548)	25965	0.441188416
negative regulation of neuron apoptotic process (GO:0043524)	25965	0.441188416
phosphatidylinositol-mediated signaling (GO:0048015)	25965	0.441188416
positive regulation of cellular protein localization (GO:1903829)	25965	0.441188416
receptor clustering (GO:0043113)	44589	0.448253438
regulation of calcineurin-NFAT signaling cascade (GO:0070884)	44589	0.448253438
regulation of calcium-mediated signaling (GO:0050848)	44589	0.448253438
carbohydrate derivative biosynthetic process (GO:1901137)	44589	0.448253438
cellular response to acid chemical (GO:0071229)	44589	0.448253438
cellular zinc ion homeostasis (GO:0006882)	44589	0.448253438
regulation of insulin secretion involved in cellular response to glucose st	44589	0.448253438
cytosolic calcium ion transport (GO:0060401)	44589	0.448253438
regulation of microtubule polymerization or depolymerization (GO:0031	44589	0.448253438
regulation of neuron migration (GO:2001222)	44589	0.448253438
regulation of phosphatase activity (GO:0010921)	44589	0.448253438
response to ketone (GO:1901654)	44589	0.448253438
RNA phosphodiester bond hydrolysis (GO:0090501)	44589	0.448253438
sarcomere organization (GO:0045214)	44589	0.448253438
leukocyte cell-cell adhesion (GO:0007159)	44589	0.448253438
sulfur compound transport (GO:0072348)	44589	0.448253438
negative regulation of phosphatase activity (GO:0010923)	44589	0.448253438
neutral amino acid transport (GO:0015804)	44589	0.448253438
nucleotide-binding oligomerization domain containing signaling pathwa	44589	0.448253438
photoperiodism (GO:0009648)	44589	0.448253438

positive regulation of cytosolic calcium ion concentration involved in ph	44589	0.448253438
positive regulation of fibroblast proliferation (GO:0048146)	44589	0.448253438
positive regulation of protein import into nucleus (GO:0042307)	44589	0.448253438
response to ionizing radiation (GO:0010212)	26330	0.448290556
regulation of protein binding (GO:0043393)	3/118	0.452187357
double-strand break repair (GO:0006302)	4/164	0.452640193
response to molecule of bacterial origin (GO:0002237)	26696	0.455341657
transcription-coupled nucleotide-excision repair (GO:0006283)	26696	0.455341657
negative regulation of cell adhesion (GO:0007162)	26696	0.455341657
neurotransmitter transport (GO:0006836)	26696	0.455341657
positive regulation of synaptic transmission (GO:0050806)	26696	0.455341657
negative regulation of canonical Wnt signaling pathway (GO:0090090)	4/165	0.457266173
actin filament polymerization (GO:0030041)	44590	0.459856336
regulation of calcium ion transmembrane transporter activity (GO:1901(	44590	0.459856336
regulation of fatty acid biosynthetic process (GO:0042304)	44590	0.459856336
determination of bilateral symmetry (GO:0009855)	44590	0.459856336
dicarboxylic acid transport (GO:0006835)	44590	0.459856336
regulation of neuronal synaptic plasticity (GO:0048168)	44590	0.459856336
establishment of mitotic spindle localization (GO:0040001)	44590	0.459856336
regulation of T cell mediated cytotoxicity (GO:0001914)	44590	0.459856336
regulation of ubiquitin-protein transferase activity (GO:0051438)	44590	0.459856336
response to zinc ion (GO:0010043)	44590	0.459856336
transition metal ion homeostasis (GO:0055076)	44590	0.459856336
MyD88-dependent toll-like receptor signaling pathway (GO:0002755)	44590	0.459856336
negative regulation of epithelial to mesenchymal transition (GO:001071(	44590	0.459856336
positive regulation of dephosphorylation (GO:0035306)	44590	0.459856336
positive regulation of leukocyte migration (GO:0002687)	44590	0.459856336
production of miRNAs involved in gene silencing by miRNA (GO:003519(	44590	0.459856336
protein K11-linked ubiquitination (GO:0070979)	44590	0.459856336
regulation of MAPK cascade (GO:0043408)	4/166	0.461879002
sphingolipid biosynthetic process (GO:0030148)	27061	0.462340727
NIK/NF-kappaB signaling (GO:0038061)	27061	0.462340727
cellular response to lipopolysaccharide (GO:0071222)	3/120	0.463102083
regulation of transcription from RNA polymerase II promoter in respons	27426	0.46928684
positive regulation of immune response (GO:0050778)	27426	0.46928684
positive regulation of lymphocyte proliferation (GO:0050671)	27426	0.46928684
protein N-linked glycosylation via asparagine (GO:0018279)	44591	0.4712158
artery morphogenesis (GO:0048844)	44591	0.4712158
regulation of cation transmembrane transport (GO:1904062)	44591	0.4712158
regulation of long-term synaptic potentiation (GO:1900271)	44591	0.4712158
regulation of macrophage activation (GO:0043030)	44591	0.4712158
regulation of natural killer cell mediated cytotoxicity (GO:0042269)	44591	0.4712158
establishment of spindle orientation (GO:0051294)	44591	0.4712158
extrinsic apoptotic signaling pathway via death domain receptors (GO:0(	44591	0.4712158
regulation of type I interferon-mediated signaling pathway (GO:006033(	44591	0.4712158
response to alcohol (GO:0097305)	44591	0.4712158
heterotypic cell-cell adhesion (GO:0034113)	44591	0.4712158

synaptic vesicle cycle (GO:0099504)	44591	0.4712158
zinc ion homeostasis (GO:0055069)	44591	0.4712158
negative regulation of gene expression, epigenetic (GO:0045814)	44591	0.4712158
plasma membrane invagination (GO:0099024)	44591	0.4712158
positive regulation of B cell proliferation (GO:0030890)	44591	0.4712158
positive regulation of DNA recombination (GO:0045911)	44591	0.4712158
positive regulation of protein import (GO:1904591)	44591	0.4712158
primary neural tube formation (GO:0014020)	44591	0.4712158
potassium ion transport (GO:0006813)	3/122	0.473921373
RNA transport (GO:0050658)	27791	0.47617913
positive regulation of epithelial cell proliferation (GO:0050679)	3/123	0.4792936
protein palmitoylation (GO:0018345)	44592	0.482336925
activation of protein kinase B activity (GO:0032148)	44592	0.482336925
regulation of cellular pH (GO:0030641)	44592	0.482336925
regulation of cellular senescence (GO:2000772)	44592	0.482336925
cellular nitrogen compound biosynthetic process (GO:0044271)	44592	0.482336925
cellular response to cAMP (GO:0071320)	44592	0.482336925
regulation of potassium ion transport (GO:0043266)	44592	0.482336925
regulation of transmembrane receptor protein serine/threonine kinase s	44592	0.482336925
tube closure (GO:0060606)	44592	0.482336925
negative regulation of response to biotic stimulus (GO:0002832)	44592	0.482336925
organelle transport along microtubule (GO:0072384)	44592	0.482336925
peptidyl-asparagine modification (GO:0018196)	44592	0.482336925
phosphatidylethanolamine metabolic process (GO:0046337)	44592	0.482336925
phospholipid translocation (GO:0045332)	44592	0.482336925
positive regulation of leukocyte cell-cell adhesion (GO:1903039)	44592	0.482336925
positive regulation of locomotion (GO:0040017)	44592	0.482336925
positive regulation of proteolysis involved in cellular protein catabolic pr	44592	0.482336925
positive regulation of Rho protein signal transduction (GO:0035025)	44592	0.482336925
positive regulation of ubiquitin-protein transferase activity (GO:005144	44592	0.482336925
cellular response to UV (GO:0034644)	28157	0.483016791
regulation of organelle assembly (GO:1902115)	28157	0.483016791
positive regulation of type I interferon production (GO:0032481)	28157	0.483016791
defense response to symbiont (GO:0140546)	3/124	0.484640057
regulation of protein phosphorylation (GO:0001932)	6/266	0.48746599
negative regulation of apoptotic signaling pathway (GO:2001234)	28522	0.489799074
negative regulation of protein serine/threonine kinase activity (GO:0071	28522	0.489799074
protein polyubiquitination (GO:0000209)	7/314	0.489922146
cellular response to oxidative stress (GO:0034599)	3/125	0.489960153
regulation of phosphorylation (GO:0042325)	3/125	0.489960153
platelet degranulation (GO:0002576)	3/125	0.489960153
7-methylguanosine mRNA capping (GO:0006370)	11689	0.493224702
7-methylguanosine RNA capping (GO:0009452)	11689	0.493224702
activation of phospholipase C activity (GO:0007202)	11689	0.493224702
regulation of cellular biosynthetic process (GO:0031326)	11689	0.493224702
regulation of centrosome duplication (GO:0010824)	11689	0.493224702
regulation of dendrite morphogenesis (GO:0048814)	11689	0.493224702

cellular response to topologically incorrect protein (GO:0035967)	11689	0.493224702
regulation of intracellular protein transport (GO:0033157)	11689	0.493224702
DNA damage checkpoint signaling (GO:0000077)	11689	0.493224702
establishment or maintenance of epithelial cell apical/basal polarity (GO	11689	0.493224702
regulation of transcription involved in G1/S transition of mitotic cell cycl	11689	0.493224702
response to amino acid (GO:0043200)	11689	0.493224702
superoxide metabolic process (GO:0006801)	11689	0.493224702
negative regulation of cell-matrix adhesion (GO:0001953)	11689	0.493224702
negative regulation of chemotaxis (GO:0050922)	11689	0.493224702
peptidyl-proline modification (GO:0018208)	11689	0.493224702
positive regulation of glucose transmembrane transport (GO:0010828)	11689	0.493224702
positive regulation of lamellipodium organization (GO:1902745)	11689	0.493224702
negative regulation of cell growth (GO:0030308)	3/126	0.495253319
recombinational repair (GO:0000725)	28887	0.496525285
axon development (GO:0061564)	28887	0.496525285
regulation of neuron differentiation (GO:0045664)	28887	0.496525285
mRNA 3'-end processing (GO:0031124)	28887	0.496525285
neuron differentiation (GO:0030182)	4/174	0.498252738
mitochondrion organization (GO:0007005)	4/175	0.502726846
regulation of protein localization to plasma membrane (GO:1903076)	29252	0.503194786
glycerophospholipid metabolic process (GO:0006650)	29252	0.503194786
lipid biosynthetic process (GO:0008610)	29252	0.503194786
negative regulation of cellular component organization (GO:0051129)	29252	0.503194786
actin filament bundle assembly (GO:0051017)	12055	0.503884013
actin filament bundle organization (GO:0061572)	12055	0.503884013
regulation of interleukin-17 production (GO:0032660)	12055	0.503884013
regulation of neurotransmitter secretion (GO:0046928)	12055	0.503884013
regulation of protein localization to cell surface (GO:2000008)	12055	0.503884013
RNA stabilization (GO:0043489)	12055	0.503884013
signal transduction by p53 class mediator (GO:0072331)	12055	0.503884013
vasculogenesis (GO:0001570)	12055	0.503884013
negative chemotaxis (GO:0050919)	12055	0.503884013
phosphatidylcholine biosynthetic process (GO:0006656)	12055	0.503884013
positive regulation of cholesterol transport (GO:0032376)	12055	0.503884013
positive regulation of organelle organization (GO:0010638)	12055	0.503884013
positive regulation of receptor signaling pathway via JAK-STAT (GO:0046	12055	0.503884013
primary alcohol metabolic process (GO:0034308)	12055	0.503884013
regulation of amyloid-beta formation (GO:1902003)	12420	0.514319643
B cell receptor signaling pathway (GO:0050853)	12420	0.514319643
regulation of cell adhesion mediated by integrin (GO:0033628)	12420	0.514319643
cardiac muscle contraction (GO:0060048)	12420	0.514319643
cellular response to amino acid stimulus (GO:0071230)	12420	0.514319643
regulation of lamellipodium assembly (GO:0010591)	12420	0.514319643
regulation of myoblast differentiation (GO:0045661)	12420	0.514319643
female gamete generation (GO:0007292)	12420	0.514319643
synaptic vesicle recycling (GO:0036465)	12420	0.514319643
termination of RNA polymerase II transcription (GO:0006369)	12420	0.514319643

tRNA methylation (GO:0030488)	12420	0.514319643
ventricular cardiac muscle tissue morphogenesis (GO:0055010)	12420	0.514319643
negative regulation of extrinsic apoptotic signaling pathway via death dc	12420	0.514319643
organelle disassembly (GO:1903008)	12420	0.514319643
phosphatidylinositol 3-kinase signaling (GO:0014065)	12420	0.514319643
phosphatidylserine metabolic process (GO:0006658)	12420	0.514319643
positive regulation of DNA binding (GO:0043388)	12420	0.514319643
positive regulation of protein dephosphorylation (GO:0035307)	12420	0.514319643
protein insertion into membrane (GO:0051205)	12420	0.514319643
protein localization to chromosome (GO:0034502)	12420	0.514319643
regulation of response to external stimulus (GO:0032101)	3/130	0.516146
protein glycosylation (GO:0006486)	3/130	0.516146
regulation of cyclin-dependent protein serine/threonine kinase activity (	29983	0.516361347
cell-cell junction organization (GO:0045216)	29983	0.516361347
RNA processing (GO:0006396)	4/179	0.52044473
cellular response to hypoxia (GO:0071456)	3/131	0.521296686
regulation of interleukin-1 beta production (GO:0032651)	30348	0.522857378
long-chain fatty acid metabolic process (GO:0001676)	30348	0.522857378
positive regulation of plasma membrane bounded cell projection assem	30348	0.522857378
acylglycerol catabolic process (GO:0046464)	12785	0.524536274
regulation of autophagosome assembly (GO:2000785)	12785	0.524536274
base-excision repair, gap-filling (GO:0006287)	12785	0.524536274
bicarbonate transport (GO:0015701)	12785	0.524536274
cellular response to amyloid-beta (GO:1904646)	12785	0.524536274
regulation of lipid biosynthetic process (GO:0046890)	12785	0.524536274
regulation of mitotic spindle organization (GO:0060236)	12785	0.524536274
regulation of phosphatidylinositol 3-kinase activity (GO:0043551)	12785	0.524536274
regulation of postsynaptic membrane potential (GO:0060078)	12785	0.524536274
regulation of protein polymerization (GO:0032271)	12785	0.524536274
regulation of T cell receptor signaling pathway (GO:0050856)	12785	0.524536274
semaphorin-plexin signaling pathway (GO:0071526)	12785	0.524536274
smoothened signaling pathway (GO:0007224)	12785	0.524536274
maturation of SSU-rRNA (GO:0030490)	12785	0.524536274
muscle cell differentiation (GO:0042692)	12785	0.524536274
negative regulation of epithelial cell migration (GO:0010633)	12785	0.524536274
negative regulation of organelle assembly (GO:1902116)	12785	0.524536274
peptidyl-tyrosine dephosphorylation (GO:0035335)	12785	0.524536274
positive regulation of lipid biosynthetic process (GO:0046889)	12785	0.524536274
positive regulation of lymphocyte activation (GO:0051251)	12785	0.524536274
negative regulation of cellular process (GO:0048523)	12/566	0.527839778
vascular transport (GO:0010232)	30713	0.529294634
regulation of cell adhesion (GO:0030155)	3/133	0.531507868
defense response to virus (GO:0051607)	3/133	0.531507868
axonal transport (GO:0098930)	13150	0.534538491
regulation of embryonic development (GO:0045995)	13150	0.534538491
dendrite morphogenesis (GO:0048813)	13150	0.534538491
regulation of osteoclast differentiation (GO:0045670)	13150	0.534538491

embryonic limb morphogenesis (GO:0030326)	13150	0.534538491
regulation of protein import into nucleus (GO:0042306)	13150	0.534538491
establishment of protein localization to plasma membrane (GO:00619513150		0.534538491
regulation of sodium ion transport (GO:0002028)	13150	0.534538491
macrophage activation (GO:0042116)	13150	0.534538491
membrane assembly (GO:0071709)	13150	0.534538491
membrane fusion (GO:0061025)	13150	0.534538491
negative regulation of cellular protein localization (GO:1903828)	13150	0.534538491
negative regulation of DNA metabolic process (GO:0051053)	13150	0.534538491
negative regulation of fat cell differentiation (GO:0045599)	13150	0.534538491
negative regulation of toll-like receptor signaling pathway (GO:0034122)	13150	0.534538491
positive regulation of bone mineralization (GO:0030501)	13150	0.534538491
positive regulation of myeloid leukocyte differentiation (GO:0002763)	13150	0.534538491
Wnt signaling pathway, planar cell polarity pathway (GO:0060071)	31079	0.535672713
glucose homeostasis (GO:0042593)	31444	0.541991256
response to interleukin-1 (GO:0070555)	31444	0.541991256
transport across blood-brain barrier (GO:0150104)	31444	0.541991256
proton transmembrane transport (GO:1902600)	13516	0.544330783
anterograde axonal transport (GO:0008089)	13516	0.544330783
regulation of glucose import (GO:0046324)	13516	0.544330783
regulation of intracellular pH (GO:0051453)	13516	0.544330783
glutamate receptor signaling pathway (GO:0007215)	13516	0.544330783
glutamine family amino acid metabolic process (GO:0009064)	13516	0.544330783
negative regulation of epithelial cell apoptotic process (GO:1904036)	13516	0.544330783
phagocytosis, engulfment (GO:0006911)	13516	0.544330783
phospholipid biosynthetic process (GO:0008654)	13516	0.544330783
positive regulation of signaling receptor activity (GO:2000273)	13516	0.544330783
protein insertion into ER membrane (GO:0045048)	13516	0.544330783
cytokine-mediated signaling pathway (GO:0019221)	13/621	0.544392215
cellular calcium ion homeostasis (GO:0006874)	3/136	0.546592999
organic substance transport (GO:0071702)	3/136	0.546592999
negative regulation of angiogenesis (GO:0016525)	31809	0.548249948
negative regulation of programmed cell death (GO:0043069)	8/381	0.549992679
regulation of apoptotic signaling pathway (GO:2001233)	13881	0.553917547
response to cAMP (GO:0051591)	13881	0.553917547
spliceosomal snRNP assembly (GO:0000387)	13881	0.553917547
lymphocyte proliferation (GO:0046651)	13881	0.553917547
mRNA destabilization (GO:0061157)	13881	0.553917547
negative regulation of innate immune response (GO:0045824)	13881	0.553917547
positive regulation of potassium ion transport (GO:0043268)	13881	0.553917547
regulation of establishment of planar polarity (GO:0090175)	32174	0.554448509
positive regulation of macromolecule metabolic process (GO:0010604)	8/384	0.558916552
cellular response to cytokine stimulus (GO:0071345)	10/482	0.560388214
regulation of cysteine-type endopeptidase activity involved in apoptotic	32540	0.560586699
regulation of endothelial cell migration (GO:0010594)	32540	0.560586699
collagen fibril organization (GO:0030199)	32540	0.560586699
regulation of type I interferon production (GO:0032479)	32540	0.560586699

SCF-dependent proteasomal ubiquitin-dependent protein catabolic proc	32540	0.560586699
post-Golgi vesicle-mediated transport (GO:0006892)	32540	0.560586699
potassium ion transmembrane transport (GO:0071805)	3/139	0.561391277
proteolysis (GO:0006508)	6/287	0.561566343
regulation of exit from mitosis (GO:0007096)	14246	0.563303085
DNA integrity checkpoint signaling (GO:0031570)	14246	0.563303085
DNA recombination (GO:0006310)	14246	0.563303085
endothelial cell migration (GO:0043542)	14246	0.563303085
response to peptide (GO:1901652)	14246	0.563303085
membrane protein proteolysis (GO:0033619)	14246	0.563303085
negative regulation of secretion by cell (GO:1903531)	14246	0.563303085
odontogenesis (GO:0042476)	14246	0.563303085
organophosphate biosynthetic process (GO:0090407)	14246	0.563303085
regulation of GTPase activity (GO:0043087)	4/189	0.563370833
axonogenesis (GO:0007409)	5/240	0.569501171
negative regulation of Wnt signaling pathway (GO:0030178)	4/191	0.57170233
regulation of nitric oxide biosynthetic process (GO:0045428)	14611	0.572491612
glycolipid biosynthetic process (GO:0009247)	14611	0.572491612
lymphocyte migration (GO:0072676)	14611	0.572491612
synaptic vesicle exocytosis (GO:0016079)	14611	0.572491612
positive regulation of catalytic activity (GO:0043085)	14611	0.572491612
positive regulation of ossification (GO:0045778)	14611	0.572491612
positive regulation of wound healing (GO:0090303)	14611	0.572491612
regulation of actin cytoskeleton organization (GO:0032956)	33270	0.57268119
positive regulation of supramolecular fiber organization (GO:1902905)	33270	0.57268119
receptor-mediated endocytosis (GO:0006898)	3/143	0.580661237
protein methylation (GO:0006479)	14977	0.581487254
acylglycerol metabolic process (GO:0006639)	14977	0.581487254
carboxylic acid transmembrane transport (GO:1905039)	14977	0.581487254
regulation of filopodium assembly (GO:0051489)	14977	0.581487254
cortical cytoskeleton organization (GO:0030865)	14977	0.581487254
heart contraction (GO:0060047)	14977	0.581487254
T cell differentiation (GO:0030217)	14977	0.581487254
positive regulation of biomineral tissue development (GO:0070169)	14977	0.581487254
positive regulation of cation transmembrane transport (GO:1904064)	14977	0.581487254
positive regulation of TOR signaling (GO:0032008)	14977	0.581487254
regulation of programmed cell death (GO:0043067)	4/194	0.584031445
visual perception (GO:0007601)	34001	0.584532206
calcium ion transmembrane import into cytosol (GO:0097553)	15342	0.590294049
regulation of double-strand break repair (GO:2000779)	15342	0.590294049
regulation of extrinsic apoptotic signaling pathway via death domain rec	15342	0.590294049
determination of left/right symmetry (GO:0007368)	15342	0.590294049
regulation of ubiquitin-dependent protein catabolic process (GO:200005	15342	0.590294049
negative regulation of protein catabolic process (GO:0042177)	15342	0.590294049
negative regulation of cellular protein metabolic process (GO:0032269)	34366	0.590366173
negative regulation of MAPK cascade (GO:0043409)	34366	0.590366173
sensory perception of light stimulus (GO:0050953)	34731	0.596139048

cellular response to retinoic acid (GO:0071300)	15707	0.598915953
lipid modification (GO:0030258)	15707	0.598915953
substantia nigra development (GO:0021762)	15707	0.598915953
myofibril assembly (GO:0030239)	15707	0.598915953
natural killer cell activation (GO:0030101)	15707	0.598915953
negative regulation of type I interferon production (GO:0032480)	15707	0.598915953
positive regulation of leukocyte mediated cytotoxicity (GO:0001912)	15707	0.598915953
positive regulation of neuron differentiation (GO:0045666)	15707	0.598915953
positive regulation of peptide hormone secretion (GO:0090277)	15707	0.598915953
positive regulation of T cell differentiation (GO:0045582)	15707	0.598915953
cellular transition metal ion homeostasis (GO:0046916)	35096	0.601850818
positive regulation of transferase activity (GO:0051347)	3/148	0.603984462
extracellular matrix organization (GO:0030198)	6/300	0.604808507
cardiac ventricle morphogenesis (GO:0003208)	16072	0.60735684
cation transmembrane transport (GO:0098655)	16072	0.60735684
regulation of endothelial cell apoptotic process (GO:2000351)	16072	0.60735684
response to amyloid-beta (GO:1904645)	16072	0.60735684
lymphocyte chemotaxis (GO:0048247)	16072	0.60735684
mitotic spindle assembly (GO:0090307)	16072	0.60735684
mRNA stabilization (GO:0048255)	16072	0.60735684
positive regulation of biosynthetic process (GO:0009891)	16072	0.60735684
positive regulation of cell-matrix adhesion (GO:0001954)	16072	0.60735684
positive regulation of osteoblast differentiation (GO:0045669)	16072	0.60735684
positive regulation of potassium ion transmembrane transport (GO:190	16072	0.60735684
double-strand break repair via homologous recombination (GO:000072	35462	0.607501497
supramolecular fiber organization (GO:0097435)	7/351	0.607719133
regulation of peptidyl-serine phosphorylation (GO:0033135)	35827	0.613091127
negative regulation of neuron death (GO:1901215)	35827	0.613091127
action potential (GO:0001508)	16438	0.615620499
cellular response to radiation (GO:0071478)	16438	0.615620499
zymogen activation (GO:0031638)	16438	0.615620499
negative regulation of T cell activation (GO:0050868)	16438	0.615620499
positive regulation of chemotaxis (GO:0050921)	16438	0.615620499
organic anion transport (GO:0015711)	36192	0.618619772
gene expression (GO:0010467)	7/356	0.622523858
alpha-amino acid metabolic process (GO:1901605)	16803	0.623710644
regulation of B cell proliferation (GO:0030888)	16803	0.623710644
regulation of double-strand break repair via homologous recombination	16803	0.623710644
erythrocyte differentiation (GO:0030218)	16803	0.623710644
negative regulation of tumor necrosis factor production (GO:0032720)	16803	0.623710644
positive regulation of nucleocytoplasmic transport (GO:0046824)	16803	0.623710644
positive regulation of translation (GO:0045727)	2/100	0.624087524
positive regulation of cell cycle process (GO:0090068)	2/101	0.629494495
positive regulation of protein localization to membrane (GO:1905477)	2/101	0.629494495
regulation of protein localization to nucleus (GO:1900180)	17168	0.63163091
regulation of synapse assembly (GO:0051963)	17168	0.63163091
regulation of wound healing (GO:0061041)	17168	0.63163091

telomere organization (GO:0032200)	17168	0.63163091
positive regulation of cell-cell adhesion (GO:0022409)	17168	0.63163091
protein O-linked glycosylation (GO:0006493)	2/102	0.634840821
cell junction assembly (GO:0034329)	2/102	0.634840821
positive regulation of cell growth (GO:0030307)	2/102	0.634840821
purine ribonucleotide biosynthetic process (GO:0009152)	17533	0.639384856
cellular response to alcohol (GO:0097306)	17533	0.639384856
cellular response to ionizing radiation (GO:0071479)	17533	0.639384856
regulation of interleukin-2 production (GO:0032663)	17533	0.639384856
regulation of protein metabolic process (GO:0051246)	17533	0.639384856
Golgi to plasma membrane transport (GO:0006893)	17533	0.639384856
myelination (GO:0042552)	17533	0.639384856
negative regulation of MAP kinase activity (GO:0043407)	17533	0.639384856
negative regulation of tumor necrosis factor superfamily cytokine produ	17533	0.639384856
nucleus organization (GO:0006997)	17533	0.639384856
translational elongation (GO:0006414)	2/104	0.645352182
cellular defense response (GO:0006968)	17899	0.646975965
regulation of interferon-beta production (GO:0032648)	17899	0.646975965
response to unfolded protein (GO:0006986)	17899	0.646975965
secondary alcohol metabolic process (GO:1902652)	17899	0.646975965
negative regulation of cell projection organization (GO:0031345)	17899	0.646975965
positive regulation of reactive oxygen species metabolic process (GO:20	17899	0.646975965
cilium assembly (GO:0060271)	6/314	0.648667669
positive regulation of cellular metabolic process (GO:0031325)	2/105	0.650517588
actin polymerization or depolymerization (GO:0008154)	18264	0.654407649
amino acid transport (GO:0006865)	18264	0.654407649
positive regulation of protein kinase B signaling (GO:0051897)	3/161	0.660506653
positive regulation of GTPase activity (GO:0043547)	4/214	0.660722399
positive regulation of protein modification process (GO:0031401)	4/214	0.660722399
regulation of axonogenesis (GO:0050770)	18629	0.66168325
regulation of interleukin-12 production (GO:0032655)	18629	0.66168325
regulation of protein modification process (GO:0031399)	18629	0.66168325
regulation of smoothened signaling pathway (GO:0008589)	18629	0.66168325
negative regulation of transport (GO:0051051)	18629	0.66168325
positive regulation of cellular process (GO:0048522)	12/625	0.665003931
positive regulation of protein phosphorylation (GO:0001934)	7/371	0.665029165
DNA replication (GO:0006260)	2/108	0.665655334
amide biosynthetic process (GO:0043604)	18994	0.668806036
regulation of exocytosis (GO:0017157)	18994	0.668806036
endocytic recycling (GO:0032456)	18994	0.668806036
glycolipid metabolic process (GO:0006664)	18994	0.668806036
sprouting angiogenesis (GO:0002040)	18994	0.668806036
negative regulation of protein metabolic process (GO:0051248)	18994	0.668806036
plasma membrane bounded cell projection morphogenesis (GO:012003	18994	0.668806036
organelle assembly (GO:0070925)	8/425	0.672137967
negative regulation of cysteine-type endopeptidase activity (GO:200011	19360	0.675779211
positive regulation of B cell activation (GO:0050871)	19360	0.675779211

positive regulation of chemokine production (GO:0032722)	19360	0.675779211
Fc-epsilon receptor signaling pathway (GO:0038095)	2/111	0.680260737
positive regulation of leukocyte chemotaxis (GO:0002690)	19725	0.68260591
Fc receptor signaling pathway (GO:0038093)	2/112	0.685012241
inorganic cation transmembrane transport (GO:0098662)	5/274	0.68510819
cellular protein-containing complex assembly (GO:0034622)	3/168	0.688432304
regulation of cardiac conduction (GO:1903779)	20090	0.689289202
glycoprotein metabolic process (GO:0009100)	20090	0.689289202
triglyceride metabolic process (GO:0006641)	20090	0.689289202
DNA metabolic process (GO:0006259)	5/277	0.69423245
chemokine-mediated signaling pathway (GO:0070098)	20455	0.695832092
nuclear-transcribed mRNA catabolic process, deadenylation-dependent	20455	0.695832092
peptidyl-tyrosine modification (GO:0018212)	20455	0.695832092
positive regulation of interleukin-1 beta production (GO:0032731)	20455	0.695832092
plasma membrane bounded cell projection assembly (GO:0120031)	5/278	0.697233438
positive regulation of protein metabolic process (GO:0051247)	2/115	0.69892034
regulation of bone mineralization (GO:0030500)	20821	0.702237524
cellular response to peptide (GO:1901653)	20821	0.702237524
regulation of reactive oxygen species metabolic process (GO:2000377)	20821	0.702237524
positive regulation of cell junction assembly (GO:1901890)	20821	0.702237524
positive regulation of gene expression, epigenetic (GO:0045815)	20821	0.702237524
protein K48-linked ubiquitination (GO:0070936)	20821	0.702237524
regulation of protein-containing complex assembly (GO:0043254)	2/116	0.703442047
ion transport (GO:0006811)	2/116	0.703442047
sphingolipid metabolic process (GO:0006665)	2/116	0.703442047
tumor necrosis factor-mediated signaling pathway (GO:0033209)	2/116	0.703442047
autophagosome assembly (GO:0000045)	21186	0.708508379
cellular iron ion homeostasis (GO:0006879)	21186	0.708508379
regulation of pathway-restricted SMAD protein phosphorylation (GO:00	21186	0.708508379
regulation of phagocytosis (GO:0050764)	21186	0.708508379
muscle organ development (GO:0007517)	21186	0.708508379
negative regulation of hydrolase activity (GO:0051346)	21186	0.708508379
negative regulation of neuron projection development (GO:0010977)	21186	0.708508379
protein polymerization (GO:0051258)	21551	0.714647477
regulation of secretion by cell (GO:1903530)	21551	0.714647477
mitotic DNA damage checkpoint signaling (GO:0044773)	21551	0.714647477
inflammatory response (GO:0006954)	4/230	0.714785784
adenylate cyclase-inhibiting G protein-coupled receptor signaling pathw	21916	0.72065758
cellular protein catabolic process (GO:0044257)	21916	0.72065758
cellular response to chemokine (GO:1990869)	21916	0.72065758
homophilic cell adhesion via plasma membrane adhesion molecules (GC	21916	0.72065758
ribonucleoprotein complex biogenesis (GO:0022613)	21916	0.72065758
macroautophagy (GO:0016236)	2/120	0.72096705
iron ion homeostasis (GO:0055072)	22282	0.726541392
O-glycan processing (GO:0016266)	22282	0.726541392
pattern recognition receptor signaling pathway (GO:0002221)	22282	0.726541392
protein lipidation (GO:0006497)	22282	0.726541392

epithelium development (GO:0060429)	2/122	0.72939792
I-kappaB kinase/NF-kappaB signaling (GO:0007249)	22647	0.732301561
positive regulation of cysteine-type endopeptidase activity (GO:200105(	22647	0.732301561
positive regulation of interleukin-1 production (GO:0032732)	22647	0.732301561
post-translational protein modification (GO:0043687)	6/345	0.734621036
regulation of tumor necrosis factor production (GO:0032680)	2/124	0.73761206
cell cycle G1/S phase transition (GO:0044843)	23012	0.737940679
COPII vesicle coating (GO:0048208)	23012	0.737940679
vesicle coating (GO:0006901)	23012	0.737940679
vesicle targeting, rough ER to cis-Golgi (GO:0048207)	23012	0.737940679
negative regulation of cytokine production (GO:0001818)	3/182	0.739047
regulation of protein secretion (GO:0050708)	2/125	0.741638915
regulation of cellular ketone metabolic process (GO:0010565)	23377	0.743461284
lipid homeostasis (GO:0055088)	23377	0.743461284
plasma membrane organization (GO:0007009)	23377	0.743461284
protein catabolic process (GO:0030163)	23377	0.743461284
regulation of cell-matrix adhesion (GO:0001952)	23743	0.74886586
cellular response to type I interferon (GO:0071357)	23743	0.74886586
chemical homeostasis (GO:0048878)	23743	0.74886586
regulation of RNA metabolic process (GO:0051252)	23743	0.74886586
tRNA modification (GO:0006400)	23743	0.74886586
type I interferon signaling pathway (GO:0060337)	23743	0.74886586
antigen receptor-mediated signaling pathway (GO:0050851)	3/185	0.74900363
positive regulation of cell death (GO:0010942)	24108	0.754156842
protein N-linked glycosylation (GO:0006487)	24473	0.75933661
anion transmembrane transport (GO:0098656)	24473	0.75933661
regulation of gene silencing by miRNA (GO:0060964)	24473	0.75933661
regulation of translational initiation (GO:0006446)	24838	0.764407497
regulation of tyrosine phosphorylation of STAT protein (GO:0042509)	24838	0.764407497
positive regulation of protein localization to nucleus (GO:1900182)	24838	0.764407497
negative regulation of cellular catabolic process (GO:0031330)	25204	0.769371786
peptidyl-tyrosine phosphorylation (GO:0018108)	25204	0.769371786
RNA metabolic process (GO:0016070)	2/133	0.771986892
carbohydrate homeostasis (GO:0033500)	25569	0.774231714
cellular response to light stimulus (GO:0071482)	25569	0.774231714
COPII-coated vesicle budding (GO:0090114)	25569	0.774231714
DNA-templated transcription, termination (GO:0006353)	25569	0.774231714
fatty acid catabolic process (GO:0009062)	25569	0.774231714
snRNA transcription by RNA polymerase II (GO:0042795)	25569	0.774231714
sterol metabolic process (GO:0016125)	25569	0.774231714
neutrophil chemotaxis (GO:0030593)	25569	0.774231714
positive regulation of peptidyl-tyrosine phosphorylation (GO:0050731)	2/134	0.775553847
cellular response to tumor necrosis factor (GO:0071356)	3/194	0.777056592
Fc-gamma receptor signaling pathway involved in phagocytosis (GO:003	25934	0.778989468
response to metal ion (GO:0010038)	25934	0.778989468
snRNA transcription (GO:0009301)	25934	0.778989468
nucleic acid metabolic process (GO:0090304)	25934	0.778989468

ribonucleoprotein complex assembly (GO:0022618)	2/136	0.782541835
negative regulation of inflammatory response to antigenic stimulus (GO:	2/136	0.782541835
cell junction organization (GO:0034330)	26299	0.783647191
extrinsic apoptotic signaling pathway (GO:0097191)	26299	0.783647191
Fc-gamma receptor signaling pathway (GO:0038094)	26299	0.783647191
negative regulation of epithelial cell proliferation (GO:0050680)	26299	0.783647191
regulation of inflammatory response to antigenic stimulus (GO:0002861	2/137	0.785963811
regulation of actin filament polymerization (GO:0030833)	26665	0.788206983
regulation of hydrolase activity (GO:0051336)	26665	0.788206983
granulocyte chemotaxis (GO:0071621)	26665	0.788206983
insulin receptor signaling pathway (GO:0008286)	26665	0.788206983
Fc receptor mediated stimulatory signaling pathway (GO:0002431)	27030	0.792670897
mitotic nuclear division (GO:0140014)	27030	0.792670897
enzyme linked receptor protein signaling pathway (GO:0007167)	2/140	0.795947357
neuron projection morphogenesis (GO:0048812)	2/140	0.795947357
fibroblast growth factor receptor signaling pathway (GO:0008543)	27395	0.797040944
nucleic acid phosphodiester bond hydrolysis (GO:0090305)	27395	0.797040944
water-soluble vitamin metabolic process (GO:0006767)	27760	0.801319094
positive regulation of interleukin-6 production (GO:0032755)	27760	0.801319094
cholesterol metabolic process (GO:0008203)	28126	0.805507275
import into nucleus (GO:0051170)	28126	0.805507275
neutrophil migration (GO:1990266)	28126	0.805507275
positive regulation of phosphatidylinositol 3-kinase signaling (GO:00140	28126	0.805507275
protein modification process (GO:0036211)	28491	0.809607374
antigen processing and presentation of exogenous peptide antigen via M	28491	0.809607374
negative regulation of blood vessel morphogenesis (GO:2000181)	28491	0.809607374
regulation of cellular response to heat (GO:1900034)	28856	0.813621239
regulation of ion transport (GO:0043269)	28856	0.813621239
positive regulation of ubiquitin-dependent protein catabolic process (GC	28856	0.813621239
regulation of mRNA stability (GO:0043488)	2/146	0.814686629
response to interferon-gamma (GO:0034341)	29221	0.81755068
negative regulation of cell cycle (GO:0045786)	29221	0.81755068
negative regulation of extrinsic apoptotic signaling pathway (GO:200123	29221	0.81755068
regulation of interleukin-8 production (GO:0032677)	29587	0.821397469
positive regulation of cellular amide metabolic process (GO:0034250)	29587	0.821397469
positive regulation of tumor necrosis factor superfamily cytokine produc	29587	0.821397469
regulation of G2/M transition of mitotic cell cycle (GO:0010389)	2/149	0.82346812
positive regulation of hydrolase activity (GO:0051345)	2/149	0.82346812
cellular protein localization (GO:0034613)	5/329	0.823731842
regulation of G protein-coupled receptor signaling pathway (GO:000827	29952	0.825163339
positive regulation of cytoskeleton organization (GO:0051495)	29952	0.825163339
epidermis development (GO:0008544)	30317	0.82884999
anaphase-promoting complex-dependent catabolic process (GO:003114	30682	0.832459083
regulation of cytokinesis (GO:0032465)	30682	0.832459083
nuclear export (GO:0051168)	30682	0.832459083
extracellular structure organization (GO:0043062)	3/216	0.834888997
positive regulation of cytokine production (GO:0001819)	5/335	0.835345164

G1/S transition of mitotic cell cycle (GO:0000082)	31048	0.835992246
retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum (	31048	0.835992246
negative regulation of defense response (GO:0031348)	31048	0.835992246
external encapsulating structure organization (GO:0045229)	3/217	0.837181424
regulation of neuron death (GO:1901214)	31413	0.839451074
positive regulation of endothelial cell migration (GO:0010595)	31413	0.839451074
calcium ion transmembrane transport (GO:0070588)	31778	0.842837126
regulation of transcription from RNA polymerase II promoter in respons	31778	0.842837126
mitotic spindle organization (GO:0007052)	2/157	0.845086627
sensory perception of mechanical stimulus (GO:0050954)	32143	0.84615193
metal ion transport (GO:0030001)	32143	0.84615193
negative regulation of binding (GO:0051100)	32143	0.84615193
T cell receptor signaling pathway (GO:0050852)	2/158	0.847613386
regulation of cation channel activity (GO:2001257)	32509	0.849396982
mitochondrial translational elongation (GO:0070125)	32509	0.849396982
mitochondrial translational termination (GO:0070126)	32509	0.849396982
cellular amino acid catabolic process (GO:0009063)	32874	0.852573746
positive regulation of binding (GO:0051099)	32874	0.852573746
protein complex oligomerization (GO:0051259)	32874	0.852573746
transmembrane receptor protein tyrosine kinase signaling pathway (GO	6/404	0.854647813
sensory perception of sound (GO:0007605)	33239	0.855683655
toll-like receptor signaling pathway (GO:0002224)	33239	0.855683655
peptide biosynthetic process (GO:0043043)	2/162	0.857350208
cellular response to fibroblast growth factor stimulus (GO:0044344)	33604	0.858728114
positive regulation of cellular component biogenesis (GO:0044089)	33604	0.858728114
regulation of heart contraction (GO:0008016)	33970	0.861708497
positive regulation of peptidyl-serine phosphorylation (GO:0033138)	33970	0.861708497
adenylate cyclase-modulating G protein-coupled receptor signaling path	2/165	0.864276692
negative regulation of cell death (GO:0060548)	34335	0.864626149
nucleosome organization (GO:0034728)	34335	0.864626149
regulation of cell cycle phase transition (GO:1901987)	34700	0.867482387
ciliary basal body-plasma membrane docking (GO:0097711)	34700	0.867482387
translational termination (GO:0006415)	35065	0.870278501
positive regulation of cell population proliferation (GO:0008284)	7/474	0.872620117
nuclear-transcribed mRNA catabolic process (GO:0000956)	2/171	0.87721391
innate immune response (GO:0045087)	4/302	0.881322211
MAPK cascade (GO:0000165)	4/303	0.882869454
cation transport (GO:0006812)	2/174	0.883247727
positive regulation of cellular protein metabolic process (GO:0032270)	1/102	0.88586147
protein targeting to ER (GO:0045047)	1/103	0.888270627
anterograde trans-synaptic signaling (GO:0098916)	3/244	0.889460489
protein transport (GO:0015031)	5/369	0.889856247
regulation of insulin secretion (GO:0050796)	1/104	0.890629051
regulation of mitotic cell cycle (GO:0007346)	2/178	0.890867047
regulation of immune response (GO:0050776)	2/179	0.892698528
mitochondrial translation (GO:0032543)	1/105	0.892937808
positive regulation of cellular biosynthetic process (GO:0031328)	2/180	0.894501457

protein processing (GO:0016485)	1/106	0.89519794
peptidyl-lysine modification (GO:0018205)	1/106	0.89519794
protein localization to nucleus (GO:0034504)	1/106	0.89519794
positive regulation of phosphorylation (GO:0042327)	3/253	0.903222863
regulation of interleukin-6 production (GO:0032675)	1/110	0.903772346
regulation of cytoskeleton organization (GO:0051493)	1/112	0.907793372
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	1/113	0.909740575
calcium ion transport (GO:0006816)	1/115	0.913512766
cellular response to lectin (GO:1990858)	1/115	0.913512766
stimulatory C-type lectin receptor signaling pathway (GO:0002223)	1/115	0.913512766
adenylate cyclase-activating G protein-coupled receptor signaling pathw	1/118	0.91887818
regulation of cellular response to stress (GO:0080135)	1/118	0.91887818
negative regulation of response to external stimulus (GO:0032102)	1/118	0.91887818
innate immune response activating cell surface receptor signaling pathw	1/119	0.920591807
cellular response to interferon-gamma (GO:0071346)	1/121	0.923911474
protein homooligomerization (GO:0051260)	1/121	0.923911474
intracellular protein transport (GO:0006886)	4/336	0.924959379
ncRNA processing (GO:0034470)	2/201	0.926421624
fatty acid metabolic process (GO:0006631)	1/124	0.92863316
protein targeting (GO:0006605)	1/125	0.930141171
synapse organization (GO:0050808)	1/126	0.93161739
microtubule cytoskeleton organization involved in mitosis (GO:1902850	1/128	0.934477114
DNA-dependent DNA replication (GO:0006261)	1/129	0.935861914
positive regulation of macromolecule biosynthetic process (GO:0010557	1/129	0.935861914
cellular response to metal ion (GO:0071248)	1/131	0.938544528
negative regulation of inflammatory response (GO:0050728)	2/212	0.939268941
translation (GO:0006412)	2/214	0.941363803
chemical synaptic transmission (GO:0007268)	3/306	0.957209276
regulation of cytokine production (GO:0001817)	1/150	0.959055887
rRNA metabolic process (GO:0016072)	1/162	0.968325138
cell-cell adhesion via plasma-membrane adhesion molecules (GO:00987	1/170	0.97330928
rRNA processing (GO:0006364)	1/173	0.97496948
defense response to bacterium (GO:0042742)	1/176	0.976526633
endoplasmic reticulum to Golgi vesicle-mediated transport (GO:000688	1/185	0.980641684
regulation of mitotic cell cycle phase transition (GO:1901990)	1/188	0.981846645
ribosome biogenesis (GO:0042254)	1/192	0.983337642
cellular protein metabolic process (GO:0044267)	3/417	0.993253509
cellular macromolecule biosynthetic process (GO:0034645)	1/314	0.998787635

of significant highly-correlated RNA-seq-based modules (green; Significant terms were highligh

Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Combined Score	Genes	KEGG
6.48E-11	0	0	3.199194863	99.73675356	SPI1;CRTC3	.
3.75E-09	0	0	3.235190233	84.23073984	SPI1;CRTC3	.
3.75E-09	0	0	2.418911927	62.9380575	ZNF692;SP	.
4.17E-08	0	0	2.304449819	53.7479254	SETD5;ZNF	.
1.00E-06	0	0	141.8695652	2825.80237	KMT2D;KM	.
2.64E-06	0	0	20.39520334	382.7999421	KMT2D;KM	.
2.59E-05	0	0	117.939759	1925.9623	KMT2D;KM	.
3.25E-05	0	0	2.546889266	40.67220126	HDAC5;ZNI	.
4.01E-05	0	0	9.211727362	144.0997508	TNRC6C;KM	.
4.84E-05	0	0	35.45652174	544.2702367	KMT2D;KM	.
9.30E-05	0	0	3.054373901	44.59755911	NOTCH1;KI	.
2.35E-04	0	0	2.651771957	36.02487552	HDAC5;ZNI	.
2.90E-04	0	0	9.506082725	126.4015711	TNRC6C;KM	.
3.60E-04	0	0	14.4119381	187.1226848	KMT2D;SET	.
3.60E-04	0	0	2.981617074	38.57490411	KMT2D;SPI	.
6.99E-04	0	0	2.996561963	36.58564634	KMT2D;SPI	.
0.004799942	0	0	16.83820998	172.1193962	KMT2D;KM	.
0.007044857	0	0	2.682059894	26.2334987	PRR5;PLEK	.
0.007984813	0	0	10.12008282	97.17091147	KMT2D;KM	.
0.010181459	0	0	1.986820958	18.49227633	NOTCH2;KI	.
0.012602445	0	0	20.90918803	189.131076	NOTCH1;TC	.
0.029127424	0	0	15.67948718	127.9610466	CEACAM1;	.
0.032522179	0	0	2.526315789	20.22657866	AMHR2;SP	.
0.035604913	0	0	7.079710145	55.74020809	PER1;LARP	.
0.04108473	0	0	28.16546763	215.4668833	ACTA1;TCA	.
0.04108473	0	0	28.16546763	215.4668833	GTF3C1;GT	.
0.059848313	0	0	3.677632823	26.61179403	SETD5;STK	.
0.06802794	0	0	2.273612926	16.0128158	SPEN;HDAC	.
0.06802794	0	0	7.597745822	53.46196561	NCOR2;NC	.
0.074740288	0	0	7.359939759	50.84654039	PER1;SPI1;	.
0.08399921	0	0	5.549587951	37.25235025	NCOA2;CEA	.
0.08399921	0	0	4.113127902	27.58427187	SKI;STK11;I	.
0.08399921	0	0	2.836891103	18.94689196	SREBF1;TFI	.
0.08399921	0	0	2.511203752	16.72677692	NOTCH2;H	.
0.08399921	0	0	17.60071942	116.4539787	CEACAM1;	.
0.08399921	0	0	2.106870229	13.92143169	SPEN;HDAC	.
0.08399921	0	0	9.403846154	61.40148719	AKAP13;TC	.
0.08399921	0	0	9.403846154	61.40148719	CEACAM1;	.
0.08399921	0	0	9.403846154	61.40148719	SPI1;GADD	.
0.096141124	0	0	15.64428457	99.25330691	SREBF1;CL	.
0.096141124	0	0	15.64428457	99.25330691	NCOR2;NC	.
0.100769015	0	0	5.052795031	31.69754753	CX3CR1;SP	.
0.103439224	0	0	2.116897507	13.17469412	MAP3K3;A	.
0.114657545	0	0	14.07913669	85.84938172	AKAP13;FH	.

0.121764571	0	0	5.885542169	35.40164575	NUMA1;TT
0.131341536	0	0	4.030177759	23.84788399	SKI;AMHR2
0.134498958	0	0	12.79856115	75.15400209	SZT2;STK1
0.139171816	0	0	2.998147576	17.43980554	NOTCH2;N
0.143052893	0	0	3.887337986	22.27662307	NCOR2;NC
0.143052893	0	0	5.474082376	31.35954249	SREBF1;EP
0.143052893	0	0	5.474082376	31.35954249	PER1;KMT2
0.146785879	0	0	11.73141487	66.4526431	NCOR2;NC
0.146785879	0	0	11.73141487	66.4526431	CX3CR1;CE
0.152065255	0	0	3.797584259	21.30625822	NOTCH2;LY
0.153149426	0	0	4.351170569	24.30138891	PER1;BRD1
0.154205643	0	0	31.22328549	170.7368599	NOTCH2;N
0.154205643	0	0	31.22328549	170.7368599	CEACAM1;
0.154205643	0	0	31.22328549	170.7368599	CX3CR1;SP
0.154205643	0	0	31.22328549	170.7368599	MYO9B;SLI
0.154205643	0	0	31.22328549	170.7368599	ERN1;CEAC
0.154205643	0	0	31.22328549	170.7368599	GTF3C1;BR
0.154205643	0	0	6.714285714	36.54148455	HDAC5;MA
0.154205643	0	0	6.714285714	36.54148455	NCOR2;PEI
0.169915225	0	0	6.482427056	34.54866433	HDAC5;SET
0.173393532	0	0	10.05447071	53.22655325	NOTCH2;N
0.177252686	0	0	6.266025641	32.71406124	CD151;PEA
0.177252686	0	0	6.266025641	32.71406124	HDAC5;AN
0.177252686	0	0	2.894830925	14.91291846	PRR5;STK1
0.177252686	0	0	9.383693046	48.11045893	NOTCH2;N
0.177252686	0	0	9.383693046	48.11045893	NCOR2;MA
0.177252686	0	0	9.383693046	48.11045893	GTF3C1;GT
0.177252686	0	0	6.063585608	31.0208664	STK11;SZT2
0.177252686	0	0	23.41626794	118.8784533	GTF3C1;GT
0.177252686	0	0	23.41626794	118.8784533	ACTA1;TCA
0.177252686	0	0	23.41626794	118.8784533	SH2B3;ZNF
0.177252686	0	0	23.41626794	118.8784533	SF3A1;SF3A
0.177252686	0	0	23.41626794	118.8784533	SLIT3;SH2B
0.177252686	0	0	23.41626794	118.8784533	SKI;NOTCH
0.177252686	0	0	23.41626794	118.8784533	CX3CR1;SP
0.177523894	0	0	4.613512875	23.35654881	GADD45A;
0.181146875	0	0	2.83649635	14.26761415	ERN1;MAP
0.181724788	0	0	5.873798077	29.45450062	FLNA;MYH
0.185023754	0	0	8.79676259	43.72599044	NOTCH1;SI
0.185023754	0	0	8.79676259	43.72599044	SREBF1;AT
0.185023754	0	0	3.022135922	14.95003399	SKI;AMHR2
0.185023754	0	0	2.480731168	12.22315126	GTF3C1;GN
0.185023754	0	0	5.695512821	28.00226222	BRD1;SPI1;
0.185023754	0	0	5.695512821	28.00226222	NCOA2;AX
0.185023754	0	0	4.438963401	21.8159513	MAFB;ZNF
0.189538178	0	0	3.268837053	15.87516236	SKI;NOTCH
0.189538178	0	0	8.278882776	39.93458579	WDR81;HC

0.189538178	0	0	8.278882776	39.93458579	SPI1;RXRA;
0.189538178	0	0	8.278882776	39.93458579	TNRC6C;A(
0.189538178	0	0	5.527714932	26.65303898	STK11;SZT2
0.189538178	0	0	2.571049841	12.38386221	NOTCH2;TI
0.189538178	0	0	2.1021523	10.09012895	FBXW5;ZFA
0.189538178	0	0	2.157635468	10.29139463	NOTCH2;SI
0.189538178	0	0	18.73205742	89.05608342	LYL1;HIPK1
0.189538178	0	0	18.73205742	89.05608342	AKNA;SPI1
0.189538178	0	0	18.73205742	89.05608342	NOTCH1;SI
0.189538178	0	0	18.73205742	89.05608342	GTF3C1;GT
0.189538178	0	0	18.73205742	89.05608342	ADARB1;PI
0.190472561	0	0	5.369505495	25.39707101	MGRN1;NE
0.190472561	0	0	5.369505495	25.39707101	SPHK1;KAT
0.202230993	0	0	3.532608696	16.45292886	NOTCH2;A
0.202230993	0	0	2.860841424	13.30554711	NOTCH2;N
0.213623083	0	0	3.084587359	14.10690799	SKI;AMHR2
0.213623083	0	0	5.078742204	23.13147821	AKNA;NOT
0.213623083	0	0	7.406664142	33.72887618	IRAK1;SH2I
0.213623083	0	0	3.986318154	17.96678538	MED12;TN
0.213623083	0	0	2.147171879	9.634378778	SPEN;SF3A
0.213623083	0	0	3.027678433	13.57482418	GAK;WDR8
0.213623083	0	0	15.6092504	69.93621438	SLIT3;SH2E
0.213623083	0	0	15.6092504	69.93621438	TCAP;CAM
0.213623083	0	0	15.6092504	69.93621438	ZDHHC5;SI
0.213623083	0	0	15.6092504	69.93621438	SREBF1;SRI
0.213623083	0	0	15.6092504	69.93621438	ERN1;MAP
0.213623083	0	0	15.6092504	69.93621438	NUMA1;RC
0.213623083	0	0	15.6092504	69.93621438	SPHK1;SRF
0.213889084	0	0	4.944838057	22.10748692	PER1;BRD1
0.216106158	0	0	3.363699103	14.95467655	STK11;LAR
0.216106158	0	0	3.919678715	17.41897281	GADD45A;
0.229767803	0	0	2.530239833	11.04808914	PITPNM1;F
0.229767803	0	0	2.530239833	11.04808914	NUMA1;SR
0.230240535	0	0	6.700582391	28.8891168	TCAP;ALPK
0.230240535	0	0	6.700582391	28.8891168	PLA2G4B;G
0.230240535	0	0	4.697115385	20.246946	FLNA;MYH
0.230240535	0	0	3.732453624	15.90747624	SKI;FAM89
0.230240535	0	0	13.37867396	56.76576117	TCAP;MEF2
0.230240535	0	0	13.37867396	56.76576117	SH2B3;ZNF
0.230240535	0	0	13.37867396	56.76576117	SREBF1;SRI
0.230240535	0	0	13.37867396	56.76576117	ZNF703;RR
0.230240535	0	0	13.37867396	56.76576117	CAPN10;HI
0.230240535	0	0	13.37867396	56.76576117	SREBF1;SRI
0.230240535	0	0	13.37867396	56.76576117	SKI;ACTA1
0.230240535	0	0	13.37867396	56.76576117	NOTCH1;SI
0.230240535	0	0	13.37867396	56.76576117	CEACAM1;
0.230240535	0	0	13.37867396	56.76576117	CEACAM1;

0.230240535	0	0	13.37867396	56.76576117	SPHK1;SRF
0.230240535	0	0	13.37867396	56.76576117	NEURL1;AN
0.230741332	0	0	4.582317073	19.40021695	SPI1;SRF;FO
0.237207031	0	0	6.395683453	26.85553992	ERN1;ZNF2
0.238648873	0	0	2.843950906	11.90458679	NCOA2;ND
0.243454833	0	0	4.472985348	18.60326151	DVL3;ATP1
0.253105235	0	0	1.879815704	7.707677119	NUMA1;M
0.253105235	0	0	3.562248996	14.57014621	SPI1;RXRA;
0.253105235	0	0	4.368738819	17.85219329	STK11;NOT
0.253105235	0	0	2.771827375	11.269517	PITPNM1;N
0.253105235	0	0	2.549462083	10.32384154	ERN1;MAP
0.253105235	0	0	2.167277914	8.769712234	SPEN;RBM
0.253105235	0	0	3.508901277	14.15847901	CX3CR1;SP
0.253105235	0	0	11.70574163	47.21767695	ZNF703;PIF
0.253105235	0	0	11.70574163	47.21767695	CEACAM1;
0.253105235	0	0	11.70574163	47.21767695	SETD5;KLF
0.253105235	0	0	11.70574163	47.21767695	SMAD6;SR
0.253105235	0	0	11.70574163	47.21767695	NOTCH1;PI
0.253105235	0	0	11.70574163	47.21767695	ADAM8;PD
0.256573364	0	0	3.03677731	12.18889794	SPI1;GADD
0.259616283	0	0	5.862110312	23.38625613	SPI1;SRF;K
0.259616283	0	0	5.862110312	23.38625613	NOTCH1;N
0.26926162	0	0	4.174145299	16.47402708	NUMA1;DV
0.270625937	0	0	3.40684477	13.38123785	GADD45A;
0.270625937	0	0	5.627338129	21.89833938	NCOA2;CE/
0.270625937	0	0	5.627338129	21.89833938	ARC;ABHD
0.270625937	0	0	5.627338129	21.89833938	GTF3C1;GT
0.270625937	0	0	5.627338129	21.89833938	SZT2;GGA3
0.270625937	0	0	3.358003442	13.01415742	SPI1;KMT2
0.270625937	0	0	10.40457204	40.02517391	AKNA;HOC
0.270625937	0	0	10.40457204	40.02517391	HDAC5;KM
0.270625937	0	0	10.40457204	40.02517391	SH2B3;ZBT
0.270625937	0	0	10.40457204	40.02517391	NEURL1;AN
0.270625937	0	0	10.40457204	40.02517391	GAK;RBSN
0.270625937	0	0	10.40457204	40.02517391	TNRC6C;AC
0.270625937	0	0	10.40457204	40.02517391	SKI;ACTA1
0.270625937	0	0	10.40457204	40.02517391	TNRC6C;AC
0.270625937	0	0	10.40457204	40.02517391	NOTCH2;N
0.270625937	0	0	10.40457204	40.02517391	CX3CR1;ZN
0.275250349	0	0	3.310537926	12.66050989	SKI;NOTCH
0.276528094	0	0	3.99611293	15.2414637	CEACAM1;
0.279570037	0	0	5.410625346	20.54717902	KMT2D;EP
0.291499815	0	0	3.912660256	14.67339209	SKI;NOTCH
0.294483715	0	0	2.246668984	8.341197519	PER1;SPI1;
0.294483715	0	0	5.209965361	19.31606216	MBOAT7;P
0.294483715	0	0	3.832613815	14.13450194	NOTCH2;A
0.294483715	0	0	3.832613815	14.13450194	ERN1;PLA2

0.294483715	0	0	3.832613815	14.13450194	LARP1;VPS
0.294483715	0	0	9.363636364	34.4429316	FLNA;GAS2
0.294483715	0	0	9.363636364	34.4429316	MAFB;RUN
0.294483715	0	0	9.363636364	34.4429316	ARHGAP21
0.294483715	0	0	9.363636364	34.4429316	CD151;PLE
0.294483715	0	0	9.363636364	34.4429316	SH2B3;ZNF
0.294483715	0	0	9.363636364	34.4429316	NCOR2;NC
0.294483715	0	0	3.175838489	11.67392704	SPI1;IRAK1
0.30169669	0	0	1.808217887	6.577447915	CD151;NO
0.30169669	0	0	3.133333333	11.36795498	EP300;ATP
0.30169669	0	0	3.133333333	11.36795498	SKI;NOTCH
0.30169669	0	0	3.755769231	13.62281398	CLCN6;TTY
0.30169669	0	0	5.023638232	18.19081279	SKI;NOTCH
0.30169669	0	0	5.023638232	18.19081279	SPHK1;KAT
0.310636407	0	0	3.68193816	13.13651687	SLIT3;CACT
0.310636407	0	0	4.85016125	17.1593354	NOTCH1;SI
0.310636407	0	0	4.85016125	17.1593354	KMT2D;AX
0.310636407	0	0	1.684447585	5.938313201	FBXW5;PPI
0.310636407	0	0	8.511961722	30.0055323	SZT2;ABL2
0.310636407	0	0	8.511961722	30.0055323	KMT2A;SH
0.310636407	0	0	8.511961722	30.0055323	MGAT5;DC
0.310636407	0	0	8.511961722	30.0055323	CX3CR1;NC
0.310636407	0	0	8.511961722	30.0055323	ZGPAT;CBL
0.310636407	0	0	8.511961722	30.0055323	HDAC5;NO
0.310636407	0	0	8.511961722	30.0055323	RXRA;KMT
0.310636407	0	0	2.459650898	8.664288976	GNA13;ARI
0.310636407	0	0	2.459650898	8.664288976	STK11;TFEI
0.310636407	0	0	2.165648741	7.620800889	ANKRD9;SI
0.310636407	0	0	3.610946746	12.67395011	GNA13;WA
0.310636407	0	0	3.610946746	12.67395011	MAFB;BLO
0.310636407	0	0	3.610946746	12.67395011	STK11;NOT
0.313245272	0	0	3.012357121	10.51162693	NOTCH1;N
0.313245272	0	0	2.441305712	8.51883217	SETD5;HDA
0.313245272	0	0	1.975392081	6.878866235	SPEN;RBM
0.313245272	0	0	2.662564944	9.262055247	ERN1;LARP
0.313245272	0	0	2.662564944	9.262055247	PITPNM1;N
0.318379921	0	0	4.6882494	16.21125276	TCAP;MYH
0.324881427	0	0	2.612989801	8.895205028	PRR5;STK1
0.324881427	0	0	2.612989801	8.895205028	NSD3;HDA
0.324881427	0	0	7.802232855	26.40830138	SZT2;ATP1
0.324881427	0	0	7.802232855	26.40830138	NOTCH1;SI
0.324881427	0	0	7.802232855	26.40830138	SETD5;SET
0.324881427	0	0	7.802232855	26.40830138	MYH11;PIK
0.324881427	0	0	7.802232855	26.40830138	FAAH;DGA
0.324881427	0	0	7.802232855	26.40830138	GTF3C1;BR
0.324881427	0	0	7.802232855	26.40830138	HDAC5;NO
0.324881427	0	0	7.802232855	26.40830138	NELFA;SUP

0.324881427	0	0	7.802232855	26.40830138	SRF;POU5F
0.324881427	0	0	4.536783476	15.33761622	ERN1;NOT(
0.324881427	0	0	4.536783476	15.33761622	SPI1;SRF;F(
0.338864127	0	0	1.999173212	6.665922245	CX3CR1;HI
0.352408956	0	0	3.352335165	11.03226046	NOTCH2;N
0.352875863	0	0	2.069610112	6.799462997	STK11;SPI1
0.356307515	0	0	7.201693044	23.44399021	NOTCH1;R
0.356307515	0	0	7.201693044	23.44399021	HIP1;PIK3C
0.356307515	0	0	7.201693044	23.44399021	FURIN;ADA
0.356307515	0	0	3.293353576	10.66775553	LYL1;HDAC
0.356307515	0	0	3.293353576	10.66775553	MED12;TN
0.356307515	0	0	3.293353576	10.66775553	HIP1;CD15
0.356307515	0	0	2.303780965	7.45716098	CX3CR1;PI
0.356307515	0	0	4.261390887	13.78367182	NOTCH1;SI
0.356307515	0	0	4.261390887	13.78367182	STK11;EP3(
0.356307515	0	0	4.261390887	13.78367182	SPI1;ADAM
0.370419822	0	0	2.763288448	8.819534225	CEACAM1;
0.374377493	0	0	2.271770894	7.217518363	ACTA1;HIP
0.379620647	0	0	2.731017092	8.60762009	NOTCH1;K
0.379620647	0	0	2.731017092	8.60762009	CD151;RXF
0.379620647	0	0	3.181388527	9.986410107	LARP1;ADA
0.379620647	0	0	6.686944634	20.96706205	SKI;ACVR2I
0.379620647	0	0	6.686944634	20.96706205	ABCC1;SLC
0.379620647	0	0	6.686944634	20.96706205	CEACAM1;
0.379620647	0	0	6.686944634	20.96706205	CEACAM1;
0.386940434	0	0	2.699487606	8.402263681	STK11;NOT
0.389538624	0	0	4.017471737	12.4466332	ANGPT4;N
0.389538624	0	0	4.017471737	12.4466332	CX3CR1;SP
0.395174332	0	0	3.90567546	11.84686137	NUMA1;CA
0.395174332	0	0	3.90567546	11.84686137	CADM4;SP
0.395174332	0	0	3.90567546	11.84686137	SREBF1;HU
0.395174332	0	0	3.90567546	11.84686137	HIP1;TNK2
0.395174332	0	0	3.90567546	11.84686137	EXD2;EME
0.395174332	0	0	3.90567546	11.84686137	STK11;NUM
0.395174332	0	0	6.240829346	18.87253421	SREBF1;SR
0.395174332	0	0	6.240829346	18.87253421	NOTCH2;N
0.395174332	0	0	6.240829346	18.87253421	MAP2K2;R
0.395174332	0	0	6.240829346	18.87253421	CX3CR1;ZN
0.395174332	0	0	6.240829346	18.87253421	KCNK6;KCN
0.395174332	0	0	6.240829346	18.87253421	STK11;ACV
0.395174332	0	0	6.240829346	18.87253421	NOTCH1;T(
0.395174332	0	0	6.240829346	18.87253421	CEACAM1;
0.395174332	0	0	6.240829346	18.87253421	PNKP;MAP
0.395174332	0	0	6.240829346	18.87253421	NOTCH1;EI
0.396855522	0	0	1.82082958	5.491951126	ERN1;NOT(
0.400008998	0	0	2.180828376	6.552653003	SREBF1;SZ
0.40040091	0	0	2.609103079	7.822992738	ERN1;SF3A

0.40040091	0	0	3.026985112	9.07040515	SREBF1;TFI
0.408071033	0	0	1.674814491	4.976503749	FBXW5;MC
0.408071033	0	0	3.799922224	11.28737339	NCOA2;CE/
0.414622928	0	0	2.978785104	8.790258257	CEACAM1;
0.4159351	0	0	5.850478469	17.08291763	MAP2K2;P
0.4159351	0	0	5.850478469	17.08291763	CEACAM1;
0.4159351	0	0	5.850478469	17.08291763	ERN1;ANG
0.4159351	0	0	5.850478469	17.08291763	GNA15;CD
0.4159351	0	0	5.850478469	17.08291763	SPI1;CBL
0.4159351	0	0	5.850478469	17.08291763	KCTD13;AE
0.4159351	0	0	5.850478469	17.08291763	PLA2G4B;L
0.4159351	0	0	5.850478469	17.08291763	MAP3K3;P
0.415977751	0	0	3.699734949	10.76459713	CX3CR1;NC
0.415977751	0	0	3.699734949	10.76459713	AMHR2;SP
0.415977751	0	0	3.699734949	10.76459713	IRAK1;MAI
0.424032721	0	0	1.909449596	5.51255151	NOTCH2;S
0.426310627	0	0	2.273959794	6.530855905	NCOR2;NC
0.426310627	0	0	2.88683432	8.263743535	IRAK1;DVL
0.426310627	0	0	1.826621289	5.219148706	CX3CR1;SZ
0.426310627	0	0	3.604685482	10.27535512	PI4KA;PIK3
0.426310627	0	0	3.604685482	10.27535512	NOTCH1;ZI
0.426310627	0	0	1.819474527	5.162345452	ZNF609;CD
0.426310627	0	0	5.506051224	15.53986795	AMHR2;AC
0.426310627	0	0	5.506051224	15.53986795	NOTCH1;PI
0.426310627	0	0	5.506051224	15.53986795	NOTCH2;N
0.426310627	0	0	5.506051224	15.53986795	CEACAM1;
0.426310627	0	0	5.506051224	15.53986795	KMT2A;ZN
0.426310627	0	0	5.506051224	15.53986795	PLA2G4B;G
0.426310627	0	0	5.506051224	15.53986795	KMT2A;HC
0.426310627	0	0	5.506051224	15.53986795	SKI;AKAP1
0.426310627	0	0	5.506051224	15.53986795	NOTCH1;H
0.426310627	0	0	5.506051224	15.53986795	NCOR2;NC
0.426310627	0	0	5.506051224	15.53986795	HDAC5;NO
0.426310627	0	0	2.842948718	8.016195974	FLNA;RELL
0.426310627	0	0	2.471147749	6.966682734	NCOA2;CE/
0.430634275	0	0	3.514388489	9.816812581	CEACAM1;
0.430634275	0	0	3.514388489	9.816812581	NOTCH1;RI
0.430634275	0	0	3.514388489	9.816812581	ERN1;FOXI
0.430634275	0	0	3.514388489	9.816812581	SZT2;FOXO
0.430634275	0	0	3.514388489	9.816812581	EXD2;EME
0.433368918	0	0	2.21990186	6.178607676	CEACAM1;
0.433368918	0	0	2.800373134	7.778399392	KMT2A;SE
0.433368918	0	0	2.800373134	7.778399392	TMEM127;
0.437929224	0	0	2.419947833	6.657757371	AXIN1;HUV
0.437929224	0	0	2.419947833	6.657757371	ANGPT4;SI
0.437929224	0	0	3.428496227	9.386433341	ERN1;AGO
0.437929224	0	0	3.428496227	9.386433341	ZGPAT;CBL

0.437929224	0	0	3.428496227	9.386433341	HIP1;ARRB	.
0.437929224	0	0	2.759049774	7.549855788	CAPN10;AI	.
0.437929224	0	0	5.199893674	14.19868534	SPHK1;SRF	.
0.437929224	0	0	5.199893674	14.19868534	CEACAM1;	.
0.437929224	0	0	5.199893674	14.19868534	STAC2;TCA	.
0.437929224	0	0	5.199893674	14.19868534	SH2B3;ZNF	.
0.437929224	0	0	5.199893674	14.19868534	RCC2;BRD4	.
0.437929224	0	0	5.199893674	14.19868534	MYH9;ADA	.
0.449467141	0	0	2.168338907	5.849367845	GAK;PPIL2;	.
0.449467141	0	0	2.718924192	7.33009885	AKAP13;KC	.
0.449467141	0	0	2.3708166	6.365981632	ARC;RBM1	.
0.449467141	0	0	3.346694073	8.981942287	NOTCH1;D	.
0.449467141	0	0	3.346694073	8.981942287	CX3CR1;SP	.
0.449467141	0	0	3.346694073	8.981942287	ERN1;MAP	.
0.449467141	0	0	3.346694073	8.981942287	HDAC5;MI	.
0.451796518	0	0	2.679945055	7.118691538	IRAK1;SPH	.
0.451796518	0	0	2.346987952	6.226145166	PER1;NCOI	.
0.451796518	0	0	4.925963233	13.02459452	AXIN1;DVL	.
0.451796518	0	0	4.925963233	13.02459452	NOTCH1;R	.
0.451796518	0	0	4.925963233	13.02459452	SREBF1;SR	.
0.451796518	0	0	4.925963233	13.02459452	ZNF703;LC	.
0.451796518	0	0	4.925963233	13.02459452	PEAK1;RCC	.
0.451796518	0	0	4.925963233	13.02459452	EP300;HIPI	.
0.451796518	0	0	4.925963233	13.02459452	GADD45A;	.
0.451796518	0	0	4.925963233	13.02459452	ATN1;NLRF	.
0.451796518	0	0	4.925963233	13.02459452	NOTCH1;EI	.
0.451796518	0	0	4.925963233	13.02459452	ERN1;MEF	.
0.456483179	0	0	2.642063922	6.915223878	SZT2;LARP	.
0.456483179	0	0	2.642063922	6.915223878	CEACAM1;	.
0.456483179	0	0	2.103179753	5.442982569	GAK;PPIL2;	.
0.456483179	0	0	3.194244604	8.24264175	SKI;DOT1L;	.
0.456483179	0	0	3.194244604	8.24264175	HDAC5;PEI	.
0.456483179	0	0	2.605235043	6.719310956	CLCN6;TTY	.
0.456483179	0	0	4.679425837	11.99017024	FBXW5;MA	.
0.456483179	0	0	4.679425837	11.99017024	FURIN;ADA	.
0.456483179	0	0	4.679425837	11.99017024	AHNAK;STA	.
0.456483179	0	0	4.679425837	11.99017024	NCOR1;EP3	.
0.456483179	0	0	4.679425837	11.99017024	DUSP18;PF	.
0.456483179	0	0	4.679425837	11.99017024	MED12;SR	.
0.456483179	0	0	4.679425837	11.99017024	CX3CR1;ZN	.
0.456483179	0	0	1.671819544	4.279421003	ANKRD9;SI	.
0.456483179	0	0	1.844279459	4.671311448	TOLLIP;SPH	.
0.456483179	0	0	3.123101519	7.90432078	ANGPT4;M	.
0.456483179	0	0	3.123101519	7.90432078	CD151;HIP	.
0.456483179	0	0	2.256255792	5.703937942	U2AF2;SPH	.
0.456483179	0	0	2.256255792	5.703937942	NCOA2;CE/	.
0.456483179	0	0	2.056807363	5.160505766	SPI1;IRAK1	.

0.456483179	0	0	2.234652897	5.582042315	ERN1;ATF6	.
0.456483179	0	0	4.456368193	11.07351863	SRF;MYH9	.
0.456483179	0	0	4.456368193	11.07351863	FURIN;ATP	.
0.456483179	0	0	4.456368193	11.07351863	PNKP;MAP	.
0.456483179	0	0	4.456368193	11.07351863	MGAT5;BC	.
0.456483179	0	0	4.456368193	11.07351863	RCC2;BRD4	.
0.456483179	0	0	4.456368193	11.07351863	DVL3;MAP	.
0.456483179	0	0	4.456368193	11.07351863	MED12;SR	.
0.456483179	0	0	4.456368193	11.07351863	HDAC5;AB	.
0.456483179	0	0	3.055051611	7.584820869	ZNF703;CS	.
0.456483179	0	0	1.912495073	4.736980857	HIP1;WDR	.
0.456483179	0	0	2.989897444	7.282772076	CADM4;ZS	.
0.456483179	0	0	2.989897444	7.282772076	NAV1;MAF	.
0.456483179	0	0	2.989897444	7.282772076	CUX1;FLNA	.
0.456483179	0	0	2.467611336	6.00428679	SPI1;IRAK1	.
0.456483179	0	0	4.253588517	10.25696882	FOXK1;PFK	.
0.456483179	0	0	4.253588517	10.25696882	FOXK1;PFK	.
0.456483179	0	0	4.253588517	10.25696882	CEACAM1;	.
0.456483179	0	0	4.253588517	10.25696882	NOTCH1;SI	.
0.456483179	0	0	4.253588517	10.25696882	ZGPAT;CBL	.
0.456483179	0	0	4.253588517	10.25696882	STK11;EP3	.
0.456483179	0	0	4.253588517	10.25696882	FOXO3;CDI	.
0.456483179	0	0	4.253588517	10.25696882	GNA13;AB	.
0.456483179	0	0	4.253588517	10.25696882	NOTCH1;A	.
0.456483179	0	0	4.253588517	10.25696882	STK11;EP3	.
0.456483179	0	0	1.524806881	3.665535365	NOTCH2;S	.
0.456483179	0	0	2.43543956	5.841130663	CX3CR1;GN	.
0.456483179	0	0	2.927458034	6.99692863	RCC2;FLNA	.
0.456483179	0	0	2.927458034	6.99692863	RREB1;ZNF	.
0.456483179	0	0	2.152205151	5.125697789	ASXL1;RXR	.
0.456483179	0	0	2.152205151	5.125697789	CD151;NEU	.
0.456483179	0	0	2.404092702	5.683653319	HDAC5;SPI	.
0.456483179	0	0	1.700026383	3.998068517	CEACAM1;	.
0.456483179	0	0	1.765531702	4.15103058	CD151;NO	.
0.456483179	0	0	2.867567171	6.726155475	SPI1;KAT6A	.
0.456483179	0	0	2.867567171	6.726155475	NUMA1;ST	.
0.456483179	0	0	4.068441856	9.526116166	MAFG;RUN	.
0.456483179	0	0	4.068441856	9.526116166	HDAC5;NO	.
0.456483179	0	0	4.068441856	9.526116166	ADAM8;RU	.
0.456483179	0	0	4.068441856	9.526116166	FOXK1;PFK	.
0.456483179	0	0	4.068441856	9.526116166	NCOR1;EP3	.
0.456483179	0	0	4.068441856	9.526116166	LNPEP;NA4	.
0.456483179	0	0	4.068441856	9.526116166	PLA2G4B;L	.
0.456483179	0	0	4.068441856	9.526116166	SUPT5H;BF	.
0.456483179	0	0	4.068441856	9.526116166	HIP1;CBL	.
0.456483179	0	0	4.068441856	9.526116166	SPHK1;AXI	.
0.456483179	0	0	2.373539435	5.531601623	SKI;NOTCH	.

0.456483179	0	0	2.113209595	4.914862083	ANGPT4;SI	.
0.456483179	0	0	2.810071942	6.469416516	IRAK1;SPHI	.
0.456483179	0	0	2.094234079	4.813454829	CUX1;EP3C	.
0.456483179	0	0	2.34375	5.38473645	LYL1;HDAC	.
0.456483179	0	0	11.68019093	26.81420401	IFFO1	.
0.456483179	0	0	11.68019093	26.81420401	VPS13D	.
0.456483179	0	0	11.68019093	26.81420401	PTPN23	.
0.456483179	0	0	11.68019093	26.81420401	SPI1	.
0.456483179	0	0	11.68019093	26.81420401	AXIN1	.
0.456483179	0	0	11.68019093	26.81420401	NOTCH1	.
0.456483179	0	0	11.68019093	26.81420401	NOTCH1	.
0.456483179	0	0	11.68019093	26.81420401	NUMA1	.
0.456483179	0	0	11.68019093	26.81420401	RFFL	.
0.456483179	0	0	11.68019093	26.81420401	CX3CR1	.
0.456483179	0	0	11.68019093	26.81420401	CX3CR1	.
0.456483179	0	0	11.68019093	26.81420401	FURIN	.
0.456483179	0	0	11.68019093	26.81420401	NOTCH1	.
0.456483179	0	0	11.68019093	26.81420401	NUMA1	.
0.456483179	0	0	11.68019093	26.81420401	ZSWIM8	.
0.456483179	0	0	11.68019093	26.81420401	VPS13D	.
0.456483179	0	0	11.68019093	26.81420401	ZNF609	.
0.456483179	0	0	11.68019093	26.81420401	SPI1	.
0.456483179	0	0	11.68019093	26.81420401	SLC15A4	.
0.456483179	0	0	11.68019093	26.81420401	SMAD6	.
0.456483179	0	0	11.68019093	26.81420401	MYH9	.
0.456483179	0	0	11.68019093	26.81420401	HIP1	.
0.456483179	0	0	11.68019093	26.81420401	NOTCH1	.
0.456483179	0	0	11.68019093	26.81420401	POU5F1	.
0.456483179	0	0	11.68019093	26.81420401	HIPK1	.
0.456483179	0	0	11.68019093	26.81420401	GDPD3	.
0.456483179	0	0	11.68019093	26.81420401	ATP13A2	.
0.456483179	0	0	11.68019093	26.81420401	MBOAT7	.
0.456483179	0	0	11.68019093	26.81420401	ABCC1	.
0.456483179	0	0	11.68019093	26.81420401	ZNF598	.
0.456483179	0	0	11.68019093	26.81420401	SLC26A6	.
0.456483179	0	0	11.68019093	26.81420401	ACVR2B	.
0.456483179	0	0	11.68019093	26.81420401	IRAK1	.
0.456483179	0	0	11.68019093	26.81420401	ERN1	.
0.456483179	0	0	11.68019093	26.81420401	AGO3	.
0.456483179	0	0	11.68019093	26.81420401	GDPD3	.
0.456483179	0	0	11.68019093	26.81420401	SLC43A2	.
0.456483179	0	0	11.68019093	26.81420401	RUNX1	.
0.456483179	0	0	11.68019093	26.81420401	SPHK1	.
0.456483179	0	0	11.68019093	26.81420401	POU5F1	.
0.456483179	0	0	11.68019093	26.81420401	SPI1	.
0.456483179	0	0	11.68019093	26.81420401	POU5F1	.
0.456483179	0	0	11.68019093	26.81420401	KLF15	.

0.456483179	0	0	11.68019093	26.81420401	SPHK1	.
0.456483179	0	0	11.68019093	26.81420401	FLNA	.
0.456483179	0	0	11.68019093	26.81420401	FURIN	.
0.456483179	0	0	11.68019093	26.81420401	DVL3	.
0.456483179	0	0	11.68019093	26.81420401	RUNX1	.
0.456483179	0	0	11.68019093	26.81420401	ARC	.
0.456483179	0	0	11.68019093	26.81420401	RCC2	.
0.456483179	0	0	11.68019093	26.81420401	RUNX1	.
0.456483179	0	0	11.68019093	26.81420401	ZNF335	.
0.456483179	0	0	11.68019093	26.81420401	ADAM8	.
0.456483179	0	0	11.68019093	26.81420401	SLC15A4	.
0.456483179	0	0	11.68019093	26.81420401	NUMA1	.
0.456483179	0	0	11.68019093	26.81420401	SLC15A4	.
0.456483179	0	0	11.68019093	26.81420401	NOTCH1	.
0.456483179	0	0	11.68019093	26.81420401	SRF	.
0.456483179	0	0	11.68019093	26.81420401	GAS2L1	.
0.456483179	0	0	11.68019093	26.81420401	GAS2L1	.
0.456483179	0	0	1.740740741	3.992466	AKAP13;M	.
0.456483179	0	0	1.929124479	4.412778766	CEACAM1;	.
0.456483179	0	0	3.898724083	8.869112109	FHOD1;W/	.
0.456483179	0	0	3.898724083	8.869112109	GAK;DNAJI	.
0.456483179	0	0	3.898724083	8.869112109	GAK;PIP5K	.
0.456483179	0	0	3.898724083	8.869112109	NFATC2;RU	.
0.456483179	0	0	3.898724083	8.869112109	SETD5;ABH	.
0.456483179	0	0	3.898724083	8.869112109	PRR5;LARP	.
0.456483179	0	0	3.898724083	8.869112109	NOTCH1;H	.
0.456483179	0	0	3.898724083	8.869112109	CSK;PPM1I	.
0.456483179	0	0	3.898724083	8.869112109	ZGPAT;CBL	.
0.456483179	0	0	3.898724083	8.869112109	NUMA1;CI	.
0.456483179	0	0	3.898724083	8.869112109	NELFA;SUP	.
0.456483179	0	0	2.314696106	5.242831751	LYL1;HDAC	.
0.456483179	0	0	2.314696106	5.242831751	AXIN1;HUV	.
0.456483179	0	0	1.915902593	4.337944555	STK11;CTD	.
0.456483179	0	0	2.754831429	6.225764304	PEAK1;RCC	.
0.456483179	0	0	2.286350844	5.105673699	GGA3;LARI	.
0.456483179	0	0	2.039287585	4.524273864	ARC;MAST	.
0.456483179	0	0	1.889991246	4.192740154	CX3CR1;IR/	.
0.456483179	0	0	3.742583732	8.276129953	SETD5;RUI	.
0.456483179	0	0	3.742583732	8.276129953	FAAH;PLBI	.
0.456483179	0	0	3.742583732	8.276129953	ZGPAT;CBL	.
0.456483179	0	0	3.742583732	8.276129953	NELFA;BRI	.
0.456483179	0	0	3.742583732	8.276129953	DOT1L;ZBT	.
0.456483179	0	0	3.742583732	8.276129953	NOTCH1;A	.
0.456483179	0	0	3.742583732	8.276129953	BRD1;FOX(	.
0.456483179	0	0	1.63995926	3.601456801	KMT2D;KM	.
0.456483179	0	0	1.63995926	3.601456801	USP35;ASX	.
0.456483179	0	0	3.598454177	7.738958042	SETD5;SUP	.

0.456483179	0	0	3.598454177	7.738958042	SPI1;CBL	.
0.456483179	0	0	3.598454177	7.738958042	ATP13A2;P	.
0.456483179	0	0	3.598454177	7.738958042	NCOR2;FO	.
0.456483179	0	0	3.598454177	7.738958042	PLA2G4B;C	.
0.456483179	0	0	3.598454177	7.738958042	KAT6A;EP3	.
0.456483179	0	0	3.598454177	7.738958042	NOTCH1;SI	.
0.456483179	0	0	3.598454177	7.738958042	KCTD13;PT	.
0.456483179	0	0	3.598454177	7.738958042	NUMA1;CD	.
0.456483179	0	0	3.598454177	7.738958042	GGA3;FLNA	.
0.456483179	0	0	3.598454177	7.738958042	GAK;VPS13	.
0.456483179	0	0	1.987134981	4.256050705	ARC;CEACA	.
0.456483179	0	0	1.748287054	3.742686279	GAK;PPIL2;	.
0.456483179	0	0	2.601385558	5.565000369	SLC15A4;SI	.
0.456483179	0	0	2.601385558	5.565000369	FAAH;ABCC	.
0.456483179	0	0	9.343675418	19.84372418	HOOK3	.
0.456483179	0	0	9.343675418	19.84372418	MCM3AP	.
0.456483179	0	0	9.343675418	19.84372418	SPI1	.
0.456483179	0	0	9.343675418	19.84372418	CEACAM1	.
0.456483179	0	0	9.343675418	19.84372418	CX3CR1	.
0.456483179	0	0	9.343675418	19.84372418	CEACAM1	.
0.456483179	0	0	9.343675418	19.84372418	RIN3	.
0.456483179	0	0	9.343675418	19.84372418	ADAM8	.
0.456483179	0	0	9.343675418	19.84372418	SLC15A4	.
0.456483179	0	0	9.343675418	19.84372418	ZBTB7A	.
0.456483179	0	0	9.343675418	19.84372418	NOTCH1	.
0.456483179	0	0	9.343675418	19.84372418	SREBF1	.
0.456483179	0	0	9.343675418	19.84372418	AKAP13	.
0.456483179	0	0	9.343675418	19.84372418	EP300	.
0.456483179	0	0	9.343675418	19.84372418	ADAM8	.
0.456483179	0	0	9.343675418	19.84372418	KLF15	.
0.456483179	0	0	9.343675418	19.84372418	KLF15	.
0.456483179	0	0	9.343675418	19.84372418	ATP13A2	.
0.456483179	0	0	9.343675418	19.84372418	SETD5	.
0.456483179	0	0	9.343675418	19.84372418	SLC26A6	.
0.456483179	0	0	9.343675418	19.84372418	TCAP	.
0.456483179	0	0	9.343675418	19.84372418	EP300	.
0.456483179	0	0	9.343675418	19.84372418	CSAD	.
0.456483179	0	0	9.343675418	19.84372418	PRR5	.
0.456483179	0	0	9.343675418	19.84372418	PISD	.
0.456483179	0	0	9.343675418	19.84372418	MRPS2	.
0.456483179	0	0	9.343675418	19.84372418	ATP13A2	.
0.456483179	0	0	9.343675418	19.84372418	NOTCH1	.
0.456483179	0	0	9.343675418	19.84372418	ABCC1	.
0.456483179	0	0	9.343675418	19.84372418	AMDHD2	.
0.456483179	0	0	9.343675418	19.84372418	SLC43A2	.
0.456483179	0	0	9.343675418	19.84372418	MAFB	.
0.456483179	0	0	9.343675418	19.84372418	PER1	.

0.456483179	0	0	9.343675418	19.84372418	FAM89B	.
0.456483179	0	0	9.343675418	19.84372418	DPH1	.
0.456483179	0	0	9.343675418	19.84372418	DPH1	.
0.456483179	0	0	9.343675418	19.84372418	RUNX1	.
0.456483179	0	0	9.343675418	19.84372418	RXRA	.
0.456483179	0	0	9.343675418	19.84372418	ACVR2B	.
0.456483179	0	0	9.343675418	19.84372418	SMCR8	.
0.456483179	0	0	9.343675418	19.84372418	HUWE1	.
0.456483179	0	0	9.343675418	19.84372418	SREBF2	.
0.456483179	0	0	9.343675418	19.84372418	DHX37	.
0.456483179	0	0	9.343675418	19.84372418	RUNX1	.
0.456483179	0	0	9.343675418	19.84372418	CX3CR1	.
0.456483179	0	0	9.343675418	19.84372418	DHX37	.
0.456483179	0	0	9.343675418	19.84372418	ADAM8	.
0.456483179	0	0	9.343675418	19.84372418	SLC15A4	.
0.456483179	0	0	2.553956835	5.365697886	SKI;BLOC1S	.
0.456483179	0	0	2.553956835	5.365697886	SPHK1;RFF	.
0.456483179	0	0	2.553956835	5.365697886	SPHK1;GBC	.
0.456483179	0	0	3.465000886	7.250686448	WDR81;WI	.
0.456483179	0	0	3.465000886	7.250686448	PLEKHG2;V	.
0.456483179	0	0	3.465000886	7.250686448	PNKP;WAS	.
0.456483179	0	0	3.465000886	7.250686448	ZNF692;EP	.
0.456483179	0	0	3.465000886	7.250686448	ERN1;ATP2	.
0.456483179	0	0	3.465000886	7.250686448	LARP1;DHX	.
0.456483179	0	0	3.465000886	7.250686448	CEACAM1;	.
0.456483179	0	0	3.465000886	7.250686448	LARP1;ADA	.
0.456483179	0	0	1.937568456	4.006914416	AKAP13;ST	.
0.456483179	0	0	1.937568456	4.006914416	NOTCH2;S	.
0.456483179	0	0	1.711511299	3.533122964	GAK;ARHG	.
0.456483179	0	0	2.508221994	5.175792052	WDR81;AT	.
0.456483179	0	0	2.129807692	4.371782898	AXIN1;DVL	.
0.456483179	0	0	1.583941606	3.247621711	USP35;ASX	.
0.456483179	0	0	3.341079973	6.80546316	GGA3;SEC1	.
0.456483179	0	0	3.341079973	6.80546316	DHX37;KRI	.
0.456483179	0	0	3.341079973	6.80546316	SF3A1;SF3A	.
0.456483179	0	0	3.341079973	6.80546316	CX3CR1;CE	.
0.456483179	0	0	3.341079973	6.80546316	NEURL1;ZE	.
0.456483179	0	0	3.341079973	6.80546316	NOTCH2;N	.
0.456483179	0	0	2.464091884	4.994709921	RBM15B;P	.
0.456483179	0	0	2.464091884	4.994709921	HIPK1;MAP	.
0.456483179	0	0	1.78150798	3.606183799	AKAP13;NC	.
0.456483179	0	0	1.279184323	2.570290624	AMHR2;PP	.
0.456483179	0	0	1.770212378	3.547141923	GAK;ARC;E	.
0.456483179	0	0	2.421483503	4.821921941	MAP3K3;P	.
0.456483179	0	0	3.225705329	6.398302565	GAK;DNAJI	.
0.456483179	0	0	3.225705329	6.398302565	ATP13A2;R	.
0.456483179	0	0	3.225705329	6.398302565	CADM4;SH	.

0.456483179	0	0	3.225705329	6.398302565	HUWE1;SR	.
0.456483179	0	0	3.225705329	6.398302565	ERN1;U2AI	.
0.456483179	0	0	7.785998409	15.41592526	DGAT1	.
0.456483179	0	0	7.785998409	15.41592526	AMDHD2	.
0.456483179	0	0	7.785998409	15.41592526	CLCN2	.
0.456483179	0	0	7.785998409	15.41592526	FLNA	.
0.456483179	0	0	7.785998409	15.41592526	NOTCH1	.
0.456483179	0	0	7.785998409	15.41592526	RUNX1	.
0.456483179	0	0	7.785998409	15.41592526	ATP13A2	.
0.456483179	0	0	7.785998409	15.41592526	WAS	.
0.456483179	0	0	7.785998409	15.41592526	ATP13A2	.
0.456483179	0	0	7.785998409	15.41592526	ATP13A2	.
0.456483179	0	0	7.785998409	15.41592526	NOTCH1	.
0.456483179	0	0	7.785998409	15.41592526	NOTCH1	.
0.456483179	0	0	7.785998409	15.41592526	SREBF2	.
0.456483179	0	0	7.785998409	15.41592526	PER1	.
0.456483179	0	0	7.785998409	15.41592526	CX3CR1	.
0.456483179	0	0	7.785998409	15.41592526	CLCN2	.
0.456483179	0	0	7.785998409	15.41592526	ATP13A2	.
0.456483179	0	0	7.785998409	15.41592526	DHX37	.
0.456483179	0	0	7.785998409	15.41592526	CX3CR1	.
0.456483179	0	0	7.785998409	15.41592526	MARK2	.
0.456483179	0	0	7.785998409	15.41592526	TCAP	.
0.456483179	0	0	7.785998409	15.41592526	CEACAM1	.
0.456483179	0	0	7.785998409	15.41592526	DENND4B	.
0.456483179	0	0	7.785998409	15.41592526	SRF	.
0.456483179	0	0	7.785998409	15.41592526	HDAC5	.
0.456483179	0	0	7.785998409	15.41592526	ARRB2	.
0.456483179	0	0	7.785998409	15.41592526	SLC15A4	.
0.456483179	0	0	7.785998409	15.41592526	LRRC32	.
0.456483179	0	0	7.785998409	15.41592526	FURIN	.
0.456483179	0	0	7.785998409	15.41592526	EP300	.
0.456483179	0	0	7.785998409	15.41592526	NFATC2	.
0.456483179	0	0	7.785998409	15.41592526	RIN3	.
0.456483179	0	0	7.785998409	15.41592526	BRD1	.
0.456483179	0	0	7.785998409	15.41592526	ATG2A	.
0.456483179	0	0	7.785998409	15.41592526	TCF3	.
0.456483179	0	0	7.785998409	15.41592526	ABCC1	.
0.456483179	0	0	7.785998409	15.41592526	SPI1	.
0.456483179	0	0	7.785998409	15.41592526	ATG2A	.
0.456483179	0	0	7.785998409	15.41592526	NOTCH2	.
0.456483179	0	0	7.785998409	15.41592526	SPI1	.
0.456483179	0	0	7.785998409	15.41592526	AGO3	.
0.456483179	0	0	7.785998409	15.41592526	NOTCH1	.
0.456483179	0	0	7.785998409	15.41592526	SMAD6	.
0.456483179	0	0	7.785998409	15.41592526	DGAT1	.
0.456483179	0	0	7.785998409	15.41592526	FAAH	.

0.456483179	0	0	7.785998409	15.41592526	SLC35F6	.
0.456483179	0	0	7.785998409	15.41592526	NOTCH1	.
0.456483179	0	0	7.785998409	15.41592526	SKI	.
0.456483179	0	0	7.785998409	15.41592526	NOTCH1	.
0.456483179	0	0	7.785998409	15.41592526	GNA15	.
0.456483179	0	0	7.785998409	15.41592526	ATG2A	.
0.456483179	0	0	7.785998409	15.41592526	BLOC1S3	.
0.456483179	0	0	7.785998409	15.41592526	NOTCH1	.
0.456483179	0	0	7.785998409	15.41592526	FLNA	.
0.456483179	0	0	7.785998409	15.41592526	IL17RA	.
0.456483179	0	0	7.785998409	15.41592526	KMT2D	.
0.456483179	0	0	7.785998409	15.41592526	RREB1	.
0.456483179	0	0	7.785998409	15.41592526	PDCD1	.
0.456483179	0	0	7.785998409	15.41592526	ZSWIM8	.
0.456483179	0	0	7.785998409	15.41592526	HUWE1	.
0.456483179	0	0	7.785998409	15.41592526	MARK4	.
0.456483179	0	0	7.785998409	15.41592526	ANAPC2	.
0.456483179	0	0	7.785998409	15.41592526	STAC2	.
0.456483179	0	0	7.785998409	15.41592526	SEC16A	.
0.456483179	0	0	1.605343955	3.172472168	GAK;HIP1;I	.
0.456483179	0	0	1.875180723	3.701566001	GAK;ARHG	.
0.456483179	0	0	2.380319473	4.65693802	ASXL1;RXR	.
0.456483179	0	0	2.380319473	4.65693802	IRAK1;MAI	.
0.456483179	0	0	2.380319473	4.65693802	CEACAM1;	.
0.456483179	0	0	2.036789298	3.955432763	HIP1;MAP2	.
0.456483179	0	0	3.118022329	6.024933641	ARC;BCL9L	.
0.456483179	0	0	3.118022329	6.024933641	PCIF1;FOX(	.
0.456483179	0	0	3.118022329	6.024933641	ZSWIM8;PI	.
0.456483179	0	0	3.118022329	6.024933641	NOTCH1;T(	.
0.456483179	0	0	3.118022329	6.024933641	ARC;CDK5I	.
0.456483179	0	0	3.118022329	6.024933641	ERN1;ZNF2	.
0.456483179	0	0	3.118022329	6.024933641	CREB3L2;R	.
0.456483179	0	0	3.118022329	6.024933641	TNRC6C;A(	.
0.456483179	0	0	3.118022329	6.024933641	BRF1;TAF4	.
0.456483179	0	0	3.118022329	6.024933641	CX3CR1;EP	.
0.456483179	0	0	3.118022329	6.024933641	NOTCH1;M	.
0.456483179	0	0	3.118022329	6.024933641	PNKP;MAP	.
0.456483179	0	0	1.726415933	3.32194446	MAST3;RPS	.
0.456483179	0	0	2.340527578	4.499304015	CAPN10;M	.
0.456483179	0	0	2.340527578	4.499304015	AMDHD2;I	.
0.456483179	0	0	2.340527578	4.499304015	NOTCH2;A	.
0.456483179	0	0	1.525969064	2.898241334	GNA13;AK	.
0.456483179	0	0	1.993248773	3.765831022	ABCC1;AD/	.
0.456483179	0	0	2.302040335	4.348598576	TBC1D2;M	.
0.456483179	0	0	2.302040335	4.348598576	ADAM8;CA	.
0.456483179	0	0	1.70531401	3.215582743	AKAP13;M	.
0.456483179	0	0	3.017286618	5.681678663	RXRA;SREB	.

0.456483179	0	0	3.017286618	5.681678663	CEACAM1;	.
0.456483179	0	0	3.017286618	5.681678663	TFEB;HOOI	.
0.456483179	0	0	3.017286618	5.681678663	PER1;NCOI	.
0.456483179	0	0	3.017286618	5.681678663	PNKP;MAP	.
0.456483179	0	0	1.972165992	3.675265497	RBM15B;M	.
0.456483179	0	0	6.673371974	12.39066339	ADARB1	.
0.456483179	0	0	6.673371974	12.39066339	AOC2	.
0.456483179	0	0	6.673371974	12.39066339	LNPEP	.
0.456483179	0	0	6.673371974	12.39066339	WAS	.
0.456483179	0	0	6.673371974	12.39066339	ATP13A2	.
0.456483179	0	0	6.673371974	12.39066339	SLIT3	.
0.456483179	0	0	6.673371974	12.39066339	SLC15A4	.
0.456483179	0	0	6.673371974	12.39066339	ZNF516	.
0.456483179	0	0	6.673371974	12.39066339	NOTCH1	.
0.456483179	0	0	6.673371974	12.39066339	ATP13A2	.
0.456483179	0	0	6.673371974	12.39066339	NOTCH1	.
0.456483179	0	0	6.673371974	12.39066339	DPH1	.
0.456483179	0	0	6.673371974	12.39066339	SREBF1	.
0.456483179	0	0	6.673371974	12.39066339	NOTCH1	.
0.456483179	0	0	6.673371974	12.39066339	CSK	.
0.456483179	0	0	6.673371974	12.39066339	STK11	.
0.456483179	0	0	6.673371974	12.39066339	DOT1L	.
0.456483179	0	0	6.673371974	12.39066339	NOTCH1	.
0.456483179	0	0	6.673371974	12.39066339	CX3CR1	.
0.456483179	0	0	6.673371974	12.39066339	NOTCH2	.
0.456483179	0	0	6.673371974	12.39066339	MYH11	.
0.456483179	0	0	6.673371974	12.39066339	PNKP	.
0.456483179	0	0	6.673371974	12.39066339	KRI1	.
0.456483179	0	0	6.673371974	12.39066339	NUMA1	.
0.456483179	0	0	6.673371974	12.39066339	SPI1	.
0.456483179	0	0	6.673371974	12.39066339	CBL	.
0.456483179	0	0	6.673371974	12.39066339	ARHGAP21	.
0.456483179	0	0	6.673371974	12.39066339	CADM4	.
0.456483179	0	0	6.673371974	12.39066339	PRDM15	.
0.456483179	0	0	6.673371974	12.39066339	RREB1	.
0.456483179	0	0	6.673371974	12.39066339	KDM5C	.
0.456483179	0	0	6.673371974	12.39066339	AGO3	.
0.456483179	0	0	6.673371974	12.39066339	FERMT3	.
0.456483179	0	0	6.673371974	12.39066339	EP300	.
0.456483179	0	0	6.673371974	12.39066339	NLRP1	.
0.456483179	0	0	6.673371974	12.39066339	MCM3AP	.
0.456483179	0	0	6.673371974	12.39066339	ACVR2B	.
0.456483179	0	0	6.673371974	12.39066339	ABHD17A	.
0.456483179	0	0	6.673371974	12.39066339	SETD5	.
0.456483179	0	0	6.673371974	12.39066339	ZNF703	.
0.456483179	0	0	6.673371974	12.39066339	LARP1	.
0.456483179	0	0	6.673371974	12.39066339	PIK3C2A	.

0.456483179	0	0	6.673371974	12.39066339	ACVR2B	.
0.456483179	0	0	6.673371974	12.39066339	NOTCH1	.
0.456483179	0	0	6.673371974	12.39066339	RUNX1	.
0.456483179	0	0	6.673371974	12.39066339	SRF	.
0.456483179	0	0	6.673371974	12.39066339	HUWE1	.
0.456483179	0	0	6.673371974	12.39066339	SUPT5H	.
0.456483179	0	0	6.673371974	12.39066339	NOTCH1	.
0.456483179	0	0	6.673371974	12.39066339	CEACAM1	.
0.456483179	0	0	6.673371974	12.39066339	NFATC2	.
0.456483179	0	0	6.673371974	12.39066339	SLIT3	.
0.456483179	0	0	6.673371974	12.39066339	PIK3C2A	.
0.456483179	0	0	6.673371974	12.39066339	NOTCH1	.
0.456483179	0	0	6.673371974	12.39066339	PTPN23	.
0.456483179	0	0	6.673371974	12.39066339	KMT2D	.
0.456483179	0	0	6.673371974	12.39066339	DVL3	.
0.456483179	0	0	6.673371974	12.39066339	MAN2A2	.
0.456483179	0	0	6.673371974	12.39066339	ABHD17A	.
0.456483179	0	0	2.264794616	4.204430315	AMHR2;SM	.
0.456483179	0	0	2.264794616	4.204430315	EP300;ABL	.
0.461257842	0	0	2.92284689	5.365355541	TTLL3;DNA	.
0.461257842	0	0	2.92284689	5.365355541	ZNF692;FC	.
0.461257842	0	0	2.92284689	5.365355541	NUMA1;RU	.
0.461257842	0	0	2.92284689	5.365355541	SLC35F6;H	.
0.461257842	0	0	2.92284689	5.365355541	SKI;DVL3	.
0.461257842	0	0	2.92284689	5.365355541	HIP1;CBL	.
0.461257842	0	0	2.92284689	5.365355541	PNKP;MAP	.
0.461257842	0	0	2.92284689	5.365355541	GGA3;EP3(	.
0.464394831	0	0	2.228731301	4.066435259	ZNF703;PI	.
0.464394831	0	0	1.538755372	2.798880324	SKI;ERN1;A	.
0.464394831	0	0	1.532395482	2.764260468	STK11;ZNF	.
0.464394831	0	0	2.193794964	3.934274555	HIPK1;MAI	.
0.464394831	0	0	2.834130781	5.073198618	DVL3;MAP	.
0.464394831	0	0	2.834130781	5.073198618	SRF;TCF3	.
0.464394831	0	0	2.834130781	5.073198618	SYN1;UNC	.
0.464394831	0	0	2.834130781	5.073198618	CX3CR1;AF	.
0.464394831	0	0	2.834130781	5.073198618	KMT2D;EP	.
0.464394831	0	0	2.834130781	5.073198618	NOTCH1;H	.
0.464394831	0	0	2.834130781	5.073198618	KCTD13;AE	.
0.464394831	0	0	1.911499215	3.419270681	ERN1;STK1	.
0.464394831	0	0	1.748426542	3.11057907	ABCC1;AD/	.
0.464394831	0	0	1.748426542	3.11057907	STK11;CTD	.
0.464394831	0	0	1.892094017	3.338855888	LARP1;P2R	.
0.464394831	0	0	1.892094017	3.338855888	HDAC5;KD	.
0.464394831	0	0	2.159933592	3.807632395	AXIN1;DVL	.
0.464394831	0	0	1.635321874	2.873007796	LARP1;RPS	.
0.464394831	0	0	1.563357546	2.740504565	CEACAM1;	.
0.464394831	0	0	5.838902148	10.21352785	SLC26A6	.

0.464394831	0	0	5.838902148	10.21352785	STK11	.
0.464394831	0	0	5.838902148	10.21352785	WAS	.
0.464394831	0	0	5.838902148	10.21352785	NUMA1	.
0.464394831	0	0	5.838902148	10.21352785	ATF6B	.
0.464394831	0	0	5.838902148	10.21352785	NOTCH1	.
0.464394831	0	0	5.838902148	10.21352785	ADAM8	.
0.464394831	0	0	5.838902148	10.21352785	RPS6KA1	.
0.464394831	0	0	5.838902148	10.21352785	CEACAM1	.
0.464394831	0	0	5.838902148	10.21352785	MAFG	.
0.464394831	0	0	5.838902148	10.21352785	IL17RA	.
0.464394831	0	0	5.838902148	10.21352785	NOTCH1	.
0.464394831	0	0	5.838902148	10.21352785	SPI1	.
0.464394831	0	0	5.838902148	10.21352785	IL17RA	.
0.464394831	0	0	5.838902148	10.21352785	UNC13D	.
0.464394831	0	0	5.838902148	10.21352785	ASXL1	.
0.464394831	0	0	5.838902148	10.21352785	EP300	.
0.464394831	0	0	5.838902148	10.21352785	BLOC1S3	.
0.464394831	0	0	5.838902148	10.21352785	BLOC1S3	.
0.464394831	0	0	5.838902148	10.21352785	NOTCH1	.
0.464394831	0	0	5.838902148	10.21352785	EP300	.
0.464394831	0	0	5.838902148	10.21352785	PFKP	.
0.464394831	0	0	5.838902148	10.21352785	CX3CR1	.
0.464394831	0	0	5.838902148	10.21352785	AMDHD2	.
0.464394831	0	0	5.838902148	10.21352785	SPHK1	.
0.464394831	0	0	5.838902148	10.21352785	ABCC1	.
0.464394831	0	0	5.838902148	10.21352785	IL17RA	.
0.464394831	0	0	5.838902148	10.21352785	SKI	.
0.464394831	0	0	5.838902148	10.21352785	SKI	.
0.464394831	0	0	5.838902148	10.21352785	AGO3	.
0.464394831	0	0	5.838902148	10.21352785	CX3CR1	.
0.464394831	0	0	5.838902148	10.21352785	NOTCH1	.
0.464394831	0	0	5.838902148	10.21352785	NOTCH1	.
0.464394831	0	0	5.838902148	10.21352785	SUPT5H	.
0.464394831	0	0	5.838902148	10.21352785	SMAD6	.
0.464394831	0	0	5.838902148	10.21352785	NFATC2	.
0.464394831	0	0	5.838902148	10.21352785	PNKP	.
0.464394831	0	0	5.838902148	10.21352785	NOTCH1	.
0.464394831	0	0	5.838902148	10.21352785	SKI	.
0.464394831	0	0	5.838902148	10.21352785	VPS13D	.
0.464394831	0	0	5.838902148	10.21352785	RUNX1	.
0.464394831	0	0	2.750633268	4.802794016	MARK4;M/	.
0.464394831	0	0	2.750633268	4.802794016	NOTCH1;SI	.
0.464394831	0	0	2.750633268	4.802794016	RIN3;ARRB	.
0.464394831	0	0	2.750633268	4.802794016	ATG2A;MA	.
0.464394831	0	0	2.750633268	4.802794016	TNRC6C;A(	.
0.464394831	0	0	2.750633268	4.802794016	FLNA;RREB	.
0.464394831	0	0	2.750633268	4.802794016	PNKP;MAP	.

0.468557796	0	0	2.127098321	3.686214143	CX3CR1;AE	.
0.468557796	0	0	1.709876	2.938958606	GNA13;WA	.
0.468557796	0	0	2.095243208	3.569744638	TBC1D2;W	.
0.468557796	0	0	2.095243208	3.569744638	SRF;MYH9;	.
0.468557796	0	0	2.67190704	4.552026534	NOTCH2;A	.
0.468557796	0	0	2.67190704	4.552026534	GAS2L1;M	.
0.468557796	0	0	2.67190704	4.552026534	ERN1;MEF	.
0.468557796	0	0	2.67190704	4.552026534	SKI;ACTA1	.
0.468557796	0	0	2.67190704	4.552026534	TFEB;MYH9	.
0.468557796	0	0	2.67190704	4.552026534	PER1;NCOI	.
0.468557796	0	0	2.67190704	4.552026534	ATP13A2;L	.
0.468557796	0	0	2.67190704	4.552026534	BRD1;FOX(	.
0.468557796	0	0	1.697398289	2.884246458	ARRDC5;AI	.
0.468557796	0	0	1.836161388	3.111146971	RBM15B;M	.
0.468557796	0	0	2.064325011	3.457966657	AMHR2;SM	.
0.468557796	0	0	2.064325011	3.457966657	NCOR1;EP3	.
0.468557796	0	0	1.818241225	3.039491733	RBM15B;M	.
0.468557796	0	0	2.597554492	4.319035757	ACTA1;TCA	.
0.468557796	0	0	2.597554492	4.319035757	CREB3L2;Z	.
0.468557796	0	0	2.597554492	4.319035757	PPP6R2;BC	.
0.468557796	0	0	2.597554492	4.319035757	ZNF703;LC	.
0.468557796	0	0	2.597554492	4.319035757	TFEB;HOOI	.
0.468557796	0	0	2.597554492	4.319035757	GAK;PIP5K	.
0.468557796	0	0	2.597554492	4.319035757	NOTCH1;SI	.
0.468557796	0	0	2.597554492	4.319035757	ACTA1;TCA	.
0.468557796	0	0	2.597554492	4.319035757	CAPN10;C2	.
0.468557796	0	0	2.597554492	4.319035757	KCTD13;PT	.
0.468557796	0	0	5.189870061	8.584536685	PLEKHJ1	.
0.468557796	0	0	5.189870061	8.584536685	RCC2	.
0.468557796	0	0	5.189870061	8.584536685	ZSWIM8	.
0.468557796	0	0	5.189870061	8.584536685	ZNF692	.
0.468557796	0	0	5.189870061	8.584536685	FERMT3	.
0.468557796	0	0	5.189870061	8.584536685	KMT2A	.
0.468557796	0	0	5.189870061	8.584536685	ERN1	.
0.468557796	0	0	5.189870061	8.584536685	PER1	.
0.468557796	0	0	5.189870061	8.584536685	P2RY1	.
0.468557796	0	0	5.189870061	8.584536685	ARC	.
0.468557796	0	0	5.189870061	8.584536685	CX3CR1	.
0.468557796	0	0	5.189870061	8.584536685	SPI1	.
0.468557796	0	0	5.189870061	8.584536685	GLS2	.
0.468557796	0	0	5.189870061	8.584536685	RBM15B	.
0.468557796	0	0	5.189870061	8.584536685	POU5F1	.
0.468557796	0	0	5.189870061	8.584536685	MARK4	.
0.468557796	0	0	5.189870061	8.584536685	ATP2A3	.
0.468557796	0	0	5.189870061	8.584536685	PFKP	.
0.468557796	0	0	5.189870061	8.584536685	CCS	.
0.468557796	0	0	5.189870061	8.584536685	RXRA	.

0.468557796	0	0	5.189870061	8.584536685	BLOC1S3	.
0.468557796	0	0	5.189870061	8.584536685	CDK5R1	.
0.468557796	0	0	5.189870061	8.584536685	SLC25A28	.
0.468557796	0	0	5.189870061	8.584536685	HOOK3	.
0.468557796	0	0	5.189870061	8.584536685	NOTCH1	.
0.468557796	0	0	5.189870061	8.584536685	AMDHD2	.
0.468557796	0	0	5.189870061	8.584536685	MGRN1	.
0.468557796	0	0	5.189870061	8.584536685	FURIN	.
0.468557796	0	0	5.189870061	8.584536685	PPM1F	.
0.468557796	0	0	5.189870061	8.584536685	NOTCH1	.
0.468557796	0	0	5.189870061	8.584536685	NCOR1	.
0.468557796	0	0	5.189870061	8.584536685	SACS	.
0.468557796	0	0	5.189870061	8.584536685	CACTIN	.
0.468557796	0	0	5.189870061	8.584536685	CACTIN	.
0.468557796	0	0	5.189870061	8.584536685	KLF15	.
0.468557796	0	0	5.189870061	8.584536685	NCOR1	.
0.468557796	0	0	5.189870061	8.584536685	ATP2A3	.
0.468557796	0	0	5.189870061	8.584536685	FURIN	.
0.468557796	0	0	5.189870061	8.584536685	SH2B3	.
0.468557796	0	0	5.189870061	8.584536685	CADM4	.
0.468557796	0	0	5.189870061	8.584536685	CDK5R1	.
0.468557796	0	0	5.189870061	8.584536685	ANKS1A	.
0.468557796	0	0	5.189870061	8.584536685	EP300	.
0.468557796	0	0	5.189870061	8.584536685	RPS6KA1	.
0.468557796	0	0	5.189870061	8.584536685	CEACAM1	.
0.468557796	0	0	5.189870061	8.584536685	TOLLIP	.
0.470832834	0	0	2.034302992	3.350639513	SPI1;PEAK1	.
0.470832834	0	0	2.034302992	3.350639513	ADAM8;AT	.
0.471797688	0	0	1.783424908	2.902113087	CX3CR1;AF	.
0.471797688	0	0	2.527221001	4.102179607	NOTCH1;H	.
0.471797688	0	0	2.527221001	4.102179607	LARP1;ND(	.
0.471797688	0	0	2.527221001	4.102179607	NFATC2;RU	.
0.471797688	0	0	2.527221001	4.102179607	NCOR1;RIN	.
0.471797688	0	0	1.649244867	2.677007104	CX3CR1;GN	.
0.471797688	0	0	2.005138746	3.247537789	GAK;SEC16	.
0.471797688	0	0	2.005138746	3.247537789	GADD45A;	.
0.471797688	0	0	1.976796028	3.148450177	SZT2;TFEB;	.
0.471797688	0	0	1.976796028	3.148450177	FHOD1;WA	.
0.471797688	0	0	1.976796028	3.148450177	ATP2A3;SY	.
0.471797688	0	0	1.484699747	2.354905923	NOTCH1;T	.
0.471797688	0	0	2.460589272	3.900003891	ATG2A;MA	.
0.471797688	0	0	2.460589272	3.900003891	SKI;AKAP13	.
0.471797688	0	0	2.460589272	3.900003891	NUMA1;CD	.
0.471797688	0	0	2.460589272	3.900003891	NOTCH1;R	.
0.471797688	0	0	2.460589272	3.900003891	CBL;EPN1	.
0.471797688	0	0	2.460589272	3.900003891	PER1;CACT	.
0.471797688	0	0	2.460589272	3.900003891	ARRB2;SH2	.

0.471797688	0	0	2.460589272	3.900003891	RBM15B;G	.
0.471797688	0	0	2.460589272	3.900003891	ARC;STAC2	.
0.471797688	0	0	2.460589272	3.900003891	PNKP;WAS	.
0.471797688	0	0	1.749910137	2.77219598	SKI;ZNF70	.
0.471797688	0	0	1.402551107	2.213812647	GNA13;AK	.
0.471797688	0	0	4.670644391	7.328158116	FHOD1	.
0.471797688	0	0	4.670644391	7.328158116	PANK1	.
0.471797688	0	0	4.670644391	7.328158116	SRF	.
0.471797688	0	0	4.670644391	7.328158116	NOTCH2	.
0.471797688	0	0	4.670644391	7.328158116	NFATC2	.
0.471797688	0	0	4.670644391	7.328158116	SKI	.
0.471797688	0	0	4.670644391	7.328158116	MAP2K2	.
0.471797688	0	0	4.670644391	7.328158116	CCS	.
0.471797688	0	0	4.670644391	7.328158116	SACS	.
0.471797688	0	0	4.670644391	7.328158116	RREB1	.
0.471797688	0	0	4.670644391	7.328158116	WDR81	.
0.471797688	0	0	4.670644391	7.328158116	PANK1	.
0.471797688	0	0	4.670644391	7.328158116	NEURL1	.
0.471797688	0	0	4.670644391	7.328158116	CMKLR1	.
0.471797688	0	0	4.670644391	7.328158116	UNC13D	.
0.471797688	0	0	4.670644391	7.328158116	HUWE1	.
0.471797688	0	0	4.670644391	7.328158116	ARRB2	.
0.471797688	0	0	4.670644391	7.328158116	UNC13D	.
0.471797688	0	0	4.670644391	7.328158116	MAP2K2	.
0.471797688	0	0	4.670644391	7.328158116	PDCD1	.
0.471797688	0	0	4.670644391	7.328158116	WAS	.
0.471797688	0	0	4.670644391	7.328158116	SLC15A4	.
0.471797688	0	0	4.670644391	7.328158116	GLS2	.
0.471797688	0	0	4.670644391	7.328158116	RUNX1	.
0.471797688	0	0	4.670644391	7.328158116	PANK1	.
0.471797688	0	0	4.670644391	7.328158116	FURIN	.
0.471797688	0	0	4.670644391	7.328158116	ABHD17A	.
0.471797688	0	0	4.670644391	7.328158116	AMDHD2	.
0.471797688	0	0	4.670644391	7.328158116	FOXO3	.
0.471797688	0	0	4.670644391	7.328158116	TCF3	.
0.471797688	0	0	4.670644391	7.328158116	PIK3C2A	.
0.471797688	0	0	4.670644391	7.328158116	MYH9	.
0.471797688	0	0	4.670644391	7.328158116	SKI	.
0.471797688	0	0	4.670644391	7.328158116	SREBF2	.
0.471797688	0	0	4.670644391	7.328158116	ARRB2	.
0.471797688	0	0	4.670644391	7.328158116	SH2B3	.
0.471797688	0	0	4.670644391	7.328158116	SH2B3	.
0.471797688	0	0	4.670644391	7.328158116	EPN1	.
0.471797688	0	0	4.670644391	7.328158116	PLBD2	.
0.471797688	0	0	4.670644391	7.328158116	ADAM8	.
0.471797688	0	0	4.670644391	7.328158116	ADAM8	.
0.471797688	0	0	4.670644391	7.328158116	PTPN23	.

0.471797688	0	0	4.670644391	7.328158116	NOTCH2	.
0.471797688	0	0	4.670644391	7.328158116	MAP2K2	.
0.471797688	0	0	4.670644391	7.328158116	BRD4	.
0.471797688	0	0	4.670644391	7.328158116	ATF6B	.
0.471797688	0	0	4.670644391	7.328158116	SREBF1	.
0.471797688	0	0	1.614873286	2.532938025	LARP1;ZNF	.
0.471797688	0	0	1.614873286	2.532938025	IRAK1;SPH	.
0.479619964	0	0	2.397374555	3.711216746	PPP6R2;SY	.
0.479619964	0	0	2.397374555	3.711216746	HOOK3;PLI	.
0.479619964	0	0	2.397374555	3.711216746	NELFA;SUP	.
0.479619964	0	0	2.397374555	3.711216746	BLOC1S3;H	.
0.479866645	0	0	1.92244013	2.961536364	KCTD13;M	.
0.479866645	0	0	1.92244013	2.961536364	PRDM15;K	.
0.479866645	0	0	1.92244013	2.961536364	ZNF703;US	.
0.479866645	0	0	1.92244013	2.961536364	NCOA2;SLI	.
0.479866645	0	0	1.92244013	2.961536364	ERN1;AHN	.
0.479866645	0	0	1.92244013	2.961536364	PLA2G4B;L	.
0.479866645	0	0	1.92244013	2.961536364	SPHK1;RPS	.
0.483853642	0	0	1.235786743	1.881100593	NOTCH2;A	.
0.483853642	0	0	1.701923077	2.590231937	WAS;ADAR	.
0.483853642	0	0	1.581895148	2.397792974	SKI;LRRK1;	.
0.483853642	0	0	1.89636399	2.873349047	SPI1;NOTC	.
0.483853642	0	0	1.89636399	2.873349047	PLA2G4B;M	.
0.483853642	0	0	1.89636399	2.873349047	SPHK1;AXI	.
0.483853642	0	0	2.337320574	3.534667096	CX3CR1;AS	.
0.483853642	0	0	2.337320574	3.534667096	SKI;ANKRD	.
0.483853642	0	0	2.337320574	3.534667096	MRPS2;FO	.
0.483853642	0	0	1.571197542	2.354611838	STK11;MAI	.
0.483853642	0	0	4.245823389	6.335327339	ZNF516	.
0.483853642	0	0	4.245823389	6.335327339	AMDHD2	.
0.483853642	0	0	4.245823389	6.335327339	NOTCH1	.
0.483853642	0	0	4.245823389	6.335327339	CDK5R1	.
0.483853642	0	0	4.245823389	6.335327339	RUNX1	.
0.483853642	0	0	4.245823389	6.335327339	NFATC2	.
0.483853642	0	0	4.245823389	6.335327339	AMDHD2	.
0.483853642	0	0	4.245823389	6.335327339	AKAP13	.
0.483853642	0	0	4.245823389	6.335327339	SREBF2	.
0.483853642	0	0	4.245823389	6.335327339	GAS2L1	.
0.483853642	0	0	4.245823389	6.335327339	RBM15B	.
0.483853642	0	0	4.245823389	6.335327339	RBSN	.
0.483853642	0	0	4.245823389	6.335327339	RUNX1	.
0.483853642	0	0	4.245823389	6.335327339	KLF15	.
0.483853642	0	0	4.245823389	6.335327339	GLS2	.
0.483853642	0	0	4.245823389	6.335327339	MRTFA	.
0.483853642	0	0	4.245823389	6.335327339	SPHK1	.
0.483853642	0	0	4.245823389	6.335327339	HOOK3	.
0.483853642	0	0	4.245823389	6.335327339	DGAT1	.

0.483853642	0	0	4.245823389	6.335327339	NOTCH1	.
0.483853642	0	0	4.245823389	6.335327339	CADM4	.
0.483853642	0	0	4.245823389	6.335327339	CEACAM1	.
0.483853642	0	0	4.245823389	6.335327339	SPI1	.
0.483853642	0	0	4.245823389	6.335327339	RIN3	.
0.483853642	0	0	4.245823389	6.335327339	RIN3	.
0.483853642	0	0	4.245823389	6.335327339	NELFA	.
0.483853642	0	0	4.245823389	6.335327339	CEACAM1	.
0.483853642	0	0	4.245823389	6.335327339	SLC26A6	.
0.483853642	0	0	4.245823389	6.335327339	ERN1	.
0.483853642	0	0	4.245823389	6.335327339	SPI1	.
0.483853642	0	0	4.245823389	6.335327339	ADAM8	.
0.488104861	0	0	2.280196056	3.369326399	EP300;ZBT	.
0.488104861	0	0	2.280196056	3.369326399	PER1;IL17F	.
0.488104861	0	0	2.280196056	3.369326399	EP300;ZBT	.
0.488104861	0	0	2.280196056	3.369326399	NOTCH1;SI	.
0.488104861	0	0	2.280196056	3.369326399	PIP5K1C;S\	.
0.488104861	0	0	2.280196056	3.369326399	GNA15;AB	.
0.490668521	0	0	1.5502274	2.270911508	MAFB;SRF;	.
0.490668521	0	0	2.225791752	3.214273136	PIP5K1C;S\	.
0.490668521	0	0	2.225791752	3.214273136	TNRC6C;M	.
0.490668521	0	0	2.225791752	3.214273136	FHOD1;PPI	.
0.490668521	0	0	1.822199383	2.627917695	ASXL1;ZNF	.
0.490668521	0	0	1.822199383	2.627917695	ADAM8;RE	.
0.490668521	0	0	1.529805496	2.190615346	ERN1;NOT	.
0.490668521	0	0	1.343577107	1.916531601	CX3CR1;IR/	.
0.490668521	0	0	1.627508361	2.317761774	HIP1;ATP2	.
0.490668521	0	0	3.891805887	5.534975898	CX3CR1	.
0.490668521	0	0	3.891805887	5.534975898	RUNX1	.
0.490668521	0	0	3.891805887	5.534975898	SMCR8	.
0.490668521	0	0	3.891805887	5.534975898	SETD5	.
0.490668521	0	0	3.891805887	5.534975898	ZNF703	.
0.490668521	0	0	3.891805887	5.534975898	SZT2	.
0.490668521	0	0	3.891805887	5.534975898	SPI1	.
0.490668521	0	0	3.891805887	5.534975898	IRAK1	.
0.490668521	0	0	3.891805887	5.534975898	FLNA	.
0.490668521	0	0	3.891805887	5.534975898	SKI	.
0.490668521	0	0	3.891805887	5.534975898	CBL	.
0.490668521	0	0	3.891805887	5.534975898	KRI1	.
0.490668521	0	0	3.891805887	5.534975898	SEC16A	.
0.490668521	0	0	3.891805887	5.534975898	CBL	.
0.490668521	0	0	3.891805887	5.534975898	ADAM8	.
0.490668521	0	0	3.891805887	5.534975898	NLRP1	.
0.490668521	0	0	3.891805887	5.534975898	GAS2L1	.
0.490668521	0	0	3.891805887	5.534975898	STK11	.
0.490668521	0	0	3.891805887	5.534975898	ATG2A	.
0.490668521	0	0	3.891805887	5.534975898	SPHK1	.

0.490668521	0	0	3.891805887	5.534975898	SPHK1	.
0.490668521	0	0	3.891805887	5.534975898	CX3CR1	.
0.490668521	0	0	3.891805887	5.534975898	NOTCH2	.
0.490668521	0	0	3.891805887	5.534975898	IRAK1	.
0.490668521	0	0	3.891805887	5.534975898	ARHGAP21	.
0.490668521	0	0	3.891805887	5.534975898	AMDHD2	.
0.490668521	0	0	3.891805887	5.534975898	SKI	.
0.490668521	0	0	3.891805887	5.534975898	SMCR8	.
0.490668521	0	0	3.891805887	5.534975898	RUNX1	.
0.490668521	0	0	3.891805887	5.534975898	RCC2	.
0.490668521	0	0	3.891805887	5.534975898	MAP3K3	.
0.490668521	0	0	3.891805887	5.534975898	ATF6B	.
0.490668521	0	0	3.891805887	5.534975898	EP300	.
0.490668521	0	0	3.891805887	5.534975898	ZNF385A	.
0.490668521	0	0	3.891805887	5.534975898	WAS	.
0.490668521	0	0	3.891805887	5.534975898	NOTCH1	.
0.490668521	0	0	3.891805887	5.534975898	NOTCH1	.
0.490668521	0	0	3.891805887	5.534975898	RCC2	.
0.490668521	0	0	3.891805887	5.534975898	CADM4	.
0.490668521	0	0	3.891805887	5.534975898	MYH9	.
0.490668521	0	0	3.891805887	5.534975898	CHERP	.
0.490668521	0	0	3.891805887	5.534975898	CHERP	.
0.490668521	0	0	3.891805887	5.534975898	ZNF609	.
0.490668521	0	0	3.891805887	5.534975898	TNRC6C	.
0.490668521	0	0	3.891805887	5.534975898	SEC16A	.
0.491472029	0	0	1.798745619	2.551997155	HIP1;ATP2	.
0.491472029	0	0	1.798745619	2.551997155	CADM4;PN	.
0.494116914	0	0	2.173917881	3.068679557	NOTCH1;EI	.
0.494116914	0	0	2.173917881	3.068679557	ADAM8;SL	.
0.495733829	0	0	1.448229494	2.038266474	TFEB;PRDM	.
0.496548391	0	0	1.775885621	2.47879874	EFNB1;ANI	.
0.496548391	0	0	1.775885621	2.47879874	SPHK1;AXI	.
0.496548391	0	0	1.440728354	2.007376754	WDR81;TC	.
0.496548391	0	0	2.124401914	2.931800327	SKI;SPHK1	.
0.496548391	0	0	2.124401914	2.931800327	PNKP;MAP	.
0.496548391	0	0	2.124401914	2.931800327	SF3A1;SF3	.
0.496548391	0	0	2.124401914	2.931800327	HOOK3;PLI	.
0.496548391	0	0	2.124401914	2.931800327	NUMA1;M	.
0.496548391	0	0	2.124401914	2.931800327	ERN1;MEF	.
0.496548391	0	0	1.433303756	1.97700527	CX3CR1;NA	.
0.496548391	0	0	1.753597122	2.408199969	AKNA;NLRI	.
0.496548391	0	0	1.753597122	2.408199969	FURIN;LNP	.
0.496548391	0	0	1.425954535	1.947141874	ANGPT4;CI	.
0.496548391	0	0	3.592252616	4.878967562	COQ8B	.
0.496548391	0	0	3.592252616	4.878967562	NLRP1	.
0.496548391	0	0	3.592252616	4.878967562	NOTCH2	.
0.496548391	0	0	3.592252616	4.878967562	SKI	.

0.496548391	0	0	3.592252616	4.878967562	SLC26A6	.
0.496548391	0	0	3.592252616	4.878967562	NOTCH1	.
0.496548391	0	0	3.592252616	4.878967562	ANKRD9	.
0.496548391	0	0	3.592252616	4.878967562	SREBF2	.
0.496548391	0	0	3.592252616	4.878967562	ZNF335	.
0.496548391	0	0	3.592252616	4.878967562	FLNA	.
0.496548391	0	0	3.592252616	4.878967562	ZNF385A	.
0.496548391	0	0	3.592252616	4.878967562	WAS	.
0.496548391	0	0	3.592252616	4.878967562	FURIN	.
0.496548391	0	0	3.592252616	4.878967562	PANK1	.
0.496548391	0	0	3.592252616	4.878967562	SETD5	.
0.496548391	0	0	3.592252616	4.878967562	ACVR2B	.
0.496548391	0	0	3.592252616	4.878967562	ASXL1	.
0.496548391	0	0	3.592252616	4.878967562	CEACAM1	.
0.496548391	0	0	3.592252616	4.878967562	SH2B3	.
0.496548391	0	0	3.592252616	4.878967562	SLC26A6	.
0.496548391	0	0	3.592252616	4.878967562	LRRC32	.
0.496548391	0	0	3.592252616	4.878967562	MFSD10	.
0.496548391	0	0	3.592252616	4.878967562	ANKS1A	.
0.496548391	0	0	3.592252616	4.878967562	SLC26A6	.
0.496548391	0	0	3.592252616	4.878967562	ERN1	.
0.496548391	0	0	3.592252616	4.878967562	NAXD	.
0.496548391	0	0	3.592252616	4.878967562	CMKLR1	.
0.496548391	0	0	3.592252616	4.878967562	U2AF2	.
0.496548391	0	0	3.592252616	4.878967562	CEACAM1	.
0.496548391	0	0	3.592252616	4.878967562	LARP1	.
0.496548391	0	0	3.592252616	4.878967562	HOOK3	.
0.496548391	0	0	3.592252616	4.878967562	PPM1F	.
0.496548391	0	0	3.592252616	4.878967562	RUNX1	.
0.496548391	0	0	3.592252616	4.878967562	RREB1	.
0.496548391	0	0	3.592252616	4.878967562	NOTCH1	.
0.496548391	0	0	3.592252616	4.878967562	C2CD2L	.
0.496548391	0	0	3.592252616	4.878967562	CMKLR1	.
0.496548391	0	0	3.592252616	4.878967562	SMCR8	.
0.496548391	0	0	3.592252616	4.878967562	SLC26A6	.
0.496548391	0	0	3.592252616	4.878967562	AGO3	.
0.496548391	0	0	3.592252616	4.878967562	RCC2	.
0.497473924	0	0	1.731858957	2.340085139	HDAC5;CE/	.
0.497473924	0	0	1.731858957	2.340085139	NCOR1;NU	.
0.497473924	0	0	2.077086656	2.80296276	NCOR2;ME	.
0.497473924	0	0	2.077086656	2.80296276	NOTCH1;SI	.
0.497473924	0	0	2.077086656	2.80296276	NOTCH1;SI	.
0.497473924	0	0	2.077086656	2.80296276	CBL;PIK3C2	.
0.497473924	0	0	2.077086656	2.80296276	AKNA;NOT	.
0.497473924	0	0	2.077086656	2.80296276	FOXO3;CDI	.
0.503720928	0	0	1.559294872	2.078729052	TNRC6C;AC	.
0.503720928	0	0	1.404347826	1.860502285	ABCC1;AKI	.

0.503720928	0	0	2.031828583	2.681558387	PNKP;HUW	.
0.503720928	0	0	2.031828583	2.681558387	SETD5;DG(	.
0.503720928	0	0	2.031828583	2.681558387	PEAK1;FER	.
0.503720928	0	0	2.031828583	2.681558387	PLA2G4B;L	.
0.503720928	0	0	1.689954061	2.210875727	NCOR1;CA	.
0.503720928	0	0	3.33549267	4.333634814	BLOC1S3	.
0.503720928	0	0	3.33549267	4.333634814	TCAP	.
0.503720928	0	0	3.33549267	4.333634814	TNK2	.
0.503720928	0	0	3.33549267	4.333634814	ZNF385A	.
0.503720928	0	0	3.33549267	4.333634814	NOTCH1	.
0.503720928	0	0	3.33549267	4.333634814	P2RY1	.
0.503720928	0	0	3.33549267	4.333634814	KCTD13	.
0.503720928	0	0	3.33549267	4.333634814	SPHK1	.
0.503720928	0	0	3.33549267	4.333634814	DVL3	.
0.503720928	0	0	3.33549267	4.333634814	TNRC6C	.
0.503720928	0	0	3.33549267	4.333634814	TNRC6C	.
0.503720928	0	0	3.33549267	4.333634814	ABL2	.
0.503720928	0	0	3.33549267	4.333634814	NDOR1	.
0.503720928	0	0	3.33549267	4.333634814	SREBF1	.
0.503720928	0	0	3.33549267	4.333634814	TCAP	.
0.503720928	0	0	3.33549267	4.333634814	PER1	.
0.503720928	0	0	3.33549267	4.333634814	HCFC1	.
0.503720928	0	0	3.33549267	4.333634814	HCFC1	.
0.503720928	0	0	3.33549267	4.333634814	KCTD13	.
0.503720928	0	0	3.33549267	4.333634814	BLOC1S3	.
0.503720928	0	0	3.33549267	4.333634814	ZNF703	.
0.503720928	0	0	3.33549267	4.333634814	COQ8B	.
0.503720928	0	0	3.33549267	4.333634814	COQ8B	.
0.503720928	0	0	3.33549267	4.333634814	FOXO3	.
0.503720928	0	0	3.33549267	4.333634814	EME2	.
0.503720928	0	0	3.33549267	4.333634814	PCIF1	.
0.503720928	0	0	3.33549267	4.333634814	WAS	.
0.503720928	0	0	3.33549267	4.333634814	U2AF2	.
0.503720928	0	0	3.33549267	4.333634814	PISD	.
0.503720928	0	0	3.33549267	4.333634814	ASCL2	.
0.503720928	0	0	3.33549267	4.333634814	ADAM8	.
0.503720928	0	0	3.33549267	4.333634814	ZNF385A	.
0.503720928	0	0	3.33549267	4.333634814	WAS	.
0.503720928	0	0	3.33549267	4.333634814	ATP13A2	.
0.503720928	0	0	3.33549267	4.333634814	KMT2A	.
0.503720928	0	0	3.33549267	4.333634814	NUMA1	.
0.503720928	0	0	3.33549267	4.333634814	TNRC6C	.
0.503720928	0	0	3.33549267	4.333634814	ZDHHC5	.
0.50501257	0	0	1.988496386	2.567035663	CEACAM1;	.
0.50501257	0	0	1.988496386	2.567035663	PCIF1;FOX(	.
0.50501257	0	0	1.988496386	2.567035663	GADD45A;	.
0.50501257	0	0	1.988496386	2.567035663	PER1;MAP	.

0.50501257	0	0	1.988496386	2.567035663	ERN1;ZNF2	.
0.50501257	0	0	1.988496386	2.567035663	ERN1;AGO	.
0.50501257	0	0	1.988496386	2.567035663	NCOR1;FLN	.
0.508111761	0	0	1.65002116	2.090364264	RBSN;PLEK	.
0.508111761	0	0	1.65002116	2.090364264	EP300;ABL	.
0.508111761	0	0	1.508684864	1.908256222	BLOC1S3;N	.
0.508111761	0	0	1.946969697	2.458893619	EP300;ZBT	.
0.508111761	0	0	1.946969697	2.458893619	DHX37;MR	.
0.508111761	0	0	1.946969697	2.458893619	PLA2G4B;L	.
0.508111761	0	0	1.496538462	1.868235701	HDAC5;CEA	.
0.508111761	0	0	1.496538462	1.868235701	ACTA1;TCA	.
0.508111761	0	0	1.630751213	2.033141328	CX3CR1;PL	.
0.508111761	0	0	1.630751213	2.033141328	ABCC1;ADA	.
0.508111761	0	0	3.112967383	3.874783274	IRAK1	.
0.508111761	0	0	3.112967383	3.874783274	SRF	.
0.508111761	0	0	3.112967383	3.874783274	ATG2A	.
0.508111761	0	0	3.112967383	3.874783274	FOXK1	.
0.508111761	0	0	3.112967383	3.874783274	SPHK1	.
0.508111761	0	0	3.112967383	3.874783274	SREBF2	.
0.508111761	0	0	3.112967383	3.874783274	CEACAM1	.
0.508111761	0	0	3.112967383	3.874783274	CEACAM1	.
0.508111761	0	0	3.112967383	3.874783274	SLC15A4	.
0.508111761	0	0	3.112967383	3.874783274	UNC13D	.
0.508111761	0	0	3.112967383	3.874783274	ARC	.
0.508111761	0	0	3.112967383	3.874783274	SYN1	.
0.508111761	0	0	3.112967383	3.874783274	CADM4	.
0.508111761	0	0	3.112967383	3.874783274	GLS2	.
0.508111761	0	0	3.112967383	3.874783274	EME2	.
0.508111761	0	0	3.112967383	3.874783274	ABCC1	.
0.508111761	0	0	3.112967383	3.874783274	EP400	.
0.508111761	0	0	3.112967383	3.874783274	ERN1	.
0.508111761	0	0	3.112967383	3.874783274	SPHK1	.
0.508111761	0	0	3.112967383	3.874783274	MAU2	.
0.508111761	0	0	3.112967383	3.874783274	CACTIN	.
0.508111761	0	0	3.112967383	3.874783274	AMDHD2	.
0.508111761	0	0	3.112967383	3.874783274	EP300	.
0.508111761	0	0	3.112967383	3.874783274	NOTCH1	.
0.508111761	0	0	3.112967383	3.874783274	RCC2	.
0.508111761	0	0	3.112967383	3.874783274	RCC2	.
0.508111761	0	0	3.112967383	3.874783274	SH2B3	.
0.508111761	0	0	3.112967383	3.874783274	CACTIN	.
0.508111761	0	0	3.112967383	3.874783274	CDK5R1	.
0.508111761	0	0	3.112967383	3.874783274	RBM15B	.
0.508111761	0	0	3.112967383	3.874783274	ANKRD11	.
0.508111761	0	0	3.112967383	3.874783274	KMT2D	.
0.508111761	0	0	3.112967383	3.874783274	PIK3C2A	.
0.508111761	0	0	3.112967383	3.874783274	ABCC1	.

0.508111761	0	0	3.112967383	3.874783274	EP300	.
0.508111761	0	0	3.112967383	3.874783274	RUNX1	.
0.508111761	0	0	3.112967383	3.874783274	PNKP	.
0.508111761	0	0	3.112967383	3.874783274	IRAK1	.
0.508111761	0	0	3.112967383	3.874783274	SEC16A	.
0.508111761	0	0	3.112967383	3.874783274	HOOK3	.
0.510327598	0	0	1.907137975	2.356676348	PI4KA;PIK3	.
0.510327598	0	0	1.907137975	2.356676348	EP300;HIPI	.
0.510327598	0	0	1.907137975	2.356676348	AKNA;NOT	.
0.510327598	0	0	1.907137975	2.356676348	U2AF2;ARF	.
0.510327598	0	0	1.907137975	2.356676348	FHOD1;PPI	.
0.510327598	0	0	1.409057918	1.74112502	ARC;BLOC1	.
0.511737957	0	0	1.48458486	1.829192713	LRRK1;PRD	.
0.513564882	0	0	1.611924254	1.977827627	RBM15B;U	.
0.513564882	0	0	1.611924254	1.977827627	LARP1;PCII	.
0.515862636	0	0	1.400548301	1.711124632	NOTCH2;N	.
0.51991944	0	0	1.868899522	2.25996817	CREB3L2;R	.
0.51991944	0	0	1.868899522	2.25996817	PNKP;MAP	.
0.51991944	0	0	1.868899522	2.25996817	GADD45A;	.
0.51991944	0	0	1.868899522	2.25996817	CEACAM1;	.
0.51991944	0	0	1.868899522	2.25996817	EP300;SMA	.
0.51991944	0	0	1.868899522	2.25996817	STAC2;ZDH	.
0.520594402	0	0	2.918257757	3.484618619	AKAP13	.
0.520594402	0	0	2.918257757	3.484618619	ANKRD9	.
0.520594402	0	0	2.918257757	3.484618619	SPHK1	.
0.520594402	0	0	2.918257757	3.484618619	ZFAND2A	.
0.520594402	0	0	2.918257757	3.484618619	AGO3	.
0.520594402	0	0	2.918257757	3.484618619	P2RY1	.
0.520594402	0	0	2.918257757	3.484618619	AGO3	.
0.520594402	0	0	2.918257757	3.484618619	NOTCH1	.
0.520594402	0	0	2.918257757	3.484618619	GGA3	.
0.520594402	0	0	2.918257757	3.484618619	NCOR1	.
0.520594402	0	0	2.918257757	3.484618619	MAP3K3	.
0.520594402	0	0	2.918257757	3.484618619	RFFL	.
0.520594402	0	0	2.918257757	3.484618619	ZNF385A	.
0.520594402	0	0	2.918257757	3.484618619	CADM4	.
0.520594402	0	0	2.918257757	3.484618619	NOTCH1	.
0.520594402	0	0	2.918257757	3.484618619	RUNX1	.
0.520594402	0	0	2.918257757	3.484618619	IL17RA	.
0.520594402	0	0	2.918257757	3.484618619	UNC13D	.
0.523075424	0	0	1.575539568	1.87261569	ANGPT4;CA	.
0.525316585	0	0	1.832160615	2.168389411	NOTCH1;TC	.
0.526029785	0	0	1.28960363	1.512276988	ESPNL;TTLI	.
0.526029785	0	0	1.198482378	1.394592743	CEACAM1;	.
0.526029785	0	0	1.317751922	1.530997882	CX3CR1;IRA	.
0.526029785	0	0	1.796834744	2.081592688	RBM15B;ZI	.
0.526029785	0	0	1.796834744	2.081592688	GADD45A;	.

0.526029785	0	0	1.796834744	2.081592688	NUMA1;H(	.
0.526029785	0	0	1.796834744	2.081592688	FLNA;KCN/	.
0.526029785	0	0	1.796834744	2.081592688	STAC2;TCA	.
0.526029785	0	0	1.796834744	2.081592688	FAAH;PLA2	.
0.526029785	0	0	1.195869837	1.38216397	TNRC6C;EF	.
0.526029785	0	0	1.235460325	1.424123774	STK11;GAL	.
0.526029785	0	0	1.54075421	1.774142624	MAP3K3;IF	.
0.526029785	0	0	1.54075421	1.774142624	ANGPT4;RI	.
0.526029785	0	0	2.746455145	3.149788495	RREB1	.
0.526029785	0	0	2.746455145	3.149788495	ADARB1	.
0.526029785	0	0	2.746455145	3.149788495	FURIN	.
0.526029785	0	0	2.746455145	3.149788495	SLC15A4	.
0.526029785	0	0	2.746455145	3.149788495	NUMA1	.
0.526029785	0	0	2.746455145	3.149788495	SRF	.
0.526029785	0	0	2.746455145	3.149788495	NCOR1	.
0.526029785	0	0	2.746455145	3.149788495	ATP13A2	.
0.526029785	0	0	2.746455145	3.149788495	SLC35F6	.
0.526029785	0	0	2.746455145	3.149788495	SUPT5H	.
0.526029785	0	0	2.746455145	3.149788495	KAT6A	.
0.526029785	0	0	2.746455145	3.149788495	SMAD6	.
0.526029785	0	0	2.746455145	3.149788495	NUMA1	.
0.526029785	0	0	2.746455145	3.149788495	SLC26A6	.
0.526029785	0	0	2.746455145	3.149788495	FLNA	.
0.526029785	0	0	2.746455145	3.149788495	LRRC32	.
0.526029785	0	0	2.746455145	3.149788495	MEX3D	.
0.526029785	0	0	2.746455145	3.149788495	CX3CR1	.
0.526029785	0	0	2.746455145	3.149788495	BLOC1S3	.
0.526029785	0	0	2.746455145	3.149788495	DGAT1	.
0.526029785	0	0	2.746455145	3.149788495	CEACAM1	.
0.526029785	0	0	2.746455145	3.149788495	SLC43A2	.
0.526029785	0	0	2.746455145	3.149788495	SKI	.
0.526029785	0	0	2.746455145	3.149788495	CACTIN	.
0.526029785	0	0	2.746455145	3.149788495	RFFL	.
0.526029785	0	0	2.746455145	3.149788495	RFFL	.
0.526029785	0	0	2.746455145	3.149788495	ANKS1A	.
0.526029785	0	0	2.746455145	3.149788495	MBOAT7	.
0.526029785	0	0	2.746455145	3.149788495	BLOC1S3	.
0.526029785	0	0	2.746455145	3.149788495	CRTC3	.
0.526029785	0	0	2.746455145	3.149788495	RUNX1	.
0.526029785	0	0	2.746455145	3.149788495	NOTCH1	.
0.526029785	0	0	2.746455145	3.149788495	ERN1	.
0.526029785	0	0	2.746455145	3.149788495	HOOK3	.
0.528446647	0	0	1.351556515	1.542848025	SPI1;MYH9	.
0.530594798	0	0	1.762841925	1.999259636	ANGPT4;G/	.
0.530594798	0	0	1.762841925	1.999259636	RPS6KA1;R	.
0.530594798	0	0	1.762841925	1.999259636	U2AF2;ARF	.
0.530594798	0	0	1.188098495	1.345525094	CEACAM1;	.

0.530594798	0	0	1.335972461	1.490929241	MYH9;FLN	.
0.530594798	0	0	1.730108099	1.921098024	AXIN1;DVL	.
0.530594798	0	0	1.730108099	1.921098024	EP300;ZBT	.
0.530594798	0	0	1.730108099	1.921098024	ATG2A;ATI	.
0.530594798	0	0	1.730108099	1.921098024	HUWE1;SR	.
0.530594798	0	0	1.180425111	1.309837016	CEACAM1;	.
0.530594798	0	0	1.259452412	1.397337935	CX3CR1;AS	.
0.530594798	0	0	2.593741713	2.860096482	NLRP1	.
0.530594798	0	0	2.593741713	2.860096482	RUNX1	.
0.530594798	0	0	2.593741713	2.860096482	RUNX1	.
0.530594798	0	0	2.593741713	2.860096482	ATP13A2	.
0.530594798	0	0	2.593741713	2.860096482	ZNF335	.
0.530594798	0	0	2.593741713	2.860096482	TCAP	.
0.530594798	0	0	2.593741713	2.860096482	SPHK1	.
0.530594798	0	0	2.593741713	2.860096482	SPHK1	.
0.530594798	0	0	2.593741713	2.860096482	EXD2	.
0.530594798	0	0	2.593741713	2.860096482	NOTCH1	.
0.530594798	0	0	2.593741713	2.860096482	GADD45A	.
0.530594798	0	0	2.593741713	2.860096482	NOTCH1	.
0.530594798	0	0	2.593741713	2.860096482	BLOC1S3	.
0.530594798	0	0	2.593741713	2.860096482	MARK2	.
0.530594798	0	0	2.593741713	2.860096482	ARRB2	.
0.530594798	0	0	2.593741713	2.860096482	CNOT3	.
0.530594798	0	0	2.593741713	2.860096482	SYN1	.
0.530594798	0	0	2.593741713	2.860096482	CADM4	.
0.530594798	0	0	2.593741713	2.860096482	P2RY1	.
0.530594798	0	0	2.593741713	2.860096482	NOTCH1	.
0.530594798	0	0	2.593741713	2.860096482	FOXO3	.
0.530594798	0	0	2.593741713	2.860096482	CX3CR1	.
0.530594798	0	0	2.593741713	2.860096482	SPHK1	.
0.530594798	0	0	2.593741713	2.860096482	ARC	.
0.530594798	0	0	2.593741713	2.860096482	NOTCH1	.
0.530594798	0	0	2.593741713	2.860096482	MARK2	.
0.530594798	0	0	2.593741713	2.860096482	MAN2A2	.
0.530594798	0	0	2.593741713	2.860096482	GGA3	.
0.530594798	0	0	2.593741713	2.860096482	PDCD1	.
0.530594798	0	0	2.593741713	2.860096482	U2AF2	.
0.530594798	0	0	2.593741713	2.860096482	CEACAM1	.
0.530594798	0	0	2.593741713	2.860096482	AMDHD2	.
0.530594798	0	0	2.593741713	2.860096482	MARK4	.
0.530594798	0	0	2.593741713	2.860096482	PPM1F	.
0.530594798	0	0	2.593741713	2.860096482	CMKLR1	.
0.530594798	0	0	2.593741713	2.860096482	ABL2	.
0.530594798	0	0	2.593741713	2.860096482	SREBF1	.
0.531425343	0	0	1.4913516	1.637925043	CCS;FURIN	.
0.531425343	0	0	1.4913516	1.637925043	ATP2A3;AT	.
0.531425343	0	0	1.4913516	1.637925043	IRAK1;ADA	.

0.531425343	0	0	1.4913516	1.637925043	CNOT3;ZNI	.
0.53653484	0	0	1.698564593	1.846839198	FAAH;PLA2	.
0.53653484	0	0	1.698564593	1.846839198	ADAM8;FU	.
0.539449138	0	0	1.475577433	1.595347235	ADAM8;FC	.
0.542224108	0	0	1.668147642	1.776235817	ARRB2;PLE	.
0.542224108	0	0	1.668147642	1.776235817	RBM15B;A	.
0.542224108	0	0	1.668147642	1.776235817	RCC2;BRD4	.
0.542224108	0	0	1.460131894	1.554093051	UVSSA;EP3	.
0.542224108	0	0	2.457103379	2.607634867	GGA3	.
0.542224108	0	0	2.457103379	2.607634867	AKAP13	.
0.542224108	0	0	2.457103379	2.607634867	ADAM8	.
0.542224108	0	0	2.457103379	2.607634867	NOTCH1	.
0.542224108	0	0	2.457103379	2.607634867	NOTCH1	.
0.542224108	0	0	2.457103379	2.607634867	CMKLR1	.
0.542224108	0	0	2.457103379	2.607634867	FHOD1	.
0.542224108	0	0	2.457103379	2.607634867	SKI	.
0.542224108	0	0	2.457103379	2.607634867	NFATC2	.
0.542224108	0	0	2.457103379	2.607634867	IRAK1	.
0.542224108	0	0	2.457103379	2.607634867	IRAK1	.
0.542224108	0	0	2.457103379	2.607634867	ABCC1	.
0.542224108	0	0	2.457103379	2.607634867	MAFB	.
0.542224108	0	0	2.457103379	2.607634867	CUX1	.
0.542224108	0	0	2.457103379	2.607634867	NR2C2	.
0.542224108	0	0	2.457103379	2.607634867	NUMA1	.
0.542224108	0	0	2.457103379	2.607634867	AGO3	.
0.545967704	0	0	1.354654404	1.427379424	GAK;TOLLI	.
0.548793705	0	0	1.445004821	1.514112059	PEAK1;RCC	.
0.550749323	0	0	1.638797952	1.709059841	SMCR8;FO	.
0.550749323	0	0	1.638797952	1.709059841	ABCC1;PITI	.
0.551674356	0	0	1.344839513	1.398755914	SRF;BLOC1	.
0.551674356	0	0	1.225988701	1.27478804	NOTCH2;N	.
0.552576288	0	0	1.430186463	1.475356168	CCS;ATP13	.
0.552576288	0	0	1.430186463	1.475356168	UPK1A;TOI	.
0.552576288	0	0	1.335164835	1.370786076	ADARB1;P	.
0.552576288	0	0	2.334128878	2.386186097	CDK5R1	.
0.552576288	0	0	2.334128878	2.386186097	SKI	.
0.552576288	0	0	2.334128878	2.386186097	NOTCH1	.
0.552576288	0	0	2.334128878	2.386186097	PEAK1	.
0.552576288	0	0	2.334128878	2.386186097	NEURL1	.
0.552576288	0	0	2.334128878	2.386186097	RFFL	.
0.552576288	0	0	2.334128878	2.386186097	ABCC1	.
0.552576288	0	0	2.334128878	2.386186097	CACTIN	.
0.552576288	0	0	2.334128878	2.386186097	FURIN	.
0.552576288	0	0	2.334128878	2.386186097	NOTCH1	.
0.552576288	0	0	2.334128878	2.386186097	HUWE1	.
0.552576288	0	0	2.334128878	2.386186097	ARC	.
0.552576288	0	0	2.334128878	2.386186097	BLOC1S3	.

0.552576288	0	0	2.334128878	2.386186097	SKI	.
0.552576288	0	0	2.334128878	2.386186097	NAXD	.
0.552576288	0	0	2.334128878	2.386186097	CSK	.
0.552576288	0	0	2.334128878	2.386186097	CNOT3	.
0.552576288	0	0	2.334128878	2.386186097	MCM3AP	.
0.552576288	0	0	2.334128878	2.386186097	SREBF2	.
0.552576288	0	0	2.334128878	2.386186097	EP300	.
0.555120716	0	0	1.141427459	1.160859472	CX3CR1;M	.
0.555521125	0	0	1.415667466	1.437779495	CX3CR1;PL	.
0.56311138	0	0	1.583083286	1.58416387	UVSSA;MA	.
0.56311138	0	0	1.583083286	1.58416387	PNKP;MAP	.
0.563362631	0	0	2.222866235	2.190801101	FLNA	.
0.563362631	0	0	2.222866235	2.190801101	CMKLR1	.
0.563362631	0	0	2.222866235	2.190801101	DGAT1	.
0.563362631	0	0	2.222866235	2.190801101	GLS2	.
0.563362631	0	0	2.222866235	2.190801101	SKI	.
0.563362631	0	0	2.222866235	2.190801101	KRI1	.
0.563362631	0	0	2.222866235	2.190801101	ABCC1	.
0.563362631	0	0	2.222866235	2.190801101	SPHK1	.
0.563362631	0	0	2.222866235	2.190801101	NDOR1	.
0.563362631	0	0	2.222866235	2.190801101	CX3CR1	.
0.563362631	0	0	2.222866235	2.190801101	PTPN23	.
0.563362631	0	0	2.222866235	2.190801101	PCIF1	.
0.563362631	0	0	2.222866235	2.190801101	NOTCH1	.
0.563362631	0	0	2.222866235	2.190801101	CEACAM1	.
0.563362631	0	0	2.222866235	2.190801101	MAFB	.
0.563362631	0	0	2.222866235	2.190801101	BOD1L1	.
0.563362631	0	0	2.222866235	2.190801101	PLA2G4B	.
0.563362631	0	0	2.222866235	2.190801101	STAC2	.
0.563362631	0	0	2.222866235	2.190801101	NEURL1	.
0.563362631	0	0	2.222866235	2.190801101	ADAM8	.
0.563362631	0	0	2.222866235	2.190801101	LARP1	.
0.563362631	0	0	1.25625081	1.23782296	ASXL1;SKI;	.
0.563450172	0	0	1.387491987	1.365990615	ATP2A3;AT	.
0.565401562	0	0	1.55661882	1.526069094	ZBTB7A;IFI	.
0.567802604	0	0	1.297809829	1.265097755	CX3CR1;P2	.
0.567802604	0	0	1.297809829	1.265097755	SEC16A;HL	.
0.570143585	0	0	1.373818592	1.331696649	TBC1D2;SII	.
0.570143585	0	0	1.373818592	1.331696649	UVSSA;PNI	.
0.571202016	0	0	1.531022041	1.470649448	GGA3;FURI	.
0.571202016	0	0	1.531022041	1.470649448	SKI;ACVR2I	.
0.571202016	0	0	1.208645677	1.157911295	NOTCH2;CI	.
0.571202016	0	0	1.360410701	1.298418178	NUMA1;KL	.
0.571202016	0	0	1.360410701	1.298418178	HDAC5;CEA	.
0.571202016	0	0	1.360410701	1.298418178	HDAC5;DO	.
0.571202016	0	0	1.360410701	1.298418178	CEACAM1;	.
0.571202016	0	0	1.360410701	1.298418178	RGS19;TNI	.

0.571202016	0	0	1.360410701	1.298418178	MAP2K2;IF	.
0.571202016	0	0	2.121718377	2.0174967	DGAT1	.
0.571202016	0	0	2.121718377	2.0174967	ACVR2B	.
0.571202016	0	0	2.121718377	2.0174967	RUNX1	.
0.571202016	0	0	2.121718377	2.0174967	HOOK3	.
0.571202016	0	0	2.121718377	2.0174967	CMKLR1	.
0.571202016	0	0	2.121718377	2.0174967	DGAT1	.
0.571202016	0	0	2.121718377	2.0174967	MAP2K2	.
0.571202016	0	0	2.121718377	2.0174967	FAM89B	.
0.571202016	0	0	2.121718377	2.0174967	AKAP13	.
0.571202016	0	0	2.121718377	2.0174967	MYH9	.
0.571202016	0	0	2.121718377	2.0174967	MGRN1	.
0.571202016	0	0	2.121718377	2.0174967	RCC2	.
0.571202016	0	0	2.121718377	2.0174967	MGRN1	.
0.571202016	0	0	2.121718377	2.0174967	RXRA	.
0.571202016	0	0	2.121718377	2.0174967	SPHK1	.
0.571202016	0	0	2.121718377	2.0174967	ARRB2	.
0.582596308	0	0	2.029365985	1.863034864	SLIT3	.
0.582596308	0	0	2.029365985	1.863034864	NOTCH1	.
0.582596308	0	0	2.029365985	1.863034864	ZNF703	.
0.582596308	0	0	2.029365985	1.863034864	NOTCH2	.
0.582596308	0	0	2.029365985	1.863034864	CX3CR1	.
0.582596308	0	0	2.029365985	1.863034864	KAT6A	.
0.582596308	0	0	2.029365985	1.863034864	NUMA1	.
0.582596308	0	0	2.029365985	1.863034864	MYH11	.
0.582596308	0	0	2.029365985	1.863034864	CADM4	.
0.582596308	0	0	2.029365985	1.863034864	CMKLR1	.
0.582596308	0	0	2.029365985	1.863034864	NDOR1	.
0.582596308	0	0	2.029365985	1.863034864	ABCC1	.
0.582596308	0	0	2.029365985	1.863034864	ABCC1	.
0.582596308	0	0	2.029365985	1.863034864	DGAT1	.
0.582596308	0	0	2.029365985	1.863034864	SPI1	.
0.582596308	0	0	2.029365985	1.863034864	WAS	.
0.582596308	0	0	2.029365985	1.863034864	IRAK1	.
0.582596308	0	0	2.029365985	1.863034864	TTLL3	.
0.582596308	0	0	2.029365985	1.863034864	PPM1F	.
0.582596308	0	0	2.029365985	1.863034864	SEC16A	.
0.58553065	0	0	1.136910633	1.037276199	SKI;STK11;I	.
0.586430994	0	0	1.210250328	1.101543037	IRAK1;AXIN	.
0.587782254	0	0	1.4590311	1.318946247	ADAM8;FU	.
0.587782254	0	0	1.4590311	1.318946247	KMT2A;SH	.
0.587782254	0	0	1.4590311	1.318946247	DVL3;PPM	.
0.587782254	0	0	1.4590311	1.318946247	PIK3C2A;CI	.
0.587782254	0	0	1.4590311	1.318946247	ADAM8;FU	.
0.587782254	0	0	1.4590311	1.318946247	SPHK1;HCF	.
0.590993003	0	0	1.309285282	1.174752703	CEACAM1;	.
0.590993003	0	0	1.309285282	1.174752703	SPHK1;MA	.

0.591927367	0	0	1.237200713	1.10158038	MAP3K3;IF	.
0.591927367	0	0	1.944709626	1.724759275	ARC	.
0.591927367	0	0	1.944709626	1.724759275	MGRN1	.
0.591927367	0	0	1.944709626	1.724759275	NOTCH2	.
0.591927367	0	0	1.944709626	1.724759275	ARRB2	.
0.591927367	0	0	1.944709626	1.724759275	ATP13A2	.
0.591927367	0	0	1.944709626	1.724759275	NUMA1	.
0.591927367	0	0	1.944709626	1.724759275	CEACAM1	.
0.591927367	0	0	1.944709626	1.724759275	RCC2	.
0.591927367	0	0	1.944709626	1.724759275	CHERP	.
0.591927367	0	0	1.944709626	1.724759275	PITPNM1	.
0.591927367	0	0	1.944709626	1.724759275	SMAD6	.
0.591927367	0	0	1.436510858	1.272783496	LARP1;ADA	.
0.591927367	0	0	1.436510858	1.272783496	NELFA;SUP	.
0.591927367	0	0	1.436510858	1.272783496	AXIN1;HUV	.
0.592641837	0	0	1.297095657	1.146034873	ATP2A3;AT	.
0.592641837	0	0	1.297095657	1.146034873	MAP2K2;G	.
0.600302598	0	0	1.285129694	1.118135843	KMT2A;WA	.
0.600809647	0	0	1.179384203	1.014226409	NOTCH2;EI	.
0.600809647	0	0	1.866825776	1.600472638	NOTCH1	.
0.600809647	0	0	1.866825776	1.600472638	PPM1F	.
0.600809647	0	0	1.866825776	1.600472638	KDM5C	.
0.600809647	0	0	1.866825776	1.600472638	NSD3	.
0.600809647	0	0	1.866825776	1.600472638	SYMPK	.
0.600809647	0	0	1.866825776	1.600472638	MYH9	.
0.600809647	0	0	1.866825776	1.600472638	SYMPK	.
0.600809647	0	0	1.866825776	1.600472638	CX3CR1	.
0.600809647	0	0	1.866825776	1.600472638	ZNF385A	.
0.600809647	0	0	1.866825776	1.600472638	SMCR8	.
0.600809647	0	0	1.866825776	1.600472638	RIN3	.
0.600809647	0	0	1.866825776	1.600472638	PLA2G4B	.
0.600809647	0	0	1.866825776	1.600472638	NEURL1	.
0.600809647	0	0	1.866825776	1.600472638	CAPN10	.
0.600809647	0	0	1.866825776	1.600472638	KMT2A	.
0.600809647	0	0	1.866825776	1.600472638	RUNX1	.
0.600809647	0	0	1.273381295	1.091027516	CNOT3;ZNI	.
0.600809647	0	0	1.212912088	1.038885871	AKAP13;AN	.
0.600809647	0	0	1.212912088	1.038885871	SPHK1;LPC	.
0.602022911	0	0	1.39348711	1.186355025	ANGPT4;AI	.
0.602022911	0	0	1.39348711	1.186355025	NELFA;SUP	.
0.602022911	0	0	1.39348711	1.186355025	U2AF2;SYN	.
0.602022911	0	0	1.39348711	1.186355025	NUMA1;CD	.
0.602022911	0	0	1.39348711	1.186355025	ADAM8;AT	.
0.605161976	0	0	1.205024814	1.018882254	CX3CR1;IR/	.
0.606744652	0	0	1.250513875	1.039076349	CX3CR1;IR/	.
0.606744652	0	0	1.123478362	0.933178014	EXD2;GADI	.
0.606744652	0	0	1.794932991	1.488343478	PPIL2	.

0.606744652	0	0	1.794932991	1.488343478	SKI	.
0.606744652	0	0	1.794932991	1.488343478	ERN1	.
0.606744652	0	0	1.794932991	1.488343478	IRAK1	.
0.606744652	0	0	1.794932991	1.488343478	ARC	.
0.606744652	0	0	1.794932991	1.488343478	PER1	.
0.606744652	0	0	1.794932991	1.488343478	CACTIN	.
0.606744652	0	0	1.794932991	1.488343478	CHERP	.
0.606744652	0	0	1.794932991	1.488343478	SLIT3	.
0.606744652	0	0	1.794932991	1.488343478	MAP2K7	.
0.606744652	0	0	1.794932991	1.488343478	BLOC1S3	.
0.606744652	0	0	1.794932991	1.488343478	FAAH	.
0.606744652	0	0	1.794932991	1.488343478	WAS	.
0.606744652	0	0	1.794932991	1.488343478	PAK4	.
0.606744652	0	0	1.794932991	1.488343478	STK11	.
0.606744652	0	0	1.794932991	1.488343478	MAP2K2	.
0.606744652	0	0	1.794932991	1.488343478	SPHK1	.
0.606744652	0	0	1.794932991	1.488343478	TCF3	.
0.606744652	0	0	1.794932991	1.488343478	SLC15A4	.
0.606744652	0	0	1.794932991	1.488343478	PIP5K1C	.
0.60887561	0	0	1.10875515	0.914276199	NUMA1;ZN	.
0.60887561	0	0	1.063512943	0.876810388	KMT2D;SL(	.
0.610147485	0	0	1.155791483	0.94976238	CX3CR1;HI	.
0.61037411	0	0	1.084078694	0.888573326	NOTCH2;C	.
0.61037411	0	0	1.352957493	1.10710245	FURIN;ATP	.
0.61037411	0	0	1.352957493	1.10710245	CX3CR1;AD	.
0.61037411	0	0	1.352957493	1.10710245	PI4KA;PIK3	.
0.61037411	0	0	1.352957493	1.10710245	NUMA1;M	.
0.611156748	0	0	1.728365597	1.386834501	FLNA	.
0.611156748	0	0	1.728365597	1.386834501	CHERP	.
0.611156748	0	0	1.728365597	1.386834501	CMKLR1	.
0.611156748	0	0	1.728365597	1.386834501	GBGT1	.
0.611156748	0	0	1.728365597	1.386834501	NEURL1	.
0.611156748	0	0	1.728365597	1.386834501	ATP13A2	.
0.611156748	0	0	1.728365597	1.386834501	C2CD2L	.
0.611156748	0	0	1.728365597	1.386834501	ATP2A3	.
0.611156748	0	0	1.728365597	1.386834501	GAS2L1	.
0.611156748	0	0	1.728365597	1.386834501	ZNF609	.
0.611156748	0	0	1.728365597	1.386834501	PPP6R2	.
0.611156748	0	0	1.728365597	1.386834501	SLIT3	.
0.611156748	0	0	1.728365597	1.386834501	ERN1	.
0.611156748	0	0	1.728365597	1.386834501	TCAP	.
0.611156748	0	0	1.728365597	1.386834501	FERMT3	.
0.611156748	0	0	1.728365597	1.386834501	SLC26A6	.
0.611156748	0	0	1.728365597	1.386834501	BOD1L1	.
0.611156748	0	0	1.728365597	1.386834501	SLC43A2	.
0.611156748	0	0	1.728365597	1.386834501	IRAK1	.
0.611156748	0	0	1.728365597	1.386834501	PER1	.

0.611156748	0	0	1.728365597	1.386834501	GNA15	.
0.611156748	0	0	1.728365597	1.386834501	SPHK1	.
0.611156748	0	0	1.728365597	1.386834501	FLNA	.
0.611156748	0	0	1.333561176	1.069934393	STK11;GAD	.
0.616094979	0	0	1.217704098	0.966441424	HDAC5;SYN	.
0.616337739	0	0	1.167067308	0.92508494	EXD2;AP5Z	.
0.617544954	0	0	1.314711234	1.034292857	IRAK1;SMA	.
0.617544954	0	0	1.314711234	1.034292857	UVSSA;EP3	.
0.617544954	0	0	1.314711234	1.034292857	NOTCH1;SI	.
0.617544954	0	0	1.314711234	1.034292857	GLS2;SYN1	.
0.617544954	0	0	1.314711234	1.034292857	ARC;KCTD1	.
0.617544954	0	0	1.15975872	0.907499162	STK11;AXIN	.
0.617544954	0	0	1.666553017	1.294646966	WAS	.
0.617544954	0	0	1.666553017	1.294646966	AHNAK	.
0.617544954	0	0	1.666553017	1.294646966	CEACAM1	.
0.617544954	0	0	1.666553017	1.294646966	NOTCH1	.
0.617544954	0	0	1.666553017	1.294646966	SLC26A6	.
0.617544954	0	0	1.666553017	1.294646966	ARC	.
0.617544954	0	0	1.666553017	1.294646966	NUMA1	.
0.617544954	0	0	1.666553017	1.294646966	CEACAM1	.
0.617544954	0	0	1.666553017	1.294646966	AXIN1	.
0.617544954	0	0	1.666553017	1.294646966	ATP13A2	.
0.617544954	0	0	1.666553017	1.294646966	ATP13A2	.
0.617544954	0	0	1.666553017	1.294646966	IRAK1	.
0.617544954	0	0	1.666553017	1.294646966	USF3	.
0.617544954	0	0	1.666553017	1.294646966	SYMPK	.
0.617544954	0	0	1.666553017	1.294646966	ADAM8	.
0.617544954	0	0	1.666553017	1.294646966	AGO3	.
0.617544954	0	0	1.666553017	1.294646966	ANAPC2	.
0.619768573	0	0	1.152540361	0.890282479	CEACAM1;	.
0.619768573	0	0	1.296384902	1.000100223	SPHK1;CSN	.
0.619768573	0	0	1.296384902	1.000100223	IRAK1;MAP	.
0.620418552	0	0	1.196765664	0.921279504	CX3CR1;IRA	.
0.623104452	0	0	1.278560661	0.967283686	NOTCH1;EI	.
0.623104452	0	0	1.278560661	0.967283686	ADAM8;SL	.
0.623104452	0	0	1.278560661	0.967283686	NFATC2;ZN	.
0.623104452	0	0	1.609003374	1.210677077	MGAT5	.
0.623104452	0	0	1.609003374	1.210677077	NOTCH1	.
0.623104452	0	0	1.609003374	1.210677077	KCNAB2	.
0.623104452	0	0	1.609003374	1.210677077	ARC	.
0.623104452	0	0	1.609003374	1.210677077	SPHK1	.
0.623104452	0	0	1.609003374	1.210677077	ARRB2	.
0.623104452	0	0	1.609003374	1.210677077	NUMA1	.
0.623104452	0	0	1.609003374	1.210677077	SPI1	.
0.623104452	0	0	1.609003374	1.210677077	CACTIN	.
0.623104452	0	0	1.609003374	1.210677077	SLIT3	.
0.623104452	0	0	1.609003374	1.210677077	ITGAD	.

0.623104452	0	0	1.609003374	1.210677077	PIP5K1C	.
0.623104452	0	0	1.609003374	1.210677077	ATP13A2	.
0.623104452	0	0	1.609003374	1.210677077	SPI1	.
0.623104452	0	0	1.609003374	1.210677077	MYH9	.
0.623104452	0	0	1.609003374	1.210677077	NFATC2	.
0.623104452	0	0	1.609003374	1.210677077	WAS	.
0.623104452	0	0	1.609003374	1.210677077	FLNA	.
0.623104452	0	0	1.609003374	1.210677077	SKI	.
0.626313051	0	0	1.176531044	0.878532027	KCNK6;KCN	.
0.628926408	0	0	1.261218156	0.935774901	ARC;U2AF2	.
0.629436515	0	0	1.166666667	0.85801558	NOTCH2;ZI	.
0.629436515	0	0	1.555290374	1.133981488	ZDHHC5	.
0.629436515	0	0	1.555290374	1.133981488	PRR5	.
0.629436515	0	0	1.555290374	1.133981488	SLC26A6	.
0.629436515	0	0	1.555290374	1.133981488	MAP3K3	.
0.629436515	0	0	1.555290374	1.133981488	SPHK1	.
0.629436515	0	0	1.555290374	1.133981488	SLC26A6	.
0.629436515	0	0	1.555290374	1.133981488	KCNAB2	.
0.629436515	0	0	1.555290374	1.133981488	ZNF703	.
0.629436515	0	0	1.555290374	1.133981488	SKI	.
0.629436515	0	0	1.555290374	1.133981488	CACTIN	.
0.629436515	0	0	1.555290374	1.133981488	ARHGAP21	.
0.629436515	0	0	1.555290374	1.133981488	MGAT5	.
0.629436515	0	0	1.555290374	1.133981488	PISD	.
0.629436515	0	0	1.555290374	1.133981488	ABCC1	.
0.629436515	0	0	1.555290374	1.133981488	IRAK1	.
0.629436515	0	0	1.555290374	1.133981488	PPM1F	.
0.629436515	0	0	1.555290374	1.133981488	AXIN1	.
0.629436515	0	0	1.555290374	1.133981488	AKAP13	.
0.629436515	0	0	1.555290374	1.133981488	AXIN1	.
0.629436515	0	0	1.244338118	0.905509655	STK11;EP3	.
0.629436515	0	0	1.244338118	0.905509655	TBC1D2;TB	.
0.629436515	0	0	1.244338118	0.905509655	IRAK1;EP3	.
0.63118531	0	0	1.156965337	0.838046469	FLNA;NLRP	.
0.633178621	0	0	1.076923077	0.773806659	CADM4;P2	.
0.633178621	0	0	1.227902292	0.876427571	CX3CR1;SL	.
0.633178621	0	0	1.227902292	0.876427571	GADD45A;	.
0.633178621	0	0	1.0640424	0.759203602	FBXW5;PPI	.
0.633178621	0	0	1.147423045	0.818607412	CCS;ATP13	.
0.633178621	0	0	1.147423045	0.818607412	CADM4;EP	.
0.633178621	0	0	1.147423045	0.818607412	FLNA;TLN1	.
0.633178621	0	0	1.505042728	1.063749789	SUPT5H	.
0.633178621	0	0	1.505042728	1.063749789	SUPT5H	.
0.633178621	0	0	1.505042728	1.063749789	GNA15	.
0.633178621	0	0	1.505042728	1.063749789	CX3CR1	.
0.633178621	0	0	1.505042728	1.063749789	FBXW5	.
0.633178621	0	0	1.505042728	1.063749789	CUX1	.

0.633178621	0	0	1.505042728	1.063749789	ERN1	.
0.633178621	0	0	1.505042728	1.063749789	ATP13A2	.
0.633178621	0	0	1.505042728	1.063749789	DOT1L	.
0.633178621	0	0	1.505042728	1.063749789	MARK2	.
0.633178621	0	0	1.505042728	1.063749789	BRD4	.
0.633178621	0	0	1.505042728	1.063749789	NEURL1	.
0.633178621	0	0	1.505042728	1.063749789	CCS	.
0.633178621	0	0	1.505042728	1.063749789	RCC2	.
0.633178621	0	0	1.505042728	1.063749789	NOTCH1	.
0.633178621	0	0	1.505042728	1.063749789	PPIL2	.
0.633178621	0	0	1.505042728	1.063749789	CAPN10	.
0.633178621	0	0	1.505042728	1.063749789	RREB1	.
0.635419352	0	0	1.138035913	0.799681781	STK11;SLIT	.
0.635597684	0	0	1.21189337	0.84847184	EXD2;AP5Z	.
0.635597684	0	0	1.21189337	0.84847184	MARK2;CD	.
0.635597684	0	0	1.21189337	0.84847184	TCF3;CDK5	.
0.635597684	0	0	1.21189337	0.84847184	U2AF2;SYN	.
0.63744535	0	0	1.097850679	0.764815288	SRF;ASCL2;	.
0.637741526	0	0	1.091374269	0.75054715	WDR81;VP	.
0.637741526	0	0	1.196294933	0.821588965	STAC2;ZDH	.
0.637741526	0	0	1.196294933	0.821588965	PLA2G4B;C	.
0.637741526	0	0	1.196294933	0.821588965	SREBF1;LP(	.
0.637741526	0	0	1.196294933	0.821588965	SACS;EP30	.
0.637741526	0	0	1.457935561	0.999282403	ESPNL	.
0.637741526	0	0	1.457935561	0.999282403	ESPNL	.
0.637741526	0	0	1.457935561	0.999282403	SPHK1	.
0.637741526	0	0	1.457935561	0.999282403	SYN1	.
0.637741526	0	0	1.457935561	0.999282403	KCNAB2	.
0.637741526	0	0	1.457935561	0.999282403	LARP1	.
0.637741526	0	0	1.457935561	0.999282403	STK11	.
0.637741526	0	0	1.457935561	0.999282403	NOTCH1	.
0.637741526	0	0	1.457935561	0.999282403	SLIT3	.
0.637741526	0	0	1.457935561	0.999282403	LPCAT1	.
0.637741526	0	0	1.457935561	0.999282403	RXRA	.
0.637741526	0	0	1.457935561	0.999282403	SMCR8	.
0.637741526	0	0	1.457935561	0.999282403	NOTCH1	.
0.637741526	0	0	1.457935561	0.999282403	GDPD3	.
0.643688387	0	0	1.413683373	0.939972683	GGA3	.
0.643688387	0	0	1.413683373	0.939972683	NFATC2	.
0.643688387	0	0	1.413683373	0.939972683	FERMT3	.
0.643688387	0	0	1.413683373	0.939972683	TCAP	.
0.643688387	0	0	1.413683373	0.939972683	NEURL1	.
0.643688387	0	0	1.413683373	0.939972683	WAS	.
0.643688387	0	0	1.413683373	0.939972683	NOTCH1	.
0.643688387	0	0	1.413683373	0.939972683	KMT2D	.
0.643688387	0	0	1.413683373	0.939972683	PIP5K1C	.
0.643688387	0	0	1.413683373	0.939972683	SYMPK	.

0.643688387	0	0	1.413683373	0.939972683	TRMT44	.
0.643688387	0	0	1.413683373	0.939972683	NOTCH1	.
0.643688387	0	0	1.413683373	0.939972683	RFFL	.
0.643688387	0	0	1.413683373	0.939972683	ATG2A	.
0.643688387	0	0	1.413683373	0.939972683	PIK3C2A	.
0.643688387	0	0	1.413683373	0.939972683	PLA2G4B	.
0.643688387	0	0	1.413683373	0.939972683	SKI	.
0.643688387	0	0	1.413683373	0.939972683	SYMPK	.
0.643688387	0	0	1.413683373	0.939972683	TRAM2	.
0.643688387	0	0	1.413683373	0.939972683	IFFO1	.
0.644805155	0	0	1.101965672	0.728802196	AKNA;NLRI	.
0.644805155	0	0	1.101965672	0.728802196	MGAT5;TE	.
0.644805155	0	0	1.166267943	0.770843016	GADD45A;	.
0.644805155	0	0	1.166267943	0.770843016	CSK;TLN1	.
0.646026014	0	0	1.066208791	0.696310663	SF3A1;SF3	.
0.646026014	0	0	1.09330036	0.712215152	ANGPT4;EI	.
0.646026014	0	0	1.151810503	0.746887548	CX3CR1;NL	.
0.646026014	0	0	1.151810503	0.746887548	FAAH;PLA2	.
0.646026014	0	0	1.151810503	0.746887548	NEURL1;M	.
0.646026014	0	0	1.372034255	0.885292336	FAAH	.
0.646026014	0	0	1.372034255	0.885292336	SMCR8	.
0.646026014	0	0	1.372034255	0.885292336	PNKP	.
0.646026014	0	0	1.372034255	0.885292336	SLC26A6	.
0.646026014	0	0	1.372034255	0.885292336	ABCC1	.
0.646026014	0	0	1.372034255	0.885292336	CEACAM1	.
0.646026014	0	0	1.372034255	0.885292336	NUMA1	.
0.646026014	0	0	1.372034255	0.885292336	WDR81	.
0.646026014	0	0	1.372034255	0.885292336	ARRB2	.
0.646026014	0	0	1.372034255	0.885292336	PLEKHG2	.
0.646026014	0	0	1.372034255	0.885292336	CEACAM1	.
0.646026014	0	0	1.372034255	0.885292336	FLNA	.
0.646026014	0	0	1.372034255	0.885292336	HIPK1	.
0.646026014	0	0	1.372034255	0.885292336	DHX37	.
0.646026014	0	0	1.372034255	0.885292336	MRTFA	.
0.646026014	0	0	1.372034255	0.885292336	PTPN23	.
0.646026014	0	0	1.372034255	0.885292336	SMCR8	.
0.646026014	0	0	1.372034255	0.885292336	DUSP18	.
0.646026014	0	0	1.372034255	0.885292336	SREBF1	.
0.646026014	0	0	1.372034255	0.885292336	ZNF335	.
0.649738048	0	0	1.010087067	0.645407749	SKI;STK11;	.
0.650843393	0	0	1.137705683	0.723819777	ABCC1;ATF	.
0.650843393	0	0	1.076369673	0.680305759	ABL2;ADAI	.
0.650843393	0	0	1.076369673	0.680305759	FLNA;NLRP	.
0.650843393	0	0	1.332765087	0.834779463	BLOC1S3	.
0.650843393	0	0	1.332765087	0.834779463	NR2C2	.
0.650843393	0	0	1.332765087	0.834779463	ARC	.
0.650843393	0	0	1.332765087	0.834779463	MAFB	.

0.650843393	0	0	1.332765087	0.834779463	SKI	.
0.650843393	0	0	1.332765087	0.834779463	FLNA	.
0.650843393	0	0	1.332765087	0.834779463	GGA3	.
0.650843393	0	0	1.332765087	0.834779463	PER1	.
0.650843393	0	0	1.332765087	0.834779463	CRTC3	.
0.650843393	0	0	1.332765087	0.834779463	GAK	.
0.650843393	0	0	1.332765087	0.834779463	HUWE1	.
0.650843393	0	0	1.332765087	0.834779463	SPI1	.
0.650843393	0	0	1.332765087	0.834779463	KMT2A	.
0.650843393	0	0	1.332765087	0.834779463	ASXL1	.
0.650843393	0	0	1.332765087	0.834779463	CACTIN	.
0.650843393	0	0	1.332765087	0.834779463	ACVR2B	.
0.650843393	0	0	1.332765087	0.834779463	RUNX1	.
0.651870698	0	0	1.123940739	0.70159968	DVL3;ARRE	.
0.657136165	0	0	1.110503532	0.680189421	STK11;FOX	.
0.657136165	0	0	1.110503532	0.680189421	IRAK1;CAC	.
0.657136165	0	0	1.110503532	0.680189421	ABCC1;ATF	.
0.657136165	0	0	1.295677539	0.788028695	UCP3	.
0.657136165	0	0	1.295677539	0.788028695	BLOC1S3	.
0.657136165	0	0	1.295677539	0.788028695	CAPN10	.
0.657136165	0	0	1.295677539	0.788028695	SLC26A6	.
0.657136165	0	0	1.295677539	0.788028695	CDK5R1	.
0.657136165	0	0	1.295677539	0.788028695	GLS2	.
0.657136165	0	0	1.295677539	0.788028695	PAK4	.
0.657136165	0	0	1.295677539	0.788028695	MYH9	.
0.657136165	0	0	1.295677539	0.788028695	LPCAT1	.
0.657136165	0	0	1.295677539	0.788028695	ARC	.
0.657136165	0	0	1.295677539	0.788028695	TRAM2	.
0.657136165	0	0	0.99668628	0.606070284	MAP3K3;SI	.
0.65908366	0	0	1.051928382	0.635418195	ATP2A3;AT	.
0.65908366	0	0	1.051928382	0.635418195	ARRDC5;AI	.
0.660726575	0	0	1.097382494	0.659553202	ANGPT4;EI	.
0.662471053	0	0	0.999869856	0.597772505	NOTCH2;A	.
0.664701056	0	0	1.260594724	0.744683016	CX3CR1	.
0.664701056	0	0	1.260594724	0.744683016	SLC26A6	.
0.664701056	0	0	1.260594724	0.744683016	GEMIN7	.
0.664701056	0	0	1.260594724	0.744683016	ELF4	.
0.664701056	0	0	1.260594724	0.744683016	MEX3D	.
0.664701056	0	0	1.260594724	0.744683016	CACTIN	.
0.664701056	0	0	1.260594724	0.744683016	FLNA	.
0.664982605	0	0	1.084566596	0.639657138	DVL3;ARRE	.
0.668537361	0	0	0.991737244	0.576948197	TNRC6C;A(	.
0.668537361	0	0	0.987391484	0.571823582	POU2F1;IR	.
0.668537361	0	0	1.072045317	0.620469133	RPS6KA1;P	.
0.668537361	0	0	1.072045317	0.620469133	ANGPT4;CI	.
0.668537361	0	0	1.072045317	0.620469133	CD151;PLE	.
0.668537361	0	0	1.072045317	0.620469133	IRAK1;EP3(	.

0.668537361	0	0	1.072045317	0.620469133	FBXW5;FB	.
0.668537361	0	0	1.072045317	0.620469133	RP2;BLOC1	.
0.668537361	0	0	1.028565383	0.59382901	KCNK6;KCN	.
0.668537361	0	0	0.995358193	0.574346919	CAPN10;AT	.
0.668537361	0	0	1.227358372	0.704426942	ANAPC2	.
0.668537361	0	0	1.227358372	0.704426942	DOT1L	.
0.668537361	0	0	1.227358372	0.704426942	IGHMBP2	.
0.668537361	0	0	1.227358372	0.704426942	MYH9	.
0.668537361	0	0	1.227358372	0.704426942	NLRP1	.
0.668537361	0	0	1.227358372	0.704426942	MYH9	.
0.668537361	0	0	1.227358372	0.704426942	NOTCH1	.
0.668537361	0	0	1.227358372	0.704426942	ANKRD11	.
0.668537361	0	0	1.227358372	0.704426942	LPCAT1	.
0.668537361	0	0	1.008056133	0.578439942	TBC1D2;RC	.
0.675454877	0	0	0.991796975	0.558376183	NOTCH2;EI	.
0.675655411	0	0	0.997171946	0.557555556	STK11;AXIN	.
0.675655411	0	0	1.195826449	0.666980806	CX3CR1	.
0.675655411	0	0	1.195826449	0.666980806	GBGT1	.
0.675655411	0	0	1.195826449	0.666980806	ADAM8	.
0.675655411	0	0	1.195826449	0.666980806	PIP5K1C	.
0.675655411	0	0	1.195826449	0.666980806	ABL2	.
0.675655411	0	0	1.195826449	0.666980806	ACVR2B	.
0.675655411	0	0	1.195826449	0.666980806	RREB1	.
0.675655411	0	0	1.04784689	0.58409721	NOTCH2;A	.
0.675655411	0	0	1.04784689	0.58409721	NUMA1;CD	.
0.682100051	0	0	0.998972251	0.543029089	GAK;PIP5K	.
0.682100051	0	0	1.165871122	0.632095948	NSD3	.
0.682100051	0	0	1.165871122	0.632095948	DGAT1	.
0.682100051	0	0	1.165871122	0.632095948	ABCC1	.
0.682100051	0	0	1.165871122	0.632095948	NEURL1	.
0.682100051	0	0	1.165871122	0.632095948	FHOD1	.
0.682100051	0	0	1.165871122	0.632095948	TCAP	.
0.682100051	0	0	1.165871122	0.632095948	SPI1	.
0.682100051	0	0	1.165871122	0.632095948	ACVR2B	.
0.682100051	0	0	1.165871122	0.632095948	FLNA	.
0.682100051	0	0	1.165871122	0.632095948	SMCR8	.
0.684726522	0	0	0.981275304	0.527730303	HIP1;GLS2;	.
0.684955754	0	0	1.02471213	0.550212415	CRYBG3;RF	.
0.688914036	0	0	1.13737703	0.599550648	CHERP	.
0.688914036	0	0	1.13737703	0.599550648	WAS	.
0.688914036	0	0	1.13737703	0.599550648	RFFL	.
0.688914036	0	0	1.13737703	0.599550648	NOTCH1	.
0.688914036	0	0	1.13737703	0.599550648	AXIN1	.
0.688914036	0	0	1.13737703	0.599550648	FLNA	.
0.688914036	0	0	1.013521947	0.534138535	LARP1;PCIF	.
0.688914036	0	0	1.013521947	0.534138535	PRDM15;S	.
0.694915925	0	0	1.002572413	0.518611999	CRYBG3;RF	.

0.694915925	0	0	1.1102398	0.569146672	ABL2	.
0.694915925	0	0	1.1102398	0.569146672	MBOAT7	.
0.694915925	0	0	1.1102398	0.569146672	SEC16A	.
0.694915925	0	0	1.1102398	0.569146672	TCAP	.
0.694915925	0	0	1.1102398	0.569146672	ELF4	.
0.694915925	0	0	1.1102398	0.569146672	CACTIN	.
0.694915925	0	0	1.1102398	0.569146672	SPI1	.
0.694915925	0	0	1.1102398	0.569146672	TCF3	.
0.694915925	0	0	1.1102398	0.569146672	CAPN10	.
0.694915925	0	0	1.1102398	0.569146672	ADAM8	.
0.697960328	0	0	0.991855849	0.503610518	ANKRD9;A	.
0.699344479	0	0	0.964276854	0.486194953	PNKP;AXIN	.
0.699344479	0	0	0.95070492	0.478055684	CD151;MI/	.
0.699344479	0	0	1.084364767	0.540706331	NOTCH1	.
0.699344479	0	0	1.084364767	0.540706331	ATP13A2	.
0.699344479	0	0	1.084364767	0.540706331	PAK4	.
0.699344479	0	0	1.084364767	0.540706331	ABCC1	.
0.699344479	0	0	1.084364767	0.540706331	ADAM8	.
0.699344479	0	0	1.084364767	0.540706331	FLNA	.
0.699344479	0	0	1.084364767	0.540706331	LARP1	.
0.699344479	0	0	1.084364767	0.540706331	RUNX1	.
0.699344479	0	0	1.084364767	0.540706331	PPM1F	.
0.699344479	0	0	1.084364767	0.540706331	ACVR2B	.
0.699344479	0	0	1.084364767	0.540706331	FLNA	.
0.699344479	0	0	0.981364895	0.489112891	EXD2;AP5Z	.
0.699344479	0	0	0.94777296	0.472031173	HIP1;GGA3	.
0.704803529	0	0	0.971092504	0.475098945	AXIN1;PPM	.
0.704803529	0	0	0.971092504	0.475098945	ADAM8;AT	.
0.705903117	0	0	1.059665871	0.514069959	GNA15	.
0.705903117	0	0	1.059665871	0.514069959	GADD45A	.
0.705903117	0	0	1.059665871	0.514069959	FURIN	.
0.705903117	0	0	1.059665871	0.514069959	CEACAM1	.
0.705903117	0	0	1.059665871	0.514069959	PPM1F	.
0.708979964	0	0	0.961031914	0.46154947	SLC26A6;M	.
0.712268034	0	0	0.933951726	0.442668206	RBM15B;M	.
0.712268034	0	0	1.036064704	0.489093748	GLS2	.
0.712268034	0	0	1.036064704	0.489093748	NFATC2	.
0.712268034	0	0	1.036064704	0.489093748	WAS	.
0.712268034	0	0	1.036064704	0.489093748	SH2B3	.
0.712268034	0	0	1.036064704	0.489093748	CACTIN	.
0.712268034	0	0	1.036064704	0.489093748	FLNA	.
0.712335913	0	0	0.951176643	0.44844617	LARP1;PCIF	.
0.71777726	0	0	0.941520468	0.43577161	NUMA1;RC	.
0.71777726	0	0	0.941520468	0.43577161	STAC2;ZDH	.
0.718388121	0	0	1.013489675	0.46564789	ATP13A2	.
0.718388121	0	0	1.013489675	0.46564789	SETD5	.
0.718388121	0	0	1.013489675	0.46564789	CADM4	.

0.718388121	0	0	1.013489675	0.46564789	DOT1L	.
0.718388121	0	0	1.013489675	0.46564789	PTPN23	.
0.720942714	0	0	0.932057416	0.423509169	TET3;GALN	.
0.720942714	0	0	0.932057416	0.423509169	FLNA;TLN1	.
0.720942714	0	0	0.932057416	0.423509169	SPHK1;RPS	.
0.722446937	0	0	0.991875286	0.44361496	PANK1	.
0.722446937	0	0	0.991875286	0.44361496	LARP1	.
0.722446937	0	0	0.991875286	0.44361496	GADD45A	.
0.722446937	0	0	0.991875286	0.44361496	RUNX1	.
0.722446937	0	0	0.991875286	0.44361496	FURIN	.
0.722446937	0	0	0.991875286	0.44361496	GGA3	.
0.722446937	0	0	0.991875286	0.44361496	SKI	.
0.722446937	0	0	0.991875286	0.44361496	SH2B3	.
0.722446937	0	0	0.991875286	0.44361496	CACTIN	.
0.722446937	0	0	0.991875286	0.44361496	NUMA1	.
0.728456631	0	0	0.913687963	0.400157952	MRPS2;ZN	.
0.728456631	0	0	0.971161496	0.422888519	CX3CR1	.
0.728456631	0	0	0.971161496	0.422888519	CACTIN	.
0.728456631	0	0	0.971161496	0.422888519	ERN1	.
0.728456631	0	0	0.971161496	0.422888519	RXRA	.
0.728456631	0	0	0.971161496	0.422888519	GAK	.
0.728456631	0	0	0.971161496	0.422888519	GADD45A	.
0.72999511	0	0	0.906832298	0.39250854	NOTCH1;T	.
0.731710009	0	0	0.904770753	0.38903961	GADD45A;	.
0.735348405	0	0	0.951293166	0.403371899	WAS	.
0.735348405	0	0	0.951293166	0.403371899	SLC43A2	.
0.740557213	0	0	0.884345688	0.366780678	CX3CR1;HI	.
0.740557213	0	0	0.886904762	0.3675524	TBC1D2;D\	.
0.740557213	0	0	0.886904762	0.3675524	P2RY1;AXII	.
0.740557213	0	0	0.93221957	0.384977143	MARK2	.
0.740557213	0	0	0.93221957	0.384977143	CMKLR1	.
0.740557213	0	0	0.93221957	0.384977143	CADM4	.
0.740557213	0	0	0.93221957	0.384977143	MGRN1	.
0.740557213	0	0	0.93221957	0.384977143	PPM1F	.
0.743560262	0	0	0.910037424	0.371260985	KMT2D;SL(	.
0.743560262	0	0	0.894766251	0.36499697	CX3CR1;AN	.
0.743889725	0	0	0.879028618	0.357749932	PNKP;IGHM	.
0.744814266	0	0	0.913893959	0.367624073	FURIN	.
0.744814266	0	0	0.913893959	0.367624073	UNC13D	.
0.744814266	0	0	0.913893959	0.367624073	PTPN23	.
0.744814266	0	0	0.913893959	0.367624073	GBGT1	.
0.744814266	0	0	0.913893959	0.367624073	SRF	.
0.744814266	0	0	0.913893959	0.367624073	FLNA	.
0.744814266	0	0	0.913893959	0.367624073	ZNF335	.
0.74815357	0	0	0.892319154	0.354510951	NCOR1;NC	.
0.75108893	0	0	0.896273178	0.35123948	RPS6KA1	.
0.75108893	0	0	0.896273178	0.35123948	NFATC2	.

0.75108893	0	0	0.896273178	0.35123948	IL17RA	.
0.755695591	0	0	0.854703481	0.329299403	NFATC2;M	.
0.757925612	0	0	0.879317332	0.335756406	CMKLR1	.
0.759951942	0	0	0.846889952	0.320394197	NFATC2;M	.
0.759951942	0	0	0.864916917	0.327092992	KCNK6;KCI	.
0.763080892	0	0	0.846522782	0.316039367	HIP1;AXIN1	.
0.763080892	0	0	0.862989481	0.321113514	ATP2A3	.
0.763080892	0	0	0.862989481	0.321113514	MAN2A2	.
0.763080892	0	0	0.862989481	0.321113514	DGAT1	.
0.768174368	0	0	0.855244507	0.312120142	EXD2;GADI	.
0.768428748	0	0	0.84725537	0.307254529	SH2B3	.
0.768428748	0	0	0.84725537	0.307254529	CNOT3	.
0.768428748	0	0	0.84725537	0.307254529	ABL2	.
0.768428748	0	0	0.84725537	0.307254529	NLRP1	.
0.769597558	0	0	0.852067611	0.307285408	NOTCH1;T	.
0.771080257	0	0	0.824279121	0.295272036	AXIN1;HUV	.
0.772271993	0	0	0.832083191	0.294127744	ACVR2B	.
0.772271993	0	0	0.832083191	0.294127744	ABCC1	.
0.772271993	0	0	0.832083191	0.294127744	GADD45A	.
0.772271993	0	0	0.832083191	0.294127744	PPM1F	.
0.772271993	0	0	0.832083191	0.294127744	EP300	.
0.772271993	0	0	0.832083191	0.294127744	RFFL	.
0.772271993	0	0	0.817006631	0.287398246	EP300;HCF	.
0.772271993	0	0	0.817006631	0.287398246	SLC15A4;SI	.
0.772271993	0	0	0.817006631	0.287398246	SPHK1;CSN	.
0.772271993	0	0	0.817006631	0.287398246	FOXO3;MA	.
0.775179328	0	0	0.81744337	0.281685585	ATG2A	.
0.775179328	0	0	0.81744337	0.281685585	ATP13A2	.
0.775179328	0	0	0.81744337	0.281685585	SMAD6	.
0.775179328	0	0	0.81744337	0.281685585	SPHK1	.
0.775179328	0	0	0.81744337	0.281685585	MEF2D	.
0.775179328	0	0	0.81744337	0.281685585	RCC2	.
0.775179328	0	0	0.81744337	0.281685585	GAK	.
0.780525207	0	0	0.80330837	0.269884217	WAS	.
0.780525207	0	0	0.80330837	0.269884217	SYN1	.
0.780525207	0	0	0.80330837	0.269884217	EME2	.
0.780525207	0	0	0.823434309	0.276486501	HDAC5;PLA	.
0.784983047	0	0	0.789652522	0.258683201	FLNA	.
0.784983047	0	0	0.789652522	0.258683201	PISD	.
0.784983047	0	0	0.789652522	0.258683201	SH2B3	.
0.784983047	0	0	0.789652522	0.258683201	CEACAM1	.
0.784983047	0	0	0.789652522	0.258683201	DHX37	.
0.784983047	0	0	0.789149299	0.258179539	ATG4B;ATF	.
0.78952004	0	0	0.77645187	0.248045177	ATP13A2	.
0.78952004	0	0	0.77645187	0.248045177	GALNT10	.
0.78952004	0	0	0.77645187	0.248045177	IRAK1	.
0.78952004	0	0	0.77645187	0.248045177	ZDHHC5	.

0.792240529	0	0	0.775917065	0.244829652	UPK1A;TOI	.
0.794241035	0	0	0.763684025	0.237935596	MAP3K14	.
0.794241035	0	0	0.763684025	0.237935596	PPM1F	.
0.794241035	0	0	0.763684025	0.237935596	NLRP1	.
0.796371789	0	0	0.822581335	0.253684503	ANKRD9;SI	.
0.798042835	0	0	0.763118676	0.232245444	CX3CR1;CA	.
0.798042835	0	0	0.751328047	0.228322462	MAP3K11	.
0.798042835	0	0	0.751328047	0.228322462	SEC16A	.
0.798042835	0	0	0.751328047	0.228322462	SEC16A	.
0.798042835	0	0	0.751328047	0.228322462	SEC16A	.
0.798854271	0	0	0.779751618	0.235792024	CEACAM1;	.
0.801269969	0	0	0.756875559	0.226224649	ADAM8;AT	.
0.801694916	0	0	0.739364322	0.219176115	NCOR2	.
0.801694916	0	0	0.739364322	0.219176115	ATP13A2	.
0.801694916	0	0	0.739364322	0.219176115	MYH9	.
0.801694916	0	0	0.739364322	0.219176115	CEACAM1	.
0.804963671	0	0	0.727774463	0.210469029	PEAK1	.
0.804963671	0	0	0.727774463	0.210469029	IRAK1	.
0.804963671	0	0	0.727774463	0.210469029	ATP13A2	.
0.804963671	0	0	0.727774463	0.210469029	AHNAK	.
0.804963671	0	0	0.727774463	0.210469029	TRMT44	.
0.804963671	0	0	0.727774463	0.210469029	IRAK1	.
0.804963671	0	0	0.766779983	0.221608194	WAS;NFAT	.
0.810113908	0	0	0.716541215	0.202175629	MARK4	.
0.814508295	0	0	0.705648369	0.194272129	MGAT5	.
0.814508295	0	0	0.705648369	0.194272129	ABCC1	.
0.814508295	0	0	0.705648369	0.194272129	POU5F1	.
0.818773472	0	0	0.695080683	0.186736386	LARP1	.
0.818773472	0	0	0.695080683	0.186736386	SH2B3	.
0.818773472	0	0	0.695080683	0.186736386	FLNA	.
0.823304859	0	0	0.68482381	0.179547763	FOXK1	.
0.823304859	0	0	0.68482381	0.179547763	ABL2	.
0.824964846	0	0	0.710361956	0.183832943	AGO3;ADA	.
0.824964846	0	0	0.674864239	0.172687014	STK11	.
0.824964846	0	0	0.674864239	0.172687014	EP300	.
0.824964846	0	0	0.674864239	0.172687014	SEC16A	.
0.824964846	0	0	0.674864239	0.172687014	SYMPK	.
0.824964846	0	0	0.674864239	0.172687014	FAAH	.
0.824964846	0	0	0.674864239	0.172687014	POU2F1	.
0.824964846	0	0	0.674864239	0.172687014	RXRA	.
0.824964846	0	0	0.674864239	0.172687014	PIP5K1C	.
0.825981411	0	0	0.704944179	0.179181206	ANGPT4;TI	.
0.827189276	0	0	0.730309993	0.184214924	CACTIN;FO	.
0.827676309	0	0	0.665189226	0.166136167	WAS	.
0.827676309	0	0	0.665189226	0.166136167	MTF1	.
0.827676309	0	0	0.665189226	0.166136167	POU2F1	.
0.827676309	0	0	0.665189226	0.166136167	EXD2	.

0.830266429	0	0	0.69435121	0.170260399	SF3A2;GEN	.
0.830266429	0	0	0.69435121	0.170260399	MYH9;FUR	.
0.830266429	0	0	0.655786749	0.15987843	FLNA	.
0.830266429	0	0	0.655786749	0.15987843	HIPK1	.
0.830266429	0	0	0.655786749	0.15987843	WAS	.
0.830266429	0	0	0.655786749	0.15987843	CEACAM1	.
0.832327887	0	0	0.689172426	0.165983409	MYH9;FUR	.
0.833130697	0	0	0.646645452	0.153898097	PLEKHG2	.
0.833130697	0	0	0.646645452	0.153898097	TBC1D10B	.
0.833130697	0	0	0.646645452	0.153898097	PIP5K1C	.
0.833130697	0	0	0.646645452	0.153898097	PIK3C2A	.
0.837060467	0	0	0.637754602	0.148180467	WAS	.
0.837060467	0	0	0.637754602	0.148180467	FLNA	.
0.839730075	0	0	0.674086402	0.153841501	TNK2;ACVR	.
0.839730075	0	0	0.674086402	0.153841501	ARC;ZNF33	.
0.840093884	0	0	0.629104044	0.142711767	CBL	.
0.840093884	0	0	0.629104044	0.142711767	EXD2	.
0.84381044	0	0	0.620684169	0.137479086	ABCC1	.
0.84381044	0	0	0.620684169	0.137479086	IL17RA	.
0.846631534	0	0	0.612485869	0.132470309	RXRA	.
0.846631534	0	0	0.612485869	0.132470309	GEMIN7	.
0.846631534	0	0	0.612485869	0.132470309	PIP5K1C	.
0.846631534	0	0	0.612485869	0.132470309	CBL	.
0.849746935	0	0	0.604500511	0.127674058	ABL2	.
0.849746935	0	0	0.604500511	0.127674058	LNPEP	.
0.849746935	0	0	0.604500511	0.127674058	ANGPT4	.
0.852763223	0	0	0.596719907	0.123079645	EP300	.
0.852763223	0	0	0.596719907	0.123079645	PER1	.
0.852763223	0	0	0.596719907	0.123079645	AXIN1	.
0.853481231	0	0	0.645800106	0.132357858	LARP1;ME	.
0.855283789	0	0	0.58913628	0.118677017	SLC26A6	.
0.855283789	0	0	0.58913628	0.118677017	SIPA1	.
0.855283789	0	0	0.58913628	0.118677017	RFFL	.
0.85810797	0	0	0.581742243	0.114456715	CACTIN	.
0.85810797	0	0	0.581742243	0.114456715	PCIF1	.
0.85810797	0	0	0.581742243	0.114456715	ADAM8	.
0.859346468	0	0	0.632522866	0.122855196	RCC2;BRD4	.
0.859346468	0	0	0.632522866	0.122855196	TBC1D2;DV	.
0.859346468	0	0	0.716049383	0.138849305	TBC1D2;GC	.
0.860040192	0	0	0.574530776	0.110409834	MGRN1	.
0.860040192	0	0	0.574530776	0.110409834	NUMA1	.
0.863481605	0	0	0.567495198	0.106527981	WAS	.
0.866035319	0	0	0.560629151	0.102803245	ANAPC2	.
0.866035319	0	0	0.560629151	0.102803245	KLHL21	.
0.866035319	0	0	0.560629151	0.102803245	U2AF2	.
0.86769963	0	0	0.654135846	0.118043066	MIA;ITGAD	.
0.86769963	0	0	0.702811245	0.126442961	IRAK1;SPH	.

0.86769963	0	0	0.553926583	0.099228159	BRD4	.
0.86769963	0	0	0.553926583	0.099228159	SCYL1	.
0.86769963	0	0	0.553926583	0.099228159	CACTIN	.
0.868532184	0	0	0.651045519	0.115700214	MIA;ITGAD	.
0.870082314	0	0	0.547381721	0.095795679	ATP13A2	.
0.870082314	0	0	0.547381721	0.095795679	ANGPT4	.
0.872785653	0	0	0.540989066	0.092499148	ATP2A3	.
0.872785653	0	0	0.540989066	0.092499148	EP300	.
0.874603837	0	0	0.599629572	0.100927335	RCC2;FLNA	.
0.874603837	0	0	0.534743368	0.089332275	ESPNL	.
0.874603837	0	0	0.534743368	0.089332275	ATP2A3	.
0.874603837	0	0	0.534743368	0.089332275	SYMPK	.
0.875711067	0	0	0.595755122	0.098496588	WAS;CSK	.
0.876343369	0	0	0.528639618	0.086289112	AHNAK	.
0.876343369	0	0	0.528639618	0.086289112	MRPS2	.
0.876343369	0	0	0.528639618	0.086289112	MRPS2	.
0.878409314	0	0	0.522673031	0.083364032	GLS2	.
0.878409314	0	0	0.522673031	0.083364032	SKI	.
0.878409314	0	0	0.522673031	0.083364032	ARC	.
0.880142126	0	0	0.698492462	0.109709284	EFNB1;TNK	.
0.88040079	0	0	0.516839035	0.080551706	ESPNL	.
0.88040079	0	0	0.516839035	0.080551706	IRAK1	.
0.881711213	0	0	0.580741627	0.089381247	IGHMBP2;I	.
0.882319546	0	0	0.511133258	0.077847088	CBL	.
0.882319546	0	0	0.511133258	0.077847088	ATP13A2	.
0.88457176	0	0	0.50555152	0.075245396	ATP2A3	.
0.88457176	0	0	0.50555152	0.075245396	AXIN1	.
0.886350424	0	0	0.569965069	0.083136425	GNA13;GN	.
0.886350424	0	0	0.50008982	0.072742097	ATP13A2	.
0.886350424	0	0	0.50008982	0.072742097	MCM3AP	.
0.888466671	0	0	0.494744325	0.070332888	ANAPC2	.
0.888466671	0	0	0.494744325	0.070332888	MARK4	.
0.890923794	0	0	0.489511368	0.06801369	MRPS2	.
0.892913608	0	0	0.693681269	0.094517516	KMT2D;SLC	.
0.897205112	0	0	0.549559752	0.071994748	DHX34;CNC	.
0.900996374	0	0	0.622160558	0.078598779	CX3CR1;IRA	.
0.902142876	0	0	0.620047595	0.077244248	MAP3K3;M	.
0.902142876	0	0	0.539890954	0.067027228	KCNK6;KCN	.
0.904400882	0	0	0.460289704	0.05578467	PCIF1	.
0.906448062	0	0	0.455753662	0.053997157	ZFAND2A	.
0.90724099	0	0	0.577300815	0.067625129	RPS6KA1;A	.
0.90724099	0	0	0.63603866	0.074222754	ARRDC5;TE	.
0.90744696	0	0	0.451305698	0.052273506	CAPN10	.
0.90744696	0	0	0.527511962	0.060959325	SPHK1;ANA	.
0.908731265	0	0	0.524504636	0.059534607	CSK;PDCD1	.
0.908731265	0	0	0.446943272	0.050611116	MRPS2	.
0.909381701	0	0	0.5215311	0.058144849	SREBF1;PC	.

0.909381701	0	0	0.442663939	0.049007512	FURIN	.
0.909381701	0	0	0.442663939	0.049007512	EP300	.
0.909381701	0	0	0.442663939	0.049007512	ZBTB7A	.
0.917118599	0	0	0.556258993	0.056619352	P2RY1;AXII	.
0.917261485	0	0	0.426331808	0.043135306	IL17RA	.
0.920926007	0	0	0.418607151	0.040495424	MARK2	.
0.922484343	0	0	0.414848278	0.039242906	DHX34	.
0.925055346	0	0	0.407528367	0.036864172	ATP2A3	.
0.925055346	0	0	0.407528367	0.036864172	EP300	.
0.925055346	0	0	0.407528367	0.036864172	EP300	.
0.929230571	0	0	0.397017726	0.033588383	GNA13	.
0.929230571	0	0	0.397017726	0.033588383	EP300	.
0.929230571	0	0	0.397017726	0.033588383	CACTIN	.
0.930544151	0	0	0.393632944	0.032568618	EP300	.
0.933059113	0	0	0.387032617	0.030629382	SLC26A6	.
0.933059113	0	0	0.387032617	0.030629382	ARC	.
0.933697187	0	0	0.557460612	0.04348497	TBC1D2;G(	.
0.934752754	0	0	0.465990238	0.035613691	AGO3;DHX	.
0.936563061	0	0	0.377534587	0.027953225	FAAH	.
0.937662528	0	0	0.374470706	0.027118759	ZFAND2A	.
0.938728973	0	0	0.371455847	0.02631136	CX3CR1	.
0.941187901	0	0	0.365568564	0.024773903	RCC2	.
0.94173728	0	0	0.362693914	0.024042015	PNKP	.
0.94173728	0	0	0.362693914	0.024042015	PCIF1	.
0.944013412	0	0	0.35707729	0.022647619	ATP13A2	.
0.944318774	0	0	0.441330599	0.027650875	MYH9;FUR	.
0.946001063	0	0	0.437121964	0.026413357	IGHMBP2;I	.
0.961494009	0	0	0.457701166	0.020016751	RPS6KA1;A	.
0.962917857	0	0	0.311239609	0.013011661	PER1	.
0.971789629	0	0	0.287863739	0.009265574	DHX37	.
0.97635495	0	0	0.274124077	0.007415984	CEACAM1	.
0.977583339	0	0	0.269301216	0.006826547	DHX37	.
0.978707354	0	0	0.26464371	0.00628615	NLRP1	.
0.98239283	0	0	0.251582443	0.004917969	SEC16A	.
0.983161031	0	0	0.247508072	0.004534385	ANAPC2	.
0.984214839	0	0	0.242274675	0.004070878	DHX37	.
0.993696333	0	0	0.333055295	0.002254568	IGHMBP2;/	.
0.998787635	0	0	0.146911481	1.78E-04	IGHMBP2	.

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Term	Overlap	P-value	Adjusted P-value	Old P-value
Lysine degradation	23255	6.33E-06	0.001404662	0
Thyroid hormone signaling pathway	11/121	4.95E-05	0.005497828	0
Notch signaling pathway	21732	2.28E-04	0.016873424	0
Human T-cell leukemia virus 1 infection	13/219	7.72E-04	0.042846934	0
Parathyroid hormone synthesis, secreti	8/106	0.001778282	0.078955723	0
MAPK signaling pathway	14/294	0.003896217	0.144160035	0
Transcriptional misregulation in cancer	10/192	0.007549529	0.239427925	0
Neurotrophin signaling pathway	7/119	0.012868813	0.357109562	0
T cell receptor signaling pathway	6/104	0.022445641	0.489815329	0
cGMP-PKG signaling pathway	8/167	0.025035735	0.489815329	0
Yersinia infection	7/137	0.025766741	0.489815329	0
Tight junction	8/169	0.026633108	0.489815329	0
Signaling pathways regulating pluripote	7/143	0.031533618	0.489815329	0
ErbB signaling pathway	31168	0.033342709	0.489815329	0
Endometrial cancer	21276	0.033443077	0.489815329	0
VEGF signaling pathway	21641	0.035302006	0.489815329	0
Thyroid cancer	13575	0.042206281	0.551164374	0
Cushing syndrome	7/155	0.045523568	0.561457334	0
Relaxin signaling pathway	6/129	0.054896228	0.613534393	0
Hepatitis B	7/162	0.055273369	0.613534393	0
Non-small cell lung cancer	26390	0.064803407	0.685064591	0
Autophagy	6/137	0.069270511	0.699002425	0
Chronic myeloid leukemia	27851	0.075837886	0.732000468	0
Cocaine addiction	17958	0.083516215	0.741623986	0
Ether lipid metabolism	17958	0.083516215	0.741623986	0
Breast cancer	6/147	0.090016109	0.75162125	0
D-Glutamine and D-glutamate metaboli	44566	0.100690974	0.75162125	0
AMPK signaling pathway	5/120	0.108766045	0.75162125	0
Hedgehog signaling pathway	20515	0.113212103	0.75162125	0
PD-L1 expression and PD-1 checkpoint p	32599	0.117583886	0.75162125	0
Platelet activation	5/124	0.120406236	0.75162125	0
Long-term depression	21976	0.131730351	0.75162125	0
GnRH signaling pathway	34060	0.132084397	0.75162125	0
TGF-beta signaling pathway	34425	0.135819929	0.75162125	0
FoxO signaling pathway	5/131	0.142101548	0.75162125	0
Basal cell carcinoma	23071	0.146263414	0.75162125	0
Fc gamma R-mediated phagocytosis	35521	0.147278192	0.75162125	0
Vascular smooth muscle contraction	5/133	0.148593341	0.75162125	0
Choline metabolism in cancer	35886	0.151178649	0.75162125	0
Glycerophospholipid metabolism	35886	0.151178649	0.75162125	0
Apelin signaling pathway	5/137	0.161943731	0.75162125	0
Melanogenesis	4/101	0.163110899	0.75162125	0
Acute myeloid leukemia	24532	0.166399335	0.75162125	0
Long-term potentiation	24532	0.166399335	0.75162125	0

Longevity regulating pathway	4/102	0.167162314	0.75162125	0
Fc epsilon RI signaling pathway	24898	0.171555753	0.75162125	0
Ubiquitin mediated proteolysis	5/140	0.172261992	0.75162125	0
Toll-like receptor signaling pathway	4/104	0.175370743	0.75162125	0
Regulation of actin cytoskeleton	7/218	0.176029127	0.75162125	0
Amphetamine addiction	25263	0.17675728	0.75162125	0
Renal cell carcinoma	25263	0.17675728	0.75162125	0
Central carbon metabolism in cancer	25628	0.182002	0.75162125	0
Prolactin signaling pathway	25628	0.182002	0.75162125	0
Spinocerebellar ataxia	5/143	0.18282679	0.75162125	0
HIF-1 signaling pathway	4/109	0.196465277	0.775070329	0
Inositol phosphate metabolism	26724	0.197976386	0.775070329	0
Phospholipase D signaling pathway	5/148	0.200943893	0.775070329	0
Gastric cancer	5/149	0.204638814	0.775070329	0
Taurine and hypotaurine metabolism	44572	0.208257029	0.775070329	0
TNF signaling pathway	4/112	0.209478467	0.775070329	0
mTOR signaling pathway	5/154	0.223440599	0.813177263	0
Cellular senescence	5/156	0.231103577	0.819904987	0
Chemical carcinogenesis	7/239	0.238163345	0.819904987	0
Growth hormone synthesis, secretion a	4/119	0.240721007	0.819904987	0
Sphingolipid signaling pathway	4/119	0.240721007	0.819904987	0
ABC transporters	16469	0.243755537	0.819904987	0
Viral carcinogenesis	6/203	0.255252846	0.845763163	0
Salmonella infection	7/249	0.269985533	0.869640671	0
Colorectal cancer	31472	0.270293722	0.869640671	0
Osteoclast differentiation	4/127	0.277604893	0.880404091	0
N-Glycan biosynthesis	18295	0.282823094	0.884320096	0
Pathways of neurodegeneration	12/475	0.297685948	0.90179695	0
Lipid and atherosclerosis	6/215	0.298265545	0.90179695	0
Phenylalanine metabolism	44578	0.302984086	0.90179695	0
Th1 and Th2 cell differentiation	33664	0.304661132	0.90179695	0
Estrogen signaling pathway	4/137	0.324818842	0.917630768	0
MicroRNAs in cancer	8/310	0.327338016	0.917630768	0
Phosphatidylinositol signaling system	35490	0.333443353	0.917630768	0
Prostate cancer	35490	0.333443353	0.917630768	0
Human cytomegalovirus infection	6/225	0.335094675	0.917630768	0
Apoptosis	4/142	0.348650499	0.917630768	0
Pantothenate and CoA biosynthesis	44582	0.359765578	0.917630768	0
Mineral absorption	21947	0.360050984	0.917630768	0
Arginine biosynthesis	44583	0.373224609	0.917630768	0
NF-kappa B signaling pathway	3/104	0.373624713	0.917630768	0
Proximal tubule bicarbonate reclamatio	44584	0.386401364	0.917630768	0
Renin-angiotensin system	44584	0.386401364	0.917630768	0
Spliceosome	4/150	0.386790389	0.917630768	0
GnRH secretion	23408	0.39014211	0.917630768	0
Glucagon signaling pathway	3/107	0.390716657	0.917630768	0
Th17 cell differentiation	3/107	0.390716657	0.917630768	0

Human papillomavirus infection	8/331	0.393808866	0.917630768	0
Insulin resistance	3/108	0.396389002	0.917630768	0
Cortisol synthesis and secretion	23774	0.397567904	0.917630768	0
Vitamin digestion and absorption	44585	0.399301747	0.917630768	0
Non-alcoholic fatty liver disease	4/155	0.410499199	0.917630768	0
alpha-Linolenic acid metabolism	44586	0.411931543	0.917630768	0
Epstein-Barr virus infection	5/202	0.419041789	0.917630768	0
Mitophagy	24869	0.419586681	0.917630768	0
Adipocytokine signaling pathway	25235	0.426835317	0.917630768	0
Epithelial cell signaling in Helicobacter p	25600	0.434036295	0.917630768	0
Pathways in cancer	12/531	0.439144503	0.917630768	0
Adherens junction	25965	0.441188416	0.917630768	0
Melanoma	26330	0.448290556	0.917630768	0
Rap1 signaling pathway	5/210	0.451959567	0.917630768	0
Linoleic acid metabolism	44590	0.459856336	0.917630768	0
Human immunodeficiency virus 1 infect	5/212	0.460116417	0.917630768	0
Wnt signaling pathway	4/166	0.461879002	0.917630768	0
Huntington disease	7/306	0.463002012	0.917630768	0
Glioma	27426	0.46928684	0.917630768	0
Thyroid hormone synthesis	27426	0.46928684	0.917630768	0
Hepatocellular carcinoma	4/168	0.471063294	0.917630768	0
Pentose phosphate pathway	44591	0.4712158	0.917630768	0
beta-Alanine metabolism	44591	0.4712158	0.917630768	0
Circadian rhythm	44592	0.482336925	0.919573442	0
Galactose metabolism	44592	0.482336925	0.919573442	0
Cell cycle	3/124	0.484640057	0.919573442	0
RNA degradation	28887	0.496525285	0.932653663	0
Fructose and mannose metabolism	12055	0.503884013	0.932653663	0
B cell receptor signaling pathway	29618	0.509806986	0.932653663	0
Alzheimer disease	8/369	0.513613115	0.932653663	0
Tuberculosis	4/180	0.524827756	0.932653663	0
Dopaminergic synapse	3/132	0.526417452	0.932653663	0
Axon guidance	4/182	0.533535686	0.932653663	0
Mucin type O-glycan biosynthesis	13150	0.534538491	0.932653663	0
Tyrosine metabolism	13150	0.534538491	0.932653663	0
Ras signaling pathway	5/232	0.539333305	0.932653663	0
Insulin secretion	31444	0.541991256	0.932653663	0
Alanine, aspartate and glutamate metal	13516	0.544330783	0.932653663	0
Insulin signaling pathway	3/137	0.55155809	0.932653663	0
Various types of N-glycan biosynthesis	14246	0.563303085	0.932653663	0
Glycine, serine and threonine metabolis	14611	0.572491612	0.932653663	0
Chemokine signaling pathway	4/192	0.575834678	0.932653663	0
Small cell lung cancer	33635	0.578637188	0.932653663	0
Kaposi sarcoma-associated herpesvirus	4/193	0.579944456	0.932653663	0
Bladder cancer	14977	0.581487254	0.932653663	0
Pathogenic Escherichia coli infection	4/197	0.596153639	0.932653663	0
Fat digestion and absorption	15707	0.598915953	0.932653663	0

Vasopressin-regulated water reabsorpti	16072	0.60735684	0.932653663	0
Focal adhesion	4/201	0.611985806	0.932653663	0
Endocytosis	5/252	0.612762061	0.932653663	0
Adrenergic signaling in cardiomyocytes	3/150	0.613070727	0.932653663	0
Aldosterone synthesis and secretion	35827	0.613091127	0.932653663	0
Basal transcription factors	16438	0.615620499	0.932653663	0
Glycosphingolipid biosynthesis	16438	0.615620499	0.932653663	0
PI3K-Akt signaling pathway	7/354	0.616638672	0.932653663	0
Progesterone-mediated oocyte matura	2/100	0.624087524	0.932653663	0
Oxytocin signaling pathway	3/154	0.630819907	0.932653663	0
Other types of O-glycan biosynthesis	17168	0.63163091	0.932653663	0
Chagas disease	2/102	0.634840821	0.932653663	0
Amino sugar and nucleotide sugar meta	17533	0.639384856	0.932653663	0
Intestinal immune network for IgA prod	17533	0.639384856	0.932653663	0
C-type lectin receptor signaling pathwa	2/104	0.645352182	0.932653663	0
Sphingolipid metabolism	17899	0.646975965	0.932653663	0
Ovarian steroidogenesis	18629	0.66168325	0.94770117	0
cAMP signaling pathway	4/216	0.667841306	0.95038955	0
Fanconi anemia pathway	19725	0.68260591	0.965213452	0
Glutamatergic synapse	2/114	0.694341704	0.97559404	0
Protein processing in endoplasmic retic	3/171	0.699862286	0.977166211	0
Viral myocarditis	21916	0.72065758	0.992086172	0
Arachidonic acid metabolism	22282	0.726541392	0.992086172	0
Glycerolipid metabolism	22282	0.726541392	0.992086172	0
Alcoholism	3/186	0.752254337	0.992086172	0
Oocyte meiosis	2/129	0.757221766	0.992086172	0
Glycolysis / Gluconeogenesis	24473	0.75933661	0.992086172	0
Retinol metabolism	24838	0.764407497	0.992086172	0
Natural killer cell mediated cytotoxicity	2/131	0.764704718	0.992086172	0
p53 signaling pathway	26665	0.788206983	0.992086172	0
Fluid shear stress and atherosclerosis	2/139	0.792666097	0.992086172	0
PPAR signaling pathway	27030	0.792670897	0.992086172	0
Pancreatic cancer	27760	0.801319094	0.992086172	0
Pertussis	27760	0.801319094	0.992086172	0
Arrhythmogenic right ventricular cardio	28126	0.805507275	0.992086172	0
Bacterial invasion of epithelial cells	28126	0.805507275	0.992086172	0
Leishmaniasis	28126	0.805507275	0.992086172	0
Proteoglycans in cancer	3/205	0.80779561	0.992086172	0
Taste transduction	31413	0.839451074	0.992086172	0
Cardiac muscle contraction	31778	0.842837126	0.992086172	0
Hepatitis C	2/157	0.845086627	0.992086172	0
Gap junction	32143	0.84615193	0.992086172	0
GABAergic synapse	32509	0.849396982	0.992086172	0
Bile secretion	32874	0.852573746	0.992086172	0
Hypertrophic cardiomyopathy	32874	0.852573746	0.992086172	0
Morphine addiction	33239	0.855683655	0.992086172	0
JAK-STAT signaling pathway	2/162	0.857350208	0.992086172	0

Hippo signaling pathway	2/163	0.859694115	0.992086172	0
IL-17 signaling pathway	34335	0.864626149	0.992086172	0
Thermogenesis	3/232	0.86840398	0.992086172	0
Cytokine-cytokine receptor interaction	4/295	0.869988214	0.992086172	0
Dilated cardiomyopathy	35065	0.870278501	0.992086172	0
Circadian entrainment	35431	0.873015754	0.992086172	0
Inflammatory mediator regulation of TR	35796	0.875695382	0.992086172	0
mRNA surveillance pathway	35796	0.875695382	0.992086172	0
Influenza A	2/172	0.879256411	0.992086172	0
Viral protein interaction with cytokine a	1/100	0.880886578	0.992086172	0
Calcium signaling pathway	3/240	0.882800831	0.992086172	0
Amoebiasis	1/102	0.88586147	0.992086172	0
Pancreatic secretion	1/102	0.88586147	0.992086172	0
Ribosome biogenesis in eukaryotes	1/108	0.899576399	0.992086172	0
Toxoplasmosis	1/112	0.907793372	0.992086172	0
Neutrophil extracellular trap formation	2/189	0.909505774	0.992086172	0
Cholinergic synapse	1/113	0.909740575	0.992086172	0
Serotonergic synapse	1/113	0.909740575	0.992086172	0
Leukocyte transendothelial migration	1/114	0.911646752	0.992086172	0
Prion disease	3/273	0.928425329	0.999917589	0
Lysosome	1/128	0.934477114	0.999917589	0
Measles	1/139	0.948201135	0.999917589	0
Amyotrophic lateral sclerosis	4/364	0.949432881	0.999917589	0
Cell adhesion molecules	1/148	0.957266891	0.999917589	0
Retrograde endocannabinoid signaling	1/148	0.957266891	0.999917589	0
Phagosome	1/152	0.960770154	0.999917589	0
Ribosome	1/158	0.965495083	0.999917589	0
Necroptosis	1/159	0.966225408	0.999917589	0
Shigellosis	2/246	0.966828915	0.999917589	0
NOD-like receptor signaling pathway	1/181	0.97891005	0.999917589	0
RNA transport	1/186	0.981051952	0.999917589	0
Diabetic cardiomyopathy	1/203	0.986837333	0.999917589	0
Coronavirus disease	1/232	0.992934344	0.999917589	0
Herpes simplex virus 1 infection	4/498	0.993525229	0.999917589	0
Parkinson disease	1/249	0.995095352	0.999917589	0
Neuroactive ligand-receptor interaction	1/341	0.999321669	0.999917589	0
Olfactory transduction	1/440	0.999917589	0.999917589	0

Old Adjusted P-value	Odds Ratio	Combined Score	Genes
0	7.918085969	94.78452568	NSD3;KMT2D;KMT2A;KMT2C;SETD1B;DOT1L;KMT2B;SE
0	4.760391198	47.18943598	NOTCH2;MED12;NCOA2;MAP2K2;NOTCH1;NCOR1;RXR/
0	6.36505867	53.37789447	NCOR2;NOTCH2;NOTCH1;ATXN1L;EP300;DVL3;DTX2
0	3.004007538	21.52823264	MAP3K3;SPI1;CRTC3;MAP2K2;ATF6B;SRF;NFATC2;CREB
0	3.86011492	24.44266272	GNA13;AKAP13;MAFB;RXRA;ATF6B;CREB3L2;ARRB2;ME
0	2.376847291	13.18615254	MAP3K3;ANGPT4;MAP2K2;GADD45A;PLA2G4B;SRF;ARF
0	2.599571161	12.70220679	LYL1;SPI1;NCOR1;RXRA;KMT2A;GADD45A;DOT1L;TCF3;/
0	2.946125908	12.82433432	MAP3K3;MAP2K2;IRAK1;RPS6KA1;FOXO3;MAP2K7;SH2
0	2.881100266	10.93855482	MAP2K2;NFATC2;PDCD1;MAP2K7;MAP3K14;PAK4
0	2.371740856	8.745678414	GNA13;MAP2K2;ATF6B;SRF;CREB3L2;ATP2A3;NFATC2;N
0	2.535853977	9.277854739	MAP2K2;IRAK1;RPS6KA1;WAS;NFATC2;PIP5K1C;MAP2K
0	2.342037026	8.491289823	STK11;WAS;SYMPK;MYH9;MYH11;MAP2K7;TJAP1;RUNX
0	2.423230309	8.376382791	MAP2K2;KAT6A;AXIN1;DVL3;TCF3;ACVR2B;POU5F1
0	2.936746988	9.987630257	MAP2K2;ABL2;CBL;MAP2K7;PAK4
0	3.476851852	11.81403134	MAP2K2;GADD45A;AXIN1;FOXO3
0	3.413461538	11.41398559	MAP2K2;PLA2G4B;SPHK1;NFATC2
0	4.135844266	13.09071733	RXRA;MAP2K2;GADD45A
0	2.22537792	6.875360979	KMT2D;MAP2K2;KMT2A;ATF6B;CREB3L2;AXIN1;DVL3
0	2.2925651	6.653736079	GNA15;MAP2K2;ATF6B;CREB3L2;ARRB2;MAP2K7
0	2.124111536	6.150288624	MAP2K2;IRAK1;ATF6B;CREB3L2;EP300;NFATC2;MAP2K7
0	2.759049774	7.549855788	MAP2K2;RXRA;GADD45A;FOXO3
0	2.15167607	5.744407056	ERN1;STK11;MAP2K2;ATG2A;ATG4B;SMCR8
0	2.605235043	6.719310956	MAP2K2;GADD45A;CBL;RUNX1
0	3.055051611	7.584820869	ATF6B;CREB3L2;CDK5R1
0	3.055051611	7.584820869	PLA2G4B;LPCAT1;GDPD3
0	1.998047076	4.810831076	NOTCH2;MAP2K2;NOTCH1;GADD45A;AXIN1;DVL3
0	11.68019093	26.81420401	GLS2
0	2.039287585	4.524273864	SREBF1;STK11;CREB3L2;FOXO3;PFKP
0	2.650604045	5.774320242	MGRN1;ARRB2;CSNK1G2
0	2.205316742	4.720708248	MAP3K3;MAP2K2;NFATC2;PDCD1
0	1.970335122	4.170970797	GNA13;PLA2G4B;P2RY1;TLN1;FERMT3
0	2.464091884	4.994709921	GNA13;MAP2K2;PLA2G4B
0	2.105769231	4.262738529	MAP3K3;MAP2K2;PLA2G4B;MAP2K7
0	2.082264957	4.157086481	AMHR2;EP300;SMAD6;ACVR2B
0	1.860202716	3.629652377	STK11;MAP2K2;GADD45A;EP300;FOXO3
0	2.340527578	4.499304015	GADD45A;AXIN1;DVL3
0	2.014784946	3.859183594	PLA2G4B;SPHK1;WAS;PIP5K1C
0	1.830948795	3.490780699	GNA13;MAP2K2;PLA2G4B;MYH9;MYH11
0	1.993248773	3.765831022	MAP2K2;PLA2G4B;WAS;PIP5K1C
0	1.993248773	3.765831022	PLA2G4B;MBOAT7;LPCAT1;PISD
0	1.775100402	3.23158154	GNA13;HDAC5;MAP2K2;SPHK1;MEF2D
0	1.93130452	3.502082663	MAP2K2;CREB3L2;EP300;DVL3
0	2.193794964	3.934274555	SPI1;MAP2K2;RUNX1
0	2.193794964	3.934274555	MAP2K2;RPS6KA1;EP300

0	1.911499215	3.419270681	STK11;ATF6B;CREB3L2;FOXO3
0	2.159933592	3.807632395	MAP2K2;PLA2G4B;MAP2K7
0	1.735385988	3.052090588	PPIL2;MGRN1;HUWE1;CBL;ANAPC2
0	1.873076923	3.26075161	MAP2K2;IRAK1;TOLLIP;MAP2K7
0	1.555867941	2.702707233	GNA13;MAP2K2;ITGAD;MYH9;MYH11;PIP5K1C;PAK4
0	2.127098321	3.686214143	ARC;ATF6B;CREB3L2
0	2.127098321	3.686214143	MAP2K2;EP300;PAK4
0	2.095243208	3.569744638	MAP2K2;GLS2;PFKP
0	2.095243208	3.569744638	MAP2K2;FOXO3;SOCS7
0	1.697398289	2.884246458	ERN1;ATXN1L;ATG2A;ATP2A3;CIC
0	1.783424908	2.902113087	ANGPT4;MAP2K2;EP300;PFKP
0	2.005138746	3.247537789	PI4KA;PIP5K1C;PIK3C2A
0	1.637627433	2.627949132	GNA13;MAP2K2;PLA2G4B;SPHK1;PIP5K1C
0	1.626171352	2.57993506	MAP2K2;RXRA;GADD45A;AXIN1;DVL3
0	4.670644391	7.328158116	CSAD
0	1.733618234	2.709878169	ATF6B;CREB3L2;MAP2K7;MAP3K14
0	1.571197542	2.354611838	PRR5;STK11;MAP2K2;RPS6KA1;DVL3
0	1.5502274	2.270911508	MAP2K2;GADD45A;NFATC2;FOXO3;HIPK1
0	1.413500877	2.02808896	NOTCH2;RXRA;MAP2K2;ATF6B;CREB3L2;RPS6KA1;ARRB
0	1.627508361	2.317761774	MAP2K2;ATF6B;CREB3L2;EP300
0	1.627508361	2.317761774	GNA13;ABCC1;MAP2K2;SPHK1
0	2.173917881	3.068679557	ABCC1;ABCA9
0	1.425954535	1.947141874	HDAC5;ATF6B;SRF;CREB3L2;UBR4;EP300
0	1.354391371	1.773422323	MAP2K2;AHNAK;IRAK1;FHOD1;FLNA;MAP2K7;PIK3C2A
0	1.689954061	2.210875727	MAP2K2;GADD45A;AXIN1
0	1.521028768	1.949284187	SPI1;NFATC2;MAP2K7;MAP3K14
0	1.946969697	2.458893619	MAN2A2;MGAT5
0	1.214394613	1.471501644	ERN1;CCS;MAP2K2;HIP1;ATXN1L;ATG2A;ATP2A3;AXIN1
0	1.343249428	1.625024337	ERN1;RXRA;POU2F1;IRAK1;NFATC2;MAP2K7
0	2.918257757	3.484618619	AOC2
0	1.575539568	1.87261569	NOTCH2;NOTCH1;NFATC2
0	1.405942741	1.580965267	NCOA2;MAP2K2;ATF6B;CREB3L2
0	1.239503633	1.3842305	NOTCH2;HDAC5;ABCC1;MAP2K2;NOTCH1;GLS2;EP300;I
0	1.4913516	1.637925043	PI4KA;PIP5K1C;PIK3C2A
0	1.4913516	1.637925043	MAP2K2;CREB3L2;EP300
0	1.281252068	1.400846924	GNA13;AKAP13;MAP2K2;ATF6B;CREB3L2;NFATC2
0	1.354654404	1.427379424	ERN1;MAP2K2;GADD45A;MAP3K14
0	2.334128878	2.386186097	PANK1
0	1.61046032	1.645100735	CLCN2;SLC26A6
0	2.222866235	2.190801101	GLS2
0	1.387491987	1.365990615	IRAK1;GADD45A;MAP3K14
0	2.121718377	2.0174967	GLS2
0	2.121718377	2.0174967	LNPEP
0	1.279899895	1.215741536	SF3A1;SF3A2;U2AF2;CHERP
0	1.506250965	1.417750015	MAP2K2;ARRB2
0	1.347260653	1.266118708	CREB3L2;EP300;PFKP
0	1.347260653	1.266118708	RXRA;NFATC2;RUNX1

0	1.157654273	1.078805977	NOTCH2;MAP2K2;NOTCH1;CREB3L2;UBR4;AXIN1;EP30(
0	1.334361083	1.234763331	SREBF1;CREB3L2;RPS6KA1
0	1.482266272	1.367226891	ATF6B;CREB3L2
0	2.029365985	1.863034864	ABCC1
0	1.237200713	1.10158038	ERN1;SREBF1;RXRA;MAP3K11
0	1.944709626	1.724759275	PLA2G4B
0	1.185432084	1.031070606	NCOR2;IRAK1;GADD45A;MAP2K7;MAP3K14
0	1.414673046	1.228622527	TFEB;FOXO3
0	1.39348711	1.186355025	STK11;RXRA
0	1.372924289	1.145879846	CSK;MAP3K14
0	1.080188145	0.888915726	NOTCH2;GNA13;SPI1;MAP2K2;NOTCH1;RXRA;GADD45A
0	1.352957493	1.10710245	WAS;EP300
0	1.333561176	1.069934393	MAP2K2;GADD45A
0	1.138701146	0.904313814	ANGPT4;MAP2K2;P2RY1;TLN1;SIPA1
0	1.666553017	1.294646966	PLA2G4B
0	1.127582795	0.875315169	MAP2K2;IRAK1;NFATC2;MAP2K7;PAK4
0	1.152540361	0.890282479	AXIN1;EP300;DVL3;NFATC2
0	1.092965251	0.841609342	ERN1;HIP1;CREB3L2;ATG2A;EP300;MAP2K7;TAF4
0	1.278560661	0.967283686	MAP2K2;GADD45A
0	1.278560661	0.967283686	ATF6B;CREB3L2
0	1.13836773	0.856920894	MAP2K2;GADD45A;AXIN1;DVL3
0	1.609003374	1.210677077	PFKP
0	1.609003374	1.210677077	AOC2
0	1.555290374	1.133981488	PER1
0	1.555290374	1.133981488	PFKP
0	1.156965337	0.838046469	GADD45A;EP300;ANAPC2
0	1.21189337	0.84847184	CNOT3;PFKP
0	1.457935561	0.999282403	PFKP
0	1.181091394	0.795728536	MAP2K2;NFATC2
0	1.033751983	0.688773432	ERN1;MAP2K2;ATG2A;ATP2A3;AXIN1;DVL3;MAP2K7;CD
0	1.060096154	0.683428251	MRC2;IRAK1;SPHK1;EP300
0	1.084769394	0.696053939	ATF6B;CREB3L2;ARRB2
0	1.048076923	0.658432652	EFNB1;NFATC2;SLIT3;PAK4
0	1.332765087	0.834779463	GALNT10
0	1.332765087	0.834779463	AOC2
0	1.027174778	0.634199816	ANGPT4;MAP2K2;PLA2G4B;ABL2;PAK4
0	1.110503532	0.680189421	ATF6B;CREB3L2
0	1.295677539	0.788028695	GLS2
0	1.044024482	0.62120304	SREBF1;MAP2K2;CBL
0	1.227358372	0.704426942	MAN2A2
0	1.195826449	0.666980806	AOC2
0	0.991816694	0.547418026	CX3CR1;WAS;ARRB2;FOXO3
0	1.036150984	0.566857083	RXRA;GADD45A
0	0.986518112	0.537477704	MAP2K2;NFATC2;EP300;MAP2K7
0	1.165871122	0.632095948	MAP2K2
0	0.965872858	0.499604363	GNA13;IRAK1;MYH9;MYH11
0	1.1102398	0.569146672	DGAT1

0	1.084364767	0.540706331	CREB3L2
0	0.94606599	0.464562099	FLNA;PIP5K1C;TLN1;PAK4
0	0.943027169	0.461874502	PIP5K1C;ARRB2;CBL;RBSN;EPN1
0	0.951059561	0.46532964	ATF6B;CREB3L2;ATP2A3
0	0.971092504	0.475098945	ATF6B;CREB3L2
0	1.059665871	0.514069959	TAF4
0	1.059665871	0.514069959	GBGT1
0	0.939432423	0.454189317	ANGPT4;STK11;RXRA;MAP2K2;ATF6B;CREB3L2;FOXO3
0	0.951176643	0.44844617	RPS6KA1;ANAPC2
0	0.925675354	0.42649091	MAP2K2;PLA2G4B;NFATC2
0	1.013489675	0.46564789	GALNT10
0	0.932057416	0.423509169	GNA15;IRAK1
0	0.991875286	0.44361496	AMDHD2
0	0.991875286	0.44361496	MAP3K14
0	0.913687963	0.400157952	NFATC2;MAP3K14
0	0.971161496	0.422888519	SPHK1
0	0.93221957	0.384977143	PLA2G4B
0	0.878447025	0.354633193	MAP2K2;CREB3L2;ATP2A3;EP300
0	0.879317332	0.335756406	EME2
0	0.831681476	0.303389976	GLS2;PLA2G4B
0	0.831277835	0.296659532	ERN1;ATF6B;MAP2K7
0	0.789652522	0.258683201	ABL2
0	0.77645187	0.248045177	PLA2G4B
0	0.77645187	0.248045177	DGAT1
0	0.762550615	0.217083518	HDAC5;ATF6B;CREB3L2
0	0.73288626	0.20381502	RPS6KA1;ANAPC2
0	0.705648369	0.194272129	PFKP
0	0.695080683	0.186736386	DGAT1
0	0.721449501	0.193540018	MAP2K2;NFATC2
0	0.646645452	0.153898097	GADD45A
0	0.679041665	0.15777751	MAP2K7;ACVR2B
0	0.637754602	0.148180467	RXRA
0	0.620684169	0.137479086	GADD45A
0	0.620684169	0.137479086	IRAK1
0	0.612485869	0.132470309	ATP2A3
0	0.612485869	0.132470309	CBL
0	0.612485869	0.132470309	IRAK1
0	0.690148871	0.147309661	MAP2K2;FLNA;CBL
0	0.547381721	0.095795679	P2RY1
0	0.540989066	0.092499148	ATP2A3
0	0.599629572	0.100927335	MAP2K2;RXRA
0	0.534743368	0.089332275	MAP2K2
0	0.528639618	0.086289112	GLS2
0	0.522673031	0.083364032	RXRA
0	0.522673031	0.083364032	ATP2A3
0	0.516839035	0.080551706	ARRB2
0	0.580741627	0.089381247	EP300;SOCS7

0	0.577104817	0.087245917	AXIN1;DVL3
0	0.50008982	0.072742097	IL17RA
0	0.607929377	0.085777776	CREB3L2;RPS6KA1;ZNF516
0	0.637357917	0.088768415	CX3CR1;AMHR2;ACVR2B;IL17RA
0	0.489511368	0.06801369	ATP2A3
0	0.48438743	0.065780626	PER1
0	0.479369141	0.063630015	PLA2G4B
0	0.479369141	0.063630015	SYMPK
0	0.546298902	0.070297041	MAP2K2;EP300
0	0.469636701	0.059562334	CX3CR1
0	0.58716571	0.073193531	GNA15;SPHK1;ATP2A3
0	0.460289704	0.05578467	GNA15
0	0.460289704	0.05578467	ATP2A3
0	0.434345237	0.045967319	REXO1
0	0.418607151	0.040495424	IRAK1
0	0.496200394	0.047066559	HDAC5;MAP2K2
0	0.414848278	0.039242906	CREB3L2
0	0.414848278	0.039242906	PLA2G4B
0	0.411155934	0.038033033	SIPA1
0	0.514521716	0.038211121	NOTCH1;ATF6B;CREB3L2
0	0.365568564	0.024773903	GGA3
0	0.336238802	0.017884082	IRAK1
0	0.513354701	0.026638201	ERN1;CCS;ATG2A;SMCR8
0	0.315506632	0.013779135	PDCD1
0	0.315506632	0.013779135	FAAH
0	0.307085619	0.012289589	MRC2
0	0.295258653	0.010367792	MRPS2
0	0.293374823	0.01007981	PLA2G4B
0	0.379166993	0.012790714	TLN1;FOXO3
0	0.2572262	0.00548291	NLRP1
0	0.250209637	0.004786476	GEMIN7
0	0.228951535	0.003033622	ATP2A3
0	0.199909081	0.001417503	IRAK1
0	0.371496419	0.002413175	POU2F1;IRAK1;ZNF316;HCFC1
0	0.186042036	9.15E-04	ERN1
0	0.135055454	9.16E-05	P2RY1
0	0.104060541	8.58E-06	ARRB2

RB2;IRAK1;RPS6KA1;FLNA;MAP3K6;MAP2K7;MAP3K14;MAP3K11

Supplementary File S6: Comprehensive details of the results of functional enrichment ana

BP	Term	Overlap	P-value	Adjusted P-value
	maturation of LSU-rRNA (GO:0000470)	44738	1.13E-11	4.85E-09
	ribosomal large subunit biogenesis (GO:004227	20972	1.70E-09	2.85E-07
	rRNA processing (GO:0006364)	8/173	2.00E-09	2.85E-07
	ribosome biogenesis (GO:0042254)	7/192	1.15E-07	1.23E-05
	rRNA metabolic process (GO:0016072)	6/162	9.15E-07	7.85E-05
	maturation of LSU-rRNA from tricistronic rRNA t	44634	2.87E-06	2.05E-04
	maturation of 5.8S rRNA (GO:0000460)	44637	5.33E-06	3.27E-04
	ncRNA processing (GO:0034470)	5/201	5.45E-05	0.002916302
	snoRNA localization (GO:0048254)	44598	6.12E-05	0.002916302
	regulation of cyclic-nucleotide phosphodiestera	44600	1.14E-04	0.004886689
	ribonucleoprotein complex biogenesis (GO:002	21976	2.52E-04	0.008814595
	sno(s)RNA 3'-end processing (GO:0031126)	44604	2.67E-04	0.008814595
	positive regulation of protein localization to chr	44604	2.67E-04	0.008814595
	regulation of translation (GO:0006417)	4/178	4.75E-04	0.014555194
	maturation of 5.8S rRNA from tricistronic rRNA	44614	9.23E-04	0.026392868
	cellular response to hexose stimulus (GO:00713	44617	0.001193823	0.032009384
	cellular response to glucose stimulus (GO:0071	11720	0.001955958	0.049359188
	tRNA aminoacylation (GO:0043039)	13912	0.002750794	0.06556058
	regulation of mRNA stability (GO:0043488)	3/146	0.003315846	0.071716244
	cellular glucose homeostasis (GO:0001678)	15738	0.003510585	0.071716244
	tRNA aminoacylation for protein translation (GO	15738	0.003510585	0.071716244
	response to glucose (GO:0009749)	17930	0.004536577	0.088028845
	ribosome assembly (GO:0042255)	18295	0.004719495	0.088028845
	regulation of protein localization (GO:0032880)	24139	0.008094901	0.106418895
	regulation of translational initiation (GO:000644	24869	0.008574669	0.106418895
	translation (GO:0006412)	3/214	0.009549137	0.106418895
	regulation of ribonuclease activity (GO:0060700	44566	0.010208974	0.106418895
	R-loop disassembly (GO:0062176)	44566	0.010208974	0.106418895
	negative regulation of hydrogen peroxide-induc	44566	0.010208974	0.106418895
	rescue of stalled ribosome (GO:0072344)	44566	0.010208974	0.106418895
	cadmium ion transmembrane transport (GO:00	44566	0.010208974	0.106418895
	cadmium ion transport (GO:0015691)	44566	0.010208974	0.106418895
	positive regulation of Golgi to plasma membran	44566	0.010208974	0.106418895
	rRNA 5'-end processing (GO:0000967)	44566	0.010208974	0.106418895
	rRNA transport (GO:0051029)	44566	0.010208974	0.106418895
	positive regulation of mitochondrial depolarizat	44566	0.010208974	0.106418895
	regulation of glomerular mesangial cell prolifera	44566	0.010208974	0.106418895
	regulation of phosphatidylinositol biosynthetic p	44566	0.010208974	0.106418895
	embryonic viscerocranium morphogenesis (GO:	44566	0.010208974	0.106418895
	endonucleolytic cleavage in 5'-ETS of tricistronic	44566	0.010208974	0.106418895
	endonucleolytic cleavage to generate mature 5'	44566	0.010208974	0.106418895
	positive regulation of cellular amide metabolic p	29618	0.011993108	0.106418895
	induction of bacterial agglutination (GO:004315	44567	0.012238541	0.106418895
	tRNA pseudouridine synthesis (GO:0031119)	44567	0.012238541	0.106418895

peptidyl-glutamine methylation (GO:0018364)	44567	0.012238541	0.106418895
protein localization to nucleolus (GO:1902570)	44567	0.012238541	0.106418895
negative regulation of cellular amide metabolic	31444	0.013442455	0.106418895
positive regulation of gastrulation (GO:2000543	44568	0.014264049	0.106418895
ribosomal large subunit export from nucleus (G	44568	0.014264049	0.106418895
ribosomal small subunit export from nucleus (G	44568	0.014264049	0.106418895
positive regulation of membrane depolarization	44568	0.014264049	0.106418895
negative regulation of protein kinase activity by	44568	0.014264049	0.106418895
rRNA-containing ribonucleoprotein complex exp	44568	0.014264049	0.106418895
iron import into cell (GO:0033212)	44568	0.014264049	0.106418895
zinc ion import across plasma membrane (GO:0	44568	0.014264049	0.106418895
mRNA pseudouridine synthesis (GO:1990481)	44568	0.014264049	0.106418895
polyadenylation-dependent snoRNA 3'-end proc	44568	0.014264049	0.106418895
negative regulation of translation (GO:0017148)	32905	0.014654082	0.106418895
negative regulation of cellular protein metaboli	34366	0.015911201	0.106418895
regulation of endodeoxyribonuclease activity (G	44569	0.016285505	0.106418895
regulation of Golgi to plasma membrane protein	44569	0.016285505	0.106418895
U4 snRNA 3'-end processing (GO:0034475)	44569	0.016285505	0.106418895
endonucleolytic cleavage in ITS1 to separate SSU	44569	0.016285505	0.106418895
regulation of protein phosphorylation (GO:0001	3/266	0.01709311	0.106418895
regulation of apoptotic process (GO:0042981)	5/742	0.017228561	0.106418895
tetrahydrofolate interconversion (GO:0035999)	44570	0.018302918	0.106418895
nuclear RNA surveillance (GO:0071027)	44570	0.018302918	0.106418895
DNA metabolic process (GO:0006259)	3/277	0.019015607	0.106418895
translational elongation (GO:0006414)	2/104	0.019247888	0.106418895
formation of translation preinitiation complex ((	44571	0.020316294	0.106418895
positive regulation of establishment of protein l	44571	0.020316294	0.106418895
positive regulation of mesenchymal cell prolifer	44571	0.020316294	0.106418895
regulation of endoplasmic reticulum unfolded p	44571	0.020316294	0.106418895
iron ion transmembrane transport (GO:003475	44571	0.020316294	0.106418895
positive regulation of protein sumoylation (GO:(	44571	0.020316294	0.106418895
telomere maintenance in response to DNA dam	44571	0.020316294	0.106418895
nuclear mRNA surveillance (GO:0071028)	44571	0.020316294	0.106418895
nuclear-transcribed mRNA catabolic process, ex	44571	0.020316294	0.106418895
dicarboxylic acid biosynthetic process (GO:0043	44571	0.020316294	0.106418895
negative regulation of centrosome duplication (	44572	0.022325642	0.106418895
positive regulation of ceramide biosynthetic prc	44572	0.022325642	0.106418895
negative regulation of oxidative stress-induced	44572	0.022325642	0.106418895
regulation of establishment of protein localizati	44572	0.022325642	0.106418895
sphingomyelin metabolic process (GO:0006684)	44572	0.022325642	0.106418895
positive regulation of protein localization to Caj	44572	0.022325642	0.106418895
tetrahydrofolate metabolic process (GO:004665	44572	0.022325642	0.106418895
positive regulation of sphingolipid biosynthetic	44572	0.022325642	0.106418895
regulation of mesenchymal cell proliferation (G	44572	0.022325642	0.106418895
regulation of mitochondrial depolarization (GO:	44572	0.022325642	0.106418895
regulation of protein localization to Cajal body (	44572	0.022325642	0.106418895
protein insertion into mitochondrial inner mem	44573	0.02433097	0.111847032

regulation of cellular response to stress (GO:008	2/118	0.024365839	0.111847032
regulation of mRNA catabolic process (GO:0061	2/122	0.025919886	0.111847032
pseudouridine synthesis (GO:0001522)	44574	0.026332285	0.111847032
pteridine-containing compound metabolic proc	44574	0.026332285	0.111847032
negative regulation of endoplasmic reticulum u	44574	0.026332285	0.111847032
negative regulation of hydrogen peroxide-induc	44574	0.026332285	0.111847032
regulation of cell aging (GO:0090342)	44574	0.026332285	0.111847032
ribosomal subunit export from nucleus (GO:000	44574	0.026332285	0.111847032
DNA deamination (GO:0045006)	44574	0.026332285	0.111847032
endonucleolytic cleavage of tricistronic rRNA tr	44574	0.026332285	0.111847032
defense response to symbiont (GO:0140546)	2/124	0.02671175	0.112346478
negative regulation of cell activation (GO:00508	44575	0.028329595	0.113583143
regulation of gastrulation (GO:0010470)	44575	0.028329595	0.113583143
positive regulation of potassium ion transmemb	44575	0.028329595	0.113583143
manganese ion transport (GO:0006828)	44575	0.028329595	0.113583143
ncRNA transcription (GO:0098781)	44575	0.028329595	0.113583143
positive regulation of chromosome organizatior	44576	0.030322908	0.116422934
positive regulation of telomerase RNA localizati	44576	0.030322908	0.116422934
embryonic cranial skeleton morphogenesis (GO	44576	0.030322908	0.116422934
protein kinase A signaling (GO:0010737)	44576	0.030322908	0.116422934
defense response to virus (GO:0051607)	2/133	0.030394799	0.116422934
ribonucleoprotein complex assembly (GO:0022(	2/136	0.03166507	0.117474131
regulation of ceramide biosynthetic process (GC	44577	0.032312232	0.117474131
negative regulation of platelet activation (GO:0(	44577	0.032312232	0.117474131
regulation of establishment of cell polarity (GO:	44577	0.032312232	0.117474131
nuclear transport (GO:0051169)	44577	0.032312232	0.117474131
platelet-derived growth factor receptor signalin	44577	0.032312232	0.117474131
negative regulation of phagocytosis (GO:00507(	44578	0.034297574	0.122548552
preassembly of GPI anchor in ER membrane (GC	44578	0.034297574	0.122548552
positive regulation of cell cycle phase transition	44579	0.036278942	0.122548552
regulation of telomerase RNA localization to Caj	44579	0.036278942	0.122548552
rRNA catabolic process (GO:0016075)	44579	0.036278942	0.122548552
rRNA transcription (GO:0009303)	44579	0.036278942	0.122548552
regulation of establishment or maintenance of (	44579	0.036278942	0.122548552
cellular response to dsRNA (GO:0071359)	44579	0.036278942	0.122548552
regulation of protein sumoylation (GO:0033233	44579	0.036278942	0.122548552
folic acid metabolic process (GO:0046655)	44580	0.038256344	0.124333118
positive regulation of establishment of protein l	44580	0.038256344	0.124333118
positive regulation of G protein-coupled recepto	44580	0.038256344	0.124333118
regulation of centriole replication (GO:0046599	44580	0.038256344	0.124333118
cytoplasmic translational initiation (GO:000218:	44580	0.038256344	0.124333118
regulation of smooth muscle cell migration (GO	44581	0.040229788	0.126901316
folic acid-containing compound metabolic proce	44581	0.040229788	0.126901316
positive regulation of embryonic development (	44581	0.040229788	0.126901316
insulin secretion (GO:0030073)	44581	0.040229788	0.126901316
regulation of signal transduction by p53 class m	2/156	0.040651389	0.127295225
negative regulation of peptidyl-serine phosphor	44582	0.042199281	0.128393557

innate immune response in mucosa (GO:00022	44582	0.042199281	0.128393557
rRNA modification (GO:0000154)	44582	0.042199281	0.128393557
zinc ion transport (GO:0006829)	44582	0.042199281	0.128393557
regulation of centrosome cycle (GO:0046605)	44583	0.044164831	0.1288892
cell projection assembly (GO:0030031)	44583	0.044164831	0.1288892
rRNA methylation (GO:0031167)	44583	0.044164831	0.1288892
zinc ion transmembrane transport (GO:0071577	44583	0.044164831	0.1288892
mRNA modification (GO:0016556)	44583	0.044164831	0.1288892
regulation of platelet activation (GO:0010543)	44583	0.044164831	0.1288892
positive regulation of cell cycle G2/M phase tra	44584	0.046126446	0.131921635
negative regulation of smoothened signaling pa	44584	0.046126446	0.131921635
positive regulation of protein autophosphorylat	44584	0.046126446	0.131921635
positive regulation of p38MAPK cascade (GO:19	44585	0.048084133	0.135711138
protein insertion into mitochondrial membrane	44585	0.048084133	0.135711138
cAMP-mediated signaling (GO:0019933)	44586	0.0500379	0.138491995
ribosomal large subunit assembly (GO:0000027)	44586	0.0500379	0.138491995
negative regulation of response to endoplasmic	44586	0.0500379	0.138491995
regulation of telomere maintenance (GO:00322	44587	0.051987755	0.140268849
regulation of biomineral tissue development (G	44587	0.051987755	0.140268849
histone methylation (GO:0016571)	44587	0.051987755	0.140268849
DNA modification (GO:0006304)	44587	0.051987755	0.140268849
peptide hormone secretion (GO:0030072)	44588	0.053933705	0.144554469
positive regulation of fibroblast proliferation (G	44589	0.055875759	0.144554469
GPI anchor metabolic process (GO:0006505)	44589	0.055875759	0.144554469
RNA phosphodiester bond hydrolysis (GO:00905	44589	0.055875759	0.144554469
cellular zinc ion homeostasis (GO:0006882)	44589	0.055875759	0.144554469
mucosal immune response (GO:0002385)	44589	0.055875759	0.144554469
regulation of GTPase activity (GO:0043087)	2/189	0.057280855	0.144554469
regulation of DNA biosynthetic process (GO:200	44590	0.057813922	0.144554469
transition metal ion homeostasis (GO:0055076)	44590	0.057813922	0.144554469
cell projection organization (GO:0030030)	44591	0.059748204	0.144554469
snRNA 3'-end processing (GO:0034472)	44591	0.059748204	0.144554469
CENP-A containing chromatin organization (GO:	44591	0.059748204	0.144554469
CENP-A containing nucleosome assembly (GO:0	44591	0.059748204	0.144554469
maturation of SSU-rRNA from tricistronic rRNA t	44591	0.059748204	0.144554469
primary neural tube formation (GO:0014020)	44591	0.059748204	0.144554469
zinc ion homeostasis (GO:0055069)	44591	0.059748204	0.144554469
ncRNA catabolic process (GO:0034661)	44591	0.059748204	0.144554469
regulation of intracellular signal transduction (G	3/437	0.059975613	0.144554469
regulation of programmed cell death (GO:0043(	2/194	0.059978311	0.144554469
regulation of cellular senescence (GO:2000772)	44592	0.061678612	0.147000692
tube closure (GO:0060606)	44592	0.061678612	0.147000692
GPI anchor biosynthetic process (GO:0006506)	11689	0.063605153	0.147495192
regulation of centrosome duplication (GO:0010	11689	0.063605153	0.147495192
chondrocyte differentiation (GO:0002062)	11689	0.063605153	0.147495192
chromatin remodeling at centromere (GO:0031(	11689	0.063605153	0.147495192
positive regulation of telomere maintenance (G	11689	0.063605153	0.147495192

exonucleolytic catabolism of deadenylated mRN	12055	0.065527834	0.149528941
positive regulation of telomere maintenance via	12055	0.065527834	0.149528941
negative chemotaxis (GO:0050919)	12055	0.065527834	0.149528941
regulation of protein kinase B signaling (GO:005	2/207	0.067192348	0.151490152
positive regulation of pri-miRNA transcription b	12420	0.067446664	0.151490152
neural tube closure (GO:0001843)	12420	0.067446664	0.151490152
base-excision repair, gap-filling (GO:0006287)	12785	0.06936165	0.154176933
nuclear-transcribed mRNA catabolic process, ex	12785	0.06936165	0.154176933
regulation of cell population proliferation (GO:0	4/764	0.070261695	0.15520828
cyclic-nucleotide-mediated signaling (GO:00199	13150	0.0712728	0.15520828
positive regulation of telomere maintenance via	13150	0.0712728	0.15520828
regulation of ossification (GO:0030278)	13150	0.0712728	0.15520828
centromere complex assembly (GO:0034508)	13516	0.07318012	0.155417185
regulation of p38MAPK cascade (GO:1900744)	13516	0.07318012	0.155417185
phospholipid biosynthetic process (GO:0008654	13516	0.07318012	0.155417185
regulation of protein autophosphorylation (GO:	13516	0.07318012	0.155417185
ncRNA metabolic process (GO:0034660)	13516	0.07318012	0.155417185
histone exchange (GO:0043486)	13881	0.075083618	0.156746897
ncRNA export from nucleus (GO:0097064)	13881	0.075083618	0.156746897
positive regulation of cell motility (GO:2000147	2/221	0.075267741	0.156746897
transcription, DNA-templated (GO:0006351)	2/221	0.075267741	0.156746897
DNA replication-independent nucleosome asser	14246	0.076983303	0.158126955
negative regulation of blood coagulation (GO:0(	14611	0.07887918	0.158126955
positive regulation of cation channel activity (G(	14611	0.07887918	0.158126955
glycolipid biosynthetic process (GO:0009247)	14611	0.07887918	0.158126955
positive regulation of intrinsic apoptotic signalir	14611	0.07887918	0.158126955
ribosomal small subunit biogenesis (GO:004227	14611	0.07887918	0.158126955
negative regulation of protein kinase B signaling	14611	0.07887918	0.158126955
nucleocytoplasmic transport (GO:0006913)	14611	0.07887918	0.158126955
gluconeogenesis (GO:0006094)	14977	0.080771259	0.158948945
response to growth factor (GO:0070848)	14977	0.080771259	0.158948945
import into cell (GO:0098657)	14977	0.080771259	0.158948945
nucleobase-containing compound catabolic pro	14977	0.080771259	0.158948945
ceramide biosynthetic process (GO:0046513)	15342	0.082659545	0.161922123
antibacterial humoral response (GO:0019731)	16072	0.086424772	0.167765734
hexose biosynthetic process (GO:0019319)	16072	0.086424772	0.167765734
regulation of pri-miRNA transcription by RNA pc	16438	0.088301727	0.170637121
regulation of DNA metabolic process (GO:0051(	16803	0.09017492	0.172701074
regulation of fibroblast proliferation (GO:00481	16803	0.09017492	0.172701074
telomere organization (GO:0032200)	17168	0.092044358	0.175497909
base-excision repair (GO:0006284)	17533	0.093910048	0.178262879
RNA catabolic process (GO:0006401)	17899	0.095771998	0.180202575
inner mitochondrial membrane organization (G(	17899	0.095771998	0.180202575
iron ion transport (GO:0006826)	18264	0.097630215	0.181895064
regulation of smoothened signaling pathway (G(	18629	0.099484706	0.181895064
negative regulation of transport (GO:0051051)	18629	0.099484706	0.181895064
cellular component assembly (GO:0022607)	2/261	0.099891122	0.181895064

positive regulation of intracellular signal transdu	3/546	0.100784999	0.181895064
amide biosynthetic process (GO:0043604)	18994	0.101335479	0.181895064
regulation of telomere maintenance via telomer	18994	0.101335479	0.181895064
glycolipid metabolic process (GO:0006664)	18994	0.101335479	0.181895064
cartilage development (GO:0051216)	18994	0.101335479	0.181895064
positive regulation of protein localization to pla	18994	0.101335479	0.181895064
regulation of intrinsic apoptotic signaling pathw	18994	0.101335479	0.181895064
cellular macromolecule catabolic process (GO:0	19360	0.10318254	0.18443879
positive regulation of cell migration (GO:00303	2/269	0.105060466	0.187016349
protein targeting to mitochondrion (GO:000662	20090	0.106865559	0.18829486
ceramide metabolic process (GO:0006672)	20090	0.106865559	0.18829486
telomere maintenance (GO:0000723)	20455	0.10870153	0.18829486
nuclear-transcribed mRNA catabolic process, de	20455	0.10870153	0.18829486
negative regulation of cellular process (GO:004	3/566	0.109252782	0.18829486
regulation of bone mineralization (GO:0030500)	20821	0.11053382	0.18829486
positive regulation of gene expression, epigenet	20821	0.11053382	0.18829486
dicarboxylic acid metabolic process (GO:004364	20821	0.11053382	0.18829486
regulation of tumor necrosis factor-mediated sig	21186	0.112362434	0.18829486
negative regulation of hydrolase activity (GO:00	21186	0.112362434	0.18829486
RNA modification (GO:0009451)	21186	0.112362434	0.18829486
cellular iron ion homeostasis (GO:0006879)	21186	0.112362434	0.18829486
membrane lipid biosynthetic process (GO:00464	21186	0.112362434	0.18829486
nucleosome assembly (GO:0006334)	21186	0.112362434	0.18829486
regulation of phagocytosis (GO:0050764)	21186	0.112362434	0.18829486
positive regulation of transcription by RNA polyr	4/908	0.114076327	0.189869714
positive regulation of apoptotic signaling pathw	21551	0.11418738	0.189869714
RNA methylation (GO:0001510)	21916	0.116008666	0.19215335
positive regulation of DNA biosynthetic process	22282	0.117826298	0.193668513
protein lipidation (GO:0006497)	22282	0.117826298	0.193668513
glucose metabolic process (GO:0006006)	22647	0.119640284	0.195899549
positive regulation of DNA metabolic process (G	23012	0.121450631	0.197357275
neuropeptide signaling pathway (GO:0007218)	23012	0.121450631	0.197357275
regulation of cell cycle (GO:0051726)	2/296	0.123023096	0.198787223
protein secretion (GO:0009306)	23377	0.123257345	0.198787223
DNA repair (GO:0006281)	2/298	0.124382891	0.199851162
tRNA modification (GO:0006400)	23743	0.125060435	0.200190025
embryonic organ development (GO:0048568)	24108	0.126859907	0.202315613
positive regulation of protein localization to nuc	24838	0.130448024	0.207267417
positive regulation of MAP kinase activity (GO:0	25204	0.132236685	0.208564477
positive regulation of protein transport (GO:005	25204	0.132236685	0.208564477
cellular response to light stimulus (GO:0071482)	25569	0.134021755	0.209073938
defense response to Gram-positive bacterium (G	25569	0.134021755	0.209073938
wound healing (GO:0042060)	25569	0.134021755	0.209073938
positive regulation of cellular protein localizatio	25934	0.135803243	0.210323434
regulation of hematopoietic stem cell differenti	25934	0.135803243	0.210323434
regulation of actin filament-based process (GO:0	26665	0.139355499	0.210951828
insulin receptor signaling pathway (GO:000828(	26665	0.139355499	0.210951828

regulation of hydrolase activity (GO:0051336)	26665	0.139355499	0.210951828
chromatin assembly (GO:0031497)	26665	0.139355499	0.210951828
defense response to Gram-negative bacterium (	26665	0.139355499	0.210951828
transcription by RNA polymerase II (GO:000636	2/320	0.139577488	0.210951828
negative regulation of gene expression (GO:001	2/322	0.14097905	0.210951828
regulation of cytokine-mediated signaling pathv	27030	0.141126281	0.210951828
negative regulation of protein binding (GO:0032	27030	0.141126281	0.210951828
sphingolipid biosynthetic process (GO:0030148)	27030	0.141126281	0.210951828
regulation of hematopoietic progenitor cell diffe	27395	0.142893508	0.211491694
nucleic acid phosphodiester bond hydrolysis (GO	27395	0.142893508	0.211491694
regulation of cell division (GO:0051302)	27760	0.144657188	0.211491694
water-soluble vitamin metabolic process (GO:00	27760	0.144657188	0.211491694
cellular protein localization (GO:0034613)	2/329	0.145909104	0.211491694
inorganic cation import across plasma membrar	28126	0.146417326	0.211491694
positive regulation of phosphatidylinositol 3-kin	28126	0.146417326	0.211491694
cellular response to UV (GO:0034644)	28126	0.146417326	0.211491694
positive regulation of protein modification by sr	28126	0.146417326	0.211491694
regulation of organelle assembly (GO:1902115)	28126	0.146417326	0.211491694
positive regulation of proteasomal ubiquitin-dep	28856	0.149927009	0.215112665
positive regulation of ubiquitin-dependent prote	28856	0.149927009	0.215112665
intracellular protein transport (GO:0006886)	2/336	0.150875866	0.215461084
glycerophospholipid metabolic process (GO:000	29221	0.151676567	0.215461084
skin development (GO:0043588)	29221	0.151676567	0.215461084
activation of cysteine-type endopeptidase activi	29587	0.153422612	0.217222113
regulation of G protein-coupled receptor signali	29952	0.15516515	0.218248686
regulation of gene expression, epigenetic (GO:0	29952	0.15516515	0.218248686
response to insulin (GO:0032868)	30682	0.158639735	0.222406688
regulation of cell cycle G2/M phase transition (G	31048	0.160371796	0.224102608
cellular response to DNA damage stimulus (GO:(	2/350	0.160911657	0.224126951
positive regulation of proteasomal protein catal	31413	0.162100378	0.225051981
negative regulation of binding (GO:0051100)	32143	0.165547132	0.22909587
negative regulation of protein kinase activity (G	32874	0.168980052	0.23309467
regulation of stem cell differentiation (GO:2000	33239	0.170691341	0.233950752
regulation of actin cytoskeleton organization (G	33239	0.170691341	0.233950752
positive regulation of cellular component biogen	33604	0.172399192	0.234791281
regulation of peptidyl-tyrosine phosphorylation	33604	0.172399192	0.234791281
protein transport (GO:0015031)	2/369	0.174726758	0.237208162
nucleosome organization (GO:0034728)	34335	0.175804607	0.237693989
positive regulation of protein phosphorylation ((	2/371	0.176192747	0.237693989
cellular transition metal ion homeostasis (GO:00	35065	0.179196349	0.240988193
regulation of MAP kinase activity (GO:0043405)	35431	0.18088711	0.242501781
negative regulation of cell population proliferati	2/379	0.182077141	0.243221146
regulation of peptidyl-serine phosphorylation (G	35796	0.182574472	0.243221146
negative regulation of programmed cell death ((	2/381	0.18355315	0.243221146
response to UV (GO:0009411)	36161	0.184258444	0.243221146
positive regulation of stress-activated MAPK cas	36161	0.184258444	0.243221146
positive regulation of translation (GO:0045727)	1/100	0.18593903	0.244686638

positive regulation of cellular protein metabolic	1/102	0.189290076	0.247577569
regulation of proteasomal ubiquitin-dependent	1/102	0.189290076	0.247577569
chromatin remodeling (GO:0006338)	1/103	0.190960549	0.249003268
cellular response to peptide hormone stimulus (	1/106	0.195951843	0.252442464
positive regulation of protein serine/threonine l	1/106	0.195951843	0.252442464
regulation of phosphatidylinositol 3-kinase signa	1/106	0.195951843	0.252442464
protein localization to nucleus (GO:0034504)	1/106	0.195951843	0.252442464
transmembrane receptor protein tyrosine kinas	2/404	0.200653153	0.257725157
regulation of cell migration (GO:0030334)	2/408	0.203648274	0.259727283
regulation of Wnt signaling pathway (GO:00301	1/111	0.204203983	0.259727283
cellular divalent inorganic cation homeostasis (G	1/111	0.204203983	0.259727283
protein-containing complex subunit organizatio	1/112	0.205844467	0.259727283
regulation of cytoskeleton organization (GO:005	1/112	0.205844467	0.259727283
phosphatidylinositol metabolic process (GO:004	1/112	0.205844467	0.259727283
positive regulation of cellular component organ	1/114	0.209115543	0.263080845
cellular amide metabolic process (GO:0043603)	1/115	0.210746149	0.264081798
regulation of protein-containing complex assem	1/116	0.212373474	0.264081798
sphingolipid metabolic process (GO:0006665)	1/116	0.212373474	0.264081798
tumor necrosis factor-mediated signaling pathw	1/116	0.212373474	0.264081798
positive regulation of protein-containing comple	1/118	0.21561831	0.26657134
regulation of protein binding (GO:0043393)	1/118	0.21561831	0.26657134
positive regulation of cysteine-type endopeptid	1/119	0.217235833	0.267799346
cellular response to organic substance (GO:007	1/123	0.223673447	0.274945297
platelet degranulation (GO:0002576)	1/125	0.226872855	0.277656251
negative regulation of cell growth (GO:0030308	1/126	0.228467731	0.277656251
negative regulation of growth (GO:0045926)	1/126	0.228467731	0.277656251
phosphatidylinositol biosynthetic process (GO:0	1/126	0.228467731	0.277656251
positive regulation of macromolecule biosynthe	1/129	0.233233126	0.281059019
cellular response to insulin stimulus (GO:00328(	1/129	0.233233126	0.281059019
DNA-dependent DNA replication (GO:0006261)	1/129	0.233233126	0.281059019
Golgi organization (GO:0007030)	1/130	0.2348152	0.282172887
RNA metabolic process (GO:0016070)	1/133	0.239542338	0.287049338
protein localization to plasma membrane (GO:0	1/136	0.244240982	0.291864571
transcription initiation from RNA polymerase II	1/140	0.250461803	0.297640203
protein localization to cell periphery (GO:19907	1/140	0.250461803	0.297640203
regulation of small GTPase mediated signal tran	1/141	0.252009185	0.298651769
chromatin organization (GO:0006325)	1/142	0.253553451	0.298964909
positive regulation of cell population proliferatio	2/474	0.253667195	0.298964909
protein-DNA complex assembly (GO:0065004)	1/143	0.255094607	0.299004334
monocarboxylic acid metabolic process (GO:003	1/143	0.255094607	0.299004334
positive regulation of gene expression (GO:001(	2/482	0.259776731	0.303662718
negative regulation of apoptotic process (GO:00	2/485	0.262068867	0.30550963
positive regulation of hydrolase activity (GO:005	1/149	0.264276557	0.307248355
negative regulation of protein phosphorylation	1/152	0.268826032	0.311692885
positive regulation of NF-kappaB transcription fa	1/155	0.273348056	0.316081714
cellular response to growth factor stimulus (GO:	1/158	0.27784279	0.319556453
organonitrogen compound biosynthetic process	1/158	0.27784279	0.319556453

positive regulation of protein kinase B signaling	1/161	0.282310397	0.323826631
regulation of MAPK cascade (GO:0043408)	1/166	0.289696555	0.331412859
cellular protein-containing complex assembly (G	1/168	0.292630208	0.332992995
DNA-templated transcription, initiation (GO:000	1/168	0.292630208	0.332992995
positive regulation of I-kappaB kinase/NF-kappa	1/171	0.297008534	0.336191718
nuclear-transcribed mRNA catabolic process (G(	1/171	0.297008534	0.336191718
positive regulation of ERK1 and ERK2 cascade (G	1/172	0.298462092	0.336947994
defense response to bacterium (GO:0042742)	1/176	0.304247059	0.342577397
protein stabilization (GO:0050821)	1/179	0.308555216	0.345412389
negative regulation of cellular macromolecule b	2/547	0.309413109	0.345412389
positive regulation of cellular biosynthetic proc	1/180	0.309985477	0.345412389
regulated exocytosis (GO:0045055)	1/180	0.309985477	0.345412389
endoplasmic reticulum to Golgi vesicle-mediate	1/185	0.317093595	0.352417493
negative regulation of Wnt signaling pathway (G	1/191	0.325529077	0.360857814
negative regulation of macromolecule metaboli	1/194	0.32970861	0.363611809
cellular response to tumor necrosis factor (GO:(	1/194	0.32970861	0.363611809
protein localization to membrane (GO:0072657)	1/195	0.331096164	0.364205781
negative regulation of intracellular signal transd	1/198	0.335242035	0.367823102
endomembrane system organization (GO:00102	1/199	0.336618413	0.368391069
positive regulation of GTPase activity (GO:0043	1/214	0.356933476	0.388640765
positive regulation of protein modification proc	1/214	0.356933476	0.388640765
extracellular structure organization (GO:004306	1/216	0.359595867	0.390015059
external encapsulating structure organization (G	1/217	0.360923026	0.390015059
regulation of cell growth (GO:0001558)	1/217	0.360923026	0.390015059
positive regulation of cellular process (GO:0048	2/625	0.36818807	0.396866035
regulation of I-kappaB kinase/NF-kappaB signali	1/224	0.370138303	0.39796825
apoptotic process (GO:0006915)	1/231	0.379223893	0.406717625
regulation of ERK1 and ERK2 cascade (GO:0070	1/238	0.388181577	0.415286525
positive regulation of DNA-binding transcription	1/246	0.398264562	0.425013675
positive regulation of signal transduction (GO:0(	1/252	0.405720228	0.431895727
positive regulation of phosphorylation (GO:004	1/253	0.406954046	0.432136846
protein-containing complex assembly (GO:0065	1/267	0.4239673	0.447985152
negative regulation of signal transduction (GO:0	1/267	0.4239673	0.447985152
positive regulation of MAPK cascade (GO:00434	1/274	0.432294416	0.454544864
inorganic cation transmembrane transport (GO:	1/274	0.432294416	0.454544864
positive regulation of transcription, DNA-templa	3/1183	0.44029872	0.46182922
positive regulation of programmed cell death (G	1/286	0.446297041	0.466979099
extracellular matrix organization (GO:0030198)	1/300	0.462207865	0.482450545
innate immune response (GO:0045087)	1/302	0.464444113	0.48359501
MAPK cascade (GO:0000165)	1/303	0.465558832	0.48359501
positive regulation of apoptotic process (GO:00	1/310	0.473298735	0.49044724
cellular macromolecule biosynthetic process (G(	1/314	0.477672322	0.493786569
protein modification by small protein conjugatio	1/409	0.571728188	0.589594694
organelle organization (GO:0006996)	1/420	0.581487254	0.5982207
organelle assembly (GO:0070925)	1/425	0.585851145	0.601268281
nervous system development (GO:0007399)	1/447	0.604530641	0.61895858
regulation of cellular macromolecule biosynthet	1/468	0.621592947	0.634912796

neutrophil degranulation (GO:0043312)	1/481	0.631793129	0.643798699
neutrophil activation involved in immune respo	1/485	0.63487732	0.64540846
neutrophil mediated immunity (GO:0002446)	1/488	0.637173909	0.646211837
positive regulation of nucleic acid-templated tra	1/511	0.654318994	0.662035019
protein ubiquitination (GO:0016567)	1/525	0.664365378	0.670618229
cytokine-mediated signaling pathway (GO:0019	1/621	0.725977522	0.73109004
regulation of transcription by RNA polymerase I	111825	0.845213012	0.849171855
regulation of gene expression (GO:0010468)	1/1079	0.897324522	0.899421075
regulation of transcription, DNA-templated (GO	125645	0.992435217	0.992435217

alysis of significant highly-correlated RNA-seq-based modules (grey60; Significa

Old P-value	Old Adjusted P-value	Odds Ratio	Combined Score	Genes	KEGG
0	0	170.9057143	4307.788562	RSL1D1;NI	.
0	0	66.91764706	1351.196727	RSL1D1;NF	.
0	0	29.08209366	582.5800423	FBL;RSL1D	.
0	0	22.00604134	351.6440283	FBL;EXOSC	.
0	0	21.76153846	302.5729961	FBL;EXOSC	.
0	0	143.1674641	1827.233166	NIFK;RPF2;	.
0	0	112.4718045	1365.65937	MAK16;WI	.
0	0	14.00439342	137.492602	FBL;EXOSC	.
0	0	255.8333333	2482.010933	FBL;NOP58	.
0	0	170.5384615	1548.508344	RACK1;SLC	.
0	0	27.56509695	228.3750478	NPM1;RPF	.
0	0	102.3025641	841.7305533	FBL;EXOSC	.
0	0	102.3025641	841.7305533	CCT5;GNL3	.
0	0	12.29263747	94.06580577	NPM1;RAC	.
0	0	51.12564103	357.2694654	UTP20;WD	.
0	0	44.45039019	299.1775464	RACK1;SLC	.
0	0	34.06666667	212.4695391	RACK1;SLC	.
0	0	28.38034188	167.3266883	IARS1;YARS	.
0	0	10.94000736	62.45696802	EXOSC5;NF	.
0	0	24.91307067	140.8079898	RACK1;SLC	.
0	0	24.91307067	140.8079898	IARS1;YARS	.
0	0	21.72613202	117.2251358	RACK1;SLC	.
0	0	21.2724359	113.9363035	NPM1;RPF	.
0	0	15.94150641	76.7825987	RSL1D1;RA	.
0	0	15.45687646	73.55839224	NPM1;EIF4	.
0	0	7.388875031	34.36790781	EEF1B2;IAF	.
0	0	124.71875	571.7716334	NPM1	.
0	0	124.71875	571.7716334	DDX21	.
0	0	124.71875	571.7716334	RACK1	.
0	0	124.71875	571.7716334	RACK1	.
0	0	124.71875	571.7716334	SLC39A14	.
0	0	124.71875	571.7716334	SLC39A14	.
0	0	124.71875	571.7716334	RACK1	.
0	0	124.71875	571.7716334	UTP20	.
0	0	124.71875	571.7716334	NPM1	.
0	0	124.71875	571.7716334	RACK1	.
0	0	124.71875	571.7716334	PDGFA	.
0	0	124.71875	571.7716334	PDGFA	.
0	0	124.71875	571.7716334	MTHFD1L	.
0	0	124.71875	571.7716334	UTP20	.
0	0	124.71875	571.7716334	UTP20	.
0	0	12.90490101	57.08383766	NPM1;RAC	.
0	0	99.77	439.3037926	RNASE2	.
0	0	99.77	439.3037926	PUS7	.

0	0	99.77	439.3037926	FBL	.
0	0	99.77	439.3037926	RPF2	.
0	0	12.13369963	52.28820472	RACK1;PUS	.
0	0	83.1375	353.3354529	RACK1	.
0	0	83.1375	353.3354529	NPM1	.
0	0	83.1375	353.3354529	NPM1	.
0	0	83.1375	353.3354529	RACK1	.
0	0	83.1375	353.3354529	NPM1	.
0	0	83.1375	353.3354529	NPM1	.
0	0	83.1375	353.3354529	SLC39A14	.
0	0	83.1375	353.3354529	SLC39A14	.
0	0	83.1375	353.3354529	PUS7	.
0	0	83.1375	353.3354529	EXOSC5	.
0	0	11.57983683	48.90207198	RACK1;PUS	.
0	0	11.07413601	45.85502866	RACK1;PUS	.
0	0	71.25714286	293.3998472	NPM1	.
0	0	71.25714286	293.3998472	RACK1	.
0	0	71.25714286	293.3998472	EXOSC5	.
0	0	71.25714286	293.3998472	UTP20	.
0	0	5.912347408	24.05781354	NPM1;RAC	.
0	0	3.622418212	14.71131688	RSL1D1;NP	.
0	0	62.346875	249.430818	MTHFD1L	.
0	0	62.346875	249.430818	EXOSC5	.
0	0	5.671820976	22.47456346	NPM1;APE	.
0	0	9.983408748	39.43799816	EEF1B2;RA	.
0	0	55.41666667	215.9217342	EIF4B	.
0	0	55.41666667	215.9217342	CCT5	.
0	0	55.41666667	215.9217342	PDGFA	.
0	0	55.41666667	215.9217342	RACK1	.
0	0	55.41666667	215.9217342	SLC39A14	.
0	0	55.41666667	215.9217342	GNL3	.
0	0	55.41666667	215.9217342	APEX1	.
0	0	55.41666667	215.9217342	EXOSC5	.
0	0	55.41666667	215.9217342	EXOSC5	.
0	0	55.41666667	215.9217342	MTHFD1L	.
0	0	49.8725	189.6162115	NPM1	.
0	0	49.8725	189.6162115	RACK1	.
0	0	49.8725	189.6162115	RACK1	.
0	0	49.8725	189.6162115	CCT5	.
0	0	49.8725	189.6162115	SGMS2	.
0	0	49.8725	189.6162115	CCT5	.
0	0	49.8725	189.6162115	MTHFD1L	.
0	0	49.8725	189.6162115	RACK1	.
0	0	49.8725	189.6162115	PDGFA	.
0	0	49.8725	189.6162115	RACK1	.
0	0	49.8725	189.6162115	CCT5	.
0	0	45.33636364	168.4701655	TIMM8A	.

0	0	8.772325376	32.58544463	RSL1D1;NP	.
0	0	8.478205128	30.9687196	EXOSC5;AF	.
0	0	41.55625	151.1383993	PUS7	.
0	0	41.55625	151.1383993	MTHFD1L	.
0	0	41.55625	151.1383993	RACK1	.
0	0	41.55625	151.1383993	RACK1	.
0	0	41.55625	151.1383993	RSL1D1	.
0	0	41.55625	151.1383993	NPM1	.
0	0	41.55625	151.1383993	EXOSC5	.
0	0	41.55625	151.1383993	UTP20	.
0	0	8.33837747	30.20703762	EXOSC5;RN	.
0	0	38.35769231	136.7009949	PDGFA	.
0	0	38.35769231	136.7009949	RACK1	.
0	0	38.35769231	136.7009949	GAL	.
0	0	38.35769231	136.7009949	SLC39A14	.
0	0	38.35769231	136.7009949	NIFK	.
0	0	35.61607143	124.5085078	GNL3	.
0	0	35.61607143	124.5085078	CCT5	.
0	0	35.61607143	124.5085078	MTHFD1L	.
0	0	35.61607143	124.5085078	GAL	.
0	0	7.761988647	27.11638145	EXOSC5;RN	.
0	0	7.587064677	26.1946526	RPF2;EIF4E	.
0	0	33.24	114.0899655	RACK1	.
0	0	33.24	114.0899655	PDGFA	.
0	0	33.24	114.0899655	RACK1	.
0	0	33.24	114.0899655	NPM1	.
0	0	33.24	114.0899655	PDGFA	.
0	0	31.1609375	105.0958914	RACK1	.
0	0	31.1609375	105.0958914	PIGW	.
0	0	29.32647059	97.26176224	NPM1	.
0	0	29.32647059	97.26176224	CCT5	.
0	0	29.32647059	97.26176224	EXOSC5	.
0	0	29.32647059	97.26176224	NIFK	.
0	0	29.32647059	97.26176224	RACK1	.
0	0	29.32647059	97.26176224	NPM1	.
0	0	29.32647059	97.26176224	GNL3	.
0	0	27.69583333	90.38385304	MTHFD1L	.
0	0	27.69583333	90.38385304	CCT5	.
0	0	27.69583333	90.38385304	SLC39A14	.
0	0	27.69583333	90.38385304	NPM1	.
0	0	27.69583333	90.38385304	EIF4B	.
0	0	26.23684211	84.30284541	PDGFA	.
0	0	26.23684211	84.30284541	MTHFD1L	.
0	0	26.23684211	84.30284541	RACK1	.
0	0	26.23684211	84.30284541	GAL	.
0	0	6.595071595	21.1221827	TAF4B;RPF	.
0	0	24.92375	78.8924444	RACK1	.

0	0	24.92375	78.8924444	RNASE2	.
0	0	24.92375	78.8924444	FBL	.
0	0	24.92375	78.8924444	SLC39A14	.
0	0	23.73571429	74.05131012	NPM1	.
0	0	23.73571429	74.05131012	PDGFA	.
0	0	23.73571429	74.05131012	FBL	.
0	0	23.73571429	74.05131012	SLC39A14	.
0	0	23.73571429	74.05131012	PUS7	.
0	0	23.73571429	74.05131012	PDGFA	.
0	0	22.65568182	69.69723344	NPM1	.
0	0	22.65568182	69.69723344	RACK1	.
0	0	22.65568182	69.69723344	PDGFA	.
0	0	21.66956522	65.76286225	RELL1	.
0	0	21.66956522	65.76286225	TIMM8A	.
0	0	20.765625	62.19251854	GAL	.
0	0	20.765625	62.19251854	RPF2	.
0	0	20.765625	62.19251854	RACK1	.
0	0	19.934	58.93979602	GNL3	.
0	0	19.934	58.93979602	SGMS2	.
0	0	19.934	58.93979602	FBL	.
0	0	19.934	58.93979602	EXOSC5	.
0	0	19.16634615	55.96572434	GAL	.
0	0	18.45555556	53.23735047	PDGFA	.
0	0	18.45555556	53.23735047	PIGW	.
0	0	18.45555556	53.23735047	RNASE2	.
0	0	18.45555556	53.23735047	SLC39A14	.
0	0	18.45555556	53.23735047	RNASE2	.
0	0	5.422185657	15.50630594	CHN2;RAC	.
0	0	17.79553571	50.72663121	PDGFA	.
0	0	17.79553571	50.72663121	SLC39A14	.
0	0	17.18103448	48.40956011	PDGFA	.
0	0	17.18103448	48.40956011	EXOSC5	.
0	0	17.18103448	48.40956011	NPM1	.
0	0	17.18103448	48.40956011	NPM1	.
0	0	17.18103448	48.40956011	UTP20	.
0	0	17.18103448	48.40956011	MTHFD1L	.
0	0	17.18103448	48.40956011	SLC39A14	.
0	0	17.18103448	48.40956011	EXOSC5	.
0	0	3.551722047	9.993896756	CHN2;TAF4	.
0	0	5.279647436	14.85572552	RSL1D1;AP	.
0	0	16.6075	46.26547336	RSL1D1	.
0	0	16.6075	46.26547336	MTHFD1L	.
0	0	16.07096774	44.27649315	PIGW	.
0	0	16.07096774	44.27649315	NPM1	.
0	0	16.07096774	44.27649315	SLC39A14	.
0	0	16.07096774	44.27649315	NPM1	.
0	0	16.07096774	44.27649315	GNL3	.

0	0	15.56796875	42.42707813	EXOSC5	.
0	0	15.56796875	42.42707813	CCT5	.
0	0	15.56796875	42.42707813	PDGFA	.
0	0	4.941588493	13.34325703	RACK1;PDC	.
0	0	15.09545455	40.70365761	GNL3	.
0	0	15.09545455	40.70365761	MTHFD1L	.
0	0	14.65073529	39.09433195	APEX1	.
0	0	14.65073529	39.09433195	EXOSC5	.
0	0	2.731009957	7.252274807	NPM1;PDC	.
0	0	14.23142857	37.58862573	GAL	.
0	0	14.23142857	37.58862573	CCT5	.
0	0	14.23142857	37.58862573	SGMS2	.
0	0	13.83541667	36.17728305	NPM1	.
0	0	13.83541667	36.17728305	RELL1	.
0	0	13.83541667	36.17728305	SGMS2	.
0	0	13.83541667	36.17728305	PDGFA	.
0	0	13.83541667	36.17728305	NIFK	.
0	0	13.46081081	34.852097	NPM1	.
0	0	13.46081081	34.852097	NPM1	.
0	0	4.622409554	11.95680363	RACK1;PDC	.
0	0	4.622409554	11.95680363	DDX21;TAF	.
0	0	13.10592105	33.6057667	NPM1	.
0	0	12.76923077	32.43177702	PDGFA	.
0	0	12.76923077	32.43177702	GAL	.
0	0	12.76923077	32.43177702	PIGW	.
0	0	12.76923077	32.43177702	RACK1	.
0	0	12.76923077	32.43177702	NPM1	.
0	0	12.76923077	32.43177702	RACK1	.
0	0	12.76923077	32.43177702	NPM1	.
0	0	12.449375	31.32429679	SLC39A14	.
0	0	12.449375	31.32429679	RACK1	.
0	0	12.449375	31.32429679	SLC39A14	.
0	0	12.449375	31.32429679	RNASE2	.
0	0	12.14512195	30.27809233	SGMS2	.
0	0	11.57906977	28.35113154	RNASE2	.
0	0	11.57906977	28.35113154	SLC39A14	.
0	0	11.31534091	27.46228274	GNL3	.
0	0	11.06333333	26.6184236	PDGFA	.
0	0	11.06333333	26.6184236	PDGFA	.
0	0	10.82228261	25.81638924	APEX1	.
0	0	10.59148936	25.05329844	APEX1	.
0	0	10.3703125	24.32652283	RNASE2	.
0	0	10.3703125	24.32652283	TIMM8A	.
0	0	10.15816327	23.6336602	SLC39A14	.
0	0	9.9545	22.97251088	RACK1	.
0	0	9.9545	22.97251088	RACK1	.
0	0	3.900603901	8.985721613	NIFK;PDGF	.

0	0	2.822913638	6.477925543	RACK1;PDC	.
0	0	9.758823529	22.34105716	SGMS2	.
0	0	9.758823529	22.34105716	CCT5	.
0	0	9.758823529	22.34105716	PIGW	.
0	0	9.758823529	22.34105716	SLC39A14	.
0	0	9.758823529	22.34105716	RACK1	.
0	0	9.758823529	22.34105716	RACK1	.
0	0	9.570673077	21.73744506	RNASE2	.
0	0	3.782195333	8.522115231	RACK1;PDC	.
0	0	9.215277778	20.60705391	TIMM8A	.
0	0	9.215277778	20.60705391	SGMS2	.
0	0	9.047272727	20.07724991	APEX1	.
0	0	9.047272727	20.07724991	EXOSC5	.
0	0	2.719827989	6.021946624	NPM1;RAC	.
0	0	8.885267857	19.56921376	SGMS2	.
0	0	8.885267857	19.56921376	DDX21	.
0	0	8.885267857	19.56921376	MTHFD1L	.
0	0	8.728947368	19.08170254	RACK1	.
0	0	8.728947368	19.08170254	SLC39A14	.
0	0	8.728947368	19.08170254	PUS7	.
0	0	8.728947368	19.08170254	SLC39A14	.
0	0	8.728947368	19.08170254	SGMS2	.
0	0	8.728947368	19.08170254	NPM1	.
0	0	8.728947368	19.08170254	RACK1	.
0	0	2.278761062	4.946933941	NPM1;GAL	.
0	0	8.578017241	18.61356393	RACK1	.
0	0	8.43220339	18.16372823	FBL	.
0	0	8.29125	17.73120117	CCT5	.
0	0	8.29125	17.73120117	PIGW	.
0	0	8.154918033	17.31505749	SLC39A14	.
0	0	8.022983871	16.91443512	GNL3	.
0	0	8.022983871	16.91443512	GAL	.
0	0	3.430141287	7.187460322	RACK1;WD	.
0	0	7.895238095	16.52852991	GAL	.
0	0	3.406618157	7.100723005	NPM1;APE	.
0	0	7.771484375	16.156591	PUS7	.
0	0	7.651538462	15.79791644	PDGFA	.
0	0	7.42238806	15.11777461	CCT5	.
0	0	7.312867647	14.79511517	PDGFA	.
0	0	7.312867647	14.79511517	RACK1	.
0	0	7.206521739	14.48332969	NPM1	.
0	0	7.206521739	14.48332969	RNASE2	.
0	0	7.206521739	14.48332969	PDGFA	.
0	0	7.103214286	14.18190957	GNL3	.
0	0	7.103214286	14.18190957	PUS7	.
0	0	6.905208333	13.60828094	PDGFA	.
0	0	6.905208333	13.60828094	SLC39A14	.

0	0	6.905208333	13.60828094	CHN2	.
0	0	6.905208333	13.60828094	NPM1	.
0	0	6.905208333	13.60828094	RNASE2	.
0	0	3.167392356	6.237024297	DDX21;TAI	.
0	0	3.147275641	6.165966121	RACK1;PUS	.
0	0	6.810273973	13.33519869	RACK1	.
0	0	6.810273973	13.33519869	RACK1	.
0	0	6.810273973	13.33519869	SGMS2	.
0	0	6.717905405	13.07073043	PUS7	.
0	0	6.717905405	13.07073043	RNASE2	.
0	0	6.628	12.81449936	RACK1	.
0	0	6.628	12.81449936	MTHFD1L	.
0	0	3.078804987	5.925995868	NPM1;TMI	.
0	0	6.540460526	12.56614975	SLC39A14	.
0	0	6.540460526	12.56614975	PDGFA	.
0	0	6.540460526	12.56614975	NPM1	.
0	0	6.540460526	12.56614975	GNL3	.
0	0	6.540460526	12.56614975	NPM1	.
0	0	6.372115385	12.0917689	RACK1	.
0	0	6.372115385	12.0917689	RACK1	.
0	0	3.013204361	5.69886696	NPM1;TMI	.
0	0	6.291139241	11.86511927	PIGW	.
0	0	6.291139241	11.86511927	PDGFA	.
0	0	6.2121875	11.64511197	RACK1	.
0	0	6.135185185	11.43147733	SLC39A14	.
0	0	6.135185185	11.43147733	DDX21	.
0	0	5.986746988	11.0223164	SLC39A14	.
0	0	5.915178571	10.8263173	NPM1	.
0	0	2.889920424	5.279594976	NPM1;APE	.
0	0	5.845294118	10.63574365	RACK1	.
0	0	5.710344828	10.2700514	RACK1	.
0	0	5.581460674	9.923695342	NPM1	.
0	0	5.519166667	9.757325781	PUS7	.
0	0	5.519166667	9.757325781	PDGFA	.
0	0	5.458241758	9.595275738	RACK1	.
0	0	5.458241758	9.595275738	PDGFA	.
0	0	2.737651086	4.775919678	NPM1;TMI	.
0	0	5.340322581	9.283521129	NPM1	.
0	0	2.722534918	4.726801771	RACK1;PDC	.
0	0	5.227368421	8.98727419	SLC39A14	.
0	0	5.17265625	8.844632572	PDGFA	.
0	0	2.66367408	4.537102195	NPM1;UTP	.
0	0	5.119072165	8.705479391	RACK1	.
0	0	2.649347135	4.491308396	NPM1;TNF	.
0	0	5.066581633	8.569696843	NPM1	.
0	0	5.066581633	8.569696843	RELL1	.
0	0	5.015151515	8.437172211	NPM1	.

0	0	4.915346535	8.181469682	NPM1	.
0	0	4.915346535	8.181469682	RACK1	.
0	0	4.866911765	8.058089471	NPM1	.
0	0	4.727142857	7.704705622	SLC39A14	.
0	0	4.727142857	7.704705622	PDGFA	.
0	0	4.727142857	7.704705622	PDGFA	.
0	0	4.727142857	7.704705622	RPF2	.
0	0	2.494833525	4.007145396	PDGFA;SLC	.
0	0	2.469748642	3.930261472	RACK1;PDC	.
0	0	4.511136364	7.166553044	RACK1	.
0	0	4.511136364	7.166553044	SLC39A14	.
0	0	4.47027027	7.065863017	NIFK	.
0	0	4.47027027	7.065863017	PDGFA	.
0	0	4.47027027	7.065863017	PIGW	.
0	0	4.390707965	6.87087989	RACK1	.
0	0	4.351973684	6.77646239	MTHFD1L	.
0	0	4.313913043	6.684015202	RACK1	.
0	0	4.313913043	6.684015202	SGMS2	.
0	0	4.313913043	6.684015202	TNFRSF6B	.
0	0	4.23974359	6.504807607	RACK1	.
0	0	4.23974359	6.504807607	RACK1	.
0	0	4.203601695	6.417940218	RACK1	.
0	0	4.064959016	6.087553018	RACK1	.
0	0	3.998991935	5.931966787	PDGFA	.
0	0	3.9668	5.856426032	RACK1	.
0	0	3.9668	5.856426032	RACK1	.
0	0	3.9668	5.856426032	PIGW	.
0	0	3.873242188	5.63834367	NPM1	.
0	0	3.873242188	5.63834367	SLC39A14	.
0	0	3.873242188	5.63834367	DDX21	.
0	0	3.843023256	5.568373364	TMED6	.
0	0	3.755113636	5.366151639	RNASE2	.
0	0	3.671111111	5.174797898	PIGW	.
0	0	3.564748201	4.935211563	TAF4B	.
0	0	3.564748201	4.935211563	PIGW	.
0	0	3.539107143	4.877915071	CHN2	.
0	0	3.513829787	4.821609151	NPM1	.
0	0	2.117231638	2.904274656	NPM1;PDG	.
0	0	3.488908451	4.766270388	NPM1	.
0	0	3.488908451	4.766270388	MTHFD1L	.
0	0	2.081089744	2.80516901	NPM1;DDX	.
0	0	2.067845198	2.769150677	NPM1;TNF	.
0	0	3.346452703	4.453322581	RACK1	.
0	0	3.279470199	4.30820993	RACK1	.
0	0	3.215097403	4.170011448	NPM1	.
0	0	3.153184713	4.038283119	RACK1	.
0	0	3.153184713	4.038283119	SGMS2	.

0	0	3.09359375	3.912616867	PDGFA	.
0	0	2.999090909	3.715637503	PDGFA	.
0	0	2.962874251	3.640914861	EIF4B	.
0	0	2.962874251	3.640914861	TAF4B	.
0	0	2.910147059	3.532902252	DDX21	.
0	0	2.910147059	3.532902252	EXOSC5	.
0	0	2.892982456	3.497940812	PDGFA	.
0	0	2.826285714	3.363040366	RNASE2	.
0	0	2.778230337	3.266794555	CCT5	.
0	0	1.826770172	2.14294385	RACK1;PUS	.
0	0	2.762569832	3.235604199	NPM1	.
0	0	2.762569832	3.235604199	PDGFA	.
0	0	2.686820652	3.085970151	TMED6	.
0	0	2.601184211	2.919318122	RACK1	.
0	0	2.560362694	2.840840224	RACK1	.
0	0	2.560362694	2.840840224	TNFRSF6B	.
0	0	2.547036082	2.815357213	PIGW	.
0	0	2.50786802	2.740855268	RACK1	.
0	0	2.495075758	2.7166517	TMED6	.
0	0	2.317605634	2.387610896	RACK1	.
0	0	2.317605634	2.387610896	RACK1	.
0	0	2.295813953	2.3480999	PDGFA	.
0	0	2.285069444	2.328692715	PDGFA	.
0	0	2.285069444	2.328692715	RACK1	.
0	0	1.591636828	1.590302099	NPM1;PDG	.
0	0	2.212556054	2.199012008	DDX21	.
0	0	2.144456522	2.079326165	YARS1	.
0	0	2.080379747	1.968626048	PDGFA	.
0	0	2.011632653	1.851987002	NPM1	.
0	0	1.962948207	1.770758794	SLC39A14	.
0	0	1.955059524	1.757706059	RACK1	.
0	0	1.850845865	1.58820889	NIFK	.
0	0	1.850845865	1.58820889	RACK1	.
0	0	1.802747253	1.511871107	PDGFA	.
0	0	1.802747253	1.511871107	SLC39A14	.
0	0	1.256400535	1.030627712	NPM1;GAL	.
0	0	1.725789474	1.3923161	RACK1	.
0	0	1.643812709	1.26859695	PDGFA	.
0	0	1.632724252	1.25215916	RNASE2	.
0	0	1.627235099	1.244048579	PDGFA	.
0	0	1.589805825	1.189220091	RACK1	.
0	0	1.569169329	1.159349846	EEF1B2	.
0	0	1.197977941	0.669779399	RACK1	.
0	0	1.165871122	0.632095948	TMED6	.
0	0	1.15182783	0.615870293	NPM1	.
0	0	1.093778027	0.550501677	TIMM8A	.
0	0	1.043468951	0.496138	PDGFA	.

0	0	1.01453125	0.465865919	RNASE2	.
0	0	1.005940083	0.457022215	RNASE2	.
0	0	0.999589322	0.45052755	RNASE2	.
0	0	0.953382353	0.404386934	NPM1	.
0	0	0.927242366	0.379170741	RACK1	.
0	0	0.779798387	0.249719692	TNFRSF6B	.
0	0	0.636309339	0.107005977	NPM1;GAL	.
0	0	0.437871058	0.047437942	RACK1	.
0	0	0.197458761	0.001499411	NPM1	.

ıntterms were highlighted)

Term	Overlap	P-value	Adjusted P-value	Old P-value
Ribosome biogenesis in eukaryotes	3/108	0.001406018	0.049210621	0
Aminoacyl-tRNA biosynthesis	24139	0.008094901	0.141660771	0
One carbon pool by folate	44581	0.040229788	0.372446658	0
Glycosylphosphatidylinositol (GPI)-anc	44587	0.051987755	0.372446658	0
RNA transport	2/186	0.05568372	0.372446658	0
Base excision repair	12055	0.065527834	0.372446658	0
Ferroptosis	14977	0.080771259	0.372446658	0
Basal transcription factors	16438	0.088301727	0.372446658	0
Sphingolipid metabolism	17899	0.095771998	0.372446658	0
Melanoma	26299	0.137581155	0.399381658	0
Glioma	27395	0.142893508	0.399381658	0
RNA degradation	28856	0.149927009	0.399381658	0
PI3K-Akt signaling pathway	2/354	0.1638024	0.399381658	0
Gap junction	32143	0.165547132	0.399381658	0
Prostate cancer	35431	0.18088711	0.399381658	0
Choline metabolism in cancer	35796	0.182574472	0.399381658	0
Sphingolipid signaling pathway	1/119	0.217235833	0.447250245	0
Fluid shear stress and atherosclerosis	1/139	0.248911297	0.451489815	0
Measles	1/139	0.248911297	0.451489815	0
Phospholipase D signaling pathway	1/148	0.262753938	0.451489815	0
mTOR signaling pathway	1/154	0.271843754	0.451489815	0
JAK-STAT signaling pathway	1/162	0.283793598	0.451489815	0
Transcriptional misregulation in cance	1/192	0.326925072	0.469580096	0
Focal adhesion	1/201	0.339362832	0.469580096	0
Proteoglycans in cancer	1/205	0.344818482	0.469580096	0
Rap1 signaling pathway	1/210	0.35157626	0.469580096	0
Regulation of actin cytoskeleton	1/218	0.362247502	0.469580096	0
Ras signaling pathway	1/232	0.380511352	0.471555807	0
Calcium signaling pathway	1/240	0.390717669	0.471555807	0
MAPK signaling pathway	1/294	0.455444322	0.501983506	0
Cytokine-cytokine receptor interactio	1/295	0.456577313	0.501983506	0
Huntington disease	1/306	0.468889426	0.501983506	0
MicroRNAs in cancer	1/310	0.473298735	0.501983506	0
Neuroactive ligand-receptor interactic	1/341	0.506281008	0.521171626	0
Pathways in cancer	1/531	0.668583244	0.668583244	0

Old Adjusted P-value	Odds Ratio	Combined Score	Genes
0	14.92781955	98.03089942	FBL;NOP58;GNL3
0	15.94150641	76.7825987	IARS1;YARS1
0	26.23684211	84.30284541	MTHFD1L
0	19.934	58.93979602	PIGW
0	5.511426979	15.91737293	EIF3J;EIF4B
0	15.56796875	42.42707813	APEX1
0	12.449375	31.32429679	SLC39A14
0	11.31534091	27.46228274	TAF4B
0	10.3703125	24.32652283	SGMS2
0	7.002816901	13.89037664	PDGFA
0	6.717905405	13.07073043	PDGFA
0	6.372115385	12.0917689	EXOSC5
0	2.856497669	5.167674103	PDGFA;EIF4B
0	5.710344828	10.2700514	PDGFA
0	5.17265625	8.844632572	PDGFA
0	5.119072165	8.705479391	PDGFA
0	4.203601695	6.417940218	SGMS2
0	3.59076087	4.99352278	PDGFA
0	3.59076087	4.99352278	RACK1
0	3.369387755	4.503312352	PDGFA
0	3.23627451	4.215337551	EIF4B
0	3.074223602	3.872009445	PDGFA
0	2.587434555	2.892814637	PDGFA
0	2.469875	2.669157956	PDGFA
0	2.420955882	2.577681644	EIF4B
0	2.362440191	2.469526383	PDGFA
0	2.274423963	2.309512849	PDGFA
0	2.135064935	2.062983581	PDGFA
0	2.062761506	1.938521494	PDGFA
0	1.677986348	1.319705733	PDGFA
0	1.672193878	1.310995371	TNFRSF6B
0	1.610983607	1.22014014	TAF4B
0	1.589805825	1.189220091	PDGFA
0	1.442573529	0.981907021	GAL
0	0.916462264	0.368962544	PDGFA

Supplementary File S6: Comprehensive details of the results of functional enrichment analysis o

BP	Term	Overlap	P-value	Adjusted P-value
	polarized epithelial cell differentiation (GO:0030859)	44634	1.95E-04	0.138839615
	import into cell (GO:0098657)	15067	3.73E-04	0.138839615
	protein deacetylation (GO:0006476)	16528	5.35E-04	0.138839615
	regulation of gene expression, epigenetic (GO:0040029	30072	6.21E-04	0.138839615
	response to progesterone (GO:0032570)	44641	6.81E-04	0.138839615
	proline transmembrane transport (GO:0035524)	44597	6.82E-04	0.138839615
	diacylglycerol metabolic process (GO:0046339)	44643	8.96E-04	0.155337506
	regulation of protein depolymerization (GO:1901879)	44598	0.001016939	0.155337506
	positive regulation of gene expression, epigenetic (GO:	20911	0.001312517	0.173023895
	positive regulation of adenylate cyclase activity (GO:00	44599	0.001415907	0.173023895
	spermidine metabolic process (GO:0008216)	44600	0.001877529	0.191195083
	store-operated calcium entry (GO:0002115)	44600	0.001877529	0.191195083
	regulation of store-operated calcium entry (GO:200125	44602	0.002984503	0.227941379
	glycine transport (GO:0015816)	44602	0.002984503	0.227941379
	lipid phosphorylation (GO:0046834)	44602	0.002984503	0.227941379
	lung epithelium development (GO:0060428)	44602	0.002984503	0.227941379
	Wnt signaling pathway, calcium modulating pathway ((	13210	0.003334934	0.239722902
	glycerolipid metabolic process (GO:0046486)	44603	0.00362777	0.24628527
	protein acylation (GO:0043543)	14305	0.004191357	0.247324882
	morphogenesis of a polarized epithelium (GO:0001738	44604	0.004329524	0.247324882
	acylglycerol metabolic process (GO:0006639)	15036	0.004829806	0.247324882
	regulation of autophagosome maturation (GO:190109(	44605	0.005088754	0.247324882
	polyamine metabolic process (GO:0006595)	44605	0.005088754	0.247324882
	vascular transport (GO:0010232)	30773	0.005388643	0.247324882
	transport across blood-brain barrier (GO:0150104)	31503	0.00585504	0.247324882
	positive regulation of cyclase activity (GO:0031281)	44606	0.005904465	0.247324882
	regulation of neuron projection arborization (GO:0150(	44607	0.00677567	0.247324882
	regulation of nuclear-transcribed mRNA catabolic proc(	44607	0.00677567	0.247324882
	establishment of apical/basal cell polarity (GO:003508(	44607	0.00677567	0.247324882
	G protein-coupled glutamate receptor signaling pathwa	44607	0.00677567	0.247324882
	positive regulation of lyase activity (GO:0051349)	44607	0.00677567	0.247324882
	positive regulation of nuclear-transcribed mRNA catab(	44607	0.00677567	0.247324882
	protein localization to cell-cell junction (GO:0150105)	44607	0.00677567	0.247324882
	nitrogen compound transport (GO:0071705)	5/143	0.007043911	0.247324882
	histone deacetylation (GO:0016575)	17227	0.007083773	0.247324882
	3'-UTR-mediated mRNA destabilization (GO:0061158)	44608	0.007701398	0.261419678
	inorganic cation transmembrane transport (GO:00986(	7/274	0.008305689	0.271994916
	regulation of metal ion transport (GO:0010959)	44609	0.008680689	0.271994916
	modified amino acid transport (GO:0072337)	44609	0.008680689	0.271994916
	organic acid transport (GO:0015849)	4/100	0.009885486	0.295219325
	positive regulation of programmed cell death (GO:004(	7/286	0.010361039	0.295219325
	glycerolipid catabolic process (GO:0046503)	44611	0.010796178	0.295219325
	response to ATP (GO:0033198)	44611	0.010796178	0.295219325
	establishment of epithelial cell polarity (GO:0090162)	44612	0.011930517	0.295219325

post-transcriptional gene silencing by RNA (GO:003519	44612	0.011930517	0.295219325
regulation of calcium ion transport (GO:0051924)	21245	0.012611761	0.295219325
positive regulation of protein binding (GO:0032092)	21245	0.012611761	0.295219325
regulation of cell-substrate junction assembly (GO:009(	44613	0.013114697	0.295219325
cellular response to steroid hormone stimulus (GO:007	44613	0.013114697	0.295219325
regulation of Wnt signaling pathway (GO:0030111)	4/111	0.014076092	0.295219325
amino acid import (GO:0043090)	44614	0.014347817	0.295219325
regulation of adenylate cyclase activity (GO:0045761)	44614	0.014347817	0.295219325
negative regulation of interleukin-2 production (GO:00	44614	0.014347817	0.295219325
protein localization to cell junction (GO:1902414)	44614	0.014347817	0.295219325
histone modification (GO:0016570)	4/114	0.015386965	0.295219325
positive regulation of apoptotic process (GO:0043065)	7/310	0.015546822	0.295219325
peptidyl-L-cysteine S-palmitoylation (GO:0018230)	44615	0.015628989	0.295219325
peptidyl-S-diacylglycerol-L-cysteine biosynthetic proces	44615	0.015628989	0.295219325
positive regulation of cholesterol efflux (GO:0010875)	44615	0.015628989	0.295219325
positive regulation of interleukin-17 production (GO:00	44615	0.015628989	0.295219325
protein deacylation (GO:0035601)	44615	0.015628989	0.295219325
amino acid import across plasma membrane (GO:0089	44616	0.016957333	0.295219325
regulation of cellular catabolic process (GO:0031329)	23802	0.017115484	0.295219325
inorganic anion transmembrane transport (GO:009866	23802	0.017115484	0.295219325
transcription by RNA polymerase II (GO:0006366)	7/320	0.018175041	0.295219325
negative regulation of cellular carbohydrate metabolic	44617	0.018331982	0.295219325
negative regulation of actin filament polymerization (G	44617	0.018331982	0.295219325
non-canonical Wnt signaling pathway (GO:0035567)	4/124	0.020301497	0.295219325
negative regulation of protein polymerization (GO:003	44619	0.021216783	0.295219325
positive regulation of gene silencing by miRNA (GO:200	44619	0.021216783	0.295219325
neutral amino acid transport (GO:0015804)	44620	0.022725255	0.295219325
regulation of reactive oxygen species biosynthetic proc	44620	0.022725255	0.295219325
response to ketone (GO:1901654)	44620	0.022725255	0.295219325
L-amino acid transport (GO:0015807)	44620	0.022725255	0.295219325
sulfur compound transport (GO:0072348)	44620	0.022725255	0.295219325
regulation of actin filament polymerization (GO:00308	26724	0.023226692	0.295219325
regulation of gluconeogenesis (GO:0006111)	47150	0.024276673	0.295219325
regulation of cell motility (GO:2000145)	4/133	0.025465419	0.295219325
negative regulation of cytoskeleton organization (GO:0	10990	0.025870223	0.295219325
negative regulation of gene expression, epigenetic (GO	10990	0.025870223	0.295219325
organic substance transport (GO:0071702)	4/136	0.027346777	0.295219325
protein palmitoylation (GO:0018345)	11355	0.027505102	0.295219325
negative regulation of osteoblast differentiation (GO:0(	11355	0.027505102	0.295219325
vitamin transport (GO:0051180)	11355	0.027505102	0.295219325
regulation of angiogenesis (GO:0045765)	5/203	0.027959792	0.295219325
establishment or maintenance of epithelial cell apical/l	11720	0.029180519	0.295219325
gene silencing by miRNA (GO:0035195)	11720	0.029180519	0.295219325
regulation of protein localization to plasma membrane	29281	0.029422035	0.295219325
regulation of cholesterol efflux (GO:0010874)	12086	0.030895691	0.295219325
regulation of interleukin-17 production (GO:0032660)	12086	0.030895691	0.295219325
positive regulation of cholesterol transport (GO:00323	12086	0.030895691	0.295219325

regulation of G protein-coupled receptor signaling path	30011	0.03133693	0.295219325
chromatin organization (GO:0006325)	4/142	0.031353261	0.295219325
receptor-mediated endocytosis (GO:0006898)	4/143	0.032052812	0.295219325
long-chain fatty acid metabolic process (GO:0001676)	30376	0.032318377	0.295219325
epithelial tube morphogenesis (GO:0060562)	12451	0.032649846	0.295219325
response to steroid hormone (GO:0048545)	12451	0.032649846	0.295219325
acylglycerol catabolic process (GO:0046464)	12816	0.034442222	0.295219325
semaphorin-plexin signaling pathway (GO:0071526)	12816	0.034442222	0.295219325
lung development (GO:0030324)	12816	0.034442222	0.295219325
negative regulation of fat cell differentiation (GO:0045	13181	0.036272066	0.295219325
retina homeostasis (GO:0001895)	13181	0.036272066	0.295219325
protein targeting to membrane (GO:0006612)	31837	0.036403283	0.295219325
glutamate receptor signaling pathway (GO:0007215)	13547	0.038138635	0.295219325
positive regulation of binding (GO:0051099)	32933	0.039632791	0.295219325
sodium ion transport (GO:0006814)	32933	0.039632791	0.295219325
protein complex oligomerization (GO:0051259)	32933	0.039632791	0.295219325
mRNA destabilization (GO:0061157)	13912	0.040041198	0.295219325
negative regulation of autophagosome maturation (GO	44566	0.041062395	0.295219325
protein sialylation (GO:1990743)	44566	0.041062395	0.295219325
ADP transport (GO:0015866)	44566	0.041062395	0.295219325
alpha-beta T cell differentiation (GO:0046632)	44566	0.041062395	0.295219325
pyrimidine nucleobase biosynthetic process (GO:00198	44566	0.041062395	0.295219325
auditory receptor cell morphogenesis (GO:0002093)	44566	0.041062395	0.295219325
auditory receptor cell stereocilium organization (GO:0(	44566	0.041062395	0.295219325
negative regulation of heterochromatin assembly (GO:(	44566	0.041062395	0.295219325
cannabinoid signaling pathway (GO:0038171)	44566	0.041062395	0.295219325
negative regulation of metallopeptidase activity (GO:19	44566	0.041062395	0.295219325
regulation of inflammatory response to wounding (GO:	44566	0.041062395	0.295219325
nephric duct development (GO:0072176)	44566	0.041062395	0.295219325
neutral lipid catabolic process (GO:0046461)	44566	0.041062395	0.295219325
regulation of NK T cell proliferation (GO:0051140)	44566	0.041062395	0.295219325
regulation of platelet-derived growth factor receptor-b	44566	0.041062395	0.295219325
regulation of postsynaptic density organization (GO:19(	44566	0.041062395	0.295219325
enamel mineralization (GO:0070166)	44566	0.041062395	0.295219325
plus-end-directed vesicle transport along microtubule (	44566	0.041062395	0.295219325
PML body organization (GO:0030578)	44566	0.041062395	0.295219325
establishment of monopolar cell polarity (GO:0061162)	44566	0.041062395	0.295219325
establishment of T cell polarity (GO:0001768)	44566	0.041062395	0.295219325
regulation of sterol transport (GO:0032371)	44566	0.041062395	0.295219325
fructose catabolic process (GO:0006001)	44566	0.041062395	0.295219325
fructose catabolic process to hydroxyacetone phospha	44566	0.041062395	0.295219325
glucose import in response to insulin stimulus (GO:004	44566	0.041062395	0.295219325
positive regulation of endothelial cell chemotaxis by VE	44566	0.041062395	0.295219325
positive regulation of histone H3-K27 methylation (GO:	44566	0.041062395	0.295219325
positive regulation of leukocyte tethering or rolling (GC	44566	0.041062395	0.295219325
isocitrate metabolic process (GO:0006102)	44566	0.041062395	0.295219325
long-chain fatty acid catabolic process (GO:0042758)	44566	0.041062395	0.295219325

positive regulation of protein catabolic process in the v	44566	0.041062395	0.295219325
positive regulation of protein localization to cilium (GO	44566	0.041062395	0.295219325
mammary gland duct morphogenesis (GO:0060603)	44566	0.041062395	0.295219325
medium-chain fatty acid catabolic process (GO:005179	44566	0.041062395	0.295219325
positive regulation of store-operated calcium channel a	44566	0.041062395	0.295219325
mesonephric duct development (GO:0072177)	44566	0.041062395	0.295219325
metanephric distal tubule development (GO:0072235)	44566	0.041062395	0.295219325
metanephric nephron tubule morphogenesis (GO:0072	44566	0.041062395	0.295219325
protein C-linked glycosylation via 2'-alpha-mannosyl-L-t	44566	0.041062395	0.295219325
protein C-linked glycosylation via tryptophan (GO:0018	44566	0.041062395	0.295219325
peptidyl-serine phosphorylation (GO:0018105)	4/156	0.041980607	0.295219325
response to organonitrogen compound (GO:0010243)	14642	0.04395142	0.295219325
carboxylic acid transmembrane transport (GO:1905039	15008	0.04595766	0.295219325
regulation of ubiquitin-dependent protein catabolic pro	15373	0.047997055	0.295219325
histone H3 acetylation (GO:0043966)	15373	0.047997055	0.295219325
negative regulation of CD8-positive, alpha-beta T cell a	44567	0.049071505	0.295219325
amino-acid betaine transport (GO:0015838)	44567	0.049071505	0.295219325
negative regulation of erythrocyte differentiation (GO:(	44567	0.049071505	0.295219325
regulation of excitatory synapse assembly (GO:190488	44567	0.049071505	0.295219325
cellular response to granulocyte macrophage colony-st	44567	0.049071505	0.295219325
regulation of hormone biosynthetic process (GO:00468	44567	0.049071505	0.295219325
neurotransmitter receptor transport, endosome to pos	44567	0.049071505	0.295219325
cobalamin transport (GO:0015889)	44567	0.049071505	0.295219325
plus-end-directed organelle transport along microtubul	44567	0.049071505	0.295219325
regulation of protein localization to cilium (GO:190356	44567	0.049071505	0.295219325
positive regulation of autophagosome maturation (GO:	44567	0.049071505	0.295219325
establishment of lymphocyte polarity (GO:0001767)	44567	0.049071505	0.295219325
establishment of mitochondrion localization, microtubu	44567	0.049071505	0.295219325
guanine nucleotide transmembrane transport (GO:190	44567	0.049071505	0.295219325
response to DNA damage checkpoint signaling (GO:007	44567	0.049071505	0.295219325
positive regulation of hemoglobin biosynthetic process	44567	0.049071505	0.295219325
response to granulocyte macrophage colony-stimulatin	44567	0.049071505	0.295219325
sialylation (GO:0097503)	44567	0.049071505	0.295219325
positive regulation of neurotransmitter secretion (GO:(	44567	0.049071505	0.295219325
positive regulation of nuclear cell cycle DNA replication	44567	0.049071505	0.295219325
T-tubule organization (GO:0033292)	44567	0.049071505	0.295219325
medium-chain fatty acid biosynthetic process (GO:0051	44567	0.049071505	0.295219325
transcription-dependent tethering of RNA polymerase	44567	0.049071505	0.295219325
transmembrane receptor protein tyrosine phosphatase	44567	0.049071505	0.295219325
metanephric collecting duct development (GO:007220	44567	0.049071505	0.295219325
proline transport (GO:0015824)	44567	0.049071505	0.295219325
regulation of cytokine production involved in inflamma	15738	0.050068921	0.295219325
positive regulation of axonogenesis (GO:0050772)	15738	0.050068921	0.295219325
lipid modification (GO:0030258)	15738	0.050068921	0.295219325
tRNA aminoacylation for protein translation (GO:00064	15738	0.050068921	0.295219325
phosphorylation (GO:0016310)	7/400	0.051071051	0.295219325
positive regulation of mRNA catabolic process (GO:006	16103	0.05217258	0.295219325

intracellular steroid hormone receptor signaling pathw	16103	0.05217258	0.295219325
mRNA catabolic process (GO:0006402)	16103	0.05217258	0.295219325
epithelial cell differentiation (GO:0030855)	3/101	0.052664182	0.295219325
membrane organization (GO:0061024)	5/242	0.052670221	0.295219325
regulation of transcription, DNA-templated (GO:00063	26/2244	0.052725104	0.295219325
negative regulation of gene expression (GO:0010629)	6/322	0.053571446	0.295219325
cell junction assembly (GO:0034329)	3/102	0.053939541	0.295219325
positive regulation of vasculature development (GO:19	3/102	0.053939541	0.295219325
amino acid transmembrane transport (GO:0003333)	16469	0.054307363	0.295219325
regulation of insulin receptor signaling pathway (GO:0(	16469	0.054307363	0.295219325
erythrocyte differentiation (GO:0030218)	16834	0.056472611	0.295219325
negative regulation of cell cycle phase transition (GO:1	44568	0.057014122	0.295219325
negative regulation of centriole replication (GO:00466(	44568	0.057014122	0.295219325
pyrimidine ribonucleotide biosynthetic process (GO:00	44568	0.057014122	0.295219325
pyrimidine-containing compound biosynthetic process	44568	0.057014122	0.295219325
receptor-mediated endocytosis of virus by host cell (G(	44568	0.057014122	0.295219325
regulation of CD8-positive, alpha-beta T cell differentia	44568	0.057014122	0.295219325
regulation of chromatin assembly or disassembly (GO:(	44568	0.057014122	0.295219325
regulation of cortisol biosynthetic process (GO:200006	44568	0.057014122	0.295219325
regulation of hemoglobin biosynthetic process (GO:004	44568	0.057014122	0.295219325
regulation of histone H3-K27 methylation (GO:006108	44568	0.057014122	0.295219325
chemical homeostasis within a tissue (GO:0048875)	44568	0.057014122	0.295219325
neurotransmitter receptor transport, endosome to pla	44568	0.057014122	0.295219325
regulation of ketone biosynthetic process (GO:001056(	44568	0.057014122	0.295219325
nicotinamide nucleotide biosynthetic process (GO:001	44568	0.057014122	0.295219325
citrulline metabolic process (GO:0000052)	44568	0.057014122	0.295219325
regulation of lysosomal protein catabolic process (GO:1	44568	0.057014122	0.295219325
regulation of metallopeptidase activity (GO:1905048)	44568	0.057014122	0.295219325
regulation of miRNA mediated inhibition of translation	44568	0.057014122	0.295219325
definitive hemopoiesis (GO:0060216)	44568	0.057014122	0.295219325
pantothenate metabolic process (GO:0015939)	44568	0.057014122	0.295219325
polyamine biosynthetic process (GO:0006596)	44568	0.057014122	0.295219325
positive regulation of amyloid-beta clearance (GO:190(	44568	0.057014122	0.295219325
regulation of vascular associated smooth muscle cell di	44568	0.057014122	0.295219325
glyceraldehyde-3-phosphate metabolic process (GO:00	44568	0.057014122	0.295219325
hemostasis (GO:0007599)	44568	0.057014122	0.295219325
positive regulation of microtubule nucleation (GO:009(	44568	0.057014122	0.295219325
positive regulation of miRNA mediated inhibition of tra	44568	0.057014122	0.295219325
L-alanine transport (GO:0015808)	44568	0.057014122	0.295219325
leukotriene transport (GO:0071716)	44568	0.057014122	0.295219325
surfactant homeostasis (GO:0043129)	44568	0.057014122	0.295219325
metanephric nephron tubule development (GO:00722	44568	0.057014122	0.295219325
positive regulation of unsaturated fatty acid biosynthet	44568	0.057014122	0.295219325
very long-chain fatty acid catabolic process (GO:00427(	44568	0.057014122	0.295219325
cation transport (GO:0006812)	4/174	0.058286487	0.295219325
regulation of cell cycle process (GO:0010564)	3/106	0.059187998	0.295219325
chromosome organization (GO:0051276)	3/106	0.059187998	0.295219325

negative regulation of mitotic cell cycle (GO:0045930)	17564	0.060891908	0.295219325
regulation of interleukin-2 production (GO:0032663)	17564	0.060891908	0.295219325
nucleus organization (GO:0006997)	17564	0.060891908	0.295219325
phosphatidic acid biosynthetic process (GO:0006654)	17564	0.060891908	0.295219325
positive regulation of blood vessel endothelial cell migr	17564	0.060891908	0.295219325
glycerophospholipid biosynthetic process (GO:0046474	4/177	0.061290559	0.295219325
negative regulation of catabolic process (GO:0009895)	17930	0.063144682	0.295219325
RNA catabolic process (GO:0006401)	17930	0.063144682	0.295219325
protein localization to presynapse (GO:1905383)	44569	0.064890794	0.295219325
ammonium transmembrane transport (GO:0072488)	44569	0.064890794	0.295219325
anterograde axonal protein transport (GO:0099641)	44569	0.064890794	0.295219325
axo-dendritic protein transport (GO:0099640)	44569	0.064890794	0.295219325
negative regulation of lipid kinase activity (GO:009021	44569	0.064890794	0.295219325
negative regulation of vascular associated smooth mus	44569	0.064890794	0.295219325
collecting duct development (GO:0072044)	44569	0.064890794	0.295219325
osteoblast development (GO:0002076)	44569	0.064890794	0.295219325
peptidyl-lysine deacetylation (GO:0034983)	44569	0.064890794	0.295219325
peptidyl-serine autophosphorylation (GO:0036289)	44569	0.064890794	0.295219325
regulation of phospholipase A2 activity (GO:0032429)	44569	0.064890794	0.295219325
positive regulation of astrocyte differentiation (GO:004	44569	0.064890794	0.295219325
positive regulation of CD4-positive, alpha-beta T cell di	44569	0.064890794	0.295219325
positive regulation of cell migration by vascular endoth	44569	0.064890794	0.295219325
regulation of transcription from RNA polymerase II pro	44569	0.064890794	0.295219325
internal protein amino acid acetylation (GO:0006475)	44569	0.064890794	0.295219325
positive regulation of neuron projection arborization (G	44569	0.064890794	0.295219325
snRNA transcription by RNA polymerase III (GO:004279	44569	0.064890794	0.295219325
lens fiber cell differentiation (GO:0070306)	44569	0.064890794	0.295219325
macromolecule modification (GO:0043412)	44569	0.064890794	0.295219325
tRNA aminoacylation for mitochondrial protein transla	44569	0.064890794	0.295219325
progesterone receptor signaling pathway (GO:0050847	44569	0.064890794	0.295219325
myeloid leukocyte mediated immunity (GO:0002444)	44569	0.064890794	0.295219325
negative regulation of alpha-beta T cell differentiation	44569	0.064890794	0.295219325
positive regulation of nucleic acid-templated transcript	8/511	0.06528571	0.295219325
amino acid transport (GO:0006865)	18295	0.06542537	0.295219325
chloride transmembrane transport (GO:1902476)	18295	0.06542537	0.295219325
phosphatidic acid metabolic process (GO:0046473)	18295	0.06542537	0.295219325
negative regulation of BMP signaling pathway (GO:003	19025	0.070068027	0.295219325
plasma membrane bounded cell projection morphoger	19025	0.070068027	0.295219325
response to peptide hormone (GO:0043434)	19025	0.070068027	0.295219325
positive regulation of protein localization to cell periph	19025	0.070068027	0.295219325
positive regulation of protein localization to plasma me	19025	0.070068027	0.295219325
myeloid cell differentiation (GO:0030099)	19025	0.070068027	0.295219325
regulation of transcription by RNA polymerase II (GO:0	25/2206	0.07014391	0.295219325
calcium ion transport (GO:0006816)	3/115	0.071833029	0.295219325
cellular amide metabolic process (GO:0043603)	3/115	0.071833029	0.295219325
alpha-amino acid biosynthetic process (GO:1901607)	44570	0.072702065	0.295219325
quaternary ammonium group transport (GO:0015697)	44570	0.072702065	0.295219325

regulation of aspartic-type endopeptidase activity invo	44570	0.072702065	0.295219325
biotin metabolic process (GO:0006768)	44570	0.072702065	0.295219325
regulation of cell adhesion molecule production (GO:0(	44570	0.072702065	0.295219325
regulation of cellular extravasation (GO:0002691)	44570	0.072702065	0.295219325
regulation of cellular response to oxidative stress (GO:1	44570	0.072702065	0.295219325
negative regulation of protein-containing complex disa	44570	0.072702065	0.295219325
negative regulation of smooth muscle cell differentiatic	44570	0.072702065	0.295219325
neurotransmitter receptor transport to postsynaptic m	44570	0.072702065	0.295219325
regulation of lipid transport (GO:0032368)	44570	0.072702065	0.295219325
detection of mechanical stimulus involved in sensory p	44570	0.072702065	0.295219325
regulation of nuclear cell cycle DNA replication (GO:00	44570	0.072702065	0.295219325
peroxisomal transport (GO:0043574)	44570	0.072702065	0.295219325
fucose catabolic process (GO:0019317)	44570	0.072702065	0.295219325
positive regulation of fatty acid beta-oxidation (GO:003	44570	0.072702065	0.295219325
icosanoid transport (GO:0071715)	44570	0.072702065	0.295219325
inner ear receptor cell development (GO:0060119)	44570	0.072702065	0.295219325
semaphorin-plexin signaling pathway involved in axon g	44570	0.072702065	0.295219325
L-fucose catabolic process (GO:0042355)	44570	0.072702065	0.295219325
L-fucose metabolic process (GO:0042354)	44570	0.072702065	0.295219325
positive regulation of angiogenesis (GO:0045766)	3/116	0.0733073	0.295219325
regulation of focal adhesion assembly (GO:0051893)	19756	0.074815045	0.295219325
regulation of proteasomal protein catabolic process (G	19756	0.074815045	0.295219325
unsaturated fatty acid metabolic process (GO:0033559	19756	0.074815045	0.295219325
regulation of protein binding (GO:0043393)	3/118	0.076296214	0.295219325
negative regulation of cell differentiation (GO:0045596	4/191	0.07636686	0.295219325
negative regulation of Wnt signaling pathway (GO:003(	4/191	0.07636686	0.295219325
regulation of blood vessel endothelial cell migration (G	20121	0.077226213	0.295219325
alanine transport (GO:0032328)	44571	0.080448474	0.295219325
amino sugar metabolic process (GO:0006040)	44571	0.080448474	0.295219325
negative regulation of glycolytic process (GO:0045820)	44571	0.080448474	0.295219325
regulation of carbohydrate biosynthetic process (GO:0(	44571	0.080448474	0.295219325
cAMP biosynthetic process (GO:0006171)	44571	0.080448474	0.295219325
negative regulation of purine nucleotide metabolic pro	44571	0.080448474	0.295219325
chloride ion homeostasis (GO:0055064)	44571	0.080448474	0.295219325
neuron projection maintenance (GO:1990535)	44571	0.080448474	0.295219325
regulation of leukocyte tethering or rolling (GO:190323	44571	0.080448474	0.295219325
regulation of microtubule nucleation (GO:0010968)	44571	0.080448474	0.295219325
DNA damage response, signal transduction by p53 clas	44571	0.080448474	0.295219325
peptidyl-lysine acetylation (GO:0018394)	44571	0.080448474	0.295219325
phagosome-lysosome fusion (GO:0090385)	44571	0.080448474	0.295219325
ectoderm development (GO:0007398)	44571	0.080448474	0.295219325
regulation of T-helper 17 type immune response (GO:2	44571	0.080448474	0.295219325
genetic imprinting (GO:0071514)	44571	0.080448474	0.295219325
immunoglobulin mediated immune response (GO:001(	44571	0.080448474	0.295219325
inner ear receptor cell stereocilium organization (GO:0(	44571	0.080448474	0.295219325
lactation (GO:0007595)	44571	0.080448474	0.295219325
lipoprotein transport (GO:0042953)	44571	0.080448474	0.295219325

low-density lipoprotein particle receptor catabolic proc	44571	0.080448474	0.295219325
low-density lipoprotein receptor particle metabolic pro	44571	0.080448474	0.295219325
positive regulation of receptor recycling (GO:0001921)	44571	0.080448474	0.295219325
monovalent inorganic anion homeostasis (GO:0055083	44571	0.080448474	0.295219325
myelin maintenance (GO:0043217)	44571	0.080448474	0.295219325
N-acetylneuraminate metabolic process (GO:0006054)	44571	0.080448474	0.295219325
negative regulation of alpha-beta T cell proliferation (G	44571	0.080448474	0.295219325
carboxylic acid transport (GO:0046942)	20852	0.082120986	0.297501491
icosanoid metabolic process (GO:0006690)	20852	0.082120986	0.297501491
regulation of signal transduction (GO:0009966)	4/198	0.084542722	0.297501491
protein targeting (GO:0006605)	3/125	0.087170368	0.297501491
negative regulation of calcium ion transmembrane trar	44572	0.088130556	0.297501491
negative regulation of centrosome duplication (GO:001	44572	0.088130556	0.297501491
regulation of biosynthetic process (GO:0009889)	44572	0.088130556	0.297501491
regulation of calcium ion transmembrane transport via	44572	0.088130556	0.297501491
B cell mediated immunity (GO:0019724)	44572	0.088130556	0.297501491
calcineurin-NFAT signaling cascade (GO:0033173)	44572	0.088130556	0.297501491
negative regulation of platelet-derived growth factor re	44572	0.088130556	0.297501491
negative regulation of potassium ion transmembrane t	44572	0.088130556	0.297501491
regulation of gene expression by genetic imprinting (G	44572	0.088130556	0.297501491
chromatin-mediated maintenance of transcription (GO	44572	0.088130556	0.297501491
regulation of mitochondrial depolarization (GO:005190	44572	0.088130556	0.297501491
regulation of mRNA 3'-end processing (GO:0031440)	44572	0.088130556	0.297501491
DNA damage response, signal transduction resulting in	44572	0.088130556	0.297501491
regulation of phospholipase activity (GO:0010517)	44572	0.088130556	0.297501491
establishment of epithelial cell apical/basal polarity (G	44572	0.088130556	0.297501491
fatty acid homeostasis (GO:0055089)	44572	0.088130556	0.297501491
regulation of T cell mediated immunity (GO:0002709)	44572	0.088130556	0.297501491
positive regulation of DNA-dependent DNA replication	44572	0.088130556	0.297501491
positive regulation of lipid localization (GO:1905954)	44572	0.088130556	0.297501491
skeletal muscle cell differentiation (GO:0035914)	44572	0.088130556	0.297501491
positive regulation of posttranscriptional gene silencing	44572	0.088130556	0.297501491
lipoprotein localization (GO:0044872)	44572	0.088130556	0.297501491
telomere maintenance via recombination (GO:000072	44572	0.088130556	0.297501491
protein kinase C signaling (GO:0070528)	44572	0.088130556	0.297501491
negative regulation of activated T cell proliferation (GO	44572	0.088130556	0.297501491
circulatory system development (GO:0072359)	3/126	0.088774831	0.298850809
peptidyl-threonine phosphorylation (GO:0018107)	21947	0.089635821	0.29985111
homophilic cell adhesion via plasma membrane adhesi	21947	0.089635821	0.29985111
regulation of endocytosis (GO:0030100)	22313	0.092184621	0.29985111
protein lipidation (GO:0006497)	22313	0.092184621	0.29985111
negative regulation of nucleic acid-templated transcrip	7/464	0.09468857	0.29985111
negative regulation of calcineurin-mediated signaling ((	44573	0.095748843	0.29985111
negative regulation of calcineurin-NFAT signaling casca	44573	0.095748843	0.29985111
regulation of actin filament depolymerization (GO:003(	44573	0.095748843	0.29985111
regulation of alcohol biosynthetic process (GO:190293(	44573	0.095748843	0.29985111
ATP transport (GO:0015867)	44573	0.095748843	0.29985111

regulation of astrocyte differentiation (GO:0048710)	44573	0.095748843	0.29985111
regulation of CD4-positive, alpha-beta T cell differentia	44573	0.095748843	0.29985111
calcineurin-mediated signaling (GO:0097720)	44573	0.095748843	0.29985111
negative regulation of receptor internalization (GO:000	44573	0.095748843	0.29985111
regulation of leukocyte cell-cell adhesion (GO:1903037	44573	0.095748843	0.29985111
nuclear body organization (GO:0030575)	44573	0.095748843	0.29985111
P-body assembly (GO:0033962)	44573	0.095748843	0.29985111
digestive system development (GO:0055123)	44573	0.095748843	0.29985111
phagolysosome assembly (GO:0001845)	44573	0.095748843	0.29985111
phospholipid homeostasis (GO:0055091)	44573	0.095748843	0.29985111
regulation of response to oxidative stress (GO:1902882	44573	0.095748843	0.29985111
glutamine metabolic process (GO:0006541)	44573	0.095748843	0.29985111
regulation of ventricular cardiac muscle cell action pote	44573	0.095748843	0.29985111
positive regulation of fatty acid oxidation (GO:0046321	44573	0.095748843	0.29985111
tricarboxylic acid metabolic process (GO:0072350)	44573	0.095748843	0.29985111
positive regulation of T-helper 17 type immune respon	44573	0.095748843	0.29985111
mitotic G1/S transition checkpoint signaling (GO:00448	44573	0.095748843	0.29985111
negative regulation of transcription, DNA-templated (G	12/948	0.099789763	0.29985111
plasma membrane organization (GO:0007009)	23408	0.099955155	0.29985111
lipid homeostasis (GO:0055088)	23408	0.099955155	0.29985111
regulation of cell adhesion (GO:0030155)	3/133	0.100347686	0.29985111
regulation of cell-matrix adhesion (GO:0001952)	23774	0.102584988	0.29985111
alpha-linolenic acid metabolic process (GO:0036109)	44574	0.10330386	0.29985111
antifungal innate immune response (GO:0061760)	44574	0.10330386	0.29985111
negative regulation of gluconeogenesis (GO:0045721)	44574	0.10330386	0.29985111
negative regulation of hippo signaling (GO:0035331)	44574	0.10330386	0.29985111
negative regulation of potassium ion transport (GO:004	44574	0.10330386	0.29985111
negative regulation of reactive oxygen species biosynth	44574	0.10330386	0.29985111
negative regulation of stem cell differentiation (GO:200	44574	0.10330386	0.29985111
chromatin organization involved in regulation of transc	44574	0.10330386	0.29985111
regulation of leukocyte adhesion to vascular endotheli	44574	0.10330386	0.29985111
cytoplasmic sequestering of protein (GO:0051220)	44574	0.10330386	0.29985111
detection of calcium ion (GO:0005513)	44574	0.10330386	0.29985111
positive regulation of adaptive immune response base	44574	0.10330386	0.29985111
positive regulation of CD4-positive, alpha-beta T cell ac	44574	0.10330386	0.29985111
fatty acid elongation (GO:0030497)	44574	0.10330386	0.29985111
glucose import (GO:0046323)	44574	0.10330386	0.29985111
positive regulation of fatty acid biosynthetic process (G	44574	0.10330386	0.29985111
positive regulation of histone deacetylation (GO:00310	44574	0.10330386	0.29985111
high-density lipoprotein particle assembly (GO:003438	44574	0.10330386	0.29985111
positive regulation of insulin receptor signaling pathwa	44574	0.10330386	0.29985111
homeostasis of number of cells (GO:0048872)	44574	0.10330386	0.29985111
positive regulation of lipid transport (GO:0032370)	44574	0.10330386	0.29985111
semaphorin-plexin signaling pathway involved in neuro	44574	0.10330386	0.29985111
positive regulation of nuclear-transcribed mRNA poly(A	44574	0.10330386	0.29985111
spinal cord development (GO:0021510)	44574	0.10330386	0.29985111
mitochondrion transport along microtubule (GO:00474	44574	0.10330386	0.29985111

protein heterotetramerization (GO:0051290)	44574	0.10330386	0.29985111
cell-cell junction assembly (GO:0007043)	24139	0.105233805	0.303571462
regulation of protein localization (GO:0032880)	24139	0.105233805	0.303571462
anion transmembrane transport (GO:0098656)	24504	0.107901111	0.303571462
peptidyl-threonine modification (GO:0018210)	24504	0.107901111	0.303571462
positive regulation of gene expression (GO:0010628)	7/482	0.109830736	0.303571462
potassium ion transmembrane transport (GO:0071805)	3/139	0.110722328	0.303571462
2-oxoglutarate metabolic process (GO:0006103)	44575	0.110796131	0.303571462
pyrimidine nucleoside biosynthetic process (GO:00461	44575	0.110796131	0.303571462
aorta development (GO:0035904)	44575	0.110796131	0.303571462
regulation of cell projection organization (GO:0031344	44575	0.110796131	0.303571462
cAMP metabolic process (GO:0046058)	44575	0.110796131	0.303571462
regulation of fatty acid beta-oxidation (GO:0031998)	44575	0.110796131	0.303571462
negative regulation of smooth muscle cell migration (G	44575	0.110796131	0.303571462
regulation of histone deacetylation (GO:0031063)	44575	0.110796131	0.303571462
neurotransmitter biosynthetic process (GO:0042136)	44575	0.110796131	0.303571462
cytoplasmic sequestering of transcription factor (GO:0(	44575	0.110796131	0.303571462
positive regulation of alpha-beta T cell differentiation (	44575	0.110796131	0.303571462
positive regulation of brown fat cell differentiation (GO	44575	0.110796131	0.303571462
positive regulation of cellular response to insulin stimu	44575	0.110796131	0.303571462
genitalia development (GO:0048806)	44575	0.110796131	0.303571462
positive regulation of granulocyte macrophage colony-	44575	0.110796131	0.303571462
positive regulation of protein deacetylation (GO:00903	44575	0.110796131	0.303571462
synaptic membrane adhesion (GO:0099560)	44575	0.110796131	0.303571462
positive regulation of protein-containing complex disas	44575	0.110796131	0.303571462
T cell differentiation in thymus (GO:0033077)	44575	0.110796131	0.303571462
transcription, DNA-templated (GO:0006351)	4/221	0.114228385	0.305488553
regulation of small GTPase mediated signal transductio	3/141	0.114269238	0.305488553
establishment of protein localization to membrane (GC	25600	0.116009109	0.305488553
fatty acid catabolic process (GO:0009062)	25600	0.116009109	0.305488553
pyrimidine nucleoside metabolic process (GO:0006213	44576	0.118226172	0.305488553
androgen receptor signaling pathway (GO:0030521)	44576	0.118226172	0.305488553
regulation of aerobic respiration (GO:1903715)	44576	0.118226172	0.305488553
regulation of clathrin-dependent endocytosis (GO:200(	44576	0.118226172	0.305488553
regulation of endothelial cell chemotaxis (GO:2001026	44576	0.118226172	0.305488553
cellular response to ATP (GO:0071318)	44576	0.118226172	0.305488553
regulation of extracellular matrix disassembly (GO:001(	44576	0.118226172	0.305488553
regulation of extracellular matrix organization (GO:190	44576	0.118226172	0.305488553
regulation of lymphocyte activation (GO:0051249)	44576	0.118226172	0.305488553
detection of mechanical stimulus involved in sensory p	44576	0.118226172	0.305488553
regulation of nuclear-transcribed mRNA poly(A) tail sho	44576	0.118226172	0.305488553
fatty acid beta-oxidation using acyl-CoA oxidase (GO:0(	44576	0.118226172	0.305488553
ganglioside biosynthetic process (GO:0001574)	44576	0.118226172	0.305488553
glucan catabolic process (GO:0009251)	44576	0.118226172	0.305488553
positive regulation of endothelial cell chemotaxis (GO:2	44576	0.118226172	0.305488553
glycogen catabolic process (GO:0005980)	44576	0.118226172	0.305488553
RNA phosphodiester bond hydrolysis, endonucleolytic (	44576	0.118226172	0.305488553

steroid hormone mediated signaling pathway (GO:004	44576	0.118226172	0.305488553
mammary gland epithelium development (GO:006118(	44576	0.118226172	0.305488553
medium-chain fatty acid metabolic process (GO:00517	44576	0.118226172	0.305488553
mitotic recombination (GO:0006312)	44576	0.118226172	0.305488553
protein tetramerization (GO:0051262)	25965	0.11874555	0.305488553
fatty acid biosynthetic process (GO:0006633)	25965	0.11874555	0.305488553
positive regulation of cellular protein localization (GO:1	25965	0.11874555	0.305488553
regulation of TOR signaling (GO:0032006)	25965	0.11874555	0.305488553
negative regulation of supramolecular fiber organizatio	26330	0.121498104	0.310681128
protein phosphorylation (GO:0006468)	7/496	0.122451634	0.310681128
negative regulation of cell adhesion (GO:0007162)	26696	0.124266315	0.310681128
regulation of actin filament-based process (GO:003297	26696	0.124266315	0.310681128
positive regulation of JNK cascade (GO:0046330)	26696	0.124266315	0.310681128
regulation of amyloid-beta clearance (GO:1900221)	44577	0.125594499	0.310681128
body fluid secretion (GO:0007589)	44577	0.125594499	0.310681128
cellular polysaccharide catabolic process (GO:0044247)	44577	0.125594499	0.310681128
cellular response to corticosteroid stimulus (GO:00713	44577	0.125594499	0.310681128
regulation of fatty acid oxidation (GO:0046320)	44577	0.125594499	0.310681128
regulation of granulocyte macrophage colony-stimulati	44577	0.125594499	0.310681128
neural tube development (GO:0021915)	44577	0.125594499	0.310681128
neuron projection organization (GO:0106027)	44577	0.125594499	0.310681128
regulation of oxidative phosphorylation (GO:0002082)	44577	0.125594499	0.310681128
regulation of Rac protein signal transduction (GO:0035(	44577	0.125594499	0.310681128
response to organophosphorus (GO:0046683)	44577	0.125594499	0.310681128
positive regulation of leukocyte adhesion to vascular e	44577	0.125594499	0.310681128
mitotic sister chromatid cohesion (GO:0007064)	44577	0.125594499	0.310681128
motor neuron axon guidance (GO:0008045)	44577	0.125594499	0.310681128
regulation of autophagy (GO:0010506)	4/231	0.128393945	0.312920575
brain development (GO:0007420)	3/150	0.13074588	0.312920575
regulation of BMP signaling pathway (GO:0030510)	27791	0.132660428	0.312920575
regulation of cell division (GO:0051302)	27791	0.132660428	0.312920575
chloride transport (GO:0006821)	27791	0.132660428	0.312920575
water-soluble vitamin metabolic process (GO:0006767)	27791	0.132660428	0.312920575
negative regulation of ATP metabolic process (GO:1903	44578	0.132901619	0.312920575
activation of protein kinase A activity (GO:0034199)	44578	0.132901619	0.312920575
adenylate cyclase-activating adrenergic receptor signal	44578	0.132901619	0.312920575
pulmonary valve morphogenesis (GO:0003184)	44578	0.132901619	0.312920575
purine ribonucleotide transport (GO:0015868)	44578	0.132901619	0.312920575
aorta morphogenesis (GO:0035909)	44578	0.132901619	0.312920575
negative regulation of peptidyl-threonine phosphorylat	44578	0.132901619	0.312920575
cellular biogenic amine biosynthetic process (GO:0042	44578	0.132901619	0.312920575
regulation of receptor recycling (GO:0001919)	44578	0.132901619	0.312920575
regulation of steroid biosynthetic process (GO:005081(	44578	0.132901619	0.312920575
positive regulation of cyclin-dependent protein serine/	44578	0.132901619	0.312920575
positive regulation of cytokine production involved in i	44578	0.132901619	0.312920575
regulation of transferase activity (GO:0051338)	44578	0.132901619	0.312920575
response to purine-containing compound (GO:001407	44578	0.132901619	0.312920575

positive regulation of regulated secretory pathway (GO	44578	0.132901619	0.312920575
mesonephric tubule development (GO:0072164)	44578	0.132901619	0.312920575
positive regulation of transcription of Notch receptor t	44578	0.132901619	0.312920575
protein heterooligomerization (GO:0051291)	44578	0.132901619	0.312920575
negative regulation of amyloid-beta formation (GO:19(	44578	0.132901619	0.312920575
actin filament organization (GO:0007015)	3/152	0.134516214	0.316113102
negative regulation of biosynthetic process (GO:00098	44579	0.140148039	0.316563593
adenine nucleotide transport (GO:0051503)	44579	0.140148039	0.316563593
negative regulation of cation transmembrane transport	44579	0.140148039	0.316563593
pulmonary valve development (GO:0003177)	44579	0.140148039	0.316563593
regulation of B cell differentiation (GO:0045577)	44579	0.140148039	0.316563593
regulation of brown fat cell differentiation (GO:009033	44579	0.140148039	0.316563593
regulation of cartilage development (GO:0061035)	44579	0.140148039	0.316563593
regulation of catabolic process (GO:0009894)	44579	0.140148039	0.316563593
cellular response to glucocorticoid stimulus (GO:00713	44579	0.140148039	0.316563593
chromatin disassembly (GO:0031498)	44579	0.140148039	0.316563593
regulation of membrane depolarization (GO:0003254)	44579	0.140148039	0.316563593
nucleosome disassembly (GO:0006337)	44579	0.140148039	0.316563593
regulation of mRNA polyadenylation (GO:1900363)	44579	0.140148039	0.316563593
regulation of oxidative stress-induced intrinsic apoptot	44579	0.140148039	0.316563593
regulation of presynapse assembly (GO:1905606)	44579	0.140148039	0.316563593
regulation of presynapse organization (GO:0099174)	44579	0.140148039	0.316563593
positive chemotaxis (GO:0050918)	44579	0.140148039	0.316563593
positive regulation of cell migration involved in sprouti	44579	0.140148039	0.316563593
positive regulation of glial cell differentiation (GO:0045	44579	0.140148039	0.316563593
intracellular estrogen receptor signaling pathway (GO:(	44579	0.140148039	0.316563593
positive regulation of stress-activated protein kinase si	44579	0.140148039	0.316563593
regulation of neuron differentiation (GO:0045664)	28887	0.141179659	0.318305431
negative regulation of cellular response to growth facto	29252	0.144045241	0.318659231
regulation of fat cell differentiation (GO:0045598)	29252	0.144045241	0.318659231
positive regulation of cell adhesion (GO:0045785)	29252	0.144045241	0.318659231
actin filament capping (GO:0051693)	44580	0.14733426	0.318659231
negative regulation of cytokine production involved in	44580	0.14733426	0.318659231
barbed-end actin filament capping (GO:0051016)	44580	0.14733426	0.318659231
regulation of centriole replication (GO:0046599)	44580	0.14733426	0.318659231
negative regulation of oxidative stress-induced intrinsic	44580	0.14733426	0.318659231
cellular response to glucagon stimulus (GO:0071377)	44580	0.14733426	0.318659231
negative regulation of T cell receptor signaling pathway	44580	0.14733426	0.318659231
detection of mechanical stimulus (GO:0050982)	44580	0.14733426	0.318659231
regulation of neuroinflammatory response (GO:015007	44580	0.14733426	0.318659231
DNA alkylation (GO:0006305)	44580	0.14733426	0.318659231
DNA methylation or demethylation (GO:0044728)	44580	0.14733426	0.318659231
establishment or maintenance of apical/basal cell polar	44580	0.14733426	0.318659231
regulation of stem cell population maintenance (GO:20	44580	0.14733426	0.318659231
fatty acid transmembrane transport (GO:1902001)	44580	0.14733426	0.318659231
regulation of synaptic vesicle exocytosis (GO:2000300)	44580	0.14733426	0.318659231
positive regulation of cilium assembly (GO:0045724)	44580	0.14733426	0.318659231

histone deubiquitination (GO:0016578)	44580	0.14733426	0.318659231
long-term memory (GO:0007616)	44580	0.14733426	0.318659231
vesicle transport along actin filament (GO:0030050)	44580	0.14733426	0.318659231
negative regulation of amyloid precursor protein catab	44580	0.14733426	0.318659231
protein autophosphorylation (GO:0046777)	3/159	0.148001351	0.319536485
cell-cell junction organization (GO:0045216)	29983	0.149812714	0.321839915
ephrin receptor signaling pathway (GO:0048013)	29983	0.149812714	0.321839915
cellular protein modification process (GO:0006464)	12/1025	0.149858356	0.321839915
regulation of interleukin-1 beta production (GO:00326	30348	0.15271381	0.32375827
regulation of osteoblast differentiation (GO:0045667)	30348	0.15271381	0.32375827
protein-DNA complex disassembly (GO:0032986)	44581	0.154460779	0.32375827
adrenergic receptor signaling pathway (GO:0071875)	44581	0.154460779	0.32375827
regulation of hippo signaling (GO:0035330)	44581	0.154460779	0.32375827
regulation of lymphocyte differentiation (GO:0045619)	44581	0.154460779	0.32375827
regulation of nuclear division (GO:0051783)	44581	0.154460779	0.32375827
regulation of protein localization to cell periphery (GO:	44581	0.154460779	0.32375827
regulation of smooth muscle cell migration (GO:00149	44581	0.154460779	0.32375827
fatty acid transport (GO:0015908)	44581	0.154460779	0.32375827
positive regulation of cyclin-dependent protein kinase a	44581	0.154460779	0.32375827
hepaticobiliary system development (GO:0061008)	44581	0.154460779	0.32375827
inositol phosphate-mediated signaling (GO:0048016)	44581	0.154460779	0.32375827
mesoderm development (GO:0007498)	44581	0.154460779	0.32375827
regulation of cytokinesis (GO:0032465)	30713	0.155625959	0.325085337
response to insulin (GO:0032868)	30713	0.155625959	0.325085337
heart development (GO:0007507)	3/164	0.157891921	0.326260039
Wnt signaling pathway, planar cell polarity pathway (G	31079	0.158548777	0.326260039
regulation of intracellular signal transduction (GO:1902	6/437	0.159764977	0.326260039
regulation of Ras protein signal transduction (GO:0046	31444	0.161481885	0.326260039
actin filament-based transport (GO:0099515)	44582	0.161528088	0.326260039
regulation of cholesterol metabolic process (GO:00901	44582	0.161528088	0.326260039
negative regulation of response to wounding (GO:1903	44582	0.161528088	0.326260039
regulation of fibroblast migration (GO:0010762)	44582	0.161528088	0.326260039
negative regulation of small GTPase mediated signal tra	44582	0.161528088	0.326260039
regulation of lipid catabolic process (GO:0050994)	44582	0.161528088	0.326260039
cobalamin metabolic process (GO:0009235)	44582	0.161528088	0.326260039
nuclear envelope organization (GO:0006998)	44582	0.161528088	0.326260039
cyclic purine nucleotide metabolic process (GO:005265	44582	0.161528088	0.326260039
response to glucagon (GO:0033762)	44582	0.161528088	0.326260039
intracellular lipid transport (GO:0032365)	44582	0.161528088	0.326260039
intrinsic apoptotic signaling pathway in response to DN	44582	0.161528088	0.326260039
linoleic acid metabolic process (GO:0043651)	44582	0.161528088	0.326260039
positive regulation of transcription from RNA polymera	44582	0.161528088	0.326260039
NAD biosynthetic process (GO:0009435)	44582	0.161528088	0.326260039
protein localization to chromatin (GO:0071168)	44582	0.161528088	0.326260039
calcium ion transmembrane transport (GO:0070588)	31809	0.164424912	0.331016875
sodium ion transmembrane transport (GO:0035725)	31809	0.164424912	0.331016875
DNA-templated transcription, initiation (GO:0006352)	3/168	0.165947833	0.332716995

regulation of establishment of planar polarity (GO:009(	32174	0.167377491	0.332716995
peptidyl-serine modification (GO:0018209)	3/169	0.167980739	0.332716995
protein mannosylation (GO:0035268)	44583	0.168536677	0.332716995
negative regulation of myeloid cell differentiation (GO:	44583	0.168536677	0.332716995
negative regulation of small molecule metabolic proces	44583	0.168536677	0.332716995
positive regulation of axon extension (GO:0045773)	44583	0.168536677	0.332716995
regulation of vacuole organization (GO:0044088)	44583	0.168536677	0.332716995
positive regulation of lipid catabolic process (GO:0050(	44583	0.168536677	0.332716995
positive regulation of peptidase activity (GO:0010952)	44583	0.168536677	0.332716995
tetrapyrrole metabolic process (GO:0033013)	44583	0.168536677	0.332716995
protein import into peroxisome membrane (GO:00450	44583	0.168536677	0.332716995
cell-cell adhesion via plasma-membrane adhesion mole	3/170	0.170020978	0.335105863
protein import (GO:0017038)	32540	0.17033926	0.335192554
supramolecular fiber organization (GO:0097435)	5/351	0.170939004	0.335831935
neuron projection development (GO:0031175)	3/171	0.172068431	0.337508222
negative regulation of cellular macromolecule biosynth	7/547	0.17425649	0.338775912
negative regulation of reactive oxygen species metabol	44584	0.175487031	0.338775912
oligosaccharide biosynthetic process (GO:0009312)	44584	0.175487031	0.338775912
DNA methylation (GO:0006306)	44584	0.175487031	0.338775912
regulation of peptidase activity (GO:0052547)	44584	0.175487031	0.338775912
ERK1 and ERK2 cascade (GO:0070371)	44584	0.175487031	0.338775912
regulation of steroid metabolic process (GO:0019218)	44584	0.175487031	0.338775912
regulation of supramolecular fiber organization (GO:19	44584	0.175487031	0.338775912
response to nutrient levels (GO:0031667)	44584	0.175487031	0.338775912
vesicle transport along microtubule (GO:0047496)	44584	0.175487031	0.338775912
regulation of actin cytoskeleton organization (GO:0032	33270	0.176288949	0.339252118
regulation of stem cell differentiation (GO:2000736)	33270	0.176288949	0.339252118
carbohydrate biosynthetic process (GO:0016051)	44585	0.182379631	0.344996764
negative regulation of NIK/NF-kappaB signaling (GO:19	44585	0.182379631	0.344996764
negative regulation of stress fiber assembly (GO:00514	44585	0.182379631	0.344996764
defense response to fungus (GO:0050832)	44585	0.182379631	0.344996764
phospholipid catabolic process (GO:0009395)	44585	0.182379631	0.344996764
positive regulation of cellular response to transforming	44585	0.182379631	0.344996764
leukotriene metabolic process (GO:0006691)	44585	0.182379631	0.344996764
mammary gland development (GO:0030879)	44585	0.182379631	0.344996764
positive regulation of transcription from RNA polymera	44585	0.182379631	0.344996764
positive regulation of transforming growth factor beta	44585	0.182379631	0.344996764
potassium ion homeostasis (GO:0055075)	44585	0.182379631	0.344996764
central nervous system development (GO:0007417)	4/268	0.186446131	0.350865969
mRNA metabolic process (GO:0016071)	34731	0.188283277	0.350865969
negative regulation of antigen receptor-mediated signa	44586	0.189214954	0.350865969
receptor catabolic process (GO:0032801)	44586	0.189214954	0.350865969
receptor signaling pathway via STAT (GO:0097696)	44586	0.189214954	0.350865969
negative regulation of endocytosis (GO:0045806)	44586	0.189214954	0.350865969
cAMP-mediated signaling (GO:0019933)	44586	0.189214954	0.350865969
regulation of cholesterol transport (GO:0032374)	44586	0.189214954	0.350865969
regulation of microtubule depolymerization (GO:00311	44586	0.189214954	0.350865969

regulation of mitochondrial fission (GO:0090140)	44586	0.189214954	0.350865969
peroxisome organization (GO:0007031)	44586	0.189214954	0.350865969
regulation of proteolysis involved in cellular protein cat	44586	0.189214954	0.350865969
in utero embryonic development (GO:0001701)	44586	0.189214954	0.350865969
negative regulation of cytokine production (GO:0001813	3/182	0.195032913	0.356935951
negative regulation of interleukin-1 beta production (G	44587	0.195993473	0.356935951
negative regulation of macroautophagy (GO:0016242)	44587	0.195993473	0.356935951
negative regulation of proteolysis involved in cellular p	44587	0.195993473	0.356935951
negative regulation of receptor-mediated endocytosis (	44587	0.195993473	0.356935951
clathrin-dependent endocytosis (GO:0072583)	44587	0.195993473	0.356935951
regulation of regulatory T cell differentiation (GO:0045	44587	0.195993473	0.356935951
positive regulation of histone methylation (GO:003106	44587	0.195993473	0.356935951
histone lysine demethylation (GO:0070076)	44587	0.195993473	0.356935951
TOR signaling (GO:0031929)	44587	0.195993473	0.356935951
metanephros development (GO:0001656)	44587	0.195993473	0.356935951
mononuclear cell differentiation (GO:1903131)	44587	0.195993473	0.356935951
protein transport (GO:0015031)	5/369	0.19638156	0.357110516
antigen processing and presentation of exogenous pep	35827	0.197351648	0.358341328
organic anion transport (GO:0015711)	36192	0.200386567	0.362161596
positive regulation of stress-activated MAPK cascade ((	36192	0.200386567	0.362161596
peroxisomal membrane transport (GO:0015919)	44588	0.202715656	0.362161596
regulation of transcription elongation from RNA polym	44588	0.202715656	0.362161596
regulation of vasculature development (GO:1901342)	44588	0.202715656	0.362161596
response to glucocorticoid (GO:0051384)	44588	0.202715656	0.362161596
L-alpha-amino acid transmembrane transport (GO:190	44588	0.202715656	0.362161596
melanosome organization (GO:0032438)	44588	0.202715656	0.362161596
monovalent inorganic cation homeostasis (GO:005506	44588	0.202715656	0.362161596
protein export from nucleus (GO:0006611)	44588	0.202715656	0.362161596
negative regulation of actin filament bundle assembly (	44588	0.202715656	0.362161596
antigen processing and presentation of peptide antiger	2/100	0.203427034	0.36290195
positive regulation of protein localization to membrane	2/101	0.206472749	0.363961263
amide transport (GO:0042886)	44589	0.20938197	0.363961263
receptor clustering (GO:0043113)	44589	0.20938197	0.363961263
regulation of B cell activation (GO:0050864)	44589	0.20938197	0.363961263
regulation of calcineurin-NFAT signaling cascade (GO:0(	44589	0.20938197	0.363961263
negative regulation of oxidative stress-induced cell dea	44589	0.20938197	0.363961263
regulation of DNA-templated transcription, elongation	44589	0.20938197	0.363961263
cellular response to epidermal growth factor stimulus (	44589	0.20938197	0.363961263
regulation of microtubule polymerization or depolymer	44589	0.20938197	0.363961263
regulation of multicellular organismal development (G(	44589	0.20938197	0.363961263
regulation of small molecule metabolic process (GO:00	44589	0.20938197	0.363961263
glycerophospholipid catabolic process (GO:0046475)	44589	0.20938197	0.363961263
glycogen metabolic process (GO:0005977)	44589	0.20938197	0.363961263
RNA phosphodiester bond hydrolysis (GO:0090501)	44589	0.20938197	0.363961263
positive regulation of microtubule polymerization (GO:	44589	0.20938197	0.363961263
internal peptidyl-lysine acetylation (GO:0018393)	44589	0.20938197	0.363961263
keratan sulfate biosynthetic process (GO:0018146)	44589	0.20938197	0.363961263

transcription by RNA polymerase III (GO:0006383)	44589	0.20938197	0.363961263
antigen processing and presentation of exogenous pep	2/103	0.212578736	0.36846981
chromatin remodeling (GO:0006338)	2/103	0.212578736	0.36846981
protein targeting to peroxisome (GO:0006625)	44590	0.215992877	0.372801265
regulation of actin polymerization or depolymerization	44590	0.215992877	0.372801265
limb development (GO:0060173)	44590	0.215992877	0.372801265
regulation of JNK cascade (GO:0046328)	2/105	0.218702203	0.376945123
negative regulation of macromolecule metabolic proce	3/194	0.220882815	0.377190949
small GTPase mediated signal transduction (GO:00072(	2/106	0.221769785	0.377190949
protein localization to nucleus (GO:0034504)	2/106	0.221769785	0.377190949
artery morphogenesis (GO:0048844)	44591	0.222548833	0.377190949
negative regulation of interleukin-1 production (GO:00	44591	0.222548833	0.377190949
plasma membrane invagination (GO:0099024)	44591	0.222548833	0.377190949
regulation of protein localization to membrane (GO:19	44591	0.222548833	0.377190949
Golgi to plasma membrane protein transport (GO:0043	44591	0.222548833	0.377190949
positive regulation of lipid kinase activity (GO:0090218	44591	0.222548833	0.377190949
ion homeostasis (GO:0050801)	44591	0.222548833	0.377190949
termination of RNA polymerase I transcription (GO:000	44591	0.222548833	0.377190949
primary neural tube formation (GO:0014020)	44591	0.222548833	0.377190949
negative regulation of transmembrane receptor protei	2/108	0.227915268	0.383949874
aminoglycan catabolic process (GO:0006026)	44592	0.229050293	0.383949874
receptor signaling pathway via JAK-STAT (GO:0007259)	44592	0.229050293	0.383949874
regulation of cellular pH (GO:0030641)	44592	0.229050293	0.383949874
organelle transport along microtubule (GO:0072384)	44592	0.229050293	0.383949874
renal water homeostasis (GO:0003091)	44592	0.229050293	0.383949874
positive regulation of leukocyte cell-cell adhesion (GO::	44592	0.229050293	0.383949874
tube closure (GO:0060606)	44592	0.229050293	0.383949874
negative regulation of intracellular signal transduction	3/198	0.229652003	0.384431161
lipid transport (GO:0006869)	2/109	0.230992632	0.385618848
modulation of chemical synaptic transmission (GO:005	2/109	0.230992632	0.385618848
aortic valve morphogenesis (GO:0003180)	11689	0.235497707	0.388889457
regulation of cell migration involved in sprouting angio	11689	0.235497707	0.388889457
regulation of cell morphogenesis (GO:0022604)	11689	0.235497707	0.388889457
response to amino acid (GO:0043200)	11689	0.235497707	0.388889457
liver development (GO:0001889)	11689	0.235497707	0.388889457
long-chain fatty acid transport (GO:0015909)	11689	0.235497707	0.388889457
transcription initiation from RNA polymerase I promote	11689	0.235497707	0.388889457
modulation by host of symbiont process (GO:0051851)	11689	0.235497707	0.388889457
regulation of cytoskeleton organization (GO:0051493)	2/112	0.240240078	0.395175722
phosphatidylinositol metabolic process (GO:0046488)	2/112	0.240240078	0.395175722
apoptotic cell clearance (GO:0043277)	12055	0.241891522	0.395175722
positive regulation of histone modification (GO:003105	12055	0.241891522	0.395175722
keratan sulfate metabolic process (GO:0042339)	12055	0.241891522	0.395175722
positive regulation of organelle organization (GO:0010(	12055	0.241891522	0.395175722
very long-chain fatty acid metabolic process (GO:0000(	12055	0.241891522	0.395175722
muscle cell development (GO:0055001)	12055	0.241891522	0.395175722
proteasomal protein catabolic process (GO:0010498)	3/205	0.245149573	0.399657081

cellular response to transforming growth factor beta st	2/114	0.246415303	0.399657081
regulation of activated T cell proliferation (GO:004600(	12420	0.248232181	0.399657081
regulation of amyloid-beta formation (GO:1902003)	12420	0.248232181	0.399657081
regulation of glucose metabolic process (GO:0010906)	12420	0.248232181	0.399657081
cellular response to vascular endothelial growth factor	12420	0.248232181	0.399657081
neural tube closure (GO:0001843)	12420	0.248232181	0.399657081
secondary alcohol biosynthetic process (GO:1902653)	12420	0.248232181	0.399657081
sister chromatid segregation (GO:0000819)	12420	0.248232181	0.399657081
transcription by RNA polymerase I (GO:0006360)	12420	0.248232181	0.399657081
protein localization to chromosome (GO:0034502)	12420	0.248232181	0.399657081
positive regulation of protein metabolic process (GO:0(	2/115	0.249505255	0.401178187
ion transport (GO:0006811)	2/116	0.252596448	0.402880297
regulation of autophagosome assembly (GO:2000785)	12785	0.254520122	0.402880297
bicarbonate transport (GO:0015701)	12785	0.254520122	0.402880297
negative regulation of organelle assembly (GO:190211(	12785	0.254520122	0.402880297
cellular response to amyloid-beta (GO:1904646)	12785	0.254520122	0.402880297
negative regulation of T cell proliferation (GO:0042130	12785	0.254520122	0.402880297
cholesterol biosynthetic process (GO:0006695)	12785	0.254520122	0.402880297
regulation of phosphatidylinositol 3-kinase activity (GO	12785	0.254520122	0.402880297
regulation of T cell receptor signaling pathway (GO:005	12785	0.254520122	0.402880297
regulation of TORC1 signaling (GO:1903432)	12785	0.254520122	0.402880297
regulation of trans-synaptic signaling (GO:0099177)	12785	0.254520122	0.402880297
smoothened signaling pathway (GO:0007224)	12785	0.254520122	0.402880297
regulation of cell migration (GO:0030334)	5/408	0.255446749	0.403684142
positive regulation of cell projection organization (GO:(	2/117	0.255688646	0.403684142
activation of adenylate cyclase activity (GO:0007190)	13150	0.260755782	0.40643312
aortic valve development (GO:0003176)	13150	0.260755782	0.40643312
regulation of cell cycle G1/S phase transition (GO:1902	13150	0.260755782	0.40643312
cyclic-nucleotide-mediated signaling (GO:0019935)	13150	0.260755782	0.40643312
regulation of microtubule-based process (GO:0032886)	13150	0.260755782	0.40643312
platelet aggregation (GO:0070527)	13150	0.260755782	0.40643312
regulation of receptor internalization (GO:0002090)	13150	0.260755782	0.40643312
establishment of protein localization to plasma membr	13150	0.260755782	0.40643312
intrinsic apoptotic signaling pathway by p53 class medi	13150	0.260755782	0.40643312
positive regulation of substrate adhesion-dependent ce	13150	0.260755782	0.40643312
cytoskeleton organization (GO:0007010)	2/120	0.264968986	0.410831465
proton transmembrane transport (GO:1902600)	13516	0.266939593	0.410831465
anterograde axonal transport (GO:0008089)	13516	0.266939593	0.410831465
regulation of erythrocyte differentiation (GO:0045646)	13516	0.266939593	0.410831465
regulation of intracellular pH (GO:0051453)	13516	0.266939593	0.410831465
phagocytosis, engulfment (GO:0006911)	13516	0.266939593	0.410831465
phagosome maturation (GO:0090382)	13516	0.266939593	0.410831465
positive regulation of calcium ion transport (GO:00519)	13516	0.266939593	0.410831465
glutamine family amino acid metabolic process (GO:00(	13516	0.266939593	0.410831465
skeletal muscle tissue development (GO:0007519)	13516	0.266939593	0.410831465
regulation of mRNA catabolic process (GO:0061013)	2/122	0.271156775	0.415042243
epithelium development (GO:0060429)	2/122	0.271156775	0.415042243

potassium ion transport (GO:0006813)	2/122	0.271156775	0.415042243
negative regulation of G0 to G1 transition (GO:007031	13881	0.273071983	0.415042243
regulation of axon extension (GO:0030516)	13881	0.273071983	0.415042243
negative regulation of ubiquitin-dependent protein cat	13881	0.273071983	0.415042243
connective tissue development (GO:0061448)	13881	0.273071983	0.415042243
response to cAMP (GO:0051591)	13881	0.273071983	0.415042243
sterol biosynthetic process (GO:0016126)	13881	0.273071983	0.415042243
positive regulation of signaling (GO:0023056)	13881	0.273071983	0.415042243
regulation of anatomical structure morphogenesis (GO	2/123	0.274250289	0.416315346
negative regulation of cellular metabolic process (GO:0	14246	0.279153378	0.419073007
cellular response to ketone (GO:1901655)	14246	0.279153378	0.419073007
regulation of heart rate by cardiac conduction (GO:008	14246	0.279153378	0.419073007
DNA recombination (GO:0006310)	14246	0.279153378	0.419073007
regulation of peptidyl-threonine phosphorylation (GO:(	14246	0.279153378	0.419073007
endothelial cell migration (GO:0043542)	14246	0.279153378	0.419073007
regulation of receptor-mediated endocytosis (GO:0048	14246	0.279153378	0.419073007
regulation of T cell differentiation (GO:0045580)	14246	0.279153378	0.419073007
vesicle cytoskeletal trafficking (GO:0099518)	14246	0.279153378	0.419073007
regulation of phosphorylation (GO:0042325)	2/125	0.280435513	0.420318537
regulation of apoptotic process (GO:0042981)	8/742	0.280670971	0.420318537
phosphatidylinositol biosynthetic process (GO:00066612	2/126	0.283526814	0.423557172
synapse organization (GO:0050808)	2/126	0.283526814	0.423557172
negative regulation of cell-substrate adhesion (GO:001	14611	0.285184198	0.424476358
carboxylic acid metabolic process (GO:0019752)	14611	0.285184198	0.424476358
digestive tract development (GO:0048565)	14611	0.285184198	0.424476358
regulation of nucleic acid-templated transcription (GO:	5/430	0.290531642	0.429714325
regulation of G0 to G1 transition (GO:0070316)	14977	0.291164862	0.429714325
regulation of mitochondrial membrane potential (GO:0	14977	0.291164862	0.429714325
epithelial cell migration (GO:0010631)	14977	0.291164862	0.429714325
hexose metabolic process (GO:0019318)	14977	0.291164862	0.429714325
T cell differentiation (GO:0030217)	14977	0.291164862	0.429714325
visual system development (GO:0150063)	14977	0.291164862	0.429714325
cellular response to insulin stimulus (GO:0032869)	2/129	0.292793101	0.431596102
protein glycosylation (GO:0006486)	2/130	0.295878683	0.435618977
ATP-dependent chromatin remodeling (GO:0043044)	15342	0.297095785	0.435835593
heterophilic cell-cell adhesion via plasma membrane ce	15342	0.297095785	0.435835593
potassium ion import across plasma membrane (GO:19	15342	0.297095785	0.435835593
cellular response to hypoxia (GO:0071456)	2/131	0.298962364	0.438047972
regulation of cell-cell adhesion (GO:0022407)	15707	0.302977377	0.442339731
regulation of cell-substrate adhesion (GO:0010810)	15707	0.302977377	0.442339731
cellular response to retinoic acid (GO:0071300)	15707	0.302977377	0.442339731
positive regulation of cytokine production (GO:000181	4/335	0.306853562	0.446058957
intracellular protein transport (GO:0006886)	4/336	0.308733581	0.446058957
branching morphogenesis of an epithelial tube (GO:004	16072	0.308810047	0.446058957
cation transmembrane transport (GO:0098655)	16072	0.308810047	0.446058957
neurogenesis (GO:0022008)	16072	0.308810047	0.446058957
response to amyloid-beta (GO:1904645)	16072	0.308810047	0.446058957

homotypic cell-cell adhesion (GO:0034109)	16072	0.308810047	0.446058957
metal ion homeostasis (GO:0055065)	16072	0.308810047	0.446058957
mitotic spindle assembly (GO:0090307)	16072	0.308810047	0.446058957
positive regulation of chemotaxis (GO:0050921)	16438	0.314594199	0.452808141
positive regulation of Notch signaling pathway (GO:004	16438	0.314594199	0.452808141
microtubule bundle formation (GO:0001578)	16438	0.314594199	0.452808141
nervous system development (GO:0007399)	5/447	0.318215772	0.457481969
establishment of protein localization to extracellular re	16803	0.320330235	0.458902165
regulation of synaptic transmission, glutamatergic (GO:	16803	0.320330235	0.458902165
positive regulation of organelle assembly (GO:1902117	16803	0.320330235	0.458902165
positive regulation of multicellular organismal process	4/345	0.32570233	0.463537967
post-translational protein modification (GO:0043687)	4/345	0.32570233	0.463537967
regulation of cellular metabolic process (GO:0031323)	17168	0.326018551	0.463537967
regulation of synapse assembly (GO:0051963)	17168	0.326018551	0.463537967
positive regulation of cell-cell adhesion (GO:0022409)	17168	0.326018551	0.463537967
regulation of T cell activation (GO:0050863)	17168	0.326018551	0.463537967
neuron projection morphogenesis (GO:0048812)	2/140	0.32660081	0.463537967
transcription initiation from RNA polymerase II promot	2/140	0.32660081	0.463537967
positive regulation of cellular catabolic process (GO:00	2/141	0.32965594	0.466384306
purine ribonucleotide biosynthetic process (GO:00091	17533	0.331659543	0.466384306
regulation of mitochondrion organization (GO:00108211	17533	0.331659543	0.466384306
regulation of protein metabolic process (GO:0051246)	17533	0.331659543	0.466384306
positive regulation of DNA repair (GO:0045739)	17533	0.331659543	0.466384306
positive regulation of endocytosis (GO:0045807)	17533	0.331659543	0.466384306
Golgi to plasma membrane transport (GO:0006893)	17533	0.331659543	0.466384306
myelination (GO:0042552)	17533	0.331659543	0.466384306
Ras protein signal transduction (GO:0007265)	2/142	0.332707327	0.466783415
protein localization to organelle (GO:0033365)	2/142	0.332707327	0.466783415
adherens junction organization (GO:0034332)	17899	0.337253603	0.468855407
receptor internalization (GO:0031623)	17899	0.337253603	0.468855407
regulation of cellular protein metabolic process (GO:00	17899	0.337253603	0.468855407
oligosaccharide metabolic process (GO:0009311)	17899	0.337253603	0.468855407
positive regulation of actin filament polymerization (GO	17899	0.337253603	0.468855407
regulation of stress-activated MAPK cascade (GO:0032	17899	0.337253603	0.468855407
response to unfolded protein (GO:0006986)	17899	0.337253603	0.468855407
secondary alcohol metabolic process (GO:1902652)	17899	0.337253603	0.468855407
positive regulation of DNA-binding transcription factor	3/246	0.338096195	0.46949267
organic hydroxy compound biosynthetic process (GO:1	18264	0.342801117	0.474408794
positive regulation of cell morphogenesis involved in di	18264	0.342801117	0.474408794
positive regulation of ion transport (GO:0043270)	18264	0.342801117	0.474408794
regulation of mRNA stability (GO:0043488)	2/146	0.344872491	0.47449902
negative regulation of transcription by RNA polymerase	7/684	0.346404343	0.47449902
positive regulation of transcription by RNA polymerase	9/908	0.347635829	0.47449902
regulation of axonogenesis (GO:0050770)	18629	0.348302472	0.47449902
regulation of epithelial cell migration (GO:0010632)	18629	0.348302472	0.47449902
negative regulation of transport (GO:0051051)	18629	0.348302472	0.47449902
regulation of protein modification process (GO:003139	18629	0.348302472	0.47449902

regulation of substrate adhesion-dependent cell spreac	18629	0.348302472	0.47449902
positive regulation of fat cell differentiation (GO:00456	18629	0.348302472	0.47449902
inositol lipid-mediated signaling (GO:0048017)	18629	0.348302472	0.47449902
sensory perception (GO:0007600)	18629	0.348302472	0.47449902
intrinsic apoptotic signaling pathway in response to DN	18629	0.348302472	0.47449902
mitotic nuclear membrane organization (GO:0101024)	18629	0.348302472	0.47449902
mitotic nuclear membrane reassembly (GO:0007084)	18629	0.348302472	0.47449902
positive regulation of signal transduction (GO:0009967	3/252	0.35178025	0.477548964
regulation of cellular macromolecule biosynthetic proc	5/468	0.352834947	0.477548964
negative regulation of cellular biosynthetic process (GC	18994	0.353758049	0.477548964
cartilage development (GO:0051216)	18994	0.353758049	0.477548964
endocytic recycling (GO:0032456)	18994	0.353758049	0.477548964
fatty acid beta-oxidation (GO:0006635)	18994	0.353758049	0.477548964
positive regulation of developmental growth (GO:0048	18994	0.353758049	0.477548964
positive regulation of hydrolase activity (GO:0051345)	2/149	0.353949984	0.477548964
regulation of canonical Wnt signaling pathway (GO:006	3/253	0.354058397	0.477548964
regulation of cytokine production (GO:0001817)	2/150	0.356966255	0.480940203
positive regulation of macroautophagy (GO:0016239)	19360	0.359168227	0.483373979
negative regulation of protein phosphorylation (GO:00	2/152	0.362983679	0.48737395
nuclear membrane reassembly (GO:0031468)	19725	0.36453338	0.48737395
regulation of megakaryocyte differentiation (GO:00456	19725	0.36453338	0.48737395
cytoplasmic microtubule organization (GO:0031122)	19725	0.36453338	0.48737395
regulation of potassium ion transmembrane transport	19725	0.36453338	0.48737395
glycosaminoglycan metabolic process (GO:0030203)	19725	0.36453338	0.48737395
positive regulation of Wnt signaling pathway (GO:0030	2/153	0.365984582	0.488779409
regulation of cardiac conduction (GO:1903779)	20090	0.369853883	0.492869623
ceramide metabolic process (GO:0006672)	20090	0.369853883	0.492869623
regulation of cell differentiation (GO:0045595)	2/156	0.374954596	0.495577282
regulation of ATP metabolic process (GO:1903578)	20455	0.375130103	0.495577282
negative regulation of metabolic process (GO:0009892	20455	0.375130103	0.495577282
glycosaminoglycan catabolic process (GO:0006027)	20455	0.375130103	0.495577282
positive regulation of interleukin-1 beta production (GO	20455	0.375130103	0.495577282
Rho protein signal transduction (GO:0007266)	20455	0.375130103	0.495577282
sensory organ development (GO:0007423)	20455	0.375130103	0.495577282
telomere maintenance (GO:0000723)	20455	0.375130103	0.495577282
arachidonic acid metabolic process (GO:0019369)	20821	0.380362408	0.497647604
cellular response to peptide (GO:1901653)	20821	0.380362408	0.497647604
regulation of mitotic nuclear division (GO:0007088)	20821	0.380362408	0.497647604
dicarboxylic acid metabolic process (GO:0043648)	20821	0.380362408	0.497647604
regulation of reactive oxygen species metabolic proces	20821	0.380362408	0.497647604
renal system development (GO:0072001)	20821	0.380362408	0.497647604
positive regulation of interferon-gamma production (G	20821	0.380362408	0.497647604
positive regulation of proteolysis (GO:0045862)	20821	0.380362408	0.497647604
monocarboxylic acid transport (GO:0015718)	20821	0.380362408	0.497647604
cellular response to growth factor stimulus (GO:00713(	2/158	0.380906197	0.497826066
receptor metabolic process (GO:0043112)	21186	0.38555116	0.501216508
chordate embryonic development (GO:0043009)	21186	0.38555116	0.501216508

eye development (GO:0001654)	21186	0.38555116	0.501216508
RNA modification (GO:0009451)	21186	0.38555116	0.501216508
muscle organ development (GO:0007517)	21186	0.38555116	0.501216508
negative regulation of autophagy (GO:0010507)	21551	0.390696721	0.506289918
fatty acid oxidation (GO:0019395)	21551	0.390696721	0.506289918
mitotic DNA damage checkpoint signaling (GO:004477	21551	0.390696721	0.506289918
adenylate cyclase-inhibiting G protein-coupled recepto	21916	0.395799447	0.510735929
apical junction assembly (GO:0043297)	21916	0.395799447	0.510735929
cellular protein catabolic process (GO:0044257)	21916	0.395799447	0.510735929
Notch signaling pathway (GO:0007219)	21916	0.395799447	0.510735929
positive regulation of macromolecule metabolic proces	4/384	0.399520017	0.514886518
regulation of DNA-templated transcription, initiation (G	22282	0.400859693	0.514886518
O-glycan processing (GO:0016266)	22282	0.400859693	0.514886518
positive regulation of transcription, DNA-templated (G	11/1183	0.401095468	0.514886518
negative regulation of canonical Wnt signaling pathwa	2/165	0.401544069	0.514886518
adenylate cyclase-modulating G protein-coupled recep	2/165	0.401544069	0.514886518
negative regulation of kinase activity (GO:0033673)	22647	0.405877811	0.517187367
double-strand break repair via nonhomologous end joi	22647	0.405877811	0.517187367
positive regulation of cysteine-type endopeptidase acti	22647	0.405877811	0.517187367
glucose metabolic process (GO:0006006)	22647	0.405877811	0.517187367
positive regulation of interleukin-1 production (GO:003	22647	0.405877811	0.517187367
response to retinoic acid (GO:0032526)	22647	0.405877811	0.517187367
negative regulation of endopeptidase activity (GO:001	23012	0.410854148	0.522438886
negative regulation of peptidase activity (GO:0010466)	23012	0.410854148	0.522438886
protein secretion (GO:0009306)	23377	0.415789052	0.524890724
negative regulation of cell cycle process (GO:0010948)	23377	0.415789052	0.524890724
negative regulation of intrinsic apoptotic signaling path	23377	0.415789052	0.524890724
regulation of cilium assembly (GO:1902017)	23377	0.415789052	0.524890724
diterpenoid metabolic process (GO:0016101)	23377	0.415789052	0.524890724
regulation of transcription initiation from RNA polymer	23377	0.415789052	0.524890724
tRNA processing (GO:0008033)	23377	0.415789052	0.524890724
chemical homeostasis (GO:0048878)	23743	0.420682864	0.528883189
steroid biosynthetic process (GO:0006694)	23743	0.420682864	0.528883189
tRNA modification (GO:0006400)	23743	0.420682864	0.528883189
mitotic G1 DNA damage checkpoint signaling (GO:0031	23743	0.420682864	0.528883189
positive regulation of cell cycle (GO:0045787)	24108	0.425535925	0.533885934
positive regulation of cell death (GO:0010942)	24108	0.425535925	0.533885934
neuron differentiation (GO:0030182)	2/174	0.427595639	0.535919868
protein N-linked glycosylation (GO:0006487)	24473	0.430348572	0.5377157
regulation of gene silencing by miRNA (GO:0060964)	24473	0.430348572	0.5377157
vascular endothelial growth factor receptor signaling p	24473	0.430348572	0.5377157
canonical Wnt signaling pathway (GO:0060070)	24838	0.43512114	0.542016344
regulation of myeloid cell differentiation (GO:0045637)	24838	0.43512114	0.542016344
regulation of translational initiation (GO:0006446)	24838	0.43512114	0.542016344
regulation of mitotic cell cycle (GO:0007346)	2/178	0.438984683	0.545133408
negative regulation of cellular catabolic process (GO:0	25204	0.439853961	0.545133408
cellular response to decreased oxygen levels (GO:0036	25204	0.439853961	0.545133408

synapse assembly (GO:0007416)	25204	0.439853961	0.545133408
positive regulation of protein polymerization (GO:0032	25204	0.439853961	0.545133408
protein stabilization (GO:0050821)	2/179	0.441812829	0.545523853
carbohydrate homeostasis (GO:0033500)	25569	0.444547363	0.545523853
neutrophil chemotaxis (GO:0030593)	25569	0.444547363	0.545523853
DNA-templated transcription, termination (GO:000635	25569	0.444547363	0.545523853
positive regulation of cell-substrate adhesion (GO:001(	25569	0.444547363	0.545523853
kidney development (GO:0001822)	25569	0.444547363	0.545523853
snRNA transcription by RNA polymerase II (GO:004279	25569	0.444547363	0.545523853
sterol metabolic process (GO:0016125)	25569	0.444547363	0.545523853
wound healing (GO:0042060)	25569	0.444547363	0.545523853
positive regulation of cellular biosynthetic process (GO	2/180	0.444633189	0.545523853
protein ubiquitination (GO:0016567)	5/525	0.446964228	0.546737494
regulation of G1/S transition of mitotic cell cycle (GO:2	25934	0.449201673	0.546737494
regulation of glycolytic process (GO:0006110)	25934	0.449201673	0.546737494
regulation of hematopoietic stem cell differentiation ((	25934	0.449201673	0.546737494
phosphatidylinositol-mediated signaling (GO:0048015)	25934	0.449201673	0.546737494
gland development (GO:0048732)	25934	0.449201673	0.546737494
histone acetylation (GO:0016573)	25934	0.449201673	0.546737494
snRNA transcription (GO:0009301)	25934	0.449201673	0.546737494
regulation of cell cycle (GO:0051726)	3/296	0.450284038	0.547509546
cell junction organization (GO:0034330)	26299	0.453817214	0.550163329
positive regulation of neurogenesis (GO:0050769)	26299	0.453817214	0.550163329
sterol homeostasis (GO:0055092)	26299	0.453817214	0.550163329
regulation of hydrolase activity (GO:0051336)	26665	0.458394309	0.553515657
regulation of Rho protein signal transduction (GO:0035	26665	0.458394309	0.553515657
granulocyte chemotaxis (GO:0071621)	26665	0.458394309	0.553515657
insulin receptor signaling pathway (GO:0008286)	26665	0.458394309	0.553515657
DNA damage response, signal transduction by p53 class	27030	0.462933274	0.557344296
regulation of stress fiber assembly (GO:0051492)	27030	0.462933274	0.557344296
mitotic nuclear division (GO:0140014)	27030	0.462933274	0.557344296
organelle organization (GO:0006996)	4/420	0.466478199	0.560554336
regulation of mitotic cell cycle phase transition (GO:19(	2/188	0.466907984	0.560554336
regulation of hematopoietic progenitor cell differentiat	27395	0.467434425	0.560554336
regulation of transcription from RNA polymerase II pro	27395	0.467434425	0.560554336
regulation of GTPase activity (GO:0043087)	2/189	0.469655418	0.562665608
cell morphogenesis involved in neuron differentiation (	27760	0.471898077	0.563143994
establishment of protein localization to organelle (GO:(	27760	0.471898077	0.563143994
positive regulation of interleukin-6 production (GO:003	27760	0.471898077	0.563143994
protein import into nucleus (GO:0006606)	27760	0.471898077	0.563143994
cholesterol metabolic process (GO:0008203)	28126	0.476324539	0.565115133
neutrophil migration (GO:1990266)	28126	0.476324539	0.565115133
regulation of organelle assembly (GO:1902115)	28126	0.476324539	0.565115133
import into nucleus (GO:0051170)	28126	0.476324539	0.565115133
inorganic cation import across plasma membrane (GO:	28126	0.476324539	0.565115133
positive regulation of tumor necrosis factor production	28126	0.476324539	0.565115133
protein modification process (GO:0036211)	28491	0.480714119	0.569217688

negative regulation of blood vessel morphogenesis (GC	28491	0.480714119	0.569217688
axon development (GO:0061564)	28856	0.485067123	0.573816094
protein polyubiquitination (GO:0000209)	3/314	0.488922186	0.57557947
negative regulation of cell cycle (GO:0045786)	29221	0.489383854	0.57557947
negative regulation of cellular component organization	29221	0.489383854	0.57557947
regulation of NIK/NF-kappaB signaling (GO:1901222)	29221	0.489383854	0.57557947
glycerophospholipid metabolic process (GO:0006650)	29221	0.489383854	0.57557947
skin development (GO:0043588)	29221	0.489383854	0.57557947
positive regulation of tumor necrosis factor superfamil	29587	0.493664612	0.580055919
regulation of cyclin-dependent protein serine/threonin	29952	0.497909695	0.583920967
positive regulation of cytoskeleton organization (GO:0(	29952	0.497909695	0.583920967
regulation of Notch signaling pathway (GO:0008593)	30317	0.502119399	0.587167374
glycoprotein biosynthetic process (GO:0009101)	30317	0.502119399	0.587167374
positive regulation of plasma membrane bounded cell	30317	0.502119399	0.587167374
proteasome-mediated ubiquitin-dependent protein cat	3/321	0.50359557	0.58833058
generation of neurons (GO:0048699)	2/202	0.504591026	0.588669162
anaphase-promoting complex-dependent catabolic pro	30682	0.506294017	0.588669162
nuclear export (GO:0051168)	30682	0.506294017	0.588669162
spindle assembly (GO:0051225)	30682	0.506294017	0.588669162
lymphocyte differentiation (GO:0030098)	30682	0.506294017	0.588669162
axon guidance (GO:0007411)	2/203	0.50721677	0.589181457
cellular response to oxygen-containing compound (GO:	3/323	0.507748782	0.589239327
negative regulation of cellular amide metabolic proces	31413	0.514539155	0.594297587
negative regulation of phosphorylation (GO:0042326)	31413	0.514539155	0.594297587
regulation of interferon-gamma production (GO:00326	31413	0.514539155	0.594297587
glucose homeostasis (GO:0042593)	31413	0.514539155	0.594297587
positive regulation of endothelial cell migration (GO:00	31413	0.514539155	0.594297587
negative regulation of angiogenesis (GO:0016525)	31778	0.518610248	0.597306054
ERAD pathway (GO:0036503)	31778	0.518610248	0.597306054
regulation of transcription from RNA polymerase II pro	31778	0.518610248	0.597306054
retrograde transport, endosome to Golgi (GO:0042147	32143	0.522647404	0.600823263
sensory perception of mechanical stimulus (GO:00509	32143	0.522647404	0.600823263
regulation of cysteine-type endopeptidase activity invo	32509	0.526650904	0.602591203
regulation of endothelial cell migration (GO:0010594)	32509	0.526650904	0.602591203
collagen fibril organization (GO:0030199)	32509	0.526650904	0.602591203
SCF-dependent proteasomal ubiquitin-dependent prot	32509	0.526650904	0.602591203
transforming growth factor beta receptor signaling pat	32509	0.526650904	0.602591203
negative regulation of inflammatory response (GO:005	2/212	0.530439945	0.605433141
negative regulation of protein kinase activity (GO:0006	32874	0.530621026	0.605433141
positive regulation of autophagy (GO:0010508)	32874	0.530621026	0.605433141
sensory perception of sound (GO:0007605)	33239	0.534558047	0.607572353
positive regulation of supramolecular fiber organizatio	33239	0.534558047	0.607572353
positive regulation of transport (GO:0051050)	33239	0.534558047	0.607572353
positive regulation of GTPase activity (GO:0043547)	2/214	0.535499525	0.607572353
negative regulation of mitotic cell cycle phase transitio	33604	0.538462241	0.607572353
cellular response to fibroblast growth factor stimulus ((	33604	0.538462241	0.607572353
regulation of lipid metabolic process (GO:0019216)	33604	0.538462241	0.607572353

regulation of peptidyl-tyrosine phosphorylation (GO:00	33604	0.538462241	0.607572353
retinoid metabolic process (GO:0001523)	33604	0.538462241	0.607572353
T cell activation (GO:0042110)	33604	0.538462241	0.607572353
positive regulation of transmembrane receptor protein	33604	0.538462241	0.607572353
Wnt signaling pathway (GO:0016055)	33604	0.538462241	0.607572353
extracellular structure organization (GO:0043062)	2/216	0.5405219	0.609333729
regulation of heart contraction (GO:0008016)	33970	0.542333881	0.610812905
external encapsulating structure organization (GO:004	2/217	0.543019082	0.611021472
regulation of kinase activity (GO:0043549)	34335	0.546173236	0.612877589
nucleosome organization (GO:0034728)	34335	0.546173236	0.612877589
hemopoiesis (GO:0030097)	34335	0.546173236	0.612877589
cellular response to lipid (GO:0071396)	2/219	0.547985339	0.614346866
ciliary basal body-plasma membrane docking (GO:0097	34700	0.549980573	0.615454451
sensory perception of light stimulus (GO:0050953)	34700	0.549980573	0.615454451
protein maturation (GO:0051604)	35431	0.557500257	0.62159244
calcium ion homeostasis (GO:0055074)	35431	0.557500257	0.62159244
positive regulation of cold-induced thermogenesis (GO	35431	0.557500257	0.62159244
glycosaminoglycan biosynthetic process (GO:0006024)	35431	0.557500257	0.62159244
regulation of I-kappaB kinase/NF-kappaB signaling (GO	2/224	0.560236216	0.624073524
cellular response to DNA damage stimulus (GO:000697	3/350	0.561974904	0.625440193
cell-matrix adhesion (GO:0007160)	1/100	0.568546218	0.631603162
regulation of transforming growth factor beta receptor	1/100	0.568546218	0.631603162
cilium organization (GO:0044782)	2/228	0.569866494	0.632494874
positive regulation of cell cycle process (GO:0090068)	1/101	0.57216695	0.634471881
protein O-linked glycosylation (GO:0006493)	1/102	0.575757478	0.634996063
regulation of cell death (GO:0010941)	1/102	0.575757478	0.634996063
regulation of proteasomal ubiquitin-dependent protein	1/102	0.575757478	0.634996063
positive regulation of cell growth (GO:0030307)	1/102	0.575757478	0.634996063
intrinsic apoptotic signaling pathway (GO:0097193)	1/102	0.575757478	0.634996063
mitotic sister chromatid segregation (GO:0000070)	1/102	0.575757478	0.634996063
cellular response to organonitrogen compound (GO:00	1/103	0.579318052	0.638346852
cellular metal ion homeostasis (GO:0006875)	1/104	0.582848919	0.6416589
neutrophil mediated immunity (GO:0002446)	4/488	0.584405092	0.642792999
activation of GTPase activity (GO:0090630)	1/105	0.586350328	0.643773675
positive regulation of cellular metabolic process (GO:0(	1/105	0.586350328	0.643773675
cellular response to peptide hormone stimulus (GO:007	1/106	0.589822521	0.64584509
peptidyl-lysine modification (GO:0018205)	1/106	0.589822521	0.64584509
positive regulation of protein serine/threonine kinase a	1/106	0.589822521	0.64584509
response to calcium ion (GO:0051592)	1/107	0.593265741	0.649033783
axonogenesis (GO:0007409)	2/240	0.597842002	0.653455211
regulation of interleukin-6 production (GO:0032675)	1/110	0.603423959	0.657205061
regulation of protein kinase activity (GO:0045859)	1/110	0.603423959	0.657205061
response to endoplasmic reticulum stress (GO:003497(	1/110	0.603423959	0.657205061
response to tumor necrosis factor (GO:0034612)	1/110	0.603423959	0.657205061
cellular divalent inorganic cation homeostasis (GO:007	1/111	0.606753672	0.659655683
Fc-epsilon receptor signaling pathway (GO:0038095)	1/111	0.606753672	0.659655683
Fc receptor signaling pathway (GO:0038093)	1/112	0.610055594	0.662655943

positive regulation of metabolic process (GO:0009893)	1/113	0.613329955	0.665030351
sulfur compound biosynthetic process (GO:0044272)	1/113	0.613329955	0.665030351
activation of protein kinase activity (GO:0032147)	1/114	0.616576985	0.667366763
positive regulation of cellular component organization	1/114	0.616576985	0.667366763
cellular response to lectin (GO:1990858)	1/115	0.61979691	0.66907405
cellular response to molecule of bacterial origin (GO:0(	1/115	0.61979691	0.66907405
stimulatory C-type lectin receptor signaling pathway (G	1/115	0.61979691	0.66907405
cytosolic transport (GO:0016482)	1/116	0.622989955	0.671334855
sphingolipid metabolic process (GO:0006665)	1/116	0.622989955	0.671334855
adenylate cyclase-activating G protein-coupled recepto	1/118	0.629296295	0.676936684
regulation of cellular response to stress (GO:0080135)	1/118	0.629296295	0.676936684
positive regulation of cysteine-type endopeptidase acti	1/119	0.632410032	0.679090561
innate immune response activating cell surface recepto	1/119	0.632410032	0.679090561
cellular response to lipopolysaccharide (GO:0071222)	1/120	0.635497769	0.681209012
macroautophagy (GO:0016236)	1/120	0.635497769	0.681209012
protein homooligomerization (GO:0051260)	1/121	0.638559723	0.683891307
fatty acid metabolic process (GO:0006631)	1/124	0.64759302	0.692352292
regulation of tumor necrosis factor production (GO:00:	1/124	0.64759302	0.692352292
platelet degranulation (GO:0002576)	1/125	0.650553965	0.694909917
negative regulation of signal transduction (GO:0009968	2/267	0.655760936	0.699860143
transmembrane receptor protein tyrosine kinase signal	3/404	0.658948512	0.702648413
positive regulation of macromolecule biosynthetic proc	1/129	0.662152485	0.705449291
regulation of primary metabolic process (GO:0080090)	1/130	0.664991815	0.706626085
positive regulation of canonical Wnt signaling pathway	1/130	0.664991815	0.706626085
G2/M transition of mitotic cell cycle (GO:0000086)	1/130	0.664991815	0.706626085
protein modification by small protein conjugation (GO:	3/409	0.667105015	0.708255716
cell cycle G2/M phase transition (GO:0044839)	1/131	0.667807423	0.708385999
transmembrane receptor protein serine/threonine kina	1/133	0.673368264	0.713665238
positive regulation of peptidyl-tyrosine phosphorylatio	1/134	0.676113886	0.715954219
plasma membrane bounded cell projection assembly (G	2/278	0.677387904	0.716682267
negative regulation of inflammatory response to antige	1/136	0.681536494	0.719825061
cellular calcium ion homeostasis (GO:0006874)	1/136	0.681536494	0.719825061
regulation of inflammatory response to antigenic stimu	1/137	0.684213859	0.721962074
regulation of gene expression (GO:0010468)	8/1079	0.684741443	0.721962074
protein dephosphorylation (GO:0006470)	1/139	0.689501648	0.726354322
enzyme linked receptor protein signaling pathway (GO:	1/140	0.692112443	0.727998844
organelle assembly (GO:0070925)	3/425	0.69225422	0.727998844
negative regulation of DNA-binding transcription factor	1/143	0.699814616	0.734685104
monocarboxylic acid metabolic process (GO:0032787)	1/143	0.699814616	0.734685104
negative regulation of cell migration (GO:0030336)	1/144	0.702339203	0.73670258
DNA repair (GO:0006281)	2/298	0.713880672	0.748166536
cellular response to organic cyclic compound (GO:0071	1/150	0.717049586	0.750498612
extracellular matrix organization (GO:0030198)	2/300	0.717334189	0.750498612
MAPK cascade (GO:0000165)	2/303	0.722449173	0.755203498
dephosphorylation (GO:0016311)	1/153	0.72413146	0.75631508
positive regulation of NF-kappaB transcription factor ac	1/155	0.728754539	0.760493635
regulation of signal transduction by p53 class mediator	1/156	0.731037117	0.762224707

mitotic spindle organization (GO:0007052)	1/157	0.7333006	0.763932935
skeletal system development (GO:0001501)	1/158	0.735545147	0.765618544
response to lipopolysaccharide (GO:0032496)	1/159	0.737770917	0.767281753
cilium assembly (GO:0060271)	2/314	0.740544055	0.769510914
peptide biosynthetic process (GO:0043043)	1/162	0.744337111	0.7727952
double-strand break repair (GO:0006302)	1/164	0.748623513	0.776585681
cellular protein-containing complex assembly (GO:003	1/168	0.756983171	0.784591548
positive regulation of I-kappaB kinase/NF-kappaB signa	1/171	0.763071027	0.790106189
cellular protein localization (GO:0034613)	2/329	0.763596898	0.790106189
positive regulation of ERK1 and ERK2 cascade (GO:007	1/172	0.765066432	0.790957005
neutrophil degranulation (GO:0043312)	3/481	0.769060413	0.794414053
defense response to bacterium (GO:0042742)	1/176	0.772882381	0.797687728
neutrophil activation involved in immune response (GC	3/485	0.773901076	0.798065076
positive regulation of developmental process (GO:0051	1/177	0.774795637	0.798313886
negative regulation of immune response (GO:0050777)	1/178	0.776692871	0.798921455
regulation of translation (GO:0006417)	1/178	0.776692871	0.798921455
regulated exocytosis (GO:0045055)	1/180	0.780439806	0.802100457
ubiquitin-dependent protein catabolic process (GO:000	2/354	0.798096549	0.819557969
gene expression (GO:0010467)	2/356	0.80065569	0.821495595
cellular response to tumor necrosis factor (GO:007135	1/194	0.804975173	0.825234615
protein localization to membrane (GO:0072657)	1/195	0.806619567	0.826227252
endomembrane system organization (GO:0010256)	1/199	0.81306046	0.832127205
modification-dependent protein catabolic process (GO:	1/201	0.81620048	0.83464183
regulation of inflammatory response (GO:0050727)	1/206	0.823823036	0.841732232
regulation of protein kinase B signaling (GO:0051896)	1/207	0.825309409	0.842546448
mitotic cell cycle phase transition (GO:0044772)	1/209	0.828244862	0.844837414
phosphate-containing compound metabolic process (G	1/212	0.832556353	0.848526992
translation (GO:0006412)	1/214	0.835370737	0.850685867
inflammatory response (GO:0006954)	1/230	0.856256884	0.871228903
regulation of ERK1 and ERK2 cascade (GO:0070372)	1/238	0.865689752	0.879753469
cellular protein metabolic process (GO:0044267)	2/417	0.866074814	0.879753469
anterograde trans-synaptic signaling (GO:0098916)	1/244	0.872358212	0.885400112
cellular component assembly (GO:0022607)	1/261	0.889517481	0.90206669
regulation of protein phosphorylation (GO:0001932)	1/266	0.894113082	0.905381762
protein-containing complex assembly (GO:0065003)	1/267	0.89500914	0.905381762
protein deubiquitination (GO:0016579)	1/267	0.89500914	0.905381762
positive regulation of cellular process (GO:0048522)	3/625	0.897307346	0.906955812
positive regulation of MAPK cascade (GO:0043410)	1/274	0.901073975	0.910010246
protein modification by small protein removal (GO:007	1/276	0.902741907	0.910941875
DNA metabolic process (GO:0006259)	1/277	0.90356536	0.91102052
innate immune response (GO:0045087)	1/302	0.922043015	0.928884225
chemical synaptic transmission (GO:0007268)	1/306	0.924653398	0.930746665
cellular macromolecule biosynthetic process (GO:0034	1/314	0.929616323	0.934972137
positive regulation of protein phosphorylation (GO:000	1/371	0.956720417	0.961441077
negative regulation of programmed cell death (GO:004	1/381	0.960265347	0.964210562
cellular response to cytokine stimulus (GO:0071345)	1/482	0.98327875	0.986125188
negative regulation of apoptotic process (GO:0043066)	1/485	0.983704259	0.986125188

positive regulation of intracellular signal transduction ((	1/546	0.990359768	0.991983309
negative regulation of cellular process (GO:0048523)	1/566	0.991886873	0.99269923
regulation of cell population proliferation (GO:0042127	1/764	0.998541348	0.998541348

f significant highly-correlated RNA-seq-based modules (pink; Significant terms

Old P-value	Old Adjusted P-value	Odds Ratio	Combined Score	Genes	KEGG
0	0	32.96341463	281.6726802	SH3BP1;SC	.
0	0	13.1294976	103.6361804	SLC36A1;S	.
0	0	11.84617687	89.23947468	HDAC10;M	.
0	0	7.918871252	58.47326049	PHF2;KAT2	.
0	0	20.13719512	146.8440601	ABHD2;CA	.
0	0	80.12121212	584.1573903	SLC36A1;S	.
0	0	18.12164634	127.1789174	DAGLA;DG	.
0	0	60.08787879	414.0630292	SH3BP1;M	.
0	0	9.158467415	60.7738382	PHF2;KAT2	.
0	0	48.06787879	315.3245455	STIM1;ORA	.
0	0	40.05454545	251.4543647	HDAC10;P	.
0	0	40.05454545	251.4543647	STIM1;ORA	.
0	0	30.03787879	174.6499058	STIM1;HOI	.
0	0	30.03787879	174.6499058	SLC36A1;S	.
0	0	30.03787879	174.6499058	DGKQ;DGK	.
0	0	30.03787879	174.6499058	RCN3;PKD	.
0	0	10.97560976	62.59722139	FZD4;NFAT	.
0	0	26.6989899	150.0252863	DGKQ;DGK	.
0	0	10.05945122	55.07278727	KAT2A;ZDH	.
0	0	24.02787879	130.76687	SCRIB;ZDH	.
0	0	9.529043646	50.81790294	ABHD2;DG	.
0	0	21.84242424	115.3437745	RUBCN;FY(	.
0	0	21.84242424	115.3437745	HDAC10;P	.
0	0	6.059202454	31.65001156	SLC5A6;SL(	.
0	0	5.910818495	30.38428112	SLC5A6;SL(	.
0	0	20.02121212	102.7497915	STIM1;ORA	.
0	0	18.48018648	92.29775811	MACF1;FZI	.
0	0	18.48018648	92.29775811	ZFP36L2;TI	.
0	0	18.48018648	92.29775811	SH3BP1;SC	.
0	0	18.48018648	92.29775811	DAGLA;HO	.
0	0	18.48018648	92.29775811	STIM1;ORA	.
0	0	18.48018648	92.29775811	ZFP36L2;TI	.
0	0	18.48018648	92.29775811	ARHGEF18	.
0	0	4.404857756	21.82867643	SLC36A1;R	.
0	0	8.227134146	40.72389093	HDAC10;M	.
0	0	17.15930736	83.50325379	ZC3H12D;Z	.
0	0	3.206039326	15.35953997	SLC36A1;S	.
0	0	16.01454545	76.01551263	STIM1;ORA	.
0	0	16.01454545	76.01551263	SLC5A6;SL(	.
0	0	5.045245399	23.29232198	SLC5A6;SL(	.
0	0	3.066263441	14.01191239	TRIO;PNM	.
0	0	14.12905526	63.98431788	ABHD2;PN	.
0	0	14.12905526	63.98431788	DGKQ;SSH	.
0	0	13.34343434	59.09347714	SH3BP1;FB	.

0	0	13.34343434	59.09347714	LIMD1;TNF.
0	0	6.57804878	28.76663276	STIM1;ORA.
0	0	6.57804878	28.76663276	LRP1;PKD1.
0	0	12.64051037	54.78424753	MACF1;LDI.
0	0	12.64051037	54.78424753	ABHD2;TRI.
0	0	4.52405252	19.28729139	MACF1;LRI.
0	0	12.00787879	50.96332839	SLC36A1;SI.
0	0	12.00787879	50.96332839	STIM1;ORA.
0	0	12.00787879	50.96332839	HOMER3;H.
0	0	12.00787879	50.96332839	ARHGEF18.
0	0	4.4	18.36663211	KAT2A;HDA.
0	0	2.819925743	11.74188614	TRIO;PNMA.
0	0	11.43549784	47.5559797	ZDHHC7;ZI.
0	0	11.43549784	47.5559797	ZDHHC7;ZI.
0	0	11.43549784	47.5559797	LRP1;ZDHH.
0	0	11.43549784	47.5559797	CARD9;ZBT.
0	0	11.43549784	47.5559797	HDAC10;HI.
0	0	10.91515152	44.50167231	SLC36A1;SI.
0	0	5.833300551	23.72853511	HSPB1;SOC.
0	0	5.833300551	23.72853511	SLC5A6;SLC.
0	0	2.728434505	10.93476329	MAF;HDAC.
0	0	10.4400527	41.75089922	SOGA1;GIT.
0	0	10.4400527	41.75089922	SSH3;SSH1.
0	0	4.031288344	15.71017518	FZD4;NFAT.
0	0	9.603878788	37.00338727	SSH3;SSH1.
0	0	9.603878788	37.00338727	LIMD1;TNF.
0	0	9.234032634	34.9441504	SLC36A1;SI.
0	0	9.234032634	34.9441504	PIKFYVE;AI.
0	0	9.234032634	34.9441504	ABHD2;CA.
0	0	9.234032634	34.9441504	SLC36A1;SI.
0	0	9.234032634	34.9441504	SLC36A1;SI.
0	0	5.164547038	19.43136628	BIN1;SSH3.
0	0	8.891582492	33.06103204	DGKQ;SOG.
0	0	3.748323584	13.75797375	MACF1;PL.
0	0	8.573593074	31.33359061	SSH3;SSH1.
0	0	8.573593074	31.33359061	DNMT3A;P.
0	0	3.662576687	13.1821871	RCN3;SCAM.
0	0	8.27753396	29.74435603	ZDHHC7;ZI.
0	0	8.27753396	29.74435603	LIMD1;HDA.
0	0	8.27753396	29.74435603	SLC5A6;TC.
0	0	3.060699588	10.94808504	PLXND1;ST.
0	0	8.001212121	28.27831545	SH3BP1;SC.
0	0	8.001212121	28.27831545	LIMD1;TNF.
0	0	4.693379791	16.54891068	LRP1;ZDHH.
0	0	7.742717498	26.92250145	LRP1;ZDHH.
0	0	7.742717498	26.92250145	CARD9;ZBT.
0	0	7.742717498	26.92250145	LRP1;ZDHH.

0	0	4.574096944	15.83990565	DGKQ;ZDH	.
0	0	3.502267271	12.12637973	KAT2A;HD/	.
0	0	3.476894558	11.96180498	PIKFYVE;LF	.
0	0	4.516692073	15.50182593	DAGLA;SLC	.
0	0	7.500378788	25.6656597	SCRIB;PKD	.
0	0	7.500378788	25.6656597	ABHD2;CA	.
0	0	7.272727273	24.49797886	DAGLA;ABI	.
0	0	7.272727273	24.49797886	PLXND1;SH	.
0	0	7.272727273	24.49797886	RCN3;PKD1	.
0	0	7.058467023	23.41086964	TRIO;ZFP36	.
0	0	7.058467023	23.41086964	WHRN;HSF	.
0	0	4.300740418	14.2487672	PIKFYVE;ZD	.
0	0	6.856450216	22.39678289	DAGLA;HO	.
0	0	4.151808242	13.40244577	LRP1;PKD1	.
0	0	4.151808242	13.40244577	SLC5A6;SLC	.
0	0	4.151808242	13.40244577	HGSNAT;KC	.
0	0	6.665656566	21.44905895	ZC3H12D;Z	.
0	0	29.86295181	95.34232789	RUBCN	.
0	0	29.86295181	95.34232789	ST3GAL1	.
0	0	29.86295181	95.34232789	SLC17A9	.
0	0	29.86295181	95.34232789	ZBTB7B	.
0	0	29.86295181	95.34232789	CAD	.
0	0	29.86295181	95.34232789	WHRN	.
0	0	29.86295181	95.34232789	WHRN	.
0	0	29.86295181	95.34232789	PHF2	.
0	0	29.86295181	95.34232789	DAGLA	.
0	0	29.86295181	95.34232789	LRP1	.
0	0	29.86295181	95.34232789	GIT1	.
0	0	29.86295181	95.34232789	PKD1	.
0	0	29.86295181	95.34232789	ABHD2	.
0	0	29.86295181	95.34232789	ZBTB7B	.
0	0	29.86295181	95.34232789	LRP1	.
0	0	29.86295181	95.34232789	LRFN4	.
0	0	29.86295181	95.34232789	STIM1	.
0	0	29.86295181	95.34232789	FYCO1	.
0	0	29.86295181	95.34232789	HIPK2	.
0	0	29.86295181	95.34232789	SCRIB	.
0	0	29.86295181	95.34232789	SCRIB	.
0	0	29.86295181	95.34232789	LRP1	.
0	0	29.86295181	95.34232789	GLYCTK	.
0	0	29.86295181	95.34232789	GLYCTK	.
0	0	29.86295181	95.34232789	ZDHHC7	.
0	0	29.86295181	95.34232789	HSPB1	.
0	0	29.86295181	95.34232789	PHF19	.
0	0	29.86295181	95.34232789	FUT7	.
0	0	29.86295181	95.34232789	IDH2	.
0	0	29.86295181	95.34232789	ABCD1	.

0	0	29.86295181	95.34232789	LRP1	.
0	0	29.86295181	95.34232789	CROCC	.
0	0	29.86295181	95.34232789	SCRIB	.
0	0	29.86295181	95.34232789	ABHD2	.
0	0	29.86295181	95.34232789	STIM1	.
0	0	29.86295181	95.34232789	PKD1	.
0	0	29.86295181	95.34232789	PKD1	.
0	0	29.86295181	95.34232789	PKD1	.
0	0	29.86295181	95.34232789	DPY19L3	.
0	0	29.86295181	95.34232789	DPY19L3	.
0	0	3.177429771	10.07419202	PIKFYVE;D	.
0	0	6.314194577	19.72977661	RCN3;MEA	.
0	0	6.151981352	18.94831635	SLC36A1;S	.
0	0	5.997878788	18.21325238	GNA12;HIF	.
0	0	5.997878788	18.21325238	KAT2A;LDB	.
0	0	23.88915663	72.01330731	ZBTB7B	.
0	0	23.88915663	72.01330731	SLC6A20	.
0	0	23.88915663	72.01330731	LDB1	.
0	0	23.88915663	72.01330731	LRFN4	.
0	0	23.88915663	72.01330731	ZFP36L2	.
0	0	23.88915663	72.01330731	DGKQ	.
0	0	23.88915663	72.01330731	SCRIB	.
0	0	23.88915663	72.01330731	TCN2	.
0	0	23.88915663	72.01330731	FYCO1	.
0	0	23.88915663	72.01330731	CROCC	.
0	0	23.88915663	72.01330731	FYCO1	.
0	0	23.88915663	72.01330731	SCRIB	.
0	0	23.88915663	72.01330731	MAP1S	.
0	0	23.88915663	72.01330731	SLC17A9	.
0	0	23.88915663	72.01330731	SMC1A	.
0	0	23.88915663	72.01330731	LDB1	.
0	0	23.88915663	72.01330731	ZFP36L2	.
0	0	23.88915663	72.01330731	ST3GAL1	.
0	0	23.88915663	72.01330731	SLC4A8	.
0	0	23.88915663	72.01330731	WIZ	.
0	0	23.88915663	72.01330731	BIN1	.
0	0	23.88915663	72.01330731	ABHD2	.
0	0	23.88915663	72.01330731	LDB1	.
0	0	23.88915663	72.01330731	TRIO	.
0	0	23.88915663	72.01330731	PKD1	.
0	0	23.88915663	72.01330731	SLC6A20	.
0	0	5.851293422	17.52084852	CARD9;AB	.
0	0	5.851293422	17.52084852	MACF1;PL	.
0	0	5.851293422	17.52084852	DGKQ;DGK	.
0	0	5.851293422	17.52084852	AARS2;VAF	.
0	0	2.164122137	6.437262351	DGKQ;GLY	.
0	0	5.711688312	16.86774771	ZFP36L2;TI	.

0	0	5.711688312	16.86774771	ARID1A;TR	.
0	0	5.711688312	16.86774771	ZC3H12D;Z	.
0	0	3.683735689	10.84425372	MAF;ZDHH	.
0	0	2.551961244	7.512221214	BIN1;FZD4	.
0	0	1.464452673	4.309391549	PHF2;HDA(	.
0	0	2.301713971	6.736516221	ZC3H12D;[	.
0	0	3.646341463	10.64692133	ARVCF;PLX	.
0	0	3.646341463	10.64692133	STIM1;HSP	.
0	0	5.578576462	16.25092579	SLC36A1;S	.
0	0	5.578576462	16.25092579	FUT7;ZBTB	.
0	0	5.451515152	15.66765193	IKZF1;HIPK	.
0	0	19.90662651	57.0216613	ZFP36L2	.
0	0	19.90662651	57.0216613	KAT2A	.
0	0	19.90662651	57.0216613	CAD	.
0	0	19.90662651	57.0216613	CAD	.
0	0	19.90662651	57.0216613	PIKFYVE	.
0	0	19.90662651	57.0216613	ZBTB7B	.
0	0	19.90662651	57.0216613	MAP1S	.
0	0	19.90662651	57.0216613	DGKQ	.
0	0	19.90662651	57.0216613	LDB1	.
0	0	19.90662651	57.0216613	PHF19	.
0	0	19.90662651	57.0216613	RCN3	.
0	0	19.90662651	57.0216613	SCRIB	.
0	0	19.90662651	57.0216613	DGKQ	.
0	0	19.90662651	57.0216613	NADSYN1	.
0	0	19.90662651	57.0216613	CAD	.
0	0	19.90662651	57.0216613	LRP1	.
0	0	19.90662651	57.0216613	LRP1	.
0	0	19.90662651	57.0216613	TNRC6B	.
0	0	19.90662651	57.0216613	ZFP36L2	.
0	0	19.90662651	57.0216613	SLC5A6	.
0	0	19.90662651	57.0216613	PAOX	.
0	0	19.90662651	57.0216613	LRP1	.
0	0	19.90662651	57.0216613	NFATC1	.
0	0	19.90662651	57.0216613	GLYCTK	.
0	0	19.90662651	57.0216613	FLI1	.
0	0	19.90662651	57.0216613	GIT1	.
0	0	19.90662651	57.0216613	TNRC6B	.
0	0	19.90662651	57.0216613	SLC36A1	.
0	0	19.90662651	57.0216613	ABCC10	.
0	0	19.90662651	57.0216613	RCN3	.
0	0	19.90662651	57.0216613	PKD1	.
0	0	19.90662651	57.0216613	ABCD1	.
0	0	19.90662651	57.0216613	ABCD1	.
0	0	2.83839769	8.067818994	SLC5A6;SL(	.
0	0	3.504025574	9.906008198	CUL9;MYO	.
0	0	3.504025574	9.906008198	HDAC10;LI	.

0	0	5.213965744	14.59209119	SCRIB;ZFP3	.
0	0	5.213965744	14.59209119	HOMER3;H	.
0	0	5.213965744	14.59209119	BIN1;LEMD	.
0	0	5.213965744	14.59209119	DGKQ;DGK	.
0	0	5.213965744	14.59209119	HSPB1;HDA	.
0	0	2.788751374	7.786554853	PIKFYVE;DC	.
0	0	5.102772405	14.09552417	ZDHHC7;GI	.
0	0	5.102772405	14.09552417	ZC3H12D;Z	.
0	0	17.06196213	46.66531114	HSPB1	.
0	0	17.06196213	46.66531114	SLC12A7	.
0	0	17.06196213	46.66531114	HSPB1	.
0	0	17.06196213	46.66531114	HSPB1	.
0	0	17.06196213	46.66531114	RUBCN	.
0	0	17.06196213	46.66531114	NFATC1	.
0	0	17.06196213	46.66531114	PKD1	.
0	0	17.06196213	46.66531114	LIMD1	.
0	0	17.06196213	46.66531114	HDAC10	.
0	0	17.06196213	46.66531114	PIKFYVE	.
0	0	17.06196213	46.66531114	LRP1	.
0	0	17.06196213	46.66531114	BIN1	.
0	0	17.06196213	46.66531114	ZBTB7B	.
0	0	17.06196213	46.66531114	HSPB1	.
0	0	17.06196213	46.66531114	CHD6	.
0	0	17.06196213	46.66531114	KAT2A	.
0	0	17.06196213	46.66531114	FZD4	.
0	0	17.06196213	46.66531114	SNAPC4	.
0	0	17.06196213	46.66531114	MAF	.
0	0	17.06196213	46.66531114	ST3GAL1	.
0	0	17.06196213	46.66531114	AARS2	.
0	0	17.06196213	46.66531114	TRERF1	.
0	0	17.06196213	46.66531114	CARD9	.
0	0	17.06196213	46.66531114	ZBTB7B	.
0	0	1.933555897	5.276639426	ZFHX3;KAT	.
0	0	4.996212121	13.62389695	SLC36A1;SI	.
0	0	4.996212121	13.62389695	SLC4A8;SLC	.
0	0	4.996212121	13.62389695	DGKQ;DGK	.
0	0	4.795878788	12.74883036	LEMD2;HIP	.
0	0	4.795878788	12.74883036	TRIO;MAP1	.
0	0	4.795878788	12.74883036	MEAK7;ZB1	.
0	0	4.795878788	12.74883036	LRP1;ZDHH	.
0	0	4.795878788	12.74883036	LRP1;ZDHH	.
0	0	4.795878788	12.74883036	IKZF1;HIPK	.
0	0	1.424918147	3.786301456	PHF2;HDAC	.
0	0	3.220982143	8.482169456	STIM1;ORA	.
0	0	3.220982143	8.482169456	SLC5A6;FU	.
0	0	14.92846386	39.13325854	CAD	.
0	0	14.92846386	39.13325854	SLC6A20	.

0	0	14.92846386	39.13325854	BIN1	.
0	0	14.92846386	39.13325854	SLC5A6	.
0	0	14.92846386	39.13325854	FUT7	.
0	0	14.92846386	39.13325854	FUT7	.
0	0	14.92846386	39.13325854	ABCD1	.
0	0	14.92846386	39.13325854	RUBCN	.
0	0	14.92846386	39.13325854	NFATC1	.
0	0	14.92846386	39.13325854	SCRIB	.
0	0	14.92846386	39.13325854	LRP1	.
0	0	14.92846386	39.13325854	WHRN	.
0	0	14.92846386	39.13325854	WIZ	.
0	0	14.92846386	39.13325854	ABCD1	.
0	0	14.92846386	39.13325854	FUT7	.
0	0	14.92846386	39.13325854	ABCD1	.
0	0	14.92846386	39.13325854	ABCC10	.
0	0	14.92846386	39.13325854	WHRN	.
0	0	14.92846386	39.13325854	PLXND1	.
0	0	14.92846386	39.13325854	FUT7	.
0	0	14.92846386	39.13325854	FUT7	.
0	0	3.192315994	8.341825238	STIM1;HSP	.
0	0	4.610955711	11.95499216	MACF1;LDI	.
0	0	4.610955711	11.95499216	GNA12;PKI	.
0	0	4.610955711	11.95499216	DAGLA;AB(	.
0	0	3.136479321	8.070575207	LRP1;PKD1	.
0	0	2.578130639	6.631484244	TRIO;LIMD	.
0	0	2.578130639	6.631484244	LRP1;FZD4	.
0	0	4.523727844	11.58534089	SH3BP1;HS	.
0	0	13.26907631	33.4399084	SLC36A1	.
0	0	13.26907631	33.4399084	ST3GAL1	.
0	0	13.26907631	33.4399084	GIT1	.
0	0	13.26907631	33.4399084	DGKQ	.
0	0	13.26907631	33.4399084	ADCY9	.
0	0	13.26907631	33.4399084	GIT1	.
0	0	13.26907631	33.4399084	SLC12A7	.
0	0	13.26907631	33.4399084	ABCD1	.
0	0	13.26907631	33.4399084	FUT7	.
0	0	13.26907631	33.4399084	GIT1	.
0	0	13.26907631	33.4399084	HIPK2	.
0	0	13.26907631	33.4399084	KAT2A	.
0	0	13.26907631	33.4399084	PIKFYVE	.
0	0	13.26907631	33.4399084	ZBTB7B	.
0	0	13.26907631	33.4399084	CARD9	.
0	0	13.26907631	33.4399084	DNMT3A	.
0	0	13.26907631	33.4399084	CARD9	.
0	0	13.26907631	33.4399084	WHRN	.
0	0	13.26907631	33.4399084	ZBTB7B	.
0	0	13.26907631	33.4399084	LRP1	.

0	0	13.26907631	33.4399084	AP2A2	.
0	0	13.26907631	33.4399084	AP2A2	.
0	0	13.26907631	33.4399084	SCRIB	.
0	0	13.26907631	33.4399084	SLC12A7	.
0	0	13.26907631	33.4399084	ABCD1	.
0	0	13.26907631	33.4399084	ST3GAL1	.
0	0	13.26907631	33.4399084	ZBTB7B	.
0	0	4.358787879	10.89505916	SLC36A1;S	.
0	0	4.358787879	10.89505916	DAGLA;AB	.
0	0	2.484219847	6.137260868	FUT7;DGK	.
0	0	2.955467813	7.211018789	PIKFYVE;ZI	.
0	0	11.94156627	29.00529984	BIN1	.
0	0	11.94156627	29.00529984	KAT2A	.
0	0	11.94156627	29.00529984	PIKFYVE	.
0	0	11.94156627	29.00529984	BIN1	.
0	0	11.94156627	29.00529984	CARD9	.
0	0	11.94156627	29.00529984	NFATC1	.
0	0	11.94156627	29.00529984	LRP1	.
0	0	11.94156627	29.00529984	BIN1	.
0	0	11.94156627	29.00529984	DNMT3A	.
0	0	11.94156627	29.00529984	ARID1A	.
0	0	11.94156627	29.00529984	ABCD1	.
0	0	11.94156627	29.00529984	ZC3H3	.
0	0	11.94156627	29.00529984	HIPK2	.
0	0	11.94156627	29.00529984	LRP1	.
0	0	11.94156627	29.00529984	SH3BP1	.
0	0	11.94156627	29.00529984	ABCD1	.
0	0	11.94156627	29.00529984	FUT7	.
0	0	11.94156627	29.00529984	WIZ	.
0	0	11.94156627	29.00529984	LRP1	.
0	0	11.94156627	29.00529984	LEMD2	.
0	0	11.94156627	29.00529984	LIMD1	.
0	0	11.94156627	29.00529984	LRP1	.
0	0	11.94156627	29.00529984	TEP1	.
0	0	11.94156627	29.00529984	DGKQ	.
0	0	11.94156627	29.00529984	SCRIB	.
0	0	2.931290898	7.098566764	KAT2A;PKI	.
0	0	4.132706374	9.968088831	CAD;HIPK2	.
0	0	4.132706374	9.968088831	PKD1;NEC1	.
0	0	4.062455059	9.684738326	RUBCN;LRI	.
0	0	4.062455059	9.684738326	ZDHHC7;ZI	.
0	0	1.854923414	4.372354953	HDAC10;LI	.
0	0	10.85542169	25.4671095	HOMER3	.
0	0	10.85542169	25.4671095	HOMER3	.
0	0	10.85542169	25.4671095	SH3BP1	.
0	0	10.85542169	25.4671095	DGKQ	.
0	0	10.85542169	25.4671095	SLC17A9	.

0	0	10.85542169	25.4671095	BIN1	.
0	0	10.85542169	25.4671095	ZBTB7B	.
0	0	10.85542169	25.4671095	NFATC1	.
0	0	10.85542169	25.4671095	ANKRD13D	.
0	0	10.85542169	25.4671095	FUT7	.
0	0	10.85542169	25.4671095	HIPK2	.
0	0	10.85542169	25.4671095	LIMD1	.
0	0	10.85542169	25.4671095	PKD1	.
0	0	10.85542169	25.4671095	PIKFYVE	.
0	0	10.85542169	25.4671095	RCN3	.
0	0	10.85542169	25.4671095	ABCD1	.
0	0	10.85542169	25.4671095	CAD	.
0	0	10.85542169	25.4671095	BIN1	.
0	0	10.85542169	25.4671095	ABCD1	.
0	0	10.85542169	25.4671095	IDH2	.
0	0	10.85542169	25.4671095	CARD9	.
0	0	10.85542169	25.4671095	FBXO31	.
0	0	1.563027295	3.602292875	ZFHX3;HDA	.
0	0	3.865298143	8.901911666	BIN1;ABCD	.
0	0	3.865298143	8.901911666	RCN3;ABCI	.
0	0	2.772467167	6.374218821	ZFHX3;FUT	.
0	0	3.803751804	8.66138505	MACF1;LDI	.
0	0	9.950301205	22.58798506	ABCD1	.
0	0	9.950301205	22.58798506	CARD9	.
0	0	9.950301205	22.58798506	SOGA1	.
0	0	9.950301205	22.58798506	LIMD1	.
0	0	9.950301205	22.58798506	BIN1	.
0	0	9.950301205	22.58798506	ABCD1	.
0	0	9.950301205	22.58798506	ZFP36L2	.
0	0	9.950301205	22.58798506	ARID1A	.
0	0	9.950301205	22.58798506	FUT7	.
0	0	9.950301205	22.58798506	PKD1	.
0	0	9.950301205	22.58798506	STIM1	.
0	0	9.950301205	22.58798506	CARD9	.
0	0	9.950301205	22.58798506	ZBTB7B	.
0	0	9.950301205	22.58798506	ABCD1	.
0	0	9.950301205	22.58798506	ZDHHC7	.
0	0	9.950301205	22.58798506	ABCD1	.
0	0	9.950301205	22.58798506	ZBTB7B	.
0	0	9.950301205	22.58798506	ZDHHC8	.
0	0	9.950301205	22.58798506	ZBTB7B	.
0	0	9.950301205	22.58798506	CARD9	.
0	0	9.950301205	22.58798506	LRP1	.
0	0	9.950301205	22.58798506	PLXND1	.
0	0	9.950301205	22.58798506	TNRC6B	.
0	0	9.950301205	22.58798506	PKD1	.
0	0	9.950301205	22.58798506	MAP1S	.

0	0	9.950301205	22.58798506	PKD1	.
0	0	3.744128788	8.430170624	ARVCF;FBF	.
0	0	3.744128788	8.430170624	AAK1;ZDHI	.
0	0	3.686340326	8.207784581	SLC5A6;SL(	.
0	0	3.686340326	8.207784581	CAD;HIPK2	.
0	0	1.782973684	3.938258769	PHF2;KAT2	.
0	0	2.649345409	5.830493282	KCNH4;KCI	.
0	0	9.184430028	20.20632858	IDH2	.
0	0	9.184430028	20.20632858	CAD	.
0	0	9.184430028	20.20632858	LRP1	.
0	0	9.184430028	20.20632858	MACF1	.
0	0	9.184430028	20.20632858	ADCY9	.
0	0	9.184430028	20.20632858	ABCD1	.
0	0	9.184430028	20.20632858	LRP1	.
0	0	9.184430028	20.20632858	ZBTB7B	.
0	0	9.184430028	20.20632858	DAGLA	.
0	0	9.184430028	20.20632858	PKD1	.
0	0	9.184430028	20.20632858	ZBTB7B	.
0	0	9.184430028	20.20632858	ZBTB7B	.
0	0	9.184430028	20.20632858	ZBTB7B	.
0	0	9.184430028	20.20632858	PKD1	.
0	0	9.184430028	20.20632858	CARD9	.
0	0	9.184430028	20.20632858	ZBTB7B	.
0	0	9.184430028	20.20632858	LRFN4	.
0	0	9.184430028	20.20632858	FYCO1	.
0	0	9.184430028	20.20632858	ZFP36L2	.
0	0	2.218314438	4.812756199	MAF;TAF1(	.
0	0	2.610683987	5.663090164	TRIO;SH3B	.
0	0	3.523172906	7.589219426	PIKFYVE;ZI	.
0	0	3.523172906	7.589219426	ABHD2;AB(	.
0	0	8.527969019	18.20854229	CAD	.
0	0	8.527969019	18.20854229	ARID1A	.
0	0	8.527969019	18.20854229	ABCD1	.
0	0	8.527969019	18.20854229	AAK1	.
0	0	8.527969019	18.20854229	HSPB1	.
0	0	8.527969019	18.20854229	SSH1	.
0	0	8.527969019	18.20854229	LRP1	.
0	0	8.527969019	18.20854229	LRP1	.
0	0	8.527969019	18.20854229	KAT2A	.
0	0	8.527969019	18.20854229	WHRN	.
0	0	8.527969019	18.20854229	TNRC6B	.
0	0	8.527969019	18.20854229	ABCD1	.
0	0	8.527969019	18.20854229	ST3GAL1	.
0	0	8.527969019	18.20854229	PYGB	.
0	0	8.527969019	18.20854229	HSPB1	.
0	0	8.527969019	18.20854229	PYGB	.
0	0	8.527969019	18.20854229	ZC3H12D	.

0	0	8.527969019	18.20854229	ABHD2	.
0	0	8.527969019	18.20854229	SCRIB	.
0	0	8.527969019	18.20854229	ABHD2	.
0	0	8.527969019	18.20854229	TEP1	.
0	0	3.471936759	7.397906699	KCNC3;PKI	.
0	0	3.471936759	7.397906699	ABHD2;AB	.
0	0	3.471936759	7.397906699	CROCC;ME	.
0	0	3.471936759	7.397906699	DGKQ;GNA	.
0	0	3.422164502	7.213432098	SSH3;SSH1	.
0	0	1.730674847	3.634484938	DGKQ;GLY	.
0	0	3.373794281	7.035468743	PLXND1;FZ	.
0	0	3.373794281	7.035468743	LRP1;SH3B	.
0	0	3.373794281	7.035468743	CARD9;HIP	.
0	0	7.959036145	16.51258703	LRP1	.
0	0	7.959036145	16.51258703	ZBTB7B	.
0	0	7.959036145	16.51258703	PYGB	.
0	0	7.959036145	16.51258703	ZFP36L2	.
0	0	7.959036145	16.51258703	ABCD1	.
0	0	7.959036145	16.51258703	CARD9	.
0	0	7.959036145	16.51258703	PKD1	.
0	0	7.959036145	16.51258703	ABCD1	.
0	0	7.959036145	16.51258703	ABCD1	.
0	0	7.959036145	16.51258703	SH3BP1	.
0	0	7.959036145	16.51258703	DGKQ	.
0	0	7.959036145	16.51258703	FUT7	.
0	0	7.959036145	16.51258703	SMC1A	.
0	0	7.959036145	16.51258703	NTN3	.
0	0	2.119510284	4.350617118	RUBCN;HS	.
0	0	2.449726232	4.98396725	ZFHX3;MA	.
0	0	3.236527437	6.537664336	LEMD2;HIP	.
0	0	3.236527437	6.537664336	MYO19;GI	.
0	0	3.236527437	6.537664336	SLC4A8;SL	.
0	0	3.236527437	6.537664336	SLC5A6;TC	.
0	0	7.46121988	15.05783203	GIT1	.
0	0	7.46121988	15.05783203	ADCY9	.
0	0	7.46121988	15.05783203	ADCY9	.
0	0	7.46121988	15.05783203	NFATC1	.
0	0	7.46121988	15.05783203	SLC17A9	.
0	0	7.46121988	15.05783203	LRP1	.
0	0	7.46121988	15.05783203	DGKQ	.
0	0	7.46121988	15.05783203	PAOX	.
0	0	7.46121988	15.05783203	SCRIB	.
0	0	7.46121988	15.05783203	DGKQ	.
0	0	7.46121988	15.05783203	PKD1	.
0	0	7.46121988	15.05783203	CARD9	.
0	0	7.46121988	15.05783203	LDB1	.
0	0	7.46121988	15.05783203	DGKQ	.

0	0	7.46121988	15.05783203	SLC4A8	.
0	0	7.46121988	15.05783203	PKD1	.
0	0	7.46121988	15.05783203	PLXND1	.
0	0	7.46121988	15.05783203	PKD1	.
0	0	7.46121988	15.05783203	BIN1	.
0	0	2.416598461	4.847866978	SH3BP1;M	.
0	0	7.021970234	13.79856469	ABCD1	.
0	0	7.021970234	13.79856469	SLC17A9	.
0	0	7.021970234	13.79856469	BIN1	.
0	0	7.021970234	13.79856469	NFATC1	.
0	0	7.021970234	13.79856469	ZFP36L2	.
0	0	7.021970234	13.79856469	ZBTB7B	.
0	0	7.021970234	13.79856469	KAT2A	.
0	0	7.021970234	13.79856469	ZDHHC7	.
0	0	7.021970234	13.79856469	ZFP36L2	.
0	0	7.021970234	13.79856469	ARID1A	.
0	0	7.021970234	13.79856469	ABCD1	.
0	0	7.021970234	13.79856469	ARID1A	.
0	0	7.021970234	13.79856469	ZC3H3	.
0	0	7.021970234	13.79856469	HSPB1	.
0	0	7.021970234	13.79856469	LRFN4	.
0	0	7.021970234	13.79856469	LRFN4	.
0	0	7.021970234	13.79856469	SCRIB	.
0	0	7.021970234	13.79856469	HDAC7	.
0	0	7.021970234	13.79856469	BIN1	.
0	0	7.021970234	13.79856469	ARID1A	.
0	0	7.021970234	13.79856469	CARD9	.
0	0	3.10995671	6.088430734	ZFHX3;BIN	.
0	0	3.06993007	5.948382017	LEMD2;HIF	.
0	0	3.06993007	5.948382017	TRIO;ZFP3(	.
0	0	3.06993007	5.948382017	ZFHX3;FUT	.
0	0	6.631526104	12.69971333	TRIOBP	.
0	0	6.631526104	12.69971333	ABCD1	.
0	0	6.631526104	12.69971333	TRIOBP	.
0	0	6.631526104	12.69971333	KAT2A	.
0	0	6.631526104	12.69971333	HSPB1	.
0	0	6.631526104	12.69971333	ADCY9	.
0	0	6.631526104	12.69971333	DGKZ	.
0	0	6.631526104	12.69971333	PKD1	.
0	0	6.631526104	12.69971333	DAGLA	.
0	0	6.631526104	12.69971333	DNMT3A	.
0	0	6.631526104	12.69971333	DNMT3A	.
0	0	6.631526104	12.69971333	SCRIB	.
0	0	6.631526104	12.69971333	KAT2A	.
0	0	6.631526104	12.69971333	ABCD1	.
0	0	6.631526104	12.69971333	SLC4A8	.
0	0	6.631526104	12.69971333	CROCC	.

0	0	6.631526104	12.69971333	KAT2A	.
0	0	6.631526104	12.69971333	KAT2A	.
0	0	6.631526104	12.69971333	MYO19	.
0	0	6.631526104	12.69971333	BIN1	.
0	0	2.307340525	4.408252246	PIKFYVE;C/	.
0	0	2.992878788	5.68158932	ARVCF;NE(	.
0	0	2.992878788	5.68158932	AP2A2;GIT	.
0	0	1.438333917	2.730050866	CUL9;SPSB	.
0	0	2.955780022	5.554471164	HSPB1;GIT	.
0	0	2.955780022	5.554471164	LIMD1;HD/	.
0	0	6.282181357	11.73395305	ARID1A	.
0	0	6.282181357	11.73395305	ADCY9	.
0	0	6.282181357	11.73395305	LIMD1	.
0	0	6.282181357	11.73395305	ZFP36L2	.
0	0	6.282181357	11.73395305	CUL9	.
0	0	6.282181357	11.73395305	ZDHHC7	.
0	0	6.282181357	11.73395305	LRP1	.
0	0	6.282181357	11.73395305	SLC27A3	.
0	0	6.282181357	11.73395305	PKD1	.
0	0	6.282181357	11.73395305	PHF2	.
0	0	6.282181357	11.73395305	NFATC1	.
0	0	6.282181357	11.73395305	IKZF1	.
0	0	2.919586105	5.43130559	MYO19;GI	.
0	0	2.919586105	5.43130559	MEAK7;ZB	.
0	0	2.235115892	4.125676436	KAT2A;PKI	.
0	0	2.88426433	5.311929409	FZD4;AP2A	.
0	0	1.677623899	3.07684852	RCN3;TRIO	.
0	0	2.84978355	5.196187912	SH3BP1;AF	.
0	0	5.967771084	10.87970162	MYO19	.
0	0	5.967771084	10.87970162	DGKQ	.
0	0	5.967771084	10.87970162	GIT1	.
0	0	5.967771084	10.87970162	GNA12	.
0	0	5.967771084	10.87970162	SH3BP1	.
0	0	5.967771084	10.87970162	ABCD1	.
0	0	5.967771084	10.87970162	TCN2	.
0	0	5.967771084	10.87970162	LEMD2	.
0	0	5.967771084	10.87970162	ADCY9	.
0	0	5.967771084	10.87970162	ADCY9	.
0	0	5.967771084	10.87970162	ABCD1	.
0	0	5.967771084	10.87970162	HIPK2	.
0	0	5.967771084	10.87970162	ABCD1	.
0	0	5.967771084	10.87970162	CHD6	.
0	0	5.967771084	10.87970162	NADSYN1	.
0	0	5.967771084	10.87970162	LEMD2	.
0	0	2.816114082	5.083934335	ORAI1;PKD	.
0	0	2.816114082	5.083934335	SLC4A8;SL(	.
0	0	2.180487805	3.916334459	HDAC10;T/	.

0	0	2.783227625	4.975029372	FZD4;AP2A	.
0	0	2.167242139	3.866156159	DGKQ;PKD	.
0	0	5.683304647	10.11970296	DPY19L3	.
0	0	5.683304647	10.11970296	LDB1	.
0	0	5.683304647	10.11970296	SOGA1	.
0	0	5.683304647	10.11970296	MACF1	.
0	0	5.683304647	10.11970296	PIKFYVE	.
0	0	5.683304647	10.11970296	ABCD1	.
0	0	5.683304647	10.11970296	RCN3	.
0	0	5.683304647	10.11970296	TCN2	.
0	0	5.683304647	10.11970296	ABCD1	.
0	0	2.154155104	3.816804073	LRFN4;PKD	.
0	0	2.751097179	4.869340715	FAM53B;A	.
0	0	1.738296582	3.070611364	CLIP2;COL	.
0	0	2.141223868	3.768260718	TRIO;MAP	.
0	0	1.563090278	2.731073517	HDAC10;LI	.
0	0	5.424698795	9.440007322	ABCD1	.
0	0	5.424698795	9.440007322	FUT7	.
0	0	5.424698795	9.440007322	DNMT3A	.
0	0	5.424698795	9.440007322	RCN3	.
0	0	5.424698795	9.440007322	ZFP36L2	.
0	0	5.424698795	9.440007322	DGKQ	.
0	0	5.424698795	9.440007322	MAP1S	.
0	0	5.424698795	9.440007322	MEAK7	.
0	0	5.424698795	9.440007322	FYCO1	.
0	0	2.689002383	4.667115564	LRP1;SH3B	.
0	0	2.689002383	4.667115564	LDB1;ZFP3	.
0	0	5.188580409	8.829225048	FUT7	.
0	0	5.188580409	8.829225048	HDAC7	.
0	0	5.188580409	8.829225048	ARHGEF18	.
0	0	5.188580409	8.829225048	CARD9	.
0	0	5.188580409	8.829225048	PNPLA6	.
0	0	5.188580409	8.829225048	HIPK2	.
0	0	5.188580409	8.829225048	ABCC10	.
0	0	5.188580409	8.829225048	ZBTB7B	.
0	0	5.188580409	8.829225048	CHD6	.
0	0	5.188580409	8.829225048	HIPK2	.
0	0	5.188580409	8.829225048	SLC12A7	.
0	0	1.819018405	3.055246821	ZFHX3;MA	.
0	0	2.572825024	4.296122927	ZC3H12D;Z	.
0	0	4.972138554	8.277972209	DGKZ	.
0	0	4.972138554	8.277972209	AP2A2	.
0	0	4.972138554	8.277972209	PKD1	.
0	0	4.972138554	8.277972209	RUBCN	.
0	0	4.972138554	8.277972209	DGKQ	.
0	0	4.972138554	8.277972209	LRP1	.
0	0	4.972138554	8.277972209	MAP1S	.

0	0	4.972138554	8.277972209	MYO19	.
0	0	4.972138554	8.277972209	ABCD1	.
0	0	4.972138554	8.277972209	PKD1	.
0	0	4.972138554	8.277972209	PKD1	.
0	0	2.008516147	3.283094279	HOMER3;A	.
0	0	4.773012048	7.778453273	GIT1	.
0	0	4.773012048	7.778453273	RUBCN	.
0	0	4.773012048	7.778453273	HIPK2	.
0	0	4.773012048	7.778453273	ANKRD13D	.
0	0	4.773012048	7.778453273	AP2A2	.
0	0	4.773012048	7.778453273	KAT2A	.
0	0	4.773012048	7.778453273	PHF19	.
0	0	4.773012048	7.778453273	PHF2	.
0	0	4.773012048	7.778453273	MEAK7	.
0	0	4.773012048	7.778453273	PKD1	.
0	0	4.773012048	7.778453273	IKZF1	.
0	0	1.650810609	2.687017455	RCN3;SCAM	.
0	0	2.492045455	4.044011932	PIKFYVE;AI	.
0	0	2.466229303	3.964480733	SLC4A8;SL(	.
0	0	2.466229303	3.964480733	CARD9;HIP	.
0	0	4.589202966	7.324143016	ABCD1	.
0	0	4.589202966	7.324143016	LDB1	.
0	0	4.589202966	7.324143016	PLXND1	.
0	0	4.589202966	7.324143016	ZFP36L2	.
0	0	4.589202966	7.324143016	SLC6A20	.
0	0	4.589202966	7.324143016	PIKFYVE	.
0	0	4.589202966	7.324143016	SLC12A7	.
0	0	4.589202966	7.324143016	PKD1	.
0	0	4.589202966	7.324143016	ARHGEF18	.
0	0	2.440940012	3.887069778	PIKFYVE;AI	.
0	0	2.416161616	3.811704769	LRP1;ZDHH	.
0	0	4.419009371	6.909541334	SLC5A6	.
0	0	4.419009371	6.909541334	SCRIB	.
0	0	4.419009371	6.909541334	ZFP36L2	.
0	0	4.419009371	6.909541334	HOMER3	.
0	0	4.419009371	6.909541334	HSPB1	.
0	0	4.419009371	6.909541334	LDB1	.
0	0	4.419009371	6.909541334	ZFP36L2	.
0	0	4.419009371	6.909541334	MAP1S	.
0	0	4.419009371	6.909541334	KAT2A	.
0	0	4.419009371	6.909541334	DGKQ	.
0	0	4.419009371	6.909541334	PNPLA6	.
0	0	4.419009371	6.909541334	PYGB	.
0	0	4.419009371	6.909541334	ZC3H12D	.
0	0	4.419009371	6.909541334	GIT1	.
0	0	4.419009371	6.909541334	KAT2A	.
0	0	4.419009371	6.909541334	ST3GAL1	.

0	0	4.419009371	6.909541334	SNAPC4	.
0	0	2.368076808	3.666831567	PIKFYVE;AI	.
0	0	2.368076808	3.666831567	KAT2A;ARI	.
0	0	4.260972461	6.529982266	ABCD1	.
0	0	4.260972461	6.529982266	SH3BP1	.
0	0	4.260972461	6.529982266	KAT2A	.
0	0	2.32185937	3.529329049	CARD9;HIP	.
0	0	1.881177372	2.840809151	ANKRD13D	.
0	0	2.299417249	3.463187825	ARHGEF18	.
0	0	2.299417249	3.463187825	PIKFYVE;FA	.
0	0	4.113834649	6.181483847	LRP1	.
0	0	4.113834649	6.181483847	GIT1	.
0	0	4.113834649	6.181483847	SH3BP1	.
0	0	4.113834649	6.181483847	ZDHHC7	.
0	0	4.113834649	6.181483847	MACF1	.
0	0	4.113834649	6.181483847	DGKZ	.
0	0	4.113834649	6.181483847	SLC4A8	.
0	0	4.113834649	6.181483847	TAF1C	.
0	0	4.113834649	6.181483847	SCRIB	.
0	0	2.255803316	3.335839875	LEMD2;HIP	.
0	0	3.976506024	5.860628975	HGSNAT	.
0	0	3.976506024	5.860628975	PKD1	.
0	0	3.976506024	5.860628975	SLC4A8	.
0	0	3.976506024	5.860628975	MAP1S	.
0	0	3.976506024	5.860628975	ADCY9	.
0	0	3.976506024	5.860628975	FUT7	.
0	0	3.976506024	5.860628975	SCRIB	.
0	0	1.842213884	2.710246915	SH3BP1;LIN	.
0	0	2.23460776	3.274525975	SLC27A3;A	.
0	0	2.23460776	3.274525975	SLC4A8;DC	.
0	0	3.848037311	5.564470136	NFATC1	.
0	0	3.848037311	5.564470136	HDAC7	.
0	0	3.848037311	5.564470136	MACF1	.
0	0	3.848037311	5.564470136	MEAK7	.
0	0	3.848037311	5.564470136	PHF2	.
0	0	3.848037311	5.564470136	ABCD1	.
0	0	3.848037311	5.564470136	TAF1C	.
0	0	3.848037311	5.564470136	CARD9	.
0	0	2.173333333	3.099426593	LRP1;SH3B	.
0	0	2.173333333	3.099426593	PIKFYVE;PI	.
0	0	3.727597892	5.29045261	LRP1	.
0	0	3.727597892	5.29045261	ZBTB7B	.
0	0	3.727597892	5.29045261	ST3GAL1	.
0	0	3.727597892	5.29045261	FYCO1	.
0	0	3.727597892	5.29045261	ABCD1	.
0	0	3.727597892	5.29045261	BIN1	.
0	0	1.777740884	2.499302358	RCN3;SPSB	.

0	0	2.134307359	2.989603164	ARHGEF18	.
0	0	3.614457831	5.036352138	SCRIB	.
0	0	3.614457831	5.036352138	BIN1	.
0	0	3.614457831	5.036352138	DGKQ	.
0	0	3.614457831	5.036352138	HSPB1	.
0	0	3.614457831	5.036352138	SCRIB	.
0	0	3.614457831	5.036352138	TM7SF2	.
0	0	3.614457831	5.036352138	SMC1A	.
0	0	3.614457831	5.036352138	TAF1C	.
0	0	3.614457831	5.036352138	LEMD2	.
0	0	2.115312416	2.93663598	LDB1;CARD	.
0	0	2.096650718	2.884911991	SLC36A1;S	.
0	0	3.507973069	4.800223982	PIKFYVE	.
0	0	3.507973069	4.800223982	SLC4A8	.
0	0	3.507973069	4.800223982	KAT2A	.
0	0	3.507973069	4.800223982	LRP1	.
0	0	3.507973069	4.800223982	SCRIB	.
0	0	3.507973069	4.800223982	TM7SF2	.
0	0	3.507973069	4.800223982	RUBCN	.
0	0	3.507973069	4.800223982	DGKZ	.
0	0	3.507973069	4.800223982	DGKQ	.
0	0	3.507973069	4.800223982	SLC4A8	.
0	0	3.507973069	4.800223982	HIPK2	.
0	0	1.488067886	2.030827718	MACF1;PL	.
0	0	2.07831357	2.834393241	PLXND1;FZ	.
0	0	3.40757315	4.58036104	ADCY9	.
0	0	3.40757315	4.58036104	NFATC1	.
0	0	3.40757315	4.58036104	PKD1	.
0	0	3.40757315	4.58036104	DGKQ	.
0	0	3.40757315	4.58036104	MACF1	.
0	0	3.40757315	4.58036104	HSPB1	.
0	0	3.40757315	4.58036104	ANKRD13D	.
0	0	3.40757315	4.58036104	MACF1	.
0	0	3.40757315	4.58036104	HIPK2	.
0	0	3.40757315	4.58036104	TRIOBP	.
0	0	2.025166923	2.689710249	BIN1;LIMD	.
0	0	3.312751004	4.375259203	SLC36A1	.
0	0	3.312751004	4.375259203	HSPB1	.
0	0	3.312751004	4.375259203	LDB1	.
0	0	3.312751004	4.375259203	SLC4A8	.
0	0	3.312751004	4.375259203	SH3BP1	.
0	0	3.312751004	4.375259203	PIKFYVE	.
0	0	3.312751004	4.375259203	ORAI1	.
0	0	3.312751004	4.375259203	CAD	.
0	0	3.312751004	4.375259203	LEMD2	.
0	0	1.991212121	2.59864755	HSPB1;ZFP	.
0	0	1.991212121	2.59864755	RCN3;PKD1	.

0	0	1.991212121	2.59864755	KCNH4;KCI	.
0	0	3.22305438	4.183588541	PHC3	.
0	0	3.22305438	4.183588541	MACF1	.
0	0	3.22305438	4.183588541	HIPK2	.
0	0	3.22305438	4.183588541	PKD1	.
0	0	3.22305438	4.183588541	DGKQ	.
0	0	3.22305438	4.183588541	TM7SF2	.
0	0	3.22305438	4.183588541	SCRIB	.
0	0	1.974655647	2.554639905	PLXND1;M	.
0	0	3.13807863	4.004169212	ANKRD13D	.
0	0	3.13807863	4.004169212	TRERF1	.
0	0	3.13807863	4.004169212	BIN1	.
0	0	3.13807863	4.004169212	HDAC10	.
0	0	3.13807863	4.004169212	DGKQ	.
0	0	3.13807863	4.004169212	PLXND1	.
0	0	3.13807863	4.004169212	AAK1	.
0	0	3.13807863	4.004169212	KAT2A	.
0	0	3.13807863	4.004169212	MYO19	.
0	0	1.942350333	2.469526515	LDB1;HSPB	.
0	0	1.309204325	1.663438644	TRIO;PNM/	.
0	0	1.926588465	2.428365692	PIKFYVE;PI	.
0	0	1.926588465	2.428365692	LRFN4;PLX	.
0	0	3.057460612	3.835951229	FZD4	.
0	0	3.057460612	3.835951229	ST3GAL1	.
0	0	3.057460612	3.835951229	PKD1	.
0	0	1.409440813	1.74212915	ZFHX3;HDA	.
0	0	2.980873494	3.677997369	PHC3	.
0	0	2.980873494	3.677997369	ABCD1	.
0	0	2.980873494	3.677997369	PLXND1	.
0	0	2.980873494	3.677997369	HECTD4	.
0	0	2.980873494	3.677997369	ZFP36L2	.
0	0	2.980873494	3.677997369	HIPK2	.
0	0	1.880792174	2.310156452	ZDHHC7;SC	.
0	0	1.866003788	2.272430167	FUT7;ST3G	.
0	0	2.908022333	3.529468697	ARID1A	.
0	0	2.908022333	3.529468697	NECTIN1	.
0	0	2.908022333	3.529468697	SLC12A7	.
0	0	1.851444679	2.235503897	LIMD1;HIP	.
0	0	2.838640275	3.389612232	FUT7	.
0	0	2.838640275	3.389612232	FZD4	.
0	0	2.838640275	3.389612232	FZD4	.
0	0	1.445851018	1.708106189	KAT2A;CAF	.
0	0	1.44142213	1.69406966	HERC2;FAM	.
0	0	2.77248529	3.257750411	PKD1	.
0	0	2.77248529	3.257750411	SLC6A20	.
0	0	2.77248529	3.257750411	DAGLA	.
0	0	2.77248529	3.257750411	LRP1	.

0	0	2.77248529	3.257750411	HSPB1	.
0	0	2.77248529	3.257750411	SLC12A7	.
0	0	2.77248529	3.257750411	SMC1A	.
0	0	2.709337349	3.133272044	HSPB1	.
0	0	2.709337349	3.133272044	AAK1	.
0	0	2.709337349	3.133272044	MAP1S	.
0	0	1.354044467	1.550415575	DAGLA;PLX	.
0	0	2.648995984	3.015624531	RCN3	.
0	0	2.648995984	3.015624531	DGKZ	.
0	0	2.648995984	3.015624531	CROCC	.
0	0	1.402731051	1.573543595	KAT2A;LRP	.
0	0	1.402731051	1.573543595	CUL9;SPSB	.
0	0	2.591278156	2.904307134	SSH1	.
0	0	2.591278156	2.904307134	LRFN4	.
0	0	2.591278156	2.904307134	FUT7	.
0	0	2.591278156	2.904307134	KAT2A	.
0	0	1.729907773	1.935795548	TRIO;MAP1	.
0	0	1.729907773	1.935795548	HDAC10;HI	.
0	0	1.717375191	1.905781167	ABCD1;TRI	.
0	0	2.536016406	2.798865145	ADCY9	.
0	0	2.536016406	2.798865145	MYO19	.
0	0	2.536016406	2.798865145	SSH1	.
0	0	2.536016406	2.798865145	HDAC10	.
0	0	2.536016406	2.798865145	LRP1	.
0	0	2.536016406	2.798865145	MACF1	.
0	0	2.536016406	2.798865145	ABCD1	.
0	0	1.705021645	1.876362803	GNA12;RG	.
0	0	1.705021645	1.876362803	PIKFYVE;CH	.
0	0	2.483057229	2.698884815	NECTIN1	.
0	0	2.483057229	2.698884815	LRP1	.
0	0	2.483057229	2.698884815	SSH1	.
0	0	2.483057229	2.698884815	FUT7	.
0	0	2.483057229	2.698884815	BIN1	.
0	0	2.483057229	2.698884815	CARD9	.
0	0	2.483057229	2.698884815	HSPB1	.
0	0	2.483057229	2.698884815	IDH2	.
0	0	1.474706414	1.599208243	FZD4;CARD	.
0	0	2.432259651	2.603988937	TM7SF2	.
0	0	2.432259651	2.603988937	TRIOBP	.
0	0	2.432259651	2.603988937	ORAI1	.
0	0	1.657323232	1.764354031	HSPB1;ZFP	.
0	0	1.237924668	1.312384058	ZFHX3;HDA	.
0	0	1.199687416	1.267589504	ZFHX3;KAT	.
0	0	2.383493976	2.51383297	PLXND1	.
0	0	2.383493976	2.51383297	MACF1	.
0	0	2.383493976	2.51383297	RUBCN	.
0	0	2.383493976	2.51383297	HSPB1	.

0	0	2.383493976	2.51383297	TRIOBP	.
0	0	2.383493976	2.51383297	ZBTB7B	.
0	0	2.383493976	2.51383297	PITPNM2	.
0	0	2.383493976	2.51383297	WHRN	.
0	0	2.383493976	2.51383297	HIPK2	.
0	0	2.383493976	2.51383297	LEMD2	.
0	0	2.383493976	2.51383297	LEMD2	.
0	0	1.438730532	1.503111693	MACF1;AA	.
0	0	1.291230035	1.345145222	ZFHX3;HD/	.
0	0	2.33664068	2.42810165	SOGA1	.
0	0	2.33664068	2.42810165	PKD1	.
0	0	2.33664068	2.42810165	DENND1C	.
0	0	2.33664068	2.42810165	ABCD1	.
0	0	2.33664068	2.42810165	MACF1	.
0	0	1.623252938	1.685909956	RCN3;SH3E	.
0	0	1.432902439	1.487773168	FZD4;FAM!	.
0	0	1.612203112	1.660753037	KAT2A;CAF	.
0	0	2.291589435	2.346506007	FYCO1	.
0	0	1.590545455	1.611854638	DGKQ;HSP	.
0	0	2.248238236	2.268780734	LEMD2	.
0	0	2.248238236	2.268780734	TNRC6B	.
0	0	2.248238236	2.268780734	CLIP2	.
0	0	2.248238236	2.268780734	BIN1	.
0	0	2.248238236	2.268780734	HGSNAT	.
0	0	1.579931768	1.58809065	MACF1;FAI	.
0	0	2.206492637	2.194681863	STIM1	.
0	0	2.206492637	2.194681863	FUT7	.
0	0	1.548917749	1.519411388	ZFHX3;BIN	.
0	0	2.16626506	2.123984704	ABCD1	.
0	0	2.16626506	2.123984704	ZDHHC7	.
0	0	2.16626506	2.123984704	HGSNAT	.
0	0	2.16626506	2.123984704	HSPB1	.
0	0	2.16626506	2.123984704	GNA12	.
0	0	2.16626506	2.123984704	HIPK2	.
0	0	2.16626506	2.123984704	TEP1	.
0	0	2.127474182	2.05648202	DAGLA	.
0	0	2.127474182	2.05648202	LRP1	.
0	0	2.127474182	2.05648202	CUL9	.
0	0	2.127474182	2.05648202	IDH2	.
0	0	2.127474182	2.05648202	PIKFYVE	.
0	0	2.127474182	2.05648202	PKD1	.
0	0	2.127474182	2.05648202	SCRIB	.
0	0	2.127474182	2.05648202	RCN3	.
0	0	2.127474182	2.05648202	SLC5A6	.
0	0	1.528904429	1.475701823	HSPB1;ZFP	.
0	0	2.090044388	1.991982396	LRP1	.
0	0	2.090044388	1.991982396	PKD1	.

0	0	2.090044388	1.991982396	HIPK2	.
0	0	2.090044388	1.991982396	AARS2	.
0	0	2.090044388	1.991982396	POU6F1	.
0	0	2.053905276	1.930308794	RUBCN	.
0	0	2.053905276	1.930308794	ABCD1	.
0	0	2.053905276	1.930308794	FBXO31	.
0	0	2.018991219	1.871297252	ADCY9	.
0	0	2.018991219	1.871297252	FBF1	.
0	0	2.018991219	1.871297252	AP2A2	.
0	0	2.018991219	1.871297252	PLXND1	.
0	0	1.256247982	1.152596732	DGKQ;SCR	.
0	0	1.985240964	1.814795729	TNRC6B	.
0	0	1.985240964	1.814795729	ST3GAL1	.
0	0	1.122730157	1.025676654	ZFHX3;KAT	.
0	0	1.462725414	1.334646239	FZD4;LIMD	.
0	0	1.462725414	1.334646239	ADCY9;GN	.
0	0	1.952597274	1.760663062	HSPB1	.
0	0	1.952597274	1.760663062	HERC2	.
0	0	1.952597274	1.760663062	CARD9	.
0	0	1.952597274	1.760663062	HECTD4	.
0	0	1.952597274	1.760663062	HSPB1	.
0	0	1.952597274	1.760663062	FZD4	.
0	0	1.921006607	1.708768031	BIN1	.
0	0	1.921006607	1.708768031	LRP1	.
0	0	1.890418818	1.65898852	RCN3	.
0	0	1.890418818	1.65898852	PHC3	.
0	0	1.890418818	1.65898852	HSPB1	.
0	0	1.890418818	1.65898852	CROCC	.
0	0	1.890418818	1.65898852	LRP1	.
0	0	1.890418818	1.65898852	TNRC6B	.
0	0	1.890418818	1.65898852	AARS2	.
0	0	1.860786898	1.611210757	SLC4A8	.
0	0	1.860786898	1.611210757	TM7SF2	.
0	0	1.860786898	1.611210757	AARS2	.
0	0	1.860786898	1.611210757	FBXO31	.
0	0	1.832066728	1.565328631	PKD1	.
0	0	1.832066728	1.565328631	LRP1	.
0	0	1.385553206	1.17713455	LDB1;FZD4	.
0	0	1.804216867	1.521243072	ST3GAL1	.
0	0	1.804216867	1.521243072	LIMD1	.
0	0	1.804216867	1.521243072	HSPB1	.
0	0	1.777198346	1.478861488	FZD4	.
0	0	1.777198346	1.478861488	TNRC6B	.
0	0	1.777198346	1.478861488	HSPB1	.
0	0	1.353787879	1.114561048	CUL9;SCRI	.
0	0	1.750974486	1.438097259	RUBCN	.
0	0	1.750974486	1.438097259	HIPK2	.

0	0	1.750974486	1.438097259	PLXND1	.
0	0	1.750974486	1.438097259	BIN1	.
0	0	1.346070878	1.099563504	AAK1;WIZ	.
0	0	1.725510739	1.398869272	HECTD4	.
0	0	1.725510739	1.398869272	PIKFYVE	.
0	0	1.725510739	1.398869272	TAF1C	.
0	0	1.725510739	1.398869272	TRIOBP	.
0	0	1.725510739	1.398869272	PKD1	.
0	0	1.725510739	1.398869272	SNAPC4	.
0	0	1.725510739	1.398869272	TM7SF2	.
0	0	1.725510739	1.398869272	MACF1	.
0	0	1.338440586	1.084813631	LDB1;PAO	.
0	0	1.146308167	0.923095274	CUL9;SPSB	.
0	0	1.700774527	1.361101505	PKD1	.
0	0	1.700774527	1.361101505	GIT1	.
0	0	1.700774527	1.361101505	LDB1	.
0	0	1.700774527	1.361101505	PITPNM2	.
0	0	1.700774527	1.361101505	PHF2	.
0	0	1.700774527	1.361101505	KAT2A	.
0	0	1.700774527	1.361101505	SNAPC4	.
0	0	1.219928411	0.973352456	BIN1;PKD1	.
0	0	1.676735109	1.324722637	SH3BP1	.
0	0	1.676735109	1.324722637	PLXND1	.
0	0	1.676735109	1.324722637	ABCD1	.
0	0	1.653363454	1.289665703	PLXND1	.
0	0	1.653363454	1.289665703	ARHGEF18	.
0	0	1.653363454	1.289665703	PIKFYVE	.
0	0	1.653363454	1.289665703	SOGA1	.
0	0	1.630632118	1.255867774	HIPK2	.
0	0	1.630632118	1.255867774	ARHGEF18	.
0	0	1.630632118	1.255867774	SMC1A	.
0	0	1.145410571	0.873425951	PIKFYVE;BI	.
0	0	1.280351906	0.97514556	PKD1;ZFP3	.
0	0	1.608515142	1.223269663	LDB1	.
0	0	1.608515142	1.223269663	LIMD1	.
0	0	1.273440285	0.962410145	PLXND1;SH	.
0	0	1.586987952	1.191815661	MAP1S	.
0	0	1.586987952	1.191815661	FAM53B	.
0	0	1.586987952	1.191815661	CARD9	.
0	0	1.586987952	1.191815661	FAM53B	.
0	0	1.566027267	1.161453288	TM7SF2	.
0	0	1.566027267	1.161453288	PIKFYVE	.
0	0	1.566027267	1.161453288	PIKFYVE	.
0	0	1.566027267	1.161453288	FAM53B	.
0	0	1.566027267	1.161453288	SLC12A7	.
0	0	1.566027267	1.161453288	HSPB1	.
0	0	1.545611015	1.132133071	ST3GAL1	.

0	0	1.545611015	1.132133071	STAB1	.
0	0	1.525718258	1.103808335	MAP1S	.
0	0	1.148262881	0.821641721	SPSB1;FBX	.
0	0	1.506329114	1.076435016	SCRIB	.
0	0	1.506329114	1.076435016	RUBCN	.
0	0	1.506329114	1.076435016	HDAC7	.
0	0	1.506329114	1.076435016	PNPLA6	.
0	0	1.506329114	1.076435016	PKD1	.
0	0	1.487424699	1.049971481	HSPB1	.
0	0	1.468987059	1.024378372	PKD1	.
0	0	1.468987059	1.024378372	BIN1	.
0	0	1.450999118	0.999618453	AAK1	.
0	0	1.450999118	0.999618453	FUT7	.
0	0	1.450999118	0.999618453	CROCC	.
0	0	1.122583985	0.770072153	SPSB1;FBX	.
0	0	1.189878788	0.813885453	LDB1;FZD4	.
0	0	1.433444622	0.975656475	FBXO31	.
0	0	1.433444622	0.975656475	PKD1	.
0	0	1.433444622	0.975656475	SMC1A	.
0	0	1.433444622	0.975656475	IKZF1	.
0	0	1.183898688	0.803650334	PLXND1;NT	.
0	0	1.115453506	0.756019225	FZD4;GIT1;	.
0	0	1.39957477	0.929994516	BIN1	.
0	0	1.39957477	0.929994516	GIT1	.
0	0	1.39957477	0.929994516	SCRIB	.
0	0	1.39957477	0.929994516	HECTD4	.
0	0	1.39957477	0.929994516	HSPB1	.
0	0	1.383230597	0.908232868	STAB1	.
0	0	1.383230597	0.908232868	RCN3	.
0	0	1.383230597	0.908232868	LIMD1	.
0	0	1.367262152	0.887145615	PIKFYVE	.
0	0	1.367262152	0.887145615	WHRN	.
0	0	1.351656627	0.866705709	CARD9	.
0	0	1.351656627	0.866705709	SH3BP1	.
0	0	1.351656627	0.866705709	COL27A1	.
0	0	1.351656627	0.866705709	FBXO31	.
0	0	1.351656627	0.866705709	ARHGEF18	.
0	0	1.132640693	0.718149168	ADCY9;GIT	.
0	0	1.336401787	0.84688745	HSPB1	.
0	0	1.336401787	0.84688745	TRIM65	.
0	0	1.321485944	0.827666408	WHRN	.
0	0	1.321485944	0.827666408	BIN1	.
0	0	1.321485944	0.827666408	LRP1	.
0	0	1.121841052	0.700651748	SH3BP1;SC	.
0	0	1.306897921	0.809019349	ZFP36L2	.
0	0	1.306897921	0.809019349	ZFP36L2	.
0	0	1.306897921	0.809019349	TM7SF2	.

0	0	1.306897921	0.809019349	DGKQ	.
0	0	1.306897921	0.809019349	LRP1	.
0	0	1.306897921	0.809019349	SCRIB	.
0	0	1.306897921	0.809019349	HIPK2	.
0	0	1.306897921	0.809019349	FZD4	.
0	0	1.111243274	0.683659226	COL27A1;A	.
0	0	1.29262703	0.790924162	STIM1	.
0	0	1.106018323	0.675346752	COL27A1;A	.
0	0	1.278663039	0.773359793	LDB1	.
0	0	1.278663039	0.773359793	ARID1A	.
0	0	1.278663039	0.773359793	ZFP36L2	.
0	0	1.095712889	0.659078695	FZD4;GIT1	.
0	0	1.264996155	0.756306189	FBF1	.
0	0	1.264996155	0.756306189	WHRN	.
0	0	1.238516566	0.723655711	LMF2	.
0	0	1.238516566	0.723655711	STIM1	.
0	0	1.238516566	0.723655711	ZBTB7B	.
0	0	1.238516566	0.723655711	ST3GAL1	.
0	0	1.070761671	0.620395853	CARD9;HSI	.
0	0	1.027236944	0.591994684	HERC2;SM	.
0	0	1.200803213	0.678060758	PKD1	.
0	0	1.200803213	0.678060758	HIPK2	.
0	0	1.051595602	0.591368116	FBF1;PKD1	.
0	0	1.18873494	0.663699792	WIZ	.
0	0	1.176905642	0.649732829	ST3GAL1	.
0	0	1.176905642	0.649732829	LRP1	.
0	0	1.176905642	0.649732829	GNA12	.
0	0	1.176905642	0.649732829	MACF1	.
0	0	1.176905642	0.649732829	HIPK2	.
0	0	1.176905642	0.649732829	SMC1A	.
0	0	1.165308292	0.636146039	SSH1	.
0	0	1.153936133	0.622926192	STIM1	.
0	0	0.981037368	0.526974902	PYGB;HGSI	.
0	0	1.142782669	0.610060631	SCRIB	.
0	0	1.142782669	0.610060631	SCRIB	.
0	0	1.131841652	0.597537237	ADCY9	.
0	0	1.131841652	0.597537237	HDAC10	.
0	0	1.131841652	0.597537237	PKD1	.
0	0	1.12110707	0.585344407	STIM1	.
0	0	0.997962821	0.513380788	MAP1S;NT	.
0	0	1.090085111	0.550640411	CARD9	.
0	0	1.090085111	0.550640411	HSPB1	.
0	0	1.090085111	0.550640411	RCN3	.
0	0	1.090085111	0.550640411	ZFP36L2	.
0	0	1.080120482	0.53966317	STIM1	.
0	0	1.080120482	0.53966317	NFATC1	.
0	0	1.070335396	0.528965306	NFATC1	.

0	0	1.060725043	0.518537797	ZBTB7B	.
0	0	1.060725043	0.518537797	ST3GAL1	.
0	0	1.051284785	0.508371981	ADCY9	.
0	0	1.051284785	0.508371981	LRP1	.
0	0	1.042010146	0.498459536	CARD9	.
0	0	1.042010146	0.498459536	GIT1	.
0	0	1.042010146	0.498459536	CARD9	.
0	0	1.032896805	0.48879247	PIKFYVE	.
0	0	1.032896805	0.48879247	FUT7	.
0	0	1.015137473	0.470164042	ADCY9	.
0	0	1.015137473	0.470164042	ABCD1	.
0	0	1.006483561	0.461188191	CARD9	.
0	0	1.006483561	0.461188191	CARD9	.
0	0	0.997975094	0.452428715	GIT1	.
0	0	0.997975094	0.452428715	HDAC10	.
0	0	0.989608434	0.443879037	CARD9	.
0	0	0.965324713	0.419426672	SLC27A3	.
0	0	0.965324713	0.419426672	HSPB1	.
0	0	0.957491255	0.411655197	TOR4A	.
0	0	0.895048599	0.377673797	LRP1;NFAT	.
0	0	0.886442431	0.369743895	SOGA1;AP	.
0	0	0.927381401	0.382321708	LDB1	.
0	0	0.920145699	0.375401546	TM7SF2	.
0	0	0.920145699	0.375401546	FAM53B	.
0	0	0.920145699	0.375401546	PHLDA1	.
0	0	0.875300372	0.354328419	CUL9;SPSB	.
0	0	0.913021316	0.368637319	PHLDA1	.
0	0	0.899096386	0.355559265	ARHGEF18	.
0	0	0.892290968	0.349237105	DGKQ	.
0	0	0.858893281	0.334548548	FBF1;PKD1	.
0	0	0.878982597	0.337006745	ADCY9	.
0	0	0.878982597	0.337006745	STIM1	.
0	0	0.872475195	0.331091032	ADCY9	.
0	0	0.881419234	0.333805775	ZFHX3;HDA	.
0	0	0.859743321	0.319640695	SSH1	.
0	0	0.853514779	0.314099283	TRIO	.
0	0	0.841420067	0.309476001	FBF1;LIMD	.
0	0	0.835355507	0.298171638	PKD1	.
0	0	0.835355507	0.298171638	SLC5A6	.
0	0	0.829471733	0.293084544	LRP1	.
0	0	0.80004095	0.269645367	HERC2;SM	.
0	0	0.795827606	0.264700445	SSH1	.
0	0	0.794590197	0.263973553	COL27A1;A	.
0	0	0.786549884	0.255713825	RGL2;ZFP3	.
0	0	0.780001585	0.251770728	SSH1	.
0	0	0.76979346	0.243576747	CARD9	.
0	0	0.764788185	0.23960129	HIPK2	.

0	0	0.759847081	0.235704234	SMC1A	.
0	0	0.75496892	0.231883689	PKD1	.
0	0	0.750152509	0.228137816	GIT1	.
0	0	0.758391608	0.227798204	FBF1;PKD1	.
0	0	0.736062261	0.217330656	RRBP1	.
0	0	0.726956907	0.210467892	HERC2	.
0	0	0.709400476	0.197507206	BIN1	.
0	0	0.696775337	0.188410951	CARD9	.
0	0	0.723046984	0.195016798	HERC2;CR(	.
0	0	0.692665398	0.185490674	CARD9	.
0	0	0.740700582	0.194497419	PYGB;HGSI	.
0	0	0.676695353	0.174335942	STAB1	.
0	0	0.734401882	0.188235444	PYGB;HGSI	.
0	0	0.672816265	0.171673092	FZD4	.
0	0	0.668981009	0.169058379	ADCY9	.
0	0	0.668981009	0.169058379	HSPB1	.
0	0	0.661439052	0.163969196	TOR4A	.
0	0	0.670833333	0.151290157	SPSB1;FBX	.
0	0	0.666974833	0.148284696	RRBP1;LMI	.
0	0	0.613022036	0.132991357	ZFP36L2	.
0	0	0.609831077	0.131054612	SCRIB	.
0	0	0.597389558	0.123629653	LEMD2	.
0	0	0.591355422	0.120101488	SPSB1	.
0	0	0.57678519	0.111780701	DAGLA	.
0	0	0.573956018	0.110197789	RCN3	.
0	0	0.568379286	0.107109054	PHLDA1	.
0	0	0.560212414	0.102661372	LIMD1	.
0	0	0.554895639	0.099814437	RRBP1	.
0	0	0.51570474	0.080029563	FUT7	.
0	0	0.49809364	0.071839393	CARD9	.
0	0	0.567155896	0.081547934	RRBP1;ST3	.
0	0	0.485646289	0.0663175	SLC12A7	.
0	0	0.45349861	0.053093857	SH3BP1	.
0	0	0.44482837	0.049786535	HSPB1	.
0	0	0.443133436	0.049152958	HGSNAT	.
0	0	0.443133436	0.049152958	KAT2A	.
0	0	0.564985099	0.061219999	ZFHX3;FUT	.
0	0	0.431616576	0.044960602	CARD9	.
0	0	0.428433735	0.043836733	KAT2A	.
0	0	0.426859612	0.043286481	SMC1A	.
0	0	0.390905816	0.031727246	CARD9	.
0	0	0.385700178	0.030214331	SLC12A7	.
0	0	0.375688056	0.027418967	RRBP1	.
0	0	0.316883751	0.014020228	DGKQ	.
0	0	0.308386176	0.012503712	HSPB1	.
0	0	0.242366556	0.004086937	ZFP36L2	.
0	0	0.240826944	0.003956781	HSPB1	.

0	0	0.213197745	0.002065247	CARD9	.
0	0	0.20543768	0.00167354	PLXND1	.
0	0	0.150562933	2.20E-04	MEAK7	.

were highlighted)

Term	Overlap	P-value	Adjusted P-value	Old P-value
Glycerolipid metabolism	22341	0.014446273	0.751904505	0
Vitamin digestion and absorption	44616	0.016957333	0.751904505	0
Peroxisome	30011	0.03133693	0.751904505	0
Phospholipase D signaling pathway	4/148	0.035687662	0.751904505	0
Regulation of actin cytoskeleton	5/218	0.036339471	0.751904505	0
Phosphatidylinositol signaling syster	35490	0.047712188	0.751904505	0
Aldosterone synthesis and secretior	35855	0.048927617	0.751904505	0
Glycerophospholipid metabolism	35855	0.048927617	0.751904505	0
ABC transporters	16469	0.054307363	0.751904505	0
Glycosphingolipid biosynthesis	16469	0.054307363	0.751904505	0
Parathyroid hormone synthesis, sec	3/106	0.059187998	0.751904505	0
Endocytosis	5/252	0.060556068	0.751904505	0
Endocrine and other factor-regulate	19391	0.072428788	0.800291666	0
Transcriptional misregulation in can	4/192	0.077509251	0.800291666	0
Platelet activation	3/124	0.085578441	0.800291666	0
Viral carcinogenesis	4/203	0.090634827	0.800291666	0
Cortisol synthesis and secretion	23774	0.102584988	0.800291666	0
Inflammatory bowel disease	23774	0.102584988	0.800291666	0
Aminoacyl-tRNA biosynthesis	24139	0.105233805	0.800291666	0
cAMP signaling pathway	4/216	0.1074217	0.800291666	0
Cushing syndrome	3/155	0.140241723	0.849967264	0
Cellular senescence	3/156	0.142168412	0.849967264	0
Glycosaminoglycan degradation	44580	0.14733426	0.849967264	0
Steroid biosynthesis	44581	0.154460779	0.849967264	0
Hippo signaling pathway	3/163	0.155897467	0.849967264	0
cGMP-PKG signaling pathway	3/167	0.163922379	0.849967264	0
Morphine addiction	33270	0.176288949	0.849967264	0
Th1 and Th2 cell differentiation	33635	0.179276171	0.849967264	0
Axon guidance	3/182	0.195032913	0.849967264	0
Choline metabolism in cancer	35827	0.197351648	0.849967264	0
Collecting duct acid secretion	44588	0.202715656	0.849967264	0
Melanogenesis	2/101	0.206472749	0.849967264	0
Protein digestion and absorption	2/103	0.212578736	0.849967264	0
C-type lectin receptor signaling path	2/104	0.215638427	0.849967264	0
Citrate cycle (TCA cycle)	44591	0.222548833	0.849967264	0
Glyoxylate and dicarboxylate metab	44591	0.222548833	0.849967264	0
Pentose phosphate pathway	44591	0.222548833	0.849967264	0
Insulin resistance	2/108	0.227915268	0.849967264	0
Glutamatergic synapse	2/114	0.246415303	0.849967264	0
Nicotinate and nicotinamide metab	12785	0.254520122	0.849967264	0
Starch and sucrose metabolism	13150	0.260755782	0.849967264	0
Mucin type O-glycan biosynthesis	13150	0.260755782	0.849967264	0
Alanine, aspartate and glutamate m	13516	0.266939593	0.849967264	0
Primary immunodeficiency	13881	0.273071983	0.849967264	0

Human T-cell leukemia virus 1 infec	3/219	0.276596282	0.849967264	0
Glycine, serine and threonine metal	14611	0.285184198	0.849967264	0
Human cytomegalovirus infection	3/225	0.2902043	0.849967264	0
Oocyte meiosis	2/129	0.292793101	0.849967264	0
Purine metabolism	2/129	0.292793101	0.849967264	0
Vascular smooth muscle contractior	2/133	0.305123292	0.849967264	0
Vasopressin-regulated water reabsc	16072	0.308810047	0.849967264	0
Calcium signaling pathway	3/240	0.324397957	0.849967264	0
Signaling pathways regulating pluri	2/143	0.335754822	0.849967264	0
Vibrio cholerae infection	18264	0.342801117	0.849967264	0
Cholesterol metabolism	18264	0.342801117	0.849967264	0
Cysteine and methionine metabolisı	18264	0.342801117	0.849967264	0
Malaria	18264	0.342801117	0.849967264	0
Ovarian steroidogenesis	18629	0.348302472	0.849967264	0
Cell adhesion molecules	2/148	0.350928845	0.849967264	0
Retrograde endocannabinoid signali	2/148	0.350928845	0.849967264	0
Glycosaminoglycan biosynthesis	19360	0.359168227	0.849967264	0
Oxytocin signaling pathway	2/154	0.368980115	0.849967264	0
Regulation of lipolysis in adipocytes	20090	0.369853883	0.849967264	0
Pyrimidine metabolism	20455	0.375130103	0.849967264	0
Glutathione metabolism	20821	0.380362408	0.849967264	0
VEGF signaling pathway	21551	0.390696721	0.849967264	0
Notch signaling pathway	21551	0.390696721	0.849967264	0
Long-term depression	21916	0.395799447	0.849967264	0
Wnt signaling pathway	2/166	0.404466502	0.849967264	0
Hepatocellular carcinoma	2/168	0.410291034	0.849967264	0
Basal cell carcinoma	23012	0.410854148	0.849967264	0
Tight junction	2/169	0.413192953	0.849967264	0
Renin secretion	25204	0.439853961	0.849967264	0
Central carbon metabolism in cance	25569	0.444547363	0.849967264	0
Epithelial cell signaling in Helicobact	25569	0.444547363	0.849967264	0
MAPK signaling pathway	3/294	0.445917509	0.849967264	0
Adherens junction	25934	0.449201673	0.849967264	0
Inositol phosphate metabolism	26665	0.458394309	0.849967264	0
Alcoholism	2/186	0.46138816	0.849967264	0
Thyroid hormone synthesis	27395	0.467434425	0.849967264	0
Neutrophil extracellular trap format	2/189	0.469655418	0.849967264	0
Gastric acid secretion	27760	0.471898077	0.849967264	0
Synaptic vesicle cycle	28491	0.480714119	0.849967264	0
B cell receptor signaling pathway	29587	0.493664612	0.849967264	0
Insulin secretion	31413	0.514539155	0.849967264	0
Gap junction	32143	0.522647404	0.849967264	0
GABAergic synapse	32509	0.526650904	0.849967264	0
PD-L1 expression and PD-1 checkpo	32509	0.526650904	0.849967264	0
Bile secretion	32874	0.530621026	0.849967264	0
Salivary secretion	33970	0.542333881	0.849967264	0
GnRH signaling pathway	33970	0.542333881	0.849967264	0

Dilated cardiomyopathy	35065	0.553756159	0.849967264	0
Circadian entrainment	35431	0.557500257	0.849967264	0
Fc gamma R-mediated phagocytosis	35431	0.557500257	0.849967264	0
Inflammatory mediator regulation c	35796	0.561213127	0.849967264	0
AGE-RAGE signaling pathway in diat	1/100	0.568546218	0.849967264	0
Progesterone-mediated oocyte mat	1/100	0.568546218	0.849967264	0
Amoebiasis	1/102	0.575757478	0.849967264	0
Longevity regulating pathway	1/102	0.575757478	0.849967264	0
Pancreatic secretion	1/102	0.575757478	0.849967264	0
Thermogenesis	2/232	0.579344512	0.849967264	0
T cell receptor signaling pathway	1/104	0.582848919	0.849967264	0
Th17 cell differentiation	1/107	0.593265741	0.849967264	0
Glucagon signaling pathway	1/107	0.593265741	0.849967264	0
Cholinergic synapse	1/113	0.613329955	0.852294909	0
Sphingolipid signaling pathway	1/119	0.632410032	0.852294909	0
Growth hormone synthesis, secretic	1/119	0.632410032	0.852294909	0
Thyroid hormone signaling pathway	1/121	0.638559723	0.852294909	0
Cell cycle	1/124	0.64759302	0.852294909	0
Osteoclast differentiation	1/127	0.656401869	0.852294909	0
Lysosome	1/128	0.659289237	0.852294909	0
Relaxin signaling pathway	1/129	0.662152485	0.852294909	0
FoxO signaling pathway	1/131	0.667807423	0.852294909	0
Natural killer cell mediated cytotoxi	1/131	0.667807423	0.852294909	0
Apelin signaling pathway	1/137	0.684213859	0.852294909	0
Autophagy	1/137	0.684213859	0.852294909	0
Yersinia infection	1/137	0.684213859	0.852294909	0
Estrogen signaling pathway	1/137	0.684213859	0.852294909	0
Insulin signaling pathway	1/137	0.684213859	0.852294909	0
Ubiquitin mediated proteolysis	1/140	0.692112443	0.852294909	0
Apoptosis	1/142	0.697268746	0.852294909	0
Spinocerebellar ataxia	1/143	0.699814616	0.852294909	0
Breast cancer	1/147	0.709787028	0.852294909	0
Gastric cancer	1/149	0.714649033	0.852294909	0
Adrenergic signaling in cardiomyocy	1/150	0.717049586	0.852294909	0
Phagosome	1/152	0.721790633	0.852294909	0
mTOR signaling pathway	1/154	0.726452707	0.852294909	0
Necroptosis	1/159	0.737770917	0.858811458	0
Hepatitis B	1/162	0.744337111	0.859738214	0
Protein processing in endoplasmic r	1/171	0.763071027	0.871858767	0
Human papillomavirus infection	2/331	0.766533547	0.871858767	0
Tuberculosis	1/180	0.780439806	0.876399818	0
NOD-like receptor signaling pathwa	1/181	0.782289771	0.876399818	0
Chemokine signaling pathway	1/192	0.801644571	0.878008989	0
Kaposi sarcoma-associated herpesvi	1/193	0.80331688	0.878008989	0
Pathogenic Escherichia coli infectior	1/197	0.809867123	0.878008989	0
Alzheimer disease	2/369	0.816603231	0.878008989	0
Proteoglycans in cancer	1/205	0.822324091	0.878008989	0

Pathways in cancer	3/531	0.82382452	0.878008989	0
Rap1 signaling pathway	1/210	0.829694149	0.878008989	0
Human immunodeficiency virus 1 in	1/212	0.832556353	0.878008989	0
Lipid and atherosclerosis	1/215	0.836760245	0.878008989	0
Ras signaling pathway	1/232	0.858675096	0.894703421	0
Chemical carcinogenesis	1/239	0.866824734	0.896922815	0
Salmonella infection	1/249	0.877663088	0.901874484	0
Herpes simplex virus 1 infection	2/498	0.922757492	0.933441583	0
Huntington disease	1/306	0.924653398	0.933441583	0
MicroRNAs in cancer	1/310	0.927176875	0.933441583	0
Pathways of neurodegeneration	1/475	0.982242454	0.982242454	0

Old Adjusted P-value	Odds Ratio	Combined Score	Genes
0	6.236858705	26.42755856	DGKQ;GLYCTK;DGKZ
0	10.91515152	44.50167231	SLC5A6;TCN2
0	4.574096944	15.83990565	IDH2;ABCD1;PAOX
0	3.355316973	11.18310458	ADCY9;DGKQ;GNA12;DGKZ
0	2.842983829	9.424067158	PIKFYVE;GNA12;SSH3;GIT1;SSH1
0	3.841268812	11.68732308	PIKFYVE;DGKQ;DGKZ
0	3.800641849	11.46810721	ADCY9;DAGLA;ORAI1
0	3.800641849	11.46810721	DGKQ;PNPLA6;DGKZ
0	5.578576462	16.25092579	ABCC10;ABCD1
0	5.578576462	16.25092579	FUT7;ST3GAL1
0	3.504025574	9.906008198	ADCY9;GNA12;PDE4A
0	2.447393412	6.862945382	ACAP3;BIN1;PSD4;AP2A2;GIT1
0	4.701604278	12.34242322	ADCY9;AP2A2
0	2.564286647	6.557798934	MAF;LDB1;KLF3;FLI1
0	2.980044346	7.32590825	ADCY9;STIM1;ORAI1
0	2.421185683	5.813065234	KAT2A;HDAC10;SCRIB;HDAC7
0	3.803751804	8.66138505	ADCY9;ORAI1
0	3.803751804	8.66138505	MAF;NFATC1
0	3.744128788	8.430170624	AARS2;VARS2
0	2.271211946	5.067058107	ADCY9;ORAI1;PDE4A;NFATC1
0	2.368541399	4.652733722	ADCY9;FZD4;ORAI1
0	2.352941176	4.58998335	NFATC1;ZFP36L2;HIPK2
0	6.631526104	12.69971333	HGSNAT
0	6.282181357	11.73395305	TM7SF2
0	2.249199695	4.180265272	FZD4;SCRIB;LIMD1
0	2.193895003	3.96735693	ADCY9;GNA12;NFATC1
0	2.689002383	4.667115564	ADCY9;PDE4A
0	2.658989899	4.570345777	MAF;NFATC1
0	2.008516147	3.283094279	SSH3;SSH1;NTN3
0	2.492045455	4.044011932	DGKQ;DGKZ
0	4.589202966	7.324143016	SLC12A7
0	2.416161616	3.811704769	ADCY9;FZD4
0	2.368076808	3.666831567	SLC36A1;COL27A1
0	2.344741533	3.597190433	CARD9;NFATC1
0	4.113834649	6.181483847	IDH2
0	4.113834649	6.181483847	GLYCTK
0	4.113834649	6.181483847	GLYCTK
0	2.255803316	3.335839875	PYGB;SLC27A3
0	2.134307359	2.989603164	ADCY9;HOMER3
0	3.507973069	4.800223982	NADSYN1
0	3.40757315	4.58036104	PYGB
0	3.40757315	4.58036104	ST3GAL1
0	3.312751004	4.375259203	CAD
0	3.22305438	4.183588541	ORAI1

0	1.661331301	2.135136843	KAT2A;ADCY9;NFATC1
0	3.057460612	3.835951229	GLYCTK
0	1.615936058	1.999187808	ADCY9;GNA12;NFATC1
0	1.880792174	2.310156452	ADCY9;SMC1A
0	1.880792174	2.310156452	ADCY9;PDE4A
0	1.822993292	2.163964768	ADCY9;GNA12
0	2.77248529	3.257750411	ADCY9
0	1.512503859	1.702753028	ADCY9;STIM1;ORAI1
0	1.692843327	1.847525331	ZFHX3;FZD4
0	2.432259651	2.603988937	ADCY9
0	2.432259651	2.603988937	LRP1
0	2.432259651	2.603988937	DNMT3A
0	2.432259651	2.603988937	LRP1
0	2.383493976	2.51383297	ADCY9
0	1.63445413	1.71155427	GLG1;NECTIN1
0	1.63445413	1.71155427	ADCY9;DAGLA
0	2.291589435	2.346506007	ST3GAL1
0	1.569457735	1.564769021	ADCY9;NFATC1
0	2.206492637	2.194681863	ADCY9
0	2.16626506	2.123984704	CAD
0	2.127474182	2.05648202	IDH2
0	2.053905276	1.930308794	HSPB1
0	2.053905276	1.930308794	KAT2A
0	2.018991219	1.871297252	GNA12
0	1.453732446	1.315898782	FZD4;NFATC1
0	1.436071559	1.279379683	FZD4;ARID1A
0	1.921006607	1.708768031	FZD4
0	1.427399746	1.261593843	ARHGEF18;SCRIB
0	1.750974486	1.438097259	ORAI1
0	1.725510739	1.398869272	IDH2
0	1.725510739	1.398869272	GIT1
0	1.228438521	0.992113118	GNA12;HSPB1;NFATC1
0	1.700774527	1.361101505	NECTIN1
0	1.653363454	1.289665703	PIKFYVE
0	1.294400527	1.001238994	HDAC10;HDAC7
0	1.608515142	1.223269663	ADCY9
0	1.273440285	0.962410145	HDAC10;HDAC7
0	1.586987952	1.191815661	ADCY9
0	1.545611015	1.132133071	AP2A2
0	1.487424699	1.049971481	NFATC1
0	1.39957477	0.929994516	ADCY9
0	1.367262152	0.887145615	ADCY9
0	1.351656627	0.866705709	ADCY9
0	1.351656627	0.866705709	NFATC1
0	1.336401787	0.84688745	ADCY9
0	1.29262703	0.790924162	ADCY9
0	1.29262703	0.790924162	ADCY9

0	1.251616994	0.739744237	ADCY9
0	1.238516566	0.723655711	ADCY9
0	1.238516566	0.723655711	BIN1
0	1.22568625	0.708023227	ADCY9
0	1.200803213	0.678060758	NFATC1
0	1.200803213	0.678060758	ADCY9
0	1.176905642	0.649732829	HSPB1
0	1.176905642	0.649732829	ADCY9
0	1.176905642	0.649732829	ADCY9
0	1.033096179	0.563923779	ADCY9;ARID1A
0	1.153936133	0.622926192	NFATC1
0	1.12110707	0.585344407	NFATC1
0	1.12110707	0.585344407	PYGB
0	1.060725043	0.518537797	ADCY9
0	1.006483561	0.461188191	GNA12
0	1.006483561	0.461188191	ADCY9
0	0.989608434	0.443879037	KAT2A
0	0.965324713	0.419426672	SMC1A
0	0.942197361	0.396648198	NFATC1
0	0.93473105	0.389402354	HGSNAT
0	0.927381401	0.382321708	ADCY9
0	0.913021316	0.368637319	HOMER3
0	0.913021316	0.368637319	NFATC1
0	0.872475195	0.331091032	ADCY9
0	0.872475195	0.331091032	RUBCN
0	0.872475195	0.331091032	NFATC1
0	0.872475195	0.331091032	ADCY9
0	0.872475195	0.331091032	PYGB
0	0.853514779	0.314099283	HERC2
0	0.841322738	0.303367827	LMNB2
0	0.835355507	0.298171638	KCNC3
0	0.812304011	0.278449947	FZD4
0	0.801245523	0.269189426	FZD4
0	0.795827606	0.264700445	ADCY9
0	0.785207053	0.255993332	PIKFYVE
0	0.774864163	0.247632557	FZD4
0	0.750152509	0.228137816	PYGB
0	0.736062261	0.217330656	NFATC1
0	0.696775337	0.188410951	RRBP1
0	0.718577876	0.191053197	FZD4;SCRIB
0	0.661439052	0.163969196	CARD9
0	0.657730924	0.161492711	CARD9
0	0.619504195	0.13696615	ADCY9
0	0.616246235	0.134961637	NFATC1
0	0.60354684	0.12727903	GNA12
0	0.64291966	0.130256773	LRP1;FZD4
0	0.579642098	0.113389987	FZD4

0	0.66882622	0.129617005	ADCY9;FZD4;GNA12
0	0.565630945	0.105602246	ADCY9
0	0.560212414	0.102661372	NFATC1
0	0.552274519	0.098425092	NFATC1
0	0.511187608	0.077886928	RGL2
0	0.495975499	0.070884062	ADCY9
0	0.475733579	0.062079657	FYCO1
0	0.472556207	0.037988235	CARD9;NECTIN1
0	0.385700178	0.030214331	AP2A2
0	0.380629313	0.028779736	DNMT3A
0	0.246034772	0.00440823	FZD4

Supplementary File S6: Comprehensive details of the results of functional enrichment analysi

BP	Term	Overlap	P-value	Adjusted P-value	Old P-value
	ribosome biogenesis (GO:0042254)	22/192	5.01E-21	5.11E-18	0
	rRNA processing (GO:0006364)	19/173	6.38E-18	3.25E-15	0
	rRNA metabolic process (GO:0016072)	18/162	4.04E-17	1.37E-14	0
	ncRNA processing (GO:0034470)	19/201	1.09E-16	2.79E-14	0
	ribonucleoprotein complex biogenesis	22190	7.93E-12	1.62E-09	0
	ribosomal large subunit biogenesis (GO	21064	1.52E-10	2.58E-08	0
	maturation of 5.8S rRNA from tricistror	44734	5.77E-09	8.40E-07	0
	maturation of LSU-rRNA from tricistron	44695	2.48E-08	3.16E-06	0
	maturation of SSU-rRNA from tricistror	44742	4.40E-08	4.98E-06	0
	ribosomal large subunit assembly (GO:(	44706	6.20E-07	6.32E-05	0
	maturation of LSU-rRNA (GO:0000470)	44707	7.63E-07	7.07E-05	0
	ribosome assembly (GO:0042255)	18415	1.05E-06	8.94E-05	0
	endonucleolytic cleavage of tricistronic	44664	1.35E-06	1.06E-04	0
	maturation of SSU-rRNA (GO:0030490)	12905	3.59E-06	2.61E-04	0
	maturation of 5.8S rRNA (GO:0000460)	44668	4.41E-06	3.00E-04	0
	ribosomal small subunit biogenesis (GC	14732	7.08E-06	4.51E-04	0
	rRNA methylation (GO:0031167)	44673	1.32E-05	7.48E-04	0
	mRNA modification (GO:0016556)	44673	1.32E-05	7.48E-04	0
	mitochondrion organization (GO:0007(	8/175	2.52E-05	0.001352902	0
	ribonucleoprotein complex assembly ((	7/136	3.87E-05	0.001970142	0
	RNA modification (GO:0009451)	21306	4.47E-05	0.002170361	0
	pseudouridine synthesis (GO:0001522)	44633	8.19E-05	0.003475761	0
	glucan biosynthetic process (GO:00092	44633	8.19E-05	0.003475761	0
	glycogen biosynthetic process (GO:000	44633	8.19E-05	0.003475761	0
	establishment of protein localization to	17624	3.07E-04	0.012353821	0
	protein-DNA complex disassembly (GO	44640	3.15E-04	0.012353821	0
	protein targeting to mitochondrion (GC	20180	5.19E-04	0.019522271	0
	response to gamma radiation (GO:001(	44644	5.49E-04	0.019522271	0
	mitochondrial transport (GO:0006839)	20546	5.56E-04	0.019522271	0
	tRNA pseudouridine synthesis (GO:003	44598	6.66E-04	0.022083288	0
	regulation of signal transduction by p5	6/156	6.72E-04	0.022083288	0
	RNA methylation (GO:0001510)	22007	7.22E-04	0.023005264	0
	glycogen metabolic process (GO:00059	44648	8.71E-04	0.026888363	0
	mRNA pseudouridine synthesis (GO:19(	44599	9.29E-04	0.027839752	0
	tRNA modification (GO:0006400)	23833	9.77E-04	0.02845394	0
	endonucleolytic cleavage in ITS1 to sep	44600	0.001233062	0.033959184	0
	rRNA base methylation (GO:0070475)	44600	0.001233062	0.033959184	0
	protein transmembrane import into int	11749	0.001292675	0.034664103	0
	positive regulation of myeloid leukocyt	13210	0.001824583	0.047673088	0
	negative regulation of peptidyl-lysine a	44602	0.001964237	0.050038937	0
	tRNA aminoacylation (GO:0043039)	13940	0.00213469	0.053054863	0
	DNA replication-independent nucleoso	14305	0.002301253	0.05583278	0
	positive regulation of macrophage diffe	44603	0.002390137	0.056640683	0
	negative regulation of histone acetylati	44604	0.00285551	0.066131011	0

tRNA aminoacylation for protein transl	15766	0.003047138	0.069000747	0
intracellular protein transmembrane tr	16132	0.003254105	0.072085508	0
DNA replication-independent nucleoso	44605	0.003359812	0.072843578	0
regulation of cell cycle (GO:0051726)	7/296	0.004009417	0.08511659	0
regulation of macrophage differentiati	44607	0.004483052	0.089573146	0
positive regulation of telomerase RNA l	44607	0.004483052	0.089573146	0
mRNA methylation (GO:0080009)	44607	0.004483052	0.089573146	0
negative regulation of histone modifica	44608	0.00510093	0.096256432	0
negative regulation of transcription reg	44608	0.00510093	0.096256432	0
regulation of monocyte differentiation	44608	0.00510093	0.096256432	0
cellular response to gamma radiation ((	44609	0.005755613	0.106635806	0
chromatin disassembly (GO:0031498)	44610	0.006446584	0.113259813	0
nucleosome disassembly (GO:0006337	44610	0.006446584	0.113259813	0
regulation of telomerase RNA localizati	44610	0.006446584	0.113259813	0
positive regulation of gene expression,	20880	0.006746308	0.116516752	0
nucleosome assembly (GO:0006334)	21245	0.007079646	0.117897174	0
positive regulation of actin cytoskeleto	44611	0.007173331	0.117897174	0
protein import into mitochondrial matr	44611	0.007173331	0.117897174	0
cobalamin metabolic process (GO:0009	44613	0.008732131	0.139031898	0
rRNA modification (GO:0000154)	44613	0.008732131	0.139031898	0
tRNA processing (GO:0008033)	23437	0.009283836	0.143444579	0
tetrapyrrole metabolic process (GO:00	44614	0.009563184	0.143444579	0
protein-containing complex assembly (	6/267	0.009611466	0.143444579	0
regulation of intracellular signal transdu	8/437	0.009711795	0.143444579	0
positive regulation of epithelial cell pro	4/123	0.009713127	0.143444579	0
cellular response to light stimulus (GO:	25628	0.011846512	0.172451369	0
RNA metabolic process (GO:0016070)	4/133	0.012661981	0.181726176	0
regulation of cellular macromolecule bi	8/468	0.014211097	0.198432238	0
cellular senescence (GO:0090398)	44619	0.01421546	0.198432238	0
regulation of cell division (GO:0051302	27820	0.01477696	0.20076963	0
water-soluble vitamin metabolic proce	27820	0.01477696	0.20076963	0
positive regulation of protein modificat	5/214	0.01513858	0.202497969	0
cellular response to UV (GO:0034644)	28185	0.015301613	0.202497969	0
Ras protein signal transduction (GO:00(	4/142	0.015758493	0.203264612	0
chromatin organization (GO:0006325)	4/142	0.015758493	0.203264612	0
beta-catenin-TCF complex assembly (G	47150	0.016299425	0.207613924	0
regulation of type I interferon-mediate	10990	0.017387345	0.216069568	0
ion homeostasis (GO:0050801)	10990	0.017387345	0.216069568	0
regulation of gene expression, epigene	30011	0.018081586	0.219346855	0
positive regulation of cytoskeleton orga	30011	0.018081586	0.219346855	0
apoptotic process (GO:0006915)	5/231	0.020354942	0.244019837	0
regulation of histone acetylation (GO:0	12086	0.020829432	0.244380834	0
negative regulation of extrinsic apopto	12451	0.022034757	0.244380834	0
cellular response to amino acid stimulu	12451	0.022034757	0.244380834	0
positive regulation of telomerase activi	12451	0.022034757	0.244380834	0
tRNA methylation (GO:0030488)	12451	0.022034757	0.244380834	0
negative regulation of gene expression	6/322	0.022195024	0.244380834	0

collagen fibril organization (GO:003019	32568	0.022414835	0.244380834	0
positive regulation of supramolecular f	33298	0.023747765	0.244380834	0
intrinsic apoptotic signaling pathway by	13181	0.024529734	0.244380834	0
regulation of actin cytoskeleton reorga	13547	0.025818531	0.244380834	0
regulation of nucleic acid-templated tra	7/430	0.026846479	0.244380834	0
response to UV (GO:0009411)	36220	0.029500624	0.244380834	0
gluconeogenesis (GO:0006094)	15008	0.03123932	0.244380834	0
cellular response to DNA damage stimu	6/350	0.031617775	0.244380834	0
positive regulation of cellular protein m	3/102	0.031830985	0.244380834	0
positive regulation of vasculature deve	3/102	0.031830985	0.244380834	0
chromatin remodeling (GO:0006338)	3/103	0.032628632	0.244380834	0
regulation of extrinsic apoptotic signali	15373	0.032658865	0.244380834	0
RNA processing (GO:0006396)	4/179	0.03325426	0.244380834	0
atrial cardiac muscle tissue morphogen	44566	0.03330053	0.244380834	0
regulation of cell proliferation involved	44566	0.03330053	0.244380834	0
negative regulation of plasminogen act	44566	0.03330053	0.244380834	0
negative regulation of RNA polymerase	44566	0.03330053	0.244380834	0
cellular response to sodium arsenite (G	44566	0.03330053	0.244380834	0
negative regulation of transforming gro	44566	0.03330053	0.244380834	0
cellular response to vitamin (GO:00712	44566	0.03330053	0.244380834	0
cellular response to vitamin D (GO:007	44566	0.03330053	0.244380834	0
centriole assembly (GO:0098534)	44566	0.03330053	0.244380834	0
regulation of miRNA metabolic process	44566	0.03330053	0.244380834	0
DNA catabolic process, exonucleolytic (	44566	0.03330053	0.244380834	0
endonucleolytic cleavage in 5'-ETS of tr	44566	0.03330053	0.244380834	0
endonucleolytic cleavage to generate m	44566	0.03330053	0.244380834	0
positive regulation of anoikis (GO:2000	44566	0.03330053	0.244380834	0
positive regulation of dopamine recept	44566	0.03330053	0.244380834	0
positive regulation of endothelial cell-m	44566	0.03330053	0.244380834	0
positive regulation of epithelial to mes	44566	0.03330053	0.244380834	0
histone H4-K20 methylation (GO:00347	44566	0.03330053	0.244380834	0
response to sodium arsenite (GO:1903	44566	0.03330053	0.244380834	0
histone H4-K20 trimethylation (GO:003	44566	0.03330053	0.244380834	0
RNA localization to Cajal body (GO:009	44566	0.03330053	0.244380834	0
rRNA 5'-end processing (GO:0000967)	44566	0.03330053	0.244380834	0
scaRNA localization to Cajal body (GO:0	44566	0.03330053	0.244380834	0
intracellular distribution of mitochondr	44566	0.03330053	0.244380834	0
lymph node development (GO:004853	44566	0.03330053	0.244380834	0
positive regulation of smooth muscle c	44566	0.03330053	0.244380834	0
small GTPase mediated signal transduc	3/106	0.035083879	0.244380834	0
branching morphogenesis of an epithel	16103	0.035572356	0.244380834	0
hexose biosynthetic process (GO:0019	16103	0.035572356	0.244380834	0
mRNA catabolic process (GO:0006402)	16103	0.035572356	0.244380834	0
amino acid transmembrane transport (	16469	0.037065516	0.244380834	0
regulation of protein ubiquitination (GO	3/109	0.037632119	0.244380834	0
regulation of telomerase activity (GO:0	16834	0.038582432	0.244380834	0
positive regulation of response to stimu	16834	0.038582432	0.244380834	0

protein-DNA complex subunit organiza	44567	0.039827364	0.244380834	0
pteridine-containing compound biosyn	44567	0.039827364	0.244380834	0
radial glial cell differentiation (GO:006(	44567	0.039827364	0.244380834	0
negative regulation of fat cell proliferat	44567	0.039827364	0.244380834	0
regulation of collagen fibril organizatio	44567	0.039827364	0.244380834	0
regulation of endothelial cell-matrix ad	44567	0.039827364	0.244380834	0
cellular response to salt (GO:1902075)	44567	0.039827364	0.244380834	0
cobalamin transport (GO:0015889)	44567	0.039827364	0.244380834	0
enzyme-directed rRNA pseudouridine s	44567	0.039827364	0.244380834	0
regulation of retrograde transport, end	44567	0.039827364	0.244380834	0
positive regulation of cell-cell adhesion	44567	0.039827364	0.244380834	0
galactose catabolic process (GO:00193	44567	0.039827364	0.244380834	0
response to gonadotropin (GO:003469	44567	0.039827364	0.244380834	0
positive regulation of kidney developm	44567	0.039827364	0.244380834	0
IMP biosynthetic process (GO:0006188	44567	0.039827364	0.244380834	0
snRNA modification (GO:0040031)	44567	0.039827364	0.244380834	0
tRNA 3'-end processing (GO:0042780)	44567	0.039827364	0.244380834	0
venous blood vessel morphogenesis (G	44567	0.039827364	0.244380834	0
protein localization to nucleolus (GO:1	44567	0.039827364	0.244380834	0
cellular response to ionizing radiation (	17564	0.041686008	0.244380834	0
cellular response to mechanical stimul	17930	0.043271912	0.244380834	0
positive regulation of angiogenesis (GO	3/116	0.043935655	0.244380834	0
aldehyde biosynthetic process (GO:004	44568	0.046310457	0.244380834	0
ammonium transport (GO:0015696)	44568	0.046310457	0.244380834	0
negative regulation of double-strand br	44568	0.046310457	0.244380834	0
aspartate transmembrane transport (G	44568	0.046310457	0.244380834	0
cellular ion homeostasis (GO:0006873)	44568	0.046310457	0.244380834	0
regulation of fat cell proliferation (GO:(	44568	0.046310457	0.244380834	0
cellular response to gonadotropin stim	44568	0.046310457	0.244380834	0
negative regulation of stress-activated	44568	0.046310457	0.244380834	0
negative regulation of T cell apoptotic p	44568	0.046310457	0.244380834	0
creatine metabolic process (GO:00066(	44568	0.046310457	0.244380834	0
death-inducing signaling complex asser	44568	0.046310457	0.244380834	0
delamination (GO:0060232)	44568	0.046310457	0.244380834	0
oxygen transport (GO:0015671)	44568	0.046310457	0.244380834	0
dorsal aorta development (GO:003590	44568	0.046310457	0.244380834	0
dorsal aorta morphogenesis (GO:0035	44568	0.046310457	0.244380834	0
positive regulation of cardiac epithelial	44568	0.046310457	0.244380834	0
regulation of transforming growth fact	44568	0.046310457	0.244380834	0
regulation of vascular associated smoo	44568	0.046310457	0.244380834	0
glyceraldehyde-3-phosphate metabolic	44568	0.046310457	0.244380834	0
hexose catabolic process (GO:0019320	44568	0.046310457	0.244380834	0
positive regulation of intracellular estr	44568	0.046310457	0.244380834	0
ribosomal large subunit export from nu	44568	0.046310457	0.244380834	0
positive regulation of miRNA metabolic	44568	0.046310457	0.244380834	0
TRAIL-activated apoptotic signaling pat	44568	0.046310457	0.244380834	0
mitochondrial DNA metabolic process (	44568	0.046310457	0.244380834	0

positive regulation of type I interferon-	44568	0.046310457	0.244380834	0
positive regulation of vascular associat	44568	0.046310457	0.244380834	0
vascular associated smooth muscle cell	44568	0.046310457	0.244380834	0
white fat cell differentiation (GO:00508	44568	0.046310457	0.244380834	0
negative regulation of protein ubiquitir	18660	0.046510094	0.244380834	0
intrinsic apoptotic signaling pathway in	18660	0.046510094	0.244380834	0
regulation of intrinsic apoptotic signalir	19025	0.048161641	0.244380834	0
negative regulation of B cell apoptotic	44569	0.0527501	0.244380834	0
adenosine to inosine editing (GO:0006	44569	0.0527501	0.244380834	0
ammonium transmembrane transport	44569	0.0527501	0.244380834	0
regulation of acetyl-CoA biosynthetic p	44569	0.0527501	0.244380834	0
regulation of acyl-CoA biosynthetic pro	44569	0.0527501	0.244380834	0
box C/D snoRNP assembly (GO:000049	44569	0.0527501	0.244380834	0
cardiac atrium development (GO:0003	44569	0.0527501	0.244380834	0
cell-cell adhesion mediated by cadherir	44569	0.0527501	0.244380834	0
regulation of epithelial to mesenchyma	44569	0.0527501	0.244380834	0
peptidyl-lysine hydroxylation (GO:0017	44569	0.0527501	0.244380834	0
regulation of protein localization to nu	44569	0.0527501	0.244380834	0
entry of bacterium into host cell (GO:0	44569	0.0527501	0.244380834	0
positive regulation of adaptive immune	44569	0.0527501	0.244380834	0
establishment of protein localization to	44569	0.0527501	0.244380834	0
regulation of stem cell division (GO:200	44569	0.0527501	0.244380834	0
positive regulation of endocytic recycli	44569	0.0527501	0.244380834	0
respiratory chain complex III assembly	44569	0.0527501	0.244380834	0
positive regulation of intracellular sterc	44569	0.0527501	0.244380834	0
positive regulation of myotube differer	44569	0.0527501	0.244380834	0
spleen development (GO:0048536)	44569	0.0527501	0.244380834	0
mitochondrial respiratory chain comple	44569	0.0527501	0.244380834	0
mitochondrial RNA processing (GO:000	44569	0.0527501	0.244380834	0
mitochondrial tRNA processing (GO:00	44569	0.0527501	0.244380834	0
vascular associated smooth muscle cell	44569	0.0527501	0.244380834	0
venous blood vessel development (GO:	44569	0.0527501	0.244380834	0
ventricular trabecula myocardium mor	44569	0.0527501	0.244380834	0
negative regulation by symbiont of hos	44569	0.0527501	0.244380834	0
regulation of protein secretion (GO:005	3/125	0.052761318	0.244380834	0
negative regulation of protein modifica	20121	0.053241798	0.24438465	0
interstrand cross-link repair (GO:00362	20121	0.053241798	0.24438465	0
positive regulation of proteolysis (GO:0	20852	0.056729652	0.253913069	0
positive regulation of macromolecule b	3/129	0.056937758	0.253913069	0
negative regulation of hydrolase activit	21217	0.058502869	0.253913069	0
negative regulation of ubiquitin proteir	44570	0.05914658	0.253913069	0
regulation of leukocyte degranulation (	44570	0.05914658	0.253913069	0
peptidyl-cysteine modification (GO:001	44570	0.05914658	0.253913069	0
epithelial to mesenchymal transition in	44570	0.05914658	0.253913069	0
regulation of RNA polymerase II regula	44570	0.05914658	0.253913069	0
galactose metabolic process (GO:0006(	44570	0.05914658	0.253913069	0
histone arginine methylation (GO:0034	44570	0.05914658	0.253913069	0

response to vitamin D (GO:0033280)	44570	0.05914658	0.253913069	0
IMP metabolic process (GO:0046040)	44570	0.05914658	0.253913069	0
inner ear receptor cell development (G	44570	0.05914658	0.253913069	0
ketone biosynthetic process (GO:0042	44570	0.05914658	0.253913069	0
mitochondrial tRNA modification (GO:(	44570	0.05914658	0.253913069	0
positive regulation of apoptotic signalir	21582	0.060295161	0.253913069	0
defense response to virus (GO:005160	3/133	0.06126662	0.253913069	0
cellular protein catabolic process (GO:(	21947	0.062106195	0.253913069	0
positive regulation of DNA biosynthetic	22313	0.06393564	0.253913069	0
negative regulation of circadian rhythm	44571	0.065500187	0.253913069	0
regulation of cell-cell adhesion mediate	44571	0.065500187	0.253913069	0
negative regulation of lymphocyte apo	44571	0.065500187	0.253913069	0
regulation of DNA methylation (GO:00	44571	0.065500187	0.253913069	0
negative regulation of protein autopho	44571	0.065500187	0.253913069	0
regulation of hair cycle (GO:0042634)	44571	0.065500187	0.253913069	0
negative regulation of transforming gro	44571	0.065500187	0.253913069	0
DNA replication-dependent nucleosom	44571	0.065500187	0.253913069	0
DNA replication-dependent nucleosom	44571	0.065500187	0.253913069	0
dosage compensation (GO:0007549)	44571	0.065500187	0.253913069	0
positive regulation of establishment of	44571	0.065500187	0.253913069	0
inner ear receptor cell stereocilium org	44571	0.065500187	0.253913069	0
positive regulation of mesenchymal cel	44571	0.065500187	0.253913069	0
rRNA pseudouridine synthesis (GO:003	44571	0.065500187	0.253913069	0
positive regulation of monocyte differe	44571	0.065500187	0.253913069	0
positive regulation of mRNA 3'-end pro	44571	0.065500187	0.253913069	0
small nucleolar ribonucleoprotein com	44571	0.065500187	0.253913069	0
smooth muscle tissue development (G(	44571	0.065500187	0.253913069	0
L-glutamate transmembrane transport	44571	0.065500187	0.253913069	0
positive regulation of vasculogenesis (G	44571	0.065500187	0.253913069	0
primary miRNA processing (GO:003105	44571	0.065500187	0.253913069	0
positive regulation of cysteine-type en(	22678	0.06578317	0.253913069	0
glucose metabolic process (GO:000600	22678	0.06578317	0.253913069	0
negative regulation of intrinsic apoptot	23408	0.069531193	0.262278194	0
protein oxidation (GO:0018158)	44572	0.071811203	0.262278194	0
regulation of cardiac muscle cell apopt(	44572	0.071811203	0.262278194	0
regulation of endocytic recycling (GO:2	44572	0.071811203	0.262278194	0
regulation of establishment of protein	44572	0.071811203	0.262278194	0
regulation of mast cell activation involv	44572	0.071811203	0.262278194	0
regulation of melanin biosynthetic proc	44572	0.071811203	0.262278194	0
regulation of mesenchymal cell prolifer	44572	0.071811203	0.262278194	0
regulation of myeloid leukocyte media	44572	0.071811203	0.262278194	0
regulation of protein localization to Caj	44572	0.071811203	0.262278194	0
positive regulation of cytoplasmic trans	44572	0.071811203	0.262278194	0
glycerol metabolic process (GO:000607	44572	0.071811203	0.262278194	0
positive regulation of integrin activatio	44572	0.071811203	0.262278194	0
positive regulation of protein localizati	44572	0.071811203	0.262278194	0
T cell homeostasis (GO:0043029)	44572	0.071811203	0.262278194	0

anion transmembrane transport (GO:0(	24504	0.075280891	0.266098433	0
negative regulation of cell division (GO	44573	0.078079913	0.266098433	0
purine nucleotide biosynthetic process	44573	0.078079913	0.266098433	0
angiotensin maturation (GO:0002003)	44573	0.078079913	0.266098433	0
regulation of angiotensin levels in bloo	44573	0.078079913	0.266098433	0
regulation of B cell apoptotic process ((	44573	0.078079913	0.266098433	0
chromatin assembly or disassembly (G(	44573	0.078079913	0.266098433	0
dosage compensation by inactivation o	44573	0.078079913	0.266098433	0
regulation of plasminogen activation ((	44573	0.078079913	0.266098433	0
regulation of pseudopodium assembly	44573	0.078079913	0.266098433	0
positive regulation of cellular senescen	44573	0.078079913	0.266098433	0
gas transport (GO:0015669)	44573	0.078079913	0.266098433	0
sno(s)RNA 3'-end processing (GO:0031	44573	0.078079913	0.266098433	0
positive regulation of protein localizati(	44573	0.078079913	0.266098433	0
positive regulation of protein maturati(	44573	0.078079913	0.266098433	0
positive regulation of pseudopodium a	44573	0.078079913	0.266098433	0
toll-like receptor 3 signaling pathway ((	44573	0.078079913	0.266098433	0
mitochondrial genome maintenance (G	44573	0.078079913	0.266098433	0
mitochondrion distribution (GO:00483	44573	0.078079913	0.266098433	0
mRNA transcription (GO:0009299)	44573	0.078079913	0.266098433	0
positive regulation of protein polymeri	25235	0.07919552	0.266796347	0
DNA-templated transcription, terminat	25600	0.081176376	0.266796347	0
sterol metabolic process (GO:0016125)	25600	0.081176376	0.266796347	0
nucleic acid metabolic process (GO:009	25965	0.083172529	0.266796347	0
pteridine-containing compound metab	44574	0.084306598	0.266796347	0
purine-containing compound salvage ((	44574	0.084306598	0.266796347	0
AMP metabolic process (GO:0046033)	44574	0.084306598	0.266796347	0
negative regulation of chromatin organ	44574	0.084306598	0.266796347	0
negative regulation of chromatin silenc	44574	0.084306598	0.266796347	0
negative regulation of gene silencing (G	44574	0.084306598	0.266796347	0
central nervous system projection neu	44574	0.084306598	0.266796347	0
pentose-phosphate shunt (GO:000609	44574	0.084306598	0.266796347	0
DNA catabolic process (GO:0006308)	44574	0.084306598	0.266796347	0
entry into host (GO:0044409)	44574	0.084306598	0.266796347	0
establishment of protein localization to	44574	0.084306598	0.266796347	0
positive regulation of cell aging (GO:00	44574	0.084306598	0.266796347	0
Golgi ribbon formation (GO:0090161)	44574	0.084306598	0.266796347	0
high-density lipoprotein particle assem	44574	0.084306598	0.266796347	0
ribosomal subunit export from nucleus	44574	0.084306598	0.266796347	0
positive regulation of neuron migratior	44574	0.084306598	0.266796347	0
positive regulation of ruffle assembly ((	44574	0.084306598	0.266796347	0
muscle tissue development (GO:00605	44574	0.084306598	0.266796347	0
protein heterotetramerization (GO:005	44574	0.084306598	0.266796347	0
extrinsic apoptotic signaling pathway ((	26330	0.085183686	0.267907951	0
response to ionizing radiation (GO:001(	26330	0.085183686	0.267907951	0
chromatin assembly (GO:0031497)	26696	0.087209558	0.271208462	0
positive regulation of transcription by F	10/908	0.087486435	0.271208462	0

proteolysis involved in cellular protein	27061	0.089249858	0.271208462	0
negative regulation of protein binding (	27061	0.089249858	0.271208462	0
regulation of peptide hormone secretic	27061	0.089249858	0.271208462	0
activation of cysteine-type endopeptid	44575	0.090491538	0.271208462	0
negative regulation of bone mineraliza	44575	0.090491538	0.271208462	0
quinone biosynthetic process (GO:1901	44575	0.090491538	0.271208462	0
antiviral innate immune response (GO:	44575	0.090491538	0.271208462	0
branching involved in blood vessel mor	44575	0.090491538	0.271208462	0
C4-dicarboxylate transport (GO:001574	44575	0.090491538	0.271208462	0
negative regulation of TORC1 signaling	44575	0.090491538	0.271208462	0
regulation of vasculogenesis (GO:2001	44575	0.090491538	0.271208462	0
respiratory electron transport chain (G	44575	0.090491538	0.271208462	0
T cell differentiation in thymus (GO:00	44575	0.090491538	0.271208462	0
thymus development (GO:0048538)	44575	0.090491538	0.271208462	0
positive regulation of phosphorylation	4/253	0.092446336	0.273530764	0
positive regulation of endothelial cell p	28157	0.095454506	0.273530764	0
negative regulation of endoplasmic ret	44576	0.09663501	0.273530764	0
C21-steroid hormone biosynthetic proc	44576	0.09663501	0.273530764	0
negative regulation of protein processi	44576	0.09663501	0.273530764	0
cellular response to arsenic-containing	44576	0.09663501	0.273530764	0
cellular response to ATP (GO:0071318)	44576	0.09663501	0.273530764	0
negative regulation of ubiquitin-protein	44576	0.09663501	0.273530764	0
regulation of integrin activation (GO:00	44576	0.09663501	0.273530764	0
contractile actin filament bundle assem	44576	0.09663501	0.273530764	0
peptidyl-arginine modification (GO:001	44576	0.09663501	0.273530764	0
regulation of phospholipase C activity (	44576	0.09663501	0.273530764	0
glucan catabolic process (GO:0009251)	44576	0.09663501	0.273530764	0
glycogen catabolic process (GO:000598	44576	0.09663501	0.273530764	0
histone H3 deacetylation (GO:0070932	44576	0.09663501	0.273530764	0
stress fiber assembly (GO:0043149)	44576	0.09663501	0.273530764	0
ubiquinone biosynthetic process (GO:0	44576	0.09663501	0.273530764	0
ubiquinone metabolic process (GO:000	44576	0.09663501	0.273530764	0
protein hydroxylation (GO:0018126)	44576	0.09663501	0.273530764	0
myoblast fusion (GO:0007520)	44576	0.09663501	0.273530764	0
negative regulation of apoptotic signali	28522	0.097549714	0.27535501	0
regulation of cellular response to heat	28887	0.099657963	0.276955816	0
positive regulation of proteasomal ubic	28887	0.099657963	0.276955816	0
positive regulation of ubiquitin-depend	28887	0.099657963	0.276955816	0
negative regulation of extrinsic apopto	29252	0.101778985	0.276955816	0
regulation of MAPK cascade (GO:00434	3/166	0.102376482	0.276955816	0
purine ribonucleoside monophosphate	44577	0.10273729	0.276955816	0
regulation of chromatin silencing (GO:0	44577	0.10273729	0.276955816	0
cellular polysaccharide catabolic proce	44577	0.10273729	0.276955816	0
negative regulation of release of cytoch	44577	0.10273729	0.276955816	0
negative regulation of type I interferon	44577	0.10273729	0.276955816	0
regulation of intrinsic apoptotic signali	44577	0.10273729	0.276955816	0
nuclear transport (GO:0051169)	44577	0.10273729	0.276955816	0

regulation of mast cell degranulation ((	44577	0.10273729	0.276955816	0
oogenesis (GO:0048477)	44577	0.10273729	0.276955816	0
DNA unwinding involved in DNA replica	44577	0.10273729	0.276955816	0
histone H2A acetylation (GO:0043968)	44577	0.10273729	0.276955816	0
transepithelial transport (GO:0070633)	44577	0.10273729	0.276955816	0
positive regulation of cellular amide m	29618	0.103912514	0.279384834	0
cellular protein-containing complex ass	3/168	0.105152199	0.281973923	0
regulation of protein phosphorylation (	4/266	0.106028616	0.283544314	0
positive regulation of protein phospho	5/371	0.106820771	0.283544314	0
positive regulation of plasma membrar	30348	0.10821605	0.283544314	0
positive regulation of gene expression	6/482	0.108383207	0.283544314	0
aorta morphogenesis (GO:0035909)	44578	0.108798652	0.283544314	0
negative regulation of execution phase	44578	0.108798652	0.283544314	0
gliogenesis (GO:0042063)	44578	0.108798652	0.283544314	0
ribosomal small subunit assembly (GO:	44578	0.108798652	0.283544314	0
stem cell development (GO:0048864)	44578	0.108798652	0.283544314	0
mesenchyme morphogenesis (GO:007	44578	0.108798652	0.283544314	0
protein heterooligomerization (GO:005	44578	0.108798652	0.283544314	0
regulation of gene expression (GO:001	11/1079	0.113076235	0.285920331	0
negative regulation of cell population p	5/379	0.114140161	0.285920331	0
regulation of neuron death (GO:19012	31444	0.114758699	0.285920331	0
positive regulation of proteasomal pro	31444	0.114758699	0.285920331	0
acidic amino acid transport (GO:00158	44579	0.114819369	0.285920331	0
regulation of adaptive immune respons	44579	0.114819369	0.285920331	0
negative regulation of fibroblast prolife	44579	0.114819369	0.285920331	0
base conversion or substitution editing	44579	0.114819369	0.285920331	0
regulation of cartilage development (G	44579	0.114819369	0.285920331	0
negative regulation of Rho protein sign	44579	0.114819369	0.285920331	0
regulation of mRNA polyadenylation (G	44579	0.114819369	0.285920331	0
positive regulation of cartilage develop	44579	0.114819369	0.285920331	0
positive regulation of cell adhesion me	44579	0.114819369	0.285920331	0
positive regulation of cell cycle phase t	44579	0.114819369	0.285920331	0
release of cytochrome c from mitocho	44579	0.114819369	0.285920331	0
positive regulation of extracellular mat	44579	0.114819369	0.285920331	0
RNA destabilization (GO:0050779)	44579	0.114819369	0.285920331	0
intracellular estrogen receptor signalin	44579	0.114819369	0.285920331	0
DNA metabolic process (GO:0006259)	4/277	0.118189371	0.285920331	0
negative regulation of binding (GO:005	32174	0.11917577	0.285920331	0
regulation of translation (GO:0006417)	3/178	0.119464426	0.285920331	0
negative regulation of immune system	44580	0.120799711	0.285920331	0
branching involved in ureteric bud mor	44580	0.120799711	0.285920331	0
cardiac atrium morphogenesis (GO:000	44580	0.120799711	0.285920331	0
cellular response to copper ion (GO:00	44580	0.120799711	0.285920331	0
regulation of insulin-like growth factor	44580	0.120799711	0.285920331	0
neural crest cell differentiation (GO:00	44580	0.120799711	0.285920331	0
regulation of mitochondrial membrane	44580	0.120799711	0.285920331	0
detection of mechanical stimulus (GO:(	44580	0.120799711	0.285920331	0

endocardial cushion morphogenesis (G	44580	0.120799711	0.285920331	0
regulation of stem cell population mair	44580	0.120799711	0.285920331	0
folic acid metabolic process (GO:00466	44580	0.120799711	0.285920331	0
positive regulation of establishment of	44580	0.120799711	0.285920331	0
positive regulation of G protein-couple	44580	0.120799711	0.285920331	0
response to ATP (GO:0033198)	44580	0.120799711	0.285920331	0
heart trabecula morphogenesis (GO:00	44580	0.120799711	0.285920331	0
positive regulation of oxidoreductase a	44580	0.120799711	0.285920331	0
mesenchymal cell development (GO:0(	44580	0.120799711	0.285920331	0
ureteric bud morphogenesis (GO:0060(	44580	0.120799711	0.285920331	0
protein stabilization (GO:0050821)	3/179	0.120933918	0.285920331	0
positive regulation of cellular biosynthe	3/180	0.122410118	0.2882768	0
negative regulation of translation (GO:(	32905	0.123634801	0.2882768	0
mitochondrial respiratory chain comple	32905	0.123634801	0.2882768	0
regulation of stem cell differentiation (	33270	0.125879455	0.2882768	0
purine ribonucleoside monophosphate	44581	0.126739947	0.2882768	0
cardiac epithelial to mesenchymal tran	44581	0.126739947	0.2882768	0
cardiac ventricle development (GO:00(	44581	0.126739947	0.2882768	0
cellular modified amino acid biosynthe	44581	0.126739947	0.2882768	0
cellular response to nitrogen compoun	44581	0.126739947	0.2882768	0
regulation of lymphocyte differentiatio	44581	0.126739947	0.2882768	0
nucleobase-containing compound bios	44581	0.126739947	0.2882768	0
regulation of nuclear division (GO:0051	44581	0.126739947	0.2882768	0
energy reserve metabolic process (GO:	44581	0.126739947	0.2882768	0
positive regulation of activated T cell p	44581	0.126739947	0.2882768	0
folic acid-containing compound metab	44581	0.126739947	0.2882768	0
positive regulation of protein processin	44581	0.126739947	0.2882768	0
mitochondrial cytochrome c oxidase as	44581	0.126739947	0.2882768	0
regulation of endothelial cell proliferati	33635	0.128133888	0.29079829	0
proteolysis (GO:0006508)	4/287	0.129747677	0.291991186	0
regulation of epithelial cell proliferatio	34001	0.130397868	0.291991186	0
regulation of anoikis (GO:2000209)	44582	0.132640344	0.291991186	0
negative regulation of protein localizati	44582	0.132640344	0.291991186	0
negative regulation of protein localizati	44582	0.132640344	0.291991186	0
nuclear-transcribed mRNA poly(A) tail s	44582	0.132640344	0.291991186	0
cyclic purine nucleotide metabolic proc	44582	0.132640344	0.291991186	0
endocardial cushion development (GO:	44582	0.132640344	0.291991186	0
extrinsic apoptotic signaling pathway ir	44582	0.132640344	0.291991186	0
regulation of transposition (GO:001052	44582	0.132640344	0.291991186	0
regulation of ubiquitin protein ligase ac	44582	0.132640344	0.291991186	0
intrinsic apoptotic signaling pathway in	44582	0.132640344	0.291991186	0
protein localization to chromatin (GO:0	44582	0.132640344	0.291991186	0
nucleosome organization (GO:0034728	34366	0.132671167	0.291991186	0
mRNA metabolic process (GO:0016071	34731	0.134953557	0.296374299	0
negative regulation of biomineral tissu	44583	0.138501167	0.299644775	0
regulation of chromosome organizatio	44583	0.138501167	0.299644775	0
regulation of endoplasmic reticulum st	44583	0.138501167	0.299644775	0

regulation of execution phase of apopt	44583	0.138501167	0.299644775	0
chaperone-mediated protein complex a	44583	0.138501167	0.299644775	0
glutamate metabolic process (GO:0006	44583	0.138501167	0.299644775	0
metallo-sulfur cluster assembly (GO:00	44583	0.138501167	0.299644775	0
negative regulation of Wnt signaling pa	3/191	0.139072962	0.300244382	0
positive regulation of cold-induced the	35462	0.139544722	0.300625943	0
negative regulation of macromolecule	3/194	0.143745836	0.303226412	0
artery development (GO:0060840)	44584	0.144322679	0.303226412	0
negative regulation of extrinsic apopto	44584	0.144322679	0.303226412	0
negative regulation of GTPase activity (	44584	0.144322679	0.303226412	0
negative regulation of signal transducti	44584	0.144322679	0.303226412	0
oligosaccharide biosynthetic process (G	44584	0.144322679	0.303226412	0
DNA catabolic process, endonucleolytic	44584	0.144322679	0.303226412	0
regulation of peptidase activity (GO:00	44584	0.144322679	0.303226412	0
ERK1 and ERK2 cascade (GO:0070371)	44584	0.144322679	0.303226412	0
glucose 6-phosphate metabolic proces	44584	0.144322679	0.303226412	0
respiratory chain complex IV assembly	44584	0.144322679	0.303226412	0
response to copper ion (GO:0046688)	44584	0.144322679	0.303226412	0
regulation of cell population proliferati	8/764	0.145553945	0.304089741	0
positive regulation of translation (GO:0	2/100	0.146494147	0.304089741	0
MAPK cascade (GO:0000165)	4/303	0.149171269	0.304089741	0
C21-steroid hormone metabolic proces	44585	0.150105142	0.304089741	0
canonical glycolysis (GO:0061621)	44585	0.150105142	0.304089741	0
carbohydrate biosynthetic process (GO	44585	0.150105142	0.304089741	0
regulation of cellular response to trans	44585	0.150105142	0.304089741	0
negative regulation of ossification (GO:	44585	0.150105142	0.304089741	0
cholesterol efflux (GO:0033344)	44585	0.150105142	0.304089741	0
DNA packaging (GO:0006323)	44585	0.150105142	0.304089741	0
regulation of ruffle assembly (GO:1900	44585	0.150105142	0.304089741	0
glucose catabolic process to pyruvate (	44585	0.150105142	0.304089741	0
heterochromatin assembly (GO:00315(	44585	0.150105142	0.304089741	0
iron-sulfur cluster assembly (GO:00162	44585	0.150105142	0.304089741	0
positive regulation of phospholipase ac	44585	0.150105142	0.304089741	0
positive regulation of protein targeting	44585	0.150105142	0.304089741	0
positive regulation of transcription fror	44585	0.150105142	0.304089741	0
ncRNA 3'-end processing (GO:0043628)	44585	0.150105142	0.304089741	0
regulation of proteasomal ubiquitin-de	2/102	0.15116639	0.305026835	0
intrinsic apoptotic signaling pathway (G	2/102	0.15116639	0.305026835	0
cellular response to organonitrogen co	2/103	0.153513674	0.308407029	0
organelle organization (GO:0006996)	5/420	0.155208691	0.308407029	0
protein quality control for misfolded or	44586	0.155848816	0.308407029	0
negative regulation of response to end	44586	0.155848816	0.308407029	0
regulation of myotube differentiation (	44586	0.155848816	0.308407029	0
outflow tract septum morphogenesis ((	44586	0.155848816	0.308407029	0
energy derivation by oxidation of orgar	44586	0.155848816	0.308407029	0
regulation of protein processing (GO:0(	44586	0.155848816	0.308407029	0
glycolytic process through glucose-6-pl	44586	0.155848816	0.308407029	0

regulation of insulin secretion (GO:005	2/104	0.155868126	0.308407029	0
regulation of angiogenesis (GO:004576	3/203	0.158068523	0.310610349	0
regulation of cell cycle process (GO:001	2/106	0.160597732	0.310610349	0
chromosome organization (GO:005127	2/106	0.160597732	0.310610349	0
protein localization to nucleus (GO:003	2/106	0.160597732	0.310610349	0
purine-containing compound biosynthe	44587	0.16155396	0.310610349	0
regulation of biomineral tissue develop	44587	0.16155396	0.310610349	0
negative regulation of intrinsic apoptot	44587	0.16155396	0.310610349	0
negative regulation of protein localizati	44587	0.16155396	0.310610349	0
negative regulation of protein transpor	44587	0.16155396	0.310610349	0
cellular response to drug (GO:0035690	44587	0.16155396	0.310610349	0
negative regulation of transposition (G	44587	0.16155396	0.310610349	0
regulation of telomere maintenance (G	44587	0.16155396	0.310610349	0
histone methylation (GO:0016571)	44587	0.16155396	0.310610349	0
positive regulation of microtubule poly	44587	0.16155396	0.310610349	0
positive regulation of T cell mediated c	44587	0.16155396	0.310610349	0
regulation of protein kinase B signaling	3/207	0.164571785	0.3143875	0
positive regulation of intracellular signa	6/546	0.164586267	0.3143875	0
DNA replication (GO:0006260)	2/108	0.165353624	0.3143875	0
camera-type eye development (GO:00	44588	0.167220829	0.3143875	0
cellular response to cadmium ion (GO:(	44588	0.167220829	0.3143875	0
cellular response to unfolded protein ((	44588	0.167220829	0.3143875	0
entrainment of circadian clock by phot	44588	0.167220829	0.3143875	0
positive regulation of BMP signaling pa	44588	0.167220829	0.3143875	0
regulation of transcription regulatory r	44588	0.167220829	0.3143875	0
positive regulation of mitotic cell cycle	44588	0.167220829	0.3143875	0
L-alpha-amino acid transmembrane tra	44588	0.167220829	0.3143875	0
positive regulation of striated muscle c	44588	0.167220829	0.3143875	0
carbohydrate derivative biosynthetic p	44589	0.17284968	0.319083014	0
cellular response to acid chemical (GO:	44589	0.17284968	0.319083014	0
regulation of extrinsic apoptotic signali	44589	0.17284968	0.319083014	0
regulation of neuron migration (GO:20	44589	0.17284968	0.319083014	0
photoperiodism (GO:0009648)	44589	0.17284968	0.319083014	0
positive regulation of fibroblast prolife	44589	0.17284968	0.319083014	0
positive regulation of microtubule poly	44589	0.17284968	0.319083014	0
internal peptidyl-lysine acetylation (GO	44589	0.17284968	0.319083014	0
L-amino acid transport (GO:0015807)	44589	0.17284968	0.319083014	0
positive regulation of response to wou	44589	0.17284968	0.319083014	0
translation (GO:0006412)	3/214	0.17614013	0.320689838	0
positive regulation of metabolic proces	2/113	0.177348297	0.320689838	0
negative regulation of myeloid leukocy	44590	0.178440764	0.320689838	0
regulation of DNA biosynthetic process	44590	0.178440764	0.320689838	0
regulation of double-strand break repa	44590	0.178440764	0.320689838	0
dicarboxylic acid transport (GO:000683	44590	0.178440764	0.320689838	0
regulation of neuronal synaptic plastici	44590	0.178440764	0.320689838	0
regulation of protein targeting to mem	44590	0.178440764	0.320689838	0
regulation of T cell mediated cytotoxici	44590	0.178440764	0.320689838	0

positive regulation of dephosphorylatic	44590	0.178440764	0.320689838	0
glycolytic process (GO:0006096)	44590	0.178440764	0.320689838	0
positive regulation of extrinsic apoptot	44590	0.178440764	0.320689838	0
response to cadmium ion (GO:004668	44590	0.178440764	0.320689838	0
telomere maintenance via telomerase	44590	0.178440764	0.320689838	0
production of miRNAs involved in gene	44590	0.178440764	0.320689838	0
artery morphogenesis (GO:0048844)	44591	0.183994333	0.322671088	0
negative regulation of gene expression	44591	0.183994333	0.322671088	0
cardiac muscle cell action potential (GC	44591	0.183994333	0.322671088	0
negative regulation of Notch signaling p	44591	0.183994333	0.322671088	0
CENP-A containing chromatin organizat	44591	0.183994333	0.322671088	0
CENP-A containing nucleosome assemb	44591	0.183994333	0.322671088	0
peptidyl-lysine trimethylation (GO:001	44591	0.183994333	0.322671088	0
positive regulation of B cell proliferatio	44591	0.183994333	0.322671088	0
extrinsic apoptotic signaling pathway v	44591	0.183994333	0.322671088	0
regulation of vasoconstriction (GO:001	44591	0.183994333	0.322671088	0
histone H3-K4 methylation (GO:00515	44591	0.183994333	0.322671088	0
RNA-dependent DNA biosynthetic proc	44591	0.183994333	0.322671088	0
termination of RNA polymerase I transc	44591	0.183994333	0.322671088	0
TRIF-dependent toll-like receptor signa	44591	0.183994333	0.322671088	0
regulation of protein-containing compl	2/116	0.184609661	0.322671088	0
ion transport (GO:0006811)	2/116	0.184609661	0.322671088	0
transcription, DNA-templated (GO:000	3/221	0.187928963	0.322928662	0
regulation of cellular response to stress	2/118	0.189474497	0.322928662	0
regulation of protein binding (GO:0043	2/118	0.189474497	0.322928662	0
positive regulation of protein-containin	2/118	0.189474497	0.322928662	0
'de novo' posttranslational protein fold	44592	0.189510638	0.322928662	0
aminoglycan catabolic process (GO:00	44592	0.189510638	0.322928662	0
negative regulation of DNA binding (GC	44592	0.189510638	0.322928662	0
regulation of cellular pH (GO:0030641)	44592	0.189510638	0.322928662	0
regulation of cellular senescence (GO:2	44592	0.189510638	0.322928662	0
negative regulation of response to DNA	44592	0.189510638	0.322928662	0
regulation of transmembrane receptor	44592	0.189510638	0.322928662	0
steroid hormone biosynthetic process (	44592	0.189510638	0.322928662	0
positive regulation of proteolysis involv	44592	0.189510638	0.322928662	0
vitamin transport (GO:0051180)	44592	0.189510638	0.322928662	0
MyD88-independent toll-like receptor s	44592	0.189510638	0.322928662	0
positive regulation of cysteine-type end	2/119	0.191913575	0.324664599	0
negative regulation of double-strand br	11689	0.194989926	0.324664599	0
regulation of cellular amide metabolic p	11689	0.194989926	0.324664599	0
regulation of cellular biosynthetic proc	11689	0.194989926	0.324664599	0
cardiac muscle tissue morphogenesis (G	11689	0.194989926	0.324664599	0
regulation of dendrite morphogenesis (	11689	0.194989926	0.324664599	0
cellular response to topologically incor	11689	0.194989926	0.324664599	0
regulation of intracellular estrogen rec	11689	0.194989926	0.324664599	0
chromatin remodeling at centromere (G	11689	0.194989926	0.324664599	0
DNA damage checkpoint signaling (GO:	11689	0.194989926	0.324664599	0

response to amino acid (GO:0043200)	11689	0.194989926	0.324664599	0
RNA biosynthetic process (GO:0032774	11689	0.194989926	0.324664599	0
transcription initiation from RNA polym	11689	0.194989926	0.324664599	0
mitochondrial membrane organization	11689	0.194989926	0.324664599	0
apoptotic mitochondrial changes (GO:0	12055	0.200432444	0.331022141	0
RNA stabilization (GO:0043489)	12055	0.200432444	0.331022141	0
signal transduction by p53 class mediat	12055	0.200432444	0.331022141	0
vasculogenesis (GO:0001570)	12055	0.200432444	0.331022141	0
muscle cell development (GO:0055001	12055	0.200432444	0.331022141	0
defense response to symbiont (GO:014	2/124	0.204168894	0.333464814	0
positive regulation of multicellular orga	4/345	0.204831715	0.333464814	0
regulation of activated T cell proliferati	12420	0.205838438	0.333464814	0
negative regulation of mitochondrion o	12420	0.205838438	0.333464814	0
organic cyclic compound biosynthetic p	12420	0.205838438	0.333464814	0
female gamete generation (GO:000729	12420	0.205838438	0.333464814	0
histone lysine methylation (GO:003496	12420	0.205838438	0.333464814	0
positive regulation of protein dephospl	12420	0.205838438	0.333464814	0
transcription by RNA polymerase I (GO	12420	0.205838438	0.333464814	0
tRNA export from nucleus (GO:000640	12420	0.205838438	0.333464814	0
tRNA-containing ribonucleoprotein con	12420	0.205838438	0.333464814	0
ventricular cardiac muscle tissue morpl	12420	0.205838438	0.333464814	0
protein targeting (GO:0006605)	2/125	0.206630806	0.334217129	0
regulation of blood circulation (GO:190	12785	0.211208149	0.338397962	0
bicarbonate transport (GO:0015701)	12785	0.211208149	0.338397962	0
blood vessel diameter maintenance (G	12785	0.211208149	0.338397962	0
negative regulation of Ras protein signa	12785	0.211208149	0.338397962	0
positive regulation of cell cycle G1/S ph	12785	0.211208149	0.338397962	0
regulation of TORC1 signaling (GO:190	12785	0.211208149	0.338397962	0
supramolecular fiber organization (GO:	4/351	0.213245616	0.341126033	0
DNA-dependent DNA replication (GO:0	2/129	0.216509386	0.342102504	0
regulation of cell cycle G1/S phase tran	13150	0.21654182	0.342102504	0
cellular response to heat (GO:0034605	13150	0.21654182	0.342102504	0
regulation of ossification (GO:0030278	13150	0.21654182	0.342102504	0
positive regulation of cytokine-mediate	13150	0.21654182	0.342102504	0
positive regulation of innate immune re	13150	0.21654182	0.342102504	0
telomere maintenance via telomere ler	13150	0.21654182	0.342102504	0
positive regulation of T cell mediated in	13150	0.21654182	0.342102504	0
negative regulation of stress-activated	13516	0.221839691	0.34617863	0
centromere complex assembly (GO:00	13516	0.221839691	0.34617863	0
regulation of intracellular pH (GO:0051	13516	0.221839691	0.34617863	0
regulation of protein autophosphorylat	13516	0.221839691	0.34617863	0
regulation of transport (GO:0051049)	13516	0.221839691	0.34617863	0
glutamine family amino acid metabolic	13516	0.221839691	0.34617863	0
positive regulation of myeloid cell diffe	13516	0.221839691	0.34617863	0
tRNA transport (GO:0051031)	13516	0.221839691	0.34617863	0
negative regulation of innate immune r	13881	0.227102001	0.350631726	0
negative regulation of TOR signaling (G	13881	0.227102001	0.350631726	0

DNA replication initiation (GO:000627(	13881	0.227102001	0.350631726	0
histone exchange (GO:0043486)	13881	0.227102001	0.350631726	0
spliceosomal snRNP assembly (GO:000	13881	0.227102001	0.350631726	0
mRNA destabilization (GO:0061157)	13881	0.227102001	0.350631726	0
ncRNA export from nucleus (GO:00970	13881	0.227102001	0.350631726	0
regulation of dendrite development (G	14246	0.232328986	0.354937387	0
negative regulation of protein secretio	14246	0.232328986	0.354937387	0
negative regulation of secretion by cell	14246	0.232328986	0.354937387	0
organophosphate biosynthetic process	14246	0.232328986	0.354937387	0
DNA integrity checkpoint signaling (GO	14246	0.232328986	0.354937387	0
regulation of T cell differentiation (GO:	14246	0.232328986	0.354937387	0
positive regulation of intracellular tran	14246	0.232328986	0.354937387	0
organic substance transport (GO:00717	2/136	0.233893052	0.356791946	0
regulation of microtubule polymerizati	14611	0.237520882	0.360706079	0
positive regulation of intrinsic apoptoti	14611	0.237520882	0.360706079	0
positive regulation of wound healing (G	14611	0.237520882	0.360706079	0
protein methylation (GO:0006479)	14977	0.242677923	0.363660005	0
regulation of cell development (GO:00(	14977	0.242677923	0.363660005	0
carbohydrate catabolic process (GO:00	14977	0.242677923	0.363660005	0
regulation of mitochondrial membrane	14977	0.242677923	0.363660005	0
regulation of protein dephosphorylatio	14977	0.242677923	0.363660005	0
regulation of release of cytochrome c f	14977	0.242677923	0.363660005	0
regulation of response to DNA damage	14977	0.242677923	0.363660005	0
response to growth factor (GO:007084	14977	0.242677923	0.363660005	0
T cell differentiation (GO:0030217)	14977	0.242677923	0.363660005	0
regulation of canonical Wnt signaling p	3/253	0.244049855	0.365178858	0
regulation of nervous system developn	15342	0.24780034	0.369705047	0
translesion synthesis (GO:0019985)	15342	0.24780034	0.369705047	0
nitrogen compound transport (GO:007	2/143	0.251357844	0.371851724	0
monocarboxylic acid metabolic process	2/143	0.251357844	0.371851724	0
negative regulation of proteolysis (GO:(	15707	0.252888365	0.371851724	0
cellular response to glucose starvation	15707	0.252888365	0.371851724	0
DNA synthesis involved in DNA repair ((	15707	0.252888365	0.371851724	0
glutathione metabolic process (GO:000	15707	0.252888365	0.371851724	0
heart looping (GO:0001947)	15707	0.252888365	0.371851724	0
positive regulation of leukocyte mediat	15707	0.252888365	0.371851724	0
positive regulation of phospholipase C	15707	0.252888365	0.371851724	0
substantia nigra development (GO:002	15707	0.252888365	0.371851724	0
cardiac ventricle morphogenesis (GO:0	16072	0.257942227	0.375490185	0
cation transmembrane transport (GO:0	16072	0.257942227	0.375490185	0
neurogenesis (GO:0022008)	16072	0.257942227	0.375490185	0
positive regulation of cell-matrix adhes	16072	0.257942227	0.375490185	0
positive regulation of mRNA catabolic p	16072	0.257942227	0.375490185	0
intracellular steroid hormone receptor	16072	0.257942227	0.375490185	0
mitotic spindle assembly (GO:0090307)	16072	0.257942227	0.375490185	0
regulation of mRNA stability (GO:0043(	2/146	0.258856439	0.376283469	0
action potential (GO:0001508)	16438	0.262962154	0.380082886	0

neural crest cell development (GO:001	16438	0.262962154	0.380082886	0
positive regulation of RNA metabolic pı	16438	0.262962154	0.380082886	0
zymogen activation (GO:0031638)	16438	0.262962154	0.380082886	0
positive regulation of transferase activi	2/148	0.263857598	0.380836958	0
regulation of B cell proliferation (GO:0(	16803	0.267948371	0.384021645	0
regulation of DNA metabolic process (G	16803	0.267948371	0.384021645	0
regulation of fibroblast proliferation (G	16803	0.267948371	0.384021645	0
postreplication repair (GO:0006301)	16803	0.267948371	0.384021645	0
posttranscriptional regulation of gene e	16803	0.267948371	0.384021645	0
cellular response to organic cyclic comp	2/150	0.268859334	0.384786041	0
determination of heart left/right asymr	17168	0.272901103	0.385695179	0
embryonic heart tube morphogenesis (	17168	0.272901103	0.385695179	0
regulation of protein localization to nu(	17168	0.272901103	0.385695179	0
epithelial to mesenchymal transition (G	17168	0.272901103	0.385695179	0
positive regulation of cell-cell adhesion	17168	0.272901103	0.385695179	0
regulation of T cell activation (GO:005(	17168	0.272901103	0.385695179	0
regulation of wound healing (GO:0061(	17168	0.272901103	0.385695179	0
histone deacetylation (GO:0016575)	17168	0.272901103	0.385695179	0
positive regulation of pathway-restricte	17168	0.272901103	0.385695179	0
positive regulation of transcription, DN	10/1183	0.277156088	0.391020946	0
purine ribonucleotide biosynthetic pro(	17533	0.277820574	0.391020946	0
histone H4 acetylation (GO:0043967)	17533	0.277820574	0.391020946	0
adherens junction organization (GO:00	17899	0.282707005	0.392477436	0
negative regulation of cell projection o	17899	0.282707005	0.392477436	0
regulation of cellular localization (GO:0	17899	0.282707005	0.392477436	0
regulation of cellular protein metabolic	17899	0.282707005	0.392477436	0
oligosaccharide metabolic process (GO	17899	0.282707005	0.392477436	0
positive regulation of actin filament po	17899	0.282707005	0.392477436	0
regulation of stress-activated MAPK ca	17899	0.282707005	0.392477436	0
response to unfolded protein (GO:000(	17899	0.282707005	0.392477436	0
RNA catabolic process (GO:0006401)	17899	0.282707005	0.392477436	0
secondary alcohol metabolic process (G	17899	0.282707005	0.392477436	0
regulation of cell differentiation (GO:0(	2/156	0.283858986	0.393540554	0
regulation of cellular component move	18264	0.287560617	0.397590595	0
organic hydroxy compound biosynthetı	18264	0.287560617	0.397590595	0
cellular response to starvation (GO:000	2/158	0.28885413	0.398837884	0
cholesterol transport (GO:0030301)	18629	0.292381628	0.401532181	0
DNA duplex unwinding (GO:0032508)	18629	0.292381628	0.401532181	0
mesenchymal cell differentiation (GO:0	18629	0.292381628	0.401532181	0
mitotic metaphase plate congression (G	18629	0.292381628	0.401532181	0
positive regulation of protein kinase B s	2/161	0.296339552	0.405376827	0
negative regulation of protein-containi	18994	0.297170255	0.405376827	0
endocytic recycling (GO:0032456)	18994	0.297170255	0.405376827	0
signal transduction in response to DNA	18994	0.297170255	0.405376827	0
sprouting angiogenesis (GO:0002040)	18994	0.297170255	0.405376827	0
positive regulation of B cell activation (	19360	0.301926715	0.410217764	0
heart morphogenesis (GO:0003007)	19360	0.301926715	0.410217764	0

IRE1-mediated unfolded protein respor	19360	0.301926715	0.410217764	0
negative regulation of canonical Wnt si	2/165	0.306302367	0.413330153	0
regulation of neuron projection develo	2/165	0.306302367	0.413330153	0
regulation of proteasomal protein cata	19725	0.306651223	0.413330153	0
regulation of proteolysis (GO:0030162)	19725	0.306651223	0.413330153	0
glycosaminoglycan metabolic process (	19725	0.306651223	0.413330153	0
inorganic anion transport (GO:0015698	19725	0.306651223	0.413330153	0
negative regulation of transcription, DI	8/948	0.310034739	0.416898194	0
negative regulation of cellular macrom	5/547	0.310218557	0.416898194	0
pyruvate metabolic process (GO:00060	20090	0.31134399	0.416898194	0
negative regulation of cytokine-mediat	20090	0.31134399	0.416898194	0
positive regulation of response to DNA	20090	0.31134399	0.416898194	0
negative regulation of transcription by	6/684	0.315745211	0.41928298	0
protein-containing complex disassembl	20455	0.316005229	0.41928298	0
blood vessel morphogenesis (GO:0048!	20455	0.316005229	0.41928298	0
nuclear-transcribed mRNA catabolic pr	20455	0.316005229	0.41928298	0
peptidyl-tyrosine modification (GO:001	20455	0.316005229	0.41928298	0
glycosaminoglycan catabolic process (G	20455	0.316005229	0.41928298	0
Rho protein signal transduction (GO:00	20455	0.316005229	0.41928298	0
regulation of transcription by RNA poly	17/2206	0.318517385	0.422066599	0
regulation of bone mineralization (GO:(	20821	0.32063515	0.422321482	0
regulation of mitotic nuclear division (G	20821	0.32063515	0.422321482	0
dicarboxylic acid metabolic process (GO	20821	0.32063515	0.422321482	0
positive regulation of interferon-gamm	20821	0.32063515	0.422321482	0
nuclear-transcribed mRNA catabolic pr	2/171	0.321196417	0.422321482	0
positive regulation of I-kappaB kinase/I	2/171	0.321196417	0.422321482	0
negative regulation of neuron projectio	21186	0.325233962	0.423261057	0
cellular iron ion homeostasis (GO:0006	21186	0.325233962	0.423261057	0
regulation of pathway-restricted SMAD	21186	0.325233962	0.423261057	0
eye development (GO:0001654)	21186	0.325233962	0.423261057	0
fat cell differentiation (GO:0045444)	21186	0.325233962	0.423261057	0
regulation of tumor necrosis factor-me	21186	0.325233962	0.423261057	0
mitochondrial respiratory chain comple	21186	0.325233962	0.423261057	0
NADH dehydrogenase complex assemb	21186	0.325233962	0.423261057	0
DNA repair (GO:0006281)	3/298	0.32644963	0.424301241	0
cation transport (GO:0006812)	2/174	0.328615702	0.426572484	0
extracellular matrix organization (GO:0	3/300	0.330143599	0.428010595	0
Notch signaling pathway (GO:0007219)	21916	0.334339087	0.432899021	0
negative regulation of cellular process (	5/566	0.335483071	0.433828996	0
regulation of mitotic cell cycle (GO:000	2/178	0.338474279	0.436515653	0
positive regulation of interleukin-8 pro	22282	0.338845811	0.436515653	0
iron ion homeostasis (GO:0055072)	22282	0.338845811	0.436515653	0
regulation of neurogenesis (GO:00507(	22647	0.343322247	0.441166923	0
I-kappaB kinase/NF-kappaB signaling (G	22647	0.343322247	0.441166923	0
cell cycle G1/S phase transition (GO:00	23012	0.347768598	0.442970252	0
negative regulation of peptidase activit	23012	0.347768598	0.442970252	0
COPII vesicle coating (GO:0048208)	23012	0.347768598	0.442970252	0

positive regulation of DNA metabolic p	23012	0.347768598	0.442970252	0
vesicle coating (GO:0006901)	23012	0.347768598	0.442970252	0
vesicle targeting, rough ER to cis-Golgi	23012	0.347768598	0.442970252	0
monocarboxylic acid biosynthetic proc	23012	0.347768598	0.442970252	0
regulation of extrinsic apoptotic signali	23377	0.352185065	0.448035682	0
BMP signaling pathway (GO:0030509)	23743	0.356571846	0.45192377	0
chemical homeostasis (GO:0048878)	23743	0.356571846	0.45192377	0
steroid biosynthetic process (GO:0006	23743	0.356571846	0.45192377	0
cell-cell junction assembly (GO:000704	24108	0.36092914	0.454619028	0
cellular component disassembly (GO:0(	24108	0.36092914	0.454619028	0
extracellular matrix disassembly (GO:0(	24108	0.36092914	0.454619028	0
positive regulation of cell cycle (GO:00	24108	0.36092914	0.454619028	0
positive regulation of T cell proliferatio	24108	0.36092914	0.454619028	0
regulation of myeloid cell differentiatio	24838	0.369556051	0.464337381	0
positive regulation of protein localizati	24838	0.369556051	0.464337381	0
cellular response to oxygen-containing	3/323	0.372524997	0.467397243	0
cellular response to decreased oxygen	25204	0.373826058	0.467397243	0
peptidyl-tyrosine phosphorylation (GO:	25204	0.373826058	0.467397243	0
positive regulation of MAP kinase activ	25204	0.373826058	0.467397243	0
COPII-coated vesicle budding (GO:0090	25569	0.378067357	0.471543008	0
wound healing (GO:0042060)	25569	0.378067357	0.471543008	0
protein tetramerization (GO:0051262)	25934	0.38228014	0.472733904	0
cellular response to BMP stimulus (GO:	25934	0.38228014	0.472733904	0
regulation of hematopoietic stem cell d	25934	0.38228014	0.472733904	0
cholesterol homeostasis (GO:0042632)	25934	0.38228014	0.472733904	0
Fc-gamma receptor signaling pathway i	25934	0.38228014	0.472733904	0
gland development (GO:0048732)	25934	0.38228014	0.472733904	0
histone acetylation (GO:0016573)	25934	0.38228014	0.472733904	0
negative regulation of nucleic acid-tem	4/464	0.382733533	0.472733904	0
cell morphogenesis involved in differer	26299	0.386464596	0.475159547	0
Fc-gamma receptor signaling pathway i	26299	0.386464596	0.475159547	0
sterol homeostasis (GO:0055092)	26299	0.386464596	0.475159547	0
negative regulation of intracellular sign	2/198	0.387028875	0.475159547	0
regulation of signal transduction (GO:0	2/198	0.387028875	0.475159547	0
regulation of actin filament polymeriza	26665	0.390620915	0.477842392	0
regulation of Rho protein signal transdu	26665	0.390620915	0.477842392	0
positive regulation of JNK cascade (GO:	26665	0.390620915	0.477842392	0
regulation of macromolecule metaboli	2/200	0.391804113	0.478715097	0
regulation of cytokine-mediated signali	27030	0.394749285	0.480011362	0
cellular response to amino acid starvati	27030	0.394749285	0.480011362	0
Fc receptor mediated stimulatory signa	27030	0.394749285	0.480011362	0
mitotic nuclear division (GO:0140014)	27030	0.394749285	0.480011362	0
intracellular protein transport (GO:000	3/336	0.396286395	0.480979929	0
positive regulation of cell population pı	4/474	0.398027267	0.480979929	0
regulation of hematopoietic progenitor	27395	0.398849892	0.480979929	0
nucleic acid phosphodiester bond hydr	27395	0.398849892	0.480979929	0
response to amino acid starvation (GO:	27395	0.398849892	0.480979929	0

positive regulation of immune respons	27395	0.398849892	0.480979929	0
positive regulation of lymphocyte proli	27395	0.398849892	0.480979929	0
actomyosin structure organization (GO	27760	0.402922922	0.482465872	0
regulation of BMP signaling pathway (G	27760	0.402922922	0.482465872	0
cellular response to hormone stimulus	27760	0.402922922	0.482465872	0
chloride transport (GO:0006821)	27760	0.402922922	0.482465872	0
establishment of protein localization to	27760	0.402922922	0.482465872	0
protein import into nucleus (GO:00066	27760	0.402922922	0.482465872	0
purine ribonucleotide metabolic proces	28126	0.406968558	0.483334453	0
cholesterol metabolic process (GO:000	28126	0.406968558	0.483334453	0
import into nucleus (GO:0051170)	28126	0.406968558	0.483334453	0
positive regulation of phosphatidylinos	28126	0.406968558	0.483334453	0
positive regulation of protein modificat	28126	0.406968558	0.483334453	0
positive regulation of tumor necrosis fa	28126	0.406968558	0.483334453	0
positive regulation of type I interferon	28126	0.406968558	0.483334453	0
negative regulation of cellular compon	29221	0.418942929	0.495822119	0
regulation of protein localization to pla	29221	0.418942929	0.495822119	0
lipid biosynthetic process (GO:000861(	29221	0.418942929	0.495822119	0
activation of cysteine-type endopeptid	29587	0.422880808	0.498744841	0
regulation of interleukin-8 production (	29587	0.422880808	0.498744841	0
positive regulation of tumor necrosis fa	29587	0.422880808	0.498744841	0
cell-cell junction organization (GO:004	29952	0.426792196	0.501616202	0
ephrin receptor signaling pathway (GO	29952	0.426792196	0.501616202	0
positive regulation of protein ubiquitin	29952	0.426792196	0.501616202	0
peptide metabolic process (GO:000651	30317	0.430677269	0.50443694	0
regulation of Notch signaling pathway (	30317	0.430677269	0.50443694	0
epidermis development (GO:0008544)	30317	0.430677269	0.50443694	0
gene expression (GO:0010467)	3/356	0.432360501	0.505827038	0
regulation of cytokinesis (GO:0032465)	30682	0.434536205	0.506627452	0
spindle assembly (GO:0051225)	30682	0.434536205	0.506627452	0
vascular transport (GO:0010232)	30682	0.434536205	0.506627452	0
G1/S transition of mitotic cell cycle (GC	31048	0.438369176	0.510512218	0
negative regulation of cellular amide m	31413	0.442176357	0.512602626	0
regulation of interferon-gamma produ	31413	0.442176357	0.512602626	0
positive regulation of endothelial cell m	31413	0.442176357	0.512602626	0
transport across blood-brain barrier (G	31413	0.442176357	0.512602626	0
regulation of I-kappaB kinase/NF-kappa	2/224	0.447711677	0.518429771	0
sensory perception of mechanical stim	32143	0.449714035	0.519567576	0
positive regulation of neuron projectio	32143	0.449714035	0.519567576	0
regulation of cysteine-type endopeptid	32509	0.453444873	0.520924832	0
regulation of endothelial cell migration	32509	0.453444873	0.520924832	0
regulation of type I interferon producti	32509	0.453444873	0.520924832	0
transforming growth factor beta recep	32509	0.453444873	0.520924832	0
protein import (GO:0017038)	32509	0.453444873	0.520924832	0
sensory perception of sound (GO:0007	33239	0.460831392	0.52821956	0
toll-like receptor signaling pathway (GC	33239	0.460831392	0.52821956	0
positive regulation of cellular compone	33604	0.464487408	0.531215116	0

positive regulation of transmembrane r	33604	0.464487408	0.531215116	0
negative regulation of cellular protein r	34335	0.471725777	0.537082197	0
negative regulation of MAPK cascade ((	34335	0.471725777	0.537082197	0
positive regulation of epithelial cell mig	34335	0.471725777	0.537082197	0
hemopoiesis (GO:0030097)	34335	0.471725777	0.537082197	0
negative regulation of programmed cel	3/381	0.476320768	0.541708552	0
cellular transition metal ion homeostas	35065	0.478867022	0.542924454	0
regulation of vesicle-mediated transpo	35065	0.478867022	0.542924454	0
regulation of ERK1 and ERK2 cascade ((	2/238	0.478988306	0.542924454	0
protein maturation (GO:0051604)	35431	0.482401628	0.545579643	0
regulation of MAP kinase activity (GO:(	35431	0.482401628	0.545579643	0
regulation of neuron apoptotic process	35796	0.485912436	0.548940989	0
organic anion transport (GO:0015711)	36161	0.489399606	0.5516573	0
positive regulation of stress-activated M	36161	0.489399606	0.5516573	0
regulation of transforming growth fact	1/100	0.492863296	0.554947734	0
cellular response to chemical stress (G(	1/101	0.496303663	0.557054691	0
positive regulation of protein localizati	1/101	0.496303663	0.557054691	0
positive regulation of DNA-binding tran	2/246	0.496374543	0.557054691	0
protein O-linked glycosylation (GO:000	1/102	0.499720862	0.558350393	0
regulation of cell death (GO:0010941)	1/102	0.499720862	0.558350393	0
cell junction assembly (GO:0034329)	1/102	0.499720862	0.558350393	0
mitotic sister chromatid segregation (G	1/102	0.499720862	0.558350393	0
steroid metabolic process (GO:000820	1/104	0.506486376	0.565289833	0
regulation of JNK cascade (GO:004632	1/105	0.509834998	0.568404664	0
protein processing (GO:0016485)	1/106	0.513161066	0.569619963	0
peptidyl-lysine modification (GO:00182	1/106	0.513161066	0.569619963	0
regulation of phosphatidylinositol 3-kin	1/106	0.513161066	0.569619963	0
positive regulation of protein serine/th	1/106	0.513161066	0.569619963	0
positive regulation of cell differentiatio	2/258	0.521758976	0.578533619	0
regulation of protein kinase activity (G(	1/110	0.526242795	0.582871096	0
cellular component assembly (GO:0022	2/261	0.527971596	0.584150984	0
regulation of Wnt signaling pathway (G	1/111	0.529458333	0.585160566	0
protein-containing complex subunit org	1/112	0.532652208	0.588052654	0
cellular protein metabolic process (GO:	3/417	0.536737518	0.59119061	0
negative regulation of cell motility (GO	1/114	0.538975541	0.59119061	0
cellular response to transforming grow	1/114	0.538975541	0.59119061	0
positive regulation of cellular compone	1/114	0.538975541	0.59119061	0
histone modification (GO:0016570)	1/114	0.538975541	0.59119061	0
positive regulation of kinase activity (G	1/114	0.538975541	0.59119061	0
negative regulation of signal transducti	2/267	0.540233832	0.591297825	0
protein deubiquitination (GO:0016579)	2/267	0.540233832	0.591297825	0
cellular amide metabolic process (GO:(	1/115	0.542105288	0.591440351	0
cellular response to lectin (GO:199085	1/115	0.542105288	0.591440351	0
stimulatory C-type lectin receptor signa	1/115	0.542105288	0.591440351	0
positive regulation of cell migration (G(	2/269	0.544272587	0.593169803	0
positive regulation of cell projection or	1/117	0.54830165	0.596922416	0
positive regulation of MAPK cascade (G	2/274	0.554262236	0.601649259	0

mRNA splicing, via spliceosome (GO:00	2/274	0.554262236	0.601649259	0
innate immune response activating cell	1/119	0.554414774	0.601649259	0
macroautophagy (GO:0016236)	1/120	0.557440469	0.604289189	0
protein modification by small protein r	2/276	0.558215011	0.604485756	0
regulation of mRNA catabolic process (	1/122	0.563430811	0.609486196	0
regulation of apoptotic process (GO:00	5/742	0.564928656	0.610458431	0
regulation of anatomical structure mor	1/123	0.566395731	0.611395392	0
fatty acid metabolic process (GO:0006(	1/124	0.569340663	0.613274984	0
regulation of tumor necrosis factor pro	1/124	0.569340663	0.613274984	0
cellular response to oxidative stress (G	1/125	0.57226574	0.615125305	0
platelet degranulation (GO:0002576)	1/125	0.57226574	0.615125305	0
positive regulation of canonical Wnt sig	1/130	0.586597935	0.628541847	0
Golgi organization (GO:0007030)	1/130	0.586597935	0.628541847	0
protein glycosylation (GO:0006486)	1/130	0.586597935	0.628541847	0
cellular response to hypoxia (GO:0071(	1/131	0.589406647	0.630225996	0
cellular response to metal ion (GO:007	1/131	0.589406647	0.630225996	0
regulation of cell adhesion (GO:003015	1/133	0.594967371	0.634175472	0
regulation of cell motility (GO:2000145	1/133	0.594967371	0.634175472	0
transmembrane receptor protein serin	1/133	0.594967371	0.634175472	0
innate immune response (GO:0045087	2/302	0.607337601	0.646684446	0
protein dephosphorylation (GO:00064	1/139	0.611204961	0.650123023	0
positive regulation of cellular process (	4/625	0.612377367	0.650690862	0
enzyme linked receptor protein signalir	1/140	0.613847686	0.651573742	0
positive regulation of apoptotic proces	2/310	0.621602712	0.658504229	0
protein-DNA complex assembly (GO:00	1/143	0.621669351	0.658504229	0
negative regulation of cell migration (G	1/144	0.624241465	0.66054211	0
cellular macromolecule biosynthetic pr	2/314	0.628585537	0.66444882	0
positive regulation of intracellular prot	1/148	0.634357497	0.669855222	0
positive regulation of hydrolase activity	1/149	0.636843975	0.67178469	0
response to cytokine (GO:0034097)	1/150	0.639313668	0.672997536	0
negative regulation of apoptotic proces	3/485	0.639314637	0.672997536	0
actin filament organization (GO:00070	1/152	0.644203151	0.676745372	0
negative regulation of protein phospho	1/152	0.644203151	0.676745372	0
dephosphorylation (GO:0016311)	1/153	0.646623163	0.677889921	0
positive regulation of Wnt signaling pat	1/153	0.646623163	0.677889921	0
positive regulation of protein kinase ac	1/154	0.649026836	0.67971053	0
mitotic spindle organization (GO:0007(	1/157	0.656140911	0.686455429	0
skeletal system development (GO:0001	1/158	0.658480315	0.68819635	0
protein autophosphorylation (GO:0046	1/159	0.66080392	0.689917208	0
positive regulation of cytokine product	2/335	0.663620202	0.692148399	0
post-translational protein modification	2/345	0.679355604	0.707835747	0
DNA-templated transcription, initiation	1/168	0.681022664	0.7088479	0
neuron projection development (GO:0(	1/171	0.687492727	0.714852132	0
positive regulation of ERK1 and ERK2 ca	1/172	0.689620333	0.716333455	0
positive regulation of developmental p	1/177	0.700044602	0.726421028	0
regulated exocytosis (GO:0045055)	1/180	0.70613157	0.731991933	0
endoplasmic reticulum to Golgi vesicle-	1/185	0.716005226	0.741472892	0

regulation of GTPase activity (GO:0043	1/189	0.723666476	0.748645826	0
negative regulation of cell differentiati	1/191	0.727419811	0.751765504	0
positive regulation of macromolecule n	2/384	0.735094184	0.758927025	0
modification-dependent protein catabo	1/201	0.74544078	0.768830116	0
generation of neurons (GO:0048699)	1/202	0.747176489	0.769841094	0
proteasomal protein catabolic process	1/205	0.752313442	0.774350906	0
mitotic cell cycle phase transition (GO:(	1/209	0.75900189	0.780277086	0
regulation of transcription, DNA-templ	13/2244	0.76033907	0.780277086	0
transmembrane receptor protein tyros	2/404	0.760368151	0.780277086	0
regulation of cell migration (GO:00303	2/408	0.765167543	0.784412199	0
protein modification by small protein c	2/409	0.766354395	0.784825262	0
positive regulation of GTPase activity ((	1/214	0.767110855	0.784825262	0
cellular response to lipid (GO:0071396)	1/219	0.774948925	0.792049102	0
positive regulation of cell motility (GO:	1/221	0.778010325	0.794381283	0
anterograde trans-synaptic signaling (G	1/244	0.810380158	0.826603985	0
RNA splicing, via transesterification rea	1/251	0.819267761	0.834833848	0
neutrophil degranulation (GO:0043312	2/481	0.839184204	0.854274429	0
cellular response to cytokine stimulus (	2/482	0.840034399	0.854286479	0
neutrophil activation involved in immu	2/485	0.842560817	0.856001468	0
neutrophil mediated immunity (GO:00(	2/488	0.845051305	0.857438932	0
inorganic cation transmembrane transp	1/274	0.845658613	0.857438932	0
positive regulation of programmed cell	1/286	0.85787067	0.868956474	0
positive regulation of nucleic acid-temp	2/511	0.862994887	0.873278838	0
mRNA processing (GO:0006397)	1/300	0.870910482	0.880414465	0
protein ubiquitination (GO:0016567)	2/525	0.872971805	0.881623656	0
chemical synaptic transmission (GO:00(	1/306	0.876128696	0.883935784	0
proteasome-mediated ubiquitin-depen	1/321	0.888276094	0.895304985	0
cellular protein localization (GO:00346	1/329	0.894263319	0.900448935	0
ubiquitin-dependent protein catabolic p	1/354	0.910995587	0.916391415	0
protein transport (GO:0015031)	1/369	0.91974403	0.924279257	0
cytokine-mediated signaling pathway ((	2/621	0.925315633	0.928962197	0
organelle assembly (GO:0070925)	1/425	0.945497122	0.948288944	0
nervous system development (GO:000	1/447	0.953197893	0.955072422	0
protein phosphorylation (GO:0006468)	1/496	0.966683791	0.967633382	0
cellular protein modification process (G	3/1025	0.971815076	0.971815076	0

s of significant highly-correlated RNA-seq-based modules (purple; S

Old Adjusted P-value	Odds Ratio	Combined Score	Genes	KEGG
0	22.55543988	1054.29354	NOP14;UTI	.
0	20.96445365	830.0666466	NOP14;UTI	.
0	21.06944444	795.3412155	NOP14;UTI	.
0	17.71395415	651.0196713	NOP14;UTI	.
0	31.704	810.3752692	BOP1;EMG	.
0	29.48958333	666.6911718	BOP1;PES1	.
0	57.7005814	1094.577815	NOP14;PES	.
0	84.85470085	1486.025809	BOP1;PES1	.
0	38.45155039	651.3708951	NOP14;UTI	.
0	38.16346154	545.4937806	BOP1;NOP	.
0	36.34432234	511.9263961	BOP1;PES1	.
0	20.95243129	288.3817534	BOP1;NOP	.
0	67.36556404	910.2737914	NOP14;RRS	.
0	25.42948718	318.8302038	NOP14;UTI	.
0	46.62830299	574.9662239	PES1;NOL9	.
0	21.79120879	258.4076713	EMG1;NOP	.
0	33.66751484	378.2278009	EMG1;NOP	.
0	33.66751484	378.2278009	DKC1;PUS1	.
0	7.430053279	78.66673923	CHCHD4;CI	.
0	8.366763566	85.01045471	PRMT5;BO	.
0	14.37735849	143.988046	METTL3;N(	.
0	45.125	424.6472363	DKC1;PUS1	.
0	45.125	424.6472363	PER2;GYS1	.
0	45.125	424.6472363	PER2;GYS1	.
0	13.75503123	111.2661602	CHCHD4;T(	.
0	26.53475936	213.9304042	GRWD1;M	.
0	11.86289478	89.73549139	CHCHD4;T(	.
0	21.47619048	161.2424272	MYC;HSF1;	.
0	11.63417499	87.20373275	TOMM40;I	.
0	74.66541353	546.0690064	PUS1;PUSL	.
0	6.113178295	44.65997051	PRMT5;BO	.
0	10.80098146	78.12213082	METTL3;N(	.
0	18.03636364	127.0865839	PER2;GYS1	.
0	59.72932331	417.0006812	DKC1;PUS1	.
0	9.913152296	68.70506099	PUS1;TRMT	.
0	49.77192982	333.3850807	NOP14;RRS	.
0	49.77192982	333.3850807	EMG1;NOP	.
0	15.54545455	103.3934632	CHCHD4;T(	.
0	13.6584022	86.13539698	FES;HSF1;F	.
0	37.32518797	232.6348858	THAP7;NO	.
0	12.87662338	79.18394198	MARS2;FA	.
0	12.51830808	76.03997818	HIRA;RUVE	.
0	33.17627402	200.2654159	HSF1;FADD	.
0	29.85714286	174.9182173	THAP7;NO	.

0	11.26420455	65.25976033	MARS2;FA	.
0	10.98891353	62.9427152	CHCHD4;T	.
0	27.14149009	154.5944083	HIRA;IPO4	.
0	3.704368512	20.44481486	PER2;BOP1	.
0	22.96356275	124.1743431	HSF1;FADI	.
0	22.96356275	124.1743431	DKC1;RUVI	.
0	22.96356275	124.1743431	METTL3;TF	.
0	21.32223416	112.5458409	THAP7;NO	.
0	21.32223416	112.5458409	PER2;ZNF5	.
0	21.32223416	112.5458409	FES;MYC	.
0	19.89974937	102.6345449	HSF1;HRAS	.
0	18.65507519	94.10002147	GRWD1;HI	.
0	18.65507519	94.10002147	GRWD1;HI	.
0	18.65507519	94.10002147	DKC1;RUVI	.
0	8.337962963	41.67947419	MYBBP1A;	.
0	8.185950413	40.52480419	HIRA;GRW	.
0	17.55683326	86.68484682	FES;HRAS	.
0	17.55683326	86.68484682	TOMM40;I	.
0	15.70716264	74.46366592	MMACHC;	.
0	15.70716264	74.46366592	DKC1;FTSJ3	.
0	7.378539493	34.52773132	ELAC2;TRM	.
0	14.92105263	69.38042566	MMACHC;	.
0	3.493540052	16.22678978	MYC;RUVB	.
0	2.853881027	13.22606655	PRMT5;BO	.
0	5.066649561	23.48025782	MYDGF;EC	.
0	6.715739484	29.78915199	MYC;METT	.
0	4.671519025	20.41057393	DKC1;MET	.
0	2.657309141	11.30348135	PRMT5;UT	.
0	11.93383459	50.75967278	HMGA1;HI	.
0	6.161892902	25.97044416	SMYD5;MY	.
0	6.161892902	25.97044416	FPGS;MM/	.
0	3.61722488	15.15801279	MYDGF;ER	.
0	6.078316953	25.40613118	MYC;METT	.
0	4.36486337	18.1158234	RRAS;CDC4	.
0	4.36486337	18.1158234	MYC;RUVB	.
0	11.04873294	45.48349532	MYC;RUVB	.
0	10.65359828	43.16851486	METTL3;FA	.
0	10.65359828	43.16851486	P2RY2;SLC	.
0	5.692174914	22.84190798	MYBBP1A;	.
0	5.692174914	22.84190798	FES;CDC42	.
0	3.342239619	13.01612337	MYC;FADD	.
0	9.621149648	37.24720613	THAP7;NO	.
0	9.320018797	35.55712265	FADD;BCL2	.
0	9.320018797	35.55712265	CASTOR1;M	.
0	9.320018797	35.55712265	DKC1;MYC	.
0	9.320018797	35.55712265	TRMT1;TRI	.
0	2.877391816	10.95678333	SMYD5;ME	.

0	5.227008457	19.85234677	BMP1;PLO	.
0	5.107696281	19.10414723	FES;CDC42	.
0	8.770897833	32.52134236	MYBBP1A;	.
0	8.519871106	31.15429562	FES;HRAS	.
0	2.513556442	9.093093565	PRMT5;UT	.
0	4.680160985	16.48981656	MYC;METT	.
0	7.644495855	26.49641671	PER2;TPI1	.
0	2.639399676	9.116580982	MYC;METT	.
0	4.537649219	15.64270661	METTL3;SA	.
0	4.537649219	15.64270661	MYDGF;EC	.
0	4.492045455	15.37431801	MYC;RUVB	.
0	7.453007519	25.50150078	FADD;BCL2	.
0	3.435550709	11.6931456	DKC1;MET	.
0	37.05410448	126.0648063	ENG	.
0	37.05410448	126.0648063	ENG	.
0	37.05410448	126.0648063	CTSZ	.
0	37.05410448	126.0648063	ZNF593	.
0	37.05410448	126.0648063	HSF1	.
0	37.05410448	126.0648063	TSKU	.
0	37.05410448	126.0648063	FES	.
0	37.05410448	126.0648063	FES	.
0	37.05410448	126.0648063	CCDC61	.
0	37.05410448	126.0648063	HRAS	.
0	37.05410448	126.0648063	REXO4	.
0	37.05410448	126.0648063	NOP14	.
0	37.05410448	126.0648063	NOP14	.
0	37.05410448	126.0648063	MYBBP1A	.
0	37.05410448	126.0648063	PRMT5	.
0	37.05410448	126.0648063	RRAS	.
0	37.05410448	126.0648063	ENG	.
0	37.05410448	126.0648063	SMYD5	.
0	37.05410448	126.0648063	HSF1	.
0	37.05410448	126.0648063	SMYD5	.
0	37.05410448	126.0648063	DKC1	.
0	37.05410448	126.0648063	NOP14	.
0	37.05410448	126.0648063	DKC1	.
0	37.05410448	126.0648063	CLUH	.
0	37.05410448	126.0648063	FADD	.
0	37.05410448	126.0648063	ENG	.
0	4.36054722	14.60789224	RRAS;GRAI	.
0	7.097386323	23.67820407	MYC;ENG	.
0	7.097386323	23.67820407	PER2;TPI1	.
0	7.097386323	23.67820407	METTL3;M	.
0	6.931981116	22.84135082	SLC25A22;	.
0	4.236492281	13.89525991	PER2;BAG2	.
0	6.774094327	22.04939407	DKC1;MYC	.
0	6.774094327	22.04939407	MYC;HMG	.

0	29.64179104	95.54145257	MYC	.
0	29.64179104	95.54145257	FPGS	.
0	29.64179104	95.54145257	METTL3	.
0	29.64179104	95.54145257	PER2	.
0	29.64179104	95.54145257	COLGALT1	.
0	29.64179104	95.54145257	RRAS	.
0	29.64179104	95.54145257	HSF1	.
0	29.64179104	95.54145257	CD320	.
0	29.64179104	95.54145257	DKC1	.
0	29.64179104	95.54145257	EIPR1	.
0	29.64179104	95.54145257	PIEZO1	.
0	29.64179104	95.54145257	PGM2	.
0	29.64179104	95.54145257	NSMF	.
0	29.64179104	95.54145257	MYC	.
0	29.64179104	95.54145257	AMPD2	.
0	29.64179104	95.54145257	DKC1	.
0	29.64179104	95.54145257	ELAC2	.
0	29.64179104	95.54145257	ENG	.
0	29.64179104	95.54145257	RRS1	.
0	6.478914678	20.58733286	HSF1;HRAS	.
0	6.340745481	19.91153576	PIEZO1;FAI	.
0	3.972646822	12.41463691	MYDGF;EC	.
0	24.70024876	75.88873531	TPI1	.
0	24.70024876	75.88873531	RHBG	.
0	24.70024876	75.88873531	HSF1	.
0	24.70024876	75.88873531	SLC25A22	.
0	24.70024876	75.88873531	P2RY2	.
0	24.70024876	75.88873531	PER2	.
0	24.70024876	75.88873531	NSMF	.
0	24.70024876	75.88873531	MYC	.
0	24.70024876	75.88873531	FADD	.
0	24.70024876	75.88873531	CKB	.
0	24.70024876	75.88873531	FADD	.
0	24.70024876	75.88873531	METTL3	.
0	24.70024876	75.88873531	MYC	.
0	24.70024876	75.88873531	ENG	.
0	24.70024876	75.88873531	ENG	.
0	24.70024876	75.88873531	ENG	.
0	24.70024876	75.88873531	TSKU	.
0	24.70024876	75.88873531	ENG	.
0	24.70024876	75.88873531	TPI1	.
0	24.70024876	75.88873531	PGM2	.
0	24.70024876	75.88873531	PAGR1	.
0	24.70024876	75.88873531	RRS1	.
0	24.70024876	75.88873531	HRAS	.
0	24.70024876	75.88873531	FADD	.
0	24.70024876	75.88873531	LONP1	.

0	24.70024876	75.88873531	FADD	.
0	24.70024876	75.88873531	ENG	.
0	24.70024876	75.88873531	ENG	.
0	24.70024876	75.88873531	PER2	.
0	6.081325763	18.65802988	PER2;BAG2	.
0	6.081325763	18.65802988	AEN;BCL2L	.
0	5.959398496	18.07600222	NOC2L;BCl	.
0	21.17057569	62.28784804	NOC2L	.
0	21.17057569	62.28784804	METTL3	.
0	21.17057569	62.28784804	RHBG	.
0	21.17057569	62.28784804	PDP2	.
0	21.17057569	62.28784804	PDP2	.
0	21.17057569	62.28784804	RUVBL1	.
0	21.17057569	62.28784804	ENG	.
0	21.17057569	62.28784804	CTNND1	.
0	21.17057569	62.28784804	ENG	.
0	21.17057569	62.28784804	PLOD1	.
0	21.17057569	62.28784804	BYSL	.
0	21.17057569	62.28784804	CTNND1	.
0	21.17057569	62.28784804	FADD	.
0	21.17057569	62.28784804	LRWD1	.
0	21.17057569	62.28784804	SMYD5	.
0	21.17057569	62.28784804	EIPR1	.
0	21.17057569	62.28784804	BCS1L	.
0	21.17057569	62.28784804	PAGR1	.
0	21.17057569	62.28784804	PIEZO1	.
0	21.17057569	62.28784804	FADD	.
0	21.17057569	62.28784804	BCS1L	.
0	21.17057569	62.28784804	ELAC2	.
0	21.17057569	62.28784804	ELAC2	.
0	21.17057569	62.28784804	ENG	.
0	21.17057569	62.28784804	ENG	.
0	21.17057569	62.28784804	ENG	.
0	21.17057569	62.28784804	BCL2L1	.
0	3.67790611	10.82031505	PER2;EIPR1	.
0	5.621222868	16.48654927	PER2;BAG2	.
0	5.621222868	16.48654927	FAAP20;AT	.
0	5.416267943	15.54175471	BAG2;FADI	.
0	3.560425685	10.20345571	MYC;METT	.
0	5.319280344	15.099732	ECM1;HRA	.
0	18.5233209	52.37907062	BAG2	.
0	18.5233209	52.37907062	FES	.
0	18.5233209	52.37907062	CHCHD4	.
0	18.5233209	52.37907062	ENG	.
0	18.5233209	52.37907062	ZNF593	.
0	18.5233209	52.37907062	PGM2	.
0	18.5233209	52.37907062	PRMT5	.

0	18.5233209	52.37907062	FES	.
0	18.5233209	52.37907062	AMPD2	.
0	18.5233209	52.37907062	TSKU	.
0	18.5233209	52.37907062	TPI1	.
0	18.5233209	52.37907062	PUS1	.
0	5.225695818	14.6763846	FADD;BCL2	.
0	3.450174825	9.634682612	FADD;BCL2	.
0	5.135338346	14.27064069	CTSZ;LONP	.
0	5.048043838	13.88150631	DKC1;MYC	.
0	16.46434494	44.87690266	PER2	.
0	16.46434494	44.87690266	PIEZO1	.
0	16.46434494	44.87690266	NOC2L	.
0	16.46434494	44.87690266	MYC	.
0	16.46434494	44.87690266	ENG	.
0	16.46434494	44.87690266	TSKU	.
0	16.46434494	44.87690266	TSKU	.
0	16.46434494	44.87690266	IPO4	.
0	16.46434494	44.87690266	IPO4	.
0	16.46434494	44.87690266	METTL3	.
0	16.46434494	44.87690266	DKC1	.
0	16.46434494	44.87690266	TSKU	.
0	16.46434494	44.87690266	MYC	.
0	16.46434494	44.87690266	DKC1	.
0	16.46434494	44.87690266	FES	.
0	16.46434494	44.87690266	HSF1	.
0	16.46434494	44.87690266	RUVBL1	.
0	16.46434494	44.87690266	ENG	.
0	16.46434494	44.87690266	SLC25A22	.
0	16.46434494	44.87690266	RRAS	.
0	16.46434494	44.87690266	METTL3	.
0	4.963659148	13.50805856	MYC;FADD	.
0	4.963659148	13.50805856	PER2;TPI1	.
0	4.803056027	12.80485038	NOC2L;BCI	.
0	14.81716418	39.02418433	CHCHD4	.
0	14.81716418	39.02418433	ENG	.
0	14.81716418	39.02418433	EIPR1	.
0	14.81716418	39.02418433	DKC1	.
0	14.81716418	39.02418433	FES	.
0	14.81716418	39.02418433	MFSD12	.
0	14.81716418	39.02418433	MYC	.
0	14.81716418	39.02418433	FES	.
0	14.81716418	39.02418433	DKC1	.
0	14.81716418	39.02418433	EIPR1	.
0	14.81716418	39.02418433	TPI1	.
0	14.81716418	39.02418433	PIEZO1	.
0	14.81716418	39.02418433	DKC1	.
0	14.81716418	39.02418433	FADD	.

0	4.580682475	11.84806782	MFSD12;SI	.
0	13.46947083	34.34745298	MYC	.
0	13.46947083	34.34745298	AMPD2	.
0	13.46947083	34.34745298	CTSZ	.
0	13.46947083	34.34745298	CTSZ	.
0	13.46947083	34.34745298	NOC2L	.
0	13.46947083	34.34745298	NOC2L	.
0	13.46947083	34.34745298	METTL3	.
0	13.46947083	34.34745298	CTSZ	.
0	13.46947083	34.34745298	CDC42EP2	.
0	13.46947083	34.34745298	HMGA1	.
0	13.46947083	34.34745298	MYC	.
0	13.46947083	34.34745298	DKC1	.
0	13.46947083	34.34745298	DKC1	.
0	13.46947083	34.34745298	BAG2	.
0	13.46947083	34.34745298	CDC42EP2	.
0	13.46947083	34.34745298	FADD	.
0	13.46947083	34.34745298	LONP1	.
0	13.46947083	34.34745298	CLUH	.
0	13.46947083	34.34745298	HSF1	.
0	4.443496802	11.26797712	FES;CDC42	.
0	4.377930119	10.9935561	PRMT5;PO	.
0	4.377930119	10.9935561	FDXR;TSKL	.
0	4.314263921	10.72887619	METTL3;DI	.
0	12.34639303	30.53627396	FPGS	.
0	12.34639303	30.53627396	AMPD2	.
0	12.34639303	30.53627396	AMPD2	.
0	12.34639303	30.53627396	HMGA1	.
0	12.34639303	30.53627396	HMGA1	.
0	12.34639303	30.53627396	HMGA1	.
0	12.34639303	30.53627396	TSKU	.
0	12.34639303	30.53627396	PGM2	.
0	12.34639303	30.53627396	REXO4	.
0	12.34639303	30.53627396	CTNND1	.
0	12.34639303	30.53627396	LRWD1	.
0	12.34639303	30.53627396	HMGA1	.
0	12.34639303	30.53627396	PRMT5	.
0	12.34639303	30.53627396	BMP1	.
0	12.34639303	30.53627396	RRS1	.
0	12.34639303	30.53627396	NSMF	.
0	12.34639303	30.53627396	HRAS	.
0	12.34639303	30.53627396	ENG	.
0	12.34639303	30.53627396	FARSA	.
0	4.252416756	10.47347004	FADD;BCL2	.
0	4.252416756	10.47347004	MYC;AEN	.
0	4.192311765	10.22689864	GRWD1;NC	.
0	1.689710468	4.1165935	PAGR1;MY	.

0	4.133876358	9.988749299	CTSZ;LONP	.
0	4.133876358	9.988749299	BAG2;CTSZ	.
0	4.133876358	9.988749299	PER2;EIPR1	.
0	11.39609644	27.37910958	FADD	.
0	11.39609644	27.37910958	ECM1	.
0	11.39609644	27.37910958	FDXR	.
0	11.39609644	27.37910958	AKAP1	.
0	11.39609644	27.37910958	ENG	.
0	11.39609644	27.37910958	SLC25A22	.
0	11.39609644	27.37910958	CASTOR1	.
0	11.39609644	27.37910958	RRAS	.
0	11.39609644	27.37910958	SLC25A22	.
0	11.39609644	27.37910958	FADD	.
0	11.39609644	27.37910958	FADD	.
0	2.405469205	5.727727564	MYDGF;ER	.
0	3.967919799	9.321062295	MYDGF;EC	.
0	10.5815565	24.72713132	BCL2L1	.
0	10.5815565	24.72713132	FDXR	.
0	10.5815565	24.72713132	CTSZ	.
0	10.5815565	24.72713132	HSF1	.
0	10.5815565	24.72713132	P2RY2	.
0	10.5815565	24.72713132	BAG2	.
0	10.5815565	24.72713132	PIEZO1	.
0	10.5815565	24.72713132	TNFAIP1	.
0	10.5815565	24.72713132	PRMT5	.
0	10.5815565	24.72713132	HRAS	.
0	10.5815565	24.72713132	PGM2	.
0	10.5815565	24.72713132	PGM2	.
0	10.5815565	24.72713132	PER2	.
0	10.5815565	24.72713132	TNFAIP1	.
0	10.5815565	24.72713132	FDXR	.
0	10.5815565	24.72713132	FDXR	.
0	10.5815565	24.72713132	PLOD1	.
0	10.5815565	24.72713132	PTGFRN	.
0	3.915512465	9.112936864	NOC2L;BCL	.
0	3.864466361	8.9115032	BAG2;HSF1	.
0	3.864466361	8.9115032	BAG2;HSPE	.
0	3.864466361	8.9115032	BAG2;HSPE	.
0	3.814729131	8.716471557	FADD;BCL2	.
0	2.747071946	6.260846889	MYDGF;RR	.
0	9.875621891	22.47276897	AMPD2	.
0	9.875621891	22.47276897	HMGA1	.
0	9.875621891	22.47276897	PGM2	.
0	9.875621891	22.47276897	BCL2L1	.
0	9.875621891	22.47276897	METTL3	.
0	9.875621891	22.47276897	BCL2L1	.
0	9.875621891	22.47276897	HMGA1	.

0	9.875621891	22.47276897	FES	.
0	9.875621891	22.47276897	METTL3	.
0	9.875621891	22.47276897	HMGA1	.
0	9.875621891	22.47276897	RUVBL1	.
0	9.875621891	22.47276897	RHBG	.
0	3.766251071	8.527568056	METTL3;SA	.
0	2.713498623	6.111739031	CHCHD4;H	.
0	2.2845988	5.126745391	MYDGF;ER	.
0	2.049075242	4.582967601	MYDGF;ER	.
0	3.672885918	8.167123097	CDC42EP2;	.
0	1.894567129	4.209883742	MYBBP1A;	.
0	9.257929104	20.53645985	ENG	.
0	9.257929104	20.53645985	BCL2L1	.
0	9.257929104	20.53645985	METTL3	.
0	9.257929104	20.53645985	PWP2	.
0	9.257929104	20.53645985	NOLC1	.
0	9.257929104	20.53645985	ENG	.
0	9.257929104	20.53645985	FARSA	.
0	1.561306935	3.403169869	PRMT5;UT	.
0	2.004422049	4.350253498	PER2;MYC;	.
0	3.541174364	7.66637203	CTSZ;NSMI	.
0	3.541174364	7.66637203	BAG2;HSPI	.
0	8.712906058	18.85817106	SLC25A22	.
0	8.712906058	18.85817106	FADD	.
0	8.712906058	18.85817106	MYC	.
0	8.712906058	18.85817106	METTL3	.
0	8.712906058	18.85817106	BMP1	.
0	8.712906058	18.85817106	TNFAIP1	.
0	8.712906058	18.85817106	HSF1	.
0	8.712906058	18.85817106	BMP1	.
0	8.712906058	18.85817106	PIEZO1	.
0	8.712906058	18.85817106	PAGR1	.
0	8.712906058	18.85817106	BCL2L1	.
0	8.712906058	18.85817106	COLGALT1	.
0	8.712906058	18.85817106	METTL3	.
0	8.712906058	18.85817106	DDX54	.
0	2.191315046	4.679481193	LONP1;LRV	.
0	3.458471761	7.356708335	BAG2;CTSZ	.
0	2.557142857	5.433255127	METTL3;SA	.
0	8.228441128	17.39180911	FADD	.
0	8.228441128	17.39180911	MYC	.
0	8.228441128	17.39180911	ENG	.
0	8.228441128	17.39180911	HSF1	.
0	8.228441128	17.39180911	IGFBP6	.
0	8.228441128	17.39180911	NOLC1	.
0	8.228441128	17.39180911	BCL2L1	.
0	8.228441128	17.39180911	PIEZO1	.

0	8.228441128	17.39180911	ENG	.
0	8.228441128	17.39180911	MYC	.
0	8.228441128	17.39180911	FPGS	.
0	8.228441128	17.39180911	DKC1	.
0	8.228441128	17.39180911	PRMT5	.
0	8.228441128	17.39180911	P2RY2	.
0	8.228441128	17.39180911	ENG	.
0	8.228441128	17.39180911	PDP2	.
0	8.228441128	17.39180911	NOLC1	.
0	8.228441128	17.39180911	MYC	.
0	2.542484504	5.371026513	BAG2;CTNI	.
0	2.527991782	5.309738947	MYC;METT	.
0	3.379528366	7.064644533	METTL3;SA	.
0	3.379528366	7.064644533	CHCHD4;B	.
0	3.341387176	6.924792806	SMYD5;ME	.
0	7.794972506	16.10143513	AMPD2	.
0	7.794972506	16.10143513	ENG	.
0	7.794972506	16.10143513	ENG	.
0	7.794972506	16.10143513	FPGS	.
0	7.794972506	16.10143513	HSF1	.
0	7.794972506	16.10143513	METTL3	.
0	7.794972506	16.10143513	AMPD2	.
0	7.794972506	16.10143513	PRMT5	.
0	7.794972506	16.10143513	MYC	.
0	7.794972506	16.10143513	FADD	.
0	7.794972506	16.10143513	FPGS	.
0	7.794972506	16.10143513	BAG2	.
0	7.794972506	16.10143513	BCS1L	.
0	3.304093567	6.788853516	MYDGF;EC	.
0	2.112804467	4.314692501	BMP1;PITR	.
0	3.267619598	6.656680202	MYC;HRAS	.
0	7.404850746	14.95864261	MYBBP1A	.
0	7.404850746	14.95864261	BCL2L1	.
0	7.404850746	14.95864261	BCL2L1	.
0	7.404850746	14.95864261	SAMD4A	.
0	7.404850746	14.95864261	AMPD2	.
0	7.404850746	14.95864261	ENG	.
0	7.404850746	14.95864261	BCL2L1	.
0	7.404850746	14.95864261	SMYD5	.
0	7.404850746	14.95864261	BAG2	.
0	7.404850746	14.95864261	AEN	.
0	7.404850746	14.95864261	LRWD1	.
0	3.231938542	6.528133329	GRWD1;HI	.
0	3.19702482	6.403079893	METTL3;HS	.
0	7.05188344	13.94070285	ECM1	.
0	7.05188344	13.94070285	MYC	.
0	7.05188344	13.94070285	BCL2L1	.

0	7.05188344	13.94070285	BCL2L1	.
0	7.05188344	13.94070285	LONP1	.
0	7.05188344	13.94070285	FPGS	.
0	7.05188344	13.94070285	NUBP2	.
0	2.378747582	4.692689941	CTNND1;IC	.
0	3.129402454	6.162951763	PER2;HSF1	.
0	2.341028082	4.540912229	ERP29;HRA	.
0	6.731004071	13.02922922	ENG	.
0	6.731004071	13.02922922	BCL2L1	.
0	6.731004071	13.02922922	HRAS	.
0	6.731004071	13.02922922	BCL2L1	.
0	6.731004071	13.02922922	ABO	.
0	6.731004071	13.02922922	REXO4	.
0	6.731004071	13.02922922	ECM1	.
0	6.731004071	13.02922922	MYC	.
0	6.731004071	13.02922922	PGM2	.
0	6.731004071	13.02922922	BCS1L	.
0	6.731004071	13.02922922	HSF1	.
0	1.592217639	3.068535378	FES;MYC;N	.
0	3.033144085	5.825971574	METTL3;SA	.
0	1.998110751	3.801725748	MYC;HSF1;	.
0	6.438027255	12.20919903	FDXR	.
0	6.438027255	12.20919903	TPI1	.
0	6.438027255	12.20919903	ABO	.
0	6.438027255	12.20919903	ENG	.
0	6.438027255	12.20919903	ECM1	.
0	6.438027255	12.20919903	TSKU	.
0	6.438027255	12.20919903	NOC2L	.
0	6.438027255	12.20919903	HRAS	.
0	6.438027255	12.20919903	TPI1	.
0	6.438027255	12.20919903	HMGA1	.
0	6.438027255	12.20919903	NUBP2	.
0	6.438027255	12.20919903	HRAS	.
0	6.438027255	12.20919903	HRAS	.
0	6.438027255	12.20919903	HSF1	.
0	6.438027255	12.20919903	ELAC2	.
0	2.972180451	5.615560846	BAG2;HSPI	.
0	2.972180451	5.615560846	MYBBP1A;	.
0	2.942604035	5.514338843	P2RY2;NSM	.
0	1.802594995	3.358206846	CLUH;MYC	.
0	6.169465174	11.46822674	LONP1	.
0	6.169465174	11.46822674	BCL2L1	.
0	6.169465174	11.46822674	PIEZO1	.
0	6.169465174	11.46822674	ENG	.
0	6.169465174	11.46822674	MYC	.
0	6.169465174	11.46822674	BAG2	.
0	6.169465174	11.46822674	TPI1	.

0	2.913607548	5.415653395	PER2;EIPR1	.
0	2.234659091	4.122335183	MYDGF;EC	.
0	2.857287449	5.225557582	PRMT5;BC	.
0	2.857287449	5.225557582	MYC;LRWD	.
0	2.857287449	5.225557582	RRS1;IPO4	.
0	5.92238806	10.7960164	AMPD2	.
0	5.92238806	10.7960164	ECM1	.
0	5.92238806	10.7960164	BCL2L1	.
0	5.92238806	10.7960164	BCL2L1	.
0	5.92238806	10.7960164	ERP29	.
0	5.92238806	10.7960164	MYC	.
0	5.92238806	10.7960164	SMYD5	.
0	5.92238806	10.7960164	MYC	.
0	5.92238806	10.7960164	PRMT5	.
0	5.92238806	10.7960164	FES	.
0	5.92238806	10.7960164	FADD	.
0	2.190396613	3.952370088	MYDGF;RR	.
0	1.664513351	3.003315443	MYDGF;EC	.
0	2.803092637	5.044638699	GRWD1;AT	.
0	5.694316877	10.18394412	TSKU	.
0	5.694316877	10.18394412	HSF1	.
0	5.694316877	10.18394412	HSF1	.
0	5.694316877	10.18394412	PER2	.
0	5.694316877	10.18394412	ENG	.
0	5.694316877	10.18394412	PER2	.
0	5.694316877	10.18394412	HSF1	.
0	5.694316877	10.18394412	SLC25A22	.
0	5.694316877	10.18394412	PIEZO1	.
0	5.483139856	9.624736148	TPI1	.
0	5.483139856	9.624736148	NSMF	.
0	5.483139856	9.624736148	BCL2L1	.
0	5.483139856	9.624736148	NSMF	.
0	5.483139856	9.624736148	PER2	.
0	5.483139856	9.624736148	MYC	.
0	5.483139856	9.624736148	FES	.
0	5.483139856	9.624736148	RUVBL1	.
0	5.483139856	9.624736148	SLC25A22	.
0	5.483139856	9.624736148	HRAS	.
0	2.116975442	3.676075794	MARS2;FA	.
0	2.676149834	4.628775004	PER2;HSF1	.
0	5.287046908	9.112217885	MYC	.
0	5.287046908	9.112217885	MYC	.
0	5.287046908	9.112217885	HSF1	.
0	5.287046908	9.112217885	SLC25A22	.
0	5.287046908	9.112217885	NSMF	.
0	5.287046908	9.112217885	HRAS	.
0	5.287046908	9.112217885	FADD	.

0	5.287046908	9.112217885	NSMF	.
0	5.287046908	9.112217885	TPI1	.
0	5.287046908	9.112217885	FADD	.
0	5.287046908	9.112217885	HSF1	.
0	5.287046908	9.112217885	DKC1	.
0	5.287046908	9.112217885	METTL3	.
0	5.104477612	8.641116555	ENG	.
0	5.104477612	8.641116555	SMYD5	.
0	5.104477612	8.641116555	SLC4A3	.
0	5.104477612	8.641116555	METTL3	.
0	5.104477612	8.641116555	RUVBL1	.
0	5.104477612	8.641116555	RUVBL1	.
0	5.104477612	8.641116555	SMYD5	.
0	5.104477612	8.641116555	CD320	.
0	5.104477612	8.641116555	FADD	.
0	5.104477612	8.641116555	PER2	.
0	5.104477612	8.641116555	PAGR1	.
0	5.104477612	8.641116555	DKC1	.
0	5.104477612	8.641116555	POLR1C	.
0	5.104477612	8.641116555	FADD	.
0	2.605329112	4.401733822	HSF1;CDC4	.
0	2.605329112	4.401733822	PIEZO1;SLC	.
0	2.048269391	3.424074004	PRMT5;PO	.
0	2.560150376	4.258812313	BAG2;HSF1	.
0	2.560150376	4.258812313	BAG2;CTSZ	.
0	2.560150376	4.258812313	CDC42EP2;	.
0	4.934079602	8.206904528	CHCHD4	.
0	4.934079602	8.206904528	NAGLU	.
0	4.934079602	8.206904528	PER2	.
0	4.934079602	8.206904528	SLC4A3	.
0	4.934079602	8.206904528	HMGA1	.
0	4.934079602	8.206904528	BCL2L1	.
0	4.934079602	8.206904528	ENG	.
0	4.934079602	8.206904528	FDXR	.
0	4.934079602	8.206904528	BAG2	.
0	4.934079602	8.206904528	CD320	.
0	4.934079602	8.206904528	FADD	.
0	2.538140222	4.189733796	MYC;FADD	.
0	4.774675012	7.805673956	HSF1	.
0	4.774675012	7.805673956	NOLC1	.
0	4.774675012	7.805673956	MFSD12	.
0	4.774675012	7.805673956	ENG	.
0	4.774675012	7.805673956	NSMF	.
0	4.774675012	7.805673956	HSF1	.
0	4.774675012	7.805673956	PAGR1	.
0	4.774675012	7.805673956	RUVBL1	.
0	4.774675012	7.805673956	ATRIP	.

0	4.774675012	7.805673956	NSMF	.
0	4.774675012	7.805673956	PRMT5	.
0	4.774675012	7.805673956	POLR1C	.
0	4.774675012	7.805673956	BCL2L1	.
0	4.625233209	7.434035694	BCL2L1	.
0	4.625233209	7.434035694	DKC1	.
0	4.625233209	7.434035694	MYBBP1A	.
0	4.625233209	7.434035694	ENG	.
0	4.625233209	7.434035694	ENG	.
0	2.433501787	3.866366421	FADD;BCL2	.
0	1.748248304	2.771964017	PER2;BMP	.
0	4.484848485	7.089037206	FADD	.
0	4.484848485	7.089037206	BCL2L1	.
0	4.484848485	7.089037206	FDXR	.
0	4.484848485	7.089037206	METTL3	.
0	4.484848485	7.089037206	PAGR1	.
0	4.484848485	7.089037206	NSMF	.
0	4.484848485	7.089037206	POLR1C	.
0	4.484848485	7.089037206	NOL6	.
0	4.484848485	7.089037206	NOL6	.
0	4.484848485	7.089037206	ENG	.
0	2.413594963	3.805808729	TOMM40;I	.
0	4.352721686	6.768095455	PER2	.
0	4.352721686	6.768095455	SLC4A3	.
0	4.352721686	6.768095455	PER2	.
0	4.352721686	6.768095455	TNFAIP1	.
0	4.352721686	6.768095455	PAGR1	.
0	4.352721686	6.768095455	CASTOR1	.
0	1.717491255	2.654057527	BMP1;CDC	.
0	2.337102599	3.576050652	HMGA1;LR	.
0	4.228144989	6.468941692	PAGR1	.
0	4.228144989	6.468941692	HSF1	.
0	4.228144989	6.468941692	ECM1	.
0	4.228144989	6.468941692	FADD	.
0	4.228144989	6.468941692	FADD	.
0	4.228144989	6.468941692	DKC1	.
0	4.228144989	6.468941692	FADD	.
0	4.110489221	6.189575773	MYC	.
0	4.110489221	6.189575773	RUVBL1	.
0	4.110489221	6.189575773	SLC4A3	.
0	4.110489221	6.189575773	ENG	.
0	4.110489221	6.189575773	FES	.
0	4.110489221	6.189575773	FPGS	.
0	4.110489221	6.189575773	FES	.
0	4.110489221	6.189575773	NOL6	.
0	3.999193223	5.928228141	METTL3	.
0	3.999193223	5.928228141	CASTOR1	.

0	3.999193223	5.928228141	LRWD1	.
0	3.999193223	5.928228141	RUVBL1	.
0	3.999193223	5.928228141	PRMT5	.
0	3.999193223	5.928228141	METTL3	.
0	3.999193223	5.928228141	NOL6	.
0	3.89375491	5.683328042	NSMF	.
0	3.89375491	5.683328042	ERP29	.
0	3.89375491	5.683328042	ERP29	.
0	3.89375491	5.683328042	TPI1	.
0	3.89375491	5.683328042	ATRIP	.
0	3.89375491	5.683328042	METTL3	.
0	3.89375491	5.683328042	EIPR1	.
0	2.214229604	3.217034955	MFSD12;CI	.
0	3.793723689	5.453476793	FES	.
0	3.793723689	5.453476793	BCL2L1	.
0	3.793723689	5.453476793	HRAS	.
0	3.69869403	5.237425219	PRMT5	.
0	3.69869403	5.237425219	PER2	.
0	3.69869403	5.237425219	TPI1	.
0	3.69869403	5.237425219	BCL2L1	.
0	3.69869403	5.237425219	NSMF	.
0	3.69869403	5.237425219	BCL2L1	.
0	3.69869403	5.237425219	MYC	.
0	3.69869403	5.237425219	MYC	.
0	3.69869403	5.237425219	FADD	.
0	1.783181818	2.514968876	CTNND1;RI	.
0	3.608299964	5.034054514	PER2	.
0	3.608299964	5.034054514	FAAP20	.
0	2.103556764	2.904754588	RHBG;CD3	.
0	2.103556764	2.904754588	PER2;CKB	.
0	3.522210377	4.842359942	ECM1	.
0	3.522210377	4.842359942	MYBBP1A	.
0	3.522210377	4.842359942	FAAP20	.
0	3.522210377	4.842359942	MMACHC	.
0	3.522210377	4.842359942	ENG	.
0	3.522210377	4.842359942	FADD	.
0	3.522210377	4.842359942	HRAS	.
0	3.522210377	4.842359942	CKB	.
0	3.440124957	4.661436895	ENG	.
0	3.440124957	4.661436895	MFSD12	.
0	3.440124957	4.661436895	METTL3	.
0	3.440124957	4.661436895	RRAS	.
0	3.440124957	4.661436895	METTL3	.
0	3.440124957	4.661436895	DDX54	.
0	3.440124957	4.661436895	CCDC61	.
0	2.059419382	2.783267525	METTL3;SA	.
0	3.361770692	4.490468929	SLC4A3	.

0	3.361770692	4.490468929	NOLC1	.
0	3.361770692	4.490468929	HRAS	.
0	3.361770692	4.490468929	FADD	.
0	2.031002163	2.705997046	DKC1;MYC	.
0	3.286898839	4.328717463	CD320	.
0	3.286898839	4.328717463	MYC	.
0	3.286898839	4.328717463	MYC	.
0	3.286898839	4.328717463	FAAP20	.
0	3.286898839	4.328717463	NOLC1	.
0	2.003352977	2.631538275	FES;P2RY2	.
0	3.215282284	4.175512865	ENG	.
0	3.215282284	4.175512865	ENG	.
0	3.215282284	4.175512865	BYSL	.
0	3.215282284	4.175512865	ENG	.
0	3.215282284	4.175512865	PIEZO1	.
0	3.215282284	4.175512865	METTL3	.
0	3.215282284	4.175512865	HRAS	.
0	3.215282284	4.175512865	PER2	.
0	3.215282284	4.175512865	ENG	.
0	1.274816709	1.635812213	PAGR1;MY	.
0	3.146713242	4.03024673	AMPD2	.
0	3.146713242	4.03024673	RUVBL1	.
0	3.081001244	3.892365161	CTNND1	.
0	3.081001244	3.892365161	TSKU	.
0	3.081001244	3.892365161	FES	.
0	3.081001244	3.892365161	NOLC1	.
0	3.081001244	3.892365161	ABO	.
0	3.081001244	3.892365161	CDC42EP2	.
0	3.081001244	3.892365161	MYC	.
0	3.081001244	3.892365161	HSF1	.
0	3.081001244	3.892365161	METTL3	.
0	3.081001244	3.892365161	TSKU	.
0	1.924714383	2.423749885	SMYD5;FES	.
0	3.017971368	3.761362905	FES	.
0	3.017971368	3.761362905	PER2	.
0	1.899845768	2.359292041	MYBBP1A;	.
0	2.957462687	3.63677822	TSKU	.
0	2.957462687	3.63677822	HMGA1	.
0	2.957462687	3.63677822	ENG	.
0	2.957462687	3.63677822	RRS1	.
0	1.863715894	2.266743238	MYDGF;EN	.
0	2.899326895	3.518188379	HSF1	.
0	2.899326895	3.518188379	EIPR1	.
0	2.899326895	3.518188379	ATRIP	.
0	2.899326895	3.518188379	ENG	.
0	2.843427095	3.405205703	CD320	.
0	2.843427095	3.405205703	ENG	.

0	2.843427095	3.405205703	MYDGF	.
0	1.817611513	2.150566204	CTNND1;IG	.
0	1.817611513	2.150566204	FES;TSKU	.
0	2.789636722	3.297474075	BAG2	.
0	2.789636722	3.297474075	FADD	.
0	2.789636722	3.297474075	NAGLU	.
0	2.789636722	3.297474075	ANO8	.
0	1.268219132	1.485174554	PER2;NCOA	.
0	1.37120352	1.604963838	PER2;MYBI	.
0	2.737838585	3.194665847	TPI1	.
0	2.737838585	3.194665847	METTL3	.
0	2.737838585	3.194665847	MYC	.
0	1.316251629	1.517400789	PER2;NCOA	.
0	2.687924016	3.096479108	MYC	.
0	2.687924016	3.096479108	ENG	.
0	2.687924016	3.096479108	SAMD4A	.
0	2.687924016	3.096479108	FES	.
0	2.687924016	3.096479108	NAGLU	.
0	2.687924016	3.096479108	CDC42EP2	.
0	1.16333594	1.330947315	ZNF593;NC	.
0	2.639792111	3.002635249	ECM1	.
0	2.639792111	3.002635249	PRMT5	.
0	2.639792111	3.002635249	FPGS	.
0	2.639792111	3.002635249	FADD	.
0	1.752547048	1.990371982	MRTO4;SA	.
0	1.752547048	1.990371982	ECM1;FAD	.
0	2.593349044	2.912876806	TSKU	.
0	2.593349044	2.912876806	MYC	.
0	2.593349044	2.912876806	ENG	.
0	2.593349044	2.912876806	TSKU	.
0	2.593349044	2.912876806	PER2	.
0	2.593349044	2.912876806	FADD	.
0	2.593349044	2.912876806	BCS1L	.
0	2.593349044	2.912876806	BCS1L	.
0	1.50770416	1.687844072	ATRIP;FAA	.
0	1.721717083	1.916040905	PIEZO1;RH	.
0	1.497398225	1.659457996	BMP1;PLO	.
0	2.505185935	2.744680634	MYC	.
0	1.323460853	1.445462482	SMYD5;MY	.
0	1.682245386	1.822388495	PRMT5;HS	.
0	2.463308458	2.665817317	FADD	.
0	2.463308458	2.665817317	MYC	.
0	2.422804013	2.590185308	PER2	.
0	2.422804013	2.590185308	TBKBP1	.
0	2.383606163	2.517607656	MYC	.
0	2.383606163	2.517607656	ECM1	.
0	2.383606163	2.517607656	CTSZ	.

0	2.383606163	2.517607656	MYC	.
0	2.383606163	2.517607656	CTSZ	.
0	2.383606163	2.517607656	CTSZ	.
0	2.383606163	2.517607656	PER2	.
0	2.345652689	2.447919602	FADD	.
0	2.308885261	2.380967569	ENG	.
0	2.308885261	2.380967569	SLC4A3	.
0	2.308885261	2.380967569	FDXR	.
0	2.273249139	2.316608249	CTNND1	.
0	2.273249139	2.316608249	BMP1	.
0	2.273249139	2.316608249	BMP1	.
0	2.273249139	2.316608249	HSF1	.
0	2.273249139	2.316608249	FADD	.
0	2.205168189	2.195140971	FES	.
0	2.205168189	2.195140971	DKC1	.
0	1.388139205	1.370719637	FES;P2RY2	.
0	2.1726295	2.137790679	MYC	.
0	2.1726295	2.137790679	FES	.
0	2.1726295	2.137790679	HRAS	.
0	2.141033961	2.082547133	CTSZ	.
0	2.141033961	2.082547133	TSKU	.
0	2.110341151	2.029307404	FARSA	.
0	2.110341151	2.029307404	ENG	.
0	2.110341151	2.029307404	METTL3	.
0	2.110341151	2.029307404	TSKU	.
0	2.110341151	2.029307404	WIPF3	.
0	2.110341151	2.029307404	FADD	.
0	2.110341151	2.029307404	RUVBL1	.
0	1.288084965	1.237097754	PER2;MYBI	.
0	2.080512928	1.977974882	METTL3	.
0	2.080512928	1.977974882	WIPF3	.
0	2.080512928	1.977974882	TSKU	.
0	1.509053245	1.432477811	NOC2L;BCI	.
0	1.509053245	1.432477811	CASTOR1;I	.
0	2.051513267	1.928458813	CDC42EP2	.
0	2.051513267	1.928458813	TNFAIP1	.
0	2.051513267	1.928458813	HRAS	.
0	1.493658388	1.399547867	MYC;TSKU	.
0	2.023308117	1.880673871	FADD	.
0	2.023308117	1.880673871	CASTOR1	.
0	2.023308117	1.880673871	WIPF3	.
0	2.023308117	1.880673871	CCDC61	.
0	1.333060333	1.233904785	ERP29;BCS	.
0	1.260029235	1.160782738	MYC;NOP2	.
0	1.995865268	1.834539763	METTL3	.
0	1.995865268	1.834539763	REXO4	.
0	1.995865268	1.834539763	CASTOR1	.

0	1.995865268	1.834539763	FADD	.
0	1.995865268	1.834539763	CD320	.
0	1.969154229	1.789980878	TNFAIP1	.
0	1.969154229	1.789980878	ENG	.
0	1.969154229	1.789980878	NSMF	.
0	1.969154229	1.789980878	ANO8	.
0	1.969154229	1.789980878	IPO4	.
0	1.969154229	1.789980878	IPO4	.
0	1.943146112	1.746925954	AMPD2	.
0	1.943146112	1.746925954	TSKU	.
0	1.943146112	1.746925954	IPO4	.
0	1.943146112	1.746925954	MYDGF	.
0	1.943146112	1.746925954	HSPBP1	.
0	1.943146112	1.746925954	FADD	.
0	1.943146112	1.746925954	POLR1C	.
0	1.86907236	1.626131413	HSF1	.
0	1.86907236	1.626131413	BCL2L1	.
0	1.86907236	1.626131413	FDXR	.
0	1.845615672	1.588456661	FADD	.
0	1.845615672	1.588456661	FADD	.
0	1.845615672	1.588456661	FADD	.
0	1.822738161	1.551985072	CTNND1	.
0	1.822738161	1.551985072	HRAS	.
0	1.822738161	1.551985072	HSPBP1	.
0	1.800418639	1.516665935	MMACHC	.
0	1.800418639	1.516665935	METTL3	.
0	1.800418639	1.516665935	PLOD1	.
0	1.256245171	1.053355981	DKC1;DDX	.
0	1.778636936	1.482451221	BCL2L1	.
0	1.778636936	1.482451221	CCDC61	.
0	1.778636936	1.482451221	SLC4A3	.
0	1.757373845	1.449295412	MYC	.
0	1.736611062	1.417155342	SAMD4A	.
0	1.736611062	1.417155342	FADD	.
0	1.736611062	1.417155342	RRAS	.
0	1.736611062	1.417155342	SLC4A3	.
0	1.33055612	1.069242658	ECM1;FAD	.
0	1.696517413	1.355760652	GRAP	.
0	1.696517413	1.355760652	FES	.
0	1.677154003	1.326430199	MYC	.
0	1.677154003	1.326430199	RRAS	.
0	1.677154003	1.326430199	POLR1C	.
0	1.677154003	1.326430199	ENG	.
0	1.677154003	1.326430199	IPO4	.
0	1.639718076	1.270327383	GRAP	.
0	1.639718076	1.270327383	FADD	.
0	1.621617189	1.24348984	CDC42EP2	.

0	1.621617189	1.24348984	ENG	.
0	1.586583213	1.192091107	SAMD4A	.
0	1.586583213	1.192091107	MYC	.
0	1.586583213	1.192091107	RRAS	.
0	1.586583213	1.192091107	RRAS	.
0	1.171657047	0.868975581	MYDGF;M	.
0	1.553024352	1.14354205	MYC	.
0	1.553024352	1.14354205	FES	.
0	1.250732764	0.92063824	RRAS;HRA	.
0	1.536769279	1.120271394	PITRM1	.
0	1.536769279	1.120271394	HRAS	.
0	1.520849361	1.09763781	NSMF	.
0	1.505254341	1.075618524	SLC4A3	.
0	1.505254341	1.075618524	HRAS	.
0	1.489974371	1.054191781	ENG	.
0	1.475	1.033336791	LONP1	.
0	1.475	1.033336791	HRAS	.
0	1.209232097	0.846975798	HSF1;PPRC	.
0	1.460322152	1.013033672	PLOD1	.
0	1.460322152	1.013033672	CTSZ	.
0	1.460322152	1.013033672	CTNND1	.
0	1.460322152	1.013033672	RRS1	.
0	1.431821475	0.974007803	FDXR	.
0	1.417982204	0.955249432	HRAS	.
0	1.404406539	0.936971611	PITRM1	.
0	1.404406539	0.936971611	PLOD1	.
0	1.404406539	0.936971611	MYDGF	.
0	1.404406539	0.936971611	HRAS	.
0	1.151844455	0.749331869	RRAS;FES	.
0	1.352594824	0.868355848	CAMKK1	.
0	1.138328447	0.727064941	NOC2L;MD	.
0	1.340230665	0.852253762	TSKU	.
0	1.328089283	0.836545625	MDN1	.
0	1.067797541	0.664432853	FDXR;ANO	.
0	1.304451195	0.806261831	ENG	.
0	1.304451195	0.806261831	ENG	.
0	1.304451195	0.806261831	CDC42EP2	.
0	1.304451195	0.806261831	RUVBL1	.
0	1.304451195	0.806261831	CAMKK1	.
0	1.112214499	0.684849649	METTL3;TS	.
0	1.112214499	0.684849649	MYC;RUVB	.
0	1.292943179	0.791662694	FPGS	.
0	1.292943179	0.791662694	HRAS	.
0	1.292943179	0.791662694	HRAS	.
0	1.103770663	0.6714293	NSMF;HRA	.
0	1.270522388	0.763494621	FES	.
0	1.083204334	0.639217676	MYDGF;HR	.

0	1.083204334	0.639217676	PRMT5;ME	.
0	1.248861624	0.736631267	HRAS	.
0	1.238304277	0.72366448	TOMM40	.
0	1.07518797	0.626846485	MYC;RUVB	.
0	1.217713087	0.698615073	SAMD4A	.
0	0.998225655	0.570042579	MYDGF;M'	.
0	1.207670663	0.686515211	NSMF	.
0	1.19779153	0.674687605	PER2	.
0	1.19779153	0.674687605	FADD	.
0	1.188071738	0.663124396	LONP1	.
0	1.188071738	0.663124396	ECM1	.
0	1.141733194	0.609018345	RUVBL1	.
0	1.141733194	0.609018345	PRMT5	.
0	1.141733194	0.609018345	PLOD1	.
0	1.132893226	0.598891463	MYC	.
0	1.132893226	0.598891463	HSF1	.
0	1.115615106	0.579281709	FES	.
0	1.115615106	0.579281709	FES	.
0	1.115615106	0.579281709	ENG	.
0	0.980701754	0.489046998	FES;AKAP1	.
0	1.066785637	0.525203024	PDP2	.
0	0.946220698	0.46403285	MYC;NOP2	.
0	1.059057232	0.516828878	FES	.
0	0.954838395	0.453981846	MYBBP1A;	.
0	1.036525121	0.492709022	GRWD1	.
0	1.029224507	0.484989137	ENG	.
0	0.942404087	0.43754235	GRWD1;AT	.
0	1.001015332	0.455604729	HRAS	.
0	0.994201291	0.448614036	HRAS	.
0	0.987478714	0.441758548	BCL2L1	.
0	0.913947567	0.408862264	MYDGF;M'	.
0	0.974300682	0.428440103	CDC42EP2	.
0	0.974300682	0.428440103	ENG	.
0	0.967841712	0.421970849	PDP2	.
0	0.967841712	0.421970849	RUVBL1	.
0	0.961467174	0.415624197	CAMKK1	.
0	0.942833907	0.397291079	CCDC61	.
0	0.936781063	0.391406475	BMP1	.
0	0.930804837	0.385630698	FES	.
0	0.882024882	0.361670138	POLR1C;FA	.
0	0.855871457	0.330888953	ANO8;DCA	.
0	0.880239521	0.338152544	POLR1C	.
0	0.864574188	0.323959431	TSKU	.
0	0.859474557	0.319392842	HRAS	.
0	0.834845658	0.297715336	BMP1	.
0	0.820728758	0.285575607	ECM1	.
0	0.798223556	0.266660797	CTSZ	.

0	0.781081296	0.252620954	HRAS	.
0	0.772780833	0.245938668	TSKU	.
0	0.766956659	0.236036009	MYC;ERP2	.
0	0.733768657	0.215566251	LONP1	.
0	0.730080939	0.212784907	PER2	.
0	0.719234709	0.204695802	TNFAIP1	.
0	0.705259759	0.194476092	MYC	.
0	0.842237914	0.23076544	PRMT5;UT	.
0	0.728051472	0.19945156	FES;HRAS	.
0	0.720730397	0.192911029	HRAS;ENG	.
0	0.718922614	0.191312899	EIPR1;TNF	.
0	0.688529185	0.182545583	HRAS	.
0	0.672566069	0.171476204	FES	.
0	0.666383989	0.1672727	HRAS	.
0	0.602604263	0.126698638	CAMKK1	.
0	0.585522388	0.116720558	METTL3	.
0	0.608598741	0.106702602	CTSZ;PGM	.
0	0.607299499	0.105859856	MYC;BCL2I	.
0	0.603434051	0.103373945	CTSZ;PGM	.
0	0.599616325	0.100950168	CTSZ;PGM	.
0	0.535563939	0.089781688	RHBG	.
0	0.51269966	0.078597845	FADD	.
0	0.571842179	0.084258951	MYC;HMG	.
0	0.488344232	0.067497027	METTL3	.
0	0.556132204	0.075551684	EIPR1;TNF	.
0	0.478590653	0.063289922	CAMKK1	.
0	0.455806903	0.05400066	TNFAIP1	.
0	0.444507645	0.049675955	ERP29	.
0	0.412498414	0.038451958	TNFAIP1	.
0	0.395380435	0.033077478	ERP29	.
0	0.467550135	0.036291417	MYC;BCL2I	.
0	0.34217474	0.01917699	CCDC61	.
0	0.32492805	0.015574693	NAGLU	.
0	0.292024725	0.009894918	FES	.
0	0.419031311	0.011979998	PDP2;ANO	.

ignificant terms were highlighted)

Term	Overlap	P-value	Adjusted P-value	Old P-value
Ribosome biogenesis in eukaryotes	6/108	9.21E-05	0.013172916	0
Aminoacyl-tRNA biosynthesis	24167	0.010097709	0.375577416	0
Acute myeloid leukemia	24532	0.010519712	0.375577416	0
Mitophagy	24898	0.01095182	0.375577416	0
Chronic myeloid leukemia	27820	0.01477696	0.375577416	0
Apoptosis	4/142	0.015758493	0.375577416	0
Starch and sucrose metabolism	13181	0.024529734	0.461506243	0
Thyroid cancer	13547	0.025818531	0.461506243	0
Bladder cancer	15008	0.03123932	0.496358088	0
Endometrial cancer	21217	0.058502869	0.647936118	0
Autophagy	3/137	0.065744951	0.647936118	0
Lysine degradation	23043	0.067648461	0.647936118	0
Glycolysis / Gluconeogenesis	24504	0.075280891	0.647936118	0
Central carbon metabolism in cancer	25600	0.081176376	0.647936118	0
RIG-I-like receptor signaling pathway	25600	0.081176376	0.647936118	0
Salmonella infection	4/249	0.088446221	0.647936118	0
Cellular senescence	3/156	0.088958433	0.647936118	0
Hepatitis C	3/157	0.090264709	0.647936118	0
Hepatitis B	3/162	0.096915709	0.647936118	0
JAK-STAT signaling pathway	3/162	0.096915709	0.647936118	0
Hepatocellular carcinoma	3/168	0.105152199	0.647936118	0
Selenocompound metabolism	44578	0.108798652	0.647936118	0
Protein processing in endoplasmic ret	3/171	0.109371062	0.647936118	0
ErbB signaling pathway	31079	0.112566508	0.647936118	0
Colorectal cancer	31444	0.114758699	0.647936118	0
Glycosaminoglycan degradation	44580	0.120799711	0.647936118	0
Axon guidance	3/182	0.125382389	0.647936118	0
Small cell lung cancer	33635	0.128133888	0.647936118	0
Transcriptional misregulation in cance	3/192	0.140624723	0.647936118	0
Kaposi sarcoma-associated herpesviru	3/193	0.142182369	0.647936118	0
Vitamin digestion and absorption	44585	0.150105142	0.647936118	0
C-type lectin receptor signaling pathw	2/104	0.155868126	0.647936118	0
Proteoglycans in cancer	3/205	0.16131003	0.647936118	0
Folate biosynthesis	44587	0.16155396	0.647936118	0
Rap1 signaling pathway	3/210	0.169501282	0.647936118	0
Human immunodeficiency virus 1 infe	3/212	0.172811459	0.647936118	0
Pentose phosphate pathway	44591	0.183994333	0.647936118	0
Human T-cell leukemia virus 1 infectio	3/219	0.184539463	0.647936118	0
Circadian rhythm	44592	0.189510638	0.647936118	0
Galactose metabolism	44592	0.189510638	0.647936118	0
RNA polymerase	44592	0.189510638	0.647936118	0
Human cytomegalovirus infection	3/225	0.194756299	0.647936118	0
Thyroid hormone signaling pathway	2/121	0.19680421	0.647936118	0
Fructose and mannose metabolism	12055	0.200432444	0.647936118	0

Ras signaling pathway	3/232	0.206849119	0.647936118	0
Lysosome	2/128	0.214035407	0.647936118	0
Purine metabolism	2/129	0.216509386	0.647936118	0
PI3K-Akt signaling pathway	4/354	0.217489046	0.647936118	0
Apelin signaling pathway	2/137	0.236384135	0.664283225	0
Insulin signaling pathway	2/137	0.236384135	0.664283225	0
Measles	2/139	0.241370712	0.664283225	0
Signaling pathways regulating pluripo	2/143	0.251357844	0.664283225	0
Breast cancer	2/147	0.261356888	0.664283225	0
Glycosphingolipid biosynthesis	16438	0.262962154	0.664283225	0
Phospholipase D signaling pathway	2/148	0.263857598	0.664283225	0
Gastric cancer	2/149	0.266358452	0.664283225	0
Other types of O-glycan biosynthesis	17168	0.272901103	0.664283225	0
Amino sugar and nucleotide sugar me	17533	0.277820574	0.664283225	0
mTOR signaling pathway	2/154	0.278860906	0.664283225	0
Arginine and proline metabolism	18264	0.287560617	0.664283225	0
Hippo signaling pathway	2/163	0.301323815	0.664283225	0
Fanconi anemia pathway	19725	0.306651223	0.664283225	0
Wnt signaling pathway	2/166	0.308789268	0.664283225	0
MAPK signaling pathway	3/294	0.319062294	0.664283225	0
Legionellosis	20821	0.32063515	0.664283225	0
VEGF signaling pathway	21551	0.329801872	0.664283225	0
Long-term depression	21916	0.334339087	0.664283225	0
NOD-like receptor signaling pathway	2/181	0.345840122	0.664283225	0
Cytosolic DNA-sensing pathway	23012	0.347768598	0.664283225	0
GnRH secretion	23377	0.352185065	0.664283225	0
Alcoholism	2/186	0.358057104	0.664283225	0
RNA transport	2/186	0.358057104	0.664283225	0
Long-term potentiation	24473	0.365257143	0.664283225	0
Fc epsilon RI signaling pathway	24838	0.369556051	0.664283225	0
Renal cell carcinoma	25204	0.373826058	0.664283225	0
Prolactin signaling pathway	25569	0.378067357	0.664283225	0
Adherens junction	25934	0.38228014	0.664283225	0
Pathogenic Escherichia coli infection	2/197	0.384635217	0.664283225	0
Melanoma	26299	0.386464596	0.664283225	0
Non-small cell lung cancer	26299	0.386464596	0.664283225	0
p53 signaling pathway	26665	0.390620915	0.664283225	0
Inositol phosphate metabolism	26665	0.390620915	0.664283225	0
Epstein-Barr virus infection	2/202	0.396562883	0.664283225	0
Glioma	27395	0.398849892	0.664283225	0
Pathways of neurodegeneration	4/475	0.399553777	0.664283225	0
Pancreatic cancer	27760	0.402922922	0.664283225	0
B cell receptor signaling pathway	29587	0.422880808	0.664283225	0
Lipid and atherosclerosis	2/215	0.427065702	0.664283225	0
Regulation of actin cytoskeleton	2/218	0.433992528	0.664283225	0
Gap junction	32143	0.449714035	0.664283225	0
PD-L1 expression and PD-1 checkpoin	32509	0.453444873	0.664283225	0

Thermogenesis	2/232	0.465713552	0.664283225	0
GnRH signaling pathway	33970	0.468118814	0.664283225	0
TGF-beta signaling pathway	34335	0.471725777	0.664283225	0
IL-17 signaling pathway	34335	0.471725777	0.664283225	0
Chemical carcinogenesis	2/239	0.48118138	0.664283225	0
Circadian entrainment	35431	0.482401628	0.664283225	0
Prostate cancer	35431	0.482401628	0.664283225	0
Pathways in cancer	4/531	0.48351335	0.664283225	0
Choline metabolism in cancer	35796	0.485912436	0.664283225	0
Inflammatory mediator regulation of	35796	0.485912436	0.664283225	0
AGE-RAGE signaling pathway in diabe	1/100	0.492863296	0.664283225	0
Melanogenesis	1/101	0.496303663	0.664283225	0
Chagas disease	1/102	0.499720862	0.664283225	0
Longevity regulating pathway	1/102	0.499720862	0.664283225	0
T cell receptor signaling pathway	1/104	0.506486376	0.664283225	0
Toll-like receptor signaling pathway	1/104	0.506486376	0.664283225	0
NF-kappa B signaling pathway	1/104	0.506486376	0.664283225	0
Endocytosis	2/252	0.509172648	0.664283225	0
Glucagon signaling pathway	1/107	0.51646473	0.664283225	0
Insulin resistance	1/108	0.519746141	0.664283225	0
TNF signaling pathway	1/112	0.532652208	0.664283225	0
Toxoplasmosis	1/112	0.532652208	0.664283225	0
Serotonergic synapse	1/113	0.535824562	0.664283225	0
Cholinergic synapse	1/113	0.535824562	0.664283225	0
Leukocyte transendothelial migration	1/114	0.538975541	0.664283225	0
Sphingolipid signaling pathway	1/119	0.554414774	0.664283225	0
Growth hormone synthesis, secretion	1/119	0.554414774	0.664283225	0
Neurotrophin signaling pathway	1/119	0.554414774	0.664283225	0
AMPK signaling pathway	1/120	0.557440469	0.664283225	0
Cell cycle	1/124	0.569340663	0.672857147	0
Relaxin signaling pathway	1/129	0.583770153	0.679718956	0
FoxO signaling pathway	1/131	0.589406647	0.679718956	0
Natural killer cell mediated cytotoxici	1/131	0.589406647	0.679718956	0
Yersinia infection	1/137	0.605865537	0.6876093	0
Estrogen signaling pathway	1/137	0.605865537	0.6876093	0
MicroRNAs in cancer	2/310	0.621602712	0.699914864	0
Oxytocin signaling pathway	1/154	0.649026836	0.725084668	0
Human papillomavirus infection	2/331	0.657156029	0.726884312	0
Necroptosis	1/159	0.66080392	0.726884312	0
Influenza A	1/172	0.689620333	0.752791661	0
Tuberculosis	1/180	0.70613157	0.760812726	0
Amyotrophic lateral sclerosis	2/364	0.707609039	0.760812726	0
Alzheimer disease	2/369	0.71469352	0.762695324	0
Chemokine signaling pathway	1/192	0.729277458	0.7724939	0
Focal adhesion	1/201	0.74544078	0.776034524	0
Viral carcinogenesis	1/203	0.748900449	0.776034524	0
Diabetic cardiomyopathy	1/203	0.748900449	0.776034524	0

cAMP signaling pathway	1/216	0.77027808	0.792444356	0
Shigellosis	1/246	0.81296283	0.828356923	0
Parkinson disease	1/249	0.816771511	0.828356923	0
Herpes simplex virus 1 infection	2/498	0.853098684	0.859106421	0
Neuroactive ligand-receptor interacti	1/341	0.90265206	0.90265206	0

Old Adjusted P-value	Odds Ratio	Combined Score	Genes
0	9.011855905	83.74210317	EMG1;UTP4;DKC1;PWP2;MDN1;NOL6
0	7.143578644	32.82793523	MARS2;FARSA;VARS1
0	7.031605114	32.02547669	PER2;MYC;HRAS
0	6.923076923	31.25249755	RRAS;HRAS;BCL2L1
0	6.161892902	25.97044416	MYC;HRAS;BCL2L1
0	4.36486337	18.1158234	CTSZ;FADD;HRAS;BCL2L1
0	8.770897833	32.52134236	GYS1;PGM2
0	8.519871106	31.15429562	MYC;HRAS
0	7.644495855	26.49641671	MYC;HRAS
0	5.319280344	15.099732	MYC;HRAS
0	3.346506106	9.109097276	RRAS;HRAS;BCL2L1
0	4.882041168	13.14943944	PLOD1;COLGALT1
0	4.580682475	11.84806782	TPI1;PGM2
0	4.377930119	10.9935561	MYC;HRAS
0	4.377930119	10.9935561	TBKBP1;FADD
0	2.445240692	5.930590391	RRAS;MYC;FADD;HRAS
0	2.928104575	7.084801025	RRAS;MYC;HRAS
0	2.908943329	6.996034065	MYC;FADD;HRAS
0	2.81675243	6.574056955	MYC;FADD;HRAS
0	2.81675243	6.574056955	MYC;HRAS;BCL2L1
0	2.713498623	6.111739031	MYC;HRAS;BCL2L1
0	9.257929104	20.53645985	MARS2
0	2.664637446	5.896866499	BAG2;ERP29;HSPBP1
0	3.584020292	7.828256738	MYC;HRAS
0	3.541174364	7.66637203	MYC;HRAS
0	8.228441128	17.39180911	NAGLU
0	2.499492128	5.189913207	RRAS;FES;HRAS
0	3.304093567	6.788853516	MYC;BCL2L1
0	2.366041366	4.641369832	PER2;MYC;BCL2L1
0	2.3534689	4.590781772	MYC;FADD;HRAS
0	6.438027255	12.20919903	MMACHC
0	2.913607548	5.415653395	RRAS;HRAS
0	2.212308731	4.036196026	RRAS;MYC;HRAS
0	5.92238806	10.7960164	FPGS
0	2.158322354	3.830795096	RRAS;CTNND1;HRAS
0	2.137451066	3.752411007	FADD;HRAS;BCL2L1
0	5.104477612	8.641116555	PGM2
0	2.067445286	3.493759139	MYC;HRAS;BCL2L1
0	4.934079602	8.206904528	PER2
0	4.934079602	8.206904528	PGM2
0	4.934079602	8.206904528	POLR1C
0	2.010954136	3.289933533	MYC;FADD;HRAS
0	2.495229671	4.056110363	MYC;HRAS
0	4.625233209	7.434035694	TPI1

0	1.948789202	3.070835073	RRAS;HRAS;BCL2L1
0	2.355770378	3.631688185	NAGLU;CTSZ
0	2.337102599	3.576050652	PGM2;AMPD2
0	1.702508179	2.597358039	GYS1;MYC;HRAS;BCL2L1
0	2.197716514	3.169760168	RRAS;HRAS
0	2.197716514	3.169760168	GYS1;HRAS
0	2.165413534	3.077964932	FADD;BCL2L1
0	2.103556764	2.904754588	MYC;HRAS
0	2.045112782	2.744272253	MYC;HRAS
0	3.361770692	4.490468929	ABO
0	2.031002163	2.705997046	RRAS;HRAS
0	2.017083525	2.668424636	MYC;HRAS
0	3.215282284	4.175512865	COLGALT1
0	3.146713242	4.03024673	PGM2
0	1.950237436	2.490535436	CASTOR1;HRAS
0	3.017971368	3.761362905	CKB
0	1.840377341	2.20766107	RASSF4;MYC
0	2.789636722	3.297474075	ATRIP
0	1.806436824	2.122737076	MYC;RUVBL1
0	1.528741018	1.746386223	RRAS;MYC;HRAS
0	2.639792111	3.002635249	HSF1
0	2.548507463	2.826965522	HRAS
0	2.505185935	2.744680634	HRAS
0	1.653799303	1.755968848	FADD;BCL2L1
0	2.383606163	2.517607656	POLR1C
0	2.345652689	2.447919602	HRAS
0	1.608450474	1.651979643	HRAS;CAMKK1
0	1.608450474	1.651979643	PRMT5;ELAC2
0	2.238692899	2.254707774	HRAS
0	2.205168189	2.195140971	HRAS
0	2.1726295	2.137790679	HRAS
0	2.141033961	2.082547133	HRAS
0	2.110341151	2.029307404	CTNND1
0	1.516869096	1.449307568	WIPF3;FADD
0	2.080512928	1.977974882	HRAS
0	2.080512928	1.977974882	HRAS
0	2.051513267	1.928458813	BCL2L1
0	2.051513267	1.928458813	TPI1
0	1.478571429	1.367561254	MYC;FADD
0	1.995865268	1.834539763	HRAS
0	1.257289185	1.153445787	TOMM40;FADD;HRAS;BCL2L1
0	1.969154229	1.789980878	BCL2L1
0	1.845615672	1.588456661	HRAS
0	1.387412192	1.180434447	HRAS;BCL2L1
0	1.367933723	1.141852527	RRAS;HRAS
0	1.696517413	1.355760652	HRAS
0	1.677154003	1.326430199	HRAS

0	1.28375286	0.981024074	COA7;HRAS
0	1.603909799	1.217420689	HRAS
0	1.586583213	1.192091107	MYC
0	1.586583213	1.192091107	FADD
0	1.245391961	0.911017906	MYC;HRAS
0	1.536769279	1.120271394	PER2
0	1.536769279	1.120271394	HRAS
0	1.120442661	0.814199186	MYC;FADD;HRAS;BCL2L1
0	1.520849361	1.09763781	HRAS
0	1.520849361	1.09763781	P2RY2
0	1.489974371	1.054191781	HRAS
0	1.475	1.033336791	HRAS
0	1.460322152	1.013033672	FADD
0	1.460322152	1.013033672	HRAS
0	1.431821475	0.974007803	HRAS
0	1.431821475	0.974007803	FADD
0	1.431821475	0.974007803	BCL2L1
0	1.179849624	0.796360893	WIPF3;HRAS
0	1.391087018	0.919158353	GYS1
0	1.37801646	0.901794335	GYS1
0	1.328089283	0.836545625	FADD
0	1.328089283	0.836545625	BCL2L1
0	1.316164712	0.821218973	HRAS
0	1.316164712	0.821218973	HRAS
0	1.304451195	0.806261831	CTNND1
0	1.248861624	0.736631267	HRAS
0	1.248861624	0.736631267	HRAS
0	1.248861624	0.736631267	HRAS
0	1.238304277	0.72366448	GYS1
0	1.19779153	0.674687605	MYC
0	1.150711287	0.619367988	HRAS
0	1.132893226	0.598891463	HRAS
0	1.132893226	0.598891463	HRAS
0	1.082583406	0.542479518	WIPF3
0	1.082583406	0.542479518	HRAS
0	0.954838395	0.453981846	MYC;HRAS
0	0.961467174	0.415624197	HRAS
0	0.892931417	0.374882791	FADD;HRAS
0	0.930804837	0.385630698	FADD
0	0.859474557	0.319392842	FADD
0	0.820728758	0.285575607	FADD
0	0.810160761	0.280205071	TOMM40;BCL2L1
0	0.798918277	0.268357825	FADD;HRAS
0	0.768695788	0.242678043	HRAS
0	0.733768657	0.215566251	HRAS
0	0.726429733	0.210046588	HRAS
0	0.726429733	0.210046588	GYS1

0	0.682054842	0.178018828	RRAS
0	0.597624124	0.123749961	BCL2L1
0	0.590304526	0.11947521	BCL2L1
0	0.587224109	0.093298194	FADD;BCL2L1
0	0.428555751	0.043891872	P2RY2

Supplementary File S6: Comprehensive details of the results of functional enrichment anal

BP	Term	Overlap	P-value
	negative regulation of leukocyte cell-cell adhesion (GO:1903038)	44638	6.69E-04
	protein phosphorylation (GO:0006468)	13/496	0.001205164
	protein localization to cell junction (GO:1902414)	44642	0.001225987
	positive regulation of actin filament polymerization (GO:0030838)	17989	0.001317698
	response to insulin (GO:0032868)	30803	0.001385735
	regulation of cation channel activity (GO:2001257)	32629	0.001791697
	regulation of AMPA receptor activity (GO:2000311)	44645	0.001792104
	regulation of megakaryocyte differentiation (GO:0045652)	19815	0.001893827
	regulation of glycogen (starch) synthase activity (GO:2000465)	44599	0.001923155
	positive regulation of voltage-gated calcium channel activity (GO:1	44599	0.001923155
	regulation of glycogen biosynthetic process (GO:0005979)	44646	0.002011415
	antigen receptor-mediated signaling pathway (GO:0050851)	7/185	0.002296719
	negative regulation of B cell apoptotic process (GO:0002903)	44600	0.002547777
	positive regulation of myeloid cell apoptotic process (GO:0033034)	44600	0.002547777
	regulation of respiratory burst (GO:0060263)	44601	0.00325474
	positive regulation of megakaryocyte differentiation (GO:0045654)	44601	0.00325474
	amino sugar metabolic process (GO:0006040)	44602	0.004042395
	secondary alcohol biosynthetic process (GO:1902653)	12479	0.00437236
	cholesterol biosynthetic process (GO:0006695)	12844	0.00474832
	actin filament network formation (GO:0051639)	44603	0.004909119
	regulation of calcium ion transmembrane transport via high voltag	44603	0.004909119
	positive regulation of leukocyte apoptotic process (GO:2000108)	44603	0.004909119
	V(D)J recombination (GO:0033151)	44603	0.004909119
	positive regulation of myeloid cell differentiation (GO:0045639)	13575	0.005557352
	protein localization to synapse (GO:0035418)	44604	0.00585331
	negative regulation of heart contraction (GO:0045822)	44604	0.00585331
	nucleotide-sugar metabolic process (GO:0009225)	44604	0.00585331
	sterol biosynthetic process (GO:0016126)	13940	0.005990927
	antifungal innate immune response (GO:0061760)	44605	0.006873392
	regulation of interleukin-5 production (GO:0032674)	44605	0.006873392
	response to nitric oxide (GO:0071731)	44605	0.006873392
	regulation of cell development (GO:0060284)	15036	0.007410629
	lipid biosynthetic process (GO:0008610)	29312	0.007787651
	glycerophospholipid biosynthetic process (GO:0046474)	6/177	0.007892188
	positive regulation of glycogen biosynthetic process (GO:0045725)	44606	0.007967811
	cellular response to insulin stimulus (GO:0032869)	5/129	0.008703925
	glycoprotein biosynthetic process (GO:0009101)	30407	0.008847298
	acetyl-CoA metabolic process (GO:0006084)	44607	0.009135034
	positive regulation of glycogen metabolic process (GO:0070875)	44607	0.009135034
	myoblast differentiation (GO:0045445)	44607	0.009135034
	axonogenesis (GO:0007409)	7/240	0.009356888
	negative regulation of T cell activation (GO:0050868)	16497	0.009588598
	glycosphingolipid biosynthetic process (GO:0006688)	44608	0.010373554
	chemical synaptic transmission (GO:0007268)	8/306	0.010511218

negative regulation of cold-induced thermogenesis (GO:0120163)	17227	0.010802794
regulation of synapse assembly (GO:0051963)	17227	0.010802794
sensory perception of mechanical stimulus (GO:0050954)	32234	0.010814779
sensory perception of sound (GO:0007605)	33329	0.012120511
regulation of fatty acid metabolic process (GO:0019217)	44610	0.013058558
regulation of oxidative stress-induced intrinsic apoptotic signaling p	44610	0.013058558
presynapse assembly (GO:0099054)	44610	0.013058558
positive regulation of developmental growth (GO:0048639)	19054	0.014211962
negative regulation of oxidative stress-induced intrinsic apoptotic s	44611	0.014502135
postsynaptic membrane organization (GO:0001941)	44611	0.014502135
N-glycan processing (GO:0006491)	44611	0.014502135
axon guidance (GO:0007411)	6/203	0.014788405
neuromuscular synaptic transmission (GO:0007274)	44612	0.016011193
positive regulation of dendrite morphogenesis (GO:0050775)	44612	0.016011193
phosphorylation (GO:0016310)	9/400	0.016919784
negative regulation of metabolic process (GO:0009892)	20515	0.01732992
negative regulation of microtubule depolymerization (GO:0007026	44613	0.017584331
phosphate-containing compound metabolic process (GO:0006796)	6/212	0.017929582
peptidyl-serine phosphorylation (GO:0018105)	5/156	0.018530241
regulation of neurotransmitter receptor activity (GO:0099601)	21245	0.019020545
negative regulation of B cell activation (GO:0050869)	44614	0.019220169
negative regulation of lymphocyte activation (GO:0051250)	44614	0.019220169
phosphatidylserine acyl-chain remodeling (GO:0036150)	44614	0.019220169
regulation of voltage-gated calcium channel activity (GO:1901385)	44614	0.019220169
skeletal system development (GO:0001501)	5/158	0.01946377
T cell receptor signaling pathway (GO:0050852)	5/158	0.01946377
protein autophosphorylation (GO:0046777)	5/159	0.019941912
cellular response to peptide hormone stimulus (GO:0071375)	4/106	0.020147043
double-strand break repair via nonhomologous end joining (GO:00(	22706	0.022666445
axon extension (GO:0048675)	44616	0.022674533
negative regulation of protein depolymerization (GO:1901880)	44616	0.022674533
defense response to fungus (GO:0050832)	44616	0.022674533
regulation of ruffle assembly (GO:1900027)	44616	0.022674533
regulation of cAMP-mediated signaling (GO:0043949)	44617	0.024490401
cAMP-mediated signaling (GO:0019933)	44617	0.024490401
regulation of microtubule depolymerization (GO:0031114)	44617	0.024490401
regulation of neutrophil chemotaxis (GO:0090022)	44617	0.024490401
peptidyl-serine modification (GO:0018209)	5/169	0.025150358
response to lipid (GO:0033993)	4/114	0.025503395
cellular response to molecule of bacterial origin (GO:0071219)	4/115	0.026227481
phosphatidylethanolamine acyl-chain remodeling (GO:0036152)	44618	0.026363654
regulation of synapse organization (GO:0050807)	44618	0.026363654
positive regulation of cellular component movement (GO:0051272	44619	0.028293013
positive regulation of erythrocyte differentiation (GO:0045648)	44619	0.028293013
positive regulation of muscle cell differentiation (GO:0051149)	44619	0.028293013
positive regulation of nucleic acid-templated transcription (GO:190	10/511	0.028673178
cellular response to lipopolysaccharide (GO:0071222)	4/120	0.03003237

negative regulation of oxidative stress-induced cell death (GO:1903	44620	0.030277218
positive regulation of nitric oxide metabolic process (GO:1904407)	44620	0.030277218
regulation of plasma membrane bounded cell projection assembly	25628	0.031016916
nervous system development (GO:0007399)	9/447	0.031645463
myeloid leukocyte differentiation (GO:0002573)	25993	0.032159487
regulation of calcium ion transmembrane transporter activity (GO::	47150	0.032315028
negative regulation of mRNA catabolic process (GO:1902373)	47150	0.032315028
negative regulation of myeloid leukocyte differentiation (GO:00027	47150	0.032315028
anterograde trans-synaptic signaling (GO:0098916)	6/244	0.032736072
phosphatidylcholine acyl-chain remodeling (GO:0036151)	10990	0.03440522
insulin receptor signaling pathway (GO:0008286)	26724	0.034509941
positive regulation of locomotion (GO:0040017)	11355	0.036546591
positive regulation of macromolecule biosynthetic process (GO:001	4/129	0.037664023
cell morphogenesis involved in neuron differentiation (GO:004866	27820	0.038197883
positive regulation of interleukin-6 production (GO:0032755)	27820	0.038197883
negative regulation of microtubule polymerization or depolymeriza	11720	0.038737955
protein K63-linked deubiquitination (GO:0070536)	11720	0.038737955
cellular response to oxygen-containing compound (GO:1901701)	7/323	0.039460637
cholesterol metabolic process (GO:0008203)	28185	0.039470161
phosphatidylcholine metabolic process (GO:0046470)	28185	0.039470161
positive regulation of endothelial cell proliferation (GO:0001938)	28185	0.039470161
neuron projection extension (GO:1990138)	12086	0.040978145
phosphatidylcholine biosynthetic process (GO:0006656)	12086	0.040978145
positive regulation of ATP metabolic process (GO:1903580)	12086	0.040978145
RNA stabilization (GO:0043489)	12086	0.040978145
regulation of cell motility (GO:2000145)	4/133	0.041381462
B cell receptor signaling pathway (GO:0050853)	12451	0.04326601
regulation of cell adhesion mediated by integrin (GO:0033628)	12451	0.04326601
phosphatidylserine metabolic process (GO:0006658)	12451	0.04326601
regulation of lipid biosynthetic process (GO:0046890)	12816	0.04560042
regulation of muscle cell differentiation (GO:0051147)	12816	0.04560042
regulation of T cell receptor signaling pathway (GO:0050856)	12816	0.04560042
regulation of trans-synaptic signaling (GO:0099177)	12816	0.04560042
positive regulation of cytokine production (GO:0001819)	7/335	0.046431662
negative regulation of B cell differentiation (GO:0045578)	44566	0.047813055
negative regulation of calcium ion-dependent exocytosis (GO:0045	44566	0.047813055
alditol phosphate metabolic process (GO:0052646)	44566	0.047813055
negative regulation of ceramide biosynthetic process (GO:1900060	44566	0.047813055
negative regulation of cGMP-mediated signaling (GO:0010754)	44566	0.047813055
negative regulation of collateral sprouting (GO:0048671)	44566	0.047813055
reelin-mediated signaling pathway (GO:0038026)	44566	0.047813055
antigen processing and presentation of lipid antigen via MHC class	44566	0.047813055
antigen processing and presentation, endogenous lipid antigen via	44566	0.047813055
antigen processing and presentation, exogenous lipid antigen via M	44566	0.047813055
regulation of barbed-end actin filament capping (GO:2000812)	44566	0.047813055
negative regulation of gonadotropin secretion (GO:0032277)	44566	0.047813055
negative regulation of interleukin-13 production (GO:0032696)	44566	0.047813055

negative regulation of interleukin-5 production (GO:0032714)	44566	0.047813055
bone marrow development (GO:0048539)	44566	0.047813055
negative regulation of macrophage differentiation (GO:0045650)	44566	0.047813055
negative regulation of myelination (GO:0031642)	44566	0.047813055
cellular response to antibiotic (GO:0071236)	44566	0.047813055
negative regulation of response to food (GO:0032096)	44566	0.047813055
regulation of germinal center formation (GO:0002634)	44566	0.047813055
negative regulation of sphingolipid biosynthetic process (GO:00901	44566	0.047813055
negative regulation of transforming growth factor beta1 productio	44566	0.047813055
negative regulation of vascular endothelial cell proliferation (GO:19	44566	0.047813055
chronic inflammatory response (GO:0002544)	44566	0.047813055
oxaloacetate metabolic process (GO:0006107)	44566	0.047813055
oxaloacetate transport (GO:0015729)	44566	0.047813055
regulation of respiratory gaseous exchange by nervous system pro	44566	0.047813055
establishment of T cell polarity (GO:0001768)	44566	0.047813055
regulation of skeletal muscle tissue development (GO:0048641)	44566	0.047813055
renal tubule development (GO:0061326)	44566	0.047813055
heart field specification (GO:0003128)	44566	0.047813055
hematopoietic stem cell migration (GO:0035701)	44566	0.047813055
hemoglobin metabolic process (GO:0020027)	44566	0.047813055
heparin metabolic process (GO:0030202)	44566	0.047813055
response to prostaglandin (GO:0034694)	44566	0.047813055
inosine metabolic process (GO:0046102)	44566	0.047813055
positive regulation of membrane permeability (GO:1905710)	44566	0.047813055
secondary heart field specification (GO:0003139)	44566	0.047813055
isopentenyl diphosphate biosynthetic process (GO:0009240)	44566	0.047813055
late endosome to Golgi transport (GO:0034499)	44566	0.047813055
long-chain fatty acid catabolic process (GO:0042758)	44566	0.047813055
sulfide oxidation (GO:0019418)	44566	0.047813055
sulfide oxidation, using sulfide:quinone oxidoreductase (GO:00702	44566	0.047813055
positive regulation of protein localization to synapse (GO:1902474)	44566	0.047813055
mature conventional dendritic cell differentiation (GO:0097029)	44566	0.047813055
membrane depolarization during AV node cell action potential (GO	44566	0.047813055
ventricular cardiac muscle cell differentiation (GO:0055012)	44566	0.047813055
postsynaptic density protein 95 clustering (GO:0097119)	44566	0.047813055
modulation by symbiont of host autophagy (GO:0075071)	44566	0.047813055
mRNA cleavage involved in gene silencing by miRNA (GO:0035279)	44566	0.047813055
calcium-dependent cell-cell adhesion via plasma membrane cell ad	13181	0.047980258
cyclic-nucleotide-mediated signaling (GO:0019935)	13181	0.047980258
positive regulation of cellular catabolic process (GO:0031331)	4/141	0.049418585
regulation of erythrocyte differentiation (GO:0045646)	13547	0.050404428
negative regulation of defense response (GO:0031348)	31107	0.050408304
B cell activation (GO:0042113)	31107	0.050408304
receptor-mediated endocytosis (GO:0006898)	4/143	0.051552994
negative regulation of phosphorylation (GO:0042326)	31472	0.051868957
regulation of interferon-gamma production (GO:0032649)	31472	0.051868957
glucose homeostasis (GO:0042593)	31472	0.051868957

regulation of protein kinase B signaling (GO:0051896)	5/207	0.052479632
regulation of dendrite development (GO:0050773)	14277	0.055381455
organophosphate biosynthetic process (GO:0090407)	14277	0.055381455
vesicle cytoskeletal trafficking (GO:0099518)	14277	0.055381455
cellular response to DNA damage stimulus (GO:0006974)	7/350	0.056195432
second-messenger-mediated signaling (GO:0019932)	32568	0.056372557
adiponectin-activated signaling pathway (GO:0033211)	44567	0.057099178
purine ribonucleoside catabolic process (GO:0046130)	44567	0.057099178
negative regulation of cellular response to hypoxia (GO:1900038)	44567	0.057099178
radial glial cell differentiation (GO:0060019)	44567	0.057099178
B cell chemotaxis (GO:0035754)	44567	0.057099178
regulation of cardiac muscle hypertrophy in response to stress (GO	44567	0.057099178
cardiac ventricle formation (GO:0003211)	44567	0.057099178
cellular response to cold (GO:0070417)	44567	0.057099178
negative regulation of relaxation of muscle (GO:1901078)	44567	0.057099178
negative regulation of sequestering of triglyceride (GO:0010891)	44567	0.057099178
regulation of hydrogen peroxide metabolic process (GO:0010310)	44567	0.057099178
nephron tubule development (GO:0072080)	44567	0.057099178
neurotransmitter-gated ion channel clustering (GO:0072578)	44567	0.057099178
neutrophil extravasation (GO:0072672)	44567	0.057099178
cobalamin transport (GO:0015889)	44567	0.057099178
regulation of macrophage apoptotic process (GO:2000109)	44567	0.057099178
dermatan sulfate proteoglycan metabolic process (GO:0050655)	44567	0.057099178
regulation of nuclease activity (GO:0032069)	44567	0.057099178
equilibrioception (GO:0050957)	44567	0.057099178
positive regulation of antigen processing and presentation (GO:000	44567	0.057099178
regulation of relaxation of cardiac muscle (GO:1901897)	44567	0.057099178
establishment of lymphocyte polarity (GO:0001767)	44567	0.057099178
positive regulation of dendritic cell antigen processing and present	44567	0.057099178
glycerol-3-phosphate metabolic process (GO:0006072)	44567	0.057099178
release of sequestered calcium ion into cytosol by sarcoplasmic ret	44567	0.057099178
positive regulation of heart rate by epinephrine-norepinephrine (G	44567	0.057099178
response to manganese ion (GO:0010042)	44567	0.057099178
histone H4-K12 acetylation (GO:0043983)	44567	0.057099178
succinate transmembrane transport (GO:0071422)	44567	0.057099178
lymphocyte apoptotic process (GO:0070227)	44567	0.057099178
maintenance of DNA repeat elements (GO:0043570)	44567	0.057099178
positive regulation of T cell differentiation in thymus (GO:0033089)	44567	0.057099178
postsynaptic density assembly (GO:0097107)	44567	0.057099178
vesicle localization (GO:0051648)	44567	0.057099178
presynaptic active zone organization (GO:1990709)	44567	0.057099178
positive regulation of autophagy (GO:0010508)	32933	0.057913868
positive regulation of double-strand break repair (GO:2000781)	14642	0.057932201
stem cell differentiation (GO:0048863)	14642	0.057932201
negative regulation of multicellular organismal process (GO:00512	5/214	0.058868976
positive regulation of supramolecular fiber organization (GO:19029	33298	0.059475007
regulation of endothelial cell proliferation (GO:0001936)	33664	0.061055834

T cell activation (GO:0042110)	33664	0.061055834
actin filament organization (GO:0007015)	4/152	0.061771806
phosphatidylinositol phosphate biosynthetic process (GO:0046854)	15373	0.063153
cellular response to lipid (GO:0071396)	5/219	0.063693677
positive regulation of protein kinase activity (GO:0045860)	4/154	0.064177858
positive regulation of cell motility (GO:2000147)	5/221	0.06568426
regulation of cell-cell adhesion (GO:0022407)	15738	0.065821038
ciliary basal body-plasma membrane docking (GO:0097711)	34759	0.065914995
negative regulation of catecholamine secretion (GO:0033604)	44568	0.0662952
negative regulation of cytoplasmic translation (GO:2000766)	44568	0.0662952
negative regulation of dendritic cell apoptotic process (GO:200066	44568	0.0662952
AV node cell action potential (GO:0086016)	44568	0.0662952
negative regulation of heart rate (GO:0010459)	44568	0.0662952
negative regulation of lymphocyte differentiation (GO:0045620)	44568	0.0662952
regulation of cGMP-mediated signaling (GO:0010752)	44568	0.0662952
negative regulation of nervous system process (GO:0031645)	44568	0.0662952
negative regulation of ruffle assembly (GO:1900028)	44568	0.0662952
regulation of glial cell differentiation (GO:0045685)	44568	0.0662952
negative regulation of stress-activated protein kinase signaling casc	44568	0.0662952
cleavage furrow formation (GO:0036089)	44568	0.0662952
regulation of lysosomal protein catabolic process (GO:1905165)	44568	0.0662952
regulation of microtubule binding (GO:1904526)	44568	0.0662952
dense core granule cytoskeletal transport (GO:0099519)	44568	0.0662952
pantothenate metabolic process (GO:0015939)	44568	0.0662952
parallel actin filament bundle assembly (GO:0030046)	44568	0.0662952
peptide transport (GO:0015833)	44568	0.0662952
piecemeal microautophagy of the nucleus (GO:0034727)	44568	0.0662952
positive regulation by symbiont of host autophagy (GO:0075044)	44568	0.0662952
epithelial cell differentiation involved in kidney development (GO:0	44568	0.0662952
regulation of respiratory system process (GO:0044065)	44568	0.0662952
positive regulation of cardiac muscle cell differentiation (GO:20007	44568	0.0662952
regulation of smooth muscle cell differentiation (GO:0051150)	44568	0.0662952
regulation of transforming growth factor beta1 production (GO:003	44568	0.0662952
positive regulation of epithelial tube formation (GO:1905278)	44568	0.0662952
release of sequestered calcium ion into cytosol by endoplasmic ret	44568	0.0662952
positive regulation of humoral immune response (GO:0002922)	44568	0.0662952
positive regulation of interleukin-5 production (GO:0032754)	44568	0.0662952
inhibition of cysteine-type endopeptidase activity (GO:0097340)	44568	0.0662952
late nucleophagy (GO:0044805)	44568	0.0662952
somatic recombination of immunoglobulin gene segments (GO:001	44568	0.0662952
succinate transport (GO:0015744)	44568	0.0662952
lysosomal microautophagy (GO:0016237)	44568	0.0662952
positive regulation of respiratory burst (GO:0060267)	44568	0.0662952
positive regulation of synaptic transmission, GABAergic (GO:00322	44568	0.0662952
miRNA loading onto RISC involved in gene silencing by miRNA (GO:	44568	0.0662952
positive regulation of urine volume (GO:0035810)	44568	0.0662952
ureter development (GO:0072189)	44568	0.0662952

vascular wound healing (GO:0061042)	44568	0.0662952
cardiac ventricle morphogenesis (GO:0003208)	16103	0.068526185
mRNA stabilization (GO:0048255)	16103	0.068526185
organonitrogen compound biosynthetic process (GO:1901566)	4/158	0.069135512
response to lipopolysaccharide (GO:0032496)	4/159	0.070405026
regulation of DNA repair (GO:0006282)	16469	0.071267471
positive regulation of nervous system development (GO:0051962)	16469	0.071267471
positive regulation of protein kinase B signaling (GO:0051897)	4/161	0.072979882
regulation of B cell proliferation (GO:0030888)	16834	0.074043944
regulation of synaptic transmission, glutamatergic (GO:0051966)	16834	0.074043944
negative regulation of appetite (GO:0032099)	44569	0.075401991
axon extension involved in axon guidance (GO:0048846)	44569	0.075401991
negative regulation of muscle cell differentiation (GO:0051148)	44569	0.075401991
regulation of collateral sprouting (GO:0048670)	44569	0.075401991
regulation of cytoplasmic translational elongation (GO:1900247)	44569	0.075401991
regulation of dendritic cell chemotaxis (GO:2000508)	44569	0.075401991
negative regulation of regulated secretory pathway (GO:1903306)	44569	0.075401991
regulation of intestinal cholesterol absorption (GO:0030300)	44569	0.075401991
neuron projection extension involved in neuron projection guidanc	44569	0.075401991
dendritic spine maintenance (GO:0097062)	44569	0.075401991
DNA damage induced protein phosphorylation (GO:0006975)	44569	0.075401991
regulation of nitric oxide metabolic process (GO:0080164)	44569	0.075401991
phosphatidylinositol-3-phosphate biosynthetic process (GO:00360	44569	0.075401991
positive regulation of cell migration by vascular endothelial growth	44569	0.075401991
fructose metabolic process (GO:0006000)	44569	0.075401991
positive regulation of dendritic cell chemotaxis (GO:2000510)	44569	0.075401991
positive regulation of extracellular matrix disassembly (GO:009009	44569	0.075401991
heparan sulfate proteoglycan biosynthetic process, polysaccharide	44569	0.075401991
positive regulation of leukocyte differentiation (GO:1902107)	44569	0.075401991
immunological synapse formation (GO:0001771)	44569	0.075401991
RNA secondary structure unwinding (GO:0010501)	44569	0.075401991
positive regulation of MHC class II biosynthetic process (GO:00453	44569	0.075401991
isoprenoid metabolic process (GO:0006720)	44569	0.075401991
mast cell activation involved in immune response (GO:0002279)	44569	0.075401991
mast cell degranulation (GO:0043303)	44569	0.075401991
venous blood vessel development (GO:0060841)	44569	0.075401991
postsynaptic density organization (GO:0097106)	44569	0.075401991
natural killer cell differentiation (GO:0001779)	44569	0.075401991
innate immune response (GO:0045087)	6/302	0.07592924
regulation of cellular metabolic process (GO:0031323)	17199	0.076854665
polyol metabolic process (GO:0019751)	17199	0.076854665
regulation of T cell activation (GO:0050863)	17199	0.076854665
MAPK cascade (GO:0000165)	6/303	0.076868414
double-strand break repair (GO:0006302)	4/164	0.076931069
heart development (GO:0007507)	4/164	0.076931069
phosphatidic acid biosynthetic process (GO:0006654)	17564	0.07969871
positive regulation of DNA repair (GO:0045739)	17564	0.07969871

inositol phosphate metabolic process (GO:0043647)	17564	0.07969871
adherens junction organization (GO:0034332)	17930	0.082575171
oligosaccharide metabolic process (GO:0009311)	17930	0.082575171
activation of GTPase activity (GO:0090630)	3/105	0.083329436
positive regulation of cellular metabolic process (GO:0031325)	3/105	0.083329436
adenosine metabolic process (GO:0046085)	44570	0.084420412
regulation of cell adhesion molecule production (GO:0060353)	44570	0.084420412
regulation of cellular extravasation (GO:0002691)	44570	0.084420412
regulation of dendritic cell antigen processing and presentation (G(	44570	0.084420412
negative regulation of smooth muscle cell differentiation (GO:0051	44570	0.084420412
regulation of glucan biosynthetic process (GO:0010962)	44570	0.084420412
cellular response to muramyl dipeptide (GO:0071225)	44570	0.084420412
cellular response to nitric oxide (GO:0071732)	44570	0.084420412
cellular response to reactive nitrogen species (GO:1902170)	44570	0.084420412
neuronal ion channel clustering (GO:0045161)	44570	0.084420412
regulation of lipid transport (GO:0032368)	44570	0.084420412
DNA topological change (GO:0006265)	44570	0.084420412
embryonic digestive tract morphogenesis (GO:0048557)	44570	0.084420412
endochondral ossification (GO:0001958)	44570	0.084420412
positive regulation of ATP biosynthetic process (GO:2001171)	44570	0.084420412
positive regulation of autophagy of mitochondrion (GO:1903599)	44570	0.084420412
regulation of skeletal muscle cell differentiation (GO:2001014)	44570	0.084420412
regulation of sterol biosynthetic process (GO:0106118)	44570	0.084420412
fructose 1,6-bisphosphate metabolic process (GO:0030388)	44570	0.084420412
positive regulation of fatty acid beta-oxidation (GO:0032000)	44570	0.084420412
response to magnesium ion (GO:0032026)	44570	0.084420412
isoprenoid biosynthetic process (GO:0008299)	44570	0.084420412
small RNA loading onto RISC (GO:0070922)	44570	0.084420412
sympathetic ganglion development (GO:0061549)	44570	0.084420412
mast cell mediated immunity (GO:0002448)	44570	0.084420412
postsynaptic membrane assembly (GO:0097104)	44570	0.084420412
muscle cell fate commitment (GO:0042693)	44570	0.084420412
chromosome organization (GO:0051276)	3/106	0.085169701
actin polymerization or depolymerization (GO:0008154)	18295	0.085483152
neuron migration (GO:0001764)	18295	0.085483152
organic hydroxy compound biosynthetic process (GO:1901617)	18295	0.085483152
phosphatidic acid metabolic process (GO:0046473)	18295	0.085483152
positive regulation of cell morphogenesis involved in differentiatio	18295	0.085483152
response to calcium ion (GO:0051592)	3/107	0.087027254
modulation of chemical synaptic transmission (GO:0050804)	3/109	0.09079352
regulation of interleukin-6 production (GO:0032675)	3/110	0.092701877
acetyl-CoA biosynthetic process (GO:0006085)	44571	0.093351317
negative regulation of cAMP-mediated signaling (GO:0043951)	44571	0.093351317
negative regulation of cell adhesion mediated by integrin (GO:0033	44571	0.093351317
adherens junction assembly (GO:0034333)	44571	0.093351317
negative regulation of cholesterol storage (GO:0010887)	44571	0.093351317
regulation of actin filament-based movement (GO:1903115)	44571	0.093351317

apical protein localization (GO:0045176)	44571	0.093351317
negative regulation of glycolytic process (GO:0045820)	44571	0.093351317
B cell homeostasis (GO:0001782)	44571	0.093351317
regulation of cell-cell adhesion mediated by integrin (GO:0033632)	44571	0.093351317
negative regulation of lymphocyte apoptotic process (GO:0070229	44571	0.093351317
negative regulation of purine nucleotide metabolic process (GO:19	44571	0.093351317
negative regulation of toll-like receptor 4 signaling pathway (GO:0(	44571	0.093351317
regulation of high voltage-gated calcium channel activity (GO:1901	44571	0.093351317
negative regulation of transforming growth factor beta production	44571	0.093351317
neuron projection maintenance (GO:1990535)	44571	0.093351317
chondroitin sulfate proteoglycan metabolic process (GO:0050654)	44571	0.093351317
chylomicron assembly (GO:0034378)	44571	0.093351317
defense response to tumor cell (GO:0002357)	44571	0.093351317
regulation of neutrophil migration (GO:1902622)	44571	0.093351317
phagosome-lysosome fusion (GO:0090385)	44571	0.093351317
positive regulation of behavior (GO:0048520)	44571	0.093351317
fructose 6-phosphate metabolic process (GO:0006002)	44571	0.093351317
positive regulation of dendritic spine morphogenesis (GO:0061003	44571	0.093351317
regulation of type B pancreatic cell development (GO:2000074)	44571	0.093351317
regulation of urine volume (GO:0035809)	44571	0.093351317
granulocyte migration (GO:0097530)	44571	0.093351317
sarcoplasmic reticulum calcium ion transport (GO:0070296)	44571	0.093351317
positive regulation of protein sumoylation (GO:0033235)	44571	0.093351317
positive regulation of skeletal muscle tissue development (GO:004	44571	0.093351317
presynaptic membrane assembly (GO:0097105)	44571	0.093351317
positive regulation of DNA-binding transcription factor activity (GO	5/246	0.093447472
heart morphogenesis (GO:0003007)	19391	0.094387486
positive regulation of metabolic process (GO:0009893)	3/113	0.098525688
sulfur compound biosynthetic process (GO:0044272)	3/113	0.098525688
glycoprotein metabolic process (GO:0009100)	20121	0.10046554
negative regulation of calcium ion transmembrane transport (GO:1	44572	0.102195548
angiogenesis involved in wound healing (GO:0060055)	44572	0.102195548
regulation of cardiac muscle cell differentiation (GO:2000725)	44572	0.102195548
cell proliferation in forebrain (GO:0021846)	44572	0.102195548
cell-cell junction maintenance (GO:0045217)	44572	0.102195548
regulation of dendritic cell apoptotic process (GO:2000668)	44572	0.102195548
cellular response to increased oxygen levels (GO:0036295)	44572	0.102195548
negative regulation of translation, ncRNA-mediated (GO:0040033)	44572	0.102195548
peptidyl-lysine monomethylation (GO:0018026)	44572	0.102195548
phosphorylated carbohydrate dephosphorylation (GO:0046838)	44572	0.102195548
positive regulation of cellular extravasation (GO:0002693)	44572	0.102195548
regulation of toll-like receptor 9 signaling pathway (GO:0034163)	44572	0.102195548
positive regulation of dendrite development (GO:1900006)	44572	0.102195548
positive regulation of integrin activation (GO:0033625)	44572	0.102195548
response to prostaglandin E (GO:0034695)	44572	0.102195548
inositol phosphate biosynthetic process (GO:0032958)	44572	0.102195548
inositol phosphate dephosphorylation (GO:0046855)	44572	0.102195548

T cell chemotaxis (GO:0010818)	44572	0.102195548
miRNA mediated inhibition of translation (GO:0035278)	44572	0.102195548
UDP-N-acetylglucosamine biosynthetic process (GO:0006048)	44572	0.102195548
postsynapse assembly (GO:0099068)	44572	0.102195548
presynaptic membrane organization (GO:0097090)	44572	0.102195548
negative regulation of cytokine production (GO:0001818)	4/182	0.102803
positive regulation of cell projection organization (GO:0031346)	3/117	0.106514338
regulation of mitotic nuclear division (GO:0007088)	20852	0.106649384
dicarboxylic acid metabolic process (GO:0043648)	20852	0.106649384
negative regulation of response to external stimulus (GO:0032102)	3/118	0.10855019
muscle organ development (GO:0007517)	21217	0.109778988
negative regulation of B cell proliferation (GO:0030889)	44573	0.110953945
negative regulation of cardiac muscle hypertrophy (GO:0010614)	44573	0.110953945
purine nucleotide biosynthetic process (GO:0006164)	44573	0.110953945
amino sugar biosynthetic process (GO:0046349)	44573	0.110953945
regulation of alcohol biosynthetic process (GO:1902930)	44573	0.110953945
regulation of B cell apoptotic process (GO:0002902)	44573	0.110953945
regulation of cell communication by electrical coupling involved in	44573	0.110953945
negative regulation of leukocyte apoptotic process (GO:2000107)	44573	0.110953945
cell cycle checkpoint signaling (GO:0000075)	44573	0.110953945
cellular response to fluid shear stress (GO:0071498)	44573	0.110953945
regulation of glycogen metabolic process (GO:0070873)	44573	0.110953945
regulation of leukocyte cell-cell adhesion (GO:1903037)	44573	0.110953945
regulation of MHC class II biosynthetic process (GO:0045346)	44573	0.110953945
digestive system development (GO:0055123)	44573	0.110953945
phagolysosome assembly (GO:0001845)	44573	0.110953945
phosphate ion transmembrane transport (GO:0035435)	44573	0.110953945
endoplasmic reticulum membrane organization (GO:0090158)	44573	0.110953945
positive regulation of actin filament depolymerization (GO:003083(	44573	0.110953945
regulation of pseudopodium assembly (GO:0031272)	44573	0.110953945
ethanol oxidation (GO:0006069)	44573	0.110953945
regulation of sister chromatid cohesion (GO:0007063)	44573	0.110953945
positive regulation of cardiocyte differentiation (GO:1905209)	44573	0.110953945
ganglion development (GO:0061548)	44573	0.110953945
regulation of vascular associated smooth muscle cell migration (GC	44573	0.110953945
positive regulation of fatty acid oxidation (GO:0046321)	44573	0.110953945
inositol phosphate catabolic process (GO:0071545)	44573	0.110953945
keratan sulfate catabolic process (GO:0042340)	44573	0.110953945
smooth muscle cell differentiation (GO:0051145)	44573	0.110953945
positive regulation of protein depolymerization (GO:1901881)	44573	0.110953945
positive regulation of pseudopodium assembly (GO:0031274)	44573	0.110953945
melanocyte differentiation (GO:0030318)	44573	0.110953945
toll-like receptor 3 signaling pathway (GO:0034138)	44573	0.110953945
mesoderm morphogenesis (GO:0048332)	44573	0.110953945
tricarboxylic acid metabolic process (GO:0072350)	44573	0.110953945
mitotic G1/S transition checkpoint signaling (GO:0044819)	44573	0.110953945
very-low-density lipoprotein particle assembly (GO:0034379)	44573	0.110953945

presynapse organization (GO:0099172)	44573	0.110953945
regulation of secretion by cell (GO:1903530)	21582	0.112932678
selective autophagy (GO:0061912)	21582	0.112932678
mitotic DNA damage checkpoint signaling (GO:0044773)	21582	0.112932678
positive regulation of epithelial cell proliferation (GO:0050679)	3/123	0.118952201
regulation of protein phosphorylation (GO:0001932)	5/266	0.119345505
alpha-linolenic acid metabolic process (GO:0036109)	44574	0.119627334
purine-containing compound salvage (GO:0043101)	44574	0.119627334
atrial cardiac muscle cell action potential (GO:0086014)	44574	0.119627334
regulation of cell communication by electrical coupling (GO:001064	44574	0.119627334
negative regulation of macrophage derived foam cell differentiatio	44574	0.119627334
cellular component maintenance (GO:0043954)	44574	0.119627334
negative regulation of reactive oxygen species biosynthetic process	44574	0.119627334
central nervous system neuron axonogenesis (GO:0021955)	44574	0.119627334
central nervous system projection neuron axonogenesis (GO:0021	44574	0.119627334
endochondral bone morphogenesis (GO:0060350)	44574	0.119627334
positive regulation of calcium ion-dependent exocytosis (GO:0045	44574	0.119627334
regulation of T cell differentiation in thymus (GO:0033081)	44574	0.119627334
response to muramyl dipeptide (GO:0032495)	44574	0.119627334
homeostasis of number of cells (GO:0048872)	44574	0.119627334
reticulophagy (GO:0061709)	44574	0.119627334
semaphorin-plexin signaling pathway involved in neuron projectior	44574	0.119627334
lipid oxidation (GO:0034440)	44574	0.119627334
positive regulation of purine nucleotide biosynthetic process (GO:1	44574	0.119627334
positive regulation of ruffle assembly (GO:1900029)	44574	0.119627334
UDP-N-acetylglucosamine metabolic process (GO:0006047)	44574	0.119627334
fatty acid metabolic process (GO:0006631)	3/124	0.121075827
regulation of neurogenesis (GO:0050767)	22678	0.122530712
cellular response to oxidative stress (GO:0034599)	3/125	0.123213416
protein localization to membrane (GO:0072657)	4/195	0.123655102
negative regulation of cell growth (GO:0030308)	3/126	0.125364777
synapse organization (GO:0050808)	3/126	0.125364777
actin cytoskeleton reorganization (GO:0031532)	23043	0.125773258
cell cycle G1/S phase transition (GO:0044843)	23043	0.125773258
monocarboxylic acid biosynthetic process (GO:0072330)	23043	0.125773258
cellular protein modification process (GO:0006464)	14/1025	0.1282057
2-oxoglutarate metabolic process (GO:0006103)	44575	0.128216537
negative regulation of interleukin-12 production (GO:0032695)	44575	0.128216537
C4-dicarboxylate transport (GO:0015740)	44575	0.128216537
cAMP metabolic process (GO:0046058)	44575	0.128216537
cardiac left ventricle morphogenesis (GO:0003214)	44575	0.128216537
cell junction maintenance (GO:0034331)	44575	0.128216537
negative regulation of pri-miRNA transcription by RNA polymerase	44575	0.128216537
regulation of fatty acid beta-oxidation (GO:0031998)	44575	0.128216537
negative regulation of smooth muscle cell migration (GO:0014912)	44575	0.128216537
negative regulation of TORC1 signaling (GO:1904262)	44575	0.128216537
negative regulation of viral transcription (GO:0032897)	44575	0.128216537

neuromuscular process controlling balance (GO:0050885)	44575	0.128216537
regulation of lamellipodium organization (GO:1902743)	44575	0.128216537
coenzyme A metabolic process (GO:0015936)	44575	0.128216537
ovarian follicle development (GO:0001541)	44575	0.128216537
pancreas development (GO:0031016)	44575	0.128216537
regulation of response to endoplasmic reticulum stress (GO:19058	44575	0.128216537
positive regulation of cardiac muscle cell proliferation (GO:006004	44575	0.128216537
positive regulation of glycoprotein biosynthetic process (GO:00105	44575	0.128216537
sulfate transport (GO:0008272)	44575	0.128216537
positive regulation of protein-containing complex disassembly (GO	44575	0.128216537
positive regulation of T cell receptor signaling pathway (GO:00508	44575	0.128216537
microvillus organization (GO:0032528)	44575	0.128216537
vascular endothelial growth factor signaling pathway (GO:0038084	44575	0.128216537
pre-miRNA processing (GO:0031054)	44575	0.128216537
negative regulation of intrinsic apoptotic signaling pathway (GO:20	23408	0.129036207
regulation of cilium assembly (GO:1902017)	23408	0.129036207
regulation of extrinsic apoptotic signaling pathway (GO:2001236)	23408	0.129036207
lipid homeostasis (GO:0055088)	23408	0.129036207
microtubule cytoskeleton organization involved in mitosis (GO:190	3/128	0.129708048
regulation of cell-matrix adhesion (GO:0001952)	23774	0.13231886
steroid biosynthetic process (GO:0006694)	23774	0.13231886
regulation of response to external stimulus (GO:0032101)	3/130	0.134104103
positive regulation of canonical Wnt signaling pathway (GO:00902	3/130	0.134104103
protein glycosylation (GO:0006486)	3/130	0.134104103
cellular response to nutrient levels (GO:0031669)	24139	0.135620526
regulation of cytoplasmic translation (GO:2000765)	44576	0.136722367
cellular response to arsenic-containing substance (GO:0071243)	44576	0.136722367
cellular response to exogenous dsRNA (GO:0071360)	44576	0.136722367
regulation of extracellular matrix disassembly (GO:0010715)	44576	0.136722367
regulation of integrin activation (GO:0033623)	44576	0.136722367
regulation of lymphocyte activation (GO:0051249)	44576	0.136722367
regulation of macrophage differentiation (GO:0045649)	44576	0.136722367
dermatan sulfate proteoglycan biosynthetic process (GO:0050651)	44576	0.136722367
phosphatidylethanolamine biosynthetic process (GO:0006646)	44576	0.136722367
regulation of sequestering of triglyceride (GO:0010889)	44576	0.136722367
positive regulation of cell killing (GO:0031343)	44576	0.136722367
regulation of synaptic transmission, GABAergic (GO:0032228)	44576	0.136722367
ganglioside biosynthetic process (GO:0001574)	44576	0.136722367
histone H4-K5 acetylation (GO:0043981)	44576	0.136722367
histone H4-K8 acetylation (GO:0043982)	44576	0.136722367
steroid hormone mediated signaling pathway (GO:0043401)	44576	0.136722367
microvillus assembly (GO:0030033)	44576	0.136722367
vitamin D metabolic process (GO:0042359)	44576	0.136722367
regulation of angiogenesis (GO:0045765)	4/203	0.137312617
regulation of myeloid cell differentiation (GO:0045637)	24869	0.142278203
apoptotic DNA fragmentation (GO:0006309)	44577	0.145145629
regulation of ATP biosynthetic process (GO:2001169)	44577	0.145145629

autophagy of nucleus (GO:0044804)	44577	0.145145629
regulation of ceramide biosynthetic process (GO:2000303)	44577	0.145145629
regulation of cholesterol storage (GO:0010885)	44577	0.145145629
negative regulation of release of cytochrome c from mitochondria	44577	0.145145629
regulation of fatty acid oxidation (GO:0046320)	44577	0.145145629
regulation of interleukin-1 production (GO:0032652)	44577	0.145145629
regulation of interleukin-13 production (GO:0032656)	44577	0.145145629
neuron cell-cell adhesion (GO:0007158)	44577	0.145145629
neuron projection organization (GO:0106027)	44577	0.145145629
dendritic cell chemotaxis (GO:0002407)	44577	0.145145629
digestive tract morphogenesis (GO:0048546)	44577	0.145145629
regulation of neurotransmitter transport (GO:0051588)	44577	0.145145629
polyol biosynthetic process (GO:0046173)	44577	0.145145629
epiboly involved in wound healing (GO:0090505)	44577	0.145145629
positive regulation of double-strand break repair via nonhomologo	44577	0.145145629
positive regulation of myeloid leukocyte cytokine production involv	44577	0.145145629
sympathetic nervous system development (GO:0048485)	44577	0.145145629
positive regulation of small molecule metabolic process (GO:00620	44577	0.145145629
mesenchyme development (GO:0060485)	44577	0.145145629
cell chemotaxis (GO:0060326)	25235	0.145632891
cellular response to calcium ion (GO:0071277)	25235	0.145632891
synapse assembly (GO:0007416)	25235	0.145632891
positive regulation of protein polymerization (GO:0032273)	25235	0.145632891
protein localization to plasma membrane (GO:0072659)	3/136	0.147593566
organic substance transport (GO:0071702)	3/136	0.147593566
mitotic cell cycle phase transition (GO:0044772)	4/209	0.147938479
carbohydrate homeostasis (GO:0033500)	25600	0.149003951
sterol metabolic process (GO:0016125)	25600	0.149003951
regulation of glycolytic process (GO:0006110)	25965	0.152390749
negative regulation of ATP metabolic process (GO:1903579)	44578	0.15348712
acyl-CoA biosynthetic process (GO:0071616)	44578	0.15348712
negative regulation of interleukin-10 production (GO:0032693)	44578	0.15348712
regulation of cell killing (GO:0031341)	44578	0.15348712
regulation of cholesterol biosynthetic process (GO:0045540)	44578	0.15348712
negative regulation of vascular associated smooth muscle cell proli	44578	0.15348712
negative regulation of viral entry into host cell (GO:0046597)	44578	0.15348712
regulation of osteoblast proliferation (GO:0033688)	44578	0.15348712
phosphate ion transport (GO:0006817)	44578	0.15348712
positive regulation of cardiac muscle tissue growth (GO:0055023)	44578	0.15348712
regulation of stem cell proliferation (GO:0072091)	44578	0.15348712
regulation of transferase activity (GO:0051338)	44578	0.15348712
positive regulation of dendrite extension (GO:1903861)	44578	0.15348712
positive regulation of heart rate (GO:0010460)	44578	0.15348712
ribosomal small subunit assembly (GO:0000028)	44578	0.15348712
RNA interference (GO:0016246)	44578	0.15348712
ruffle organization (GO:0031529)	44578	0.15348712
positive regulation of regulated secretory pathway (GO:1903307)	44578	0.15348712

maturation of 5.8S rRNA (GO:0000460)	44578	0.15348712
membrane depolarization during cardiac muscle cell action potenti	44578	0.15348712
vasculature development (GO:0001944)	44578	0.15348712
positive regulation of protein phosphorylation (GO:0001934)	6/371	0.155503869
negative regulation of supramolecular fiber organization (GO:1902	26330	0.155792662
positive regulation of neurogenesis (GO:0050769)	26330	0.155792662
protein localization to cell periphery (GO:1990778)	3/140	0.156822221
positive regulation of GTPase activity (GO:0043547)	4/214	0.157029382
regulation of actin filament polymerization (GO:0030833)	26696	0.159209078
endoplasmic reticulum organization (GO:0007029)	26696	0.159209078
positive regulation of JNK cascade (GO:0046330)	26696	0.159209078
chromatin organization (GO:0006325)	3/142	0.161502643
negative regulation of biosynthetic process (GO:0009890)	44579	0.16174763
regulation of B cell differentiation (GO:0045577)	44579	0.16174763
regulation of dendrite extension (GO:1903859)	44579	0.16174763
cellular response to dsRNA (GO:0071359)	44579	0.16174763
dendritic cell migration (GO:0036336)	44579	0.16174763
DNA conformation change (GO:0071103)	44579	0.16174763
phosphatidylglycerol acyl-chain remodeling (GO:0036148)	44579	0.16174763
phosphatidylinositol acyl-chain remodeling (GO:0036149)	44579	0.16174763
regulation of protein sumoylation (GO:0033233)	44579	0.16174763
regulation of protein-containing complex disassembly (GO:004324	44579	0.16174763
positive regulation of CREB transcription factor activity (GO:00327	44579	0.16174763
regulation of vascular endothelial cell proliferation (GO:1905562)	44579	0.16174763
positive regulation of excitatory postsynaptic potential (GO:20004	44579	0.16174763
positive regulation of extracellular matrix organization (GO:190305	44579	0.16174763
positive regulation of fatty acid metabolic process (GO:0045923)	44579	0.16174763
positive regulation of myoblast differentiation (GO:0045663)	44579	0.16174763
positive regulation of nervous system process (GO:0031646)	44579	0.16174763
positive regulation of nitric-oxide synthase activity (GO:0051000)	44579	0.16174763
T cell migration (GO:0072678)	44579	0.16174763
positive regulation of synaptic transmission, glutamatergic (GO:005	44579	0.16174763
microtubule depolymerization (GO:0007019)	44579	0.16174763
negative regulation of nucleic acid-templated transcription (GO:19	7/464	0.168829429
phospholipid metabolic process (GO:0006644)	27791	0.169539381
water-soluble vitamin metabolic process (GO:0006767)	27791	0.169539381
purine ribonucleoside bisphosphate metabolic process (GO:003403	44580	0.169927941
negative regulation of cytokine production involved in inflammator	44580	0.169927941
regulation of autophagy of mitochondrion (GO:1903146)	44580	0.169927941
negative regulation of T cell receptor signaling pathway (GO:00508	44580	0.169927941
neural crest cell differentiation (GO:0014033)	44580	0.169927941
nucleotide-sugar biosynthetic process (GO:0009226)	44580	0.169927941
peptidyl-lysine dimethylation (GO:0018027)	44580	0.169927941
regulation of oligodendrocyte differentiation (GO:0048713)	44580	0.169927941
ethanol metabolic process (GO:0006067)	44580	0.169927941
excitatory postsynaptic potential (GO:0060079)	44580	0.169927941
glycerolipid catabolic process (GO:0046503)	44580	0.169927941

response to fatty acid (GO:0070542)	44580	0.169927941
heparan sulfate proteoglycan biosynthetic process (GO:0015012)	44580	0.169927941
histone H4-K16 acetylation (GO:0043984)	44580	0.169927941
positive regulation of leukocyte activation (GO:0002696)	44580	0.169927941
positive regulation of neutrophil chemotaxis (GO:0090023)	44580	0.169927941
striated muscle cell differentiation (GO:0051146)	44580	0.169927941
telomere capping (GO:0016233)	44580	0.169927941
vesicle transport along actin filament (GO:0030050)	44580	0.169927941
purine ribonucleotide metabolic process (GO:0009150)	28157	0.173007895
regulation of organelle assembly (GO:1902115)	28157	0.173007895
positive regulation of phosphatidylinositol 3-kinase signaling (GO:0	28157	0.173007895
positive regulation of protein modification by small protein conjuga	28157	0.173007895
positive regulation of transferase activity (GO:0051347)	3/148	0.175789963
protein modification process (GO:0036211)	28522	0.176488004
negative regulation of blood vessel morphogenesis (GO:2000181)	28522	0.176488004
adrenergic receptor signaling pathway (GO:0071875)	44581	0.178028828
negative regulation of lipid storage (GO:0010888)	44581	0.178028828
negative regulation of osteoclast differentiation (GO:0045671)	44581	0.178028828
regulation of granulocyte chemotaxis (GO:0071622)	44581	0.178028828
negative regulation of viral life cycle (GO:1903901)	44581	0.178028828
regulation of lymphocyte differentiation (GO:0045619)	44581	0.178028828
nucleobase-containing compound biosynthetic process (GO:00346	44581	0.178028828
regulation of nuclear division (GO:0051783)	44581	0.178028828
embryonic digestive tract development (GO:0048566)	44581	0.178028828
energy reserve metabolic process (GO:0006112)	44581	0.178028828
ganglioside metabolic process (GO:0001573)	44581	0.178028828
positive regulation of lymphocyte differentiation (GO:0045621)	44581	0.178028828
inositol phosphate-mediated signaling (GO:0048016)	44581	0.178028828
skeletal muscle contraction (GO:0003009)	44581	0.178028828
positive regulation of nitrogen compound metabolic process (GO:0	44581	0.178028828
lipopolysaccharide-mediated signaling pathway (GO:0031663)	44581	0.178028828
positive regulation of protein processing (GO:0010954)	44581	0.178028828
mesoderm formation (GO:0001707)	44581	0.178028828
post-transcriptional gene silencing by RNA (GO:0035194)	44581	0.178028828
production of small RNA involved in gene silencing by RNA (GO:007	44581	0.178028828
positive regulation of hydrolase activity (GO:0051345)	3/149	0.178205077
regulation of ion transport (GO:0043269)	28887	0.179979158
actin filament-based transport (GO:0099515)	44582	0.186051057
actin nucleation (GO:0045010)	44582	0.186051057
regulation of cardiac muscle cell proliferation (GO:0060043)	44582	0.186051057
regulation of cholesterol metabolic process (GO:0090181)	44582	0.186051057
negative regulation of peptidyl-serine phosphorylation (GO:003313	44582	0.186051057
regulation of dendritic spine development (GO:0060998)	44582	0.186051057
cellular response to inorganic substance (GO:0071241)	44582	0.186051057
neuron apoptotic process (GO:0051402)	44582	0.186051057
chondroitin sulfate biosynthetic process (GO:0030206)	44582	0.186051057
cobalamin metabolic process (GO:0009235)	44582	0.186051057

endocardial cushion development (GO:0003197)	44582	0.186051057
positive regulation of antigen receptor-mediated signaling pathwa	44582	0.186051057
focal adhesion assembly (GO:0048041)	44582	0.186051057
positive regulation of glycolytic process (GO:0045821)	44582	0.186051057
positive regulation of immune system process (GO:0002684)	44582	0.186051057
positive regulation of phosphatase activity (GO:0010922)	44582	0.186051057
spindle assembly checkpoint signaling (GO:0071173)	44582	0.186051057
linoleic acid metabolic process (GO:0043651)	44582	0.186051057
positive regulation of purine nucleotide metabolic process (GO:190	44582	0.186051057
mitotic spindle assembly checkpoint signaling (GO:0007094)	44582	0.186051057
mitotic spindle checkpoint signaling (GO:0071174)	44582	0.186051057
myotube differentiation (GO:0014902)	44582	0.186051057
positive regulation of tumor necrosis factor superfamily cytokine p	29618	0.186992437
positive regulation of Wnt signaling pathway (GO:0030177)	3/153	0.187955481
negative regulation of cellular process (GO:0048523)	8/566	0.189216515
cell-cell junction organization (GO:0045216)	29983	0.190513506
regulation of G protein-coupled receptor signaling pathway (GO:00	29983	0.190513506
positive regulation of cytoskeleton organization (GO:0051495)	29983	0.190513506
positive regulation of protein ubiquitination (GO:0031398)	29983	0.190513506
negative regulation of mitotic metaphase/anaphase transition (GO	44583	0.19399539
negative regulation of phosphate metabolic process (GO:0045936)	44583	0.19399539
osteoclast differentiation (GO:0030316)	44583	0.19399539
positive regulation of axon extension (GO:0045773)	44583	0.19399539
positive regulation of calcium ion transmembrane transporter activ	44583	0.19399539
fatty-acyl-CoA metabolic process (GO:0035337)	44583	0.19399539
female gonad development (GO:0008585)	44583	0.19399539
positive regulation of dendritic spine development (GO:0060999)	44583	0.19399539
regulation of vacuole organization (GO:0044088)	44583	0.19399539
glutathione derivative biosynthetic process (GO:1901687)	44583	0.19399539
glutathione derivative metabolic process (GO:1901685)	44583	0.19399539
regulation of viral release from host cell (GO:1902186)	44583	0.19399539
positive regulation of granulocyte chemotaxis (GO:0071624)	44583	0.19399539
positive regulation of lipid catabolic process (GO:0050996)	44583	0.19399539
positive regulation of neutrophil migration (GO:1902624)	44583	0.19399539
positive regulation of peptidase activity (GO:0010952)	44583	0.19399539
tetrapyrrole metabolic process (GO:0033013)	44583	0.19399539
regulation of interleukin-1 beta production (GO:0032651)	30348	0.194043505
positive regulation of plasma membrane bounded cell projection a	30348	0.194043505
long-chain fatty acid metabolic process (GO:0001676)	30348	0.194043505
spindle assembly (GO:0051225)	30713	0.19758193
mitotic spindle organization (GO:0007052)	3/157	0.197840901
cellular response to starvation (GO:0009267)	3/158	0.200331974
regulation of cell cycle G2/M phase transition (GO:1902749)	31079	0.201128283
G1/S transition of mitotic cell cycle (GO:0000082)	31079	0.201128283
negative regulation of G protein-coupled receptor signaling pathwa	44584	0.201862577
negative regulation of GTPase activity (GO:0034260)	44584	0.201862577
negative regulation of reactive oxygen species metabolic process ((	44584	0.201862577

cytoskeleton-dependent intracellular transport (GO:0030705)	44584	0.201862577
DNA catabolic process, endonucleolytic (GO:0000737)	44584	0.201862577
regulation of peptidase activity (GO:0052547)	44584	0.201862577
regulation of release of sequestered calcium ion into cytosol by sar	44584	0.201862577
regulation of toll-like receptor 4 signaling pathway (GO:0034143)	44584	0.201862577
positive regulation of morphogenesis of an epithelium (GO:190533	44584	0.201862577
positive regulation of receptor internalization (GO:0002092)	44584	0.201862577
mitotic cell cycle checkpoint signaling (GO:0007093)	44584	0.201862577
transmembrane receptor protein tyrosine kinase signaling pathwa	6/404	0.20290844
regulation of neuron death (GO:1901214)	31444	0.204682078
positive regulation of endothelial cell migration (GO:0010595)	31444	0.204682078
negative regulation of angiogenesis (GO:0016525)	31809	0.208242834
purine ribonucleotide catabolic process (GO:0009154)	44585	0.209653365
apoptotic nuclear changes (GO:0030262)	44585	0.209653365
canonical glycolysis (GO:0061621)	44585	0.209653365
cardiac muscle cell differentiation (GO:0055007)	44585	0.209653365
negative regulation of ossification (GO:0030279)	44585	0.209653365
neuromuscular junction development (GO:0007528)	44585	0.209653365
dendritic cell differentiation (GO:0097028)	44585	0.209653365
phospholipid catabolic process (GO:0009395)	44585	0.209653365
positive regulation of carbohydrate metabolic process (GO:004591	44585	0.209653365
glucose catabolic process to pyruvate (GO:0061718)	44585	0.209653365
positive regulation of lamellipodium assembly (GO:0010592)	44585	0.209653365
immune response-activating cell surface receptor signaling pathwa	44585	0.209653365
positive regulation of p38MAPK cascade (GO:1900745)	44585	0.209653365
wound healing, spreading of cells (GO:0044319)	44585	0.209653365
protein K48-linked deubiquitination (GO:0071108)	44585	0.209653365
positive regulation of neuron projection development (GO:001097	32174	0.211810082
regulation of endothelial cell migration (GO:0010594)	32540	0.215383359
3'-phosphoadenosine 5'-phosphosulfate metabolic process (GO:00	44586	0.217368492
negative regulation of antigen receptor-mediated signaling pathwa	44586	0.217368492
negative regulation of cellular carbohydrate metabolic process (GO	44586	0.217368492
regulation of dopamine secretion (GO:0014059)	44586	0.217368492
cellular polysaccharide biosynthetic process (GO:0033692)	44586	0.217368492
negative regulation of response to endoplasmic reticulum stress (G	44586	0.217368492
negative regulation of sequestering of calcium ion (GO:0051283)	44586	0.217368492
chemical synaptic transmission, postsynaptic (GO:0099565)	44586	0.217368492
organophosphate ester transport (GO:0015748)	44586	0.217368492
outflow tract septum morphogenesis (GO:0003148)	44586	0.217368492
phosphatidylglycerol metabolic process (GO:0046471)	44586	0.217368492
endosome transport via multivesicular body sorting pathway (GO:0	44586	0.217368492
energy derivation by oxidation of organic compounds (GO:001598(	44586	0.217368492
regulation of rhodopsin mediated signaling pathway (GO:0022400)	44586	0.217368492
regulation of ryanodine-sensitive calcium-release channel activity (	44586	0.217368492
fat-soluble vitamin metabolic process (GO:0006775)	44586	0.217368492
glycolytic process through glucose-6-phosphate (GO:0061620)	44586	0.217368492
positive regulation of lipid metabolic process (GO:0045834)	44586	0.217368492

in utero embryonic development (GO:0001701)	44586	0.217368492
protein complex oligomerization (GO:0051259)	32905	0.218962212
regulation of MAPK cascade (GO:0043408)	3/166	0.220516324
toll-like receptor signaling pathway (GO:0002224)	33270	0.222546195
proteoglycan metabolic process (GO:0006029)	44587	0.225008689
purine-containing compound biosynthetic process (GO:0072522)	44587	0.225008689
cellular response to drug (GO:0035690)	44587	0.225008689
negative regulation of signaling receptor activity (GO:2000272)	44587	0.225008689
regulation of myelination (GO:0031641)	44587	0.225008689
DNA geometric change (GO:0032392)	44587	0.225008689
endothelial cell development (GO:0001885)	44587	0.225008689
regulation of regulatory T cell differentiation (GO:0045589)	44587	0.225008689
regulation of viral life cycle (GO:1903900)	44587	0.225008689
positive regulation of filopodium assembly (GO:0051491)	44587	0.225008689
positive regulation of glucose import (GO:0046326)	44587	0.225008689
positive regulation of interleukin-2 production (GO:0032743)	44587	0.225008689
histone methylation (GO:0016571)	44587	0.225008689
positive regulation of microtubule polymerization or depolymerizat	44587	0.225008689
positive regulation of T cell mediated cytotoxicity (GO:0001916)	44587	0.225008689
regulation of lipid metabolic process (GO:0019216)	33635	0.22613487
acute inflammatory response (GO:0002526)	44588	0.232574679
regulation of cardiac muscle cell contraction (GO:0086004)	44588	0.232574679
bile acid biosynthetic process (GO:0006699)	44588	0.232574679
regulation of cell junction assembly (GO:1901888)	44588	0.232574679
calcium-ion regulated exocytosis (GO:0017156)	44588	0.232574679
negative regulation of plasma membrane bounded cell projection a	44588	0.232574679
chondroitin sulfate proteoglycan biosynthetic process (GO:005065(	44588	0.232574679
dendritic spine organization (GO:0097061)	44588	0.232574679
peptidyl-lysine methylation (GO:0018022)	44588	0.232574679
positive regulation of calcium ion transmembrane transport (GO:19	44588	0.232574679
regulation of vasculature development (GO:1901342)	44588	0.232574679
release of sequestered calcium ion into cytosol (GO:0051209)	44588	0.232574679
positive regulation of nitric oxide biosynthetic process (GO:004542	44588	0.232574679
positive regulation of nuclear division (GO:0051785)	44588	0.232574679
positive regulation of striated muscle cell differentiation (GO:0051	44588	0.232574679
microtubule polymerization or depolymerization (GO:0031109)	44588	0.232574679
modulation of excitatory postsynaptic potential (GO:0098815)	44588	0.232574679
presynaptic endocytosis (GO:0140238)	44588	0.232574679
regulation of kinase activity (GO:0043549)	34366	0.233324588
positive regulation of epithelial cell migration (GO:0010634)	34366	0.233324588
positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:004	3/171	0.233335654
regulation of canonical Wnt signaling pathway (GO:0060828)	4/253	0.234039896
positive regulation of phosphorylation (GO:0042327)	4/253	0.234039896
negative regulation of axonogenesis (GO:0050771)	44589	0.24006718
calcium ion import (GO:0070509)	44589	0.24006718
regulation of DNA damage response, signal transduction by p53 cla	44589	0.24006718
regulation of multicellular organismal development (GO:2000026)	44589	0.24006718

regulation of postsynapse organization (GO:0099175)	44589	0.24006718
regulation of protein transport (GO:0051223)	44589	0.24006718
regulation of reactive oxygen species biosynthetic process (GO:190	44589	0.24006718
regulation of small molecule metabolic process (GO:0062012)	44589	0.24006718
positive regulation of cytosolic calcium ion concentration involved	44589	0.24006718
glycerophospholipid catabolic process (GO:0046475)	44589	0.24006718
response to ketone (GO:1901654)	44589	0.24006718
positive regulation of monooxygenase activity (GO:0032770)	44589	0.24006718
keratan sulfate biosynthetic process (GO:0018146)	44589	0.24006718
positive regulation of phosphatidylinositol 3-kinase activity (GO:00	44589	0.24006718
sulfur compound transport (GO:0072348)	44589	0.24006718
positive regulation of synapse assembly (GO:0051965)	44589	0.24006718
protein depolymerization (GO:0051261)	44589	0.24006718
protein localization to cell surface (GO:0034394)	44589	0.24006718
glycosaminoglycan biosynthetic process (GO:0006024)	35462	0.244133873
actin filament polymerization (GO:0030041)	44590	0.247486901
aggrephagy (GO:0035973)	44590	0.247486901
beta-catenin-TCF complex assembly (GO:1904837)	44590	0.247486901
negative regulation of interferon-gamma production (GO:0032689)	44590	0.247486901
regulation of double-strand break repair via nonhomologous end jc	44590	0.247486901
regulation of fatty acid biosynthetic process (GO:0042304)	44590	0.247486901
regulation of response to biotic stimulus (GO:0002831)	44590	0.247486901
establishment of endothelial barrier (GO:0061028)	44590	0.247486901
regulation of T cell mediated cytotoxicity (GO:0001914)	44590	0.247486901
glial cell differentiation (GO:0010001)	44590	0.247486901
regulation of ubiquitin-protein transferase activity (GO:0051438)	44590	0.247486901
glycolytic process (GO:0006096)	44590	0.247486901
positive regulation of extrinsic apoptotic signaling pathway (GO:20	44590	0.247486901
response to zinc ion (GO:0010043)	44590	0.247486901
positive regulation of leukocyte migration (GO:0002687)	44590	0.247486901
positive regulation of viral genome replication (GO:0045070)	44590	0.247486901
production of miRNAs involved in gene silencing by miRNA (GO:00	44590	0.247486901
negative regulation of neuron death (GO:1901215)	35827	0.247741953
regulation of peptidyl-serine phosphorylation (GO:0033135)	35827	0.247741953
cellular component assembly (GO:0022607)	4/261	0.250879837
positive regulation of stress-activated MAPK cascade (GO:0032874	36192	0.25135188
artery morphogenesis (GO:0048844)	44591	0.254834547
regulation of catecholamine secretion (GO:0050433)	44591	0.254834547
chondroitin sulfate metabolic process (GO:0030204)	44591	0.254834547
plasma membrane invagination (GO:0099024)	44591	0.254834547
positive regulation of B cell proliferation (GO:0030890)	44591	0.254834547
fatty-acyl-CoA biosynthetic process (GO:0046949)	44591	0.254834547
respiratory tube development (GO:0030323)	44591	0.254834547
response to alcohol (GO:0097305)	44591	0.254834547
heterotypic cell-cell adhesion (GO:0034113)	44591	0.254834547
positive regulation of lipid kinase activity (GO:0090218)	44591	0.254834547
positive regulation of phosphate metabolic process (GO:0045937)	44591	0.254834547

maintenance of blood-brain barrier (GO:0035633)	44591	0.254834547
primary neural tube formation (GO:0014020)	44591	0.254834547
mRNA splice site selection (GO:0006376)	44591	0.254834547
regulation of intracellular signal transduction (GO:1902531)	6/437	0.254846878
positive regulation of cellular biosynthetic process (GO:0031328)	3/180	0.256727029
cellular response to chemical stress (GO:0062197)	2/101	0.258575774
activation of protein kinase B activity (GO:0032148)	44592	0.262110814
proteoglycan biosynthetic process (GO:0030166)	44592	0.262110814
purine nucleoside bisphosphate metabolic process (GO:0034032)	44592	0.262110814
regulation of calcium ion-dependent exocytosis (GO:0017158)	44592	0.262110814
regulation of developmental growth (GO:0048638)	44592	0.262110814
regulation of macrophage derived foam cell differentiation (GO:00	44592	0.262110814
phosphatidylethanolamine metabolic process (GO:0046337)	44592	0.262110814
ribonucleoside bisphosphate metabolic process (GO:0033875)	44592	0.262110814
positive regulation of mononuclear cell migration (GO:0071677)	44592	0.262110814
tube closure (GO:0060606)	44592	0.262110814
positive regulation of ubiquitin-protein transferase activity (GO:00	44592	0.262110814
vitamin transport (GO:0051180)	44592	0.262110814
protein acetylation (GO:0006473)	44592	0.262110814
calcium-mediated signaling (GO:0019722)	2/102	0.262189008
cell junction assembly (GO:0034329)	2/102	0.262189008
positive regulation of cell growth (GO:0030307)	2/102	0.262189008
protein-containing complex assembly (GO:0065003)	4/267	0.263676028
positive regulation of transcription, DNA-templated (GO:0045893)	14/1183	0.265038722
chromatin remodeling (GO:0006338)	2/103	0.265802623
negative regulation of developmental growth (GO:0048640)	11689	0.269316392
B cell proliferation (GO:0042100)	11689	0.269316392
regulation of cellular biosynthetic process (GO:0031326)	11689	0.269316392
regulation of chemotaxis (GO:0050920)	11689	0.269316392
regulation of dendrite morphogenesis (GO:0048814)	11689	0.269316392
regulation of dendritic spine morphogenesis (GO:0061001)	11689	0.269316392
regulation of intracellular protein transport (GO:0033157)	11689	0.269316392
chondrocyte differentiation (GO:0002062)	11689	0.269316392
regulation of NMDA receptor activity (GO:2000310)	11689	0.269316392
gene silencing by miRNA (GO:0035195)	11689	0.269316392
positive regulation of glucose transmembrane transport (GO:0010	11689	0.269316392
positive regulation of lamellipodium organization (GO:1902745)	11689	0.269316392
skeletal muscle organ development (GO:0060538)	11689	0.269316392
superoxide metabolic process (GO:0006801)	11689	0.269316392
steroid metabolic process (GO:0008202)	2/104	0.26941627
endoplasmic reticulum to Golgi vesicle-mediated transport (GO:00	3/185	0.269861719
positive regulation of transcription by RNA polymerase II (GO:0045	11/908	0.272873649
regulation of JNK cascade (GO:0046328)	2/105	0.273029607
bile acid metabolic process (GO:0008206)	12055	0.276451963
negative regulation of smooth muscle cell proliferation (GO:00486	12055	0.276451963
regulation of neurotransmitter secretion (GO:0046928)	12055	0.276451963
positive regulation of cholesterol transport (GO:0032376)	12055	0.276451963

keratan sulfate metabolic process (GO:0042339)	12055	0.276451963
mitotic G2 DNA damage checkpoint signaling (GO:0007095)	12055	0.276451963
regulation of cell cycle process (GO:0010564)	2/106	0.276642297
regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)	2/106	0.276642297
negative regulation of blood vessel endothelial cell migration (GO:(	12420	0.283518205
autophagosome maturation (GO:0097352)	12420	0.283518205
negative regulation of mitochondrion organization (GO:0010823)	12420	0.283518205
cell-substrate junction assembly (GO:0007044)	12420	0.283518205
cellular response to amino acid stimulus (GO:0071230)	12420	0.283518205
neural tube closure (GO:0001843)	12420	0.283518205
regulation of lamellipodium assembly (GO:0010591)	12420	0.283518205
organelle disassembly (GO:1903008)	12420	0.283518205
regulation of myoblast differentiation (GO:0045661)	12420	0.283518205
phosphatidylinositol 3-kinase signaling (GO:0014065)	12420	0.283518205
epithelial tube morphogenesis (GO:0060562)	12420	0.283518205
positive regulation of DNA binding (GO:0043388)	12420	0.283518205
positive regulation of interleukin-12 production (GO:0032735)	12420	0.283518205
response to steroid hormone (GO:0048545)	12420	0.283518205
histone lysine methylation (GO:0034968)	12420	0.283518205
sister chromatid segregation (GO:0000819)	12420	0.283518205
striated muscle tissue development (GO:0014706)	12420	0.283518205
synaptic vesicle recycling (GO:0036465)	12420	0.283518205
DNA metabolic process (GO:0006259)	4/277	0.28526362
negative regulation of cellular macromolecule biosynthetic process	7/547	0.286004999
negative regulation of cell cycle G1/S phase transition (GO:190280	12785	0.290515788
negative regulation of epithelial cell migration (GO:0010633)	12785	0.290515788
negative regulation of T cell proliferation (GO:0042130)	12785	0.290515788
oxoacid metabolic process (GO:0043436)	12785	0.290515788
regulation of phosphatidylinositol 3-kinase activity (GO:0043551)	12785	0.290515788
regulation of postsynaptic membrane potential (GO:0060078)	12785	0.290515788
regulation of regulated secretory pathway (GO:1903305)	12785	0.290515788
regulation of TORC1 signaling (GO:1903432)	12785	0.290515788
respiratory system development (GO:0060541)	12785	0.290515788
response to exogenous dsRNA (GO:0043330)	12785	0.290515788
positive regulation of lipid biosynthetic process (GO:0046889)	12785	0.290515788
positive regulation of lymphocyte activation (GO:0051251)	12785	0.290515788
semaphorin-plexin signaling pathway (GO:0071526)	12785	0.290515788
smoothened signaling pathway (GO:0007224)	12785	0.290515788
lung development (GO:0030324)	12785	0.290515788
muscle cell differentiation (GO:0042692)	12785	0.290515788
regulation of protein kinase activity (GO:0045859)	2/110	0.291080108
negative regulation of macromolecule metabolic process (GO:0010	3/194	0.29367968
negative regulation of cellular protein localization (GO:1903828)	13150	0.297445375
negative regulation of fat cell differentiation (GO:0045599)	13150	0.297445375
regulation of cardiac muscle contraction (GO:0055117)	13150	0.297445375
regulation of embryonic development (GO:0045995)	13150	0.297445375
negative regulation of toll-like receptor signaling pathway (GO:003	13150	0.297445375

regulation of microtubule-based process (GO:0032886)	13150	0.297445375
dendrite morphogenesis (GO:0048813)	13150	0.297445375
regulation of ossification (GO:0030278)	13150	0.297445375
regulation of osteoclast differentiation (GO:0045670)	13150	0.297445375
regulation of receptor internalization (GO:0002090)	13150	0.297445375
positive regulation of bone mineralization (GO:0030501)	13150	0.297445375
regulation of sodium ion transport (GO:0002028)	13150	0.297445375
positive regulation of mitotic nuclear division (GO:0045840)	13150	0.297445375
macrophage activation (GO:0042116)	13150	0.297445375
membrane assembly (GO:0071709)	13150	0.297445375
positive regulation of T cell mediated immunity (GO:0002711)	13150	0.297445375
mitochondrion disassembly (GO:0061726)	13150	0.297445375
Wnt signaling pathway, calcium modulating pathway (GO:0007223	13150	0.297445375
regulation of cytoskeleton organization (GO:0051493)	2/112	0.298286876
phosphatidylinositol metabolic process (GO:0046488)	2/112	0.298286876
proton transmembrane transport (GO:1902600)	13516	0.304307624
negative regulation of endothelial cell proliferation (GO:0001937)	13516	0.304307624
negative regulation of epithelial cell apoptotic process (GO:190403	13516	0.304307624
negative regulation of G1/S transition of mitotic cell cycle (GO:200(	13516	0.304307624
negative regulation of stress-activated MAPK cascade (GO:003287:	13516	0.304307624
regulation of glucose import (GO:0046324)	13516	0.304307624
regulation of microtubule cytoskeleton organization (GO:0070507)	13516	0.304307624
regulation of p38MAPK cascade (GO:1900744)	13516	0.304307624
phospholipid biosynthetic process (GO:0008654)	13516	0.304307624
positive regulation of calcium ion transport (GO:0051928)	13516	0.304307624
regulation of vascular associated smooth muscle cell proliferation (	13516	0.304307624
positive regulation of exocytosis (GO:0045921)	13516	0.304307624
skeletal muscle tissue development (GO:0007519)	13516	0.304307624
lysosome localization (GO:0032418)	13516	0.304307624
negative regulation of intracellular signal transduction (GO:190253	3/198	0.304314702
regulation of signal transduction (GO:0009966)	3/198	0.304314702
activation of protein kinase activity (GO:0032147)	2/114	0.305482371
positive regulation of kinase activity (GO:0033674)	2/114	0.305482371
endomembrane system organization (GO:0010256)	3/199	0.306976527
calcium ion transport (GO:0006816)	2/115	0.30907518
cellular amide metabolic process (GO:0043603)	2/115	0.30907518
cellular response to lectin (GO:1990858)	2/115	0.30907518
stimulatory C-type lectin receptor signaling pathway (GO:0002223)	2/115	0.30907518
positive regulation of protein metabolic process (GO:0051247)	2/115	0.30907518
negative regulation of endothelial cell migration (GO:0010596)	13881	0.311103186
negative regulation of G0 to G1 transition (GO:0070317)	13881	0.311103186
regulation of axon extension (GO:0030516)	13881	0.311103186
regulation of cell communication (GO:0010646)	13881	0.311103186
negative regulation of TOR signaling (GO:0032007)	13881	0.311103186
positive regulation of cell development (GO:0010720)	13881	0.311103186
positive regulation of insulin secretion (GO:0032024)	13881	0.311103186
lymphocyte proliferation (GO:0046651)	13881	0.311103186

synaptic vesicle endocytosis (GO:0048488)	13881	0.311103186
generation of neurons (GO:0048699)	3/202	0.314967167
negative regulation of lymphocyte proliferation (GO:0050672)	14246	0.317832705
negative regulation of secretion by cell (GO:1903531)	14246	0.317832705
regulation of heart rate by cardiac conduction (GO:0086091)	14246	0.317832705
odontogenesis (GO:0042476)	14246	0.317832705
regulation of nitric-oxide synthase activity (GO:0050999)	14246	0.317832705
endothelial cell migration (GO:0043542)	14246	0.317832705
regulation of protein tyrosine kinase activity (GO:0061097)	14246	0.317832705
regulation of T cell differentiation (GO:0045580)	14246	0.317832705
regulation of viral entry into host cell (GO:0046596)	14246	0.317832705
replication fork processing (GO:0031297)	14246	0.317832705
positive regulation of intracellular transport (GO:0032388)	14246	0.317832705
protein acylation (GO:0043543)	14246	0.317832705
negative regulation of transcription, DNA-templated (GO:0045892)	11/948	0.320408822
positive regulation of macromolecule metabolic process (GO:0010	5/384	0.320533646
innate immune response activating cell surface receptor signaling p	2/119	0.323407138
autophagy of mitochondrion (GO:0000422)	14611	0.32449682
bone development (GO:0060348)	14611	0.32449682
carboxylic acid metabolic process (GO:0019752)	14611	0.32449682
negative regulation of protein kinase B signaling (GO:0051898)	14611	0.32449682
digestive tract development (GO:0048565)	14611	0.32449682
regulation of nitric oxide biosynthetic process (GO:0045428)	14611	0.32449682
positive regulation of cation channel activity (GO:2001259)	14611	0.32449682
fatty acid derivative biosynthetic process (GO:1901570)	14611	0.32449682
glycolipid biosynthetic process (GO:0009247)	14611	0.32449682
positive regulation of ossification (GO:0045778)	14611	0.32449682
sulfur compound catabolic process (GO:0044273)	14611	0.32449682
regulation of inflammatory response (GO:0050727)	3/206	0.325628398
regulation of cell population proliferation (GO:0042127)	9/764	0.329135216
cellular response to cytokine stimulus (GO:0071345)	6/482	0.330541626
negative regulation of cell-cell adhesion (GO:0022408)	14977	0.331096164
carbohydrate catabolic process (GO:0016052)	14977	0.331096164
carboxylic acid transmembrane transport (GO:1905039)	14977	0.331096164
regulation of filopodium assembly (GO:0051489)	14977	0.331096164
regulation of G0 to G1 transition (GO:0070316)	14977	0.331096164
endosome organization (GO:0007032)	14977	0.331096164
epithelial cell migration (GO:0010631)	14977	0.331096164
regulation of release of cytochrome c from mitochondria (GO:0090	14977	0.331096164
regulation of response to DNA damage stimulus (GO:2001020)	14977	0.331096164
positive regulation of biomineral tissue development (GO:0070169	14977	0.331096164
gluconeogenesis (GO:0006094)	14977	0.331096164
regulation of viral transcription (GO:0046782)	14977	0.331096164
hexose metabolic process (GO:0019318)	14977	0.331096164
JNK cascade (GO:0007254)	14977	0.331096164
T cell differentiation (GO:0030217)	14977	0.331096164
extracellular matrix organization (GO:0030198)	4/300	0.335736133

ATP-dependent chromatin remodeling (GO:0043044)	15342	0.337631363
calcium ion transmembrane import into cytosol (GO:0097553)	15342	0.337631363
regulation of double-strand break repair (GO:2000779)	15342	0.337631363
ceramide biosynthetic process (GO:0046513)	15342	0.337631363
regulation of nervous system development (GO:0051960)	15342	0.337631363
positive regulation of epithelial to mesenchymal transition (GO:001	15342	0.337631363
histone H3 acetylation (GO:0043966)	15342	0.337631363
positive regulation of protein tyrosine kinase activity (GO:0061098	15342	0.337631363
regulation of anatomical structure morphogenesis (GO:0022603)	2/123	0.337663925
non-canonical Wnt signaling pathway (GO:0035567)	2/124	0.341214549
negative regulation of inflammatory response (GO:0050728)	3/212	0.341618478
regulation of cell-substrate adhesion (GO:0010810)	15707	0.344103037
regulation of cytokine production involved in inflammatory respon	15707	0.344103037
cellular glucose homeostasis (GO:0001678)	15707	0.344103037
cellular response to retinoic acid (GO:0071300)	15707	0.344103037
development of primary male sexual characteristics (GO:0046546)	15707	0.344103037
DNA-dependent DNA replication maintenance of fidelity (GO:0045(	15707	0.344103037
positive regulation of axonogenesis (GO:0050772)	15707	0.344103037
glutathione metabolic process (GO:0006749)	15707	0.344103037
heart looping (GO:0001947)	15707	0.344103037
positive regulation of leukocyte mediated cytotoxicity (GO:000191	15707	0.344103037
positive regulation of neuron differentiation (GO:0045666)	15707	0.344103037
positive regulation of peptide hormone secretion (GO:0090277)	15707	0.344103037
lipid modification (GO:0030258)	15707	0.344103037
male gonad development (GO:0008584)	15707	0.344103037
positive regulation of T cell differentiation (GO:0045582)	15707	0.344103037
natural killer cell activation (GO:0030101)	15707	0.344103037
regulation of phosphorylation (GO:0042325)	2/125	0.344759283
regulation of transcription, DNA-templated (GO:0006355)	24/2244	0.346649139
positive regulation of protein modification process (GO:0031401)	3/214	0.34694403
negative regulation of growth (GO:0045926)	2/126	0.348297903
circulatory system development (GO:0072359)	2/126	0.348297903
phosphatidylinositol biosynthetic process (GO:0006661)	2/126	0.348297903
embryonic organ morphogenesis (GO:0048562)	16072	0.350511801
positive regulation of biosynthetic process (GO:0009891)	16072	0.350511801
positive regulation of cell-matrix adhesion (GO:0001954)	16072	0.350511801
hexose biosynthetic process (GO:0019319)	16072	0.350511801
intracellular steroid hormone receptor signaling pathway (GO:003(	16072	0.350511801
positive regulation of osteoblast differentiation (GO:0045669)	16072	0.350511801
lymphocyte chemotaxis (GO:0048247)	16072	0.350511801
positive regulation of receptor-mediated endocytosis (GO:004826(	16072	0.350511801
positive regulation of stress fiber assembly (GO:0051496)	16072	0.350511801
mRNA catabolic process (GO:0006402)	16072	0.350511801
extracellular structure organization (GO:0043062)	3/216	0.352265735
external encapsulating structure organization (GO:0045229)	3/217	0.354924851
regulation of pri-miRNA transcription by RNA polymerase II (GO:19	16438	0.356858262
mitotic G2/M transition checkpoint (GO:0044818)	16438	0.356858262

regulation of primary metabolic process (GO:0080090)	2/130	0.362386982
G2/M transition of mitotic cell cycle (GO:0000086)	2/130	0.362386982
Golgi organization (GO:0007030)	2/130	0.362386982
erythrocyte differentiation (GO:0030218)	16803	0.363143024
spliceosomal complex assembly (GO:0000245)	16803	0.363143024
vesicle organization (GO:0016050)	16803	0.363143024
cell cycle G2/M phase transition (GO:0044839)	2/131	0.365891874
cellular response to metal ion (GO:0071248)	2/131	0.365891874
regulation of cell migration (GO:0030334)	5/408	0.366769853
protein modification by small protein conjugation (GO:0032446)	5/409	0.368703657
regulation of DNA binding (GO:0051101)	17168	0.369366683
determination of heart left/right asymmetry (GO:0061371)	17168	0.369366683
embryonic heart tube morphogenesis (GO:0003143)	17168	0.369366683
regulation of protein localization to nucleus (GO:1900180)	17168	0.369366683
glycosphingolipid metabolic process (GO:0006687)	17168	0.369366683
positive regulation of pathway-restricted SMAD protein phosphory	17168	0.369366683
telomere organization (GO:0032200)	17168	0.369366683
regulation of cell adhesion (GO:0030155)	2/133	0.372879428
regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043122)	3/224	0.373495637
negative regulation of mitotic cell cycle (GO:0045930)	17533	0.37552983
regulation of interleukin-10 production (GO:0032653)	17533	0.37552983
regulation of interleukin-2 production (GO:0032663)	17533	0.37552983
histone H4 acetylation (GO:0043967)	17533	0.37552983
myelination (GO:0042552)	17533	0.37552983
negative regulation of catabolic process (GO:0009895)	17899	0.381633051
receptor internalization (GO:0031623)	17899	0.381633051
cellular response to mechanical stimulus (GO:0071260)	17899	0.381633051
regulation of smooth muscle cell proliferation (GO:0048660)	17899	0.381633051
regulation of stress-activated MAPK cascade (GO:0032872)	17899	0.381633051
secondary alcohol metabolic process (GO:1902652)	17899	0.381633051
ribonucleoprotein complex assembly (GO:0022618)	2/136	0.383302406
positive regulation of ion transport (GO:0043270)	18264	0.387676926
inflammatory response (GO:0006954)	3/230	0.389333716
apoptotic process (GO:0006915)	3/231	0.391964536
regulation of epithelial cell migration (GO:0010632)	18629	0.393662028
regulation of interleukin-12 production (GO:0032655)	18629	0.393662028
positive regulation of actin filament bundle assembly (GO:0032233	18629	0.393662028
gonad development (GO:0008406)	18629	0.393662028
inositol lipid-mediated signaling (GO:0048017)	18629	0.393662028
sensory perception (GO:0007600)	18629	0.393662028
intrinsic apoptotic signaling pathway in response to DNA damage (	18629	0.393662028
mesenchymal cell differentiation (GO:0048762)	18629	0.393662028
mitotic nuclear membrane organization (GO:0101024)	18629	0.393662028
mitotic nuclear membrane reassembly (GO:0007084)	18629	0.393662028
neuron projection morphogenesis (GO:0048812)	2/140	0.397083443
enzyme linked receptor protein signaling pathway (GO:0007167)	2/140	0.397083443
cartilage development (GO:0051216)	18994	0.399588926

negative regulation of protein-containing complex assembly (GO:0(	18994	0.399588926
regulation of exocytosis (GO:0017157)	18994	0.399588926
endocytic recycling (GO:0032456)	18994	0.399588926
plasma membrane bounded cell projection morphogenesis (GO:01	18994	0.399588926
regulation of release of sequestered calcium ion into cytosol (GO:0	18994	0.399588926
response to peptide hormone (GO:0043434)	18994	0.399588926
sprouting angiogenesis (GO:0002040)	18994	0.399588926
positive regulation of protein localization to cell periphery (GO:190	18994	0.399588926
positive regulation of protein localization to plasma membrane (GC	18994	0.399588926
myeloid cell differentiation (GO:0030099)	18994	0.399588926
organelle assembly (GO:0070925)	5/425	0.3996344
regulation of small GTPase mediated signal transduction (GO:0051(	2/141	0.400506843
regulation of DNA replication (GO:0006275)	19360	0.405458183
positive regulation of B cell activation (GO:0050871)	19360	0.405458183
IRE1-mediated unfolded protein response (GO:0036498)	19360	0.405458183
nitrogen compound transport (GO:0071705)	2/143	0.407326329
monocarboxylic acid metabolic process (GO:0032787)	2/143	0.407326329
regulation of nucleic acid-templated transcription (GO:1903506)	5/430	0.409278793
regulation of humoral immune response (GO:0002920)	19725	0.411270357
nuclear membrane reassembly (GO:0031468)	19725	0.411270357
positive regulation of leukocyte chemotaxis (GO:0002690)	19725	0.411270357
inorganic anion transport (GO:0015698)	19725	0.411270357
striated muscle contraction (GO:0006941)	19725	0.411270357
unsaturated fatty acid metabolic process (GO:0033559)	19725	0.411270357
pyruvate metabolic process (GO:0006090)	20090	0.417026
negative regulation of cysteine-type endopeptidase activity involve	20090	0.417026
regulation of blood vessel endothelial cell migration (GO:0043535)	20090	0.417026
regulation of gene silencing by RNA (GO:0060966)	20090	0.417026
ceramide metabolic process (GO:0006672)	20090	0.417026
regulation of posttranscriptional gene silencing (GO:0060147)	20090	0.417026
interstrand cross-link repair (GO:0036297)	20090	0.417026
positive regulation of response to DNA damage stimulus (GO:2001(	20090	0.417026
regulation of mRNA stability (GO:0043488)	2/146	0.417485091
positive regulation of cytosolic calcium ion concentration (GO:0007	2/147	0.420851999
protein-containing complex disassembly (GO:0032984)	20455	0.42272566
autophagosome organization (GO:1905037)	20455	0.42272566
peptidyl-tyrosine modification (GO:0018212)	20455	0.42272566
glycosaminoglycan catabolic process (GO:0006027)	20455	0.42272566
positive regulation of interleukin-1 beta production (GO:0032731)	20455	0.42272566
telomere maintenance (GO:0000723)	20455	0.42272566
regulation of cytosolic calcium ion concentration (GO:0051480)	2/148	0.424209012
regulation of G2/M transition of mitotic cell cycle (GO:0010389)	2/149	0.427556003
regulation of bone mineralization (GO:0030500)	20821	0.428369877
cellular response to peptide (GO:1901653)	20821	0.428369877
regulation of reactive oxygen species metabolic process (GO:20003	20821	0.428369877
positive regulation of cell junction assembly (GO:1901890)	20821	0.428369877
renal system development (GO:0072001)	20821	0.428369877

positive regulation of interferon-gamma production (GO:0032729)	20821	0.428369877
positive regulation of proteolysis (GO:0045862)	20821	0.428369877
regulation of cytokine production (GO:0001817)	2/150	0.430892848
receptor metabolic process (GO:0043112)	21186	0.433959189
autophagosome assembly (GO:0000045)	21186	0.433959189
regulation of calcium ion transport (GO:0051924)	21186	0.433959189
negative regulation of hydrolase activity (GO:0051346)	21186	0.433959189
chordate embryonic development (GO:0043009)	21186	0.433959189
nucleosome assembly (GO:0006334)	21186	0.433959189
regulation of pathway-restricted SMAD protein phosphorylation (G	21186	0.433959189
fat cell differentiation (GO:0045444)	21186	0.433959189
positive regulation of mitochondrion organization (GO:0010822)	21186	0.433959189
regulation of apoptotic process (GO:0042981)	8/742	0.436973503
negative regulation of protein phosphorylation (GO:0001933)	2/152	0.437535621
protein polymerization (GO:0051258)	21551	0.439494127
phospholipid transport (GO:0015914)	21551	0.439494127
positive regulation of apoptotic signaling pathway (GO:2001235)	21551	0.439494127
fatty acid oxidation (GO:0019395)	21551	0.439494127
response to reactive oxygen species (GO:0000302)	21551	0.439494127
positive regulation of intracellular signal transduction (GO:1902533	6/546	0.441638028
peptidyl-threonine phosphorylation (GO:0018107)	21916	0.444975218
response to organic cyclic compound (GO:0014070)	21916	0.444975218
homophilic cell adhesion via plasma membrane adhesion molecule	21916	0.444975218
positive regulation of NF-kappaB transcription factor activity (GO:0	2/155	0.447420773
regulation of DNA-templated transcription, initiation (GO:2000142)	22282	0.450402982
negative regulation of response to stimulus (GO:0048585)	22282	0.450402982
pattern recognition receptor signaling pathway (GO:0002221)	22282	0.450402982
positive regulation of interleukin-8 production (GO:0032757)	22282	0.450402982
positive regulation of cysteine-type endopeptidase activity (GO:20(	22647	0.455777935
glucose metabolic process (GO:0006006)	22647	0.455777935
positive regulation of interleukin-1 production (GO:0032732)	22647	0.455777935
response to retinoic acid (GO:0032526)	22647	0.455777935
I-kappaB kinase/NF-kappaB signaling (GO:0007249)	22647	0.455777935
stress-activated MAPK cascade (GO:0051403)	22647	0.455777935
negative regulation of endopeptidase activity (GO:0010951)	23012	0.461100589
negative regulation of peptidase activity (GO:0010466)	23012	0.461100589
cellular response to reactive oxygen species (GO:0034614)	23012	0.461100589
positive regulation of DNA metabolic process (GO:0051054)	23012	0.461100589
positive regulation of viral process (GO:0048524)	23012	0.461100589
positive regulation of cell differentiation (GO:0045597)	3/258	0.461644614
negative regulation of cell cycle process (GO:0010948)	23377	0.46637145
regulation of cellular ketone metabolic process (GO:0010565)	23377	0.46637145
regulation of innate immune response (GO:0045088)	23377	0.46637145
diterpenoid metabolic process (GO:0016101)	23377	0.46637145
regulation of transcription initiation from RNA polymerase II promo	23377	0.46637145
chemical homeostasis (GO:0048878)	23743	0.47159102
inorganic anion transmembrane transport (GO:0098661)	23743	0.47159102

mitotic G1 DNA damage checkpoint signaling (GO:0031571)	23743	0.47159102
cell-cell junction assembly (GO:0007043)	24108	0.476759795
cellular component disassembly (GO:0022411)	24108	0.476759795
extracellular matrix disassembly (GO:0022617)	24108	0.476759795
positive regulation of cell death (GO:0010942)	24108	0.476759795
negative regulation of canonical Wnt signaling pathway (GO:00900	2/165	0.479653428
regulation of neuron projection development (GO:0010975)	2/165	0.479653428
regulation of cellular macromolecule biosynthetic process (GO:200	5/468	0.48156855
protein N-linked glycosylation (GO:0006487)	24473	0.481878266
anion transmembrane transport (GO:0098656)	24473	0.481878266
regulation of gene silencing by miRNA (GO:0060964)	24473	0.481878266
peptidyl-threonine modification (GO:0018210)	24473	0.481878266
positive regulation of catabolic process (GO:0009896)	24473	0.481878266
regulation of viral genome replication (GO:0045069)	24473	0.481878266
vascular endothelial growth factor receptor signaling pathway (GO:	24473	0.481878266
regulation of gene expression (GO:0010468)	11/1079	0.483827192
protein deubiquitination (GO:0016579)	3/267	0.484131778
negative regulation of transforming growth factor beta receptor sig	24838	0.486946922
interferon-gamma-mediated signaling pathway (GO:0060333)	24838	0.486946922
positive regulation of protein localization to nucleus (GO:1900182)	24838	0.486946922
regulation of transcription by RNA polymerase II (GO:0006357)	22/2206	0.489033827
positive regulation of cell migration (GO:0030335)	3/269	0.489069014
cellular response to decreased oxygen levels (GO:0036294)	25204	0.491966243
peptidyl-tyrosine phosphorylation (GO:0018108)	25204	0.491966243
positive regulation of protein transport (GO:0051222)	25204	0.491966243
cell-cell adhesion via plasma-membrane adhesion molecules (GO:0	2/170	0.495335913
negative regulation of viral process (GO:0048525)	25569	0.496936709
neutrophil chemotaxis (GO:0030593)	25569	0.496936709
defense response to Gram-positive bacterium (GO:0050830)	25569	0.496936709
fatty acid catabolic process (GO:0009062)	25569	0.496936709
positive regulation of cell-substrate adhesion (GO:0010811)	25569	0.496936709
positive regulation of MAPK cascade (GO:0043410)	3/274	0.501311323
negative regulation of neuron apoptotic process (GO:0043524)	25934	0.501858792
regulation of endopeptidase activity (GO:0052548)	25934	0.501858792
regulation of G1/S transition of mitotic cell cycle (GO:2000045)	25934	0.501858792
regulation of hematopoietic stem cell differentiation (GO:1902036)	25934	0.501858792
cholesterol homeostasis (GO:0042632)	25934	0.501858792
phosphatidylinositol-mediated signaling (GO:0048015)	25934	0.501858792
fatty acid biosynthetic process (GO:0006633)	25934	0.501858792
positive regulation of cellular protein localization (GO:1903829)	25934	0.501858792
histone acetylation (GO:0016573)	25934	0.501858792
response to metal ion (GO:0010038)	25934	0.501858792
neutrophil degranulation (GO:0043312)	5/481	0.505659879
protein modification by small protein removal (GO:0070646)	3/276	0.506166796
cell junction organization (GO:0034330)	26299	0.506732961
cell morphogenesis involved in differentiation (GO:0000904)	26299	0.506732961
cytoskeleton-dependent cytokinesis (GO:0061640)	26299	0.506732961

response to ionizing radiation (GO:0010212)	26299	0.506732961
sterol homeostasis (GO:0055092)	26299	0.506732961
positive regulation of protein secretion (GO:0050714)	26299	0.506732961
positive regulation of secretion by cell (GO:1903532)	26299	0.506732961
negative regulation of cell population proliferation (GO:0008285)	4/379	0.506942434
positive regulation of gene expression (GO:0010628)	5/482	0.5074955
plasma membrane bounded cell projection assembly (GO:0120031	3/278	0.510997964
negative regulation of programmed cell death (GO:0043069)	4/381	0.51106743
negative regulation of cell adhesion (GO:0007162)	26665	0.511559679
regulation of actin filament-based process (GO:0032970)	26665	0.511559679
chromatin assembly (GO:0031497)	26665	0.511559679
defense response to Gram-negative bacterium (GO:0050829)	26665	0.511559679
granulocyte chemotaxis (GO:0071621)	26665	0.511559679
response to molecule of bacterial origin (GO:0002237)	26665	0.511559679
positive regulation of synaptic transmission (GO:0050806)	26665	0.511559679
negative regulation of apoptotic process (GO:0043066)	5/485	0.512986299
neutrophil activation involved in immune response (GO:0002283)	5/485	0.512986299
defense response to bacterium (GO:0042742)	2/176	0.513756557
negative regulation of protein binding (GO:0032091)	27030	0.516339406
cellular response to amino acid starvation (GO:0034198)	27030	0.516339406
regulation of stress fiber assembly (GO:0051492)	27030	0.516339406
sphingolipid biosynthetic process (GO:0030148)	27030	0.516339406
mitotic nuclear division (GO:0140014)	27030	0.516339406
positive regulation of developmental process (GO:0051094)	2/177	0.5167836
neutrophil mediated immunity (GO:0002446)	5/488	0.518452411
regulation of hematopoietic progenitor cell differentiation (GO:190	27395	0.521072598
response to amino acid starvation (GO:1990928)	27395	0.521072598
positive regulation of immune response (GO:0050778)	27395	0.521072598
positive regulation of lymphocyte proliferation (GO:0050671)	27395	0.521072598
integrin-mediated signaling pathway (GO:0007229)	27395	0.521072598
positive regulation of T cell activation (GO:0050870)	27395	0.521072598
regulation of immune response (GO:0050776)	2/179	0.52280032
regulation of cell division (GO:0051302)	27760	0.525759705
regulation of epithelial to mesenchymal transition (GO:0010717)	27760	0.525759705
cellular response to hormone stimulus (GO:0032870)	27760	0.525759705
regulation of T cell proliferation (GO:0042129)	27760	0.525759705
positive regulation of growth (GO:0045927)	27760	0.525759705
positive regulation of programmed cell death (GO:0043068)	3/286	0.530071937
neutrophil migration (GO:1990266)	28126	0.530401174
positive regulation of tumor necrosis factor production (GO:00327(	28126	0.530401174
positive regulation of type I interferon production (GO:0032481)	28126	0.530401174
negative regulation of apoptotic signaling pathway (GO:2001234)	28491	0.534997447
recombinational repair (GO:0000725)	28856	0.539548961
axon development (GO:0061564)	28856	0.539548961
regulation of neuron differentiation (GO:0045664)	28856	0.539548961
negative regulation of cell cycle (GO:0045786)	29221	0.54405615
negative regulation of cellular component organization (GO:00511	29221	0.54405615

negative regulation of extrinsic apoptotic signaling pathway (GO:20	29221	0.54405615
regulation of fat cell differentiation (GO:0045598)	29221	0.54405615
regulation of protein localization to plasma membrane (GO:190307	29221	0.54405615
positive regulation of cell adhesion (GO:0045785)	29221	0.54405615
glycerophospholipid metabolic process (GO:0006650)	29221	0.54405615
negative regulation of protein modification process (GO:0031400)	29587	0.548519444
regulation of interleukin-8 production (GO:0032677)	29587	0.548519444
phospholipase C-activating G protein-coupled receptor signaling pa	29587	0.548519444
positive regulation of cellular amide metabolic process (GO:00342	29587	0.548519444
regulation of mitotic cell cycle phase transition (GO:1901990)	2/188	0.549250856
regulation of GTPase activity (GO:0043087)	2/189	0.552126006
ephrin receptor signaling pathway (GO:0048013)	29952	0.552939267
regulation of cell cycle (GO:0051726)	3/296	0.553324588
regulation of defense response (GO:0031347)	30317	0.557316042
peptide metabolic process (GO:0006518)	30317	0.557316042
regulation of osteoblast differentiation (GO:0045667)	30317	0.557316042
negative regulation of cell differentiation (GO:0045596)	2/191	0.557837687
negative regulation of Wnt signaling pathway (GO:0030178)	2/191	0.557837687
DNA repair (GO:0006281)	3/298	0.557893414
regulation of cytokinesis (GO:0032465)	30682	0.561650186
lymphocyte differentiation (GO:0030098)	30682	0.561650186
vascular transport (GO:0010232)	30682	0.561650186
positive regulation of protein catabolic process (GO:0045732)	31048	0.56594211
Wnt signaling pathway, planar cell polarity pathway (GO:0060071)	31048	0.56594211
cytokine-mediated signaling pathway (GO:0019221)	6/621	0.566535453
negative regulation of cellular amide metabolic process (GO:00342	31413	0.570192226
transport across blood-brain barrier (GO:0150104)	31413	0.570192226
positive regulation of cellular process (GO:0048522)	6/625	0.572842494
regulation of establishment of planar polarity (GO:0090175)	32143	0.578568645
retrograde transport, endosome to Golgi (GO:0042147)	32143	0.578568645
metal ion transport (GO:0030001)	32143	0.578568645
cellular protein metabolic process (GO:0044267)	4/417	0.582420067
regulation of cysteine-type endopeptidase activity involved in apop	32509	0.582695748
regulation of type I interferon production (GO:0032479)	32509	0.582695748
regulation of macromolecule metabolic process (GO:0060255)	2/200	0.582899142
protein ubiquitination (GO:0016567)	5/525	0.583567857
positive regulation of apoptotic process (GO:0043065)	3/310	0.584713004
negative regulation of translation (GO:0017148)	32874	0.586782639
positive regulation of binding (GO:0051099)	32874	0.586782639
regulation of actin cytoskeleton organization (GO:0032956)	33239	0.590829707
regulation of stem cell differentiation (GO:2000736)	33239	0.590829707
cilium assembly (GO:0060271)	3/314	0.593421704
negative regulation of mitotic cell cycle phase transition (GO:19019	33604	0.59483734
regulation of peptidyl-tyrosine phosphorylation (GO:0050730)	33604	0.59483734
retinoid metabolic process (GO:0001523)	33604	0.59483734
positive regulation of transmembrane receptor protein serine/thre	33604	0.59483734
regulation of epithelial cell proliferation (GO:0050678)	33970	0.598805919

regulation of heart contraction (GO:0008016)	33970	0.598805919
negative regulation of cell death (GO:0060548)	34335	0.602735823
negative regulation of MAPK cascade (GO:0043409)	34335	0.602735823
nucleosome organization (GO:0034728)	34335	0.602735823
sensory perception of light stimulus (GO:0050953)	34700	0.606627427
regulation of vesicle-mediated transport (GO:0060627)	35065	0.610481102
negative regulation of gene expression (GO:0010629)	3/322	0.610483862
double-strand break repair via homologous recombination (GO:00(	35431	0.614297216
positive regulation of cold-induced thermogenesis (GO:0120162)	35431	0.614297216
regulation of neuron apoptotic process (GO:0043523)	35796	0.618076133
positive regulation of defense response (GO:0031349)	35796	0.618076133
RNA splicing (GO:0008380)	35796	0.618076133
cellular protein localization (GO:0034613)	3/329	0.62501904
cell-matrix adhesion (GO:0007160)	1/100	0.625523817
organic acid transport (GO:0015849)	1/100	0.625523817
regulation of transforming growth factor beta receptor signaling pa	1/100	0.625523817
positive regulation of translation (GO:0045727)	1/100	0.625523817
regulation of cell growth (GO:0001558)	2/217	0.62735686
epithelial cell differentiation (GO:0030855)	1/101	0.629193295
positive regulation of cell cycle process (GO:0090068)	1/101	0.629193295
positive regulation of protein localization to membrane (GO:19054	1/101	0.629193295
regulation of cell death (GO:0010941)	1/102	0.632826997
regulation of protein catabolic process (GO:0042176)	1/102	0.632826997
positive regulation of cellular protein metabolic process (GO:00322	1/102	0.632826997
intrinsic apoptotic signaling pathway (GO:0097193)	1/102	0.632826997
positive regulation of vasculature development (GO:1904018)	1/102	0.632826997
mitotic sister chromatid segregation (GO:0000070)	1/102	0.632826997
cellular response to organonitrogen compound (GO:0071417)	1/103	0.636425273
regulation of insulin secretion (GO:0050796)	1/104	0.639988464
negative regulation of transmembrane receptor protein serine/thr	1/108	0.653897146
cilium organization (GO:0044782)	2/228	0.654123033
positive regulation of multicellular organismal process (GO:005124	3/345	0.65683818
post-translational protein modification (GO:0043687)	3/345	0.65683818
regulation of protein ubiquitination (GO:0031396)	1/109	0.657289957
lipid transport (GO:0006869)	1/109	0.657289957
response to endoplasmic reticulum stress (GO:0034976)	1/110	0.660649677
response to tumor necrosis factor (GO:0034612)	1/110	0.660649677
regulation of autophagy (GO:0010506)	2/231	0.661153194
Fc-epsilon receptor signaling pathway (GO:0038095)	1/111	0.663976628
regulation of Wnt signaling pathway (GO:0030111)	1/111	0.663976628
protein-containing complex subunit organization (GO:0043933)	1/112	0.667271127
Fc receptor signaling pathway (GO:0038093)	1/112	0.667271127
supramolecular fiber organization (GO:0097435)	3/351	0.668262362
cellular response to transforming growth factor beta stimulus (GO:	1/114	0.673764027
positive regulation of cellular component organization (GO:005113	1/114	0.673764027
positive regulation of angiogenesis (GO:0045766)	1/116	0.680130861
sphingolipid metabolic process (GO:0006665)	1/116	0.680130861

positive regulation of cysteine-type endopeptidase activity involve	1/119	0.689450051
macroautophagy (GO:0016236)	1/120	0.692496023
cellular response to interferon-gamma (GO:0071346)	1/121	0.695512271
protein homooligomerization (GO:0051260)	1/121	0.695512271
epithelium development (GO:0060429)	1/122	0.698499083
cellular response to organic substance (GO:0071310)	1/123	0.701456745
regulation of tumor necrosis factor production (GO:0032680)	1/124	0.70438554
protein targeting (GO:0006605)	1/125	0.707285749
regulation of protein secretion (GO:0050708)	1/125	0.707285749
plasma membrane bounded cell projection organization (GO:0120	1/128	0.715817617
cellular response to hypoxia (GO:0071456)	1/131	0.72410204
RNA metabolic process (GO:0016070)	1/133	0.729491054
positive regulation of peptidyl-tyrosine phosphorylation (GO:00507	1/134	0.732146159
cellular calcium ion homeostasis (GO:0006874)	1/136	0.737378835
central nervous system development (GO:0007417)	2/268	0.738702129
transcription initiation from RNA polymerase II promoter (GO:0006	1/140	0.747541024
protein-DNA complex assembly (GO:0065004)	1/143	0.75490505
neuron development (GO:0048666)	1/143	0.75490505
negative regulation of cell migration (GO:0030336)	1/144	0.75731192
positive regulation of intracellular protein transport (GO:0090316)	1/148	0.766706516
cellular response to organic cyclic compound (GO:0071407)	1/150	0.77126723
response to cytokine (GO:0034097)	1/150	0.77126723
proteolysis (GO:0006508)	2/287	0.772326501
regulation of cell differentiation (GO:0045595)	1/156	0.784423938
regulation of signal transduction by p53 class mediator (GO:19017	1/156	0.784423938
cellular response to growth factor stimulus (GO:0071363)	1/158	0.788639976
negative regulation of transcription by RNA polymerase II (GO:000	5/684	0.800816549
cellular protein-containing complex assembly (GO:0034622)	1/168	0.808520887
DNA-templated transcription, initiation (GO:0006352)	1/168	0.808520887
neuron projection development (GO:0031175)	1/171	0.814113973
nuclear-transcribed mRNA catabolic process (GO:0000956)	1/171	0.814113973
positive regulation of ERK1 and ERK2 cascade (GO:0070374)	1/172	0.815941976
rRNA processing (GO:0006364)	1/173	0.817752093
neuron differentiation (GO:0030182)	1/174	0.819544498
regulation of mitotic cell cycle (GO:0007346)	1/178	0.826540429
regulation of translation (GO:0006417)	1/178	0.826540429
RNA processing (GO:0006396)	1/179	0.828246831
regulated exocytosis (GO:0045055)	1/180	0.829936531
intracellular protein transport (GO:0006886)	2/336	0.842200191
cellular response to tumor necrosis factor (GO:0071356)	1/194	0.851926934
regulation of programmed cell death (GO:0043067)	1/194	0.851926934
ncRNA processing (GO:0034470)	1/201	0.861836728
protein transport (GO:0015031)	2/369	0.877697007
regulation of ERK1 and ERK2 cascade (GO:0070372)	1/238	0.904235865
membrane organization (GO:0061024)	1/242	0.907960272
positive regulation of signal transduction (GO:0009967)	1/252	0.916652772
organelle organization (GO:0006996)	2/420	0.918374134

inorganic cation transmembrane transport (GO:0098662)	1/274	0.933007033
positive regulation of cell population proliferation (GO:0008284)	2/474	0.947429789
cellular macromolecule biosynthetic process (GO:0034645)	1/314	0.954992769
transcription by RNA polymerase II (GO:0006366)	1/320	0.957602511

lysis of significant highly-correlated RNA-seq-based modules (red; Significant terms were highli

Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Combined Score	Genes	KEGG
0.273886039	0	0	20.61458333	150.7017457	PPARA;LAX	.
0.273886039	0	0	2.857438628	19.20524438	CDKL5;PRK	.
0.273886039	0	0	16.27138158	109.0834903	NLGN2;BSN	.
0.273886039	0	0	9.196044212	60.98695727	CARMIL2;S	.
0.273886039	0	0	6.570952698	43.24688562	EPM2AIP1;	.
0.273886039	0	0	6.178258145	39.07496278	CACNB2;M	.
0.273886039	0	0	14.05042614	88.86002121	MEF2C;NL(	.
0.273886039	0	0	8.27434555	51.8731579	MEF2C;AG	.
0.273886039	0	0	41.03626943	256.6321285	EPM2AIP1;	.
0.273886039	0	0	41.03626943	256.6321285	CACNB2;ST	.
0.273886039	0	0	13.4388587	83.44075483	EPM2AIP1;	.
0.273886039	0	0	4.105576142	24.94660433	MEF2C;PDI	.
0.273886039	0	0	34.19516408	204.2317809	ORMDL3;B	.
0.273886039	0	0	34.19516408	204.2317809	MEF2C;PIK	.
0.306148963	0	0	29.30866025	167.869541	INSR;NOXC	.
0.306148963	0	0	29.30866025	167.869541	HMGB2;RA	.
0.321227131	0	0	25.64378238	141.3207791	CSGALNAC	.
0.321227131	0	0	9.966733871	54.14380814	ACLY;EBP;M	.
0.321227131	0	0	9.654785156	51.65275644	ACLY;EBP;M	.
0.321227131	0	0	22.79332182	121.1843605	CARMIL2;S	.
0.321227131	0	0	22.79332182	121.1843605	CACNB2;SE	.
0.321227131	0	0	22.79332182	121.1843605	MEF2C;PIK	.
0.321227131	0	0	22.79332182	121.1843605	PRKDC;HM	.
0.322012304	0	0	9.0859375	47.1799431	PRKDC;HM	.
0.322012304	0	0	20.51295337	105.451922	NLGN2;BSN	.
0.322012304	0	0	20.51295337	105.451922	SPTBN4;PD	.
0.322012304	0	0	20.51295337	105.451922	CSGALNAC	.
0.322012304	0	0	8.825892857	45.1665878	ACLY;EBP;M	.
0.333692111	0	0	18.64719736	92.86486111	CLEC4D;BC	.
0.333692111	0	0	18.64719736	92.86486111	PDE4D;TNI	.
0.333692111	0	0	18.64719736	92.86486111	CCR7;FOXC	.
0.342615857	0	0	8.127878289	39.8659423	ADGRA2;H	.
0.342615857	0	0	5.43648388	26.39530339	ACLY;PCYT	.
0.342615857	0	0	3.645038522	17.64884574	PCYT2;PLA	.
0.342615857	0	0	17.09240069	82.596386	EPM2AIP1;	.
0.343466259	0	0	4.176782683	19.81457839	PRKDC;INS	.
0.343466259	0	0	5.229239844	24.7219799	CSGALNAC	.
0.343466259	0	0	15.77680351	74.08216381	ACLY;MVK	.
0.343466259	0	0	15.77680351	74.08216381	EPM2AIP1;	.
0.343466259	0	0	15.77680351	74.08216381	MAPK12;P	.
0.343466259	0	0	3.127659574	14.61130742	SPTBN4;SP	.
0.343591418	0	0	7.352306548	34.16749653	LAX1;PAG1	.
0.346303022	0	0	14.64914878	66.92457204	ST8SIA4;ST	.
0.346303022	0	0	2.800416323	12.75677055	CACNB2;NI	.

0.346303022	0	0	7.017400568	31.77444214	NPR3;ARR
0.346303022	0	0	7.017400568	31.77444214	MEF2C;NL
0.346303022	0	0	4.916728995	22.25725372	SPTBN4;M
0.352477306	0	0	4.746464464	20.94546487	SPTBN4;M
0.352477306	0	0	12.81670984	55.60288073	PPARA;ADI
0.352477306	0	0	12.81670984	55.60288073	VNN1;NOL
0.352477306	0	0	12.81670984	55.60288073	NLGN2;BSI
0.352477306	0	0	6.299744898	26.79704381	SYT4;CDKL
0.352477306	0	0	12.06217617	51.06473313	VNN1;NOL
0.352477306	0	0	12.06217617	51.06473313	NLGN2;LHI
0.352477306	0	0	12.06217617	51.06473313	ST8SIA4;ST
0.352477306	0	0	3.159777617	13.31502439	SPTBN4;SP
0.352477306	0	0	11.39147956	47.09769932	STAC3;RIM
0.352477306	0	0	11.39147956	47.09769932	CDKL5;LRP
0.352477306	0	0	2.402524544	9.800550301	CDKL5;PRK
0.352477306	0	0	5.823113208	23.61459205	ARRDC3;NI
0.352477306	0	0	10.7913826	43.60524771	KATNB1;TT
0.352477306	0	0	3.020342117	12.14571169	ITPKC;INPP
0.352477306	0	0	3.425235274	13.66104126	PRKDC;ULK
0.352477306	0	0	5.610795455	22.23129331	MEF2C;NL
0.352477306	0	0	10.25129534	40.51101829	INHA;TNFR
0.352477306	0	0	10.25129534	40.51101829	LAX1;PAG1
0.352477306	0	0	10.25129534	40.51101829	PLA2G4D;L
0.352477306	0	0	10.25129534	40.51101829	CACNB2;ST
0.352477306	0	0	3.380116959	13.3149583	ACAN;EBP;
0.352477306	0	0	3.380116959	13.3149583	PDE4D;PIK
0.352477306	0	0	3.357997266	13.14632976	CDKL5;INSI
0.352477306	0	0	4.045375218	15.79596754	PRKDC;INS
0.352477306	0	0	5.22934322	19.80284115	BABAM2;P
0.352477306	0	0	9.318417334	35.28430714	NRP2;ULK2
0.352477306	0	0	9.318417334	35.28430714	KATNB1;TT
0.352477306	0	0	9.318417334	35.28430714	CLEC4D;BC
0.352477306	0	0	9.318417334	35.28430714	CARMIL2;E
0.352477306	0	0	8.912818202	33.0618677	RASD2;PDI
0.352477306	0	0	8.912818202	33.0618677	PDE4D;PDI
0.352477306	0	0	8.912818202	33.0618677	KATNB1;TT
0.352477306	0	0	8.912818202	33.0618677	CCR7;JAM3
0.352477306	0	0	3.151636714	11.6071097	PRKDC;ULK
0.352477306	0	0	3.749643027	13.75722914	PAQR7;HM
0.352477306	0	0	3.715673789	13.52857328	MEF2C;TRI
0.352477306	0	0	8.541018998	31.05317173	PLA2G4D;L
0.352477306	0	0	8.541018998	31.05317173	MEF2C;CDI
0.352477306	0	0	8.198963731	29.23045673	SPOCK2;CC
0.352477306	0	0	8.198963731	29.23045673	PRKDC;HM
0.352477306	0	0	8.198963731	29.23045673	MEF2C;MA
0.352477306	0	0	2.082753412	7.39750935	MEF2C;CAI
0.352477306	0	0	3.554612746	12.460622	MEF2C;TRI

0.352477306	0	0	7.883220407	27.57045754	VNN1;NOL	.
0.352477306	0	0	7.883220407	27.57045754	INSR;TMEM	.
0.352477306	0	0	4.603078358	15.98751554	CDKL5;TBC	.
0.352477306	0	0	2.139527176	7.388130736	ACAN;MEF	.
0.352477306	0	0	4.53515625	15.58754874	EFNA2;PIK	.
0.352477306	0	0	7.590865477	26.05354227	CACNB2;PI	.
0.352477306	0	0	7.590865477	26.05354227	AXIN2;TEN	.
0.352477306	0	0	7.590865477	26.05354227	LRRC17;INI	.
0.352477306	0	0	2.609977324	8.92423727	CACNB2;NI	.
0.352477306	0	0	7.319393042	24.66303868	PLA2G4D;L	.
0.352477306	0	0	4.405133929	14.829918	INSR;FOXO	.
0.352477306	0	0	7.066642844	23.38470387	SPOCK2;CC	.
0.352477306	0	0	3.297172775	10.8115942	EPM2AIP1;	.
0.352477306	0	0	4.223458904	13.78948848	SPTBN4;M	.
0.352477306	0	0	4.223458904	13.78948848	BCL10;RAB	.
0.352477306	0	0	6.83074266	22.20630318	KATNB1;TT	.
0.352477306	0	0	6.83074266	22.20630318	BABAM2;U	.
0.352477306	0	0	2.296374226	7.422918605	MEF2C;TRI	.
0.352477306	0	0	4.166173986	13.46595056	ACLY;EBP;M	.
0.352477306	0	0	4.166173986	13.46595056	PLA2G4D;L	.
0.352477306	0	0	4.166173986	13.46595056	NRP2;HMG	.
0.352477306	0	0	6.610061842	21.11727304	NRP2;ULK2	.
0.352477306	0	0	6.610061842	21.11727304	LPCAT3;PC	.
0.352477306	0	0	6.610061842	21.11727304	INSR;PPAR	.
0.352477306	0	0	6.610061842	21.11727304	AXIN2;TEN	.
0.352477306	0	0	3.194285482	10.17355095	SPOCK2;M	.
0.352477306	0	0	6.403173575	20.10844905	MEF2C;PIK	.
0.352477306	0	0	6.403173575	20.10844905	ADA;JAM3	.
0.352477306	0	0	6.403173575	20.10844905	PLA2G4D;L	.
0.352477306	0	0	6.208823991	19.1718449	PPARA;ADI	.
0.352477306	0	0	6.208823991	19.1718449	MEF2C;MA	.
0.352477306	0	0	6.208823991	19.1718449	PVRIG;BCL	.
0.352477306	0	0	6.208823991	19.1718449	NLGN2;LRP	.
0.352477306	0	0	2.210998313	6.787264416	PRKDC;PDE	.
0.352477306	0	0	25.51675258	77.5825775	INHA	.
0.352477306	0	0	25.51675258	77.5825775	SYT4	.
0.352477306	0	0	25.51675258	77.5825775	GPD1	.
0.352477306	0	0	25.51675258	77.5825775	ORMDL3	.
0.352477306	0	0	25.51675258	77.5825775	PDE10A	.
0.352477306	0	0	25.51675258	77.5825775	ULK2	.
0.352477306	0	0	25.51675258	77.5825775	LRP8	.
0.352477306	0	0	25.51675258	77.5825775	CD1E	.
0.352477306	0	0	25.51675258	77.5825775	CD1E	.
0.352477306	0	0	25.51675258	77.5825775	CD1E	.
0.352477306	0	0	25.51675258	77.5825775	CARMIL2	.
0.352477306	0	0	25.51675258	77.5825775	INHA	.
0.352477306	0	0	25.51675258	77.5825775	TNFRSF21	.

0.352477306	0	0	25.51675258	77.5825775	TNFRSF21	.
0.352477306	0	0	25.51675258	77.5825775	LRRC17	.
0.352477306	0	0	25.51675258	77.5825775	INHA	.
0.352477306	0	0	25.51675258	77.5825775	TNFRSF21	.
0.352477306	0	0	25.51675258	77.5825775	MEF2C	.
0.352477306	0	0	25.51675258	77.5825775	PPARA	.
0.352477306	0	0	25.51675258	77.5825775	MEF2C	.
0.352477306	0	0	25.51675258	77.5825775	ORMDL3	.
0.352477306	0	0	25.51675258	77.5825775	LAPTM4B	.
0.352477306	0	0	25.51675258	77.5825775	MEF2C	.
0.352477306	0	0	25.51675258	77.5825775	VNN1	.
0.352477306	0	0	25.51675258	77.5825775	ACLY	.
0.352477306	0	0	25.51675258	77.5825775	SLC25A30	.
0.352477306	0	0	25.51675258	77.5825775	NLGN2	.
0.352477306	0	0	25.51675258	77.5825775	CCR7	.
0.352477306	0	0	25.51675258	77.5825775	MEF2C	.
0.352477306	0	0	25.51675258	77.5825775	MEF2C	.
0.352477306	0	0	25.51675258	77.5825775	MEF2C	.
0.352477306	0	0	25.51675258	77.5825775	JAM3	.
0.352477306	0	0	25.51675258	77.5825775	INHA	.
0.352477306	0	0	25.51675258	77.5825775	CSGALNAC	.
0.352477306	0	0	25.51675258	77.5825775	CCR7	.
0.352477306	0	0	25.51675258	77.5825775	ADA	.
0.352477306	0	0	25.51675258	77.5825775	JAM3	.
0.352477306	0	0	25.51675258	77.5825775	MEF2C	.
0.352477306	0	0	25.51675258	77.5825775	MVK	.
0.352477306	0	0	25.51675258	77.5825775	RAB7B	.
0.352477306	0	0	25.51675258	77.5825775	AIG1	.
0.352477306	0	0	25.51675258	77.5825775	SUOX	.
0.352477306	0	0	25.51675258	77.5825775	SUOX	.
0.352477306	0	0	25.51675258	77.5825775	NLGN2	.
0.352477306	0	0	25.51675258	77.5825775	CCR7	.
0.352477306	0	0	25.51675258	77.5825775	CACNB2	.
0.352477306	0	0	25.51675258	77.5825775	MEF2C	.
0.352477306	0	0	25.51675258	77.5825775	NLGN2	.
0.352477306	0	0	25.51675258	77.5825775	ULK2	.
0.352477306	0	0	25.51675258	77.5825775	AGO1	.
0.352477306	0	0	6.025906736	18.30047173	CDH23;CDI	.
0.352477306	0	0	6.025906736	18.30047173	PDE4D;PDI	.
0.352477306	0	0	3.006534949	9.041939516	INSR;ORMI	.
0.352477306	0	0	5.853441895	17.48818936	PRKDC;HM	.
0.352477306	0	0	3.758193598	11.22797675	MVK;LPCA	.
0.352477306	0	0	3.758193598	11.22797675	MEF2C;PIK	.
0.352477306	0	0	2.962974123	8.78564788	COLEC12;C	.
0.352477306	0	0	3.712725904	10.98608514	PRKDC;PP/	.
0.352477306	0	0	3.712725904	10.98608514	PDE4D;CCI	.
0.352477306	0	0	3.712725904	10.98608514	INSR;ADIP(	.

0.352477306	0	0	2.553804065	7.52690371	RASD2;INS	.
0.352477306	0	0	5.536479485	16.01986143	CDKL5;LRP	.
0.352477306	0	0	5.536479485	16.01986143	ITPKC;PCY	.
0.352477306	0	0	5.536479485	16.01986143	SYT4;MYO	.
0.352477306	0	0	2.112679114	6.082233765	BABAM2;P	.
0.352477306	0	0	3.582667151	10.30293679	INPP5A;CC	.
0.352477306	0	0	20.41237113	58.43991553	ADIPOR2	.
0.352477306	0	0	20.41237113	58.43991553	ADA	.
0.352477306	0	0	20.41237113	58.43991553	NOL3	.
0.352477306	0	0	20.41237113	58.43991553	GPR157	.
0.352477306	0	0	20.41237113	58.43991553	PIK3CD	.
0.352477306	0	0	20.41237113	58.43991553	FOXO1	.
0.352477306	0	0	20.41237113	58.43991553	MEF2C	.
0.352477306	0	0	20.41237113	58.43991553	FOXO1	.
0.352477306	0	0	20.41237113	58.43991553	PDE4D	.
0.352477306	0	0	20.41237113	58.43991553	PPARA	.
0.352477306	0	0	20.41237113	58.43991553	NOXO1	.
0.352477306	0	0	20.41237113	58.43991553	MEF2C	.
0.352477306	0	0	20.41237113	58.43991553	LHFPL4	.
0.352477306	0	0	20.41237113	58.43991553	PIK3CD	.
0.352477306	0	0	20.41237113	58.43991553	CUBN	.
0.352477306	0	0	20.41237113	58.43991553	MEF2C	.
0.352477306	0	0	20.41237113	58.43991553	CSGALNAC	.
0.352477306	0	0	20.41237113	58.43991553	HMGB2	.
0.352477306	0	0	20.41237113	58.43991553	CDH23	.
0.352477306	0	0	20.41237113	58.43991553	CCR7	.
0.352477306	0	0	20.41237113	58.43991553	PDE4D	.
0.352477306	0	0	20.41237113	58.43991553	CCR7	.
0.352477306	0	0	20.41237113	58.43991553	CCR7	.
0.352477306	0	0	20.41237113	58.43991553	GPD1	.
0.352477306	0	0	20.41237113	58.43991553	NOL3	.
0.352477306	0	0	20.41237113	58.43991553	PDE4D	.
0.352477306	0	0	20.41237113	58.43991553	D2HGDH	.
0.352477306	0	0	20.41237113	58.43991553	JADE1	.
0.352477306	0	0	20.41237113	58.43991553	SLC25A30	.
0.352477306	0	0	20.41237113	58.43991553	TNFRSF21	.
0.352477306	0	0	20.41237113	58.43991553	AXIN2	.
0.352477306	0	0	20.41237113	58.43991553	VNN1	.
0.352477306	0	0	20.41237113	58.43991553	NLGN2	.
0.352477306	0	0	20.41237113	58.43991553	MYO1A	.
0.352477306	0	0	20.41237113	58.43991553	BSN	.
0.352477306	0	0	3.541307471	10.0884711	ORMDL3;F	.
0.352477306	0	0	5.390509954	15.35477001	PRKDC;SPI	.
0.352477306	0	0	5.390509954	15.35477001	MEF2C;FO	.
0.352477306	0	0	2.467388567	6.988732648	MEF2C;AR	.
0.352477306	0	0	3.500887784	9.880202398	KATNB1;C	.
0.352477306	0	0	3.461376404	9.677892573	NRP2;HM	.

0.352477306	0	0	3.461376404	9.677892573	PIK3CD;CC	.
0.352477306	0	0	2.78151974	7.744608311	CARMIL2;M	.
0.352477306	0	0	5.120466321	14.14372607	ITPKC;PIK3	.
0.352477306	0	0	2.409124447	6.633933662	MEF2C;TRI	.
0.352477306	0	0	2.744153578	7.535711966	INSR;MINK	.
0.352477306	0	0	2.386574074	6.498392911	CARMIL2;II	.
0.352477306	0	0	4.99532415	13.59135668	MINK1;AD/	.
0.352477306	0	0	3.347995924	9.104504355	HAUS5;PCI	.
0.352477306	0	0	17.00945017	46.15748661	SYT4	.
0.352477306	0	0	17.00945017	46.15748661	CPEB2	.
0.352477306	0	0	17.00945017	46.15748661	CCR7	.
0.352477306	0	0	17.00945017	46.15748661	CACNB2	.
0.352477306	0	0	17.00945017	46.15748661	SPTBN4	.
0.352477306	0	0	17.00945017	46.15748661	INHA	.
0.352477306	0	0	17.00945017	46.15748661	PDE10A	.
0.352477306	0	0	17.00945017	46.15748661	TNFRSF21	.
0.352477306	0	0	17.00945017	46.15748661	EVL	.
0.352477306	0	0	17.00945017	46.15748661	TNFRSF21	.
0.352477306	0	0	17.00945017	46.15748661	FOXO1	.
0.352477306	0	0	17.00945017	46.15748661	SPIRE2	.
0.352477306	0	0	17.00945017	46.15748661	LAPTM4B	.
0.352477306	0	0	17.00945017	46.15748661	TTBK2	.
0.352477306	0	0	17.00945017	46.15748661	SYT4	.
0.352477306	0	0	17.00945017	46.15748661	VNN1	.
0.352477306	0	0	17.00945017	46.15748661	SPIRE2	.
0.352477306	0	0	17.00945017	46.15748661	CDH17	.
0.352477306	0	0	17.00945017	46.15748661	ULK2	.
0.352477306	0	0	17.00945017	46.15748661	ULK2	.
0.352477306	0	0	17.00945017	46.15748661	MEF2C	.
0.352477306	0	0	17.00945017	46.15748661	NLGN2	.
0.352477306	0	0	17.00945017	46.15748661	MEF2C	.
0.352477306	0	0	17.00945017	46.15748661	FOXO4	.
0.352477306	0	0	17.00945017	46.15748661	LAPTM4B	.
0.352477306	0	0	17.00945017	46.15748661	PIK3CD	.
0.352477306	0	0	17.00945017	46.15748661	NOL3	.
0.352477306	0	0	17.00945017	46.15748661	CCR7	.
0.352477306	0	0	17.00945017	46.15748661	PDE4D	.
0.352477306	0	0	17.00945017	46.15748661	NOL3	.
0.352477306	0	0	17.00945017	46.15748661	ULK2	.
0.352477306	0	0	17.00945017	46.15748661	PRKDC	.
0.352477306	0	0	17.00945017	46.15748661	SLC25A30	.
0.352477306	0	0	17.00945017	46.15748661	ULK2	.
0.352477306	0	0	17.00945017	46.15748661	INSR	.
0.352477306	0	0	17.00945017	46.15748661	NLGN2	.
0.352477306	0	0	17.00945017	46.15748661	AGO1	.
0.352477306	0	0	17.00945017	46.15748661	NPR3	.
0.352477306	0	0	17.00945017	46.15748661	FOXF1	.

0.352477306	0	0	17.00945017	46.15748661	ADIPOR2	.
0.352477306	0	0	4.87614113	13.07068816	MEF2C;FO	.
0.352477306	0	0	4.87614113	13.07068816	AXIN2;TEN	.
0.352477306	0	0	2.672332903	7.139636418	LPCAT3;GS	.
0.352477306	0	0	2.654956933	7.044903348	MEF2C;TRI	.
0.352477306	0	0	4.762501506	12.579268	BABAM2;A	.
0.352477306	0	0	4.762501506	12.579268	NUMBL;NL	.
0.352477306	0	0	2.620869043	6.860312018	RASD2;INS	.
0.352477306	0	0	4.65402732	12.11488233	MEF2C;TN	.
0.352477306	0	0	4.65402732	12.11488233	MEF2C;NL	.
0.352477306	0	0	14.57879234	37.68503515	PPARA	.
0.352477306	0	0	14.57879234	37.68503515	NRP2	.
0.352477306	0	0	14.57879234	37.68503515	FOXO4	.
0.352477306	0	0	14.57879234	37.68503515	ULK2	.
0.352477306	0	0	14.57879234	37.68503515	CPEB2	.
0.352477306	0	0	14.57879234	37.68503515	CCR7	.
0.352477306	0	0	14.57879234	37.68503515	SYT4	.
0.352477306	0	0	14.57879234	37.68503515	LPCAT3	.
0.352477306	0	0	14.57879234	37.68503515	NRP2	.
0.352477306	0	0	14.57879234	37.68503515	INSR	.
0.352477306	0	0	14.57879234	37.68503515	MAPK12	.
0.352477306	0	0	14.57879234	37.68503515	TMEM106	.
0.352477306	0	0	14.57879234	37.68503515	PIK3CD	.
0.352477306	0	0	14.57879234	37.68503515	PIK3CD	.
0.352477306	0	0	14.57879234	37.68503515	ALDOC	.
0.352477306	0	0	14.57879234	37.68503515	CCR7	.
0.352477306	0	0	14.57879234	37.68503515	CARMIL2	.
0.352477306	0	0	14.57879234	37.68503515	CSGALNAC	.
0.352477306	0	0	14.57879234	37.68503515	PRKDC	.
0.352477306	0	0	14.57879234	37.68503515	CCR7	.
0.352477306	0	0	14.57879234	37.68503515	AGO1	.
0.352477306	0	0	14.57879234	37.68503515	TMEM106	.
0.352477306	0	0	14.57879234	37.68503515	MVK	.
0.352477306	0	0	14.57879234	37.68503515	PIK3CD	.
0.352477306	0	0	14.57879234	37.68503515	PIK3CD	.
0.352477306	0	0	14.57879234	37.68503515	FOXF1	.
0.352477306	0	0	14.57879234	37.68503515	NLGN2	.
0.352477306	0	0	14.57879234	37.68503515	PIK3CD	.
0.352477306	0	0	2.092342342	5.393961115	COLEC12;V	.
0.352477306	0	0	4.550374208	11.6755281	ACLY;PPAR	.
0.352477306	0	0	4.550374208	11.6755281	ITPKC;INPF	.
0.352477306	0	0	4.550374208	11.6755281	LAX1;PAG1	.
0.352477306	0	0	2.08519053	5.349890417	SPTBN4;M	.
0.352477306	0	0	2.571335079	6.595077104	BABAM2;P	.
0.352477306	0	0	2.571335079	6.595077104	MEF2C;FO	.
0.352477306	0	0	4.451227754	11.25938894	PLA2G4D;(	.
0.352477306	0	0	4.451227754	11.25938894	BABAM2;S	.

0.352477306	0	0	4.451227754	11.25938894	ITPKC;INPP	.
0.352477306	0	0	4.356300298	10.86481436	CDH17;JAM	.
0.352477306	0	0	4.356300298	10.86481436	ST8SIA4;ST	.
0.352477306	0	0	3.018229167	7.500158883	TBC1D9B;A	.
0.352477306	0	0	3.018229167	7.500158883	ACLY;INSR;	.
0.352477306	0	0	12.75579897	31.53164691	ADA	.
0.352477306	0	0	12.75579897	31.53164691	COLEC12	.
0.352477306	0	0	12.75579897	31.53164691	JAM3	.
0.352477306	0	0	12.75579897	31.53164691	CCR7	.
0.352477306	0	0	12.75579897	31.53164691	FOXO4	.
0.352477306	0	0	12.75579897	31.53164691	PPP1R3F	.
0.352477306	0	0	12.75579897	31.53164691	TRIM41	.
0.352477306	0	0	12.75579897	31.53164691	FOXO1	.
0.352477306	0	0	12.75579897	31.53164691	FOXO1	.
0.352477306	0	0	12.75579897	31.53164691	SPTBN4	.
0.352477306	0	0	12.75579897	31.53164691	PPARA	.
0.352477306	0	0	12.75579897	31.53164691	HMGB2	.
0.352477306	0	0	12.75579897	31.53164691	FOXF1	.
0.352477306	0	0	12.75579897	31.53164691	MEF2C	.
0.352477306	0	0	12.75579897	31.53164691	PPARA	.
0.352477306	0	0	12.75579897	31.53164691	CAMKK2	.
0.352477306	0	0	12.75579897	31.53164691	MEF2C	.
0.352477306	0	0	12.75579897	31.53164691	LPCAT3	.
0.352477306	0	0	12.75579897	31.53164691	ALDOC	.
0.352477306	0	0	12.75579897	31.53164691	PPARA	.
0.352477306	0	0	12.75579897	31.53164691	D2HGDH	.
0.352477306	0	0	12.75579897	31.53164691	MVK	.
0.352477306	0	0	12.75579897	31.53164691	AGO1	.
0.352477306	0	0	12.75579897	31.53164691	NRP2	.
0.352477306	0	0	12.75579897	31.53164691	PIK3CD	.
0.352477306	0	0	12.75579897	31.53164691	NLGN2	.
0.352477306	0	0	12.75579897	31.53164691	MEF2C	.
0.352477306	0	0	2.988774272	7.361678376	SATB1;HM	.
0.352477306	0	0	4.265328152	10.49030148	SPIRE2;EVI	.
0.352477306	0	0	4.265328152	10.49030148	MEF2C;CD	.
0.352477306	0	0	4.265328152	10.49030148	CYP39A1;E	.
0.352477306	0	0	4.265328152	10.49030148	PLA2G4D;C	.
0.352477306	0	0	4.265328152	10.49030148	CDKL5;PRK	.
0.352477306	0	0	2.959885817	7.226661681	SYT4;MEF2	.
0.352477306	0	0	2.903744104	6.966568088	MEF2C;NL(	.
0.352477306	0	0	2.87646028	6.84127694	BCL10;RAB	.
0.352477306	0	0	11.33791523	26.88656558	ACLY	.
0.352477306	0	0	11.33791523	26.88656558	PDE4D	.
0.352477306	0	0	11.33791523	26.88656558	JAM3	.
0.352477306	0	0	11.33791523	26.88656558	JAM3	.
0.352477306	0	0	11.33791523	26.88656558	PPARA	.
0.352477306	0	0	11.33791523	26.88656558	PDE4D	.

0.352477306	0	0	11.33791523	26.88656558	JAM3	.
0.352477306	0	0	11.33791523	26.88656558	PPARA	.
0.352477306	0	0	11.33791523	26.88656558	MEF2C	.
0.352477306	0	0	11.33791523	26.88656558	ADA	.
0.352477306	0	0	11.33791523	26.88656558	ORMDL3	.
0.352477306	0	0	11.33791523	26.88656558	PPARA	.
0.352477306	0	0	11.33791523	26.88656558	RAB7B	.
0.352477306	0	0	11.33791523	26.88656558	CACNB2	.
0.352477306	0	0	11.33791523	26.88656558	LAPTM4B	.
0.352477306	0	0	11.33791523	26.88656558	INSR	.
0.352477306	0	0	11.33791523	26.88656558	CSGALNAC	.
0.352477306	0	0	11.33791523	26.88656558	LPCAT3	.
0.352477306	0	0	11.33791523	26.88656558	DLEC1	.
0.352477306	0	0	11.33791523	26.88656558	JAM3	.
0.352477306	0	0	11.33791523	26.88656558	RAB7B	.
0.352477306	0	0	11.33791523	26.88656558	MEF2C	.
0.352477306	0	0	11.33791523	26.88656558	GFPT1	.
0.352477306	0	0	11.33791523	26.88656558	LRP8	.
0.352477306	0	0	11.33791523	26.88656558	FOXO1	.
0.352477306	0	0	11.33791523	26.88656558	NPR3	.
0.352477306	0	0	11.33791523	26.88656558	JAM3	.
0.352477306	0	0	11.33791523	26.88656558	NOL3	.
0.352477306	0	0	11.33791523	26.88656558	RASD2	.
0.352477306	0	0	11.33791523	26.88656558	MEF2C	.
0.352477306	0	0	11.33791523	26.88656558	NLGN2	.
0.352477306	0	0	2.136274296	5.063730163	TRIM41;BC	.
0.355132916	0	0	4.013816926	9.473999852	INSR;TBX1	.
0.356807023	0	0	2.797585227	6.483230244	ACLY;INSR;	.
0.356807023	0	0	2.797585227	6.483230244	CSGALNAC	.
0.356807023	0	0	3.861961091	8.874556791	ST8SIA4;ST	.
0.356807023	0	0	10.20360825	23.27307496	SESTD1	.
0.356807023	0	0	10.20360825	23.27307496	ADIPOR2	.
0.356807023	0	0	10.20360825	23.27307496	MEF2C	.
0.356807023	0	0	10.20360825	23.27307496	NUMBL	.
0.356807023	0	0	10.20360825	23.27307496	NLGN2	.
0.356807023	0	0	10.20360825	23.27307496	CCR7	.
0.356807023	0	0	10.20360825	23.27307496	FOXO1	.
0.356807023	0	0	10.20360825	23.27307496	AGO1	.
0.356807023	0	0	10.20360825	23.27307496	SMYD2	.
0.356807023	0	0	10.20360825	23.27307496	INPP5A	.
0.356807023	0	0	10.20360825	23.27307496	JAM3	.
0.356807023	0	0	10.20360825	23.27307496	RAB7B	.
0.356807023	0	0	10.20360825	23.27307496	LRP8	.
0.356807023	0	0	10.20360825	23.27307496	CDH17	.
0.356807023	0	0	10.20360825	23.27307496	CCR7	.
0.356807023	0	0	10.20360825	23.27307496	ITPKC	.
0.356807023	0	0	10.20360825	23.27307496	INPP5A	.

0.356807023	0	0	10.20360825	23.27307496	PIK3CD	.
0.356807023	0	0	10.20360825	23.27307496	AGO1	.
0.356807023	0	0	10.20360825	23.27307496	GFPT1	.
0.356807023	0	0	10.20360825	23.27307496	NLGN2	.
0.356807023	0	0	10.20360825	23.27307496	NLGN2	.
0.356807023	0	0	2.309194659	5.253281009	CCR7;PPAF	.
0.356807023	0	0	2.698876096	6.044067373	CARMIL2;C	.
0.356807023	0	0	3.721149317	8.328708428	INSR;RCC1	.
0.356807023	0	0	3.721149317	8.328708428	ACLY;D2HC	.
0.356807023	0	0	2.675271739	5.94055496	MVK;LPCA	.
0.356807023	0	0	3.654515174	8.073869693	MEF2C;MA	.
0.356807023	0	0	9.275538894	20.39357155	TNFRSF21	.
0.356807023	0	0	9.275538894	20.39357155	FOXO1	.
0.356807023	0	0	9.275538894	20.39357155	ADA	.
0.356807023	0	0	9.275538894	20.39357155	GFPT1	.
0.356807023	0	0	9.275538894	20.39357155	LPCAT3	.
0.356807023	0	0	9.275538894	20.39357155	ORMDL3	.
0.356807023	0	0	9.275538894	20.39357155	PDE4D	.
0.356807023	0	0	9.275538894	20.39357155	CCR7	.
0.356807023	0	0	9.275538894	20.39357155	ZWINT	.
0.356807023	0	0	9.275538894	20.39357155	MEF2C	.
0.356807023	0	0	9.275538894	20.39357155	PPP1R3F	.
0.356807023	0	0	9.275538894	20.39357155	PPARA	.
0.356807023	0	0	9.275538894	20.39357155	TMEM106A	.
0.356807023	0	0	9.275538894	20.39357155	FOXF1	.
0.356807023	0	0	9.275538894	20.39357155	RAB7B	.
0.356807023	0	0	9.275538894	20.39357155	SLC25A30	.
0.356807023	0	0	9.275538894	20.39357155	LPCAT3	.
0.356807023	0	0	9.275538894	20.39357155	CARMIL2	.
0.356807023	0	0	9.275538894	20.39357155	CCR7	.
0.356807023	0	0	9.275538894	20.39357155	ACSS2	.
0.356807023	0	0	9.275538894	20.39357155	AXIN2	.
0.356807023	0	0	9.275538894	20.39357155	MEF2C	.
0.356807023	0	0	9.275538894	20.39357155	NRP2	.
0.356807023	0	0	9.275538894	20.39357155	MEF2C	.
0.356807023	0	0	9.275538894	20.39357155	PPARA	.
0.356807023	0	0	9.275538894	20.39357155	INPP5A	.
0.356807023	0	0	9.275538894	20.39357155	ACAN	.
0.356807023	0	0	9.275538894	20.39357155	MEF2C	.
0.356807023	0	0	9.275538894	20.39357155	KATNB1	.
0.356807023	0	0	9.275538894	20.39357155	CCR7	.
0.356807023	0	0	9.275538894	20.39357155	MEF2C	.
0.356807023	0	0	9.275538894	20.39357155	COLEC12	.
0.356807023	0	0	9.275538894	20.39357155	TBX19	.
0.356807023	0	0	9.275538894	20.39357155	ACLY	.
0.356807023	0	0	9.275538894	20.39357155	PRKDC	.
0.356807023	0	0	9.275538894	20.39357155	LPCAT3	.

0.356807023	0	0	9.275538894	20.39357155	NLGN2	.
0.36085707	0	0	3.590219071	7.830136429	MEF2C;STX	.
0.36085707	0	0	3.590219071	7.830136429	ULK2;PCNT	.
0.36085707	0	0	3.590219071	7.830136429	BABAM2;P	.
0.36503664	0	0	2.563151042	5.457034537	NRP2;HMG	.
0.36503664	0	0	1.97055858	4.188880588	SPTBN4;PR	.
0.36503664	0	0	8.502147766	18.05323882	FADS2	.
0.36503664	0	0	8.502147766	18.05323882	ADA	.
0.36503664	0	0	8.502147766	18.05323882	CACNB2	.
0.36503664	0	0	8.502147766	18.05323882	PDE4D	.
0.36503664	0	0	8.502147766	18.05323882	PPARA	.
0.36503664	0	0	8.502147766	18.05323882	INSR	.
0.36503664	0	0	8.502147766	18.05323882	PPARA	.
0.36503664	0	0	8.502147766	18.05323882	SPTBN4	.
0.36503664	0	0	8.502147766	18.05323882	SPTBN4	.
0.36503664	0	0	8.502147766	18.05323882	MEF2C	.
0.36503664	0	0	8.502147766	18.05323882	SYT4	.
0.36503664	0	0	8.502147766	18.05323882	VNN1	.
0.36503664	0	0	8.502147766	18.05323882	TRIM41	.
0.36503664	0	0	8.502147766	18.05323882	LPCAT3	.
0.36503664	0	0	8.502147766	18.05323882	ULK2	.
0.36503664	0	0	8.502147766	18.05323882	NRP2	.
0.36503664	0	0	8.502147766	18.05323882	ADIPOR2	.
0.36503664	0	0	8.502147766	18.05323882	PPARA	.
0.36503664	0	0	8.502147766	18.05323882	CARMIL2	.
0.36503664	0	0	8.502147766	18.05323882	GFPT1	.
0.36503664	0	0	2.541838843	5.366681606	ACLY;PPAR	.
0.36503664	0	0	3.410189983	7.159330918	NUMBL;HN	.
0.36503664	0	0	2.520876025	5.278304344	CPEB2;FOX	.
0.36503664	0	0	2.150598942	4.495308851	SPTBN4;CA	.
0.36503664	0	0	2.500254065	5.191846508	JADE1;ULK	.
0.36503664	0	0	2.500254065	5.191846508	CACNB2;NI	.
0.36503664	0	0	3.354115349	6.95400193	PTK7;MINK	.
0.36503664	0	0	3.354115349	6.95400193	CDK3;RCC1	.
0.36503664	0	0	3.354115349	6.95400193	CYP39A1;A	.
0.36503664	0	0	1.437863064	2.953542232	CDKL5;PRK	.
0.36503664	0	0	7.847739889	16.11953042	D2HGDH	.
0.36503664	0	0	7.847739889	16.11953042	CCR7	.
0.36503664	0	0	7.847739889	16.11953042	SLC25A30	.
0.36503664	0	0	7.847739889	16.11953042	PDE4D	.
0.36503664	0	0	7.847739889	16.11953042	FOXF1	.
0.36503664	0	0	7.847739889	16.11953042	NLGN2	.
0.36503664	0	0	7.847739889	16.11953042	PPARA	.
0.36503664	0	0	7.847739889	16.11953042	PPARA	.
0.36503664	0	0	7.847739889	16.11953042	MEF2C	.
0.36503664	0	0	7.847739889	16.11953042	CASTOR2	.
0.36503664	0	0	7.847739889	16.11953042	TRIM31	.

0.36503664	0	0	7.847739889	16.11953042	CDH23	.
0.36503664	0	0	7.847739889	16.11953042	CARMIL2	.
0.36503664	0	0	7.847739889	16.11953042	ACLY	.
0.36503664	0	0	7.847739889	16.11953042	INHA	.
0.36503664	0	0	7.847739889	16.11953042	FOXF1	.
0.36503664	0	0	7.847739889	16.11953042	LPCAT3	.
0.36503664	0	0	7.847739889	16.11953042	MEF2C	.
0.36503664	0	0	7.847739889	16.11953042	CCR7	.
0.36503664	0	0	7.847739889	16.11953042	SLC25A30	.
0.36503664	0	0	7.847739889	16.11953042	INSR	.
0.36503664	0	0	7.847739889	16.11953042	BCL10	.
0.36503664	0	0	7.847739889	16.11953042	MINK1	.
0.36503664	0	0	7.847739889	16.11953042	PIK3CD	.
0.36503664	0	0	7.847739889	16.11953042	AGO1	.
0.36503664	0	0	3.299849574	6.756977356	VNN1;NOL	.
0.36503664	0	0	3.299849574	6.756977356	CDKL5;TBC	.
0.36503664	0	0	3.299849574	6.756977356	BCL10;NOL	.
0.36503664	0	0	3.299849574	6.756977356	TLCD3A;OF	.
0.366248804	0	0	2.46	5.02447408	RCC1;PCNT	.
0.369420399	0	0	3.247306522	6.56780949	MINK1;CCF	.
0.369420399	0	0	3.247306522	6.56780949	CYP39A1;E	.
0.369420399	0	0	2.42101378	4.864152951	ADGRA2;G	.
0.369420399	0	0	2.42101378	4.864152951	ADGRA2;P	.
0.369420399	0	0	2.42101378	4.864152951	GFPT1;ST8	.
0.369420399	0	0	3.19640544	6.386080981	PPARA;FOX	.
0.369420399	0	0	7.286818851	14.49933348	CPEB2	.
0.369420399	0	0	7.286818851	14.49933348	CPEB2	.
0.369420399	0	0	7.286818851	14.49933348	COLEC12	.
0.369420399	0	0	7.286818851	14.49933348	CARMIL2	.
0.369420399	0	0	7.286818851	14.49933348	JAM3	.
0.369420399	0	0	7.286818851	14.49933348	PAG1	.
0.369420399	0	0	7.286818851	14.49933348	INHA	.
0.369420399	0	0	7.286818851	14.49933348	CSGALNAC	.
0.369420399	0	0	7.286818851	14.49933348	PCYT2	.
0.369420399	0	0	7.286818851	14.49933348	PPARA	.
0.369420399	0	0	7.286818851	14.49933348	NOXO1	.
0.369420399	0	0	7.286818851	14.49933348	NLGN2	.
0.369420399	0	0	7.286818851	14.49933348	ST8SIA4	.
0.369420399	0	0	7.286818851	14.49933348	JADE1	.
0.369420399	0	0	7.286818851	14.49933348	JADE1	.
0.369420399	0	0	7.286818851	14.49933348	CALCOCO1	.
0.369420399	0	0	7.286818851	14.49933348	MINK1	.
0.369420399	0	0	7.286818851	14.49933348	CUBN	.
0.370350339	0	0	2.063300797	4.096673571	ADGRA2;A	.
0.375303941	0	0	3.099230648	6.043409776	MEF2C;AG	.
0.375303941	0	0	6.800687285	13.12544685	HMGB2	.
0.375303941	0	0	6.800687285	13.12544685	PPARA	.

0.375303941	0	0	6.800687285	13.12544685	ULK2	.
0.375303941	0	0	6.800687285	13.12544685	ORMDL3	.
0.375303941	0	0	6.800687285	13.12544685	PPARA	.
0.375303941	0	0	6.800687285	13.12544685	NOL3	.
0.375303941	0	0	6.800687285	13.12544685	PPARA	.
0.375303941	0	0	6.800687285	13.12544685	CCR7	.
0.375303941	0	0	6.800687285	13.12544685	TNFRSF21	.
0.375303941	0	0	6.800687285	13.12544685	NLGN2	.
0.375303941	0	0	6.800687285	13.12544685	INSR	.
0.375303941	0	0	6.800687285	13.12544685	CCR7	.
0.375303941	0	0	6.800687285	13.12544685	FOXF1	.
0.375303941	0	0	6.800687285	13.12544685	MEF2C	.
0.375303941	0	0	6.800687285	13.12544685	ITPKC	.
0.375303941	0	0	6.800687285	13.12544685	CARMIL2	.
0.375303941	0	0	6.800687285	13.12544685	PRKDC	.
0.375303941	0	0	6.800687285	13.12544685	BCL10	.
0.375303941	0	0	6.800687285	13.12544685	NRP2	.
0.375303941	0	0	6.800687285	13.12544685	PPARA	.
0.375303941	0	0	6.800687285	13.12544685	FOXF1	.
0.375303941	0	0	3.052818808	5.881763014	HMGB2;CC	.
0.375303941	0	0	3.052818808	5.881763014	SYT4;MEF2	.
0.375303941	0	0	3.052818808	5.881763014	NLGN2;SP(	.
0.375303941	0	0	3.052818808	5.881763014	CCR7;EVL	.
0.378065656	0	0	2.311090226	4.421792656	CACNB2;SF	.
0.378065656	0	0	2.311090226	4.421792656	CUBN;ARR	.
0.378065656	0	0	2.002298557	3.826309995	CDK3;RCC1	.
0.378065656	0	0	3.007772021	5.726143602	INSR;ADIP(	.
0.378065656	0	0	3.007772021	5.726143602	CYP39A1;E	.
0.378065656	0	0	2.964030938	5.576253158	INSR;PPAR	.
0.378065656	0	0	6.375322165	11.94823751	PPARA	.
0.378065656	0	0	6.375322165	11.94823751	ACLY	.
0.378065656	0	0	6.375322165	11.94823751	TNFRSF21	.
0.378065656	0	0	6.375322165	11.94823751	NOXO1	.
0.378065656	0	0	6.375322165	11.94823751	LPCAT3	.
0.378065656	0	0	6.375322165	11.94823751	MEF2C	.
0.378065656	0	0	6.375322165	11.94823751	TRIM31	.
0.378065656	0	0	6.375322165	11.94823751	NPR3	.
0.378065656	0	0	6.375322165	11.94823751	SLC25A30	.
0.378065656	0	0	6.375322165	11.94823751	MEF2C	.
0.378065656	0	0	6.375322165	11.94823751	HMGB2	.
0.378065656	0	0	6.375322165	11.94823751	PPP1R3F	.
0.378065656	0	0	6.375322165	11.94823751	SYT4	.
0.378065656	0	0	6.375322165	11.94823751	PDE4D	.
0.378065656	0	0	6.375322165	11.94823751	PRKDC	.
0.378065656	0	0	6.375322165	11.94823751	AGO1	.
0.378065656	0	0	6.375322165	11.94823751	CCR7	.
0.378065656	0	0	6.375322165	11.94823751	SYT4	.

0.378065656	0	0	6.375322165	11.94823751	PRKDC	.
0.378065656	0	0	6.375322165	11.94823751	CACNB2	.
0.378065656	0	0	6.375322165	11.94823751	FOXF1	.
0.379766276	0	0	1.690802348	3.146726328	INSR;CCR7	.
0.379766276	0	0	2.9215396	5.431811865	KATNB1;TT	.
0.379766276	0	0	2.9215396	5.431811865	NUMBL;CD	.
0.379766276	0	0	2.243156934	4.155767789	CACNB2;SF	.
0.379766276	0	0	1.954126153	3.617717412	TBC1D9B;C	.
0.379766276	0	0	2.880245202	5.292557076	CCR7;EVL	.
0.379766276	0	0	2.880245202	5.292557076	LMAN1L;LF	.
0.379766276	0	0	2.880245202	5.292557076	MINK1;CCF	.
0.379766276	0	0	2.210656475	4.030543543	SATB1;HM	.
0.379766276	0	0	6	10.93030799	PPARA	.
0.379766276	0	0	6	10.93030799	INHA	.
0.379766276	0	0	6	10.93030799	SYT4	.
0.379766276	0	0	6	10.93030799	COLEC12	.
0.379766276	0	0	6	10.93030799	CCR7	.
0.379766276	0	0	6	10.93030799	HMGB2	.
0.379766276	0	0	6	10.93030799	PLA2G4D	.
0.379766276	0	0	6	10.93030799	PLA2G4D	.
0.379766276	0	0	6	10.93030799	RASD2	.
0.379766276	0	0	6	10.93030799	INSR	.
0.379766276	0	0	6	10.93030799	LRP8	.
0.379766276	0	0	6	10.93030799	MEF2C	.
0.379766276	0	0	6	10.93030799	NLGN2	.
0.379766276	0	0	6	10.93030799	CARMIL2	.
0.379766276	0	0	6	10.93030799	PPARA	.
0.379766276	0	0	6	10.93030799	MEF2C	.
0.379766276	0	0	6	10.93030799	NLGN2	.
0.379766276	0	0	6	10.93030799	NPR3	.
0.379766276	0	0	6	10.93030799	PIK3CD	.
0.379766276	0	0	6	10.93030799	NLGN2	.
0.379766276	0	0	6	10.93030799	KATNB1	.
0.385733863	0	0	1.576376926	2.804163898	ZBTB14;SF	.
0.385733863	0	0	2.763058395	4.903516965	PCYT2;PLA	.
0.385733863	0	0	2.763058395	4.903516965	CUBN;VNN	.
0.385733863	0	0	5.666380298	10.04298369	BPNT2	.
0.385733863	0	0	5.666380298	10.04298369	PPARA	.
0.385733863	0	0	5.666380298	10.04298369	CAMKK2	.
0.385733863	0	0	5.666380298	10.04298369	PVRIG	.
0.385733863	0	0	5.666380298	10.04298369	MEF2C	.
0.385733863	0	0	5.666380298	10.04298369	GFPT1	.
0.385733863	0	0	5.666380298	10.04298369	SMYD2	.
0.385733863	0	0	5.666380298	10.04298369	TNFRSF21	.
0.385733863	0	0	5.666380298	10.04298369	ACSS2	.
0.385733863	0	0	5.666380298	10.04298369	MEF2C	.
0.385733863	0	0	5.666380298	10.04298369	PLA2G4D	.

0.385733863	0	0	5.666380298	10.04298369	FOXO1	.
0.385733863	0	0	5.666380298	10.04298369	CSGALNAC	.
0.385733863	0	0	5.666380298	10.04298369	JADE1	.
0.385733863	0	0	5.666380298	10.04298369	CLEC4D	.
0.385733863	0	0	5.666380298	10.04298369	CCR7	.
0.385733863	0	0	5.666380298	10.04298369	MEF2C	.
0.385733863	0	0	5.666380298	10.04298369	PRKDC	.
0.385733863	0	0	5.666380298	10.04298369	MYO1A	.
0.388131173	0	0	2.726079447	4.782682992	ACLY;BPNT	.
0.388131173	0	0	2.726079447	4.782682992	CDKL5;TBC	.
0.388131173	0	0	2.726079447	4.782682992	INSR;PIK3C	.
0.388131173	0	0	2.726079447	4.782682992	RASD2;BCL	.
0.388131173	0	0	2.118534483	3.682998871	EPM2AIP1;	.
0.388131173	0	0	2.69007363	4.665939083	PRKDC;ST8	.
0.388131173	0	0	2.69007363	4.665939083	AGO1;FOX	.
0.388131173	0	0	5.367878459	9.263937187	PDE4D	.
0.388131173	0	0	5.367878459	9.263937187	PPARA	.
0.388131173	0	0	5.367878459	9.263937187	LRRC17	.
0.388131173	0	0	5.367878459	9.263937187	JAM3	.
0.388131173	0	0	5.367878459	9.263937187	TRIM31	.
0.388131173	0	0	5.367878459	9.263937187	PRKDC	.
0.388131173	0	0	5.367878459	9.263937187	ADA	.
0.388131173	0	0	5.367878459	9.263937187	RCC1	.
0.388131173	0	0	5.367878459	9.263937187	FOXF1	.
0.388131173	0	0	5.367878459	9.263937187	GFPT1	.
0.388131173	0	0	5.367878459	9.263937187	ST8SIA4	.
0.388131173	0	0	5.367878459	9.263937187	PRKDC	.
0.388131173	0	0	5.367878459	9.263937187	INPP5A	.
0.388131173	0	0	5.367878459	9.263937187	STAC3	.
0.388131173	0	0	5.367878459	9.263937187	TMEM106/	.
0.388131173	0	0	5.367878459	9.263937187	BCL10	.
0.388131173	0	0	5.367878459	9.263937187	LPCAT3	.
0.388131173	0	0	5.367878459	9.263937187	TBX19	.
0.388131173	0	0	5.367878459	9.263937187	AGO1	.
0.388131173	0	0	5.367878459	9.263937187	AGO1	.
0.388131173	0	0	2.103916952	3.628878618	CDKL5;HM	.
0.39142866	0	0	2.655003028	4.553102458	SPTBN4;SY	.
0.392166444	0	0	5.099226804	8.575543809	MYO1A	.
0.392166444	0	0	5.099226804	8.575543809	SPIRE2	.
0.392166444	0	0	5.099226804	8.575543809	MEF2C	.
0.392166444	0	0	5.099226804	8.575543809	LPCAT3	.
0.392166444	0	0	5.099226804	8.575543809	PDE4D	.
0.392166444	0	0	5.099226804	8.575543809	MEF2C	.
0.392166444	0	0	5.099226804	8.575543809	FOXO1	.
0.392166444	0	0	5.099226804	8.575543809	TNFRSF21	.
0.392166444	0	0	5.099226804	8.575543809	CSGALNAC	.
0.392166444	0	0	5.099226804	8.575543809	CUBN	.

0.392166444	0	0	5.099226804	8.575543809	FOXF1	.
0.392166444	0	0	5.099226804	8.575543809	BCL10	.
0.392166444	0	0	5.099226804	8.575543809	TESK2	.
0.392166444	0	0	5.099226804	8.575543809	INSR	.
0.392166444	0	0	5.099226804	8.575543809	PIK3CD	.
0.392166444	0	0	5.099226804	8.575543809	MEF2C	.
0.392166444	0	0	5.099226804	8.575543809	ZWINT	.
0.392166444	0	0	5.099226804	8.575543809	FADS2	.
0.392166444	0	0	5.099226804	8.575543809	INSR	.
0.392166444	0	0	5.099226804	8.575543809	ZWINT	.
0.392166444	0	0	5.099226804	8.575543809	ZWINT	.
0.392166444	0	0	5.099226804	8.575543809	MEF2C	.
0.393599465	0	0	2.587525415	4.338470503	BCL10;TME	.
0.394109953	0	0	2.047395833	3.422324804	ADGRA2;P	.
0.394109953	0	0	1.475629157	2.456720883	LPCAT3;JAI	.
0.394109953	0	0	2.555051813	4.236358155	NLGN2;CDI	.
0.394109953	0	0	2.555051813	4.236358155	USP20;GRI	.
0.394109953	0	0	2.555051813	4.236358155	CCR7;EVL	.
0.394109953	0	0	2.555051813	4.236358155	ARRDC3;BC	.
0.394109953	0	0	4.856161021	7.963719877	ZWINT	.
0.394109953	0	0	4.856161021	7.963719877	INHA	.
0.394109953	0	0	4.856161021	7.963719877	EFNA2	.
0.394109953	0	0	4.856161021	7.963719877	CDKL5	.
0.394109953	0	0	4.856161021	7.963719877	STAC3	.
0.394109953	0	0	4.856161021	7.963719877	ACLY	.
0.394109953	0	0	4.856161021	7.963719877	INHA	.
0.394109953	0	0	4.856161021	7.963719877	LRP8	.
0.394109953	0	0	4.856161021	7.963719877	LAPTM4B	.
0.394109953	0	0	4.856161021	7.963719877	GSTT1	.
0.394109953	0	0	4.856161021	7.963719877	GSTT1	.
0.394109953	0	0	4.856161021	7.963719877	TRIM31	.
0.394109953	0	0	4.856161021	7.963719877	CCR7	.
0.394109953	0	0	4.856161021	7.963719877	PPARA	.
0.394109953	0	0	4.856161021	7.963719877	CCR7	.
0.394109953	0	0	4.856161021	7.963719877	MAPK12	.
0.394109953	0	0	4.856161021	7.963719877	CUBN	.
0.394109953	0	0	2.523380029	4.137517829	CCR7;TMEI	.
0.394109953	0	0	2.523380029	4.137517829	CARMIL2;C	.
0.394109953	0	0	2.523380029	4.137517829	FADS2;AIG	.
0.400740991	0	0	2.492480728	4.041811598	RCC1;HAUS	.
0.400740991	0	0	1.993810877	3.230556012	RCC1;PCNT	.
0.401325203	0	0	1.980846774	3.184764675	CASTOR2;F	.
0.401325203	0	0	2.462325988	3.949108826	HAUS5;PCI	.
0.401325203	0	0	2.462325988	3.949108826	CDK3;RCC1	.
0.401325203	0	0	4.635192127	7.417086688	ADA	.
0.401325203	0	0	4.635192127	7.417086688	CPEB2	.
0.401325203	0	0	4.635192127	7.417086688	PPARA	.

0.401325203	0	0	4.635192127	7.417086688	MAP6D1	.
0.401325203	0	0	4.635192127	7.417086688	HMGB2	.
0.401325203	0	0	4.635192127	7.417086688	MAPK12	.
0.401325203	0	0	4.635192127	7.417086688	PDE4D	.
0.401325203	0	0	4.635192127	7.417086688	RAB7B	.
0.401325203	0	0	4.635192127	7.417086688	PIK3CD	.
0.401325203	0	0	4.635192127	7.417086688	INSR	.
0.401325203	0	0	4.635192127	7.417086688	ZWINT	.
0.402872299	0	0	1.547977985	2.46902556	NRP2;EFNA	.
0.405324378	0	0	2.432889218	3.859285704	MEF2C;INF	.
0.405324378	0	0	2.432889218	3.859285704	NRP2;PIK3	.
0.406608653	0	0	2.404145078	3.772224816	AGO1;FOX	.
0.406608653	0	0	4.43343792	6.926358967	PDE4D	.
0.406608653	0	0	4.43343792	6.926358967	HMGB2	.
0.406608653	0	0	4.43343792	6.926358967	ALDOC	.
0.406608653	0	0	4.43343792	6.926358967	MEF2C	.
0.406608653	0	0	4.43343792	6.926358967	MEF2C	.
0.406608653	0	0	4.43343792	6.926358967	CACNB2	.
0.406608653	0	0	4.43343792	6.926358967	CCR7	.
0.406608653	0	0	4.43343792	6.926358967	PLA2G4D	.
0.406608653	0	0	4.43343792	6.926358967	INSR	.
0.406608653	0	0	4.43343792	6.926358967	ALDOC	.
0.406608653	0	0	4.43343792	6.926358967	CARMIL2	.
0.406608653	0	0	4.43343792	6.926358967	LAX1	.
0.406608653	0	0	4.43343792	6.926358967	MINK1	.
0.406608653	0	0	4.43343792	6.926358967	CARMIL2	.
0.406608653	0	0	4.43343792	6.926358967	USP20	.
0.410262771	0	0	2.376069406	3.687814746	PTK7;LRP8	.
0.410463715	0	0	2.348639152	3.605949706	NRP2;PIK3	.
0.410463715	0	0	4.248496564	6.483890804	BPNT2	.
0.410463715	0	0	4.248496564	6.483890804	PVRIG	.
0.410463715	0	0	4.248496564	6.483890804	PPARA	.
0.410463715	0	0	4.248496564	6.483890804	SYT4	.
0.410463715	0	0	4.248496564	6.483890804	CSGALNAC	.
0.410463715	0	0	4.248496564	6.483890804	LPCAT3	.
0.410463715	0	0	4.248496564	6.483890804	CCR7	.
0.410463715	0	0	4.248496564	6.483890804	MEF2C	.
0.410463715	0	0	4.248496564	6.483890804	PCTP	.
0.410463715	0	0	4.248496564	6.483890804	NRP2	.
0.410463715	0	0	4.248496564	6.483890804	PLA2G4D	.
0.410463715	0	0	4.248496564	6.483890804	LAPTM4B	.
0.410463715	0	0	4.248496564	6.483890804	GFPT1	.
0.410463715	0	0	4.248496564	6.483890804	GRK4	.
0.410463715	0	0	4.248496564	6.483890804	PDE4D	.
0.410463715	0	0	4.248496564	6.483890804	CUBN	.
0.410463715	0	0	4.248496564	6.483890804	ALDOC	.
0.410463715	0	0	4.248496564	6.483890804	PPARA	.

0.410463715	0	0	4.248496564	6.483890804	FOXF1	.
0.412955049	0	0	2.321832313	3.526529198	BCL10;NOI	.
0.415365541	0	0	1.882860429	2.846477434	INSR;MINK	.
0.415506842	0	0	2.295627874	3.449457691	COLEC12;B	.
0.415506842	0	0	4.078350515	6.083333948	CSGALNAC	.
0.415506842	0	0	4.078350515	6.083333948	ADA	.
0.415506842	0	0	4.078350515	6.083333948	MEF2C	.
0.415506842	0	0	4.078350515	6.083333948	PPARA	.
0.415506842	0	0	4.078350515	6.083333948	TNFRSF21	.
0.415506842	0	0	4.078350515	6.083333948	HMGB2	.
0.415506842	0	0	4.078350515	6.083333948	PDE4D	.
0.415506842	0	0	4.078350515	6.083333948	FANCA	.
0.415506842	0	0	4.078350515	6.083333948	TRIM31	.
0.415506842	0	0	4.078350515	6.083333948	CCR7	.
0.415506842	0	0	4.078350515	6.083333948	INSR	.
0.415506842	0	0	4.078350515	6.083333948	PDE4D	.
0.415506842	0	0	4.078350515	6.083333948	SMYD2	.
0.415506842	0	0	4.078350515	6.083333948	KATNB1	.
0.415506842	0	0	4.078350515	6.083333948	CD1E	.
0.41707473	0	0	2.270005757	3.374644326	MVK;PPAR	.
0.419558134	0	0	3.921292625	5.719377463	VNN1	.
0.419558134	0	0	3.921292625	5.719377463	PDE4D	.
0.419558134	0	0	3.921292625	5.719377463	CYP39A1	.
0.419558134	0	0	3.921292625	5.719377463	MEF2C	.
0.419558134	0	0	3.921292625	5.719377463	SYT4	.
0.419558134	0	0	3.921292625	5.719377463	EVL	.
0.419558134	0	0	3.921292625	5.719377463	CSGALNAC	.
0.419558134	0	0	3.921292625	5.719377463	INSR	.
0.419558134	0	0	3.921292625	5.719377463	SMYD2	.
0.419558134	0	0	3.921292625	5.719377463	CACNB2	.
0.419558134	0	0	3.921292625	5.719377463	ADGRA2	.
0.419558134	0	0	3.921292625	5.719377463	CCR7	.
0.419558134	0	0	3.921292625	5.719377463	INSR	.
0.419558134	0	0	3.921292625	5.719377463	INSR	.
0.419558134	0	0	3.921292625	5.719377463	MEF2C	.
0.419558134	0	0	3.921292625	5.719377463	KATNB1	.
0.419558134	0	0	3.921292625	5.719377463	NLGN2	.
0.419558134	0	0	3.921292625	5.719377463	NLGN2	.
0.419558134	0	0	2.22043253	3.231450333	INSR;CAMI	.
0.419558134	0	0	2.22043253	3.231450333	NRP2;PIK3	.
0.419558134	0	0	1.826357887	2.657857154	CCR7;BCL1	.
0.419821267	0	0	1.644778065	2.388651451	ADGRA2;P	.
0.419821267	0	0	1.644778065	2.388651451	INSR;BCL1(	.
0.421588221	0	0	3.775868652	5.387547135	ULK2	.
0.421588221	0	0	3.775868652	5.387547135	CACNB2	.
0.421588221	0	0	3.775868652	5.387547135	SMYD2	.
0.421588221	0	0	3.775868652	5.387547135	INSR	.

0.421588221	0	0	3.775868652	5.387547135	CDKL5	.
0.421588221	0	0	3.775868652	5.387547135	STXBP5	.
0.421588221	0	0	3.775868652	5.387547135	PPARA	.
0.421588221	0	0	3.775868652	5.387547135	PPARA	.
0.421588221	0	0	3.775868652	5.387547135	GPR157	.
0.421588221	0	0	3.775868652	5.387547135	PLA2G4D	.
0.421588221	0	0	3.775868652	5.387547135	CCR7	.
0.421588221	0	0	3.775868652	5.387547135	NPR3	.
0.421588221	0	0	3.775868652	5.387547135	ACAN	.
0.421588221	0	0	3.775868652	5.387547135	CCR7	.
0.421588221	0	0	3.775868652	5.387547135	SLC25A30	.
0.421588221	0	0	3.775868652	5.387547135	NLGN2	.
0.421588221	0	0	3.775868652	5.387547135	KATNB1	.
0.421588221	0	0	3.775868652	5.387547135	JAM3	.
0.425144401	0	0	2.149986365	3.031563646	CSGALNAC	.
0.425144401	0	0	3.640832106	5.084049295	SPIRE2	.
0.425144401	0	0	3.640832106	5.084049295	PCNT	.
0.425144401	0	0	3.640832106	5.084049295	AXIN2	.
0.425144401	0	0	3.640832106	5.084049295	INHA	.
0.425144401	0	0	3.640832106	5.084049295	PRKDC	.
0.425144401	0	0	3.640832106	5.084049295	ADIPOR2	.
0.425144401	0	0	3.640832106	5.084049295	LRP8	.
0.425144401	0	0	3.640832106	5.084049295	PDE4D	.
0.425144401	0	0	3.640832106	5.084049295	CD1E	.
0.425144401	0	0	3.640832106	5.084049295	GPR157	.
0.425144401	0	0	3.640832106	5.084049295	ARRDC3	.
0.425144401	0	0	3.640832106	5.084049295	ALDOC	.
0.425144401	0	0	3.640832106	5.084049295	BCL10	.
0.425144401	0	0	3.640832106	5.084049295	D2HGDH	.
0.425144401	0	0	3.640832106	5.084049295	JAM3	.
0.425144401	0	0	3.640832106	5.084049295	PPARA	.
0.425144401	0	0	3.640832106	5.084049295	AGO1	.
0.425144401	0	0	2.127482729	2.968620438	MEF2C;INF	.
0.425144401	0	0	2.127482729	2.968620438	SPTBN4;PD	.
0.429020751	0	0	1.592926844	2.202669277	NLGN2;FAI	.
0.429020751	0	0	2.105443085	2.90740932	MINK1;CCF	.
0.429020751	0	0	3.515108425	4.805648067	FOXF1	.
0.429020751	0	0	3.515108425	4.805648067	SYT4	.
0.429020751	0	0	3.515108425	4.805648067	CSGALNAC	.
0.429020751	0	0	3.515108425	4.805648067	SPIRE2	.
0.429020751	0	0	3.515108425	4.805648067	MEF2C	.
0.429020751	0	0	3.515108425	4.805648067	ACLY	.
0.429020751	0	0	3.515108425	4.805648067	FOXF1	.
0.429020751	0	0	3.515108425	4.805648067	CCR7	.
0.429020751	0	0	3.515108425	4.805648067	JAM3	.
0.429020751	0	0	3.515108425	4.805648067	CCR7	.
0.429020751	0	0	3.515108425	4.805648067	BCL10	.

0.429020751	0	0	3.515108425	4.805648067	JAM3	.
0.429020751	0	0	3.515108425	4.805648067	BCL10	.
0.429020751	0	0	3.515108425	4.805648067	NOL3	.
0.429020751	0	0	1.427024638	1.950874525	RASD2;CAS	.
0.431702992	0	0	1.73269774	2.356021725	EPM2AIP1;	.
0.432669361	0	0	2.062699534	2.789938286	CPEB2;FOX	.
0.432669361	0	0	3.397766323	4.549568026	INSR	.
0.432669361	0	0	3.397766323	4.549568026	CSGALNAC	.
0.432669361	0	0	3.397766323	4.549568026	ACLY	.
0.432669361	0	0	3.397766323	4.549568026	SYT4	.
0.432669361	0	0	3.397766323	4.549568026	INSR	.
0.432669361	0	0	3.397766323	4.549568026	PPARA	.
0.432669361	0	0	3.397766323	4.549568026	PCYT2	.
0.432669361	0	0	3.397766323	4.549568026	ACLY	.
0.432669361	0	0	3.397766323	4.549568026	CCR7	.
0.432669361	0	0	3.397766323	4.549568026	BCL10	.
0.432669361	0	0	3.397766323	4.549568026	ARRDC3	.
0.432669361	0	0	3.397766323	4.549568026	CUBN	.
0.432669361	0	0	3.397766323	4.549568026	FOXO1	.
0.432669361	0	0	2.041968912	2.733562609	CCR7;CAM	.
0.432669361	0	0	2.041968912	2.733562609	NLGN2;SP(	.
0.432669361	0	0	2.041968912	2.733562609	SYT4;CDKL	.
0.434646684	0	0	1.556108534	2.074345731	FANCA;AN	.
0.435990845	0	0	1.233069772	1.637367879	MEF2C;CA	.
0.435990845	0	0	2.021648797	2.678687213	SATB1;SM/	.
0.435990845	0	0	3.287994679	4.313416363	ULK2	.
0.435990845	0	0	3.287994679	4.313416363	MEF2C	.
0.435990845	0	0	3.287994679	4.313416363	ADIPOR2	.
0.435990845	0	0	3.287994679	4.313416363	ADGRA2	.
0.435990845	0	0	3.287994679	4.313416363	CDKL5	.
0.435990845	0	0	3.287994679	4.313416363	LRP8	.
0.435990845	0	0	3.287994679	4.313416363	PCNT	.
0.435990845	0	0	3.287994679	4.313416363	MEF2C	.
0.435990845	0	0	3.287994679	4.313416363	MEF2C	.
0.435990845	0	0	3.287994679	4.313416363	AGO1	.
0.435990845	0	0	3.287994679	4.313416363	INSR	.
0.435990845	0	0	3.287994679	4.313416363	CARMIL2	.
0.435990845	0	0	3.287994679	4.313416363	MEF2C	.
0.435990845	0	0	3.287994679	4.313416363	NOXO1	.
0.435990845	0	0	2.001727116	2.625260355	CYP39A1;C	.
0.436242628	0	0	1.684666896	2.206653528	SPTBN4;SP	.
0.440417533	0	0	1.260166739	1.636637034	MEF2C;CA	.
0.440417533	0	0	1.982192263	2.573232521	MINK1;CCI	.
0.442451283	0	0	3.185083763	4.095120179	CYP39A1	.
0.442451283	0	0	3.185083763	4.095120179	MEF2C	.
0.442451283	0	0	3.185083763	4.095120179	MEF2C	.
0.442451283	0	0	3.185083763	4.095120179	LPCAT3	.

0.442451283	0	0	3.185083763	4.095120179	ACAN	.
0.442451283	0	0	3.185083763	4.095120179	BABAM2	.
0.442451283	0	0	1.963033081	2.522556307	RCC1;KLHL	.
0.442451283	0	0	1.963033081	2.522556307	INSR;PIK3C	.
0.444937329	0	0	3.088409872	3.89287561	MEF2C	.
0.444937329	0	0	3.088409872	3.89287561	LIX1	.
0.444937329	0	0	3.088409872	3.89287561	NOL3	.
0.444937329	0	0	3.088409872	3.89287561	TESK2	.
0.444937329	0	0	3.088409872	3.89287561	CASTOR2	.
0.444937329	0	0	3.088409872	3.89287561	BCL10	.
0.444937329	0	0	3.088409872	3.89287561	CARMIL2	.
0.444937329	0	0	3.088409872	3.89287561	ULK2	.
0.444937329	0	0	3.088409872	3.89287561	MEF2C	.
0.444937329	0	0	3.088409872	3.89287561	PIK3CD	.
0.444937329	0	0	3.088409872	3.89287561	MEF2C	.
0.444937329	0	0	3.088409872	3.89287561	HMGB2	.
0.444937329	0	0	3.088409872	3.89287561	CCR7	.
0.444937329	0	0	3.088409872	3.89287561	PAQR7	.
0.444937329	0	0	3.088409872	3.89287561	SMYD2	.
0.444937329	0	0	3.088409872	3.89287561	ZWINT	.
0.444937329	0	0	3.088409872	3.89287561	MEF2C	.
0.444937329	0	0	3.088409872	3.89287561	NLGN2	.
0.447210154	0	0	1.4983411	1.879431491	PRKDC;FAN	.
0.447519202	0	0	1.328358944	1.662767982	ZBTB14;SFI	.
0.447519202	0	0	2.99742268	3.705106255	JADE1	.
0.447519202	0	0	2.99742268	3.705106255	EVL	.
0.447519202	0	0	2.99742268	3.705106255	TNFRSF21	.
0.447519202	0	0	2.99742268	3.705106255	BPNT2	.
0.447519202	0	0	2.99742268	3.705106255	CCR7	.
0.447519202	0	0	2.99742268	3.705106255	MEF2C	.
0.447519202	0	0	2.99742268	3.705106255	SYT4	.
0.447519202	0	0	2.99742268	3.705106255	CASTOR2	.
0.447519202	0	0	2.99742268	3.705106255	FOXF1	.
0.447519202	0	0	2.99742268	3.705106255	COLEC12	.
0.447519202	0	0	2.99742268	3.705106255	PPARA	.
0.447519202	0	0	2.99742268	3.705106255	PRKDC	.
0.447519202	0	0	2.99742268	3.705106255	NRP2	.
0.447519202	0	0	2.99742268	3.705106255	TTBK2	.
0.447519202	0	0	2.99742268	3.705106255	FOXF1	.
0.447519202	0	0	2.99742268	3.705106255	MEF2C	.
0.447930024	0	0	1.889944348	2.3324876	CCR7;CAM	.
0.449002296	0	0	1.604548429	1.96599804	MEF2C;SFN	.
0.449002296	0	0	2.911634757	3.530429016	TTBK2	.
0.449002296	0	0	2.911634757	3.530429016	FOXO1	.
0.449002296	0	0	2.911634757	3.530429016	PDE4D	.
0.449002296	0	0	2.911634757	3.530429016	INSR	.
0.449002296	0	0	2.911634757	3.530429016	RAB7B	.

0.449002296	0	0	2.911634757	3.530429016	MAP6D1	.
0.449002296	0	0	2.911634757	3.530429016	MINK1	.
0.449002296	0	0	2.911634757	3.530429016	MEF2C	.
0.449002296	0	0	2.911634757	3.530429016	LRRC17	.
0.449002296	0	0	2.911634757	3.530429016	INSR	.
0.449002296	0	0	2.911634757	3.530429016	MEF2C	.
0.449002296	0	0	2.911634757	3.530429016	SPTBN4	.
0.449002296	0	0	2.911634757	3.530429016	INSR	.
0.449002296	0	0	2.911634757	3.530429016	TMEM106A	.
0.449002296	0	0	2.911634757	3.530429016	NLGN2	.
0.449002296	0	0	2.911634757	3.530429016	CD1E	.
0.449002296	0	0	2.911634757	3.530429016	ULK2	.
0.449002296	0	0	2.911634757	3.530429016	AGO1	.
0.44937112	0	0	1.855393311	2.244468517	ARHGEF19	.
0.44937112	0	0	1.855393311	2.244468517	PLA2G4D;P	.
0.451225248	0	0	2.830612829	3.367625851	SLC25A27	.
0.451225248	0	0	2.830612829	3.367625851	MEF2C	.
0.451225248	0	0	2.830612829	3.367625851	PPARA	.
0.451225248	0	0	2.830612829	3.367625851	JADE1	.
0.451225248	0	0	2.830612829	3.367625851	FOXO1	.
0.451225248	0	0	2.830612829	3.367625851	INSR	.
0.451225248	0	0	2.830612829	3.367625851	MAP6D1	.
0.451225248	0	0	2.830612829	3.367625851	MINK1	.
0.451225248	0	0	2.830612829	3.367625851	PCYT2	.
0.451225248	0	0	2.830612829	3.367625851	CACNB2	.
0.451225248	0	0	2.830612829	3.367625851	MEF2C	.
0.451225248	0	0	2.830612829	3.367625851	STXBP5	.
0.451225248	0	0	2.830612829	3.367625851	MEF2C	.
0.451225248	0	0	2.830612829	3.367625851	PIK3CD	.
0.451225248	0	0	1.571314103	1.869381245	PDE10A;PD	.
0.451225248	0	0	1.571314103	1.869381245	USP20;CAS	.
0.452065849	0	0	1.82207624	2.160733172	INSR;MINK	.
0.452065849	0	0	1.82207624	2.160733172	INSR;CCR7	.
0.453692146	0	0	1.563217474	1.846134815	LAPTM4B;S	.
0.453692146	0	0	1.805859966	2.120387918	CACNB2;CD	.
0.453692146	0	0	1.805859966	2.120387918	VNN1;ORM	.
0.453692146	0	0	1.805859966	2.120387918	CLEC4D;BC	.
0.453692146	0	0	1.805859966	2.120387918	CLEC4D;BC	.
0.453692146	0	0	1.805859966	2.120387918	BCL10;FOX	.
0.453692146	0	0	2.753970465	3.215620285	MEF2C	.
0.453692146	0	0	2.753970465	3.215620285	FOXO4	.
0.453692146	0	0	2.753970465	3.215620285	CDKL5	.
0.453692146	0	0	2.753970465	3.215620285	GRK4	.
0.453692146	0	0	2.753970465	3.215620285	CASTOR2	.
0.453692146	0	0	2.753970465	3.215620285	NUMBL	.
0.453692146	0	0	2.753970465	3.215620285	NLGN2	.
0.453692146	0	0	2.753970465	3.215620285	MEF2C	.

0.453692146	0	0	2.753970465	3.215620285	NLGN2	.
0.457739924	0	0	1.539415829	1.778466907	MEF2C;CD	.
0.457739924	0	0	2.68136191	3.073457784	TNFRSF21	.
0.457739924	0	0	2.68136191	3.073457784	SYT4	.
0.457739924	0	0	2.68136191	3.073457784	CACNB2	.
0.457739924	0	0	2.68136191	3.073457784	AXIN2	.
0.457739924	0	0	2.68136191	3.073457784	NPR3	.
0.457739924	0	0	2.68136191	3.073457784	ADGRA2	.
0.457739924	0	0	2.68136191	3.073457784	LRP8	.
0.457739924	0	0	2.68136191	3.073457784	FANCA	.
0.457739924	0	0	2.68136191	3.073457784	TRIM31	.
0.457739924	0	0	2.68136191	3.073457784	TONSL	.
0.457739924	0	0	2.68136191	3.073457784	PCNT	.
0.457739924	0	0	2.68136191	3.073457784	FOXO1	.
0.460747982	0	0	1.203818848	1.370135489	MEF2C;ZB	.
0.460747982	0	0	1.348840439	1.534667526	MEF2C;CA	.
0.461159315	0	0	1.743766884	1.968439495	CLEC4D;BC	.
0.461159315	0	0	2.61247687	2.940289271	ULK2	.
0.461159315	0	0	2.61247687	2.940289271	LRRC17	.
0.461159315	0	0	2.61247687	2.940289271	CSGALNAC	.
0.461159315	0	0	2.61247687	2.940289271	PPARA	.
0.461159315	0	0	2.61247687	2.940289271	FOXF1	.
0.461159315	0	0	2.61247687	2.940289271	INSR	.
0.461159315	0	0	2.61247687	2.940289271	STAC3	.
0.461159315	0	0	2.61247687	2.940289271	ACLY	.
0.461159315	0	0	2.61247687	2.940289271	ST8SIA5	.
0.461159315	0	0	2.61247687	2.940289271	MEF2C	.
0.461159315	0	0	2.61247687	2.940289271	ACAN	.
0.462330886	0	0	1.508774631	1.692842768	MVK;LPCA	.
0.462673842	0	0	1.220892972	1.356762028	PRKDC;INS	.
0.462673842	0	0	1.289115646	1.427080255	NUMBL;PI	.
0.462673842	0	0	2.547036082	2.815357213	PPARA	.
0.462673842	0	0	2.547036082	2.815357213	ALDOC	.
0.462673842	0	0	2.547036082	2.815357213	SLC25A30	.
0.462673842	0	0	2.547036082	2.815357213	CCR7	.
0.462673842	0	0	2.547036082	2.815357213	FOXO4	.
0.462673842	0	0	2.547036082	2.815357213	LAPTM4B	.
0.462673842	0	0	2.547036082	2.815357213	ADGRA2	.
0.462673842	0	0	2.547036082	2.815357213	NOL3	.
0.462673842	0	0	2.547036082	2.815357213	SMYD2	.
0.462673842	0	0	2.547036082	2.815357213	MEF2C	.
0.462673842	0	0	2.547036082	2.815357213	ALDOC	.
0.462673842	0	0	2.547036082	2.815357213	TRIM31	.
0.462673842	0	0	2.547036082	2.815357213	ALDOC	.
0.462673842	0	0	2.547036082	2.815357213	MINK1	.
0.462673842	0	0	2.547036082	2.815357213	PIK3CD	.
0.46751077	0	0	1.380288666	1.506488108	ACAN;SPO	.

0.46751077	0	0	2.484787528	2.69798384	SMARCA2	.
0.46751077	0	0	2.484787528	2.69798384	CCR7	.
0.46751077	0	0	2.484787528	2.69798384	SPIRE2	.
0.46751077	0	0	2.484787528	2.69798384	ST8SIA4	.
0.46751077	0	0	2.484787528	2.69798384	HMGB2	.
0.46751077	0	0	2.484787528	2.69798384	AXIN2	.
0.46751077	0	0	2.484787528	2.69798384	JADE1	.
0.46751077	0	0	2.484787528	2.69798384	LRP8	.
0.46751077	0	0	1.685779129	1.830257451	MEF2C;AD	.
0.468665223	0	0	1.671876327	1.797674693	AGO1;ARH	.
0.468665223	0	0	1.465011962	1.573511812	MVK;LPCA	.
0.468665223	0	0	2.425503191	2.587561101	MINK1	.
0.468665223	0	0	2.425503191	2.587561101	PPARA	.
0.468665223	0	0	2.425503191	2.587561101	FOXO1	.
0.468665223	0	0	2.425503191	2.587561101	PTK7	.
0.468665223	0	0	2.425503191	2.587561101	MAMLD1	.
0.468665223	0	0	2.425503191	2.587561101	TONSL	.
0.468665223	0	0	2.425503191	2.587561101	CDKL5	.
0.468665223	0	0	2.425503191	2.587561101	GSTT1	.
0.468665223	0	0	2.425503191	2.587561101	MEF2C	.
0.468665223	0	0	2.425503191	2.587561101	CD1E	.
0.468665223	0	0	2.425503191	2.587561101	MEF2C	.
0.468665223	0	0	2.425503191	2.587561101	NLGN2	.
0.468665223	0	0	2.425503191	2.587561101	LPCAT3	.
0.468665223	0	0	2.425503191	2.587561101	MAMLD1	.
0.468665223	0	0	2.425503191	2.587561101	VNN1	.
0.468665223	0	0	2.425503191	2.587561101	PIK3CD	.
0.469134467	0	0	1.658199587	1.765831394	BCL10;INH	.
0.470580071	0	0	1.111743322	1.177827722	MEF2C;CA	.
0.470580071	0	0	1.450977488	1.535992884	INSR;AXIN2	.
0.470580071	0	0	1.64474344	1.734706172	JADE1;SM/	.
0.470580071	0	0	1.64474344	1.734706172	MEF2C;FO	.
0.470580071	0	0	1.64474344	1.734706172	ITPKC;PIK3	.
0.470580071	0	0	2.368976265	2.483542101	FOXF1	.
0.470580071	0	0	2.368976265	2.483542101	PPARA	.
0.470580071	0	0	2.368976265	2.483542101	CCR7	.
0.470580071	0	0	2.368976265	2.483542101	ALDOC	.
0.470580071	0	0	2.368976265	2.483542101	CALCOCO1	.
0.470580071	0	0	2.368976265	2.483542101	MEF2C	.
0.470580071	0	0	2.368976265	2.483542101	PIK3CD	.
0.470580071	0	0	2.368976265	2.483542101	INSR	.
0.470580071	0	0	2.368976265	2.483542101	EVL	.
0.470580071	0	0	2.368976265	2.483542101	AGO1	.
0.472513307	0	0	1.437206573	1.499537446	ACAN;SPO	.
0.475656189	0	0	1.43041764	1.481696969	ACAN;SPO	.
0.477397053	0	0	2.315018744	2.385433746	PPARA	.
0.477397053	0	0	2.315018744	2.385433746	BABAM2	.

0.483227454	0	0	1.593021373	1.616984598	MVK;PPAR	.
0.483227454	0	0	1.593021373	1.616984598	HAUS5;PCI	.
0.483227454	0	0	1.593021373	1.616984598	SPTBN5;LM	.
0.483227454	0	0	2.263459336	2.292790412	INHA	.
0.483227454	0	0	2.263459336	2.292790412	NOL3	.
0.483227454	0	0	2.263459336	2.292790412	LAPTM4B	.
0.486025834	0	0	1.580592039	1.589154764	HAUS5;PCI	.
0.486025834	0	0	1.580592039	1.589154764	SYT4;MEF2	.
0.486762459	0	0	1.266945279	1.270772379	CARMIL2;II	.
0.486774832	0	0	1.263744138	1.260915948	TRIM41;PR	.
0.486774832	0	0	2.214141641	2.205208481	HMGB2	.
0.486774832	0	0	2.214141641	2.205208481	MEF2C	.
0.486774832	0	0	2.214141641	2.205208481	MEF2C	.
0.486774832	0	0	2.214141641	2.205208481	ORMDL3	.
0.486774832	0	0	2.214141641	2.205208481	ST8SIA5	.
0.486774832	0	0	2.214141641	2.205208481	INHA	.
0.486774832	0	0	2.214141641	2.205208481	PRKDC	.
0.490974225	0	0	1.556302654	1.535292819	MINK1;CCI	.
0.491355711	0	0	1.384615385	1.363637016	CCR7;BCL1	.
0.49188198	0	0	2.166922571	2.122321603	ZWINT	.
0.49188198	0	0	2.166922571	2.122321603	TNFRSF21	.
0.49188198	0	0	2.166922571	2.122321603	PDE4D	.
0.49188198	0	0	2.166922571	2.122321603	JADE1	.
0.49188198	0	0	2.166922571	2.122321603	TNFRSF21	.
0.497279431	0	0	2.121670962	2.043796579	PPARA	.
0.497279431	0	0	2.121670962	2.043796579	GRK4	.
0.497279431	0	0	2.121670962	2.043796579	BCL10	.
0.497279431	0	0	2.121670962	2.043796579	PRKDC	.
0.497279431	0	0	2.121670962	2.043796579	FOXO1	.
0.497279431	0	0	2.121670962	2.043796579	EBP	.
0.499022596	0	0	1.521228057	1.458752786	PRKDC;NO	.
0.504281567	0	0	2.078266358	1.96932977	CACNB2	.
0.505999346	0	0	1.347604626	1.271220268	VNN1;PIK3	.
0.506810395	0	0	1.341625548	1.256544905	JADE1;FOX	.
0.506810395	0	0	2.036597938	1.898643958	EVL	.
0.506810395	0	0	2.036597938	1.898643958	CCR7	.
0.506810395	0	0	2.036597938	1.898643958	EVL	.
0.506810395	0	0	2.036597938	1.898643958	MAMLD1	.
0.506810395	0	0	2.036597938	1.898643958	PIK3CD	.
0.506810395	0	0	2.036597938	1.898643958	CDH23	.
0.506810395	0	0	2.036597938	1.898643958	PRKDC	.
0.506810395	0	0	2.036597938	1.898643958	MEF2C	.
0.506810395	0	0	2.036597938	1.898643958	RCC1	.
0.506810395	0	0	2.036597938	1.898643958	RCC1	.
0.508410628	0	0	1.476834122	1.364017044	SPTBN4;M	.
0.508410628	0	0	1.476834122	1.364017044	INSR;MPZL	.
0.508410628	0	0	1.996563574	1.831485594	MEF2C	.

0.508410628	0	0	1.996563574	1.831485594	JAM3	.
0.508410628	0	0	1.996563574	1.831485594	STXBP5	.
0.508410628	0	0	1.996563574	1.831485594	ANKRD50	.
0.508410628	0	0	1.996563574	1.831485594	MINK1	.
0.508410628	0	0	1.996563574	1.831485594	PDE4D	.
0.508410628	0	0	1.996563574	1.831485594	EPM2AIP1	.
0.508410628	0	0	1.996563574	1.831485594	ADGRA2	.
0.508410628	0	0	1.996563574	1.831485594	STAC3	.
0.508410628	0	0	1.996563574	1.831485594	STAC3	.
0.508410628	0	0	1.996563574	1.831485594	INHA	.
0.508410628	0	0	1.214598997	1.114036454	RCC1;ULK2	.
0.509090202	0	0	1.466134864	1.341549212	ARHGEF19	.
0.514081352	0	0	1.958068993	1.767622378	ZBTB38	.
0.514081352	0	0	1.958068993	1.767622378	MEF2C	.
0.514081352	0	0	1.958068993	1.767622378	GFPT1	.
0.515581266	0	0	1.445191636	1.297985319	CUBN;ARR	.
0.515581266	0	0	1.445191636	1.297985319	VNN1;PPAI	.
0.517526661	0	0	1.2	1.072030452	MEF2C;INS	.
0.517526661	0	0	1.921027038	1.706841126	CCR7	.
0.517526661	0	0	1.921027038	1.706841126	RCC1	.
0.517526661	0	0	1.921027038	1.706841126	CCR7	.
0.517526661	0	0	1.921027038	1.706841126	SLC25A30	.
0.517526661	0	0	1.921027038	1.706841126	STAC3	.
0.517526661	0	0	1.921027038	1.706841126	FADS2	.
0.5212825	0	0	1.885357006	1.648945887	ALDOC	.
0.5212825	0	0	1.885357006	1.648945887	NOL3	.
0.5212825	0	0	1.885357006	1.648945887	MEF2C	.
0.5212825	0	0	1.885357006	1.648945887	AGO1	.
0.5212825	0	0	1.885357006	1.648945887	ORMDL3	.
0.5212825	0	0	1.885357006	1.648945887	AGO1	.
0.5212825	0	0	1.885357006	1.648945887	FANCA	.
0.5212825	0	0	1.885357006	1.648945887	BABAM2	.
0.521423288	0	0	1.414867588	1.235895957	AXIN2;TEN	.
0.524919239	0	0	1.405038413	1.216024292	CCR7;GPR1	.
0.524919239	0	0	1.850984067	1.593756272	LIX1	.
0.524919239	0	0	1.850984067	1.593756272	ULK2	.
0.524919239	0	0	1.850984067	1.593756272	INSR	.
0.524919239	0	0	1.850984067	1.593756272	ACAN	.
0.524919239	0	0	1.850984067	1.593756272	TMEM106	.
0.524919239	0	0	1.850984067	1.593756272	PRKDC	.
0.526326927	0	0	1.395343885	1.196547837	CDH23;CCI	.
0.528007097	0	0	1.385781256	1.177456757	HAUS5;PCI	.
0.528007097	0	0	1.817838733	1.541105976	MEF2C	.
0.528007097	0	0	1.817838733	1.541105976	TRIM41	.
0.528007097	0	0	1.817838733	1.541105976	NOXO1	.
0.528007097	0	0	1.817838733	1.541105976	NLGN2	.
0.528007097	0	0	1.817838733	1.541105976	FOXF1	.

0.528007097	0	0	1.817838733	1.541105976	PDE4D	.
0.528007097	0	0	1.817838733	1.541105976	MAPK12	.
0.530551243	0	0	1.37634785	1.158741518	PIK3CD;CC	.
0.530551243	0	0	1.785856394	1.490841459	GRK4	.
0.530551243	0	0	1.785856394	1.490841459	ULK2	.
0.530551243	0	0	1.785856394	1.490841459	CACNB2	.
0.530551243	0	0	1.785856394	1.490841459	CPEB2	.
0.530551243	0	0	1.785856394	1.490841459	FOXF1	.
0.530551243	0	0	1.785856394	1.490841459	HMGB2	.
0.530551243	0	0	1.785856394	1.490841459	INHA	.
0.530551243	0	0	1.785856394	1.490841459	FOXO1	.
0.530551243	0	0	1.785856394	1.490841459	CAMKK2	.
0.533802859	0	0	1.111541768	0.920226222	BABAM2;M	.
0.53405605	0	0	1.357858377	1.122401873	PRKDC;PDI	.
0.534280018	0	0	1.754976893	1.442820774	SPIRE2	.
0.534280018	0	0	1.754976893	1.442820774	PCTP	.
0.534280018	0	0	1.754976893	1.442820774	BCL10	.
0.534280018	0	0	1.754976893	1.442820774	ADIPOR2	.
0.534280018	0	0	1.754976893	1.442820774	CAMKK2	.
0.536452971	0	0	1.132569077	0.925608698	RASD2;INS	.
0.539201049	0	0	1.725144155	1.396912516	PRKDC	.
0.539201049	0	0	1.725144155	1.396912516	PAQR7	.
0.539201049	0	0	1.725144155	1.396912516	CDH17	.
0.54172829	0	0	1.331030512	1.070489009	BCL10;RAB	.
0.543589805	0	0	1.696305842	1.352994883	AGO1	.
0.543589805	0	0	1.696305842	1.352994883	LPCAT3	.
0.543589805	0	0	1.696305842	1.352994883	BCL10	.
0.543589805	0	0	1.696305842	1.352994883	BCL10	.
0.547442771	0	0	1.668413047	1.310954839	BCL10	.
0.547442771	0	0	1.668413047	1.310954839	ALDOC	.
0.547442771	0	0	1.668413047	1.310954839	TMEM106/	.
0.547442771	0	0	1.668413047	1.310954839	PTK7	.
0.547442771	0	0	1.668413047	1.310954839	BCL10	.
0.547442771	0	0	1.668413047	1.310954839	MINK1	.
0.551634647	0	0	1.64142002	1.270687355	SPOCK2	.
0.551634647	0	0	1.64142002	1.270687355	SPOCK2	.
0.551634647	0	0	1.64142002	1.270687355	CAMKK2	.
0.551634647	0	0	1.64142002	1.270687355	BABAM2	.
0.551634647	0	0	1.64142002	1.270687355	PPARA	.
0.551846818	0	0	1.197916667	0.925941569	MEF2C;AXI	.
0.555291956	0	0	1.615283914	1.232094729	FOXO4	.
0.555291956	0	0	1.615283914	1.232094729	PPARA	.
0.555291956	0	0	1.615283914	1.232094729	LRP8	.
0.555291956	0	0	1.615283914	1.232094729	LRP8	.
0.555291956	0	0	1.615283914	1.232094729	AGO1	.
0.560177178	0	0	1.589964562	1.195085975	TLCD3A	.
0.560177178	0	0	1.589964562	1.195085975	SLC25A30	.

0.560177178	0	0	1.589964562	1.195085975	PRKDC	.
0.564534611	0	0	1.565424266	1.159576269	JAM3	.
0.564534611	0	0	1.565424266	1.159576269	NOXO1	.
0.564534611	0	0	1.565424266	1.159576269	NOXO1	.
0.564534611	0	0	1.565424266	1.159576269	AXIN2	.
0.566141132	0	0	1.248736451	0.917436008	JADE1;AXI	.
0.566141132	0	0	1.248736451	0.917436008	CDKL5;PTK	.
0.566141132	0	0	1.099352052	0.8033039	MEF2C;INS	.
0.566141132	0	0	1.541627616	1.125486449	GFPT1	.
0.566141132	0	0	1.541627616	1.125486449	SLC25A30	.
0.566141132	0	0	1.541627616	1.125486449	AGO1	.
0.566141132	0	0	1.541627616	1.125486449	PRKDC	.
0.566141132	0	0	1.541627616	1.125486449	FOXO1	.
0.566141132	0	0	1.541627616	1.125486449	PPARA	.
0.566141132	0	0	1.541627616	1.125486449	NRP2	.
0.567902047	0	0	1.048826535	0.761476884	MEF2C;CAI	.
0.567902047	0	0	1.156545928	0.838956266	BABAM2;U	.
0.569871786	0	0	1.518541314	1.092742561	PPARA	.
0.569871786	0	0	1.518541314	1.092742561	TRIM31	.
0.569871786	0	0	1.518541314	1.092742561	ORMDL3	.
0.571466511	0	0	1.026016854	0.733934087	MEF2C;CAI	.
0.571466511	0	0	1.147732613	0.820917665	CARMIL2;II	.
0.573516031	0	0	1.496134021	1.06127545	CPEB2	.
0.573516031	0	0	1.496134021	1.06127545	INSR	.
0.573516031	0	0	1.496134021	1.06127545	PCNT	.
0.576630491	0	0	1.211263262	0.850935618	CDH23;CDI	.
0.576630491	0	0	1.474376214	1.031020386	TRIM31	.
0.576630491	0	0	1.474376214	1.031020386	PIK3CD	.
0.576630491	0	0	1.474376214	1.031020386	HMGB2	.
0.576630491	0	0	1.474376214	1.031020386	AIG1	.
0.576630491	0	0	1.474376214	1.031020386	CCR7	.
0.577444558	0	0	1.12626845	0.777719864	INSR;CCR7	.
0.577444558	0	0	1.453240059	1.001916725	MEF2C	.
0.577444558	0	0	1.453240059	1.001916725	SPOCK2	.
0.577444558	0	0	1.453240059	1.001916725	JADE1	.
0.577444558	0	0	1.453240059	1.001916725	PRKDC	.
0.577444558	0	0	1.453240059	1.001916725	CYP39A1	.
0.577444558	0	0	1.453240059	1.001916725	PIK3CD	.
0.577444558	0	0	1.453240059	1.001916725	ACLY	.
0.577444558	0	0	1.453240059	1.001916725	ORMDL3	.
0.577444558	0	0	1.453240059	1.001916725	JADE1	.
0.577444558	0	0	1.453240059	1.001916725	D2HGDH	.
0.578868258	0	0	1.068609023	0.728674887	ACLY;VNN1	.
0.578868258	0	0	1.11790293	0.761167839	BABAM2;U	.
0.578868258	0	0	1.432699289	0.973907599	NLGN2	.
0.578868258	0	0	1.432699289	0.973907599	MEF2C	.
0.578868258	0	0	1.432699289	0.973907599	SPIRE2	.

0.578868258	0	0	1.432699289	0.973907599	BABAM2	.
0.578868258	0	0	1.432699289	0.973907599	CYP39A1	.
0.578868258	0	0	1.432699289	0.973907599	NLGN2	.
0.578868258	0	0	1.432699289	0.973907599	STXBP5	.
0.578868258	0	0	1.085095986	0.737168448	SMYD2;FO	.
0.579060445	0	0	1.066313583	0.72324578	MEF2C;CAI	.
0.579741955	0	0	1.109659091	0.745013655	MINK1;PCI	.
0.579741955	0	0	1.079228408	0.724436106	BABAM2;P	.
0.579741955	0	0	1.412729095	0.946939635	JAM3	.
0.579741955	0	0	1.412729095	0.946939635	ARHGEF19	.
0.579741955	0	0	1.412729095	0.946939635	HMGB2	.
0.579741955	0	0	1.412729095	0.946939635	HMGB2	.
0.579741955	0	0	1.412729095	0.946939635	PIK3CD	.
0.579741955	0	0	1.412729095	0.946939635	HMGB2	.
0.579741955	0	0	1.412729095	0.946939635	NLGN2	.
0.580484496	0	0	1.059484649	0.70721251	BABAM2;N	.
0.580484496	0	0	1.059484649	0.70721251	ACLY;VNN1	.
0.580919323	0	0	1.169138229	0.778652782	COLEC12;H	.
0.581654795	0	0	1.39330603	0.920962698	TTBK2	.
0.581654795	0	0	1.39330603	0.920962698	CASTOR2	.
0.581654795	0	0	1.39330603	0.920962698	EVL	.
0.581654795	0	0	1.39330603	0.920962698	ST8SIA5	.
0.581654795	0	0	1.39330603	0.920962698	ZWINT	.
0.58171976	0	0	1.162398224	0.767335172	INSR;LRP8	.
0.583162092	0	0	1.052740547	0.691552674	ACLY;VNN1	.
0.583492753	0	0	1.374407913	0.895929655	PRKDC	.
0.583492753	0	0	1.374407913	0.895929655	CASTOR2	.
0.583492753	0	0	1.374407913	0.895929655	CCR7	.
0.583492753	0	0	1.374407913	0.895929655	MEF2C	.
0.583492753	0	0	1.374407913	0.895929655	CDH17	.
0.583492753	0	0	1.374407913	0.895929655	CCR7	.
0.584992179	0	0	1.149146688	0.745285618	COLEC12;L	.
0.586124709	0	0	1.356013746	0.871796159	KLHL13	.
0.586124709	0	0	1.356013746	0.871796159	AXIN2	.
0.586124709	0	0	1.356013746	0.871796159	MEF2C	.
0.586124709	0	0	1.356013746	0.871796159	TNFRSF21	.
0.586124709	0	0	1.356013746	0.871796159	INSR	.
0.589552265	0	0	1.07784894	0.684156586	ARHGEF19	.
0.589552265	0	0	1.338103635	0.848520453	PIK3CD	.
0.589552265	0	0	1.338103635	0.848520453	TMEM106A	.
0.589552265	0	0	1.338103635	0.848520453	PRKDC	.
0.594222256	0	0	1.320658723	0.826063189	NOL3	.
0.597953745	0	0	1.303661116	0.804387259	TONSL	.
0.597953745	0	0	1.303661116	0.804387259	SPTBN4	.
0.597953745	0	0	1.303661116	0.804387259	MEF2C	.
0.599856781	0	0	1.287093827	0.783457644	INHA	.
0.599856781	0	0	1.287093827	0.783457644	CARMIL2	.

0.599856781	0	0	1.287093827	0.783457644	NOL3	.
0.599856781	0	0	1.287093827	0.783457644	FOXO1	.
0.599856781	0	0	1.287093827	0.783457644	STAC3	.
0.599856781	0	0	1.287093827	0.783457644	CCR7	.
0.599856781	0	0	1.287093827	0.783457644	PLA2G4D	.
0.603010783	0	0	1.270940722	0.763241274	PRKDC	.
0.603010783	0	0	1.270940722	0.763241274	BCL10	.
0.603010783	0	0	1.270940722	0.763241274	GPR157	.
0.603010783	0	0	1.270940722	0.763241274	PRKDC	.
0.603374116	0	0	1.093041395	0.654950413	HAUS5;PCI	.
0.606090182	0	0	1.087140838	0.645738813	CDKL5;CPE	.
0.606521125	0	0	1.255186458	0.743706897	EFNA2	.
0.606521125	0	0	1.04052901	0.615795984	FOXO4;INH	.
0.608868447	0	0	1.239816445	0.72482496	LRP8	.
0.608868447	0	0	1.239816445	0.72482496	GSTT1	.
0.608868447	0	0	1.239816445	0.72482496	MEF2C	.
0.608868447	0	0	1.075527044	0.627771415	PPARA;FOX	.
0.608868447	0	0	1.075527044	0.627771415	JADE1;AXIN	.
0.608868447	0	0	1.033368644	0.603060867	BABAM2;P	.
0.611637865	0	0	1.224816793	0.706567496	KLHL13	.
0.611637865	0	0	1.224816793	0.706567496	PIK3CD	.
0.611637865	0	0	1.224816793	0.706567496	INSR	.
0.615421153	0	0	1.210174276	0.688908025	FOXO1	.
0.615421153	0	0	1.210174276	0.688908025	ARHGEF19	.
0.615621557	0	0	0.99057943	0.562862703	NUMBL;PII	.
0.61870173	0	0	1.195876289	0.671821459	ORMDL3	.
0.61870173	0	0	1.195876289	0.671821459	INSR	.
0.62112965	0	0	0.983973126	0.548215195	COLEC12;A	.
0.625985486	0	0	1.168266382	0.63927312	ARHGEF19	.
0.625985486	0	0	1.168266382	0.63927312	RAB7B	.
0.625985486	0	0	1.168266382	0.63927312	CDH23	.
0.628862515	0	0	0.983329742	0.531551997	PRKDC;TM	.
0.628862515	0	0	1.154932052	0.62376737	BCL10	.
0.628862515	0	0	1.154932052	0.62376737	PRKDC	.
0.628862515	0	0	1.02616842	0.553865279	HMG20B;T	.
0.629132969	0	0	0.975961538	0.525647557	TRIM41;PR	.
0.6299163	0	0	0.992365635	0.532537283	ARHGEF19	.
0.631242224	0	0	1.141897371	0.608746424	CPEB2	.
0.631242224	0	0	1.141897371	0.608746424	HMGB2	.
0.634688586	0	0	1.129152348	0.594190957	ARHGEF19	.
0.634688586	0	0	1.129152348	0.594190957	PRKDC	.
0.636721335	0	0	0.979401125	0.511100474	HAUS5;PCI	.
0.636721335	0	0	1.116687436	0.580082595	JADE1	.
0.636721335	0	0	1.116687436	0.580082595	LRP8	.
0.636721335	0	0	1.116687436	0.580082595	LRP8	.
0.636721335	0	0	1.116687436	0.580082595	INHA	.
0.640058884	0	0	1.104493501	0.566403862	PRKDC	.

0.640058884	0	0	1.104493501	0.566403862	PDE4D	.
0.642889733	0	0	1.0925618	0.553138127	INPP5A	.
0.642889733	0	0	1.0925618	0.553138127	FOXO1	.
0.642889733	0	0	1.0925618	0.553138127	HMGB2	.
0.64658235	0	0	1.080883966	0.54026955	CDH23	.
0.649772428	0	0	1.06945198	0.527783045	STXBP5	.
0.649772428	0	0	0.954447492	0.471023101	MEF2C;SFM	.
0.652907705	0	0	1.058258162	0.51566423	TONSL	.
0.652907705	0	0	1.058258162	0.51566423	ADIPOR2	.
0.655535293	0	0	1.047295143	0.503899393	MEF2C	.
0.655535293	0	0	1.047295143	0.503899393	MEF2C	.
0.655535293	0	0	1.047295143	0.503899393	NOL3	.
0.661104877	0	0	0.933617715	0.438775272	TBC1D9B;A	.
0.661104877	0	0	1.026033531	0.481379917	TESK2	.
0.661104877	0	0	1.026033531	0.481379917	SLC25A30	.
0.661104877	0	0	1.026033531	0.481379917	PPARA	.
0.661104877	0	0	1.026033531	0.481379917	PRKDC	.
0.662576894	0	0	0.944210146	0.440228298	JADE1;SMA	.
0.663120384	0	0	1.015721649	0.470600869	ALDOC	.
0.663120384	0	0	1.015721649	0.470600869	INSR	.
0.663120384	0	0	1.015721649	0.470600869	STAC3	.
0.664159436	0	0	1.005613963	0.460126915	AXIN2	.
0.664159436	0	0	1.005613963	0.460126915	FOXO1	.
0.664159436	0	0	1.005613963	0.460126915	PRKDC	.
0.664159436	0	0	1.005613963	0.460126915	PRKDC	.
0.664159436	0	0	1.005613963	0.460126915	PIK3CD	.
0.664159436	0	0	1.005613963	0.460126915	ZWINT	.
0.667470408	0	0	0.995704467	0.449947171	MEF2C	.
0.670739999	0	0	0.985987389	0.440051228	NLGN2	.
0.684600254	0	0	0.94893535	0.40311268	PPARA	.
0.684600254	0	0	0.897748636	0.381058225	PCNT;TTBK	.
0.686006508	0	0	0.889208699	0.37375006	PIK3CD;AX	.
0.686006508	0	0	0.889208699	0.37375006	TMEM132/	.
0.686006508	0	0	0.940101184	0.394494681	BCL10	.
0.686006508	0	0	0.940101184	0.394494681	PCTP	.
0.688558009	0	0	0.931429112	0.386106771	ANKS4B	.
0.688558009	0	0	0.931429112	0.386106771	TNFRSF21	.
0.688605922	0	0	0.885851981	0.366538712	ORMDL3;F	.
0.690590757	0	0	0.922914714	0.377941262	BCL10	.
0.690590757	0	0	0.922914714	0.377941262	PTK7	.
0.693059383	0	0	0.914553729	0.369990785	FANCA	.
0.693059383	0	0	0.914553729	0.369990785	BCL10	.
0.693610244	0	0	0.873608118	0.35212909	MYO1A;KA	.
0.698357342	0	0	0.898275705	0.354706922	MEF2C	.
0.698357342	0	0	0.898275705	0.354706922	INSR	.
0.703986895	0	0	0.882563873	0.340201946	PIK3CD	.
0.703986895	0	0	0.882563873	0.340201946	ORMDL3	.

0.713142493	0	0	0.859994758	0.319798533	BCL10	.
0.715801178	0	0	0.852724595	0.313336026	LIX1	.
0.717932763	0	0	0.845575601	0.307034102	TRIM31	.
0.717932763	0	0	0.845575601	0.307034102	BCL10	.
0.720521672	0	0	0.838544773	0.300887821	ALDOC	.
0.723076987	0	0	0.831629204	0.294892424	CCR7	.
0.725599068	0	0	0.824826083	0.289043335	TMEM106	.
0.727590603	0	0	0.81813269	0.283336142	KATNB1	.
0.727590603	0	0	0.81813269	0.283336142	STXBP5	.
0.735864422	0	0	0.798684958	0.267024238	CCR7	.
0.743872744	0	0	0.780134814	0.251845427	CPEB2	.
0.748897705	0	0	0.768236489	0.242308068	AGO1	.
0.75111109	0	0	0.762421518	0.237704056	LRP8	.
0.755963996	0	0	0.751050019	0.228810014	CDH23	.
0.756805108	0	0	0.761190541	0.230534557	ACAN;ADG	.
0.76533962	0	0	0.729288734	0.212198294	PPARA	.
0.771828873	0	0	0.713772325	0.200686582	HMGB2	.
0.771828873	0	0	0.713772325	0.200686582	MEF2C	.
0.773764046	0	0	0.708744863	0.197016941	EVL	.
0.78283128	0	0	0.689319027	0.183118419	PCNT	.
0.786420854	0	0	0.679997232	0.176609129	MEF2C	.
0.786420854	0	0	0.679997232	0.176609129	CCR7	.
0.786967762	0	0	0.709753659	0.183363359	ACAN;LRP8	.
0.798213676	0	0	0.653475224	0.158667488	SPOCK2	.
0.798213676	0	0	0.653475224	0.158667488	SMYD2	.
0.801961598	0	0	0.645085035	0.153172452	MEF2C	.
0.813793994	0	0	0.741260367	0.164651263	MEF2C;SAT	.
0.820515128	0	0	0.606148528	0.128836122	ANKS4B	.
0.820515128	0	0	0.606148528	0.128836122	PPARA	.
0.825078471	0	0	0.595360825	0.122438875	MINK1	.
0.825078471	0	0	0.595360825	0.122438875	AGO1	.
0.826374612	0	0	0.591849038	0.120389217	CCR7	.
0.827650907	0	0	0.588378087	0.118379349	PRKDC	.
0.828907574	0	0	0.584947262	0.116408356	MEF2C	.
0.834861306	0	0	0.571611626	0.1088957	RCC1	.
0.834861306	0	0	0.571611626	0.1088957	PRKDC	.
0.836023797	0	0	0.568371366	0.10710621	NOL3	.
0.837167882	0	0	0.56516731	0.105350606	SYT4	.
0.848969382	0	0	0.604107846	0.103747993	TBC1D9B;K	.
0.857625442	0	0	0.523796806	0.083940802	TNFRSF21	.
0.857625442	0	0	0.523796806	0.083940802	LRP8	.
0.867021575	0	0	0.505283505	0.07513032	AGO1	.
0.882387439	0	0	0.548855727	0.071600337	TBC1D9B;A	.
0.908461266	0	0	0.42559485	0.042842523	CCR7	.
0.911594536	0	0	0.418445481	0.040402859	LPCAT3	.
0.919708281	0	0	0.401568982	0.034947157	NLGN2	.
0.9208215	0	0	0.480625728	0.040925481	SPTBN5;LN	.

0.934870562	0	0	0.368792719	0.025573024	SLC25A27	.
0.948690507	0	0	0.424453324	0.022921518	MEF2C;INS	.
0.955627738	0	0	0.32100392	0.014782715	INHA	.
0.957602511	0	0	0.314869276	0.013640925	PPARA	.

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Term	Overlap	P-value	Adjusted P-value
Longevity regulating pathway	5/102	0.003248503	0.276602973
Sulfur metabolism	44602	0.004042395	0.276602973
Insulin resistance	5/108	0.004149045	0.276602973
AMPK signaling pathway	5/120	0.006462133	0.323106637
FoxO signaling pathway	5/131	0.009266743	0.331648476
Insulin signaling pathway	5/137	0.011104844	0.331648476
Morphine addiction	33329	0.012120511	0.331648476
Phosphatidylinositol signaling system	35521	0.01502522	0.331648476
Glycerophospholipid metabolism	35886	0.015548315	0.331648476
Non-alcoholic fatty liver disease	5/155	0.018074765	0.331648476
C-type lectin receptor signaling pathway	4/104	0.018927452	0.331648476
VEGF signaling pathway	21610	0.019898909	0.331648476
alpha-Linolenic acid metabolism	44617	0.024490401	0.3767754
Fc epsilon RI signaling pathway	24898	0.02879737	0.398615908
Adipocytokine signaling pathway	25263	0.029896193	0.398615908
Inositol phosphate metabolism	26724	0.034509941	0.431374258
Purine metabolism	4/129	0.037664023	0.44310615
Autophagy	4/137	0.045299748	0.48004217
Fluid shear stress and atherosclerosis	4/139	0.047334134	0.48004217
Diabetic cardiomyopathy	5/203	0.04902008	0.48004217
Aldosterone-regulated sodium reabsorption	13547	0.050404428	0.48004217
Rap1 signaling pathway	5/210	0.055165691	0.484489738
Phosphonate and phosphinate metabolism	44567	0.057099178	0.484489738
Oxytocin signaling pathway	4/154	0.064177858	0.484489738
mTOR signaling pathway	4/154	0.064177858	0.484489738
MAPK signaling pathway	6/294	0.068653932	0.484489738
Inflammatory mediator regulation of TRP channels	35855	0.070946025	0.484489738
Type II diabetes mellitus	16834	0.074043944	0.484489738
AGE-RAGE signaling pathway in diabetic complications	3/100	0.074393451	0.484489738
Progesterone-mediated oocyte maturation	3/100	0.074393451	0.484489738
Ras signaling pathway	5/232	0.077248147	0.484489738
Amoebiasis	3/102	0.077914096	0.484489738
T cell receptor signaling pathway	3/104	0.081506632	0.484489738
Hepatocellular carcinoma	4/168	0.082363256	0.484489738
Ovarian steroidogenesis	18660	0.088421774	0.504408443
HIF-1 signaling pathway	3/109	0.09079352	0.504408443
Shigellosis	5/246	0.093447472	0.50512147
Regulation of lipolysis in adipocytes	20121	0.10046554	0.515380844
Leukocyte transendothelial migration	3/114	0.100499265	0.515380844
Endometrial cancer	21217	0.109778988	0.548894941
Non-homologous end-joining	44574	0.119627334	0.576551556
Platelet activation	3/124	0.121075827	0.576551556
Glycolysis / Gluconeogenesis	24504	0.138940529	0.64623502
Epithelial cell signaling in Helicobacter pylori infection	25600	0.149003951	0.662239783

Prolactin signaling pathway	25600	0.149003951	0.662239783
Primary bile acid biosynthesis	44578	0.15348712	0.667335304
cAMP signaling pathway	4/216	0.160723214	0.667830132
PPAR signaling pathway	27061	0.162639396	0.667830132
Signaling pathways regulating pluripotency of stem cells	3/143	0.163858708	0.667830132
Cell adhesion molecules	3/148	0.175789963	0.667830132
Phospholipase D signaling pathway	3/148	0.175789963	0.667830132
Steroid biosynthesis	44581	0.178028828	0.667830132
Gastric cancer	3/149	0.178205077	0.667830132
Phagosome	3/152	0.18550476	0.667830132
Pantothenate and CoA biosynthesis	44582	0.186051057	0.667830132
B cell receptor signaling pathway	29618	0.186992437	0.667830132
Terpenoid backbone biosynthesis	44583	0.19399539	0.673646666
Cellular senescence	3/156	0.195357533	0.673646666
Colorectal cancer	31444	0.204682078	0.684360305
Chemical carcinogenesis	4/239	0.205308092	0.684360305
Vitamin digestion and absorption	44585	0.209653365	0.687388083
PD-L1 expression and PD-1 checkpoint pathway in cancer	32540	0.215383359	0.68874202
Salmonella infection	4/249	0.225727742	0.68874202
Tight junction	3/169	0.228190994	0.68874202
GnRH signaling pathway	34001	0.229727809	0.68874202
Biosynthesis of unsaturated fatty acids	44588	0.232574679	0.68874202
Phototransduction	44589	0.24006718	0.68874202
Fc gamma R-mediated phagocytosis	35462	0.244133873	0.68874202
Prostate cancer	35462	0.244133873	0.68874202
Linoleic acid metabolism	44590	0.247486901	0.68874202
Choline metabolism in cancer	35827	0.247741953	0.68874202
Citrate cycle (TCA cycle)	44591	0.254834547	0.68874202
Glyoxylate and dicarboxylate metabolism	44591	0.254834547	0.68874202
Pentose phosphate pathway	44591	0.254834547	0.68874202
Chagas disease	2/102	0.262189008	0.699170688
Toll-like receptor signaling pathway	2/104	0.26941627	0.708795512
Fructose and mannose metabolism	12055	0.276451963	0.708795512
Parathyroid hormone synthesis, secretion and action	2/106	0.276642297	0.708795512
Glucagon signaling pathway	2/107	0.280254012	0.708795512
Propanoate metabolism	12420	0.283518205	0.708795512
Chemokine signaling pathway	3/192	0.288371507	0.712028413
Alzheimer disease	5/369	0.292005158	0.712207702
TNF signaling pathway	2/112	0.298286876	0.716017938
Pathogenic Escherichia coli infection	3/197	0.301653966	0.716017938
Alanine, aspartate and glutamate metabolism	13516	0.304307624	0.716017938
Primary immunodeficiency	13881	0.311103186	0.71977427
Growth hormone synthesis, secretion and action	2/119	0.323407138	0.71977427
Neurotrophin signaling pathway	2/119	0.323407138	0.71977427
Sphingolipid signaling pathway	2/119	0.323407138	0.71977427
Thyroid hormone signaling pathway	2/121	0.330545918	0.71977427
Ferroptosis	14977	0.331096164	0.71977427

Homologous recombination	14977	0.331096164	0.71977427
Osteoclast differentiation	2/127	0.351830194	0.747656122
Glycosphingolipid biosynthesis	16438	0.356858262	0.747656122
Oocyte meiosis	2/129	0.358874939	0.747656122
Relaxin signaling pathway	2/129	0.358874939	0.747656122
Carbohydrate digestion and absorption	17168	0.369366683	0.753809557
Pyruvate metabolism	17168	0.369366683	0.753809557
Amino sugar and nucleotide sugar metabolism	17533	0.37552983	0.755709013
Cocaine addiction	17899	0.381633051	0.755709013
Ether lipid metabolism	17899	0.381633051	0.755709013
Yersinia infection	2/137	0.38676046	0.758353843
Apoptosis	2/142	0.403921188	0.775859674
Glycosaminoglycan biosynthesis	19360	0.405458183	0.775859674
Spinocerebellar ataxia	2/143	0.407326329	0.775859674
Fanconi anemia pathway	19725	0.411270357	0.775981805
Breast cancer	2/147	0.420851999	0.776250102
Glutathione metabolism	20821	0.428369877	0.776250102
Adrenergic signaling in cardiomyocytes	2/150	0.430892848	0.776250102
Notch signaling pathway	21551	0.439494127	0.776250102
Long-term depression	21916	0.444975218	0.776250102
Arachidonic acid metabolism	22282	0.450402982	0.776250102
Hepatitis C	2/157	0.453956944	0.776250102
Basal cell carcinoma	23012	0.461100589	0.776250102
Lysine degradation	23012	0.461100589	0.776250102
GnRH secretion	23377	0.46637145	0.776250102
Hepatitis B	2/162	0.47010285	0.776250102
Acute myeloid leukemia	24473	0.481878266	0.776250102
cGMP-PKG signaling pathway	2/167	0.485962057	0.776250102
Mitophagy	24838	0.486946922	0.776250102
Renal cell carcinoma	25204	0.491966243	0.776250102
Central carbon metabolism in cancer	25569	0.496936709	0.776250102
RIG-I-like receptor signaling pathway	25569	0.496936709	0.776250102
Prion disease	3/273	0.498874599	0.776250102
Adherens junction	25934	0.501858792	0.776250102
Melanoma	26299	0.506732961	0.776250102
Non-small cell lung cancer	26299	0.506732961	0.776250102
Glioma	27395	0.521072598	0.776250102
Chronic myeloid leukemia	27760	0.525759705	0.776250102
Metabolism of xenobiotics by cytochrome P450	27760	0.525759705	0.776250102
Pancreatic cancer	27760	0.525759705	0.776250102
Pertussis	27760	0.525759705	0.776250102
Tuberculosis	2/180	0.525789906	0.776250102
Arrhythmogenic right ventricular cardiomyopathy	28126	0.530401174	0.776250102
Bacterial invasion of epithelial cells	28126	0.530401174	0.776250102
Leishmaniasis	28126	0.530401174	0.776250102
Axon guidance	2/182	0.53173132	0.776250102
Cytokine-cytokine receptor interaction	3/295	0.551029806	0.789913239

Neutrophil extracellular trap formation	2/189	0.552126006	0.789913239
Peroxisome	29952	0.552939267	0.789913239
Transcriptional misregulation in cancer	2/192	0.560674171	0.791527427
Kaposi sarcoma-associated herpesvirus infection	2/193	0.563497724	0.791527427
ErbB signaling pathway	31048	0.56594211	0.791527427
Cardiac muscle contraction	31778	0.574400937	0.795155249
Gap junction	32143	0.578568645	0.795155249
Hypertrophic cardiomyopathy	32874	0.586782639	0.795155249
Epstein-Barr virus infection	2/202	0.588325214	0.795155249
Small cell lung cancer	33604	0.59483734	0.795155249
Th1 and Th2 cell differentiation	33604	0.59483734	0.795155249
Proteoglycans in cancer	2/205	0.596366437	0.795155249
IL-17 signaling pathway	34335	0.602735823	0.798325594
Dilated cardiomyopathy	35065	0.610481102	0.801405941
Human immunodeficiency virus 1 infection	2/212	0.614672324	0.801405941
Hematopoietic cell lineage	36161	0.621818215	0.801405941
Lipid and atherosclerosis	2/215	0.622322079	0.801405941
Viral protein interaction with cytokine and cytokine receptor	1/100	0.625523817	0.801405941
Human papillomavirus infection	3/331	0.629103664	0.801405941
NF-kappa B signaling pathway	1/104	0.639988464	0.802226459
Human cytomegalovirus infection	2/225	0.646977768	0.802226459
Th17 cell differentiation	1/107	0.65047092	0.802226459
Drug metabolism	1/108	0.653897146	0.802226459
Coronavirus disease	2/232	0.663471111	0.802226459
Thermogenesis	2/232	0.663471111	0.802226459
Toxoplasmosis	1/112	0.667271127	0.802226459
Cholinergic synapse	1/113	0.67053349	0.802226459
Serotonergic synapse	1/113	0.67053349	0.802226459
Glutamatergic synapse	1/114	0.673764027	0.802226459
PI3K-Akt signaling pathway	3/354	0.673870226	0.802226459
Pathways of neurodegeneration	4/475	0.683805403	0.809237163
Amyotrophic lateral sclerosis	3/364	0.692061721	0.81419026
Cell cycle	1/124	0.70438554	0.822327743
Endocytosis	2/252	0.707201859	0.822327743
Lysosome	1/128	0.715817617	0.827534817
Natural killer cell mediated cytotoxicity	1/131	0.72410204	0.828967107
Dopaminergic synapse	1/132	0.726809767	0.828967107
Vascular smooth muscle contraction	1/133	0.729491054	0.828967107
Apelin signaling pathway	1/137	0.739956908	0.830601138
Estrogen signaling pathway	1/137	0.739956908	0.830601138
Measles	1/139	0.745037759	0.830601138
Ubiquitin mediated proteolysis	1/140	0.747541024	0.830601138
Pathways in cancer	4/531	0.76417857	0.842534633
Retrograde endocannabinoid signaling	1/148	0.766706516	0.842534633
Cushing syndrome	1/155	0.782284649	0.854389503
Necroptosis	1/159	0.790717131	0.854389503
JAK-STAT signaling pathway	1/162	0.796827523	0.854389503

Hippo signaling pathway	1/163	0.798824616	0.854389503
Huntington disease	2/306	0.802133019	0.854389503
Wnt signaling pathway	1/166	0.804699466	0.854389503
MicroRNAs in cancer	2/310	0.807951486	0.854389503
Protein processing in endoplasmic reticulum	1/171	0.814113973	0.854389503
Influenza A	1/172	0.815941976	0.854389503
NOD-like receptor signaling pathway	1/181	0.831609692	0.866260096
Alcoholism	1/186	0.839732995	0.870189632
Focal adhesion	1/201	0.861836728	0.886712712
Viral carcinogenesis	1/203	0.864544894	0.886712712
Regulation of actin cytoskeleton	1/218	0.883241528	0.897860356
Human T-cell leukemia virus 1 infection	1/219	0.88439245	0.897860356
Calcium signaling pathway	1/240	0.906116441	0.915269132
Parkinson disease	1/249	0.914134501	0.918728141
Herpes simplex virus 1 infection	2/498	0.95691434	0.95691434

Old P-value	Old Adjusted P-value	Odds Ratio	Combined Score	Genes
0	0	5.346717309	30.63434344	INSR;PIK3CD;ADIPOR2;FOXO1;CAMKK2
0	0	25.64378238	141.3207791	BPNT2;SUOX
0	0	5.033725089	27.60936392	INSR;GFPT1;PIK3CD;PPARA;FOXO1
0	0	4.505720824	22.71692464	INSR;PIK3CD;ADIPOR2;FOXO1;CAMKK2
0	0	4.110066834	19.24055171	INSR;PIK3CD;FOXO4;FOXO1;MAPK12
0	0	3.922049442	17.65068871	PPP1R3F;INPP5A;INSR;PIK3CD;FOXO1
0	0	4.746464464	20.94546487	PDE10A;GRK4;PDE4D;PDE7B
0	0	4.438889827	18.63457106	ITPKC;INPP5A;PIK3CD;BPNT2
0	0	4.391444803	18.28511098	PCYT2;PLA2G4D;LPCAT3;GPD1
0	0	3.448245614	13.83863213	INSR;PIK3CD;PPARA;ADIPOR2;MAPK12
0	0	4.126701571	16.37121086	CLEC4D;PIK3CD;BCL10;MAPK12
0	0	5.510323661	21.58443589	PLA2G4D;PIK3CD;MAPK12
0	0	8.912818202	33.0618677	FADS2;PLA2G4D
0	0	4.745192308	16.83343315	PLA2G4D;PIK3CD;MAPK12
0	0	4.673058712	16.40254883	PPARA;ADIPOR2;CAMKK2
0	0	4.405133929	14.829918	ITPKC;INPP5A;PIK3CD
0	0	3.297172775	10.8115942	PDE10A;PDE4D;PDE7B;ADA
0	0	3.097586899	9.585339613	ULK2;PIK3CD;RAB7B;CAMKK2
0	0	3.051386465	9.308326429	MEF2C;PIK3CD;GSTT1;MAPK12
0	0	2.605927698	7.858240833	INSR;GFPT1;PIK3CD;PPARA;MAPK12
0	0	5.853441895	17.48818936	INSR;PIK3CD
0	0	2.516046213	7.290027659	EFNA2;INSR;PIK3CD;EVL;MAPK12
0	0	20.41237113	58.43991553	PCYT2
0	0	2.744153578	7.535711966	CACNB2;MEF2C;PLA2G4D;CAMKK2
0	0	2.744153578	7.535711966	CASTOR2;INSR;ULK2;PIK3CD
0	0	2.151344797	5.762757566	CACNB2;MEF2C;EFNA2;PLA2G4D;INSR;MAPK
0	0	3.241776316	8.577208162	PLA2G4D;PIK3CD;MAPK12
0	0	4.65402732	12.11488233	INSR;PIK3CD
0	0	3.174613402	8.248875345	PIK3CD;FOXO1;MAPK12
0	0	3.174613402	8.248875345	PIK3CD;CPEB2;MAPK12
0	0	2.269649896	5.811965927	EFNA2;PLA2G4D;INSR;PIK3CD;FOXO4
0	0	3.110164141	7.937600406	PIK3CD;CD1E;RAB7B
0	0	3.048267327	7.642222267	PIK3CD;BCL10;MAPK12
0	0	2.508108798	6.261784228	PIK3CD;GSTT1;AXIN2;SMARCA2
0	0	4.178069155	10.13447924	PLA2G4D;INSR
0	0	2.903744104	6.966568088	INSR;PIK3CD;ALDOC
0	0	2.136274296	5.063730163	PIK3CD;BCL10;FOXO4;FOXO1;MAPK12
0	0	3.861961091	8.874556791	INSR;PIK3CD
0	0	2.772240991	6.369514397	PIK3CD;MAPK12;JAM3
0	0	3.654515174	8.073869693	PIK3CD;AXIN2
0	0	8.502147766	18.05323882	PRKDC
0	0	2.541838843	5.366681606	PLA2G4D;PIK3CD;MAPK12
0	0	3.147070546	6.211402355	ACSS2;ALDOC
0	0	3.007772021	5.726143602	MAPK12;JAM3

0	0	3.007772021	5.726143602	PIK3CD;MAPK12
0	0	6.375322165	11.94823751	CYP39A1
0	0	1.935493431	3.538220499	PDE10A;PDE4D;PIK3CD;PPARA
0	0	2.84009787	5.158242048	FADS2;PPARA
0	0	2.194754464	3.969763809	PIK3CD;AXIN2;MAPK12
0	0	2.118534483	3.682998871	NLGN2;MPZL1;JAM3
0	0	2.118534483	3.682998871	PLA2G4D;INSR;PIK3CD
0	0	5.367878459	9.263937187	EBP
0	0	2.103916952	3.628878618	PIK3CD;AXIN2;CDH17
0	0	2.061241611	3.472521666	COLEC12;TUBAL3;RAB7B
0	0	5.099226804	8.575543809	VNN1
0	0	2.587525415	4.338470503	PIK3CD;BCL10
0	0	4.856161021	7.963719877	MVK
0	0	2.006944444	3.27718754	PIK3CD;FOXO1;MAPK12
0	0	2.432889218	3.859285704	PIK3CD;AXIN2
0	0	1.744012476	2.761196491	PAQR7;PIK3CD;GSTT1;PPARA
0	0	4.43343792	6.926358967	CUBN
0	0	2.348639152	3.605949706	PIK3CD;MAPK12
0	0	1.671973501	2.488608311	TUBAL3;PIK3CD;RAB7B;MAPK12
0	0	1.848550452	2.731366961	TUBAL3;CD1E;JAM3
0	0	2.244946763	3.302002646	PLA2G4D;MAPK12
0	0	3.921292625	5.719377463	FADS2
0	0	3.775868652	5.387547135	RGS9
0	0	2.149986365	3.031563646	PLA2G4D;PIK3CD
0	0	2.149986365	3.031563646	PIK3CD;FOXO1
0	0	3.640832106	5.084049295	PLA2G4D
0	0	2.127482729	2.968620438	PLA2G4D;PIK3CD
0	0	3.515108425	4.805648067	ACLY
0	0	3.515108425	4.805648067	ACSS2
0	0	3.515108425	4.805648067	ALDOC
0	0	2.041968912	2.733562609	PIK3CD;MAPK12
0	0	2.001727116	2.625260355	PIK3CD;MAPK12
0	0	3.185083763	4.095120179	ALDOC
0	0	1.963033081	2.522556307	MEF2C;PDE4D
0	0	1.944238835	2.473186314	PPARA;FOXO1
0	0	3.088409872	3.89287561	ACSS2
0	0	1.621693122	2.016584598	GRK4;PIK3CD;CCR7
0	0	1.405508965	1.730158786	TUBAL3;INSR;ULK2;PIK3CD;AXIN2
0	0	1.855393311	2.244468517	PIK3CD;MAPK12
0	0	1.579494201	1.892983883	TUBAL3;MYO1A;MAPK12
0	0	2.830612829	3.367625851	GFPT1
0	0	2.753970465	3.215620285	ADA
0	0	1.743766884	1.968439495	PIK3CD;MAPK12
0	0	1.743766884	1.968439495	PIK3CD;MAPK12
0	0	1.743766884	1.968439495	PIK3CD;MAPK12
0	0	1.714285714	1.897730905	PIK3CD;FOXO1
0	0	2.547036082	2.815357213	LPCAT3

0	0	2.547036082	2.815357213	BABAM2
0	0	1.631502591	1.704278414	PIK3CD;MAPK12
0	0	2.315018744	2.385433746	ST8SIA5
0	0	1.605646444	1.645436469	CPEB2;MAPK12
0	0	1.605646444	1.645436469	PIK3CD;MAPK12
0	0	2.214141641	2.205208481	PIK3CD
0	0	2.214141641	2.205208481	ACSS2
0	0	2.166922571	2.122321603	GFPT1
0	0	2.121670962	2.043796579	RGS9
0	0	2.121670962	2.043796579	PLA2G4D
0	0	1.50988294	1.434312913	PIK3CD;MAPK12
0	0	1.455588453	1.319542605	TUBAL3;PIK3CD
0	0	1.958068993	1.767622378	CSGALNACT1
0	0	1.445191636	1.297985319	ULK2;PIK3CD
0	0	1.921027038	1.706841126	FANCA
0	0	1.405038413	1.216024292	PIK3CD;AXIN2
0	0	1.817838733	1.541105976	GSTT1
0	0	1.37634785	1.158741518	CACNB2;MAPK12
0	0	1.754976893	1.442820774	NUMBL
0	0	1.725144155	1.396912516	PLA2G4D
0	0	1.696305842	1.352994883	PLA2G4D
0	0	1.313722213	1.037515956	PIK3CD;PPARA
0	0	1.64142002	1.270687355	AXIN2
0	0	1.64142002	1.270687355	SMYD2
0	0	1.615283914	1.232094729	PIK3CD
0	0	1.27234456	0.960370482	PIK3CD;MAPK12
0	0	1.541627616	1.125486449	PIK3CD
0	0	1.233474643	0.890105806	MEF2C;INSR
0	0	1.518541314	1.092742561	RAB7B
0	0	1.496134021	1.06127545	PIK3CD
0	0	1.474376214	1.031020386	PIK3CD
0	0	1.474376214	1.031020386	MAPK12
0	0	1.130497685	0.786148678	TUBAL3;PIK3CD;MAPK12
0	0	1.453240059	1.001916725	INSR
0	0	1.432699289	0.973907599	PIK3CD
0	0	1.432699289	0.973907599	PIK3CD
0	0	1.374407913	0.895929655	PIK3CD
0	0	1.356013746	0.871796159	PIK3CD
0	0	1.356013746	0.871796159	GSTT1
0	0	1.356013746	0.871796159	PIK3CD
0	0	1.356013746	0.871796159	MAPK12
0	0	1.14263259	0.734545434	BCL10;MAPK12
0	0	1.338103635	0.848520453	CACNB2
0	0	1.338103635	0.848520453	PIK3CD
0	0	1.338103635	0.848520453	MAPK12
0	0	1.129821531	0.713614436	EFNA2;PIK3CD
0	0	1.044145976	0.622275895	CCR7;INHA;TNFRSF21

0	0	1.087140838	0.645738813	PIK3CD;MAPK12
0	0	1.255186458	0.743706897	MVK
0	0	1.069811835	0.619009542	MEF2C;FOXO1
0	0	1.064156471	0.610391622	PIK3CD;MAPK12
0	0	1.210174276	0.688908025	PIK3CD
0	0	1.181910813	0.655284011	CACNB2
0	0	1.168266382	0.63927312	TUBAL3
0	0	1.141897371	0.608746424	CACNB2
0	0	1.015803109	0.53885856	PIK3CD;MAPK12
0	0	1.116687436	0.580082595	PIK3CD
0	0	1.116687436	0.580082595	MAPK12
0	0	1.000638097	0.517229806	PIK3CD;MAPK12
0	0	1.0925618	0.553138127	MAPK12
0	0	1.06945198	0.527783045	CACNB2
0	0	0.966938071	0.470575845	PIK3CD;MAPK12
0	0	1.036555859	0.492475451	CD1E
0	0	0.953173271	0.452087708	PIK3CD;MAPK12
0	0	1.026033531	0.481379917	CCR7
0	0	0.927829649	0.430011213	PIK3CD;AXIN2;FOXO1
0	0	0.985987389	0.440051228	BCL10
0	0	0.90996538	0.396238371	PIK3CD;MAPK12
0	0	0.957936199	0.411968783	MAPK12
0	0	0.94893535	0.40311268	GSTT1
0	0	0.881955395	0.361839811	PIK3CD;MAPK12
0	0	0.881955395	0.361839811	SMARCA2;MAPK12
0	0	0.914553729	0.369990785	MAPK12
0	0	0.906342047	0.362248267	PIK3CD
0	0	0.906342047	0.362248267	PLA2G4D
0	0	0.898275705	0.354706922	PLA2G4D
0	0	0.866007835	0.341828647	EFNA2;INSR;PIK3CD
0	0	0.859661409	0.326741742	TUBAL3;ULK2;AXIN2;MAPK12
0	0	0.841585873	0.309771042	TUBAL3;ULK2;MAPK12
0	0	0.824826083	0.289043335	PRKDC
0	0	0.810569948	0.280813155	GRK4;PSD3
0	0	0.798684958	0.267024238	LAPTM4B
0	0	0.780134814	0.251845427	PIK3CD
0	0	0.774140238	0.247020799	MAPK12
0	0	0.768236489	0.242308068	PLA2G4D
0	0	0.745489691	0.224514156	MEF2C
0	0	0.745489691	0.224514156	PIK3CD
0	0	0.734610787	0.216210925	PIK3CD
0	0	0.729288734	0.212198294	KLHL13
0	0	0.76608681	0.206041949	PIK3CD;GSTT1;AXIN2;FOXO1
0	0	0.689319027	0.183118419	MAPK12
0	0	0.657752042	0.161502202	AXIN2
0	0	0.640969594	0.150509265	PLA2G4D
0	0	0.628930012	0.142840717	PIK3CD

0	0	0.625015909	0.140387237	AXIN2
0	0	0.664746387	0.146563832	TUBAL3;ULK2
0	0	0.613558263	0.13331787	AXIN2
0	0	0.655978736	0.139889607	EFNA2;PIK3CD
0	0	0.595360825	0.122438875	LMAN1L
0	0	0.591849038	0.120389217	PIK3CD
0	0	0.561998855	0.103628131	MAPK12
0	0	0.546670382	0.095487627	CAMKK2
0	0	0.505283505	0.07513032	PIK3CD
0	0	0.500229662	0.07280945	PIK3CD
0	0	0.465295263	0.057769471	PIK3CD
0	0	0.463137236	0.056898432	PIK3CD
0	0	0.421990251	0.041602947	ITPKC
0	0	0.406489026	0.036493594	TUBAL3
0	0	0.403413839	0.01776691	PIK3CD;ZNF613

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Supplementary File S6: Comprehensive details of the results of functional enrichment an

BP	Term	Overlap	P-value	Adjusted P-value
	androgen metabolic process (GO:0008209)	44613	1.97E-04	0.020513108
	steroid hormone biosynthetic process (GO:012(	11355	4.34E-04	0.022575285
	steroid metabolic process (GO:0008202)	2/104	0.004786758	0.07770337
	negative regulation of cell size (GO:0045792)	44567	0.005985691	0.07770337
	aromatic amino acid transport (GO:0015801)	44567	0.005985691	0.07770337
	thyroid hormone transport (GO:0070327)	44568	0.006979996	0.07770337
	negative regulation by symbiont of host progra	44569	0.007973357	0.07770337
	nitrogen compound transport (GO:0071705)	2/143	0.008864977	0.07770337
	estrogen biosynthetic process (GO:0006703)	44570	0.008965773	0.07770337
	androgen biosynthetic process (GO:0006702)	44570	0.008965773	0.07770337
	hormone transport (GO:0009914)	44570	0.008965773	0.07770337
	negative regulation of exocytosis (GO:0045920)	44570	0.008965773	0.07770337
	phagosome-lysosome fusion (GO:0090385)	44571	0.009957248	0.079657981
	protein polyglutamylation (GO:0018095)	44572	0.01094778	0.081326364
	phagolysosome assembly (GO:0001845)	44573	0.011937371	0.082765769
	regulation of extracellular matrix organization (	44576	0.014900504	0.091156023
	positive regulation of exosomal secretion (GO:1	44576	0.014900504	0.091156023
	piRNA metabolic process (GO:0034587)	44580	0.018838221	0.092458647
	regulation of exosomal secretion (GO:1903541)	44580	0.018838221	0.092458647
	protein targeting to lysosome (GO:0006622)	44581	0.019820311	0.092458647
	early endosome to late endosome transport (G	44581	0.019820311	0.092458647
	regulation of cell size (GO:0008361)	44585	0.023739344	0.092458647
	peptidyl-glutamic acid modification (GO:00182(	44585	0.023739344	0.092458647
	peripheral nervous system development (GO:0(	44586	0.024716774	0.092458647
	regulation of synapse organization (GO:005080	44587	0.025693274	0.092458647
	negative regulation of axonogenesis (GO:00507	44589	0.027643489	0.092458647
	phagosome acidification (GO:0090383)	44589	0.027643489	0.092458647
	regulation of postsynapse organization (GO:009	44589	0.027643489	0.092458647
	protein localization to lysosome (GO:0061462)	44589	0.027643489	0.092458647
	estrogen metabolic process (GO:0008210)	44591	0.029589996	0.092458647
	organic cyclic compound biosynthetic process (	12420	0.033471909	0.092458647
	secondary alcohol biosynthetic process (GO:19(	12420	0.033471909	0.092458647
	negative regulation of neurogenesis (GO:00507	12785	0.03444008	0.092458647
	cholesterol biosynthetic process (GO:0006695)	12785	0.03444008	0.092458647
	intracellular pH reduction (GO:0051452)	12785	0.03444008	0.092458647
	establishment of protein localization to plasma	13150	0.03540733	0.092458647
	positive regulation of exocytosis (GO:0045921)	13516	0.036373659	0.092458647
	phagosome maturation (GO:0090382)	13516	0.036373659	0.092458647
	ncRNA metabolic process (GO:0034660)	13516	0.036373659	0.092458647
	negative regulation of TOR signaling (GO:00320	13881	0.037339069	0.092458647
	sterol biosynthetic process (GO:0016126)	13881	0.037339069	0.092458647
	regulation of apoptotic signaling pathway (GO:2	13881	0.037339069	0.092458647
	negative regulation of epidermal growth factor	16072	0.043112259	0.104271511
	myelination (GO:0042552)	17533	0.046942764	0.109977183

amino acid transport (GO:0006865)	18264	0.04885255	0.109977183
negative regulation of transport (GO:0051051)	18629	0.049806079	0.109977183
regulation of axonogenesis (GO:0050770)	18629	0.049806079	0.109977183
endocytic recycling (GO:0032456)	18994	0.0507587	0.109977183
autophagosome organization (GO:1905037)	20455	0.054560118	0.112372137
negative regulation of neuron projection devel	21186	0.056455399	0.112372137
autophagosome assembly (GO:0000045)	21186	0.056455399	0.112372137
selective autophagy (GO:0061912)	21551	0.057401686	0.112372137
homophilic cell adhesion via plasma membrane	21916	0.058347071	0.112372137
cellular protein catabolic process (GO:0044257	21916	0.058347071	0.112372137
negative regulation of kinase activity (GO:0033	22647	0.06023514	0.113074002
positive regulation of viral process (GO:004852	23012	0.061177825	0.113074002
regulation of extrinsic apoptotic signaling pathv	23377	0.062119612	0.113074002
steroid biosynthetic process (GO:0006694)	23743	0.063060501	0.113074002
positive regulation of catabolic process (GO:00	24473	0.06493959	0.114469786
synapse assembly (GO:0007416)	25204	0.066815099	0.115812838
regulation of TOR signaling (GO:0032006)	25934	0.068687033	0.117105762
nervous system development (GO:0007399)	2/447	0.072676705	0.121909312
cholesterol metabolic process (GO:0008203)	28126	0.074281457	0.122623358
lipid biosynthetic process (GO:0008610)	29221	0.077066683	0.12523336
positive regulation of protein catabolic process	31048	0.081691043	0.127469916
neutrophil degranulation (GO:0043312)	2/481	0.082498962	0.127469916
neutrophil activation involved in immune respo	2/485	0.083681174	0.127469916
retrograde transport, endosome to Golgi (GO:0	32143	0.084455084	0.127469916
neutrophil mediated immunity (GO:0002446)	2/488	0.084571386	0.127469916
negative regulation of protein kinase activity (G	32874	0.086293386	0.128207316
positive regulation of cellular component bioge	33604	0.08812818	0.129089165
hemopoiesis (GO:0030097)	34335	0.089959474	0.129941463
antigen processing and presentation of exogen	35796	0.093611586	0.130876197
organic acid transport (GO:0015849)	1/100	0.095432416	0.130876197
antigen processing and presentation of peptide	1/100	0.095432416	0.130876197
cell junction assembly (GO:0034329)	1/102	0.097249772	0.130876197
regulation of protein catabolic process (GO:004	1/102	0.097249772	0.130876197
antigen processing and presentation of exogen	1/103	0.098157148	0.130876197
activation of GTPase activity (GO:0090630)	1/105	0.099969302	0.131605157
regulation of protein kinase activity (GO:00458	1/110	0.104484565	0.135829935
positive regulation of protein metabolic proces	1/115	0.108978304	0.139352995
cytosolic transport (GO:0016482)	1/116	0.109874477	0.139352995
synapse organization (GO:0050808)	1/126	0.118789239	0.148844348
negative regulation of inflammatory response t	1/136	0.127619141	0.155392317
organic substance transport (GO:0071702)	1/136	0.127619141	0.155392317
regulation of inflammatory response to antigen	1/137	0.128497493	0.155392317
regulation of cellular component organization (	1/139	0.130251678	0.155703155
regulation of small GTPase mediated signal trar	1/141	0.132002508	0.156002964
negative regulation of protein phosphorylation	1/152	0.141572381	0.165432895
adenylate cyclase-modulating G protein-couple	1/165	0.15275301	0.176514589
cell-cell adhesion via plasma-membrane adhesi	1/170	0.157016302	0.179447202

negative regulation of immune response (GO:0	1/178	0.163795207	0.185159799
negative regulation of intracellular signal transc	1/198	0.180516629	0.201868058
negative regulation of inflammatory response (	1/212	0.192032086	0.212011716
positive regulation of GTPase activity (GO:0043	1/214	0.193664548	0.212011716
intracellular protein transport (GO:0006886)	1/336	0.287529058	0.311489813
protein transport (GO:0015031)	1/369	0.311076071	0.333524859
negative regulation of programmed cell death (	1/381	0.319453839	0.339012238
phosphorylation (GO:0016310)	1/400	0.332521003	0.349314993
organelle organization (GO:0006996)	1/420	0.346018236	0.35972859
organelle assembly (GO:0070925)	1/425	0.349351804	0.35972859
regulation of intracellular signal transduction (G	1/437	0.357286629	0.364292249
protein phosphorylation (GO:0006468)	1/496	0.39498063	0.398815393
cellular protein modification process (GO:0006	1/1025	0.651009352	0.651009352

alysis of significant highly-correlated RNA-seq-based modules (salmon; Signific

Old P-value	Old Adjusted P-value	Odds Ratio	Combined Score	Genes	KEGG
0	0	116.7309942	995.8416923	HSD17B3;H	.
0	0	76.44061303	591.8141768	HSD17B3;H	.
0	0	21.65359477	115.6713806	HSD17B3;H	.
0	0	210.2631579	1076.207481	DEPTOR	.
0	0	210.2631579	1076.207481	SLC16A10	.
0	0	175.2105263	869.8689178	SLC16A10	.
0	0	150.1729323	725.5830081	RAB7A	.
0	0	15.63356974	73.87873089	SLC16A10;	.
0	0	131.3947368	619.4395814	HSD17B7	.
0	0	131.3947368	619.4395814	HSD17B3	.
0	0	131.3947368	619.4395814	SLC16A10	.
0	0	131.3947368	619.4395814	RAB7A	.
0	0	116.7894737	538.3357754	RAB7A	.
0	0	105.1052632	474.5101771	TTLL1	.
0	0	95.54545455	423.0830518	RAB7A	.
0	0	75.06015038	315.7300333	ANGPTL7	.
0	0	75.06015038	315.7300333	RAB7A	.
0	0	58.36842105	231.8316322	ASZ1	.
0	0	58.36842105	231.8316322	RAB7A	.
0	0	55.29362881	216.8089753	RAB7A	.
0	0	55.29362881	216.8089753	RAB7A	.
0	0	45.66819222	170.827423	DEPTOR	.
0	0	45.66819222	170.827423	TTLL1	.
0	0	43.76315789	161.9356388	NFASC	.
0	0	42.01052632	153.8226357	ARHGAP22	.
0	0	38.89473684	139.5685146	LINGO1	.
0	0	38.89473684	139.5685146	RAB7A	.
0	0	38.89473684	139.5685146	ARHGAP22	.
0	0	38.89473684	139.5685146	RAB7A	.
0	0	36.20871143	127.4662135	HSD17B7	.
0	0	31.81339713	108.0716599	HSD17B3	.
0	0	31.81339713	108.0716599	HSD17B7	.
0	0	30.87616099	104.0074062	LINGO1	.
0	0	30.87616099	104.0074062	HSD17B7	.
0	0	30.87616099	104.0074062	RAB7A	.
0	0	29.9924812	100.1999734	RAB7A	.
0	0	29.15789474	96.62665093	RAB7A	.
0	0	29.15789474	96.62665093	RAB7A	.
0	0	29.15789474	96.62665093	ASZ1	.
0	0	28.36842105	93.26728562	DEPTOR	.
0	0	28.36842105	93.26728562	HSD17B7	.
0	0	28.36842105	93.26728562	DEPTOR	.
0	0	24.40269278	76.72079425	RAB7A	.
0	0	22.32138858	68.27724817	NFASC	.

0	0	21.40816327	64.63014669	SLC16A10	.
0	0	20.97894737	62.92883309	RAB7A	.
0	0	20.97894737	62.92883309	LINGO1	.
0	0	20.56656347	61.30218505	RAB7A	.
0	0	19.06698565	55.45541451	RAB7A	.
0	0	18.39612188	52.87605302	LINGO1	.
0	0	18.39612188	52.87605302	RAB7A	.
0	0	18.07803993	51.66128207	RAB7A	.
0	0	17.77074041	50.4928242	KIRREL3	.
0	0	17.77074041	50.4928242	RAB7A	.
0	0	17.18636756	48.28508895	DEPTOR	.
0	0	16.90831919	47.24134485	RAB7A	.
0	0	16.63909774	46.23495323	DEPTOR	.
0	0	16.37828947	45.2640346	HSD17B3	.
0	0	15.88038278	43.42169605	RAB7A	.
0	0	15.41176471	41.70155665	KIRREL3	.
0	0	14.96992481	40.09237541	DEPTOR	.
0	0	4.877652934	12.78791036	KIRREL3;NI	.
0	0	13.78393352	35.83676501	HSD17B7	.
0	0	13.25849434	33.98263763	HSD17B3	.
0	0	12.46616541	31.22538725	RAB7A	.
0	0	4.523544421	11.28610567	NFASC;RAE	.
0	0	4.485162181	11.12652681	NFASC;RAE	.
0	0	12.03448276	29.74365058	RAB7A	.
0	0	4.456790123	11.00898153	NFASC;RAE	.
0	0	11.76286221	28.81903982	DEPTOR	.
0	0	11.50318103	27.94080033	RAB7A	.
0	0	11.25466893	27.10569961	KIRREL3	.
0	0	10.7883885	25.55338909	RAB7A	.
0	0	10.56937799	24.83103039	SLC16A10	.
0	0	10.56937799	24.83103039	RAB7A	.
0	0	10.35904117	24.14146207	KIRREL3	.
0	0	10.35904117	24.14146207	RAB7A	.
0	0	10.25696594	23.80832097	RAB7A	.
0	0	10.05870445	23.16411122	ARHGAP22	.
0	0	9.5948817	21.67211205	DEPTOR	.
0	0	9.171745152	20.33014962	RAB7A	.
0	0	9.091533181	20.07789357	RAB7A	.
0	0	8.36	17.81018125	KIRREL3	.
0	0	7.736842105	15.92787486	VIPR2	.
0	0	7.736842105	15.92787486	RAB7A	.
0	0	7.679566563	15.75728705	VIPR2	.
0	0	7.567505721	15.42474639	ANGPTL7	.
0	0	7.458646617	15.10326978	ARHGAP22	.
0	0	6.91146741	13.5115329	DEPTOR	.
0	0	6.359435173	11.94895247	VIPR2	.
0	0	6.169729056	11.42267121	KIRREL3	.

0	0	5.888492417	10.65309758	VIPR2	.
0	0	5.285332621	9.04813205	DEPTOR	.
0	0	4.931154901	8.136863222	VIPR2	.
0	0	4.884358784	8.018298921	ARHGAP22	.
0	0	3.086410055	3.846998259	RAB7A	.
0	0	2.804919908	3.275354896	RAB7A	.
0	0	2.71468144	3.097838347	RAB7A	.
0	0	2.58290463	2.843912967	LMTK3	.
0	0	2.457103379	2.607634867	RAB7A	.
0	0	2.427507448	2.552950909	RAB7A	.
0	0	2.359246741	2.428176705	ARHGAP22	.
0	0	2.071770335	1.924505902	LMTK3	.
0	0	0.974300987	0.418200451	LMTK3	.

ant terms were highlighted)

Term	Overlap	P-value	Adjusted P-value	Old P-value	Old Adjusted P-value
Steroid hormone biosynthesis	22313	0.001678125	0.026850006	0	0
Autophagy	2/137	0.008163347	0.065306778	0	0
Steroid biosynthesis	44581	0.019820311	0.105708327	0	0
Ovarian steroidogenesis	18629	0.049806079	0.199224316	0	0
Mitophagy	24838	0.065877792	0.208438623	0	0
Amoebiasis	1/102	0.097249772	0.208438623	0	0
Protein digestion and absorptio	1/103	0.098157148	0.208438623	0	0
Thyroid hormone signaling path	1/121	0.114342514	0.208438623	0	0
Cell adhesion molecules	1/148	0.138104084	0.208438623	0	0
Phagosome	1/152	0.141572381	0.208438623	0	0
mTOR signaling pathway	1/154	0.143301554	0.208438623	0	0
Tuberculosis	1/180	0.165481823	0.220642431	0	0
cAMP signaling pathway	1/216	0.195293876	0.239031858	0	0
Salmonella infection	1/249	0.221730401	0.239031858	0	0
Endocytosis	1/252	0.224092367	0.239031858	0	0
Neuroactive ligand-receptor int	1/341	0.291145282	0.291145282	0	0

Odds Ratio	Combined Score	Genes
37.51600753	239.7302132	HSD17B3;HSD17B7
16.33333333	78.53231621	DEPTOR;RAB7A
55.29362881	216.8089753	HSD17B7
20.97894737	62.92883309	HSD17B7
15.64257659	42.54708713	RAB7A
10.35904117	24.14146207	RAB7A
10.25696594	23.80832097	SLC16A10
8.710526316	18.88927133	SLC16A10
7.100966702	14.05812214	NFASC
6.91146741	13.5115329	RAB7A
6.820433437	13.25076606	DEPTOR
5.822111144	10.47336034	RAB7A
4.838433293	7.902370194	VIPR2
4.187606112	6.307761967	RAB7A
4.13692598	6.187587605	RAB7A
3.040247678	3.751461592	VIPR2

Supplementary File S7: The results of the assigning the miRNA-seq-based modules to the RNA-se

RNA-seq-based / miRNA-seq-based modules	R_MEbrown	P_MEbrown	R_MEblue	P_MEblue
MEmidnightblue	0.636968792	5.75E-06	-0.41321272	0.006531354
MEsalmon	0.695615382	3.17E-07	0.002755003	0.986184798
MEpink	0.085855111	0.588774289	0.095753711	0.546364896
MEyellow	-0.354875066	0.021106699	0.739690719	2.19E-08
MEblue	-0.215935794	0.169610081	0.513649809	0.000503186
MEred	0.261227041	0.09471975	0.196027592	0.213433935
MEbrown	-0.096789922	0.54201109	0.734005729	3.18E-08
MEgreenyellow	0.377125863	0.01381801	0.074248517	0.640278225
MEblack	0.189999174	0.228129655	0.401716706	0.008365178
MElightcyan	0.3005975	0.053075989	0.349531749	0.023270871
MEgrey60	-0.360189927	0.019123941	0.017927203	0.910280842
MEpurple	-0.214964445	0.171584449	-0.144797889	0.360237568
MEgreen	0.287439332	0.064925697	-0.378757924	0.013380309
MEturquoise	0.278284438	0.074342732		
MEcyan	-0.061237452	0.700052823	-0.024171096	0.879233225
MEmagenta	-0.412112591	0.006690319	0.132890562	0.401486813
MEtan	-0.245589464	0.116954305	0.191251701	0.225020709
MEgrey	0.13576109	0.391301622	-0.156882097	0.321104613

q-based modules (R = correlation; P = p-value)

R_MEturquoise	P_MEturquoise	R_MEgrey	P_MEgrey
-0.616604227	1.37E-05	-0.097681625	0.538277835
-0.736982991	2.62E-08	-0.296154406	0.056865409
-0.134527676	0.395659389	0.020221918	0.898852627
0.198591502	0.207387528	-0.015713589	0.921322129
0.083764701	0.597913725	-0.275718175	0.07716641
-0.394958956	0.009637525	-0.322847202	0.037037323
-0.084199651	0.596006989	0.191914386	0.223387665
-0.53436176	0.000267264	0.231276765	0.140569075
-0.30119536	0.052581956	0.077807278	0.624293201
-0.395547371	0.009520509	-0.193192871	0.220260198
0.42238181	0.005328745	0.187045022	0.235578449
0.313925708	0.042911106	0.337438045	0.028859726
-0.208464741	0.185222841	0.28515349	0.067183213
-0.109177709	0.491288292	0.300761486	0.052940112
0.188594137	0.231652027	-0.055915878	0.725051513
0.465716473	0.001882829	-0.259591386	0.096880025
0.21274538	0.176156897	-0.103224141	0.515355361
-0.108943691	0.492223202	-0.330875459	0.032330664

Supplementary File S8: information from the results of target prediction analysis and inter

bta-miR-10b	UBAP1
bta-miR-10b	ECE1
bta-miR-10b	PSTPIP2
bta-miR-10b	ETS2
bta-miR-10b	NUDT3
bta-miR-10b	EPG5
bta-miR-10b	DNAJB6
bta-miR-10b	CSF1
bta-miR-10b	ADAM19
bta-miR-10b	HDAC4
bta-miR-10b	TMBIM1
bta-miR-10b	LRCH1
bta-miR-10b	SLC46A2
bta-miR-10b	TNFRSF1B
bta-miR-10b	CYTH1
bta-miR-10b	SH3BP2
bta-miR-10b	LOC514257
bta-miR-10b	LOC529196
bta-miR-10b	DCBLD1
bta-miR-10b	CALM1
bta-miR-10b	AOAH
bta-miR-10b	VCAN
bta-miR-10b	LPIN2
bta-miR-10b	DTX3L
bta-miR-10b	E2F3
bta-miR-10b	PLEKHF2
bta-miR-10b	MOCS1
bta-miR-10b	LENG8
bta-miR-10b	LOC100337457
bta-miR-10b	ICAM1
bta-miR-10b	LYSMD1
bta-miR-10b	STK3
bta-miR-10b	CD46
bta-miR-10b	SLC1A2
bta-miR-10b	MTMR3
bta-miR-10b	CDKN1A
bta-miR-10b	IFIT3
bta-miR-10b	MLXIP
bta-miR-10b	SIK3
bta-miR-10b	SLC8A1
bta-miR-10b	BCL2L11
bta-miR-10b	SYNE3

bta-miR-27b	PELI1
bta-miR-27b	VEGFA
bta-miR-27b	E2F2
bta-miR-27b	SBNO2
bta-miR-27b	NIN
bta-miR-27b	CYLD
bta-miR-27b	TLE3
bta-miR-27b	GRIPAP1
bta-miR-27b	IL10RB
bta-miR-27b	ANTXR2
bta-miR-27b	CRISPLD2
bta-miR-27b	ADGRE5
bta-miR-27b	CSF1
bta-miR-27b	BID
bta-miR-27b	SEMA4D
bta-miR-27b	MCL1
bta-miR-27b	HDAC4
bta-miR-27b	ANKFY1
bta-miR-27b	RYBP
bta-miR-27b	SLC46A2
bta-miR-27b	GADD45B
bta-miR-27b	ELL
bta-miR-27b	PCGF5
bta-miR-27b	LOC514257
bta-miR-27b	B4GALT5
bta-miR-27b	COPZ1
bta-miR-27b	COP1
bta-miR-27b	RND1
bta-miR-27b	PHACTR2
bta-miR-27b	STK19
bta-miR-27b	SF3B1
bta-miR-27b	BACH1
bta-miR-27b	MAD2L2
bta-miR-27b	RAP1GAP
bta-miR-27b	TPM4
bta-miR-27b	SRI
bta-miR-27b	LOC509283
bta-miR-27b	IL17RC
bta-miR-27b	LAPTM5
bta-miR-27b	SLC1A2
bta-miR-27b	PHF12
bta-miR-27b	BOLA-DMB

bta-miR-10b	ATXN7
bta-miR-10b	SMNDC1
bta-miR-10b	ZNF408
bta-miR-10b	PTBP3
bta-miR-10b	FNBP1
bta-miR-10b	SH3PXD2B
bta-miR-10b	DPH3
bta-miR-10b	IL15
bta-miR-10b	DUSP5
bta-miR-10b	ALKBH1
bta-miR-10b	NIPAL4
bta-miR-10b	LOC507247
bta-miR-10b	MAEA
bta-miR-10b	HERPUD1
bta-miR-10b	ARHGAP35
bta-miR-10b	GPCPD1
bta-miR-10b	MEGF9
bta-miR-10b	H2AW
bta-miR-10b	LMTK2
bta-miR-10b	IRF5
bta-miR-10b	PLEKHO2
bta-miR-10b	IL10

bta-miR-27b	CREBRF
bta-miR-27b	SP140L
bta-miR-27b	SERINC2
bta-miR-27b	TNIP2
bta-miR-27b	CCDC69
bta-miR-27b	SSH2
bta-miR-27b	KDM3A
bta-miR-27b	DDX17
bta-miR-27b	PLA2G4A
bta-miR-27b	HEG1
bta-miR-27b	DPH3
bta-miR-27b	IL1R1
bta-miR-27b	SLC13A3
bta-miR-27b	NGP
bta-miR-27b	FRAT1
bta-miR-27b	SDCBP
bta-miR-27b	TRIM25
bta-miR-27b	PLAGL2
bta-miR-27b	C1H3orf38
bta-miR-27b	SRGAP2
bta-miR-27b	MNT
bta-miR-27b	C7H19orf38
bta-miR-27b	OSBPL2
bta-miR-27b	TTC19
bta-miR-27b	PTPN9
bta-miR-27b	POGZ
bta-miR-27b	CMPK2
bta-miR-27b	ELOVL5
bta-miR-27b	RETREG3
bta-miR-27b	ZSWIM6
bta-miR-27b	MYSM1
bta-miR-27b	MALT1
bta-miR-27b	HPCAL1

ractions between blue miRNA-seq-based module miRNAs and turquoise RNA-seq-based modu

bta-miR-29a	ARRDC4
bta-miR-29a	ADAM19
bta-miR-29a	SLC2A9
bta-miR-29a	BTG2
bta-miR-29a	ILRUN
bta-miR-29a	ELL
bta-miR-29a	EGR3
bta-miR-29a	TAP1
bta-miR-29a	ARIH2
bta-miR-29a	MAP2K3
bta-miR-29a	KCNJ2
bta-miR-29a	ANKRD33B
bta-miR-29a	PPM1D
bta-miR-29a	EGR2
bta-miR-29a	SLC25A37
bta-miR-29a	MLXIP
bta-miR-29a	TET2
bta-miR-29a	LOC112442378
bta-miR-29a	KCTD7
bta-miR-29a	PARP11
bta-miR-29a	IFNAR1
bta-miR-29a	ATP8B4
bta-miR-29a	SSH2
bta-miR-29a	CCL8
bta-miR-29a	GCH1
bta-miR-29a	GPAT3
bta-miR-29a	RSPRY1
bta-miR-29a	OTUD4
bta-miR-29a	SRRM2
bta-miR-29a	PPP4R2
bta-miR-29a	SNRK
bta-miR-29a	APOL3
bta-miR-29a	SPRYD3
bta-miR-29a	RAB11FIP1
bta-miR-29a	SIK1
bta-miR-29a	CD164
bta-miR-29a	ZSWIM7
bta-miR-29a	MAP4K4
bta-miR-29a	RNF175
bta-miR-29a	RET
bta-miR-29a	SNX20
bta-miR-29a	HIPK3
bta-miR-30a-5p	STAT3
bta-miR-30a-5p	PSTPIP2
bta-miR-30a-5p	NFKB1
bta-miR-30a-5p	GRIPAP1
bta-miR-30a-5p	CD47
bta-miR-30a-5p	LOC617141
bta-miR-30a-5p	CRKL
bta-miR-30a-5p	ANKFY1
bta-miR-30a-5p	PXN
bta-miR-30a-5p	PPP1R16B
bta-miR-30a-5p	TREML2
bta-miR-30a-5p	CHIC2
bta-miR-30a-5p	HIVEP3
bta-miR-30a-5p	IL12B
bta-miR-30a-5p	SHISA5
bta-miR-30a-5p	SLC1A5
bta-miR-30a-5p	TAPT1
bta-miR-30a-5p	WSB1
bta-miR-30a-5p	TLR4
bta-miR-30a-5p	FMR1
bta-miR-30a-5p	TDRD10
bta-miR-30a-5p	SLC4A7
bta-miR-30a-5p	SLC8A1
bta-miR-30a-5p	SYNE3
bta-miR-30a-5p	DCAF11
bta-miR-30a-5p	R3HCC1L
bta-miR-30a-5p	PTGER2
bta-miR-30a-5p	NFIX
bta-miR-30a-5p	TIRAP
bta-miR-30a-5p	SEMA7A
bta-miR-30a-5p	GPCPD1
bta-miR-30a-5p	ARHGAP17
bta-miR-30a-5p	LMTK2
bta-miR-30a-5p	KLF6
bta-miR-30a-5p	ZC3H12C

bta-miR-29a	USP3
bta-miR-29a	CAMK1D
bta-miR-29a	DIXDC1

ıle RNAs (mRNAs and lncRNAs)

bta-miR-31	STAT3
bta-miR-31	ACSL4
bta-miR-31	ADAM17
bta-miR-31	RAB27A
bta-miR-31	ARHGEF2
bta-miR-31	VEGFA
bta-miR-31	LOC527744
bta-miR-31	NUDT3
bta-miR-31	CYLD
bta-miR-31	GABARAPL1
bta-miR-31	RNF41
bta-miR-31	MFSD14A
bta-miR-31	FAS
bta-miR-31	SLC45A4
bta-miR-31	ANTXR2
bta-miR-31	ZFAND3
bta-miR-31	CRISPLD2
bta-miR-31	ADGRE5
bta-miR-31	NLRP12
bta-miR-31	NABP1
bta-miR-31	PTAFR
bta-miR-31	CXCR2
bta-miR-31	RIC1
bta-miR-31	ADAM19
bta-miR-31	RELA
bta-miR-31	IGSF6
bta-miR-31	LRCH1
bta-miR-31	THEMIS2
bta-miR-31	VPS4B
bta-miR-31	OSM
bta-miR-31	DUSP16
bta-miR-31	BAZ2A
bta-miR-31	TACC3
bta-miR-31	QKI
bta-miR-31	NDFIP2
bta-miR-31	H3-3B
bta-miR-31	PXN
bta-miR-31	GALC
bta-miR-31	ZNFX1
bta-miR-31	ZDHHC18
bta-miR-31	ZNF655
bta-miR-31	CYTH1

bta-miR-96	CD55
bta-miR-96	MARCKSL1
bta-miR-96	PIK3AP1
bta-miR-96	PTK2B
bta-miR-96	TMEM88
bta-miR-96	GRIPAP1
bta-miR-96	PDXK
bta-miR-96	ACVR1B
bta-miR-96	CXCR2
bta-miR-96	TNFSF13B
bta-miR-96	BAZ2A
bta-miR-96	MORC3
bta-miR-96	QKI
bta-miR-96	KDM4A
bta-miR-96	IL6
bta-miR-96	EDEM1
bta-miR-96	KCNJ2
bta-miR-96	FOSL2
bta-miR-96	CSRNP1
bta-miR-96	PPP1R3B
bta-miR-96	KAT5
bta-miR-96	VAT1L
bta-miR-96	TATDN2
bta-miR-96	MTMR3
bta-miR-96	SLC25A37
bta-miR-96	TGM2
bta-miR-96	VEZF1
bta-miR-96	PGS1
bta-miR-96	RBM43
bta-miR-96	SFPQ
bta-miR-96	YIPF4
bta-miR-96	ORAI2
bta-miR-96	PAQR8
bta-miR-96	R3HCC1L
bta-miR-96	NOD1
bta-miR-96	LFNG
bta-miR-96	ETV3
bta-miR-96	ESYT2
bta-miR-96	TLE4
bta-miR-96	TIMM17A
bta-miR-96	TFEC
bta-miR-96	SH3BGRL

bta-miR-31	SH3BP2
bta-miR-31	SLC6A2
bta-miR-31	TREML2
bta-miR-31	B4GALT5
bta-miR-31	HIVEP3
bta-miR-31	EGR3
bta-miR-31	RND1
bta-miR-31	CDS2
bta-miR-31	CFLAR
bta-miR-31	PAM
bta-miR-31	PHACTR2
bta-miR-31	PLAU
bta-miR-31	EMP1
bta-miR-31	EDEM1
bta-miR-31	SLA
bta-miR-31	INPP4A
bta-miR-31	SF3B1
bta-miR-31	MPHOSPH8
bta-miR-31	FEM1C
bta-miR-31	LOC100297725
bta-miR-31	LOC521224
bta-miR-31	HIP1R
bta-miR-31	IL6R
bta-miR-31	SNX10
bta-miR-31	KCNJ2
bta-miR-31	ANKRD33B
bta-miR-31	IL1B
bta-miR-31	JAK1
bta-miR-31	PAPOLG
bta-miR-31	SCNN1D
bta-miR-31	LOC509283
bta-miR-31	ICAM4
bta-miR-31	SLC6A9
bta-miR-31	IKBKE
bta-miR-31	IL1RAP
bta-miR-31	SLC1A2
bta-miR-31	PRKAB1
bta-miR-31	PARP9
bta-miR-31	MTMR3
bta-miR-31	CDKN1A
bta-miR-31	SMURF1
bta-miR-31	HES4
bta-miR-31	MLXIP
bta-miR-31	UBE2G1
bta-miR-31	TGM2
bta-miR-31	RNASE10
bta-miR-31	CREBRF

bta-miR-96	SERPINB2
bta-miR-96	KLF7
bta-miR-96	CASS4
bta-miR-96	ARHGAP35
bta-miR-96	N4BP2L2
bta-miR-96	FBXL3
bta-miR-96	SRGAP2
bta-miR-96	HECA
bta-miR-96	ATXN1
bta-miR-96	GLS
bta-miR-96	FCMR
bta-miR-96	CMPK2
bta-miR-96	RETREG3
bta-miR-96	FASLG
bta-miR-96	CABYR
bta-miR-96	TNFAIP8

bta-miR-31	USB1
bta-miR-31	GPX3
bta-miR-31	NIPBL
bta-miR-31	MIER3
bta-miR-31	PXK
bta-miR-31	DNASE1L1
bta-miR-31	VEZF1
bta-miR-31	ALCAM
bta-miR-31	TET2
bta-miR-31	IRF1
bta-miR-31	CORO2A
bta-miR-31	INTS6
bta-miR-31	PGS1
bta-miR-31	TFIP11
bta-miR-31	RASSF2
bta-miR-31	PARP11
bta-miR-31	YIPF4
bta-miR-31	ATXN7
bta-miR-31	IFNAR1
bta-miR-31	ATP8B4
bta-miR-31	RAF1
bta-miR-31	KPNA3
bta-miR-31	RNF114
bta-miR-31	STK40
bta-miR-31	IL22RA2
bta-miR-31	RELT
bta-miR-31	KDM3A
bta-miR-31	IL2RB
bta-miR-31	CTIF
bta-miR-31	FNBP1
bta-miR-31	CYP27B1
bta-miR-31	EDN1
bta-miR-31	RSPRY1
bta-miR-31	USP36
bta-miR-31	DLL1
bta-miR-31	HCLS1
bta-miR-31	ALDH2
bta-miR-31	DHRS3
bta-miR-31	OTUD4
bta-miR-31	FSD2
bta-miR-31	TIMM17A
bta-miR-31	TMEM229B
bta-miR-31	NACC2
bta-miR-31	TIRAP
bta-miR-31	SHROOM4
bta-miR-31	FRAT1
bta-miR-31	F13A1

bta-miR-31	RAP1GAP2
bta-miR-31	CTDSP2
bta-miR-31	FOXN3
bta-miR-31	CDC42SE2
bta-miR-31	KLF7
bta-miR-31	SPRYD3
bta-miR-31	MARCHF7
bta-miR-31	COTL1
bta-miR-31	SLC2A1
bta-miR-31	GZF1
bta-miR-31	CEBPD
bta-miR-31	HECA
bta-miR-31	LOC100336941
bta-miR-31	PAN3
bta-miR-31	GPCPD1
bta-miR-31	ANKRD44
bta-miR-31	SEH1L
bta-miR-31	RAB8B
bta-miR-31	C7H19orf38
bta-miR-31	NAMPT
bta-miR-31	PLEKHA4
bta-miR-31	RABGAP1L
bta-miR-31	CYP4V2
bta-miR-31	CHM
bta-miR-31	CYBB
bta-miR-31	HECW2
bta-miR-31	BCR
bta-miR-31	KRAS
bta-miR-31	KLF6
bta-miR-31	IFI16
bta-miR-31	MYSM1
bta-miR-31	ZMIZ2
bta-miR-31	OTULINL
bta-miR-31	ENTPD1
bta-miR-31	ITGA2B
bta-miR-31	TP53INP2

bta-miR-99a-3p	PTPRC
bta-miR-99a-3p	IKBKB
bta-miR-99a-3p	MKNK1
bta-miR-99a-3p	NAIP
bta-miR-99a-3p	MFSD14A
bta-miR-99a-3p	CRISPLD2
bta-miR-99a-3p	SLC25A19
bta-miR-99a-3p	ADGRE5
bta-miR-99a-3p	IL23A
bta-miR-99a-3p	LOC407171
bta-miR-99a-3p	LRCH1
bta-miR-99a-3p	LAMB3
bta-miR-99a-3p	PREX1
bta-miR-99a-3p	ANKFY1
bta-miR-99a-3p	ILRUN
bta-miR-99a-3p	LRP10
bta-miR-99a-3p	VDR
bta-miR-99a-3p	PPP1R16B
bta-miR-99a-3p	SH3BP2
bta-miR-99a-3p	IL2RA
bta-miR-99a-3p	MLKL
bta-miR-99a-3p	CDS2
bta-miR-99a-3p	PKNOX1
bta-miR-99a-3p	PIK3R6
bta-miR-99a-3p	KDM8
bta-miR-99a-3p	SPATA13
bta-miR-99a-3p	SCYL3
bta-miR-99a-3p	GPR146
bta-miR-99a-3p	IL1B
bta-miR-99a-3p	JAK1
bta-miR-99a-3p	TMEM120A
bta-miR-99a-3p	WAC
bta-miR-99a-3p	CD74
bta-miR-99a-3p	TMEM198
bta-miR-99a-3p	KAT5
bta-miR-99a-3p	CD46
bta-miR-99a-3p	SDC4
bta-miR-99a-3p	ACTB
bta-miR-99a-3p	NYX
bta-miR-99a-3p	VEZF1
bta-miR-99a-3p	TAGLN2
bta-miR-99a-3p	LOC509881

bta-miR-99a-5p	IL1RN
bta-miR-99a-5p	TNFRSF1A
bta-miR-99a-5p	WLS
bta-miR-99a-5p	SLC2A3
bta-miR-99a-5p	RNF41
bta-miR-99a-5p	CMIP
bta-miR-99a-5p	BRF2
bta-miR-99a-5p	SH3BP2
bta-miR-99a-5p	TAPT1
bta-miR-99a-5p	HIP1R
bta-miR-99a-5p	IL6R
bta-miR-99a-5p	ABTB2
bta-miR-99a-5p	NYX
bta-miR-99a-5p	TSPAN2
bta-miR-99a-5p	SSH2
bta-miR-99a-5p	DAAM2
bta-miR-99a-5p	TIMM17A
bta-miR-99a-5p	ITGA5
bta-miR-99a-5p	TIRAP
bta-miR-99a-5p	CLEC5A
bta-miR-99a-5p	RAP1GAP2
bta-miR-99a-5p	LOC507247
bta-miR-99a-5p	PLAGL2
bta-miR-99a-5p	ARHGAP35
bta-miR-99a-5p	SMAD7
bta-miR-99a-5p	ATXN1
bta-miR-99a-5p	MNT
bta-miR-99a-5p	FAM43A
bta-miR-99a-5p	RSAD2
bta-miR-99a-5p	PLEKHO2

bta-miR-99a-3p	KDM7A
bta-miR-99a-3p	PIM1
bta-miR-99a-3p	PFKFB4
bta-miR-99a-3p	IL2RB
bta-miR-99a-3p	CCL8
bta-miR-99a-3p	NFIX
bta-miR-99a-3p	LOC100138271
bta-miR-99a-3p	ROCK1
bta-miR-99a-3p	DAAM2
bta-miR-99a-3p	LOC507247
bta-miR-99a-3p	CASS4
bta-miR-99a-3p	ZBP1
bta-miR-99a-3p	SIK1
bta-miR-99a-3p	BRWD3
bta-miR-99a-3p	LMTK2
bta-miR-99a-3p	SPRED1
bta-miR-99a-3p	MALT1

bta-miR-100	MGC157082
bta-miR-100	SLC2A3
bta-miR-100	ATXN7L3
bta-miR-100	TRIB1
bta-miR-100	RIN2
bta-miR-100	CMIP
bta-miR-100	BRF2
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bta-miR-100	LOC104968422
bta-miR-100	ADGRG3
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bta-miR-100	ETNK1
bta-miR-100	PXK
bta-miR-100	SSH2
bta-miR-100	RHBDD2
bta-miR-100	IL22RA2
bta-miR-100	DDX17
bta-miR-100	TIMM17A
bta-miR-100	ITGA5
bta-miR-100	MAP3K8
bta-miR-100	ARHGAP35
bta-miR-100	ATXN1
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bta-miR-100	SLC38A2
bta-miR-100	ELOVL5
bta-miR-100	GANC

bta-miR-125a	STAT3
bta-miR-125a	IL1RN
bta-miR-125a	LOC616254
bta-miR-125a	N4BP1
bta-miR-125a	LOC527744
bta-miR-125a	NAIP
bta-miR-125a	GABARAPL1
bta-miR-125a	ATXN7L3
bta-miR-125a	SLC45A4
bta-miR-125a	ZFAND3
bta-miR-125a	ACVR1B
bta-miR-125a	MAPKAPK3
bta-miR-125a	CRISPLD2
bta-miR-125a	NDEL1
bta-miR-125a	PHF1
bta-miR-125a	LPAR3
bta-miR-125a	CD14
bta-miR-125a	USP32
bta-miR-125a	RIN2
bta-miR-125a	SLC2A9
bta-miR-125a	IL10RA
bta-miR-125a	CRKL
bta-miR-125a	ST6GALNAC6
bta-miR-125a	PIK3R5
bta-miR-125a	PREX1
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bta-miR-125a	ADAR
bta-miR-125a	RYBP
bta-miR-125a	CLIP1
bta-miR-125a	DUSP16
bta-miR-125a	BAZ2A
bta-miR-125a	ILRUN
bta-miR-125a	DAGLB
bta-miR-125a	RASGEF1B
bta-miR-125a	VDR
bta-miR-125a	QKI
bta-miR-125a	ARF6
bta-miR-125a	FOXS1
bta-miR-125a	JUNB
bta-miR-125a	PPP1R16B
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bta-miR-125a	RALGDS

bta-miR-125a	TREML2
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bta-miR-125a	B4GALT5
bta-miR-125a	MLKL
bta-miR-125a	MST1R
bta-miR-125a	RLF
bta-miR-125a	CFLAR
bta-miR-125a	TMEM268
bta-miR-125a	PPARD
bta-miR-125a	EMP1
bta-miR-125a	BOLA-DRA
bta-miR-125a	TRAF3
bta-miR-125a	SNAI1
bta-miR-125a	WDR77
bta-miR-125a	ZC3H12A
bta-miR-125a	LENG8
bta-miR-125a	WAC
bta-miR-125a	VASP
bta-miR-125a	PPP1R3B
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bta-miR-125a	MIF4GD
bta-miR-125a	NEK6
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bta-miR-125a	VCPIP1
bta-miR-125a	SLC6A9
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bta-miR-125a	NR1H2
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bta-miR-125a	KCNJ15
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bta-miR-125a	PGS1

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bta-miR-125a	PARP11
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bta-miR-125a	KDM7A
bta-miR-125a	IFNAR1
bta-miR-125a	PAQR8
bta-miR-125a	R3HCC1L
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bta-miR-125a	RAB3D
bta-miR-125a	ZSWIM4
bta-miR-125a	IL22RA2
bta-miR-125a	FAM241A
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bta-miR-125a	RAB37
bta-miR-125a	HEG1
bta-miR-125a	FAM3B
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bta-miR-125a	GAB2
bta-miR-125a	SRSF5
bta-miR-125a	RIPOR3
bta-miR-125a	SLC13A5
bta-miR-125a	P2RY8
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bta-miR-125a	TIRAP
bta-miR-125a	NIPAL4
bta-miR-125a	IL1A
bta-miR-125a	SLC16A3
bta-miR-125a	RAP1GAP2
bta-miR-125a	SRRM2
bta-miR-125a	CDC42SE2
bta-miR-125a	RPIA
bta-miR-125a	MARCHF7
bta-miR-125a	RARG
bta-miR-125a	SLC2A1
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bta-miR-125a	SRGAP2
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bta-miR-125a	ATXN1

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bta-miR-125a	EIF4E3
bta-miR-125a	GPCPD1
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bta-miR-125a	SLC38A2
bta-miR-125a	EIF4A1
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bta-miR-125a	ZSWIM6
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bta-miR-125a	RET
bta-miR-125a	MYSM1
bta-miR-125a	USP3
bta-miR-125a	FAR2
bta-miR-125a	TTYH2
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bta-miR-127	STAT3
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bta-miR-127	PTPRJ
bta-miR-127	MCEMP1
bta-miR-127	E2F2
bta-miR-127	NUDT3
bta-miR-127	CYLD
bta-miR-127	TLE3
bta-miR-127	DNAJB6
bta-miR-127	ATXN7L3
bta-miR-127	LPAR3
bta-miR-127	LOC617141
bta-miR-127	ADAM19
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bta-miR-127	SLC2A9
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bta-miR-127	MMP25
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bta-miR-127	RASSF5
bta-miR-127	GALC
bta-miR-127	RETN
bta-miR-127	LOC514257
bta-miR-127	MLKL
bta-miR-127	AMMECR1
bta-miR-127	VNN2
bta-miR-127	AOAH
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bta-miR-127	CACHD1
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bta-miR-127	E2F3
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bta-miR-127	DRAXIN
bta-miR-127	LENG8
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bta-miR-127	WAC

bta-miR-141	DCAF12
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bta-miR-141	DNAJB6
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bta-miR-141	CRISPLD2
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bta-miR-141	LCP2
bta-miR-141	CASP4
bta-miR-141	USP15
bta-miR-141	VDR
bta-miR-141	STAT6
bta-miR-141	CALM1
bta-miR-141	MED13
bta-miR-141	ARL5B
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bta-miR-141	WDR4
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bta-miR-141	ALKBH1
bta-miR-141	LOC515333
bta-miR-141	SDCBP
bta-miR-141	LOC507247
bta-miR-141	HECA
bta-miR-141	TRIM8
bta-miR-141	IL13RA1
bta-miR-141	HECW2
bta-miR-141	RET
bta-miR-141	GNG4

bta-miR-127	CD74
bta-miR-127	KYNU
bta-miR-127	VCPIP1
bta-miR-127	OSTM1
bta-miR-127	VAT1L
bta-miR-127	DAPP1
bta-miR-127	SLC1A2
bta-miR-127	PML
bta-miR-127	SLC25A37
bta-miR-127	MLXIP
bta-miR-127	SLC7A5
bta-miR-127	CWC22
bta-miR-127	CREBRF
bta-miR-127	SP140L
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bta-miR-127	RELT
bta-miR-127	RHBDF2
bta-miR-127	RAB37
bta-miR-127	DDX17
bta-miR-127	NFIX
bta-miR-127	HEG1
bta-miR-127	FAM3B
bta-miR-127	GOSR1
bta-miR-127	TBC1D2B
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bta-miR-127	OTUD4
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bta-miR-127	TMEM229B
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bta-miR-127	SLC16A3
bta-miR-127	GPR31
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bta-miR-127	LOC100336941
bta-miR-127	GPCPD1
bta-miR-127	RAB8B
bta-miR-127	STEAP3
bta-miR-127	C25H16orf54
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bta-miR-127	FCMR
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bta-miR-127	CSGALNACT2
bta-miR-127	FOS
bta-miR-127	ZC3H12C
bta-miR-127	KIAA0232
bta-miR-127	TTYH2
bta-miR-127	CAMK1D

bta-miR-143	E2F2
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bta-miR-143	NUDT3
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bta-miR-143	GABARAPL1
bta-miR-143	SKAP2
bta-miR-143	TBC1D9
bta-miR-143	GPR141
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bta-miR-143	SIRT1
bta-miR-143	RND1
bta-miR-143	CFLAR
bta-miR-143	STK38L
bta-miR-143	STARD8
bta-miR-143	MED13
bta-miR-143	WSB1
bta-miR-143	BACH1
bta-miR-143	SPATA13
bta-miR-143	MPHOSPH8
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bta-miR-143	LOC521224
bta-miR-143	IPCEF1
bta-miR-143	GOLGA7
bta-miR-143	TRAF2
bta-miR-143	RAB3GAP1
bta-miR-143	HRH2
bta-miR-143	WAC
bta-miR-143	CD101
bta-miR-143	SLC1A2
bta-miR-143	SMURF1
bta-miR-143	SLC7A5
bta-miR-143	CWC22
bta-miR-143	SP140L
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bta-miR-143	ETNK1
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bta-miR-143	GRAMD1C
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bta-miR-143	FRYL
bta-miR-143	LOC100848815

bta-miR-148a	DENND5A
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bta-miR-148a	RAB27A
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bta-miR-148a	NUDT3
bta-miR-148a	IFNAR2
bta-miR-148a	TRIB1
bta-miR-148a	KHNYN
bta-miR-148a	USP15
bta-miR-148a	QKI
bta-miR-148a	EGR3
bta-miR-148a	CFLAR
bta-miR-148a	EHBP1L1
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bta-miR-148a	PPP1R3B
bta-miR-148a	ICAM1
bta-miR-148a	CD46
bta-miR-148a	SLC1A2
bta-miR-148a	SMURF1
bta-miR-148a	SLC4A7
bta-miR-148a	MIER3
bta-miR-148a	TET2
bta-miR-148a	GRAMD1C
bta-miR-148a	DAZAP2
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bta-miR-148a	KPNA3
bta-miR-148a	GPAT3
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bta-miR-148a	TBC1D2B
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bta-miR-143	YIPF4
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bta-miR-143	KPNA3
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bta-miR-143	PARP8
bta-miR-143	PIK3CA
bta-miR-143	BACH2
bta-miR-143	EPC1
bta-miR-143	TIRAP
bta-miR-143	ZNF331
bta-miR-143	PPP4R2
bta-miR-143	R3HDM4
bta-miR-143	RUFY4
bta-miR-143	CDC42SE2
bta-miR-143	SPRYD3
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bta-miR-143	ENPP2
bta-miR-143	FCMR
bta-miR-143	CHP1
bta-miR-143	ZSWIM6
bta-miR-143	USP3
bta-miR-143	CAMK1D
bta-miR-143	IL10

bta-miR-150	MAPKAPK2
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bta-miR-150	LOC616254
bta-miR-150	KLF10
bta-miR-150	ETS2
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bta-miR-150	CD82
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bta-miR-150	PHF1
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bta-miR-150	BIN2
bta-miR-150	CLIP1
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bta-miR-150	SLC6A2
bta-miR-150	COPZ1
bta-miR-150	MLKL
bta-miR-150	RND1
bta-miR-150	GDI1
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bta-miR-151-3p	FGR
bta-miR-151-3p	ITM2C
bta-miR-151-3p	CYLD
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bta-miR-151-3p	ATXN7L3
bta-miR-151-3p	FAS
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bta-miR-151-3p	LPAR3
bta-miR-151-3p	JAK3
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bta-miR-151-3p	SEMA4D
bta-miR-151-3p	CD14
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bta-miR-151-3p	PIK3R5
bta-miR-151-3p	IKZF5
bta-miR-151-3p	ADAR
bta-miR-151-3p	RYBP
bta-miR-151-3p	USP15
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bta-miR-151-3p	RIPK3
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bta-miR-151-3p	KSR1
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bta-miR-151-3p	LOC521224
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bta-miR-151-3p	ICAM4
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bta-miR-151-3p	ICAM1
bta-miR-151-3p	CRTC2

bta-miR-150	CFLAR
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bta-miR-150	EDEM1
bta-miR-150	KSR1
bta-miR-150	WSB1
bta-miR-150	SLA
bta-miR-150	LOC507055
bta-miR-150	LOC104968422
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bta-miR-150	GOLGA7
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bta-miR-150	STARD3
bta-miR-150	CD46
bta-miR-150	IFI35
bta-miR-150	CDKN1A
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bta-miR-150	NYX
bta-miR-150	SLC8A1
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bta-miR-150	ORAI2
bta-miR-150	ATXN7
bta-miR-150	PAQR8
bta-miR-150	MAP3K2
bta-miR-150	SSH2
bta-miR-150	RNF114
bta-miR-150	STK40
bta-miR-150	LAIR1
bta-miR-150	YRDC
bta-miR-150	FNBP1
bta-miR-150	PIAS1

bta-miR-151-3p	TATDN2
bta-miR-151-3p	SLC4A7
bta-miR-151-3p	TRIM35
bta-miR-151-3p	UBE2G1
bta-miR-151-3p	SP140L
bta-miR-151-3p	PGAM5
bta-miR-151-3p	CDC42SE1
bta-miR-151-3p	PARP11
bta-miR-151-3p	ORAI2
bta-miR-151-3p	ATXN7
bta-miR-151-3p	ATP8B4
bta-miR-151-3p	LAIR1
bta-miR-151-3p	IL22RA2
bta-miR-151-3p	PRKCD
bta-miR-151-3p	FNBP1
bta-miR-151-3p	RAB37
bta-miR-151-3p	DGKD
bta-miR-151-3p	PNKD
bta-miR-151-3p	CDADC1
bta-miR-151-3p	GAB2
bta-miR-151-3p	TTC33
bta-miR-151-3p	ERAP2
bta-miR-151-3p	DEDD2
bta-miR-151-3p	TFEC
bta-miR-151-3p	SHROOM4
bta-miR-151-3p	NIPAL4
bta-miR-151-3p	OSCP1
bta-miR-151-3p	MED30
bta-miR-151-3p	FAM13B
bta-miR-151-3p	R3HDM4
bta-miR-151-3p	FOXN3
bta-miR-151-3p	KLF7
bta-miR-151-3p	APOL3
bta-miR-151-3p	PLAGL2
bta-miR-151-3p	CASS4
bta-miR-151-3p	IQSEC1
bta-miR-151-3p	TAL1
bta-miR-151-3p	SRGAP2
bta-miR-151-3p	HECA
bta-miR-151-3p	RAB11FIP1
bta-miR-151-3p	CD164
bta-miR-151-3p	STEAP3
bta-miR-151-3p	SLC38A2
bta-miR-151-3p	PNP
bta-miR-151-3p	ELOVL5
bta-miR-151-3p	IFI16
bta-miR-151-3p	MYSM1

bta-miR-150	DDX17
bta-miR-150	HEG1
bta-miR-150	DLL1
bta-miR-150	SHOC2
bta-miR-150	ETV3
bta-miR-150	TBC1D2B
bta-miR-150	IL15
bta-miR-150	FNIP1
bta-miR-150	TNFSF14
bta-miR-150	RAPGEF1
bta-miR-150	NR4A1
bta-miR-150	RC3H2
bta-miR-150	RAP1GAP2
bta-miR-150	CTDSP2
bta-miR-150	FOXN3
bta-miR-150	KLF7
bta-miR-150	MOCOS
bta-miR-150	C1H3orf38
bta-miR-150	ZBTB2
bta-miR-150	PI4K2A
bta-miR-150	PTPN9
bta-miR-150	FRAT2
bta-miR-150	POGZ
bta-miR-150	TMEM165
bta-miR-150	RETREG3
bta-miR-150	LOC512486
bta-miR-150	FASLG
bta-miR-150	USPL1
bta-miR-150	FOS
bta-miR-150	KRAS
bta-miR-150	LMTK2
bta-miR-150	HIPK3
bta-miR-150	CA5B
bta-miR-150	S1PR2
bta-miR-150	GANC
bta-miR-150	FAR2
bta-miR-150	SNAPC1

bta-miR-151-3p	ART1
bta-miR-151-3p	SCARA5
bta-miR-151-3p	ZMIZ2
bta-miR-151-3p	CAMK1D

bta-miR-152	MXD1
bta-miR-152	ACVR1B
bta-miR-152	ADGRE5
bta-miR-152	CSF1
bta-miR-152	MAML2
bta-miR-152	SLC2A9
bta-miR-152	ST6GALNAC6
bta-miR-152	PREX1
bta-miR-152	RNF144B
bta-miR-152	DNAJB12
bta-miR-152	ANKFY1
bta-miR-152	DUSP16
bta-miR-152	RASSF5
bta-miR-152	RICTOR
bta-miR-152	KIAA1191
bta-miR-152	LOC514257
bta-miR-152	SIDT2
bta-miR-152	B4GALT5
bta-miR-152	ALYREF
bta-miR-152	CALM1
bta-miR-152	STOM
bta-miR-152	WARS1
bta-miR-152	FLCN
bta-miR-152	SLA
bta-miR-152	SIRPB2
bta-miR-152	PRKAA1
bta-miR-152	PLEKHF2
bta-miR-152	HIP1R
bta-miR-152	ANKRD33B
bta-miR-152	IL15RA
bta-miR-152	FMR1
bta-miR-152	CD101
bta-miR-152	CD46
bta-miR-152	MYLIP
bta-miR-152	SLC4A7
bta-miR-152	SDC4
bta-miR-152	UBE2G1
bta-miR-152	SLC7A5
bta-miR-152	NOD2
bta-miR-152	KDM5A
bta-miR-152	DAZAP2
bta-miR-152	PARP11

bta-miR-182	CD55
bta-miR-182	FNBP4
bta-miR-182	WTAP
bta-miR-182	CYLD
bta-miR-182	PDE4B
bta-miR-182	CD53
bta-miR-182	TUT7
bta-miR-182	TNIP3
bta-miR-182	ANKFY1
bta-miR-182	MORC3
bta-miR-182	PIAS2
bta-miR-182	PPP1R16B
bta-miR-182	B4GALT5
bta-miR-182	MLKL
bta-miR-182	LOC529196
bta-miR-182	PHACTR2
bta-miR-182	ARIH2
bta-miR-182	B3GNT3
bta-miR-182	FOSL2
bta-miR-182	KMT5B
bta-miR-182	KYNU
bta-miR-182	SLC1A2
bta-miR-182	SMURF1
bta-miR-182	SLC4A7
bta-miR-182	NOD2
bta-miR-182	TET2
bta-miR-182	BCL2L11
bta-miR-182	CEP76
bta-miR-182	TEX2
bta-miR-182	TRIP10
bta-miR-182	KDM7A
bta-miR-182	FNBP1
bta-miR-182	PRDM1
bta-miR-182	DDX17
bta-miR-182	HEG1
bta-miR-182	CDADC1
bta-miR-182	GJB2
bta-miR-182	WWC2
bta-miR-182	TIMM17A
bta-miR-182	TMEM229B
bta-miR-182	SH3BGRL
bta-miR-182	FCRL5

bta-miR-152	RBM43
bta-miR-152	ORAI2
bta-miR-152	LAIR1
bta-miR-152	PTBP3
bta-miR-152	FNBP1
bta-miR-152	LOC100138271
bta-miR-152	SPRED2
bta-miR-152	TNFSF14
bta-miR-152	PIK3CA
bta-miR-152	NR4A1
bta-miR-152	SH3BGRL
bta-miR-152	FOXN3
bta-miR-152	KLF7
bta-miR-152	EIF4E3
bta-miR-152	FAM43A
bta-miR-152	OSBPL2
bta-miR-152	DPYD
bta-miR-152	FRAT2
bta-miR-152	MAP4K4
bta-miR-152	FCMR
bta-miR-152	CHP1
bta-miR-152	USPL1
bta-miR-152	HECW2
bta-miR-152	HIPK3
bta-miR-152	FAR2

bta-miR-182	GPR31
bta-miR-182	CASS4
bta-miR-182	ZBTB2
bta-miR-182	EIF4E3
bta-miR-182	ARHGAP17
bta-miR-182	PTPN9
bta-miR-182	TMEM140
bta-miR-182	CHST15
bta-miR-182	CYBB
bta-miR-182	CMPK2
bta-miR-182	CSGALNACT2
bta-miR-182	ANKRD13A
bta-miR-182	HIPK3
bta-miR-182	FRMD4A
bta-miR-182	DIXDC1

bta-miR-183	N4BP1
bta-miR-183	STEAP4
bta-miR-183	NUDT3
bta-miR-183	PARM1
bta-miR-183	TAB2
bta-miR-183	MAPKAPK3
bta-miR-183	RUBCNL
bta-miR-183	VPS37A
bta-miR-183	TOP1
bta-miR-183	ST6GALNAC6
bta-miR-183	PIK3R5
bta-miR-183	ADAR
bta-miR-183	RILPL2
bta-miR-183	SLCO4A1
bta-miR-183	TBXAS1
bta-miR-183	DUSP16
bta-miR-183	DAGLB
bta-miR-183	TNFAIP2
bta-miR-183	TNFRSF1B
bta-miR-183	MBOAT1
bta-miR-183	GALC
bta-miR-183	EFHD2
bta-miR-183	SLC6A2
bta-miR-183	LOC514257
bta-miR-183	LITAF
bta-miR-183	COP1
bta-miR-183	PHACTR2
bta-miR-183	IL12B
bta-miR-183	STOM
bta-miR-183	VSIR
bta-miR-183	SIRPB2
bta-miR-183	SPATA13
bta-miR-183	BRAF
bta-miR-183	ICOSLG
bta-miR-183	SESN2
bta-miR-183	JAK1
bta-miR-183	CD101
bta-miR-183	LOC100337457
bta-miR-183	SLC1A2
bta-miR-183	TATDN2
bta-miR-183	AIF1
bta-miR-183	SLC4A7

bta-miR-193b	ACSL4
bta-miR-193b	GTPBP1
bta-miR-193b	SLC2A3
bta-miR-193b	GRIPAP1
bta-miR-193b	ATXN7L3
bta-miR-193b	CD82
bta-miR-193b	SKAP2
bta-miR-193b	CRISPLD2
bta-miR-193b	PTAFR
bta-miR-193b	SPTSSA
bta-miR-193b	ETV6
bta-miR-193b	TRAF1
bta-miR-193b	ST6GALNAC6
bta-miR-193b	THEMIS2
bta-miR-193b	ZNF263
bta-miR-193b	USP15
bta-miR-193b	BAZ2A
bta-miR-193b	MAX
bta-miR-193b	TAPBPL
bta-miR-193b	NUP98
bta-miR-193b	RASSF5
bta-miR-193b	LOC618409
bta-miR-193b	TREML2
bta-miR-193b	LOC514257
bta-miR-193b	DCBLD1
bta-miR-193b	MCF2L2
bta-miR-193b	IL17REL
bta-miR-193b	EMP1
bta-miR-193b	KSR1
bta-miR-193b	SLA
bta-miR-193b	NCF4
bta-miR-193b	MPHOSPH8
bta-miR-193b	RHOG
bta-miR-193b	IPCEF1
bta-miR-193b	SESN2
bta-miR-193b	IL6R
bta-miR-193b	SNX10
bta-miR-193b	GPR146
bta-miR-193b	VGF
bta-miR-193b	KCNJ2
bta-miR-193b	HRH2
bta-miR-193b	NAB2

bta-miR-183	MLXIP
bta-miR-183	NUB1
bta-miR-183	SLC39A13
bta-miR-183	TMBIM4
bta-miR-183	ETNK1
bta-miR-183	DNASE1L1
bta-miR-183	ALCAM
bta-miR-183	SLC8A1
bta-miR-183	IRF1
bta-miR-183	BCL2L11
bta-miR-183	GRAMD1C
bta-miR-183	LOC112442378
bta-miR-183	CCDC69
bta-miR-183	SFPQ
bta-miR-183	DDIT3
bta-miR-183	SYNE3
bta-miR-183	YIPF4
bta-miR-183	ATXN7
bta-miR-183	ATP8B4
bta-miR-183	IFIT2
bta-miR-183	MICU1
bta-miR-183	ZNF408
bta-miR-183	FAM241A
bta-miR-183	IL2RB
bta-miR-183	CTIF
bta-miR-183	FNBP1
bta-miR-183	LOC518134
bta-miR-183	SH3PXD2B
bta-miR-183	ELK3
bta-miR-183	TTC33
bta-miR-183	WDR4
bta-miR-183	DPH3
bta-miR-183	DGAT2
bta-miR-183	TLE4
bta-miR-183	PIK3CA
bta-miR-183	SHE
bta-miR-183	NGP
bta-miR-183	SYNGR2
bta-miR-183	LOC783604
bta-miR-183	CLEC5A
bta-miR-183	HSPA5
bta-miR-183	PPP4R2
bta-miR-183	DIAPH2
bta-miR-183	TCF7L2
bta-miR-183	EIF4E3
bta-miR-183	ANKRD44
bta-miR-183	STEAP3

bta-miR-193b	ARID4B
bta-miR-193b	LOC100337457
bta-miR-193b	CD46
bta-miR-193b	MTMR3
bta-miR-193b	NR1H2
bta-miR-193b	HES4
bta-miR-193b	MLXIP
bta-miR-193b	SLC39A13
bta-miR-193b	RNASE10
bta-miR-193b	SP140L
bta-miR-193b	TMBIM4
bta-miR-193b	VEZF1
bta-miR-193b	TEX2
bta-miR-193b	CD5
bta-miR-193b	INTS6
bta-miR-193b	CCDC69
bta-miR-193b	KCTD7
bta-miR-193b	FRYL
bta-miR-193b	LOC509881
bta-miR-193b	ORAI2
bta-miR-193b	IER3
bta-miR-193b	IFIT2
bta-miR-193b	TM9SF4
bta-miR-193b	FCGR2B
bta-miR-193b	ATG16L1
bta-miR-193b	RELT
bta-miR-193b	CTIF
bta-miR-193b	PIAS1
bta-miR-193b	NOD1
bta-miR-193b	GCH1
bta-miR-193b	C5AR1
bta-miR-193b	FAM3B
bta-miR-193b	VEGFC
bta-miR-193b	UBTF
bta-miR-193b	TMEM229B
bta-miR-193b	MX2
bta-miR-193b	KRR1
bta-miR-193b	SHROOM4
bta-miR-193b	R3HDM4
bta-miR-193b	STK4
bta-miR-193b	DMXL2
bta-miR-193b	APOL3
bta-miR-193b	SPRYD3
bta-miR-193b	NR2C2AP
bta-miR-193b	NLK
bta-miR-193b	N4BP3
bta-miR-193b	ARHGAP35

bta-miR-183	IL13RA1
bta-miR-183	RABGAP1L
bta-miR-183	PTPN9
bta-miR-183	CYP4V2
bta-miR-183	CXCL8
bta-miR-183	HECW2
bta-miR-183	GSN
bta-miR-183	IRF5
bta-miR-183	CHI3L2
bta-miR-183	USP3
bta-miR-183	SLC30A1
bta-miR-183	CAMK1D

bta-miR-193b	ACVRL1
bta-miR-193b	EIF4E3
bta-miR-193b	FAM43A
bta-miR-193b	C25H16orf54
bta-miR-193b	SLC38A2
bta-miR-193b	FRAT2
bta-miR-193b	LOC107131273
bta-miR-193b	FCMR
bta-miR-193b	RETREG3
bta-miR-193b	BFAR
bta-miR-193b	RARA
bta-miR-193b	RET
bta-miR-193b	KIAA0232
bta-miR-193b	OTULINL
bta-miR-193b	TNF

bta-miR-200a	DCAF12
bta-miR-200a	NAB1
bta-miR-200a	IFNGR2
bta-miR-200a	ETS2
bta-miR-200a	XKR8
bta-miR-200a	ABT1
bta-miR-200a	CASP4
bta-miR-200a	THEMIS2
bta-miR-200a	NDFIP2
bta-miR-200a	LOC529196
bta-miR-200a	CDS2
bta-miR-200a	PHACTR2
bta-miR-200a	INPP4A
bta-miR-200a	IFIT3
bta-miR-200a	SMG9
bta-miR-200a	ZBTB42
bta-miR-200a	PLXNA1
bta-miR-200a	YIPF4
bta-miR-200a	STAT5A
bta-miR-200a	STAT5B
bta-miR-200a	FLT4
bta-miR-200a	FAM241A
bta-miR-200a	PTBP3
bta-miR-200a	DLL1
bta-miR-200a	GALNT11
bta-miR-200a	FSD2
bta-miR-200a	CALCOCO2
bta-miR-200a	SDCBP
bta-miR-200a	SRGAP2
bta-miR-200a	HECA
bta-miR-200a	RAB11FIP1
bta-miR-200a	NUP210
bta-miR-200a	RAB8B
bta-miR-200a	CD164
bta-miR-200a	RBM47
bta-miR-200a	LMTK2
bta-miR-200a	WDR45
bta-miR-200a	GNG4

bta-miR-200b	NUDT3
bta-miR-200b	PSEN1
bta-miR-200b	EPG5
bta-miR-200b	XKR8
bta-miR-200b	BID
bta-miR-200b	RIC1
bta-miR-200b	ANKFY1
bta-miR-200b	ELL
bta-miR-200b	LOC514257
bta-miR-200b	COPZ1
bta-miR-200b	LOC529196
bta-miR-200b	WARS1
bta-miR-200b	ZBTB49
bta-miR-200b	PLEKHF2
bta-miR-200b	NUMB
bta-miR-200b	SNX10
bta-miR-200b	ANKRD33B
bta-miR-200b	PHLDB1
bta-miR-200b	IFIT3
bta-miR-200b	SLC25A37
bta-miR-200b	SMG9
bta-miR-200b	VEZF1
bta-miR-200b	CCDC69
bta-miR-200b	YIPF4
bta-miR-200b	SH3PXD2B
bta-miR-200b	USP36
bta-miR-200b	FSD2
bta-miR-200b	LOC507247
bta-miR-200b	CD164
bta-miR-200b	C7H19orf38
bta-miR-200b	TTC19
bta-miR-200b	HYLS1

bta-miR-200c	DHX8
bta-miR-200c	FGR
bta-miR-200c	TLE3
bta-miR-200c	RIOK3
bta-miR-200c	TBC1D9
bta-miR-200c	ABT1
bta-miR-200c	TOP1
bta-miR-200c	POLR2C
bta-miR-200c	USP15
bta-miR-200c	TNFAIP2
bta-miR-200c	RASSF5
bta-miR-200c	POLB
bta-miR-200c	TXNDC16
bta-miR-200c	RICTOR
bta-miR-200c	PDP1
bta-miR-200c	LOC529196
bta-miR-200c	RND1
bta-miR-200c	DCBLD1
bta-miR-200c	STK19
bta-miR-200c	ARIH2
bta-miR-200c	NUMB
bta-miR-200c	PRKCB
bta-miR-200c	ANKRD33B
bta-miR-200c	CSRNP1
bta-miR-200c	IFIT3
bta-miR-200c	CREBRF
bta-miR-200c	CD38
bta-miR-200c	IRF1
bta-miR-200c	C5AR2
bta-miR-200c	USP34
bta-miR-200c	BLZF1
bta-miR-200c	MS4A8
bta-miR-200c	PARP11
bta-miR-200c	KDM7A
bta-miR-200c	IFIT2
bta-miR-200c	STK40
bta-miR-200c	SRPRA
bta-miR-200c	CTIF
bta-miR-200c	FNBP1
bta-miR-200c	PARD3
bta-miR-200c	DCSTAMP
bta-miR-200c	RAPGEF1

bta-miR-204	CD55
bta-miR-204	DHX8
bta-miR-204	TMEM88
bta-miR-204	DCAF12
bta-miR-204	MCEMP1
bta-miR-204	HIC1
bta-miR-204	ETS2
bta-miR-204	LOC527744
bta-miR-204	SLC2A3
bta-miR-204	CYTH4
bta-miR-204	TREM1
bta-miR-204	GABARAPL1
bta-miR-204	RNF41
bta-miR-204	MXD1
bta-miR-204	ACVR1B
bta-miR-204	CNP
bta-miR-204	IRAK2
bta-miR-204	CRISPLD2
bta-miR-204	ADGRE5
bta-miR-204	TLR2
bta-miR-204	PTAFR
bta-miR-204	TBC1D9
bta-miR-204	USP32
bta-miR-204	RUBCNL
bta-miR-204	SIRPA
bta-miR-204	SERTAD1
bta-miR-204	TOP1
bta-miR-204	LRCH1
bta-miR-204	PREX1
bta-miR-204	RYBP
bta-miR-204	S100A9
bta-miR-204	BTG2
bta-miR-204	SLC46A2
bta-miR-204	P2RY14
bta-miR-204	BAZ2A
bta-miR-204	TAPBPL
bta-miR-204	DAGLB
bta-miR-204	VDR
bta-miR-204	QKI
bta-miR-204	RASSF5
bta-miR-204	ARF6
bta-miR-204	ARHGAP31

bta-miR-200c	FCRL5
bta-miR-200c	GPR31
bta-miR-200c	CDC42SE2
bta-miR-200c	SRGAP2
bta-miR-200c	NUP210
bta-miR-200c	HYLS1
bta-miR-200c	CHP1
bta-miR-200c	LMTK2
bta-miR-200c	FAR2
bta-miR-200c	ENTPD1
bta-miR-200c	CAMK1D
bta-miR-200c	DIXDC1

bta-miR-204	ELL
bta-miR-204	ZNF655
bta-miR-204	LIMK2
bta-miR-204	PPP1R16B
bta-miR-204	SH3BP2
bta-miR-204	SMIM3
bta-miR-204	IL2RA
bta-miR-204	ZBTB12
bta-miR-204	LOC514257
bta-miR-204	MOB3C
bta-miR-204	COPZ1
bta-miR-204	ALYREF
bta-miR-204	HIVEP3
bta-miR-204	LOC529196
bta-miR-204	MST1R
bta-miR-204	TAF5L
bta-miR-204	TMEM268
bta-miR-204	IL12B
bta-miR-204	STK19
bta-miR-204	FGD3
bta-miR-204	SLA
bta-miR-204	PTGS2
bta-miR-204	SIRPB2
bta-miR-204	ARL5B
bta-miR-204	RASSF1
bta-miR-204	LPIN2
bta-miR-204	KCNJ2
bta-miR-204	FMR1
bta-miR-204	CSRNP1
bta-miR-204	CRLF3
bta-miR-204	ITGB7
bta-miR-204	MIF4GD
bta-miR-204	CASP7
bta-miR-204	CD101
bta-miR-204	TMEM198
bta-miR-204	LAPTM5
bta-miR-204	VAT1L
bta-miR-204	ADGRG3
bta-miR-204	SDC4
bta-miR-204	GTPBP4
bta-miR-204	TFB1M
bta-miR-204	ANKRD12
bta-miR-204	USB1
bta-miR-204	EMILIN2
bta-miR-204	CCNJL
bta-miR-204	LMNB1
bta-miR-204	NYX

bta-miR-204	TET2
bta-miR-204	SELP
bta-miR-204	IRF1
bta-miR-204	ZFYVE28
bta-miR-204	FXR2
bta-miR-204	SYNE3
bta-miR-204	LOC509881
bta-miR-204	TIPARP
bta-miR-204	IER3
bta-miR-204	PIM1
bta-miR-204	IFNAR1
bta-miR-204	PFKFB4
bta-miR-204	ERBIN
bta-miR-204	ARAP1
bta-miR-204	FBRS
bta-miR-204	IL2RB
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bta-miR-204	DDX17
bta-miR-204	EDN1
bta-miR-204	GPAT3
bta-miR-204	NFIX
bta-miR-204	HEG1
bta-miR-204	USP36
bta-miR-204	HCLS1
bta-miR-204	PARD3
bta-miR-204	ETV3
bta-miR-204	UBTF
bta-miR-204	FAM104A
bta-miR-204	GRTP1
bta-miR-204	GRK6
bta-miR-204	DAAM2
bta-miR-204	ELF1
bta-miR-204	WWC2
bta-miR-204	TIMM17A
bta-miR-204	NACC2
bta-miR-204	TNFSF14
bta-miR-204	PIK3CA
bta-miR-204	SLC13A5
bta-miR-204	EPC1
bta-miR-204	TIRAP
bta-miR-204	MAP3K8
bta-miR-204	F13A1
bta-miR-204	HSPA5
bta-miR-204	SLC16A3
bta-miR-204	RAP1GAP2
bta-miR-204	SRRM2
bta-miR-204	FOXN3

bta-miR-204	SNRK
bta-miR-204	APOL3
bta-miR-204	B4GALT4
bta-miR-204	N4BP3
bta-miR-204	COTL1
bta-miR-204	RARG
bta-miR-204	SRGAP2
bta-miR-204	CEBPD
bta-miR-204	EIF4E3
bta-miR-204	ITPR2
bta-miR-204	STEAP3
bta-miR-204	NDRG1
bta-miR-204	NAMPT
bta-miR-204	MEGF9
bta-miR-204	ZSWIM7
bta-miR-204	HEXIM1
bta-miR-204	FCMR
bta-miR-204	RETREG3
bta-miR-204	CDKN2D
bta-miR-204	USPL1
bta-miR-204	ZSWIM6
bta-miR-204	SLC4A2
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bta-miR-204	ENTPD1
bta-miR-204	TP53INP2

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bta-miR-205	RAB27A
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bta-miR-205	VEGFA
bta-miR-205	PSEN1
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bta-miR-205	MAPKAPK3
bta-miR-205	CRISPLD2
bta-miR-205	JAK3
bta-miR-205	CD48
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bta-miR-205	PIK3R5
bta-miR-205	RNF122
bta-miR-205	SUSD2
bta-miR-205	BAZ2A
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bta-miR-205	SIRPB1
bta-miR-205	FOXS1
bta-miR-205	SLC39A8
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bta-miR-205	LOC514257

bta-miR-224	STAT3
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bta-miR-224	STX11
bta-miR-224	LOC616254
bta-miR-224	N4BP1
bta-miR-224	TAP2
bta-miR-224	SPTLC2
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bta-miR-224	NECAP1
bta-miR-224	VDR
bta-miR-224	POR
bta-miR-224	SH3BP2
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bta-miR-224	STK38L
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bta-miR-224	SLA
bta-miR-224	ANKRD33B
bta-miR-224	LENG8
bta-miR-224	GTF2H1
bta-miR-224	ICAM4
bta-miR-224	PDCL
bta-miR-224	SENP7
bta-miR-224	HES4
bta-miR-224	CWC22
bta-miR-224	CNN2
bta-miR-224	SLC8A1
bta-miR-224	IRF1
bta-miR-224	DAZAP2
bta-miR-224	GRAMD4
bta-miR-224	SYNE3
bta-miR-224	PHC2
bta-miR-224	LYSMD3
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bta-miR-205	IL17REL
bta-miR-205	SLA
bta-miR-205	SIRPB2
bta-miR-205	LOC104968422
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bta-miR-205	FLOT2
bta-miR-205	ICOSLG
bta-miR-205	GAB3
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bta-miR-205	NUMB
bta-miR-205	TPM4
bta-miR-205	SESN2
bta-miR-205	GPR146
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bta-miR-205	CDKN1B
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bta-miR-205	ARRDC2
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bta-miR-205	IL18RAP
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bta-miR-224	MAP3K8
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bta-miR-224	ANKRD44
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bta-miR-205	OTUD4
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bta-miR-205	RABGAP1L
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bta-miR-205	PRR5L
bta-miR-205	S1PR2
bta-miR-205	SDC3
bta-miR-205	TTYH2

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bta-miR-335	UBTF
bta-miR-335	PLAGL2
bta-miR-335	RETREG3

bta-miR-375	PTPRJ
bta-miR-375	STEAP4
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bta-miR-375	DNAJB6
bta-miR-375	ATXN7L3
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bta-miR-375	HDAC4
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bta-miR-375	PTPN2
bta-miR-375	PIK3R5
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bta-miR-375	ATP8B4
bta-miR-375	CTIF
bta-miR-375	FNBP1
bta-miR-375	NFIX
bta-miR-375	FAM3B
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bta-miR-375	SLC4A2
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bta-miR-375	ANKRD13A
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bta-miR-375	FAR2
bta-miR-375	GNG4

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bta-miR-429	ABT1
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bta-miR-429	CD274
bta-miR-429	PTGS2
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bta-miR-429	DRAXIN
bta-miR-429	FOSL2
bta-miR-429	YIPF4
bta-miR-429	HEG1
bta-miR-429	DLL1
bta-miR-429	PLCG2
bta-miR-429	TIMM17A
bta-miR-429	EPC1
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bta-miR-429	SLC16A3
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bta-miR-429	ELOVL5
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bta-miR-429	HIPK3

bta-miR-450b	ITM2C
bta-miR-450b	CYLD
bta-miR-450b	LOC509283
bta-miR-450b	IRF1
bta-miR-450b	INTS6
bta-miR-450b	APOL3
bta-miR-450b	TM6SF1

bta-miR-451	ACVR1B
bta-miR-451	TNIP3
bta-miR-451	MOB3C
bta-miR-451	SNX10
bta-miR-451	STK10
bta-miR-451	SP140L
bta-miR-451	KCTD7
bta-miR-451	GAB2
bta-miR-451	DPH3
bta-miR-451	TNFSF14
bta-miR-451	TBL1X
bta-miR-451	F13A1
bta-miR-451	HIPK3
bta-miR-451	FRMD4A
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bta-miR-451	TTYH2
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bta-miR-455-5p	BATF3
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bta-miR-455-5p	LOC617141
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bta-miR-455-5p	TRAF1
bta-miR-455-5p	LRCH1
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bta-miR-455-5p	SUSD2
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bta-miR-455-5p	ZNFX1
bta-miR-455-5p	BRF2
bta-miR-455-5p	PPP1R16B
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bta-miR-455-5p	KIAA1191
bta-miR-455-5p	LOC514257
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bta-miR-455-5p	FEM1C
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bta-miR-455-5p	JAK1
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bta-miR-455-5p	RNF114
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bta-miR-455-5p	IL1R1
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bta-miR-455-5p	TBL1X
bta-miR-455-5p	RAP1GAP2
bta-miR-455-5p	LOC507247
bta-miR-455-5p	HERPUD1
bta-miR-455-5p	NR2C2AP
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bta-miR-455-5p	LOC100336941
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bta-miR-455-5p	LOC789148
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bta-miR-455-5p	ZC3H12C
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bta-miR-455-5p	USP3
bta-miR-455-5p	KIAA0232
bta-miR-455-5p	GANC
bta-miR-455-5p	TTYH2

bta-miR-486	SUSD6
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bta-miR-486	MOB3C
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bta-miR-504	ANKFY1
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bta-miR-486	ARL5B
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bta-miR-486	TPM4
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bta-miR-504	TAF5L
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bta-miR-504	CSRNP1
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bta-miR-486	SLC2A1
bta-miR-486	SMAD7
bta-miR-486	SRGAP2
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bta-miR-615	RIPK3
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bta-miR-615	FNBP1
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bta-miR-3431	KLF6
bta-miR-3431	IRF5
bta-miR-3431	ANKRD13A
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bta-miR-3431	TTYH2
bta-miR-3431	GNG4
bta-miR-3431	OTULINL
bta-miR-3431	TP53INP2
bta-miR-3431	DIXDC1

Supplementary File S9: Complete list of the turquoise RNA-seq-based module genes, hub genes, Tl

Module_info	Module_size	Gene_id	Gene_symbol	Module_label	Module_color
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		ENSBTAG00000000016	LTA	1	turquoise
		ENSBTAG00000000065	CRLS1	1	turquoise
		ENSBTAG00000000088	ALCAM	1	turquoise
		ENSBTAG00000000095	CD274	1	turquoise
		ENSBTAG00000000098	SETDB1	1	turquoise
		ENSBTAG00000000113	ARHGEF2	1	turquoise
		ENSBTAG00000000115	VPS54	1	turquoise
		ENSBTAG00000000128	FGF18	1	turquoise
		ENSBTAG00000000131	SENP3	1	turquoise
		ENSBTAG00000000132	EIF4A1	1	turquoise
		ENSBTAG00000000137	FRYL	1	turquoise
		ENSBTAG00000000152	RANBP2	1	turquoise
		ENSBTAG00000000163	DDIT4	1	turquoise
		ENSBTAG00000000176	SP3	1	turquoise
		ENSBTAG00000000181	SUSD3	1	turquoise
		ENSBTAG00000000199	PDP1	1	turquoise
		ENSBTAG00000000202	SLC25A19	1	turquoise
		ENSBTAG00000000203	ATP6V1G1	1	turquoise
		ENSBTAG00000000204	TMEM268	1	turquoise
		ENSBTAG00000000210	ARHGAP31	1	turquoise
		ENSBTAG00000000222	ARID4B	1	turquoise
		ENSBTAG00000000225	POLB	1	turquoise
		ENSBTAG00000000226	DKK4	1	turquoise
		ENSBTAG00000000240	AKAP7	1	turquoise
		ENSBTAG00000000241	STAU1	1	turquoise
		ENSBTAG00000000242	NA	1	turquoise
		ENSBTAG00000000244	NRXN2	1	turquoise
		ENSBTAG00000000256	NA	1	turquoise
		ENSBTAG00000000266	NAB1	1	turquoise
		ENSBTAG00000000275	PARP11	1	turquoise
		ENSBTAG00000000277	IL18	1	turquoise
		ENSBTAG00000000283	CSF1	1	turquoise
		ENSBTAG00000000288	UPF2	1	turquoise
		ENSBTAG00000000290	ATP11B	1	turquoise
		ENSBTAG00000000292	TCIRG1	1	turquoise
		ENSBTAG00000000308	ITCH	1	turquoise
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ENSBTAG00000043553	GPX3	1	turquoise
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ENSBTAG00000045861	TARM1	1	turquoise
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ENSBTAG00000046152	MGAM	1	turquoise
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ENSBTAG00000046158	CFB	1	turquoise
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ENSBTAG00000046431	NA	1	turquoise
ENSBTAG00000046449	NA	1	turquoise

ENSBTAG00000046450	NA	1	turquoise
ENSBTAG00000046461	NA	1	turquoise
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ENSBTAG00000046841	IRF2BP2	1	turquoise
ENSBTAG00000046862	MARCKSL1	1	turquoise
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ENSBTAG00000046900	GGT1	1	turquoise
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ENSBTAG00000046941	LOC786015	1	turquoise
ENSBTAG00000046956	STYX	1	turquoise
ENSBTAG00000046981	NA	1	turquoise
ENSBTAG00000047030	LOC515276	1	turquoise
ENSBTAG00000047055	NA	1	turquoise
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ENSBTAG00000047133	NA	1	turquoise
ENSBTAG00000047158	LRFN1	1	turquoise
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ENSBTAG00000047379	NA	1	turquoise
ENSBTAG00000047383	LOC784305	1	turquoise
ENSBTAG00000047389	NA	1	turquoise
ENSBTAG00000047424	TRIP10	1	turquoise
ENSBTAG00000047432	LOC781224	1	turquoise
ENSBTAG00000047448	C25H16orf54	1	turquoise
ENSBTAG00000047473	LOC100301263	1	turquoise
ENSBTAG00000047488	KCNK9	1	turquoise
ENSBTAG00000047495	CD81	1	turquoise
ENSBTAG00000047502	FKBP5	1	turquoise
ENSBTAG00000047520	MPV17L	1	turquoise
ENSBTAG00000047534	NA	1	turquoise
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ENSBTAG00000047561	NA	1	turquoise
ENSBTAG00000047570	NA	1	turquoise
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ENSBTAG00000047766	NA	1	turquoise
ENSBTAG00000047776	NA	1	turquoise
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ENSBTAG00000047805	NA	1	turquoise
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ENSBTAG00000047871	KLF17	1	turquoise
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ENSBTAG00000048122	CFD	1	turquoise
ENSBTAG00000048137	NA	1	turquoise
ENSBTAG00000048145	NA	1	turquoise
ENSBTAG00000048154	NA	1	turquoise
ENSBTAG00000048155	FCN1	1	turquoise
ENSBTAG00000048184	NA	1	turquoise
ENSBTAG00000048226	NA	1	turquoise
ENSBTAG00000048229	NA	1	turquoise
ENSBTAG00000048249	NA	1	turquoise
ENSBTAG00000048272	NA	1	turquoise
ENSBTAG00000048273	C6H4orf3	1	turquoise
ENSBTAG00000048306	NA	1	turquoise
ENSBTAG00000048314	NA	1	turquoise

Fs, hub TFs, and hub lncRNAs

TFs_info	Gene_id	Gene_symbol	Modulememberships_info_Ge	Gene_symbol
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	ENSBTAG00000000176	SP3	ENSBTAG00000011982	BATF3
	ENSBTAG00000000222	ARID4B	ENSBTAG00000006984	CD55
	ENSBTAG00000000507	NR4A1	ENSBTAG00000021523	STAT3
	ENSBTAG00000000569	HES1	ENSBTAG00000012671	TNIP1
	ENSBTAG00000000816	PRDM1	ENSBTAG00000020034	LYN
	ENSBTAG00000001042	MXD1	ENSBTAG00000047495	CD81
	ENSBTAG00000001146	HIVEP2	ENSBTAG00000016116	NA
	ENSBTAG00000001160	GMEB1	ENSBTAG00000014090	ARID5A
	ENSBTAG00000001252	HIVEP1	ENSBTAG00000008339	DHX8
	ENSBTAG00000001509	ELK3	ENSBTAG00000023144	PTPRC
	ENSBTAG00000001511	BCL6	ENSBTAG00000046862	MARCKSL1
	ENSBTAG00000001562	NFE2	ENSBTAG00000018986	ACSL4
	ENSBTAG00000001864	NR4A3	ENSBTAG00000019665	IL1RN
	ENSBTAG00000002020	CREBRF	ENSBTAG00000006322	DENND5A
	ENSBTAG00000002129	KLF5	ENSBTAG00000007599	IKBKB
	ENSBTAG00000002333	HOPX	ENSBTAG00000038107	MAPKAPK2
	ENSBTAG00000002690	BLZF1	ENSBTAG00000004211	TNFRSF1A
	ENSBTAG00000003264	NR1H2	ENSBTAG00000019872	PIK3AP1
	ENSBTAG00000003541	ZNF614	ENSBTAG00000006616	PTPN1
	ENSBTAG00000003602	RBPJ	ENSBTAG00000036224	MGC157082
	ENSBTAG00000003650	NR4A2	ENSBTAG00000007932	HCK
	ENSBTAG00000003845	CSRNP1	ENSBTAG00000006378	RIPK1
	ENSBTAG00000004037	JUN	ENSBTAG00000003857	SUSD6
	ENSBTAG00000004136	NFE2L3	ENSBTAG00000001602	IL4R
	ENSBTAG00000004139	BACH1	ENSBTAG00000026376	NA
	ENSBTAG00000004189	MLXIP	ENSBTAG00000011784	FGR
	ENSBTAG00000004193	VEZF1	ENSBTAG00000031950	RAB3IP
	ENSBTAG00000004322	FOS	ENSBTAG00000010644	CHST11
	ENSBTAG00000004380	STAT2	ENSBTAG00000012962	SARS1
	ENSBTAG00000004710	HNF1B	ENSBTAG00000012047	JAK2
	ENSBTAG00000004953	ELK4	ENSBTAG00000001141	ADAM17
	ENSBTAG00000004954	TOX	ENSBTAG00000035907	DDX3X
	ENSBTAG00000004989	IRF5	ENSBTAG00000005493	TBC1D14
	ENSBTAG00000005029	TAL1	ENSBTAG00000005958	PTK2B
	ENSBTAG00000005038	ZBTB42	ENSBTAG00000047561	NA
	ENSBTAG00000005067	UBTF	ENSBTAG00000014762	ISG20
	ENSBTAG00000005354	LRRFIP1	ENSBTAG00000010324	GTPBP1
	ENSBTAG00000005443	MIER1	ENSBTAG00000011236	STX11
	ENSBTAG00000005461	SOX15	ENSBTAG00000007239	TNFAIP6
	ENSBTAG00000005474	CREB1	ENSBTAG00000002977	ECE1
	ENSBTAG00000005524	HBP1	ENSBTAG00000001492	FYB1
	ENSBTAG00000005564	PIAS1	ENSBTAG00000014439	KMO
	ENSBTAG00000005606	HOXC9	ENSBTAG00000018252	ARRDC4

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ENSBTAG00000009863	BHLHE40
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ENSBTAG00000019938	N4BP1
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ENSBTAG00000004736	GRB2
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ENSBTAG00000001051	NA
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ENSBTAG00000007974	WTAP
ENSBTAG00000010047	TIAM2
ENSBTAG00000047904	LOC527744
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ENSBTAG00000008853	HNRNPF
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ENSBTAG00000012938	JARID2	ENSBTAG00000019684	NUDT3
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ENSBTAG00000013702	ZNF296	ENSBTAG00000048062	KDM6B
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ENSBTAG00000013895	RELA	ENSBTAG00000007901	LOC508459
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ENSBTAG00000014090	ARID5A	ENSBTAG00000004556	SLC2A3
ENSBTAG00000014123	ZNF507	ENSBTAG00000027326	TP53RK
ENSBTAG00000014153	PKNOX1	ENSBTAG00000031396	NA
ENSBTAG00000014199	TBX21	ENSBTAG00000015413	RASA2
ENSBTAG00000014211	FOXP4	ENSBTAG00000009658	PLEK
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ENSBTAG00000014829	MYRFL	ENSBTAG00000020860	CHD1
ENSBTAG00000015007	NCOA1	ENSBTAG00000003037	NA
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ENSBTAG00000016169	ID1	ENSBTAG00000030416	LOC538810
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ENSBTAG00000016328	SFPQ	ENSBTAG00000007788	GRIPAP1
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ENSBTAG00000016462	TCF4	ENSBTAG00000002432	ABHD13
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ENSBTAG00000016546	PARP12	ENSBTAG00000038428	RELB
ENSBTAG00000016723	GFI1	ENSBTAG00000004608	LOC100138951
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ENSBTAG00000017393	L3MBTL3	ENSBTAG00000018186	PDXK
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ENSBTAG00000017542	PPARD
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ENSBTAG00000017580	RFX5
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ENSBTAG00000017682	TET2
ENSBTAG00000017731	ZFAT
ENSBTAG00000017824	IRF8
ENSBTAG00000017840	BAZ2A
ENSBTAG00000017872	ZNF304
ENSBTAG00000017994	MAX
ENSBTAG00000018024	NR1D2
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0.974146736	4.13E-28		ENSBTAG00000016116	NA
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0.973380425	7.46E-28		ENSBTAG00000023144	PTPRC
0.972376598	1.58E-27		ENSBTAG00000046862	MARCKSL1
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0.957770756	8.26E-24		ENSBTAG00000005958	PTK2B
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0.943326405	3.00E-21	ENSBTAG00000005339	VEGFA
0.943201283	3.13E-21	ENSBTAG00000009012	PTX3
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0.94140895	5.82E-21	ENSBTAG00000001051	NA
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0.941183139	6.28E-21	ENSBTAG00000007974	WTAP
0.940432941	8.09E-21	ENSBTAG00000010047	TIAM2
0.940329744	8.37E-21	ENSBTAG00000047904	LOC527744
0.94023175	8.65E-21	ENSBTAG00000020780	SBNO2
0.940154583	8.87E-21	ENSBTAG00000008853	HNRNPF
0.940147406	8.90E-21	ENSBTAG00000020281	NIN

0.939725179	1.02E-20	ENSBTAG00000012976	WLS
0.93957924	1.07E-20	ENSBTAG00000013305	NA
0.939286012	1.18E-20	ENSBTAG00000013451	RHOH
0.938982764	1.31E-20	ENSBTAG00000019933	MKNK1
0.938854839	1.36E-20	ENSBTAG00000004873	CCNL2
0.938782736	1.39E-20	ENSBTAG00000019684	NUDT3
0.93868418	1.44E-20	ENSBTAG00000016830	DAXX
0.938627986	1.47E-20	ENSBTAG00000048062	KDM6B
0.938422837	1.57E-20	ENSBTAG00000015919	PARM1
0.938294265	1.63E-20	ENSBTAG00000007901	LOC508459
0.938119815	1.73E-20	ENSBTAG00000015034	IK
0.937981234	1.81E-20	ENSBTAG00000004556	SLC2A3
0.937756295	1.94E-20	ENSBTAG00000027326	TP53RK
0.937601796	2.04E-20	ENSBTAG00000031396	NA
0.937483694	2.12E-20	ENSBTAG00000015413	RASA2
0.937392453	2.18E-20	ENSBTAG00000009658	PLEK
0.937272261	2.26E-20	ENSBTAG00000001824	SLC2A6
0.937262996	2.27E-20	ENSBTAG00000006291	CYLD
0.937163762	2.34E-20	ENSBTAG00000015580	TLE3
0.937142262	2.36E-20	ENSBTAG00000014237	CYTH4
0.936942992	2.51E-20	ENSBTAG00000011757	PSEN1
0.936426851	2.96E-20	ENSBTAG00000003038	TAP2
0.936373041	3.01E-20	ENSBTAG00000017593	TREM1
0.93603239	3.34E-20	ENSBTAG00000015212	IFNAR2
0.935975069	3.40E-20	ENSBTAG00000016260	LRRK2
0.935553496	3.88E-20	ENSBTAG00000020164	BAZ1A
0.935443024	4.01E-20	ENSBTAG00000003326	NAIP
0.935342101	4.14E-20	ENSBTAG00000016593	FMNL3
0.93519666	4.33E-20	ENSBTAG00000011765	GABARAPL1
0.935176746	4.35E-20	ENSBTAG00000020860	CHD1
0.935069743	4.50E-20	ENSBTAG00000003037	NA
0.934836932	4.83E-20	ENSBTAG00000008636	PDE4B
0.934834129	4.83E-20	ENSBTAG00000026754	RNF41
0.934541867	5.28E-20	ENSBTAG00000020480	SPTLC2
0.934332072	5.63E-20	ENSBTAG00000005474	CREB1
0.934220358	5.82E-20	ENSBTAG00000030416	LOC538810
0.934174735	5.91E-20	ENSBTAG00000001042	MXD1
0.934122272	6.00E-20	ENSBTAG00000007788	GRIPAP1
0.934055572	6.12E-20	ENSBTAG00000012067	EPG5
0.933743161	6.72E-20	ENSBTAG00000002432	ABHD13
0.93364758	6.92E-20	ENSBTAG00000000771	DNAJB6
0.933542252	7.14E-20	ENSBTAG00000038428	RELB
0.933369574	7.52E-20	ENSBTAG00000004608	LOC100138951
0.93311473	8.11E-20	ENSBTAG00000019018	LOC112441484
0.933084253	8.18E-20	ENSBTAG00000019662	ATXN7L3
0.932934677	8.55E-20	ENSBTAG00000018186	PDXK
0.932628204	9.37E-20	ENSBTAG00000015776	MFSD14A

0.9326168	9.40E-20	ENSBTAG00000046690	LOC107133338
0.93245649	9.85E-20	ENSBTAG00000010785	FAS
0.932188802	1.07E-19	ENSBTAG00000019404	IL10RB
0.932155631	1.08E-19	ENSBTAG00000008597	SLC45A4
0.932125743	1.09E-19	ENSBTAG00000003305	NCF1
0.931835927	1.18E-19	ENSBTAG00000001749	SENP2
0.931782491	1.20E-19	ENSBTAG00000014324	ANTXR2
0.931464628	1.32E-19	ENSBTAG00000006136	NA
0.931430937	1.33E-19	ENSBTAG00000000527	ZFAND3
0.931232906	1.41E-19	ENSBTAG00000000504	GTF2B
0.930918225	1.54E-19	ENSBTAG00000008223	NLRC4
0.930828677	1.58E-19	ENSBTAG00000023179	TRIB1
0.930690901	1.64E-19	ENSBTAG00000013290	DYSF
0.930651314	1.66E-19	ENSBTAG00000013454	TAB2
0.930577475	1.70E-19	ENSBTAG00000013555	ACVR1B
0.930423627	1.77E-19	ENSBTAG00000025762	CNP
0.930317665	1.83E-19	ENSBTAG00000007581	ADORA2B
0.930199023	1.89E-19	ENSBTAG00000031252	CD82
0.930195255	1.89E-19	ENSBTAG00000004547	OLR1
0.930116708	1.94E-19	ENSBTAG00000016532	MAPKAPK3
0.92974198	2.15E-19	ENSBTAG00000006566	FFAR2
0.929490982	2.31E-19	ENSBTAG00000005650	SKAP2
0.929422309	2.36E-19	ENSBTAG00000033565	NA
0.929334803	2.41E-19	ENSBTAG00000006654	TANK
0.929049687	2.61E-19	ENSBTAG00000006193	IRAK2
0.929046417	2.62E-19	ENSBTAG00000014829	MYRFL
0.929026456	2.63E-19	ENSBTAG00000047766	NA
0.928741973	2.85E-19	ENSBTAG00000006132	DENND3
0.928568122	2.99E-19	ENSBTAG00000021176	CRISPLD2
0.928281913	3.24E-19	ENSBTAG00000045861	TARM1
0.92821448	3.30E-19	ENSBTAG00000000152	RANBP2
0.928125723	3.38E-19	ENSBTAG00000009496	STAT5A
0.928074016	3.43E-19	ENSBTAG00000000202	SLC25A19
0.928003734	3.49E-19	ENSBTAG00000026753	CXCR1
0.927957928	3.54E-19	ENSBTAG00000006017	NFKB2
0.927851782	3.64E-19	ENSBTAG00000009064	CSF2RB
0.927802432	3.69E-19	ENSBTAG00000016566	ITGA9
0.92751774	3.99E-19	ENSBTAG00000005043	NA
0.927463727	4.05E-19	ENSBTAG00000009863	BHLHE40
0.927441656	4.08E-19	ENSBTAG00000015742	ICAM3
0.927396698	4.13E-19	ENSBTAG00000021818	ADGRE5
0.927265655	4.28E-19	ENSBTAG00000010042	RIOK3
0.927020787	4.57E-19	ENSBTAG00000006523	SOD2
0.926890545	4.73E-19	ENSBTAG00000011994	NDEL1
0.926719655	4.96E-19	ENSBTAG00000000283	CSF1
0.926710012	4.97E-19	ENSBTAG00000001634	PHF1
0.926488805	5.28E-19	ENSBTAG00000005182	BoLA

0.926324191	5.52E-19	ENSBTAG00000020801	CYRIB
0.926157376	5.77E-19	ENSBTAG00000000937	ITPRID2
0.926129094	5.81E-19	ENSBTAG00000038149	NLRP12
0.925902647	6.17E-19	ENSBTAG00000008800	XKR8
0.925877444	6.22E-19	ENSBTAG00000019015	IFITM3
0.925551755	6.78E-19	ENSBTAG00000017722	F5
0.925374878	7.11E-19	ENSBTAG00000031905	LOC107131731
0.924921863	8.01E-19	ENSBTAG00000027760	NA
0.92486831	8.12E-19	ENSBTAG00000007208	HDAC11
0.924831874	8.20E-19	ENSBTAG00000008008	TLR2
0.924676376	8.54E-19	ENSBTAG00000021435	MAFF
0.924665137	8.57E-19	ENSBTAG00000018073	TSPO
0.924622104	8.67E-19	ENSBTAG00000031701	TAGAP
0.924540041	8.85E-19	ENSBTAG00000003791	LPAR3
0.924527131	8.88E-19	ENSBTAG00000000671	PARP3
0.924398236	9.19E-19	ENSBTAG00000020904	JAK3
0.924129605	9.86E-19	ENSBTAG00000019017	LOC112444847
0.924120453	9.88E-19	ENSBTAG00000011578	CD44
0.923710979	1.10E-18	ENSBTAG00000013689	MCTP2
0.923496288	1.16E-18	ENSBTAG00000016944	ADORA2A
0.923331368	1.21E-18	ENSBTAG00000038154	HSH2D
0.923179634	1.26E-18	ENSBTAG00000018036	CNOT7
0.923176337	1.26E-18	ENSBTAG00000011238	CD48
0.922352318	1.56E-18	ENSBTAG00000026148	LOC100300051
0.922139034	1.64E-18	ENSBTAG00000018653	NABP1
0.921707727	1.83E-18	ENSBTAG00000015636	SHFL
0.921553529	1.91E-18	ENSBTAG00000037962	MAML2
0.921244456	2.06E-18	ENSBTAG00000008624	NA
0.921037789	2.17E-18	ENSBTAG00000027051	PTAFR
0.920957888	2.21E-18	ENSBTAG00000038042	CXCR2
0.920780911	2.31E-18	ENSBTAG00000003585	CD47
0.920773366	2.32E-18	ENSBTAG00000013988	BID
0.920735751	2.34E-18	ENSBTAG00000015061	LOC617141
0.920608605	2.41E-18	ENSBTAG00000018951	TBC1D9
0.92051567	2.47E-18	ENSBTAG00000005136	ABI1
0.920128487	2.72E-18	ENSBTAG00000001283	RIC1
0.920062775	2.76E-18	ENSBTAG00000001941	SEMA4D
0.920009474	2.80E-18	ENSBTAG00000002135	CD69
0.919863903	2.90E-18	ENSBTAG00000015154	MCL1
0.919710682	3.01E-18	ENSBTAG00000003851	CCNL1
0.919490636	3.18E-18	ENSBTAG00000003836	ADAM19
0.919431762	3.23E-18	ENSBTAG00000013981	SPTSSA
0.919290543	3.34E-18	ENSBTAG00000015032	CD14
0.919210682	3.41E-18	ENSBTAG00000017764	HDAC4
0.91920877	3.41E-18	ENSBTAG00000000812	CD300A
0.919190771	3.42E-18	ENSBTAG00000001246	ATP1A1
0.919120533	3.48E-18	ENSBTAG00000010153	ANXA3

0.91889692	3.68E-18	ENSBTAG00000002154	GPR141
0.918823746	3.74E-18	ENSBTAG00000003935	TMBIM1
0.918402466	4.15E-18	ENSBTAG00000011103	SLC8B1
0.91828224	4.27E-18	ENSBTAG00000010784	ABT1
0.918265473	4.29E-18	ENSBTAG00000006466	CD53
0.918224776	4.33E-18	ENSBTAG00000001778	NFKBIB
0.918088927	4.47E-18	ENSBTAG00000045880	SIGLEC5
0.917850017	4.74E-18	ENSBTAG00000009381	LCP2
0.917712973	4.89E-18	ENSBTAG00000004378	IL23A
0.917625634	5.00E-18	ENSBTAG00000009233	NA
0.917571783	5.06E-18	ENSBTAG00000004043	LOC407171
0.916770414	6.13E-18	ENSBTAG00000004380	STAT2
0.916658542	6.29E-18	ENSBTAG00000014605	ETV6
0.916518324	6.50E-18	ENSBTAG00000012419	BCL2L15
0.916441402	6.62E-18	ENSBTAG00000019272	LPCAT2
0.91634028	6.78E-18	ENSBTAG00000012640	S100A8
0.916288099	6.86E-18	ENSBTAG00000020089	USP32
0.91626306	6.90E-18	ENSBTAG00000020382	RIN2
0.915862201	7.58E-18	ENSBTAG00000039197	SLC2A9
0.915853983	7.60E-18	ENSBTAG00000013371	RUBCNL
0.915739669	7.81E-18	ENSBTAG00000045904	PIM3
0.915704574	7.87E-18	ENSBTAG00000020093	CUL4A
0.915571606	8.12E-18	ENSBTAG00000010355	VPS37A
0.915480309	8.29E-18	ENSBTAG00000039160	VAV1
0.915470152	8.31E-18	ENSBTAG00000045948	NA
0.915466476	8.32E-18	ENSBTAG00000007213	SIRPA
0.915389487	8.47E-18	ENSBTAG00000006155	CCRL2
0.915252375	8.74E-18	ENSBTAG00000020884	CASP4
0.915219718	8.81E-18	ENSBTAG00000008951	ALPL
0.915005858	9.26E-18	ENSBTAG00000010493	SERTAD1
0.914968839	9.34E-18	ENSBTAG00000007960	TOP1
0.914064078	1.15E-17	ENSBTAG00000010563	PTPN2
0.914021388	1.16E-17	ENSBTAG00000013895	RELA
0.913239544	1.39E-17	ENSBTAG00000024503	FCER1G
0.913121997	1.42E-17	ENSBTAG00000003012	TRAF1
0.913100283	1.43E-17	ENSBTAG00000031718	OGFR
0.912914795	1.49E-17	ENSBTAG00000018223	CHI3L1
0.912447002	1.66E-17	ENSBTAG00000001737	TUT7
0.912437258	1.66E-17	ENSBTAG00000010316	ICAM5
0.912242241	1.74E-17	ENSBTAG00000006343	IL1R2
0.911989719	1.84E-17	ENSBTAG00000013334	NA
0.911784126	1.92E-17	ENSBTAG00000005215	IL10RA
0.911200344	2.19E-17	ENSBTAG00000018869	IGSF6
0.911007123	2.29E-17	ENSBTAG00000017280	C3
0.910936085	2.32E-17	ENSBTAG00000020458	STX6
0.910790462	2.40E-17	ENSBTAG00000001573	JMJD1C
0.910467316	2.57E-17	ENSBTAG00000045548	CRKL

0.910131999	2.77E-17	ENSBTAG00000002959	LRCH1
0.910112377	2.78E-17	ENSBTAG00000044129	ST6GALNAC6
0.910043211	2.82E-17	ENSBTAG00000024918	BIRC3
0.90999861	2.85E-17	ENSBTAG00000011409	CD72
0.909766773	3.00E-17	ENSBTAG00000010982	UBE2B
0.909635631	3.09E-17	ENSBTAG00000047107	TNIP3
0.90962216	3.09E-17	ENSBTAG00000016542	LAMB3
0.90959591	3.11E-17	ENSBTAG00000013410	MARK3
0.90953123	3.16E-17	ENSBTAG00000005978	PIK3R5
0.909504035	3.18E-17	ENSBTAG00000021087	UBR1
0.90898624	3.55E-17	ENSBTAG00000045907	NA
0.908904967	3.61E-17	ENSBTAG00000015609	PREX1
0.908766447	3.72E-17	ENSBTAG00000003536	MARCHF6
0.908688345	3.79E-17	ENSBTAG00000006223	THEMIS2
0.908597403	3.86E-17	ENSBTAG00000010666	KHNYN
0.908536834	3.91E-17	ENSBTAG00000010492	VPS4B
0.908536299	3.91E-17	ENSBTAG00000005443	MIER1
0.908365201	4.06E-17	ENSBTAG00000023847	IKZF5
0.908343552	4.08E-17	ENSBTAG00000011563	TNFSF13B
0.908245463	4.16E-17	ENSBTAG00000013524	CMIP
0.908126487	4.27E-17	ENSBTAG00000009055	RNF144B
0.908003733	4.38E-17	ENSBTAG00000012172	MIDN
0.907533669	4.84E-17	ENSBTAG00000007519	ADAR
0.907491909	4.89E-17	ENSBTAG00000013651	DNAJB12
0.907262739	5.13E-17	ENSBTAG00000021091	ANKFY1
0.907260895	5.13E-17	ENSBTAG00000047676	PRODH
0.907204059	5.19E-17	ENSBTAG00000001856	POLR2C
0.907188521	5.21E-17	ENSBTAG00000031962	NA
0.907069458	5.34E-17	ENSBTAG00000010945	SEC24B
0.906796414	5.66E-17	ENSBTAG00000022689	RYBP
0.906701608	5.77E-17	ENSBTAG00000007804	RILPL2
0.906487185	6.04E-17	ENSBTAG00000006505	S100A9
0.906459028	6.08E-17	ENSBTAG00000016411	RNF122
0.906212403	6.40E-17	ENSBTAG00000018625	ZNF263
0.906176552	6.45E-17	ENSBTAG00000016388	SLCO4A1
0.906121249	6.52E-17	ENSBTAG00000015711	BTG2
0.905963356	6.74E-17	ENSBTAG00000008897	BIN2
0.905872987	6.87E-17	ENSBTAG00000006730	SUSD2
0.905856759	6.89E-17	ENSBTAG00000037413	TMEM164
0.905728382	7.08E-17	ENSBTAG00000010238	LTB4R
0.905492035	7.43E-17	ENSBTAG00000031397	NA
0.905100761	8.06E-17	ENSBTAG00000026192	NA
0.904632814	8.87E-17	ENSBTAG00000016779	CLIP1
0.904470884	9.17E-17	ENSBTAG00000047680	IRF7
0.904382506	9.34E-17	ENSBTAG00000021326	CCL20
0.904285687	9.53E-17	ENSBTAG00000020225	TBXAS1
0.904038324	1.00E-16	ENSBTAG00000011465	MYBPH

0.903615233	1.09E-16	ENSBTAG00000010428	USP15
0.903273735	1.17E-16	ENSBTAG00000016163	OSM
0.903242007	1.18E-16	ENSBTAG00000010763	DUSP16
0.903039666	1.23E-16	ENSBTAG00000013670	SLC46A2
0.903018787	1.23E-16	ENSBTAG00000020990	P2RY14
0.903003653	1.24E-16	ENSBTAG00000017840	BAZ2A
0.902881324	1.27E-16	ENSBTAG00000023026	LOC281376
0.902602353	1.34E-16	ENSBTAG00000034493	ILRUN
0.902595151	1.34E-16	ENSBTAG00000020303	FBXO38
0.902567135	1.35E-16	ENSBTAG00000001518	ISG20L2
0.902504729	1.37E-16	ENSBTAG00000017994	MAX
0.901818732	1.57E-16	ENSBTAG00000025953	NA
0.901734584	1.59E-16	ENSBTAG00000016074	ZNF143
0.901642194	1.62E-16	ENSBTAG00000010372	MTMR7
0.901602302	1.64E-16	ENSBTAG00000011876	MORC3
0.901367464	1.71E-16	ENSBTAG00000016424	MMP25
0.901302168	1.74E-16	ENSBTAG00000012787	SDE2
0.901061068	1.82E-16	ENSBTAG00000016378	LRP10
0.900672196	1.97E-16	ENSBTAG00000014728	TAPBPL
0.900350138	2.09E-16	ENSBTAG00000021452	TRANK1
0.900322761	2.11E-16	ENSBTAG00000009236	DAGLB
0.900274479	2.13E-16	ENSBTAG00000011044	TACC3
0.900255303	2.13E-16	ENSBTAG00000008432	NUP98
0.900244457	2.14E-16	ENSBTAG00000006561	RASGEF1B
0.900142439	2.18E-16	ENSBTAG00000018430	GSAP
0.900094439	2.20E-16	ENSBTAG00000040392	MGC139164
0.900012237	2.24E-16	ENSBTAG00000024097	MRPS15
0.899869661	2.30E-16	ENSBTAG00000035995	TNFAIP2
0.89986846	2.30E-16	ENSBTAG00000020237	NECAP1
0.899574813	2.44E-16	ENSBTAG00000014261	TARS1
0.89945693	2.49E-16	ENSBTAG00000004196	FMNL1
0.899443144	2.50E-16	ENSBTAG00000024928	TNFRSF1B
0.899352885	2.54E-16	ENSBTAG00000003528	NA
0.898753283	2.86E-16	ENSBTAG00000045881	MIR1260B
0.898288148	3.12E-16	ENSBTAG00000015375	SH2D3C
0.898224715	3.16E-16	ENSBTAG00000014548	NIBAN1
0.898186652	3.18E-16	ENSBTAG00000020736	CD40
0.898160503	3.20E-16	ENSBTAG00000009171	LOC527385
0.897876921	3.38E-16	ENSBTAG00000012779	CYRIA
0.8976394	3.54E-16	ENSBTAG00000016414	VDR
0.8975273	3.61E-16	ENSBTAG00000007176	NA
0.897480076	3.64E-16	ENSBTAG00000014087	KMT5C
0.897344659	3.74E-16	ENSBTAG00000011593	QKI
0.896423156	4.45E-16	ENSBTAG00000017016	H3-5
0.896390299	4.48E-16	ENSBTAG00000031483	NA
0.896225446	4.62E-16	ENSBTAG00000010427	RASSF5
0.896182927	4.66E-16	ENSBTAG00000022681	EOGT

0.895452984	5.34E-16	ENSBTAG00000045980	ARF6
0.895274695	5.52E-16	ENSBTAG00000010928	CSRNP2
0.895253341	5.54E-16	ENSBTAG00000008998	NA
0.89517231	5.62E-16	ENSBTAG00000014227	NDFIP2
0.894946217	5.87E-16	ENSBTAG00000000225	POLB
0.894557159	6.30E-16	ENSBTAG00000000163	DDIT4
0.894316851	6.59E-16	ENSBTAG00000011192	GPR87
0.894194153	6.74E-16	ENSBTAG00000009691	SH2B2
0.894119545	6.83E-16	ENSBTAG00000024909	H3-3B
0.893931967	7.07E-16	ENSBTAG00000025462	GADD45B
0.893854631	7.17E-16	ENSBTAG00000007718	TGIF1
0.893848849	7.18E-16	ENSBTAG00000018398	GPR4
0.893660635	7.43E-16	ENSBTAG00000000210	ARHGAP31
0.893487251	7.67E-16	ENSBTAG00000018108	PXN
0.893065648	8.28E-16	ENSBTAG00000007833	PIAS2
0.892830162	8.65E-16	ENSBTAG00000031214	LOC618409
0.892750377	8.77E-16	ENSBTAG00000009036	SUPT6H
0.892646505	8.94E-16	ENSBTAG00000001510	CDK17
0.892627729	8.97E-16	ENSBTAG00000016519	MBOAT1
0.892003463	1.00E-15	ENSBTAG00000046419	TPC3
0.891839168	1.03E-15	ENSBTAG00000039520	SIRPB1
0.891813992	1.04E-15	ENSBTAG00000019414	CLK4
0.891517383	1.10E-15	ENSBTAG00000018015	IL27
0.891208892	1.16E-15	ENSBTAG00000017763	NA
0.891189685	1.16E-15	ENSBTAG00000012737	GPR65
0.891070463	1.19E-15	ENSBTAG00000002951	CD244
0.890984719	1.21E-15	ENSBTAG00000001124	GALC
0.890932301	1.22E-15	ENSBTAG00000010722	NA
0.890784074	1.25E-15	ENSBTAG00000009206	FOXS1
0.890678771	1.27E-15	ENSBTAG00000004587	DUSP6
0.890645464	1.28E-15	ENSBTAG00000013705	NFKBIE
0.890606969	1.29E-15	ENSBTAG00000010399	TXNDC16
0.890561755	1.30E-15	ENSBTAG00000008269	NA
0.89038707	1.34E-15	ENSBTAG00000002078	KDM4A
0.89030785	1.36E-15	ENSBTAG00000020166	ZNFX1
0.890111336	1.41E-15	ENSBTAG00000012046	JUNB
0.888872389	1.75E-15	ENSBTAG00000018280	SLC28A3
0.888810533	1.77E-15	ENSBTAG00000009048	EFHD2
0.888419491	1.89E-15	ENSBTAG00000018667	RCL1
0.888237392	1.95E-15	ENSBTAG00000018013	EMP3
0.888183211	1.97E-15	ENSBTAG00000011204	NINJ1
0.888152223	1.98E-15	ENSBTAG00000003587	ELL
0.888107204	2.00E-15	ENSBTAG00000009426	EZH2
0.888104962	2.00E-15	ENSBTAG00000003316	SYAP1
0.887801323	2.11E-15	ENSBTAG00000015868	LIG4
0.887596333	2.18E-15	ENSBTAG00000015190	RMC1
0.887542373	2.20E-15	ENSBTAG00000046672	ZDHHC18

0.887444159	2.24E-15	ENSBTAG00000005668	SLC39A8
0.887140041	2.36E-15	ENSBTAG00000030951	ZNF655
0.886857176	2.48E-15	ENSBTAG00000010662	LIMK2
0.886603795	2.59E-15	ENSBTAG00000027665	BRF2
0.886468553	2.65E-15	ENSBTAG00000004716	RETN
0.886335489	2.71E-15	ENSBTAG00000006663	CYTH1
0.886254128	2.75E-15	ENSBTAG00000006125	PLK3
0.886075376	2.83E-15	ENSBTAG00000015752	SP110
0.885891027	2.92E-15	ENSBTAG00000010244	CLIC5
0.885799091	2.97E-15	ENSBTAG00000016828	TAPBP
0.885562202	3.09E-15	ENSBTAG00000018314	MED11
0.885512131	3.12E-15	ENSBTAG00000038062	FUT4
0.885068171	3.36E-15	ENSBTAG00000015821	AMPD3
0.884707486	3.57E-15	ENSBTAG00000000653	PPP1R16B
0.884517424	3.69E-15	ENSBTAG00000017082	POR
0.88450013	3.70E-15	ENSBTAG00000013996	SH3BP2
0.884431479	3.74E-15	ENSBTAG00000006697	RICTOR
0.884390588	3.77E-15	ENSBTAG00000003825	PTPN12
0.884080398	3.97E-15	ENSBTAG00000011608	KIAA1191
0.884010603	4.01E-15	ENSBTAG00000004964	PCGF5
0.883605968	4.29E-15	ENSBTAG00000003353	SLC6A2
0.883560381	4.33E-15	ENSBTAG00000047740	NA
0.883399966	4.44E-15	ENSBTAG00000018638	CC2D2A
0.883273049	4.54E-15	ENSBTAG00000006335	STAT6
0.883023321	4.73E-15	ENSBTAG00000038128	BOLA-DQA5
0.882930187	4.80E-15	ENSBTAG00000010487	SMIM3
0.882747075	4.95E-15	ENSBTAG00000020892	IL2RA
0.882338963	5.29E-15	ENSBTAG00000011304	XRN2
0.882336774	5.30E-15	ENSBTAG00000004194	RALGDS
0.882218044	5.40E-15	ENSBTAG00000032031	ZBTB12
0.88207753	5.53E-15	ENSBTAG00000013740	SP2
0.88191823	5.67E-15	ENSBTAG00000015707	TREML2
0.881771276	5.81E-15	ENSBTAG00000031548	LOC514257
0.881281028	6.29E-15	ENSBTAG00000000199	PDP1
0.88102502	6.56E-15	ENSBTAG00000010818	AEBP2
0.881003681	6.58E-15	ENSBTAG00000008260	NA
0.880749766	6.86E-15	ENSBTAG00000006707	ACSL5
0.88069966	6.92E-15	ENSBTAG00000000256	NA
0.880631558	6.99E-15	ENSBTAG00000005622	LITAF
0.880606732	7.02E-15	ENSBTAG00000046566	NA
0.88029087	7.39E-15	ENSBTAG00000007192	SIDT2
0.880242571	7.45E-15	ENSBTAG00000018423	DDX5
0.88023133	7.46E-15	ENSBTAG00000016095	PRICKLE3
0.880227442	7.47E-15	ENSBTAG00000023551	MOB3C
0.88014269	7.57E-15	ENSBTAG00000012626	B4GALT5
0.880015707	7.72E-15	ENSBTAG00000004154	SKIL
0.879935671	7.82E-15	ENSBTAG00000032660	CHIC2

0.879840914	7.94E-15	ENSBTAG00000005384	COPZ1
0.879798576	8.00E-15	ENSBTAG00000008498	ALYREF
0.879642555	8.20E-15	ENSBTAG00000000277	IL18
0.879561934	8.31E-15	ENSBTAG00000048229	NA
0.879459378	8.45E-15	ENSBTAG00000007304	CLK3
0.879389863	8.54E-15	ENSBTAG00000012216	MLKL
0.879112184	8.93E-15	ENSBTAG00000015749	STEAP1
0.878730876	9.49E-15	ENSBTAG00000008840	HM13
0.878655893	9.60E-15	ENSBTAG00000004443	NA
0.878446282	9.93E-15	ENSBTAG00000022288	AMMECR1
0.878413147	9.98E-15	ENSBTAG00000014023	SIRT1
0.878225421	1.03E-14	ENSBTAG00000047345	NA
0.877990754	1.07E-14	ENSBTAG00000036016	FAM111B
0.877822629	1.10E-14	ENSBTAG00000031385	COP1
0.87781398	1.10E-14	ENSBTAG00000034366	RGS2
0.87743129	1.17E-14	ENSBTAG00000020745	HIVEP3
0.877393104	1.17E-14	ENSBTAG00000017462	ATF4
0.877175435	1.21E-14	ENSBTAG00000013919	BOLA-DRB3
0.877173598	1.21E-14	ENSBTAG00000016913	AVIL
0.877098993	1.23E-14	ENSBTAG00000005018	NFAM1
0.877064974	1.23E-14	ENSBTAG00000025405	BATF
0.876735803	1.30E-14	ENSBTAG00000013364	LIPM
0.876620528	1.32E-14	ENSBTAG00000003842	RABGEF1
0.876606491	1.33E-14	ENSBTAG00000018422	RIPK3
0.876276869	1.40E-14	ENSBTAG00000019293	EGR3
0.876121903	1.43E-14	ENSBTAG00000031355	LOC529196
0.876051411	1.45E-14	ENSBTAG00000018773	RND1
0.876047328	1.45E-14	ENSBTAG00000015046	MST1R
0.876016672	1.45E-14	ENSBTAG00000039016	NA
0.875617933	1.55E-14	ENSBTAG00000012125	GDI1
0.875611688	1.55E-14	ENSBTAG00000047338	DCBLD1
0.875408258	1.60E-14	ENSBTAG00000005816	IRF9
0.875283934	1.63E-14	ENSBTAG00000000131	SENP3
0.874956516	1.71E-14	ENSBTAG00000000095	CD274
0.874950168	1.72E-14	ENSBTAG00000006066	CDS2
0.874893698	1.73E-14	ENSBTAG00000017969	CA4
0.874620017	1.80E-14	ENSBTAG00000010394	MCF2L2
0.874587555	1.81E-14	ENSBTAG00000015882	UBE2J2
0.874518896	1.83E-14	ENSBTAG00000017002	RBCK1
0.874301712	1.90E-14	ENSBTAG00000009664	NA
0.874246496	1.91E-14	ENSBTAG00000014153	PKNOX1
0.873997189	1.99E-14	ENSBTAG00000001154	NA
0.87393096	2.01E-14	ENSBTAG00000045808	IL17REL
0.873903323	2.01E-14	ENSBTAG00000019695	RLF
0.873892093	2.02E-14	ENSBTAG00000038938	LOC781710
0.873824215	2.04E-14	ENSBTAG00000010998	CFLAR
0.873460229	2.15E-14	ENSBTAG00000013929	RRAD

0.873231524	2.23E-14	ENSBTAG00000010156	TPT1
0.873111973	2.27E-14	ENSBTAG00000008143	STK17A
0.873052597	2.29E-14	ENSBTAG00000006581	CCDC82
0.873034211	2.30E-14	ENSBTAG00000012387	PAM
0.872939174	2.33E-14	ENSBTAG00000001785	TGM3
0.872767864	2.39E-14	ENSBTAG00000025644	CALM1
0.872767252	2.39E-14	ENSBTAG00000014921	IL6
0.872495276	2.49E-14	ENSBTAG00000026403	CREBBP
0.872464084	2.51E-14	ENSBTAG00000018011	NA
0.872403456	2.53E-14	ENSBTAG00000034225	TAF5L
0.872141787	2.63E-14	ENSBTAG00000016498	PHACTR2
0.872069422	2.66E-14	ENSBTAG00000008953	TAP1
0.872057049	2.66E-14	ENSBTAG00000012124	GPBP1
0.872047178	2.67E-14	ENSBTAG00000000204	TMEM268
0.872045563	2.67E-14	ENSBTAG00000011798	STK38L
0.871983478	2.69E-14	ENSBTAG00000007191	NA
0.871972671	2.70E-14	ENSBTAG00000033702	STARD8
0.871970715	2.70E-14	ENSBTAG00000004741	IL12B
0.871927958	2.72E-14	ENSBTAG00000009183	SHISA5
0.871836995	2.75E-14	ENSBTAG00000017287	DRAM1
0.871745216	2.79E-14	ENSBTAG00000009384	AGTRAP
0.871528198	2.88E-14	ENSBTAG00000003719	TDRD7
0.871368034	2.95E-14	ENSBTAG00000011721	MED13
0.871190793	3.03E-14	ENSBTAG00000004787	METRNL
0.87103977	3.10E-14	ENSBTAG00000020580	TCN1
0.871038435	3.10E-14	ENSBTAG00000005589	STK19
0.870764894	3.23E-14	ENSBTAG00000001592	INSIG1
0.870730548	3.25E-14	ENSBTAG00000010777	CARS1
0.87071307	3.26E-14	ENSBTAG00000016344	PIK3R6
0.8706789	3.27E-14	ENSBTAG00000000957	CDKN2AIP
0.870654153	3.29E-14	ENSBTAG00000006939	FGD3
0.870568849	3.33E-14	ENSBTAG00000018059	CD80
0.870495074	3.36E-14	ENSBTAG00000012928	PPP4C
0.870246468	3.49E-14	ENSBTAG00000003386	NA
0.870012765	3.61E-14	ENSBTAG00000016381	REM2
0.86978626	3.74E-14	ENSBTAG00000020536	HERC6
0.869778418	3.74E-14	ENSBTAG00000016357	VNN2
0.869656972	3.81E-14	ENSBTAG00000003074	SLC16A6
0.869525974	3.88E-14	ENSBTAG00000013577	SLC1A5
0.869321738	4.00E-14	ENSBTAG00000019451	TAPT1
0.869318683	4.00E-14	ENSBTAG00000038375	STOM
0.869092079	4.14E-14	ENSBTAG00000039413	NA
0.869013693	4.19E-14	ENSBTAG00000019303	NA
0.868883877	4.27E-14	ENSBTAG00000005180	RBMS1
0.868847444	4.29E-14	ENSBTAG00000017542	PPARD
0.868561687	4.47E-14	ENSBTAG00000005488	ARIH2
0.868361647	4.61E-14	ENSBTAG00000005947	PLAU

0.868286397	4.66E-14	ENSBTAG00000036078	EMP1
0.868269862	4.67E-14	ENSBTAG00000003639	ELMO2
0.868042504	4.82E-14	ENSBTAG00000040350	XIAP
0.867994372	4.86E-14	ENSBTAG00000004679	WARS1
0.867804781	4.99E-14	ENSBTAG00000019059	ATG16L2
0.86767287	5.09E-14	ENSBTAG00000012904	EDEM1
0.867407222	5.29E-14	ENSBTAG00000000292	TCIRG1
0.867271614	5.39E-14	ENSBTAG00000016435	NOM1
0.867208733	5.44E-14	ENSBTAG00000010645	BOLA-DRA
0.867204607	5.45E-14	ENSBTAG00000021144	PSTPIP1
0.867026439	5.59E-14	ENSBTAG00000019386	BOLA-NC1
0.867010635	5.60E-14	ENSBTAG00000015694	NA
0.867002938	5.61E-14	ENSBTAG00000001579	AGO2
0.866959866	5.64E-14	ENSBTAG00000006601	KSR1
0.866944673	5.66E-14	ENSBTAG00000013368	ANKRD22
0.866900696	5.69E-14	ENSBTAG00000008010	FLCN
0.866611342	5.93E-14	ENSBTAG00000008428	UPP1
0.866482053	6.05E-14	ENSBTAG00000007875	SAFB
0.866287727	6.22E-14	ENSBTAG00000008463	NA
0.86624434	6.25E-14	ENSBTAG00000005008	WSB1
0.866017156	6.46E-14	ENSBTAG00000019428	CCR1
0.866003192	6.47E-14	ENSBTAG00000019530	KDM8
0.865465499	6.99E-14	ENSBTAG00000007828	SLA
0.86522053	7.24E-14	ENSBTAG00000038233	LOC507055
0.86521223	7.25E-14	ENSBTAG00000009065	MAP3K5
0.865094297	7.37E-14	ENSBTAG00000018119	AOAH
0.864940197	7.53E-14	ENSBTAG00000014127	PTGS2
0.864871401	7.61E-14	ENSBTAG00000010888	VSIR
0.864741251	7.75E-14	ENSBTAG00000007280	NA
0.864647505	7.85E-14	ENSBTAG00000020330	BTG1
0.864601004	7.90E-14	ENSBTAG00000004814	INPP4A
0.864569148	7.94E-14	ENSBTAG00000017833	RNF19A
0.864435507	8.09E-14	ENSBTAG00000021287	SLC16A7
0.864381685	8.15E-14	ENSBTAG00000017310	EVA1C
0.864301275	8.25E-14	ENSBTAG00000006539	SIRPB2
0.864295261	8.25E-14	ENSBTAG00000047133	NA
0.864281175	8.27E-14	ENSBTAG00000007531	NCF4
0.864194966	8.37E-14	ENSBTAG00000013900	TRIM21
0.863891794	8.74E-14	ENSBTAG00000007334	NFKBID
0.863871638	8.76E-14	ENSBTAG00000014953	LOC104968422
0.863851334	8.79E-14	ENSBTAG00000020760	SNAP29
0.863752692	8.91E-14	ENSBTAG00000009554	EHBP1L1
0.86366472	9.02E-14	ENSBTAG00000019474	NA
0.863531126	9.19E-14	ENSBTAG00000008915	SF3B1
0.863495663	9.24E-14	ENSBTAG00000004139	BACH1
0.86332821	9.46E-14	ENSBTAG00000019545	SPATA13
0.862743633	1.03E-13	ENSBTAG00000001562	NFE2

0.862740927	1.03E-13	ENSBTAG00000009341	CCDC146
0.862715159	1.03E-13	ENSBTAG00000010665	CBLN3
0.862577654	1.05E-13	ENSBTAG00000046158	CFB
0.862493758	1.06E-13	ENSBTAG00000014680	ZBTB49
0.862167924	1.11E-13	ENSBTAG00000000013	PRKAA1
0.862161884	1.11E-13	ENSBTAG00000021761	BRAF
0.861935975	1.15E-13	ENSBTAG00000014906	VCAN
0.861934089	1.15E-13	ENSBTAG00000047088	NA
0.861835953	1.16E-13	ENSBTAG00000010073	FLOT2
0.861683513	1.19E-13	ENSBTAG00000043964	ARL5B
0.86165964	1.19E-13	ENSBTAG00000018523	TRIM38
0.861491334	1.22E-13	ENSBTAG00000003922	MPHOSPH8
0.86126063	1.26E-13	ENSBTAG00000030503	H2AJ
0.861158433	1.28E-13	ENSBTAG00000016455	CACHD1
0.861060669	1.30E-13	ENSBTAG00000013275	MAD2L2
0.860682818	1.36E-13	ENSBTAG00000020963	RASSF1
0.860655515	1.37E-13	ENSBTAG00000004353	NA
0.860461532	1.41E-13	ENSBTAG00000019123	MEFV
0.860404198	1.42E-13	ENSBTAG00000005430	MB21D2
0.860191643	1.46E-13	ENSBTAG00000012321	ZFAND6
0.859893689	1.52E-13	ENSBTAG00000014880	ICOSLG
0.859850039	1.53E-13	ENSBTAG00000004526	NA
0.859617554	1.58E-13	ENSBTAG00000012060	LPIN2
0.859570065	1.59E-13	ENSBTAG00000009933	DTX3L
0.859151629	1.68E-13	ENSBTAG00000021703	MED12L
0.859050987	1.70E-13	ENSBTAG00000017850	ARHGEF6
0.858955832	1.73E-13	ENSBTAG00000013475	TRAF3
0.85890659	1.74E-13	ENSBTAG00000008699	FEM1C
0.858900558	1.74E-13	ENSBTAG00000045914	LOC100297725
0.858838145	1.75E-13	ENSBTAG00000013044	GAB3
0.858621527	1.81E-13	ENSBTAG00000012894	NA
0.858551559	1.82E-13	ENSBTAG00000005448	LOC521224
0.858511357	1.83E-13	ENSBTAG00000018730	ZBTB17
0.858420044	1.86E-13	ENSBTAG00000015150	IL12A
0.858345016	1.88E-13	ENSBTAG00000007584	INPP1
0.858309689	1.88E-13	ENSBTAG00000005973	OVGP1
0.858272201	1.89E-13	ENSBTAG00000006999	RYR1
0.858218688	1.91E-13	ENSBTAG00000044194	ZDHHC2
0.858185869	1.92E-13	ENSBTAG00000003650	NR4A2
0.858063858	1.95E-13	ENSBTAG00000019517	ELN
0.857620302	2.07E-13	ENSBTAG00000000347	RHOG
0.857574024	2.08E-13	ENSBTAG00000032260	DCUN1D3
0.857124485	2.21E-13	ENSBTAG00000009207	KMT2E
0.857119179	2.21E-13	ENSBTAG00000002743	OSGEP
0.857056792	2.23E-13	ENSBTAG00000038710	NA
0.856998597	2.25E-13	ENSBTAG00000008952	RAP1GAP
0.856852395	2.29E-13	ENSBTAG00000021045	E2F3

0.856640453	2.36E-13	ENSBTAG00000003489	IPCEF1
0.856625122	2.36E-13	ENSBTAG00000038335	LOC534155
0.856595591	2.37E-13	ENSBTAG00000019581	PLEKHF2
0.856461141	2.41E-13	ENSBTAG00000000241	STAU1
0.856352965	2.45E-13	ENSBTAG00000014794	SCYL3
0.856283933	2.47E-13	ENSBTAG00000007158	TSPAN31
0.85605011	2.55E-13	ENSBTAG00000010171	NA
0.856004473	2.56E-13	ENSBTAG00000037937	LOC101903126
0.855848326	2.62E-13	ENSBTAG00000035183	NA
0.855725858	2.66E-13	ENSBTAG00000005841	NA
0.855628588	2.69E-13	ENSBTAG00000011683	NUMB
0.855591184	2.71E-13	ENSBTAG00000015318	NECTIN2
0.855534316	2.73E-13	ENSBTAG00000020921	PRKCB
0.855053974	2.91E-13	ENSBTAG00000020428	PAF1
0.855036347	2.91E-13	ENSBTAG00000027626	GOLGA7
0.854911467	2.96E-13	ENSBTAG00000004553	TPM4
0.854687505	3.05E-13	ENSBTAG00000012997	SMPDL3B
0.854332331	3.19E-13	ENSBTAG00000010576	MAP2K3
0.854043353	3.32E-13	ENSBTAG00000021595	HIP1R
0.853853933	3.40E-13	ENSBTAG00000002363	SESN2
0.853790588	3.43E-13	ENSBTAG00000011825	TRIR
0.853528023	3.55E-13	ENSBTAG00000018474	IL6R
0.853499015	3.56E-13	ENSBTAG00000010449	MOCS1
0.853355066	3.63E-13	ENSBTAG00000020620	RGS2
0.853254741	3.68E-13	ENSBTAG00000001822	SNX10
0.853251072	3.68E-13	ENSBTAG00000005647	GPR132
0.8532173	3.69E-13	ENSBTAG00000005062	TEC
0.85307649	3.76E-13	ENSBTAG00000014297	MOV10
0.853010058	3.79E-13	ENSBTAG00000046014	GPR146
0.852980447	3.81E-13	ENSBTAG00000015952	ADAP1
0.852536096	4.03E-13	ENSBTAG00000009868	VGF
0.852453212	4.08E-13	ENSBTAG00000007103	ITGAL
0.852083146	4.28E-13	ENSBTAG00000007895	SLC20A1
0.851972602	4.34E-13	ENSBTAG00000039037	SERPINB4
0.851967318	4.34E-13	ENSBTAG00000008294	KCNJ2
0.851802632	4.43E-13	ENSBTAG00000035226	NA
0.851337274	4.71E-13	ENSBTAG00000006240	TLR4
0.850949795	4.94E-13	ENSBTAG00000012916	NA
0.85092723	4.96E-13	ENSBTAG00000018165	RIPOR2
0.850885015	4.99E-13	ENSBTAG00000031441	FXYD5
0.850882606	4.99E-13	ENSBTAG00000010390	SRI
0.850675072	5.12E-13	ENSBTAG00000037830	NA
0.850670827	5.12E-13	ENSBTAG00000011337	ANKRD33B
0.850619786	5.16E-13	ENSBTAG00000007922	RNF24
0.850349098	5.34E-13	ENSBTAG00000010497	TRAF2
0.85031651	5.36E-13	ENSBTAG00000014554	SNAI1
0.850247507	5.41E-13	ENSBTAG00000014465	SERPINE1

0.849966557	5.60E-13	ENSBTAG00000015271	RIPK2
0.849940177	5.62E-13	ENSBTAG00000013449	RAB3GAP1
0.849634307	5.84E-13	ENSBTAG00000032369	NMI
0.849493972	5.95E-13	ENSBTAG00000014102	WDR77
0.849028406	6.31E-13	ENSBTAG00000018254	CDKN1B
0.848901887	6.41E-13	ENSBTAG00000005745	HPSE
0.848644658	6.62E-13	ENSBTAG00000021820	DDX39A
0.848590146	6.66E-13	ENSBTAG00000042258	NA
0.848427828	6.80E-13	ENSBTAG00000006078	IL15RA
0.848423215	6.81E-13	ENSBTAG00000011316	ZC3H12A
0.848386491	6.84E-13	ENSBTAG00000046750	B3GNT3
0.847639208	7.51E-13	ENSBTAG00000044071	HRH2
0.847615514	7.53E-13	ENSBTAG00000014359	DRAXIN
0.847576916	7.56E-13	ENSBTAG00000001321	IL1B
0.847565095	7.57E-13	ENSBTAG00000011689	LENG8
0.847248458	7.88E-13	ENSBTAG00000012552	FMR1
0.847174796	7.95E-13	ENSBTAG00000006608	GGT5
0.847108672	8.02E-13	ENSBTAG00000003147	JAK1
0.847002524	8.12E-13	ENSBTAG00000016139	TMEM120A
0.8469847	8.14E-13	ENSBTAG00000023929	FOSL2
0.846689643	8.44E-13	ENSBTAG00000018263	WAC
0.846360542	8.79E-13	ENSBTAG00000012989	UBE2L6
0.846352274	8.80E-13	ENSBTAG00000011421	CD37
0.846242389	8.92E-13	ENSBTAG00000048155	FCN1
0.845858011	9.36E-13	ENSBTAG00000010422	MDM2
0.845589756	9.67E-13	ENSBTAG00000009427	PPM1D
0.845530557	9.74E-13	ENSBTAG00000019604	VASP
0.845461325	9.82E-13	ENSBTAG00000039335	ARRDC2
0.845296844	1.00E-12	ENSBTAG00000003845	CSRNP1
0.84527396	1.01E-12	ENSBTAG00000010606	PPP1R3B
0.845114334	1.03E-12	ENSBTAG00000019110	PNRC1
0.845110177	1.03E-12	ENSBTAG00000014421	NA
0.844725028	1.07E-12	ENSBTAG00000013882	CHMP2A
0.844662926	1.08E-12	ENSBTAG00000009123	ING5
0.844581207	1.09E-12	ENSBTAG00000005588	DXO
0.844551435	1.10E-12	ENSBTAG00000000098	SETDB1
0.844536288	1.10E-12	ENSBTAG00000022895	NA
0.844395183	1.12E-12	ENSBTAG00000007414	PAPOLG
0.844342379	1.13E-12	ENSBTAG00000018487	CFAP45
0.843951481	1.18E-12	ENSBTAG00000006324	NAB2
0.8439425	1.18E-12	ENSBTAG00000018381	CRLF3
0.843767024	1.21E-12	ENSBTAG00000018993	ITGB7
0.84349791	1.25E-12	ENSBTAG00000017674	SCNN1D
0.84327793	1.28E-12	ENSBTAG00000032289	ARHGAP15
0.843125882	1.31E-12	ENSBTAG00000002647	RGS10
0.842953156	1.33E-12	ENSBTAG00000002615	LONRF3
0.842826143	1.35E-12	ENSBTAG00000035735	BIRC2

0.842585084	1.39E-12	ENSBTAG00000015228	CD74
0.842460909	1.41E-12	ENSBTAG00000005160	GTF2H1
0.842448032	1.42E-12	ENSBTAG00000005757	FUS
0.842228677	1.45E-12	ENSBTAG00000005413	NLRC5
0.842122034	1.47E-12	ENSBTAG00000022489	LOC509283
0.841999752	1.49E-12	ENSBTAG00000002282	EIF1
0.84183631	1.52E-12	ENSBTAG00000033669	IL17RC
0.841821091	1.53E-12	ENSBTAG00000047432	LOC781224
0.841107229	1.66E-12	ENSBTAG00000000222	ARID4B
0.840735787	1.74E-12	ENSBTAG00000044676	LOC112446843
0.840698566	1.75E-12	ENSBTAG00000023610	U2AF1L4
0.840672223	1.75E-12	ENSBTAG00000008099	CCR5
0.840622751	1.76E-12	ENSBTAG00000009614	NRROS
0.840518213	1.78E-12	ENSBTAG00000008140	FAP
0.840351423	1.82E-12	ENSBTAG00000030168	MIF4GD
0.840194116	1.85E-12	ENSBTAG00000015086	HSD11B1
0.840070381	1.88E-12	ENSBTAG00000010649	MEF2A
0.840066946	1.88E-12	ENSBTAG00000001185	KMT5B
0.839983672	1.90E-12	ENSBTAG00000001136	NA
0.839969147	1.90E-12	ENSBTAG00000019470	NEK6
0.83985993	1.93E-12	ENSBTAG00000010314	ICAM4
0.839582457	1.99E-12	ENSBTAG00000006615	CASP7
0.839086851	2.11E-12	ENSBTAG00000018203	CD101
0.839011827	2.13E-12	ENSBTAG00000033748	IL18RAP
0.839003025	2.13E-12	ENSBTAG00000016367	RBM18
0.838729823	2.20E-12	ENSBTAG00000010328	KCNK17
0.838377891	2.29E-12	ENSBTAG00000018451	PTMS
0.838333215	2.31E-12	ENSBTAG00000008851	SIGLEC8
0.837764886	2.46E-12	ENSBTAG00000002435	PTPRE
0.837656821	2.49E-12	ENSBTAG00000008320	SEPTIN5
0.837401023	2.57E-12	ENSBTAG00000024561	H3-3A
0.83733035	2.59E-12	ENSBTAG00000017457	STK10
0.836990067	2.69E-12	ENSBTAG00000011698	TYK2
0.836821854	2.75E-12	ENSBTAG00000002027	FAM167B
0.836662986	2.80E-12	ENSBTAG00000047605	LOC100337457
0.83653584	2.84E-12	ENSBTAG00000032277	KYNU
0.836397822	2.89E-12	ENSBTAG00000006695	VCPIP1
0.836214435	2.95E-12	ENSBTAG00000020540	TMEM198
0.836201164	2.95E-12	ENSBTAG00000016546	PARP12
0.835904206	3.05E-12	ENSBTAG00000004558	C10H15orf48
0.835891158	3.06E-12	ENSBTAG00000048122	CFD
0.835879728	3.06E-12	ENSBTAG00000020515	FHIP1B
0.835751352	3.11E-12	ENSBTAG00000000725	USP42
0.835742313	3.11E-12	ENSBTAG00000010303	ICAM1
0.835706462	3.12E-12	ENSBTAG00000045515	NA
0.835688001	3.13E-12	ENSBTAG00000046245	NA
0.835597035	3.16E-12	ENSBTAG00000000226	DKK4

0.835455635	3.22E-12	ENSBTAG00000010134	OSTM1
0.835384455	3.24E-12	ENSBTAG00000030675	PDCL
0.835299319	3.27E-12	ENSBTAG00000015730	BOLA-DMA
0.834713823	3.50E-12	ENSBTAG00000005477	LAPTM5
0.834673202	3.52E-12	ENSBTAG00000011415	ETF1
0.834513732	3.58E-12	ENSBTAG00000005578	KAT5
0.834234888	3.70E-12	ENSBTAG00000011882	SLC24A3
0.834092891	3.76E-12	ENSBTAG00000011729	STARD3
0.833950792	3.82E-12	ENSBTAG00000003934	PSPC1
0.833770744	3.90E-12	ENSBTAG00000016698	SLAMF8
0.833551078	3.99E-12	ENSBTAG00000046450	NA
0.833257929	4.13E-12	ENSBTAG00000008690	SLC6A9
0.833248217	4.13E-12	ENSBTAG00000016932	SENP7
0.83307573	4.21E-12	ENSBTAG00000018146	VAT1L
0.833041977	4.23E-12	ENSBTAG00000010334	SYTL3
0.833012293	4.24E-12	ENSBTAG00000008142	IFIH1
0.832973209	4.26E-12	ENSBTAG00000020395	LYSMD1
0.832867422	4.31E-12	ENSBTAG00000007921	DAPP1
0.832807347	4.34E-12	ENSBTAG00000026234	STK3
0.832781232	4.36E-12	ENSBTAG00000010408	IKBKE
0.832472987	4.51E-12	ENSBTAG00000047570	NA
0.832353969	4.57E-12	ENSBTAG00000013205	IL1RAP
0.832269544	4.61E-12	ENSBTAG00000016879	DENND11
0.832251258	4.62E-12	ENSBTAG00000046409	EGR2
0.832150269	4.68E-12	ENSBTAG00000005397	CD46
0.831155829	5.23E-12	ENSBTAG00000002962	PPM1M
0.830943476	5.35E-12	ENSBTAG00000006487	RPS9
0.830935379	5.36E-12	ENSBTAG00000012628	SLC1A2
0.830839002	5.41E-12	ENSBTAG00000009389	HNRNPH1
0.830656257	5.52E-12	ENSBTAG00000006221	ADGRG3
0.830592228	5.56E-12	ENSBTAG00000017942	CRTC2
0.830457653	5.65E-12	ENSBTAG00000000639	APRT
0.830433349	5.66E-12	ENSBTAG00000011881	TDRD10
0.830429327	5.66E-12	ENSBTAG00000015889	CLCN7
0.830375165	5.70E-12	ENSBTAG00000019479	TATDN2
0.830266632	5.77E-12	ENSBTAG00000005940	PRKAB1
0.830178154	5.82E-12	ENSBTAG00000021791	PARP9
0.829926972	5.99E-12	ENSBTAG00000007389	IFI35
0.829760399	6.10E-12	ENSBTAG00000001252	HIVEP1
0.829406924	6.34E-12	ENSBTAG00000015976	PHF12
0.829333685	6.39E-12	ENSBTAG00000016197	PHLDB1
0.829186457	6.50E-12	ENSBTAG00000047659	NA
0.829048689	6.60E-12	ENSBTAG00000003506	STEAP2
0.828821858	6.76E-12	ENSBTAG00000022394	SAA2
0.828522115	6.99E-12	ENSBTAG00000001030	MTMR3
0.828420215	7.07E-12	ENSBTAG00000010125	STAT5B
0.828261997	7.19E-12	ENSBTAG00000002650	ZPR1

0.828186418	7.25E-12	ENSBTAG00000012451	BOLA-DMB
0.828049059	7.36E-12	ENSBTAG00000045936	NA
0.82797917	7.42E-12	ENSBTAG00000017793	KLRG2
0.82791083	7.47E-12	ENSBTAG00000008353	CDKN1A
0.827810764	7.55E-12	ENSBTAG00000007118	SMURF1
0.827705075	7.64E-12	ENSBTAG00000008540	SLC22A1
0.827675525	7.67E-12	ENSBTAG00000039634	NA
0.827613156	7.72E-12	ENSBTAG00000009768	IFIT3
0.827590936	7.74E-12	ENSBTAG00000020173	INPP5D
0.827572527	7.75E-12	ENSBTAG00000020766	ABCA7
0.827305982	7.98E-12	ENSBTAG00000010309	XPO6
0.827293647	7.99E-12	ENSBTAG00000001160	GMEB1
0.827283671	8.00E-12	ENSBTAG00000012638	S100A12
0.827157795	8.11E-12	ENSBTAG00000014511	C16H1orf159
0.827112563	8.15E-12	ENSBTAG00000020554	AIF1
0.827080234	8.18E-12	ENSBTAG00000006780	NAPSA
0.827009549	8.24E-12	ENSBTAG00000004472	NA
0.826976994	8.27E-12	ENSBTAG00000013201	ALOX5AP
0.826755272	8.47E-12	ENSBTAG00000003264	NR1H2
0.826629848	8.59E-12	ENSBTAG00000018498	PQBP1
0.826318453	8.88E-12	ENSBTAG00000015779	PML
0.826170144	9.02E-12	ENSBTAG00000017363	SAT1
0.826073531	9.12E-12	ENSBTAG00000019099	SLC25A37
0.825618137	9.58E-12	ENSBTAG00000014705	HES4
0.825607743	9.59E-12	ENSBTAG00000004953	ELK4
0.825213673	1.00E-11	ENSBTAG00000013125	PLAUR
0.824677986	1.06E-11	ENSBTAG00000011815	SMG9
0.824593377	1.07E-11	ENSBTAG00000001790	SAFB2
0.824577989	1.07E-11	ENSBTAG00000004115	MYLIP
0.824032162	1.13E-11	ENSBTAG00000018227	SLC4A7
0.823993004	1.14E-11	ENSBTAG00000025812	NA
0.823880983	1.15E-11	ENSBTAG00000045647	NA
0.823513934	1.20E-11	ENSBTAG00000047339	BCOR
0.823439857	1.21E-11	ENSBTAG00000005181	SYS1
0.823408757	1.21E-11	ENSBTAG00000004189	MLXIP
0.823009119	1.26E-11	ENSBTAG00000009958	TRIM35
0.822978673	1.27E-11	ENSBTAG00000015127	SDC4
0.822884878	1.28E-11	ENSBTAG00000011263	EIF6
0.822650961	1.31E-11	ENSBTAG00000004540	NUB1
0.822467635	1.34E-11	ENSBTAG00000021394	FITM1
0.822466527	1.34E-11	ENSBTAG00000021395	PSME1
0.822433419	1.34E-11	ENSBTAG00000018086	TBC1D10A
0.822331621	1.36E-11	ENSBTAG00000002758	NA
0.822122647	1.39E-11	ENSBTAG00000005923	ABTB2
0.822017282	1.40E-11	ENSBTAG00000014433	UBE2G1
0.821920318	1.42E-11	ENSBTAG00000018419	ADCY4
0.821911418	1.42E-11	ENSBTAG00000027064	BTBD11

0.821800721	1.44E-11	ENSBTAG00000018975	KCNT1
0.82173392	1.45E-11	ENSBTAG00000039310	NA
0.821568504	1.47E-11	ENSBTAG00000008573	ZFP36
0.821302645	1.51E-11	ENSBTAG00000006731	SLC7A5
0.821221144	1.53E-11	ENSBTAG00000027655	NA
0.820458611	1.65E-11	ENSBTAG00000000483	HYAL1
0.820253105	1.69E-11	ENSBTAG00000019436	SLC39A13
0.820066788	1.72E-11	ENSBTAG00000021726	CWC22
0.820039333	1.73E-11	ENSBTAG00000014917	GTPBP4
0.819861847	1.76E-11	ENSBTAG00000010433	NA
0.819847291	1.76E-11	ENSBTAG00000016208	TGM2
0.819748248	1.78E-11	ENSBTAG00000008954	PSMB9
0.819631286	1.80E-11	ENSBTAG00000031895	TFB1M
0.819221295	1.88E-11	ENSBTAG00000000381	S1PR4
0.819102425	1.90E-11	ENSBTAG00000032869	RNASE10
0.81900993	1.92E-11	ENSBTAG00000009717	FGL2
0.81895535	1.93E-11	ENSBTAG00000002020	CREBRF
0.81863179	2.00E-11	ENSBTAG00000002755	ANKRD12
0.818628584	2.00E-11	ENSBTAG00000002623	SAMSN1
0.818536615	2.02E-11	ENSBTAG00000020936	NOD2
0.818397271	2.05E-11	ENSBTAG00000033395	C25H16orf91
0.818090478	2.11E-11	ENSBTAG00000011406	TESK1
0.818030105	2.12E-11	ENSBTAG00000020472	KDM5A
0.817576986	2.22E-11	ENSBTAG00000026944	NA
0.816884992	2.39E-11	ENSBTAG00000019617	PTPN22
0.816739803	2.42E-11	ENSBTAG00000046266	TNFSF9
0.816710432	2.43E-11	ENSBTAG00000015758	USB1
0.81666351	2.44E-11	ENSBTAG00000046662	TRPM5
0.816582541	2.46E-11	ENSBTAG00000037702	SP140L
0.816430032	2.50E-11	ENSBTAG00000033735	WASHC4
0.816398905	2.51E-11	ENSBTAG00000026199	ACTB
0.816398019	2.51E-11	ENSBTAG00000021766	HBEGF
0.816307517	2.53E-11	ENSBTAG00000006751	TENT2
0.816290735	2.54E-11	ENSBTAG00000026993	TMBIM4
0.815735392	2.68E-11	ENSBTAG00000003743	NA
0.815708793	2.69E-11	ENSBTAG00000022395	LOC104968478
0.81566313	2.70E-11	ENSBTAG00000043553	GPX3
0.815552833	2.73E-11	ENSBTAG00000042836	LOC112442823
0.815516561	2.74E-11	ENSBTAG00000010511	KAT8
0.815245364	2.82E-11	ENSBTAG00000003880	EMILIN2
0.815229585	2.82E-11	ENSBTAG00000029901	MIR23A
0.815112993	2.86E-11	ENSBTAG00000019742	FOXJ2
0.815033901	2.88E-11	ENSBTAG00000023054	SLC25A16
0.814978261	2.90E-11	ENSBTAG00000045854	LOC100852077
0.814956199	2.90E-11	ENSBTAG00000033218	NA
0.814944075	2.91E-11	ENSBTAG00000015119	SIK3
0.814413379	3.06E-11	ENSBTAG00000000579	NIPBL

0.814181446	3.14E-11	ENSBTAG00000047488	KCNK9
0.814168268	3.14E-11	ENSBTAG00000019227	LOC789748
0.813990287	3.20E-11	ENSBTAG00000032374	SELENOK
0.813910121	3.22E-11	ENSBTAG00000018198	TLR9
0.81378031	3.27E-11	ENSBTAG00000001120	CORO6
0.81372551	3.28E-11	ENSBTAG00000046343	CCNJL
0.813670711	3.30E-11	ENSBTAG00000011197	IPMK
0.813018342	3.52E-11	ENSBTAG00000013569	CD38
0.812726482	3.63E-11	ENSBTAG00000007513	PGAM5
0.812302128	3.78E-11	ENSBTAG00000011467	BATF2
0.812274	3.79E-11	ENSBTAG00000014248	MIER3
0.812149378	3.84E-11	ENSBTAG00000022813	TMEM150B
0.812001882	3.90E-11	ENSBTAG00000012615	NA
0.811234826	4.20E-11	ENSBTAG00000015632	TNFRSF18
0.81105227	4.28E-11	ENSBTAG00000015805	SIPA1L1
0.811005222	4.30E-11	ENSBTAG00000021480	SAG
0.810719932	4.42E-11	ENSBTAG00000020764	CNN2
0.810702631	4.43E-11	ENSBTAG00000036392	MIR371
0.810514397	4.51E-11	ENSBTAG00000022779	OLFM4
0.81035088	4.58E-11	ENSBTAG00000002882	LMNB1
0.810263751	4.62E-11	ENSBTAG00000005833	ETNK1
0.810009707	4.74E-11	ENSBTAG00000019989	PXK
0.809985201	4.75E-11	ENSBTAG00000046407	NYX
0.809820617	4.83E-11	ENSBTAG00000000806	ATAD1
0.809516229	4.97E-11	ENSBTAG00000007455	DNASE1L1
0.809442731	5.01E-11	ENSBTAG00000004193	VEZF1
0.809387984	5.04E-11	ENSBTAG00000035081	SERINC2
0.809332395	5.06E-11	ENSBTAG00000030071	MIR24-2
0.809160184	5.15E-11	ENSBTAG00000014238	ATP6V1E1
0.809149632	5.15E-11	ENSBTAG00000015363	CDC42SE1
0.808803677	5.33E-11	ENSBTAG00000004635	LLGL1
0.808479772	5.50E-11	ENSBTAG00000043243	LOC112449172
0.808431723	5.53E-11	ENSBTAG00000010871	NA
0.808417721	5.53E-11	ENSBTAG00000000088	ALCAM
0.808355202	5.57E-11	ENSBTAG00000007343	NA
0.807794661	5.88E-11	ENSBTAG00000002068	TAGLN2
0.807605015	5.98E-11	ENSBTAG00000013861	SLC8A1
0.807604143	5.99E-11	ENSBTAG00000047871	KLF17
0.806905111	6.40E-11	ENSBTAG00000017682	TET2
0.806888128	6.41E-11	ENSBTAG00000035224	NA
0.806870838	6.42E-11	ENSBTAG00000000290	ATP11B
0.806694962	6.53E-11	ENSBTAG00000016401	OPTN
0.806508023	6.65E-11	ENSBTAG00000004386	SOCS1
0.806494197	6.66E-11	ENSBTAG00000015994	LRRC63
0.806447911	6.69E-11	ENSBTAG00000012335	UBA7
0.80569618	7.19E-11	ENSBTAG00000003397	CTBP2
0.805534181	7.30E-11	ENSBTAG00000020755	SELP

0.80505414	7.64E-11	ENSBTAG00000013074	PPP1R15B
0.80484509	7.79E-11	ENSBTAG00000010148	LOC505856
0.804803756	7.82E-11	ENSBTAG00000042264	LOC112444803
0.804788263	7.83E-11	ENSBTAG00000031231	IRF1
0.804666757	7.92E-11	ENSBTAG00000007659	CORO2A
0.804525911	8.03E-11	ENSBTAG00000002082	MARCKS
0.8043378	8.18E-11	ENSBTAG00000020350	DUSP2
0.804007265	8.43E-11	ENSBTAG00000006683	ZFYVE28
0.803590006	8.77E-11	ENSBTAG00000012201	NA
0.803471036	8.87E-11	ENSBTAG00000024105	BCL2L11
0.802925944	9.34E-11	ENSBTAG00000014328	MGC138914
0.802856007	9.40E-11	ENSBTAG00000002773	CD300LF
0.802559401	9.66E-11	ENSBTAG00000018912	ARHGEF1
0.802336878	9.87E-11	ENSBTAG00000005038	ZBTB42
0.802276709	9.92E-11	ENSBTAG00000010547	CEP76
0.801805749	1.04E-10	ENSBTAG00000018000	CLN3
0.801649005	1.05E-10	ENSBTAG00000037735	C5AR2
0.801513122	1.07E-10	ENSBTAG00000004971	GRAMD1C
0.801192597	1.10E-10	ENSBTAG00000032686	HOMEZ
0.801186726	1.10E-10	ENSBTAG00000000973	KCNJ15
0.80108542	1.11E-10	ENSBTAG00000029996	MIR27A
0.800874255	1.13E-10	ENSBTAG00000038536	LOC616948
0.800739069	1.15E-10	ENSBTAG00000004349	DAZAP2
0.800634961	1.16E-10	ENSBTAG00000005462	FXR2
0.800587661	1.16E-10	ENSBTAG00000003764	AKIRIN2
0.800575656	1.16E-10	ENSBTAG00000038737	P2RY6
0.800407149	1.18E-10	ENSBTAG00000030845	MPEG1
0.800321703	1.19E-10	ENSBTAG00000016912	TSFM
0.800307921	1.19E-10	ENSBTAG00000029930	MIR22
0.800291755	1.19E-10	ENSBTAG00000004723	TEX2
0.800274554	1.20E-10	ENSBTAG00000013362	DNM2
0.799959482	1.23E-10	ENSBTAG00000013730	CD5
0.79951895	1.28E-10	ENSBTAG00000006027	USP34
0.799156274	1.33E-10	ENSBTAG00000002970	INTS6
0.799102012	1.33E-10	ENSBTAG00000011582	NA
0.798938035	1.35E-10	ENSBTAG00000020095	MS4A3
0.798666812	1.39E-10	ENSBTAG00000015126	TNIP2
0.798613656	1.39E-10	ENSBTAG00000009159	PLXNA1
0.798568211	1.40E-10	ENSBTAG00000038494	NA
0.798518098	1.40E-10	ENSBTAG00000000336	LOC112442378
0.798407724	1.42E-10	ENSBTAG00000027937	NA
0.798300077	1.43E-10	ENSBTAG00000007073	CPB2
0.798008607	1.47E-10	ENSBTAG00000002096	FCGR3A
0.797656671	1.52E-10	ENSBTAG00000022396	NA
0.797292705	1.57E-10	ENSBTAG00000000675	PGS1
0.797261571	1.58E-10	ENSBTAG00000012778	CAPN2
0.797167633	1.59E-10	ENSBTAG00000002834	CCDC69

0.797134595	1.59E-10	ENSBTAG00000002912	NA
0.79668105	1.66E-10	ENSBTAG00000002690	BLZF1
0.796479624	1.69E-10	ENSBTAG00000012288	TFIP11
0.796391725	1.70E-10	ENSBTAG00000012182	DIRAS3
0.796321738	1.72E-10	ENSBTAG00000047424	TRIP10
0.795866131	1.79E-10	ENSBTAG00000017346	RASSF2
0.795830549	1.79E-10	ENSBTAG00000019313	ZMIZ1
0.795628118	1.83E-10	ENSBTAG00000006189	ACTG1
0.795331109	1.88E-10	ENSBTAG00000003895	NA
0.795056065	1.92E-10	ENSBTAG00000015961	TSPAN2
0.794771694	1.97E-10	ENSBTAG00000017435	KCTD7
0.794694919	1.99E-10	ENSBTAG00000000176	SP3
0.794542459	2.01E-10	ENSBTAG00000009289	MS4A8
0.794524628	2.02E-10	ENSBTAG00000006650	ZNF668
0.794114528	2.09E-10	ENSBTAG00000000137	FRYL
0.794073485	2.10E-10	ENSBTAG00000015042	WDR55
0.794058038	2.10E-10	ENSBTAG00000004662	SLC16A12
0.793762345	2.16E-10	ENSBTAG00000014393	CLK2
0.793486175	2.21E-10	ENSBTAG00000019115	NA
0.793427924	2.22E-10	ENSBTAG00000018851	MYCBP2
0.793332174	2.24E-10	ENSBTAG00000015312	LTBR
0.793085367	2.29E-10	ENSBTAG00000021803	GRAMD4
0.793059373	2.30E-10	ENSBTAG00000016169	ID1
0.793019809	2.31E-10	ENSBTAG00000012277	SRRD
0.793001366	2.31E-10	ENSBTAG00000045293	LOC112442824
0.792881787	2.33E-10	ENSBTAG00000000275	PARP11
0.792798063	2.35E-10	ENSBTAG00000013586	CCR2
0.792769184	2.36E-10	ENSBTAG00000021286	SLC37A1
0.792753133	2.36E-10	ENSBTAG00000029904	MIR222
0.79249603	2.42E-10	ENSBTAG00000039529	BTBD19
0.792482222	2.42E-10	ENSBTAG00000000735	BCL2A1
0.792478249	2.42E-10	ENSBTAG00000031849	TMEM119
0.79241832	2.43E-10	ENSBTAG00000016217	RBM43
0.792006993	2.52E-10	ENSBTAG00000016328	SFPQ
0.791978614	2.53E-10	ENSBTAG00000008259	ACOD1
0.79189546	2.55E-10	ENSBTAG00000021911	PTPRG
0.791868243	2.55E-10	ENSBTAG00000031544	DDIT3
0.791776527	2.57E-10	ENSBTAG00000047093	NA
0.791679195	2.60E-10	ENSBTAG00000000563	MYD88
0.791525908	2.63E-10	ENSBTAG00000005427	NRDE2
0.79148678	2.64E-10	ENSBTAG00000032209	CXHXorf65
0.791429056	2.65E-10	ENSBTAG00000004789	LGR6
0.791246154	2.70E-10	ENSBTAG00000003526	SYNE3
0.791187228	2.71E-10	ENSBTAG00000048023	NA
0.791171608	2.72E-10	ENSBTAG00000037605	LOC100848815
0.791068128	2.74E-10	ENSBTAG00000013834	NA
0.79103569	2.75E-10	ENSBTAG00000024901	LOC509881

0.790932392	2.77E-10	ENSBTAG00000020538	HERC5
0.790802105	2.80E-10	ENSBTAG00000014707	ISG15
0.790561274	2.86E-10	ENSBTAG00000012120	TIPARP
0.790266779	2.94E-10	ENSBTAG00000012038	NA
0.78996325	3.02E-10	ENSBTAG00000033041	YIPF4
0.789881697	3.04E-10	ENSBTAG00000018332	PPTC7
0.789677199	3.09E-10	ENSBTAG00000003128	SPATA6
0.78964918	3.10E-10	ENSBTAG00000012050	ORAI2
0.789603626	3.11E-10	ENSBTAG00000040586	NA
0.789442324	3.16E-10	ENSBTAG00000011287	ATXN7
0.789279623	3.20E-10	ENSBTAG00000011358	IER3
0.789128963	3.25E-10	ENSBTAG00000019672	LOC574091
0.788869505	3.32E-10	ENSBTAG00000011898	LTO1
0.788816441	3.34E-10	ENSBTAG00000003495	KDM7A
0.78853148	3.42E-10	ENSBTAG00000048314	NA
0.788376627	3.46E-10	ENSBTAG00000014471	PALM2
0.788343953	3.47E-10	ENSBTAG00000046612	ZNF292
0.788154592	3.53E-10	ENSBTAG00000007927	SLAMF1
0.787944928	3.60E-10	ENSBTAG00000029942	NA
0.787944527	3.60E-10	ENSBTAG00000000396	PIM1
0.787864583	3.62E-10	ENSBTAG00000021647	FCAR
0.787820541	3.64E-10	ENSBTAG00000000551	SMNDC1
0.787783215	3.65E-10	ENSBTAG00000017826	SCLY
0.787602089	3.70E-10	ENSBTAG00000017731	ZFAT
0.787510536	3.73E-10	ENSBTAG00000021819	IFNAR1
0.787484304	3.74E-10	ENSBTAG00000014490	DDX39B
0.787379602	3.78E-10	ENSBTAG00000021392	DCAF11
0.787126554	3.86E-10	ENSBTAG00000025494	PAQR8
0.787036578	3.89E-10	ENSBTAG00000006894	NOS2
0.786897978	3.94E-10	ENSBTAG00000047926	OVCA2
0.786458101	4.09E-10	ENSBTAG00000007361	NA
0.786445331	4.09E-10	ENSBTAG00000011936	ATP8B4
0.786367556	4.12E-10	ENSBTAG00000009960	FLOT1
0.786335032	4.13E-10	ENSBTAG00000037537	LOC618463
0.786080259	4.22E-10	ENSBTAG00000006044	KLHL5
0.785936532	4.27E-10	ENSBTAG00000021856	R3HCC1L
0.78592884	4.28E-10	ENSBTAG00000006752	PFKFB4
0.785742664	4.35E-10	ENSBTAG00000046383	NA
0.785401574	4.47E-10	ENSBTAG00000014898	HK3
0.785384159	4.48E-10	ENSBTAG00000018994	TNFSF10
0.784679611	4.76E-10	ENSBTAG00000034918	IFIT2
0.784085486	5.00E-10	ENSBTAG00000005807	MICU1
0.78399396	5.04E-10	ENSBTAG00000007199	NA
0.783902636	5.08E-10	ENSBTAG00000000415	ERBIN
0.783858867	5.10E-10	ENSBTAG00000005354	LRRFIP1
0.783846906	5.10E-10	ENSBTAG00000004603	PHC2
0.783680192	5.18E-10	ENSBTAG00000017863	SRGN

0.783359523	5.32E-10	ENSBTAG00000014349	RNF126
0.783166122	5.41E-10	ENSBTAG00000001652	SLCO3A1
0.783103798	5.44E-10	ENSBTAG00000005450	NA
0.782836397	5.56E-10	ENSBTAG00000000746	KAT2B
0.782768984	5.59E-10	ENSBTAG00000002051	ARAP1
0.782742507	5.60E-10	ENSBTAG00000034643	NA
0.782494661	5.72E-10	ENSBTAG00000004216	MAP3K2
0.782439493	5.75E-10	ENSBTAG00000045748	RAF1
0.782363883	5.78E-10	ENSBTAG00000001462	FLT4
0.78230217	5.81E-10	ENSBTAG00000017970	ZYX
0.782290774	5.82E-10	ENSBTAG00000012622	TRA2A
0.782116764	5.90E-10	ENSBTAG00000011011	SSH2
0.782109733	5.91E-10	ENSBTAG00000001015	TM9SF4
0.78204078	5.94E-10	ENSBTAG00000025898	TBC1D8
0.78202773	5.95E-10	ENSBTAG00000021842	FCGR2B
0.781843541	6.04E-10	ENSBTAG00000019884	PKD1L3
0.781839563	6.04E-10	ENSBTAG00000007836	PPA1
0.781572939	6.18E-10	ENSBTAG00000037608	NA
0.781422333	6.26E-10	ENSBTAG00000027557	ZNF408
0.781311742	6.32E-10	ENSBTAG00000039764	NA
0.781041292	6.46E-10	ENSBTAG00000005146	NA
0.780747087	6.62E-10	ENSBTAG00000004850	KPNA3
0.780746075	6.62E-10	ENSBTAG00000027317	RNF114
0.78059018	6.71E-10	ENSBTAG00000005089	RHBDD2
0.780541854	6.73E-10	ENSBTAG00000003928	ATG16L1
0.780539559	6.74E-10	ENSBTAG00000010242	LAMP1
0.780529061	6.74E-10	ENSBTAG00000015969	STK40
0.780030512	7.03E-10	ENSBTAG00000045742	NA
0.780002129	7.04E-10	ENSBTAG00000002148	RAB3D
0.779777859	7.17E-10	ENSBTAG00000019800	NA
0.779609397	7.28E-10	ENSBTAG00000020714	DDX19B
0.779505787	7.34E-10	ENSBTAG00000002163	PTGER2
0.779454066	7.37E-10	ENSBTAG00000029765	NA
0.779376382	7.42E-10	ENSBTAG00000027713	LYSMD3
0.779361737	7.43E-10	ENSBTAG00000026080	LAIR1
0.779246153	7.50E-10	ENSBTAG00000044741	LOC112441677
0.779084263	7.60E-10	ENSBTAG00000008485	NA
0.779011176	7.64E-10	ENSBTAG00000014105	SRPRA
0.778902843	7.71E-10	ENSBTAG00000001060	CXCR4
0.77864079	7.88E-10	ENSBTAG00000002527	ZSWIM4
0.77828104	8.12E-10	ENSBTAG00000012010	PANX1
0.778116439	8.23E-10	ENSBTAG00000045673	LOC613345
0.778016871	8.29E-10	ENSBTAG00000006864	LOC107131209
0.777998897	8.31E-10	ENSBTAG00000017118	FAM8A1
0.777879845	8.39E-10	ENSBTAG00000017000	IL22RA2
0.77771713	8.50E-10	ENSBTAG00000033315	DNAJC1
0.77768927	8.52E-10	ENSBTAG00000044059	NA

0.777353054	8.76E-10	ENSBTAG00000031789	FBRS
0.777228219	8.85E-10	ENSBTAG00000046693	NA
0.777145005	8.91E-10	ENSBTAG00000017375	FAM241A
0.776948066	9.05E-10	ENSBTAG00000019255	NFE2L2
0.776784804	9.17E-10	ENSBTAG00000047200	NA
0.776723377	9.22E-10	ENSBTAG00000016494	RELT
0.776704944	9.23E-10	ENSBTAG00000006510	YRDC
0.776424764	9.45E-10	ENSBTAG00000037554	NA
0.776060177	9.73E-10	ENSBTAG00000009482	AFF4
0.775891625	9.86E-10	ENSBTAG00000013580	KDM3A
0.775361364	1.03E-09	ENSBTAG00000011483	SCARF1
0.775044814	1.06E-09	ENSBTAG00000003436	RHBDF2
0.774678708	1.09E-09	ENSBTAG00000001325	UPB1
0.774372255	1.12E-09	ENSBTAG00000009785	SAMD4B
0.774284471	1.12E-09	ENSBTAG00000000920	DNAH17
0.77422593	1.13E-09	ENSBTAG00000009677	PARP10
0.774171954	1.13E-09	ENSBTAG00000016345	IL2RB
0.774015465	1.15E-09	ENSBTAG00000014113	CCL8
0.773918851	1.16E-09	ENSBTAG00000008719	PRKCD
0.773733341	1.17E-09	ENSBTAG00000022022	GUCD1
0.773664444	1.18E-09	ENSBTAG00000016750	PTBP3
0.773529333	1.19E-09	ENSBTAG00000018901	CTIF
0.773506984	1.20E-09	ENSBTAG00000020313	FNBP1
0.773385262	1.21E-09	ENSBTAG00000005564	PIAS1
0.773302864	1.22E-09	ENSBTAG00000020759	NCLN
0.772770369	1.27E-09	ENSBTAG00000019314	USP25
0.772388815	1.31E-09	ENSBTAG00000038235	NOD1
0.772289919	1.32E-09	ENSBTAG00000003820	GRAMD1A
0.772134782	1.33E-09	ENSBTAG00000000816	PRDM1
0.772094138	1.34E-09	ENSBTAG00000007089	FRG1
0.771989783	1.35E-09	ENSBTAG00000045814	NA
0.771697549	1.38E-09	ENSBTAG00000008092	RAB37
0.771693679	1.38E-09	ENSBTAG00000020616	DGKD
0.771627362	1.39E-09	ENSBTAG00000011667	PM20D2
0.771476026	1.41E-09	ENSBTAG00000025401	DOK3
0.771462238	1.41E-09	ENSBTAG00000003936	PNKD
0.771439226	1.41E-09	ENSBTAG00000006685	IL10
0.771383707	1.42E-09	ENSBTAG00000016906	CYP27B1
0.771160515	1.44E-09	ENSBTAG00000040151	GCH1
0.770707818	1.49E-09	ENSBTAG00000003541	ZNF614
0.770631224	1.50E-09	ENSBTAG00000008603	TASL
0.770626462	1.50E-09	ENSBTAG00000009887	DDX17
0.770355247	1.54E-09	ENSBTAG00000019339	NA
0.770314299	1.54E-09	ENSBTAG00000008545	ATF3
0.770255676	1.55E-09	ENSBTAG00000013711	NA
0.770109347	1.57E-09	ENSBTAG00000018731	LOC524181
0.769945947	1.59E-09	ENSBTAG00000008096	EDN1

0.769884059	1.59E-09	ENSBTAG00000013215	MREG
0.769777901	1.61E-09	ENSBTAG00000001034	IL18R1
0.7697768	1.61E-09	ENSBTAG00000020872	C5AR1
0.769739071	1.61E-09	ENSBTAG00000023648	LOC618664
0.769713897	1.62E-09	ENSBTAG00000003039	PSMB8
0.769688503	1.62E-09	ENSBTAG00000013298	PLA2G4A
0.769640148	1.63E-09	ENSBTAG00000009488	NXF1
0.769602759	1.63E-09	ENSBTAG00000017592	GPAT3
0.769482375	1.65E-09	ENSBTAG00000018229	NFIX
0.769362433	1.66E-09	ENSBTAG00000038981	LOC518134
0.769052705	1.70E-09	ENSBTAG00000009019	SH3PXD2B
0.768957689	1.71E-09	ENSBTAG00000021396	HEG1
0.768931054	1.72E-09	ENSBTAG00000014543	PLXNA4
0.768898942	1.72E-09	ENSBTAG00000016603	LOC786914
0.7685916	1.76E-09	ENSBTAG00000030921	FAM3B
0.768355451	1.80E-09	ENSBTAG00000004842	RSPRY1
0.768164672	1.82E-09	ENSBTAG00000040361	LFNG
0.768094249	1.83E-09	ENSBTAG00000001509	ELK3
0.767985854	1.85E-09	ENSBTAG00000021505	USP36
0.767877395	1.87E-09	ENSBTAG00000002271	CDADC1
0.767824306	1.87E-09	ENSBTAG00000011343	XAF1
0.767644877	1.90E-09	ENSBTAG00000037533	C4A
0.767642352	1.90E-09	ENSBTAG00000031476	DLL1
0.767351006	1.94E-09	ENSBTAG00000001009	HCLS1
0.767302049	1.95E-09	ENSBTAG00000021962	BCLAF3
0.767217218	1.96E-09	ENSBTAG00000014737	VEGFC
0.766664162	2.05E-09	ENSBTAG00000020019	XCR1
0.766633457	2.05E-09	ENSBTAG00000014991	PARD3
0.766427963	2.09E-09	ENSBTAG00000004659	COQ10B
0.766220297	2.12E-09	ENSBTAG00000018704	BTG3
0.76618921	2.13E-09	ENSBTAG00000016711	PPIF
0.766148399	2.13E-09	ENSBTAG00000046939	NA
0.766036811	2.15E-09	ENSBTAG00000017656	ST3GAL3
0.766000068	2.16E-09	ENSBTAG00000015060	GBP5
0.765961515	2.16E-09	ENSBTAG00000003923	GPBAR1
0.765947793	2.17E-09	ENSBTAG00000021105	IRAK4
0.765829506	2.19E-09	ENSBTAG00000024849	LOC100138271
0.765741533	2.20E-09	ENSBTAG00000007709	SHOC2
0.765704687	2.21E-09	ENSBTAG00000019175	SOBP
0.76567235	2.21E-09	ENSBTAG00000002922	GAB2
0.765383413	2.26E-09	ENSBTAG00000001887	STAM2
0.765231523	2.29E-09	ENSBTAG00000008649	ETV3
0.765155611	2.30E-09	ENSBTAG00000021260	GALNT11
0.764630702	2.40E-09	ENSBTAG00000001294	PPP1R15A
0.764482982	2.43E-09	ENSBTAG00000004961	GOSR1
0.7643043	2.46E-09	ENSBTAG00000011075	PLPBP
0.764207977	2.48E-09	ENSBTAG00000000012	TTC33

0.763319372	2.65E-09	ENSBTAG00000005067	UBTF
0.763235956	2.67E-09	ENSBTAG00000020942	RNF166
0.763048701	2.71E-09	ENSBTAG00000004492	SWT1
0.76287796	2.74E-09	ENSBTAG00000011435	NPEPPS
0.762815066	2.75E-09	ENSBTAG00000042868	LOC112442805
0.762598653	2.80E-09	ENSBTAG00000025233	CBARP
0.76237001	2.85E-09	ENSBTAG00000020649	CIITA
0.762288791	2.87E-09	ENSBTAG00000001881	SLC10A1
0.761877696	2.96E-09	ENSBTAG00000012322	INKA1
0.761807858	2.97E-09	ENSBTAG00000008743	ALDH2
0.76168388	3.00E-09	ENSBTAG00000031889	NA
0.761636518	3.01E-09	ENSBTAG00000012052	PADI4
0.761629265	3.01E-09	ENSBTAG00000002764	IGFLR1
0.761583678	3.02E-09	ENSBTAG00000008479	CXCL13
0.761234934	3.10E-09	ENSBTAG00000039275	ERAP2
0.761018585	3.16E-09	ENSBTAG00000012720	ANKRD2
0.761010488	3.16E-09	ENSBTAG00000017713	KTN1
0.760819324	3.20E-09	ENSBTAG00000016081	NA
0.760765975	3.22E-09	ENSBTAG00000017425	GJB2
0.760408946	3.30E-09	ENSBTAG00000016073	UGCG
0.760146232	3.37E-09	ENSBTAG00000014002	CEP95
0.760076027	3.39E-09	ENSBTAG00000005761	DEDD2
0.75961665	3.51E-09	ENSBTAG00000021490	WDR4
0.759450247	3.55E-09	ENSBTAG00000003916	DPH3
0.757856868	4.00E-09	ENSBTAG00000007881	LOC100139670
0.757675242	4.05E-09	ENSBTAG00000047379	NA
0.757655096	4.06E-09	ENSBTAG00000025258	LOC515676
0.757513059	4.10E-09	ENSBTAG00000011596	SRSF5
0.757446223	4.12E-09	ENSBTAG00000042135	LOC112448925
0.757257265	4.18E-09	ENSBTAG00000020294	PTPN6
0.756870894	4.30E-09	ENSBTAG00000016355	DGAT2
0.75679937	4.32E-09	ENSBTAG00000004514	NA
0.756611849	4.38E-09	ENSBTAG00000006088	FAM104A
0.756607112	4.38E-09	ENSBTAG00000003366	DDX58
0.75635495	4.47E-09	ENSBTAG00000006043	LOC515755
0.756346671	4.47E-09	ENSBTAG00000011143	KPNA1
0.756247701	4.50E-09	ENSBTAG00000015649	TMEM156
0.756115161	4.55E-09	ENSBTAG00000012022	TBC1D2B
0.756081148	4.56E-09	ENSBTAG00000007075	LOC616942
0.756018237	4.58E-09	ENSBTAG00000010246	GRTP1
0.755990592	4.59E-09	ENSBTAG00000023851	FAM102A
0.755914451	4.61E-09	ENSBTAG00000043994	GRK6
0.755820957	4.65E-09	ENSBTAG00000021240	DCSTAMP
0.755802829	4.65E-09	ENSBTAG00000018200	IL15
0.755755985	4.67E-09	ENSBTAG00000025443	FNIP1
0.755738677	4.67E-09	ENSBTAG00000038124	FCGR2A
0.755716274	4.68E-09	ENSBTAG00000005273	IL1R1

0.755704081	4.69E-09	ENSBTAG00000008403	ROCK1
0.755115379	4.89E-09	ENSBTAG00000012297	RIPOR3
0.75483974	4.99E-09	ENSBTAG00000007883	NA
0.754522755	5.11E-09	ENSBTAG00000021381	DAAM2
0.754409352	5.15E-09	ENSBTAG00000004118	ALAS1
0.754190568	5.23E-09	ENSBTAG00000018035	TGFBR1
0.753998979	5.31E-09	ENSBTAG00000017233	NA
0.753777256	5.39E-09	ENSBTAG00000002129	KLF5
0.753766805	5.40E-09	ENSBTAG00000018238	ABTB1
0.75375604	5.40E-09	ENSBTAG00000022137	NA
0.753613341	5.46E-09	ENSBTAG00000035641	NA
0.753427057	5.53E-09	ENSBTAG00000005483	ESYT2
0.753406257	5.54E-09	ENSBTAG00000003532	TLE4
0.753177449	5.64E-09	ENSBTAG00000045767	LAT2
0.753047966	5.69E-09	ENSBTAG00000000878	RB1CC1
0.753002057	5.71E-09	ENSBTAG00000024493	DHRS3
0.752747006	5.81E-09	ENSBTAG00000019857	OTUD4
0.752617265	5.87E-09	ENSBTAG00000002103	PLCG2
0.752612519	5.87E-09	ENSBTAG00000020344	SLC44A3
0.752412652	5.96E-09	ENSBTAG00000013108	HK2
0.752321111	6.00E-09	ENSBTAG00000008406	TREX1
0.752169872	6.06E-09	ENSBTAG00000007356	ELF1
0.75176514	6.24E-09	ENSBTAG00000011524	XRN1
0.751664491	6.29E-09	ENSBTAG00000012191	WWC2
0.751443402	6.39E-09	ENSBTAG00000012266	NA
0.750867667	6.66E-09	ENSBTAG00000045529	NCR1
0.750712096	6.73E-09	ENSBTAG00000018898	ARID4A
0.750642973	6.77E-09	ENSBTAG00000015018	FSD2
0.750563452	6.80E-09	ENSBTAG00000030589	TMCO6
0.749737051	7.22E-09	ENSBTAG00000044856	LOC112442840
0.749548524	7.32E-09	ENSBTAG00000031387	FZR1
0.749546596	7.32E-09	ENSBTAG00000020283	DUSP5
0.749360925	7.42E-09	ENSBTAG00000047059	TIMM17A
0.74934569	7.42E-09	ENSBTAG00000012900	TMEM229B
0.749128455	7.54E-09	ENSBTAG00000020490	NACC2
0.748925593	7.65E-09	ENSBTAG00000019456	SPRED2
0.748643284	7.80E-09	ENSBTAG00000007935	CALCOCO2
0.748636733	7.81E-09	ENSBTAG00000004908	CHRNE
0.74861473	7.82E-09	ENSBTAG00000004066	PARP8
0.748535938	7.86E-09	ENSBTAG00000005814	PSME2
0.748364049	7.96E-09	ENSBTAG00000012223	TNFSF14
0.748336506	7.98E-09	ENSBTAG00000009232	PIK3CA
0.748109732	8.11E-09	ENSBTAG00000014903	ABCA3
0.747923728	8.21E-09	ENSBTAG00000017091	CMTR1
0.747894273	8.23E-09	ENSBTAG00000020713	BACH2
0.747782458	8.30E-09	ENSBTAG00000011957	CREBL2
0.747756822	8.31E-09	ENSBTAG00000024177	NA

0.747608291	8.40E-09	ENSBTAG00000004680	SLC13A5
0.747224026	8.63E-09	ENSBTAG00000048306	NA
0.747088957	8.71E-09	ENSBTAG00000010002	IRF2
0.746897102	8.83E-09	ENSBTAG00000013745	ITGA5
0.746892238	8.83E-09	ENSBTAG00000046981	NA
0.746630806	9.00E-09	ENSBTAG00000047839	P2RY8
0.746592822	9.02E-09	ENSBTAG00000005861	CCNT1
0.746585741	9.03E-09	ENSBTAG00000038619	LOC512672
0.74652116	9.07E-09	ENSBTAG00000037634	GBP4
0.746511448	9.07E-09	ENSBTAG00000014560	HLX
0.74647576	9.10E-09	ENSBTAG00000000873	SLC13A3
0.746443391	9.12E-09	ENSBTAG00000015092	NA
0.746388777	9.15E-09	ENSBTAG00000008471	MX2
0.746105104	9.34E-09	ENSBTAG00000008133	ALKBH1
0.745572452	9.69E-09	ENSBTAG00000001552	EPC1
0.745485271	9.75E-09	ENSBTAG00000020542	SHE
0.745423237	9.79E-09	ENSBTAG00000031998	CXCL16
0.745268866	9.90E-09	ENSBTAG00000031519	NGP
0.745239826	9.92E-09	ENSBTAG00000045592	NA
0.74468448	1.03E-08	ENSBTAG00000003508	CFAP69
0.744564827	1.04E-08	ENSBTAG00000015844	TFPI2
0.744423307	1.05E-08	ENSBTAG00000017068	DDA1
0.744296836	1.06E-08	ENSBTAG00000014228	TFEC
0.74363988	1.11E-08	ENSBTAG00000019069	SYNGR2
0.743582025	1.11E-08	ENSBTAG00000002416	LOC783604
0.742943773	1.16E-08	ENSBTAG00000011591	KRR1
0.742935895	1.16E-08	ENSBTAG00000021504	TIRAP
0.74283596	1.17E-08	ENSBTAG00000002996	SHROOM4
0.742735889	1.18E-08	ENSBTAG00000011829	NF1
0.74264582	1.19E-08	ENSBTAG00000030913	MX1
0.742428221	1.21E-08	ENSBTAG00000020791	RAPGEF1
0.742398521	1.21E-08	ENSBTAG00000020453	CLEC5A
0.742380831	1.21E-08	ENSBTAG00000042713	LOC112443329
0.742273254	1.22E-08	ENSBTAG00000007357	CHSY1
0.74207717	1.24E-08	ENSBTAG00000031851	SELPLG
0.741999273	1.24E-08	ENSBTAG00000000507	NR4A1
0.741925911	1.25E-08	ENSBTAG00000010235	NOP9
0.741868837	1.25E-08	ENSBTAG00000010587	SH3BGRL
0.741379266	1.30E-08	ENSBTAG00000029803	MIR221
0.74109064	1.32E-08	ENSBTAG00000018309	NA
0.741060971	1.33E-08	ENSBTAG00000023198	SERPINB2
0.740838929	1.35E-08	ENSBTAG00000001146	HIVEP2
0.740557079	1.37E-08	ENSBTAG00000007867	STAT1
0.740503788	1.38E-08	ENSBTAG00000030836	ZBTB21
0.74004382	1.42E-08	ENSBTAG00000020213	NIPAL4
0.739702895	1.45E-08	ENSBTAG00000023867	RC3H2
0.739678369	1.46E-08	ENSBTAG00000018112	TBL1X

0.739632304	1.46E-08	ENSBTAG00000007994	OSCP1
0.739597419	1.46E-08	ENSBTAG00000011600	MAP3K8
0.739589999	1.47E-08	ENSBTAG00000007956	FRAT1
0.739577285	1.47E-08	ENSBTAG00000032603	LOC515333
0.739366666	1.49E-08	ENSBTAG00000007268	F13A1
0.739282231	1.50E-08	ENSBTAG00000035584	NA
0.739110715	1.51E-08	ENSBTAG00000016804	LYST
0.738809167	1.55E-08	ENSBTAG00000020674	LTB
0.738751987	1.55E-08	ENSBTAG00000014526	MOB3A
0.738688019	1.56E-08	ENSBTAG00000018232	STOML3
0.738458413	1.58E-08	ENSBTAG00000006937	NA
0.738437552	1.59E-08	ENSBTAG00000007662	HSPA5
0.738376521	1.59E-08	ENSBTAG00000016513	ZNF331
0.738240097	1.61E-08	ENSBTAG00000003352	NA
0.738141815	1.62E-08	ENSBTAG00000010349	IL1A
0.738006971	1.63E-08	ENSBTAG00000039012	MFSD6L
0.737801233	1.65E-08	ENSBTAG00000026254	MED30
0.737435145	1.70E-08	ENSBTAG00000047710	NA
0.737302589	1.71E-08	ENSBTAG00000017461	SLC16A3
0.737010687	1.75E-08	ENSBTAG00000020000	RAP1GAP2
0.736973782	1.75E-08	ENSBTAG00000019910	SDCBP
0.736816192	1.77E-08	ENSBTAG00000000964	FCRL5
0.736297686	1.83E-08	ENSBTAG00000009948	TRIM25
0.736237893	1.84E-08	ENSBTAG00000046580	DHX58
0.736115693	1.85E-08	ENSBTAG00000012683	SRRM2
0.735915677	1.88E-08	ENSBTAG00000002147	PPP4R2
0.735858954	1.89E-08	ENSBTAG00000024903	KCNJ16
0.735740097	1.90E-08	ENSBTAG00000023963	RHBDD1
0.735716899	1.90E-08	ENSBTAG00000020041	FAM13B
0.735695555	1.91E-08	ENSBTAG00000019073	TRAF7
0.735694086	1.91E-08	ENSBTAG00000029905	NA
0.735638781	1.91E-08	ENSBTAG00000046406	R3HDM4
0.735528634	1.93E-08	ENSBTAG00000000995	TENT5A
0.735481217	1.93E-08	ENSBTAG00000016508	CTDSP2
0.735130426	1.98E-08	ENSBTAG00000015562	PLBD1
0.734935197	2.01E-08	ENSBTAG00000014529	GBP4
0.734906608	2.01E-08	ENSBTAG00000046294	NA
0.734796734	2.03E-08	ENSBTAG00000012417	ARL14EP
0.734276836	2.10E-08	ENSBTAG00000003327	RUFY4
0.734247864	2.10E-08	ENSBTAG00000003257	STK4
0.734130846	2.12E-08	ENSBTAG00000046090	LOC507247
0.734058792	2.13E-08	ENSBTAG00000046684	FOXN3
0.73404081	2.13E-08	ENSBTAG00000014857	LOC107131333
0.733687422	2.18E-08	ENSBTAG00000000737	DMXL2
0.733624219	2.19E-08	ENSBTAG00000014497	GPR31
0.733343615	2.23E-08	ENSBTAG00000002069	BOLA
0.733247505	2.24E-08	ENSBTAG00000005961	CDC42SE2

0.733127875	2.26E-08	ENSBTAG00000019345	RFK
0.732644256	2.34E-08	ENSBTAG00000048004	NA
0.732583959	2.35E-08	ENSBTAG00000044097	KLF7
0.732552709	2.35E-08	ENSBTAG00000047875	NA
0.731986433	2.44E-08	ENSBTAG00000019929	ITGAV
0.731968609	2.44E-08	ENSBTAG00000006135	MAP1LC3A
0.731486618	2.52E-08	ENSBTAG00000009982	IGSF8
0.731419725	2.53E-08	ENSBTAG00000012575	MAEA
0.731352209	2.54E-08	ENSBTAG00000003325	SNRK
0.73130026	2.55E-08	ENSBTAG00000000990	PSMA2
0.730916907	2.62E-08	ENSBTAG00000008959	NA
0.730520155	2.69E-08	ENSBTAG00000015772	STOML1
0.730496919	2.69E-08	ENSBTAG00000002866	RPIA
0.73036432	2.71E-08	ENSBTAG00000040244	APOL3
0.730301771	2.73E-08	ENSBTAG00000016896	HERPUD1
0.730261283	2.73E-08	ENSBTAG00000020257	PTPN5
0.730211242	2.74E-08	ENSBTAG00000042616	NA
0.730157808	2.75E-08	ENSBTAG00000002937	ADGRE3
0.729527072	2.87E-08	ENSBTAG00000021464	SPRYD3
0.729397151	2.89E-08	ENSBTAG00000031797	MANF
0.729312511	2.91E-08	ENSBTAG00000001763	NR2C2AP
0.729162264	2.94E-08	ENSBTAG00000018334	PLAGL2
0.728963778	2.97E-08	ENSBTAG00000016661	USP18
0.728879251	2.99E-08	ENSBTAG00000016852	SNIP1
0.728696834	3.03E-08	ENSBTAG00000012252	MOCOS
0.728446321	3.08E-08	ENSBTAG00000006729	NA
0.728432169	3.08E-08	ENSBTAG00000014825	NLK
0.728063253	3.15E-08	ENSBTAG00000008755	MARCHF7
0.727744146	3.22E-08	ENSBTAG00000014555	CASS4
0.72746316	3.28E-08	ENSBTAG00000003602	RBPJ
0.727280626	3.32E-08	ENSBTAG00000001390	B4GALT4
0.727235421	3.33E-08	ENSBTAG00000006368	N4BP3
0.726672814	3.45E-08	ENSBTAG00000016315	COTL1
0.726345275	3.52E-08	ENSBTAG00000038815	DIAPH2
0.726145618	3.57E-08	ENSBTAG00000014122	FOXRED1
0.725848945	3.64E-08	ENSBTAG00000003237	IQSEC1
0.725845996	3.64E-08	ENSBTAG00000046235	SRSF12
0.725806546	3.65E-08	ENSBTAG00000015543	ARHGAP35
0.725795471	3.65E-08	ENSBTAG00000007592	RARG
0.725625564	3.69E-08	ENSBTAG00000018137	NA
0.725482266	3.72E-08	ENSBTAG00000013843	ACVRL1
0.725052382	3.83E-08	ENSBTAG00000021574	TCF7L2
0.725025747	3.83E-08	ENSBTAG00000023279	N4BP2L2
0.724889682	3.87E-08	ENSBTAG00000018872	F12
0.724856396	3.88E-08	ENSBTAG00000009617	SLC2A1
0.724769643	3.90E-08	ENSBTAG00000003449	KCP
0.724736586	3.91E-08	ENSBTAG00000012406	ZBP1

0.724688338	3.92E-08	ENSBTAG00000045156	LOC112449177
0.724648462	3.93E-08	ENSBTAG00000039086	NA
0.724378365	4.00E-08	ENSBTAG00000004974	ZDHHC23
0.724252114	4.03E-08	ENSBTAG00000012441	SMAD7
0.724055599	4.08E-08	ENSBTAG00000044830	MIR339A
0.724005077	4.09E-08	ENSBTAG00000005029	TAL1
0.723803573	4.14E-08	ENSBTAG00000010874	GHSR
0.723573366	4.21E-08	ENSBTAG00000018848	FBXL3
0.723550471	4.21E-08	ENSBTAG00000008908	GZF1
0.723336117	4.27E-08	ENSBTAG00000011672	GABRR2
0.722986298	4.37E-08	ENSBTAG00000007970	C1H3orf38
0.722977733	4.37E-08	ENSBTAG00000021338	OAF
0.722875367	4.40E-08	ENSBTAG00000014172	FGD2
0.72287333	4.40E-08	ENSBTAG00000014790	ZBTB2
0.722780492	4.42E-08	ENSBTAG00000001483	SRGAP2
0.722715672	4.44E-08	ENSBTAG00000011131	NMUR2
0.722692852	4.45E-08	ENSBTAG00000046307	CEBPD
0.722651551	4.46E-08	ENSBTAG00000011446	SEMA7A
0.722543397	4.49E-08	ENSBTAG00000037800	APOBEC3Z1
0.722511681	4.50E-08	ENSBTAG00000024595	HECA
0.722295407	4.56E-08	ENSBTAG00000019675	ATXN1
0.72222101	4.58E-08	ENSBTAG00000015124	ARGLU1
0.721880893	4.68E-08	ENSBTAG00000016204	C1RL
0.721841955	4.69E-08	ENSBTAG00000007330	STXBP3
0.72177024	4.71E-08	ENSBTAG00000046885	NA
0.721723929	4.73E-08	ENSBTAG00000011684	RAB11FIP1
0.721438111	4.81E-08	ENSBTAG00000036391	MIR212
0.721372737	4.83E-08	ENSBTAG00000011437	SIK1
0.72127201	4.86E-08	ENSBTAG00000013184	CEP120
0.721051836	4.93E-08	ENSBTAG00000006859	LOC100336941
0.720894893	4.98E-08	ENSBTAG00000003665	NUP210
0.720679864	5.05E-08	ENSBTAG00000002010	PI4K2A
0.720477253	5.11E-08	ENSBTAG00000010166	MIC2
0.720235534	5.19E-08	ENSBTAG00000025129	MNT
0.720233109	5.19E-08	ENSBTAG00000018862	EIF4E3
0.720139961	5.22E-08	ENSBTAG00000008556	POU2F2
0.719567699	5.41E-08	ENSBTAG00000009912	PAN3
0.719560335	5.42E-08	ENSBTAG00000006089	C19H17orf80
0.719441063	5.46E-08	ENSBTAG00000008462	FAM43A
0.719417254	5.46E-08	ENSBTAG00000008293	GPCPD1
0.719212975	5.53E-08	ENSBTAG00000006128	DYNLT4
0.718918848	5.64E-08	ENSBTAG00000035975	NA
0.718794212	5.68E-08	ENSBTAG00000034676	HIGD1A
0.718654103	5.73E-08	ENSBTAG00000047604	HSD17B1
0.71801485	5.96E-08	ENSBTAG00000008967	RAP1B
0.71749335	6.16E-08	ENSBTAG00000024641	NA
0.717325626	6.22E-08	ENSBTAG00000031696	ANKRD44

0.717309811	6.23E-08	ENSBTAG00000000242	NA
0.717170955	6.28E-08	ENSBTAG00000021071	TRIM8
0.717136563	6.30E-08	ENSBTAG00000010792	SEH1L
0.717091322	6.31E-08	ENSBTAG00000000377	BMX
0.716982739	6.36E-08	ENSBTAG00000008648	PRDX5
0.716742713	6.45E-08	ENSBTAG00000011146	RAB8B
0.71637115	6.60E-08	ENSBTAG00000014306	DOP1B
0.716188702	6.67E-08	ENSBTAG00000002313	ITPR2
0.715937577	6.78E-08	ENSBTAG00000016060	CREM
0.715596697	6.92E-08	ENSBTAG00000020141	FREM1
0.715494438	6.97E-08	ENSBTAG00000017992	CD164
0.715416469	7.00E-08	ENSBTAG00000039937	NA
0.715380426	7.01E-08	ENSBTAG00000002243	SNX15
0.715193626	7.10E-08	ENSBTAG00000045885	MIR3064
0.714778422	7.28E-08	ENSBTAG00000004224	C7H19orf38
0.714518353	7.39E-08	ENSBTAG00000012208	BOLA
0.714471681	7.42E-08	ENSBTAG00000001519	METTL25B
0.714263348	7.51E-08	ENSBTAG00000017402	OSBPL2
0.714230469	7.53E-08	ENSBTAG00000011147	RNF13
0.714111387	7.58E-08	ENSBTAG00000001395	C1H21orf91
0.714087886	7.59E-08	ENSBTAG00000007111	STEAP3
0.714046013	7.61E-08	ENSBTAG00000012002	BCAR1
0.713989256	7.64E-08	ENSBTAG00000043268	LOC112441945
0.713943173	7.66E-08	ENSBTAG00000010065	TRPC5
0.713835475	7.71E-08	ENSBTAG00000017786	FCRL6
0.712598558	8.31E-08	ENSBTAG00000013270	TTC19
0.712374605	8.43E-08	ENSBTAG00000000711	NDRG1
0.71223035	8.50E-08	ENSBTAG00000006441	ATP5PB
0.712083056	8.58E-08	ENSBTAG00000016656	PARP14
0.711937595	8.65E-08	ENSBTAG00000001388	NA
0.711807664	8.72E-08	ENSBTAG00000047448	C25H16orf54
0.711664928	8.80E-08	ENSBTAG00000005476	NA
0.711597215	8.83E-08	ENSBTAG00000015509	NAMPT
0.71128539	9.00E-08	ENSBTAG00000007101	F3
0.711276227	9.00E-08	ENSBTAG00000019338	IL13RA1
0.711242564	9.02E-08	ENSBTAG00000031358	DPYD
0.711148881	9.07E-08	ENSBTAG00000013380	CEP192
0.710760958	9.29E-08	ENSBTAG00000010993	ZNF839
0.710625408	9.36E-08	ENSBTAG00000013706	MEGF9
0.710441677	9.47E-08	ENSBTAG00000020043	ARHGAP17
0.710323585	9.54E-08	ENSBTAG00000004987	NUP210L
0.710268443	9.57E-08	ENSBTAG00000011105	SLC38A2
0.710257124	9.57E-08	ENSBTAG00000009924	MR1
0.710143783	9.64E-08	ENSBTAG00000009177	PLEKHA4
0.710046808	9.70E-08	ENSBTAG00000039524	NA
0.709399599	1.01E-07	ENSBTAG00000017670	LOC511531
0.709319221	1.01E-07	ENSBTAG00000000132	EIF4A1

0.709285363	1.01E-07	ENSBTAG00000027809	RABGAP1L
0.709227573	1.02E-07	ENSBTAG00000037964	H2AW
0.708935985	1.04E-07	ENSBTAG00000001728	IGSF10
0.708595191	1.06E-07	ENSBTAG00000044099	ZSWIM7
0.708370674	1.07E-07	ENSBTAG00000008327	NA
0.708277312	1.08E-07	ENSBTAG00000039856	NA
0.708034945	1.09E-07	ENSBTAG00000039691	NA
0.707953982	1.10E-07	ENSBTAG00000001346	STRA8
0.707947401	1.10E-07	ENSBTAG00000016984	PTPN9
0.70794267	1.10E-07	ENSBTAG00000001576	TMEM140
0.707552212	1.13E-07	ENSBTAG00000017711	NA
0.707157068	1.15E-07	ENSBTAG00000011828	ARID3B
0.706957948	1.17E-07	ENSBTAG00000039319	CYP4F2
0.706452023	1.20E-07	ENSBTAG00000031750	PLAC8B
0.706374055	1.21E-07	ENSBTAG00000046701	FRAT2
0.70637306	1.21E-07	ENSBTAG00000038640	NA
0.706237846	1.22E-07	ENSBTAG00000002356	RBM47
0.706205121	1.22E-07	ENSBTAG00000012317	PNP
0.706153355	1.22E-07	ENSBTAG00000004136	NFE2L3
0.7060811	1.23E-07	ENSBTAG00000042974	LOC112441942
0.705951178	1.24E-07	ENSBTAG00000018722	PLEKHM2
0.705924195	1.24E-07	ENSBTAG00000021263	CYP4V2
0.705654866	1.26E-07	ENSBTAG00000010023	FAM107B
0.705419782	1.28E-07	ENSBTAG00000014628	OAS2
0.705202116	1.29E-07	ENSBTAG00000009470	CLIC4
0.705130377	1.30E-07	ENSBTAG00000013165	ENPP2
0.704770771	1.33E-07	ENSBTAG00000005989	LAP3
0.704733849	1.33E-07	ENSBTAG00000014614	ACTA2
0.704501322	1.35E-07	ENSBTAG00000000484	HYAL2
0.704430471	1.35E-07	ENSBTAG00000021289	POGZ
0.704009773	1.39E-07	ENSBTAG00000016526	PIH1D1
0.703868601	1.40E-07	ENSBTAG00000026070	LOC107131273
0.703692455	1.41E-07	ENSBTAG00000006851	LOC617565
0.703619396	1.42E-07	ENSBTAG00000025445	LOC789148
0.703570223	1.42E-07	ENSBTAG00000046700	NA
0.703536708	1.43E-07	ENSBTAG00000013023	MAP4K4
0.703492592	1.43E-07	ENSBTAG00000007863	GLS
0.703445523	1.43E-07	ENSBTAG00000037457	MBD2
0.702357604	1.53E-07	ENSBTAG00000006846	LGALS9
0.702306139	1.53E-07	ENSBTAG00000046765	POLR2A
0.702076449	1.55E-07	ENSBTAG00000007577	UBXN7
0.702010003	1.56E-07	ENSBTAG00000030974	TUBA4A
0.701996811	1.56E-07	ENSBTAG00000003758	TKT
0.701995009	1.56E-07	ENSBTAG00000010859	HYLS1
0.701587388	1.60E-07	ENSBTAG00000012938	JARID2
0.701237137	1.63E-07	ENSBTAG00000006056	HEXIM1
0.701039904	1.65E-07	ENSBTAG00000046699	STAT4

0.700831164	1.67E-07	ENSBTAG00000019796	FCMR
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0.700374165	1.71E-07	ENSBTAG00000003312	CHST15
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0.698642996	1.89E-07	ENSBTAG00000001269	TMEM165
0.698546234	1.90E-07	ENSBTAG00000033255	DUSP11
0.698377247	1.92E-07	ENSBTAG00000026233	NA
0.69825643	1.93E-07	ENSBTAG00000007130	ESF1
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0.697546748	2.01E-07	ENSBTAG00000002869	ARL4A
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0.697452465	2.02E-07	ENSBTAG00000015209	MXD4
0.697290664	2.04E-07	ENSBTAG00000010420	PCDH17
0.696908181	2.09E-07	ENSBTAG00000038650	MS4A7
0.696720066	2.11E-07	ENSBTAG00000014217	HHEX
0.6964982	2.14E-07	ENSBTAG00000038084	NA
0.696127537	2.18E-07	ENSBTAG00000043876	LOC112446144
0.695963322	2.20E-07	ENSBTAG00000024272	NA
0.695890787	2.21E-07	ENSBTAG00000047801	CRELD2
0.69555699	2.25E-07	ENSBTAG00000005165	CSGALNACT2
0.694783038	2.36E-07	ENSBTAG00000004484	CEP83
0.693704258	2.50E-07	ENSBTAG00000032493	RETREG3
0.693689675	2.51E-07	ENSBTAG00000020796	UBE2D1
0.693327938	2.56E-07	ENSBTAG00000010731	CDKN2D
0.693174902	2.58E-07	ENSBTAG00000014310	HEATR5B
0.693045049	2.60E-07	ENSBTAG00000021521	BFAR
0.692769827	2.64E-07	ENSBTAG00000027173	CHP1
0.692543852	2.67E-07	ENSBTAG00000016230	BRWD3
0.692541796	2.67E-07	ENSBTAG00000025471	TNF
0.692490383	2.68E-07	ENSBTAG00000038500	NA
0.692426529	2.69E-07	ENSBTAG00000032163	LTV1
0.692194024	2.72E-07	ENSBTAG00000001143	LOC512486
0.69213535	2.73E-07	ENSBTAG00000016061	RSAD2
0.6919797	2.76E-07	ENSBTAG00000003197	NA
0.691863671	2.77E-07	ENSBTAG00000019426	RNF175
0.691809392	2.78E-07	ENSBTAG00000021341	BTBD1
0.691389805	2.85E-07	ENSBTAG00000038576	GBP6
0.691370859	2.85E-07	ENSBTAG00000013196	STK17B
0.691267637	2.87E-07	ENSBTAG00000042475	LOC112448304
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0.690931095	2.92E-07	ENSBTAG00000001178	USPL1

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0.689003435	3.25E-07	ENSBTAG00000009778	KRAS
0.688812412	3.29E-07	ENSBTAG00000037452	LOC790312
0.68862194	3.32E-07	ENSBTAG00000005638	CABYR
0.688418103	3.36E-07	ENSBTAG00000005408	CLK1
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0.687141125	3.60E-07	ENSBTAG00000004135	LMTK2
0.687141014	3.60E-07	ENSBTAG00000001029	RASGRP2
0.68698914	3.63E-07	ENSBTAG00000046188	ELANE
0.686613842	3.71E-07	ENSBTAG00000015188	KLF6
0.686529113	3.72E-07	ENSBTAG00000000570	RET
0.686418662	3.75E-07	ENSBTAG00000008732	ZC3H12C
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0.686017586	3.83E-07	ENSBTAG00000011398	PRR7
0.685849199	3.86E-07	ENSBTAG00000019915	GSN
0.684895164	4.07E-07	ENSBTAG00000003961	SNX20
0.684818657	4.09E-07	ENSBTAG00000007816	LOC787045
0.684678601	4.12E-07	ENSBTAG00000011511	IFI16
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0.684091535	4.25E-07	ENSBTAG00000014508	FBXO40
0.683353639	4.42E-07	ENSBTAG00000004989	IRF5
0.682486353	4.63E-07	ENSBTAG00000014376	ANKRD13A
0.681738088	4.82E-07	ENSBTAG00000014884	HIPK3
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0.681294658	4.94E-07	ENSBTAG00000013578	CHI3L2
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0.680569426	5.14E-07	ENSBTAG00000017228	TP53I11
0.680537119	5.14E-07	ENSBTAG00000008411	PLEKHO2
0.680258346	5.22E-07	ENSBTAG00000025219	LOC100848263
0.680228021	5.23E-07	ENSBTAG00000020418	CA5B
0.680152125	5.25E-07	ENSBTAG00000027916	MALT1
0.680092222	5.27E-07	ENSBTAG00000002563	WDR45
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0.679887499	5.33E-07	ENSBTAG00000047575	NA
0.67972559	5.37E-07	ENSBTAG00000008805	USP3
0.679701932	5.38E-07	ENSBTAG00000019375	SCARF2
0.679404553	5.46E-07	ENSBTAG00000015083	FBXO9
0.679296192	5.50E-07	ENSBTAG00000010909	SLC30A1
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0.67925155	5.51E-07	ENSBTAG00000039950	NA
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0.679089486	5.56E-07	ENSBTAG00000019636	SCARA5
0.679013896	5.58E-07	ENSBTAG00000008279	FRMD4A
0.67900884	5.58E-07	ENSBTAG00000003341	DOK2
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0.678004703	5.88E-07	ENSBTAG00000015638	IL20RA
0.677990664	5.89E-07	ENSBTAG00000002738	S1PR2
0.677963638	5.90E-07	ENSBTAG00000011997	ZMIZ2
0.677891508	5.92E-07	ENSBTAG00000038488	TMSB4X
0.67784938	5.93E-07	ENSBTAG00000008909	PNPT1
0.677695306	5.98E-07	ENSBTAG00000026676	SDC3
0.677574959	6.02E-07	ENSBTAG00000008866	GANC
0.677516763	6.04E-07	ENSBTAG00000002845	CDH10
0.67750888	6.04E-07	ENSBTAG00000011095	FAR2
0.677506744	6.04E-07	ENSBTAG00000005251	LOC516599
0.677414564	6.07E-07	ENSBTAG00000019975	IL7R
0.677179703	6.15E-07	ENSBTAG00000012926	TM6SF1
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0.651276002	2.25E-06
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0.650944315	2.29E-06
0.650876432	2.30E-06
0.650541557	2.33E-06
0.650540423	2.33E-06
0.650537656	2.33E-06
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6.75E-30	1	ENSBTAG00000015363	CDC42SE1	0.808355202
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1.85E-06

MEturquoise
5.57E-11

Supplementary File S10: Details from gene significance (GS) for SCC related to the turquoise I

Ensembl_id	Gene_symbol	R_gene_significance_SCC	P_gene_significance_SCC
ENSBTAG00000000009	FOXF1	-0.30486444	0.046831231
ENSBTAG00000000012	TTC33	0.29307642	0.056479568
ENSBTAG00000000013	PRKAA1	0.470003667	0.001472283
ENSBTAG00000000015	FOXRED2	-0.088248825	0.573616127
ENSBTAG00000000016	LTA	-0.042684663	0.785792726
ENSBTAG00000000020	TRPV3	-0.240127839	0.120897945
ENSBTAG00000000021	WASHC3	-0.402155646	0.007510588
ENSBTAG00000000022	NUP37	-0.527275948	0.000280157
ENSBTAG00000000030	RDM1	-0.630831676	5.77E-06
ENSBTAG00000000031	TRPV4	-0.089251254	0.569253297
ENSBTAG00000000032	ABI3	-0.320006913	0.036442788
ENSBTAG00000000033	PHOSPHO1	-0.528196344	0.000272118
ENSBTAG00000000040	MAFG	0.564267852	8.11E-05
ENSBTAG00000000042	PYCR1	0.037470727	0.811450453
ENSBTAG00000000049	CCDC77	-0.383167293	0.011207049
ENSBTAG00000000053	FILIP1	-0.399101239	0.008022306
ENSBTAG00000000054	SNAPC4	0.171682802	0.270973424
ENSBTAG00000000056	STRADA	-0.458583819	0.00198307
ENSBTAG00000000064	FEN1	-0.531645338	0.00024381
ENSBTAG00000000065	CRLS1	0.198844156	0.20114528
ENSBTAG00000000067	SDF2L1	0.202662935	0.192450889
ENSBTAG00000000074	NFIA	-0.242035741	0.117883873
ENSBTAG00000000078	GLIPR2	0.300398926	0.05031567
ENSBTAG00000000079	CCSAP	-0.333872702	0.02866602
ENSBTAG00000000080	GRWD1	0.569206305	6.80E-05
ENSBTAG00000000084	MRPS30	-0.405055325	0.007051112
ENSBTAG00000000087	HSD17B12	0.077699106	0.620428432
ENSBTAG00000000088	ALCAM	0.390600356	0.0096076
ENSBTAG00000000090	SEC31B	-0.70790664	1.10E-07
ENSBTAG00000000095	CD274	0.456497973	0.002091653
ENSBTAG00000000098	SETDB1	0.654138333	1.96E-06
ENSBTAG00000000105	RIT1	-0.403773265	0.007251177
ENSBTAG00000000113	ARHGEF2	0.543938912	0.000163216
ENSBTAG00000000115	VPS54	-0.046730374	0.766035579
ENSBTAG00000000120	USP43	-0.270417706	0.079458768
ENSBTAG00000000128	FGF18	0.326452273	0.032636227
ENSBTAG00000000130	TNFSF13	0.209584421	0.177376918
ENSBTAG00000000131	SENP3	0.643009065	3.32E-06
ENSBTAG00000000132	EIF4A1	0.294730244	0.055037069
ENSBTAG00000000133	CD68	-0.404038325	0.007209417
ENSBTAG00000000137	FRYL	0.392823905	0.009168972
ENSBTAG00000000140	EPHX1	-0.148252387	0.342739572
ENSBTAG00000000141	NFU1	-0.530807813	0.000250428
ENSBTAG00000000144	LOC100335205	-0.366754631	0.015560472

ENSBTAG00000000146	FARP1	-0.265557699	0.08522917
ENSBTAG00000000152	RANBP2	0.440723788	0.003097313
ENSBTAG00000000153	LRFN3	0.013969254	0.929155408
ENSBTAG00000000156	NA	-0.619274301	9.54E-06
ENSBTAG00000000160	CBS	0.030540284	0.845854845
ENSBTAG00000000163	DDIT4	0.55664499	0.00010602
ENSBTAG00000000169	ASZ1	-0.33114308	0.030077155
ENSBTAG00000000170	GSTT4	-0.38806877	0.010128801
ENSBTAG00000000175	N4BP2	-0.529910726	0.000257696
ENSBTAG00000000176	SP3	0.445719891	0.002740624
ENSBTAG00000000181	SUSD3	0.474276325	0.001313551
ENSBTAG00000000182	SPINT2	-0.375281255	0.013147567
ENSBTAG00000000183	NA	-0.3099664	0.043092154
ENSBTAG00000000185	SLC6A14	-0.33522356	0.027988236
ENSBTAG00000000186	FLAD1	-0.363422052	0.016600515
ENSBTAG00000000191	SLC25A20	-0.33919327	0.026072994
ENSBTAG00000000199	PDP1	0.696226494	2.17E-07
ENSBTAG00000000202	SLC25A19	0.669972569	8.93E-07
ENSBTAG00000000203	ATP6V1G1	0.203022992	0.191645073
ENSBTAG00000000204	TMEM268	0.541210589	0.000178659
ENSBTAG00000000205	MMD	-0.591894956	2.91E-05
ENSBTAG00000000207	PUDP	-0.38796963	0.010149695
ENSBTAG00000000210	ARHGAP31	0.523830736	0.000312186
ENSBTAG00000000211	SHROOM2	0.000295802	0.998497949
ENSBTAG00000000218	MAP2K5	-0.596697617	2.41E-05
ENSBTAG00000000220	NA	-0.262577411	0.088925876
ENSBTAG00000000222	ARID4B	0.365761494	0.015864475
ENSBTAG00000000224	TSPAN15	0.044829914	0.775299029
ENSBTAG00000000225	POLB	0.370996471	0.014316962
ENSBTAG00000000226	DKK4	0.59535729	2.54E-05
ENSBTAG00000000231	BMPR1A	-0.256004217	0.097518059
ENSBTAG00000000240	AKAP7	0.303559076	0.047828955
ENSBTAG00000000241	STAU1	0.39410857	0.008923481
ENSBTAG00000000242	NA	0.282947149	0.065987895
ENSBTAG00000000243	HEBP2	-0.090123008	0.565471645
ENSBTAG00000000244	NRXN2	0.18750064	0.228586895
ENSBTAG00000000245	NHSL1	-0.267015536	0.083465018
ENSBTAG00000000250	HDHD3	0.292752004	0.056766053
ENSBTAG00000000251	ALAD	-0.141271978	0.366192659
ENSBTAG00000000253	PTPRF	-0.383213838	0.011196365
ENSBTAG00000000256	NA	0.502195553	0.000600467
ENSBTAG00000000266	NAB1	0.544638	0.000159459
ENSBTAG00000000275	PARP11	0.352673866	0.020363906
ENSBTAG00000000277	IL18	0.609322284	1.45E-05
ENSBTAG00000000281	MND1	-0.605380504	1.70E-05
ENSBTAG00000000283	CSF1	0.576918842	5.13E-05
ENSBTAG00000000285	GUF1	-0.36080218	0.017458847

ENSBTAG00000000286	PFKM	-0.357396532	0.01863035
ENSBTAG00000000287	GNPDA2	-0.559100902	9.73E-05
ENSBTAG00000000288	UPF2	0.191441045	0.218778071
ENSBTAG00000000290	ATP11B	0.417113515	0.005391185
ENSBTAG00000000292	TCIRG1	0.680883243	5.05E-07
ENSBTAG00000000295	CLHC1	-0.487074804	0.000925056
ENSBTAG00000000296	IMPDH1	0.213726873	0.168770811
ENSBTAG00000000297	ZNF330	-0.368562588	0.01501971
ENSBTAG00000000301	LOC538702	0.140672297	0.368251433
ENSBTAG00000000305	LMO4	-0.146761459	0.347669504
ENSBTAG00000000306	ITK	-0.274333349	0.075035931
ENSBTAG00000000308	ITCH	0.04489722	0.774970424
ENSBTAG00000000312	GRINA	0.231294631	0.135613388
ENSBTAG00000000313	NUDT13	-0.624160861	7.73E-06
ENSBTAG00000000320	UBAP1	0.558601568	9.91E-05
ENSBTAG00000000321	TBL2	-0.193634941	0.213444834
ENSBTAG00000000329	MEGF10	-0.017153579	0.913062169
ENSBTAG00000000332	ERF	0.515280959	0.000406385
ENSBTAG00000000333	ARHGAP20	0.40964119	0.006374031
ENSBTAG00000000336	LOC112442378	0.490322531	0.000844462
ENSBTAG00000000342	PLOD3	-0.29016222	0.059095001
ENSBTAG00000000343	ZNHIT1	-0.521555481	0.000335109
ENSBTAG00000000347	RHOG	0.593117893	2.77E-05
ENSBTAG00000000356	CCDC137	0.398402656	0.008143476
ENSBTAG00000000357	PRAG1	-0.458438948	0.001990447
ENSBTAG00000000359	EIF3J	0.289122895	0.060050852
ENSBTAG00000000369	EPS8	-0.67136175	8.32E-07
ENSBTAG00000000371	DIS3L	-0.613339506	1.23E-05
ENSBTAG00000000376	P2RX3	-0.37797757	0.012454188
ENSBTAG00000000377	BMX	0.53218469	0.000239632
ENSBTAG00000000379	GOLT1B	-0.456361143	0.002098956
ENSBTAG00000000380	NA	0.132551822	0.396808076
ENSBTAG00000000381	S1PR4	0.501323196	0.000615961
ENSBTAG00000000386	NA	0.361827834	0.01711846
ENSBTAG00000000390	TPST1	-0.604976207	1.73E-05
ENSBTAG00000000394	BACE2	-0.322075943	0.035183062
ENSBTAG00000000396	PIM1	0.483709266	0.001015742
ENSBTAG00000000404	NAXE	-0.421603361	0.004866331
ENSBTAG00000000406	GPATCH4	0.061623323	0.694646539
ENSBTAG00000000413	NRTN	-0.494390963	0.000752377
ENSBTAG00000000415	ERBIN	0.372707002	0.013839951
ENSBTAG00000000418	TOX3	-0.15358848	0.325450105
ENSBTAG00000000422	TSHZ1	-0.380903608	0.011737244
ENSBTAG00000000428	BAK1	0.551452263	0.00012673
ENSBTAG00000000429	DGCR2	0.542703611	0.000170052
ENSBTAG00000000431	NA	-0.197563495	0.204121844
ENSBTAG00000000432	NA	-0.359480885	0.017905753

ENSBTAG00000000434	CRYAB	-0.345410862	0.023293131
ENSBTAG00000000435	TARBP2	-0.176316757	0.258052968
ENSBTAG00000000436	TNFAIP3	0.280136188	0.068840038
ENSBTAG00000000440	HSPB2	-0.17279229	0.267841774
ENSBTAG00000000442	RBP4	0.026758734	0.86475173
ENSBTAG00000000446	ATP11A	0.402753336	0.007413821
ENSBTAG00000000447	FRA10AC1	-0.650699175	2.31E-06
ENSBTAG00000000448	BDH1	-0.3259146	0.032940691
ENSBTAG00000000451	TMEM126A	-0.086781881	0.580028007
ENSBTAG00000000454	TMEM106C	-0.302889776	0.04834715
ENSBTAG00000000460	SYTL2	-0.521258074	0.000338215
ENSBTAG00000000462	CCDC102A	0.135241352	0.387210727
ENSBTAG00000000472	ZNF570	-0.488483073	0.000889303
ENSBTAG00000000475	IMMP1L	-0.672303383	7.92E-07
ENSBTAG00000000477	TLR5	-0.193965769	0.21264852
ENSBTAG00000000480	IFRD2	0.268507058	0.081689704
ENSBTAG00000000483	HYAL1	0.492464234	0.000794804
ENSBTAG00000000484	HYAL2	0.430251878	0.003979501
ENSBTAG00000000489	WDR54	-0.503178904	0.000583421
ENSBTAG00000000490	RTKN	-0.419768497	0.005075186
ENSBTAG00000000494	PDE4D	-0.416086336	0.005517952
ENSBTAG00000000495	HAVCR2	-0.586818346	3.54E-05
ENSBTAG00000000496	SLC12A8	0.11908002	0.446918439
ENSBTAG00000000497	AKR1A1	-0.097304621	0.534768837
ENSBTAG00000000501	KLHL13	-0.248472821	0.108132623
ENSBTAG00000000504	GTF2B	0.511434681	0.000456544
ENSBTAG00000000505	KYAT3	0.372448633	0.013911123
ENSBTAG00000000507	NR4A1	0.453459847	0.002259196
ENSBTAG00000000510	ATG101	0.306468532	0.045628339
ENSBTAG00000000512	SNTA1	-0.379326372	0.012119194
ENSBTAG00000000517	ANKRD29	-0.505797066	0.00054013
ENSBTAG00000000521	PLEKHA8	-0.692911262	2.62E-07
ENSBTAG00000000524	CSTB	-0.081500084	0.603377731
ENSBTAG00000000527	ZFAND3	0.541460623	0.000177191
ENSBTAG00000000532	EXO5	-0.685978972	3.84E-07
ENSBTAG00000000533	ZNF684	-0.521579444	0.00033486
ENSBTAG00000000536	ZNF395	-0.332127347	0.029561835
ENSBTAG00000000539	LRRC28	-0.492130151	0.000802374
ENSBTAG00000000542	CFAP36	-0.687973495	3.44E-07
ENSBTAG00000000551	SMNDC1	0.349079569	0.021772313
ENSBTAG00000000552	DISP2	0.109948617	0.482761213
ENSBTAG00000000555	ACO1	-0.369825906	0.01465138
ENSBTAG00000000559	PLTP	-0.203197965	0.191254344
ENSBTAG00000000561	OCLN	-0.316766603	0.038489815
ENSBTAG00000000562	TOMM20	-0.076266367	0.62690749
ENSBTAG00000000563	MYD88	0.512197132	0.00044618
ENSBTAG00000000565	RFX7	-0.352439584	0.020453316

ENSBTAG00000000566	CCDC14	-0.535259282	0.000217025
ENSBTAG00000000569	HES1	0.215387848	0.165406217
ENSBTAG00000000570	RET	0.431068419	0.003903578
ENSBTAG00000000571	ARHGAP27	0.560646509	9.22E-05
ENSBTAG00000000575	TNC	0.148636776	0.341475556
ENSBTAG00000000576	ADGRG2	-0.231503449	0.135250813
ENSBTAG00000000579	NIPBL	0.362265602	0.016974892
ENSBTAG00000000581	DOCK10	-0.128408139	0.411861808
ENSBTAG00000000582	LY6G6E	-0.204167442	0.189099646
ENSBTAG00000000585	LY6G6C	-0.311548547	0.041983291
ENSBTAG00000000586	CPLANE1	-0.094090564	0.548408969
ENSBTAG00000000590	POLE	-0.425619519	0.004435134
ENSBTAG00000000595	FBN3	-0.015457497	0.921630123
ENSBTAG00000000598	CST3	-0.132588338	0.396676855
ENSBTAG00000000601	COL11A2	-0.5664858	7.50E-05
ENSBTAG00000000603	JAM2	-0.360705395	0.01749126
ENSBTAG00000000604	GPNMB	-0.558761148	9.85E-05
ENSBTAG00000000605	ATP5PF	-0.349884784	0.021449901
ENSBTAG00000000609	LOC509829	0.238517599	0.123486645
ENSBTAG00000000621	CATSPERG	-0.000224645	0.998859276
ENSBTAG00000000625	SMAD6	0.37126847	0.01424019
ENSBTAG00000000628	NA	-0.270920649	0.078879517
ENSBTAG00000000629	MMS22L	-0.587697473	3.42E-05
ENSBTAG00000000632	RAD54B	-0.391867956	0.009355392
ENSBTAG00000000634	MLPH	-0.282913255	0.066021718
ENSBTAG00000000638	CDT1	-0.336805631	0.027211404
ENSBTAG00000000639	APRT	0.745358674	9.84E-09
ENSBTAG00000000641	SKAP1	-0.617264129	1.04E-05
ENSBTAG00000000653	PPP1R16B	0.324766425	0.0335987
ENSBTAG00000000655	MIPOL1	-0.319640983	0.036669389
ENSBTAG00000000656	NFATC1	-0.089967311	0.566146202
ENSBTAG00000000658	NA	0.178924457	0.250966067
ENSBTAG00000000660	FAM83D	-0.185429282	0.23386221
ENSBTAG00000000662	TCF20	0.454269846	0.002213409
ENSBTAG00000000664	SLC22A15	-0.263359517	0.087943941
ENSBTAG00000000666	GHDC	-0.274278076	0.075096987
ENSBTAG00000000667	APOL3	-0.276042525	0.073167109
ENSBTAG00000000668	SLC22A5	-0.378962989	0.01220868
ENSBTAG00000000670	RRP9	0.593423441	2.74E-05
ENSBTAG00000000671	PARP3	0.663854911	1.22E-06
ENSBTAG00000000672	OTULINL	0.441811704	0.003016351
ENSBTAG00000000675	PGS1	0.449895653	0.002470744
ENSBTAG00000000679	PGM3	-0.471332165	0.001421197
ENSBTAG00000000682	RAPGEF6	0.067419874	0.667513131
ENSBTAG00000000683	WDR37	0.459842221	0.001919997
ENSBTAG00000000684	ARHGEF10L	0.470781428	0.001442181
ENSBTAG00000000687	POC1B	-0.462502063	0.001792486

ENSBTAG00000000697	RRP8	0.277767972	0.071317878
ENSBTAG00000000700	PARVA	-0.275586218	0.073662411
ENSBTAG00000000704	GUSB	-0.657324298	1.68E-06
ENSBTAG00000000706	ADAMTS1	-0.097466807	0.534084933
ENSBTAG00000000710	PIP5K1C	0.162730071	0.29712522
ENSBTAG00000000711	NDRG1	0.561012969	9.10E-05
ENSBTAG00000000713	AGFG2	-0.505876205	0.000538868
ENSBTAG00000000715	LOC530077	-0.258634515	0.094006274
ENSBTAG00000000717	PLPP2	0.056756002	0.71772665
ENSBTAG00000000718	TMPRSS9	-0.29100471	0.058329133
ENSBTAG00000000720	CTSL	-0.317845731	0.037797892
ENSBTAG00000000725	USP42	0.590408928	3.08E-05
ENSBTAG00000000731	WFIKKN2	0.385320711	0.010721818
ENSBTAG00000000735	BCL2A1	0.379353846	0.012112451
ENSBTAG00000000736	LRP8	-0.249184389	0.107093618
ENSBTAG00000000737	DMXL2	0.25459509	0.099440493
ENSBTAG00000000738	DAPK1	-0.371340877	0.014219812
ENSBTAG00000000742	AMOTL2	-0.363344978	0.016625247
ENSBTAG00000000746	KAT2B	0.55193646	0.000124654
ENSBTAG00000000748	GAR1	-0.010153373	0.948476718
ENSBTAG00000000752	SGO1	-0.67828356	5.80E-07
ENSBTAG00000000754	PPP2R5A	0.16145827	0.300967737
ENSBTAG00000000758	PACC1	-0.578755104	4.79E-05
ENSBTAG00000000759	NENF	-0.549759887	0.000134233
ENSBTAG00000000764	GIPC1	-0.085395654	0.586116638
ENSBTAG00000000770	PGM2L1	-0.555284456	0.000111126
ENSBTAG00000000771	DNAJB6	0.500032081	0.000639549
ENSBTAG00000000778	HSP90AB1	0.236932312	0.126075713
ENSBTAG00000000781	HIP1	0.237202101	0.125632247
ENSBTAG00000000782	KDR	-0.040483164	0.796600653
ENSBTAG00000000783	TGFA	0.324147706	0.033957745
ENSBTAG00000000785	PASK	-0.366927649	0.015508019
ENSBTAG00000000786	NQO2	0.217019343	0.162148918
ENSBTAG00000000793	LAMC2	-0.354506583	0.019675735
ENSBTAG00000000795	NMNAT2	-0.210791224	0.174837906
ENSBTAG00000000799	ICA1	-0.768202666	1.82E-09
ENSBTAG00000000802	LYVE1	-0.17465706	0.262632409
ENSBTAG00000000803	ZNF667	-0.513690474	0.000426492
ENSBTAG00000000804	MOB3B	-0.176365115	0.257920342
ENSBTAG00000000806	ATAD1	0.404584655	0.007123999
ENSBTAG00000000807	TMED3	-0.392737822	0.009185627
ENSBTAG00000000809	IRX1	-0.335790372	0.02770783
ENSBTAG00000000812	CD300A	0.587287179	3.47E-05
ENSBTAG00000000813	HOMER3	0.257923523	0.094945762
ENSBTAG00000000815	EPHA2	-0.192267885	0.216757356
ENSBTAG00000000816	PRDM1	0.328598963	0.031443668
ENSBTAG00000000817	SYNJ2	-0.021133444	0.892997256

ENSBTAG00000000819	RFX3	-0.113196833	0.469841872
ENSBTAG00000000820	GNG11	0.439728326	0.00317306
ENSBTAG00000000824	TSEN54	-0.05190142	0.740996185
ENSBTAG00000000825	MRPS26	-0.146351529	0.349032558
ENSBTAG00000000828	CAPN6	-0.360749803	0.017476382
ENSBTAG00000000829	SHPK	-0.428911457	0.004106935
ENSBTAG00000000831	CTNS	-0.194465637	0.21144924
ENSBTAG00000000833	TAX1BP3	-0.053122316	0.735121604
ENSBTAG00000000835	NA	-0.330711178	0.030305615
ENSBTAG00000000836	KRT8	-0.318141114	0.037610282
ENSBTAG00000000837	PARP1	-0.606220097	1.64E-05
ENSBTAG00000000838	CCDC88C	-0.243065586	0.116280713
ENSBTAG00000000842	UBASH3B	-0.331472036	0.029904107
ENSBTAG00000000843	NDRG2	-0.605825303	1.67E-05
ENSBTAG00000000851	CYP20A1	-0.510754579	0.00046597
ENSBTAG00000000853	NA	-0.019915513	0.899131166
ENSBTAG00000000854	SEC16B	-0.166689321	0.285366165
ENSBTAG00000000855	NXN	-0.600478503	2.07E-05
ENSBTAG00000000856	FBXL6	-0.317260032	0.038172159
ENSBTAG00000000859	SLC38A1	-0.059593662	0.704239195
ENSBTAG00000000868	ZFP1	-0.830300118	5.75E-12
ENSBTAG00000000873	SLC13A3	0.373338974	0.013667165
ENSBTAG00000000874	CAST	0.139020786	0.373957021
ENSBTAG00000000875	CEP131	-0.162141935	0.298898224
ENSBTAG00000000877	ETFBKMT	-0.468007694	0.001552097
ENSBTAG00000000878	RB1CC1	0.429853867	0.004016974
ENSBTAG00000000879	C14H8orf33	-0.068778851	0.661210383
ENSBTAG00000000892	CGAS	-0.112404033	0.472978045
ENSBTAG00000000894	PGK1	0.145178829	0.352949909
ENSBTAG00000000895	TAF9B	-0.131609038	0.400204742
ENSBTAG00000000897	IQGAP2	-0.064547828	0.680907378
ENSBTAG00000000898	F2RL2	-0.634394796	4.92E-06
ENSBTAG00000000899	TMEM17	-0.255671563	0.09796929
ENSBTAG00000000900	LRRC8C	0.157418814	0.313382604
ENSBTAG00000000905	RAB6B	0.314626989	0.039892358
ENSBTAG00000000913	UQCR10	-0.133395989	0.39378097
ENSBTAG00000000917	BMP1	0.146553024	0.348362161
ENSBTAG00000000918	ERMARD	-0.588485408	3.32E-05
ENSBTAG00000000920	DNAH17	0.264171338	0.086933624
ENSBTAG00000000928	SPECC1	-0.482755032	0.001042855
ENSBTAG00000000930	NA	0.009243724	0.953087357
ENSBTAG00000000933	CCDC183	-0.348703284	0.021924366
ENSBTAG00000000936	SLC39A2	0.136435382	0.38299402
ENSBTAG00000000937	ITPRID2	0.583454681	4.02E-05
ENSBTAG00000000942	SIPA1L2	-0.371236522	0.014249189
ENSBTAG00000000943	ZNF286A	-0.464013489	0.001723417
ENSBTAG00000000944	LPCAT1	0.061431935	0.695549104

ENSBTAG00000000945	ATP2C2	-0.313835545	0.04042162
ENSBTAG00000000946	MEAK7	0.064116192	0.682928908
ENSBTAG00000000949	DNAJC9	-0.481912047	0.001067342
ENSBTAG00000000951	JAKMIP3	-0.058471615	0.709561879
ENSBTAG00000000957	CDKN2AIP	0.38628063	0.010511382
ENSBTAG00000000959	ZSWIM1	0.233680564	0.131513496
ENSBTAG00000000961	NEURL2	0.338202311	0.02654057
ENSBTAG00000000962	STAP1	-0.291332269	0.058033516
ENSBTAG00000000964	FCRL5	0.34900818	0.021801093
ENSBTAG00000000970	ASIC1	-0.411966347	0.006052787
ENSBTAG00000000973	KCNJ15	0.299622812	0.050942078
ENSBTAG00000000974	IARS1	0.311688487	0.041886342
ENSBTAG00000000977	CADM1	-0.555828496	0.000109058
ENSBTAG00000000986	USH1C	-0.392703573	0.009192261
ENSBTAG00000000987	OTOG	0.205553412	0.186049287
ENSBTAG00000000988	BRCA2	-0.569618776	6.70E-05
ENSBTAG00000000990	PSMA2	0.294509276	0.055228073
ENSBTAG00000000993	N4BP2L1	-0.107478946	0.492706912
ENSBTAG00000000995	TENT5A	0.531394877	0.000245772
ENSBTAG00000001002	TCF7	-0.00492215	0.975009751
ENSBTAG00000001005	ZNF280B	-0.530598787	0.000252105
ENSBTAG00000001008	PRF1	-0.234967061	0.129341585
ENSBTAG00000001009	HCLS1	0.448179034	0.002578717
ENSBTAG00000001015	TM9SF4	0.639221944	3.95E-06
ENSBTAG00000001022	AMDHD2	0.168431166	0.280290183
ENSBTAG00000001023	ZNF598	0.529813495	0.000258495
ENSBTAG00000001024	ARID1A	0.166077036	0.287164572
ENSBTAG00000001027	SERPINH1	-0.246974988	0.110344787
ENSBTAG00000001029	RASGRP2	0.42878529	0.004119111
ENSBTAG00000001030	MTMR3	0.54728875	0.000145913
ENSBTAG00000001032	PYGM	-0.086413436	0.581643514
ENSBTAG00000001034	IL18R1	0.408304127	0.006565365
ENSBTAG00000001036	HIBADH	-0.50839909	0.000499983
ENSBTAG00000001037	MAP4K2	0.106052945	0.498497379
ENSBTAG00000001042	MXD1	0.535203999	0.000217414
ENSBTAG00000001050	LDLRAP1	-0.513022515	0.0004352
ENSBTAG00000001051	NA	0.650036071	2.39E-06
ENSBTAG00000001060	CXCR4	0.430310233	0.003974033
ENSBTAG00000001061	PRKCA	-0.406263852	0.006866908
ENSBTAG00000001066	PILRA	0.160521854	0.303817228
ENSBTAG00000001068	ZCWPW1	-0.497106727	0.000696012
ENSBTAG00000001077	OSBPL5	-0.382280295	0.011412308
ENSBTAG00000001078	SRL	-0.442755308	0.00294764
ENSBTAG00000001081	PALLD	-0.341227433	0.025134649
ENSBTAG00000001082	SH2D5	0.469469012	0.001493297
ENSBTAG00000001083	MAP3K20	-0.061125385	0.696995627
ENSBTAG00000001084	OR10H1	0.233682959	0.131509428

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ENSBTAG00000001092	PHOSPHO2	-0.5765085	5.21E-05
ENSBTAG00000001093	KLHL23	-0.511386531	0.000457206
ENSBTAG00000001094	MTUS2	0.072403956	0.644511379
ENSBTAG00000001097	FKBP7	-0.465101401	0.001675171
ENSBTAG00000001101	IFNLR1	-0.39636078	0.008506724
ENSBTAG00000001102	SERPINB10	0.198921888	0.200965599
ENSBTAG00000001104	CMTM4	0.414138173	0.005765504
ENSBTAG00000001107	CACYBP	-0.199613739	0.199371319
ENSBTAG00000001110	SLC16A5	0.440545335	0.003110774
ENSBTAG00000001112	SMOX	-0.383384466	0.011157277
ENSBTAG00000001113	NDUFAF7	-0.614417319	1.17E-05
ENSBTAG00000001114	PRKD3	-0.440667566	0.003101549
ENSBTAG00000001116	P4HA2	-0.266860249	0.083651568
ENSBTAG00000001117	ANKRD50	-0.494381188	0.000752587
ENSBTAG00000001119	ANKRD13B	-0.171396326	0.271785941
ENSBTAG00000001120	CORO6	0.450128831	0.002456389
ENSBTAG00000001124	GALC	0.65373298	2.00E-06
ENSBTAG00000001125	ADAMDEC1	0.156600849	0.315935483
ENSBTAG00000001126	BMP2K	0.418251698	0.005253683
ENSBTAG00000001131	SLC12A9	0.623732552	7.88E-06
ENSBTAG00000001133	VWA8	-0.649286377	2.48E-06
ENSBTAG00000001136	NA	0.390923434	0.009542771
ENSBTAG00000001138	NA	-0.213916783	0.168383632
ENSBTAG00000001139	ACHE	-0.327863712	0.031848005
ENSBTAG00000001140	IAH1	-0.521173231	0.000339106
ENSBTAG00000001141	ADAM17	0.583321839	4.04E-05
ENSBTAG00000001142	GNE	-0.537497595	0.000201799
ENSBTAG00000001143	LOC512486	0.358230165	0.018337639
ENSBTAG00000001146	HIVEP2	0.332501889	0.029367671
ENSBTAG00000001151	APLP1	-0.079300281	0.613221105
ENSBTAG00000001153	TLE2	-0.066563496	0.671496557
ENSBTAG00000001154	NA	0.465101633	0.001675161
ENSBTAG00000001156	ST3GAL1	-0.117289889	0.453827918
ENSBTAG00000001160	GMEB1	0.627763425	6.61E-06
ENSBTAG00000001161	SINHCAF	0.168693776	0.279530056
ENSBTAG00000001164	ACAD10	-0.516040028	0.000397092
ENSBTAG00000001165	AIFM2	-0.633322854	5.16E-06
ENSBTAG00000001173	PLXNA2	-0.039548909	0.801198743
ENSBTAG00000001174	MRPL15	0.205560239	0.18603435
ENSBTAG00000001178	USPL1	0.402484476	0.007457216
ENSBTAG00000001179	TEP1	0.244733792	0.113718886
ENSBTAG00000001181	RPS6KC1	-0.266497672	0.084088404
ENSBTAG00000001183	KLHL33	-0.50555894	0.000543945
ENSBTAG00000001185	KMT5B	0.422296407	0.004789415
ENSBTAG00000001186	SH2D4A	-0.291272656	0.058087226

ENSBTAG00000001187	RASL10A	-0.364294038	0.016322864
ENSBTAG00000001189	AP1B1	-0.322016164	0.03521895
ENSBTAG00000001191	CCL17	-0.201130773	0.195906708
ENSBTAG00000001192	STX12	-0.448837039	0.002536848
ENSBTAG00000001195	KCNH4	0.044006046	0.779324496
ENSBTAG00000001197	SLAMF7	-0.03829792	0.807366062
ENSBTAG00000001198	GIMAP7	-0.306420106	0.045664283
ENSBTAG00000001204	JCAD	-0.391893064	0.009350454
ENSBTAG00000001207	SERPINB8	-0.048547411	0.757208752
ENSBTAG00000001209	PHLDB2	-0.309827955	0.043190307
ENSBTAG00000001219	NA	-0.447025358	0.002653594
ENSBTAG00000001228	CEND1	-0.144161674	0.356369258
ENSBTAG00000001229	SLC25A22	0.457169183	0.002056153
ENSBTAG00000001231	CDHR1	-0.389094217	0.009914834
ENSBTAG00000001233	MPZL3	0.011784763	0.940212138
ENSBTAG00000001235	CD200R1L	-0.143635671	0.358145369
ENSBTAG00000001242	ADRB1	-0.215961817	0.164254921
ENSBTAG00000001243	AP3M2	0.003993891	0.979721523
ENSBTAG00000001244	PLAT	-0.159971911	0.305498707
ENSBTAG00000001246	ATP1A1	0.561553254	8.93E-05
ENSBTAG00000001250	TFAP2A	-0.354991183	0.019497076
ENSBTAG00000001252	HIVEP1	0.613743354	1.21E-05
ENSBTAG00000001255	CRYBB3	0.04709595	0.764257284
ENSBTAG00000001257	AGTPBP1	-0.579897703	4.59E-05
ENSBTAG00000001258	TMEM50B	0.270399097	0.079480264
ENSBTAG00000001269	TMEM165	0.442559209	0.002961805
ENSBTAG00000001273	NLRP3	0.50290942	0.000588049
ENSBTAG00000001274	PPM1L	-0.377690859	0.012526405
ENSBTAG00000001282	RALGAPA1	-0.66407072	1.20E-06
ENSBTAG00000001283	RIC1	0.462706174	0.001783018
ENSBTAG00000001286	ELMO3	0.126817426	0.417726245
ENSBTAG00000001288	MAOB	0.426082976	0.004387587
ENSBTAG00000001289	MRPL18	-0.549297935	0.00013635
ENSBTAG00000001292	LTF	-0.05915774	0.706305449
ENSBTAG00000001294	PPP1R15A	0.42437996	0.004564516
ENSBTAG00000001295	DEPDC5	0.437685865	0.003333578
ENSBTAG00000001298	STAMBPL1	-0.116408269	0.457251958
ENSBTAG00000001301	LRRC32	-0.095513739	0.542348795
ENSBTAG00000001302	MRPS28	0.049217095	0.753963163
ENSBTAG00000001303	HSPB8	-0.346799232	0.022707477
ENSBTAG00000001305	ATP2B2	-0.299335651	0.051175436
ENSBTAG00000001308	LOC522763	0.146979702	0.346945158
ENSBTAG00000001311	MORF4L2	0.184992078	0.234986208
ENSBTAG00000001314	TRMT6	0.199255943	0.200194698
ENSBTAG00000001321	IL1B	0.468367071	0.00153745
ENSBTAG00000001325	UPB1	0.31272573	0.041173426
ENSBTAG00000001333	PPARG	-0.726511706	3.49E-08

ENSBTAG00000001335	GHR	-0.090421724	0.564178499
ENSBTAG00000001338	CCR3	0.003277813	0.983356759
ENSBTAG00000001341	NA	-0.207126648	0.182629404
ENSBTAG00000001343	DEPDC1	-0.369529621	0.014737069
ENSBTAG00000001346	STRA8	0.630956958	5.74E-06
ENSBTAG00000001349	KIF1C	-0.411781768	0.006077765
ENSBTAG00000001350	LOC101906045	-0.26485002	0.086095942
ENSBTAG00000001354	INPP5E	-0.468387453	0.001536623
ENSBTAG00000001359	B3GNT7	-0.155950321	0.317975148
ENSBTAG00000001361	NA	-0.458368377	0.00199405
ENSBTAG00000001364	DPH6	-0.445666049	0.002744267
ENSBTAG00000001368	LGALS3BP	0.248500457	0.108092128
ENSBTAG00000001374	METTL27	-0.31939381	0.036823103
ENSBTAG00000001385	ZSCAN2	-0.247917634	0.108948608
ENSBTAG00000001388	NA	0.62735059	6.73E-06
ENSBTAG00000001390	B4GALT4	0.606107038	1.65E-05
ENSBTAG00000001395	C1H21orf91	0.33263549	0.029298668
ENSBTAG00000001396	ADAMTS7	0.036004221	0.818703639
ENSBTAG00000001408	CNRIP1	-0.300737898	0.05004404
ENSBTAG00000001410	GRAMD1B	-0.464248536	0.001712891
ENSBTAG00000001414	KCTD12	0.463205785	0.001760029
ENSBTAG00000001422	NA	-0.547842035	0.00014322
ENSBTAG00000001424	MSH6	-0.7039955	1.39E-07
ENSBTAG00000001441	NA	-0.303115055	0.048172226
ENSBTAG00000001444	TNXB	-0.592953324	2.79E-05
ENSBTAG00000001446	ABRACL	0.364242872	0.016339047
ENSBTAG00000001447	NA	0.288492462	0.06063664
ENSBTAG00000001457	TMEM267	-0.380840562	0.011752312
ENSBTAG00000001462	FLT4	0.69441295	2.41E-07
ENSBTAG00000001465	P2RY1	0.720592011	5.08E-08
ENSBTAG00000001468	SAMD4A	0.31048365	0.042727043
ENSBTAG00000001470	DTX2	0.561783672	8.86E-05
ENSBTAG00000001471	POC1A	-0.69664791	2.12E-07
ENSBTAG00000001473	ARVCF	0.186756282	0.230473144
ENSBTAG00000001475	MCUR1	-0.439950457	0.003156018
ENSBTAG00000001476	NA	0.147081594	0.346607295
ENSBTAG00000001481	IGSF9	-0.226782035	0.143626323
ENSBTAG00000001483	SRGAP2	0.35929416	0.017969682
ENSBTAG00000001484	LZTFL1	-0.56063774	9.22E-05
ENSBTAG00000001489	TUBA1A	-0.47133911	0.001420935
ENSBTAG00000001492	FYB1	0.526710121	0.000285205
ENSBTAG00000001497	MRAS	-0.512243324	0.000445559
ENSBTAG00000001500	FIGNL1	-0.456955098	0.002067417
ENSBTAG00000001504	NOP14	0.616633873	1.07E-05
ENSBTAG00000001505	GRK4	-0.342869021	0.02439807
ENSBTAG00000001509	ELK3	0.559060369	9.75E-05
ENSBTAG00000001510	CDK17	0.437689043	0.003333323

ENSBTAG00000001511	BCL6	0.610306623	1.39E-05
ENSBTAG00000001512	ZFP64	-0.277508257	0.071593842
ENSBTAG00000001517	KRT18	-0.296263239	0.053726511
ENSBTAG00000001518	ISG20L2	0.618392121	9.91E-06
ENSBTAG00000001519	METTL25B	0.499755296	0.00064471
ENSBTAG00000001520	MRPL24	-0.068293905	0.663456873
ENSBTAG00000001521	UQCRB	-0.240976865	0.119549577
ENSBTAG00000001523	YES1	-0.308883665	0.043864643
ENSBTAG00000001529	NSD3	0.478592405	0.001168822
ENSBTAG00000001533	HACE1	0.46033591	0.001895741
ENSBTAG00000001535	LIPH	-0.289108994	0.06006372
ENSBTAG00000001537	TSKU	0.369898783	0.014630368
ENSBTAG00000001543	BRI3BP	-0.256201796	0.097250809
ENSBTAG00000001545	SLC34A2	-0.075936814	0.628401734
ENSBTAG00000001548	NA	-0.370975867	0.014322792
ENSBTAG00000001551	PLEKHG3	0.6184511	9.88E-06
ENSBTAG00000001552	EPC1	0.208166167	0.180394471
ENSBTAG00000001562	NFE2	0.544970761	0.000157698
ENSBTAG00000001564	PDE4DIP	-0.52769917	0.000276434
ENSBTAG00000001567	LRRK1	0.345045463	0.023449347
ENSBTAG00000001568	PPIC	-0.387697667	0.010207203
ENSBTAG00000001570	CSF2	-0.027522424	0.860929119
ENSBTAG00000001572	NSUN7	-0.328586395	0.031450544
ENSBTAG00000001573	JMJD1C	0.459910986	0.001916602
ENSBTAG00000001576	TMEM140	0.316077453	0.038937086
ENSBTAG00000001578	ADPGK	0.427993492	0.004196249
ENSBTAG00000001579	AGO2	0.467371279	0.00157834
ENSBTAG00000001586	OTUD7B	-0.062191772	0.69196826
ENSBTAG00000001592	INSIG1	0.576619526	5.19E-05
ENSBTAG00000001593	OGFOD2	-0.482876052	0.001039381
ENSBTAG00000001595	MT1E	-0.559956962	9.45E-05
ENSBTAG00000001597	PITPNM2	-0.032103344	0.838068284
ENSBTAG00000001598	MAP7	-0.225155009	0.146599498
ENSBTAG00000001599	SV2A	-0.340118931	0.025642441
ENSBTAG00000001602	IL4R	0.532555758	0.000236795
ENSBTAG00000001604	NA	-0.361174081	0.017334769
ENSBTAG00000001607	TMEM41B	-0.127472327	0.415306126
ENSBTAG00000001608	NA	-0.63630155	4.52E-06
ENSBTAG00000001609	MAP2K6	-0.032866249	0.834273279
ENSBTAG00000001610	SLC4A1	0.045008902	0.774425248
ENSBTAG00000001614	ZNF174	-0.486904224	0.000929472
ENSBTAG00000001616	ZNF592	0.497138564	0.000695374
ENSBTAG00000001618	ALPK3	0.193975717	0.212624606
ENSBTAG00000001619	SERINC5	-0.186766254	0.230447805
ENSBTAG00000001621	NA	-0.370274894	0.014522334
ENSBTAG00000001626	CTPS1	-0.355462346	0.01932468
ENSBTAG00000001629	SCMH1	-0.225340843	0.146257636

ENSBTAG00000001631	KIFC1	-0.564206651	8.13E-05
ENSBTAG00000001634	PHF1	0.66237152	1.31E-06
ENSBTAG00000001635	CUTA	-0.082262019	0.599984358
ENSBTAG00000001637	FUNDC1	-0.109763497	0.483503056
ENSBTAG00000001640	EPB41L1	-0.234733028	0.129734679
ENSBTAG00000001644	MDN1	0.179762075	0.248717713
ENSBTAG00000001647	PLEKHJ1	0.627772506	6.61E-06
ENSBTAG00000001652	SLCO3A1	0.465033994	0.001678125
ENSBTAG00000001656	TMEM254	0.006801668	0.965472194
ENSBTAG00000001657	PICALM	-0.334651894	0.028273425
ENSBTAG00000001662	EHD3	-0.150650183	0.334901737
ENSBTAG00000001675	ITPKA	-0.378890358	0.012226634
ENSBTAG00000001683	NA	0.130071234	0.405781112
ENSBTAG00000001692	NDST1	-0.421887765	0.004834638
ENSBTAG00000001693	RPAP1	-0.449801113	0.002476586
ENSBTAG00000001694	TYRO3	-0.414066046	0.005774852
ENSBTAG00000001702	TMEM107	-0.492359456	0.000797172
ENSBTAG00000001710	CMTM8	0.291405903	0.057967227
ENSBTAG00000001712	CMTM7	0.486854013	0.000930776
ENSBTAG00000001714	MFSD9	-0.253562603	0.100867468
ENSBTAG00000001717	AURKB	-0.457239804	0.002052449
ENSBTAG00000001724	PTGR3	-0.679537715	5.43E-07
ENSBTAG00000001725	CXCL10	0.345310183	0.023336086
ENSBTAG00000001727	PRXL2B	-0.367126112	0.015448036
ENSBTAG00000001728	IGSF10	0.396950393	0.008400427
ENSBTAG00000001729	DUSP10	0.402483073	0.007457443
ENSBTAG00000001737	TUT7	0.463585962	0.001742711
ENSBTAG00000001748	TRIM45	-0.513378025	0.000430546
ENSBTAG00000001749	SENP2	0.510528138	0.000469147
ENSBTAG00000001752	FUCA2	-0.433340202	0.003698968
ENSBTAG00000001763	NR2C2AP	0.57486474	5.53E-05
ENSBTAG00000001770	ST8SIA5	-0.694444267	2.40E-07
ENSBTAG00000001774	SPRY2	-0.223640094	0.149408328
ENSBTAG00000001775	RINL	0.314948652	0.039678877
ENSBTAG00000001776	SIRT2	-0.3375347	0.026859492
ENSBTAG00000001778	NFKBIB	0.529015424	0.000265139
ENSBTAG00000001781	TOMM40	0.514169248	0.000420347
ENSBTAG00000001785	TGM3	0.427717465	0.004223435
ENSBTAG00000001786	HYKK	-0.587087948	3.50E-05
ENSBTAG00000001788	PDPN	-0.255627763	0.098028822
ENSBTAG00000001790	SAFB2	0.478855857	0.001160466
ENSBTAG00000001793	HSD11B1L	0.06624179	0.672995273
ENSBTAG00000001795	LONP1	0.259961811	0.092271641
ENSBTAG00000001796	CATSPERD	-0.296949243	0.053148227
ENSBTAG00000001801	SYT4	-0.417109296	0.005391701
ENSBTAG00000001805	TWSG1	-0.251140919	0.104276016
ENSBTAG00000001808	LACTB2	-0.48897404	0.000877131

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ENSBTAG00000001815	ARHGEF5	-0.284180769	0.06476618
ENSBTAG00000001817	TMEM161A	-0.288980475	0.06018279
ENSBTAG00000001818	MEF2B	-0.380107619	0.0119287
ENSBTAG00000001821	PRRC2C	0.354864021	0.019543825
ENSBTAG00000001822	SNX10	0.546096501	0.000151871
ENSBTAG00000001823	STC2	-0.079766736	0.611128183
ENSBTAG00000001824	SLC2A6	0.614517762	1.17E-05
ENSBTAG00000001826	SASH1	-0.292722746	0.056791948
ENSBTAG00000001828	SCRN2	-0.402682086	0.0074253
ENSBTAG00000001829	SLC17A9	0.151247564	0.332966484
ENSBTAG00000001832	MRPL10	-0.605330531	1.70E-05
ENSBTAG00000001834	PNKP	0.613675823	1.21E-05
ENSBTAG00000001835	GJA1	0.184226373	0.236963602
ENSBTAG00000001836	NA	-0.123196116	0.431252033
ENSBTAG00000001838	LRRC36	0.008057181	0.9591037
ENSBTAG00000001839	OCIAD2	-0.469710196	0.001483785
ENSBTAG00000001842	GSTM3	-0.51517984	0.000407637
ENSBTAG00000001843	WBP1	-0.560737655	9.19E-05
ENSBTAG00000001844	MOGS	-0.417045257	0.00539953
ENSBTAG00000001847	CNTLN	-0.486395058	0.000942767
ENSBTAG00000001848	KATNB1	-0.584490668	3.86E-05
ENSBTAG00000001856	POLR2C	0.457811714	0.002022669
ENSBTAG00000001858	NA	-0.366879947	0.015522465
ENSBTAG00000001861	SESTD1	-0.199851525	0.198825434
ENSBTAG00000001864	NR4A3	0.164916617	0.290593128
ENSBTAG00000001867	SACS	0.151333871	0.332687464
ENSBTAG00000001868	PCYT2	-0.168442452	0.28025749
ENSBTAG00000001872	ORC6	-0.22968405	0.138434188
ENSBTAG00000001874	DOCK3	0.057614618	0.713636466
ENSBTAG00000001877	HMGN5	-0.505463813	0.000545476
ENSBTAG00000001879	PER2	0.345927529	0.023073728
ENSBTAG00000001881	SLC10A1	0.467234996	0.001584011
ENSBTAG00000001882	CD79A	-0.042874869	0.784860772
ENSBTAG00000001885	NA	-0.37001313	0.014597451
ENSBTAG00000001886	PABIR2	-0.628606804	6.37E-06
ENSBTAG00000001887	STAM2	0.420820814	0.004954472
ENSBTAG00000001888	MED13L	0.442681372	0.002952973
ENSBTAG00000001889	C22H3orf14	-0.58825702	3.35E-05
ENSBTAG00000001890	RUBCN	-0.226469088	0.144194705
ENSBTAG00000001894	NEDD1	-0.665294796	1.13E-06
ENSBTAG00000001898	CCDC112	0.038357211	0.807073496
ENSBTAG00000001904	ZNF276	0.577519191	5.02E-05
ENSBTAG00000001906	FANCA	-0.603026469	1.87E-05
ENSBTAG00000001908	DLD	-0.52865719	0.000268171
ENSBTAG00000001912	TRPV5	-0.186215983	0.231848949
ENSBTAG00000001919	ZNF652	-0.625024956	7.45E-06

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ENSBTAG00000001927	ATP6V1C2	-0.097084655	0.535697073
ENSBTAG00000001928	PDIA6	0.454221581	0.002216114
ENSBTAG00000001931	TRABD	0.60321813	1.86E-05
ENSBTAG00000001932	CRAT	-0.340047404	0.025675498
ENSBTAG00000001938	CKS2	-0.629712699	6.06E-06
ENSBTAG00000001941	SEMA4D	0.586489552	3.58E-05
ENSBTAG00000001945	ARG2	0.054919384	0.726501814
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ENSBTAG00000001950	RDH11	-0.134597676	0.38949513
ENSBTAG00000001952	PROM2	-0.16806298	0.281358175
ENSBTAG00000001957	TRMT11	-0.519582736	0.000356199
ENSBTAG00000001961	MAP1B	0.41120326	0.006156632
ENSBTAG00000001969	CCDC39	-0.378865236	0.012232848
ENSBTAG00000001992	CYP51A1	0.172459329	0.268779067
ENSBTAG00000002002	NA	-0.737222067	1.72E-08
ENSBTAG00000002006	THBS1	-0.452942041	0.002288902
ENSBTAG00000002008	NA	-0.530993423	0.000248947
ENSBTAG00000002009	NA	-0.005331246	0.972933471
ENSBTAG00000002010	PI4K2A	0.587553622	3.44E-05
ENSBTAG00000002015	RPS6KA6	-0.286778022	0.062252745
ENSBTAG00000002019	SERPINB5	-0.303759761	0.047674457
ENSBTAG00000002020	CREBRF	0.38735507	0.010280044
ENSBTAG00000002025	AMIGO2	0.079823899	0.610871909
ENSBTAG00000002027	FAM167B	0.593231084	2.76E-05
ENSBTAG00000002028	DIPK1A	-0.48258465	0.001047764
ENSBTAG00000002029	IGSF5	-0.130252933	0.405119921
ENSBTAG00000002034	MFSD2B	0.030142531	0.847838643
ENSBTAG00000002035	NA	0.177970321	0.253543775
ENSBTAG00000002037	ATXN7L1	-0.545113376	0.000156949
ENSBTAG00000002041	SASH3	-0.272188848	0.077433588
ENSBTAG00000002044	SIRT3	-0.335338689	0.027931091
ENSBTAG00000002049	HADH	-0.659885791	1.48E-06
ENSBTAG00000002050	COA7	0.348411645	0.022042825
ENSBTAG00000002051	ARAP1	0.562258955	8.71E-05
ENSBTAG00000002052	PLOD1	0.368795475	0.014951225
ENSBTAG00000002056	MARS2	0.106666366	0.496002238
ENSBTAG00000002058	ASF1A	-0.718123184	5.92E-08
ENSBTAG00000002065	TFAP2C	0.038411476	0.806805752
ENSBTAG00000002068	TAGLN2	0.562764628	8.56E-05
ENSBTAG00000002069	BOLA	0.286902613	0.062134156
ENSBTAG00000002070	KLC3	-0.188606298	0.225804672
ENSBTAG00000002078	KDM4A	0.624278694	7.69E-06
ENSBTAG00000002080	CCN3	-0.280144221	0.068831751
ENSBTAG00000002082	MARCKS	0.442658002	0.002954661
ENSBTAG00000002083	AUTS2	-0.429407319	0.004059384
ENSBTAG00000002085	IL36G	-0.356098984	0.019093777

ENSBTAG00000002087	IL36A	-0.428451022	0.004151523
ENSBTAG00000002089	NA	-0.299318165	0.051189673
ENSBTAG00000002092	PI16	0.011871906	0.93977084
ENSBTAG00000002096	FCGR3A	0.430867306	0.003922159
ENSBTAG00000002100	GZMM	-0.210002699	0.176493921
ENSBTAG00000002101	GDE1	-0.321644907	0.035442503
ENSBTAG00000002103	PLCG2	0.412583788	0.005969878
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ENSBTAG00000002113	NA	-0.621153564	8.81E-06
ENSBTAG00000002117	KIF18A	-0.641497156	3.56E-06
ENSBTAG00000002123	MYO3A	-0.27467508	0.07465931
ENSBTAG00000002125	GNAL	0.256450041	0.096915827
ENSBTAG00000002126	PFKFB2	-0.327009358	0.032323221
ENSBTAG00000002127	TCP11L2	-0.011340019	0.942464617
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ENSBTAG00000002136	FCHO1	-0.189964497	0.22241894
ENSBTAG00000002144	ADRB2	0.221080855	0.154242958
ENSBTAG00000002147	PPP4R2	0.318680212	0.037269846
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ENSBTAG00000002154	GPR141	0.671803647	8.13E-07
ENSBTAG00000002163	PTGER2	0.651492221	2.23E-06
ENSBTAG00000002164	AXDND1	0.410132163	0.006304995
ENSBTAG00000002169	NA	-0.577040998	5.11E-05
ENSBTAG00000002177	PIKFYVE	-0.09523028	0.543553254
ENSBTAG00000002178	PPL	-0.318319147	0.037497575
ENSBTAG00000002179	CDIN1	-0.414913675	0.00566583
ENSBTAG00000002182	COX17	0.312375708	0.041412888
ENSBTAG00000002184	NA	-0.405728258	0.006948024
ENSBTAG00000002188	C25H16orf89	-0.324377388	0.033824093
ENSBTAG00000002190	DOCK8	0.249269592	0.10696972
ENSBTAG00000002191	RRP12	0.15611718	0.317451187
ENSBTAG00000002194	MYZAP	-0.305978946	0.045992787
ENSBTAG00000002199	CORIN	-0.331841521	0.029710723
ENSBTAG00000002202	CRAMP1	0.21648142	0.163217695
ENSBTAG00000002211	MAPK8IP3	-0.469488938	0.001492509
ENSBTAG00000002215	GFPT2	-0.350270832	0.02129675
ENSBTAG00000002219	ATAD3A	0.170930172	0.2731115
ENSBTAG00000002223	POP4	-0.453856681	0.002236661
ENSBTAG00000002224	UHRF1	-0.369924526	0.014622952
ENSBTAG00000002226	FBXO31	-0.17185592	0.270483194
ENSBTAG00000002227	LRIG3	-0.142913276	0.360593345
ENSBTAG00000002233	CPNE2	0.212219255	0.171867315
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ENSBTAG00000002243	SNX15	0.417211375	0.005379241

ENSBTAG00000002249	NAALADL1	0.347545258	0.022397903
ENSBTAG00000002251	NA	0.142485957	0.362046145
ENSBTAG00000002256	YEATS4	-0.2194482	0.157386398
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ENSBTAG00000002278	FBN1	-0.301093782	0.049760133
ENSBTAG00000002279	LUC7L3	0.216313502	0.16355237
ENSBTAG00000002282	EIF1	0.463590295	0.001742515
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ENSBTAG00000002286	DNAJC18	-0.552048362	0.000124179
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ENSBTAG00000002292	SMARCA1	-0.54849314	0.00014011
ENSBTAG00000002296	STING1	0.33551145	0.027845522
ENSBTAG00000002298	CKAP2L	-0.138520975	0.375694077
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ENSBTAG00000002302	CD59	-0.636181631	4.54E-06
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ENSBTAG00000002311	REEP6	-0.456223606	0.002106319
ENSBTAG00000002313	ITPR2	0.345122658	0.023416272
ENSBTAG00000002316	NIPA1	-0.528398093	0.000270384
ENSBTAG00000002321	AMT	-0.091450107	0.559737135
ENSBTAG00000002326	LGALS3	-0.394675057	0.008817038
ENSBTAG00000002328	KDM2B	-0.027779069	0.859645194
ENSBTAG00000002329	ASAP2	-0.407038967	0.006750968
ENSBTAG00000002331	DLGAP5	-0.276397187	0.072783953
ENSBTAG00000002332	LSM5	-0.327262061	0.032182056
ENSBTAG00000002333	HOPX	0.260336013	0.091787099
ENSBTAG00000002340	STEAP4	0.549724301	0.000134395
ENSBTAG00000002341	ETS1	-0.112902753	0.471003906
ENSBTAG00000002345	SETD1A	0.439518679	0.003189218
ENSBTAG00000002346	HSD3B7	0.05005976	0.749885173
ENSBTAG00000002347	MAST3	0.362138554	0.017016453
ENSBTAG00000002348	SLC4A4	-0.400000892	0.007868551
ENSBTAG00000002349	STX1B	0.291480108	0.057900486
ENSBTAG00000002350	PIK3R2	-0.484467426	0.000994649
ENSBTAG00000002352	GGA2	-0.318317124	0.037498854
ENSBTAG00000002355	LOC112441543	0.234792802	0.129634194
ENSBTAG00000002356	RBM47	0.410269242	0.006285836
ENSBTAG00000002357	TICAM2	0.247226801	0.109970495
ENSBTAG00000002361	TMCC2	-0.4193036	0.005129326
ENSBTAG00000002362	APOLD1	-0.005418755	0.972489355
ENSBTAG00000002363	SESN2	0.308071225	0.044451649
ENSBTAG00000002367	HCFC1R1	-0.28070594	0.068254197
ENSBTAG00000002381	ZDHHC5	0.617647471	1.02E-05

ENSBTAG00000002382	DDX10	-0.024758184	0.87477963
ENSBTAG00000002385	SLC35E4	0.621139813	8.81E-06
ENSBTAG00000002394	TMEM44	-0.120301258	0.442238021
ENSBTAG00000002395	HPS3	-0.456326105	0.00210083
ENSBTAG00000002398	NA	-0.660536173	1.44E-06
ENSBTAG00000002402	IGF2R	0.475092746	0.001285012
ENSBTAG00000002408	FHAD1	-0.156151044	0.317344916
ENSBTAG00000002411	CTNND1	0.41110145	0.006170603
ENSBTAG00000002416	LOC783604	0.504527799	0.000560744
ENSBTAG00000002417	RAB30	-0.529096732	0.000264455
ENSBTAG00000002418	TICRR	-0.336083848	0.027563564
ENSBTAG00000002422	BCL9	-0.203018673	0.191654724
ENSBTAG00000002425	SCN9A	0.279288511	0.069719005
ENSBTAG00000002428	PPA2	-0.61452223	1.17E-05
ENSBTAG00000002430	COL17A1	-0.185455515	0.233794885
ENSBTAG00000002432	ABHD13	0.495443589	0.000730063
ENSBTAG00000002435	PTPRE	0.649781651	2.42E-06
ENSBTAG00000002440	KIF7	-0.051642304	0.742244861
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ENSBTAG00000002450	NA	0.50769782	0.00051053
ENSBTAG00000002451	TTC39A	-0.354913224	0.019525725
ENSBTAG00000002455	KLHL8	0.525116682	0.000299864
ENSBTAG00000002464	PLCH2	-0.361409318	0.017256671
ENSBTAG00000002467	NA	-0.213647261	0.168933313
ENSBTAG00000002470	CCDC78	-0.558018109	0.000101084
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ENSBTAG00000002473	ANGPTL4	-0.640007852	3.82E-06
ENSBTAG00000002477	MRM2	0.120671674	0.440823752
ENSBTAG00000002478	AGMAT	0.407144325	0.006735341
ENSBTAG00000002480	NUDT1	-0.042531545	0.786543177
ENSBTAG00000002481	HAGHL	-0.474473035	0.001306623
ENSBTAG00000002485	TNS1	0.147737481	0.344437284
ENSBTAG00000002490	CHPT1	-0.534334031	0.000223617
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ENSBTAG00000002503	BSCL2	-0.434375011	0.003608921
ENSBTAG00000002508	GNG3	-0.178971523	0.250839372
ENSBTAG00000002522	SYT5	-0.278503077	0.070541328
ENSBTAG00000002524	MRI1	-0.112485904	0.472653664
ENSBTAG00000002526	BDH2	-0.735464781	1.94E-08
ENSBTAG00000002527	ZSWIM4	0.463848961	0.00173082
ENSBTAG00000002531	ARHGAP10	-0.314208091	0.040171778
ENSBTAG00000002539	TRIOBP	-0.019863572	0.899392894
ENSBTAG00000002554	TCAF1	-0.405101836	0.007043945
ENSBTAG00000002557	MRPL19	-0.513287732	0.000431724
ENSBTAG00000002561	CCDC120	0.019955136	0.898931523

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ENSBTAG00000002563	WDR45	0.455464325	0.002147381
ENSBTAG00000002564	DLG4	-0.25676707	0.09648932
ENSBTAG00000002566	PGPEP1	-0.434442734	0.003603095
ENSBTAG00000002570	PPP1R21	-0.606424875	1.63E-05
ENSBTAG00000002576	GLDN	0.071054942	0.650705993
ENSBTAG00000002579	FBL	0.405018579	0.007056779
ENSBTAG00000002580	MYH14	-0.20388851	0.189717809
ENSBTAG00000002594	ZNF436	-0.079253633	0.613430578
ENSBTAG00000002596	VSTM1	-0.261283085	0.090569561
ENSBTAG00000002599	MGARP	-0.517566321	0.000378984
ENSBTAG00000002600	EFCAB7	-0.69264728	2.66E-07
ENSBTAG00000002606	LGR4	-0.311822679	0.041793547
ENSBTAG00000002610	FKBP3	-0.569228603	6.79E-05
ENSBTAG00000002612	FANCM	-0.601711237	1.97E-05
ENSBTAG00000002613	MIS18BP1	-0.411012285	0.006182861
ENSBTAG00000002614	RUFY2	-0.651499117	2.23E-06
ENSBTAG00000002615	LONRF3	0.606795817	1.61E-05
ENSBTAG00000002620	DNA2	-0.29957711	0.05097916
ENSBTAG00000002623	SAMSN1	0.325663486	0.033083687
ENSBTAG00000002624	PSTPIP2	0.537348158	0.000202785
ENSBTAG00000002626	ARHGAP6	-0.512791154	0.000438253
ENSBTAG00000002628	SLC44A2	0.235024808	0.129244727
ENSBTAG00000002630	MRTFA	0.24632544	0.11131474
ENSBTAG00000002631	SCNN1A	-0.112106427	0.474158178
ENSBTAG00000002632	CSN2	-0.306708498	0.045450566
ENSBTAG00000002633	SEPTIN9	-0.233887171	0.131162873
ENSBTAG00000002639	ZDHHC7	0.025646879	0.870322496
ENSBTAG00000002640	KALRN	0.02920033	0.852541568
ENSBTAG00000002641	NA	0.512197764	0.000446172
ENSBTAG00000002647	RGS10	0.572445661	6.05E-05
ENSBTAG00000002650	ZPR1	0.673147242	7.59E-07
ENSBTAG00000002651	PKP2	-0.096029884	0.540158919
ENSBTAG00000002655	ZWINT	-0.492124468	0.000802504
ENSBTAG00000002660	NA	-0.573139588	5.90E-05
ENSBTAG00000002663	BCAS3	-0.524864771	0.000302243
ENSBTAG00000002668	ZNF711	-0.333216197	0.029000298
ENSBTAG00000002669	RASSF4	0.268104956	0.082165385
ENSBTAG00000002670	DEPP1	0.235359544	0.12868435
ENSBTAG00000002682	MARK4	0.277211964	0.071909702
ENSBTAG00000002683	PFKP	0.359664253	0.017843162
ENSBTAG00000002685	PITRM1	0.379066131	0.012183224
ENSBTAG00000002688	ATP1B1	-0.062356041	0.691194984
ENSBTAG00000002689	NME7	-0.383203135	0.011198821
ENSBTAG00000002690	BLZF1	0.373988018	0.013491624
ENSBTAG00000002699	KIT	-0.232644185	0.133282853
ENSBTAG00000002702	TSPAN32	0.3399146	0.025736969

ENSBTAG00000002703	ATP6V1A	-0.170353855	0.274756195
ENSBTAG00000002705	REC8	0.298388252	0.051951443
ENSBTAG00000002706	GSTZ1	-0.802635272	9.60E-11
ENSBTAG00000002707	IPO4	0.499688256	0.000645966
ENSBTAG00000002708	MRPL42	-0.199691659	0.199192321
ENSBTAG00000002714	GNAI1	-0.052638203	0.737449244
ENSBTAG00000002719	ORC1	-0.315901204	0.039052155
ENSBTAG00000002721	TUT4	-0.545866901	0.000153043
ENSBTAG00000002724	HORMAD1	0.427249145	0.004269911
ENSBTAG00000002736	DNMT1	-0.357887057	0.018457641
ENSBTAG00000002737	WFIKKN1	-0.542078001	0.000173612
ENSBTAG00000002738	S1PR2	0.47357895	0.001338372
ENSBTAG00000002742	MSH2	-0.673869257	7.31E-07
ENSBTAG00000002743	OSGEP	0.646913496	2.77E-06
ENSBTAG00000002745	APEX1	0.376401141	0.01285569
ENSBTAG00000002747	ABCA5	-0.372478768	0.013902806
ENSBTAG00000002755	ANKRD12	0.498060998	0.000677122
ENSBTAG00000002756	CDCA2	-0.555551559	0.000110106
ENSBTAG00000002758	NA	0.554546738	0.000113987
ENSBTAG00000002763	KMT2B	0.421753163	0.004849615
ENSBTAG00000002764	IGFLR1	0.595439086	2.53E-05
ENSBTAG00000002765	CYP24A1	0.302205565	0.048881571
ENSBTAG00000002767	GNB4	-0.285870158	0.063122325
ENSBTAG00000002770	TCN2	-0.037100904	0.813278115
ENSBTAG00000002773	CD300LF	0.599775505	2.13E-05
ENSBTAG00000002774	PTPN23	0.384820064	0.010832994
ENSBTAG00000002779	GABRP	-0.301254977	0.049631967
ENSBTAG00000002781	NA	-0.031506321	0.841040664
ENSBTAG00000002782	ZC3H7B	-0.357268173	0.018675767
ENSBTAG00000002783	PCYOX1	-0.612770846	1.26E-05
ENSBTAG00000002786	LOC781494	-0.312789694	0.041129788
ENSBTAG00000002788	RAB27B	-0.184493188	0.236273285
ENSBTAG00000002796	KLHL3	0.13587955	0.384953556
ENSBTAG00000002798	NABP2	0.427579692	0.004237061
ENSBTAG00000002808	PSMA3	-0.269388433	0.080654579
ENSBTAG00000002809	CAPN10	0.452800707	0.00229707
ENSBTAG00000002816	SARM1	0.541213937	0.000178639
ENSBTAG00000002817	SLC46A1	-0.115046223	0.462569229
ENSBTAG00000002820	RBBP7	-0.604914485	1.73E-05
ENSBTAG00000002821	NA	-0.424166567	0.004587119
ENSBTAG00000002823	MPZL1	-0.274959521	0.074346964
ENSBTAG00000002824	DPEP3	-0.609509234	1.44E-05
ENSBTAG00000002826	CLSPN	-0.391003937	0.009526676
ENSBTAG00000002827	ACAT2	-0.033679217	0.830233321
ENSBTAG00000002830	U2AF2	0.620573569	9.03E-06
ENSBTAG00000002834	CCDC69	0.502319418	0.000598295
ENSBTAG00000002835	SMAD1	-0.305120101	0.046637811

ENSBTAG00000002842	HEATR4	0.418908923	0.005175682
ENSBTAG00000002843	ACOT4	-0.561240225	9.03E-05
ENSBTAG00000002844	PPFIA3	-0.001672968	0.991504991
ENSBTAG00000002845	CDH10	0.453628674	0.002249584
ENSBTAG00000002846	TRAF3IP3	0.409651204	0.006372616
ENSBTAG00000002847	D2HGDH	-0.333932867	0.028635547
ENSBTAG00000002849	IRF6	-0.265031611	0.085872877
ENSBTAG00000002850	HEATR9	-0.11440963	0.465065753
ENSBTAG00000002858	ACBD7	-0.401638822	0.00759514
ENSBTAG00000002859	NA	-0.292195738	0.057259989
ENSBTAG00000002866	RPIA	0.635226523	4.74E-06
ENSBTAG00000002869	ARL4A	0.252133841	0.102867968
ENSBTAG00000002880	SORBS1	-0.059264439	0.705799508
ENSBTAG00000002882	LMNB1	0.354962905	0.019507464
ENSBTAG00000002885	MSR1	-0.619659623	9.39E-06
ENSBTAG00000002888	TMTC2	-0.163809439	0.293888996
ENSBTAG00000002894	TNFSF4	-0.705960702	1.24E-07
ENSBTAG00000002900	LOC511898	0.502265644	0.000599237
ENSBTAG00000002904	ZNF787	0.469149751	0.001505972
ENSBTAG00000002908	GNG4	0.287468547	0.061597749
ENSBTAG00000002910	ECHDC2	-0.429488084	0.004051685
ENSBTAG00000002912	NA	0.400069006	0.007857015
ENSBTAG00000002917	PRKAG2	0.19533382	0.209377506
ENSBTAG00000002918	RAD51	-0.655983875	1.79E-06
ENSBTAG00000002920	KAT6B	0.227545642	0.142246387
ENSBTAG00000002922	GAB2	0.496221492	0.000713955
ENSBTAG00000002923	CX3CR1	0.124942237	0.424699894
ENSBTAG00000002929	IRF4	-0.063112228	0.687639343
ENSBTAG00000002937	ADGRE3	0.386814974	0.010395781
ENSBTAG00000002938	CPED1	-0.398867866	0.008062611
ENSBTAG00000002939	FURIN	0.566386292	7.53E-05
ENSBTAG00000002941	FES	0.561195641	9.05E-05
ENSBTAG00000002942	SLC2A10	0.434748999	0.003576852
ENSBTAG00000002944	ATP5MC3	-0.300541283	0.05020145
ENSBTAG00000002947	LY9	-0.072597666	0.643623806
ENSBTAG00000002951	CD244	0.52218445	0.000328625
ENSBTAG00000002952	TBX19	-0.589367579	3.21E-05
ENSBTAG00000002953	TXN	-0.416524274	0.005463592
ENSBTAG00000002955	NA	-0.452298331	0.002326311
ENSBTAG00000002956	ZNF674	-0.67913833	5.54E-07
ENSBTAG00000002959	LRCH1	0.513566185	0.0004281
ENSBTAG00000002962	PPM1M	0.503681482	0.000574878
ENSBTAG00000002964	TXLNB	0.096454822	0.538359212
ENSBTAG00000002970	INTS6	0.330952257	0.030177917
ENSBTAG00000002974	FMO2	0.033645963	0.83039849
ENSBTAG00000002976	CD177	-0.208163062	0.180401118
ENSBTAG00000002977	ECE1	0.600548811	2.07E-05

ENSBTAG00000002980	GPT2	-0.122743862	0.432958224
ENSBTAG00000002981	PIMREG	-0.345348515	0.023319724
ENSBTAG00000002995	GMPPA	-0.467999309	0.001552441
ENSBTAG00000002996	SHROOM4	0.425657052	0.004431267
ENSBTAG00000003012	TRAF1	0.525519414	0.000296096
ENSBTAG00000003014	TRPV2	-0.489450135	0.000865471
ENSBTAG00000003015	SESN1	-0.243776317	0.115183973
ENSBTAG00000003016	PTPN7	0.463444489	0.001749138
ENSBTAG00000003018	FSTL3	-0.569743432	6.67E-05
ENSBTAG00000003033	GADD45G	0.547130964	0.000146689
ENSBTAG00000003035	IMPACT	-0.208946701	0.178729256
ENSBTAG00000003037	NA	0.62904036	6.25E-06
ENSBTAG00000003038	TAP2	0.595735835	2.50E-05
ENSBTAG00000003039	PSMB8	0.517085353	0.000384608
ENSBTAG00000003043	GNG2	-0.561104616	9.07E-05
ENSBTAG00000003045	BAMBI	0.257236411	0.095860561
ENSBTAG00000003049	MICALL2	-0.175374988	0.260644913
ENSBTAG00000003061	NA	-0.426223551	0.004373254
ENSBTAG00000003063	SYNJ1	0.628531234	6.39E-06
ENSBTAG00000003068	MSMO1	-0.116511738	0.456849383
ENSBTAG00000003069	MAN1C1	-0.561455409	8.96E-05
ENSBTAG00000003072	ACADVL	-0.496937925	0.000699402
ENSBTAG00000003074	SLC16A6	0.618501605	9.86E-06
ENSBTAG00000003075	DVL2	0.504507432	0.00056108
ENSBTAG00000003076	NT5DC1	-0.427935211	0.004201976
ENSBTAG00000003081	RWDD4	-0.45004242	0.0024617
ENSBTAG00000003083	SLC50A1	-0.455872333	0.002125229
ENSBTAG00000003088	LANCL3	0.10406523	0.506626507
ENSBTAG00000003089	RHPN2	-0.317693226	0.037895054
ENSBTAG00000003097	DENND4C	-0.59887256	2.21E-05
ENSBTAG00000003100	SMTN	0.009035058	0.954145217
ENSBTAG00000003109	ITM2B	0.013996083	0.929019692
ENSBTAG00000003113	NA	0.303944131	0.047532875
ENSBTAG00000003128	SPATA6	0.444663716	0.002812861
ENSBTAG00000003140	CRYGS	-0.194119095	0.212280158
ENSBTAG00000003143	TBCCD1	-0.485038644	0.000979016
ENSBTAG00000003144	KIAA0825	-0.584120847	3.92E-05
ENSBTAG00000003147	JAK1	0.351394918	0.020856021
ENSBTAG00000003148	MCM3AP	0.6064007	1.63E-05
ENSBTAG00000003151	DNAJB11	0.37208178	0.014012714
ENSBTAG00000003152	IFI27	0.255891823	0.097670336
ENSBTAG00000003155	IFI27L2	-0.070006535	0.655536358
ENSBTAG00000003160	LRCH4	0.215274461	0.165634345
ENSBTAG00000003161	YBEY	-0.498357049	0.000671355
ENSBTAG00000003162	CRYZ	-0.451620089	0.002366309
ENSBTAG00000003166	AXL	-0.121426267	0.43795041
ENSBTAG00000003169	FBXO24	-0.222224955	0.152067697

ENSBTAG00000003171	SHANK2	-0.276437938	0.072740029
ENSBTAG00000003174	NDUFAF4	-0.271648452	0.078047154
ENSBTAG00000003176	JAM3	-0.428626932	0.004134439
ENSBTAG00000003180	TMEM201	-0.2244462	0.147908832
ENSBTAG00000003183	NTN4	-0.447885209	0.002597609
ENSBTAG00000003189	CCDC6	-0.246976822	0.110342057
ENSBTAG00000003191	FSCN1	0.392486477	0.009234406
ENSBTAG00000003192	TBC1D16	-0.430375336	0.00396794
ENSBTAG00000003196	PAPSS2	-0.52853199	0.000269238
ENSBTAG00000003197	NA	0.159912115	0.305681893
ENSBTAG00000003200	CSPG4B	-0.118021463	0.450997229
ENSBTAG00000003212	NNAT	-0.017223468	0.912709319
ENSBTAG00000003215	KIF3B	-0.408236223	0.006575214
ENSBTAG00000003221	ATF7IP	0.306454665	0.045638629
ENSBTAG00000003222	ASNS	0.211971673	0.17237971
ENSBTAG00000003229	RPL23	0.430456606	0.003960345
ENSBTAG00000003231	LIM2	-0.379563234	0.012061167
ENSBTAG00000003237	IQSEC1	0.453022441	0.002284267
ENSBTAG00000003239	UTP20	0.291751565	0.057656857
ENSBTAG00000003240	C8H9orf152	0.095508539	0.54237088
ENSBTAG00000003242	ACAD9	-0.599841735	2.13E-05
ENSBTAG00000003244	CFAP92	-0.560004531	9.43E-05
ENSBTAG00000003245	BCAR3	0.284376509	0.064573993
ENSBTAG00000003255	CD4	-0.192746936	0.215592536
ENSBTAG00000003256	TOMM34	0.160467864	0.303982041
ENSBTAG00000003257	STK4	0.413408568	0.005860665
ENSBTAG00000003261	AURKC	-0.013819228	0.929914359
ENSBTAG00000003263	TBCA	-0.266016466	0.084670908
ENSBTAG00000003264	NR1H2	0.55123351	0.000127678
ENSBTAG00000003265	ADD3	-0.48787092	0.00090469
ENSBTAG00000003275	NA	-0.277601144	0.071495048
ENSBTAG00000003276	PRKCH	-0.106034175	0.49857383
ENSBTAG00000003279	NDUFA10	-0.294474037	0.055258582
ENSBTAG00000003289	LOC616364	0.461822218	0.001824343
ENSBTAG00000003290	SLC9A7	-0.143987876	0.356955514
ENSBTAG00000003291	RIMKLB	-0.139636827	0.371822615
ENSBTAG00000003297	OASL	-0.267363764	0.083047865
ENSBTAG00000003298	LZTS2	0.33941323	0.025970143
ENSBTAG00000003300	MFGE8	-0.225377531	0.146190213
ENSBTAG00000003305	NCF1	0.601474553	1.99E-05
ENSBTAG00000003312	CHST15	0.40298112	0.007377227
ENSBTAG00000003313	TNFRSF9	-0.389146665	0.009903995
ENSBTAG00000003314	SKA3	0.152332016	0.329471135
ENSBTAG00000003316	SYAP1	0.306887504	0.04531832
ENSBTAG00000003322	TTLL7	0.120526736	0.441376836
ENSBTAG00000003323	NOL6	0.522355499	0.000326882
ENSBTAG00000003325	SNRK	0.483564253	0.001019821

ENSBTAG00000003326	NAIP	0.559270191	9.68E-05
ENSBTAG00000003327	RUFY4	0.406799219	0.006786647
ENSBTAG00000003328	TAMM41	-0.553375682	0.000118666
ENSBTAG00000003329	FST	-0.29607275	0.053887982
ENSBTAG00000003330	ATL3	-0.461188661	0.001854481
ENSBTAG00000003336	TPD52L1	-0.39586096	0.008597736
ENSBTAG00000003339	ZBTB10	0.048985774	0.755083782
ENSBTAG00000003341	DOK2	0.506527998	0.00052857
ENSBTAG00000003345	FAT4	-0.181659351	0.243675276
ENSBTAG00000003352	NA	0.348415061	0.022041435
ENSBTAG00000003353	SLC6A2	0.494623572	0.000747395
ENSBTAG00000003358	MCFD2	-0.427124145	0.004282391
ENSBTAG00000003359	ELOVL5	0.348645033	0.021947984
ENSBTAG00000003361	METTL15	-0.528814005	0.00026684
ENSBTAG00000003362	HSP90B1	0.310666962	0.042598254
ENSBTAG00000003366	DDX58	0.233470987	0.131869875
ENSBTAG00000003375	TC2N	-0.203166548	0.191324459
ENSBTAG00000003386	NA	0.47199039	0.001396474
ENSBTAG00000003390	SF3A1	0.581418166	4.34E-05
ENSBTAG00000003396	MAFB	0.589990572	3.13E-05
ENSBTAG00000003397	CTBP2	0.612995443	1.24E-05
ENSBTAG00000003403	PADI2	-0.070410461	0.653673677
ENSBTAG00000003405	TP53I3	-0.632214263	5.43E-06
ENSBTAG00000003408	NA	-0.083311373	0.595324592
ENSBTAG00000003415	ESD	-0.619328966	9.52E-06
ENSBTAG00000003417	PHKG2	0.42232501	0.004786263
ENSBTAG00000003422	SNX5	-0.587063346	3.50E-05
ENSBTAG00000003424	BET1	-0.552173762	0.000123648
ENSBTAG00000003425	MGME1	-0.664835573	1.16E-06
ENSBTAG00000003436	RHBDF2	0.525029409	0.000300686
ENSBTAG00000003443	USP46	-0.627247029	6.76E-06
ENSBTAG00000003444	SYDE2	-0.075201024	0.631743195
ENSBTAG00000003446	EPHB4	-0.087638274	0.576280859
ENSBTAG00000003447	NA	-0.47296417	0.001360598
ENSBTAG00000003449	KCP	0.469381596	0.001496758
ENSBTAG00000003450	ATP6V1H	-0.531924504	0.000241639
ENSBTAG00000003454	RGS20	-0.194812684	0.210619381
ENSBTAG00000003455	ANKRD6	-0.040375424	0.797130571
ENSBTAG00000003457	ATF5	-0.142111622	0.363321705
ENSBTAG00000003458	CDCA7	-0.21871606	0.158811107
ENSBTAG00000003470	TTYH1	-0.628109085	6.51E-06
ENSBTAG00000003474	RAB15	-0.100578177	0.521047811
ENSBTAG00000003489	IPCEF1	0.523743223	0.000313041
ENSBTAG00000003491	SLC25A23	-0.236539308	0.126723813
ENSBTAG00000003494	DNAAF9	-0.316566843	0.038619028
ENSBTAG00000003495	KDM7A	0.533341656	0.000230887
ENSBTAG00000003496	AIG1	-0.134733914	0.389010964

ENSBTAG00000003499	ENPP4	0.469243359	0.001502246
ENSBTAG00000003505	DCN	-0.336242173	0.027485995
ENSBTAG00000003506	STEAP2	0.624970147	7.47E-06
ENSBTAG00000003508	CFAP69	0.574589229	5.59E-05
ENSBTAG00000003510	MMRN2	0.504796512	0.000556322
ENSBTAG00000003511	SLAIN1	-0.248807332	0.107643231
ENSBTAG00000003512	MYH7B	-0.058390971	0.709944958
ENSBTAG00000003514	HSF4	-0.098262059	0.530737676
ENSBTAG00000003519	NOL3	-0.234205966	0.13062323
ENSBTAG00000003521	KIAA0895L	-0.282401089	0.066534489
ENSBTAG00000003525	STXBP1	0.174170422	0.263985325
ENSBTAG00000003526	SYNE3	0.626962307	6.85E-06
ENSBTAG00000003528	NA	0.540355314	0.000183766
ENSBTAG00000003531	ABCA13	0.289073127	0.060096931
ENSBTAG00000003532	TLE4	0.432472422	0.00377599
ENSBTAG00000003536	MARCHF6	0.548208189	0.000141464
ENSBTAG00000003541	ZNF614	0.446681953	0.002676249
ENSBTAG00000003544	S1PR5	-0.281244865	0.067703692
ENSBTAG00000003545	TAF1D	0.115618348	0.460331681
ENSBTAG00000003548	GSTP1	-0.234233465	0.130576758
ENSBTAG00000003550	C29H11orf54	-0.570281903	6.54E-05
ENSBTAG00000003553	ZFP36L2	0.144754897	0.354372597
ENSBTAG00000003556	ZFYVE21	-0.256748522	0.096514234
ENSBTAG00000003557	CCDC117	-0.088360683	0.573128538
ENSBTAG00000003559	PPP1R13B	0.036460481	0.816445395
ENSBTAG00000003565	TRIM3	-0.086277046	0.582242052
ENSBTAG00000003572	F11	0.033565725	0.83079705
ENSBTAG00000003576	POLL	-0.261857197	0.089837608
ENSBTAG00000003578	DPCD	-0.450037838	0.002461982
ENSBTAG00000003579	FBXW4	-0.436604084	0.003421445
ENSBTAG00000003580	PSD	-0.028119005	0.857945138
ENSBTAG00000003581	SETD7	-0.200547899	0.197232817
ENSBTAG00000003585	CD47	0.524514479	0.000305579
ENSBTAG00000003586	MAN1A2	0.342392251	0.024610117
ENSBTAG00000003587	ELL	0.564256942	8.12E-05
ENSBTAG00000003588	ZFAND1	0.233834728	0.131251805
ENSBTAG00000003598	NA	0.352970983	0.020250988
ENSBTAG00000003601	ZMAT1	-0.595403743	2.54E-05
ENSBTAG00000003602	RBPJ	0.527203204	0.000280802
ENSBTAG00000003604	ADAMTSL4	0.043144785	0.783538769
ENSBTAG00000003606	GLI4	-0.717607648	6.11E-08
ENSBTAG00000003607	FAM20C	-0.222800051	0.150982807
ENSBTAG00000003608	SYCP2	-0.103336939	0.50962169
ENSBTAG00000003609	PBDC1	-0.107035842	0.494502467
ENSBTAG00000003610	DENND1A	-0.1245562	0.426143616
ENSBTAG00000003616	DCLRE1B	-0.457745108	0.002026117
ENSBTAG00000003619	SEC24D	-0.649085412	2.50E-06

ENSBTAG00000003622	ZKSCAN7	-0.367689386	0.015278862
ENSBTAG00000003629	ASPA	-0.458017729	0.002012035
ENSBTAG00000003632	CYP39A1	-0.126669408	0.418274337
ENSBTAG00000003634	CISD1	-0.457952623	0.00201539
ENSBTAG00000003636	LIPA	-0.532906183	0.000234144
ENSBTAG00000003639	ELMO2	0.548030713	0.000142313
ENSBTAG00000003642	PRDX1	-0.47359062	0.001337953
ENSBTAG00000003644	HSPBP1	0.237758258	0.124721758
ENSBTAG00000003650	NR4A2	0.420131546	0.005033254
ENSBTAG00000003651	OTOP1	-0.509512672	0.000483635
ENSBTAG00000003661	SLC35F2	-0.256796646	0.096449604
ENSBTAG00000003665	NUP210	0.409818833	0.006348977
ENSBTAG00000003667	TLN2	-0.222260674	0.15200015
ENSBTAG00000003668	RADX	-0.299761474	0.050829704
ENSBTAG00000003669	BNC2	0.13132743	0.401222577
ENSBTAG00000003675	ADGRL1	-0.213690152	0.168845751
ENSBTAG00000003682	DNAJB13	-0.087151549	0.578409177
ENSBTAG00000003692	UCP2	-0.261205991	0.090668203
ENSBTAG00000003693	SUN2	0.458824884	0.001970848
ENSBTAG00000003696	BICDL1	-0.381888072	0.011504091
ENSBTAG00000003699	ZFP3	-0.289909528	0.059326272
ENSBTAG00000003700	SLC5A10	0.03395031	0.828887112
ENSBTAG00000003701	NA	-0.450558328	0.002430141
ENSBTAG00000003705	FAM83G	-0.055063599	0.725811502
ENSBTAG00000003707	GRAP	0.449407498	0.002501036
ENSBTAG00000003709	ITGB8	-0.461127557	0.001857411
ENSBTAG00000003711	EPAS1	-0.225269662	0.146388511
ENSBTAG00000003712	FAM89B	0.166635941	0.285522662
ENSBTAG00000003718	HACL1	-0.652249301	2.15E-06
ENSBTAG00000003719	TDRD7	0.396624364	0.008459062
ENSBTAG00000003733	TM4SF5	-0.345736922	0.023154467
ENSBTAG00000003741	NEURL1	0.46736997	0.001578395
ENSBTAG00000003743	NA	0.47090577	0.00143742
ENSBTAG00000003748	CNOT2	-0.209076673	0.178453043
ENSBTAG00000003749	KCNMB4	-0.349869283	0.021456069
ENSBTAG00000003751	MACC1	-0.257077288	0.096073378
ENSBTAG00000003754	NA	0.553597705	0.000117765
ENSBTAG00000003758	TKT	0.554950185	0.000112414
ENSBTAG00000003759	PCNX3	0.532361989	0.000238272
ENSBTAG00000003760	NA	0.370963602	0.014326263
ENSBTAG00000003762	GNB5	-0.71557888	6.93E-08
ENSBTAG00000003763	MYO5C	-0.536010004	0.000211806
ENSBTAG00000003764	AKIRIN2	0.388005401	0.010142152
ENSBTAG00000003773	SLC25A13	-0.343397384	0.02416486
ENSBTAG00000003777	TIE1	-0.310459176	0.042744261
ENSBTAG00000003779	ZC4H2	-0.060869917	0.698201918
ENSBTAG00000003788	RCC1	-0.610138377	1.40E-05

ENSBTAG00000003791	LPAR3	0.507339042	0.000516004
ENSBTAG00000003793	NGLY1	-0.007915672	0.959821377
ENSBTAG00000003794	GNAO1	0.136921187	0.381286189
ENSBTAG00000003800	LRRC27	-0.31882369	0.037179667
ENSBTAG00000003802	TEKT3	-0.419835919	0.005067376
ENSBTAG00000003804	SCCPDH	-0.606541258	1.62E-05
ENSBTAG00000003806	ECM1	0.311985229	0.041681367
ENSBTAG00000003808	HDAC9	-0.550650016	0.000130238
ENSBTAG00000003813	BCS1L	0.303613182	0.047787262
ENSBTAG00000003815	EDEM2	-0.544484344	0.000160278
ENSBTAG00000003819	STK36	-0.434306105	0.003614857
ENSBTAG00000003820	GRAMD1A	0.523637821	0.000314073
ENSBTAG00000003822	CROCC	-0.05216494	0.739726966
ENSBTAG00000003825	PTPN12	0.486087431	0.000950881
ENSBTAG00000003826	SCN1B	-0.286975861	0.06206452
ENSBTAG00000003829	HPN	-0.235684502	0.128142083
ENSBTAG00000003832	MFAP2	-0.390623726	0.009602898
ENSBTAG00000003833	SLC35G2	-0.585390075	3.73E-05
ENSBTAG00000003836	ADAM19	0.530717614	0.00025115
ENSBTAG00000003837	RSPO1	-0.357139274	0.01872147
ENSBTAG00000003838	NA	0.011161978	0.943366466
ENSBTAG00000003840	GUCY1B1	-0.498172459	0.000674946
ENSBTAG00000003842	RABGEF1	0.356887603	0.018810975
ENSBTAG00000003845	CSRNP1	0.429767821	0.004025116
ENSBTAG00000003851	CCNL1	0.542676145	0.000170207
ENSBTAG00000003855	FAM120C	-0.453668862	0.002247302
ENSBTAG00000003857	SUSD6	0.589505969	3.19E-05
ENSBTAG00000003861	GPATCH11	-0.403918885	0.007228209
ENSBTAG00000003863	PCED1A	-0.250354801	0.105401213
ENSBTAG00000003865	CASR	-0.185165316	0.234540393
ENSBTAG00000003871	CYP2B6	-0.25839331	0.09432419
ENSBTAG00000003876	MCU	0.274287649	0.075086409
ENSBTAG00000003877	ZCCHC24	-0.247588333	0.109434808
ENSBTAG00000003878	ZUP1	0.078549988	0.616593951
ENSBTAG00000003880	EMILIN2	0.396719459	0.008441923
ENSBTAG00000003887	ECHDC1	-0.671517373	8.25E-07
ENSBTAG00000003889	PER1	-0.036897357	0.81428446
ENSBTAG00000003891	NA	0.421442808	0.004884303
ENSBTAG00000003892	LOC537017	0.098717595	0.528824934
ENSBTAG00000003894	NDRG4	-0.322431231	0.034970388
ENSBTAG00000003895	NA	0.494295759	0.000754425
ENSBTAG00000003901	DNMT3B	-0.343402386	0.024162662
ENSBTAG00000003902	ZNF512	-0.576491558	5.21E-05
ENSBTAG00000003907	TSPAN14	0.497027801	0.000697595
ENSBTAG00000003908	MAPRE1	0.276436619	0.07274145
ENSBTAG00000003914	MVB12A	-0.6030534	1.87E-05
ENSBTAG00000003915	LARP6	-0.202840783	0.192052561

ENSBTAG00000003916	DPH3	0.48521263	0.000974298
ENSBTAG00000003920	TGM1	-0.077594987	0.620898326
ENSBTAG00000003922	MPHOSPH8	0.44490922	0.002795923
ENSBTAG00000003923	GPBAR1	0.576749708	5.16E-05
ENSBTAG00000003928	ATG16L1	0.329252716	0.031087718
ENSBTAG00000003934	PSPC1	0.459880544	0.001918105
ENSBTAG00000003935	TMBIM1	0.44980282	0.00247648
ENSBTAG00000003936	PNKD	0.574721446	5.56E-05
ENSBTAG00000003942	PIP4K2C	-0.348857644	0.021861884
ENSBTAG00000003943	TTC39B	-0.358951835	0.018087381
ENSBTAG00000003946	NECAB3	-0.467112146	0.001589138
ENSBTAG00000003947	SSBP4	0.257468706	0.095550534
ENSBTAG00000003948	FDPS	0.381435326	0.01161082
ENSBTAG00000003950	PROC	-0.431741388	0.00384196
ENSBTAG00000003952	FBXL2	-0.509962759	0.000477165
ENSBTAG00000003953	ZNF316	0.405784999	0.006939391
ENSBTAG00000003955	MYO7A	-0.205625031	0.185892619
ENSBTAG00000003956	SGCA	-0.592193683	2.87E-05
ENSBTAG00000003957	NA	0.272766941	0.076781413
ENSBTAG00000003958	TMEM220	-0.276698444	0.072459735
ENSBTAG00000003959	ARHGAP24	-0.565100747	7.88E-05
ENSBTAG00000003960	CCP110	-0.365495116	0.015946865
ENSBTAG00000003961	SNX20	0.323372386	0.034412119
ENSBTAG00000003963	FER1L5	-0.621771241	8.57E-06
ENSBTAG00000003965	LIPT1	-0.348777812	0.02189418
ENSBTAG00000003966	DUSP3	-0.153488399	0.32576926
ENSBTAG00000003970	MITD1	0.148224141	0.34283257
ENSBTAG00000003971	E2F1	-0.300136914	0.050526443
ENSBTAG00000003975	LMAN2L	-0.444733009	0.002808071
ENSBTAG00000003977	SLC52A3	-0.03678028	0.814863428
ENSBTAG00000003981	RRP1	0.533682518	0.000228366
ENSBTAG00000003983	TOM1L2	-0.399741704	0.007912585
ENSBTAG00000003986	CXXC5	-0.15007207	0.3367812
ENSBTAG00000003989	GSTO1	-0.51928265	0.00035951
ENSBTAG00000003990	ITPRIP	0.242462265	0.117217889
ENSBTAG00000003994	IGFBP3	-0.091757436	0.558413022
ENSBTAG00000003997	UBE2D4	-0.598004778	2.29E-05
ENSBTAG00000004005	WDR7	0.246760147	0.11066489
ENSBTAG00000004009	PMM1	-0.425726512	0.004424118
ENSBTAG00000004010	PAPPA	-0.442184622	0.00298903
ENSBTAG00000004011	GALK2	-0.469552991	0.001489979
ENSBTAG00000004015	KAT6A	0.563780766	8.26E-05
ENSBTAG00000004017	PLEKHG2	0.311786315	0.041818676
ENSBTAG00000004018	DGKA	-0.186574549	0.230935279
ENSBTAG00000004019	PMEL	-0.655331711	1.85E-06
ENSBTAG00000004022	PLAG1	-0.215129576	0.165926176
ENSBTAG00000004029	NA	0.049896102	0.750676657

ENSBTAG00000004034	SESN3	-0.657372893	1.68E-06
ENSBTAG00000004035	SDK1	-0.351703379	0.020736427
ENSBTAG00000004037	JUN	0.5873762	3.46E-05
ENSBTAG00000004038	ABAT	0.372266453	0.013961495
ENSBTAG00000004041	ANKRD10	-0.043392272	0.782327148
ENSBTAG00000004043	LOC407171	0.620368742	9.11E-06
ENSBTAG00000004046	DTX4	-0.451840816	0.002353226
ENSBTAG00000004051	SBDS	0.124110871	0.427812497
ENSBTAG00000004064	BPNT1	0.282039079	0.066898827
ENSBTAG00000004066	PARP8	0.389834926	0.009762702
ENSBTAG00000004073	MTA3	-0.528697872	0.000267825
ENSBTAG00000004075	IDI1	0.167196535	0.283881935
ENSBTAG00000004085	ASF1B	-0.574503722	5.61E-05
ENSBTAG00000004086	SPINT1	-0.180236967	0.24744904
ENSBTAG00000004091	GTF3C4	0.178554191	0.251964283
ENSBTAG00000004092	AK8	-0.601941372	1.96E-05
ENSBTAG00000004093	NA	-0.49419332	0.000756634
ENSBTAG00000004097	A2ML1	-0.564283994	8.11E-05
ENSBTAG00000004099	CCDC170	0.362562976	0.016877949
ENSBTAG00000004100	TTI1	-0.439828611	0.003165356
ENSBTAG00000004104	RUNX2	-0.538829798	0.000193202
ENSBTAG00000004108	CENPX	-0.387410648	0.010268197
ENSBTAG00000004111	LRRC45	-0.270592541	0.07925703
ENSBTAG00000004112	GAMT	-0.219052582	0.158155088
ENSBTAG00000004114	MAP3K11	0.482375083	0.001053829
ENSBTAG00000004115	MYLIP	0.324012089	0.034036866
ENSBTAG00000004118	ALAS1	0.230060113	0.137771682
ENSBTAG00000004124	CPOX	0.381744148	0.011537928
ENSBTAG00000004135	LMTK2	0.42188523	0.00483492
ENSBTAG00000004136	NFE2L3	0.292446964	0.057036489
ENSBTAG00000004138	BICRA	0.241341523	0.118973946
ENSBTAG00000004139	BACH1	0.504706627	0.000557798
ENSBTAG00000004140	STKLD1	-0.492891696	0.000785211
ENSBTAG00000004150	NRG1	0.282001758	0.066936478
ENSBTAG00000004154	SKIL	0.535449949	0.000215689
ENSBTAG00000004155	SPATA20	-0.343669278	0.024045578
ENSBTAG00000004165	NA	-0.436668649	0.003416144
ENSBTAG00000004168	STON1	-0.131382367	0.401023895
ENSBTAG00000004172	SETD1B	0.357971186	0.018428156
ENSBTAG00000004177	TANC1	-0.533931545	0.00022654
ENSBTAG00000004178	ACOX2	-0.084646872	0.589417286
ENSBTAG00000004184	WDSUB1	-0.619007718	9.65E-06
ENSBTAG00000004189	MLXIP	0.479920253	0.001127244
ENSBTAG00000004190	ARHGAP29	-0.276020116	0.073191372
ENSBTAG00000004193	VEZF1	0.52281638	0.000322225
ENSBTAG00000004194	RALGDS	0.542481397	0.000171309
ENSBTAG00000004196	FMNL1	0.597550338	2.33E-05

ENSBTAG00000004208	PLEKHG6	0.46814772	0.001546376
ENSBTAG00000004211	TNFRSF1A	0.576963186	5.12E-05
ENSBTAG00000004216	MAP3K2	0.347959969	0.022227347
ENSBTAG00000004218	NA	-0.272273732	0.077337555
ENSBTAG00000004222	SAT2	-0.501845352	0.000606644
ENSBTAG00000004224	C7H19orf38	0.470139786	0.001466975
ENSBTAG00000004225	TSR1	0.482947403	0.001037338
ENSBTAG00000004226	SHBG	-0.506330533	0.000531671
ENSBTAG00000004227	TBCK	-0.63751763	4.27E-06
ENSBTAG00000004237	BTC	-0.213000063	0.170258539
ENSBTAG00000004240	TMPO	-0.60605382	1.66E-05
ENSBTAG00000004243	LYPLA1	0.403048355	0.007366455
ENSBTAG00000004246	SPSB1	-0.066634178	0.671167441
ENSBTAG00000004247	RPH3A	0.075113532	0.632141011
ENSBTAG00000004248	MLYCD	-0.419174203	0.005144484
ENSBTAG00000004249	TANC2	-0.311207569	0.042220282
ENSBTAG00000004256	ODC1	0.517154169	0.000383799
ENSBTAG00000004257	TAF4B	0.458303044	0.00199739
ENSBTAG00000004259	HPCAL1	0.377150941	0.012663369
ENSBTAG00000004269	SGK1	0.263772384	0.087428992
ENSBTAG00000004270	FCER2	-0.073579593	0.639132194
ENSBTAG00000004272	ISG12(B)	-0.343689387	0.024036776
ENSBTAG00000004273	CST7	-0.12331977	0.430786187
ENSBTAG00000004275	DKK3	-0.153253542	0.32651898
ENSBTAG00000004277	EVC2	-0.114216842	0.46582323
ENSBTAG00000004280	SRPX	-0.25043376	0.105287778
ENSBTAG00000004281	ACSS1	-0.299945811	0.050680623
ENSBTAG00000004283	PPFIBP1	-0.276450563	0.072726425
ENSBTAG00000004286	CDC45	-0.293713608	0.055920254
ENSBTAG00000004287	EVC	-0.258508145	0.09417273
ENSBTAG00000004288	GSTA4	-0.463515336	0.001745917
ENSBTAG00000004294	EVI5L	-0.342183762	0.024703325
ENSBTAG00000004295	NDUFA8	-0.374964727	0.01323108
ENSBTAG00000004297	ACOXL	-0.086729661	0.580256853
ENSBTAG00000004300	LRRC8E	-0.12286099	0.43251598
ENSBTAG00000004305	RGS16	0.24748516	0.109587477
ENSBTAG00000004315	HDLBP	-0.050518177	0.747669531
ENSBTAG00000004316	BOD1L1	0.425634947	0.004433544
ENSBTAG00000004318	ARL3	-0.584864623	3.81E-05
ENSBTAG00000004321	SFXN2	-0.13013832	0.405536919
ENSBTAG00000004322	FOS	0.501738493	0.00060854
ENSBTAG00000004328	CHST10	-0.34867411	0.021936192
ENSBTAG00000004329	RELL1	0.493958726	0.000761715
ENSBTAG00000004337	PDE1B	-0.617972437	1.01E-05
ENSBTAG00000004339	LOC508153	0.454786233	0.002184648
ENSBTAG00000004343	CCS	0.043143475	0.783545182
ENSBTAG00000004344	ACSL1	-0.063072355	0.687826663

ENSBTAG00000004347	ADGRF5	-0.391796061	0.009369543
ENSBTAG00000004349	DAZAP2	0.440851139	0.003087738
ENSBTAG00000004353	NA	0.422336998	0.004784943
ENSBTAG00000004358	DARS2	-0.450459387	0.002436165
ENSBTAG00000004361	ZBTB37	-0.313370499	0.040735274
ENSBTAG00000004364	THNSL2	-0.491630659	0.000813813
ENSBTAG00000004367	COQ10A	-0.728743927	3.02E-08
ENSBTAG00000004368	NFATC3	-0.475889133	0.001257706
ENSBTAG00000004371	CS	-0.371645553	0.014134336
ENSBTAG00000004374	CNPY2	-0.308150294	0.044394241
ENSBTAG00000004375	ESRP2	-0.376277825	0.012887557
ENSBTAG00000004377	PHLDB3	0.073956398	0.637411952
ENSBTAG00000004378	IL23A	0.46036543	0.0018943
ENSBTAG00000004379	ETHE1	-0.166345256	0.286375851
ENSBTAG00000004380	STAT2	0.448911154	0.00253217
ENSBTAG00000004381	TACSTD2	-0.349028372	0.021792949
ENSBTAG00000004383	FNBP1L	0.08105177	0.605378231
ENSBTAG00000004386	SOCS1	0.530806965	0.000250435
ENSBTAG00000004388	SLITRK6	-0.253721558	0.100646763
ENSBTAG00000004392	C29H11orf24	0.650593551	2.33E-06
ENSBTAG00000004394	PKIB	-0.669731876	9.04E-07
ENSBTAG00000004398	IMMP2L	-0.51990304	0.000352696
ENSBTAG00000004399	LRRN3	-0.436280144	0.003448148
ENSBTAG00000004400	PRRC2B	0.321372416	0.035607326
ENSBTAG00000004403	CD320	0.236460336	0.126854346
ENSBTAG00000004406	MSI2	0.29989521	0.050721512
ENSBTAG00000004409	IVD	-0.347606116	0.022372806
ENSBTAG00000004413	RHOBTB3	-0.549344381	0.000136135
ENSBTAG00000004421	CHST14	-0.596062662	2.47E-05
ENSBTAG00000004422	ALG14	-0.348638293	0.021950718
ENSBTAG00000004423	ARHGAP42	-0.194008965	0.212544697
ENSBTAG00000004428	H2AZ1	-0.523332622	0.00031708
ENSBTAG00000004430	SGPP1	0.368214276	0.015122633
ENSBTAG00000004440	SLC15A1	0.008130745	0.958730626
ENSBTAG00000004443	NA	0.611402281	1.33E-05
ENSBTAG00000004448	CKAP5	-0.630761038	5.79E-06
ENSBTAG00000004457	ORAI1	0.13129255	0.401348747
ENSBTAG00000004458	MORN3	-0.260337976	0.091784562
ENSBTAG00000004459	TMEM45A	-0.532521094	0.000237059
ENSBTAG00000004460	RFWD3	-0.691115756	2.89E-07
ENSBTAG00000004471	ST3GAL6	0.034606962	0.825628278
ENSBTAG00000004472	NA	0.577623023	5.00E-05
ENSBTAG00000004475	CDK5R1	0.522722012	0.000323174
ENSBTAG00000004476	ADHFE1	-0.45591104	0.002123138
ENSBTAG00000004484	CEP83	0.381281836	0.011647195
ENSBTAG00000004490	TRIM31	-0.479905259	0.001127706
ENSBTAG00000004492	SWT1	0.329319039	0.031051794

ENSBTAG00000004494	B4GALNT1	0.332259759	0.029493071
ENSBTAG00000004495	UBA5	-0.627917932	6.56E-06
ENSBTAG00000004496	NA	-0.009882142	0.949851312
ENSBTAG00000004499	RGS3	0.028198645	0.857546941
ENSBTAG00000004502	CLUAP1	-0.626609126	6.95E-06
ENSBTAG00000004505	NLRC3	-0.342843779	0.024409259
ENSBTAG00000004509	SLX4	-0.383468663	0.011138031
ENSBTAG00000004511	VAV2	0.203298058	0.191031081
ENSBTAG00000004514	NA	0.489815471	0.000856617
ENSBTAG00000004515	KCNK1	-0.398211515	0.008176903
ENSBTAG00000004517	TARBP1	-0.665509112	1.12E-06
ENSBTAG00000004518	GRHL2	-0.283289027	0.065647499
ENSBTAG00000004524	SPPL2B	-0.279216011	0.069794592
ENSBTAG00000004526	NA	0.575916062	5.32E-05
ENSBTAG00000004532	FGFR1OP2	0.347436044	0.022443001
ENSBTAG00000004538	PRDM9	-0.260057601	0.092147417
ENSBTAG00000004540	NUB1	0.441851358	0.003013436
ENSBTAG00000004541	LPAR5	-0.285072049	0.063894736
ENSBTAG00000004544	TXNDC9	-0.115032053	0.462624718
ENSBTAG00000004547	OLR1	0.595481344	2.53E-05
ENSBTAG00000004552	PBXIP1	0.472477881	0.00137841
ENSBTAG00000004553	TPM4	0.425836403	0.004412828
ENSBTAG00000004555	LRP2	-0.04088013	0.794648966
ENSBTAG00000004556	SLC2A3	0.549784359	0.000134121
ENSBTAG00000004557	DHRS9	0.099150668	0.527009649
ENSBTAG00000004558	C10H15orf48	0.505556607	0.000543983
ENSBTAG00000004560	CLEC4F	0.057217428	0.71552758
ENSBTAG00000004562	CD207	0.287813336	0.061272763
ENSBTAG00000004565	NA	0.018259213	0.907482106
ENSBTAG00000004568	GALNS	-0.242711336	0.116830302
ENSBTAG00000004572	RNF183	-0.132770188	0.39602374
ENSBTAG00000004575	FAM126A	-0.172821319	0.26776016
ENSBTAG00000004580	MS4A1	-0.167128302	0.28408131
ENSBTAG00000004585	NA	-0.282112267	0.066825042
ENSBTAG00000004587	DUSP6	0.631029671	5.72E-06
ENSBTAG00000004588	KCNN4	-0.488752296	0.00088261
ENSBTAG00000004590	PPIH	-0.57985783	4.60E-05
ENSBTAG00000004597	PIM2	-0.397454166	0.008310514
ENSBTAG00000004601	ABHD10	-0.450643341	0.002424974
ENSBTAG00000004603	PHC2	0.5780281	4.92E-05
ENSBTAG00000004608	LOC100138951	0.534211352	0.000224504
ENSBTAG00000004613	CSGALNACT1	-0.188370142	0.226396959
ENSBTAG00000004624	NA	-0.602113311	1.94E-05
ENSBTAG00000004625	PYGB	-0.218265856	0.159691834
ENSBTAG00000004631	KIAA0586	-0.62754431	6.67E-06
ENSBTAG00000004635	LLGL1	0.608890037	1.47E-05
ENSBTAG00000004639	HARBI1	-0.520399949	0.000347322

ENSBTAG00000004640	SPAM1	0.140232036	0.369767307
ENSBTAG00000004641	PLEKHA6	-0.31281191	0.041114641
ENSBTAG00000004645	ADAMTSL3	0.139633068	0.371835615
ENSBTAG00000004650	ZNF516	0.225914154	0.14520667
ENSBTAG00000004651	NME1	-0.218853117	0.158543687
ENSBTAG00000004652	LPAR2	0.073378257	0.640052133
ENSBTAG00000004653	ADGRA3	-0.466894513	0.001598257
ENSBTAG00000004654	PWP1	-0.734326549	2.09E-08
ENSBTAG00000004657	NA	0.000764943	0.996115708
ENSBTAG00000004659	COQ10B	0.29605883	0.053899797
ENSBTAG00000004660	SPATS2	-0.4429032	0.002936996
ENSBTAG00000004662	SLC16A12	0.364598372	0.01622689
ENSBTAG00000004664	COQ4	-0.408274242	0.006569698
ENSBTAG00000004674	HAAO	0.389248886	0.0098829
ENSBTAG00000004679	WARS1	0.543699673	0.00016452
ENSBTAG00000004680	SLC13A5	0.337635998	0.026810897
ENSBTAG00000004685	SRGAP3	-0.341938527	0.024813338
ENSBTAG00000004688	DHCR24	-0.099075393	0.527324953
ENSBTAG00000004690	NA	-0.551969906	0.000124512
ENSBTAG00000004705	ILDR1	-0.582252704	4.20E-05
ENSBTAG00000004706	SUV39H1	-0.634846861	4.82E-06
ENSBTAG00000004710	HNF1B	0.456487345	0.002092219
ENSBTAG00000004714	MCEMP1	0.462616119	0.001787189
ENSBTAG00000004716	RETN	0.473850132	0.001328671
ENSBTAG00000004722	THUMPD2	-0.628250168	6.47E-06
ENSBTAG00000004723	TEX2	0.533271716	0.000231407
ENSBTAG00000004727	PAQR4	-0.066222541	0.67308499
ENSBTAG00000004729	PKMYT1	-0.1890592	0.22467176
ENSBTAG00000004732	SPTB	0.362102936	0.01702812
ENSBTAG00000004735	CCNE1	-0.628521761	6.39E-06
ENSBTAG00000004736	GRB2	0.575921077	5.32E-05
ENSBTAG00000004741	IL12B	0.576830973	5.15E-05
ENSBTAG00000004742	RUNX1	0.218680457	0.158880627
ENSBTAG00000004746	HELZ	0.523868941	0.000311813
ENSBTAG00000004749	NEK4	-0.330915958	0.030197116
ENSBTAG00000004750	VSTM2L	-0.293617643	0.056004205
ENSBTAG00000004751	SPTBN4	-0.580533164	4.49E-05
ENSBTAG00000004757	LTBP4	-0.296620915	0.053424372
ENSBTAG00000004768	RAI1	0.098991735	0.527675483
ENSBTAG00000004769	NEIL2	-0.229787459	0.138251779
ENSBTAG00000004770	SCN4A	0.365356967	0.015989736
ENSBTAG00000004772	THEM4	-0.009532175	0.951625143
ENSBTAG00000004777	S100B	-0.020382339	0.896779372
ENSBTAG00000004782	PTPRCAP	-0.112436918	0.472847738
ENSBTAG00000004786	TMEM134	-0.601168824	2.02E-05
ENSBTAG00000004787	METRNL	0.651446309	2.23E-06
ENSBTAG00000004788	SDR39U1	-0.684049893	4.26E-07

ENSBTAG00000004789	LGR6	0.437098986	0.003380998
ENSBTAG00000004790	UBE2T	-0.386022133	0.010567699
ENSBTAG00000004792	CHMP4C	-0.269831177	0.080138485
ENSBTAG00000004797	TRMT44	0.523323177	0.000317173
ENSBTAG00000004802	CEP170B	0.212099635	0.172114742
ENSBTAG00000004806	PHKB	-0.726453934	3.50E-08
ENSBTAG00000004813	SUSD1	0.319788079	0.036578162
ENSBTAG00000004814	INPP4A	0.542702655	0.000170057
ENSBTAG00000004815	LOC509006	-0.087396642	0.577337005
ENSBTAG00000004822	SOX10	-0.357284858	0.018669859
ENSBTAG00000004826	ACP5	-0.389266757	0.009879216
ENSBTAG00000004832	KIF21A	-0.349262814	0.021698586
ENSBTAG00000004838	IRX5	-0.349951737	0.021423273
ENSBTAG00000004840	C1S	0.375932679	0.012977107
ENSBTAG00000004842	RSPRY1	0.447902006	0.002596525
ENSBTAG00000004848	OLFML2A	-0.318502761	0.037381625
ENSBTAG00000004849	IGSF3	0.204959191	0.187352781
ENSBTAG00000004850	KPNA3	0.314667496	0.039865423
ENSBTAG00000004851	NCKAP5L	-0.241856402	0.118164748
ENSBTAG00000004852	PLEKHO1	0.587617609	3.43E-05
ENSBTAG00000004854	SLC24A5	-0.46465549	0.0016948
ENSBTAG00000004856	RNF130	-0.598839112	2.21E-05
ENSBTAG00000004862	TUB	-0.159205311	0.307852522
ENSBTAG00000004869	CXADR	-0.345167189	0.02339721
ENSBTAG00000004873	CCNL2	0.63646077	4.48E-06
ENSBTAG00000004877	TRAIP	-0.453107687	0.002279362
ENSBTAG00000004879	FOXO4	-0.515001123	0.00040986
ENSBTAG00000004881	MTHFD2	0.430726057	0.003935256
ENSBTAG00000004884	SLC4A5	-0.253965276	0.100309086
ENSBTAG00000004885	DDR2	0.260661737	0.091366934
ENSBTAG00000004894	GIMAP5	-0.196340814	0.206992314
ENSBTAG00000004895	AFAP1L2	-0.361423419	0.017251999
ENSBTAG00000004896	ABLIM3	-0.632293469	5.41E-06
ENSBTAG00000004899	ABLIM1	-0.467430112	0.001575898
ENSBTAG00000004901	PIK3C2A	0.144392946	0.355590036
ENSBTAG00000004903	KRT15	-0.246642901	0.110839878
ENSBTAG00000004905	KRT19	-0.392200904	0.009290097
ENSBTAG00000004906	CCNE2	-0.21625935	0.163660405
ENSBTAG00000004907	MINK1	-0.601838687	1.96E-05
ENSBTAG00000004908	CHRNE	0.547201799	0.00014634
ENSBTAG00000004917	KLRK1	-0.336796348	0.027215909
ENSBTAG00000004922	AGPAT5	-0.379862732	0.011988135
ENSBTAG00000004925	NA	-0.414072771	0.005773979
ENSBTAG00000004926	LRR1	-0.636405909	4.50E-06
ENSBTAG00000004931	POLE2	-0.612824302	1.25E-05
ENSBTAG00000004933	KLHDC2	-0.658535238	1.58E-06
ENSBTAG00000004939	NA	-0.534891995	0.00021962

ENSBTAG00000004941	TEX35	-0.596217362	2.46E-05
ENSBTAG00000004942	EXOSC9	-0.535185297	0.000217546
ENSBTAG00000004943	CCNA2	-0.377372161	0.012607098
ENSBTAG00000004945	BBS7	-0.485221502	0.000974058
ENSBTAG00000004948	LRATD1	-0.417541521	0.005339116
ENSBTAG00000004950	BRB	-0.252593007	0.102221776
ENSBTAG00000004953	ELK4	0.464664281	0.001694411
ENSBTAG00000004954	TOX	-0.17778432	0.254048335
ENSBTAG00000004956	CHEK2	-0.381135273	0.011682018
ENSBTAG00000004961	GOSR1	0.337828756	0.026718629
ENSBTAG00000004962	BCORL1	0.265287026	0.085559888
ENSBTAG00000004964	PCGF5	0.465924076	0.001639485
ENSBTAG00000004966	NA	-0.525335479	0.000297812
ENSBTAG00000004970	LRRC24	0.350628639	0.021155622
ENSBTAG00000004971	GRAMD1C	0.536131028	0.000210976
ENSBTAG00000004974	ZDHHC23	0.33285535	0.029185405
ENSBTAG00000004976	CDCA7L	-0.120606202	0.441073545
ENSBTAG00000004987	NUP210L	0.621200273	8.79E-06
ENSBTAG00000004988	CCKAR	0.432853088	0.003742032
ENSBTAG00000004989	IRF5	0.429912768	0.004011409
ENSBTAG00000004990	NEO1	-0.471281879	0.001423102
ENSBTAG00000004991	ELP1	-0.283341575	0.065595303
ENSBTAG00000004993	NXT1	-0.338237955	0.026523632
ENSBTAG00000004994	NA	0.381867312	0.011508966
ENSBTAG00000004997	CTNNAL1	0.012180456	0.938208463
ENSBTAG00000004999	RESF1	0.054119885	0.730332635
ENSBTAG00000005002	GALE	-0.383096082	0.01122341
ENSBTAG00000005005	CSN1S2	-0.34214762	0.024719513
ENSBTAG00000005007	NA	-0.75485981	4.99E-09
ENSBTAG00000005008	WSB1	0.635517097	4.68E-06
ENSBTAG00000005010	MXD3	-0.138226443	0.376719942
ENSBTAG00000005012	HSPH1	0.199721575	0.199123629
ENSBTAG00000005015	SFXN3	-0.306467456	0.045629137
ENSBTAG00000005018	NFAM1	0.675751685	6.62E-07
ENSBTAG00000005019	PRSS50	0.0549897	0.726165208
ENSBTAG00000005028	HIRIP3	-0.532052785	0.000240647
ENSBTAG00000005029	TAL1	0.375147077	0.013182913
ENSBTAG00000005031	DOC2A	-0.155585402	0.319122943
ENSBTAG00000005033	TLCD3B	-0.540624589	0.000182144
ENSBTAG00000005034	CAPN5	-0.202995616	0.191706256
ENSBTAG00000005038	ZBTB42	0.496609462	0.000706041
ENSBTAG00000005042	SYN1	-0.033678817	0.830235309
ENSBTAG00000005043	NA	0.491476871	0.000817364
ENSBTAG00000005049	BLK	-0.16506268	0.290160121
ENSBTAG00000005055	TXK	-0.209150818	0.178295608
ENSBTAG00000005062	TEC	0.54122173	0.000178594
ENSBTAG00000005066	HSPBAP1	0.090619766	0.563321929

ENSBTAG00000005067	UBTF	0.675982678	6.54E-07
ENSBTAG00000005069	TM7SF2	-0.160352947	0.304333039
ENSBTAG00000005072	CUBN	-0.320365615	0.03622178
ENSBTAG00000005078	UCHL1	-0.448956347	0.002529321
ENSBTAG00000005083	TULP4	-0.394592958	0.008832396
ENSBTAG00000005089	RHBDD2	0.6737729	7.34E-07
ENSBTAG00000005090	CEMIP2	-0.454028833	0.002226946
ENSBTAG00000005091	DGKG	0.27380737	0.075618527
ENSBTAG00000005092	ROR2	0.313716615	0.040501645
ENSBTAG00000005093	CES2	-0.297869709	0.052380175
ENSBTAG00000005096	COX7A2	0.120807968	0.440304004
ENSBTAG00000005104	MGAT5B	-0.192167317	0.217002441
ENSBTAG00000005105	PAFAH2	-0.247678174	0.109301998
ENSBTAG00000005110	CADPS2	-0.337642752	0.026807659
ENSBTAG00000005111	BMP2	-0.276504873	0.072667928
ENSBTAG00000005115	SLC31A2	0.066437416	0.672083773
ENSBTAG00000005119	PSMD1	-0.579833475	4.60E-05
ENSBTAG00000005120	TESPA1	0.019794747	0.899739711
ENSBTAG00000005124	JADE3	0.588579918	3.31E-05
ENSBTAG00000005129	CEP55	-0.386601563	0.010441819
ENSBTAG00000005136	ABI1	0.504462809	0.000561818
ENSBTAG00000005138	BCL9L	0.32926682	0.031080076
ENSBTAG00000005140	NBL1	-0.47740775	0.001207062
ENSBTAG00000005141	PELI2	0.161384542	0.301191464
ENSBTAG00000005142	RPL37	0.179216941	0.250179429
ENSBTAG00000005143	NA	0.079925156	0.610418064
ENSBTAG00000005144	PNPLA2	-0.35415504	0.0198062
ENSBTAG00000005145	PEAK1	0.019729529	0.900068367
ENSBTAG00000005146	NA	0.440958776	0.003079666
ENSBTAG00000005147	HPS5	-0.082304761	0.599794248
ENSBTAG00000005150	HMGB3	-0.518050238	0.000373399
ENSBTAG00000005154	APCDD1	-0.315425679	0.039364002
ENSBTAG00000005155	ARL13B	0.073054962	0.641530435
ENSBTAG00000005160	GTF2H1	0.472979834	0.001360028
ENSBTAG00000005161	ATP8B2	-0.390367397	0.00965458
ENSBTAG00000005162	STX19	-0.109338027	0.485210325
ENSBTAG00000005164	GZMK	-0.263728822	0.087483214
ENSBTAG00000005165	CSGALNACT2	0.481529077	0.001078635
ENSBTAG00000005170	ADGRG5	-0.005073032	0.974243959
ENSBTAG00000005180	RBMS1	0.447441777	0.00262635
ENSBTAG00000005181	SYS1	0.606128552	1.65E-05
ENSBTAG00000005182	BoLA	0.604980017	1.73E-05
ENSBTAG00000005183	MVK	-0.289559767	0.059647576
ENSBTAG00000005186	DBNDD2	0.246219937	0.111472896
ENSBTAG00000005193	CRTAM	-0.602883467	1.88E-05
ENSBTAG00000005198	FGF1	-0.237062398	0.125861737
ENSBTAG00000005203	C1H3orf33	-0.411131422	0.006166487

ENSBTAG00000005205	DSE	-0.296623881	0.053421872
ENSBTAG00000005206	TMEM14A	-0.466823823	0.001601229
ENSBTAG00000005213	ZWILCH	-0.397739142	0.00826002
ENSBTAG00000005215	IL10RA	0.494770534	0.000744262
ENSBTAG00000005218	PDE3B	0.240098082	0.12094541
ENSBTAG00000005219	KLHL4	-0.467029684	0.001592588
ENSBTAG00000005221	WNK1	-0.213524117	0.169184889
ENSBTAG00000005234	LYPD1	-0.04035543	0.797228919
ENSBTAG00000005239	NA	-0.624343466	7.67E-06
ENSBTAG00000005240	NA	-0.201259377	0.195614967
ENSBTAG00000005244	RASL11A	-0.277999385	0.071072694
ENSBTAG00000005250	BGN	-0.213814382	0.168592322
ENSBTAG00000005251	LOC516599	0.218577507	0.159081778
ENSBTAG00000005259	UCP3	0.036325467	0.817113492
ENSBTAG00000005260	SPP1	-0.598787398	2.22E-05
ENSBTAG00000005261	FCGBP	-0.403387797	0.00731228
ENSBTAG00000005262	NA	0.16856241	0.279910127
ENSBTAG00000005268	PLA2G4D	-0.412063173	0.00603972
ENSBTAG00000005269	CCNB2	-0.44470475	0.002810024
ENSBTAG00000005273	IL1R1	0.360297732	0.017628345
ENSBTAG00000005275	PKIG	-0.547972156	0.000142594
ENSBTAG00000005278	WEE1	-0.275824815	0.073403096
ENSBTAG00000005280	ADA	0.037943138	0.809117237
ENSBTAG00000005286	NA	0.256023322	0.097492191
ENSBTAG00000005288	GFRA3	-0.502963064	0.000587125
ENSBTAG00000005289	CHERP	0.622871209	8.18E-06
ENSBTAG00000005293	CDC25C	-0.515291884	0.00040625
ENSBTAG00000005294	NA	-0.26705023	0.083423384
ENSBTAG00000005299	EDNRB	-0.584290147	3.89E-05
ENSBTAG00000005300	TMEM51	-0.432405211	0.003782013
ENSBTAG00000005304	SRM	-0.413546247	0.005842604
ENSBTAG00000005309	TGDS	-0.586051782	3.64E-05
ENSBTAG00000005310	GPR180	-0.611563513	1.32E-05
ENSBTAG00000005311	POLR3H	-0.423767937	0.004629603
ENSBTAG00000005313	EPHB3	-0.289400448	0.059794392
ENSBTAG00000005328	ICE2	-0.311900694	0.041739676
ENSBTAG00000005339	VEGFA	0.547230577	0.000146198
ENSBTAG00000005340	SERGEF	-0.501682579	0.000609535
ENSBTAG00000005347	GPN3	-0.523881321	0.000311693
ENSBTAG00000005351	RFXAP	-0.536955895	0.000205393
ENSBTAG00000005354	LRRFIP1	0.535794994	0.000213289
ENSBTAG00000005355	BAG2	0.612657777	1.26E-05
ENSBTAG00000005356	DENND2B	-0.171616341	0.271161781
ENSBTAG00000005359	TGFB2	-0.305886415	0.046061931
ENSBTAG00000005362	RAB23	-0.720608992	5.07E-08
ENSBTAG00000005364	HMBS	-0.313409395	0.040708965
ENSBTAG00000005367	VRK3	-0.429113197	0.004087531

ENSBTAG00000005370	TMTC1	-0.352423244	0.020459565
ENSBTAG00000005371	DPAGT1	-0.075551022	0.630152834
ENSBTAG00000005373	TPM1	-0.339817259	0.025782103
ENSBTAG00000005379	SLC41A1	-0.264685632	0.086298265
ENSBTAG00000005382	NA	-0.001080758	0.994512063
ENSBTAG00000005384	COPZ1	0.439545571	0.003187141
ENSBTAG00000005385	POP5	0.014510193	0.926419417
ENSBTAG00000005393	TIPRL	-0.614645475	1.16E-05
ENSBTAG00000005397	CD46	0.400034596	0.007862841
ENSBTAG00000005403	ADI1	-0.243277608	0.115952714
ENSBTAG00000005408	CLK1	0.327079696	0.032283878
ENSBTAG00000005412	NEDD4L	-0.07175963	0.647467162
ENSBTAG00000005413	NLRC5	0.512650376	0.00044012
ENSBTAG00000005414	NA	0.575262686	5.45E-05
ENSBTAG00000005416	PPIL3	-0.542894443	0.000168979
ENSBTAG00000005424	KCNC1	-0.44749824	0.002622675
ENSBTAG00000005427	NRDE2	0.613001824	1.24E-05
ENSBTAG00000005430	MB21D2	0.390629145	0.009601808
ENSBTAG00000005431	LMCD1	-0.342659036	0.024491274
ENSBTAG00000005432	CAPG	0.279714313	0.069276384
ENSBTAG00000005442	DNAI4	-0.347165582	0.022555011
ENSBTAG00000005443	MIER1	0.4423455	0.00297731
ENSBTAG00000005444	UGGT1	0.330110756	0.030625598
ENSBTAG00000005445	SLC35D1	-0.412672465	0.005958052
ENSBTAG00000005448	LOC521224	0.629200584	6.20E-06
ENSBTAG00000005450	NA	0.470362261	0.001458336
ENSBTAG00000005456	TTK	-0.319429549	0.036800844
ENSBTAG00000005461	SOX15	0.341175689	0.025158165
ENSBTAG00000005462	FXR2	0.43931101	0.003205294
ENSBTAG00000005464	ADCY6	-0.194713951	0.210855241
ENSBTAG00000005474	CREB1	0.521604969	0.000334595
ENSBTAG00000005475	TCAF2	0.050571923	0.747409892
ENSBTAG00000005476	NA	0.241473526	0.118766089
ENSBTAG00000005477	LAPTM5	0.608798061	1.48E-05
ENSBTAG00000005482	TMEM135	-0.43462872	0.003587139
ENSBTAG00000005483	ESYT2	0.41250814	0.005979983
ENSBTAG00000005488	ARIH2	0.66701365	1.04E-06
ENSBTAG00000005490	P4HTM	-0.448812007	0.00253843
ENSBTAG00000005491	NA	0.07438416	0.635461347
ENSBTAG00000005493	TBC1D14	0.648744094	2.54E-06
ENSBTAG00000005496	RP2	0.345817309	0.023120388
ENSBTAG00000005497	RPRD1A	0.362785419	0.016805739
ENSBTAG00000005498	SQLE	0.290482976	0.058802475
ENSBTAG00000005501	COBLL1	-0.401059828	0.007690836
ENSBTAG00000005504	TP53INP2	0.301330292	0.049572176
ENSBTAG00000005514	TRIO	-0.031323426	0.841951677
ENSBTAG00000005517	NOP58	0.327479646	0.032060915

ENSBTAG00000005523	XYLT1	-0.005246055	0.973365822
ENSBTAG00000005524	HBP1	0.123874185	0.428700973
ENSBTAG00000005527	GIPR	-0.111407387	0.476936283
ENSBTAG00000005530	NA	-0.228301322	0.140890448
ENSBTAG00000005532	PEX6	-0.161885534	0.299673297
ENSBTAG00000005533	PPP2R5D	-0.46893828	0.00151442
ENSBTAG00000005534	ENO3	0.412710624	0.005952969
ENSBTAG00000005536	MEA1	-0.102454144	0.513264219
ENSBTAG00000005547	VCPKMT	0.116312921	0.457623106
ENSBTAG00000005557	AFDN	-0.448448638	0.002561489
ENSBTAG00000005560	ST18	-0.183488696	0.238879297
ENSBTAG00000005564	PIAS1	0.325383313	0.033243834
ENSBTAG00000005571	PHF20	-0.305453253	0.046386737
ENSBTAG00000005572	ZNF205	-0.228295375	0.140901082
ENSBTAG00000005574	CLU	-0.538719126	0.000193904
ENSBTAG00000005577	RNASEH2C	-0.561998544	8.79E-05
ENSBTAG00000005578	KAT5	0.401965458	0.007541607
ENSBTAG00000005580	SZT2	0.221539258	0.153368687
ENSBTAG00000005583	HYI	-0.516815964	0.000387791
ENSBTAG00000005586	GATM	-0.540463751	0.000183111
ENSBTAG00000005588	DXO	0.676165347	6.48E-07
ENSBTAG00000005589	STK19	0.558050329	0.000100971
ENSBTAG00000005592	MCOLN1	-0.428645149	0.004132673
ENSBTAG00000005603	CXCL11	0.023506602	0.881063236
ENSBTAG00000005606	HOXC9	0.100419386	0.521709328
ENSBTAG00000005607	ERCC6L	-0.589031837	3.25E-05
ENSBTAG00000005615	CEACAM1	0.196281787	0.207131601
ENSBTAG00000005617	SLC41A3	-0.282404218	0.066531347
ENSBTAG00000005622	LITAF	0.44951132	0.002494566
ENSBTAG00000005628	CD52	-0.323596198	0.034280445
ENSBTAG00000005629	CRYBG2	-0.51189613	0.000450246
ENSBTAG00000005630	VWA7	-0.334270588	0.028464985
ENSBTAG00000005631	VARS1	0.224949478	0.146978279
ENSBTAG00000005633	ARHGEF28	-0.241593271	0.118577772
ENSBTAG00000005635	TTC39C	0.290723818	0.058583592
ENSBTAG00000005638	CABYR	0.2618382	0.089861754
ENSBTAG00000005647	GPR132	0.532436403	0.000237704
ENSBTAG00000005650	SKAP2	0.548344451	0.000140815
ENSBTAG00000005666	LRRC20	-0.537120824	0.000204293
ENSBTAG00000005668	SLC39A8	0.491893405	0.000807778
ENSBTAG00000005670	ARHGEF19	-0.271792548	0.077883175
ENSBTAG00000005674	NEU1	0.252080755	0.102942878
ENSBTAG00000005675	SLC44A4	-0.187850093	0.227705022
ENSBTAG00000005678	AACS	-0.062849323	0.68887479
ENSBTAG00000005681	ME1	-0.229798054	0.1382331
ENSBTAG00000005682	UBAC2	0.383911295	0.011037322
ENSBTAG00000005683	ELAC1	-0.705304844	1.29E-07

ENSBTAG00000005688	MRPS2	0.434290644	0.00361619
ENSBTAG00000005691	FGF2	-0.355501473	0.019310422
ENSBTAG00000005696	DBF4B	-0.558661121	9.88E-05
ENSBTAG00000005699	SCML4	-0.47595209	0.001255569
ENSBTAG00000005700	MAP3K9	-0.41087566	0.006201685
ENSBTAG00000005704	IL1RL2	-0.321290394	0.035657061
ENSBTAG00000005708	KIF20B	-0.691908783	2.77E-07
ENSBTAG00000005716	CRABP2	-0.127083267	0.416742893
ENSBTAG00000005718	PLIN2	-0.366691191	0.015579743
ENSBTAG00000005722	NA	-0.485208711	0.000974404
ENSBTAG00000005723	NEPRO	0.144739011	0.354425977
ENSBTAG00000005725	IDO2	0.26240944	0.089137869
ENSBTAG00000005729	FBXL4	-0.620022229	9.24E-06
ENSBTAG00000005730	GPAT4	0.58645105	3.59E-05
ENSBTAG00000005733	CHD6	-0.133521476	0.393332136
ENSBTAG00000005734	GATA6	0.097634003	0.533380344
ENSBTAG00000005738	ATP8B1	-0.550655893	0.000130212
ENSBTAG00000005745	HPSE	0.620211891	9.17E-06
ENSBTAG00000005754	PPM1K	-0.469691714	0.001484512
ENSBTAG00000005756	ZDHHC24	-0.46757535	0.001569883
ENSBTAG00000005757	FUS	0.477190616	0.00121419
ENSBTAG00000005760	TBC1D4	-0.509896377	0.000478114
ENSBTAG00000005761	DEDD2	0.500770295	0.000625965
ENSBTAG00000005762	LYNX1	-0.237764927	0.12471087
ENSBTAG00000005765	SYNGR1	-0.421688668	0.004856806
ENSBTAG00000005766	IL4I1	-0.361437257	0.017247415
ENSBTAG00000005769	NPHP3	0.103251788	0.509972466
ENSBTAG00000005773	PGM2	0.362311906	0.016959766
ENSBTAG00000005776	ZNF185	-0.332131341	0.029559759
ENSBTAG00000005780	LDB1	0.399673635	0.007924184
ENSBTAG00000005785	DPY19L1	-0.477352932	0.001208858
ENSBTAG00000005786	ATXN3	-0.186317201	0.231590785
ENSBTAG00000005787	IFT57	-0.591747051	2.92E-05
ENSBTAG00000005788	VANGL1	-0.463781339	0.001733871
ENSBTAG00000005791	UROS	-0.451219515	0.002390215
ENSBTAG00000005793	PEA15	0.065296879	0.677404503
ENSBTAG00000005796	DCAF8	-0.641189946	3.61E-06
ENSBTAG00000005807	MICU1	0.566928277	7.38E-05
ENSBTAG00000005810	NA	-0.115302834	0.461564918
ENSBTAG00000005812	TP73	-0.433834059	0.003655751
ENSBTAG00000005814	PSME2	0.470427551	0.001455809
ENSBTAG00000005815	RNF31	0.414592446	0.005706934
ENSBTAG00000005816	IRF9	0.460157924	0.001904455
ENSBTAG00000005819	CCDC61	0.325314556	0.033283233
ENSBTAG00000005825	NEIL3	-0.322418755	0.034977838
ENSBTAG00000005827	FIG4	-0.525695847	0.000294459
ENSBTAG00000005828	MERTK	-0.222853734	0.150881828

ENSBTAG00000005832	GRK2	0.419226712	0.005138328
ENSBTAG00000005833	ETNK1	0.304690823	0.046962951
ENSBTAG00000005838	ULK3	-0.089942329	0.566254472
ENSBTAG00000005841	NA	0.670565374	8.67E-07
ENSBTAG00000005842	ABCC10	-0.088049733	0.574484439
ENSBTAG00000005843	REXO2	-0.402102613	0.007519227
ENSBTAG00000005845	MPI	-0.380068005	0.011938297
ENSBTAG00000005846	FAM219B	-0.128602645	0.411147969
ENSBTAG00000005850	DLK2	0.101619188	0.516721327
ENSBTAG00000005859	LALBA	-0.238992794	0.122718403
ENSBTAG00000005861	CCNT1	0.444137037	0.002849505
ENSBTAG00000005862	SMC4	-0.672809575	7.72E-07
ENSBTAG00000005865	MAPK6	0.301819037	0.049185583
ENSBTAG00000005866	NA	-0.155831447	0.318348758
ENSBTAG00000005868	HEBP1	-0.096865852	0.536621169
ENSBTAG00000005870	FANCL	-0.553524839	0.00011806
ENSBTAG00000005882	NA	0.158739179	0.309289397
ENSBTAG00000005884	WDR31	-0.403052872	0.007365732
ENSBTAG00000005888	MDGA1	-0.20169665	0.194625298
ENSBTAG00000005891	FCRL1	-0.438987335	0.003230493
ENSBTAG00000005892	ZAP70	-0.393628487	0.009014552
ENSBTAG00000005897	FNTB	-0.40016129	0.007841407
ENSBTAG00000005903	LRP5	0.670143583	8.86E-07
ENSBTAG00000005907	NDUFB6	-0.401397939	0.007634827
ENSBTAG00000005915	SFMBT2	-0.386855307	0.0103871
ENSBTAG00000005917	PARD6G	-0.339760634	0.025808388
ENSBTAG00000005923	ABTB2	0.386829948	0.010392557
ENSBTAG00000005928	MINPP1	-0.590778436	3.04E-05
ENSBTAG00000005929	NA	-0.383444607	0.011143527
ENSBTAG00000005934	TTYH3	0.459999293	0.00191225
ENSBTAG00000005940	PRKAB1	0.540973678	0.000180061
ENSBTAG00000005945	NXPE4	-0.208097686	0.1805411
ENSBTAG00000005947	PLAU	0.532328174	0.000238531
ENSBTAG00000005951	HIC2	0.364816548	0.01615838
ENSBTAG00000005952	CEBPE	0.390403289	0.009647329
ENSBTAG00000005953	ESX1	0.247303302	0.109856976
ENSBTAG00000005955	RSPH3	-0.226248876	0.144595654
ENSBTAG00000005957	CSE1L	-0.729116417	2.94E-08
ENSBTAG00000005958	PTK2B	0.649496615	2.45E-06
ENSBTAG00000005960	EPB41L2	0.617293247	1.04E-05
ENSBTAG00000005961	CDC42SE2	0.290687417	0.058616632
ENSBTAG00000005970	XBP1	0.290028403	0.059217385
ENSBTAG00000005973	OVGP1	0.528957292	0.000265629
ENSBTAG00000005976	HSD17B7	0.029700554	0.850044102
ENSBTAG00000005978	PIK3R5	0.65130097	2.25E-06
ENSBTAG00000005979	HELLS	-0.527297922	0.000279963
ENSBTAG00000005980	RREB1	0.443032584	0.002927712

ENSBTAG00000005984	DAAM1	-0.100331262	0.522076627
ENSBTAG00000005989	LAP3	0.457287641	0.002049943
ENSBTAG00000005990	S1PR1	0.24603311	0.111753377
ENSBTAG00000005994	SPESP1	-0.340048848	0.02567483
ENSBTAG00000005997	ABCB1	-0.002821564	0.985673121
ENSBTAG00000005998	NOCT	0.190667233	0.220680962
ENSBTAG00000006001	STAP2	-0.326743515	0.032472279
ENSBTAG00000006005	MPND	-0.255776733	0.097826458
ENSBTAG00000006013	NT5DC3	-0.47478673	0.001295644
ENSBTAG00000006016	GTPBP2	0.541341377	0.00017789
ENSBTAG00000006017	NFKB2	0.503996293	0.000569583
ENSBTAG00000006021	CEP250	-0.531817763	0.000242467
ENSBTAG00000006022	ATP6V0E2	-0.32144577	0.035562894
ENSBTAG00000006025	AHSA2	0.023058386	0.883315291
ENSBTAG00000006026	BEX3	-0.417424826	0.005353269
ENSBTAG00000006027	USP34	0.379062064	0.012184227
ENSBTAG00000006034	RNF113A	-0.432338297	0.003788019
ENSBTAG00000006036	ERP27	0.129034061	0.409567199
ENSBTAG00000006039	ARHGDIB	0.444186406	0.002846053
ENSBTAG00000006043	LOC515755	0.503017243	0.000586193
ENSBTAG00000006044	KLHL5	0.456464847	0.002093419
ENSBTAG00000006050	BOLA1	-0.644458234	3.11E-06
ENSBTAG00000006052	PLCD3	-0.319597227	0.036696562
ENSBTAG00000006054	ACBD4	-0.505191451	0.00054988
ENSBTAG00000006056	HEXIM1	0.213681705	0.168862992
ENSBTAG00000006064	BRME1	-0.0566781	0.718098141
ENSBTAG00000006066	CDS2	0.46853249	0.001530749
ENSBTAG00000006067	VMAC	-0.472155401	0.001390336
ENSBTAG00000006068	CC2D1A	-0.245321009	0.112827368
ENSBTAG00000006069	CAPS	-0.348950602	0.021824328
ENSBTAG00000006071	CTTN	-0.222502958	0.151542546
ENSBTAG00000006072	LRRC59	-0.181411374	0.244330374
ENSBTAG00000006073	PODNL1	-0.29775359	0.052476571
ENSBTAG00000006075	SUCLG1	-0.44720279	0.002641955
ENSBTAG00000006078	IL15RA	0.530773133	0.000250705
ENSBTAG00000006080	MAST1	-0.174065761	0.264276897
ENSBTAG00000006082	DNASE2	-0.557132902	0.000104242
ENSBTAG00000006086	MMP28	-0.33639899	0.027409343
ENSBTAG00000006088	FAM104A	0.523805585	0.000312431
ENSBTAG00000006089	C19H17orf80	0.573706116	5.77E-05
ENSBTAG00000006107	SLF1	-0.671819029	8.12E-07
ENSBTAG00000006110	NA	-0.008238581	0.958183762
ENSBTAG00000006117	FLYWCH1	-0.554293112	0.000114986
ENSBTAG00000006118	RSRC2	0.155225666	0.320256985
ENSBTAG00000006122	HUWE1	0.149319142	0.339238764
ENSBTAG00000006124	MAU2	0.265340457	0.085494526
ENSBTAG00000006125	PLK3	0.586663886	3.56E-05

ENSBTAG00000006126	GTF3C1	0.218963989	0.1583276
ENSBTAG00000006128	DYNLT4	0.590352382	3.09E-05
ENSBTAG00000006130	CLEC14A	-0.112448879	0.472800347
ENSBTAG00000006132	DENND3	0.551776891	0.000125335
ENSBTAG00000006133	NA	-0.320498284	0.036140317
ENSBTAG00000006135	MAP1LC3A	0.476134939	0.001249383
ENSBTAG00000006136	NA	0.553910169	0.000116509
ENSBTAG00000006138	SEMA3C	-0.207951751	0.18085385
ENSBTAG00000006139	TRPM4	-0.29439739	0.055324989
ENSBTAG00000006143	CREB3L1	-0.155690773	0.318791247
ENSBTAG00000006152	NA	-0.154982806	0.32102402
ENSBTAG00000006155	CCRL2	0.557189505	0.000104037
ENSBTAG00000006156	BST1	0.276175743	0.073023002
ENSBTAG00000006157	NA	0.620904534	8.90E-06
ENSBTAG00000006158	DZIP3	-0.502906564	0.000588098
ENSBTAG00000006160	SUOX	-0.426844837	0.004310393
ENSBTAG00000006161	MET	-0.294036145	0.055638833
ENSBTAG00000006162	RAB11FIP5	-0.113902382	0.467060178
ENSBTAG00000006165	PRDX4	-0.39933285	0.007982477
ENSBTAG00000006167	BTBD8	-0.102316606	0.513832889
ENSBTAG00000006173	CCDC116	0.072277833	0.64508953
ENSBTAG00000006185	SPC24	-0.401685205	0.007587518
ENSBTAG00000006187	MFAP4	-0.303312779	0.048019121
ENSBTAG00000006189	ACTG1	0.503374733	0.000580079
ENSBTAG00000006193	IRAK2	0.503835048	0.00057229
ENSBTAG00000006194	FOSL1	0.378254736	0.012384713
ENSBTAG00000006201	DTWD1	-0.604794717	1.74E-05
ENSBTAG00000006204	XPNPEP3	-0.360247104	0.017645432
ENSBTAG00000006208	ADCY7	0.621843444	8.55E-06
ENSBTAG00000006209	EXT1	-0.281704424	0.06723704
ENSBTAG00000006212	GTF2IRD1	-0.568017346	7.10E-05
ENSBTAG00000006213	NA	-0.520672105	0.00034441
ENSBTAG00000006214	LOXL2	-0.097859654	0.532430136
ENSBTAG00000006221	ADGRG3	0.597897674	2.30E-05
ENSBTAG00000006222	TFDP2	-0.233107781	0.1324892
ENSBTAG00000006223	THEMIS2	0.563128832	8.45E-05
ENSBTAG00000006225	RPA2	-0.43341973	0.003691978
ENSBTAG00000006227	IDH3A	0.446504088	0.002688049
ENSBTAG00000006233	NIM1K	0.086551736	0.581036876
ENSBTAG00000006235	INTS3	-0.279728195	0.069261991
ENSBTAG00000006236	NA	0.417208223	0.005379626
ENSBTAG00000006240	TLR4	0.352594651	0.0203941
ENSBTAG00000006243	GCNT7	0.379662634	0.012036886
ENSBTAG00000006246	CBX5	-0.575317286	5.44E-05
ENSBTAG00000006253	FLNC	-0.312540048	0.041300317
ENSBTAG00000006255	MDM4	0.034870457	0.824321414
ENSBTAG00000006256	PTPRO	0.189956824	0.222437969

ENSBTAG00000006260	KIAA1614	-0.677006679	6.20E-07
ENSBTAG00000006261	GPR17	-0.242695568	0.116854811
ENSBTAG00000006262	LIMS2	-0.43936224	0.003201322
ENSBTAG00000006263	GP2	-0.161550424	0.300688245
ENSBTAG00000006270	HSP90AA1	0.292174808	0.05727864
ENSBTAG00000006272	NTHL1	-0.098901754	0.528052629
ENSBTAG00000006276	C1QTNF1	-0.512516408	0.000441904
ENSBTAG00000006280	RBFOX3	0.054719789	0.727457568
ENSBTAG00000006282	POU2AF1	-0.04809884	0.75938504
ENSBTAG00000006287	NEDD9	0.358580917	0.018215645
ENSBTAG00000006291	CYLD	0.471457125	0.001416474
ENSBTAG00000006296	VMA21	-0.579499594	4.66E-05
ENSBTAG00000006305	AK1	-0.449639688	0.002486587
ENSBTAG00000006307	HSD17B11	-0.226724782	0.143730183
ENSBTAG00000006320	DBT	-0.377922944	0.01246792
ENSBTAG00000006322	DENND5A	0.503523187	0.000577556
ENSBTAG00000006323	SNX9	0.453541452	0.002254546
ENSBTAG00000006324	NAB2	0.704924582	1.31E-07
ENSBTAG00000006326	ALDH1L2	-0.285738365	0.06324936
ENSBTAG00000006335	STAT6	0.666602632	1.06E-06
ENSBTAG00000006338	NA	-0.232909478	0.132828252
ENSBTAG00000006339	LOC785479	-0.544955881	0.000157776
ENSBTAG00000006342	ATP5IF1	-0.385776888	0.010621368
ENSBTAG00000006343	IL1R2	0.550723386	0.000129913
ENSBTAG00000006345	ART1	0.308210457	0.0443506
ENSBTAG00000006347	UTP4	0.502678269	0.000592044
ENSBTAG00000006349	EXTL1	-0.100920939	0.519621295
ENSBTAG00000006353	TXNL4B	-0.164556281	0.291663143
ENSBTAG00000006354	HP	0.257686357	0.095260753
ENSBTAG00000006359	EPHA1	0.199518193	0.199590962
ENSBTAG00000006360	CD180	0.105011585	0.502747867
ENSBTAG00000006364	GLMP	-0.238433369	0.123623195
ENSBTAG00000006367	CCN2	-0.498584231	0.00066696
ENSBTAG00000006368	N4BP3	0.44498579	0.002790658
ENSBTAG00000006371	RMND5B	-0.177381678	0.25514288
ENSBTAG00000006372	KLHL42	-0.135393809	0.386670815
ENSBTAG00000006373	NA	0.016286843	0.917439434
ENSBTAG00000006374	NHP2	-0.125653047	0.422048784
ENSBTAG00000006377	MYO1G	-0.463270862	0.001757053
ENSBTAG00000006378	RIPK1	0.550661803	0.000130185
ENSBTAG00000006379	BPHL	-0.408495869	0.006537625
ENSBTAG00000006391	NDUFAB1	-0.10928098	0.485439471
ENSBTAG00000006392	TTC7B	-0.46895005	0.001513949
ENSBTAG00000006393	FECH	-0.576574072	5.20E-05
ENSBTAG00000006396	GPI	-0.316675545	0.038548671
ENSBTAG00000006397	NA	-0.013499999	0.931529484
ENSBTAG00000006398	TOMM7	-0.620174319	9.18E-06

ENSBTAG00000006403	NA	0.535096629	0.000218171
ENSBTAG00000006404	CENPT	-0.321340165	0.035626875
ENSBTAG00000006405	PALB2	-0.280209218	0.068764724
ENSBTAG00000006410	DCTN5	-0.499956719	0.000640951
ENSBTAG00000006411	NA	-0.401095374	0.007684932
ENSBTAG00000006414	NUTF2	-0.126221529	0.419935256
ENSBTAG00000006429	ACO2	-0.118467664	0.449275476
ENSBTAG00000006434	SYNPO2	-0.484252791	0.00100058
ENSBTAG00000006439	DOCK11	0.346353933	0.02289396
ENSBTAG00000006441	ATP5PB	0.31057026	0.042666154
ENSBTAG00000006443	PRDM11	-0.367142924	0.015442963
ENSBTAG00000006447	ACSM3	-0.380567499	0.011817764
ENSBTAG00000006448	ERI2	-0.606671692	1.61E-05
ENSBTAG00000006449	REXO5	-0.605432019	1.70E-05
ENSBTAG00000006452	CD3D	-0.390213751	0.009685672
ENSBTAG00000006453	CD3G	-0.449588455	0.002489769
ENSBTAG00000006466	CD53	0.470303605	0.001460609
ENSBTAG00000006470	TTBK2	-0.463506597	0.001746314
ENSBTAG00000006471	OSBPL11	0.462471112	0.001793925
ENSBTAG00000006474	EPCAM	-0.348735362	0.021911369
ENSBTAG00000006478	C8H9orf64	-0.572274157	6.08E-05
ENSBTAG00000006485	TREML1	-0.626126053	7.10E-06
ENSBTAG00000006487	RPS9	0.555677324	0.000109629
ENSBTAG00000006489	MYO5A	-0.561095706	9.08E-05
ENSBTAG00000006490	BOLA-DOA	0.458289777	0.001998069
ENSBTAG00000006491	AGL	-0.553938057	0.000116397
ENSBTAG00000006492	PI4K2B	-0.559478616	9.61E-05
ENSBTAG00000006497	NA	-0.165265026	0.289560952
ENSBTAG00000006500	RBM15B	0.564209604	8.13E-05
ENSBTAG00000006504	TCHP	-0.587564161	3.44E-05
ENSBTAG00000006505	S100A9	0.565392093	7.80E-05
ENSBTAG00000006510	YRDC	0.586111155	3.63E-05
ENSBTAG00000006511	MTF1	0.46685592	0.001599879
ENSBTAG00000006515	ESPN	-0.303110428	0.048175814
ENSBTAG00000006519	TNFRSF25	0.161771845	0.300017378
ENSBTAG00000006520	NA	-0.270225307	0.079681236
ENSBTAG00000006523	SOD2	0.568988815	6.85E-05
ENSBTAG00000006525	FDXR	0.585136298	3.77E-05
ENSBTAG00000006526	BCL2L1	0.480993739	0.001094598
ENSBTAG00000006528	BBS9	-0.234750478	0.129705338
ENSBTAG00000006530	COX7ALP1	-0.03848375	0.806449187
ENSBTAG00000006531	DIP2C	-0.443397024	0.0029017
ENSBTAG00000006532	CDK5RAP2	-0.423178725	0.004693026
ENSBTAG00000006534	GTPBP8	-0.537935597	0.000198935
ENSBTAG00000006538	PTHLH	-0.267801934	0.082525281
ENSBTAG00000006539	SIRPB2	0.544246015	0.000161556
ENSBTAG00000006541	ATP2A1	-0.430702048	0.003937486

ENSBTAG00000006548	MCCC1	-0.588311079	3.34E-05
ENSBTAG00000006549	CALHM6	0.386587207	0.010444923
ENSBTAG00000006551	ESCO2	-0.365906671	0.015819725
ENSBTAG00000006552	LAMP3	-0.08860786	0.572051763
ENSBTAG00000006558	NA	0.490831509	0.000832416
ENSBTAG00000006561	RASGEF1B	0.506130569	0.000534828
ENSBTAG00000006563	KLHL40	-0.258431879	0.094273299
ENSBTAG00000006566	FFAR2	0.460634628	0.001881197
ENSBTAG00000006570	SEC22C	-0.45650923	0.002091053
ENSBTAG00000006572	CARD9	0.145671321	0.351301512
ENSBTAG00000006573	KLHL18	0.429944258	0.004008437
ENSBTAG00000006579	P4HA3	-0.274089731	0.075305332
ENSBTAG00000006581	CCDC82	0.572020899	6.14E-05
ENSBTAG00000006587	ZNF367	-0.652228659	2.15E-06
ENSBTAG00000006589	CFTR	0.079998532	0.610089276
ENSBTAG00000006590	NUDT16L1	-0.385877609	0.010599298
ENSBTAG00000006591	NA	-0.331563115	0.029856341
ENSBTAG00000006592	SGSM1	-0.412994628	0.005915258
ENSBTAG00000006601	KSR1	0.590584404	3.06E-05
ENSBTAG00000006606	RFLNB	0.261301019	0.090546627
ENSBTAG00000006607	CCNG1	-0.594184903	2.66E-05
ENSBTAG00000006608	GGT5	0.470024887	0.001471454
ENSBTAG00000006609	ERRFI1	-0.154146827	0.323673145
ENSBTAG00000006612	SCAF1	0.300843896	0.049959343
ENSBTAG00000006613	METTL17	-0.481608709	0.001076278
ENSBTAG00000006615	CASP7	0.482934392	0.00103771
ENSBTAG00000006616	PTPN1	0.523610358	0.000314343
ENSBTAG00000006618	HLF	-0.489459476	0.000865243
ENSBTAG00000006619	MATK	-0.04040749	0.796972848
ENSBTAG00000006621	NA	-0.043457204	0.782009347
ENSBTAG00000006625	NDC1	-0.634124468	4.98E-06
ENSBTAG00000006626	TMEM132B	-0.407569813	0.006672546
ENSBTAG00000006631	GLI1	0.10040355	0.521775319
ENSBTAG00000006633	IRF3	0.213455654	0.169324875
ENSBTAG00000006638	BCL2L12	0.377070023	0.012684006
ENSBTAG00000006645	LPAR6	-0.002134598	0.989161046
ENSBTAG00000006650	ZNF668	0.588443207	3.32E-05
ENSBTAG00000006654	TANK	0.447409815	0.002628432
ENSBTAG00000006657	ZDHHC8	-0.095417857	0.542756069
ENSBTAG00000006662	NA	-0.308689415	0.044004416
ENSBTAG00000006663	CYTH1	0.410636561	0.006234747
ENSBTAG00000006665	ERP29	0.279297328	0.069709818
ENSBTAG00000006667	EPB41	-0.434596284	0.003589917
ENSBTAG00000006673	TMEM179	-0.423179651	0.004692926
ENSBTAG00000006677	NA	0.161377637	0.301212424
ENSBTAG00000006679	MITF	-0.164647806	0.291391118
ENSBTAG00000006680	NKIRAS1	0.01298225	0.934149586

ENSBTAG00000006683	ZFYVE28	0.448266768	0.0025731
ENSBTAG00000006685	IL10	0.433922012	0.003648101
ENSBTAG00000006688	RPS6KL1	-0.000573158	0.997089567
ENSBTAG00000006695	VCPIP1	0.392476349	0.009236376
ENSBTAG00000006697	RICTOR	0.349182681	0.021730801
ENSBTAG00000006702	EIF3E	0.047408638	0.762737208
ENSBTAG00000006703	PTGDR	-0.304221714	0.047320356
ENSBTAG00000006707	ACSL5	0.608604666	1.49E-05
ENSBTAG00000006713	ZDHHC6	-0.554963796	0.000112361
ENSBTAG00000006716	PTGS1	-0.417320377	0.005365965
ENSBTAG00000006719	ZFAND4	-0.190280947	0.221635144
ENSBTAG00000006720	GJA5	-0.274362017	0.075004278
ENSBTAG00000006721	POLR1F	0.397603408	0.008284037
ENSBTAG00000006729	NA	0.358989396	0.018074435
ENSBTAG00000006730	SUSD2	0.412361	0.005999679
ENSBTAG00000006731	SLC7A5	0.64809804	2.62E-06
ENSBTAG00000006734	BICD1	-0.271420426	0.078307195
ENSBTAG00000006738	GPR68	-0.430633036	0.003943902
ENSBTAG00000006740	SCYL1	0.661093208	1.40E-06
ENSBTAG00000006743	RBBP8	-0.311878272	0.041755153
ENSBTAG00000006745	FGG	-0.34816394	0.02214386
ENSBTAG00000006747	LTBP3	0.393874897	0.008967709
ENSBTAG00000006748	DMXL1	-0.621376121	8.72E-06
ENSBTAG00000006751	TENT2	0.315501274	0.039314292
ENSBTAG00000006752	PFKFB4	0.545816256	0.000153303
ENSBTAG00000006754	DBP	-0.425573827	0.004439846
ENSBTAG00000006758	NA	-0.288263027	0.060850954
ENSBTAG00000006762	SH3RF2	0.183531652	0.238767455
ENSBTAG00000006770	MTBP	0.012805565	0.935043875
ENSBTAG00000006771	FRY	0.143125183	0.35987421
ENSBTAG00000006775	SLC12A7	0.153072051	0.327099083
ENSBTAG00000006777	TLCD1	-0.261205169	0.090669255
ENSBTAG00000006780	NAPSA	0.285286654	0.063686306
ENSBTAG00000006784	PLA2G4B	0.126551004	0.418713066
ENSBTAG00000006790	SPTBN5	-0.328797852	0.031335024
ENSBTAG00000006792	EHD4	0.135908793	0.384850318
ENSBTAG00000006795	GCSH	-0.443019083	0.00292868
ENSBTAG00000006797	MARCHF3	0.122170833	0.435125442
ENSBTAG00000006801	TMEM106A	-0.034031822	0.82848243
ENSBTAG00000006804	KIRREL3	0.156323308	0.316804669
ENSBTAG00000006805	ZNF180	-0.2366175	0.126594668
ENSBTAG00000006806	KRT17	-0.184215795	0.236990999
ENSBTAG00000006812	FAM181B	-0.116089437	0.458493667
ENSBTAG00000006817	CBL	0.243370466	0.115809284
ENSBTAG00000006821	PECR	-0.37993051	0.011971659
ENSBTAG00000006823	CMYA5	0.399664392	0.007925761
ENSBTAG00000006828	RAPGEF3	-0.556700288	0.000105817

ENSBTAG00000006832	SLC5A6	0.0616453	0.694542926
ENSBTAG00000006835	MCAM	-0.457060749	0.002061852
ENSBTAG00000006838	AIFM1	-0.638223645	4.14E-06
ENSBTAG00000006843	UTP15	0.338471123	0.026413049
ENSBTAG00000006844	LEF1	-0.313074965	0.040935629
ENSBTAG00000006846	LGALS9	0.491577845	0.000815031
ENSBTAG00000006848	DHX34	0.081979921	0.601239747
ENSBTAG00000006851	LOC617565	0.264888318	0.086048861
ENSBTAG00000006852	ACYP2	-0.610223364	1.40E-05
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ENSBTAG00000006862	MEIS3	-0.023362321	0.881788074
ENSBTAG00000006864	LOC107131209	0.533826575	0.000227308
ENSBTAG00000006870	RASGEF1A	0.074970117	0.632793322
ENSBTAG00000006882	IQGAP3	-0.296107307	0.05385866
ENSBTAG00000006883	EIF4B	0.395998903	0.008572535
ENSBTAG00000006886	FAM117A	-0.383059819	0.01123175
ENSBTAG00000006893	BBX	-0.174278965	0.26368316
ENSBTAG00000006894	NOS2	0.545882908	0.000152961
ENSBTAG00000006896	ABCA9	0.156495409	0.316265516
ENSBTAG00000006901	NIPSNAP3A	-0.468799422	0.00151999
ENSBTAG00000006904	TNS2	0.250904381	0.10461361
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ENSBTAG00000006907	NEB	-0.213911774	0.168393835
ENSBTAG00000006910	ASRGL1	0.413075574	0.005904548
ENSBTAG00000006921	ABCA6	0.271652262	0.078042815
ENSBTAG00000006925	CENPL	-0.542943377	0.000168705
ENSBTAG00000006928	OAT	-0.395701361	0.008626974
ENSBTAG00000006933	PPP1R10	0.189710971	0.223048261
ENSBTAG00000006934	CYP11A1	-0.084337031	0.590785484
ENSBTAG00000006936	MRPS18B	-0.346072717	0.023012386
ENSBTAG00000006937	NA	0.290652016	0.058648779
ENSBTAG00000006938	PPM1F	0.504777228	0.000556638
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ENSBTAG00000006945	CCDC50	-0.519767897	0.00035417
ENSBTAG00000006948	GARNL3	-0.332596165	0.029318965
ENSBTAG00000006951	LMO2	0.423742271	0.00463235
ENSBTAG00000006954	ZNF432	-0.577554518	5.01E-05
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ENSBTAG00000006958	C23H6orf136	-0.537723743	0.000200316
ENSBTAG00000006961	NLRP13	0.281094507	0.067856925
ENSBTAG00000006963	RPL12	-0.260903735	0.091055736
ENSBTAG00000006965	NLRP8	0.205309586	0.186583365
ENSBTAG00000006966	NRM	-0.519444149	0.000357725
ENSBTAG00000006969	TUBB	-0.569827421	6.65E-05
ENSBTAG00000006972	TRIP13	-0.463357739	0.001753089
ENSBTAG00000006974	PLEKHA7	-0.357747366	0.018506687

ENSBTAG00000006978	HSD17B4	-0.617755338	1.02E-05
ENSBTAG00000006984	CD55	0.596209571	2.46E-05
ENSBTAG00000006985	TM7SF3	-0.509852931	0.000478736
ENSBTAG00000006989	SEMA4F	0.108489249	0.488625551
ENSBTAG00000006995	SPTBN1	-0.403537918	0.007288431
ENSBTAG00000006998	RASGRP4	0.340743225	0.025355419
ENSBTAG00000006999	RYR1	0.442610815	0.002958071
ENSBTAG00000007000	ENOSF1	-0.460648426	0.001880527
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ENSBTAG00000007003	TYMS	-0.489675799	0.000859992
ENSBTAG00000007008	MOK	-0.616709059	1.06E-05
ENSBTAG00000007012	ZNF3	-0.434074097	0.003634906
ENSBTAG00000007013	TOM1L1	-0.289348353	0.059842461
ENSBTAG00000007016	CNPY4	-0.717742008	6.06E-08
ENSBTAG00000007020	ZNF502	-0.612975739	1.24E-05
ENSBTAG00000007031	OXSM	-0.633399099	5.15E-06
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ENSBTAG00000007039	FBXO25	0.174150981	0.264039468
ENSBTAG00000007051	CLDN23	-0.238860036	0.122932668
ENSBTAG00000007053	ZFHX2	-0.283761648	0.065179224
ENSBTAG00000007058	ATG2A	0.249766594	0.106249184
ENSBTAG00000007070	BLOC1S3	0.496648481	0.000705249
ENSBTAG00000007071	RAI14	-0.187179	0.229400648
ENSBTAG00000007073	CPB2	0.604835344	1.74E-05
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ENSBTAG00000007075	LOC616942	0.521845481	0.000332105
ENSBTAG00000007077	ABHD1	0.30807925	0.04444582
ENSBTAG00000007084	MAP3K14	0.310859636	0.042463229
ENSBTAG00000007089	FRG1	0.313918409	0.040365939
ENSBTAG00000007093	NA	0.120989992	0.439610394
ENSBTAG00000007096	GAS8	-0.436924958	0.003395173
ENSBTAG00000007097	THTPA	-0.291786639	0.057625439
ENSBTAG00000007099	AP1G2	-0.381130917	0.011683055
ENSBTAG00000007101	F3	0.359292745	0.017970167
ENSBTAG00000007102	GTSE1	-0.53450442	0.000222389
ENSBTAG00000007103	ITGAL	0.539949167	0.000186236
ENSBTAG00000007105	PWP2	0.628512361	6.39E-06
ENSBTAG00000007107	TMEM143	-0.40370089	0.007262616
ENSBTAG00000007111	STEAP3	0.548634146	0.000139444
ENSBTAG00000007112	HSPB11	-0.333239513	0.028988372
ENSBTAG00000007115	GSR	-0.433387128	0.003694842
ENSBTAG00000007116	ARRDC3	-0.483747403	0.001014671
ENSBTAG00000007118	SMURF1	0.603031295	1.87E-05
ENSBTAG00000007121	TK1	-0.652876856	2.09E-06
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ENSBTAG00000007127	NA	0.090127561	0.565451925

ENSBTAG00000007130	ESF1	0.35539662	0.019348652
ENSBTAG00000007131	GADL1	0.22841852	0.140681016
ENSBTAG00000007137	RFC5	-0.540499195	0.000182897
ENSBTAG00000007142	CPPED1	-0.618645928	9.80E-06
ENSBTAG00000007147	CUEDC1	0.378932743	0.012216154
ENSBTAG00000007148	F2	0.281447851	0.067497257
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ENSBTAG00000007156	AGAP2	0.301300039	0.049596186
ENSBTAG00000007158	TSPAN31	0.46146909	0.001841088
ENSBTAG00000007159	ESR1	-0.374715244	0.01329722
ENSBTAG00000007160	CDK4	-0.296131543	0.053838103
ENSBTAG00000007166	CAMKK1	0.545076331	0.000157143
ENSBTAG00000007169	P2RX1	0.156848621	0.315160799
ENSBTAG00000007170	SLC38A7	-0.177539276	0.254714089
ENSBTAG00000007172	GOT2	-0.533817708	0.000227373
ENSBTAG00000007176	NA	0.39254921	0.00922221
ENSBTAG00000007177	EMP2	-0.26131792	0.090525018
ENSBTAG00000007181	KIFC3	0.455236465	0.002159841
ENSBTAG00000007184	NUDT7	0.38985228	0.009759161
ENSBTAG00000007186	ARHGAP39	-0.534762263	0.000220544
ENSBTAG00000007187	INF2	-0.3755443	0.013078508
ENSBTAG00000007191	NA	0.52523012	0.000298799
ENSBTAG00000007192	SIDT2	0.450075159	0.002459687
ENSBTAG00000007193	NA	0.299261112	0.051236149
ENSBTAG00000007196	TAGLN	-0.039381223	0.802024745
ENSBTAG00000007199	NA	0.354177187	0.019797959
ENSBTAG00000007204	KRT80	-0.349024131	0.02179466
ENSBTAG00000007206	STRIP2	-0.524825755	0.000302613
ENSBTAG00000007208	HDAC11	0.458297772	0.00199766
ENSBTAG00000007213	SIRPA	0.634694315	4.86E-06
ENSBTAG00000007214	ELL2	0.139029713	0.373926041
ENSBTAG00000007217	TMEM94	-0.306643719	0.0454985
ENSBTAG00000007220	CASKIN2	-0.338244861	0.026520351
ENSBTAG00000007228	CBX7	0.19863714	0.201624358
ENSBTAG00000007235	NTNG2	-0.270965973	0.078827481
ENSBTAG00000007237	BUB1B	-0.360903689	0.017424906
ENSBTAG00000007238	NA	-0.374440696	0.013370331
ENSBTAG00000007239	TNFAIP6	0.543240377	0.00016705
ENSBTAG00000007244	NID1	-0.242675918	0.116885358
ENSBTAG00000007245	IFT140	-0.504707185	0.000557789
ENSBTAG00000007246	TMEM204	-0.079744595	0.611227458
ENSBTAG00000007247	NUF2	-0.471746539	0.001405588
ENSBTAG00000007253	TSPAN33	-0.09321146	0.552168394
ENSBTAG00000007268	F13A1	0.565432248	7.79E-05
ENSBTAG00000007269	EIF2B1	-0.471408162	0.001418323
ENSBTAG00000007271	TCTN2	-0.582801826	4.12E-05

ENSBTAG00000007275	TREM2	-0.461508666	0.001839204
ENSBTAG00000007280	NA	0.49428386	0.000754681
ENSBTAG00000007288	CDK19	-0.177212612	0.255603409
ENSBTAG00000007300	FHL3	-0.058981478	0.707141518
ENSBTAG00000007302	SLC2A5	-0.321032712	0.035813684
ENSBTAG00000007304	CLK3	0.659745627	1.49E-06
ENSBTAG00000007306	RAB3C	-0.339584574	0.025890259
ENSBTAG00000007307	SELE	0.059518201	0.704596729
ENSBTAG00000007312	CD209	-0.006861226	0.965170043
ENSBTAG00000007315	LARS2	-0.261661219	0.090086949
ENSBTAG00000007318	ZNF687	0.367446603	0.015351586
ENSBTAG00000007321	SREK1	0.019386635	0.901796605
ENSBTAG00000007330	STXBP3	0.402609083	0.007437077
ENSBTAG00000007331	PLOD2	-0.562451876	8.65E-05
ENSBTAG00000007333	NA	-0.436720521	0.003411891
ENSBTAG00000007334	NFKBID	0.54703267	0.000147174
ENSBTAG00000007335	TPD52	-0.496512766	0.000708006
ENSBTAG00000007336	HCST	0.359324275	0.017959358
ENSBTAG00000007343	NA	0.607523358	1.56E-05
ENSBTAG00000007346	COMMD4	-0.524208387	0.000308521
ENSBTAG00000007348	STRA6	0.124074625	0.427948491
ENSBTAG00000007352	KCNC4	-0.036097422	0.818242229
ENSBTAG00000007356	ELF1	0.372758748	0.013825733
ENSBTAG00000007357	CHSY1	0.319023728	0.037054239
ENSBTAG00000007361	NA	0.653352129	2.04E-06
ENSBTAG00000007362	XPC	-0.366168816	0.01573919
ENSBTAG00000007363	LSM3	-0.521983999	0.000330679
ENSBTAG00000007364	PMS2	-0.43328781	0.003703579
ENSBTAG00000007365	NEIL1	-0.431577902	0.00385685
ENSBTAG00000007366	HAUS8	-0.358111584	0.018379038
ENSBTAG00000007368	MAN2C1	-0.675508884	6.71E-07
ENSBTAG00000007369	PDLIM2	-0.057360321	0.714847039
ENSBTAG00000007371	SCAMP1	-0.071762614	0.647453465
ENSBTAG00000007374	LHFPL2	-0.422387359	0.0047794
ENSBTAG00000007375	MIF	-0.373926635	0.013508144
ENSBTAG00000007378	CLIP4	-0.060509008	0.69990734
ENSBTAG00000007382	NA	-0.502619886	0.000593057
ENSBTAG00000007388	ZC3H12D	-0.012828079	0.934929916
ENSBTAG00000007389	IFI35	0.42825738	0.004170402
ENSBTAG00000007390	VAT1	-0.456559997	0.00208835
ENSBTAG00000007393	RND2	-0.658253792	1.61E-06
ENSBTAG00000007395	ALS2	-0.606024921	1.66E-05
ENSBTAG00000007397	FOLH1B	0.327686239	0.031946243
ENSBTAG00000007399	LAMP2	-0.089599403	0.567741639
ENSBTAG00000007402	ZFAND2A	0.62333763	8.01E-06
ENSBTAG00000007409	NA	0.222170543	0.152170639
ENSBTAG00000007413	CEP41	-0.562504986	8.64E-05

ENSBTAG00000007414	PAPOLG	0.40056227	0.007773903
ENSBTAG00000007415	SLC7A8	-0.570118068	6.58E-05
ENSBTAG00000007424	LIF	0.307787688	0.044658006
ENSBTAG00000007427	PPRC1	0.504802083	0.000556231
ENSBTAG00000007428	CDKL5	-0.529923138	0.000257594
ENSBTAG00000007429	SPNS2	-0.290302603	0.058966831
ENSBTAG00000007430	MYBBP1A	0.356129452	0.019082785
ENSBTAG00000007433	MYO9A	0.36378993	0.016482895
ENSBTAG00000007434	CD300LG	-0.244831067	0.113570835
ENSBTAG00000007435	NOLC1	0.512287275	0.000444969
ENSBTAG00000007436	GGT6	-0.172155222	0.269637026
ENSBTAG00000007438	STT3B	-0.554462747	0.000114317
ENSBTAG00000007439	TENM4	-0.377914836	0.012469959
ENSBTAG00000007443	NA	-0.561186219	9.05E-05
ENSBTAG00000007446	NGF	0.055483038	0.723805
ENSBTAG00000007447	LOC531462	0.179253542	0.250081106
ENSBTAG00000007449	HS3ST1	-0.181235875	0.244794719
ENSBTAG00000007450	C2	0.120839698	0.440183051
ENSBTAG00000007454	RPL10	0.420922033	0.004942994
ENSBTAG00000007455	DNASE1L1	0.60396154	1.80E-05
ENSBTAG00000007461	C20H5orf34	-0.552776347	0.000121127
ENSBTAG00000007480	CIRBP	-0.21777703	0.16065214
ENSBTAG00000007482	NA	0.234941964	0.129383696
ENSBTAG00000007484	ACADS	-0.589260144	3.22E-05
ENSBTAG00000007485	GRHL1	-0.104501485	0.504836631
ENSBTAG00000007490	SULF2	0.041846203	0.789904455
ENSBTAG00000007494	SMARCA2	-0.488103312	0.000898821
ENSBTAG00000007498	ZGPAT	0.587918097	3.39E-05
ENSBTAG00000007501	NA	-0.349492436	0.021606495
ENSBTAG00000007502	CKMT1A	-0.338024338	0.026625279
ENSBTAG00000007507	FAAH	0.186841232	0.230257339
ENSBTAG00000007508	SRBD1	-0.696754291	2.11E-07
ENSBTAG00000007510	PXMP2	-0.339581627	0.025891631
ENSBTAG00000007512	PLA2G15	-0.588560453	3.31E-05
ENSBTAG00000007513	PGAM5	0.655540731	1.83E-06
ENSBTAG00000007519	ADAR	0.484518066	0.000993254
ENSBTAG00000007523	STX4	0.138041079	0.377366427
ENSBTAG00000007530	TRIM10	-0.012436118	0.936914069
ENSBTAG00000007531	NCF4	0.594708765	2.61E-05
ENSBTAG00000007532	TRIM15	-0.225664259	0.145664077
ENSBTAG00000007534	GGH	-0.786879702	3.94E-10
ENSBTAG00000007543	TAF1B	-0.475144841	0.00128321
ENSBTAG00000007544	MARVELD3	-0.25031018	0.105465359
ENSBTAG00000007545	PHLPP2	-0.142179203	0.363091222
ENSBTAG00000007546	NA	0.236137368	0.127389228
ENSBTAG00000007550	OLFM2	0.139074113	0.373771972
ENSBTAG00000007554	IFI6	-0.357123509	0.018727066

ENSBTAG00000007558	IL9R	-0.154887745	0.32132457
ENSBTAG00000007559	URI1	0.398110922	0.008194542
ENSBTAG00000007564	BBS12	-0.416817759	0.005427423
ENSBTAG00000007567	TMX3	-0.442730477	0.00294943
ENSBTAG00000007569	TNFRSF11A	-0.30832649	0.044266531
ENSBTAG00000007577	UBXN7	0.419630935	0.005091154
ENSBTAG00000007578	SHTN1	-0.365389594	0.015979602
ENSBTAG00000007581	ADORA2B	0.586622536	3.56E-05
ENSBTAG00000007584	INPP1	0.514150382	0.000420588
ENSBTAG00000007592	RARG	0.415217718	0.005627162
ENSBTAG00000007593	AIDA	-0.113252091	0.469623694
ENSBTAG00000007595	BROX	-0.479002454	0.001155839
ENSBTAG00000007596	GEM	-0.279137245	0.069876784
ENSBTAG00000007599	IKBKB	0.594745962	2.60E-05
ENSBTAG00000007605	FKBP4	0.013958554	0.929209532
ENSBTAG00000007608	BMT2	-0.312843037	0.041093425
ENSBTAG00000007609	ITFG2	0.555596341	0.000109936
ENSBTAG00000007615	CNTN3	-0.440119879	0.003143074
ENSBTAG00000007616	TMED6	-0.04136603	0.792261723
ENSBTAG00000007619	PUSL1	0.366214422	0.015725214
ENSBTAG00000007622	CTSD	-0.161532633	0.300742188
ENSBTAG00000007623	CPTP	-0.35764985	0.01854099
ENSBTAG00000007624	FRMD4B	0.245512357	0.11253801
ENSBTAG00000007626	IL2RG	0.560676481	9.21E-05
ENSBTAG00000007630	RNF170	-0.63970792	3.87E-06
ENSBTAG00000007632	FAM151B	-0.499421132	0.00065099
ENSBTAG00000007634	HOOK3	0.266035827	0.08464741
ENSBTAG00000007635	PLCL1	-0.317987659	0.037707653
ENSBTAG00000007636	IRAK3	0.181661717	0.243669033
ENSBTAG00000007642	NA	-0.205225232	0.186768388
ENSBTAG00000007644	GNG7	0.108773915	0.487478751
ENSBTAG00000007651	TARS3	-0.232909154	0.132828807
ENSBTAG00000007652	RFTN2	-0.278742611	0.070289736
ENSBTAG00000007654	CHST7	0.107766913	0.49154181
ENSBTAG00000007657	SCARA3	-0.317676429	0.037905767
ENSBTAG00000007659	CORO2A	0.487607594	0.000911381
ENSBTAG00000007661	MYO1F	0.401943937	0.007545125
ENSBTAG00000007662	HSPA5	0.403155251	0.007349357
ENSBTAG00000007665	NPR3	-0.457007808	0.002064639
ENSBTAG00000007666	IGF2BP2	0.147875695	0.343981067
ENSBTAG00000007668	AGPAT4	-0.215233409	0.165716995
ENSBTAG00000007675	NPHP1	0.239328471	0.12217789
ENSBTAG00000007678	MKX	-0.078189763	0.618216077
ENSBTAG00000007681	DHFR	-0.578417104	4.85E-05
ENSBTAG00000007689	LPIN1	-0.14930209	0.339294552
ENSBTAG00000007692	NA	-0.054750084	0.727312476
ENSBTAG00000007693	SLC45A3	-0.348286348	0.022093883

ENSBTAG00000007695	CSN1S1	-0.294044694	0.05563139
ENSBTAG00000007700	PHYH	-0.585753672	3.68E-05
ENSBTAG00000007702	RPP38	-0.078685971	0.615982078
ENSBTAG00000007704	ELOVL7	-0.258490254	0.094196314
ENSBTAG00000007705	COLEC12	-0.226833145	0.143533654
ENSBTAG00000007708	NLGN3	0.163902283	0.293611691
ENSBTAG00000007709	SHOC2	0.282826016	0.066108837
ENSBTAG00000007718	TGIF1	0.611133364	1.34E-05
ENSBTAG00000007719	MFSD6	0.497282456	0.000692498
ENSBTAG00000007728	PES1	0.649157798	2.49E-06
ENSBTAG00000007739	REX1BD	-0.565396235	7.80E-05
ENSBTAG00000007743	PUS7	0.322173235	0.035124718
ENSBTAG00000007746	AHR	0.112926532	0.470909887
ENSBTAG00000007749	TONSL	-0.438081489	0.003301941
ENSBTAG00000007753	KIFC2	0.050178942	0.749308945
ENSBTAG00000007755	APOBEC3H	-0.337292461	0.026975995
ENSBTAG00000007758	PDE10A	-0.427363792	0.004258492
ENSBTAG00000007762	ASIC3	-0.529574608	0.000260468
ENSBTAG00000007763	SLC1A4	0.330851594	0.030231183
ENSBTAG00000007766	CDK5	-0.489821463	0.000856472
ENSBTAG00000007773	VCAM1	-0.255511043	0.098187603
ENSBTAG00000007777	OGG1	-0.56937691	6.76E-05
ENSBTAG00000007780	CAMK1	-0.542470379	0.000171371
ENSBTAG00000007783	MYBL2	-0.242860439	0.116598742
ENSBTAG00000007784	NAA50	-0.090070746	0.565698026
ENSBTAG00000007788	GRIPAP1	0.545928071	0.00015273
ENSBTAG00000007791	KCNQ5	-0.432614487	0.003763285
ENSBTAG00000007793	NA	0.223456196	0.14975197
ENSBTAG00000007799	MTFR2	-0.429576418	0.004043279
ENSBTAG00000007804	RILPL2	0.527597835	0.000277322
ENSBTAG00000007807	HSPA2	0.01531313	0.922359828
ENSBTAG00000007812	NDUFA13	-0.321409343	0.035584953
ENSBTAG00000007814	WWTR1	-0.635713479	4.64E-06
ENSBTAG00000007816	LOC787045	0.338472557	0.026412371
ENSBTAG00000007817	BRCC3	-0.513785445	0.000425267
ENSBTAG00000007820	LOC101905254	-0.534378433	0.000223296
ENSBTAG00000007823	TG	0.030446181	0.8463241
ENSBTAG00000007825	MARK2	0.605771623	1.67E-05
ENSBTAG00000007828	SLA	0.537737839	0.000200224
ENSBTAG00000007829	CSAD	0.22156744	0.153315056
ENSBTAG00000007830	PLEKHM3	-0.328295879	0.031609826
ENSBTAG00000007833	PIAS2	0.417269068	0.005372211
ENSBTAG00000007834	PPP1R16A	-0.481149309	0.001089938
ENSBTAG00000007835	GPT	-0.484858565	0.00098392
ENSBTAG00000007836	PPA1	0.32527257	0.033307311
ENSBTAG00000007837	SELENOI	-0.163407199	0.295092342
ENSBTAG00000007838	MFSD3	-0.653977167	1.98E-06

ENSBTAG00000007840	HMGCR	0.264598834	0.086405241
ENSBTAG00000007841	WTIP	0.030338579	0.846860735
ENSBTAG00000007842	GCLM	-0.518225787	0.000371392
ENSBTAG00000007844	CETN2	-0.604334815	1.78E-05
ENSBTAG00000007847	EED	-0.599881524	2.12E-05
ENSBTAG00000007850	ITIH4	-0.265096622	0.085793127
ENSBTAG00000007855	NA	0.00818741	0.958443263
ENSBTAG00000007860	ASPM	-0.295810624	0.054110815
ENSBTAG00000007863	GLS	0.556198368	0.000107672
ENSBTAG00000007865	GNPDA1	-0.299847443	0.050760133
ENSBTAG00000007867	STAT1	0.374236162	0.01342502
ENSBTAG00000007870	FKBP14	-0.493076666	0.000781092
ENSBTAG00000007872	PSIP1	-0.438276692	0.003286428
ENSBTAG00000007875	SAFB	0.477083492	0.00121772
ENSBTAG00000007876	MAPK8	0.261501025	0.090291161
ENSBTAG00000007878	ARHGAP22	-0.039909372	0.799423872
ENSBTAG00000007881	LOC100139670	0.318132273	0.037615886
ENSBTAG00000007882	CACNA1B	-0.018381136	0.906867033
ENSBTAG00000007883	NA	0.305145532	0.046618606
ENSBTAG00000007884	SREBF1	0.480618467	0.001105914
ENSBTAG00000007888	EFR3B	-0.452765496	0.002299109
ENSBTAG00000007893	SCPEP1	-0.412703404	0.005953931
ENSBTAG00000007895	SLC20A1	0.638464372	4.09E-06
ENSBTAG00000007898	CYBRD1	-0.199063825	0.200637795
ENSBTAG00000007901	LOC508459	0.589480382	3.19E-05
ENSBTAG00000007909	NOTCH2	0.26507267	0.085822502
ENSBTAG00000007916	FOXJ1	-0.538457974	0.000195568
ENSBTAG00000007921	DAPP1	0.537715114	0.000200372
ENSBTAG00000007922	RNF24	0.490353462	0.000843726
ENSBTAG00000007923	LAMTOR3	0.147696226	0.34457353
ENSBTAG00000007927	SLAMF1	0.483971798	0.001008393
ENSBTAG00000007931	SLC38A6	-0.364194049	0.016354501
ENSBTAG00000007932	HCK	0.636066551	4.57E-06
ENSBTAG00000007935	CALCOCO2	0.445423295	0.002760743
ENSBTAG00000007937	PRIM2	-0.457871424	0.002019582
ENSBTAG00000007939	CHMP2B	-0.354644099	0.019624897
ENSBTAG00000007942	TENT4B	-0.094538489	0.546498143
ENSBTAG00000007956	FRAT1	0.453686637	0.002246293
ENSBTAG00000007958	TNS4	-0.391429175	0.009442043
ENSBTAG00000007960	TOP1	0.460151451	0.001904772
ENSBTAG00000007961	TADA3	-0.414772096	0.005683914
ENSBTAG00000007962	ATP9A	-0.126235338	0.419883992
ENSBTAG00000007966	TTLL3	-0.173828943	0.264937437
ENSBTAG00000007970	C1H3orf38	0.281501088	0.067443199
ENSBTAG00000007974	WTAP	0.565981178	7.63E-05
ENSBTAG00000007979	TNPO1	-0.562805691	8.55E-05
ENSBTAG00000007981	GRK5	0.178681761	0.251620063

ENSBTAG00000007986	NSD2	-0.465066961	0.00167668
ENSBTAG00000007992	NA	-0.307305278	0.045010891
ENSBTAG00000007993	CORO1C	-0.468938235	0.001514422
ENSBTAG00000007994	OSCP1	0.465175797	0.001671916
ENSBTAG00000007996	HTR6	0.384672782	0.010865888
ENSBTAG00000007998	TMCO4	0.502526207	0.000594686
ENSBTAG00000008001	NUCKS1	-0.647215902	2.73E-06
ENSBTAG00000008004	NCF2	-0.181588575	0.243862128
ENSBTAG00000008006	RASGRP3	-0.640498633	3.73E-06
ENSBTAG00000008008	TLR2	0.563325273	8.39E-05
ENSBTAG00000008010	FLCN	0.640301003	3.76E-06
ENSBTAG00000008016	STX17	-0.592511958	2.84E-05
ENSBTAG00000008021	LOC112441507	0.08561275	0.585161216
ENSBTAG00000008022	PTGFRN	0.174673637	0.262586404
ENSBTAG00000008023	RHBDL2	-0.445313393	0.002768231
ENSBTAG00000008026	OXT	-0.271136492	0.078631944
ENSBTAG00000008028	CHN1	-0.554268454	0.000115083
ENSBTAG00000008032	ACTR3B	-0.566825122	7.41E-05
ENSBTAG00000008036	CELSR1	-0.209769165	0.17698653
ENSBTAG00000008040	SPART	0.442018607	0.003001166
ENSBTAG00000008047	ZDHHC15	-0.51726477	0.000382501
ENSBTAG00000008048	GCFC2	0.233048184	0.132591028
ENSBTAG00000008057	PARVG	-0.286902692	0.062134081
ENSBTAG00000008061	RILPL1	-0.367539144	0.015323831
ENSBTAG00000008063	PPARA	-0.548511709	0.000140022
ENSBTAG00000008065	CDPF1	-0.420911396	0.004944199
ENSBTAG00000008066	LOC101904413	-0.500365547	0.000633381
ENSBTAG00000008074	C1QTNF6	-0.026958584	0.863751093
ENSBTAG00000008077	SLC37A4	-0.377444831	0.012588659
ENSBTAG00000008078	TRIM59	-0.565656727	7.72E-05
ENSBTAG00000008079	NRBP2	0.141455333	0.365564561
ENSBTAG00000008082	CEP350	0.266973521	0.08351546
ENSBTAG00000008084	ZNF382	-0.466986392	0.001594402
ENSBTAG00000008088	KIF18B	-0.426862181	0.00430865
ENSBTAG00000008091	SELENBP1	-0.355686563	0.019243092
ENSBTAG00000008092	RAB37	0.377255366	0.01263678
ENSBTAG00000008093	NA	-0.483705904	0.001015836
ENSBTAG00000008096	EDN1	0.37695706	0.012712862
ENSBTAG00000008098	DCLK2	-0.228072373	0.141300245
ENSBTAG00000008099	CCR5	0.560187773	9.37E-05
ENSBTAG00000008100	GOLGA7B	0.224449728	0.147902294
ENSBTAG00000008103	ALDH1A1	-0.170553929	0.274184485
ENSBTAG00000008105	RBM38	0.235222689	0.128913238
ENSBTAG00000008111	ESYT3	-0.307139456	0.045132712
ENSBTAG00000008115	TNFAIP1	0.478578177	0.001169275
ENSBTAG00000008116	POLDIP2	-0.522980524	0.000320581
ENSBTAG00000008118	RPF1	0.141545874	0.365254645

ENSBTAG00000008124	GK	0.1935072	0.213752865
ENSBTAG00000008125	KCNAB2	0.386091598	0.01055254
ENSBTAG00000008126	NPHP4	-0.32241298	0.034981287
ENSBTAG00000008129	CLSTN3	0.122673958	0.433222279
ENSBTAG00000008132	SOX13	0.412274985	0.00601122
ENSBTAG00000008133	ALKBH1	0.432471344	0.003776086
ENSBTAG00000008140	FAP	0.344398438	0.023728113
ENSBTAG00000008142	IFIH1	0.354593908	0.01964344
ENSBTAG00000008143	STK17A	0.431800997	0.003836543
ENSBTAG00000008147	MICAL1	0.246458773	0.111115112
ENSBTAG00000008150	PKIA	-0.190572942	0.220913611
ENSBTAG00000008151	MAP3K3	0.388824083	0.00997082
ENSBTAG00000008154	LIMD2	0.263271074	0.088054558
ENSBTAG00000008165	ITGA2B	0.572875786	5.95E-05
ENSBTAG00000008167	TTC3	-0.363306923	0.01663747
ENSBTAG00000008168	STARD6	-0.82898893	6.64E-12
ENSBTAG00000008169	C24H18orf54	-0.652123659	2.16E-06
ENSBTAG00000008170	POLA1	-0.456113392	0.002112236
ENSBTAG00000008172	EGLN3	0.21811165	0.159994321
ENSBTAG00000008175	ZNF713	-0.346116643	0.022993854
ENSBTAG00000008180	SPDL1	-0.633570313	5.11E-06
ENSBTAG00000008181	CHAF1A	-0.492135645	0.000802249
ENSBTAG00000008182	FOSB	0.368044066	0.015173145
ENSBTAG00000008184	CCT6A	-0.135897635	0.384889707
ENSBTAG00000008190	SUMF2	-0.47551933	0.001270321
ENSBTAG00000008193	NA	-0.225905001	0.145223405
ENSBTAG00000008195	PHKG1	0.140423022	0.36910926
ENSBTAG00000008198	RGL3	-0.47399583	0.001323485
ENSBTAG00000008201	ODAD3	-0.681981818	4.76E-07
ENSBTAG00000008203	NA	-0.374143268	0.013449921
ENSBTAG00000008216	RRM2	-0.34465741	0.023616207
ENSBTAG00000008223	NLRC4	0.588522415	3.31E-05
ENSBTAG00000008224	PAIP2	-0.278864636	0.070161841
ENSBTAG00000008232	DAB2IP	-0.268276068	0.081962698
ENSBTAG00000008237	TOLLIP	0.499718324	0.000645402
ENSBTAG00000008238	S100A7	0.18220622	0.242234781
ENSBTAG00000008243	LRRC40	-0.592688257	2.82E-05
ENSBTAG00000008248	DMD	-0.556771297	0.000105557
ENSBTAG00000008250	SPRY4	0.176521433	0.25749194
ENSBTAG00000008259	ACOD1	0.490526446	0.000839618
ENSBTAG00000008260	NA	0.423332746	0.004676374
ENSBTAG00000008267	CNOT11	0.277675609	0.071415924
ENSBTAG00000008269	NA	0.492803536	0.000787181
ENSBTAG00000008271	MEDAG	-0.254204784	0.099978091
ENSBTAG00000008274	NA	-0.318901628	0.037130757
ENSBTAG00000008275	GREB1L	-0.038932186	0.804237691
ENSBTAG00000008278	TMEM187	-0.094294093	0.547540329

ENSBTAG00000008279	FRMD4A	0.591866531	2.91E-05
ENSBTAG00000008280	HNF4G	-0.270163306	0.079753031
ENSBTAG00000008283	FLI1	0.131475003	0.400689009
ENSBTAG00000008288	ANKRD26	-0.535502326	0.000215323
ENSBTAG00000008289	ZBTB4	-0.566332067	7.54E-05
ENSBTAG00000008291	PROCR	-0.528755684	0.000267335
ENSBTAG00000008292	SNRPD1	0.11940053	0.44568746
ENSBTAG00000008293	GPCPD1	0.503090203	0.000584941
ENSBTAG00000008294	KCNJ2	0.530176818	0.000255521
ENSBTAG00000008300	FN1	-0.090805225	0.562520333
ENSBTAG00000008301	WNK2	-0.136892989	0.381385193
ENSBTAG00000008302	RINT1	-0.707185745	1.15E-07
ENSBTAG00000008309	ATP13A2	0.534832797	0.000220041
ENSBTAG00000008313	KLF15	-0.081319612	0.604182703
ENSBTAG00000008314	SDHB	-0.31247365	0.041345769
ENSBTAG00000008320	SEPTIN5	0.569386659	6.76E-05
ENSBTAG00000008323	SNAP25	-0.473308621	0.001348105
ENSBTAG00000008327	NA	0.358204027	0.018346758
ENSBTAG00000008328	LOC526163	0.325783444	0.033015314
ENSBTAG00000008329	CYTIP	0.001313901	0.993328217
ENSBTAG00000008330	RNF19B	0.515216984	0.000407177
ENSBTAG00000008331	TMEM54	-0.342141313	0.024722339
ENSBTAG00000008333	ETV4	0.027271453	0.862185
ENSBTAG00000008339	DHX8	0.544149803	0.000162074
ENSBTAG00000008340	ATOX1	-0.607734991	1.55E-05
ENSBTAG00000008346	NA	0.174548663	0.262933367
ENSBTAG00000008347	MRPL48	-0.596918337	2.39E-05
ENSBTAG00000008348	NOL4L	0.468872617	0.001517052
ENSBTAG00000008349	ZNF311	-0.585512041	3.72E-05
ENSBTAG00000008350	KLHL21	0.195981291	0.207841699
ENSBTAG00000008353	CDKN1A	0.373798757	0.013542613
ENSBTAG00000008361	PON2	-0.553889638	0.000116591
ENSBTAG00000008362	CTDSP1	0.601658686	1.98E-05
ENSBTAG00000008365	NA	-0.323821092	0.034148551
ENSBTAG00000008366	STAC2	-0.088696816	0.571664468
ENSBTAG00000008367	NA	-0.592501669	2.84E-05
ENSBTAG00000008371	FBXL20	-0.568060133	7.09E-05
ENSBTAG00000008373	ITGA10	-0.119927264	0.443668485
ENSBTAG00000008385	KLHL36	0.367656089	0.015288819
ENSBTAG00000008388	THOC2	0.30627572	0.045771587
ENSBTAG00000008389	HTRA1	-0.404089723	0.007201344
ENSBTAG00000008390	DNAJC10	-0.593151552	2.77E-05
ENSBTAG00000008395	APBA3	0.646328997	2.85E-06
ENSBTAG00000008397	ZNF555	-0.618403921	9.90E-06
ENSBTAG00000008399	ATRIP	0.673437436	7.47E-07
ENSBTAG00000008401	PFKFB3	0.006989062	0.964521507
ENSBTAG00000008403	ROCK1	0.28436511	0.064585172

ENSBTAG00000008406	TREX1	0.53462184	0.000221547
ENSBTAG00000008409	MYC	0.486874089	0.000930254
ENSBTAG00000008411	PLEKHO2	0.403173053	0.007346513
ENSBTAG00000008416	ABHD5	-0.532264415	0.00023902
ENSBTAG00000008419	PDE2A	0.217326897	0.161540141
ENSBTAG00000008421	SCRIB	0.016994736	0.913864186
ENSBTAG00000008428	UPP1	0.575936278	5.32E-05
ENSBTAG00000008429	LRP4	0.450821566	0.002414175
ENSBTAG00000008431	MOGAT1	-0.621175265	8.80E-06
ENSBTAG00000008432	NUP98	0.457007171	0.002064673
ENSBTAG00000008434	GCAT	-0.554658478	0.000113549
ENSBTAG00000008436	CDC25B	-0.488363577	0.000892288
ENSBTAG00000008438	ARFIP1	-0.553245271	0.000119197
ENSBTAG00000008441	SOCS3	0.614172349	1.18E-05
ENSBTAG00000008443	LARP1	0.230400519	0.137174025
ENSBTAG00000008448	MEIS1	-0.516224899	0.000394858
ENSBTAG00000008453	LBR	0.151047675	0.333613262
ENSBTAG00000008462	FAM43A	0.293624477	0.055998224
ENSBTAG00000008463	NA	0.540090899	0.000185371
ENSBTAG00000008464	ABCB9	-0.362271878	0.016972841
ENSBTAG00000008465	ACCS	-0.576256408	5.26E-05
ENSBTAG00000008466	CCNB1IP1	-0.041227311	0.792943066
ENSBTAG00000008468	NA	-0.257253695	0.095837467
ENSBTAG00000008470	MPHOSPH9	-0.634823109	4.83E-06
ENSBTAG00000008471	MX2	0.28394821	0.06499511
ENSBTAG00000008479	CXCL13	0.440445225	0.003118348
ENSBTAG00000008483	CALCRL	-0.427996664	0.004195937
ENSBTAG00000008485	NA	0.258047977	0.094780791
ENSBTAG00000008487	VPS37D	-0.437057128	0.003384403
ENSBTAG00000008490	CRYZL1	-0.471525987	0.001413877
ENSBTAG00000008492	ZMYM3	-0.533378324	0.000230614
ENSBTAG00000008493	AQP3	-0.615292544	1.13E-05
ENSBTAG00000008494	TMEM171	-0.244248439	0.114459776
ENSBTAG00000008497	RGS14	0.419259975	0.005134432
ENSBTAG00000008498	ALYREF	0.475830602	0.001259695
ENSBTAG00000008499	TROAP	-0.422665179	0.004748921
ENSBTAG00000008507	SPHK1	0.412411971	0.00599285
ENSBTAG00000008510	FBXO42	-0.188230062	0.22674879
ENSBTAG00000008513	RHEX	-0.290230627	0.059032518
ENSBTAG00000008518	MED25	-0.122218382	0.434945381
ENSBTAG00000008520	NFIC	0.339052151	0.026139159
ENSBTAG00000008528	SLC25A1	-0.191965063	0.217495917
ENSBTAG00000008530	SLC36A4	-0.564832527	7.95E-05
ENSBTAG00000008533	GLCCI1	-0.212788378	0.170693616
ENSBTAG00000008535	SOCS7	0.138764951	0.374845559
ENSBTAG00000008537	FAM219A	-0.571520357	6.25E-05
ENSBTAG00000008540	SLC22A1	0.396919911	0.008405894

ENSBTAG00000008541	MGST1	-0.217550315	0.161098948
ENSBTAG00000008542	SSPO	-0.175042561	0.261563948
ENSBTAG00000008543	GTF2H5	-0.515488333	0.000403827
ENSBTAG00000008544	SALL1	-0.028777229	0.854655098
ENSBTAG00000008545	ATF3	0.497070334	0.000696742
ENSBTAG00000008548	FAM98A	-0.54797677	0.000142572
ENSBTAG00000008550	GIMAP7	-0.364030195	0.016406457
ENSBTAG00000008551	TUSC1	-0.431161712	0.003894985
ENSBTAG00000008553	B4GALNT3	-0.277333127	0.071780406
ENSBTAG00000008554	NINJ2	0.022989992	0.883659018
ENSBTAG00000008555	P2RY10	-0.521757537	0.000333014
ENSBTAG00000008556	POU2F2	0.568896404	6.88E-05
ENSBTAG00000008562	POGLUT1	-0.485497422	0.000966619
ENSBTAG00000008567	DLEC1	-0.238835375	0.122972502
ENSBTAG00000008571	CUX2	-0.454677091	0.002190699
ENSBTAG00000008573	ZFP36	0.564002458	8.19E-05
ENSBTAG00000008575	CGNL1	-0.345278379	0.02334967
ENSBTAG00000008577	GRSF1	-0.651338269	2.24E-06
ENSBTAG00000008578	LSM4	-0.328816025	0.031325112
ENSBTAG00000008579	RCC2	0.563885753	8.23E-05
ENSBTAG00000008583	PALD1	-0.235158228	0.129021151
ENSBTAG00000008584	CLN8	-0.168675098	0.279584077
ENSBTAG00000008585	ARHGEF10	-0.430640122	0.003943242
ENSBTAG00000008590	SPAG7	-0.129683474	0.407194226
ENSBTAG00000008591	CAMTA2	0.384649666	0.010871058
ENSBTAG00000008592	FCGR1A	-0.552135278	0.000123811
ENSBTAG00000008596	PRICKLE1	-0.344600623	0.023640708
ENSBTAG00000008597	SLC45A4	0.620109168	9.21E-06
ENSBTAG00000008600	TRAF3IP2	0.144273123	0.355993625
ENSBTAG00000008603	TASL	0.424524156	0.004549298
ENSBTAG00000008607	ARID3A	0.494158771	0.000757381
ENSBTAG00000008609	SEPTIN8	-0.414411823	0.00573016
ENSBTAG00000008611	IGFBP4	-0.265578725	0.085203522
ENSBTAG00000008612	C1R	0.524136547	0.000309215
ENSBTAG00000008613	TCP11L1	-0.446006824	0.002721283
ENSBTAG00000008614	KASH5	-0.114249117	0.465696374
ENSBTAG00000008621	PRKAR1A	-0.200181419	0.198069838
ENSBTAG00000008624	NA	0.595480168	2.53E-05
ENSBTAG00000008625	PLEKHF1	-0.259046189	0.093465589
ENSBTAG00000008631	CORO1A	0.371047218	0.014302612
ENSBTAG00000008633	SLX1A	-0.199850524	0.198827729
ENSBTAG00000008636	PDE4B	0.44481456	0.002802443
ENSBTAG00000008638	FAM110A	0.273194129	0.076302259
ENSBTAG00000008648	PRDX5	0.536216466	0.000210391
ENSBTAG00000008649	ETV3	0.367232815	0.015415867
ENSBTAG00000008650	CAMK1D	0.42908974	0.004089783
ENSBTAG00000008654	HOOK2	-0.195909045	0.208012676

ENSBTAG00000008656	KBTBD6	0.06414296	0.682803478
ENSBTAG00000008661	C15H11orf52	-0.094172453	0.548059398
ENSBTAG00000008665	DIXDC1	0.246021665	0.111770577
ENSBTAG00000008674	FAM136A	-0.393600897	0.00901981
ENSBTAG00000008682	TLR3	0.381287801	0.011645779
ENSBTAG00000008683	LDHA	-0.042909038	0.784693383
ENSBTAG00000008686	NA	0.005872113	0.970188684
ENSBTAG00000008690	SLC6A9	0.558544874	9.92E-05
ENSBTAG00000008692	UQCR11	-0.223157491	0.150311382
ENSBTAG00000008695	TCF3	0.532131992	0.000240037
ENSBTAG00000008699	FEM1C	0.422451678	0.004772328
ENSBTAG00000008700	CRCT1	-0.3188484	0.037164155
ENSBTAG00000008703	EIF2AK2	0.169541502	0.277085524
ENSBTAG00000008704	FIGN	-0.153581517	0.325472302
ENSBTAG00000008705	CABLES1	0.166571859	0.285710604
ENSBTAG00000008709	POGLUT3	-0.50236341	0.000597526
ENSBTAG00000008711	BOK	-0.308223497	0.044341146
ENSBTAG00000008713	DCAF4	0.665575363	1.12E-06
ENSBTAG00000008716	SSB	-0.405325411	0.007009579
ENSBTAG00000008717	SERPINE2	-0.197389545	0.204528514
ENSBTAG00000008718	GALNT17	0.210429826	0.175595501
ENSBTAG00000008719	PRKCD	0.592176591	2.88E-05
ENSBTAG00000008721	MANSC1	-0.491813328	0.000809613
ENSBTAG00000008726	NCS1	-0.355843971	0.019185988
ENSBTAG00000008728	MRTFB	-0.139708053	0.371576306
ENSBTAG00000008729	DENND10	0.240501827	0.120302596
ENSBTAG00000008730	SFXN4	-0.36117733	0.017333688
ENSBTAG00000008732	ZC3H12C	0.40330387	0.007325643
ENSBTAG00000008733	MAGED1	-0.638389269	4.11E-06
ENSBTAG00000008734	PM20D1	-0.344045511	0.023881332
ENSBTAG00000008735	VASH1	-0.298731309	0.051669361
ENSBTAG00000008743	ALDH2	0.456010919	0.002117751
ENSBTAG00000008744	PDK2	-0.589330441	3.21E-05
ENSBTAG00000008747	DCXR	-0.533218221	0.000231806
ENSBTAG00000008755	MARCHF7	0.303966948	0.047515377
ENSBTAG00000008756	ELF3	-0.434867704	0.003566726
ENSBTAG00000008758	KIF20A	-0.421286803	0.00490182
ENSBTAG00000008759	CDC23	-0.534618087	0.000221574
ENSBTAG00000008761	TRAFD1	0.27701767	0.072117423
ENSBTAG00000008762	HECTD4	-0.064436264	0.681429669
ENSBTAG00000008764	SMYD5	0.232844217	0.132939974
ENSBTAG00000008765	PRADC1	-0.389366077	0.009858763
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ENSBTAG00000008771	MYEF2	-0.61963286	9.40E-06
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ENSBTAG00000008783	HTR7	0.137881144	0.377924748

ENSBTAG00000008787	FAM171A1	-0.385027287	0.010786858
ENSBTAG00000008789	HMG20B	-0.35012141	0.021355919
ENSBTAG00000008792	RNASE6	0.504017906	0.000569221
ENSBTAG00000008793	RNASE1	-0.398563795	0.008115387
ENSBTAG00000008794	ATF6B	0.660557284	1.43E-06
ENSBTAG00000008797	ARHGEF38	0.015049585	0.923692082
ENSBTAG00000008800	XKR8	0.674829223	6.95E-07
ENSBTAG00000008804	SAAL1	-0.645132966	3.01E-06
ENSBTAG00000008805	USP3	0.237778238	0.124689141
ENSBTAG00000008808	CCDC17	0.416414309	0.005477197
ENSBTAG00000008809	PTBP2	0.218596083	0.159045469
ENSBTAG00000008812	PFDN4	-0.175386297	0.260613685
ENSBTAG00000008814	ADGRA2	-0.510684171	0.000466956
ENSBTAG00000008816	TRIM2	-0.423901676	0.004615311
ENSBTAG00000008817	LAMA4	-0.123338527	0.430715548
ENSBTAG00000008826	RBBP9	-0.306871091	0.045330432
ENSBTAG00000008827	SPOCK2	-0.659478826	1.51E-06
ENSBTAG00000008836	NA	-0.554378791	0.000114647
ENSBTAG00000008839	AMER1	0.579090434	4.73E-05
ENSBTAG00000008840	HM13	0.462910221	0.001773597
ENSBTAG00000008842	JPH1	-0.052326596	0.738948698
ENSBTAG00000008844	EXTL3	-0.527253651	0.000280355
ENSBTAG00000008849	SORT1	-0.328342083	0.031584449
ENSBTAG00000008851	SIGLEC8	0.513065885	0.00043463
ENSBTAG00000008852	SIGLEC10	-0.235287478	0.128804841
ENSBTAG00000008853	HNRNPF	0.585144279	3.77E-05
ENSBTAG00000008854	RFX1	0.548450322	0.000140312
ENSBTAG00000008858	ARHGAP8	-0.271778783	0.077898828
ENSBTAG00000008860	RIPOR1	-0.311942833	0.041710602
ENSBTAG00000008862	GOLGB1	-0.672533685	7.83E-07
ENSBTAG00000008864	LY96	0.170065719	0.275580914
ENSBTAG00000008866	GANC	0.315151339	0.039544837
ENSBTAG00000008868	CAPN3	-0.405071771	0.007048577
ENSBTAG00000008870	KCNS1	0.328414205	0.031544871
ENSBTAG00000008877	APBA1	0.100117179	0.522969456
ENSBTAG00000008880	POGLUT2	-0.47164536	0.001409386
ENSBTAG00000008883	ZNF207	0.217888814	0.160432169
ENSBTAG00000008884	MAPRE3	-0.59655859	2.42E-05
ENSBTAG00000008893	ANO10	-0.387657154	0.010215794
ENSBTAG00000008897	BIN2	0.597124233	2.37E-05
ENSBTAG00000008902	ZNF345	-0.785030864	4.62E-10
ENSBTAG00000008908	GZF1	0.528595516	0.000268696
ENSBTAG00000008909	PNPT1	0.239113776	0.122523389
ENSBTAG00000008915	SF3B1	0.413046642	0.005908374
ENSBTAG00000008916	CYFIP2	-0.002997674	0.984778999
ENSBTAG00000008921	NEXN	-0.277615161	0.071480149
ENSBTAG00000008931	CREG1	-0.590426748	3.08E-05

ENSBTAG00000008934	ESPL1	-0.26873748	0.08141809
ENSBTAG00000008937	NA	0.624877122	7.50E-06
ENSBTAG00000008938	SRC	0.52521793	0.000298913
ENSBTAG00000008939	DNMBP	0.32093254	0.035874722
ENSBTAG00000008945	SDSL	0.176214921	0.258332408
ENSBTAG00000008947	TKTL2	-0.118159388	0.450464637
ENSBTAG00000008948	P2RX7	-0.608977604	1.47E-05
ENSBTAG00000008951	ALPL	0.682976494	4.51E-07
ENSBTAG00000008952	RAP1GAP	0.584380805	3.88E-05
ENSBTAG00000008953	TAP1	0.541896693	0.000174656
ENSBTAG00000008954	PSMB9	0.53223818	0.000239221
ENSBTAG00000008956	CD8B	-0.386262003	0.010515431
ENSBTAG00000008958	NSMAF	0.533000495	0.000233435
ENSBTAG00000008959	NA	0.475692109	0.001264413
ENSBTAG00000008963	CIT	-0.440580181	0.003108142
ENSBTAG00000008966	TSPAN7	-0.459065791	0.0019587
ENSBTAG00000008967	RAP1B	0.338137757	0.02657127
ENSBTAG00000008993	INTS6L	0.070617231	0.652720973
ENSBTAG00000008994	FPGS	0.37489154	0.013250453
ENSBTAG00000008996	SFI1	0.217171235	0.161848053
ENSBTAG00000008997	ENG	0.595199967	2.56E-05
ENSBTAG00000008998	NA	0.539497973	0.000189016
ENSBTAG00000009002	LOC509941	-0.438236499	0.003289617
ENSBTAG00000009005	NA	-0.441883628	0.003011065
ENSBTAG00000009006	PISD	0.35869304	0.018176792
ENSBTAG00000009012	PTX3	0.465500629	0.001657769
ENSBTAG00000009013	NA	0.307830166	0.044627041
ENSBTAG00000009019	SH3PXD2B	0.512826123	0.00043779
ENSBTAG00000009020	CRIM1	0.079064929	0.614278259
ENSBTAG00000009023	TMTC3	-0.590445951	3.08E-05
ENSBTAG00000009024	KCND1	0.170387349	0.274660431
ENSBTAG00000009026	PACS1	-0.549745704	0.000134297
ENSBTAG00000009029	LOC507443	-0.239108805	0.122531397
ENSBTAG00000009035	CENPE	-0.520423897	0.000347065
ENSBTAG00000009036	SUPT6H	0.594854013	2.59E-05
ENSBTAG00000009037	GALNT12	0.210971703	0.174460449
ENSBTAG00000009046	TBX6	-0.233921389	0.13110487
ENSBTAG00000009047	YPEL3	-0.14192821	0.363947678
ENSBTAG00000009048	EFHD2	0.641462676	3.57E-06
ENSBTAG00000009049	LOC507581	-0.448486093	0.002559104
ENSBTAG00000009050	ADIPOR2	-0.21371955	0.168785755
ENSBTAG00000009051	MMP19	-0.717593225	6.12E-08
ENSBTAG00000009055	RNF144B	0.527894511	0.000274731
ENSBTAG00000009058	TMEM177	-0.349507177	0.021600595
ENSBTAG00000009064	CSF2RB	0.594930977	2.58E-05
ENSBTAG00000009065	MAP3K5	0.446628134	0.002679815
ENSBTAG00000009072	ZNF572	-0.49161492	0.000814176

ENSBTAG00000009075	RNF207	-0.405691672	0.006953595
ENSBTAG00000009078	MIA	0.452069201	0.002339756
ENSBTAG00000009080	ITGB6	-0.408417756	0.006548914
ENSBTAG00000009085	SLC35A5	0.166764747	0.285145131
ENSBTAG00000009086	LOXL1	0.091573242	0.559206438
ENSBTAG00000009091	RNASEL	-0.005990924	0.969585784
ENSBTAG00000009097	FANCI	-0.635298905	4.73E-06
ENSBTAG00000009101	SH2B3	0.619702252	9.37E-06
ENSBTAG00000009107	CBX8	-0.400761405	0.007740565
ENSBTAG00000009111	NA	-0.120237824	0.442480464
ENSBTAG00000009112	TRAM2	0.331554241	0.029860992
ENSBTAG00000009123	ING5	0.525945034	0.000292161
ENSBTAG00000009125	ALDH1A3	-0.357380091	0.018636162
ENSBTAG00000009126	YBX2	-0.313103559	0.040916209
ENSBTAG00000009127	TSPYL4	-0.53488354	0.00021968
ENSBTAG00000009129	POLI	-0.539742262	0.000187507
ENSBTAG00000009132	TMPRSS2	0.177899384	0.253736124
ENSBTAG00000009137	NKG7	-0.193783327	0.213087408
ENSBTAG00000009139	LDLRAD4	0.202609942	0.19256969
ENSBTAG00000009145	SLC7A4	-0.280886977	0.068068876
ENSBTAG00000009150	SPON1	-0.380560442	0.01181946
ENSBTAG00000009151	PYGO1	-0.582961292	4.09E-05
ENSBTAG00000009153	MLXIPL	-0.170397326	0.27463191
ENSBTAG00000009159	PLXNA1	0.403330568	0.00732139
ENSBTAG00000009165	LPIN3	-0.570662601	6.45E-05
ENSBTAG00000009167	SLC15A4	0.331146486	0.030075359
ENSBTAG00000009171	LOC527385	0.501157181	0.000618949
ENSBTAG00000009172	BCAT2	-0.105900268	0.499119401
ENSBTAG00000009174	HSD17B14	-0.357002591	0.018770036
ENSBTAG00000009177	PLEKHA4	0.331613098	0.029830154
ENSBTAG00000009181	INPP5A	-0.208010238	0.180728462
ENSBTAG00000009182	CLCN1	0.034974095	0.823807526
ENSBTAG00000009183	SHISA5	0.562424423	8.66E-05
ENSBTAG00000009187	DNAJC28	-0.489377969	0.000867229
ENSBTAG00000009191	TUSC3	-0.25537591	0.098371677
ENSBTAG00000009194	OSBPL10	-0.215191267	0.16580187
ENSBTAG00000009201	CORO7	0.377067319	0.012684696
ENSBTAG00000009206	FOXS1	0.525226807	0.00029883
ENSBTAG00000009207	KMT2E	0.446504677	0.00268801
ENSBTAG00000009208	TCTN1	-0.619638067	9.40E-06
ENSBTAG00000009209	BEND5	-0.37461378	0.0133242
ENSBTAG00000009210	ZBTB44	0.061882095	0.693426861
ENSBTAG00000009211	UBE2S	0.368103283	0.015155556
ENSBTAG00000009212	APOA2	0.381566903	0.011579715
ENSBTAG00000009214	ETS2	0.540369031	0.000183683
ENSBTAG00000009215	NR1I3	0.145465917	0.351988437
ENSBTAG00000009216	HVCN1	0.089997655	0.566014708

ENSBTAG00000009218	ANLN	-0.421340814	0.004895749
ENSBTAG00000009223	SFN	0.550884978	0.000129201
ENSBTAG00000009226	SCUBE3	0.142161236	0.363152488
ENSBTAG00000009231	NSDHL	0.047631162	0.761655987
ENSBTAG00000009232	PIK3CA	0.326635646	0.032532922
ENSBTAG00000009233	NA	0.536586084	0.000207879
ENSBTAG00000009236	DAGLB	0.517502601	0.000379724
ENSBTAG00000009239	SLC16A10	0.16764727	0.282567211
ENSBTAG00000009245	PPP2CB	-0.555795248	0.000109184
ENSBTAG00000009246	DPY30	-0.694139011	2.44E-07
ENSBTAG00000009255	NA	0.137496971	0.379267874
ENSBTAG00000009256	ITGA4	-0.11077854	0.479442743
ENSBTAG00000009257	CERKL	0.027802411	0.859528436
ENSBTAG00000009258	NEK11	-0.298978138	0.051467167
ENSBTAG00000009263	MFSD1	-0.255671176	0.097969816
ENSBTAG00000009266	NA	-0.259340476	0.093080552
ENSBTAG00000009267	UHRF1BP1	-0.27354169	0.075914154
ENSBTAG00000009271	PNMA1	0.38063232	0.011802199
ENSBTAG00000009272	MIDEAS	0.210340833	0.175782419
ENSBTAG00000009278	MSL3	-0.532333193	0.000238493
ENSBTAG00000009284	GLS2	0.43784591	0.003320748
ENSBTAG00000009286	ZC3H4	0.200739462	0.196796293
ENSBTAG00000009287	EBP	-0.510543687	0.000468928
ENSBTAG00000009289	MS4A8	0.246807186	0.110594743
ENSBTAG00000009290	NA	-0.585341628	3.74E-05
ENSBTAG00000009293	EVL	-0.518178811	0.000371928
ENSBTAG00000009294	DEGS2	-0.438951414	0.0032333
ENSBTAG00000009297	PANX2	-0.482133924	0.001060848
ENSBTAG00000009298	XYLT2	-0.396015676	0.008569475
ENSBTAG00000009299	AFTPH	-0.04726401	0.763440183
ENSBTAG00000009315	CDON	-0.159315929	0.307512163
ENSBTAG00000009331	CPAMD8	-0.457686495	0.002029156
ENSBTAG00000009334	NDUFA5	-0.539534384	0.000188791
ENSBTAG00000009336	LXN	-0.60451008	1.76E-05
ENSBTAG00000009337	PNMA8A	0.022475363	0.886246042
ENSBTAG00000009340	KATNAL1	0.218080675	0.160055132
ENSBTAG00000009341	CCDC146	0.306187654	0.045837137
ENSBTAG00000009343	AAK1	-0.306815306	0.045371621
ENSBTAG00000009351	ATXN10	-0.571067639	6.36E-05
ENSBTAG00000009353	EVI2B	0.298410448	0.051933156
ENSBTAG00000009354	EVI2A	-0.100450519	0.521579593
ENSBTAG00000009357	IL34	-0.03968083	0.800549064
ENSBTAG00000009358	MTSS2	-0.332988872	0.029116798
ENSBTAG00000009359	LOC782705	0.265401457	0.08541995
ENSBTAG00000009362	SYNE1	0.207887595	0.180991466
ENSBTAG00000009363	GINS3	-0.535184691	0.00021755
ENSBTAG00000009366	ARF5	-0.259139464	0.093343417

ENSBTAG00000009368	RRAGC	0.184611554	0.23596748
ENSBTAG00000009374	PARP2	-0.588679275	3.29E-05
ENSBTAG00000009376	DPH1	0.437068427	0.003383483
ENSBTAG00000009381	LCP2	0.531603971	0.000244133
ENSBTAG00000009383	KIF11	-0.512331128	0.000444381
ENSBTAG00000009384	AGTRAP	0.525275526	0.000298373
ENSBTAG00000009386	NA	-0.093045138	0.552881023
ENSBTAG00000009389	HNRNPH1	0.513374047	0.000430598
ENSBTAG00000009390	MINDY4	-0.18297425	0.240221484
ENSBTAG00000009392	NA	-0.459646866	0.001929671
ENSBTAG00000009393	GAL	0.198356454	0.2022752
ENSBTAG00000009394	NSMCE2	0.238906128	0.122858246
ENSBTAG00000009396	EXO1	0.113365059	0.469177826
ENSBTAG00000009407	MBTD1	-0.16188484	0.299675397
ENSBTAG00000009412	SIAE	-0.340544551	0.025446469
ENSBTAG00000009417	ZFAND5	-0.407340199	0.00670637
ENSBTAG00000009419	TRIM29	-0.386834968	0.010391477
ENSBTAG00000009421	CD1E	-0.113521729	0.468559845
ENSBTAG00000009423	NIPAL1	-0.417707321	0.005319063
ENSBTAG00000009426	EZH2	0.533732284	0.000228
ENSBTAG00000009427	PPM1D	0.540508134	0.000182844
ENSBTAG00000009428	GAN	-0.167646428	0.282569664
ENSBTAG00000009434	PAQR6	0.250533929	0.105144009
ENSBTAG00000009436	TMEM79	0.34811722	0.022162959
ENSBTAG00000009441	RBBP6	0.127691198	0.414499091
ENSBTAG00000009455	IL12RB2	-0.486914541	0.000929204
ENSBTAG00000009459	MTCL1	-0.175648536	0.259890271
ENSBTAG00000009461	STYXL1	-0.251690344	0.103495074
ENSBTAG00000009462	MDH2	-0.210166167	0.176149694
ENSBTAG00000009469	SREK1IP1	0.126240523	0.419864741
ENSBTAG00000009470	CLIC4	0.431429442	0.003870415
ENSBTAG00000009477	PIR	-0.438158538	0.00329581
ENSBTAG00000009479	UQCRQ	-0.341843444	0.024856103
ENSBTAG00000009482	AFF4	0.37650579	0.0128287
ENSBTAG00000009486	TMEM179B	-0.216471375	0.163237702
ENSBTAG00000009488	NXF1	0.384669701	0.010866577
ENSBTAG00000009493	BCL3	0.615608126	1.11E-05
ENSBTAG00000009494	CBLC	-0.266466655	0.084125855
ENSBTAG00000009495	BCAM	-0.317807764	0.037822062
ENSBTAG00000009496	STAT5A	0.526833798	0.000284095
ENSBTAG00000009502	LUZP1	0.253386605	0.101112269
ENSBTAG00000009512	EPS8L1	-0.335681737	0.027761391
ENSBTAG00000009513	TGFBI	0.25507325	0.098784916
ENSBTAG00000009517	DBI	-0.153500399	0.325730981
ENSBTAG00000009519	TRIM23	-0.714834145	7.25E-08
ENSBTAG00000009522	EIF4E	0.029186514	0.852610566
ENSBTAG00000009527	TCEANC2	0.058554075	0.709170242

ENSBTAG00000009539	NA	-0.068587205	0.662097825
ENSBTAG00000009541	SUCLG2	-0.576483282	5.21E-05
ENSBTAG00000009543	ESYT1	-0.539752733	0.000187442
ENSBTAG00000009545	PPEF1	-0.43084783	0.003923963
ENSBTAG00000009548	MAD2L1BP	-0.083606968	0.594014848
ENSBTAG00000009552	ATP2B1	-0.073476084	0.639605081
ENSBTAG00000009554	EHBP1L1	0.557298154	0.000103646
ENSBTAG00000009562	ZNF593	0.407659698	0.006659346
ENSBTAG00000009568	KANK2	-0.38189742	0.011501896
ENSBTAG00000009569	DOCK6	-0.481668159	0.001074521
ENSBTAG00000009573	CSTPP1	-0.553563428	0.000117904
ENSBTAG00000009575	TBC1D32	-0.354855868	0.019546825
ENSBTAG00000009576	PACSIN3	-0.267418807	0.082982077
ENSBTAG00000009578	PTK2	0.110600338	0.480154276
ENSBTAG00000009579	CEP85	-0.412463557	0.005985945
ENSBTAG00000009581	UBXN11	-0.539718027	0.000187656
ENSBTAG00000009586	CDC25A	-0.35196836	0.020634151
ENSBTAG00000009598	CHM	0.384977011	0.010798036
ENSBTAG00000009602	TMEM120B	-0.171525703	0.271418795
ENSBTAG00000009603	UQCRH	0.066132892	0.673502875
ENSBTAG00000009607	LARGE2	-0.39381921	0.008978277
ENSBTAG00000009611	PHF21A	0.148288725	0.342619957
ENSBTAG00000009614	NRROS	0.564816904	7.96E-05
ENSBTAG00000009615	ANXA2	0.443459782	0.002897241
ENSBTAG00000009617	SLC2A1	0.392968275	0.009141097
ENSBTAG00000009618	NEK2	-0.353575505	0.020022864
ENSBTAG00000009632	LARP7	-0.045169659	0.773640703
ENSBTAG00000009637	SLC12A2	0.099881056	0.523955078
ENSBTAG00000009639	SMPD3	-0.749331702	7.43E-09
ENSBTAG00000009641	MTHFD1	-0.241587803	0.118586367
ENSBTAG00000009642	AKAP5	-0.11142533	0.476864867
ENSBTAG00000009646	ALDH7A1	-0.444238338	0.002842425
ENSBTAG00000009649	DRC1	-0.458900532	0.001967026
ENSBTAG00000009654	LPAR1	-0.243952893	0.114912714
ENSBTAG00000009655	TNS3	0.54963781	0.000134789
ENSBTAG00000009656	BOLA-DQA2	0.290777262	0.058535109
ENSBTAG00000009657	MTMR1	-0.498010761	0.000678105
ENSBTAG00000009658	PLEK	0.503315014	0.000581096
ENSBTAG00000009661	RNASEH2A	-0.648432058	2.58E-06
ENSBTAG00000009663	YBX3	0.210724897	0.17497677
ENSBTAG00000009664	NA	0.543268984	0.000166892
ENSBTAG00000009665	UTRN	0.09601577	0.540218743
ENSBTAG00000009668	TMEM184B	0.395623976	0.008641181
ENSBTAG00000009677	PARP10	0.510956795	0.000463149
ENSBTAG00000009679	PLEKHG1	-0.456844724	0.002073246
ENSBTAG00000009681	PPP2R3C	0.227504926	0.142319716
ENSBTAG00000009683	PSMA6	-0.330120208	0.03062054

ENSBTAG00000009685	ERI1	-0.656994911	1.71E-06
ENSBTAG00000009689	RWDD1	-0.397686135	0.008269392
ENSBTAG00000009691	SH2B2	0.563460029	8.35E-05
ENSBTAG00000009694	PUS10	-0.031738873	0.839882604
ENSBTAG00000009696	ACTN2	0.338529326	0.026385506
ENSBTAG00000009698	ABCD3	-0.636288025	4.52E-06
ENSBTAG00000009703	MYH7	-0.428393152	0.004157157
ENSBTAG00000009704	CECR2	-0.008435309	0.957186149
ENSBTAG00000009708	SMYD4	-0.583891934	3.95E-05
ENSBTAG00000009711	RPA1	-0.590323504	3.09E-05
ENSBTAG00000009713	ATP5MK	-0.22599674	0.145055737
ENSBTAG00000009714	ARHGAP33	-0.075142528	0.632009159
ENSBTAG00000009717	FGL2	0.452895845	0.002291569
ENSBTAG00000009719	CALHM2	-0.27747973	0.071624206
ENSBTAG00000009725	AOX1	-0.283522658	0.065415684
ENSBTAG00000009733	FBP1	-0.492598813	0.000791773
ENSBTAG00000009734	XPA	-0.335079303	0.028059976
ENSBTAG00000009736	CDC42BPG	-0.02403934	0.878387701
ENSBTAG00000009737	LTC4S	-0.050562214	0.747456793
ENSBTAG00000009738	MGAT4B	-0.480423735	0.001111826
ENSBTAG00000009746	MPHOSPH6	-0.554809513	0.00011296
ENSBTAG00000009749	USP2	0.27201819	0.077626942
ENSBTAG00000009760	LOC515736	0.215252294	0.165678971
ENSBTAG00000009762	BEAN1	-0.645720832	2.93E-06
ENSBTAG00000009765	MTMR14	-0.527614182	0.000277178
ENSBTAG00000009768	IFIT3	0.391480041	0.009431962
ENSBTAG00000009770	GPD2	0.127883519	0.413790693
ENSBTAG00000009772	LIX1	-0.371528947	0.014166998
ENSBTAG00000009773	KREMEN1	0.185317003	0.234150513
ENSBTAG00000009777	NUP35	-0.583396205	4.03E-05
ENSBTAG00000009778	KRAS	0.468540674	0.001530418
ENSBTAG00000009780	GTF2I	-0.439897458	0.003160077
ENSBTAG00000009782	NA	-0.365249544	0.016023139
ENSBTAG00000009785	SAMD4B	0.552659806	0.000121611
ENSBTAG00000009786	SCIN	-0.339975826	0.025708614
ENSBTAG00000009797	RIMBP2	-0.332144118	0.029553119
ENSBTAG00000009803	SNCB	-0.314908225	0.039705656
ENSBTAG00000009806	INVS	-0.550626893	0.00013034
ENSBTAG00000009811	BOP1	0.559760291	9.51E-05
ENSBTAG00000009812	CXCL5	-0.525922397	0.000292369
ENSBTAG00000009819	CDC20	-0.357955497	0.018433651
ENSBTAG00000009826	GPD1L	-0.333624027	0.028792262
ENSBTAG00000009830	PLEKHB1	-0.262331859	0.089235915
ENSBTAG00000009832	NOBOX	-0.213107981	0.170037041
ENSBTAG00000009834	NA	0.061894949	0.6933663
ENSBTAG00000009835	CACNA1G	-0.138953312	0.374191243
ENSBTAG00000009837	ANKS4B	-0.196825619	0.205850788

ENSBTAG00000009838	RRP15	0.483729092	0.001015185
ENSBTAG00000009839	GSTK1	-0.30408749	0.047423022
ENSBTAG00000009841	CNDP2	-0.065585549	0.676056345
ENSBTAG00000009844	CCN1	-0.368138584	0.015145078
ENSBTAG00000009845	ITPK1	0.308257904	0.044316208
ENSBTAG00000009846	MTHFD1L	0.05624774	0.720151541
ENSBTAG00000009848	GPR171	0.149234829	0.33951465
ENSBTAG00000009849	PLAC8A	0.132202811	0.398063539
ENSBTAG00000009850	GIMAP7	-0.413967236	0.005787678
ENSBTAG00000009852	NAV3	-0.260957884	0.090986215
ENSBTAG00000009855	FAN1	-0.446380027	0.002696307
ENSBTAG00000009856	ACAP3	-0.049762433	0.751323295
ENSBTAG00000009861	FRS3	-0.54480978	0.000158548
ENSBTAG00000009863	BHLHE40	0.574913136	5.52E-05
ENSBTAG00000009867	GARIN1B	-0.722897741	4.39E-08
ENSBTAG00000009868	VGF	0.52232309	0.000327211
ENSBTAG00000009872	SPHK2	-0.216393564	0.163392739
ENSBTAG00000009873	NRN1	-0.094958273	0.544710256
ENSBTAG00000009877	MCMBP	-0.38875048	0.009986121
ENSBTAG00000009879	PCGF6	-0.50866292	0.000496065
ENSBTAG00000009881	ENTPD6	0.085256959	0.586727384
ENSBTAG00000009886	KDELR3	-0.341036716	0.025221413
ENSBTAG00000009887	DDX17	0.403699184	0.007262886
ENSBTAG00000009888	DRAM2	0.200972856	0.196265366
ENSBTAG00000009889	ZNF181	-0.71752448	6.15E-08
ENSBTAG00000009895	ZNF599	-0.501534211	0.00061218
ENSBTAG00000009902	AKR1B1	-0.627664606	6.64E-06
ENSBTAG00000009904	SPIC	-0.580471559	4.50E-05
ENSBTAG00000009912	PAN3	0.312220952	0.041519124
ENSBTAG00000009915	AP2A2	-0.024965971	0.873737152
ENSBTAG00000009917	PIP5K1B	0.047349236	0.763025913
ENSBTAG00000009918	GSE1	0.532447019	0.000237623
ENSBTAG00000009924	MR1	0.316201671	0.038856154
ENSBTAG00000009933	DTX3L	0.38338964	0.011156093
ENSBTAG00000009941	MBIP	-0.559976977	9.44E-05
ENSBTAG00000009942	PLCL2	0.022265036	0.887303688
ENSBTAG00000009943	XCL2	-0.257687626	0.095259065
ENSBTAG00000009945	BRICD5	-0.143758658	0.357729609
ENSBTAG00000009948	TRIM25	0.375605221	0.013062557
ENSBTAG00000009949	DARS1	-0.434867582	0.003566737
ENSBTAG00000009951	PGP	0.320920667	0.035881963
ENSBTAG00000009956	CENPM	-0.448285446	0.002571905
ENSBTAG00000009958	TRIM35	0.521674593	0.000333872
ENSBTAG00000009959	SLC6A8	0.300156401	0.050510743
ENSBTAG00000009960	FLOT1	0.714330769	7.48E-08
ENSBTAG00000009965	ECI1	-0.1752224	0.261066495
ENSBTAG00000009966	XRCC3	-0.057406843	0.71462552

ENSBTAG00000009972	INHA	-0.356039247	0.019115344
ENSBTAG00000009975	PBX4	-0.213609687	0.169010045
ENSBTAG00000009982	IGSF8	0.642095547	3.47E-06
ENSBTAG00000009983	KIF23	-0.214103377	0.168003838
ENSBTAG00000009984	SGPL1	-0.488362334	0.000892319
ENSBTAG00000009987	ITGB3	-0.666793993	1.05E-06
ENSBTAG00000009994	EML5	0.061113439	0.697052018
ENSBTAG00000009996	DOT1L	0.276203592	0.072992905
ENSBTAG00000009997	ANO1	-0.299838852	0.050767082
ENSBTAG00000009998	GALNT16	-0.111543527	0.476394568
ENSBTAG00000010002	IRF2	0.458069908	0.00200935
ENSBTAG00000010006	EMC2	-0.073977937	0.637313675
ENSBTAG00000010007	MAPK13	0.145566269	0.351652731
ENSBTAG00000010015	NMRAL1	-0.54760246	0.000144381
ENSBTAG00000010018	ATP7A	0.201954582	0.19404319
ENSBTAG00000010020	LOC533921	-0.403771557	0.007251447
ENSBTAG00000010023	FAM107B	0.382384475	0.011388034
ENSBTAG00000010027	CHDH	0.187668886	0.228162019
ENSBTAG00000010030	NA	-0.373411968	0.013647327
ENSBTAG00000010033	NA	0.070020722	0.655470901
ENSBTAG00000010042	RIOK3	0.493386148	0.000774244
ENSBTAG00000010047	TIAM2	0.478431251	0.00117396
ENSBTAG00000010048	SPC25	-0.701557236	1.60E-07
ENSBTAG00000010050	NA	-0.213662662	0.168901868
ENSBTAG00000010052	EXD2	0.650115385	2.38E-06
ENSBTAG00000010059	C8H9orf72	-0.320373511	0.036216927
ENSBTAG00000010060	SLC43A3	-0.405662449	0.006958047
ENSBTAG00000010063	KDM3B	0.280448809	0.068518098
ENSBTAG00000010065	TRPC5	0.25679012	0.096458367
ENSBTAG00000010069	EGR1	0.478736119	0.001164257
ENSBTAG00000010073	FLOT2	0.663061662	1.27E-06
ENSBTAG00000010077	FANCD2	-0.519915382	0.000352561
ENSBTAG00000010083	HADHB	-0.606318146	1.64E-05
ENSBTAG00000010091	ARL6	-0.506378832	0.000530911
ENSBTAG00000010096	SLC5A2	-0.377198719	0.012651198
ENSBTAG00000010101	BYSL	0.49928618	0.000653542
ENSBTAG00000010106	CCND3	-0.141821344	0.364312701
ENSBTAG00000010107	WHRN	0.043809499	0.780285685
ENSBTAG00000010109	CDK1	-0.585313473	3.75E-05
ENSBTAG00000010113	ZBTB24	-0.23125445	0.135683237
ENSBTAG00000010118	HAT1	-0.740616671	1.37E-08
ENSBTAG00000010119	ALDH1A2	-0.096899973	0.536477011
ENSBTAG00000010120	HERC3	-0.37951637	0.012072629
ENSBTAG00000010123	APOE	-0.636384044	4.50E-06
ENSBTAG00000010124	ATG4C	-0.386200656	0.010528778
ENSBTAG00000010125	STAT5B	0.49851721	0.000668254
ENSBTAG00000010126	PCIF1	0.492584764	0.000792089

ENSBTAG00000010128	NAP1L5	0.252903646	0.101786375
ENSBTAG00000010130	ZNF335	0.553499497	0.000118163
ENSBTAG00000010134	OSTM1	0.537540477	0.000201517
ENSBTAG00000010135	PEDS1	-0.436635241	0.003418886
ENSBTAG00000010144	MTERF2	-0.491023236	0.000827919
ENSBTAG00000010146	PLXNB3	-0.438377329	0.003278456
ENSBTAG00000010148	LOC505856	0.563274337	8.41E-05
ENSBTAG00000010152	MID1	-0.350124556	0.021354672
ENSBTAG00000010153	ANXA3	0.540712661	0.000181616
ENSBTAG00000010155	LOC504773	0.214080652	0.168050061
ENSBTAG00000010156	TPT1	0.594558516	2.62E-05
ENSBTAG00000010158	NA	-0.339788149	0.025795613
ENSBTAG00000010161	CCL21	0.080123878	0.609527792
ENSBTAG00000010164	ESPNL	-0.037852767	0.809563448
ENSBTAG00000010166	MIC2	0.392600146	0.009212319
ENSBTAG00000010167	TEX14	-0.010349975	0.94748044
ENSBTAG00000010171	NA	0.413358018	0.005867309
ENSBTAG00000010174	SPATA46	0.030147962	0.847811552
ENSBTAG00000010175	COL8A2	-0.547113326	0.000146776
ENSBTAG00000010179	COL5A3	-0.298414216	0.051930051
ENSBTAG00000010180	URB2	0.346316784	0.022909575
ENSBTAG00000010191	PAK1	0.209588494	0.177368305
ENSBTAG00000010193	RAB7A	-0.076205984	0.627181166
ENSBTAG00000010195	PKN3	-0.355467814	0.019322687
ENSBTAG00000010196	NUP43	-0.618022401	1.01E-05
ENSBTAG00000010206	UAP1	0.51438006	0.000417667
ENSBTAG00000010208	ZER1	-0.3267799	0.032451844
ENSBTAG00000010215	CREB3L3	-0.540865009	0.000180707
ENSBTAG00000010217	ZNF318	0.019972102	0.898846037
ENSBTAG00000010219	KRBA1	-0.463848343	0.001730848
ENSBTAG00000010228	NA	-0.311691206	0.04188446
ENSBTAG00000010234	DHRS1	-0.551880249	0.000124894
ENSBTAG00000010235	NOP9	0.59271915	2.82E-05
ENSBTAG00000010236	CIDEB	0.289168892	0.060008291
ENSBTAG00000010238	LTB4R	0.602500004	1.91E-05
ENSBTAG00000010239	GARIN2	-0.325318602	0.033280914
ENSBTAG00000010242	LAMP1	0.441181538	0.003063018
ENSBTAG00000010243	RBM33	0.291624253	0.057771016
ENSBTAG00000010244	CLIC5	0.60096681	2.03E-05
ENSBTAG00000010246	GRTP1	0.511535888	0.000455156
ENSBTAG00000010247	FKTN	-0.528135531	0.000272643
ENSBTAG00000010252	ZNF397	-0.433035939	0.003725816
ENSBTAG00000010253	SYTL1	-0.137756684	0.37835957
ENSBTAG00000010254	MAP3K6	0.379865342	0.0119875
ENSBTAG00000010256	TMEM170B	-0.077834134	0.619819261
ENSBTAG00000010264	FBXL18	0.267022793	0.083456309
ENSBTAG00000010265	MGST3	-0.374236891	0.013424825

ENSBTAG00000010270	LOC512541	-0.257794121	0.095117527
ENSBTAG00000010273	EREG	0.154101375	0.323817572
ENSBTAG00000010276	RECQL4	-0.467520768	0.001572141
ENSBTAG00000010278	STPG1	-0.498317523	0.000672123
ENSBTAG00000010279	DUSP14	-0.447907643	0.002596162
ENSBTAG00000010285	MMRN1	0.046112992	0.769041435
ENSBTAG00000010286	NPAT	-0.553040504	0.000120037
ENSBTAG00000010293	PARD3B	-0.351142438	0.02095434
ENSBTAG00000010300	NA	-0.28597278	0.063023548
ENSBTAG00000010303	ICAM1	0.506401232	0.000530559
ENSBTAG00000010304	CHKA	0.428367119	0.004159694
ENSBTAG00000010309	XPO6	0.508452769	0.000499183
ENSBTAG00000010314	ICAM4	0.57075249	6.43E-05
ENSBTAG00000010316	ICAM5	0.490219038	0.00084693
ENSBTAG00000010318	FDX2	0.041866811	0.789803324
ENSBTAG00000010322	HYOU1	0.335859687	0.0276737
ENSBTAG00000010324	GTPBP1	0.572341097	6.07E-05
ENSBTAG00000010326	LOC520638	-0.531719179	0.000243234
ENSBTAG00000010328	KCNK17	0.598045359	2.28E-05
ENSBTAG00000010334	SYTL3	0.467448287	0.001575144
ENSBTAG00000010338	FBXO36	-0.553835021	0.00011681
ENSBTAG00000010339	ABHD11	-0.037108102	0.813242531
ENSBTAG00000010344	SLC16A14	-0.000726183	0.996312527
ENSBTAG00000010345	XPNPEP2	-0.439479655	0.003192233
ENSBTAG00000010347	EZR	0.400544478	0.007776887
ENSBTAG00000010348	GATD1	0.330228369	0.0305627
ENSBTAG00000010349	IL1A	0.443702708	0.002880038
ENSBTAG00000010350	USP53	0.1500833	0.336744632
ENSBTAG00000010351	SNX25	0.026937094	0.863858681
ENSBTAG00000010353	ATP7B	-0.437364823	0.003359445
ENSBTAG00000010355	VPS37A	0.531350795	0.000246119
ENSBTAG00000010356	RAB12	0.285467533	0.063511052
ENSBTAG00000010357	ST6GAL1	-0.427096973	0.004285109
ENSBTAG00000010360	LRIG1	-0.267841561	0.082478146
ENSBTAG00000010362	NOSTRIN	-0.356392908	0.018987959
ENSBTAG00000010365	SQOR	0.437308463	0.003364005
ENSBTAG00000010366	HCRTR1	-0.497886593	0.00068054
ENSBTAG00000010367	TTC13	-0.460600238	0.001882866
ENSBTAG00000010370	CLBA1	-0.603593548	1.83E-05
ENSBTAG00000010371	CHAC1	0.22284608	0.150896221
ENSBTAG00000010372	MTMR7	0.528602939	0.000268633
ENSBTAG00000010373	CACTIN	0.650661814	2.32E-06
ENSBTAG00000010376	TMEM184C	-0.245963484	0.111858043
ENSBTAG00000010379	CRTC1	-0.526064027	0.000291069
ENSBTAG00000010384	CDC6	-0.095629888	0.541855632
ENSBTAG00000010387	MINDY3	-0.141994514	0.363721313
ENSBTAG00000010388	MGAT4A	-0.295617038	0.054275856

ENSBTAG00000010389	STBD1	-0.339204017	0.026067962
ENSBTAG00000010390	SRI	0.563848441	8.24E-05
ENSBTAG00000010392	ESRRG	-0.276904909	0.072238193
ENSBTAG00000010394	MCF2L2	0.407954281	0.006616242
ENSBTAG00000010395	DOCK9	0.079738709	0.611253849
ENSBTAG00000010399	TXNDC16	0.681901819	4.78E-07
ENSBTAG00000010402	MYH9	0.270215977	0.079692037
ENSBTAG00000010403	FAAP24	-0.542375237	0.000171912
ENSBTAG00000010408	IKBKE	0.525015936	0.000300813
ENSBTAG00000010411	ADAMTS8	-0.224628591	0.147571094
ENSBTAG00000010413	TMEM169	-0.16195642	0.299458887
ENSBTAG00000010416	RIN3	0.338269142	0.026508819
ENSBTAG00000010419	CYP2R1	-0.510692793	0.000466835
ENSBTAG00000010420	PCDH17	0.407055133	0.006748568
ENSBTAG00000010422	MDM2	0.447988916	0.002590927
ENSBTAG00000010423	LIFR	-0.227116531	0.143020633
ENSBTAG00000010426	XRCC5	-0.554737926	0.000113239
ENSBTAG00000010427	RASSF5	0.655538692	1.83E-06
ENSBTAG00000010428	USP15	0.447084883	0.002649685
ENSBTAG00000010431	LURAP1L	-0.180469028	0.246830679
ENSBTAG00000010433	NA	0.469362208	0.001497527
ENSBTAG00000010442	PANK1	0.160832367	0.302870438
ENSBTAG00000010444	ERBB3	-0.323333458	0.034435065
ENSBTAG00000010447	LSP1	0.280500696	0.06846478
ENSBTAG00000010449	MOCS1	0.419846407	0.005066162
ENSBTAG00000010450	WIZ	-0.048398575	0.757930644
ENSBTAG00000010452	PODXL	-0.256231254	0.097211011
ENSBTAG00000010457	NUAK1	-0.102633162	0.512524512
ENSBTAG00000010458	LOC613822	-0.442853511	0.002940568
ENSBTAG00000010460	MARK1	-0.474001072	0.001323298
ENSBTAG00000010463	NA	-0.308641328	0.044039074
ENSBTAG00000010464	MN1	0.05482196	0.726968275
ENSBTAG00000010467	SUPT5H	0.522156905	0.000328907
ENSBTAG00000010470	UQCC3	-0.458342641	0.001995365
ENSBTAG00000010472	TNFAIP8L3	0.490772161	0.000833813
ENSBTAG00000010482	PITPNM1	0.441534864	0.003036775
ENSBTAG00000010484	LRRN4CL	-0.344633206	0.023626647
ENSBTAG00000010487	SMIM3	0.637262688	4.32E-06
ENSBTAG00000010492	VPS4B	0.518007998	0.000373884
ENSBTAG00000010493	SERTAD1	0.558209133	0.000100414
ENSBTAG00000010496	STAG3	-0.369251511	0.014817888
ENSBTAG00000010497	TRAF2	0.562099878	8.76E-05
ENSBTAG00000010498	SLC40A1	-0.633168086	5.20E-06
ENSBTAG00000010503	TIMM9	-0.208432859	0.179824259
ENSBTAG00000010508	BLVRB	-0.56429652	8.11E-05
ENSBTAG00000010509	CDK3	-0.112695228	0.471824844
ENSBTAG00000010511	KAT8	0.49458351	0.000748251

ENSBTAG00000010515	FBXW5	0.439206273	0.003213429
ENSBTAG00000010517	EVPL	-0.418445351	0.005230594
ENSBTAG00000010520	NA	0.362806965	0.016798758
ENSBTAG00000010521	PVRIG	-0.339980058	0.025706655
ENSBTAG00000010526	PLPP1	-0.614003439	1.19E-05
ENSBTAG00000010527	NA	0.064169278	0.682680164
ENSBTAG00000010529	FZD6	-0.288466439	0.060660917
ENSBTAG00000010531	CYP1B1	0.028015171	0.858464354
ENSBTAG00000010542	SPIRE1	-0.331442557	0.029919581
ENSBTAG00000010547	CEP76	0.253772026	0.100576766
ENSBTAG00000010549	IFRD1	0.270839108	0.078973206
ENSBTAG00000010550	EIF5A2	-0.591450117	2.96E-05
ENSBTAG00000010555	LSMEM1	0.218945257	0.158364094
ENSBTAG00000010559	DHRS7B	-0.281437497	0.067507775
ENSBTAG00000010563	PTPN2	0.46303659	0.001767784
ENSBTAG00000010564	ELOVL6	-0.216162638	0.163853478
ENSBTAG00000010568	ZBED5	-0.56742866	7.25E-05
ENSBTAG00000010576	MAP2K3	0.534988538	0.000218935
ENSBTAG00000010577	PAICS	-0.400234756	0.007829002
ENSBTAG00000010578	IL17B	-0.672849723	7.70E-07
ENSBTAG00000010581	MAGI1	0.044612523	0.776360654
ENSBTAG00000010582	BRD3	0.371451345	0.01418877
ENSBTAG00000010587	SH3BGRL	0.446475339	0.002689961
ENSBTAG00000010590	FAM118A	0.3104534	0.042748325
ENSBTAG00000010591	ZNF365	-0.320898367	0.035895565
ENSBTAG00000010597	GGCT	-0.067333751	0.667913325
ENSBTAG00000010602	DDX56	0.554609937	0.000113739
ENSBTAG00000010604	PNO1	0.379014678	0.012195917
ENSBTAG00000010606	PPP1R3B	0.527638548	0.000276965
ENSBTAG00000010609	FAM221A	-0.530382121	0.000253853
ENSBTAG00000010612	TMED4	-0.422781108	0.004736252
ENSBTAG00000010616	MBD6	0.296392066	0.053617529
ENSBTAG00000010620	ATP6V1B1	0.008239042	0.958181425
ENSBTAG00000010626	SH3GLB2	-0.070377139	0.653827262
ENSBTAG00000010630	ABHD18	-0.238082138	0.124193818
ENSBTAG00000010634	NDNF	-0.144728235	0.354462189
ENSBTAG00000010637	ARSG	-0.348458219	0.022023872
ENSBTAG00000010639	MAP2K7	0.221574376	0.153301859
ENSBTAG00000010640	NA	-0.366390048	0.015671494
ENSBTAG00000010641	APH1B	-0.158454103	0.310170255
ENSBTAG00000010644	CHST11	0.615404503	1.12E-05
ENSBTAG00000010645	BOLA-DRA	0.45509146	0.002167803
ENSBTAG00000010649	MEF2A	0.525950478	0.000292111
ENSBTAG00000010653	MIGA2	-0.263791366	0.087405373
ENSBTAG00000010658	PFKL	-0.347098974	0.022582667
ENSBTAG00000010659	CUX1	0.30485914	0.046835247
ENSBTAG00000010660	CACNA1C	-0.190243723	0.221727243

ENSBTAG00000010661	DPYSL3	-0.298927018	0.05150899
ENSBTAG00000010662	LIMK2	0.381110924	0.011687812
ENSBTAG00000010663	ADAM15	0.547551477	0.000144629
ENSBTAG00000010664	PRKCQ	0.025525275	0.870932156
ENSBTAG00000010665	CBLN3	0.423480399	0.00466046
ENSBTAG00000010666	KHNYN	0.562354636	8.68E-05
ENSBTAG00000010667	PIK3IP1	-0.468176695	0.001545194
ENSBTAG00000010668	GEMIN7	0.540940505	0.000180258
ENSBTAG00000010670	VSIG8	0.427744302	0.004220785
ENSBTAG00000010671	GLI3	-0.285568899	0.063413006
ENSBTAG00000010672	PCCA	-0.433863704	0.003653171
ENSBTAG00000010673	EFNA4	-0.306680048	0.045471613
ENSBTAG00000010677	LIMCH1	0.040414218	0.796939752
ENSBTAG00000010681	NR1H3	0.019135924	0.903060514
ENSBTAG00000010682	DDR1	-0.304319274	0.047245845
ENSBTAG00000010693	LMO7	-0.358791029	0.018142894
ENSBTAG00000010698	VARS2	0.105475443	0.500852275
ENSBTAG00000010709	DLAT	-0.458867015	0.001968719
ENSBTAG00000010711	LOC101906280	-0.129261277	0.408736044
ENSBTAG00000010715	MRPL37	-0.281243798	0.067704778
ENSBTAG00000010717	SSBP3	-0.195859696	0.208129523
ENSBTAG00000010718	RALGPS2	-0.552514706	0.000122216
ENSBTAG00000010720	MIB2	-0.383364678	0.011161804
ENSBTAG00000010721	MCM3	-0.596974467	2.38E-05
ENSBTAG00000010722	NA	0.43959199	0.003183559
ENSBTAG00000010729	KRI1	0.213930699	0.168355286
ENSBTAG00000010731	CDKN2D	0.228166954	0.141130847
ENSBTAG00000010736	BBS5	-0.699103686	1.84E-07
ENSBTAG00000010738	CCL14	-0.031388482	0.841627602
ENSBTAG00000010741	KLHL41	-0.572614246	6.01E-05
ENSBTAG00000010742	PKD2L1	-0.327017436	0.032318701
ENSBTAG00000010743	FASTKD1	-0.479218583	0.001149048
ENSBTAG00000010745	THRA	-0.291049624	0.058288528
ENSBTAG00000010756	ST7	-0.148347735	0.342425763
ENSBTAG00000010760	REV3L	-0.503877552	0.000571575
ENSBTAG00000010763	DUSP16	0.500578308	0.000629473
ENSBTAG00000010766	OIP5	0.177614327	0.25451006
ENSBTAG00000010772	TPGS1	-0.055548369	0.723492637
ENSBTAG00000010774	NUSAP1	0.070224924	0.654529012
ENSBTAG00000010777	CARS1	0.579717789	4.62E-05
ENSBTAG00000010778	NDUFAF1	-0.54419457	0.000161833
ENSBTAG00000010784	ABT1	0.51780285	0.000376245
ENSBTAG00000010785	FAS	0.484927867	0.00098203
ENSBTAG00000010786	TACC2	-0.214514449	0.167169327
ENSBTAG00000010787	RFC3	-0.585714737	3.69E-05
ENSBTAG00000010788	PPM1E	0.370603895	0.014428387
ENSBTAG00000010792	SEH1L	0.424556713	0.004545868

ENSBTAG00000010793	CCDC80	-0.214731863	0.166729174
ENSBTAG00000010795	ATG14	-0.461969908	0.00181738
ENSBTAG00000010798	SLC23A1	-0.248494451	0.108100927
ENSBTAG00000010801	CMBL	-0.216102627	0.163973367
ENSBTAG00000010802	KCNK7	0.320138557	0.03636155
ENSBTAG00000010805	POMT1	-0.256654729	0.096640289
ENSBTAG00000010809	HID1	-0.267171543	0.083277931
ENSBTAG00000010813	NA	0.117080321	0.454640575
ENSBTAG00000010815	CAMKK2	-0.08076989	0.606637518
ENSBTAG00000010818	AEBP2	0.509342079	0.000486108
ENSBTAG00000010820	WNT11	-0.39435082	0.008877828
ENSBTAG00000010821	ACER2	-0.390057482	0.009717384
ENSBTAG00000010828	LOC617313	-0.667129511	1.03E-06
ENSBTAG00000010830	LRP1	0.130217278	0.405249618
ENSBTAG00000010835	CRELD1	-0.370716277	0.014396415
ENSBTAG00000010836	NA	0.079063451	0.614284899
ENSBTAG00000010841	FMO5	-0.630394521	5.88E-06
ENSBTAG00000010846	CNNM3	-0.182439979	0.241620805
ENSBTAG00000010849	ANKRD23	-0.151806895	0.331160811
ENSBTAG00000010850	SERTAD4	-0.342838999	0.024411378
ENSBTAG00000010852	LOC107131749	0.384114925	0.010991254
ENSBTAG00000010859	HYLS1	0.163232352	0.295616409
ENSBTAG00000010871	NA	0.375507381	0.013088181
ENSBTAG00000010874	GHSR	0.556137346	0.0001079
ENSBTAG00000010877	ARMC12	0.562288506	8.70E-05
ENSBTAG00000010878	NA	-0.080093536	0.609663688
ENSBTAG00000010882	ANKRD9	0.367478236	0.015342094
ENSBTAG00000010884	NKAP	-0.557942747	0.00010135
ENSBTAG00000010888	VSIR	0.589183273	3.23E-05
ENSBTAG00000010890	PRMT5	0.266523919	0.084056722
ENSBTAG00000010899	TIMP2	-0.284784152	0.064175201
ENSBTAG00000010904	PAGR1	0.647281838	2.72E-06
ENSBTAG00000010906	RPS6KA5	-0.295760823	0.054153234
ENSBTAG00000010909	SLC30A1	0.381097269	0.011691063
ENSBTAG00000010913	SRXN1	-0.045095361	0.77400327
ENSBTAG00000010915	CRTC3	0.386000791	0.01057236
ENSBTAG00000010916	LHFPL4	-0.097466615	0.53408574
ENSBTAG00000010923	RAB9A	-0.17029686	0.2749192
ENSBTAG00000010927	CBFA2T3	-0.053464042	0.733479973
ENSBTAG00000010928	CSRNP2	0.507609927	0.000511866
ENSBTAG00000010932	DNAJC12	-0.602485287	1.91E-05
ENSBTAG00000010935	EML4	0.156598695	0.315942224
ENSBTAG00000010937	APOO	-0.342584685	0.024524347
ENSBTAG00000010943	SLC22A23	-0.522631073	0.00032409
ENSBTAG00000010945	SEC24B	0.432967444	0.003731883
ENSBTAG00000010948	CLIC2	-0.584961596	3.80E-05
ENSBTAG00000010949	PROSER1	0.304260703	0.047290567

ENSBTAG00000010954	ART3	0.068558045	0.662232896
ENSBTAG00000010956	SCARB2	-0.529303682	0.000262722
ENSBTAG00000010957	LHPP	-0.216680351	0.162821853
ENSBTAG00000010958	NA	-0.10991012	0.482915436
ENSBTAG00000010961	LYRM7	-0.033011681	0.833550256
ENSBTAG00000010963	IL16	0.133242783	0.394329348
ENSBTAG00000010964	STARD5	-0.459771432	0.001923498
ENSBTAG00000010971	LIMS1	-0.276589783	0.072576546
ENSBTAG00000010976	KANK1	-0.459571883	0.001933395
ENSBTAG00000010978	PROX1	-0.340921211	0.025274081
ENSBTAG00000010981	CIB2	0.135320928	0.386928863
ENSBTAG00000010982	UBE2B	0.465194203	0.001671111
ENSBTAG00000010986	KCNQ1	-0.312104327	0.041599329
ENSBTAG00000010987	NFKBIZ	0.30789881	0.04457704
ENSBTAG00000010989	PIK3R1	-0.301200787	0.049675024
ENSBTAG00000010990	LHX2	-0.221111373	0.15418464
ENSBTAG00000010991	TTR	-0.066885922	0.66999575
ENSBTAG00000010992	CTSH	0.506928542	0.00052233
ENSBTAG00000010993	ZNF839	0.393959095	0.008951751
ENSBTAG00000010998	CFLAR	0.409840419	0.006345939
ENSBTAG00000010999	IL17RD	0.023696704	0.880108348
ENSBTAG00000011000	HDAC10	0.129709652	0.407098735
ENSBTAG00000011001	ERG	-0.135879926	0.384952231
ENSBTAG00000011002	CCDC136	0.235812848	0.127928381
ENSBTAG00000011003	IKZF3	-0.236705949	0.126448702
ENSBTAG00000011007	TTYH2	0.592548156	2.84E-05
ENSBTAG00000011011	SSH2	0.413740655	0.005817184
ENSBTAG00000011014	CHST3	0.325020372	0.033452241
ENSBTAG00000011017	ABI2	0.062344392	0.691249807
ENSBTAG00000011019	LOC618367	-0.352916109	0.020271802
ENSBTAG00000011027	PTGR1	0.105548733	0.500553103
ENSBTAG00000011042	TMEM129	0.04980348	0.751124706
ENSBTAG00000011043	RAC2	0.507270632	0.000517053
ENSBTAG00000011044	TACC3	0.482766332	0.00104253
ENSBTAG00000011045	MRPS36	-0.275301201	0.073973123
ENSBTAG00000011051	NA	-0.359717176	0.017825131
ENSBTAG00000011052	NA	-0.458643173	0.001980055
ENSBTAG00000011056	IDS	-0.193837087	0.212958016
ENSBTAG00000011059	CDKN2C	-0.568387465	7.00E-05
ENSBTAG00000011063	CTSO	-0.640842219	3.67E-06
ENSBTAG00000011064	ADCK5	0.414326946	0.005741102
ENSBTAG00000011067	IL17RA	0.442430023	0.00297117
ENSBTAG00000011072	ADK	-0.547456203	0.000145093
ENSBTAG00000011075	PLPBP	0.644541028	3.09E-06
ENSBTAG00000011079	C18H19orf48	0.181071861	0.245229214
ENSBTAG00000011082	IGF1	-0.636780685	4.42E-06
ENSBTAG00000011083	POLD1	-0.351213818	0.020926505

ENSBTAG00000011088	SLC6A6	0.318820704	0.037181542
ENSBTAG00000011091	SGIP1	-0.062509661	0.690472119
ENSBTAG00000011095	FAR2	0.408842768	0.006487696
ENSBTAG00000011100	CTSC	0.261686429	0.090054844
ENSBTAG00000011102	TPCN1	-0.135234461	0.387235144
ENSBTAG00000011103	SLC8B1	0.61149544	1.32E-05
ENSBTAG00000011104	RTN4	-0.57585784	5.34E-05
ENSBTAG00000011105	SLC38A2	0.433933322	0.003647118
ENSBTAG00000011108	USP54	-0.419113551	0.005151602
ENSBTAG00000011112	KCNK5	-0.364930348	0.016122743
ENSBTAG00000011115	NA	-0.107770705	0.491526478
ENSBTAG00000011121	CLCN4	-0.478683528	0.001165926
ENSBTAG00000011125	MYO9B	0.511972535	0.000449211
ENSBTAG00000011126	STK38	0.204603295	0.188136584
ENSBTAG00000011129	QSOX2	0.42642483	0.004352802
ENSBTAG00000011131	NMUR2	0.461542542	0.001837594
ENSBTAG00000011132	CCDC83	-0.276266283	0.072925189
ENSBTAG00000011133	AP1S3	-0.012667198	0.935744267
ENSBTAG00000011136	NR2F6	-0.490223027	0.000846835
ENSBTAG00000011137	MORN4	-0.646865633	2.77E-06
ENSBTAG00000011138	NA	-0.173405032	0.266122548
ENSBTAG00000011140	FAM162A	-0.574678416	5.57E-05
ENSBTAG00000011143	KPNA1	0.210820833	0.17477594
ENSBTAG00000011145	NDUFA4	-0.014491471	0.926514093
ENSBTAG00000011146	RAB8B	0.193848453	0.212930667
ENSBTAG00000011147	RNF13	0.404590707	0.007123058
ENSBTAG00000011149	SIGIRR	-0.06890066	0.660646572
ENSBTAG00000011150	PFN2	-0.552563226	0.000122013
ENSBTAG00000011154	SDC1	-0.311012884	0.042356082
ENSBTAG00000011156	ATP8A1	-0.103056071	0.510779173
ENSBTAG00000011162	ZKSCAN2	-0.075706771	0.629445649
ENSBTAG00000011170	JAKMIP1	-0.202046497	0.19383605
ENSBTAG00000011171	NA	-0.322536312	0.03490769
ENSBTAG00000011172	ALMS1	-0.480129848	0.001120803
ENSBTAG00000011178	NA	-0.08985076	0.566651402
ENSBTAG00000011182	PDLIM1	-0.245078612	0.113194732
ENSBTAG00000011184	FTH1	0.37083178	0.014363617
ENSBTAG00000011186	BEST1	0.446921112	0.002660454
ENSBTAG00000011187	FAM13A	-0.027624324	0.8604193
ENSBTAG00000011189	TJAP1	0.25208068	0.102942983
ENSBTAG00000011190	FLNA	0.350387858	0.021250506
ENSBTAG00000011192	GPR87	0.473191778	0.001352332
ENSBTAG00000011193	C1QC	-0.545862742	0.000153065
ENSBTAG00000011195	NA	-0.360205425	0.01765951
ENSBTAG00000011196	C1QB	-0.529184403	0.00026372
ENSBTAG00000011197	IPMK	0.402276976	0.007490857
ENSBTAG00000011202	CARD19	0.3346617	0.028268513

ENSBTAG00000011204	NINJ1	0.428197086	0.004176295
ENSBTAG00000011205	PPP1R42	-0.501821673	0.000607064
ENSBTAG00000011206	GALNT1	0.213886754	0.168444812
ENSBTAG00000011209	SYT11	0.111131436	0.478035317
ENSBTAG00000011214	THAP3	0.33160541	0.029834181
ENSBTAG00000011215	ACTN4	0.153180512	0.326752329
ENSBTAG00000011224	CITED2	-0.319943382	0.036482047
ENSBTAG00000011226	SLC4A2	0.492648526	0.000790656
ENSBTAG00000011227	TRPC6	0.074535071	0.634773771
ENSBTAG00000011228	FASTK	-0.231711721	0.134889906
ENSBTAG00000011229	TMUB1	-0.520842129	0.000342602
ENSBTAG00000011234	FOXO3	0.111340388	0.477203
ENSBTAG00000011236	STX11	0.601000527	2.03E-05
ENSBTAG00000011238	CD48	0.577727101	4.98E-05
ENSBTAG00000011240	NA	-0.20588579	0.185322997
ENSBTAG00000011244	TESK2	-0.402551867	0.007446318
ENSBTAG00000011252	RAD50	-0.64862089	2.55E-06
ENSBTAG00000011256	MYO1B	-0.411980599	0.006050862
ENSBTAG00000011257	ASAH1	0.184830105	0.235403554
ENSBTAG00000011258	ACOT9	-0.227008966	0.1432152
ENSBTAG00000011262	NA	-0.611946121	1.30E-05
ENSBTAG00000011263	EIF6	0.558317794	0.000100035
ENSBTAG00000011266	ZBTB16	-0.116347662	0.457487853
ENSBTAG00000011268	TMEM64	0.027117306	0.862956532
ENSBTAG00000011274	ENO2	-0.178600751	0.251838615
ENSBTAG00000011278	XYLB	-0.476599599	0.001233782
ENSBTAG00000011280	TBKBP1	0.519128135	0.000361226
ENSBTAG00000011283	RBPJL	0.428153981	0.004180513
ENSBTAG00000011284	SLC39A1	-0.208852514	0.178929611
ENSBTAG00000011287	ATXN7	0.438106292	0.003299966
ENSBTAG00000011291	DLG3	-0.227427905	0.14245851
ENSBTAG00000011299	NA	-0.085750928	0.584553475
ENSBTAG00000011304	XRN2	0.506131635	0.000534811
ENSBTAG00000011307	DNM1	-0.475801818	0.001260674
ENSBTAG00000011310	NALF2	0.097029299	0.53593079
ENSBTAG00000011313	CASP8AP2	-0.551729689	0.000125537
ENSBTAG00000011316	ZC3H12A	0.500089814	0.000638477
ENSBTAG00000011321	NUGGC	-0.014497821	0.926481982
ENSBTAG00000011322	HIPK1	0.329652266	0.030871818
ENSBTAG00000011324	EMILIN1	-0.298513688	0.051848159
ENSBTAG00000011325	KHK	0.275604297	0.073642738
ENSBTAG00000011327	OLFML3	0.063498079	0.6858276
ENSBTAG00000011328	NA	-0.555071943	0.000111943
ENSBTAG00000011330	NA	-0.10230493	0.513881183
ENSBTAG00000011334	NADK2	-0.612193078	1.29E-05
ENSBTAG00000011337	ANKRD33B	0.504307405	0.000564394
ENSBTAG00000011338	NREP	-0.415212438	0.005627832

ENSBTAG00000011340	NSL1	-0.70475814	1.33E-07
ENSBTAG00000011343	XAF1	0.345228517	0.023370978
ENSBTAG00000011344	TMEM110	-0.452671252	0.002304574
ENSBTAG00000011345	SFMBT1	0.293710338	0.055923113
ENSBTAG00000011349	CDH24	-0.470799904	0.001441473
ENSBTAG00000011354	NUDT9	-0.452338787	0.002323944
ENSBTAG00000011356	CAMSAP3	-0.309194983	0.043641385
ENSBTAG00000011358	IER3	0.511588857	0.000454431
ENSBTAG00000011359	CD7	-0.256074895	0.097422393
ENSBTAG00000011373	MAML3	0.305842087	0.046095086
ENSBTAG00000011382	SLC9A3R1	0.425314769	0.004466643
ENSBTAG00000011387	NA	0.541711018	0.000175731
ENSBTAG00000011389	TMEM104	-0.469613246	0.001487602
ENSBTAG00000011392	MYBPC1	-0.373877484	0.013521383
ENSBTAG00000011397	UNC13B	-0.352653109	0.020371814
ENSBTAG00000011398	PRR7	0.443870895	0.002868181
ENSBTAG00000011400	DBN1	-0.530359569	0.000254036
ENSBTAG00000011403	RUSC2	-0.4113712	0.006133646
ENSBTAG00000011405	CEP72	-0.493642007	0.000768623
ENSBTAG00000011406	TESK1	0.566193949	7.58E-05
ENSBTAG00000011409	CD72	0.486379272	0.000943182
ENSBTAG00000011411	SIT1	0.099915161	0.523812659
ENSBTAG00000011412	LAMB1	-0.278010992	0.071060414
ENSBTAG00000011413	CCDC107	-0.22833779	0.140825257
ENSBTAG00000011415	ETF1	0.45182867	0.002353944
ENSBTAG00000011416	ARHGEF39	-0.406962131	0.006762385
ENSBTAG00000011417	NA	0.427575261	0.0042375
ENSBTAG00000011419	HSPA9	0.054018172	0.730820463
ENSBTAG00000011420	CA9	0.236406264	0.126943779
ENSBTAG00000011421	CD37	0.602031662	1.95E-05
ENSBTAG00000011424	TPM2	-0.161919202	0.299571447
ENSBTAG00000011434	NPR2	-0.388724069	0.009991617
ENSBTAG00000011435	NPEPPS	0.489689583	0.000859658
ENSBTAG00000011437	SIK1	0.413543016	0.005843028
ENSBTAG00000011442	SPAG8	-0.015649544	0.920659519
ENSBTAG00000011444	HINT2	-0.630267062	5.92E-06
ENSBTAG00000011445	TMEM8B	-0.579291903	4.70E-05
ENSBTAG00000011446	SEMA7A	0.482105852	0.001061668
ENSBTAG00000011447	FAM171A2	-0.428138792	0.004182
ENSBTAG00000011454	FKBP10	-0.361407455	0.017257288
ENSBTAG00000011455	POLA2	-0.692189406	2.72E-07
ENSBTAG00000011463	MID1IP1	0.573507345	5.82E-05
ENSBTAG00000011465	MYBPH	0.663171107	1.26E-06
ENSBTAG00000011466	NAXD	0.659836787	1.49E-06
ENSBTAG00000011467	BATF2	0.568443312	6.99E-05
ENSBTAG00000011470	NA	0.243172179	0.116115726
ENSBTAG00000011471	CARS2	-0.497434345	0.000689474

ENSBTAG00000011473	MYL9	-0.357367808	0.018640505
ENSBTAG00000011476	NA	-0.282422807	0.066512681
ENSBTAG00000011479	INPP5K	0.357031045	0.018759917
ENSBTAG00000011481	IL12RB1	-0.356006863	0.019127044
ENSBTAG00000011482	SLC43A2	-0.135060332	0.387852369
ENSBTAG00000011483	SCARF1	0.539025322	0.000191969
ENSBTAG00000011491	WDR81	0.599287276	2.17E-05
ENSBTAG00000011494	PYGL	-0.349152767	0.021742838
ENSBTAG00000011495	DIP2A	-0.522169004	0.000328783
ENSBTAG00000011504	ZP2	0.074180929	0.636387782
ENSBTAG00000011508	H3-3D	0.314671599	0.039862695
ENSBTAG00000011511	IFI16	0.326480325	0.032620406
ENSBTAG00000011512	NA	-0.619985188	9.26E-06
ENSBTAG00000011515	SELL	0.589267487	3.22E-05
ENSBTAG00000011517	CCDC106	0.017497828	0.911324313
ENSBTAG00000011518	RARB	-0.169184169	0.278114229
ENSBTAG00000011524	XRN1	0.274585273	0.074758142
ENSBTAG00000011528	SMIM11	-0.591437259	2.96E-05
ENSBTAG00000011532	MLLT6	-0.029256633	0.852260396
ENSBTAG00000011538	KIF1A	-0.342045291	0.024765394
ENSBTAG00000011540	SPG21	-0.448973525	0.002528239
ENSBTAG00000011541	RBL1	-0.587404502	3.46E-05
ENSBTAG00000011543	PDCD1	0.53221849	0.000239372
ENSBTAG00000011545	GDA	0.31641527	0.038717309
ENSBTAG00000011548	AMPD1	0.179254616	0.250078222
ENSBTAG00000011551	CPNE9	-0.548698872	0.00013914
ENSBTAG00000011553	FAHD2A	-0.637211371	4.33E-06
ENSBTAG00000011554	SURF6	0.426060692	0.004389863
ENSBTAG00000011558	GPAT2	0.045017312	0.774384197
ENSBTAG00000011562	STK32C	-0.150611963	0.335025791
ENSBTAG00000011563	TNFSF13B	0.490722909	0.000834974
ENSBTAG00000011578	CD44	0.591411171	2.96E-05
ENSBTAG00000011580	DAG1	-0.194489814	0.211391354
ENSBTAG00000011581	BSN	-0.164044192	0.293188171
ENSBTAG00000011582	NA	0.521709457	0.000333511
ENSBTAG00000011583	APEH	-0.475147835	0.001283106
ENSBTAG00000011584	CHST2	-0.177830391	0.253923296
ENSBTAG00000011585	MST1	-0.716600175	6.51E-08
ENSBTAG00000011586	HABP4	-0.361335035	0.0172813
ENSBTAG00000011589	CDC14B	-0.586560108	3.57E-05
ENSBTAG00000011590	GLIPR1	0.449749289	0.002479793
ENSBTAG00000011591	KRR1	0.37241086	0.013921554
ENSBTAG00000011593	QKI	0.443091363	0.002923503
ENSBTAG00000011596	SRSF5	0.286471223	0.062545533
ENSBTAG00000011600	MAP3K8	0.343006171	0.024337355
ENSBTAG00000011601	ST3GAL5	-0.354403117	0.019714058
ENSBTAG00000011602	RASAL3	-0.232036393	0.134328723

ENSBTAG00000011608	KIAA1191	0.622765418	8.22E-06
ENSBTAG00000011613	PLS3	-0.554012078	0.000116102
ENSBTAG00000011614	PDE7A	0.08715516	0.578393374
ENSBTAG00000011616	MPO	-0.448770189	0.002541075
ENSBTAG00000011620	PIGU	-0.196731163	0.206072848
ENSBTAG00000011623	VMP1	0.25490245	0.099018708
ENSBTAG00000011628	EGFR	-0.271416806	0.078311329
ENSBTAG00000011635	CENPN	-0.341223345	0.025136506
ENSBTAG00000011636	NA	-0.72739146	3.29E-08
ENSBTAG00000011638	NA	0.495163894	0.000735934
ENSBTAG00000011639	STK11	0.380801462	0.011761665
ENSBTAG00000011640	PLPP3	-0.612995862	1.24E-05
ENSBTAG00000011646	ZNF512B	-0.131759468	0.399661648
ENSBTAG00000011647	SLC25A15	-0.601715653	1.97E-05
ENSBTAG00000011648	TMLHE	-0.607220967	1.58E-05
ENSBTAG00000011651	HECTD2	-0.540732518	0.000181497
ENSBTAG00000011667	PM20D2	0.48720457	0.000921708
ENSBTAG00000011668	KCTD14	-0.310262022	0.042883173
ENSBTAG00000011671	NA	0.301086676	0.049765789
ENSBTAG00000011672	GABRR2	0.59487681	2.59E-05
ENSBTAG00000011677	NA	0.673625262	7.40E-07
ENSBTAG00000011680	PAPLN	0.112493335	0.472624231
ENSBTAG00000011683	NUMB	0.572860883	5.96E-05
ENSBTAG00000011684	RAB11FIP1	0.46537353	0.001663291
ENSBTAG00000011689	LENG8	0.521651851	0.000334108
ENSBTAG00000011693	LENG9	0.24014028	0.120878105
ENSBTAG00000011698	TYK2	0.511443718	0.00045642
ENSBTAG00000011700	PLLP	0.239691026	0.12159611
ENSBTAG00000011706	TNR	0.109916381	0.482890352
ENSBTAG00000011713	MYO15B	-0.494971241	0.000740002
ENSBTAG00000011715	RECQL5	-0.478854064	0.001160523
ENSBTAG00000011721	MED13	0.408460232	0.006542773
ENSBTAG00000011723	GRIK5	-0.284658628	0.06429779
ENSBTAG00000011726	CRYL1	-0.202887476	0.191948079
ENSBTAG00000011727	ETAA1	-0.677308137	6.10E-07
ENSBTAG00000011729	STARD3	0.703087483	1.46E-07
ENSBTAG00000011730	TCAP	0.513083478	0.000434399
ENSBTAG00000011734	ANKRD1	-0.313547504	0.040615658
ENSBTAG00000011738	TFR2	-0.372442231	0.013912891
ENSBTAG00000011742	NA	0.226362997	0.144387767
ENSBTAG00000011744	USP31	0.305453384	0.046386638
ENSBTAG00000011752	SYNM	0.024195306	0.87760466
ENSBTAG00000011754	LAMTOR2	0.071889497	0.646870977
ENSBTAG00000011756	NA	0.354337919	0.019738239
ENSBTAG00000011757	PSEN1	0.53957275	0.000188553
ENSBTAG00000011758	NA	-0.501036245	0.000621135
ENSBTAG00000011759	C1QL1	-0.575393345	5.43E-05

ENSBTAG00000011762	ANKRD52	-0.040142912	0.798274481
ENSBTAG00000011765	GABARAPL1	0.5085247	0.000498114
ENSBTAG00000011766	C7	0.211568647	0.173216168
ENSBTAG00000011770	TJP2	-0.289790842	0.059435146
ENSBTAG00000011771	FICD	0.369819343	0.014653273
ENSBTAG00000011779	MAL2	-0.362620847	0.016859138
ENSBTAG00000011782	CHGB	-0.214599351	0.166997344
ENSBTAG00000011784	FGR	0.591969524	2.90E-05
ENSBTAG00000011786	CLUH	0.582272606	4.20E-05
ENSBTAG00000011788	CXHXorf38	-0.539017513	0.000192018
ENSBTAG00000011793	FDX1	-0.460841234	0.001871195
ENSBTAG00000011795	TXNRD3	-0.413530352	0.005844687
ENSBTAG00000011798	STK38L	0.501130817	0.000619425
ENSBTAG00000011802	COL6A1	-0.130476658	0.404306649
ENSBTAG00000011803	MYH3	0.347613944	0.02236958
ENSBTAG00000011805	PLIN3	-0.697023491	2.07E-07
ENSBTAG00000011809	NA	-0.181801856	0.24329935
ENSBTAG00000011815	SMG9	0.518660907	0.000366458
ENSBTAG00000011818	COL26A1	0.167423824	0.28321847
ENSBTAG00000011819	NA	-0.700773149	1.67E-07
ENSBTAG00000011823	CLSTN1	-0.62383119	7.85E-06
ENSBTAG00000011825	TRIR	0.593948083	2.68E-05
ENSBTAG00000011826	PEX26	-0.307262514	0.045042282
ENSBTAG00000011828	ARID3B	0.585791847	3.68E-05
ENSBTAG00000011829	NF1	0.348972917	0.02181532
ENSBTAG00000011831	SPPL2A	0.16302535	0.296237628
ENSBTAG00000011833	GRIA3	-0.121324233	0.438338327
ENSBTAG00000011838	PCED1B	-0.232081015	0.134251731
ENSBTAG00000011839	HMGCS1	0.021377184	0.891770429
ENSBTAG00000011841	TCTN3	-0.106433641	0.496948109
ENSBTAG00000011851	FYN	0.494332368	0.000753637
ENSBTAG00000011854	SLC38A5	-0.095655353	0.541747538
ENSBTAG00000011861	CFAP161	-0.038466306	0.806535247
ENSBTAG00000011864	NA	-0.110282719	0.481423854
ENSBTAG00000011866	PCBD1	-0.299240902	0.051252621
ENSBTAG00000011873	KCNE3	-0.003351705	0.982981619
ENSBTAG00000011875	CLIP2	0.020085907	0.898272647
ENSBTAG00000011876	MORC3	0.432010855	0.003817526
ENSBTAG00000011879	B4GALT2	-0.432317565	0.003789881
ENSBTAG00000011880	CHAF1B	0.192995439	0.214990008
ENSBTAG00000011881	TDRD10	0.459975895	0.001913403
ENSBTAG00000011882	SLC24A3	0.544250902	0.00016153
ENSBTAG00000011885	NNT	-0.666330964	1.08E-06
ENSBTAG00000011887	CD22	0.089216474	0.569404413
ENSBTAG00000011889	NOC4L	0.452339933	0.002323877
ENSBTAG00000011892	SRGAP1	-0.650164435	2.37E-06
ENSBTAG00000011893	HDHD2	-0.491279807	0.000821934

ENSBTAG00000011894	C22H3orf62	-0.088022892	0.574601547
ENSBTAG00000011898	LTO1	0.605756548	1.68E-05
ENSBTAG00000011904	HCFC1	0.335099498	0.028049924
ENSBTAG00000011905	RRAS2	-0.536016918	0.000211759
ENSBTAG00000011911	NA	-0.510071689	0.00047561
ENSBTAG00000011912	SLC25A25	0.637100553	4.36E-06
ENSBTAG00000011917	GPAM	-0.586073093	3.64E-05
ENSBTAG00000011922	PLEC	0.488665807	0.000884755
ENSBTAG00000011926	NA	-0.281818901	0.067121195
ENSBTAG00000011928	NA	-0.571026245	6.37E-05
ENSBTAG00000011930	DDX54	0.527454661	0.00027858
ENSBTAG00000011931	CD63	-0.451009813	0.002402815
ENSBTAG00000011934	PCK2	0.294236133	0.055464911
ENSBTAG00000011935	RASSF6	-0.332682931	0.029274197
ENSBTAG00000011936	ATP8B4	0.464870037	0.00168533
ENSBTAG00000011940	ZNF831	0.049421192	0.752974846
ENSBTAG00000011945	NA	-0.573655889	5.79E-05
ENSBTAG00000011951	MRTO4	0.686233969	3.78E-07
ENSBTAG00000011954	SEC11C	-0.578515032	4.84E-05
ENSBTAG00000011957	CREBL2	0.306058697	0.04593326
ENSBTAG00000011961	PPBP	-0.557212771	0.000103953
ENSBTAG00000011966	LAMC1	-0.572094407	6.12E-05
ENSBTAG00000011969	HSPB1	-0.042628663	0.786067169
ENSBTAG00000011970	FNIP2	0.462476725	0.001793664
ENSBTAG00000011971	NRP2	-0.466253177	0.001625399
ENSBTAG00000011973	NA	-0.554674252	0.000113488
ENSBTAG00000011975	SERPINB1	0.198932194	0.200941784
ENSBTAG00000011976	CYP4B1	0.118085831	0.450748633
ENSBTAG00000011981	MYBL1	0.086066691	0.58316572
ENSBTAG00000011982	BATF3	0.569204456	6.80E-05
ENSBTAG00000011984	RSKR	0.026454938	0.866273219
ENSBTAG00000011985	NA	0.086569171	0.58096042
ENSBTAG00000011986	PLSCR4	0.384731968	0.010852659
ENSBTAG00000011987	ERG28	-0.568892031	6.88E-05
ENSBTAG00000011988	KIAA0100	0.16012299	0.305036183
ENSBTAG00000011990	ALOX15	-0.092448836	0.555439534
ENSBTAG00000011994	NDEL1	0.459656998	0.001929168
ENSBTAG00000011997	ZMIZ2	0.544196943	0.00016182
ENSBTAG00000011998	DUT	-0.499614433	0.000647351
ENSBTAG00000012002	BCAR1	0.296113033	0.053853803
ENSBTAG00000012003	PPIA	-0.250762222	0.104816905
ENSBTAG00000012004	TGFB3	-0.126774054	0.417886805
ENSBTAG00000012005	IFT43	-0.410068651	0.006313889
ENSBTAG00000012007	SOCS2	-0.217862718	0.160483502
ENSBTAG00000012010	PANX1	0.522227823	0.000328182
ENSBTAG00000012012	CYB5A	-0.562310045	8.70E-05
ENSBTAG00000012016	LMTK3	-0.423819151	0.004624125

ENSBTAG00000012019	NA	0.146731061	0.347770469
ENSBTAG00000012020	TRAF5	-0.477995903	0.00118794
ENSBTAG00000012022	TBC1D2B	0.322994961	0.034635111
ENSBTAG00000012024	SLC29A2	0.132365365	0.397478514
ENSBTAG00000012029	KLRB1	-0.015816072	0.919817978
ENSBTAG00000012030	TTLL1	-0.135181283	0.387423581
ENSBTAG00000012031	ATG9B	-0.316794159	0.038472018
ENSBTAG00000012032	PDE4A	0.335536372	0.027833196
ENSBTAG00000012036	HR	-0.133472041	0.393508916
ENSBTAG00000012038	NA	0.36829345	0.015099185
ENSBTAG00000012039	PHACTR1	-0.201465948	0.195146998
ENSBTAG00000012040	GIT1	-0.01842924	0.906624376
ENSBTAG00000012043	PADI3	0.429143947	0.00408458
ENSBTAG00000012046	JUNB	0.59982263	2.13E-05
ENSBTAG00000012047	JAK2	0.540646378	0.000182013
ENSBTAG00000012050	ORAI2	0.427346372	0.004260226
ENSBTAG00000012052	PADI4	0.470205158	0.001464431
ENSBTAG00000012054	LOC508879	0.362236788	0.016984311
ENSBTAG00000012057	CBLIF	0.193962084	0.212657378
ENSBTAG00000012058	GMDS	-0.575933703	5.32E-05
ENSBTAG00000012059	MVD	0.314338334	0.04008473
ENSBTAG00000012060	LPIN2	0.57525368	5.46E-05
ENSBTAG00000012061	POU3F1	-0.366930689	0.015507098
ENSBTAG00000012062	PRDX2	-0.643813944	3.20E-06
ENSBTAG00000012064	ZNF473	0.482218196	0.001058391
ENSBTAG00000012066	PECAM1	-0.024409539	0.876529267
ENSBTAG00000012067	EPG5	0.511486331	0.000455835
ENSBTAG00000012068	BRIP1	-0.516778654	0.000388234
ENSBTAG00000012069	CCDC167	-0.496704869	0.000704107
ENSBTAG00000012073	VOPP1	-0.443709624	0.00287955
ENSBTAG00000012074	MYB	0.080345959	0.60853353
ENSBTAG00000012082	TNFRSF12A	0.055774773	0.72241048
ENSBTAG00000012083	IRX3	-0.374624214	0.013321424
ENSBTAG00000012087	NA	0.275759087	0.07347446
ENSBTAG00000012090	GGTA1	-0.104867561	0.503337172
ENSBTAG00000012096	BCKDHB	-0.655301412	1.86E-06
ENSBTAG00000012101	SYMPK	0.579055634	4.74E-05
ENSBTAG00000012107	SLC25A28	0.130419813	0.4045132
ENSBTAG00000012111	PRDM5	-0.213977465	0.168260051
ENSBTAG00000012112	SLC7A6	-0.040347195	0.797269431
ENSBTAG00000012120	TIPARP	0.366838808	0.015534934
ENSBTAG00000012121	NOXA1	-0.347498286	0.02241729
ENSBTAG00000012124	GPBP1	0.395093477	0.008739119
ENSBTAG00000012125	GDI1	0.634357363	4.93E-06
ENSBTAG00000012126	PNPLA7	-0.047470161	0.762438232
ENSBTAG00000012128	AASS	0.002152626	0.989069509
ENSBTAG00000012137	NTN1	-0.065811446	0.675002054

ENSBTAG00000012142	RAD18	-0.723256099	4.29E-08
ENSBTAG00000012156	NAIF1	0.495320987	0.000732632
ENSBTAG00000012157	CCDC158	0.014979414	0.924046839
ENSBTAG00000012164	CP	-0.255537446	0.098151668
ENSBTAG00000012168	RANBP6	-0.683053041	4.50E-07
ENSBTAG00000012172	MIDN	0.591507863	2.95E-05
ENSBTAG00000012176	QPCTL	-0.299635641	0.050931673
ENSBTAG00000012180	BMF	0.286752624	0.062276942
ENSBTAG00000012182	DIRAS3	0.513202287	0.000432841
ENSBTAG00000012184	PTTG1	-0.476321075	0.001243112
ENSBTAG00000012185	CLEC4E	0.227824764	0.14174443
ENSBTAG00000012186	DKKL1	-0.182189444	0.242278886
ENSBTAG00000012189	NA	0.126347263	0.419468607
ENSBTAG00000012191	WWC2	0.542474768	0.000171346
ENSBTAG00000012193	TTC28	0.026912504	0.863981793
ENSBTAG00000012194	DENND2C	-0.001528108	0.992240537
ENSBTAG00000012197	AP5Z1	0.601386635	2.00E-05
ENSBTAG00000012200	ANKRD13D	-0.056699995	0.717993722
ENSBTAG00000012201	NA	0.519127582	0.000361232
ENSBTAG00000012205	CPT1C	-0.384168134	0.010979243
ENSBTAG00000012208	BOLA	0.276725847	0.072430301
ENSBTAG00000012211	HOXA5	-0.27539301	0.073872925
ENSBTAG00000012215	CPNE7	-0.276629077	0.072534288
ENSBTAG00000012216	MLKL	0.520979674	0.000341146
ENSBTAG00000012219	CSPG4	-0.232293593	0.133885398
ENSBTAG00000012223	TNFSF14	0.552122469	0.000123865
ENSBTAG00000012225	KPNA2	-0.626952508	6.85E-06
ENSBTAG00000012228	SEMA4A	0.064940251	0.679071413
ENSBTAG00000012234	RHBG	0.47848027	0.001172395
ENSBTAG00000012239	SLC37A3	0.007757576	0.960623212
ENSBTAG00000012241	POLD2	-0.382294741	0.011408939
ENSBTAG00000012244	TUBA1B	-0.451342271	0.002382866
ENSBTAG00000012249	PRR15L	-0.260239498	0.091911884
ENSBTAG00000012251	MTR	-0.336737867	0.027244306
ENSBTAG00000012252	MOCOS	0.545674562	0.000154032
ENSBTAG00000012253	AGO1	-0.607690977	1.55E-05
ENSBTAG00000012260	MTRF1	-0.32111322	0.03576469
ENSBTAG00000012263	ASAP3	0.006848161	0.965236322
ENSBTAG00000012265	VWF	-0.373173849	0.013712133
ENSBTAG00000012266	NA	0.59380304	2.70E-05
ENSBTAG00000012267	ZFC3H1	0.245488823	0.112573568
ENSBTAG00000012271	NA	0.010513506	0.946651806
ENSBTAG00000012272	TMEM19	-0.476387021	0.001240898
ENSBTAG00000012273	FAM131A	0.254382885	0.099732502
ENSBTAG00000012274	CIZ1	-0.323705788	0.034216121
ENSBTAG00000012275	ENDOU	-0.438191513	0.00329319
ENSBTAG00000012276	LOC784446	-0.191169597	0.219444295

ENSBTAG00000012277	SRRD	0.678903648	5.61E-07
ENSBTAG00000012278	MTMR12	-0.404510481	0.007135544
ENSBTAG00000012280	PGLYRP2	-0.314422158	0.040028788
ENSBTAG00000012284	CLCN2	-0.038804823	0.804865638
ENSBTAG00000012288	TFIP11	0.524206909	0.000308535
ENSBTAG00000012291	TBC1D22A	0.141173673	0.366529675
ENSBTAG00000012297	RIPOR3	0.105156209	0.502156455
ENSBTAG00000012305	ADGRL2	-0.344191515	0.023817847
ENSBTAG00000012307	DTNA	-0.254502952	0.099567201
ENSBTAG00000012314	LDLR	0.30864152	0.044038935
ENSBTAG00000012317	PNP	0.397085284	0.00837627
ENSBTAG00000012321	ZFAND6	0.341377708	0.025066459
ENSBTAG00000012322	INKA1	0.392995662	0.009135818
ENSBTAG00000012330	B2M	0.164703846	0.291224643
ENSBTAG00000012335	UBA7	0.404326425	0.007164263
ENSBTAG00000012338	FAH	-0.631158062	5.69E-06
ENSBTAG00000012342	LIMA1	-0.492088492	0.000803323
ENSBTAG00000012343	TSPAN5	0.116219155	0.457988256
ENSBTAG00000012348	LRRC71	-0.565274964	7.83E-05
ENSBTAG00000012349	LAX1	-0.403100277	0.007358146
ENSBTAG00000012357	VPS13B	0.306618306	0.045517316
ENSBTAG00000012361	ARHGEF11	0.541430699	0.000177366
ENSBTAG00000012365	ANP32A	-0.228279988	0.140928597
ENSBTAG00000012366	MRPS23	-0.486820077	0.000931658
ENSBTAG00000012371	CPD	0.129247916	0.408784892
ENSBTAG00000012372	TMEM53	-0.343657697	0.024050649
ENSBTAG00000012375	KLHL9	-0.601571623	1.98E-05
ENSBTAG00000012377	ECHDC3	-0.461919077	0.001819774
ENSBTAG00000012382	KCTD9	-0.626912806	6.86E-06
ENSBTAG00000012383	CHMP5	-0.151471348	0.332243313
ENSBTAG00000012384	TFEB	0.636038393	4.57E-06
ENSBTAG00000012387	PAM	0.514812395	0.000412218
ENSBTAG00000012397	DCK	-0.125933579	0.421005059
ENSBTAG00000012405	PEAR1	-0.326174953	0.032792971
ENSBTAG00000012406	ZBP1	0.371446681	0.014190079
ENSBTAG00000012408	RAB27A	0.424760203	0.004524482
ENSBTAG00000012409	POSTN	-0.151065176	0.333556602
ENSBTAG00000012412	URB1	0.393355887	0.009066619
ENSBTAG00000012417	ARL14EP	0.340881892	0.025292031
ENSBTAG00000012419	BCL2L15	0.525853086	0.000293007
ENSBTAG00000012432	FDFT1	0.102307621	0.513870052
ENSBTAG00000012433	DENND1B	-0.64845046	2.58E-06
ENSBTAG00000012441	SMAD7	0.480736206	0.001102352
ENSBTAG00000012442	CTSB	-0.42056679	0.004983381
ENSBTAG00000012443	DIAPH3	-0.428893235	0.004108692
ENSBTAG00000012446	MTHFSD	-0.466774233	0.001603317
ENSBTAG00000012448	CCDC91	-0.246881391	0.110484156

ENSBTAG00000012449	AFF3	-0.237835616	0.124595507
ENSBTAG00000012451	BOLA-DMB	0.53808288	0.000197981
ENSBTAG00000012456	HEPACAM2	0.076666604	0.62509474
ENSBTAG00000012460	ELF5	-0.284955244	0.064008408
ENSBTAG00000012463	ZMAT3	-0.476148856	0.001248913
ENSBTAG00000012464	AFAP1	-0.247088631	0.11017575
ENSBTAG00000012482	CDCP1	-0.236106895	0.127439782
ENSBTAG00000012490	ETFA	-0.465042927	0.001677734
ENSBTAG00000012496	MTMR11	-0.484498079	0.000993804
ENSBTAG00000012499	RPGRIP1L	-0.433270791	0.003705078
ENSBTAG00000012500	RARA	0.385962719	0.01058068
ENSBTAG00000012504	GAS2L1	0.385939606	0.010585733
ENSBTAG00000012505	ARHGEF17	0.149059682	0.340088205
ENSBTAG00000012507	PDZD3	0.05503008	0.72597193
ENSBTAG00000012508	NECAB2	0.108437606	0.48883375
ENSBTAG00000012509	DYRK1B	-0.447231334	0.002640087
ENSBTAG00000012512	GPR137	-0.434919504	0.003562315
ENSBTAG00000012518	PCDH1	-0.308423845	0.044196094
ENSBTAG00000012519	XDH	0.607735223	1.55E-05
ENSBTAG00000012522	ZNF283	-0.296088584	0.053874545
ENSBTAG00000012525	ABO	0.647034268	2.75E-06
ENSBTAG00000012526	APBB1IP	0.430925328	0.003916791
ENSBTAG00000012529	IFNG	-0.113886445	0.467122913
ENSBTAG00000012537	CASP6	0.204560032	0.188232022
ENSBTAG00000012543	EDA	-0.219493616	0.15729833
ENSBTAG00000012544	IFNGR1	0.178427146	0.252307404
ENSBTAG00000012545	GOLM2	-0.496932535	0.000699511
ENSBTAG00000012552	FMR1	0.540425475	0.000183342
ENSBTAG00000012557	OSGEPL1	-0.512737975	0.000438958
ENSBTAG00000012558	ADAMTS12	-0.008073387	0.959021514
ENSBTAG00000012561	ORMDL1	-0.417410908	0.005354959
ENSBTAG00000012566	MAP10	-0.512228754	0.000445755
ENSBTAG00000012575	MAEA	0.443311998	0.00290775
ENSBTAG00000012577	UVSSA	0.282850105	0.066084772
ENSBTAG00000012584	GJB3	-0.289613013	0.059598573
ENSBTAG00000012586	HSPD1	-0.080802176	0.606493225
ENSBTAG00000012589	HSPE1	0.153111347	0.326973428
ENSBTAG00000012595	RIDA	0.421806232	0.004843705
ENSBTAG00000012599	SMAD3	0.205292889	0.186619979
ENSBTAG00000012605	GPR157	-0.507454154	0.000514242
ENSBTAG00000012615	NA	0.440845776	0.003088141
ENSBTAG00000012619	CNPPD1	0.590518579	3.07E-05
ENSBTAG00000012621	RTN4RL2	-0.305265666	0.046527973
ENSBTAG00000012622	TRA2A	0.34589146	0.023088988
ENSBTAG00000012626	B4GALT5	0.531359961	0.000246047
ENSBTAG00000012628	SLC1A2	0.500509612	0.000630732
ENSBTAG00000012629	ZNF362	-0.599339387	2.17E-05

ENSBTAG00000012638	S100A12	0.556303741	0.000107281
ENSBTAG00000012640	S100A8	0.552518808	0.000122199
ENSBTAG00000012646	PLCXD2	0.097752471	0.532881376
ENSBTAG00000012649	LSM8	-0.425690369	0.004427836
ENSBTAG00000012656	OVOL1	-0.341299668	0.025101852
ENSBTAG00000012657	ZSWIM8	0.453553609	0.002253853
ENSBTAG00000012658	TMA16	-0.071670915	0.647874555
ENSBTAG00000012659	LRIF1	0.057558281	0.713904593
ENSBTAG00000012667	CAMK2G	-0.463148085	0.00176267
ENSBTAG00000012668	NA	0.051717432	0.741882754
ENSBTAG00000012671	TNIP1	0.58945907	3.20E-05
ENSBTAG00000012673	CDK18	-0.409180092	0.006439461
ENSBTAG00000012674	CNKSR3	-0.281750635	0.067190258
ENSBTAG00000012675	MYO19	0.098162811	0.531154856
ENSBTAG00000012676	KRT79	-0.602858112	1.88E-05
ENSBTAG00000012678	COLGALT1	0.695443339	2.27E-07
ENSBTAG00000012683	SRRM2	0.493312666	0.000775865
ENSBTAG00000012684	CCL19	-0.131428025	0.400858816
ENSBTAG00000012687	INSR	-0.428895618	0.004108462
ENSBTAG00000012693	PKD1L2	-0.454636412	0.002192958
ENSBTAG00000012695	LCK	-0.353231217	0.020152519
ENSBTAG00000012700	CD247	-0.245268751	0.11290649
ENSBTAG00000012703	GLO1	-0.359412865	0.017929019
ENSBTAG00000012708	SERPINI1	-0.545866235	0.000153047
ENSBTAG00000012715	KIF26B	-0.136734612	0.381941552
ENSBTAG00000012718	NA	-0.255116669	0.098725551
ENSBTAG00000012719	UBTD1	0.541201712	0.000178712
ENSBTAG00000012720	ANKRD2	0.509828297	0.000479089
ENSBTAG00000012721	HOGA1	-0.417745326	0.005314476
ENSBTAG00000012723	HAUS4	-0.497668463	0.000684836
ENSBTAG00000012724	AJUBA	-0.257380942	0.095667575
ENSBTAG00000012725	C10H14orf93	-0.403658859	0.007269266
ENSBTAG00000012726	PSMB5	-0.536794854	0.000206472
ENSBTAG00000012736	PTRH1	-0.603838962	1.81E-05
ENSBTAG00000012737	GPR65	0.627052949	6.82E-06
ENSBTAG00000012738	ZNF827	-0.316752408	0.038498985
ENSBTAG00000012739	C1QBP	-0.047784988	0.760908822
ENSBTAG00000012741	CCPG1	-0.068356678	0.663165915
ENSBTAG00000012742	SLC22A18	-0.314775776	0.039793495
ENSBTAG00000012745	PPAN	0.578140158	4.90E-05
ENSBTAG00000012749	CUL7	-0.230827303	0.136427435
ENSBTAG00000012752	MRPL2	-0.214816366	0.166558325
ENSBTAG00000012753	BRF1	0.520302502	0.00034837
ENSBTAG00000012757	GCNT1	-0.204556908	0.188238914
ENSBTAG00000012760	NDUFB3	-0.249325869	0.106887946
ENSBTAG00000012761	PTK7	-0.530252183	0.000254908
ENSBTAG00000012768	HMGXB3	0.061740968	0.694091947

ENSBTAG00000012774	RAB7B	-0.215503797	0.165173171
ENSBTAG00000012777	SRF	0.566112387	7.60E-05
ENSBTAG00000012778	CAPN2	0.480374427	0.001113328
ENSBTAG00000012779	CYRIA	0.547898115	0.00014295
ENSBTAG00000012780	LPO	-0.015515905	0.921334916
ENSBTAG00000012781	TP53BP2	-0.061991645	0.692910749
ENSBTAG00000012784	RACGAP1	-0.690068233	3.07E-07
ENSBTAG00000012787	SDE2	0.526000183	0.000291655
ENSBTAG00000012794	PAH	-0.210148953	0.176185919
ENSBTAG00000012798	KCNH8	-0.026037511	0.868364579
ENSBTAG00000012800	MMAA	-0.30449245	0.047113819
ENSBTAG00000012804	REEP5	-0.34307958	0.024304909
ENSBTAG00000012805	TSPAN13	-0.054074464	0.730550469
ENSBTAG00000012808	MASP2	-0.159122542	0.308107351
ENSBTAG00000012815	CLEC12A	0.298475957	0.051879209
ENSBTAG00000012817	JAG1	-0.07493253	0.632964326
ENSBTAG00000012818	PDLIM5	-0.439130238	0.003219346
ENSBTAG00000012820	STX3	0.144484503	0.355281837
ENSBTAG00000012822	MGC137036	0.332427038	0.02940639
ENSBTAG00000012827	NA	-0.237130328	0.125750109
ENSBTAG00000012828	TBC1D15	-0.284162482	0.064784159
ENSBTAG00000012829	EBI3	-0.407831133	0.006634231
ENSBTAG00000012834	ARSI	-0.463058919	0.001766759
ENSBTAG00000012837	NA	0.141916682	0.363987042
ENSBTAG00000012844	LRSAM1	-0.507933266	0.000506967
ENSBTAG00000012847	NIBAN2	0.152796373	0.327981471
ENSBTAG00000012848	PTPRU	-0.277259955	0.071858467
ENSBTAG00000012849	COL4A1	-0.262186912	0.089419321
ENSBTAG00000012851	SLC5A1	-0.231610795	0.135064708
ENSBTAG00000012852	DICER1	-0.459062937	0.001958843
ENSBTAG00000012854	GSDMB	-0.552824419	0.000120928
ENSBTAG00000012855	LPL	-0.106911059	0.495008724
ENSBTAG00000012861	KIF4A	-0.504879058	0.00055497
ENSBTAG00000012880	DNLZ	0.375401466	0.013115969
ENSBTAG00000012885	ACAT1	-0.71947411	5.44E-08
ENSBTAG00000012887	FCER1A	0.175256451	0.260972375
ENSBTAG00000012894	NA	0.471177036	0.00142708
ENSBTAG00000012897	ITGA7	-0.093059773	0.552818301
ENSBTAG00000012898	RPS27L	-0.674419085	7.10E-07
ENSBTAG00000012899	IFNGR2	0.646463206	2.83E-06
ENSBTAG00000012900	TMEM229B	0.516451617	0.000392134
ENSBTAG00000012902	ARL8B	-0.053819688	0.731772718
ENSBTAG00000012904	EDEM1	0.416875852	0.005420289
ENSBTAG00000012907	ODF2L	-0.434910011	0.003563123
ENSBTAG00000012915	ZNF404	-0.463890092	0.001728967
ENSBTAG00000012916	NA	0.431337871	0.003878804
ENSBTAG00000012918	CRISP3	-0.253161414	0.10142616

ENSBTAG00000012919	MMP15	-0.325929264	0.032932356
ENSBTAG00000012920	TMEM70	-0.460242747	0.001900298
ENSBTAG00000012921	KIF24	-0.274933524	0.074375469
ENSBTAG00000012922	PHF2	-0.132764792	0.396043113
ENSBTAG00000012925	NCAPH	-0.100460606	0.521537566
ENSBTAG00000012926	TM6SF1	0.363718043	0.016505824
ENSBTAG00000012927	ALDOA	-0.298982695	0.05146344
ENSBTAG00000012928	PPP4C	0.63636008	4.50E-06
ENSBTAG00000012929	CEP85L	-0.306231763	0.045804296
ENSBTAG00000012936	THYN1	-0.532297787	0.000238764
ENSBTAG00000012937	ACAD8	-0.635491073	4.69E-06
ENSBTAG00000012938	JARID2	0.408606562	0.006521657
ENSBTAG00000012940	TMEM25	-0.451369625	0.002381232
ENSBTAG00000012941	IFT46	-0.556780623	0.000105523
ENSBTAG00000012943	PPARGC1B	0.337890412	0.026689172
ENSBTAG00000012944	USP35	0.247787713	0.109140235
ENSBTAG00000012954	ERAS	-0.250018729	0.105885065
ENSBTAG00000012962	SARS1	0.596876423	2.39E-05
ENSBTAG00000012966	SCRN3	0.014456467	0.926691118
ENSBTAG00000012970	FAM53B	0.194125285	0.212265297
ENSBTAG00000012972	CYP2U1	-0.548849547	0.000138433
ENSBTAG00000012975	VDAC2	-0.407978438	0.006612718
ENSBTAG00000012976	WLS	0.621537277	8.66E-06
ENSBTAG00000012977	COMTD1	0.051092352	0.744897226
ENSBTAG00000012980	RRAGB	-0.478972902	0.001156771
ENSBTAG00000012981	HEXA	-0.557089434	0.000104399
ENSBTAG00000012985	FCSK	-0.217445271	0.161306274
ENSBTAG00000012987	ULK1	-0.073316861	0.640332766
ENSBTAG00000012989	UBE2L6	0.417928144	0.005292457
ENSBTAG00000012990	PUS1	0.62602224	7.13E-06
ENSBTAG00000012991	NA	-0.155380295	0.319769217
ENSBTAG00000012995	MCUB	-0.410251924	0.006288254
ENSBTAG00000012997	SMPDL3B	0.535283031	0.000216858
ENSBTAG00000013001	LOC784914	-0.430058511	0.003997669
ENSBTAG00000013004	ITIH5	0.05307133	0.735366637
ENSBTAG00000013007	FAM210B	-0.56588744	7.66E-05
ENSBTAG00000013008	PMCH	-0.387250654	0.010302333
ENSBTAG00000013009	AURKA	-0.584616483	3.85E-05
ENSBTAG00000013013	GMPS	-0.603249248	1.85E-05
ENSBTAG00000013017	GNAT2	0.408545883	0.006530406
ENSBTAG00000013018	AMPD2	0.664143957	1.20E-06
ENSBTAG00000013023	MAP4K4	0.306905542	0.045305011
ENSBTAG00000013029	ARNTL	-0.303855211	0.047601116
ENSBTAG00000013031	TMEM62	-0.553798755	0.000116956
ENSBTAG00000013036	YDJC	-0.349463014	0.021618277
ENSBTAG00000013044	GAB3	0.499555757	0.000648454
ENSBTAG00000013045	DKC1	0.615386661	1.12E-05

ENSBTAG00000013054	MFSD2A	-0.171376641	0.271841831
ENSBTAG00000013057	CBLB	-0.70981428	9.83E-08
ENSBTAG00000013064	RGS18	0.215042361	0.166102027
ENSBTAG00000013070	EAF2	-0.183477298	0.238908978
ENSBTAG00000013071	GPR153	-0.290498139	0.058788676
ENSBTAG00000013074	PPP1R15B	0.346630956	0.022777798
ENSBTAG00000013078	LOC104968411	-0.291342028	0.058024726
ENSBTAG00000013081	PSPH	-0.029841443	0.849340944
ENSBTAG00000013093	ALDH3B1	0.644500996	3.10E-06
ENSBTAG00000013096	UNC119	-0.415475259	0.005594588
ENSBTAG00000013098	PIGS	-0.382768674	0.011298899
ENSBTAG00000013099	ALDOC	-0.366131092	0.015750758
ENSBTAG00000013100	SPAG5	-0.472604217	0.001373763
ENSBTAG00000013105	SYT3	0.025410222	0.871509039
ENSBTAG00000013107	SHANK1	-0.243142637	0.116161433
ENSBTAG00000013108	HK2	0.56064726	9.22E-05
ENSBTAG00000013109	STIM1	-0.163461038	0.294931094
ENSBTAG00000013110	FARP2	-0.191963633	0.217499409
ENSBTAG00000013111	RRM1	-0.673107663	7.60E-07
ENSBTAG00000013114	ZMYND8	-0.235155175	0.129026265
ENSBTAG00000013116	PLCB4	-0.510594026	0.000468221
ENSBTAG00000013118	CD86	-0.559915307	9.46E-05
ENSBTAG00000013125	PLAUR	0.382636221	0.011329561
ENSBTAG00000013126	EMG1	0.541126164	0.000179157
ENSBTAG00000013127	LPCAT3	-0.405697638	0.006952686
ENSBTAG00000013132	MTX3	-0.425492948	0.004448197
ENSBTAG00000013133	TBC1D10C	0.203707223	0.190120342
ENSBTAG00000013136	EFCAB11	-0.580549296	4.48E-05
ENSBTAG00000013138	TDP1	-0.696738512	2.11E-07
ENSBTAG00000013141	ACTRT3	-0.333401428	0.028905657
ENSBTAG00000013143	BAG4	-0.370775981	0.014379454
ENSBTAG00000013145	DDHD2	-0.61972787	9.36E-06
ENSBTAG00000013148	CLDN1	-0.126450228	0.419086679
ENSBTAG00000013152	NIPSNAP1	-0.339879819	0.025753088
ENSBTAG00000013159	PHF11	0.440739918	0.003096099
ENSBTAG00000013162	HSPA8	0.170494689	0.274353681
ENSBTAG00000013165	ENPP2	0.340163561	0.025621833
ENSBTAG00000013166	SMYD2	-0.171285035	0.272102023
ENSBTAG00000013167	SIGLEC1	0.216210437	0.163758033
ENSBTAG00000013168	RPA3	-0.547103273	0.000146826
ENSBTAG00000013177	APEX2	-0.553349553	0.000118772
ENSBTAG00000013180	POT1	-0.573954309	5.72E-05
ENSBTAG00000013184	CEP120	0.222474212	0.151596788
ENSBTAG00000013185	TIMD4	0.209720137	0.177090071
ENSBTAG00000013187	DLG5	-0.351104037	0.020969328
ENSBTAG00000013191	AGRN	-0.238538193	0.123453277
ENSBTAG00000013192	CEP19	-0.369271378	0.014812102

ENSBTAG00000013196	STK17B	0.265605174	0.085171267
ENSBTAG00000013197	PSEN2	-0.242670733	0.116893419
ENSBTAG00000013198	NA	-0.648656523	2.55E-06
ENSBTAG00000013201	ALOX5AP	0.650303085	2.36E-06
ENSBTAG00000013204	ATP13A3	0.568493784	6.98E-05
ENSBTAG00000013205	IL1RAP	0.362521439	0.016891462
ENSBTAG00000013208	SLC25A4	-0.543893453	0.000163463
ENSBTAG00000013215	MREG	0.363283504	0.016644996
ENSBTAG00000013221	RTTN	-0.592981157	2.79E-05
ENSBTAG00000013222	CD109	-0.596134539	2.46E-05
ENSBTAG00000013224	RMND1	-0.39109635	0.009508228
ENSBTAG00000013235	TINAGL1	-0.391028314	0.009521807
ENSBTAG00000013240	SLC3A2	0.533147616	0.000232333
ENSBTAG00000013244	HDAC6	-0.314285543	0.040119994
ENSBTAG00000013245	ITPR3	-0.390551841	0.009617367
ENSBTAG00000013254	XPO1	-0.229768234	0.138285678
ENSBTAG00000013259	POLR3A	-0.030254522	0.847279995
ENSBTAG00000013264	RPS24	0.191225437	0.219307131
ENSBTAG00000013270	TTC19	0.367943407	0.015203085
ENSBTAG00000013271	NCOR1	0.505417908	0.000546216
ENSBTAG00000013273	PIGL	-0.021686877	0.890211994
ENSBTAG00000013274	CENPV	-0.202748938	0.192258194
ENSBTAG00000013275	MAD2L2	0.481642725	0.001075272
ENSBTAG00000013278	MAGIX	-0.221411829	0.153611355
ENSBTAG00000013281	SPATA21	0.118623675	0.448674328
ENSBTAG00000013283	PRR19	-0.400899532	0.007717514
ENSBTAG00000013284	SGK3	0.249435738	0.106728434
ENSBTAG00000013287	SMO	-0.205096266	0.187051518
ENSBTAG00000013288	SUGP2	-0.409465375	0.006398911
ENSBTAG00000013290	DYSF	0.702076171	1.55E-07
ENSBTAG00000013292	SIDT1	-0.385046192	0.010782657
ENSBTAG00000013294	DYRK3	-0.015750695	0.920148344
ENSBTAG00000013298	PLA2G4A	0.343004198	0.024338228
ENSBTAG00000013301	GGT7	-0.343604376	0.024074007
ENSBTAG00000013303	ACSS2	-0.357937436	0.01843998
ENSBTAG00000013305	NA	0.474340696	0.00131128
ENSBTAG00000013306	ZBTB7C	-0.270300234	0.079594541
ENSBTAG00000013316	BRPF3	0.034650246	0.825413568
ENSBTAG00000013319	SMCO1	-0.437782913	0.003325793
ENSBTAG00000013320	TSPAN1	-0.031808295	0.839536961
ENSBTAG00000013322	POMGNT1	-0.522806964	0.00032232
ENSBTAG00000013326	ANAPC10	-0.528539992	0.00026917
ENSBTAG00000013334	NA	0.517179873	0.000383497
ENSBTAG00000013337	DHDH	-0.53334319	0.000230875
ENSBTAG00000013341	GYG2	-0.057180251	0.715704674
ENSBTAG00000013343	FTL	-0.566569309	7.48E-05
ENSBTAG00000013362	DNM2	0.532812531	0.00023485

ENSBTAG00000013364	LIPM	0.438591698	0.00326153
ENSBTAG00000013366	NRIP3	0.134392309	0.390225632
ENSBTAG00000013367	PPT1	-0.328356359	0.031576612
ENSBTAG00000013368	ANKRD22	0.446981366	0.002656487
ENSBTAG00000013369	COL14A1	-0.651631349	2.21E-06
ENSBTAG00000013371	RUBCNL	0.461189156	0.001854458
ENSBTAG00000013380	CEP192	0.181649485	0.243701318
ENSBTAG00000013391	ANKH	-0.41546773	0.005595538
ENSBTAG00000013392	PLD2	-0.349941762	0.021427239
ENSBTAG00000013401	ARHGEF40	-0.247479596	0.109595716
ENSBTAG00000013402	NA	0.271830977	0.07783949
ENSBTAG00000013403	AGBL5	-0.609543124	1.43E-05
ENSBTAG00000013405	CIBAR1	-0.544143427	0.000162109
ENSBTAG00000013406	CSRP2	-0.218818346	0.158611499
ENSBTAG00000013407	PLXNB1	0.125190711	0.423772099
ENSBTAG00000013410	MARK3	0.521774979	0.000332833
ENSBTAG00000013411	ENO1	0.447793012	0.002603561
ENSBTAG00000013412	NFAT5	0.453085169	0.002280657
ENSBTAG00000013413	CCDC51	-0.334592153	0.028303367
ENSBTAG00000013414	BLVRA	-0.416278167	0.005494083
ENSBTAG00000013417	GLYCAM1	-0.228538964	0.140466025
ENSBTAG00000013419	HTATIP2	-0.271035649	0.078747536
ENSBTAG00000013420	FSD1L	-0.63161674	5.57E-06
ENSBTAG00000013429	CLEC4G	-0.275912846	0.073307603
ENSBTAG00000013436	HAUS5	-0.490379208	0.000843113
ENSBTAG00000013439	ARHGEF26	-0.633731136	5.07E-06
ENSBTAG00000013449	RAB3GAP1	0.370311081	0.014511975
ENSBTAG00000013451	RHOH	0.432312922	0.003790298
ENSBTAG00000013452	AQP9	-0.152992423	0.327353804
ENSBTAG00000013454	TAB2	0.528329499	0.000270972
ENSBTAG00000013462	L1CAM	-0.301551124	0.049397198
ENSBTAG00000013464	CEP97	-0.530133227	0.000255876
ENSBTAG00000013465	NXPE3	0.211327193	0.173718687
ENSBTAG00000013468	AHNAK	0.326853411	0.032410592
ENSBTAG00000013475	TRAF3	0.531261082	0.000246826
ENSBTAG00000013478	MARVELD1	0.211001915	0.17439732
ENSBTAG00000013483	TAF1A	0.271472104	0.078248202
ENSBTAG00000013485	ZFYVE19	-0.440144179	0.003141221
ENSBTAG00000013486	KICS2	-0.184518235	0.236208552
ENSBTAG00000013489	CYP27A1	-0.548301735	0.000141018
ENSBTAG00000013492	PRKAG3	-0.136873648	0.381453109
ENSBTAG00000013495	WDFY3	0.115341323	0.46141438
ENSBTAG00000013496	CPM	-0.416865362	0.005421576
ENSBTAG00000013501	DHRS13	0.480259875	0.001116823
ENSBTAG00000013505	NA	-0.579501104	4.66E-05
ENSBTAG00000013515	INTS13	-0.632438785	5.37E-06
ENSBTAG00000013523	OSBPL7	-0.576622842	5.19E-05

ENSBTAG00000013524	CMIP	0.590906159	3.02E-05
ENSBTAG00000013527	PGD	-0.561085308	9.08E-05
ENSBTAG00000013530	DDAH2	-0.675775409	6.62E-07
ENSBTAG00000013531	CENPS	-0.605179616	1.72E-05
ENSBTAG00000013533	CLIC1	-0.210563338	0.175315347
ENSBTAG00000013535	DFFA	-0.587957172	3.39E-05
ENSBTAG00000013536	P2RY11	-0.013198148	0.933056938
ENSBTAG00000013537	FER1L6	-0.167488306	0.283030429
ENSBTAG00000013544	LGALS8	0.288426981	0.060697744
ENSBTAG00000013548	GABRE	-0.318164976	0.03759516
ENSBTAG00000013550	PRKCG	-0.493330125	0.00077548
ENSBTAG00000013555	ACVR1B	0.592369216	2.85E-05
ENSBTAG00000013556	UNC13D	0.424396365	0.004562783
ENSBTAG00000013557	ERAP1	0.282001961	0.066936274
ENSBTAG00000013562	SKP2	-0.500656469	0.000628042
ENSBTAG00000013568	UEVLD	-0.659772626	1.49E-06
ENSBTAG00000013569	CD38	0.439653128	0.003178847
ENSBTAG00000013573	BIRC5	-0.480800485	0.001100412
ENSBTAG00000013577	SLC1A5	0.627556758	6.67E-06
ENSBTAG00000013578	CHI3L2	0.179635515	0.249056556
ENSBTAG00000013580	KDM3A	0.441415514	0.003045618
ENSBTAG00000013586	CCR2	0.587940148	3.39E-05
ENSBTAG00000013588	ZNF532	-0.292121877	0.057325832
ENSBTAG00000013592	ZNF248	-0.521077415	0.000340114
ENSBTAG00000013596	NR1H4	0.092053007	0.557140953
ENSBTAG00000013600	PSMG1	-0.137357537	0.379756054
ENSBTAG00000013611	SCLT1	-0.490530179	0.000839529
ENSBTAG00000013612	MBLAC2	-0.558964066	9.78E-05
ENSBTAG00000013614	TMEM38A	0.463701567	0.001737475
ENSBTAG00000013615	CHORDC1	0.266118983	0.084546548
ENSBTAG00000013620	UCHL5	-0.60527177	1.71E-05
ENSBTAG00000013624	LMNB2	0.098143048	0.531237949
ENSBTAG00000013629	GET1	-0.500263599	0.000635261
ENSBTAG00000013631	GLUL	-0.054226648	0.729820704
ENSBTAG00000013636	DGKZ	-0.127065602	0.416808195
ENSBTAG00000013641	BAG3	0.40941393	0.006406207
ENSBTAG00000013645	RFFL	0.28374803	0.06519268
ENSBTAG00000013650	SLC66A1	0.455819533	0.002128084
ENSBTAG00000013651	DNAJB12	0.487147715	0.000923173
ENSBTAG00000013663	CMSS1	-0.321032085	0.035814066
ENSBTAG00000013664	FILIP1L	-0.525832662	0.000293195
ENSBTAG00000013666	SLC25A29	0.30452159	0.047091633
ENSBTAG00000013669	KIF22	-0.364834771	0.016152669
ENSBTAG00000013670	SLC46A2	0.614793516	1.15E-05
ENSBTAG00000013671	UTP14A	0.52426448	0.00030798
ENSBTAG00000013676	DYNC2LI1	-0.612571192	1.27E-05
ENSBTAG00000013678	OSGIN2	-0.661309706	1.38E-06

ENSBTAG00000013686	WSCD2	-0.731696183	2.49E-08
ENSBTAG00000013689	MCTP2	0.555122878	0.000111747
ENSBTAG00000013693	NA	-0.60692222	1.60E-05
ENSBTAG00000013697	CLASRP	0.553933304	0.000116416
ENSBTAG00000013698	ODAD4	-0.310805342	0.042501242
ENSBTAG00000013702	ZNF296	0.59574925	2.50E-05
ENSBTAG00000013705	NFKBIE	0.53323607	0.000231673
ENSBTAG00000013706	MEGF9	0.53265597	0.000236034
ENSBTAG00000013708	SNX8	0.265157235	0.085718825
ENSBTAG00000013711	NA	0.361818588	0.017121503
ENSBTAG00000013715	BRINP2	-0.039388463	0.801989077
ENSBTAG00000013716	NR2C2	0.195817126	0.208230353
ENSBTAG00000013717	PRAP1	-0.38879222	0.009977441
ENSBTAG00000013721	PSMD10	-0.440474658	0.00311612
ENSBTAG00000013722	AARS2	-0.023107296	0.8830695
ENSBTAG00000013724	ATG4A	-0.636543027	4.47E-06
ENSBTAG00000013725	RBSN	0.614889625	1.15E-05
ENSBTAG00000013726	RNPEP	-0.395636756	0.008638833
ENSBTAG00000013730	CD5	0.432601666	0.00376443
ENSBTAG00000013735	TBCE	-0.428513301	0.004145468
ENSBTAG00000013736	PROM1	-0.38890836	0.009953324
ENSBTAG00000013740	SP2	0.552013264	0.000124328
ENSBTAG00000013744	SYNPO	-0.302724715	0.04847564
ENSBTAG00000013745	ITGA5	0.5810397	4.40E-05
ENSBTAG00000013750	B3GALNT2	-0.437232225	0.003370181
ENSBTAG00000013755	ITGB5	-0.550593265	0.000130489
ENSBTAG00000013761	STMN1	-0.554322593	0.000114869
ENSBTAG00000013769	NECTIN3	-0.149809706	0.337636307
ENSBTAG00000013773	PKP4	-0.63870789	4.05E-06
ENSBTAG00000013774	CCDC9B	-0.352267326	0.020519266
ENSBTAG00000013782	DNAJB2	-0.446969208	0.002657287
ENSBTAG00000013790	MAP3K1	0.281524136	0.067419806
ENSBTAG00000013791	FFAR3	0.012168484	0.93826908
ENSBTAG00000013792	UBALD2	0.588049813	3.37E-05
ENSBTAG00000013793	NEDD4	0.069751856	0.656711855
ENSBTAG00000013806	EFHB	-0.065262551	0.67756489
ENSBTAG00000013813	KLHL17	-0.351513841	0.020809845
ENSBTAG00000013820	NA	0.520215268	0.000349311
ENSBTAG00000013821	RIOK1	0.443231466	0.002913491
ENSBTAG00000013822	NA	-0.069684048	0.65702497
ENSBTAG00000013824	WWC3	0.574061469	5.70E-05
ENSBTAG00000013825	BCAT1	-0.383090756	0.011224635
ENSBTAG00000013834	NA	0.399720146	0.007916257
ENSBTAG00000013836	LOC100297513	-0.616860948	1.06E-05
ENSBTAG00000013837	TUBE1	-0.486593559	0.000937564
ENSBTAG00000013842	ACTR6	-0.606335209	1.64E-05
ENSBTAG00000013843	ACVRL1	0.59580069	2.50E-05

ENSBTAG00000013851	BCL10	-0.299746925	0.050841485
ENSBTAG00000013855	ORMDL3	-0.669242387	9.27E-07
ENSBTAG00000013856	SSBP2	-0.213199966	0.169848412
ENSBTAG00000013857	SH2D3A	0.34042366	0.025502004
ENSBTAG00000013860	GADD45A	0.144078384	0.356650139
ENSBTAG00000013861	SLC8A1	0.53954936	0.000188698
ENSBTAG00000013863	DUSP1	0.355722342	0.0192301
ENSBTAG00000013869	SH3BP4	-0.231490937	0.135272518
ENSBTAG00000013879	NA	-0.595632405	2.51E-05
ENSBTAG00000013880	WWC1	-0.265703698	0.085051197
ENSBTAG00000013882	CHMP2A	0.458741259	0.00197508
ENSBTAG00000013884	SIPA1	0.577145169	5.09E-05
ENSBTAG00000013885	ADSS2	0.410630633	0.006235568
ENSBTAG00000013888	FOXA1	-0.286647118	0.062377537
ENSBTAG00000013895	RELA	0.608825312	1.48E-05
ENSBTAG00000013900	TRIM21	0.500737689	0.000626559
ENSBTAG00000013901	PTDSS1	-0.204683309	0.187960163
ENSBTAG00000013905	SMC3	-0.481041999	0.00109315
ENSBTAG00000013909	BOC	-0.123135342	0.431481092
ENSBTAG00000013910	POLR3GL	-0.406573565	0.006820377
ENSBTAG00000013912	TXNRD1	-0.577655674	4.99E-05
ENSBTAG00000013915	DSN1	-0.596869069	2.39E-05
ENSBTAG00000013916	HERC2	-0.166969224	0.284546478
ENSBTAG00000013917	NA	0.370024174	0.014594275
ENSBTAG00000013919	BOLA-DRB3	0.514863103	0.000411583
ENSBTAG00000013920	NA	-0.308834628	0.043899894
ENSBTAG00000013922	MOSPD1	-0.470835922	0.001440093
ENSBTAG00000013923	QPCT	-0.047271255	0.763404965
ENSBTAG00000013926	FCGRT	-0.395814724	0.008606198
ENSBTAG00000013927	GSTCD	-0.646108214	2.88E-06
ENSBTAG00000013928	WFDC2	-0.338405149	0.026444299
ENSBTAG00000013929	RRAD	0.532797074	0.000234966
ENSBTAG00000013937	SPICE1	-0.553809058	0.000116914
ENSBTAG00000013938	PHC3	-0.262144609	0.089472903
ENSBTAG00000013942	DAGLA	0.017120087	0.913231267
ENSBTAG00000013943	ZNF703	0.454601314	0.002194909
ENSBTAG00000013949	AHCTF1	-0.345968542	0.023056386
ENSBTAG00000013953	CALD1	-0.399534893	0.007947872
ENSBTAG00000013955	TRAPPC9	-0.463609666	0.001741637
ENSBTAG00000013957	GALNT3	0.454825692	0.002182464
ENSBTAG00000013958	PAK4	0.006585498	0.966568925
ENSBTAG00000013960	PSAT1	0.417482237	0.005346302
ENSBTAG00000013961	MYSM1	0.401298486	0.007651266
ENSBTAG00000013971	PI4KA	0.409429638	0.006403979
ENSBTAG00000013973	SERPIND1	0.42956958	0.004043929
ENSBTAG00000013974	TMEM215	-0.394490589	0.008851579
ENSBTAG00000013976	AGBL3	-0.16003728	0.305298527

ENSBTAG00000013981	SPTSSA	0.505516795	0.000544623
ENSBTAG00000013982	UACA	-0.466212378	0.00162714
ENSBTAG00000013983	ZC2HC1C	-0.66461045	1.17E-06
ENSBTAG00000013988	BID	0.47277699	0.00136743
ENSBTAG00000013992	ACYP1	-0.253309019	0.101220331
ENSBTAG00000013996	SH3BP2	0.5734794	5.82E-05
ENSBTAG00000014001	MAP1A	-0.54082866	0.000180923
ENSBTAG00000014002	CEP95	0.557662122	0.000102343
ENSBTAG00000014005	PPIP5K1	-0.348303778	0.022086775
ENSBTAG00000014006	TOR3A	-0.56168358	8.89E-05
ENSBTAG00000014007	ELMOD2	-0.66931324	9.24E-07
ENSBTAG00000014015	PLA2G6	-0.572550797	6.02E-05
ENSBTAG00000014016	IKZF1	0.19611074	0.207535592
ENSBTAG00000014021	UBN2	-0.336071402	0.027569669
ENSBTAG00000014023	SIRT1	0.402652938	0.00743
ENSBTAG00000014026	PAG1	-0.395257109	0.008708809
ENSBTAG00000014027	TRIM36	0.174769782	0.262319689
ENSBTAG00000014030	FGD6	0.283858413	0.065083678
ENSBTAG00000014031	TLR6	0.146593701	0.348226922
ENSBTAG00000014034	NA	-0.309483904	0.043435017
ENSBTAG00000014038	CDKL2	-0.177174919	0.255706162
ENSBTAG00000014042	TLR10	-0.01024176	0.94802881
ENSBTAG00000014046	BPI	0.065577414	0.676094324
ENSBTAG00000014048	SHLD1	-0.199324497	0.200036754
ENSBTAG00000014053	MAK	-0.278994744	0.070025678
ENSBTAG00000014054	CFAP206	-0.522606939	0.000324334
ENSBTAG00000014057	SLC35A1	-0.516318544	0.000393731
ENSBTAG00000014059	ATP2B4	-0.279730869	0.069259219
ENSBTAG00000014064	FGFR2	-0.261950678	0.089718861
ENSBTAG00000014068	VDAC3	0.085820315	0.584248395
ENSBTAG00000014069	PDK4	-0.604278477	1.78E-05
ENSBTAG00000014083	AMIGO1	-0.353659817	0.01999122
ENSBTAG00000014087	KMT5C	0.553822662	0.00011686
ENSBTAG00000014088	MBNL3	-0.597510493	2.33E-05
ENSBTAG00000014089	PPCDC	-0.711647697	8.80E-08
ENSBTAG00000014090	ARID5A	0.560766365	9.18E-05
ENSBTAG00000014091	ARHGEF3	-0.467402699	0.001577036
ENSBTAG00000014092	CELF6	-0.259449854	0.092937757
ENSBTAG00000014093	IDH2	0.135663841	0.385715606
ENSBTAG00000014095	HAUS7	-0.368644119	0.014995704
ENSBTAG00000014099	YTHDC2	0.295274095	0.054569226
ENSBTAG00000014102	WDR77	0.596592713	2.42E-05
ENSBTAG00000014103	SH3GL2	-0.415685779	0.005568082
ENSBTAG00000014105	SRPRA	0.433246076	0.003707255
ENSBTAG00000014111	INPP4B	-0.110155149	0.481934269
ENSBTAG00000014112	EXOC4	-0.597896892	2.30E-05
ENSBTAG00000014113	CCL8	0.466041256	0.001634458

ENSBTAG00000014117	CCDC9	0.614386202	1.17E-05
ENSBTAG00000014119	PRKCZ	-0.378040733	0.012438326
ENSBTAG00000014122	FOXRED1	0.439585122	0.003184089
ENSBTAG00000014123	ZNF507	0.362321373	0.016956675
ENSBTAG00000014124	MLLT3	-0.451799327	0.00235568
ENSBTAG00000014126	UNKL	0.34717779	0.022549945
ENSBTAG00000014127	PTGS2	0.450040324	0.002461829
ENSBTAG00000014136	FAAP20	0.388231781	0.010094525
ENSBTAG00000014137	CEP164	-0.481638944	0.001075384
ENSBTAG00000014138	MTM1	-0.139532301	0.372184254
ENSBTAG00000014140	ATP1B3	0.374647122	0.013315329
ENSBTAG00000014147	PRSS54	-0.029813009	0.849482843
ENSBTAG00000014149	LCN2	0.560944843	9.13E-05
ENSBTAG00000014150	BBLN	-0.319202896	0.03694219
ENSBTAG00000014151	RCSD1	-0.151541193	0.332017807
ENSBTAG00000014153	PKNOX1	0.480304712	0.001115454
ENSBTAG00000014156	AMN1	-0.168457845	0.2802129
ENSBTAG00000014159	TTL	-0.384990795	0.01079497
ENSBTAG00000014169	PCDH19	0.512134949	0.000447018
ENSBTAG00000014171	NAPEPLD	-0.356142648	0.019078026
ENSBTAG00000014172	FGD2	0.488226065	0.000895734
ENSBTAG00000014178	RALGAPA2	-0.355398782	0.019347863
ENSBTAG00000014179	SLC12A5	0.080003747	0.610065913
ENSBTAG00000014186	NCOA5	0.617011386	1.05E-05
ENSBTAG00000014191	QSOX1	-0.118904796	0.447592207
ENSBTAG00000014194	ADARB2	-0.334286538	0.02845695
ENSBTAG00000014199	TBX21	0.117530225	0.45289692
ENSBTAG00000014204	S100A16	-0.242040015	0.117877185
ENSBTAG00000014207	ADAMTS10	-0.22001434	0.156291128
ENSBTAG00000014208	RPL35A	-0.002698867	0.986296074
ENSBTAG00000014211	FOXP4	0.377483423	0.012578876
ENSBTAG00000014215	CCDC86	0.468655301	0.001525791
ENSBTAG00000014217	HHEX	0.548273732	0.000141151
ENSBTAG00000014220	LOC518526	-0.495135878	0.000736524
ENSBTAG00000014224	IGSF9B	-0.044290367	0.777934639
ENSBTAG00000014225	SLC5A9	-0.300954845	0.049870815
ENSBTAG00000014227	NDFIP2	0.391995802	0.009330273
ENSBTAG00000014228	TFEC	0.36731292	0.015391755
ENSBTAG00000014230	VRK1	-0.440806836	0.003091066
ENSBTAG00000014233	CCT8	-0.050941676	0.745624431
ENSBTAG00000014234	CCDC196	-0.275821429	0.073406771
ENSBTAG00000014237	CYTH4	0.516399291	0.000392761
ENSBTAG00000014238	ATP6V1E1	0.285858736	0.063133326
ENSBTAG00000014239	CCNB1	-0.273526323	0.07593128
ENSBTAG00000014246	CENPH	-0.650618507	2.32E-06
ENSBTAG00000014247	FAM83F	-0.227330313	0.142634518
ENSBTAG00000014248	MIER3	0.417834502	0.005303726

ENSBTAG00000014249	IVNS1ABP	0.229069183	0.139522479
ENSBTAG00000014250	ZC3HAV1L	-0.257174078	0.095943883
ENSBTAG00000014252	SPTLC3	-0.295210544	0.054623729
ENSBTAG00000014259	NA	0.281703389	0.067238089
ENSBTAG00000014261	TARS1	0.529248179	0.000263186
ENSBTAG00000014265	SREBF2	0.490280092	0.000845473
ENSBTAG00000014267	ZCCHC14	0.338639866	0.026333261
ENSBTAG00000014270	UNC5B	-0.006007819	0.969500056
ENSBTAG00000014272	MMUT	-0.531065783	0.000248372
ENSBTAG00000014291	WNT2B	0.264343042	0.086721099
ENSBTAG00000014294	ST7L	-0.19105071	0.219736525
ENSBTAG00000014297	MOV10	0.435527997	0.003510856
ENSBTAG00000014299	RHOC	-0.165363446	0.289269809
ENSBTAG00000014304	TMEM47	-0.23747907	0.125178197
ENSBTAG00000014306	DOP1B	0.401161107	0.007674022
ENSBTAG00000014310	HEATR5B	0.148486953	0.341967888
ENSBTAG00000014313	PYROXD2	-0.571909748	6.17E-05
ENSBTAG00000014322	FAM234B	-0.182561318	0.24130252
ENSBTAG00000014324	ANTXR2	0.454953345	0.002175411
ENSBTAG00000014326	CDCA8	-0.413087688	0.005902947
ENSBTAG00000014328	MGC138914	0.466955831	0.001595683
ENSBTAG00000014329	LOC512548	-0.240653394	0.120061949
ENSBTAG00000014331	UBL4A	-0.39011622	0.009705454
ENSBTAG00000014334	ZFYVE26	0.180238214	0.247445714
ENSBTAG00000014335	LOC112441470	-0.163755264	0.29405088
ENSBTAG00000014343	IFT22	-0.66226962	1.32E-06
ENSBTAG00000014349	RNF126	0.587498055	3.45E-05
ENSBTAG00000014351	EIF2AK4	-0.397190959	0.008357387
ENSBTAG00000014353	SRP14	-0.648558859	2.56E-06
ENSBTAG00000014354	FXYD6	0.073202143	0.640857264
ENSBTAG00000014355	MYCBPAP	-0.492206277	0.000800644
ENSBTAG00000014357	SDC2	-0.269854624	0.080111226
ENSBTAG00000014358	EVA1B	0.536527316	0.000208277
ENSBTAG00000014359	DRAXIN	0.390081417	0.009712521
ENSBTAG00000014365	LOC112447333	0.166027894	0.287309231
ENSBTAG00000014367	PRKX	0.375870251	0.012993361
ENSBTAG00000014368	SLAMF6	0.008793258	0.955371148
ENSBTAG00000014371	CHPF2	0.317619148	0.037942323
ENSBTAG00000014372	SMARCD3	0.086974403	0.579184669
ENSBTAG00000014373	CETN3	-0.603473294	1.84E-05
ENSBTAG00000014374	CARD6	0.038617991	0.805787011
ENSBTAG00000014375	TMCC3	-0.462686868	0.001783911
ENSBTAG00000014376	ANKRD13A	0.339894926	0.025746086
ENSBTAG00000014377	CHD3	0.230889648	0.136318625
ENSBTAG00000014380	MCM2	-0.386749738	0.010409836
ENSBTAG00000014389	SP4	0.150524856	0.335308627
ENSBTAG00000014390	MTMR9	0.606870388	1.60E-05

ENSBTAG00000014393	CLK2	0.668868746	9.45E-07
ENSBTAG00000014396	KLF10	0.543664051	0.000164715
ENSBTAG00000014400	E2F2	0.607247817	1.58E-05
ENSBTAG00000014401	SORBS3	-0.438841968	0.003241867
ENSBTAG00000014402	GIMAP8	0.206076973	0.184906154
ENSBTAG00000014405	OSBPL6	-0.262865992	0.088562578
ENSBTAG00000014407	INO80D	0.023547893	0.880855813
ENSBTAG00000014411	NA	-0.606714475	1.61E-05
ENSBTAG00000014412	ELAVL3	0.008182126	0.95847006
ENSBTAG00000014417	CASTOR2	-0.46112313	0.001857624
ENSBTAG00000014420	AGER	0.238734347	0.123135784
ENSBTAG00000014421	NA	0.432220353	0.003798624
ENSBTAG00000014424	DDN	0.03209872	0.838091297
ENSBTAG00000014429	KMT2D	0.251880627	0.103225656
ENSBTAG00000014432	HNMT	-0.446401027	0.002694908
ENSBTAG00000014433	UBE2G1	0.428447501	0.004151866
ENSBTAG00000014434	CCHCR1	-0.560783791	9.18E-05
ENSBTAG00000014435	TCF19	-0.455582893	0.002140923
ENSBTAG00000014439	KMO	0.504235449	0.000565591
ENSBTAG00000014440	PSMA4	-0.045918446	0.769989317
ENSBTAG00000014441	CD96	-0.30676038	0.045412204
ENSBTAG00000014447	RPS6KA1	0.637490115	4.28E-06
ENSBTAG00000014448	VKORC1L1	-0.518837344	0.000364474
ENSBTAG00000014453	PLK1	-0.146890762	0.347240237
ENSBTAG00000014454	NA	-0.259555445	0.092800068
ENSBTAG00000014455	PDZD2	-0.105286967	0.501622055
ENSBTAG00000014458	MROH1	-0.384736908	0.010851556
ENSBTAG00000014459	MAP6D1	-0.129270581	0.408702034
ENSBTAG00000014461	ANAPC13	-0.40374634	0.007255431
ENSBTAG00000014465	SERPINE1	0.549845188	0.000133845
ENSBTAG00000014467	GLIS3	0.041639383	0.790919551
ENSBTAG00000014468	AP1S1	-0.419126877	0.005150038
ENSBTAG00000014469	NBEAL1	-0.23419343	0.130644418
ENSBTAG00000014471	PALM2	0.530071936	0.000256376
ENSBTAG00000014472	LCMT2	0.086148265	0.582807452
ENSBTAG00000014479	TUBGCP4	-0.629835523	6.03E-06
ENSBTAG00000014484	TMEM26	-0.468468408	0.001533342
ENSBTAG00000014485	POF1B	-0.176087037	0.258683611
ENSBTAG00000014490	DDX39B	0.645411977	2.97E-06
ENSBTAG00000014493	TRIP4	-0.580800385	4.44E-05
ENSBTAG00000014494	RNASET2	0.042981838	0.784336784
ENSBTAG00000014496	CCR6	0.346062513	0.023016693
ENSBTAG00000014497	GPR31	0.369980401	0.014606866
ENSBTAG00000014498	UNC93A	-0.391475916	0.00943278
ENSBTAG00000014501	FERMT2	-0.393819205	0.008978278
ENSBTAG00000014502	BRAT1	-0.206451	0.18409258
ENSBTAG00000014503	IQCE	-0.231887447	0.134585954

ENSBTAG00000014506	ZNF503	0.260729746	0.091279395
ENSBTAG00000014508	FBXO40	0.332643743	0.02929441
ENSBTAG00000014511	C16H1orf159	0.691022009	2.91E-07
ENSBTAG00000014512	WDR19	-0.629333418	6.17E-06
ENSBTAG00000014515	RFC1	-0.285075727	0.06389116
ENSBTAG00000014520	LIAS	-0.502522739	0.000594746
ENSBTAG00000014521	UGDH	-0.277743779	0.07134355
ENSBTAG00000014526	MOB3A	0.638311406	4.12E-06
ENSBTAG00000014529	GBP4	0.425723655	0.004424411
ENSBTAG00000014536	SFXN1	-0.054134166	0.73026415
ENSBTAG00000014537	NA	-0.380030441	0.011947404
ENSBTAG00000014538	HPCAL4	0.006788658	0.965538202
ENSBTAG00000014540	PERM1	-0.366771864	0.015555241
ENSBTAG00000014541	PDGFA	0.334879735	0.028159474
ENSBTAG00000014543	PLXNA4	0.386369632	0.010492051
ENSBTAG00000014546	CLEC7A	-0.175576792	0.260088052
ENSBTAG00000014548	NIBAN1	0.489872884	0.000855233
ENSBTAG00000014549	GNL3	0.403899545	0.007231256
ENSBTAG00000014550	GLT8D1	-0.568234352	7.04E-05
ENSBTAG00000014551	TNFAIP8	0.277599696	0.071496587
ENSBTAG00000014553	ATP6V0D1	0.46437495	0.001707253
ENSBTAG00000014554	SNAI1	0.470146139	0.001466727
ENSBTAG00000014555	CASS4	0.115762942	0.459767108
ENSBTAG00000014558	DDX21	0.537772492	0.000199998
ENSBTAG00000014560	HLX	0.580606732	4.47E-05
ENSBTAG00000014564	XXYLT1	-0.064914169	0.679193382
ENSBTAG00000014567	MYLK	-0.310258269	0.042885821
ENSBTAG00000014576	GUCY1A1	-0.309012622	0.043772051
ENSBTAG00000014580	FCRLB	0.020339993	0.896992668
ENSBTAG00000014585	PTGIR	0.476679576	0.001231115
ENSBTAG00000014587	NA	-0.19209159	0.217187114
ENSBTAG00000014588	RSL1D1	0.511637925	0.00045376
ENSBTAG00000014593	NA	-0.009376308	0.952415245
ENSBTAG00000014595	LIG1	-0.677731524	5.97E-07
ENSBTAG00000014596	EFHD1	-0.392229261	0.009284554
ENSBTAG00000014597	ZSWIM9	-0.364519316	0.016251775
ENSBTAG00000014599	LRRC66	-0.654577158	1.92E-06
ENSBTAG00000014600	ADCY8	0.39029079	0.009670072
ENSBTAG00000014601	SGCB	-0.690648161	2.97E-07
ENSBTAG00000014602	CAMTA1	-0.08627232	0.582262794
ENSBTAG00000014605	ETV6	0.467076049	0.001590647
ENSBTAG00000014608	KDM1B	-0.30748079	0.044882242
ENSBTAG00000014611	SORL1	-0.002814389	0.985709552
ENSBTAG00000014612	DOCK2	0.510781418	0.000465595
ENSBTAG00000014614	ACTA2	0.318199316	0.037573406
ENSBTAG00000014615	SLC26A2	-0.181982687	0.242822887
ENSBTAG00000014616	SEPSECS	-0.117777123	0.451941586

ENSBTAG00000014623	MCM8	-0.569855243	6.64E-05
ENSBTAG00000014628	OAS2	0.202916753	0.191882588
ENSBTAG00000014633	ABCD4	-0.246499396	0.111054343
ENSBTAG00000014636	ZFHX3	0.055062415	0.725817172
ENSBTAG00000014642	NAPRT	0.341618879	0.024957347
ENSBTAG00000014644	DUS2	-0.439100776	0.003221642
ENSBTAG00000014646	MZT2B	-0.000913446	0.995361636
ENSBTAG00000014655	MYO1A	-0.33459104	0.028303925
ENSBTAG00000014665	ADAMTS2	0.530674175	0.000251499
ENSBTAG00000014668	NAGK	-0.238133044	0.124110991
ENSBTAG00000014669	NDUFA12	-0.493046786	0.000781756
ENSBTAG00000014676	SHROOM1	-0.366869586	0.015525605
ENSBTAG00000014678	PAEP	-0.296443076	0.053574426
ENSBTAG00000014679	DHX57	-0.495563462	0.00072756
ENSBTAG00000014680	ZBTB49	0.473474599	0.001342122
ENSBTAG00000014682	NA	-0.395301149	0.008700667
ENSBTAG00000014687	TP53I13	-0.53767789	0.000200616
ENSBTAG00000014689	CSPP1	-0.44966951	0.002484737
ENSBTAG00000014693	TMEM88	0.57545298	5.42E-05
ENSBTAG00000014698	CARD11	-0.266274609	0.084358033
ENSBTAG00000014705	HES4	0.389676471	0.009795077
ENSBTAG00000014707	ISG15	0.369777749	0.014665278
ENSBTAG00000014713	RARRES1	-0.527112413	0.000281608
ENSBTAG00000014714	TUBGCP5	-0.588496652	3.32E-05
ENSBTAG00000014718	NA	-0.332759527	0.029234725
ENSBTAG00000014725	CD27	-0.271140142	0.078627762
ENSBTAG00000014726	NA	-0.663967222	1.21E-06
ENSBTAG00000014727	RFC4	-0.550425464	0.000131235
ENSBTAG00000014728	TAPBPL	0.562689135	8.58E-05
ENSBTAG00000014729	MRPL51	-0.480555793	0.001107813
ENSBTAG00000014730	NCAPD2	-0.462094173	0.00181154
ENSBTAG00000014733	NOP2	0.657500953	1.67E-06
ENSBTAG00000014737	VEGFC	0.594125831	2.67E-05
ENSBTAG00000014742	LRWD1	0.524029666	0.00031025
ENSBTAG00000014750	EPB41L4A	-0.131236178	0.401552714
ENSBTAG00000014761	PGA5	0.265759615	0.084983112
ENSBTAG00000014762	ISG20	0.53233124	0.000238508
ENSBTAG00000014764	CD9	-0.329489968	0.030959368
ENSBTAG00000014768	ZNF786	-0.506463207	0.000529586
ENSBTAG00000014769	GMEB2	0.558035941	0.000101021
ENSBTAG00000014773	HMMR	-0.72823254	3.12E-08
ENSBTAG00000014779	NISCH	0.095210842	0.543635896
ENSBTAG00000014782	STAB1	-0.071961686	0.646539672
ENSBTAG00000014784	NT5DC2	-0.623245402	8.05E-06
ENSBTAG00000014788	AKAP12	-0.141046456	0.366966091
ENSBTAG00000014790	ZBTB2	0.633872707	5.04E-06
ENSBTAG00000014791	CTH	-0.003525967	0.982096939

ENSBTAG00000014793	C16H1orf112	-0.150236494	0.33624599
ENSBTAG00000014794	SCYL3	0.500528524	0.000630385
ENSBTAG00000014797	SEC22A	-0.426363834	0.004358991
ENSBTAG00000014798	CXCR3	-0.280098345	0.06887909
ENSBTAG00000014799	ARMC7	0.180721471	0.246159191
ENSBTAG00000014804	HNRNPDL	-0.170291055	0.274935805
ENSBTAG00000014805	ENOPH1	-0.174560481	0.262900545
ENSBTAG00000014806	ATP2A3	0.520361816	0.000347732
ENSBTAG00000014809	ANXA6	0.200414789	0.197536545
ENSBTAG00000014814	BICRAL	0.206280273	0.184463624
ENSBTAG00000014818	MYLK3	0.265481623	0.085322022
ENSBTAG00000014824	MMP14	-0.352989069	0.020244131
ENSBTAG00000014825	NLK	0.200491735	0.19736093
ENSBTAG00000014828	CACNA1A	0.077445324	0.621574024
ENSBTAG00000014829	MYRFL	0.535052202	0.000218485
ENSBTAG00000014831	PPP1R3C	-0.543753019	0.000164229
ENSBTAG00000014835	SPARC	-0.303967406	0.047515026
ENSBTAG00000014841	GBA	-0.064329016	0.681931889
ENSBTAG00000014855	MICAL2	0.049408037	0.753038538
ENSBTAG00000014857	LOC107131333	0.520891459	0.000342079
ENSBTAG00000014863	GYPC	-0.14776508	0.344346156
ENSBTAG00000014878	COX7A1	0.000583371	0.997037705
ENSBTAG00000014879	FAM185A	-0.614015532	1.19E-05
ENSBTAG00000014880	ICOSLG	0.523234848	0.000318049
ENSBTAG00000014881	PHF23	0.557250798	0.000103816
ENSBTAG00000014882	DNMT3L	0.249700594	0.106344654
ENSBTAG00000014884	HIPK3	0.278274626	0.070781941
ENSBTAG00000014885	MYOM3	0.086337861	0.581975137
ENSBTAG00000014889	DCBLD2	0.052856087	0.73640136
ENSBTAG00000014897	UNC5A	-0.026390344	0.866596787
ENSBTAG00000014898	HK3	0.573426323	5.83E-05
ENSBTAG00000014900	CNOT3	0.340876241	0.025294611
ENSBTAG00000014903	ABCA3	0.65053912	2.33E-06
ENSBTAG00000014904	SIRT5	-0.484960203	0.000981149
ENSBTAG00000014906	VCAN	0.525447255	0.000296768
ENSBTAG00000014907	IL11RA	-0.629119979	6.23E-06
ENSBTAG00000014912	FMOD	0.128072557	0.413095059
ENSBTAG00000014915	ETV5	0.253517119	0.100930689
ENSBTAG00000014917	GTPBP4	0.627256981	6.76E-06
ENSBTAG00000014921	IL6	0.524616493	0.000304604
ENSBTAG00000014922	SHB	-0.207696318	0.181402196
ENSBTAG00000014923	BBS2	-0.659922964	1.48E-06
ENSBTAG00000014932	ARSL	-0.256277301	0.097148829
ENSBTAG00000014936	SLC25A51	-0.542408988	0.00017172
ENSBTAG00000014943	KDM5C	0.579939529	4.59E-05
ENSBTAG00000014944	TBXA2R	-0.167299346	0.283581701
ENSBTAG00000014945	IQSEC2	-0.169769904	0.276429304

ENSBTAG00000014947	PTPN13	0.040906557	0.794519083
ENSBTAG00000014953	LOC104968422	0.515165643	0.000407814
ENSBTAG00000014956	JSRP1	-0.256470978	0.096887615
ENSBTAG00000014958	PRKAR2B	-0.239764526	0.121478422
ENSBTAG00000014960	SCHIP1	-0.264180019	0.08692287
ENSBTAG00000014966	PLXNB2	-0.290255002	0.059010266
ENSBTAG00000014970	LAMTOR5	0.354436663	0.019701626
ENSBTAG00000014971	SEC61G	0.222633126	0.151297116
ENSBTAG00000014972	PTGER4	0.322426175	0.034973407
ENSBTAG00000014974	GRAMD2B	0.406567637	0.006821265
ENSBTAG00000014975	SLC4A3	0.061345395	0.695957354
ENSBTAG00000014979	MFSD12	0.609942021	1.41E-05
ENSBTAG00000014981	OTUB2	0.43364395	0.003672335
ENSBTAG00000014982	TEKTIP1	0.639212766	3.96E-06
ENSBTAG00000014983	IL23R	-0.138425415	0.376026733
ENSBTAG00000014991	PARD3	0.249178594	0.107102049
ENSBTAG00000014996	NA	-0.53501644	0.000218738
ENSBTAG00000015006	NA	-0.465017656	0.001678842
ENSBTAG00000015007	NCOA1	0.061514447	0.695159936
ENSBTAG00000015008	CPA3	-0.531635385	0.000243887
ENSBTAG00000015010	TBC1D23	0.370959321	0.014327475
ENSBTAG00000015012	PTRHD1	-0.569346531	6.77E-05
ENSBTAG00000015013	C2CD2L	0.543785662	0.000164051
ENSBTAG00000015014	CENPO	-0.590012015	3.13E-05
ENSBTAG00000015015	HINFP	-0.334453906	0.028372756
ENSBTAG00000015016	CALCOCO1	-0.635770558	4.63E-06
ENSBTAG00000015017	GAL3ST4	-0.350201431	0.021324214
ENSBTAG00000015018	FSD2	0.402251409	0.007495011
ENSBTAG00000015019	STN1	-0.669208855	9.29E-07
ENSBTAG00000015024	GXYLT1	-0.096037986	0.540124579
ENSBTAG00000015026	ABL2	0.001110739	0.994359824
ENSBTAG00000015032	CD14	0.518817395	0.000364698
ENSBTAG00000015034	IK	0.502877271	0.000588603
ENSBTAG00000015037	GAREM2	-0.031703296	0.840059749
ENSBTAG00000015038	HADHA	-0.650341552	2.35E-06
ENSBTAG00000015042	WDR55	0.61679406	1.06E-05
ENSBTAG00000015043	MFNG	0.422146918	0.004805915
ENSBTAG00000015044	CARD10	-0.275443214	0.073818179
ENSBTAG00000015046	MST1R	0.657037245	1.71E-06
ENSBTAG00000015050	HCN2	-0.385457139	0.010691692
ENSBTAG00000015052	PROX2	-0.64529095	2.99E-06
ENSBTAG00000015053	CFL2	-0.117488985	0.4530566
ENSBTAG00000015058	CDH4	0.227315336	0.142661542
ENSBTAG00000015060	GBP5	0.485616975	0.000963411
ENSBTAG00000015061	LOC617141	0.525661346	0.000294779
ENSBTAG00000015066	LANCL1	-0.688173588	3.40E-07
ENSBTAG00000015074	PTGDS	-0.066903573	0.669913626

ENSBTAG00000015076	LATS1	-0.618009869	1.01E-05
ENSBTAG00000015083	FBXO9	0.300249342	0.050435914
ENSBTAG00000015085	CLIC3	-0.159539943	0.306823629
ENSBTAG00000015086	HSD11B1	0.349675224	0.021533422
ENSBTAG00000015089	LGALS1	-0.446081007	0.002716303
ENSBTAG00000015092	NA	0.585822314	3.67E-05
ENSBTAG00000015094	VNN1	-0.413896455	0.005796881
ENSBTAG00000015097	CACFD1	-0.342714031	0.024466835
ENSBTAG00000015098	RABEPK	-0.052363316	0.73877195
ENSBTAG00000015101	HMGB2	-0.464483958	0.001702404
ENSBTAG00000015104	CCDC28B	-0.264471064	0.086562902
ENSBTAG00000015106	DSP	-0.352976098	0.020249048
ENSBTAG00000015107	SLC16A1	0.125939246	0.420983991
ENSBTAG00000015108	USHBP1	-0.420149622	0.005031174
ENSBTAG00000015109	TOB2	0.297870778	0.052379288
ENSBTAG00000015113	CITED4	-0.08748591	0.576946724
ENSBTAG00000015114	CALR	0.360561743	0.017539463
ENSBTAG00000015115	ACP4	-0.463330612	0.001754326
ENSBTAG00000015119	SIK3	0.43006779	0.003996795
ENSBTAG00000015124	ARGLU1	0.402201138	0.007503185
ENSBTAG00000015126	TNIP2	0.551707441	0.000125632
ENSBTAG00000015127	SDC4	0.5382601	0.000196837
ENSBTAG00000015129	KLK10	-0.233441468	0.131920128
ENSBTAG00000015131	SLC29A1	-0.353799582	0.019938856
ENSBTAG00000015133	CCR7	-0.330694249	0.030314599
ENSBTAG00000015142	MAPKBP1	-0.455343015	0.002154007
ENSBTAG00000015148	METTL3	0.490520727	0.000839753
ENSBTAG00000015150	IL12A	0.485627121	0.000963139
ENSBTAG00000015154	MCL1	0.451749712	0.002358618
ENSBTAG00000015155	HACD3	-0.604826435	1.74E-05
ENSBTAG00000015157	GRAP2	-0.197069852	0.205277386
ENSBTAG00000015158	INTS14	-0.677839504	5.94E-07
ENSBTAG00000015160	PLD4	0.021420948	0.891550176
ENSBTAG00000015163	TM4SF1	-0.562187512	8.73E-05
ENSBTAG00000015164	SLC27A5	-0.549136585	0.000137096
ENSBTAG00000015165	DPY19L3	-0.185189961	0.23447702
ENSBTAG00000015169	UBXN4	-0.607840656	1.54E-05
ENSBTAG00000015172	MCM6	-0.690533385	2.99E-07
ENSBTAG00000015177	PRSS23	-0.369635999	0.014706254
ENSBTAG00000015178	ECI2	-0.587460976	3.45E-05
ENSBTAG00000015181	EPM2A	-0.636599418	4.46E-06
ENSBTAG00000015182	STARD10	0.151246624	0.332969522
ENSBTAG00000015183	TPCN2	0.435392548	0.003522254
ENSBTAG00000015184	SYDE1	-0.201552228	0.194951773
ENSBTAG00000015186	ILVBL	-0.271344909	0.078393464
ENSBTAG00000015188	KLF6	0.593804874	2.70E-05
ENSBTAG00000015190	RMC1	0.682865354	4.54E-07

ENSBTAG00000015192	FAM193B	-0.032328639	0.836947192
ENSBTAG00000015193	NA	-0.416259532	0.005496397
ENSBTAG00000015195	NPC1	0.568123073	7.07E-05
ENSBTAG00000015200	L2HGDH	-0.685750499	3.88E-07
ENSBTAG00000015202	DMAC2L	-0.560758661	9.19E-05
ENSBTAG00000015205	NCK2	0.039005153	0.803877994
ENSBTAG00000015208	CARMIL3	0.123121002	0.431535151
ENSBTAG00000015209	MXD4	0.305263056	0.04652994
ENSBTAG00000015212	IFNAR2	0.585207417	3.76E-05
ENSBTAG00000015218	NA	-0.173003488	0.267248368
ENSBTAG00000015220	AGO4	-0.418630697	0.005208579
ENSBTAG00000015221	PCCB	-0.625207172	7.39E-06
ENSBTAG00000015222	RSRP1	-0.189089627	0.224595788
ENSBTAG00000015224	TCOF1	0.084756931	0.588931628
ENSBTAG00000015228	CD74	0.527841327	0.000275194
ENSBTAG00000015230	PLA2G12A	-0.620523826	9.05E-06
ENSBTAG00000015235	HMCN1	-0.261577883	0.090193139
ENSBTAG00000015240	UBR4	0.474093692	0.001320011
ENSBTAG00000015241	EPHX2	0.370165414	0.014553711
ENSBTAG00000015242	SLC18B1	-0.31937118	0.036837202
ENSBTAG00000015251	ALG13	-0.72348672	4.23E-08
ENSBTAG00000015254	GLB1	-0.48903909	0.00087553
ENSBTAG00000015255	ST6GALNAC2	-0.125314983	0.423308499
ENSBTAG00000015258	P2RX5	0.433387718	0.00369479
ENSBTAG00000015261	CARD14	-0.001252457	0.993640215
ENSBTAG00000015265	TIGD2	-0.42546508	0.004451077
ENSBTAG00000015266	SDHAF2	0.459723475	0.001925872
ENSBTAG00000015268	PICK1	-0.240227246	0.120739483
ENSBTAG00000015271	RIPK2	0.473479919	0.00134193
ENSBTAG00000015272	TSC22D4	0.216271902	0.163635359
ENSBTAG00000015276	SLC26A11	0.340235414	0.025588683
ENSBTAG00000015277	PCF11	0.089204031	0.569458478
ENSBTAG00000015280	KIF2C	-0.283725816	0.065214634
ENSBTAG00000015286	GOLGA1	-0.619918985	9.28E-06
ENSBTAG00000015293	NXPH3	-0.269439205	0.080595264
ENSBTAG00000015296	PTPRB	-0.149423881	0.338896234
ENSBTAG00000015297	BANK1	0.225913502	0.145207862
ENSBTAG00000015299	NA	-0.178059534	0.253302006
ENSBTAG00000015303	PALS2	0.364593492	0.016228425
ENSBTAG00000015304	ANXA9	0.45161039	0.002366885
ENSBTAG00000015311	PTPRR	-0.007321557	0.962834821
ENSBTAG00000015312	LTBR	0.662734403	1.29E-06
ENSBTAG00000015314	ASL	-0.625090077	7.43E-06
ENSBTAG00000015316	NPM1	0.183297716	0.239376966
ENSBTAG00000015318	NECTIN2	0.548194309	0.00014153
ENSBTAG00000015321	TRERF1	-0.082717201	0.597961124
ENSBTAG00000015326	GSDME	0.377952805	0.012460412

ENSBTAG00000015330	NA	-0.139577314	0.372028493
ENSBTAG00000015334	ZHX1	-0.698635484	1.89E-07
ENSBTAG00000015337	TSPAN12	-0.354145374	0.019809797
ENSBTAG00000015338	DSCC1	-0.259124656	0.093362804
ENSBTAG00000015340	ANGPTL7	0.251009028	0.104464151
ENSBTAG00000015341	DEPTOR	-0.040474365	0.796643929
ENSBTAG00000015343	DYNC2I2	-0.586559393	3.57E-05
ENSBTAG00000015346	NASP	-0.633751482	5.07E-06
ENSBTAG00000015361	CNTFR	-0.561456337	8.96E-05
ENSBTAG00000015363	CDC42SE1	0.54598307	0.000152449
ENSBTAG00000015366	SFRP4	-0.449695624	0.002483117
ENSBTAG00000015368	SEPTIN4	-0.181805125	0.243290732
ENSBTAG00000015369	MLLT11	-0.411649877	0.006095668
ENSBTAG00000015375	SH2D3C	0.576027489	5.30E-05
ENSBTAG00000015381	ARHGAP18	-0.330548259	0.030392165
ENSBTAG00000015386	REL	0.112868376	0.471139843
ENSBTAG00000015388	RPL18	0.58495758	3.80E-05
ENSBTAG00000015390	FN3KRP	-0.600904528	2.04E-05
ENSBTAG00000015392	TTF2	-0.540615995	0.000182195
ENSBTAG00000015394	NA	-0.391974387	0.009334477
ENSBTAG00000015395	NA	0.070192169	0.654680059
ENSBTAG00000015398	TJP1	-0.298955865	0.051485386
ENSBTAG00000015401	ATG4B	0.518101201	0.000372815
ENSBTAG00000015402	GREB1	-0.366615465	0.015602772
ENSBTAG00000015403	TPP1	-0.285304477	0.06366902
ENSBTAG00000015405	DCHS1	0.156188202	0.317228334
ENSBTAG00000015406	ZNF750	-0.23005006	0.137789362
ENSBTAG00000015408	DTYMK	-0.397745228	0.008258944
ENSBTAG00000015413	RASA2	0.531686945	0.000243485
ENSBTAG00000015414	TBCD	-0.436952434	0.003392931
ENSBTAG00000015416	PEBP4	-0.462515948	0.00179184
ENSBTAG00000015419	ARHGEF37	-0.418475391	0.005227021
ENSBTAG00000015424	WDR12	0.318514827	0.037374016
ENSBTAG00000015426	PDLIM4	-0.577214629	5.07E-05
ENSBTAG00000015427	CFDP1	-0.654106453	1.97E-06
ENSBTAG00000015432	TMEM231	-0.46211003	0.001810796
ENSBTAG00000015434	DSTN	-0.314715355	0.039833618
ENSBTAG00000015436	SLC27A4	-0.415836447	0.00554918
ENSBTAG00000015438	RRBP1	-0.221467207	0.153505862
ENSBTAG00000015449	PPEF2	-0.071789893	0.647328216
ENSBTAG00000015450	CPEB3	-0.277571271	0.071526809
ENSBTAG00000015457	FGFR1	-0.293018925	0.056530256
ENSBTAG00000015467	FAM184A	0.021327789	0.892019029
ENSBTAG00000015474	SRSF11	0.242999926	0.11638243
ENSBTAG00000015478	SRD5A1	-0.610749935	1.37E-05
ENSBTAG00000015481	MTIF2	-0.49231733	0.000798125
ENSBTAG00000015490	HS1BP3	-0.308880695	0.043866778

ENSBTAG00000015497	NA	-0.061768409	0.693962609
ENSBTAG00000015498	ELOVL4	0.564556323	8.03E-05
ENSBTAG00000015505	FADS2	-0.261357512	0.090474413
ENSBTAG00000015509	NAMPT	0.215862414	0.16445389
ENSBTAG00000015511	FADS3	-0.278755142	0.070276594
ENSBTAG00000015512	HEXB	-0.139408412	0.372613157
ENSBTAG00000015513	DOCK5	-0.433600353	0.003676147
ENSBTAG00000015516	CCDC28A	-0.700604845	1.69E-07
ENSBTAG00000015520	SLC11A1	0.312645613	0.041228137
ENSBTAG00000015521	GEMIN6	-0.256037133	0.097473496
ENSBTAG00000015522	MRPS31	-0.181013541	0.245383837
ENSBTAG00000015527	MYO1D	-0.257074903	0.09607657
ENSBTAG00000015529	CHCHD4	0.633559638	5.11E-06
ENSBTAG00000015534	LYPLAL1	-0.585929831	3.66E-05
ENSBTAG00000015537	RASAL2	-0.115699261	0.460015708
ENSBTAG00000015538	LEMD2	0.220140376	0.156048054
ENSBTAG00000015541	DLC1	0.200667992	0.196959076
ENSBTAG00000015543	ARHGAP35	0.368872791	0.014928548
ENSBTAG00000015546	RIOX2	-0.383053208	0.011233271
ENSBTAG00000015553	SCAI	-0.28695698	0.062082465
ENSBTAG00000015557	LOC528040	0.28396046	0.064983035
ENSBTAG00000015559	ERI3	-0.589466299	3.19E-05
ENSBTAG00000015562	PLBD1	0.211084176	0.174225519
ENSBTAG00000015565	NA	0.006817342	0.965392678
ENSBTAG00000015567	TIMM44	0.185790699	0.232935826
ENSBTAG00000015569	ENKUR	-0.061409649	0.69565423
ENSBTAG00000015571	GCLC	-0.012509276	0.936543705
ENSBTAG00000015576	NPAS1	-0.029999931	0.848550092
ENSBTAG00000015580	TLE3	0.521663537	0.000333987
ENSBTAG00000015582	HMOX1	-0.058753947	0.708221276
ENSBTAG00000015584	BMI1	-0.446632368	0.002679534
ENSBTAG00000015588	TMEM209	-0.589100662	3.24E-05
ENSBTAG00000015590	CILK1	-0.331416525	0.029933251
ENSBTAG00000015591	SQSTM1	0.022822678	0.884499972
ENSBTAG00000015592	GPR84	0.52736334	0.000279385
ENSBTAG00000015595	MCM5	-0.640727069	3.69E-06
ENSBTAG00000015596	SLCO2B1	-0.401830122	0.007563748
ENSBTAG00000015599	PRKD2	0.117923433	0.451375982
ENSBTAG00000015602	MRNIP	-0.534529518	0.000222209
ENSBTAG00000015604	ZNF385A	0.493674325	0.000767915
ENSBTAG00000015606	NA	-0.00371255	0.981149732
ENSBTAG00000015607	ERMP1	-0.160035496	0.305303989
ENSBTAG00000015609	PREX1	0.608682074	1.49E-05
ENSBTAG00000015611	TBC1D9B	-0.461854927	0.001822799
ENSBTAG00000015614	LNX2	-0.502709992	0.000591494
ENSBTAG00000015615	THEMIS	-0.185175403	0.234514454
ENSBTAG00000015618	GDF15	-0.193005135	0.214966525

ENSBTAG00000015632	TNFRSF18	0.432905614	0.003737367
ENSBTAG00000015635	TNFRSF4	0.219993709	0.156330944
ENSBTAG00000015636	SHFL	0.655369931	1.85E-06
ENSBTAG00000015637	BPNT2	-0.392515828	0.009228698
ENSBTAG00000015638	IL20RA	0.291463156	0.057915728
ENSBTAG00000015644	EID2	-0.071455669	0.64886342
ENSBTAG00000015649	TMEM156	0.400788678	0.007736009
ENSBTAG00000015651	NA	-0.610567717	1.38E-05
ENSBTAG00000015655	APBB1	-0.037977672	0.808946739
ENSBTAG00000015659	CIAO1	-0.678759314	5.65E-07
ENSBTAG00000015662	IMPG2	0.142693048	0.361341635
ENSBTAG00000015663	STIP1	0.102531001	0.512946576
ENSBTAG00000015667	TMEM127	0.204327974	0.188744528
ENSBTAG00000015669	ADAT1	0.16195362	0.299467355
ENSBTAG00000015678	NEMP2	0.510410476	0.000470806
ENSBTAG00000015683	HSPA4	-0.023490553	0.881143857
ENSBTAG00000015692	HSPA4L	-0.030296127	0.847072474
ENSBTAG00000015694	NA	0.504869087	0.000555133
ENSBTAG00000015698	FYCO1	-0.187053299	0.229719211
ENSBTAG00000015707	TREML2	0.570179654	6.57E-05
ENSBTAG00000015708	CXCR6	-0.203136213	0.191392177
ENSBTAG00000015710	CD3E	-0.426933216	0.004301516
ENSBTAG00000015711	BTG2	0.567193452	7.31E-05
ENSBTAG00000015716	ERO1A	0.390496879	0.009628443
ENSBTAG00000015718	CASP8	0.13424932	0.390734727
ENSBTAG00000015719	PIGF	-0.402685118	0.007424811
ENSBTAG00000015720	WWP1	-0.554587747	0.000113826
ENSBTAG00000015721	RAVER1	0.528232277	0.000271808
ENSBTAG00000015727	IFI47	0.064489728	0.681179356
ENSBTAG00000015730	BOLA-DMA	0.578474173	4.84E-05
ENSBTAG00000015734	RMDN1	-0.474821319	0.001294438
ENSBTAG00000015739	MRC2	0.01757386	0.910940536
ENSBTAG00000015742	ICAM3	0.556243108	0.000107506
ENSBTAG00000015745	RAB3IL1	-0.170130364	0.275395742
ENSBTAG00000015749	STEAP1	0.606851758	1.60E-05
ENSBTAG00000015752	SP110	0.602663537	1.90E-05
ENSBTAG00000015758	USB1	0.562721597	8.57E-05
ENSBTAG00000015761	COQ5	-0.60980806	1.42E-05
ENSBTAG00000015764	EML2	-0.070725739	0.652221234
ENSBTAG00000015766	ZFPM1	-0.184865386	0.235312604
ENSBTAG00000015769	VSIG4	-0.665688982	1.11E-06
ENSBTAG00000015772	STOML1	0.26086058	0.091111171
ENSBTAG00000015776	MFSD14A	0.538605564	0.000194626
ENSBTAG00000015778	SASS6	-0.247637282	0.109362432
ENSBTAG00000015779	PML	0.362798362	0.016801545
ENSBTAG00000015782	SCAP	-0.160123327	0.305035152
ENSBTAG00000015788	CCDC171	-0.467396236	0.001577304

ENSBTAG00000015792	CFAP54	0.2013725	0.1953586
ENSBTAG00000015793	RAB38	-0.512900148	0.000436812
ENSBTAG00000015794	NES	-0.237799032	0.124655201
ENSBTAG00000015801	EFNB1	0.409363734	0.006413333
ENSBTAG00000015802	CREB3L2	-0.102496454	0.513089344
ENSBTAG00000015804	SIGMAR1	-0.107443313	0.492851178
ENSBTAG00000015805	SIPA1L1	0.590649554	3.05E-05
ENSBTAG00000015807	GALT	-0.57818473	4.90E-05
ENSBTAG00000015808	ZNF609	0.240843622	0.119760432
ENSBTAG00000015815	CFP	0.480792516	0.001100653
ENSBTAG00000015818	LOC112441463	0.223073163	0.150469588
ENSBTAG00000015821	AMPD3	0.451517633	0.002372403
ENSBTAG00000015825	CCDC65	0.016596467	0.91587546
ENSBTAG00000015828	FKBP11	0.315532977	0.03929346
ENSBTAG00000015829	ENPP5	0.515595807	0.000402507
ENSBTAG00000015835	PIWIL2	-0.072982769	0.641860729
ENSBTAG00000015837	P2RY12	0.188079745	0.227126748
ENSBTAG00000015844	TFPI2	0.423746421	0.004631906
ENSBTAG00000015856	CFAP126	0.165145399	0.289915083
ENSBTAG00000015860	FGD1	-0.558251388	0.000100267
ENSBTAG00000015865	CAPN14	0.244437425	0.114170856
ENSBTAG00000015868	LIG4	0.439826964	0.003165482
ENSBTAG00000015872	PROKR2	0.09239652	0.555664268
ENSBTAG00000015874	CASP3	-0.258244587	0.094520623
ENSBTAG00000015875	FOXM1	-0.386892137	0.010379178
ENSBTAG00000015879	TULP3	0.226597892	0.143960567
ENSBTAG00000015882	UBE2J2	0.529459062	0.000261427
ENSBTAG00000015888	PDE7B	-0.480355651	0.0011139
ENSBTAG00000015889	CLCN7	0.666662696	1.06E-06
ENSBTAG00000015893	EPN3	-0.404929543	0.007070527
ENSBTAG00000015894	WWOX	-0.42840384	0.004156116
ENSBTAG00000015896	CC2D1B	-0.005289806	0.97314378
ENSBTAG00000015899	NA	-0.634499325	4.90E-06
ENSBTAG00000015902	PTGFR	0.177911735	0.253702625
ENSBTAG00000015904	RORA	-0.454616396	0.00219407
ENSBTAG00000015905	ARHGAP32	0.030896774	0.844077648
ENSBTAG00000015908	MBOAT7	0.635341832	4.72E-06
ENSBTAG00000015909	PDE8A	0.11280053	0.471408189
ENSBTAG00000015912	DMKN	0.164026252	0.293241688
ENSBTAG00000015913	MFHAS1	0.085944956	0.58370056
ENSBTAG00000015915	SBSN	-0.432762296	0.003750107
ENSBTAG00000015919	PARM1	0.561688493	8.89E-05
ENSBTAG00000015926	ABLIM2	-0.158346059	0.310504518
ENSBTAG00000015930	DNAL1	-0.653019455	2.07E-06
ENSBTAG00000015936	BRINP1	-0.568127245	7.07E-05
ENSBTAG00000015938	ARAP3	0.447510509	0.002621877
ENSBTAG00000015939	NECTIN1	-0.304006653	0.047484941

ENSBTAG00000015942	DNAJA4	0.188041932	0.227221892
ENSBTAG00000015950	ISOC2	-0.242254895	0.117541325
ENSBTAG00000015952	ADAP1	0.605780323	1.67E-05
ENSBTAG00000015961	TSPAN2	0.390477841	0.009632282
ENSBTAG00000015963	DMAC1	-0.400034222	0.007862904
ENSBTAG00000015968	ACSF3	0.178411764	0.252348968
ENSBTAG00000015969	STK40	0.493375445	0.00077448
ENSBTAG00000015972	GLRX2	-0.244638532	0.113864012
ENSBTAG00000015974	FLVCR1	0.302634064	0.048546324
ENSBTAG00000015976	PHF12	0.418184114	0.005261762
ENSBTAG00000015978	ANXA1	0.099646025	0.524937052
ENSBTAG00000015979	SEZ6	0.095090053	0.544149573
ENSBTAG00000015980	FASN	-0.067921416	0.665184391
ENSBTAG00000015981	ETV1	-0.293806043	0.055839485
ENSBTAG00000015982	KCTD13	0.475768882	0.001261796
ENSBTAG00000015984	CADM4	-0.106164542	0.498042974
ENSBTAG00000015986	NDE1	0.251698671	0.103483273
ENSBTAG00000015988	MYH11	-0.200683694	0.196923304
ENSBTAG00000015991	CDH1	-0.241285713	0.11906191
ENSBTAG00000015994	LRRC63	0.515715324	0.000401044
ENSBTAG00000015996	GPC1	-0.437358416	0.003359963
ENSBTAG00000016005	PPP3CA	-0.489345848	0.000868013
ENSBTAG00000016006	ANKRD11	0.510039377	0.000476071
ENSBTAG00000016007	ADH5	-0.607621435	1.55E-05
ENSBTAG00000016010	KLHL7	-0.657658286	1.65E-06
ENSBTAG00000016013	ASB14	-0.086559718	0.581001876
ENSBTAG00000016028	ZNF691	-0.140306354	0.36951116
ENSBTAG00000016032	NA	-0.137451661	0.379426472
ENSBTAG00000016034	EXOSC5	0.39133755	0.009460224
ENSBTAG00000016038	GCC2	-0.390620628	0.009603521
ENSBTAG00000016041	B3GNT8	-0.035557144	0.820917844
ENSBTAG00000016042	TM6SF2	0.257553872	0.095437063
ENSBTAG00000016045	TRIB2	-0.171789818	0.270670312
ENSBTAG00000016048	CPT1B	-0.575048919	5.50E-05
ENSBTAG00000016053	ARSA	0.104598307	0.504439826
ENSBTAG00000016060	CREM	0.181259857	0.24473123
ENSBTAG00000016061	RSAD2	0.237843963	0.12458189
ENSBTAG00000016062	C21H14orf28	-0.22516862	0.146574439
ENSBTAG00000016070	LINGO2	-0.215769269	0.164640493
ENSBTAG00000016072	SHC2	-0.316546331	0.038632316
ENSBTAG00000016073	UGCG	0.35488163	0.019537346
ENSBTAG00000016074	ZNF143	0.63114248	5.69E-06
ENSBTAG00000016080	VPS13D	0.265582432	0.085199001
ENSBTAG00000016081	NA	0.500346347	0.000633734
ENSBTAG00000016085	IRAK1	0.687319376	3.57E-07
ENSBTAG00000016091	KLHL25	-0.571097122	6.35E-05
ENSBTAG00000016092	SPATS2L	-0.527908868	0.000274606

ENSBTAG00000016094	SLC36A1	-0.017400248	0.911816879
ENSBTAG00000016095	PRICKLE3	0.648123024	2.62E-06
ENSBTAG00000016096	SYP	-0.214631638	0.166931976
ENSBTAG00000016097	CACNA1F	-0.435064117	0.003550026
ENSBTAG00000016103	CBFB	0.118243442	0.450140232
ENSBTAG00000016108	BTBD2	-0.379291258	0.012127817
ENSBTAG00000016109	DHRS12	-0.093420517	0.551273272
ENSBTAG00000016116	NA	0.604438426	1.77E-05
ENSBTAG00000016124	PACSIN1	-0.202017327	0.19390177
ENSBTAG00000016128	GGA3	0.628170284	6.49E-06
ENSBTAG00000016131	NCAPG2	-0.584222175	3.90E-05
ENSBTAG00000016137	ZNF608	-0.070682521	0.652420259
ENSBTAG00000016139	TMEM120A	0.664213523	1.20E-06
ENSBTAG00000016140	PPFIBP2	-0.224372305	0.148045827
ENSBTAG00000016147	CETN4	-0.426295026	0.004365982
ENSBTAG00000016152	DAB2	-0.679808338	5.35E-07
ENSBTAG00000016155	GDPD3	0.234559338	0.130026995
ENSBTAG00000016158	ACAN	-0.200687919	0.196913678
ENSBTAG00000016163	OSM	0.570781505	6.42E-05
ENSBTAG00000016165	KRT7	-0.333066335	0.029077056
ENSBTAG00000016168	APLP2	0.039707542	0.800417532
ENSBTAG00000016169	ID1	0.436231238	0.003452196
ENSBTAG00000016175	NA	-0.421893523	0.004833998
ENSBTAG00000016185	ENAH	-0.388805604	0.00997466
ENSBTAG00000016191	ZNF32	-0.68470139	4.11E-07
ENSBTAG00000016193	FASTKD2	-0.580314158	4.52E-05
ENSBTAG00000016194	FBXO32	-0.268589194	0.081592805
ENSBTAG00000016197	PHLDB1	0.629284663	6.18E-06
ENSBTAG00000016198	EP300	0.523644972	0.000314003
ENSBTAG00000016204	C1RL	0.611429754	1.33E-05
ENSBTAG00000016206	MAOA	0.534957638	0.000219154
ENSBTAG00000016208	TGM2	0.371358894	0.014214745
ENSBTAG00000016211	GCDH	-0.466644111	0.001608806
ENSBTAG00000016213	SYCE2	-0.55990997	9.46E-05
ENSBTAG00000016217	RBM43	0.517064667	0.000384852
ENSBTAG00000016218	PTGES2	0.124127486	0.427750167
ENSBTAG00000016220	WIPF3	0.430569505	0.003949816
ENSBTAG00000016221	AMOT	-0.439710418	0.003174437
ENSBTAG00000016224	RPS7	0.392820716	0.009169588
ENSBTAG00000016228	NMD3	-0.115472968	0.460899703
ENSBTAG00000016229	KLF9	0.326829129	0.032424213
ENSBTAG00000016230	BRWD3	0.267563098	0.08280981
ENSBTAG00000016231	POFUT1	-0.192848125	0.215347049
ENSBTAG00000016234	DUOX2	-0.516614824	0.000390183
ENSBTAG00000016236	SLC12A6	-0.392981438	0.00913856
ENSBTAG00000016240	RNF157	-0.228729084	0.140127157
ENSBTAG00000016243	RBL2	-0.399742766	0.007912404

ENSBTAG00000016250	AKTIP	-0.375098745	0.013195665
ENSBTAG00000016254	HDAC5	0.437009652	0.003388268
ENSBTAG00000016255	PLEK2	0.182672769	0.241010421
ENSBTAG00000016260	LRRK2	0.551965238	0.000124532
ENSBTAG00000016263	SLC25A14	-0.465640795	0.001651697
ENSBTAG00000016265	DNAJA1	0.284675644	0.064281161
ENSBTAG00000016266	SDHD	-0.018928052	0.904108637
ENSBTAG00000016267	SERPING1	0.336464916	0.027377171
ENSBTAG00000016268	XRCC1	-0.644545555	3.09E-06
ENSBTAG00000016269	ME2	0.308534756	0.044115961
ENSBTAG00000016276	HAL	0.320069332	0.036404251
ENSBTAG00000016277	MTARC2	-0.427573963	0.004237629
ENSBTAG00000016282	EIF5	0.057394235	0.714685553
ENSBTAG00000016283	TMEM63C	-0.314207859	0.040171933
ENSBTAG00000016284	IL7	-0.034171521	0.827788968
ENSBTAG00000016290	MOB1B	-0.316756514	0.038496332
ENSBTAG00000016296	GPD1	-0.359900436	0.017762814
ENSBTAG00000016297	CCNYL1	0.255250046	0.098543364
ENSBTAG00000016302	SLC25A27	-0.0761817	0.627291242
ENSBTAG00000016305	ATP13A4	-0.189836123	0.222737446
ENSBTAG00000016307	CDC7	-0.549345625	0.00013613
ENSBTAG00000016312	LGALS4	-0.566697823	7.44E-05
ENSBTAG00000016313	ECH1	-0.658837629	1.56E-06
ENSBTAG00000016315	COTL1	0.549898819	0.000133602
ENSBTAG00000016316	ZZEF1	0.430976854	0.003912028
ENSBTAG00000016319	CYB5D2	-0.364495062	0.016259416
ENSBTAG00000016328	SFPQ	0.326173733	0.032793663
ENSBTAG00000016335	NPM3	0.409467242	0.006398646
ENSBTAG00000016337	ACOT13	-0.389164465	0.009900319
ENSBTAG00000016343	KCNIP2	-0.610885209	1.36E-05
ENSBTAG00000016344	PIK3R6	0.454284755	0.002212574
ENSBTAG00000016345	IL2RB	0.296376171	0.053630966
ENSBTAG00000016347	LOC784385	0.253024378	0.101617537
ENSBTAG00000016349	TEAD2	-0.111659608	0.475932926
ENSBTAG00000016352	STX10	-0.246361501	0.111260722
ENSBTAG00000016354	IER2	0.445789808	0.0027359
ENSBTAG00000016355	DGAT2	0.475430693	0.001273361
ENSBTAG00000016357	VNN2	0.468005979	0.001552168
ENSBTAG00000016359	SLCO4C1	0.445841829	0.00273239
ENSBTAG00000016362	POU6F1	-0.073801487	0.638118948
ENSBTAG00000016367	RBM18	0.655723325	1.82E-06
ENSBTAG00000016369	TSEN15	-0.71149344	8.89E-08
ENSBTAG00000016373	TTC26	-0.542209739	0.000172857
ENSBTAG00000016374	OGFRL1	0.052634445	0.737467323
ENSBTAG00000016378	LRP10	0.575541888	5.40E-05
ENSBTAG00000016381	REM2	0.407871897	0.006628272
ENSBTAG00000016388	SLCO4A1	0.488888123	0.000879251

ENSBTAG00000016391	LOC100295568	0.260237557	0.091914394
ENSBTAG00000016401	OPTN	0.441837059	0.003014487
ENSBTAG00000016406	MCM10	-0.519258257	0.00035978
ENSBTAG00000016407	IRX6	-0.272388205	0.077208195
ENSBTAG00000016411	RNF122	0.508763666	0.000494577
ENSBTAG00000016412	NA	-0.091414519	0.559890559
ENSBTAG00000016414	VDR	0.577616386	5.00E-05
ENSBTAG00000016415	LTA4H	-0.566933155	7.38E-05
ENSBTAG00000016424	MMP25	0.532081078	0.000240429
ENSBTAG00000016429	TMEM205	-0.40880948	0.006492473
ENSBTAG00000016430	METTL8	-0.428687995	0.004128523
ENSBTAG00000016435	NOM1	0.643537785	3.24E-06
ENSBTAG00000016442	MAP4K3	-0.502356485	0.000597647
ENSBTAG00000016444	RETREG1	-0.050794905	0.746333002
ENSBTAG00000016448	ZBTB40	0.508420012	0.000499671
ENSBTAG00000016451	HSPA14	-0.073701548	0.638575223
ENSBTAG00000016455	CACHD1	0.26791221	0.082394164
ENSBTAG00000016456	CDC42BPB	-0.375428863	0.013108776
ENSBTAG00000016462	TCF4	-0.08303909	0.596532165
ENSBTAG00000016465	DHCR7	-0.190357068	0.221446889
ENSBTAG00000016467	SLC22A17	-0.416591996	0.005455227
ENSBTAG00000016469	TNKS1BP1	-0.413674241	0.005825857
ENSBTAG00000016470	NADSYN1	0.010189394	0.948294179
ENSBTAG00000016471	PDPR	-0.347252287	0.022519052
ENSBTAG00000016472	NA	-0.43567738	0.003498323
ENSBTAG00000016477	PEAK3	0.342023005	0.024775395
ENSBTAG00000016481	CALU	-0.364420854	0.016282813
ENSBTAG00000016486	SORBS2	-0.299961724	0.050667771
ENSBTAG00000016494	RELT	0.510059148	0.000475789
ENSBTAG00000016495	LINS1	-0.579659699	4.63E-05
ENSBTAG00000016496	ZNF641	-0.329881737	0.030748383
ENSBTAG00000016497	FAM168A	-0.249728277	0.106304601
ENSBTAG00000016498	PHACTR2	0.441267668	0.003056603
ENSBTAG00000016502	LOC786562	-0.111945796	0.474795794
ENSBTAG00000016504	AGAP1	-0.402504025	0.007454053
ENSBTAG00000016506	ST3GAL4	-0.432051396	0.003813862
ENSBTAG00000016508	CTDSP2	0.614540325	1.17E-05
ENSBTAG00000016512	TTC21B	-0.494138597	0.000757817
ENSBTAG00000016513	ZNF331	0.279483618	0.069515915
ENSBTAG00000016516	CYB5R3	-0.471134332	0.001428704
ENSBTAG00000016519	MBOAT1	0.429512176	0.00404939
ENSBTAG00000016522	C21H15orf40	-0.262263814	0.089321978
ENSBTAG00000016523	DNAH10	0.014303907	0.927462684
ENSBTAG00000016525	ITGA1	-0.283661343	0.065278385
ENSBTAG00000016526	PIH1D1	0.593601095	2.72E-05
ENSBTAG00000016528	NOC2L	0.307755863	0.044681217
ENSBTAG00000016529	SLC25A30	-0.66480849	1.16E-06

ENSBTAG00000016532	MAPKAPK3	0.55780307	0.000101843
ENSBTAG00000016534	BCL11A	-0.009736167	0.950591167
ENSBTAG00000016541	CAMK1G	-0.434384921	0.003608068
ENSBTAG00000016542	LAMB3	0.449190754	0.00251459
ENSBTAG00000016546	PARP12	0.441128334	0.003066987
ENSBTAG00000016548	TEX12	-0.459914433	0.001916432
ENSBTAG00000016549	CARMIL1	-0.628736157	6.33E-06
ENSBTAG00000016553	EME2	0.545833533	0.000153214
ENSBTAG00000016554	C1H3orf52	-0.289988456	0.059253958
ENSBTAG00000016558	SPSB3	0.499795796	0.000643953
ENSBTAG00000016559	NUDT22	-0.460724355	0.001876847
ENSBTAG00000016561	NUBP2	0.566589351	7.47E-05
ENSBTAG00000016563	GOLGA4	-0.334342264	0.028428895
ENSBTAG00000016564	NPRL3	-0.363978216	0.016422968
ENSBTAG00000016566	ITGA9	0.54603832	0.000152167
ENSBTAG00000016571	FAM234A	-0.250303495	0.10547497
ENSBTAG00000016577	AXIN1	0.480539468	0.001108309
ENSBTAG00000016580	TEF	-0.235899314	0.12778456
ENSBTAG00000016584	RPF2	0.415863734	0.005545762
ENSBTAG00000016588	PGAP6	-0.186023579	0.232340235
ENSBTAG00000016589	PRPF40B	-0.403717721	0.007259955
ENSBTAG00000016590	NME4	-0.624036613	7.78E-06
ENSBTAG00000016592	CAPN15	0.483718842	0.001015473
ENSBTAG00000016593	FMNL3	0.608926637	1.47E-05
ENSBTAG00000016594	PIGQ	-0.359046258	0.018054851
ENSBTAG00000016595	CYSTM1	-0.034819564	0.824573794
ENSBTAG00000016598	DYNC1H1	0.448122373	0.002582351
ENSBTAG00000016603	LOC786914	0.505643764	0.000542584
ENSBTAG00000016609	DQX1	-0.013801857	0.930002241
ENSBTAG00000016615	ABHD6	-0.225875335	0.145277654
ENSBTAG00000016618	DSTYK	-0.560067816	9.41E-05
ENSBTAG00000016619	MIS18A	-0.63738435	4.30E-06
ENSBTAG00000016620	SIGLEC15	-0.317422353	0.038068132
ENSBTAG00000016622	TCAIM	-0.420337965	0.005009547
ENSBTAG00000016625	TMEM131L	-0.143134444	0.359842802
ENSBTAG00000016629	ADCY9	-0.125774403	0.421597098
ENSBTAG00000016630	NA	-0.192819149	0.215417326
ENSBTAG00000016640	HEATR3	-0.324941012	0.033497953
ENSBTAG00000016644	LVRN	-0.128281956	0.412325279
ENSBTAG00000016649	CCND2	0.16557468	0.288645583
ENSBTAG00000016650	TIGAR	0.48663226	0.000936552
ENSBTAG00000016656	PARP14	0.211146832	0.174094742
ENSBTAG00000016658	ABHD4	-0.652846844	2.09E-06
ENSBTAG00000016661	USP18	0.195118239	0.209890618
ENSBTAG00000016664	SLC2A4RG	-0.578292103	4.88E-05
ENSBTAG00000016676	PTER	-0.580144754	4.55E-05
ENSBTAG00000016679	ETFDH	-0.439904162	0.003159563

ENSBTAG00000016680	PPID	0.178532808	0.252022011
ENSBTAG00000016683	NFKBIA	0.326497846	0.032610528
ENSBTAG00000016688	NA	-0.039570051	0.801094616
ENSBTAG00000016694	KIAA0319L	-0.410925136	0.006194862
ENSBTAG00000016696	NCDN	-0.437993057	0.00330899
ENSBTAG00000016698	SLAMF8	0.551661018	0.000125831
ENSBTAG00000016704	SLC37A2	-0.359887379	0.017767248
ENSBTAG00000016707	FKBP9	-0.752911961	5.74E-09
ENSBTAG00000016709	NT5C3A	0.262024304	0.089625421
ENSBTAG00000016711	PPIF	0.673477436	7.46E-07
ENSBTAG00000016712	CLCA3	-0.659830432	1.49E-06
ENSBTAG00000016713	TMEM30B	-0.289668101	0.059547908
ENSBTAG00000016714	NA	-0.564439872	8.07E-05
ENSBTAG00000016716	RRS1	0.31823123	0.037553198
ENSBTAG00000016717	CEP68	0.037026323	0.813646812
ENSBTAG00000016720	RAB1A	-0.066723397	0.6707521
ENSBTAG00000016722	PGGHG	0.449016433	0.002525538
ENSBTAG00000016723	GFI1	-0.060782907	0.698612937
ENSBTAG00000016724	NPEPL1	-0.399305071	0.007987245
ENSBTAG00000016726	KIF15	-0.461318695	0.00184826
ENSBTAG00000016728	PLEKHG5	0.123466714	0.430232963
ENSBTAG00000016731	TMEM42	-0.531857257	0.00024216
ENSBTAG00000016733	NOL9	0.395641595	0.008637945
ENSBTAG00000016737	CDK8	-0.378492059	0.012325488
ENSBTAG00000016738	DTX1	-0.187610542	0.228309296
ENSBTAG00000016739	RASAL1	-0.348425631	0.022037132
ENSBTAG00000016740	ACLY	-0.262572304	0.088932315
ENSBTAG00000016742	WFDC3	-0.278478862	0.070566802
ENSBTAG00000016746	UBE2C	-0.285740994	0.063246823
ENSBTAG00000016750	PTBP3	0.374021657	0.013482579
ENSBTAG00000016751	MYO6	-0.500902024	0.000623568
ENSBTAG00000016754	KLHL38	-0.257011624	0.096161305
ENSBTAG00000016757	ZKSCAN1	-0.008119326	0.958788537
ENSBTAG00000016761	NOX1	-0.257752726	0.095172525
ENSBTAG00000016762	SLC25A12	-0.393690441	0.009002755
ENSBTAG00000016770	GAPT	0.190538819	0.220997848
ENSBTAG00000016771	PLK2	-0.280814463	0.068143057
ENSBTAG00000016775	SLC27A1	-0.007670905	0.961062807
ENSBTAG00000016776	BAHCC1	0.192464672	0.216278339
ENSBTAG00000016779	CLIP1	0.536663429	0.000207357
ENSBTAG00000016782	SLC39A10	0.263948999	0.087209426
ENSBTAG00000016784	DNAH7	-0.150266905	0.336147059
ENSBTAG00000016785	LOC523484	-0.623769885	7.87E-06
ENSBTAG00000016795	RUFY3	-0.213776021	0.16867055
ENSBTAG00000016797	CSNK1G2	0.491569086	0.000815233
ENSBTAG00000016799	ERN1	0.188977346	0.224876223
ENSBTAG00000016800	SEMA6D	-0.237162135	0.125697866

ENSBTAG00000016804	LYST	0.463750058	0.001735283
ENSBTAG00000016805	SGMS2	0.095089425	0.544152245
ENSBTAG00000016813	SH3D19	-0.379999567	0.011954893
ENSBTAG00000016819	FABP3	-0.580479446	4.49E-05
ENSBTAG00000016824	WDR46	0.342075575	0.024751808
ENSBTAG00000016827	RGL2	0.090624301	0.563302323
ENSBTAG00000016828	TAPBP	0.498540022	0.000667814
ENSBTAG00000016830	DAXX	0.651281373	2.25E-06
ENSBTAG00000016836	PDK1	-0.329967082	0.03070258
ENSBTAG00000016841	ATP10B	0.31608918	0.03892944
ENSBTAG00000016844	ADGB	-0.158022936	0.31150555
ENSBTAG00000016847	ARL4D	-0.297868539	0.052381145
ENSBTAG00000016852	SNIP1	0.397142583	0.008366027
ENSBTAG00000016854	AK7	-0.443416234	0.002900334
ENSBTAG00000016857	ADAMTS15	-0.442110387	0.002994451
ENSBTAG00000016864	LBP	0.357756924	0.018503327
ENSBTAG00000016867	HSD17B3	-0.182533827	0.241374606
ENSBTAG00000016874	DNAJB1	0.518802346	0.000364867
ENSBTAG00000016876	LOC101905801	-0.30153804	0.049407551
ENSBTAG00000016878	WDR59	0.08787948	0.575227449
ENSBTAG00000016879	DENND11	0.583451718	4.02E-05
ENSBTAG00000016881	ANPEP	0.056563678	0.718643896
ENSBTAG00000016883	SGF29	-0.192264561	0.216765453
ENSBTAG00000016886	MT3	-0.181886667	0.243075808
ENSBTAG00000016890	ANKS1A	0.136646844	0.382250079
ENSBTAG00000016891	TCP11	-0.280455604	0.068511114
ENSBTAG00000016895	NIPA2	-0.087419749	0.577235968
ENSBTAG00000016896	HERPUD1	0.554630436	0.000113659
ENSBTAG00000016904	MARCHF9	-0.323819625	0.03414941
ENSBTAG00000016906	CYP27B1	0.374039222	0.013477858
ENSBTAG00000016908	METTL1	0.671027896	8.46E-07
ENSBTAG00000016910	EEF1AKMT3	0.381279369	0.01164778
ENSBTAG00000016911	ARHGAP23	0.453310265	0.002267742
ENSBTAG00000016912	TSFM	0.532638495	0.000236167
ENSBTAG00000016913	AVIL	0.4321985	0.003800592
ENSBTAG00000016915	FLT1	0.183392379	0.239130198
ENSBTAG00000016918	MYOF	0.108599392	0.488181664
ENSBTAG00000016920	EOMES	-0.16878365	0.279270226
ENSBTAG00000016931	E2F7	-0.176202882	0.258365457
ENSBTAG00000016932	SENP7	0.365725895	0.015875465
ENSBTAG00000016933	IL27RA	0.506059601	0.000535953
ENSBTAG00000016936	MISP3	-0.361883279	0.01710022
ENSBTAG00000016939	C11H2orf42	0.097480479	0.534027298
ENSBTAG00000016943	NEK7	-0.42955249	0.004045554
ENSBTAG00000016944	ADORA2A	0.524372699	0.000306938
ENSBTAG00000016948	PTH1R	-0.198577755	0.201761935
ENSBTAG00000016952	PSMD5	-0.680465895	5.16E-07

ENSBTAG00000016957	NA	0.04075024	0.795287437
ENSBTAG00000016958	PHF19	-0.103851683	0.507503819
ENSBTAG00000016959	LAPTM4B	-0.375550991	0.013076755
ENSBTAG00000016963	ADAMTS6	-0.321910307	0.035282573
ENSBTAG00000016967	RARS2	-0.506224029	0.000533351
ENSBTAG00000016969	ORC3	-0.419883545	0.005061866
ENSBTAG00000016972	RAB11FIP4	0.178562063	0.251943033
ENSBTAG00000016973	PRSS8	-0.095023012	0.544434777
ENSBTAG00000016975	H2AZ2	-0.575742083	5.36E-05
ENSBTAG00000016981	FBXO4	0.007203138	0.963435521
ENSBTAG00000016982	MCOLN3	-0.511453394	0.000456287
ENSBTAG00000016984	PTPN9	0.217588123	0.161024373
ENSBTAG00000016991	EFNB2	0.12454192	0.426197075
ENSBTAG00000016995	HDHD5	-0.407922642	0.006620859
ENSBTAG00000016997	SIGLEC11	-0.100768352	0.520256095
ENSBTAG00000016998	ARL11	0.256359334	0.097038124
ENSBTAG00000017000	IL22RA2	0.376329183	0.012874277
ENSBTAG00000017002	RBCK1	0.570142707	6.57E-05
ENSBTAG00000017007	TRIB3	0.280300205	0.068670982
ENSBTAG00000017011	CCDC125	-0.489881551	0.000855024
ENSBTAG00000017016	H3-5	0.569327981	6.77E-05
ENSBTAG00000017019	PRKDC	-0.515910918	0.000398659
ENSBTAG00000017021	MCM4	-0.521963559	0.000330889
ENSBTAG00000017024	PPARGC1A	-0.2933247	0.056261101
ENSBTAG00000017026	DEPDC1B	-0.369047586	0.014877387
ENSBTAG00000017027	MMACHC	0.388912015	0.009952566
ENSBTAG00000017033	LSR	-0.474762313	0.001296496
ENSBTAG00000017038	HPS4	-0.173383312	0.266183367
ENSBTAG00000017040	LY6E	-0.119649019	0.444734372
ENSBTAG00000017051	ACP6	-0.675308033	6.78E-07
ENSBTAG00000017054	NA	0.254061342	0.100176224
ENSBTAG00000017056	PKLR	0.374919243	0.013243117
ENSBTAG00000017061	SMARCAD1	-0.581374493	4.35E-05
ENSBTAG00000017062	NA	-0.219973688	0.156369589
ENSBTAG00000017063	EPB41L4B	-0.340594323	0.025423633
ENSBTAG00000017068	DDA1	0.517160646	0.000383723
ENSBTAG00000017069	GASK1B	-0.057790258	0.712800739
ENSBTAG00000017074	ANO8	0.40225592	0.007494278
ENSBTAG00000017075	STX1A	-0.140940195	0.367330853
ENSBTAG00000017077	CTSV	-0.474241436	0.001314783
ENSBTAG00000017082	POR	0.589732597	3.16E-05
ENSBTAG00000017085	AGA	-0.334170076	0.028515659
ENSBTAG00000017086	GRB10	0.093485604	0.55099473
ENSBTAG00000017090	SMCR8	0.523848529	0.000312012
ENSBTAG00000017091	CMTR1	0.282036058	0.066901875
ENSBTAG00000017095	DENND4A	-0.203782924	0.189952181
ENSBTAG00000017103	MAP3K13	-0.545972888	0.000152501

ENSBTAG00000017104	MUC1	-0.025754843	0.869781283
ENSBTAG00000017112	CDYL2	0.070784447	0.651950913
ENSBTAG00000017116	RASD2	-0.133100522	0.394838952
ENSBTAG00000017118	FAM8A1	0.355615357	0.019268971
ENSBTAG00000017120	PHB1	-0.167587838	0.282740337
ENSBTAG00000017122	HSPG2	-0.099849589	0.524086494
ENSBTAG00000017123	ZNF93	0.041037199	0.79387708
ENSBTAG00000017124	GPSM2	-0.42792558	0.004202923
ENSBTAG00000017125	PABPC4	-0.423477592	0.004660762
ENSBTAG00000017132	TTC22	-0.255051156	0.098815134
ENSBTAG00000017133	GINS4	-0.212240534	0.171823325
ENSBTAG00000017135	CTSS	0.066262448	0.672898998
ENSBTAG00000017136	SSTR2	-0.441660633	0.003027482
ENSBTAG00000017138	TMEM71	-0.080482242	0.607923735
ENSBTAG00000017140	CIP2A	-0.460219087	0.001901456
ENSBTAG00000017143	PDIA4	0.299403767	0.051120005
ENSBTAG00000017150	EHF	-0.213467226	0.169301209
ENSBTAG00000017151	SH3TC2	-0.72043706	5.13E-08
ENSBTAG00000017158	VSNL1	-0.139970534	0.370669457
ENSBTAG00000017170	NA	-0.148613246	0.341552848
ENSBTAG00000017174	SCN11A	-0.415117289	0.005639909
ENSBTAG00000017179	USP12	-0.270292866	0.079603063
ENSBTAG00000017181	MACROD1	-0.528072103	0.000273191
ENSBTAG00000017187	TMEM255A	0.131763264	0.399647949
ENSBTAG00000017195	FANCC	-0.605708444	1.68E-05
ENSBTAG00000017196	PDIA3	0.227423087	0.142467196
ENSBTAG00000017205	CCN6	-0.444146227	0.002848862
ENSBTAG00000017211	SERINC4	0.38841691	0.010055719
ENSBTAG00000017212	HYPK	0.589930568	3.14E-05
ENSBTAG00000017215	WDR76	-0.406818653	0.006783749
ENSBTAG00000017218	ACER3	0.149316338	0.339247937
ENSBTAG00000017219	DDX51	0.389828905	0.00976393
ENSBTAG00000017223	MEST	0.151808724	0.331154914
ENSBTAG00000017228	TP53I11	0.312080276	0.041615886
ENSBTAG00000017232	KIF13B	0.38446733	0.010911915
ENSBTAG00000017233	NA	0.376722496	0.012772961
ENSBTAG00000017239	GABBR1	0.145448936	0.352045265
ENSBTAG00000017240	DGKQ	0.169027338	0.278566506
ENSBTAG00000017242	FADS6	-0.509471089	0.000484237
ENSBTAG00000017243	GATA3	-0.440202637	0.003136768
ENSBTAG00000017245	COPG2	-0.468577044	0.001528948
ENSBTAG00000017248	LOC787187	-0.137709079	0.378525963
ENSBTAG00000017253	MECR	-0.395152717	0.008728135
ENSBTAG00000017255	ATAD2B	0.128768206	0.41054092
ENSBTAG00000017256	CD2	-0.355759821	0.019216498
ENSBTAG00000017263	MXI1	-0.025439668	0.871361389
ENSBTAG00000017266	ITGA6	-0.404956074	0.007066428

ENSBTAG00000017267	COX5A	-0.029110672	0.852989356
ENSBTAG00000017268	PROCA1	-0.5433651	0.00016636
ENSBTAG00000017271	MASTL	-0.339043369	0.026143281
ENSBTAG00000017273	LRRC25	0.259110134	0.093381821
ENSBTAG00000017280	C3	0.404266359	0.007173657
ENSBTAG00000017281	OPLAH	-0.475678697	0.001264871
ENSBTAG00000017284	RHBDL1	-0.498873506	0.000661401
ENSBTAG00000017287	DRAM1	0.517974279	0.000374271
ENSBTAG00000017289	MCF2L	0.232864443	0.132905342
ENSBTAG00000017296	POLN	-0.539153964	0.000191161
ENSBTAG00000017298	AAMDC	-0.499422455	0.000650965
ENSBTAG00000017306	AKNA	0.400400339	0.007801103
ENSBTAG00000017310	EVA1C	0.539765744	0.000187362
ENSBTAG00000017313	ADA2	0.587783977	3.41E-05
ENSBTAG00000017325	ATG13	0.144443029	0.355421428
ENSBTAG00000017326	OMA1	-0.469455933	0.001493815
ENSBTAG00000017329	GMNN	-0.522552425	0.000324885
ENSBTAG00000017330	NA	-0.187279708	0.229145644
ENSBTAG00000017335	HGFAC	-0.408969401	0.006469552
ENSBTAG00000017339	RUNX1T1	-0.013898564	0.929513005
ENSBTAG00000017346	RASSF2	0.283330228	0.065606571
ENSBTAG00000017349	PCDHGA8	-0.360910922	0.01742249
ENSBTAG00000017354	MPP7	-0.556378056	0.000107005
ENSBTAG00000017363	SAT1	0.362139961	0.017015992
ENSBTAG00000017365	ZBTB47	-0.260986271	0.090949786
ENSBTAG00000017366	GRB7	-0.293558364	0.056056114
ENSBTAG00000017367	IFIT5	0.230369378	0.137228619
ENSBTAG00000017368	YBX1	-0.20635075	0.18431039
ENSBTAG00000017370	ARFGEF3	-0.333590599	0.028809268
ENSBTAG00000017371	RELL2	0.60049313	2.07E-05
ENSBTAG00000017375	FAM241A	0.276693339	0.07246522
ENSBTAG00000017380	NA	-0.212826371	0.17061547
ENSBTAG00000017388	SVBP	-0.357919883	0.018446131
ENSBTAG00000017393	L3MBTL3	0.369228722	0.014824527
ENSBTAG00000017402	OSBPL2	0.506445385	0.000529866
ENSBTAG00000017405	RORC	-0.153499734	0.325733103
ENSBTAG00000017409	DLX3	-0.257406027	0.09563411
ENSBTAG00000017412	SOCS6	-0.370432268	0.014477331
ENSBTAG00000017421	SLC3A1	-0.586539516	3.57E-05
ENSBTAG00000017425	GJB2	0.610328398	1.39E-05
ENSBTAG00000017429	PREPL	-0.669001496	9.39E-07
ENSBTAG00000017435	KCTD7	0.338727993	0.026291671
ENSBTAG00000017437	TMEM237	-0.575570086	5.39E-05
ENSBTAG00000017446	E2F8	-0.469092035	0.001508274
ENSBTAG00000017448	EFEMP1	0.313645219	0.040549748
ENSBTAG00000017450	KLHL24	-0.370326611	0.014507531
ENSBTAG00000017452	RCAN3	-0.394591884	0.008832597

ENSBTAG00000017455	ADAM9	0.160569808	0.303670887
ENSBTAG00000017456	NYAP1	-0.299320775	0.051187548
ENSBTAG00000017457	STK10	0.532101745	0.00024027
ENSBTAG00000017459	DUSP18	0.212149426	0.172011721
ENSBTAG00000017461	SLC16A3	0.455840229	0.002126965
ENSBTAG00000017462	ATF4	0.585034698	3.79E-05
ENSBTAG00000017463	RPS19BP1	0.547193015	0.000146383
ENSBTAG00000017465	GNS	-0.381962648	0.011486591
ENSBTAG00000017468	NUCB2	-0.590233295	3.10E-05
ENSBTAG00000017469	CCDC88A	-0.6711822	8.40E-07
ENSBTAG00000017482	ISYNA1	0.225515076	0.145937649
ENSBTAG00000017486	ADARB1	0.228622776	0.140316564
ENSBTAG00000017488	KLF3	0.114991473	0.462783658
ENSBTAG00000017490	PLD1	-0.464562027	0.001698939
ENSBTAG00000017492	PCMTD1	0.264394612	0.086657346
ENSBTAG00000017493	JADE1	-0.299640571	0.050927675
ENSBTAG00000017502	RIMKLA	-0.507547247	0.000512821
ENSBTAG00000017507	SV2C	-0.322071606	0.035185664
ENSBTAG00000017512	MAPT	0.025068968	0.873220491
ENSBTAG00000017514	CCND1	-0.215655095	0.164869433
ENSBTAG00000017515	NA	-0.341941037	0.024812211
ENSBTAG00000017517	ZNF236	0.45783109	0.002021667
ENSBTAG00000017527	CRYBG1	-0.074132757	0.636607455
ENSBTAG00000017528	SNAI3	0.273835729	0.075587025
ENSBTAG00000017529	CA8	-0.29879158	0.05161993
ENSBTAG00000017530	PLGRKT	-0.67244506	7.87E-07
ENSBTAG00000017533	LRRC1	-0.205833131	0.18543793
ENSBTAG00000017542	PPARD	0.592222064	2.87E-05
ENSBTAG00000017543	ATP23	-0.097918977	0.532180468
ENSBTAG00000017551	DROSHA	-0.54578665	0.000153455
ENSBTAG00000017554	RTN4IP1	-0.377233178	0.012642426
ENSBTAG00000017557	QRSL1	0.010527116	0.946582842
ENSBTAG00000017560	CEBPG	0.442766786	0.002946812
ENSBTAG00000017561	HHIPL2	-0.212168299	0.171972683
ENSBTAG00000017564	CGN	-0.228204373	0.14106387
ENSBTAG00000017566	TUFT1	0.200203425	0.198019506
ENSBTAG00000017569	C20H5orf22	-0.729182323	2.93E-08
ENSBTAG00000017571	PLEKHA5	0.202149366	0.193604411
ENSBTAG00000017574	LMNA	-0.151296235	0.332809119
ENSBTAG00000017580	RFX5	0.464304589	0.001710389
ENSBTAG00000017582	CHEK1	-0.583167676	4.06E-05
ENSBTAG00000017584	PLCG1	-0.472998532	0.001359347
ENSBTAG00000017592	GPAT3	0.307685732	0.044732399
ENSBTAG00000017593	TREM1	0.59457229	2.62E-05
ENSBTAG00000017594	ZHX3	-0.351022939	0.021001011
ENSBTAG00000017595	HS2ST1	-0.369144601	0.014849056
ENSBTAG00000017597	ESCO1	-0.268809563	0.081333267

ENSBTAG00000017602	TMEM45B	-0.23814645	0.124089188
ENSBTAG00000017604	RAB13	-0.219045831	0.158168229
ENSBTAG00000017616	ADSS1	-0.379853196	0.011990454
ENSBTAG00000017626	GFPT1	-0.47840736	0.001174723
ENSBTAG00000017632	AEN	0.388504462	0.010037412
ENSBTAG00000017633	EIF1AX	-0.322758134	0.03477564
ENSBTAG00000017644	KIF17	-0.306916812	0.045296697
ENSBTAG00000017648	TIFAB	0.400098046	0.0078521
ENSBTAG00000017655	PALMD	-0.370389368	0.014489587
ENSBTAG00000017656	ST3GAL3	0.436831289	0.003402824
ENSBTAG00000017659	BFSP2	0.379785598	0.012006908
ENSBTAG00000017660	LOC100297302	-0.614459237	1.17E-05
ENSBTAG00000017661	RFX2	0.281153646	0.067796622
ENSBTAG00000017662	EEF2K	-0.223148853	0.150327582
ENSBTAG00000017664	HGF	-0.550671753	0.000130141
ENSBTAG00000017665	DHRS4	-0.050805133	0.746283618
ENSBTAG00000017666	ABCC5	-0.647732868	2.66E-06
ENSBTAG00000017670	LOC511531	0.364507466	0.016255508
ENSBTAG00000017672	HAS1	0.096020587	0.540198324
ENSBTAG00000017674	SCNN1D	0.58243861	4.18E-05
ENSBTAG00000017676	TPK1	-0.536468325	0.000208677
ENSBTAG00000017677	SCG3	-0.099710798	0.524666334
ENSBTAG00000017680	NOS3	-0.289018302	0.060147724
ENSBTAG00000017681	RIN1	-0.251328067	0.104009503
ENSBTAG00000017682	TET2	0.588466173	3.32E-05
ENSBTAG00000017685	JUP	-0.315665198	0.039206674
ENSBTAG00000017690	CARNS1	-0.573693251	5.78E-05
ENSBTAG00000017691	KIAA0040	0.197946061	0.203229455
ENSBTAG00000017701	LOC618939	0.363942555	0.016434304
ENSBTAG00000017704	ABCG2	-0.562795072	8.55E-05
ENSBTAG00000017706	SLC39A3	-0.175360549	0.260684786
ENSBTAG00000017710	ECHS1	-0.314303069	0.040108285
ENSBTAG00000017711	NA	0.286682475	0.062343811
ENSBTAG00000017713	KTN1	0.403812408	0.007244997
ENSBTAG00000017715	HOMER2	-0.039204569	0.802895149
ENSBTAG00000017718	CCL22	-0.377954556	0.012459972
ENSBTAG00000017719	AKAP6	-0.636699065	4.44E-06
ENSBTAG00000017721	METTL13	0.301436065	0.049488304
ENSBTAG00000017722	F5	0.535256243	0.000217046
ENSBTAG00000017727	KIFAP3	-0.553964303	0.000116293
ENSBTAG00000017731	ZFAT	0.522395376	0.000326476
ENSBTAG00000017733	CA2	-0.469495603	0.001492246
ENSBTAG00000017738	EMID1	-0.036255407	0.81746022
ENSBTAG00000017739	TNK1	0.012708808	0.935533636
ENSBTAG00000017740	TUBAL3	-0.579338617	4.69E-05
ENSBTAG00000017741	HACD4	-0.479001554	0.001155868
ENSBTAG00000017745	IL6ST	0.30584744	0.046091081

ENSBTAG00000017746	SLIT3	0.48917146	0.000872279
ENSBTAG00000017747	PLSCR3	-0.205533746	0.186092324
ENSBTAG00000017748	RNF44	-0.322949048	0.034662319
ENSBTAG00000017751	RGS9	-0.259335223	0.093087414
ENSBTAG00000017752	DYNLRB2	-0.444961064	0.002792357
ENSBTAG00000017753	APP	-0.412030528	0.006044123
ENSBTAG00000017761	SMC1A	-0.449638577	0.002486656
ENSBTAG00000017763	NA	0.480522566	0.001108822
ENSBTAG00000017764	HDAC4	0.530737195	0.000250993
ENSBTAG00000017765	GSTM1	-0.616733382	1.06E-05
ENSBTAG00000017766	NA	-0.180936553	0.245588058
ENSBTAG00000017771	EPN2	-0.459601766	0.00193191
ENSBTAG00000017775	SDCCAG8	-0.292822861	0.056703382
ENSBTAG00000017783	TSPYL2	-0.704970241	1.31E-07
ENSBTAG00000017785	FRMPD4	-0.17682645	0.256657388
ENSBTAG00000017786	FCRL6	0.521462585	0.000336076
ENSBTAG00000017788	AKT3	-0.429027583	0.004095756
ENSBTAG00000017790	B9D1	-0.257208482	0.095897887
ENSBTAG00000017793	KLRG2	0.510731372	0.000466295
ENSBTAG00000017797	LY75	-0.307528061	0.044847644
ENSBTAG00000017801	ATP6AP2	-0.213239	0.169768412
ENSBTAG00000017802	THRB	-0.482741254	0.001043251
ENSBTAG00000017804	BNIP3	0.015935516	0.919214428
ENSBTAG00000017805	CRACR2B	0.084710055	0.589138455
ENSBTAG00000017812	ALS2CL	-0.345135423	0.023410806
ENSBTAG00000017815	STX8	-0.645018392	3.03E-06
ENSBTAG00000017818	MOG	-0.227664161	0.142033088
ENSBTAG00000017819	PMVK	0.471067247	0.001431257
ENSBTAG00000017824	IRF8	0.413268805	0.005879049
ENSBTAG00000017826	SCLY	0.551817432	0.000125162
ENSBTAG00000017830	RBMS2	-0.476293945	0.001244025
ENSBTAG00000017831	ERLIN2	0.241323132	0.119002927
ENSBTAG00000017833	RNF19A	0.404155506	0.007191022
ENSBTAG00000017835	C7H5orf63	-0.384286211	0.01095263
ENSBTAG00000017836	ZFP57	-0.242731684	0.11679868
ENSBTAG00000017839	NA	0.281352328	0.067594341
ENSBTAG00000017840	BAZ2A	0.647434245	2.70E-06
ENSBTAG00000017843	LOC112445051	-0.184925848	0.235156796
ENSBTAG00000017844	STIL	-0.437622902	0.003338637
ENSBTAG00000017846	F11R	-0.346455548	0.022851293
ENSBTAG00000017850	ARHGEF6	0.460446937	0.001890324
ENSBTAG00000017851	RXRA	0.55207835	0.000124052
ENSBTAG00000017852	ALDH9A1	-0.111814965	0.475315456
ENSBTAG00000017855	ITM2C	0.575973072	5.31E-05
ENSBTAG00000017856	TSTD1	0.268187588	0.082067456
ENSBTAG00000017860	HIPK2	-0.528495327	0.000269552
ENSBTAG00000017863	SRGN	0.31775226	0.037857419

ENSBTAG00000017866	CD36	-0.500537677	0.000630217
ENSBTAG00000017867	YPEL1	0.125939979	0.420981265
ENSBTAG00000017868	DHX40	-0.641458354	3.57E-06
ENSBTAG00000017869	CAV1	-0.344765519	0.023569621
ENSBTAG00000017871	GNA12	-0.092325439	0.555969678
ENSBTAG00000017872	ZNF304	0.047753365	0.761062405
ENSBTAG00000017877	NECTIN4	-0.247720378	0.109239651
ENSBTAG00000017879	C9H6orf163	-0.018781397	0.904848187
ENSBTAG00000017889	CCT5	0.402681661	0.007425368
ENSBTAG00000017894	CAD	0.206941403	0.183029739
ENSBTAG00000017895	CLEC10A	-0.047858495	0.760551859
ENSBTAG00000017921	NELFA	0.381125263	0.0116844
ENSBTAG00000017922	DOLPP1	-0.435315754	0.00352873
ENSBTAG00000017925	LMF2	0.175005542	0.261666426
ENSBTAG00000017942	CRTC2	0.50548782	0.000545089
ENSBTAG00000017943	GALNT6	-0.222665415	0.151236281
ENSBTAG00000017949	NA	0.046256253	0.768343639
ENSBTAG00000017950	SLC4A8	-0.24832064	0.108355827
ENSBTAG00000017956	KCTD15	-0.284938101	0.064025105
ENSBTAG00000017958	AHI1	-0.736647408	1.79E-08
ENSBTAG00000017964	LRRC51	0.199241414	0.200228185
ENSBTAG00000017967	PTGES3	-0.093199329	0.552220355
ENSBTAG00000017969	CA4	0.479199897	0.001149634
ENSBTAG00000017970	ZYX	0.622880071	8.17E-06
ENSBTAG00000017981	ADRB3	0.536209045	0.000210442
ENSBTAG00000017983	PRELID3A	-0.093444393	0.551171087
ENSBTAG00000017992	CD164	0.502183487	0.000600679
ENSBTAG00000017994	MAX	0.564269407	8.11E-05
ENSBTAG00000018000	CLN3	0.641368408	3.58E-06
ENSBTAG00000018002	DTX3	-0.073500768	0.639492296
ENSBTAG00000018007	NR2F2	-0.321895351	0.03529157
ENSBTAG00000018011	NA	0.600839402	2.04E-05
ENSBTAG00000018013	EMP3	0.53463224	0.000221473
ENSBTAG00000018015	IL27	0.593086336	2.78E-05
ENSBTAG00000018016	NUPR1	0.450525487	0.002432139
ENSBTAG00000018019	BCL11B	-0.253941124	0.100342511
ENSBTAG00000018022	SPINDOC	-0.544480842	0.000160297
ENSBTAG00000018024	NR1D2	0.214764743	0.166662682
ENSBTAG00000018025	IQCG	0.255239478	0.098557791
ENSBTAG00000018031	PODXL2	-0.489034034	0.000875654
ENSBTAG00000018035	TGFBR1	0.4430779	0.002924466
ENSBTAG00000018036	CNOT7	0.546637182	0.000149142
ENSBTAG00000018040	PSMB10	0.473185763	0.001352549
ENSBTAG00000018041	ACADSB	-0.463897668	0.001728626
ENSBTAG00000018046	B3GNT2	0.315023822	0.039629122
ENSBTAG00000018048	MED15	0.545292474	0.000156012
ENSBTAG00000018049	MKNK2	0.164666025	0.29133699

ENSBTAG00000018050	CDR2	0.221755917	0.152956736
ENSBTAG00000018052	PTPRS	0.015473714	0.92154816
ENSBTAG00000018059	CD80	0.47092258	0.001436777
ENSBTAG00000018061	LNPK	-0.354082246	0.019833306
ENSBTAG00000018062	KIAA1522	-0.467243026	0.001583676
ENSBTAG00000018064	FAM221A	-0.302741391	0.048462646
ENSBTAG00000018065	YARS1	0.506966237	0.000521746
ENSBTAG00000018067	S100PBP	-0.656183427	1.78E-06
ENSBTAG00000018069	TNFSF15	-0.03385103	0.829380068
ENSBTAG00000018073	TSPO	0.586706763	3.55E-05
ENSBTAG00000018077	LYPD3	-0.237713095	0.124795508
ENSBTAG00000018082	QPRT	-0.002529238	0.98715732
ENSBTAG00000018084	CASTOR1	0.686150041	3.80E-07
ENSBTAG00000018085	GTSF1	-0.20200605	0.193927184
ENSBTAG00000018086	TBC1D10A	0.736950164	1.75E-08
ENSBTAG00000018088	SETBP1	-0.365540638	0.015932759
ENSBTAG00000018093	KMT2A	0.125905719	0.421108648
ENSBTAG00000018094	ZNF689	-0.527423007	0.000278858
ENSBTAG00000018101	AHCY	0.179588873	0.24918151
ENSBTAG00000018103	HMGB1	-0.537398172	0.000202455
ENSBTAG00000018105	ACVR2B	0.442463469	0.002968743
ENSBTAG00000018108	PXN	0.552689899	0.000121486
ENSBTAG00000018112	TBL1X	0.397390765	0.008321784
ENSBTAG00000018115	PEBP1	-0.546896247	0.00014785
ENSBTAG00000018116	MTFP1	0.524358062	0.000307079
ENSBTAG00000018119	AOAH	0.477294005	0.001210791
ENSBTAG00000018125	KIF5C	0.002351005	0.988062259
ENSBTAG00000018130	MAP2	-0.519404837	0.000358159
ENSBTAG00000018133	SEMA3A	-0.562699676	8.58E-05
ENSBTAG00000018134	AREG	0.217752225	0.160700981
ENSBTAG00000018137	NA	0.426373065	0.004358054
ENSBTAG00000018138	GK5	0.50919747	0.000488213
ENSBTAG00000018142	DTL	-0.179909937	0.248322232
ENSBTAG00000018143	C16H1orf116	-0.357919527	0.018446256
ENSBTAG00000018146	VAT1L	0.411174614	0.00616056
ENSBTAG00000018151	HELQ	-0.224061815	0.148622468
ENSBTAG00000018152	MYADM	0.535249752	0.000217092
ENSBTAG00000018156	KRTCAP3	-0.061012264	0.697529681
ENSBTAG00000018157	NA	-0.377363958	0.01260918
ENSBTAG00000018159	CASP2	-0.039994129	0.79900668
ENSBTAG00000018164	FNDC4	-0.374332456	0.013399249
ENSBTAG00000018165	RIPOR2	0.432174594	0.003802746
ENSBTAG00000018169	ITGB4	-0.216534007	0.163112987
ENSBTAG00000018175	HEXD	-0.311303338	0.042153609
ENSBTAG00000018176	CYBC1	-0.106384203	0.497149161
ENSBTAG00000018179	PCDH8	-0.389195647	0.009893882
ENSBTAG00000018181	CCDC8	0.123755671	0.429146242

ENSBTAG00000018186	PDXK	0.602923732	1.88E-05
ENSBTAG00000018188	NDUFC2	-0.462710455	0.001782819
ENSBTAG00000018189	CSTB	-0.150803902	0.334403091
ENSBTAG00000018192	ALG8	-0.48262519	0.001046594
ENSBTAG00000018198	TLR9	0.429741887	0.004027573
ENSBTAG00000018199	ZBTB8A	-0.172118848	0.269739768
ENSBTAG00000018200	IL15	0.355061297	0.01947134
ENSBTAG00000018201	TKFC	-0.454338227	0.002209581
ENSBTAG00000018202	CYB561A3	0.14203977	0.363566855
ENSBTAG00000018203	CD101	0.440212591	0.003136011
ENSBTAG00000018205	PHC1	-0.532144226	0.000239943
ENSBTAG00000018206	NIPAL2	-0.04713859	0.764049946
ENSBTAG00000018213	TBCEL	-0.68352843	4.38E-07
ENSBTAG00000018216	SKA1	-0.590598854	3.06E-05
ENSBTAG00000018220	RGSL1	-0.23665718	0.126529168
ENSBTAG00000018223	CHI3L1	0.632270362	5.41E-06
ENSBTAG00000018224	GLP1R	-0.558778452	9.84E-05
ENSBTAG00000018225	SIPA1L3	-0.185812245	0.232880678
ENSBTAG00000018227	SLC4A7	0.467709808	0.001564332
ENSBTAG00000018229	NFIX	0.571930642	6.16E-05
ENSBTAG00000018232	STOML3	0.165613888	0.288529817
ENSBTAG00000018235	SLC45A2	-0.359794035	0.017798973
ENSBTAG00000018236	EPB41L5	-0.55190327	0.000124795
ENSBTAG00000018237	MYO16	-0.576309634	5.25E-05
ENSBTAG00000018238	ABTB1	0.490374102	0.000843234
ENSBTAG00000018240	CYP2S1	0.292118883	0.057328502
ENSBTAG00000018245	SLC1A3	-0.728586138	3.05E-08
ENSBTAG00000018246	RAB39A	-0.187625508	0.228271511
ENSBTAG00000018248	MGLL	-0.03492063	0.824072621
ENSBTAG00000018249	KCNN3	-0.33719481	0.027023079
ENSBTAG00000018252	ARRDC4	0.460125333	0.001906054
ENSBTAG00000018254	CDKN1B	0.41182658	0.006071693
ENSBTAG00000018255	ACTN1	0.429856259	0.004016748
ENSBTAG00000018256	SMC6	-0.372477005	0.013903292
ENSBTAG00000018257	APIP	-0.219936882	0.156440651
ENSBTAG00000018261	PDHX	0.026403254	0.866532115
ENSBTAG00000018263	WAC	0.400175402	0.007839023
ENSBTAG00000018270	NFATC2	0.291441764	0.057934966
ENSBTAG00000018272	RERE	-0.095298128	0.543264843
ENSBTAG00000018274	FADD	0.520744545	0.000343639
ENSBTAG00000018275	LOC507930	-0.01371996	0.930416575
ENSBTAG00000018278	ATP5PO	-0.372617099	0.013864681
ENSBTAG00000018279	SPATA5L1	-0.527568061	0.000277583
ENSBTAG00000018280	SLC28A3	0.537295364	0.000203134
ENSBTAG00000018281	GPX7	-0.306798829	0.045383792
ENSBTAG00000018283	ACAA1	-0.439528021	0.003188496
ENSBTAG00000018284	KBTBD11	-0.204275243	0.188861124

ENSBTAG00000018285	VAMP5	0.513183883	0.000433082
ENSBTAG00000018289	TMEM150A	0.080360211	0.608469748
ENSBTAG00000018290	IL9	0.21919629	0.157875547
ENSBTAG00000018291	C11H2orf68	-0.376674521	0.012785283
ENSBTAG00000018297	PLEKHH1	-0.179179049	0.250281246
ENSBTAG00000018299	PIGH	0.177713831	0.254239727
ENSBTAG00000018307	SEMA3F	-0.210273608	0.175923709
ENSBTAG00000018309	NA	0.414502874	0.005718442
ENSBTAG00000018313	MBNL2	-0.707572285	1.12E-07
ENSBTAG00000018314	MED11	0.501576453	0.000611426
ENSBTAG00000018315	PELP1	0.219390062	0.157499189
ENSBTAG00000018316	ZMYND15	-0.38085327	0.011749274
ENSBTAG00000018320	RPLP1	0.259437532	0.092953835
ENSBTAG00000018321	PAOX	-0.029055333	0.853265762
ENSBTAG00000018324	AGO3	0.314634901	0.039887096
ENSBTAG00000018326	FXYD7	-0.105240714	0.501811057
ENSBTAG00000018331	CLEC3B	0.060595464	0.699498673
ENSBTAG00000018332	PPTC7	0.45439934	0.002206165
ENSBTAG00000018334	PLAGL2	0.483044389	0.001034566
ENSBTAG00000018339	ATP5MC1	-0.252028472	0.103016696
ENSBTAG00000018342	TJP3	-0.105071055	0.502504634
ENSBTAG00000018343	NCR3	0.06614257	0.673457756
ENSBTAG00000018358	STAC3	-0.152311307	0.329537667
ENSBTAG00000018362	TMEM109	-0.273055924	0.07645702
ENSBTAG00000018364	TMEM132A	-0.21557772	0.165024716
ENSBTAG00000018366	SLC15A3	0.331005551	0.030149748
ENSBTAG00000018367	CD6	-0.331107776	0.030095776
ENSBTAG00000018372	STARD7	-0.591422801	2.96E-05
ENSBTAG00000018373	DPYSL2	-0.088424444	0.572850687
ENSBTAG00000018379	TMEM175	-0.089060906	0.570080564
ENSBTAG00000018381	CRLF3	0.611607524	1.32E-05
ENSBTAG00000018382	SMS	-0.165783961	0.288027995
ENSBTAG00000018383	ATAD5	-0.666490754	1.07E-06
ENSBTAG00000018386	TEFM	-0.214453066	0.16729375
ENSBTAG00000018387	EIPR1	0.549255379	0.000136546
ENSBTAG00000018394	SDR42E1	-0.547467545	0.000145038
ENSBTAG00000018395	KIAA1217	-0.266191712	0.084458408
ENSBTAG00000018397	HHLA2	-0.212426191	0.17143988
ENSBTAG00000018398	GPR4	0.363479914	0.016581968
ENSBTAG00000018399	MYH15	-0.480809431	0.001100143
ENSBTAG00000018400	BRMS1L	-0.630797681	5.78E-06
ENSBTAG00000018403	ARHGAP9	0.232055305	0.134296087
ENSBTAG00000018404	PRKG1	-0.54408397	0.00016243
ENSBTAG00000018410	EBPL	-0.405546486	0.006975741
ENSBTAG00000018413	TENT5B	-0.693209218	2.57E-07
ENSBTAG00000018415	TTLL4	-0.411199246	0.006157182
ENSBTAG00000018416	CCDC42	-0.030240894	0.847347973

ENSBTAG00000018419	ADCY4	0.546545426	0.000149602
ENSBTAG00000018420	POLG2	-0.46073071	0.001876539
ENSBTAG00000018422	RIPK3	0.589775526	3.16E-05
ENSBTAG00000018423	DDX5	0.424532621	0.004548406
ENSBTAG00000018424	ACKR3	0.546367025	0.0001505
ENSBTAG00000018426	MRRF	-0.409837607	0.006346334
ENSBTAG00000018430	GSAP	0.443609512	0.002886627
ENSBTAG00000018431	NAV2	0.04198158	0.789240195
ENSBTAG00000018436	UBE2J1	0.115875413	0.459328221
ENSBTAG00000018438	RRAGD	-0.193297269	0.214259759
ENSBTAG00000018445	GRIN3A	0.108631784	0.488051161
ENSBTAG00000018446	GCA	0.070988437	0.651011987
ENSBTAG00000018447	RABGGTB	0.157136011	0.314263753
ENSBTAG00000018449	NUMA1	0.42208444	0.004812826
ENSBTAG00000018451	PTMS	0.569784539	6.66E-05
ENSBTAG00000018453	ANKRD37	-0.06775816	0.665942076
ENSBTAG00000018454	UFSP2	-0.278022687	0.071048042
ENSBTAG00000018464	ZDHHC14	0.366222508	0.015722738
ENSBTAG00000018467	BBOF1	-0.444808349	0.002802871
ENSBTAG00000018469	ALDH6A1	-0.522916037	0.000321226
ENSBTAG00000018471	SSR3	-0.555837578	0.000109024
ENSBTAG00000018473	MARCO	0.327766465	0.031901804
ENSBTAG00000018474	IL6R	0.567205277	7.31E-05
ENSBTAG00000018479	PTPMT1	-0.210035363	0.176425098
ENSBTAG00000018483	NDUFS3	-0.092204147	0.556491009
ENSBTAG00000018487	CFAP45	0.547272791	0.000145991
ENSBTAG00000018488	AFF1	0.363314752	0.016634955
ENSBTAG00000018498	PQBP1	0.427129856	0.00428182
ENSBTAG00000018499	ANXA8L1	-0.275172134	0.074114164
ENSBTAG00000018502	ARMC9	-0.571335853	6.30E-05
ENSBTAG00000018513	FHL1	-0.271849552	0.077818381
ENSBTAG00000018517	VLDLR	0.272863381	0.076673037
ENSBTAG00000018523	TRIM38	0.537546911	0.000201475
ENSBTAG00000018524	AMHR2	0.083056322	0.596455708
ENSBTAG00000018531	JCHAIN	-0.413350893	0.005868246
ENSBTAG00000018534	ESS2	0.565186343	7.85E-05
ENSBTAG00000018538	CEP70	-0.564165192	8.14E-05
ENSBTAG00000018546	LRBA	-0.491483385	0.000817213
ENSBTAG00000018548	INTS7	-0.646188582	2.86E-06
ENSBTAG00000018555	NA	-0.544103197	0.000162326
ENSBTAG00000018560	NA	0.086448724	0.581488701
ENSBTAG00000018562	LDAF1	0.113330742	0.469313246
ENSBTAG00000018569	CUL4B	-0.58881013	3.28E-05
ENSBTAG00000018572	FLT3	-0.207033022	0.182831662
ENSBTAG00000018577	SLC7A1	0.511732397	0.000452472
ENSBTAG00000018578	LOXL3	-0.310007881	0.04306278
ENSBTAG00000018589	RFC2	-0.56628616	7.55E-05

ENSBTAG00000018596	PTPN21	-0.421860617	0.004837656
ENSBTAG00000018599	PROSER3	-0.100220303	0.522539284
ENSBTAG00000018600	VGLL4	-0.572798552	5.97E-05
ENSBTAG00000018616	IPO11	-0.625813885	7.20E-06
ENSBTAG00000018622	PCBP4	-0.257627819	0.095338623
ENSBTAG00000018625	ZNF263	0.392174318	0.009295297
ENSBTAG00000018629	CWF19L2	-0.141314591	0.366046626
ENSBTAG00000018633	RABAC1	-0.487626616	0.000910896
ENSBTAG00000018635	ATP1A3	0.177329606	0.255284664
ENSBTAG00000018637	HDDC3	-0.558360525	9.99E-05
ENSBTAG00000018638	CC2D2A	0.54983159	0.000133907
ENSBTAG00000018642	RCCD1	-0.476061057	0.001251879
ENSBTAG00000018643	PRC1	-0.523392868	0.000316484
ENSBTAG00000018644	PDZRN3	-0.194392128	0.211625306
ENSBTAG00000018653	NABP1	0.512573818	0.000441139
ENSBTAG00000018655	MYDGF	0.286515269	0.062503431
ENSBTAG00000018658	TNRC6C	0.190061032	0.222179636
ENSBTAG00000018660	PPP6R2	0.377314756	0.012621679
ENSBTAG00000018661	TMC6	0.441881056	0.003011254
ENSBTAG00000018663	GPRC5C	-0.342186162	0.024702251
ENSBTAG00000018667	RCL1	0.657680147	1.65E-06
ENSBTAG00000018669	NA	0.11019344	0.481781033
ENSBTAG00000018682	SETD4	-0.665009695	1.15E-06
ENSBTAG00000018688	CBR3	-0.323844314	0.034134956
ENSBTAG00000018691	RHOU	-0.188761092	0.225417021
ENSBTAG00000018694	ACSS3	-0.611249377	1.34E-05
ENSBTAG00000018697	WDR44	-0.040920789	0.794449136
ENSBTAG00000018704	BTG3	0.421154964	0.004916667
ENSBTAG00000018705	ADCY3	-0.284962561	0.064001283
ENSBTAG00000018706	PCTP	-0.457638497	0.002031648
ENSBTAG00000018708	NA	0.382603928	0.011337047
ENSBTAG00000018710	TTF1	0.431142487	0.003896754
ENSBTAG00000018711	DENND4B	0.300974822	0.049854889
ENSBTAG00000018718	NA	0.357951809	0.018434943
ENSBTAG00000018722	PLEKHM2	0.402609265	0.007437047
ENSBTAG00000018723	SLC25A34	0.306078963	0.045918143
ENSBTAG00000018724	TMEM82	-0.113375925	0.469134951
ENSBTAG00000018725	FBLIM1	-0.291223285	0.058131738
ENSBTAG00000018729	SPEN	0.281753731	0.067187124
ENSBTAG00000018730	ZBTB17	0.541775631	0.000175356
ENSBTAG00000018731	LOC524181	0.322444692	0.034962351
ENSBTAG00000018732	HSPA12B	0.400170314	0.007839883
ENSBTAG00000018737	GLMN	-0.271408152	0.078321212
ENSBTAG00000018744	MGAT5	0.244918243	0.113438277
ENSBTAG00000018745	CEP290	-0.68011697	5.26E-07
ENSBTAG00000018746	NA	-0.451243152	0.002388798
ENSBTAG00000018749	NUDT16	-0.463442604	0.001749223

ENSBTAG00000018761	SLC35F6	0.350387331	0.021250714
ENSBTAG00000018768	HMGN1	-0.589508074	3.19E-05
ENSBTAG00000018770	HSDL1	-0.38117882	0.011671662
ENSBTAG00000018772	TAF1C	0.135496023	0.386309082
ENSBTAG00000018773	RND1	0.352415531	0.020462515
ENSBTAG00000018774	NUAK2	-0.511924125	0.000449867
ENSBTAG00000018775	TPX2	-0.681688669	4.84E-07
ENSBTAG00000018784	CTSZ	0.553885681	0.000116607
ENSBTAG00000018785	TUBB1	0.448823203	0.002537723
ENSBTAG00000018795	PMS1	-0.368825841	0.014942315
ENSBTAG00000018799	GPSM1	-0.288546421	0.060586324
ENSBTAG00000018804	CELSR2	0.168417647	0.28032935
ENSBTAG00000018806	PSRC1	-0.263377015	0.087922069
ENSBTAG00000018807	MYBPHL	0.204650893	0.188031622
ENSBTAG00000018808	SLC25A35	-0.268663553	0.081505156
ENSBTAG00000018809	RANGRF	-0.234001977	0.130968343
ENSBTAG00000018810	THBS2	-0.320879309	0.035907193
ENSBTAG00000018813	IDH3B	-0.341689003	0.024925695
ENSBTAG00000018819	TENM1	0.164228458	0.292638825
ENSBTAG00000018823	GRN	-0.059461588	0.704865
ENSBTAG00000018825	SSH1	-0.082714872	0.597971469
ENSBTAG00000018828	ATN1	0.444693356	0.002810812
ENSBTAG00000018837	SLC39A11	-0.440853918	0.00308753
ENSBTAG00000018841	PTPN3	-0.19499634	0.210181143
ENSBTAG00000018843	SERPINA1	-0.363127289	0.016695269
ENSBTAG00000018848	FBXL3	0.357071583	0.018745509
ENSBTAG00000018851	MYCBP2	0.504873627	0.000555059
ENSBTAG00000018854	SOD1	-0.609285034	1.45E-05
ENSBTAG00000018862	EIF4E3	0.404152071	0.007191561
ENSBTAG00000018863	PRIMPOL	-0.142034655	0.36358431
ENSBTAG00000018864	CENPU	-0.609125427	1.46E-05
ENSBTAG00000018868	METTL9	0.071958198	0.646555676
ENSBTAG00000018869	IGSF6	0.585366578	3.74E-05
ENSBTAG00000018870	OTOA	0.324022048	0.03403105
ENSBTAG00000018872	F12	0.617422895	1.03E-05
ENSBTAG00000018880	TRPV1	-0.400742635	0.007743702
ENSBTAG00000018894	PEX11G	-0.445303889	0.00276888
ENSBTAG00000018898	ARID4A	0.410754482	0.006218422
ENSBTAG00000018900	CARMIL2	-0.213760671	0.168701859
ENSBTAG00000018901	CTIF	0.287270287	0.061785243
ENSBTAG00000018902	ZC2HC1A	-0.555614262	0.000109868
ENSBTAG00000018904	ENKD1	-0.703331974	1.44E-07
ENSBTAG00000018905	MAN2A2	0.49723028	0.00069354
ENSBTAG00000018908	GFOD2	-0.287942854	0.061151036
ENSBTAG00000018909	CREB5	-0.271358125	0.078378362
ENSBTAG00000018912	ARHGEF1	0.593699728	2.71E-05
ENSBTAG00000018914	RAB25	-0.208260573	0.180192477

ENSBTAG00000018920	TRIM47	-0.077668881	0.620564821
ENSBTAG00000018922	TRMT10B	-0.065768499	0.675202445
ENSBTAG00000018926	LEAP2	0.266507977	0.084075964
ENSBTAG00000018936	LSS	-0.201130566	0.195907178
ENSBTAG00000018937	HMOX2	-0.52775979	0.000275905
ENSBTAG00000018938	CDIP1	-0.5978209	2.30E-05
ENSBTAG00000018940	CRACR2A	0.05398492	0.73097997
ENSBTAG00000018942	SSX2IP	-0.144448679	0.355402411
ENSBTAG00000018945	AMOTL1	-0.396420656	0.008495876
ENSBTAG00000018946	NIBAN3	0.679372706	5.47E-07
ENSBTAG00000018948	HIF3A	-0.256080964	0.097414182
ENSBTAG00000018951	TBC1D9	0.627533036	6.68E-06
ENSBTAG00000018960	NA	-0.573873978	5.74E-05
ENSBTAG00000018966	PLCE1	-0.352916107	0.020271803
ENSBTAG00000018969	POLR1C	0.12445971	0.426504903
ENSBTAG00000018971	RAD51B	-0.588788416	3.28E-05
ENSBTAG00000018972	GARS1	0.197727198	0.203739648
ENSBTAG00000018975	KCNT1	0.539914836	0.000186447
ENSBTAG00000018981	NA	-0.460311898	0.001896915
ENSBTAG00000018984	PIK3CD	-0.193478769	0.213821465
ENSBTAG00000018986	ACSL4	0.563151106	8.44E-05
ENSBTAG00000018991	TSGA10	-0.093908774	0.549185381
ENSBTAG00000018993	ITGB7	0.66111757	1.40E-06
ENSBTAG00000018994	TNFSF10	0.346788743	0.022711855
ENSBTAG00000018999	MGRN1	0.29573723	0.054173339
ENSBTAG00000019001	PRDM10	0.200200698	0.198025743
ENSBTAG00000019002	SLC2A12	-0.169558013	0.277038052
ENSBTAG00000019010	EIF2B3	-0.496403629	0.00071023
ENSBTAG00000019011	PGM1	-0.589068328	3.24E-05
ENSBTAG00000019014	MAGEF1	-0.484337139	0.000998245
ENSBTAG00000019015	IFITM3	0.525278072	0.000298349
ENSBTAG00000019017	LOC112444847	0.443960818	0.002861859
ENSBTAG00000019018	LOC112441484	0.547180675	0.000146444
ENSBTAG00000019023	NANS	-0.349430378	0.021631352
ENSBTAG00000019024	JAZF1	-0.127615959	0.414776417
ENSBTAG00000019025	NDUFA11	-0.474335049	0.001311479
ENSBTAG00000019026	EXTL2	-0.381655133	0.011558898
ENSBTAG00000019028	STOX1	0.083352894	0.59514054
ENSBTAG00000019033	CD84	-0.592990392	2.79E-05
ENSBTAG00000019036	ARHGAP28	-0.137409686	0.379573431
ENSBTAG00000019040	PLBD2	-0.069980394	0.655656976
ENSBTAG00000019044	BAIAP2	-0.597034018	2.38E-05
ENSBTAG00000019049	AATK	-0.142760932	0.361110879
ENSBTAG00000019052	ANK3	-0.34687295	0.022676728
ENSBTAG00000019054	EPSTI1	0.277432488	0.071674511
ENSBTAG00000019058	IQSEC3	0.29471167	0.055053104
ENSBTAG00000019059	ATG16L2	0.492038769	0.000804456

ENSBTAG00000019061	ELF4	0.54463205	0.00015949
ENSBTAG00000019065	EEPD1	-0.637698314	4.24E-06
ENSBTAG00000019066	FAM167A	-0.049419789	0.75298164
ENSBTAG00000019067	TMC8	0.254422329	0.099678175
ENSBTAG00000019069	SYNGR2	0.585720425	3.69E-05
ENSBTAG00000019070	PMP22	-0.529889952	0.000257867
ENSBTAG00000019071	COMMD10	-0.594681309	2.61E-05
ENSBTAG00000019072	PSD4	0.410073619	0.006313193
ENSBTAG00000019073	TRAF7	0.582391451	4.18E-05
ENSBTAG00000019075	METAP1D	-0.02907868	0.853149148
ENSBTAG00000019076	PAK6	-0.497645984	0.00068528
ENSBTAG00000019079	PLCB2	-0.098041976	0.531662988
ENSBTAG00000019081	NA	0.150274464	0.336122472
ENSBTAG00000019086	TELO2	-0.376876203	0.012733552
ENSBTAG00000019090	PLEKHH3	-0.188795729	0.225330343
ENSBTAG00000019091	RNPC3	0.006318672	0.967922743
ENSBTAG00000019093	AMY2B	-0.581491581	4.33E-05
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ENSBTAG00000019099	SLC25A37	0.536083148	0.000211304
ENSBTAG00000019104	FAAP100	-0.508633588	0.0004965
ENSBTAG00000019107	GAS7	0.150851522	0.334248709
ENSBTAG00000019110	PNRC1	0.34686775	0.022678896
ENSBTAG00000019115	NA	0.521653523	0.000334091
ENSBTAG00000019120	WDHD1	-0.470814357	0.001440919
ENSBTAG00000019121	IFT122	-0.673436806	7.47E-07
ENSBTAG00000019123	MEFV	0.435662882	0.003499537
ENSBTAG00000019124	NA	-0.394223348	0.008901825
ENSBTAG00000019125	SLC1A1	-0.28652438	0.062494725
ENSBTAG00000019129	BTD	-0.672921428	7.67E-07
ENSBTAG00000019131	CELF3	0.050018344	0.750085447
ENSBTAG00000019132	DMP1	0.035537032	0.821017482
ENSBTAG00000019138	KIF3C	-0.502577108	0.000593801
ENSBTAG00000019146	OSBP2	-0.320425422	0.036185038
ENSBTAG00000019150	PLD3	-0.674697336	7.00E-07
ENSBTAG00000019152	NYAP2	-0.204694284	0.187935974
ENSBTAG00000019153	JMJD6	0.322926571	0.034675645
ENSBTAG00000019156	CCT2	0.270667444	0.079170725
ENSBTAG00000019161	NPRL2	-0.267374724	0.083034763
ENSBTAG00000019162	MRM3	0.366218172	0.015724066
ENSBTAG00000019164	RHOBTB1	-0.387145929	0.010324729
ENSBTAG00000019166	NSMCE4A	-0.685763055	3.88E-07
ENSBTAG00000019167	INPPL1	-0.305951488	0.046013296
ENSBTAG00000019174	ZNF710	0.418043001	0.005278665
ENSBTAG00000019175	SOBP	0.538872835	0.00019293
ENSBTAG00000019177	BIN1	0.09667954	0.537408655
ENSBTAG00000019181	BAIAP2L1	-0.190788104	0.220382976
ENSBTAG00000019187	ZNF462	-0.2534606	0.101009291

ENSBTAG00000019188	GAK	0.497572676	0.00068673
ENSBTAG00000019193	SETD5	0.227009352	0.143214502
ENSBTAG00000019194	SHLD2	-0.417638408	0.00532739
ENSBTAG00000019197	TASOR2	0.58381362	3.96E-05
ENSBTAG00000019203	S100A4	0.321593712	0.035473422
ENSBTAG00000019208	ZFTA	-0.401410649	0.007632729
ENSBTAG00000019209	RAD1	-0.48911291	0.000873716
ENSBTAG00000019214	USP14	-0.583699989	3.98E-05
ENSBTAG00000019217	KIF13A	0.076255421	0.626957097
ENSBTAG00000019218	ATP6V0A1	-0.26370689	0.087510523
ENSBTAG00000019225	SLC39A14	0.077805313	0.619949267
ENSBTAG00000019227	LOC789748	0.636613908	4.45E-06
ENSBTAG00000019229	TMEM144	-0.555057344	0.000112
ENSBTAG00000019232	TYW5	-0.389961132	0.009736981
ENSBTAG00000019235	MAGOHB	-0.554896548	0.000112622
ENSBTAG00000019237	TXNDC5	-0.488256695	0.000894966
ENSBTAG00000019242	CHRNB1	-0.30280712	0.048411458
ENSBTAG00000019246	SC5D	0.138034204	0.377390414
ENSBTAG00000019247	NA	0.133569996	0.393158672
ENSBTAG00000019249	HS3ST6	0.241906423	0.118086357
ENSBTAG00000019251	EPB41L3	0.106503242	0.496665133
ENSBTAG00000019252	KDF1	-0.222206621	0.152102378
ENSBTAG00000019255	NFE2L2	0.556398583	0.000106929
ENSBTAG00000019256	GLA	-0.260266958	0.091876367
ENSBTAG00000019262	TOP2A	-0.460503462	0.001887571
ENSBTAG00000019266	NA	-0.511798145	0.000451577
ENSBTAG00000019269	COL6A2	-0.162523451	0.297747328
ENSBTAG00000019272	LPCAT2	0.509866866	0.000478537
ENSBTAG00000019274	ATIC	-0.191665462	0.218228334
ENSBTAG00000019276	NA	-0.453512791	0.002256178
ENSBTAG00000019278	KNTC1	-0.457146527	0.002057342
ENSBTAG00000019280	CRYBB1	-0.438825786	0.003243135
ENSBTAG00000019282	CRYBA4	-0.125673285	0.42197344
ENSBTAG00000019283	FAM186B	-0.489010155	0.000876242
ENSBTAG00000019289	ITGA2	-0.321138636	0.035749234
ENSBTAG00000019293	EGR3	0.569265153	6.79E-05
ENSBTAG00000019295	MDH1	-0.47888121	0.001159665
ENSBTAG00000019298	STRADB	-0.358158729	0.01836257
ENSBTAG00000019302	BCL2	-0.015415948	0.921840126
ENSBTAG00000019303	NA	0.554915695	0.000112548
ENSBTAG00000019309	NA	-0.662799304	1.28E-06
ENSBTAG00000019310	FOXK1	0.354489201	0.019682169
ENSBTAG00000019313	ZMIZ1	0.501189462	0.000618367
ENSBTAG00000019314	USP25	0.347236291	0.022525682
ENSBTAG00000019315	PLA2G7	-0.462586074	0.001788583
ENSBTAG00000019321	CCDC57	-0.216521583	0.16313772
ENSBTAG00000019325	TRMT1	0.322721065	0.034797678

ENSBTAG00000019327	NRAP	0.160279571	0.304557289
ENSBTAG00000019329	LYL1	0.408057513	0.006601194
ENSBTAG00000019330	PROK2	0.296788964	0.053282888
ENSBTAG00000019334	KLC2	-0.485345097	0.000970719
ENSBTAG00000019336	DVL3	0.309059351	0.043738539
ENSBTAG00000019337	ACVR1C	-0.317806515	0.037822857
ENSBTAG00000019338	IL13RA1	0.335509469	0.027846502
ENSBTAG00000019339	NA	0.420511443	0.004989699
ENSBTAG00000019340	NA	-0.374888996	0.013251127
ENSBTAG00000019342	OSBPL3	-0.278181029	0.070880708
ENSBTAG00000019343	MDFI	-0.250031723	0.105866327
ENSBTAG00000019345	RFK	0.472594004	0.001374138
ENSBTAG00000019347	PLXDC1	-0.528722552	0.000267616
ENSBTAG00000019348	NA	0.037780144	0.809922071
ENSBTAG00000019353	STIM2	-0.004939528	0.974921551
ENSBTAG00000019354	PAX8	0.06361463	0.685280681
ENSBTAG00000019358	RNF214	-0.612996722	1.24E-05
ENSBTAG00000019362	NOA1A	-0.337181375	0.027029562
ENSBTAG00000019365	BACE1	-0.630953098	5.74E-06
ENSBTAG00000019369	TSPAN4	-0.490195513	0.000847492
ENSBTAG00000019370	LOC781001	0.214609005	0.166977795
ENSBTAG00000019371	CNR2	-0.013314639	0.93246743
ENSBTAG00000019373	CAPRIN2	-0.130824775	0.403043066
ENSBTAG00000019375	SCARF2	0.02904284	0.853328164
ENSBTAG00000019376	FNDC3B	0.346582931	0.0227979
ENSBTAG00000019382	PKDCC	-0.184837615	0.235384193
ENSBTAG00000019385	SCN3A	-0.120308868	0.442208938
ENSBTAG00000019386	BOLA-NC1	0.534688786	0.000221068
ENSBTAG00000019387	NIFK	0.171712387	0.270889603
ENSBTAG00000019390	CA12	0.115349522	0.461382316
ENSBTAG00000019399	CNKSR1	-0.263421206	0.087866851
ENSBTAG00000019403	MALSU1	0.198090969	0.202892153
ENSBTAG00000019404	IL10RB	0.536335822	0.000209577
ENSBTAG00000019406	IGF2BP3	0.037430591	0.811648754
ENSBTAG00000019407	NA	-0.337655573	0.026801515
ENSBTAG00000019414	CLK4	0.449039051	0.002524115
ENSBTAG00000019417	ARMCX2	-0.328933649	0.031261023
ENSBTAG00000019418	UBE3D	-0.36837652	0.015074617
ENSBTAG00000019421	DACT1	-0.246535623	0.111000174
ENSBTAG00000019422	NA	-0.263548172	0.08770835
ENSBTAG00000019426	RNF175	0.336514756	0.027352871
ENSBTAG00000019427	KIAA0232	0.207814389	0.181148583
ENSBTAG00000019428	CCR1	0.458425552	0.001991131
ENSBTAG00000019432	LOC616254	0.582055259	4.24E-05
ENSBTAG00000019434	PDCD4	-0.499342196	0.000652482
ENSBTAG00000019436	SLC39A13	0.641352891	3.59E-06
ENSBTAG00000019437	SLFN11	-0.214813141	0.166564842

ENSBTAG00000019448	CLDN7	-0.363274601	0.016647857
ENSBTAG00000019451	TAPT1	0.497717208	0.000683874
ENSBTAG00000019453	PTGES	0.046928472	0.765071808
ENSBTAG00000019455	MYO5B	-0.291947337	0.057481665
ENSBTAG00000019456	SPRED2	0.390819527	0.00956358
ENSBTAG00000019457	MRPL22	-0.486217515	0.000947442
ENSBTAG00000019459	CHAC2	-0.415886321	0.005542935
ENSBTAG00000019461	NUMBL	-0.438781896	0.003246577
ENSBTAG00000019462	COQ8B	0.354390694	0.019718664
ENSBTAG00000019464	NA	-0.158113849	0.311223696
ENSBTAG00000019465	ITPKC	-0.277125649	0.072001923
ENSBTAG00000019470	NEK6	0.526793822	0.000284453
ENSBTAG00000019474	NA	0.555308131	0.000111035
ENSBTAG00000019478	NAAA	-0.576235522	5.26E-05
ENSBTAG00000019479	TATDN2	0.473999873	0.001323341
ENSBTAG00000019480	PDE6D	-0.51193033	0.000449783
ENSBTAG00000019486	CLDN12	-0.548933336	0.000138042
ENSBTAG00000019492	FANCE	-0.507592423	0.000512133
ENSBTAG00000019495	TEAD3	-0.115556963	0.460571476
ENSBTAG00000019496	CDKN3	-0.229105572	0.139457896
ENSBTAG00000019498	ITGA3	-0.357702244	0.018522553
ENSBTAG00000019516	COMT	-0.413470983	0.005852472
ENSBTAG00000019517	ELN	0.48136636	0.001083465
ENSBTAG00000019519	PWWP2B	0.280529246	0.068435457
ENSBTAG00000019524	ITGAD	0.328190953	0.031667519
ENSBTAG00000019529	ATP8A2	-0.17684484	0.256607128
ENSBTAG00000019530	KDM8	0.406297337	0.006861864
ENSBTAG00000019533	ADTRP	-0.5962457	2.45E-05
ENSBTAG00000019537	MARCHF8	0.213620552	0.168987854
ENSBTAG00000019540	NA	-0.345603407	0.023211163
ENSBTAG00000019542	MRPL39	-0.754577979	5.09E-09
ENSBTAG00000019545	SPATA13	0.441945178	0.003006547
ENSBTAG00000019547	NA	0.462360013	0.001799101
ENSBTAG00000019550	TBC1D2	0.042450301	0.78694144
ENSBTAG00000019556	MIIP	0.243186773	0.116093151
ENSBTAG00000019565	NCOA4	-0.156111834	0.317467965
ENSBTAG00000019567	IL21R	0.690632726	2.97E-07
ENSBTAG00000019568	IFT74	-0.496740385	0.000703388
ENSBTAG00000019569	CD151	0.153060054	0.327137452
ENSBTAG00000019574	MAPK12	-0.323256893	0.03448023
ENSBTAG00000019579	NA	-0.515856393	0.000399323
ENSBTAG00000019581	PLEKHF2	0.613564084	1.21E-05
ENSBTAG00000019585	MYOM1	-0.265232142	0.085627069
ENSBTAG00000019588	BLA-DQB	0.124624339	0.425888584
ENSBTAG00000019589	CFAP410	-0.415547913	0.005585428
ENSBTAG00000019596	GPRC5B	-0.306730634	0.045434195
ENSBTAG00000019600	OOEP	-0.290233841	0.059029583

ENSBTAG00000019604	VASP	0.615791412	1.11E-05
ENSBTAG00000019606	IFT52	0.505690192	0.00054184
ENSBTAG00000019612	RNASE4	0.004098386	0.979191077
ENSBTAG00000019614	FAM76A	-0.394189988	0.008908115
ENSBTAG00000019615	PHTF1	-0.427057014	0.004289107
ENSBTAG00000019617	PTPN22	0.45086025	0.002411837
ENSBTAG00000019621	NDRG3	-0.550807179	0.000129544
ENSBTAG00000019625	EHHADH	-0.677659544	5.99E-07
ENSBTAG00000019630	RGL1	-0.392554855	0.009221114
ENSBTAG00000019633	SHROOM3	-0.281907801	0.067031341
ENSBTAG00000019634	PIDD1	-0.178984678	0.250803968
ENSBTAG00000019636	SCARA5	0.391796884	0.009369381
ENSBTAG00000019646	TRIM41	-0.440055041	0.003148022
ENSBTAG00000019648	RACK1	0.200194651	0.198039573
ENSBTAG00000019652	STK26	0.22830289	0.140887645
ENSBTAG00000019662	ATXN7L3	0.633555687	5.11E-06
ENSBTAG00000019663	DECR1	-0.65687701	1.72E-06
ENSBTAG00000019665	IL1RN	0.548959385	0.00013792
ENSBTAG00000019667	RNF187	-0.538391204	0.000195995
ENSBTAG00000019669	CD163	0.618888208	9.70E-06
ENSBTAG00000019670	NA	-0.321244565	0.035684876
ENSBTAG00000019672	LOC574091	0.402674491	0.007426524
ENSBTAG00000019674	CLIP3	-0.467794941	0.001560827
ENSBTAG00000019675	ATXN1	0.335746663	0.02772937
ENSBTAG00000019678	ALKBH6	-0.582055623	4.24E-05
ENSBTAG00000019684	NUDT3	0.566938364	7.38E-05
ENSBTAG00000019687	NMRK1	-0.361169742	0.017336212
ENSBTAG00000019689	NA	-0.297411999	0.052760971
ENSBTAG00000019692	BCL2L2	-0.279661514	0.069331147
ENSBTAG00000019695	RLF	0.420554892	0.004984738
ENSBTAG00000019700	PC	-0.299963998	0.050665934
ENSBTAG00000019704	HLTF	-0.66229053	1.32E-06
ENSBTAG00000019708	ACSL6	0.144108051	0.356550077
ENSBTAG00000019711	IRAG2	-0.016584834	0.915934214
ENSBTAG00000019712	ST14	-0.217693995	0.160815679
ENSBTAG00000019716	CXCL8	0.280571587	0.068391986
ENSBTAG00000019721	REXO4	0.551320157	0.000127301
ENSBTAG00000019722	GUCY2C	-0.334167893	0.02851676
ENSBTAG00000019728	CD164L2	-0.343089551	0.024300505
ENSBTAG00000019729	COQ3	-0.611678065	1.31E-05
ENSBTAG00000019730	SFRS18	0.116270168	0.457789576
ENSBTAG00000019734	CD276	-0.276981572	0.072156068
ENSBTAG00000019738	MDM1	-0.59022899	3.10E-05
ENSBTAG00000019741	C3AR1	0.46339657	0.001751319
ENSBTAG00000019742	FOXJ2	0.567845311	7.14E-05
ENSBTAG00000019743	CHTF18	-0.36346089	0.016588064
ENSBTAG00000019745	LMF1	-0.036905302	0.814245178

ENSBTAG00000019746	CCDC66	-0.315842763	0.039090372
ENSBTAG00000019750	TMEM106B	-0.335600694	0.027801404
ENSBTAG00000019754	CAVIN3	0.073739082	0.638403843
ENSBTAG00000019761	MANBA	-0.162436554	0.298009212
ENSBTAG00000019767	MIER2	0.468376201	0.001537079
ENSBTAG00000019770	APOA4	-0.351229998	0.020920199
ENSBTAG00000019771	PALM	-0.104892217	0.50323626
ENSBTAG00000019777	CDCA3	-0.333648892	0.028779619
ENSBTAG00000019781	CLASP1	-0.601800276	1.97E-05
ENSBTAG00000019782	TPI1	0.147185359	0.346263432
ENSBTAG00000019783	NA	0.661355354	1.38E-06
ENSBTAG00000019785	CIC	0.255500235	0.098202315
ENSBTAG00000019788	TEAD4	-0.183782874	0.238114081
ENSBTAG00000019790	MSH5	-0.277450487	0.071655342
ENSBTAG00000019791	GRHL3	-0.352462147	0.020444691
ENSBTAG00000019794	SYPL1	0.09112288	0.561148586
ENSBTAG00000019796	FCMR	0.254636983	0.099382922
ENSBTAG00000019798	PIGR	-0.130218572	0.405244909
ENSBTAG00000019800	NA	0.494591846	0.000748072
ENSBTAG00000019805	RHBDF1	-0.276553525	0.072615557
ENSBTAG00000019806	YPEL2	-0.513973344	0.000422852
ENSBTAG00000019807	COL27A1	-0.063724268	0.684766349
ENSBTAG00000019808	CCSER1	0.312812015	0.04111457
ENSBTAG00000019810	AARS1	0.299461351	0.051073181
ENSBTAG00000019814	PGBD2	0.310139894	0.042969407
ENSBTAG00000019818	CASZ1	-0.161373921	0.301223705
ENSBTAG00000019819	FUT8	-0.385512426	0.010679504
ENSBTAG00000019822	TPPP3	0.238507024	0.123503782
ENSBTAG00000019824	NA	-0.395558769	0.008653168
ENSBTAG00000019828	TAB1	-0.181559841	0.243938015
ENSBTAG00000019836	GSKIP	-0.402964128	0.007379951
ENSBTAG00000019839	LTBP1	-0.348723892	0.021916016
ENSBTAG00000019843	HAUS6	-0.628767007	6.32E-06
ENSBTAG00000019844	ZNF467	0.510844261	0.000464717
ENSBTAG00000019847	CPEB2	-0.548407313	0.000140516
ENSBTAG00000019848	NA	-0.645041477	3.02E-06
ENSBTAG00000019857	OTUD4	0.371564775	0.014156956
ENSBTAG00000019859	B3GALT2	-0.120680227	0.440791127
ENSBTAG00000019864	MAPK15	-0.159834807	0.305918834
ENSBTAG00000019866	NRP1	0.557841503	0.000101707
ENSBTAG00000019867	COMMD1	-0.44932207	0.00250637
ENSBTAG00000019871	TRMT2A	0.484977638	0.000980675
ENSBTAG00000019872	PIK3AP1	0.513564724	0.000428119
ENSBTAG00000019884	PKD1L3	0.405895995	0.006922531
ENSBTAG00000019887	DHODH	-0.079488009	0.612378427
ENSBTAG00000019888	HIRA	0.465843984	0.00164293
ENSBTAG00000019892	HAS2	-0.267574162	0.082796612

ENSBTAG00000019900	LNPEP	0.426589414	0.00433614
ENSBTAG00000019901	RAD54L	-0.520513112	0.000346108
ENSBTAG00000019903	RAMP2	0.550852799	0.000129343
ENSBTAG00000019907	WNK4	-0.119757311	0.444319365
ENSBTAG00000019908	CUL9	0.174642354	0.262673228
ENSBTAG00000019910	SDCBP	0.375366258	0.013125217
ENSBTAG00000019915	GSN	0.506709284	0.000525738
ENSBTAG00000019916	CLMN	-0.446095429	0.002715335
ENSBTAG00000019920	BICDL2	-0.334040537	0.028581077
ENSBTAG00000019929	ITGAV	0.371124877	0.014280676
ENSBTAG00000019933	MKNK1	0.63264342	5.32E-06
ENSBTAG00000019938	N4BP1	0.466066978	0.001633356
ENSBTAG00000019940	RASGRF1	-0.257616241	0.095354032
ENSBTAG00000019947	SYT7	-0.181748552	0.243439919
ENSBTAG00000019951	PCYOX1L	-0.395504773	0.008663105
ENSBTAG00000019952	ARMC8	-0.495199172	0.000735191
ENSBTAG00000019953	CYBB	0.496138669	0.000715655
ENSBTAG00000019954	ABHD2	-0.02960715	0.850510327
ENSBTAG00000019956	CMPK1	-0.627149703	6.79E-06
ENSBTAG00000019958	NXNL2	-0.191463247	0.218723642
ENSBTAG00000019960	TM4SF18	-0.466545489	0.001612978
ENSBTAG00000019964	GAS6	-0.573863343	5.74E-05
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ENSBTAG00000019967	RASA3	0.451056558	0.002400001
ENSBTAG00000019975	IL7R	0.347388579	0.022462625
ENSBTAG00000019977	PCDH10	-0.053869913	0.731531721
ENSBTAG00000019979	CMPK2	0.228759927	0.14007224
ENSBTAG00000019984	GINS1	-0.556986979	0.000104771
ENSBTAG00000019988	GNA15	0.469589943	0.001488521
ENSBTAG00000019989	PXK	0.425363797	0.00446156
ENSBTAG00000019993	APLN	-0.087470963	0.577012063
ENSBTAG00000020000	RAP1GAP2	0.331817922	0.029723043
ENSBTAG00000020015	DFFB	0.627874291	6.58E-06
ENSBTAG00000020018	FRK	-0.310745512	0.042543165
ENSBTAG00000020019	XCR1	0.539956714	0.00018619
ENSBTAG00000020023	MTHFS	0.217596524	0.161007805
ENSBTAG00000020030	FITM2	-0.491920687	0.000807154
ENSBTAG00000020031	PKD2	-0.482329828	0.001055143
ENSBTAG00000020034	LYN	0.493175183	0.000778906
ENSBTAG00000020035	RCAN1	0.107180913	0.493914235
ENSBTAG00000020040	LPCAT4	-0.283591853	0.065347152
ENSBTAG00000020041	FAM13B	0.462155334	0.001808671
ENSBTAG00000020043	ARHGAP17	0.433856362	0.00365381
ENSBTAG00000020046	CLMP	-0.192945666	0.215110597
ENSBTAG00000020048	MAPK10	0.103154182	0.510374697
ENSBTAG00000020050	MLEC	-0.435883965	0.003481055
ENSBTAG00000020053	ZEB1	-0.145818202	0.350810804

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ENSBTAG00000020059	GEN1	-0.652721054	2.10E-06
ENSBTAG00000020060	TXNIP	0.09223872	0.556342384
ENSBTAG00000020061	KCNJ12	0.409062211	0.006456282
ENSBTAG00000020062	TMC4	-0.134665002	0.389255821
ENSBTAG00000020066	ZW10	-0.719670703	5.38E-08
ENSBTAG00000020067	LLGL2	-0.211393977	0.17357959
ENSBTAG00000020070	ABCC3	-0.060474428	0.700070818
ENSBTAG00000020073	NCEH1	-0.627090193	6.81E-06
ENSBTAG00000020074	NKPD1	-0.304611458	0.047023263
ENSBTAG00000020080	MYBPC2	0.147568968	0.344994014
ENSBTAG00000020087	CAMK2A	-0.512585165	0.000440988
ENSBTAG00000020089	USP32	0.500331737	0.000634004
ENSBTAG00000020090	EPHX3	-0.381234813	0.011658358
ENSBTAG00000020093	CUL4A	0.464472654	0.001702907
ENSBTAG00000020095	MS4A3	0.462580077	0.001788862
ENSBTAG00000020097	PERP	-0.302314106	0.048796476
ENSBTAG00000020100	ARHGAP11A	-0.454081679	0.002223972
ENSBTAG00000020116	JSP.1	0.151529762	0.332054706
ENSBTAG00000020117	ZBTB7A	0.542177762	0.00017304
ENSBTAG00000020119	RNF43	-0.225991287	0.145065699
ENSBTAG00000020125	RBFOX2	-0.505429369	0.000546031
ENSBTAG00000020126	MYO10	-0.259248521	0.093200731
ENSBTAG00000020127	TKTL1	-0.075778835	0.62911855
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ENSBTAG00000020133	PPP3CC	-0.733383467	2.22E-08
ENSBTAG00000020141	FREM1	0.396937921	0.008402664
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ENSBTAG00000020147	BBS1	-0.691181092	2.88E-07
ENSBTAG00000020148	TEK	-0.443067714	0.002925196
ENSBTAG00000020149	RNASEH2B	-0.116494918	0.45691481
ENSBTAG00000020153	NIT1	-0.650904049	2.29E-06
ENSBTAG00000020161	KLHL22	0.103934465	0.507163637
ENSBTAG00000020164	BAZ1A	0.441118291	0.003067737
ENSBTAG00000020166	ZNFX1	0.380182097	0.011910674
ENSBTAG00000020172	DENND2D	0.391979515	0.00933347
ENSBTAG00000020173	INPP5D	0.505165634	0.000550299
ENSBTAG00000020178	ARSK	-0.688871945	3.27E-07
ENSBTAG00000020179	AAAS	-0.574948726	5.52E-05
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ENSBTAG00000020190	KREMEN2	0.051586367	0.742514504
ENSBTAG00000020193	DCLRE1A	-0.639744744	3.86E-06
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ENSBTAG00000020205	PDE8B	-0.316685298	0.038542364
ENSBTAG00000020213	NIPAL4	0.284340981	0.064608842

ENSBTAG00000020214	LRRC8B	-0.24878949	0.10766929
ENSBTAG00000020218	ANXA7	-0.58519999	3.76E-05
ENSBTAG00000020219	MSS51	0.230313344	0.137326896
ENSBTAG00000020225	TBXAS1	0.444810282	0.002802738
ENSBTAG00000020227	FAM72A	-0.570731429	6.44E-05
ENSBTAG00000020232	REXO1	0.621674935	8.61E-06
ENSBTAG00000020233	CCDC186	0.364340759	0.016308099
ENSBTAG00000020236	NA	-0.200745448	0.196782663
ENSBTAG00000020237	NECAP1	0.533171643	0.000232153
ENSBTAG00000020242	LOC529792	0.292342608	0.057129243
ENSBTAG00000020244	EFNA1	-0.189718173	0.223030366
ENSBTAG00000020247	ADCYAP1R1	-0.241575713	0.11860537
ENSBTAG00000020252	NLGN2	-0.663280501	1.25E-06
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ENSBTAG00000020257	PTPN5	0.400999449	0.007700876
ENSBTAG00000020260	NA	-0.44391072	0.002865379
ENSBTAG00000020261	CDH26	0.054591392	0.728072607
ENSBTAG00000020266	SLC19A2	0.005685026	0.971138074
ENSBTAG00000020269	MISP	-0.297299365	0.052855019
ENSBTAG00000020270	NFKB1	0.49532549	0.000732537
ENSBTAG00000020279	ALG9	-0.609645221	1.43E-05
ENSBTAG00000020281	NIN	0.607446055	1.56E-05
ENSBTAG00000020282	DCTD	-0.500806812	0.0006253
ENSBTAG00000020283	DUSP5	0.347823638	0.022283295
ENSBTAG00000020286	GAREM1	-0.355848252	0.019184437
ENSBTAG00000020292	NA	-0.265498849	0.085300991
ENSBTAG00000020294	PTPN6	0.579559704	4.65E-05
ENSBTAG00000020297	SLC66A3	-0.014613808	0.92589544
ENSBTAG00000020301	BLM	-0.585602564	3.70E-05
ENSBTAG00000020303	FBXO38	0.567594369	7.21E-05
ENSBTAG00000020311	USP20	-0.296337953	0.053663284
ENSBTAG00000020312	NCOA2	0.035920374	0.819118797
ENSBTAG00000020313	FNBP1	0.400042083	0.007861573
ENSBTAG00000020314	COG2	-0.471341127	0.001420858
ENSBTAG00000020315	DENND5B	-0.110671689	0.479869314
ENSBTAG00000020319	ALOX5	-0.547699649	0.000143909
ENSBTAG00000020329	FAM161B	0.109677017	0.483849815
ENSBTAG00000020330	BTG1	0.383730343	0.011078398
ENSBTAG00000020331	COQ6	-0.192079901	0.217215629
ENSBTAG00000020334	ENTPD5	-0.34892058	0.021836451
ENSBTAG00000020338	CCT6B	-0.376012672	0.012956306
ENSBTAG00000020344	SLC44A3	0.38410142	0.010994304
ENSBTAG00000020345	CNN3	0.201246065	0.195645152
ENSBTAG00000020346	CCDC92	-0.671111884	8.43E-07
ENSBTAG00000020348	ASTL	0.298806211	0.051607936
ENSBTAG00000020350	DUSP2	0.547559665	0.000144589
ENSBTAG00000020352	PAQR5	0.011527603	0.941514512

ENSBTAG00000020355	KLF4	0.401765897	0.007574275
ENSBTAG00000020357	GOLPH3L	-0.633283935	5.17E-06
ENSBTAG00000020359	PLEKHM1	-0.287742639	0.061339287
ENSBTAG00000020368	NA	-0.059254942	0.705844532
ENSBTAG00000020369	NOXO1	-0.626614857	6.95E-06
ENSBTAG00000020371	ACOT8	-0.195341566	0.209359087
ENSBTAG00000020374	THSD1	-0.245898188	0.111956268
ENSBTAG00000020382	RIN2	0.570692443	6.44E-05
ENSBTAG00000020385	NA	-0.461276216	0.00185029
ENSBTAG00000020394	TNFAIP8L2	-0.008206106	0.958348452
ENSBTAG00000020395	LYSMD1	0.583390635	4.03E-05
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ENSBTAG00000020414	DHX37	0.478381902	0.001175537
ENSBTAG00000020416	PGAP1	-0.507968326	0.000506438
ENSBTAG00000020418	CA5B	0.253589412	0.100830217
ENSBTAG00000020423	EP400	0.303298559	0.048030119
ENSBTAG00000020426	TFAP2B	-0.083547515	0.594278173
ENSBTAG00000020428	PAF1	0.441516198	0.003038157
ENSBTAG00000020430	GLT1D1	0.221825896	0.152823853
ENSBTAG00000020432	MIS12	-0.058884439	0.707601951
ENSBTAG00000020433	NLRP1	0.153614725	0.325366441
ENSBTAG00000020434	C18H19orf12	-0.285445972	0.063531922
ENSBTAG00000020436	KIF27	-0.60888874	1.47E-05
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ENSBTAG00000020446	THOP1	0.061419884	0.69560595
ENSBTAG00000020448	NA	-0.305695922	0.046204544
ENSBTAG00000020450	CLDND2	-0.188254755	0.226686741
ENSBTAG00000020453	CLEC5A	0.337551915	0.026851228
ENSBTAG00000020454	LZTS3	0.049097004	0.754544874
ENSBTAG00000020455	ITPR1	0.032691729	0.835141086
ENSBTAG00000020458	STX6	0.530975091	0.000249093
ENSBTAG00000020465	FERMT1	-0.469660002	0.00148576
ENSBTAG00000020468	MICU3	-0.112705957	0.471782383
ENSBTAG00000020469	TMED8	-0.396014068	0.008569768
ENSBTAG00000020471	SAMD15	-0.376252089	0.012894217
ENSBTAG00000020472	KDM5A	0.436669585	0.003416067
ENSBTAG00000020477	AHSA1	0.122397305	0.434268198
ENSBTAG00000020480	SPTLC2	0.536059621	0.000211466
ENSBTAG00000020481	GXYLT2	-0.348421567	0.022038786
ENSBTAG00000020489	SEMA6A	0.017176149	0.912948219
ENSBTAG00000020490	NACC2	0.464506556	0.001701401
ENSBTAG00000020495	SH3YL1	-0.374201698	0.013434254
ENSBTAG00000020498	ACP1	-0.603684444	1.82E-05
ENSBTAG00000020499	LOC112443425	0.27418339	0.07520167
ENSBTAG00000020503	MTRFR	-0.495590662	0.000726993
ENSBTAG00000020504	CDK2AP1	-0.60134768	2.00E-05
ENSBTAG00000020510	EPHA10	-0.133768936	0.392447913

ENSBTAG00000020515	FHIP1B	0.630629945	5.82E-06
ENSBTAG00000020518	PARK7	-0.59167343	2.93E-05
ENSBTAG00000020520	RASD1	0.118346497	0.449742668
ENSBTAG00000020523	SLC10A5	0.327326721	0.032146017
ENSBTAG00000020524	UPK3BL1	0.195818551	0.208226978
ENSBTAG00000020527	IDH1	-0.491306614	0.000821311
ENSBTAG00000020535	PYCARD	0.50996649	0.000477111
ENSBTAG00000020536	HERC6	0.352091624	0.020586719
ENSBTAG00000020538	HERC5	0.304541812	0.047076242
ENSBTAG00000020539	CHPF	-0.425250244	0.004473339
ENSBTAG00000020540	TMEM198	0.55904435	9.75E-05
ENSBTAG00000020541	PIGY	-0.585965597	3.65E-05
ENSBTAG00000020542	SHE	0.365725337	0.015875637
ENSBTAG00000020543	UPK1A	-0.192426745	0.216370602
ENSBTAG00000020551	ABCD1	0.112497914	0.472606093
ENSBTAG00000020552	PRDM2	0.370153137	0.014557233
ENSBTAG00000020554	AIF1	0.617920181	1.01E-05
ENSBTAG00000020566	BCR	0.248171379	0.108575088
ENSBTAG00000020569	CACNA2D1	-0.26885969	0.08127432
ENSBTAG00000020573	SCUBE2	0.075731198	0.629334768
ENSBTAG00000020575	IFITM5	0.156015048	0.317771831
ENSBTAG00000020580	TCN1	0.586690714	3.55E-05
ENSBTAG00000020582	PRSS22	-0.102036356	0.514992605
ENSBTAG00000020583	AASDH	-0.380117755	0.011926245
ENSBTAG00000020584	IFT81	-0.133788533	0.392377939
ENSBTAG00000020589	ENTPD1	0.524970415	0.000301243
ENSBTAG00000020591	VAMP4	-0.390001528	0.009728761
ENSBTAG00000020596	TMEM126B	-0.038049308	0.808593095
ENSBTAG00000020597	FMO3	-0.627098128	6.80E-06
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ENSBTAG00000020600	RHOD	-0.289235614	0.059946594
ENSBTAG00000020601	ZNF366	-0.238918877	0.122837668
ENSBTAG00000020602	IDO1	0.255494024	0.098210771
ENSBTAG00000020605	SMTNL2	-0.454289263	0.002212321
ENSBTAG00000020607	ABCB6	-0.368408464	0.015065178
ENSBTAG00000020611	GLB1L	0.338769445	0.026272127
ENSBTAG00000020612	NEK3	-0.694850419	2.35E-07
ENSBTAG00000020614	PRKCE	0.239365484	0.1221184
ENSBTAG00000020616	DGKD	0.399892446	0.00788695
ENSBTAG00000020619	PKD1	-0.072277058	0.645093083
ENSBTAG00000020620	RGS2	0.532862484	0.000234473
ENSBTAG00000020626	ERCC6L2	-0.56971128	6.68E-05
ENSBTAG00000020632	NQO1	-0.657897755	1.63E-06
ENSBTAG00000020634	FBXO7	0.230168886	0.137580499
ENSBTAG00000020635	VPS45	-0.559010116	9.76E-05
ENSBTAG00000020638	TIMP3	-0.042378298	0.787294449
ENSBTAG00000020642	ZDHHC13	0.312866832	0.041077213

ENSBTAG00000020643	BARX2	-0.273628086	0.07581792
ENSBTAG00000020646	NA	-0.641043918	3.64E-06
ENSBTAG00000020649	CIITA	0.574573847	5.59E-05
ENSBTAG00000020654	BAZ2B	-0.00864089	0.956143713
ENSBTAG00000020657	FAT1	-0.007218793	0.963356105
ENSBTAG00000020658	LNX1	0.08889015	0.570823154
ENSBTAG00000020661	ABCA1	0.413255503	0.005880801
ENSBTAG00000020665	GFRA2	-0.414805464	0.005679648
ENSBTAG00000020669	NA	0.162913301	0.29657424
ENSBTAG00000020674	LTB	0.32967348	0.03086039
ENSBTAG00000020676	MMP9	-0.275368134	0.073900064
ENSBTAG00000020685	NA	-0.483084542	0.001033421
ENSBTAG00000020689	PPP1R13L	-0.416133863	0.00551203
ENSBTAG00000020696	HECW2	0.237770842	0.124701213
ENSBTAG00000020699	TSPAN11	-0.671295121	8.35E-07
ENSBTAG00000020700	CLCN6	0.317611539	0.037947181
ENSBTAG00000020701	MEF2C	-0.304709962	0.046948415
ENSBTAG00000020705	PRSS12	0.49977124	0.000644412
ENSBTAG00000020707	ADGRG6	-0.29859946	0.051777629
ENSBTAG00000020709	MAP1S	0.102404415	0.513469792
ENSBTAG00000020710	CENPQ	-0.542293813	0.000172376
ENSBTAG00000020713	BACH2	0.21916095	0.157944257
ENSBTAG00000020714	DDX19B	0.311375154	0.042103669
ENSBTAG00000020729	DHRS7	-0.340804745	0.02532728
ENSBTAG00000020731	PRRG4	-0.275610517	0.07363597
ENSBTAG00000020733	RPS15A	0.269982532	0.079962649
ENSBTAG00000020735	SMG1	0.3621629	0.017008482
ENSBTAG00000020736	CD40	0.550140739	0.00013251
ENSBTAG00000020739	NXT2	-0.528993782	0.000265322
ENSBTAG00000020742	NA	0.277795355	0.071288831
ENSBTAG00000020745	HIVEP3	0.600611318	2.06E-05
ENSBTAG00000020747	ASS1	0.29518633	0.054644507
ENSBTAG00000020749	PRXL2C	-0.651165299	2.26E-06
ENSBTAG00000020751	HSF1	0.520013979	0.00035149
ENSBTAG00000020754	ZNF526	-0.04995181	0.750407215
ENSBTAG00000020755	SELP	0.382854722	0.011279017
ENSBTAG00000020758	MAP3K12	-0.337913859	0.026677977
ENSBTAG00000020759	NCLN	0.639144223	3.97E-06
ENSBTAG00000020760	SNAP29	0.596456786	2.43E-05
ENSBTAG00000020764	CNN2	0.478183167	0.001181908
ENSBTAG00000020766	ABCA7	0.550397939	0.000131358
ENSBTAG00000020767	NA	0.363945556	0.01643335
ENSBTAG00000020772	ARHGAP45	0.485614811	0.000963469
ENSBTAG00000020773	CTSW	-0.300517063	0.050220868
ENSBTAG00000020774	NA	-0.138192832	0.376837117
ENSBTAG00000020777	ERCC3	0.106650924	0.496064973
ENSBTAG00000020780	SBNO2	0.622405619	8.34E-06

ENSBTAG00000020783	MAPK14	0.174732235	0.262423825
ENSBTAG00000020789	STS	-0.109680134	0.483837315
ENSBTAG00000020791	RAPGEF1	0.370407589	0.01448438
ENSBTAG00000020793	KCNA4	-0.15717406	0.31414511
ENSBTAG00000020796	UBE2D1	0.281866077	0.0670735
ENSBTAG00000020800	BEND7	-0.461695014	0.001830359
ENSBTAG00000020801	CYRIB	0.531767421	0.000242858
ENSBTAG00000020802	DNAH12	-0.472113647	0.001391887
ENSBTAG00000020807	FAU	0.533924628	0.00022659
ENSBTAG00000020810	CYB561	0.022698914	0.885122112
ENSBTAG00000020814	C2CD4B	-0.393940373	0.008955297
ENSBTAG00000020824	KRT10	-0.399242251	0.007998036
ENSBTAG00000020825	IRAK1BP1	-0.434618796	0.003587989
ENSBTAG00000020826	CHIC1	-0.40210446	0.007518926
ENSBTAG00000020828	NA	-0.470339976	0.001459199
ENSBTAG00000020829	PTPRK	-0.36979946	0.014659011
ENSBTAG00000020835	KIAA0513	0.350159382	0.021340869
ENSBTAG00000020837	ARHGEF16	-0.483350983	0.001025847
ENSBTAG00000020848	PIK3CG	0.600978965	2.03E-05
ENSBTAG00000020852	SLC16A11	-0.304397914	0.047185855
ENSBTAG00000020853	SLC16A13	-0.314416125	0.040032813
ENSBTAG00000020855	PTPN4	-0.63436155	4.93E-06
ENSBTAG00000020860	CHD1	0.48445196	0.000995075
ENSBTAG00000020865	PELI1	0.529528618	0.000260849
ENSBTAG00000020872	C5AR1	0.534849993	0.000219919
ENSBTAG00000020880	ARMH4	-0.290598215	0.058697661
ENSBTAG00000020884	CASP4	0.498869838	0.000661471
ENSBTAG00000020890	TRIM66	-0.448740914	0.002542927
ENSBTAG00000020892	IL2RA	0.414309289	0.005743381
ENSBTAG00000020893	MATN3	0.086653953	0.5805887
ENSBTAG00000020894	LAPTM4A	-0.557279685	0.000103712
ENSBTAG00000020895	LOXL4	-0.064822419	0.679622499
ENSBTAG00000020900	RPUSD4	0.611747092	1.31E-05
ENSBTAG00000020904	JAK3	0.613896029	1.20E-05
ENSBTAG00000020907	PSMC3IP	0.221990122	0.152512338
ENSBTAG00000020911	FNBP4	0.512061329	0.000448011
ENSBTAG00000020914	CPNE8	-0.507623954	0.000511653
ENSBTAG00000020921	PRKCB	0.639839922	3.84E-06
ENSBTAG00000020923	GDF1	-0.483300827	0.001027269
ENSBTAG00000020924	FBXW9	-0.480941985	0.001096152
ENSBTAG00000020927	HSD17B8	-0.045996494	0.769609006
ENSBTAG00000020930	GEMIN2	-0.636029891	4.57E-06
ENSBTAG00000020931	CHN2	0.221671031	0.15311804
ENSBTAG00000020934	SHF	-0.4325222	0.003771534
ENSBTAG00000020935	HIF1A	0.243787499	0.115166781
ENSBTAG00000020936	NOD2	0.594295576	2.65E-05
ENSBTAG00000020937	SNAPC1	0.172533682	0.268569572

ENSBTAG00000020942	RNF166	0.694385237	2.41E-07
ENSBTAG00000020944	PIEZO1	0.648297019	2.59E-06
ENSBTAG00000020954	TRIM7	-0.091882943	0.557872703
ENSBTAG00000020957	FZD5	-0.567345085	7.27E-05
ENSBTAG00000020961	DUSP19	-0.635119256	4.76E-06
ENSBTAG00000020963	RASSF1	0.536237559	0.000210247
ENSBTAG00000020965	ZMYND10	0.576976398	5.12E-05
ENSBTAG00000020969	DCAF6	-0.212313053	0.171673476
ENSBTAG00000020975	SYNGAP1	-0.28796102	0.061133979
ENSBTAG00000020980	CAT	-0.628295614	6.46E-06
ENSBTAG00000020983	RRAS	0.488702381	0.000883848
ENSBTAG00000020988	KIZ	-0.729977927	2.78E-08
ENSBTAG00000020990	P2RY14	0.48612981	0.00094976
ENSBTAG00000020994	C19H17orf75	-0.738144965	1.62E-08
ENSBTAG00000020998	RUVBL1	0.301813554	0.049189907
ENSBTAG00000020999	DDB2	-0.272383502	0.077213506
ENSBTAG00000021000	USF3	-0.091642299	0.558908912
ENSBTAG00000021002	ACP2	-0.166982511	0.284507607
ENSBTAG00000021007	FOLR1	-0.521184649	0.000338986
ENSBTAG00000021008	ZNF219	-0.653826012	1.99E-06
ENSBTAG00000021013	TUBB4A	-0.379640576	0.012042271
ENSBTAG00000021019	SLC30A4	-0.391304899	0.00946671
ENSBTAG00000021021	C21H15orf39	0.352214052	0.020539699
ENSBTAG00000021023	ZMYM4	-0.752390157	5.97E-09
ENSBTAG00000021024	MACF1	-0.146449154	0.348707652
ENSBTAG00000021025	P3H2	-0.337898828	0.026685153
ENSBTAG00000021029	PRR5L	0.173397548	0.266143503
ENSBTAG00000021035	CTSK	-0.372126975	0.014000164
ENSBTAG00000021036	MARCHF2	-0.484764501	0.000986491
ENSBTAG00000021041	PRAM1	0.530820875	0.000250323
ENSBTAG00000021045	E2F3	0.454430221	0.002204441
ENSBTAG00000021048	ADM	-0.07926017	0.613401221
ENSBTAG00000021052	GNB1L	0.376269486	0.012889715
ENSBTAG00000021060	FTSJ3	0.490023602	0.000851609
ENSBTAG00000021064	NA	0.535377723	0.000216194
ENSBTAG00000021065	MFSD13A	0.219009079	0.158239782
ENSBTAG00000021066	NA	-0.298767902	0.051639344
ENSBTAG00000021068	SUFU	-0.477764642	0.001195426
ENSBTAG00000021069	PBK	-0.482286138	0.001056413
ENSBTAG00000021071	TRIM8	0.533701761	0.000228224
ENSBTAG00000021072	DTNB	-0.153378943	0.326118537
ENSBTAG00000021073	KIAA1549	-0.006079027	0.969138723
ENSBTAG00000021076	TNRC6B	-0.248177903	0.108565497
ENSBTAG00000021077	BOLA-DQB	0.132379719	0.397426877
ENSBTAG00000021078	PYROXD1	-0.405917008	0.006919344
ENSBTAG00000021079	C3H1orf210	-0.230999799	0.136126539
ENSBTAG00000021082	TMEM125	-0.320526225	0.03612318

ENSBTAG00000021087	UBR1	0.41607288	0.005519629
ENSBTAG00000021090	ABCC1	0.329335488	0.031042889
ENSBTAG00000021091	ANKFY1	0.507948223	0.000506741
ENSBTAG00000021092	ATP6V0D2	-0.432775378	0.003748942
ENSBTAG00000021096	RTEL1	-0.452159711	0.002334437
ENSBTAG00000021097	PELI3	-0.28917479	0.060002835
ENSBTAG00000021100	PPP1R3F	-0.376224404	0.012901383
ENSBTAG00000021102	GALM	-0.688072358	3.42E-07
ENSBTAG00000021105	IRAK4	0.347405895	0.022455464
ENSBTAG00000021107	STXBP5	-0.502572655	0.000593878
ENSBTAG00000021111	POU5F1	0.390474251	0.009633006
ENSBTAG00000021115	ZNF692	0.256809599	0.096432215
ENSBTAG00000021116	EXOC6	0.117787445	0.451901671
ENSBTAG00000021121	PPIL2	0.608750265	1.48E-05
ENSBTAG00000021130	MFSD10	0.241487518	0.118744074
ENSBTAG00000021133	TENM3	-0.235019924	0.129252917
ENSBTAG00000021134	DPP9	0.571388256	6.28E-05
ENSBTAG00000021135	RMI1	-0.540637081	0.000182069
ENSBTAG00000021140	RMND5A	-0.415520148	0.005588927
ENSBTAG00000021141	CD8A	-0.270043705	0.079891667
ENSBTAG00000021143	DNMT3A	0.173178672	0.266756814
ENSBTAG00000021144	PSTPIP1	0.627666745	6.64E-06
ENSBTAG00000021145	MAP4K1	0.089052844	0.570115614
ENSBTAG00000021151	MYH10	0.024913824	0.873998758
ENSBTAG00000021156	TBC1D31	-0.503855161	0.000571951
ENSBTAG00000021157	NA	0.318842224	0.037168032
ENSBTAG00000021158	SATB1	-0.363689059	0.016515076
ENSBTAG00000021160	AP1M2	-0.17917526	0.250291429
ENSBTAG00000021162	CKAP2	-0.629582761	6.10E-06
ENSBTAG00000021165	VPS9D1	0.479656399	0.0011354
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ENSBTAG00000021176	CRISPLD2	0.507867833	0.000507955
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ENSBTAG00000021181	BUB1	-0.148756232	0.341083324
ENSBTAG00000021182	DOCK4	0.525820264	0.00029331
ENSBTAG00000021183	MAP3K21	-0.554793693	0.000113022
ENSBTAG00000021187	ID2	0.430927208	0.003916617
ENSBTAG00000021191	EHD2	-0.259703119	0.092607766
ENSBTAG00000021193	FBXO5	-0.225484112	0.145994479
ENSBTAG00000021199	COA8	-0.390437509	0.00964042
ENSBTAG00000021202	ACOT7	0.137846448	0.378045934
ENSBTAG00000021204	TES	-0.202382305	0.193080605
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ENSBTAG00000021208	RRM2B	-0.410043094	0.006317471
ENSBTAG00000021210	HES2	0.044968217	0.774623839
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ENSBTAG00000021215	VWA5A	-0.483229345	0.001029299

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ENSBTAG00000021222	ZNF771	0.076698401	0.624950821
ENSBTAG00000021223	CRY2	-0.013195936	0.933068131
ENSBTAG00000021224	ZSWIM6	0.516369932	0.000393114
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ENSBTAG00000021240	DCSTAMP	0.485258552	0.000973056
ENSBTAG00000021245	SPRY1	0.33013084	0.03061485
ENSBTAG00000021249	LAT	-0.240330896	0.120574425
ENSBTAG00000021250	RALBP1	-0.436127821	0.003460768
ENSBTAG00000021251	RIPK4	-0.215160992	0.165862866
ENSBTAG00000021253	PRDM15	0.524867967	0.000302213
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ENSBTAG00000021272	ABCG1	-0.085935183	0.583743508
ENSBTAG00000021273	SEMA4B	0.460858397	0.001870366
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ENSBTAG00000021286	SLC37A1	0.43559342	0.003505362
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ENSBTAG00000021289	POGZ	0.46948461	0.001492681
ENSBTAG00000021291	STXBP6	-0.4865614	0.000938405
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ENSBTAG00000021302	CHAD	-0.471206674	0.001425955
ENSBTAG00000021308	NA	-0.260006873	0.092213187
ENSBTAG00000021313	RUNDC3B	0.110872495	0.479067815
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ENSBTAG00000021341	BTBD1	0.23559364	0.128293535
ENSBTAG00000021343	ARHGEF12	-0.452836311	0.00229501
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ENSBTAG00000021368	LOC782884	-0.436548686	0.003425998
ENSBTAG00000021372	SEPTIN11	-0.059648381	0.703979975
ENSBTAG00000021374	FARSA	0.475750535	0.001262421
ENSBTAG00000021377	S100A14	-0.298905228	0.051526826
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ENSBTAG00000021392	DCAF11	0.578972346	4.75E-05
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ENSBTAG00000021395	PSME1	0.596850617	2.39E-05
ENSBTAG00000021396	HEG1	0.539484432	0.0001891
ENSBTAG00000021398	MTRES1	-0.548190715	0.000141547
ENSBTAG00000021416	PRXL2A	-0.593819114	2.70E-05
ENSBTAG00000021417	DMWD	-0.280332961	0.06863726
ENSBTAG00000021423	LKAAEAR1	-0.436971385	0.003391386
ENSBTAG00000021424	CSK	0.642188675	3.45E-06
ENSBTAG00000021425	LMAN1L	-0.35407642	0.019835476
ENSBTAG00000021427	HOXB3	-0.40182751	0.007564176
ENSBTAG00000021430	UPK3B	0.431144844	0.003896537
ENSBTAG00000021433	LOC508131	-0.666420755	1.07E-06
ENSBTAG00000021434	EDN2	-0.192133857	0.217084026
ENSBTAG00000021435	MAFF	0.531992194	0.000241115
ENSBTAG00000021437	GPR174	-0.35715816	0.018714768
ENSBTAG00000021438	ZNF821	0.124266027	0.427230631
ENSBTAG00000021442	CRTAP	-0.660784558	1.42E-06
ENSBTAG00000021445	ST8SIA4	-0.138364851	0.376237657
ENSBTAG00000021452	TRANK1	0.484653903	0.000989521
ENSBTAG00000021454	NA	0.156324463	0.316801049
ENSBTAG00000021462	CSF3	0.354362435	0.019729144
ENSBTAG00000021464	SPRYD3	0.59183884	2.91E-05
ENSBTAG00000021467	IGFBP6	0.711110122	9.09E-08
ENSBTAG00000021468	MED24	-0.163103221	0.296003835
ENSBTAG00000021469	CTTNBP2	-0.489789879	0.000857234
ENSBTAG00000021472	ZC3H3	0.033848813	0.829391073
ENSBTAG00000021474	GSDMD	0.416616754	0.005452172
ENSBTAG00000021480	SAG	0.464593193	0.001697558
ENSBTAG00000021484	TSPAN18	-0.207784859	0.181211988
ENSBTAG00000021485	C3H1orf54	-0.079047814	0.614355166
ENSBTAG00000021487	CIART	0.360989062	0.017396404
ENSBTAG00000021490	WDR4	0.558102047	0.000100789
ENSBTAG00000021497	CDH23	-0.709534436	1.00E-07
ENSBTAG00000021501	LOC784768	-0.084085378	0.591897769
ENSBTAG00000021504	TIRAP	0.315897611	0.039054504
ENSBTAG00000021505	USP36	0.440629084	0.003104451
ENSBTAG00000021506	ARL6IP5	-0.608611198	1.49E-05
ENSBTAG00000021508	LMOD3	-0.374891939	0.013250347
ENSBTAG00000021512	ZBTB7B	0.296135671	0.053834603
ENSBTAG00000021514	DNPEP	0.337825192	0.026720333
ENSBTAG00000021516	GSTA1	0.08113526	0.605005458
ENSBTAG00000021517	TMEM216	-0.05475818	0.727273705
ENSBTAG00000021518	TMPRSS4	-0.202679438	0.192413903
ENSBTAG00000021521	BFAR	0.348333541	0.022074641
ENSBTAG00000021523	STAT3	0.595369095	2.54E-05
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ENSBTAG00000021535	CROT	-0.537182402	0.000203883
ENSBTAG00000021538	MYO1E	-0.596700768	2.41E-05
ENSBTAG00000021540	WDR11	-0.669975116	8.93E-07
ENSBTAG00000021543	MDFIC	-0.544909638	0.00015802
ENSBTAG00000021549	NA	-0.393673836	0.009005915
ENSBTAG00000021550	MAMDC4	0.068481137	0.662589182
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ENSBTAG00000021568	VWCE	-0.339577399	0.0258936
ENSBTAG00000021569	DDB1	-0.552095846	0.000123978
ENSBTAG00000021573	DCAF12	0.553540963	0.000117995
ENSBTAG00000021574	TCF7L2	0.505973963	0.000537312
ENSBTAG00000021577	ZFYVE16	0.310389999	0.042792961
ENSBTAG00000021581	FHOD3	-0.295067904	0.054746223
ENSBTAG00000021582	NCAPG	-0.537067855	0.000204645
ENSBTAG00000021583	TPGS2	-0.225710756	0.14557889
ENSBTAG00000021587	SMPDL3A	0.109213559	0.485710364
ENSBTAG00000021592	WRN	-0.507179633	0.000518452
ENSBTAG00000021594	NA	-0.230145141	0.137622216
ENSBTAG00000021595	HIP1R	0.402495756	0.007455391
ENSBTAG00000021596	ICOS	-0.329769323	0.030808801
ENSBTAG00000021601	PARD6B	-0.27745677	0.071648651
ENSBTAG00000021602	CTTNBP2NL	0.238892006	0.122881046
ENSBTAG00000021606	ERCC8	-0.449723984	0.00248136
ENSBTAG00000021607	NDUFAF2	-0.387727352	0.010200913
ENSBTAG00000021609	ADGRF1	-0.278592582	0.070447234
ENSBTAG00000021611	IFTAP	-0.544352254	0.000160985
ENSBTAG00000021614	TASP1	-0.380936848	0.011729307
ENSBTAG00000021617	ZC3HAV1	-0.195006377	0.21015721
ENSBTAG00000021620	PITHD1	-0.590167215	3.11E-05
ENSBTAG00000021630	MTFMT	-0.539149041	0.000191192
ENSBTAG00000021632	MSRA	-0.647136049	2.74E-06
ENSBTAG00000021635	NUDT17	-0.071642325	0.648005867
ENSBTAG00000021636	GPR155	-0.312744461	0.041160644
ENSBTAG00000021639	ARC	0.255883959	0.097680999
ENSBTAG00000021645	MBD4	-0.690346157	3.02E-07
ENSBTAG00000021647	FCAR	0.548206733	0.00014147
ENSBTAG00000021651	UQCRC2	-0.447461339	0.002625076
ENSBTAG00000021656	SPECC1L	-0.287365675	0.061694978
ENSBTAG00000021658	TAMALIN	0.103838662	0.507557338
ENSBTAG00000021663	SMIM8	-0.354342886	0.019736396
ENSBTAG00000021664	TACR2	-0.481224512	0.001087691
ENSBTAG00000021668	METTL4	-0.489173171	0.000872237
ENSBTAG00000021669	SOGA1	-0.049285105	0.753633788
ENSBTAG00000021671	METTL18	-0.560521834	9.26E-05
ENSBTAG00000021672	RGS1	-0.283680862	0.065259079
ENSBTAG00000021673	NDC80	-0.317019856	0.038326509
ENSBTAG00000021677	TRIM37	-0.510515189	0.000469329

ENSBTAG00000021678	SLC31A1	-0.490144992	0.0008487
ENSBTAG00000021680	SKA2	-0.721296688	4.86E-08
ENSBTAG00000021681	PRR11	-0.37640556	0.01285455
ENSBTAG00000021685	EEF1A2	-0.516397029	0.000392788
ENSBTAG00000021686	MELK	-0.610459889	1.38E-05
ENSBTAG00000021687	JADE2	-0.008820477	0.955233146
ENSBTAG00000021693	RPP25	0.148390706	0.342284397
ENSBTAG00000021694	SPAST	-0.643172996	3.30E-06
ENSBTAG00000021695	GLYCTK	-0.014836094	0.924771457
ENSBTAG00000021696	CCIN	-0.042969979	0.784394872
ENSBTAG00000021697	PDGFB	-0.648844141	2.53E-06
ENSBTAG00000021700	MADD	-0.407672231	0.006657507
ENSBTAG00000021703	MED12L	0.360723196	0.017485295
ENSBTAG00000021706	TBX3	-0.223943593	0.148842464
ENSBTAG00000021707	MYBPC3	-0.371605236	0.014145622
ENSBTAG00000021708	CEP128	-0.601895449	1.96E-05
ENSBTAG00000021709	SPI1	0.642349713	3.43E-06
ENSBTAG00000021713	MAMLD1	-0.310653813	0.042607482
ENSBTAG00000021714	TEKT2	-0.193390346	0.214034915
ENSBTAG00000021726	CWC22	0.432786391	0.003747962
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ENSBTAG00000021752	DNAJB4	-0.324014992	0.03403517
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ENSBTAG00000021766	HBEGF	0.430449739	0.003960986
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ENSBTAG00000021772	NA	-0.67657252	6.34E-07
ENSBTAG00000021775	SLC4A9	0.216568083	0.163045163
ENSBTAG00000021776	NDUFV1	-0.143581566	0.358328367
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ENSBTAG00000021779	MGST2	-0.272484066	0.077099997
ENSBTAG00000021787	PAQR7	-0.429504632	0.004050109
ENSBTAG00000021790	APOOL	-0.483327478	0.001026513
ENSBTAG00000021791	PARP9	0.427469774	0.00424796
ENSBTAG00000021798	ERBB2	-0.30467152	0.046977614
ENSBTAG00000021799	RCN3	0.089686367	0.56736433
ENSBTAG00000021801	INPP5F	-0.090745125	0.562780041
ENSBTAG00000021803	GRAMD4	0.575479615	5.41E-05
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ENSBTAG00000021815	STARD13	-0.305451458	0.046388086
ENSBTAG00000021818	ADGRE5	0.555450811	0.00011049
ENSBTAG00000021819	IFNAR1	0.386957086	0.01036522

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ENSBTAG00000021829	GM2A	-0.561399304	8.98E-05
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ENSBTAG00000021837	RGS19	0.425272017	0.004471079
ENSBTAG00000021838	ESRP1	-0.326590103	0.032558553
ENSBTAG00000021841	CHD7	-0.277359717	0.071752055
ENSBTAG00000021842	FCGR2B	0.398323307	0.008157338
ENSBTAG00000021843	UBQLN2	-0.245358768	0.112770225
ENSBTAG00000021846	CELSR3	-0.326730586	0.032479542
ENSBTAG00000021850	NCKIPSD	-0.41084788	0.006205518
ENSBTAG00000021856	R3HCC1L	0.4414925	0.003039911
ENSBTAG00000021857	ARHGAP21	-0.003764033	0.980888376
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ENSBTAG00000021867	BFSP1	-0.282108088	0.066829253
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ENSBTAG00000021879	VCL	-0.19966808	0.199246476
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ENSBTAG00000021884	CXXC1	0.539645827	0.000188101
ENSBTAG00000021887	DPYS	0.519319317	0.000359104
ENSBTAG00000021897	B4GALT3	0.071768283	0.647427434
ENSBTAG00000021899	PDE9A	-0.589034374	3.25E-05
ENSBTAG00000021901	TRPM2	-0.269317827	0.080737122
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ENSBTAG00000021918	EZH1	0.243235592	0.116017657
ENSBTAG00000021919	NAV1	0.520932349	0.000341646
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ENSBTAG00000021932	RNASEK	-0.153265487	0.326480825
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ENSBTAG00000021934	RETSAT	-0.388189001	0.010103511
ENSBTAG00000021939	ELAC2	0.329245169	0.031091808
ENSBTAG00000021940	CCDC149	-0.589252073	3.22E-05
ENSBTAG00000021944	RTRAF	-0.562435583	8.66E-05
ENSBTAG00000021953	LARGE1	-0.429378809	0.004062105

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ENSBTAG00000021964	CDH17	-0.27756187	0.071536807
ENSBTAG00000021965	SUB1	-0.276560626	0.072607916
ENSBTAG00000021967	TMEM168	0.102044239	0.514959966
ENSBTAG00000021968	MID2	0.19170649	0.218127936
ENSBTAG00000021969	KLHL29	-0.221134021	0.154141373
ENSBTAG00000021975	PATJ	-0.31307409	0.040936223
ENSBTAG00000021976	NDUFS1	-0.407365762	0.006702597
ENSBTAG00000021978	PARVB	-0.364063756	0.016395804
ENSBTAG00000021979	EEF1B2	0.065465517	0.676616804
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ENSBTAG00000021992	CAVIN4	0.06713621	0.668831596
ENSBTAG00000021993	SPDEF	-0.121669858	0.437025082
ENSBTAG00000021994	CACNA2D4	-0.17199433	0.270091673
ENSBTAG00000021996	GATAD1	-0.400743829	0.007743503
ENSBTAG00000021997	ITSN1	-0.3608986	0.017426606
ENSBTAG00000021999	CPT1A	0.243924461	0.114956359
ENSBTAG00000022000	CACNB2	-0.577074812	5.10E-05
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ENSBTAG00000022005	TLDC2	0.049354229	0.753299065
ENSBTAG00000022006	TRIM65	0.492722143	0.000789004
ENSBTAG00000022007	SAMHD1	0.04100848	0.794018198
ENSBTAG00000022019	LOC101905136	0.05235693	0.738802689
ENSBTAG00000022022	GUCD1	0.465425715	0.001661022
ENSBTAG00000022027	DDT	-0.14527931	0.352613209
ENSBTAG00000022028	DERL3	-0.064817795	0.679644132
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ENSBTAG00000022039	CMKLR1	-0.005742816	0.970844806
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ENSBTAG00000022109	SCOC	-0.521700642	0.000333603
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ENSBTAG00000022137	NA	0.645458805	2.96E-06
ENSBTAG00000022147	EPS8L2	-0.307585958	0.044805298
ENSBTAG00000022150	NA	-0.138887317	0.374420415
ENSBTAG00000022155	FSTL1	-0.015428919	0.921774566
ENSBTAG00000022161	TLR7	0.077190257	0.622726308
ENSBTAG00000022185	IGHMBP2	0.602576606	1.91E-05
ENSBTAG00000022209	CABP2	-0.022023084	0.8885206
ENSBTAG00000022227	PLSCR2	0.304234183	0.047310827
ENSBTAG00000022238	B4GAT1	-0.45950624	0.001936661
ENSBTAG00000022244	ACTN3	-0.450426983	0.002438141

ENSBTAG00000022275	LOC100337136	0.352410557	0.020464417
ENSBTAG00000022288	AMMECR1	0.520661641	0.000344522
ENSBTAG00000022292	TIMM8A	0.391219517	0.009483689
ENSBTAG00000022294	FADS1	0.147911325	0.343863522
ENSBTAG00000022373	LOC112441455	0.261298955	0.090549266
ENSBTAG00000022381	TET3	0.660185944	1.46E-06
ENSBTAG00000022394	SAA2	0.498138011	0.000675618
ENSBTAG00000022395	LOC104968478	0.57562412	5.38E-05
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ENSBTAG00000022489	LOC509283	0.434628045	0.003587196
ENSBTAG00000022509	DNAH9	-0.545811929	0.000153325
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ENSBTAG00000022520	BRCA1	-0.330847563	0.030233318
ENSBTAG00000022534	NA	0.097093975	0.535657727
ENSBTAG00000022539	POLR2K	0.377940107	0.012463604
ENSBTAG00000022564	AKR1C4	-0.509372125	0.000485671
ENSBTAG00000022570	LOC782922	-0.390884838	0.009550496
ENSBTAG00000022590	NA	0.258986858	0.093543365
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ENSBTAG00000022613	CYCS	-0.105986009	0.498770034
ENSBTAG00000022622	CISH	0.245530452	0.112510677
ENSBTAG00000022632	TCTA	-0.430252938	0.003979402
ENSBTAG00000022635	LAMB2	-0.560723467	9.20E-05
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ENSBTAG00000022715	NA	0.611075751	1.35E-05
ENSBTAG00000022733	EPM2AIP1	-0.232857942	0.132916472
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ENSBTAG00000022779	OLFM4	0.543060628	0.00016805
ENSBTAG00000022799	NOTCH1	0.46590788	0.001640181
ENSBTAG00000022807	KIR3DS1	-0.150366079	0.335824554
ENSBTAG00000022813	TMEM150B	0.569606334	6.70E-05
ENSBTAG00000022825	BRI3	0.326298176	0.032723248
ENSBTAG00000022837	LOC100337093	-0.21597675	0.164225046
ENSBTAG00000022847	HEATR5A	-0.645079158	3.02E-06
ENSBTAG00000022890	MBP	0.175706859	0.259729564
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ENSBTAG00000022895	NA	0.549650785	0.00013473
ENSBTAG00000022920	RNF128	-0.390745766	0.009578375
ENSBTAG00000022927	RAC3	-0.354733722	0.019591825
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ENSBTAG00000022991	NBEA	-0.283406146	0.065531209
ENSBTAG00000023026	LOC281376	0.595178338	2.56E-05
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ENSBTAG00000023106	LOC534913	-0.622929527	8.16E-06
ENSBTAG00000023144	PTPRC	0.584387081	3.88E-05
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ENSBTAG00000023147	LINGO1	-0.00708057	0.964057291
ENSBTAG00000023169	NINL	0.0571789	0.715711109
ENSBTAG00000023179	TRIB1	0.607906829	1.53E-05
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ENSBTAG00000023198	SERPINB2	0.378343572	0.012362515
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ENSBTAG00000023283	JAML	0.334595311	0.028301783
ENSBTAG00000023309	LOC100337390	0.078470322	0.616952539
ENSBTAG00000023338	NA	-0.405743786	0.00694566
ENSBTAG00000023367	LOC101906366	-0.389519633	0.009827212
ENSBTAG00000023375	METTL6	-0.181601813	0.243827174
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ENSBTAG00000023407	NA	-0.179355805	0.249806534
ENSBTAG00000023411	INHCA	-0.185541773	0.233573604
ENSBTAG00000023416	PPP2R3A	-0.444478774	0.002825681
ENSBTAG00000023419	SULT2A1	-0.314465017	0.04000021
ENSBTAG00000023426	FAIM	-0.476359068	0.001241836
ENSBTAG00000023453	C18H19orf54	-0.413627048	0.005832027
ENSBTAG00000023464	NA	-0.48939688	0.000866768
ENSBTAG00000023472	PPP1R14A	-0.261939554	0.089732985
ENSBTAG00000023507	NA	0.327558598	0.032017052
ENSBTAG00000023523	GKAP1	-0.255088867	0.098763561
ENSBTAG00000023551	MOB3C	0.607059939	1.59E-05
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ENSBTAG00000023601	POLR1G	0.062140211	0.692211038
ENSBTAG00000023607	HACD2	0.269339579	0.080711685
ENSBTAG00000023610	U2AF1L4	0.658038025	1.62E-06
ENSBTAG00000023611	ZBTB32	0.08584772	0.584127923
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ENSBTAG00000023648	LOC618664	0.470735638	0.001443938
ENSBTAG00000023652	PROS1	-0.46722208	0.001584549
ENSBTAG00000023659	MT2A	-0.08107377	0.605279995
ENSBTAG00000023675	ZNF654	0.142030954	0.36359694
ENSBTAG00000023730	TUBB3	-0.45583163	0.00212743
ENSBTAG00000023736	CDC42EP3	0.027721079	0.859935269

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ENSBTAG00000023776	NA	-0.316908248	0.038398407
ENSBTAG00000023787	TOR4A	0.310650084	0.042610099
ENSBTAG00000023788	EXD3	-0.05291768	0.73610522
ENSBTAG00000023806	COBL	-0.171459331	0.271607104
ENSBTAG00000023814	ECT2	-0.66904484	9.37E-07
ENSBTAG00000023823	LOC100847700	-0.069486613	0.657936985
ENSBTAG00000023831	ELP4	-0.463518322	0.001745781
ENSBTAG00000023832	ADAM8	0.34309258	0.024299167
ENSBTAG00000023843	RALGPS1	-0.450397423	0.002439945
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ENSBTAG00000023851	FAM102A	0.347603279	0.022373976
ENSBTAG00000023860	NA	-0.622743981	8.22E-06
ENSBTAG00000023867	RC3H2	0.348038148	0.022195316
ENSBTAG00000023891	RBM20	0.026133258	0.867884795
ENSBTAG00000023929	FOSL2	0.451259523	0.002387818
ENSBTAG00000023933	SEC16A	0.458958357	0.001964109
ENSBTAG00000023938	CENPA	0.18912244	0.224513879
ENSBTAG00000023947	AVPI1	0.010564278	0.946394546
ENSBTAG00000023963	RHBDD1	0.41057364	0.006243473
ENSBTAG00000023967	NA	-0.32539883	0.033234948
ENSBTAG00000023970	LOC783508	-0.157075337	0.314453005
ENSBTAG00000023976	ARHGAP25	0.284202943	0.064744387
ENSBTAG00000024015	PTPRM	-0.327013992	0.032320628
ENSBTAG00000024027	TRMT10C	-0.136107084	0.384150694
ENSBTAG00000024042	MORN2	-0.533209203	0.000231873
ENSBTAG00000024091	MALL	-0.249183744	0.107094556
ENSBTAG00000024096	LSM10	-0.194309018	0.211824491
ENSBTAG00000024097	MRPS15	0.507062283	0.000520261
ENSBTAG00000024105	BCL2L11	0.29052776	0.058761725
ENSBTAG00000024107	INPP5B	-0.038215914	0.807770754
ENSBTAG00000024125	LOC100295881	0.275467332	0.07379189
ENSBTAG00000024157	DYNC2I1	-0.330880271	0.030216001
ENSBTAG00000024162	SLC19A1	0.099587634	0.525181151
ENSBTAG00000024177	NA	0.420398652	0.005002596
ENSBTAG00000024199	KMT2C	0.458522174	0.001986206
ENSBTAG00000024219	TRPV6	-0.232003856	0.134384884
ENSBTAG00000024240	ACADM	-0.594023566	2.68E-05
ENSBTAG00000024269	TGFBR3	-0.425830712	0.004413412
ENSBTAG00000024272	NA	0.378512899	0.012320299
ENSBTAG00000024291	GARIN1A	-0.495038059	0.000738589
ENSBTAG00000024378	MRPS21	-0.61870783	9.78E-06
ENSBTAG00000024379	LRRC17	-0.123663139	0.429494073
ENSBTAG00000024387	PNPLA8	0.005880634	0.970145444
ENSBTAG00000024407	LOC787530	0.122386003	0.434310957
ENSBTAG00000024426	PPP1R9A	-0.453673481	0.002247039
ENSBTAG00000024431	PEX1	-0.500350785	0.000633652

ENSBTAG00000024449	CENPF	-0.399990054	0.007870389
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ENSBTAG00000024470	SH2D2A	-0.087041278	0.578891854
ENSBTAG00000024476	CKS1B	-0.441426775	0.003044783
ENSBTAG00000024482	RABGAP1L	-0.171303196	0.272050427
ENSBTAG00000024490	NA	-0.157498256	0.313135362
ENSBTAG00000024492	LOC526769	0.097816329	0.532612511
ENSBTAG00000024493	DHRS3	0.493684153	0.0007677
ENSBTAG00000024496	CELA2A	0.109690789	0.483794588
ENSBTAG00000024503	FCER1G	0.584213879	3.90E-05
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ENSBTAG00000024539	SPSB1	-0.404908781	0.007073736
ENSBTAG00000024561	H3-3A	0.429669332	0.004034453
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ENSBTAG00000024585	NA	-0.517692891	0.000377516
ENSBTAG00000024595	HECA	0.517839575	0.000375821
ENSBTAG00000024603	NCOR2	0.597410735	2.34E-05
ENSBTAG00000024623	LOC782120	-0.518292658	0.00037063
ENSBTAG00000024633	PIK3C2B	-0.380951772	0.011725744
ENSBTAG00000024641	NA	0.350436021	0.021231498
ENSBTAG00000024643	VEPH1	0.086541178	0.581083179
ENSBTAG00000024663	LAD1	-0.297293169	0.052860197
ENSBTAG00000024675	CYSLTR1	0.035856461	0.819435286
ENSBTAG00000024688	PHIP	-0.205877284	0.185341558
ENSBTAG00000024708	CABIN1	-0.242600645	0.117002432
ENSBTAG00000024715	PTPRJ	0.530427619	0.000253485
ENSBTAG00000024726	HJURP	-0.384489109	0.010907028
ENSBTAG00000024751	ULBP17	-0.304411	0.047175878
ENSBTAG00000024756	DENND6B	0.147223485	0.346137137
ENSBTAG00000024803	ENDOD1	-0.427098399	0.004284966
ENSBTAG00000024815	ANKRD28	0.042686956	0.785781492
ENSBTAG00000024822	SETX	0.382742425	0.01130497
ENSBTAG00000024849	LOC100138271	0.297487995	0.052697592
ENSBTAG00000024851	TRIM14	0.236892606	0.126141078
ENSBTAG00000024869	CX3CL1	-0.302480497	0.048666257
ENSBTAG00000024874	NA	-0.39979264	0.007903915
ENSBTAG00000024878	ANKRD31	-0.129064515	0.409455742
ENSBTAG00000024884	CCNF	-0.429129508	0.004085965
ENSBTAG00000024901	LOC509881	0.509704335	0.00048087
ENSBTAG00000024903	KCNJ16	0.255001638	0.098882886
ENSBTAG00000024904	NA	-0.140487496	0.368887272
ENSBTAG00000024909	H3-3B	0.53232558	0.000238551
ENSBTAG00000024915	SECTM1A	0.468902928	0.001515837
ENSBTAG00000024918	BIRC3	0.494308487	0.000754151
ENSBTAG00000024928	TNFRSF1B	0.57470082	5.57E-05
ENSBTAG00000024934	NA	0.515877815	0.000399062
ENSBTAG00000024950	ACE	0.423797461	0.004626444

ENSBTAG00000024958	FAM214A	-0.378765865	0.012257459
ENSBTAG00000024960	LOC512286	0.738442866	1.58E-08
ENSBTAG00000024974	HEXIM2	-0.139840027	0.371120183
ENSBTAG00000024979	HSPB9	0.01597444	0.919017754
ENSBTAG00000024984	FSBP	-0.513013491	0.000435319
ENSBTAG00000025001	MRPL45	-0.209095729	0.17841257
ENSBTAG00000025005	METTL7A	-0.479952006	0.001126266
ENSBTAG00000025009	NA	-0.505489301	0.000545065
ENSBTAG00000025021	LOC614741	0.158877347	0.308863042
ENSBTAG00000025023	NA	0.094042457	0.54861438
ENSBTAG00000025028	NA	-0.395465609	0.008670319
ENSBTAG00000025035	PRLR	-0.310871715	0.042454776
ENSBTAG00000025062	MAGEE2	-0.120072645	0.443112123
ENSBTAG00000025071	TENM2	0.110262795	0.48150355
ENSBTAG00000025078	LRRC75A	-0.086791704	0.579984966
ENSBTAG00000025099	RNF145	0.203929002	0.189627982
ENSBTAG00000025101	ASGR2	-0.254744428	0.099235386
ENSBTAG00000025124	ZNF300	0.005319479	0.972993188
ENSBTAG00000025126	NA	-0.447686771	0.002610436
ENSBTAG00000025129	MNT	0.579831478	4.60E-05
ENSBTAG00000025130	HIC1	0.599932234	2.12E-05
ENSBTAG00000025140	DOC2B	-0.637295224	4.32E-06
ENSBTAG00000025161	AGPAT2	-0.360077818	0.01770267
ENSBTAG00000025167	ABHD15	-0.395613664	0.008643076
ENSBTAG00000025181	CCDC85C	-0.349981419	0.021411478
ENSBTAG00000025182	FBXL21	-0.658313078	1.60E-06
ENSBTAG00000025210	COL4A2	-0.015495757	0.92143675
ENSBTAG00000025213	OMG	0.006458294	0.967214319
ENSBTAG00000025219	LOC100848263	0.424604944	0.004540791
ENSBTAG00000025221	TEX30	-0.054221094	0.72984733
ENSBTAG00000025233	CBARP	0.556028874	0.000108305
ENSBTAG00000025250	CCL3	0.415611155	0.005577465
ENSBTAG00000025257	CCL4	0.40860771	0.006521492
ENSBTAG00000025258	LOC515676	0.42251231	0.004765671
ENSBTAG00000025263	FHIP1A	0.152260972	0.329699417
ENSBTAG00000025274	NA	-0.387086519	0.010337453
ENSBTAG00000025277	ABHD17A	0.472360079	0.001382756
ENSBTAG00000025280	NA	-0.107842241	0.49123727
ENSBTAG00000025308	STON2	-0.708632908	1.06E-07
ENSBTAG00000025310	NA	0.010317908	0.947642935
ENSBTAG00000025320	AKAP1	0.548957843	0.000137927
ENSBTAG00000025329	IRF2BPL	0.603354318	1.85E-05
ENSBTAG00000025345	ARL10	-0.714515299	7.40E-08
ENSBTAG00000025391	NA	0.316202684	0.038855495
ENSBTAG00000025398	LOC504548	-0.195173241	0.209759622
ENSBTAG00000025401	DOK3	0.506772767	0.000524749
ENSBTAG00000025405	BATF	0.498561001	0.000667409

ENSBTAG00000025424	NOTCH4	0.103334695	0.509630932
ENSBTAG00000025425	RAB24	0.569744188	6.67E-05
ENSBTAG00000025441	HSPA1A	0.484678786	0.000988838
ENSBTAG00000025442	HSPA1L	0.428139328	0.004181947
ENSBTAG00000025443	FNIP1	0.396638492	0.008456514
ENSBTAG00000025445	LOC789148	0.402172528	0.00750784
ENSBTAG00000025450	SYNE2	0.470422454	0.001456006
ENSBTAG00000025452	SF3A2	0.316396522	0.038729479
ENSBTAG00000025458	DPF3	-0.489638727	0.00086089
ENSBTAG00000025462	GADD45B	0.515500087	0.000403682
ENSBTAG00000025471	TNF	0.512451028	0.000442776
ENSBTAG00000025477	KIF3A	-0.316660215	0.038558587
ENSBTAG00000025494	PAQR8	0.586551905	3.57E-05
ENSBTAG00000025496	SORD	-0.317946752	0.037733643
ENSBTAG00000025516	GNL1	0.198079748	0.202918256
ENSBTAG00000025526	MDC1	-0.158006551	0.311556364
ENSBTAG00000025540	ALKBH7	-0.255047254	0.098820473
ENSBTAG00000025597	GRIN3B	0.05818351	0.710930783
ENSBTAG00000025604	NA	0.06428693	0.682129007
ENSBTAG00000025622	DEF6	-0.082531815	0.598784782
ENSBTAG00000025642	NA	-0.034347503	0.826915578
ENSBTAG00000025644	CALM1	0.549374915	0.000135995
ENSBTAG00000025659	ZNF618	-0.227697795	0.141972602
ENSBTAG00000025664	RNASE2	0.503998398	0.000569548
ENSBTAG00000025666	LOC112448430	0.213421644	0.169394445
ENSBTAG00000025752	P3H4	-0.609041262	1.46E-05
ENSBTAG00000025756	LOC528919	0.088209523	0.573787491
ENSBTAG00000025762	CNP	0.538888008	0.000192834
ENSBTAG00000025775	INSL3	0.130858915	0.402919269
ENSBTAG00000025778	EMC9	-0.525416041	0.000297059
ENSBTAG00000025782	TNFSF8	0.523235626	0.000318041
ENSBTAG00000025803	INSYN1	-0.157951999	0.311725586
ENSBTAG00000025809	ABHD8	-0.367969322	0.015195372
ENSBTAG00000025812	NA	0.443199286	0.002915788
ENSBTAG00000025822	CALML4	-0.569211242	6.80E-05
ENSBTAG00000025826	SLC24A1	0.044821587	0.775339687
ENSBTAG00000025830	R3HCC1	-0.71840628	5.82E-08
ENSBTAG00000025848	RBM3	-0.129023776	0.409604843
ENSBTAG00000025853	HOMER1	0.05999035	0.702360731
ENSBTAG00000025856	JMY	-0.030867611	0.844223002
ENSBTAG00000025868	TLN1	0.526095879	0.000290778
ENSBTAG00000025898	TBC1D8	0.363940232	0.016435043
ENSBTAG00000025903	GLDC	-0.531120861	0.000247935
ENSBTAG00000025931	NEU3	-0.468852678	0.001517852
ENSBTAG00000025942	HPGD	-0.342188466	0.024701219
ENSBTAG00000025953	NA	0.422627873	0.004753003
ENSBTAG00000025964	MAST4	-0.359360073	0.017947093

ENSBTAG00000026008	METTL5	-0.58634565	3.60E-05
ENSBTAG00000026032	ZYG11A	-0.108941826	0.486802967
ENSBTAG00000026067	SH2D1A	-0.378197453	0.012399045
ENSBTAG00000026070	LOC107131273	0.583544767	4.00E-05
ENSBTAG00000026080	LAIR1	0.639433187	3.92E-06
ENSBTAG00000026097	LIMD1	-0.070069751	0.655244703
ENSBTAG00000026111	LBH	-0.351435624	0.020840206
ENSBTAG00000026114	UBE2F	-0.389285195	0.009875416
ENSBTAG00000026141	NA	-0.269171812	0.080908032
ENSBTAG00000026148	LOC100300051	0.423156218	0.004695464
ENSBTAG00000026156	VGLL3	-0.217186901	0.161817046
ENSBTAG00000026172	LRATD2	0.144253293	0.356060441
ENSBTAG00000026180	NA	-0.431494399	0.003864475
ENSBTAG00000026181	UGT1A6	-0.412086486	0.006036577
ENSBTAG00000026192	NA	0.575826358	5.34E-05
ENSBTAG00000026199	ACTB	0.583696881	3.98E-05
ENSBTAG00000026232	NA	-0.627497061	6.69E-06
ENSBTAG00000026233	NA	0.251552695	0.103690303
ENSBTAG00000026234	STK3	0.483527905	0.001020846
ENSBTAG00000026236	AZGP1	-0.329463132	0.030973863
ENSBTAG00000026248	POP7	-0.217968855	0.160274796
ENSBTAG00000026254	MED30	0.113047361	0.470432306
ENSBTAG00000026275	CCL24	-0.224416533	0.14796382
ENSBTAG00000026278	CLDN4	-0.345655648	0.023188966
ENSBTAG00000026283	ASPH	-0.586425779	3.59E-05
ENSBTAG00000026286	GTF2IRD2	-0.191748978	0.218023996
ENSBTAG00000026307	ZNF629	-0.29014814	0.059107869
ENSBTAG00000026309	ZHX2	0.106561458	0.496428505
ENSBTAG00000026326	SPN	0.346679436	0.02275752
ENSBTAG00000026340	LOC101905222	0.082060235	0.600882221
ENSBTAG00000026356	DGAT1	0.394167801	0.0089123
ENSBTAG00000026369	ENC1	0.18225767	0.242099555
ENSBTAG00000026371	SNX29	-0.190679771	0.220650037
ENSBTAG00000026375	RMI2	-0.363791676	0.016482338
ENSBTAG00000026376	NA	0.543179245	0.00016739
ENSBTAG00000026394	UBALD1	0.503448343	0.000578827
ENSBTAG00000026403	CREBBP	0.543513446	0.000165542
ENSBTAG00000026417	NA	0.172203267	0.269501361
ENSBTAG00000026418	NA	0.210433407	0.175587983
ENSBTAG00000026429	DECR2	-0.552165365	0.000123684
ENSBTAG00000026437	NA	-0.061525086	0.695109762
ENSBTAG00000026461	CACNA1H	-0.088930223	0.570648846
ENSBTAG00000026497	A4GALT	-0.146860625	0.347340257
ENSBTAG00000026501	MGC127055	0.534634195	0.000221459
ENSBTAG00000026502	CYP2D14	0.686411419	3.75E-07
ENSBTAG00000026505	LOC539789	-0.46233989	0.00180004
ENSBTAG00000026527	NA	-0.302879499	0.048355141

ENSBTAG00000026531	NA	0.079931489	0.610389683
ENSBTAG00000026580	HTR1E	-0.499423372	0.000650948
ENSBTAG00000026586	PPP1R14C	-0.223571822	0.149535838
ENSBTAG00000026604	LYRM2	-0.682786814	4.56E-07
ENSBTAG00000026613	MSTO1	-0.296826738	0.053251127
ENSBTAG00000026624	ETFRF1	-0.49087303	0.000831441
ENSBTAG00000026637	CCDC162P	0.010520404	0.94661685
ENSBTAG00000026645	LOC526787	0.360283449	0.017633164
ENSBTAG00000026657	IFT27	-0.360258588	0.017641555
ENSBTAG00000026673	KPNA5	-0.320634132	0.036057059
ENSBTAG00000026676	SDC3	0.501576499	0.000611425
ENSBTAG00000026704	CENPW	-0.414093547	0.005771286
ENSBTAG00000026716	IBTK	-0.303514773	0.047863117
ENSBTAG00000026753	CXCR1	0.501983319	0.000604204
ENSBTAG00000026754	RNF41	0.52601268	0.00029154
ENSBTAG00000026758	LOC788425	-0.237418152	0.125277957
ENSBTAG00000026768	TH	-0.017046787	0.913601367
ENSBTAG00000026769	ASCL2	0.299561137	0.050992125
ENSBTAG00000026772	ZNF142	-0.161462634	0.300954498
ENSBTAG00000026779	LYZ	0.431106769	0.003900044
ENSBTAG00000026796	LOC507756	0.114227094	0.465782933
ENSBTAG00000026812	AOX2	-0.582860127	4.11E-05
ENSBTAG00000026819	HDAC7	0.08411153	0.591782138
ENSBTAG00000026825	TMEM37	-0.528527821	0.000269274
ENSBTAG00000026842	ZRANB3	-0.521533793	0.000335335
ENSBTAG00000026851	FMNL2	-0.475194678	0.001281488
ENSBTAG00000026882	NA	-0.590583007	3.06E-05
ENSBTAG00000026893	EXOC3L4	-0.169346834	0.277645631
ENSBTAG00000026915	NEK1	-0.702609215	1.50E-07
ENSBTAG00000026916	PRR13	-0.431978458	0.003820456
ENSBTAG00000026919	PXDC1	-0.186906985	0.230090395
ENSBTAG00000026936	ZGRF1	-0.620121659	9.20E-06
ENSBTAG00000026944	NA	0.554664505	0.000113526
ENSBTAG00000026962	XPOT	-0.435276003	0.003532087
ENSBTAG00000026963	NCALD	-0.254467255	0.099616324
ENSBTAG00000026971	CDCA5	-0.13664781	0.382246682
ENSBTAG00000026986	NA	0.270999842	0.078788612
ENSBTAG00000026993	TMBIM4	0.391854467	0.009358045
ENSBTAG00000027024	ARHGAP5	-0.009039791	0.95412122
ENSBTAG00000027049	SDHAF4	-0.281426523	0.067518924
ENSBTAG00000027051	PTAFR	0.605584671	1.69E-05
ENSBTAG00000027059	ARPIN	-0.541914361	0.000174554
ENSBTAG00000027064	BTBD11	0.561615646	8.91E-05
ENSBTAG00000027074	SV2B	-0.364906542	0.016130192
ENSBTAG00000027081	ATP10A	-0.129443686	0.408069496
ENSBTAG00000027126	MUC15	-0.083649488	0.593826551
ENSBTAG00000027151	ARHGAP26	-0.370739586	0.014389791

ENSBTAG00000027173	CHP1	0.232581019	0.133391264
ENSBTAG00000027181	LAMA3	-0.14686299	0.34733241
ENSBTAG00000027182	NR3C2	0.065413931	0.676857721
ENSBTAG00000027201	RAPH1	-0.040861475	0.794740657
ENSBTAG00000027204	LOC100300510	-0.405308478	0.007012177
ENSBTAG00000027205	PGBD5	-0.049100865	0.754526169
ENSBTAG00000027225	NA	0.223934034	0.148860261
ENSBTAG00000027246	UBD	-0.033216182	0.832533801
ENSBTAG00000027317	RNF114	0.362303927	0.016962372
ENSBTAG00000027319	NA	0.515381468	0.000405143
ENSBTAG00000027321	CCDC18	-0.588497593	3.32E-05
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ENSBTAG00000027327	OCSTAMP	0.597401232	2.34E-05
ENSBTAG00000027337	CTSA	0.068669652	0.661715989
ENSBTAG00000027348	OOSP2	-0.264920311	0.086009544
ENSBTAG00000027386	SOX12	0.192152819	0.217037787
ENSBTAG00000027397	PPP1R3D	0.336781012	0.027223354
ENSBTAG00000027407	TNFRSF6B	0.248452246	0.10816278
ENSBTAG00000027412	NA	-0.668706408	9.53E-07
ENSBTAG00000027438	NA	-0.369223281	0.014826112
ENSBTAG00000027442	NFIB	-0.31710994	0.038268556
ENSBTAG00000027444	SVIL	0.196915844	0.20563883
ENSBTAG00000027446	RSU1	-0.643444786	3.26E-06
ENSBTAG00000027464	FGFRL1	-0.578394584	4.86E-05
ENSBTAG00000027513	CXCL2	0.163289141	0.29544613
ENSBTAG00000027557	ZNF408	0.536747007	0.000206794
ENSBTAG00000027569	APBB2	-0.270857647	0.078951897
ENSBTAG00000027626	GOLGA7	0.418562178	0.005216708
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ENSBTAG00000027642	C15H11orf42	0.499977761	0.000640559
ENSBTAG00000027655	NA	0.355217782	0.019414004
ENSBTAG00000027665	BRF2	0.531811827	0.000242513
ENSBTAG00000027676	IL18BP	0.019815003	0.899637637
ENSBTAG00000027684	FOLR2	-0.65472334	1.91E-06
ENSBTAG00000027694	TTC30A	-0.136617523	0.382353181
ENSBTAG00000027713	LYSMD3	0.386199232	0.010529088
ENSBTAG00000027715	LOC101906134	-0.441506412	0.003038881
ENSBTAG00000027722	IPO7	-0.226612872	0.143933356
ENSBTAG00000027728	NUDT12	-0.626018855	7.13E-06
ENSBTAG00000027760	NA	0.508124631	0.000504087
ENSBTAG00000027764	EID1	-0.551831371	0.000125102
ENSBTAG00000027766	C1QTNF5	-0.198934352	0.200936798
ENSBTAG00000027795	GFM1	-0.538212337	0.000197145
ENSBTAG00000027803	NA	0.237873254	0.124534116
ENSBTAG00000027809	RABGAP1L	0.336225332	0.027494237
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ENSBTAG00000027916	MALT1	0.557328735	0.000103536
ENSBTAG00000027923	NA	-0.139662385	0.371734221
ENSBTAG00000027924	SNX18	0.000729454	0.996295921
ENSBTAG00000027937	NA	0.524722932	0.00030359
ENSBTAG00000028359	LOC112442867	-0.286858625	0.062176004
ENSBTAG00000028421	LOC112442826	0.520844146	0.000342581
ENSBTAG00000028443	LOC112443528	-0.184503142	0.236247557
ENSBTAG00000028704	NA	-0.162345822	0.298282814
ENSBTAG00000029237	NA	-0.671385772	8.31E-07
ENSBTAG00000029683	LOC112449179	-0.366396867	0.015669412
ENSBTAG00000029765	NA	0.487417068	0.00091625
ENSBTAG00000029803	MIR221	0.350798648	0.021088842
ENSBTAG00000029828	MIR421	0.180670866	0.246293701
ENSBTAG00000029830	MIR146A	0.29280682	0.056717565
ENSBTAG00000029855	MIR101-1	0.303190377	0.048113855
ENSBTAG00000029897	MIR21	0.097180996	0.535290426
ENSBTAG00000029901	MIR23A	0.528920499	0.00026594
ENSBTAG00000029904	MIR222	0.227863784	0.141674363
ENSBTAG00000029905	NA	0.430862085	0.003922643
ENSBTAG00000029930	MIR22	0.359083498	0.018042036
ENSBTAG00000029942	NA	0.477872492	0.00119193
ENSBTAG00000029982	MIR142	0.233547068	0.131740419
ENSBTAG00000029994	MIRLET7I	0.100896087	0.519724662
ENSBTAG00000029996	MIR27A	0.445277796	0.00277066
ENSBTAG00000030071	MIR24-2	0.337999789	0.026636981
ENSBTAG00000030124	NA	0.050899202	0.745829461
ENSBTAG00000030162	AXIN2	-0.485368789	0.00097008
ENSBTAG00000030168	MIF4GD	0.652976518	2.08E-06
ENSBTAG00000030172	PRPSAP1	0.166376483	0.286284115
ENSBTAG00000030173	QRICH2	0.32496707	0.033482938
ENSBTAG00000030175	FBF1	-0.209972365	0.17655785
ENSBTAG00000030179	MAPK8IP2	-0.504384496	0.000563115
ENSBTAG00000030180	SHANK3	-0.071910756	0.646773406
ENSBTAG00000030182	MAPK11	0.24739993	0.109713719
ENSBTAG00000030190	COL6A3	0.272694261	0.07686317
ENSBTAG00000030193	GPR35	0.546270563	0.000150988
ENSBTAG00000030198	TMEM232	-0.354308584	0.019749128
ENSBTAG00000030227	NA	-0.281798589	0.067141737
ENSBTAG00000030230	NA	0.325312769	0.033284258
ENSBTAG00000030246	ENTPD8	-0.213907244	0.168403065
ENSBTAG00000030247	NSMF	0.382941707	0.01125895
ENSBTAG00000030255	PDXP	-0.296322871	0.053676043
ENSBTAG00000030257	SH3BP1	0.010756324	0.945421515
ENSBTAG00000030258	CDC42EP1	-0.654397336	1.94E-06
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ENSBTAG00000030317	PPP1R26	-0.229348505	0.139027307

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ENSBTAG00000030322	NA	0.028906578	0.854008849
ENSBTAG00000030334	AOC2	0.123880317	0.428677941
ENSBTAG00000030335	ALDH4A1	0.233904811	0.131132969
ENSBTAG00000030340	IFFO2	-0.246655741	0.110820704
ENSBTAG00000030347	TUBG2	-0.594138414	2.66E-05
ENSBTAG00000030369	IFFO1	0.164255035	0.292559647
ENSBTAG00000030393	RDH13	0.07061435	0.652734245
ENSBTAG00000030416	LOC538810	0.547875687	0.000143058
ENSBTAG00000030424	CLEC1A	0.036664428	0.815436435
ENSBTAG00000030425	ID3	0.124460872	0.426500552
ENSBTAG00000030426	LOC100848575	-0.18761047	0.228309479
ENSBTAG00000030432	TTC8	-0.752312197	6.00E-09
ENSBTAG00000030434	FUCA1	-0.567801415	7.15E-05
ENSBTAG00000030435	PNRC2	-0.464510964	0.001701205
ENSBTAG00000030439	NA	0.384886679	0.010818145
ENSBTAG00000030456	SPATA7	-0.562481846	8.64E-05
ENSBTAG00000030503	H2AJ	0.548516067	0.000140001
ENSBTAG00000030507	LOC783993	-0.649633111	2.43E-06
ENSBTAG00000030517	SMIM33	-0.016277961	0.9174843
ENSBTAG00000030518	ECSCR	0.336100113	0.027555587
ENSBTAG00000030521	IER5L	0.469872013	0.001477433
ENSBTAG00000030523	ZPBP2	-0.327880718	0.031838605
ENSBTAG00000030533	NA	-0.340980197	0.025247173
ENSBTAG00000030543	SLC6A16	0.031036949	0.843379043
ENSBTAG00000030556	ZNF217	0.024583667	0.875655351
ENSBTAG00000030563	PRRG2	-0.605857169	1.67E-05
ENSBTAG00000030566	GLE1	-0.567531514	7.22E-05
ENSBTAG00000030575	BHLHE41	0.115452418	0.460980024
ENSBTAG00000030578	PTOV1	-0.337878857	0.02669469
ENSBTAG00000030589	TMCO6	0.583789795	3.97E-05
ENSBTAG00000030593	RFTN1	-0.278129666	0.070934953
ENSBTAG00000030608	NA	-0.488075364	0.000899525
ENSBTAG00000030632	ALG10	-0.649528615	2.45E-06
ENSBTAG00000030646	KCTD17	-0.094143854	0.548181472
ENSBTAG00000030650	TST	-0.520074019	0.000350838
ENSBTAG00000030667	ODAD1	-0.404798612	0.007090786
ENSBTAG00000030670	PCNT	-0.532451419	0.000237589
ENSBTAG00000030671	HOOK1	-0.013210903	0.932992387
ENSBTAG00000030674	AK4	-0.287393686	0.061668492
ENSBTAG00000030675	PDCL	0.488668888	0.000884679
ENSBTAG00000030690	RADIL	-0.156435402	0.316453439
ENSBTAG00000030704	NA	0.466572258	0.001611845
ENSBTAG00000030706	ALG6	-0.545082571	0.00015711
ENSBTAG00000030710	ITGB3BP	-0.465804253	0.001644641
ENSBTAG00000030735	NA	-0.26951799	0.08050329
ENSBTAG00000030749	DNAJC6	0.155813363	0.318405622

ENSBTAG00000030757	ELFN1	-0.29244256	0.057040401
ENSBTAG00000030769	KPTN	-0.15649831	0.316256433
ENSBTAG00000030775	PCBP3	-0.617881802	1.01E-05
ENSBTAG00000030805	NA	-0.492384311	0.00079661
ENSBTAG00000030820	NT5M	-0.517301727	0.000382069
ENSBTAG00000030824	L3HYPDH	-0.540347948	0.00018381
ENSBTAG00000030836	ZBTB21	0.511596968	0.00045432
ENSBTAG00000030838	LOC112446467	0.13536696	0.386765866
ENSBTAG00000030845	MPEG1	0.595613623	2.51E-05
ENSBTAG00000030855	CHCHD6	-0.405683	0.006954916
ENSBTAG00000030864	FAM228B	-0.322262093	0.035071501
ENSBTAG00000030885	SSC5D	-0.252426813	0.102455303
ENSBTAG00000030892	LOC790134	0.135647469	0.385773482
ENSBTAG00000030897	XRCC2	-0.032209325	0.837540871
ENSBTAG00000030898	MS4A13	-0.304081697	0.047427458
ENSBTAG00000030913	MX1	0.275977973	0.073237018
ENSBTAG00000030921	FAM3B	0.442355228	0.002976603
ENSBTAG00000030930	HMCES	0.110098894	0.482159435
ENSBTAG00000030932	IFI44L	0.149015563	0.340232776
ENSBTAG00000030939	ZNF575	-0.42762775	0.004232304
ENSBTAG00000030940	GIMAP7	-0.212954569	0.170351976
ENSBTAG00000030951	ZNF655	0.636495177	4.48E-06
ENSBTAG00000030962	EEFSEC	0.142819209	0.360912852
ENSBTAG00000030965	MCM7	-0.127875561	0.413819993
ENSBTAG00000030973	TUBA1D	0.132091816	0.398463291
ENSBTAG00000030974	TUBA4A	0.300006873	0.050631318
ENSBTAG00000030977	ULK2	-0.669089142	9.35E-07
ENSBTAG00000030999	NA	-0.240690671	0.120002818
ENSBTAG00000031001	MEGF8	-0.406845622	0.006779729
ENSBTAG00000031010	ACAD11	-0.44631775	0.002700461
ENSBTAG00000031012	PIGK	-0.500203387	0.000636374
ENSBTAG00000031014	LDAH	-0.670138964	8.86E-07
ENSBTAG00000031020	TLR8	0.380398008	0.011858547
ENSBTAG00000031031	OR10P1	0.279496554	0.069502466
ENSBTAG00000031044	MIGA1	-0.681499431	4.89E-07
ENSBTAG00000031059	LRRC61	-0.334506793	0.028346194
ENSBTAG00000031069	SNX24	-0.441098999	0.003069178
ENSBTAG00000031071	ZNF624	-0.55246554	0.000122422
ENSBTAG00000031076	NA	-0.764066603	2.50E-09
ENSBTAG00000031082	NA	-0.144480842	0.35529416
ENSBTAG00000031134	YWHAH	-0.385146366	0.010760422
ENSBTAG00000031160	NA	-0.295065699	0.054748118
ENSBTAG00000031166	ZDBF2	0.048439084	0.757734144
ENSBTAG00000031178	SLC9A9	-0.526884993	0.000283636
ENSBTAG00000031184	CDKN1C	-0.270425631	0.079449615
ENSBTAG00000031185	ATRAID	-0.499295937	0.000653357
ENSBTAG00000031209	SLC22A4	-0.042310508	0.787626841

ENSBTAG00000031214	LOC618409	0.50818742	0.000503146
ENSBTAG00000031217	MYL6B	-0.326209889	0.032773191
ENSBTAG00000031231	IRF1	0.465354556	0.001664117
ENSBTAG00000031242	NA	-0.662476059	1.30E-06
ENSBTAG00000031249	PSMG4	-0.606091286	1.65E-05
ENSBTAG00000031252	CD82	0.455415157	0.002150064
ENSBTAG00000031256	NA	0.339859875	0.025762335
ENSBTAG00000031261	REPS2	-0.519732247	0.00035456
ENSBTAG00000031265	SVOPL	0.363010403	0.01673297
ENSBTAG00000031279	SELENOM	-0.35830664	0.018310982
ENSBTAG00000031287	TMEM158	0.433118727	0.003718494
ENSBTAG00000031295	HSDL2	-0.395348185	0.008691978
ENSBTAG00000031327	TRMT61A	0.411482184	0.006118497
ENSBTAG00000031332	RBKS	0.004523431	0.977033525
ENSBTAG00000031335	BABAM2	-0.469077482	0.001508855
ENSBTAG00000031340	SLC6A20	0.283950861	0.064992497
ENSBTAG00000031348	CCR9	-0.222783856	0.15101328
ENSBTAG00000031352	ZNF554	-0.21522169	0.165740594
ENSBTAG00000031355	LOC529196	0.428864888	0.004111426
ENSBTAG00000031358	DPYD	0.153755048	0.324919357
ENSBTAG00000031359	NA	-0.188035899	0.227237075
ENSBTAG00000031363	TLE5	-0.036780669	0.814861508
ENSBTAG00000031385	COP1	0.593341117	2.75E-05
ENSBTAG00000031387	FZR1	0.561778801	8.86E-05
ENSBTAG00000031396	NA	0.4441317	0.002849879
ENSBTAG00000031397	NA	0.525246299	0.000298647
ENSBTAG00000031402	ASXL1	0.558033631	0.00010103
ENSBTAG00000031430	NA	0.12325516	0.431029559
ENSBTAG00000031433	TEX9	-0.385463577	0.010690272
ENSBTAG00000031439	CDC14A	0.005652947	0.971300863
ENSBTAG00000031441	FXYD5	0.589190698	3.23E-05
ENSBTAG00000031444	LY86	0.507117254	0.000519413
ENSBTAG00000031447	PRSS45	-0.067390622	0.667649045
ENSBTAG00000031453	CCM2L	0.285376664	0.063599047
ENSBTAG00000031461	SNX7	-0.350105264	0.02136232
ENSBTAG00000031462	FAM209A	0.051274051	0.744020585
ENSBTAG00000031468	LOC614881	0.728746906	3.02E-08
ENSBTAG00000031476	DLL1	0.546483054	0.000149915
ENSBTAG00000031483	NA	0.550656918	0.000130207
ENSBTAG00000031497	FGFBP1	-0.120544341	0.441309634
ENSBTAG00000031500	SHMT2	-0.408837978	0.006488383
ENSBTAG00000031503	NDUFA4L2	-0.299121241	0.051350235
ENSBTAG00000031509	PFAS	-0.332613484	0.029310024
ENSBTAG00000031519	NGP	0.415227376	0.005625937
ENSBTAG00000031524	NA	0.305808983	0.046119858
ENSBTAG00000031544	DDIT3	0.541513733	0.00017688
ENSBTAG00000031548	LOC514257	0.660839016	1.41E-06

ENSBTAG00000031553	SLC49A3	-0.180625819	0.246413477
ENSBTAG00000031558	NA	0.490530539	0.000839521
ENSBTAG00000031561	RSRC1	-0.610375981	1.39E-05
ENSBTAG00000031569	GOLM1	-0.349464636	0.021617628
ENSBTAG00000031572	IFT80	-0.574066892	5.70E-05
ENSBTAG00000031575	VAV3	-0.592585786	2.83E-05
ENSBTAG00000031579	SGO2	-0.552858599	0.000120787
ENSBTAG00000031590	SSH3	0.006458363	0.96721397
ENSBTAG00000031595	FTCDNL1	-0.368820795	0.014943796
ENSBTAG00000031598	NIPSNAP2	-0.538785516	0.000193483
ENSBTAG00000031648	NA	-0.11599325	0.458868631
ENSBTAG00000031655	NA	-0.458222441	0.002001518
ENSBTAG00000031673	ARRDC5	-0.023340382	0.881898302
ENSBTAG00000031682	NA	-0.484040385	0.001006481
ENSBTAG00000031696	ANKRD44	0.382800764	0.011291481
ENSBTAG00000031697	KLHDC1	-0.650062796	2.39E-06
ENSBTAG00000031701	TAGAP	0.609313518	1.45E-05
ENSBTAG00000031707	FRMD6	-0.11697749	0.455039619
ENSBTAG00000031711	NA	-0.58705136	3.51E-05
ENSBTAG00000031715	PCMTD2	-0.485194198	0.000974796
ENSBTAG00000031718	OGFR	0.645409365	2.97E-06
ENSBTAG00000031725	TNFSF12	-0.090259999	0.564878439
ENSBTAG00000031731	HIGD1A	0.183099686	0.239893752
ENSBTAG00000031746	NA	0.314441984	0.040015566
ENSBTAG00000031749	SLC35E2	-0.295797773	0.054121759
ENSBTAG00000031750	PLAC8B	0.459668138	0.001928616
ENSBTAG00000031752	TMEM256	-0.4658335	0.001643381
ENSBTAG00000031753	BTN1A1	-0.217085621	0.162017586
ENSBTAG00000031756	NA	0.54315989	0.000167497
ENSBTAG00000031773	NA	0.310184164	0.042938132
ENSBTAG00000031777	GDPD5	-0.373302251	0.013677155
ENSBTAG00000031778	H2BC5	0.628576315	6.38E-06
ENSBTAG00000031785	NA	0.480289609	0.001115915
ENSBTAG00000031789	FBRS	0.462224868	0.001805415
ENSBTAG00000031795	NA	0.608640715	1.49E-05
ENSBTAG00000031797	MANF	0.439148439	0.003217929
ENSBTAG00000031800	PPDPF	-0.5101713	0.000474193
ENSBTAG00000031806	ZNF48	-0.478739358	0.001164154
ENSBTAG00000031809	DENND1C	0.040616267	0.795946116
ENSBTAG00000031810	WDR88	-0.115636155	0.460262135
ENSBTAG00000031814	SDS	0.466070327	0.001633212
ENSBTAG00000031837	IMPDH2	-0.519564413	0.000356401
ENSBTAG00000031849	TMEM119	0.397652525	0.008275339
ENSBTAG00000031851	SELPLG	0.546420681	0.000150229
ENSBTAG00000031852	TBC1D10B	0.544354009	0.000160976
ENSBTAG00000031863	NA	-0.360237109	0.017648807
ENSBTAG00000031869	ZSCAN26	-0.50696431	0.000521776

ENSBTAG00000031873	ZSCAN16	-0.546031763	0.000152201
ENSBTAG00000031874	ZNF165	0.016184182	0.917958062
ENSBTAG00000031885	TMEM251	-0.092005563	0.557345053
ENSBTAG00000031886	H2BC15	0.555133426	0.000111706
ENSBTAG00000031889	NA	0.627242274	6.76E-06
ENSBTAG00000031895	TFB1M	0.438271751	0.00328682
ENSBTAG00000031905	LOC107131731	0.520899039	0.000341999
ENSBTAG00000031916	NA	-0.444639655	0.002814526
ENSBTAG00000031933	ALOX12E	-0.114735246	0.463787887
ENSBTAG00000031940	RSBN1	0.168807972	0.279199937
ENSBTAG00000031941	PEPD	-0.11208642	0.474237572
ENSBTAG00000031950	RAB3IP	0.520412386	0.000347188
ENSBTAG00000031962	NA	0.605787262	1.67E-05
ENSBTAG00000031993	NA	-0.324136851	0.033964073
ENSBTAG00000031998	CXCL16	0.251693447	0.103490676
ENSBTAG00000032007	LRP11	-0.269508414	0.080514465
ENSBTAG00000032014	NA	0.086401145	0.581697439
ENSBTAG00000032017	NA	-0.226520473	0.144101265
ENSBTAG00000032018	ZNF19	-0.740558745	1.37E-08
ENSBTAG00000032031	ZBTB12	0.428351848	0.004161183
ENSBTAG00000032047	LOC100296211	-0.193621884	0.213476306
ENSBTAG00000032051	SULT1C4	-0.23231634	0.133846243
ENSBTAG00000032068	PLA2G4F	-0.254075975	0.100155998
ENSBTAG00000032071	SYCP1	0.15497032	0.321063486
ENSBTAG00000032084	GPR183	-0.017998051	0.908799786
ENSBTAG00000032089	CDC42EP2	0.187357284	0.228949342
ENSBTAG00000032121	SUGCT	-0.313998562	0.04031214
ENSBTAG00000032122	CD19	-0.170642725	0.273931003
ENSBTAG00000032125	NA	0.079009932	0.614525403
ENSBTAG00000032137	PNPLA6	-0.025605533	0.870529778
ENSBTAG00000032140	SBK1	-0.050054132	0.749912389
ENSBTAG00000032152	TMPRSS6	-0.272281096	0.077329227
ENSBTAG00000032156	NA	-0.205379852	0.186429343
ENSBTAG00000032163	LTV1	0.464298449	0.001710663
ENSBTAG00000032166	GTPBP10	-0.496927641	0.000699609
ENSBTAG00000032183	NELL2	-0.34621141	0.022953915
ENSBTAG00000032200	NA	-0.558285112	0.000100149
ENSBTAG00000032209	CXHXorf65	0.457235409	0.002052679
ENSBTAG00000032253	RAD54L2	0.242621507	0.116969977
ENSBTAG00000032260	DCUN1D3	0.568020103	7.10E-05
ENSBTAG00000032265	RTP4	0.099375643	0.526067841
ENSBTAG00000032277	KYNU	0.475086854	0.001285216
ENSBTAG00000032281	LOC515547	0.468035012	0.00155098
ENSBTAG00000032288	GCK	-0.258968334	0.093567657
ENSBTAG00000032289	ARHGAP15	0.451976756	0.0023452
ENSBTAG00000032304	ACY1	-0.261410921	0.090406182
ENSBTAG00000032331	SLC48A1	-0.589591926	3.18E-05

ENSBTAG00000032340	KNSTRN	-0.645767553	2.92E-06
ENSBTAG00000032364	NA	-0.453220326	0.002272895
ENSBTAG00000032366	SLC23A2	0.032611413	0.835540529
ENSBTAG00000032369	NMI	0.455835221	0.002127236
ENSBTAG00000032372	HASPIN	-0.573174419	5.89E-05
ENSBTAG00000032373	LOC101905757	0.217168239	0.161853983
ENSBTAG00000032374	SELENOK	0.457874581	0.002019419
ENSBTAG00000032396	KCTD19	0.259462795	0.092920873
ENSBTAG00000032425	NA	-0.543470376	0.000165779
ENSBTAG00000032427	FHOD1	0.419765498	0.005075534
ENSBTAG00000032433	DENR	0.136761767	0.381846125
ENSBTAG00000032450	NA	0.138689244	0.375108736
ENSBTAG00000032455	H2BC18	-0.173702238	0.265291294
ENSBTAG00000032493	RETREG3	0.384638332	0.010873594
ENSBTAG00000032503	ITPRIPL2	0.417633334	0.005328004
ENSBTAG00000032515	PLA2R1	-0.695443706	2.27E-07
ENSBTAG00000032518	SPRED1	0.341902869	0.024829369
ENSBTAG00000032531	MUSTN1	-0.194576217	0.211184574
ENSBTAG00000032534	RHOF	0.031059282	0.843267753
ENSBTAG00000032544	NA	0.279999068	0.068981622
ENSBTAG00000032548	SYBU	-0.409639063	0.006374331
ENSBTAG00000032558	TTC7A	-0.072736522	0.642987874
ENSBTAG00000032603	LOC515333	0.378894392	0.012225636
ENSBTAG00000032609	NA	-0.48014221	0.001120424
ENSBTAG00000032657	TEAD1	-0.325750818	0.033033898
ENSBTAG00000032660	CHIC2	0.468868581	0.001517214
ENSBTAG00000032680	TMEM63B	-0.241238481	0.119136391
ENSBTAG00000032686	HOMEZ	0.498029963	0.000677729
ENSBTAG00000032702	LOC783144	0.40113948	0.00767761
ENSBTAG00000032719	TFRC	-0.424858161	0.004514218
ENSBTAG00000032764	NA	0.292065023	0.057376555
ENSBTAG00000032808	FASLG	0.432510745	0.003772559
ENSBTAG00000032821	SCEL	-0.305384578	0.046438403
ENSBTAG00000032859	NA	-0.520442675	0.000346863
ENSBTAG00000032869	RNASE10	0.541358122	0.000177791
ENSBTAG00000032887	SUPT3H	-0.481143733	0.001090104
ENSBTAG00000032893	NA	-0.602632897	1.90E-05
ENSBTAG00000032899	NA	-0.438319262	0.003283054
ENSBTAG00000032902	LOC512464	-0.0446358	0.776246963
ENSBTAG00000032914	SLC11A2	0.301781335	0.049215318
ENSBTAG00000032933	TTC23L	-0.465325725	0.001665373
ENSBTAG00000032951	ABHD17C	-0.202323281	0.193213236
ENSBTAG00000032961	IER3IP1	-0.326957153	0.032352448
ENSBTAG00000032996	P4HA1	0.195008423	0.210152333
ENSBTAG00000033008	MYOZ1	-0.382798434	0.011292019
ENSBTAG00000033015	FAHD1	0.1520562	0.330357953
ENSBTAG00000033041	YIPF4	0.432685314	0.003756965

ENSBTAG00000033076	NA	-0.460372984	0.001893931
ENSBTAG00000033078	CNEP1R1	-0.204889058	0.187507053
ENSBTAG00000033089	HACD1	-0.162163642	0.298832663
ENSBTAG00000033107	NA	-0.039208123	0.802877635
ENSBTAG00000033136	COX20	-0.208451288	0.179784904
ENSBTAG00000033137	PSD3	-0.569176218	6.81E-05
ENSBTAG00000033160	FAM114A1	-0.571947065	6.16E-05
ENSBTAG00000033174	TFAP4	-0.540875771	0.000180643
ENSBTAG00000033180	SMYD3	-0.554461666	0.000114321
ENSBTAG00000033182	HGSNAT	-0.014060699	0.928692833
ENSBTAG00000033186	OXCT1	-0.549206656	0.000136771
ENSBTAG00000033190	PGM5	-0.238238156	0.123940102
ENSBTAG00000033197	EPDR1	-0.308146744	0.044396817
ENSBTAG00000033214	TBC1D19	-0.534826649	0.000220085
ENSBTAG00000033218	NA	0.470042435	0.001470769
ENSBTAG00000033221	CCDC152	-0.665271791	1.13E-06
ENSBTAG00000033222	CALR3	-0.247589006	0.109433813
ENSBTAG00000033248	CDH3	-0.330318261	0.030514699
ENSBTAG00000033255	DUSP11	0.192346388	0.216566175
ENSBTAG00000033267	LIN9	-0.673311539	7.52E-07
ENSBTAG00000033268	ZFHX4	0.164540848	0.291709028
ENSBTAG00000033284	NA	-0.031122219	0.842954135
ENSBTAG00000033299	IGFALS	0.015306826	0.922391693
ENSBTAG00000033304	TCIM	-0.368170183	0.015135704
ENSBTAG00000033313	SLC38A9	-0.636465573	4.48E-06
ENSBTAG00000033315	DNAJC1	0.376294791	0.012883169
ENSBTAG00000033316	PDCD1LG2	0.268486083	0.081714464
ENSBTAG00000033333	CDK10	-0.534397962	0.000223155
ENSBTAG00000033334	SPATA2L	0.389847498	0.009760137
ENSBTAG00000033345	STAR	-0.683433252	4.40E-07
ENSBTAG00000033351	PACRGL	-0.313026772	0.040968377
ENSBTAG00000033395	C25H16orf91	0.693176734	2.58E-07
ENSBTAG00000033398	HKDC1	-0.294222095	0.055477105
ENSBTAG00000033412	NA	-0.622944224	8.15E-06
ENSBTAG00000033429	FAM229B	-0.561643329	8.90E-05
ENSBTAG00000033441	SHCBP1	-0.470759459	0.001443024
ENSBTAG00000033464	SPA17	-0.526487991	0.000287209
ENSBTAG00000033486	C17H4orf46	-0.535971231	0.000212073
ENSBTAG00000033504	MAK16	0.484040161	0.001006487
ENSBTAG00000033510	MPZL2	-0.221326328	0.153774336
ENSBTAG00000033529	NA	0.322466928	0.034949079
ENSBTAG00000033545	EBD	-0.149861372	0.337467807
ENSBTAG00000033547	C17H4orf45	0.463034963	0.001767859
ENSBTAG00000033562	LHX1	0.09933595	0.526233947
ENSBTAG00000033563	NA	-0.65173344	2.20E-06
ENSBTAG00000033565	NA	0.468783361	0.001520636
ENSBTAG00000033603	IP6K3	-0.485664281	0.000962145

ENSBTAG00000033621	SMCO4	-0.034702235	0.825155695
ENSBTAG00000033662	NCKAP1	-0.305250112	0.046539699
ENSBTAG00000033669	IL17RC	0.541379591	0.000177666
ENSBTAG00000033677	NA	-0.217363624	0.161467554
ENSBTAG00000033679	HLCS	-0.411506024	0.006115247
ENSBTAG00000033680	NA	-0.38715666	0.010322433
ENSBTAG00000033685	CCNJ	-0.39750658	0.008301207
ENSBTAG00000033690	BARD1	-0.489525021	0.000863649
ENSBTAG00000033702	STARD8	0.520072378	0.000350856
ENSBTAG00000033727	RBPMS	-0.603291546	1.85E-05
ENSBTAG00000033731	PRCP	-0.361769958	0.017137517
ENSBTAG00000033735	WASHC4	0.264185571	0.086915992
ENSBTAG00000033740	NA	-0.461104992	0.001858494
ENSBTAG00000033747	SIL1	-0.506209525	0.00053358
ENSBTAG00000033748	IL18RAP	0.361813833	0.017123068
ENSBTAG00000033801	VRK2	-0.725739791	3.66E-08
ENSBTAG00000033803	FABP7	-0.211201823	0.173980024
ENSBTAG00000033806	LOC613401	-0.260587141	0.091463027
ENSBTAG00000033886	CIST1	-0.233292049	0.132174723
ENSBTAG00000034075	SLC7A11	-0.28856655	0.060567563
ENSBTAG00000034090	NA	-0.740348643	1.39E-08
ENSBTAG00000034113	GALNT10	0.543196631	0.000167293
ENSBTAG00000034138	LOC786974	0.048068429	0.759532654
ENSBTAG00000034159	FCRLA	-0.168716044	0.279465664
ENSBTAG00000034174	NA	-0.123255244	0.431029244
ENSBTAG00000034182	LOC782966	-0.496263325	0.000713098
ENSBTAG00000034192	KIAA2012	-0.205934059	0.185217693
ENSBTAG00000034193	BCO2	-0.15544184	0.319575207
ENSBTAG00000034222	CAB39L	-0.292742822	0.056774179
ENSBTAG00000034225	TAF5L	0.646668592	2.80E-06
ENSBTAG00000034246	ACRBP	-0.261015734	0.090911988
ENSBTAG00000034255	EIF5B	0.153051341	0.32716532
ENSBTAG00000034295	LAG3	-0.461241215	0.001851965
ENSBTAG00000034302	NA	0.366518149	0.015632409
ENSBTAG00000034323	LOC107131287	-0.282729253	0.066205575
ENSBTAG00000034347	RBM11	-0.580905894	4.42E-05
ENSBTAG00000034349	IFI44	0.137475219	0.379344008
ENSBTAG00000034366	RGS2	0.53440772	0.000223085
ENSBTAG00000034384	VWA3B	0.280698936	0.068261374
ENSBTAG00000034385	GPR162	-0.038242233	0.807640864
ENSBTAG00000034393	FAM149A	-0.203707312	0.190120144
ENSBTAG00000034396	PIGW	0.39484622	0.008785092
ENSBTAG00000034435	NKD2	-0.162832134	0.29681823
ENSBTAG00000034442	LNP1	-0.599559579	2.15E-05
ENSBTAG00000034449	NA	0.443342483	0.00290558
ENSBTAG00000034493	ILRUN	0.571628037	6.23E-05
ENSBTAG00000034498	LY6D	-0.225193431	0.146528768

ENSBTAG00000034501	CFI	-0.067153441	0.668751479
ENSBTAG00000034503	NA	-0.207365849	0.182113387
ENSBTAG00000034529	HMGA1	0.449340921	0.002505192
ENSBTAG00000034580	NA	0.502681361	0.000591991
ENSBTAG00000034609	NA	-0.398815838	0.00807162
ENSBTAG00000034613	MROH6	-0.019348044	0.901991139
ENSBTAG00000034633	ERO1B	0.11995391	0.443566482
ENSBTAG00000034643	NA	0.709386899	1.01E-07
ENSBTAG00000034645	PON3	-0.238632814	0.123300047
ENSBTAG00000034656	LOC781416	0.284634061	0.064321804
ENSBTAG00000034659	UBTD2	0.196489586	0.206641544
ENSBTAG00000034676	HIGD1A	0.324147725	0.033957734
ENSBTAG00000034689	ZNRF1	0.169106455	0.278338285
ENSBTAG00000034693	SYT1	-0.233886121	0.131164652
ENSBTAG00000034712	RAB33A	-0.377668748	0.012531989
ENSBTAG00000034776	DDAH1	-0.162372827	0.298201365
ENSBTAG00000034785	DNAJC15	-0.651872181	2.19E-06
ENSBTAG00000034827	PDGFD	-0.401110664	0.007682393
ENSBTAG00000034844	LOC100295757	-0.036865142	0.814443761
ENSBTAG00000034848	F2RL1	-0.356258664	0.019036228
ENSBTAG00000034850	NA	0.316313787	0.038783225
ENSBTAG00000034871	NA	-0.654777784	1.90E-06
ENSBTAG00000034875	ALPK1	0.534362595	0.00022341
ENSBTAG00000034883	CCR4	-0.45236187	0.002322595
ENSBTAG00000034885	RGCC	0.479305665	0.001146322
ENSBTAG00000034918	IFIT2	0.35603455	0.019117041
ENSBTAG00000034954	NA	-4.97E-05	0.999747665
ENSBTAG00000034963	MKS1	-0.697863465	1.98E-07
ENSBTAG00000034985	PHLDA1	0.017829223	0.909651729
ENSBTAG00000034991	NA	-0.603845617	1.81E-05
ENSBTAG00000034992	MCTS1	-0.395258696	0.008708515
ENSBTAG00000034998	SIMC1	-0.475127401	0.001283813
ENSBTAG00000035081	SERINC2	0.535330285	0.000216527
ENSBTAG00000035129	NA	-0.545197648	0.000156508
ENSBTAG00000035144	PLCXD1	0.345374172	0.023308777
ENSBTAG00000035175	DONSON	-0.632273713	5.41E-06
ENSBTAG00000035183	NA	0.603747241	1.82E-05
ENSBTAG00000035206	NA	0.16125614	0.301581358
ENSBTAG00000035224	NA	0.444715481	0.002809282
ENSBTAG00000035226	NA	0.535814821	0.000213152
ENSBTAG00000035244	ANKRD39	-0.241725086	0.118370732
ENSBTAG00000035247	MCEE	-0.335067307	0.028065948
ENSBTAG00000035319	NA	-0.580084084	4.56E-05
ENSBTAG00000035379	LOC511386	0.191243081	0.219263803
ENSBTAG00000035392	NA	0.036074419	0.818356104
ENSBTAG00000035572	NA	-0.640462857	3.74E-06
ENSBTAG00000035584	NA	0.278260669	0.070796662

ENSBTAG00000035587	ARRB2	0.534987261	0.000218944
ENSBTAG00000035615	UPF3B	-0.444853349	0.00279977
ENSBTAG00000035641	NA	0.676031849	6.53E-07
ENSBTAG00000035660	LOC514680	-0.222964024	0.150674524
ENSBTAG00000035662	CAMK4	-0.363135028	0.016692776
ENSBTAG00000035726	NA	-0.601958655	1.95E-05
ENSBTAG00000035735	BIRC2	0.248910459	0.107492696
ENSBTAG00000035744	LOC785873	0.516254132	0.000394506
ENSBTAG00000035777	NA	0.315074656	0.039595505
ENSBTAG00000035782	METTL22	-0.217390056	0.16141533
ENSBTAG00000035827	ATG7	0.350290183	0.021289097
ENSBTAG00000035844	PLAAT1	-0.381847964	0.011513512
ENSBTAG00000035858	MCC	0.386930575	0.010370916
ENSBTAG00000035868	LOC614923	-0.086118337	0.582938885
ENSBTAG00000035907	DDX3X	0.47561429	0.001267071
ENSBTAG00000035945	NA	-0.344466103	0.023698831
ENSBTAG00000035958	RHOBTB2	-0.476573485	0.001234654
ENSBTAG00000035975	NA	0.561883749	8.83E-05
ENSBTAG00000035995	TNFAIP2	0.62207888	8.46E-06
ENSBTAG00000035998	CKB	0.119320116	0.445996128
ENSBTAG00000036016	FAM111B	0.489443231	0.000865639
ENSBTAG00000036028	BEX2	-0.610426931	1.38E-05
ENSBTAG00000036061	LOC100336795	-0.168724182	0.279442134
ENSBTAG00000036078	EMP1	0.531237616	0.000247012
ENSBTAG00000036087	ARMC2	-0.583479755	4.01E-05
ENSBTAG00000036101	KYAT1	-0.298955263	0.051485878
ENSBTAG00000036127	AS3MT	0.462027413	0.001814675
ENSBTAG00000036222	NA	-0.336765316	0.027230975
ENSBTAG00000036224	MGC157082	0.583812673	3.96E-05
ENSBTAG00000036257	LOC107131241	-0.332056635	0.029598612
ENSBTAG00000036260	LPXN	-0.274133676	0.07525668
ENSBTAG00000036262	GBE1	-0.392609344	0.009210533
ENSBTAG00000036298	LOC515578	0.103628005	0.508423575
ENSBTAG00000036367	MIR374B	0.247718646	0.109242209
ENSBTAG00000036391	MIR212	0.319066356	0.037027555
ENSBTAG00000036392	MIR371	0.301606475	0.049353418
ENSBTAG00000036418	MIR223	0.209388403	0.177791807
ENSBTAG00000036437	MIR33B	0.585835869	3.67E-05
ENSBTAG00000037179	LOC112443347	-0.215948351	0.164281865
ENSBTAG00000037375	LOC512684	-0.497921989	0.000679845
ENSBTAG00000037377	ABHD14B	-0.226656127	0.143854801
ENSBTAG00000037383	AKAP13	0.499947648	0.000641119
ENSBTAG00000037389	TRIM44	-0.45452946	0.002198908
ENSBTAG00000037397	PRSS36	0.080045334	0.609879601
ENSBTAG00000037400	TNRC18	0.432116933	0.003807945
ENSBTAG00000037404	LRFN4	-0.148018283	0.343510803
ENSBTAG00000037413	TMEM164	0.61681448	1.06E-05

ENSBTAG00000037415	LOC100295347	-0.298085048	0.052201788
ENSBTAG00000037421	NA	0.361593484	0.017195736
ENSBTAG00000037440	NA	-0.472861839	0.001364329
ENSBTAG00000037452	LOC790312	0.349864455	0.021457991
ENSBTAG00000037456	AHDC1	-0.19823651	0.202553772
ENSBTAG00000037457	MBD2	0.22010404	0.156118103
ENSBTAG00000037465	TRIM34	0.367811389	0.015242428
ENSBTAG00000037470	NA	0.609340986	1.45E-05
ENSBTAG00000037489	CRCP	-0.645851811	2.91E-06
ENSBTAG00000037490	NA	0.333822496	0.028691471
ENSBTAG00000037496	NA	-0.190833249	0.220271749
ENSBTAG00000037510	LOC615733	-0.284397224	0.06455368
ENSBTAG00000037523	B3GALT6	0.530409555	0.000253631
ENSBTAG00000037526	FABP4	-0.630548164	5.84E-06
ENSBTAG00000037527	OAS1Z	0.158532178	0.309928851
ENSBTAG00000037533	C4A	0.420746432	0.004962922
ENSBTAG00000037537	LOC618463	0.580814211	4.44E-05
ENSBTAG00000037539	LOC534578	-0.156268837	0.316975435
ENSBTAG00000037549	NA	-0.603333148	1.85E-05
ENSBTAG00000037554	NA	0.458546492	0.001984969
ENSBTAG00000037558	GRO1	0.25601691	0.097500873
ENSBTAG00000037565	LOC788142	-0.43809826	0.003300606
ENSBTAG00000037566	ZNF500	-0.219386069	0.157506939
ENSBTAG00000037571	EBAG9	-0.46568192	0.001649919
ENSBTAG00000037581	MZF1	0.210696992	0.175035217
ENSBTAG00000037595	NA	0.054600884	0.728027133
ENSBTAG00000037600	NA	0.12413488	0.427722431
ENSBTAG00000037605	LOC100848815	0.326145494	0.032809659
ENSBTAG00000037608	NA	0.476280938	0.001244462
ENSBTAG00000037634	GBP4	0.376682855	0.012783142
ENSBTAG00000037640	PID1	-0.210446793	0.175559882
ENSBTAG00000037649	VIPR2	-0.271964339	0.077688034
ENSBTAG00000037650	RTL9	0.102057506	0.514905039
ENSBTAG00000037651	S100A2	-0.206225935	0.184581829
ENSBTAG00000037661	NA	-0.667756287	1.00E-06
ENSBTAG00000037673	GSTM1	-0.145003158	0.353539026
ENSBTAG00000037679	PPP1R3E	0.149425014	0.338892529
ENSBTAG00000037693	NA	-0.156243773	0.31705403
ENSBTAG00000037702	SP140L	0.389667568	0.009796899
ENSBTAG00000037726	PLCD1	-0.564053271	8.18E-05
ENSBTAG00000037729	CERS1	-0.561979259	8.80E-05
ENSBTAG00000037735	C5AR2	0.491413866	0.000818823
ENSBTAG00000037743	LOC112446756	0.38836993	0.010065555
ENSBTAG00000037756	TET1	-0.0258345	0.86938201
ENSBTAG00000037757	EBF4	-0.600554852	2.07E-05
ENSBTAG00000037765	TNFAIP8L1	0.39282793	0.009168194
ENSBTAG00000037768	MMP3	-0.477021698	0.001219761

ENSBTAG00000037775	LOC100141266	-0.500302803	0.000634537
ENSBTAG00000037778	CXCL3	0.109285322	0.485422029
ENSBTAG00000037799	LOC515697	0.25946978	0.092911762
ENSBTAG00000037800	APOBEC3Z1	0.242671155	0.116892763
ENSBTAG00000037803	ZNF197	-0.571973729	6.15E-05
ENSBTAG00000037811	CCL2	0.149810367	0.33763415
ENSBTAG00000037819	SFT2D2	-0.67569855	6.64E-07
ENSBTAG00000037821	LOC112443487	0.179063012	0.250593217
ENSBTAG00000037826	LOC407148	0.039131584	0.80325483
ENSBTAG00000037830	NA	0.628247556	6.47E-06
ENSBTAG00000037832	ASPHD2	-0.098714394	0.528838363
ENSBTAG00000037856	MGC152281	-0.172756927	0.267941218
ENSBTAG00000037882	NA	-0.580655379	4.46E-05
ENSBTAG00000037885	PCDHB1	0.204553449	0.188246546
ENSBTAG00000037888	LYPD5	-0.537885793	0.000199259
ENSBTAG00000037902	FAM229A	0.421674001	0.004858442
ENSBTAG00000037929	ADAMDEC1	-0.523040619	0.000319981
ENSBTAG00000037931	NA	-0.085534236	0.58550667
ENSBTAG00000037937	LOC101903126	0.597665151	2.32E-05
ENSBTAG00000037951	KLHL6	-0.217612796	0.16097572
ENSBTAG00000037962	MAML2	0.557462025	0.000103057
ENSBTAG00000037964	H2AW	0.43682992	0.003402936
ENSBTAG00000037971	NA	-0.20909285	0.178418685
ENSBTAG00000037981	LOC530973	-0.496878389	0.000700601
ENSBTAG00000037989	NA	0.429631926	0.004038004
ENSBTAG00000038011	SH3RF3	-0.629247401	6.19E-06
ENSBTAG00000038025	NA	-0.264085338	0.087040223
ENSBTAG00000038033	KRT6B	-0.145169682	0.352980567
ENSBTAG00000038034	ZNF628	0.529472749	0.000261313
ENSBTAG00000038042	CXCR2	0.503703682	0.000574503
ENSBTAG00000038047	NA	0.249599031	0.106491696
ENSBTAG00000038048	MRC1	-0.464814743	0.001687766
ENSBTAG00000038050	ZNF420	-0.696304593	2.16E-07
ENSBTAG00000038051	LOC532875	-0.524503568	0.000305683
ENSBTAG00000038055	KLF16	0.603541529	1.83E-05
ENSBTAG00000038062	FUT4	0.614985849	1.14E-05
ENSBTAG00000038063	LIPJ	-0.409352458	0.006414935
ENSBTAG00000038067	NA	-0.382188723	0.01143368
ENSBTAG00000038079	C16H1orf21	-0.691810934	2.78E-07
ENSBTAG00000038084	NA	0.397592891	0.008285901
ENSBTAG00000038085	NA	0.190138238	0.221988374
ENSBTAG00000038088	NA	-0.538380549	0.000196064
ENSBTAG00000038107	MAPKAPK2	0.631069781	5.71E-06
ENSBTAG00000038111	NA	-0.52970414	0.000259397
ENSBTAG00000038112	LOC100850276	-0.082301871	0.599807102
ENSBTAG00000038117	ATG10	-0.697976803	1.97E-07
ENSBTAG00000038124	FCGR2A	0.392476322	0.009236381

ENSBTAG00000038128	BOLA-DQA5	0.572250892	6.09E-05
ENSBTAG00000038131	NA	-0.578485253	4.84E-05
ENSBTAG00000038134	NA	-0.643639712	3.23E-06
ENSBTAG00000038141	ADGRG1	-0.349840524	0.021467518
ENSBTAG00000038148	SOWAHB	-0.151111431	0.333406881
ENSBTAG00000038149	NLRP12	0.47220163	0.001388621
ENSBTAG00000038154	HSH2D	0.446525663	0.002686615
ENSBTAG00000038156	DYNLT3	-0.56541343	7.79E-05
ENSBTAG00000038178	ZNF25	-0.582169887	4.22E-05
ENSBTAG00000038181	FOCAD	-0.461476144	0.001840752
ENSBTAG00000038186	GLRX	0.210379588	0.175701001
ENSBTAG00000038221	EFNA2	0.037867452	0.809490937
ENSBTAG00000038233	LOC507055	0.549631092	0.00013482
ENSBTAG00000038235	NOD1	0.577377941	5.04E-05
ENSBTAG00000038238	LOC101902340	0.171184397	0.272388056
ENSBTAG00000038241	REPIN1	0.013704726	0.930493649
ENSBTAG00000038251	NAA16	-0.199813018	0.198913763
ENSBTAG00000038262	NA	-0.505821633	0.000539738
ENSBTAG00000038263	LOC782529	-0.143091189	0.359989515
ENSBTAG00000038283	TMEM243	-0.460838471	0.001871328
ENSBTAG00000038284	NA	-0.664289203	1.19E-06
ENSBTAG00000038306	CBX2	-0.484664441	0.000989232
ENSBTAG00000038316	GPATCH8	0.276804276	0.072346108
ENSBTAG00000038321	LIPE	0.454404403	0.002205882
ENSBTAG00000038322	LOC510613	-0.078633691	0.616217287
ENSBTAG00000038330	LOC516108	0.193248298	0.214378122
ENSBTAG00000038335	LOC534155	0.520015257	0.000351476
ENSBTAG00000038366	CD1B5	-0.546346479	0.000150604
ENSBTAG00000038375	STOM	0.6219473	8.51E-06
ENSBTAG00000038379	LOC101902561	-0.004044383	0.979465213
ENSBTAG00000038381	SLC26A6	0.575432843	5.42E-05
ENSBTAG00000038384	KRT5	-0.364298762	0.016321371
ENSBTAG00000038397	BOLA-DRB2	0.483884824	0.001010822
ENSBTAG00000038407	NA	-0.272608469	0.076959763
ENSBTAG00000038415	SLC6A12	-0.6063744	1.63E-05
ENSBTAG00000038422	NA	-0.572987411	5.93E-05
ENSBTAG00000038426	CD1B	-0.436585084	0.003423006
ENSBTAG00000038428	RELB	0.549753901	0.00013426
ENSBTAG00000038430	LOC788801	-0.553715039	0.000117292
ENSBTAG00000038439	NA	-0.511917702	0.000449954
ENSBTAG00000038476	NA	0.316536868	0.038638448
ENSBTAG00000038477	GGCX	-0.367002671	0.015485321
ENSBTAG00000038480	FPGT	-0.421768994	0.004847852
ENSBTAG00000038487	ZNF613	-0.064010036	0.683426414
ENSBTAG00000038488	TMSB4X	0.63022157	5.93E-06
ENSBTAG00000038490	CLEC4A	-0.101913336	0.515502094
ENSBTAG00000038494	NA	0.592479163	2.84E-05

ENSBTAG00000038495	DCLK1	-0.237289716	0.125488482
ENSBTAG00000038496	CR2	-0.476853899	0.001225318
ENSBTAG00000038500	NA	0.340240718	0.025586238
ENSBTAG00000038502	NA	-0.143216157	0.359565745
ENSBTAG00000038527	LOC783382	0.389231106	0.009886567
ENSBTAG00000038532	FOLR3	-0.679146822	5.54E-07
ENSBTAG00000038536	LOC616948	0.435723738	0.003494441
ENSBTAG00000038540	LOC785216	-0.624994002	7.46E-06
ENSBTAG00000038576	GBP6	0.512623553	0.000440477
ENSBTAG00000038584	OLFM1	-0.110102585	0.48214466
ENSBTAG00000038600	LRRC15	-0.247747729	0.10919926
ENSBTAG00000038604	NA	-0.204436177	0.188505434
ENSBTAG00000038613	NA	-0.324798161	0.033580368
ENSBTAG00000038617	SH3D21	-0.34518136	0.023391146
ENSBTAG00000038619	LOC512672	0.289822192	0.059406372
ENSBTAG00000038620	CIR1	-0.440691538	0.003099742
ENSBTAG00000038625	LOC513659	0.330261287	0.030545115
ENSBTAG00000038639	NA	-0.121360591	0.438200078
ENSBTAG00000038640	NA	0.258063283	0.094760517
ENSBTAG00000038650	MS4A7	0.286885645	0.062150296
ENSBTAG00000038662	GJB6	0.406317053	0.006858896
ENSBTAG00000038680	LOC538435	-0.239057463	0.122614132
ENSBTAG00000038682	FAM83H	-0.523782555	0.000312656
ENSBTAG00000038698	NA	0.452395819	0.002320611
ENSBTAG00000038706	MT1E	-0.481791586	0.001070883
ENSBTAG00000038710	NA	0.450749838	0.002418516
ENSBTAG00000038715	NA	-0.54969139	0.000134545
ENSBTAG00000038716	SKI	0.57984213	4.60E-05
ENSBTAG00000038733	EFS	-0.39033984	0.00966015
ENSBTAG00000038737	P2RY6	0.491676736	0.000812752
ENSBTAG00000038756	GLB1L3	-0.322375066	0.035003938
ENSBTAG00000038770	LOC513767	0.051744851	0.741750609
ENSBTAG00000038794	TMEM245	-0.363119701	0.016697715
ENSBTAG00000038797	NA	0.476932454	0.001222714
ENSBTAG00000038815	DIAPH2	0.24984616	0.106134176
ENSBTAG00000038845	TYSND1	-0.164266938	0.29252419
ENSBTAG00000038869	ZNF383	-0.551437361	0.000126794
ENSBTAG00000038878	AOX4	-0.381280239	0.011647574
ENSBTAG00000038888	ZBTB9	-0.370727408	0.014393251
ENSBTAG00000038889	RILP	-0.279520937	0.069477122
ENSBTAG00000038893	LOC101904477	-0.482730482	0.001043561
ENSBTAG00000038896	RPS26	0.041617528	0.791026839
ENSBTAG00000038903	NA	0.095510576	0.54236223
ENSBTAG00000038910	SECTM1	0.370950223	0.014330051
ENSBTAG00000038913	NA	-0.550718222	0.000129936
ENSBTAG00000038916	NA	0.041520724	0.791502099
ENSBTAG00000038929	BCAS4	0.310893334	0.042439649

ENSBTAG00000038931	TSTD3	-0.264759348	0.086207493
ENSBTAG00000038938	LOC781710	0.499135894	0.000656394
ENSBTAG00000038945	PADI6	-0.48960347	0.000861745
ENSBTAG00000038949	MRPL30	-0.726708801	3.44E-08
ENSBTAG00000038951	NA	-0.650595349	2.33E-06
ENSBTAG00000038970	ZBTB14	-0.508300832	0.000501449
ENSBTAG00000038981	LOC518134	0.308120356	0.04441597
ENSBTAG00000038990	TRAF4	-0.095770942	0.541257015
ENSBTAG00000038992	STK11IP	0.557830443	0.000101746
ENSBTAG00000039012	MFSD6L	0.211510326	0.173337449
ENSBTAG00000039014	DEF8	0.06588475	0.674660064
ENSBTAG00000039015	TMEM145	-0.039964185	0.799154063
ENSBTAG00000039016	NA	0.715810218	6.83E-08
ENSBTAG00000039023	NA	-0.674790314	6.96E-07
ENSBTAG00000039028	PI3	-0.027076129	0.863162651
ENSBTAG00000039035	NA	0.612858115	1.25E-05
ENSBTAG00000039037	SERPINB4	0.489851538	0.000855747
ENSBTAG00000039041	NA	-0.041867179	0.789801518
ENSBTAG00000039046	NA	0.32171216	0.035401921
ENSBTAG00000039050	P2RY2	0.654734671	1.91E-06
ENSBTAG00000039071	ANKRD16	-0.07832461	0.617608637
ENSBTAG00000039075	ZNF527	-0.768870945	1.73E-09
ENSBTAG00000039080	SLC22A3	0.404728511	0.007101653
ENSBTAG00000039086	NA	0.466057112	0.001633778
ENSBTAG00000039090	MAGEH1	-0.536956182	0.000205391
ENSBTAG00000039117	TOGARAM1	-0.600055322	2.11E-05
ENSBTAG00000039119	NA	-0.256711689	0.096563722
ENSBTAG00000039121	PTP4A2	-0.2630423	0.088341187
ENSBTAG00000039122	PLA2G5	0.334775774	0.028211421
ENSBTAG00000039129	LOC510798	-0.441542163	0.003036235
ENSBTAG00000039130	LOC613956	-0.105591662	0.500377909
ENSBTAG00000039132	NA	-0.410270341	0.006285683
ENSBTAG00000039160	VAV1	0.664213465	1.20E-06
ENSBTAG00000039161	ALDH3A2	-0.483282288	0.001027795
ENSBTAG00000039163	NA	0.000215419	0.998906126
ENSBTAG00000039190	SLC9A5	-0.405867453	0.006926864
ENSBTAG00000039195	NHS	-0.191493979	0.218648316
ENSBTAG00000039196	LOC510860	-0.333120761	0.02904916
ENSBTAG00000039197	SLC2A9	0.557243488	0.000103843
ENSBTAG00000039231	NA	-0.456798015	0.002075718
ENSBTAG00000039234	LIPK	-0.502662104	0.000592325
ENSBTAG00000039242	ZNF10	-0.628112332	6.51E-06
ENSBTAG00000039245	GK2	-0.043020654	0.784146669
ENSBTAG00000039260	RPTN	-0.278181374	0.070880343
ENSBTAG00000039275	ERAP2	0.681237986	4.96E-07
ENSBTAG00000039283	NA	0.087682639	0.57608704
ENSBTAG00000039287	ZFP69	-0.53783171	0.000199611

ENSBTAG00000039292	ADRA2A	-0.161891841	0.299654217
ENSBTAG00000039307	YAP1	-0.279966668	0.069015111
ENSBTAG00000039310	NA	0.409629376	0.0063757
ENSBTAG00000039316	NA	-0.659188329	1.53E-06
ENSBTAG00000039319	CYP4F2	0.454791913	0.002184333
ENSBTAG00000039326	LOC520336	0.332162908	0.029543355
ENSBTAG00000039329	RAET1G	0.066765793	0.670554771
ENSBTAG00000039335	ARRDC2	0.566491108	7.50E-05
ENSBTAG00000039340	SCN4B	0.135466909	0.386412094
ENSBTAG00000039341	LOC100296121	-0.477699522	0.001197542
ENSBTAG00000039347	CLEC4D	-0.013163501	0.933232275
ENSBTAG00000039353	NA	0.081156687	0.604909807
ENSBTAG00000039355	MADCAM1	0.049640788	0.751911914
ENSBTAG00000039366	LOC515418	-0.358728316	0.018164583
ENSBTAG00000039380	NA	-0.273386096	0.076087706
ENSBTAG00000039406	LOC613570	-0.666441937	1.07E-06
ENSBTAG00000039413	NA	0.585405229	3.73E-05
ENSBTAG00000039425	KRT6A	-0.095415575	0.542765764
ENSBTAG00000039426	DPEP2	-0.112107569	0.474153647
ENSBTAG00000039442	SEC62	0.245193209	0.113020942
ENSBTAG00000039446	LOC100850808	-0.073727021	0.638458915
ENSBTAG00000039453	LOC100847773	0.162850699	0.296762413
ENSBTAG00000039462	PCLAF	-0.383063069	0.011231002
ENSBTAG00000039466	CDR2L	-0.619757842	9.35E-06
ENSBTAG00000039470	NA	-0.254182844	0.100008376
ENSBTAG00000039477	TPBG	-0.170685389	0.273809268
ENSBTAG00000039486	NA	-0.139264852	0.373110533
ENSBTAG00000039509	GPRC5A	-0.321700958	0.035408678
ENSBTAG00000039512	NA	0.402714461	0.007420082
ENSBTAG00000039513	GCNT2	-0.127425601	0.41547853
ENSBTAG00000039520	SIRPB1	0.630297605	5.91E-06
ENSBTAG00000039524	NA	0.328048997	0.031745709
ENSBTAG00000039529	BTBD19	0.611648053	1.32E-05
ENSBTAG00000039531	LCN12	-0.240544661	0.120234551
ENSBTAG00000039552	PLK4	-0.548951139	0.000137959
ENSBTAG00000039555	COX7C	-0.20054031	0.197250125
ENSBTAG00000039563	LOC528282	-0.28837361	0.060747584
ENSBTAG00000039571	PROSER2	-0.274496599	0.074855828
ENSBTAG00000039582	NDUFC1	-0.334772298	0.028213159
ENSBTAG00000039588	LOC511617	-0.067840106	0.665561715
ENSBTAG00000039593	FAM98C	-0.289362793	0.059829134
ENSBTAG00000039594	ZNF862	0.364183394	0.016357875
ENSBTAG00000039599	HOXB4	-0.526299326	0.000288921
ENSBTAG00000039601	SAP25	0.124609703	0.425943358
ENSBTAG00000039618	ARL14EPL	-0.2323805	0.133735847
ENSBTAG00000039620	SAPCD1	0.005635666	0.971388561
ENSBTAG00000039634	NA	0.513796796	0.000425121

ENSBTAG00000039657	H2AC6	0.645779642	2.92E-06
ENSBTAG00000039664	LOC101906101	-0.360005797	0.017727069
ENSBTAG00000039671	LOC539876	-0.535763647	0.000213506
ENSBTAG00000039682	MTUS1	-0.614235592	1.18E-05
ENSBTAG00000039684	CAVIN1	-0.378635735	0.012289751
ENSBTAG00000039686	NA	-0.421554751	0.004871766
ENSBTAG00000039691	NA	0.600625195	2.06E-05
ENSBTAG00000039708	AJM1	-0.200766563	0.196734592
ENSBTAG00000039709	PARPBP	-0.358486015	0.018248585
ENSBTAG00000039711	ZFP62	-0.647639594	2.68E-06
ENSBTAG00000039714	LOC523126	0.005926805	0.969911152
ENSBTAG00000039719	PHGDH	-0.326597477	0.032554402
ENSBTAG00000039720	TMEM225B	0.632475289	5.36E-06
ENSBTAG00000039728	LOC100295775	0.275546374	0.073705786
ENSBTAG00000039731	RND3	-0.411766539	0.00607983
ENSBTAG00000039738	ADORA3	-0.382076435	0.011459934
ENSBTAG00000039740	LY6G5B	0.231892709	0.13457686
ENSBTAG00000039764	NA	0.539561751	0.000188621
ENSBTAG00000039766	FBRSL1	0.335944361	0.027632055
ENSBTAG00000039784	PRR5	0.566324752	7.54E-05
ENSBTAG00000039787	CSN3	-0.267080696	0.083386838
ENSBTAG00000039789	NA	0.366968145	0.015495763
ENSBTAG00000039793	HDGF	0.391237286	0.009480153
ENSBTAG00000039803	MYO7B	0.208289195	0.180131266
ENSBTAG00000039812	NA	0.56468612	8.00E-05
ENSBTAG00000039819	RPH3AL	-0.232073817	0.134264149
ENSBTAG00000039820	CLDN8	-0.278680079	0.070355347
ENSBTAG00000039823	NA	-0.140422692	0.3691104
ENSBTAG00000039856	NA	0.422876393	0.004725862
ENSBTAG00000039861	OAS1Y	0.157714657	0.312462502
ENSBTAG00000039875	NA	-0.099616706	0.525059612
ENSBTAG00000039886	LOC509184	-0.281748543	0.067192376
ENSBTAG00000039888	MAGED2	-0.579980865	4.58E-05
ENSBTAG00000039892	NA	0.497372063	0.000690713
ENSBTAG00000039922	ARAP2	-0.427002422	0.004294575
ENSBTAG00000039928	NA	-0.173668172	0.265386483
ENSBTAG00000039932	NA	-0.210799187	0.174821239
ENSBTAG00000039935	KCNC3	-0.26792712	0.08237645
ENSBTAG00000039937	NA	0.390695456	0.009588478
ENSBTAG00000039950	NA	0.237899801	0.12449083
ENSBTAG00000039954	COPZ2	-0.67039007	8.74E-07
ENSBTAG00000039958	GYS1	0.747969956	8.19E-09
ENSBTAG00000039962	DCTPP1	-0.441991438	0.003003156
ENSBTAG00000039967	KRT78	-0.375601983	0.013063405
ENSBTAG00000039971	LOC514658	-0.325823112	0.032992729
ENSBTAG00000039980	CLECL1	-0.028805705	0.85451282
ENSBTAG00000039992	TUBA1C	-0.539657937	0.000188026

ENSBTAG00000039993	CD1D	0.568929777	6.87E-05
ENSBTAG00000040001	MARVELD2	-0.283383027	0.065554151
ENSBTAG00000040006	SRSF3	0.125344659	0.42319783
ENSBTAG00000040028	OBSCN	-0.284547705	0.064406274
ENSBTAG00000040042	GRIN2C	-0.423668558	0.004640247
ENSBTAG00000040043	NA	-0.492960529	0.000783676
ENSBTAG00000040055	CAB39	-0.448884225	0.002533869
ENSBTAG00000040056	LTB4R2	0.249341892	0.106864671
ENSBTAG00000040058	ORC5	-0.439633514	0.003180358
ENSBTAG00000040061	ZBTB38	-0.621695279	8.60E-06
ENSBTAG00000040063	NA	-0.150924314	0.334012808
ENSBTAG00000040065	RAD51AP1	-0.546570748	0.000149475
ENSBTAG00000040067	HIPK4	-0.62147046	8.69E-06
ENSBTAG00000040070	SCGB1D	-0.198655263	0.201582385
ENSBTAG00000040072	ZNF140	-0.573735969	5.77E-05
ENSBTAG00000040078	FLVCR2	-0.120308978	0.442208518
ENSBTAG00000040088	SLC9B2	-0.406598474	0.006816647
ENSBTAG00000040108	NA	-0.642227933	3.44E-06
ENSBTAG00000040116	H1-10	-0.248004311	0.108820908
ENSBTAG00000040128	FZD4	-0.047454275	0.762515427
ENSBTAG00000040151	GCH1	0.541668092	0.000175981
ENSBTAG00000040161	TM4SF19	-0.225561922	0.145851702
ENSBTAG00000040169	LOC509810	-0.648046088	2.62E-06
ENSBTAG00000040190	CCDC88B	0.637601052	4.26E-06
ENSBTAG00000040206	ZNF770	-0.488522696	0.000888315
ENSBTAG00000040209	ZNF112	-0.385110746	0.010768324
ENSBTAG00000040242	NA	0.31409311	0.040248753
ENSBTAG00000040244	APOL3	0.619744279	9.35E-06
ENSBTAG00000040279	KRT24	0.116893565	0.455365438
ENSBTAG00000040298	GSTT1	-0.217188992	0.161812907
ENSBTAG00000040304	LOC616094	-0.267311451	0.083110429
ENSBTAG00000040323	NA	0.46579622	0.001644987
ENSBTAG00000040331	LOC512867	-0.240510272	0.120289179
ENSBTAG00000040333	QDPR	-0.697207775	2.05E-07
ENSBTAG00000040334	MEX3D	0.446196193	0.002708585
ENSBTAG00000040338	OBSL1	-0.364013176	0.016411862
ENSBTAG00000040350	XIAP	0.436845856	0.003401633
ENSBTAG00000040356	SPIRE2	-0.305892602	0.046057305
ENSBTAG00000040360	CCDC166	-0.218607546	0.159023067
ENSBTAG00000040361	LFNG	0.515176572	0.000407678
ENSBTAG00000040392	MGC139164	0.555443817	0.000110517
ENSBTAG00000040398	CRACD	-0.231171651	0.135827258
ENSBTAG00000040427	ARHGAP19	-0.607432339	1.56E-05
ENSBTAG00000040432	CLDN3	-0.322723188	0.034796416
ENSBTAG00000040435	NA	-0.424963531	0.0045032
ENSBTAG00000040460	KRT23	-0.230081115	0.137734753
ENSBTAG00000040473	NA	-0.246372869	0.111243697

ENSBTAG00000040477	CHD5	-0.283479545	0.065458413
ENSBTAG00000040485	NA	-0.25913199	0.093353203
ENSBTAG00000040507	ARHGEF18	0.089205092	0.569453869
ENSBTAG00000040512	PCP4L1	-0.313908293	0.040372733
ENSBTAG00000040518	LOC112443216	-0.542945349	0.000168694
ENSBTAG00000040555	FBXL19	-0.10304325	0.510832042
ENSBTAG00000040559	NA	-0.238583721	0.123379531
ENSBTAG00000040564	NA	-0.407329642	0.006707929
ENSBTAG00000040569	NLRX1	-0.133920917	0.39190543
ENSBTAG00000040575	KCTD5	0.221663368	0.153132608
ENSBTAG00000040580	NA	-0.074119985	0.636665702
ENSBTAG00000040584	DSC2	-0.315491392	0.039320788
ENSBTAG00000040585	NR6A1	0.326473403	0.032624309
ENSBTAG00000040586	NA	0.439938268	0.003156951
ENSBTAG00000040595	NA	-0.134920818	0.388347317
ENSBTAG00000040607	SLA2	0.047742019	0.761117506
ENSBTAG00000042134	NA	0.239159786	0.122449285
ENSBTAG00000042135	LOC112448925	0.671429063	8.29E-07
ENSBTAG00000042180	LOC112441892	0.252769706	0.101973934
ENSBTAG00000042183	LOC112446498	-0.079115354	0.614051695
ENSBTAG00000042217	LOC112441903	0.359486971	0.017903673
ENSBTAG00000042258	NA	0.582902792	4.10E-05
ENSBTAG00000042264	LOC112444803	0.637960603	4.19E-06
ENSBTAG00000042339	LOC112441895	0.50462656	0.000559115
ENSBTAG00000042370	NA	0.277001586	0.07213464
ENSBTAG00000042475	LOC112448304	0.624023587	7.78E-06
ENSBTAG00000042479	LOC112444954	0.250778493	0.104793622
ENSBTAG00000042524	NA	-0.011988472	0.939180569
ENSBTAG00000042553	LOC112443669	0.106791516	0.495493972
ENSBTAG00000042616	NA	0.276615768	0.072548599
ENSBTAG00000042625	LOC112444675	0.21257766	0.171127502
ENSBTAG00000042644	LOC112449391	0.236243753	0.127212853
ENSBTAG00000042645	LOC112446104	0.436058488	0.003466525
ENSBTAG00000042711	LOC112444971	0.158327736	0.310561228
ENSBTAG00000042713	LOC112443329	0.520399401	0.000347328
ENSBTAG00000042753	LOC112443378	0.052934098	0.736026289
ENSBTAG00000042757	LOC112448166	-0.072491386	0.644110718
ENSBTAG00000042833	LOC112448169	0.302441258	0.048696941
ENSBTAG00000042836	LOC112442823	0.752553875	5.90E-09
ENSBTAG00000042837	LOC112444676	0.224127023	0.148501228
ENSBTAG00000042868	LOC112442805	0.547082411	0.000146929
ENSBTAG00000042871	LOC112443652	0.165503646	0.288855401
ENSBTAG00000042883	LOC112442425	-0.123220902	0.431158632
ENSBTAG00000042974	LOC112441942	0.377969739	0.012456156
ENSBTAG00000042986	LOC112443648	0.34101972	0.025229157
ENSBTAG00000042989	LOC112443901	-0.216073266	0.164032046
ENSBTAG00000043036	LOC112449405	0.177181634	0.255687853

ENSBTAG00000043122	LOC112441672	0.039920759	0.799367819
ENSBTAG00000043151	LOC112443902	0.254538152	0.09951878
ENSBTAG00000043166	LOC112443650	0.203155947	0.191348121
ENSBTAG00000043229	NA	0.038612599	0.805813604
ENSBTAG00000043240	LOC112442436	-0.068720217	0.661481848
ENSBTAG00000043243	LOC112449172	0.581662226	4.30E-05
ENSBTAG00000043250	NA	-0.112505357	0.472576609
ENSBTAG00000043264	LOC112449400	-0.114000766	0.466672991
ENSBTAG00000043268	LOC112441945	0.432112085	0.003808382
ENSBTAG00000043347	NA	0.469019049	0.001511189
ENSBTAG00000043350	LOC112449403	-0.119220651	0.446378089
ENSBTAG00000043369	LOC112446907	0.633318147	5.17E-06
ENSBTAG00000043376	NA	0.1863572	0.231488816
ENSBTAG00000043378	LOC112441944	0.377574542	0.012555805
ENSBTAG00000043414	NA	0.423907948	0.004614642
ENSBTAG00000043432	LOC112441894	0.319581836	0.036706123
ENSBTAG00000043453	LOC112442485	0.498476412	0.000669043
ENSBTAG00000043462	LOC112441682	0.293060454	0.056493641
ENSBTAG00000043480	LOC112441683	-0.047779475	0.760935596
ENSBTAG00000043482	NA	-0.146000482	0.350202416
ENSBTAG00000043486	LOC112441934	0.312900959	0.041053971
ENSBTAG00000043509	LOC112444953	-0.250213209	0.105604861
ENSBTAG00000043530	LOC112447190	0.186563415	0.230963613
ENSBTAG00000043545	NA	-0.164325551	0.292349632
ENSBTAG00000043546	ND6	-0.232056319	0.134294338
ENSBTAG00000043547	NA	-0.116654557	0.456294017
ENSBTAG00000043549	NA	0.165802492	0.287973351
ENSBTAG00000043550	CYTB	-0.211299442	0.173776511
ENSBTAG00000043553	GPX3	0.552954827	0.000120389
ENSBTAG00000043555	NA	0.151961037	0.330664272
ENSBTAG00000043556	COX2	-0.118549014	0.44896196
ENSBTAG00000043557	NA	-0.140036813	0.37044068
ENSBTAG00000043558	ND1	-0.266676204	0.083873085
ENSBTAG00000043559	ND4L	-0.220617339	0.155130683
ENSBTAG00000043561	COX1	-0.331030018	0.030136822
ENSBTAG00000043564	ATP8	-0.216037589	0.164103368
ENSBTAG00000043565	NA	0.08862679	0.571969332
ENSBTAG00000043567	NA	-0.354303981	0.019750836
ENSBTAG00000043568	ND3	-0.265742393	0.085004078
ENSBTAG00000043570	NA	-0.074939089	0.632934487
ENSBTAG00000043571	ND2	-0.131585695	0.400289058
ENSBTAG00000043572	NA	0.483040197	0.001034686
ENSBTAG00000043573	NA	-0.166690476	0.28536278
ENSBTAG00000043577	ND4	-0.156733927	0.315519251
ENSBTAG00000043580	NA	-0.346863728	0.022680573
ENSBTAG00000043582	NA	-0.322659756	0.034834154
ENSBTAG00000043584	ATP6	-0.189751058	0.222948673

ENSBTAG00000043602	NA	-0.308436558	0.044186903
ENSBTAG00000043615	LOC112447901	0.338134953	0.026572604
ENSBTAG00000043639	NA	0.061631089	0.694609924
ENSBTAG00000043683	NA	0.418014812	0.005282047
ENSBTAG00000043706	NA	0.15244197	0.329118021
ENSBTAG00000043729	NA	-0.171211806	0.272310136
ENSBTAG00000043876	LOC112446144	0.375377335	0.013122307
ENSBTAG00000043907	NA	0.099651232	0.524915284
ENSBTAG00000043914	NA	0.008541034	0.956650043
ENSBTAG00000043949	PAWR	-0.275683896	0.073556164
ENSBTAG00000043951	IMPA2	-0.227501059	0.142326682
ENSBTAG00000043953	SPIB	-0.19927206	0.200157558
ENSBTAG00000043959	PDGFC	-0.662510929	1.30E-06
ENSBTAG00000043961	MPDZ	0.094306074	0.547489217
ENSBTAG00000043963	FHDC1	-0.301410942	0.049508214
ENSBTAG00000043964	ARL5B	0.457185702	0.002055286
ENSBTAG00000043971	NOTCH3	0.376198478	0.012908098
ENSBTAG00000043981	SBF2	-0.71550879	6.96E-08
ENSBTAG00000043994	GRK6	0.529094574	0.000264473
ENSBTAG00000044000	PRIM1	-0.545860176	0.000153078
ENSBTAG00000044006	GINS2	-0.373372286	0.013658108
ENSBTAG00000044007	KLF12	-0.041570268	0.791258853
ENSBTAG00000044010	NA	0.225345957	0.146248236
ENSBTAG00000044017	MSRB3	0.30950904	0.043417101
ENSBTAG00000044019	KAT2A	0.247519247	0.109537019
ENSBTAG00000044022	KIAA1671	-0.062657932	0.689774682
ENSBTAG00000044023	CDK6	0.136513477	0.382719175
ENSBTAG00000044033	EDIL3	-0.322239862	0.035084809
ENSBTAG00000044038	TEN1	-0.063891399	0.683982573
ENSBTAG00000044044	CLOCK	-0.349357117	0.021660726
ENSBTAG00000044048	LMBR1L	0.11633581	0.457533993
ENSBTAG00000044053	SLC17A5	-0.575393591	5.43E-05
ENSBTAG00000044055	THSD7B	0.163874338	0.293695139
ENSBTAG00000044056	C19H17orf98	-0.263296529	0.088022709
ENSBTAG00000044058	MFSD8	-0.346412651	0.022869297
ENSBTAG00000044059	NA	0.359024074	0.01806249
ENSBTAG00000044061	FAXC	-0.267218357	0.083221855
ENSBTAG00000044063	B4GALT6	-0.322013466	0.03522057
ENSBTAG00000044064	RNF144A	-0.183127164	0.239821999
ENSBTAG00000044065	PITPNC1	-0.37429346	0.01340968
ENSBTAG00000044070	SNX30	-0.11348083	0.468721127
ENSBTAG00000044071	HRH2	0.458392663	0.00199281
ENSBTAG00000044077	POLR3G	-0.662915682	1.28E-06
ENSBTAG00000044078	TESC	0.097903	0.532247703
ENSBTAG00000044079	SMIM4	-0.362953971	0.016751197
ENSBTAG00000044082	MARCHF1	0.321518922	0.03551863
ENSBTAG00000044083	LIMK1	0.263343994	0.087963348

ENSBTAG00000044087	NA	-0.702677743	1.50E-07
ENSBTAG00000044097	KLF7	0.479521899	0.001139577
ENSBTAG00000044099	ZSWIM7	0.381044595	0.011703608
ENSBTAG00000044105	FOXO1	-0.580866004	4.43E-05
ENSBTAG00000044106	SPIDR	-0.469208547	0.001503631
ENSBTAG00000044112	MSRB2	-0.471508888	0.001414522
ENSBTAG00000044121	NUBPL	-0.449574295	0.002490649
ENSBTAG00000044126	SNTB1	-0.397402387	0.008319717
ENSBTAG00000044129	ST6GALNAC6	0.505931265	0.000537991
ENSBTAG00000044138	METTL23	0.177712555	0.254243191
ENSBTAG00000044150	UCK2	0.0884456	0.572758507
ENSBTAG00000044153	SH3PXD2A	-0.352771597	0.020326705
ENSBTAG00000044155	BSPRY	-0.282572102	0.066362924
ENSBTAG00000044158	LDLRAD3	0.400677934	0.007754524
ENSBTAG00000044160	MCCC2	-0.533998393	0.000226052
ENSBTAG00000044161	NMU	-0.19300246	0.214973003
ENSBTAG00000044172	LMLN	-0.444197757	0.002845259
ENSBTAG00000044173	EHBP1	-0.62421923	7.71E-06
ENSBTAG00000044175	CENPK	-0.379829572	0.011996202
ENSBTAG00000044178	ZMPSTE24	-0.630666478	5.81E-06
ENSBTAG00000044179	CERS6	-0.21149323	0.173373015
ENSBTAG00000044192	MAF	-0.033362769	0.83180537
ENSBTAG00000044194	ZDHHC2	0.500157149	0.000637229
ENSBTAG00000044197	EDARADD	0.350973891	0.021020191
ENSBTAG00000044198	THAP7	0.637014027	4.37E-06
ENSBTAG00000044204	CD79B	-0.239571828	0.121787151
ENSBTAG00000044208	DUSP4	0.04908637	0.754596387
ENSBTAG00000044240	NA	-0.000703275	0.996428851
ENSBTAG00000044284	MIR2357	0.374920664	0.013242741
ENSBTAG00000044419	NA	0.324291552	0.033873991
ENSBTAG00000044427	NA	0.061188226	0.696699012
ENSBTAG00000044492	NA	-0.113241235	0.469666554
ENSBTAG00000044526	MIR1584	0.578386166	4.86E-05
ENSBTAG00000044676	LOC112446843	0.487891262	0.000904175
ENSBTAG00000044681	NA	0.312307472	0.041459703
ENSBTAG00000044741	LOC112441677	0.535854549	0.000212878
ENSBTAG00000044830	MIR339A	0.228728398	0.140128379
ENSBTAG00000044856	LOC112442840	0.59891556	2.21E-05
ENSBTAG00000044861	LOC112446116	-0.056040804	0.721139599
ENSBTAG00000045039	LOC112444215	0.437746105	0.003328744
ENSBTAG00000045156	LOC112449177	0.45342984	0.002260908
ENSBTAG00000045172	MIR2358	0.539625181	0.000188229
ENSBTAG00000045293	LOC112442824	0.439052395	0.003225414
ENSBTAG00000045327	LOC112444391	0.071472531	0.648785936
ENSBTAG00000045337	MIR2376	0.139282848	0.37304816
ENSBTAG00000045449	MIR2349	0.36082067	0.01745266
ENSBTAG00000045475	NA	0.239754023	0.121495234

ENSBTAG00000045492	NA	0.159400024	0.307253571
ENSBTAG00000045494	NA	-0.106404339	0.497067271
ENSBTAG00000045500	SGSM2	-0.225481231	0.145999767
ENSBTAG00000045507	NA	-0.218864683	0.158521135
ENSBTAG00000045509	FAM217B	0.142590796	0.361689386
ENSBTAG00000045515	NA	0.514520891	0.000415885
ENSBTAG00000045518	NA	-0.044325375	0.777763553
ENSBTAG00000045523	LOC509118	-0.320907548	0.035889964
ENSBTAG00000045529	NCR1	0.418309484	0.005246784
ENSBTAG00000045532	NA	-0.103541531	0.50877938
ENSBTAG00000045538	NA	-0.100710727	0.520495932
ENSBTAG00000045543	NA	0.45282055	0.002295922
ENSBTAG00000045547	NA	0.206608208	0.183751388
ENSBTAG00000045548	CRKL	0.54133162	0.000177947
ENSBTAG00000045550	TSPAN6	-0.079373877	0.612890689
ENSBTAG00000045565	NHSL2	0.339722842	0.025825944
ENSBTAG00000045567	PRR15	-0.184226317	0.236963748
ENSBTAG00000045577	NA	-0.040435988	0.796832677
ENSBTAG00000045581	NA	-0.386701686	0.010420199
ENSBTAG00000045584	NA	-0.231916102	0.134536438
ENSBTAG00000045588	LOC100298356	0.312661604	0.041217212
ENSBTAG00000045592	NA	0.305346344	0.046467187
ENSBTAG00000045604	TTC9	-0.507177934	0.000518478
ENSBTAG00000045608	NA	0.318628931	0.037302121
ENSBTAG00000045609	NA	0.241738072	0.11835035
ENSBTAG00000045613	NA	-0.182073034	0.242585071
ENSBTAG00000045622	NA	-0.693669941	2.51E-07
ENSBTAG00000045625	NTN3	-0.058452209	0.709654054
ENSBTAG00000045630	NA	-0.68798654	3.44E-07
ENSBTAG00000045632	NA	-0.132049059	0.398617345
ENSBTAG00000045642	NA	0.199174155	0.200383248
ENSBTAG00000045647	NA	0.384160863	0.010980883
ENSBTAG00000045656	NA	0.286489965	0.062527615
ENSBTAG00000045657	NA	-0.132178131	0.398152402
ENSBTAG00000045658	NA	-0.503027844	0.000586011
ENSBTAG00000045661	NA	0.156627467	0.315852201
ENSBTAG00000045673	LOC613345	0.492671478	0.00079014
ENSBTAG00000045674	NA	0.113207624	0.469799259
ENSBTAG00000045685	NA	0.375471689	0.01309754
ENSBTAG00000045702	NA	0.217182766	0.161825229
ENSBTAG00000045703	COX15	-0.348213451	0.022123634
ENSBTAG00000045710	NA	-0.058435686	0.709732543
ENSBTAG00000045727	EPPK1	-0.143912177	0.357211047
ENSBTAG00000045728	NA	-0.381316117	0.011639062
ENSBTAG00000045742	NA	0.341371018	0.025069492
ENSBTAG00000045744	NKRF	0.122983446	0.432053891
ENSBTAG00000045747	NA	0.038543718	0.806153362

ENSBTAG00000045748	RAF1	0.556897243	0.000105097
ENSBTAG00000045751	LOC520016	0.582654378	4.14E-05
ENSBTAG00000045754	SMIM1	-0.440524368	0.003112359
ENSBTAG00000045762	SCAMP4	0.058138825	0.711143184
ENSBTAG00000045767	LAT2	0.609048467	1.46E-05
ENSBTAG00000045770	KRT77	-0.495589046	0.000727027
ENSBTAG00000045772	NA	-0.091519939	0.55943614
ENSBTAG00000045781	NA	0.145230487	0.352776785
ENSBTAG00000045783	NA	-0.210606994	0.175223811
ENSBTAG00000045787	CDS1	-0.201580386	0.19488809
ENSBTAG00000045788	NA	0.606322022	1.64E-05
ENSBTAG00000045794	NA	-0.712011912	8.61E-08
ENSBTAG00000045795	KIR2DS1	-0.065594903	0.676012676
ENSBTAG00000045808	IL17REL	0.43891494	0.003236153
ENSBTAG00000045814	NA	0.437320349	0.003363043
ENSBTAG00000045818	NA	0.108221544	0.489705295
ENSBTAG00000045822	C15H11orf96	0.52708865	0.000281819
ENSBTAG00000045824	SOX9	-0.174714494	0.262473042
ENSBTAG00000045825	NA	0.07224479	0.645241037
ENSBTAG00000045832	PHLPP1	-0.262049585	0.089593355
ENSBTAG00000045834	RASSF7	0.219383081	0.157512737
ENSBTAG00000045836	NA	-0.2742084	0.075174009
ENSBTAG00000045849	KCNK13	0.284338305	0.064611467
ENSBTAG00000045854	LOC100852077	0.536931626	0.000205555
ENSBTAG00000045857	MCRIP2	-0.319946528	0.036480102
ENSBTAG00000045858	LOC504207	0.291053933	0.058284633
ENSBTAG00000045859	NA	-0.12420762	0.427449618
ENSBTAG00000045861	TARM1	0.506375241	0.000530968
ENSBTAG00000045862	FERMT3	0.389308062	0.009870706
ENSBTAG00000045867	RPGR	-0.144585396	0.354942403
ENSBTAG00000045868	NA	-0.44743308	0.002626916
ENSBTAG00000045877	TSC22D3	0.220069572	0.156184574
ENSBTAG00000045879	CALHM5	-0.235848284	0.127869425
ENSBTAG00000045880	SIGLEC5	0.657772387	1.64E-06
ENSBTAG00000045881	MIR1260B	0.651673008	2.21E-06
ENSBTAG00000045885	MIR3064	0.407448867	0.006690344
ENSBTAG00000045886	NA	-0.248402167	0.108236207
ENSBTAG00000045888	NA	-0.488926751	0.000878297
ENSBTAG00000045892	NA	-0.30023329	0.050448832
ENSBTAG00000045895	NFASC	-0.246426062	0.111164062
ENSBTAG00000045901	CLDN6	-0.19755195	0.204148816
ENSBTAG00000045904	PIM3	0.479219222	0.001149028
ENSBTAG00000045907	NA	0.544038169	0.000162678
ENSBTAG00000045909	FAM174A	-0.3173102	0.038139983
ENSBTAG00000045914	LOC100297725	0.456858543	0.002072516
ENSBTAG00000045926	NA	0.00138794	0.992952268
ENSBTAG00000045929	LOC512440	0.067817939	0.665664594

ENSBTAG00000045936	NA	0.418982761	0.005166982
ENSBTAG00000045937	NA	-0.08328556	0.595439026
ENSBTAG00000045948	NA	0.501688424	0.000609431
ENSBTAG00000045952	NA	0.158501877	0.310022527
ENSBTAG00000045955	TSSK1B	-0.477457201	0.001205443
ENSBTAG00000045965	NA	-0.035748952	0.81996772
ENSBTAG00000045966	GPRIN3	-0.442059121	0.0029982
ENSBTAG00000045971	NA	-0.454677933	0.002190652
ENSBTAG00000045976	NA	-0.324934502	0.033501705
ENSBTAG00000045980	ARF6	0.515603409	0.000402414
ENSBTAG00000045981	DIRAS1	-0.119233605	0.446328333
ENSBTAG00000045987	NA	-0.412579364	0.005970469
ENSBTAG00000045989	CDC42EP5	0.46467245	0.001694049
ENSBTAG00000046003	NA	0.054632482	0.727875763
ENSBTAG00000046010	BHLHA15	-0.288755363	0.060391805
ENSBTAG00000046012	SOWAHD	0.237657472	0.124886386
ENSBTAG00000046014	GPR146	0.547381131	0.00014546
ENSBTAG00000046029	NA	-0.309895831	0.043142162
ENSBTAG00000046030	NA	0.2480973	0.108684033
ENSBTAG00000046037	SLC25A5	-0.03481688	0.824587103
ENSBTAG00000046041	NA	0.126131373	0.420270042
ENSBTAG00000046047	LOC100851913	-0.264311074	0.086760636
ENSBTAG00000046049	NA	-0.460726541	0.001876741
ENSBTAG00000046050	NA	-0.113139242	0.470069317
ENSBTAG00000046052	ANKRD63	-0.347107063	0.022579308
ENSBTAG00000046054	NA	0.353980763	0.019871146
ENSBTAG00000046057	NA	-0.201072835	0.196038242
ENSBTAG00000046062	NA	0.472563453	0.001375261
ENSBTAG00000046063	NA	0.00214436	0.989111481
ENSBTAG00000046076	NA	-0.291634557	0.05776177
ENSBTAG00000046088	LOC101902204	-0.52837379	0.000270592
ENSBTAG00000046090	LOC507247	0.46991704	0.00147567
ENSBTAG00000046100	NA	0.254640698	0.099377819
ENSBTAG00000046110	CLCF1	-0.095754603	0.54132634
ENSBTAG00000046117	NA	0.567988136	7.11E-05
ENSBTAG00000046118	NA	-0.174734286	0.262418137
ENSBTAG00000046120	NA	0.036761818	0.814954736
ENSBTAG00000046121	LOC100196897	-0.293427532	0.056170815
ENSBTAG00000046129	RAB34	-0.313223403	0.040834896
ENSBTAG00000046133	NA	-0.058252548	0.710602674
ENSBTAG00000046140	NPDC1	-0.22991337	0.138029917
ENSBTAG00000046144	NA	0.3784481	0.01233644
ENSBTAG00000046150	NA	0.078847485	0.615255656
ENSBTAG00000046152	MGAM	0.393150028	0.009106109
ENSBTAG00000046153	NA	-0.045944416	0.769862764
ENSBTAG00000046155	RGN	-0.509777774	0.000479814
ENSBTAG00000046156	NA	-0.26227367	0.089309508

ENSBTAG00000046158	CFB	0.389682193	0.009793906
ENSBTAG00000046162	ZNF385C	-0.422650697	0.004750505
ENSBTAG00000046174	GNA13	0.147308343	0.345856146
ENSBTAG00000046176	SPEG	-0.300977231	0.049852968
ENSBTAG00000046188	ELANE	0.181948474	0.242912985
ENSBTAG00000046189	RNASE13	-0.672506677	7.84E-07
ENSBTAG00000046192	AK6	-0.247170021	0.110054808
ENSBTAG00000046210	NA	0.239849438	0.121342567
ENSBTAG00000046211	NA	0.199990245	0.19850746
ENSBTAG00000046218	KLF11	-0.369270187	0.014812449
ENSBTAG00000046223	ANAPC2	0.527529425	0.000277922
ENSBTAG00000046227	NA	0.115790958	0.459657764
ENSBTAG00000046235	SRSF12	0.490926791	0.000830179
ENSBTAG00000046239	LCOR	0.42970807	0.004030778
ENSBTAG00000046245	NA	0.361032988	0.017381754
ENSBTAG00000046255	ATXN1L	0.068301336	0.663422425
ENSBTAG00000046257	GIMAP4	-0.247714823	0.109247855
ENSBTAG00000046263	ADAMTSL5	-0.326633502	0.032534128
ENSBTAG00000046264	NA	-0.064100948	0.683000339
ENSBTAG00000046266	TNFSF9	0.578628026	4.82E-05
ENSBTAG00000046273	TLCD3A	-0.302180862	0.048900955
ENSBTAG00000046286	CCNB3	-0.605368139	1.70E-05
ENSBTAG00000046288	NA	0.49131374	0.000821146
ENSBTAG00000046294	NA	0.49113693	0.000825262
ENSBTAG00000046295	CCER2	-0.14787299	0.343989993
ENSBTAG00000046303	NA	0.588301604	3.34E-05
ENSBTAG00000046307	CEBPD	0.487825994	0.000905828
ENSBTAG00000046320	CXCR5	-0.1639828	0.293371344
ENSBTAG00000046321	NA	-0.638628435	4.06E-06
ENSBTAG00000046323	NA	-0.340780981	0.025338147
ENSBTAG00000046324	LOC100297676	0.159906854	0.305698014
ENSBTAG00000046325	NA	-0.608256126	1.51E-05
ENSBTAG00000046328	XG	-0.003380783	0.982833998
ENSBTAG00000046332	ACTA1	0.503011885	0.000586285
ENSBTAG00000046333	C6H4orf54	0.019030363	0.903592747
ENSBTAG00000046337	TUBB6	-0.388139665	0.010113882
ENSBTAG00000046338	NA	-0.389028852	0.009928356
ENSBTAG00000046339	VASN	-0.633421699	5.14E-06
ENSBTAG00000046343	CCNJL	0.408150655	0.006587642
ENSBTAG00000046350	PKP1	-0.26632615	0.084295673
ENSBTAG00000046351	NA	-0.03242046	0.83649037
ENSBTAG00000046356	NA	0.366753662	0.015560766
ENSBTAG00000046357	SLC29A3	-0.136461515	0.382902036
ENSBTAG00000046359	PHRF1	0.470920179	0.001436869
ENSBTAG00000046362	BBIP1	-0.477712227	0.001197129
ENSBTAG00000046364	NA	-0.558416456	9.97E-05
ENSBTAG00000046375	LOC407163	0.160374848	0.304266125

ENSBTAG00000046383	NA	0.345088773	0.023430786
ENSBTAG00000046389	KLRD1	-0.301572028	0.04938066
ENSBTAG00000046406	R3HDM4	0.588092832	3.37E-05
ENSBTAG00000046407	NYX	0.449623833	0.002487572
ENSBTAG00000046409	EGR2	0.639553678	3.90E-06
ENSBTAG00000046412	NA	-0.043532625	0.781640249
ENSBTAG00000046416	NA	0.503353441	0.000580441
ENSBTAG00000046419	TPC3	0.718930727	5.63E-08
ENSBTAG00000046429	NA	-0.11827625	0.450013645
ENSBTAG00000046431	NA	0.365207154	0.016036337
ENSBTAG00000046444	NA	0.017445661	0.911587639
ENSBTAG00000046449	NA	0.491572646	0.000815151
ENSBTAG00000046450	NA	0.475641417	0.001266144
ENSBTAG00000046452	NA	-0.296025366	0.053928208
ENSBTAG00000046456	NA	-0.216594241	0.162993113
ENSBTAG00000046461	NA	0.523341071	0.000316996
ENSBTAG00000046467	PTP4A3	0.218208231	0.159804821
ENSBTAG00000046481	ZNF740	-0.00863735	0.956161665
ENSBTAG00000046482	LOC538679	-0.486000896	0.000953175
ENSBTAG00000046484	NA	0.163164227	0.295820761
ENSBTAG00000046502	ACBD6	-0.480972145	0.001095246
ENSBTAG00000046503	NCOA7	-0.522588514	0.00032452
ENSBTAG00000046509	TENT5C	0.302869378	0.048363013
ENSBTAG00000046514	ASMTL	0.082754584	0.597795093
ENSBTAG00000046516	FUT7	0.379673067	0.01203434
ENSBTAG00000046533	RAB31	0.489743626	0.000858351
ENSBTAG00000046537	NA	-0.058262569	0.710555051
ENSBTAG00000046545	MEF2D	0.537010369	0.000205029
ENSBTAG00000046547	CIDEA	-0.52722977	0.000280566
ENSBTAG00000046548	ST6GALNAC4	0.56241143	8.67E-05
ENSBTAG00000046552	GGACT	-0.505725266	0.000541278
ENSBTAG00000046555	WAS	0.693327294	2.56E-07
ENSBTAG00000046556	NA	-0.324760153	0.033602324
ENSBTAG00000046566	NA	0.419870472	0.005063378
ENSBTAG00000046569	CISD3	-0.31733365	0.038124951
ENSBTAG00000046570	NA	-0.42818998	0.00417699
ENSBTAG00000046573	PGBD1	-0.424818714	0.004518349
ENSBTAG00000046580	DHX58	0.305335134	0.046475629
ENSBTAG00000046587	CST6	-0.307903192	0.044573849
ENSBTAG00000046588	DNAJB9	0.199393041	0.199878918
ENSBTAG00000046594	NA	-0.27205988	0.077579673
ENSBTAG00000046595	NA	0.025322684	0.871948
ENSBTAG00000046607	JMJD7	0.279362369	0.06964207
ENSBTAG00000046611	NA	0.143574492	0.358352298
ENSBTAG00000046612	ZNF292	0.457742122	0.002026272
ENSBTAG00000046616	NA	0.250557586	0.105110076
ENSBTAG00000046622	NA	0.266541702	0.084035261

ENSBTAG00000046623	LOC782136	-0.160541082	0.303758544
ENSBTAG00000046633	NA	-0.515388763	0.000405053
ENSBTAG00000046640	NA	0.494221145	0.000756034
ENSBTAG00000046644	HRAS	0.54795137	0.000142694
ENSBTAG00000046655	NA	0.275627523	0.073617468
ENSBTAG00000046662	TRPM5	0.398767639	0.008079974
ENSBTAG00000046664	TSC22D1	0.130541313	0.404071792
ENSBTAG00000046668	ANG2	-0.322540497	0.034905195
ENSBTAG00000046671	WFS1	-0.322328774	0.03503161
ENSBTAG00000046672	ZDHHC18	0.577297311	5.06E-05
ENSBTAG00000046677	RTN4R	0.163761574	0.294032022
ENSBTAG00000046678	NA	-0.052535251	0.737944543
ENSBTAG00000046680	NA	0.130721282	0.403418484
ENSBTAG00000046684	FOXN3	0.584786629	3.82E-05
ENSBTAG00000046690	LOC107133338	0.428080937	0.004187668
ENSBTAG00000046693	NA	0.607216077	1.58E-05
ENSBTAG00000046695	NA	-0.166193557	0.28682176
ENSBTAG00000046699	STAT4	0.234052459	0.130882872
ENSBTAG00000046700	NA	0.541896279	0.000174658
ENSBTAG00000046701	FRAT2	0.420720816	0.004965835
ENSBTAG00000046708	PDP2	0.672067935	8.02E-07
ENSBTAG00000046721	NA	0.417471845	0.005347563
ENSBTAG00000046724	CBX6	0.167294415	0.283596096
ENSBTAG00000046730	NA	-0.079907286	0.610498151
ENSBTAG00000046744	PALM3	-0.078412964	0.617210773
ENSBTAG00000046750	B3GNT3	0.560438803	9.29E-05
ENSBTAG00000046758	RNF223	-0.199654666	0.199277288
ENSBTAG00000046760	BRD1	0.534263192	0.000224129
ENSBTAG00000046765	POLR2A	0.372670861	0.013849888
ENSBTAG00000046766	NA	0.166438307	0.286102554
ENSBTAG00000046771	FNDC7	-0.2342638	0.130525507
ENSBTAG00000046773	MCOLN2	0.007103963	0.96393862
ENSBTAG00000046794	NA	-0.576240925	5.26E-05
ENSBTAG00000046803	GAS1	-0.263334782	0.087974866
ENSBTAG00000046814	ACOT2	-0.526440905	0.000287635
ENSBTAG00000046837	ZNF358	-0.588245412	3.35E-05
ENSBTAG00000046839	NA	-0.348112269	0.022164984
ENSBTAG00000046840	DEXI	-0.15915384	0.308010973
ENSBTAG00000046841	IRF2BP2	0.583366882	4.03E-05
ENSBTAG00000046850	NA	-0.190135085	0.221996184
ENSBTAG00000046852	NA	-0.080011257	0.610032265
ENSBTAG00000046862	MARCKSL1	0.604134864	1.79E-05
ENSBTAG00000046866	NA	-0.310745565	0.042543127
ENSBTAG00000046871	NA	-0.64454797	3.09E-06
ENSBTAG00000046874	NA	0.053509558	0.733261406
ENSBTAG00000046875	AP5B1	0.456064977	0.00211484
ENSBTAG00000046882	NA	0.132992422	0.395226441

ENSBTAG00000046885	NA	0.416689163	0.005443245
ENSBTAG00000046886	NA	-0.576798965	5.15E-05
ENSBTAG00000046888	NA	0.017335181	0.912145344
ENSBTAG00000046900	GGT1	0.238509533	0.123499716
ENSBTAG00000046901	NA	-0.512368763	0.000443877
ENSBTAG00000046910	NA	-0.437186307	0.003373905
ENSBTAG00000046912	NA	0.109896912	0.482968354
ENSBTAG00000046922	TWIST1	-0.363728935	0.016502348
ENSBTAG00000046926	NA	0.032769711	0.834753294
ENSBTAG00000046934	NA	-0.145288974	0.352580839
ENSBTAG00000046939	NA	0.647374968	2.71E-06
ENSBTAG00000046941	LOC786015	0.132406182	0.397331693
ENSBTAG00000046952	LOC784931	0.175058403	0.261520101
ENSBTAG00000046956	STYX	0.065299924	0.677390274
ENSBTAG00000046957	DOK6	-0.416317645	0.005489182
ENSBTAG00000046971	NA	-0.068744533	0.661369266
ENSBTAG00000046974	NA	-0.475145438	0.001283189
ENSBTAG00000046977	PLA2G2D4	0.530100568	0.000256142
ENSBTAG00000046979	LGMN	-0.575060893	5.49E-05
ENSBTAG00000046980	KLRF2	-0.26555069	0.085237722
ENSBTAG00000046981	NA	0.326619528	0.032541991
ENSBTAG00000046996	EPN1	0.563811527	8.25E-05
ENSBTAG00000047000	NA	-0.25614182	0.097331874
ENSBTAG00000047002	NA	-0.526165083	0.000290145
ENSBTAG00000047003	ASXL3	0.134678048	0.389209459
ENSBTAG00000047008	NA	0.279272451	0.069735744
ENSBTAG00000047009	ANKRD66	-0.592256684	2.87E-05
ENSBTAG00000047014	NA	-0.181289148	0.244653704
ENSBTAG00000047024	NA	-0.231401569	0.135427618
ENSBTAG00000047030	LOC515276	0.00679081	0.965527281
ENSBTAG00000047036	GPR39	-0.15934986	0.307407807
ENSBTAG00000047042	NA	-0.090071783	0.565693534
ENSBTAG00000047046	NA	-0.052679253	0.737251784
ENSBTAG00000047053	NA	-0.43852349	0.003266907
ENSBTAG00000047055	NA	0.284925738	0.064037147
ENSBTAG00000047059	TIMM17A	0.540964077	0.000180118
ENSBTAG00000047061	NDOR1	0.334192459	0.028504368
ENSBTAG00000047062	LRP3	-0.215736258	0.164706663
ENSBTAG00000047064	NA	-0.264065304	0.08706507
ENSBTAG00000047077	ENTPD7	0.564202227	8.13E-05
ENSBTAG00000047088	NA	0.558607184	9.90E-05
ENSBTAG00000047093	NA	0.547088047	0.000146901
ENSBTAG00000047098	NA	-0.616348049	1.08E-05
ENSBTAG00000047103	IDNK	-0.074370564	0.635523308
ENSBTAG00000047107	TNIP3	0.503185719	0.000583304
ENSBTAG00000047116	NA	-0.266264691	0.084370037
ENSBTAG00000047119	NA	-0.304515065	0.0470966

ENSBTAG00000047121	LOC100847119	-0.196122441	0.207507939
ENSBTAG00000047122	NA	0.058280397	0.710470335
ENSBTAG00000047128	NA	0.157690261	0.312538313
ENSBTAG00000047133	NA	0.538930696	0.000192565
ENSBTAG00000047135	GORASP1	-0.327709868	0.031933149
ENSBTAG00000047136	LOC101902490	-0.076647205	0.625182552
ENSBTAG00000047147	CRYBG3	0.211240774	0.173898799
ENSBTAG00000047148	NA	-0.414767295	0.005684529
ENSBTAG00000047150	NA	-0.542027816	0.0001739
ENSBTAG00000047154	NA	-0.045499487	0.772031727
ENSBTAG00000047157	NA	0.017080481	0.913431238
ENSBTAG00000047158	LRFN1	0.501602203	0.000610967
ENSBTAG00000047166	SH2D7	0.190524899	0.221032215
ENSBTAG00000047190	NA	0.276237356	0.072956429
ENSBTAG00000047196	NA	-0.687766661	3.48E-07
ENSBTAG00000047200	NA	0.580712884	4.46E-05
ENSBTAG00000047206	H1-4	0.102037544	0.514987687
ENSBTAG00000047210	NA	-0.652049459	2.17E-06
ENSBTAG00000047213	GPRASP1	0.228739734	0.140108192
ENSBTAG00000047214	TRAPPC1	-0.446200525	0.002708295
ENSBTAG00000047216	NA	-0.100625016	0.520852759
ENSBTAG00000047225	BCL2L14	-0.734530032	2.06E-08
ENSBTAG00000047226	NA	-0.412440205	0.00598907
ENSBTAG00000047227	NA	-0.11418674	0.465941562
ENSBTAG00000047229	CRIP1	-0.22036852	0.155608759
ENSBTAG00000047238	ITGAM	0.336056253	0.027577102
ENSBTAG00000047242	NA	0.173319022	0.266363434
ENSBTAG00000047254	ABCA2	-0.022622515	0.885506192
ENSBTAG00000047265	PPP1R14B	0.023776327	0.879708448
ENSBTAG00000047274	KIF21B	0.426753889	0.004319546
ENSBTAG00000047275	NA	0.476272004	0.001244763
ENSBTAG00000047277	NA	-0.221164917	0.154082361
ENSBTAG00000047282	NA	0.021149135	0.89291827
ENSBTAG00000047284	NA	-0.073860466	0.637849735
ENSBTAG00000047287	MTARC1	-0.138930215	0.374271439
ENSBTAG00000047293	NRIP1	-0.119710503	0.44449872
ENSBTAG00000047299	DGCR6L	-0.261682242	0.090060176
ENSBTAG00000047302	LOC514978	-0.606462391	1.63E-05
ENSBTAG00000047319	NA	-0.092820122	0.553845831
ENSBTAG00000047322	NA	-0.297796316	0.052441085
ENSBTAG00000047330	FABP5	-0.582556451	4.16E-05
ENSBTAG00000047336	LOC100847115	-0.064990339	0.678837206
ENSBTAG00000047338	DCBLD1	0.5356945	0.000213986
ENSBTAG00000047339	BCOR	0.422872174	0.004726322
ENSBTAG00000047341	LOC100299503	0.248988288	0.107379195
ENSBTAG00000047343	NA	-0.505425219	0.000546098
ENSBTAG00000047344	OR2AT2C	-0.225774072	0.145462946

ENSBTAG00000047345	NA	0.557008848	0.000104691
ENSBTAG00000047347	NA	-0.422742019	0.004740521
ENSBTAG00000047354	NA	0.054457583	0.72871375
ENSBTAG00000047357	RNF208	-0.292091836	0.057352629
ENSBTAG00000047359	NA	0.188398504	0.22632577
ENSBTAG00000047362	RCN1	-0.496611008	0.00070601
ENSBTAG00000047363	NA	0.097058646	0.535806877
ENSBTAG00000047367	CMTR2	0.130238455	0.405172583
ENSBTAG00000047370	NA	-0.114733861	0.463793315
ENSBTAG00000047373	LOC112447652	-0.175782315	0.259521743
ENSBTAG00000047379	NA	0.426655582	0.004329458
ENSBTAG00000047380	CALCB	-0.276698929	0.072459214
ENSBTAG00000047381	NA	-0.133486622	0.393456771
ENSBTAG00000047383	LOC784305	0.193014638	0.214943508
ENSBTAG00000047389	NA	0.122892658	0.432396457
ENSBTAG00000047401	NA	0.145571801	0.351634231
ENSBTAG00000047405	NA	0.184726461	0.235670872
ENSBTAG00000047406	NA	-0.053826788	0.731738647
ENSBTAG00000047411	NA	0.105043422	0.502617645
ENSBTAG00000047412	TNFSF18	-0.319939849	0.036484231
ENSBTAG00000047416	HEPH	-0.188064717	0.227164558
ENSBTAG00000047421	NA	0.163044649	0.296179675
ENSBTAG00000047424	TRIP10	0.450589253	0.00242826
ENSBTAG00000047432	LOC781224	0.476437184	0.001239215
ENSBTAG00000047441	NA	-0.081597247	0.602944544
ENSBTAG00000047448	C25H16orf54	0.537549893	0.000201455
ENSBTAG00000047449	LOC104968634	-0.071234194	0.649881526
ENSBTAG00000047450	SFR1	-0.447498463	0.00262266
ENSBTAG00000047462	NA	-0.468220595	0.001543405
ENSBTAG00000047473	LOC100301263	0.154128853	0.323730253
ENSBTAG00000047481	NA	-0.001973612	0.98997845
ENSBTAG00000047488	KCNK9	0.47215035	0.001390524
ENSBTAG00000047495	CD81	0.595754647	2.50E-05
ENSBTAG00000047499	IRX2	-0.331300301	0.029994346
ENSBTAG00000047501	NA	-0.227714951	0.141941755
ENSBTAG00000047502	FKBP5	0.48505261	0.000978636
ENSBTAG00000047520	MPV17L	0.376706749	0.012777005
ENSBTAG00000047529	NA	-0.327825862	0.031868936
ENSBTAG00000047531	ARHGAP4	0.602928285	1.88E-05
ENSBTAG00000047532	TRIQK	-0.19962538	0.199344569
ENSBTAG00000047534	NA	0.227101069	0.143048589
ENSBTAG00000047536	NA	-0.50151913	0.00061245
ENSBTAG00000047537	NA	0.137572762	0.379002673
ENSBTAG00000047538	RIMBP3B	0.285694594	0.063291595
ENSBTAG00000047545	RTL5	-0.387377848	0.010275188
ENSBTAG00000047547	NA	0.129940059	0.406258836
ENSBTAG00000047548	NA	0.061502754	0.69521508

ENSBTAG00000047560	C2CD4C	-0.102622442	0.512568793
ENSBTAG00000047561	NA	0.536559651	0.000208058
ENSBTAG00000047567	VEGFB	-0.385366908	0.010711608
ENSBTAG00000047570	NA	0.471159242	0.001427757
ENSBTAG00000047572	ZNF789	-0.518957776	0.000363126
ENSBTAG00000047575	NA	0.29339372	0.056200489
ENSBTAG00000047579	NA	-0.486209421	0.000947656
ENSBTAG00000047582	CSNK1E	0.164489741	0.291861012
ENSBTAG00000047591	C23H6orf141	-0.393042802	0.009126737
ENSBTAG00000047598	NA	-0.563975859	8.20E-05
ENSBTAG00000047604	HSD17B1	0.6642781	1.19E-06
ENSBTAG00000047605	LOC100337457	0.592666835	2.82E-05
ENSBTAG00000047606	NA	0.154799221	0.321604607
ENSBTAG00000047608	MRPS22	-0.478970235	0.001156855
ENSBTAG00000047609	NA	-0.612788374	1.25E-05
ENSBTAG00000047621	NA	-0.538777128	0.000193536
ENSBTAG00000047633	NA	0.408593034	0.006523607
ENSBTAG00000047646	NA	-0.192296911	0.216686654
ENSBTAG00000047647	LOC784731	-0.172224914	0.269440249
ENSBTAG00000047648	SYT2	-0.455209412	0.002161324
ENSBTAG00000047650	NXPH4	0.123860196	0.42875352
ENSBTAG00000047654	NA	0.311725316	0.041860858
ENSBTAG00000047659	NA	0.421523186	0.004875298
ENSBTAG00000047663	NA	-0.088086197	0.574325363
ENSBTAG00000047667	NA	0.001431683	0.992730156
ENSBTAG00000047668	NA	-0.210122684	0.176241212
ENSBTAG00000047673	THUMPD1	-0.472112851	0.001391917
ENSBTAG00000047675	LOC618268	-0.098798338	0.528486257
ENSBTAG00000047676	PRODH	0.593200407	2.76E-05
ENSBTAG00000047680	IRF7	0.417340096	0.005363566
ENSBTAG00000047685	NA	-0.195647276	0.208633001
ENSBTAG00000047697	NA	-0.166894324	0.284765671
ENSBTAG00000047699	NA	0.284503042	0.064449997
ENSBTAG00000047700	NA	-0.252868695	0.101835291
ENSBTAG00000047703	NA	0.559131066	9.72E-05
ENSBTAG00000047707	BOLA-DOB	0.033299335	0.832120574
ENSBTAG00000047710	NA	0.284263734	0.064684666
ENSBTAG00000047727	NA	-0.387551724	0.010238179
ENSBTAG00000047734	RUSF1	-0.368666089	0.014989241
ENSBTAG00000047739	TSC22D1	-0.428002954	0.00419532
ENSBTAG00000047740	NA	0.57247026	6.04E-05
ENSBTAG00000047744	NA	-0.261583585	0.090185871
ENSBTAG00000047752	OTUD1	-0.230438594	0.137107296
ENSBTAG00000047754	NA	-0.073838585	0.637949608
ENSBTAG00000047755	FNDC10	0.021498668	0.891159051
ENSBTAG00000047756	CNTROB	-0.283944994	0.06499828
ENSBTAG00000047764	LOC100848700	-0.060242713	0.701166612

ENSBTAG00000047766	NA	0.627927885	6.56E-06
ENSBTAG00000047768	COX7B	-0.211039885	0.174318004
ENSBTAG00000047776	NA	0.768107017	1.83E-09
ENSBTAG00000047783	NA	-0.417775046	0.005310891
ENSBTAG00000047787	LOC619131	0.115660616	0.460166608
ENSBTAG00000047788	NA	-0.112195918	0.473803146
ENSBTAG00000047790	NA	-0.045679953	0.771151777
ENSBTAG00000047793	TSSC4	0.491127061	0.000825492
ENSBTAG00000047794	DNAH1	0.110173225	0.481861927
ENSBTAG00000047801	CRELD2	0.550517027	0.000130828
ENSBTAG00000047805	NA	0.222716712	0.151139669
ENSBTAG00000047807	SAPCD2	-0.218123304	0.159971446
ENSBTAG00000047809	NA	-0.452928564	0.00228968
ENSBTAG00000047816	LOC100300483	-0.044752853	0.775675311
ENSBTAG00000047822	NA	-0.321392662	0.035595058
ENSBTAG00000047827	RENBP	0.296783912	0.053287137
ENSBTAG00000047837	NA	-0.0747211	0.633926605
ENSBTAG00000047838	NA	0.009596269	0.951300262
ENSBTAG00000047839	P2RY8	0.569964603	6.62E-05
ENSBTAG00000047848	NA	-0.047285394	0.763336231
ENSBTAG00000047852	NA	-0.088670829	0.571777595
ENSBTAG00000047871	KLF17	0.545876188	0.000152996
ENSBTAG00000047875	NA	0.428494161	0.004147328
ENSBTAG00000047876	SH3TC1	0.670938989	8.50E-07
ENSBTAG00000047879	KCNA3	-0.263922732	0.087242053
ENSBTAG00000047880	NA	-0.280039293	0.068940064
ENSBTAG00000047883	NA	0.201677502	0.194668562
ENSBTAG00000047894	SLC32A1	-0.150297657	0.336047034
ENSBTAG00000047902	ULBP21	-0.140668367	0.368264949
ENSBTAG00000047904	LOC527744	0.486683152	0.000935224
ENSBTAG00000047908	NA	0.084258057	0.591134445
ENSBTAG00000047914	CDHR5	0.096948457	0.536272202
ENSBTAG00000047918	NA	-0.10656169	0.496427562
ENSBTAG00000047926	OVCA2	0.561854971	8.84E-05
ENSBTAG00000047939	ZNF75D	-0.340281333	0.025567517
ENSBTAG00000047942	DESI1	0.047645685	0.761585433
ENSBTAG00000047947	NA	0.041169073	0.793229155
ENSBTAG00000047953	NLRP2	0.21042782	0.175599714
ENSBTAG00000047954	ZNF75D	-0.065737056	0.675349175
ENSBTAG00000047956	NAGLU	0.603689148	1.82E-05
ENSBTAG00000047957	NA	-0.387530625	0.010242663
ENSBTAG00000047958	DPP7	-0.035680059	0.820308952
ENSBTAG00000047970	NA	0.328656014	0.031412472
ENSBTAG00000047972	INAVA	0.313798077	0.040446817
ENSBTAG00000047988	NA	0.683571569	4.37E-07
ENSBTAG00000047991	TAF4	0.501828415	0.000606944
ENSBTAG00000047996	NA	0.061177335	0.696750413

ENSBTAG00000047998	COL5A1	-0.349363699	0.021658086
ENSBTAG00000048000	NA	-0.063811177	0.684358743
ENSBTAG00000048004	NA	0.408177184	0.006583787
ENSBTAG00000048010	NUDT14	-0.321185412	0.035720803
ENSBTAG00000048011	GPR160	0.220410173	0.155528652
ENSBTAG00000048023	NA	0.310779856	0.042519096
ENSBTAG00000048029	MMP1	-0.009465966	0.951960756
ENSBTAG00000048041	ACTR1B	-0.566590434	7.47E-05
ENSBTAG00000048042	NA	-0.716442306	6.57E-08
ENSBTAG00000048049	NA	-0.420882095	0.00494752
ENSBTAG00000048054	UAP1L1	-0.562992759	8.49E-05
ENSBTAG00000048059	TMEM86A	0.177398457	0.255097205
ENSBTAG00000048062	KDM6B	0.580478721	4.49E-05
ENSBTAG00000048067	EPOP	-0.364472188	0.016266625
ENSBTAG00000048077	MAGED4B	-0.180504831	0.246735369
ENSBTAG00000048098	PKP3	-0.362172123	0.017005463
ENSBTAG00000048107	CANX	-0.030643208	0.845341667
ENSBTAG00000048112	NA	-0.118691594	0.448412753
ENSBTAG00000048114	LOC100848331	-0.499086047	0.000657343
ENSBTAG00000048122	CFD	0.384699617	0.010859888
ENSBTAG00000048125	ENTPD2	-0.0959938	0.540311876
ENSBTAG00000048135	IGCGAMMA	-0.220421358	0.155507147
ENSBTAG00000048137	NA	0.056939008	0.716854207
ENSBTAG00000048140	DNAAF5	-0.276875914	0.072269273
ENSBTAG00000048145	NA	0.399419898	0.007967552
ENSBTAG00000048148	NA	0.115543357	0.460624636
ENSBTAG00000048152	TUBG1	-0.546746182	0.000148597
ENSBTAG00000048154	NA	0.368458204	0.015050492
ENSBTAG00000048155	FCN1	0.489748431	0.000858235
ENSBTAG00000048160	TIGD5	0.331949647	0.029654327
ENSBTAG00000048171	TAP	-0.057622091	0.7136009
ENSBTAG00000048174	NA	0.026016012	0.868472314
ENSBTAG00000048179	LOC782835	0.327156954	0.032240709
ENSBTAG00000048184	NA	0.133546245	0.393243579
ENSBTAG00000048185	NA	0.184665192	0.235828994
ENSBTAG00000048188	NA	-0.229122951	0.13942706
ENSBTAG00000048191	NA	0.007470706	0.96207826
ENSBTAG00000048205	NA	-0.145555697	0.351688087
ENSBTAG00000048226	NA	0.308755357	0.043956927
ENSBTAG00000048228	SNHG12	0.229357435	0.139011497
ENSBTAG00000048229	NA	0.596208059	2.46E-05
ENSBTAG00000048230	NA	-0.20325008	0.191138076
ENSBTAG00000048234	NA	-0.522809394	0.000322295
ENSBTAG00000048245	NA	0.235253867	0.128861066
ENSBTAG00000048246	DPP4	-0.267251179	0.083182557
ENSBTAG00000048249	NA	0.305031421	0.046704828
ENSBTAG00000048250	HSTN	-0.193031876	0.214901762

ENSBTAG00000048255	NA	0.154908085	0.321260246
ENSBTAG00000048265	NA	-0.323659095	0.034243516
ENSBTAG00000048271	MICAL3	-0.395001	0.008756289
ENSBTAG00000048272	NA	0.059313971	0.705564679
ENSBTAG00000048273	C6H4orf3	0.231812268	0.134715928
ENSBTAG00000048306	NA	0.289242843	0.059939912
ENSBTAG00000048314	NA	0.259106932	0.093386014

RNA-seq-based module (R = correlation; P= p-value)

Supplementary File S11: List of the hub miRNAs of the blue miRNA-seq-based module

Module_info	Module_size	miRNA_id	Module_label	Module_color
blue	38	bta-miR-100	2	blue
		bta-miR-10b	2	blue
		bta-miR-125a	2	blue
		bta-miR-127	2	blue
		bta-miR-1388-5p	2	blue
		bta-miR-141	2	blue
		bta-miR-143	2	blue
		bta-miR-148a	2	blue
		bta-miR-150	2	blue
		bta-miR-151-3p	2	blue
		bta-miR-152	2	blue
		bta-miR-182	2	blue
		bta-miR-183	2	blue
		bta-miR-193b	2	blue
		bta-miR-200a	2	blue
		bta-miR-200b	2	blue
		bta-miR-200c	2	blue
		bta-miR-204	2	blue
		bta-miR-205	2	blue
		bta-miR-224	2	blue
		bta-miR-2285t	2	blue
		bta-miR-27b	2	blue
		bta-miR-29a	2	blue
		bta-miR-30a-5p	2	blue
		bta-miR-31	2	blue
		bta-miR-335	2	blue
		bta-miR-3431	2	blue
		bta-miR-375	2	blue
		bta-miR-429	2	blue
		bta-miR-450b	2	blue
		bta-miR-451	2	blue
		bta-miR-455-5p	2	blue
		bta-miR-486	2	blue
		bta-miR-504	2	blue
		bta-miR-615	2	blue
		bta-miR-96	2	blue
		bta-miR-99a-3p	2	blue
		bta-miR-99a-5p	2	blue

Modulememberships_info_miRNA_id	MEblue	MEblue	HubmiRNAs_info
bta-miR-200a	0.928817336	7.62E-19	19
bta-miR-182	0.893636358	1.68E-15	
bta-miR-429	0.874820089	3.66E-14	
bta-miR-200b	0.870454822	6.96E-14	
bta-miR-205	0.863049728	1.97E-13	
bta-miR-30a-5p	0.855615079	5.28E-13	
bta-miR-141	0.83547703	5.91E-12	
bta-miR-29a	0.790749317	4.66E-10	
bta-miR-200c	0.790041799	4.95E-10	
bta-miR-183	0.770615478	2.39E-09	
bta-miR-450b	0.752136142	9.33E-09	
bta-miR-375	0.73037795	4.02E-08	
bta-miR-127	0.722821996	6.46E-08	
bta-miR-99a-5p	0.721902097	6.84E-08	
bta-miR-31	0.713835057	1.11E-07	
bta-miR-125a	0.676352344	8.82E-07	
bta-miR-504	0.673715817	1.01E-06	
bta-miR-193b	0.66306478	1.71E-06	
bta-miR-143	0.651044877	3.03E-06	
bta-miR-3431	0.632063525	7.13E-06	
bta-miR-27b	0.61579777	1.42E-05	
bta-miR-151-3p	0.610847977	1.74E-05	
bta-miR-486	0.602771571	2.40E-05	
bta-miR-99a-3p	0.600506688	2.62E-05	
bta-miR-152/bta-miR-2957	0.599376775	2.74E-05	
bta-miR-1388-5p	0.549406158	0.000164411	
bta-miR-30f	0.546571418	0.000180492	
bta-miR-224	0.515709896	0.000473344	
bta-miR-96	0.513722701	0.000502102	
bta-miR-424-3p	0.490978319	0.000961949	
bta-miR-204	0.488167321	0.001039236	
bta-miR-615	0.482182813	0.001222432	
bta-miR-455-5p	0.470220354	0.001676561	
bta-miR-424-5p	0.464692806	0.001932724	
bta-miR-542-5p/bta-miR-3601	0.457993746	0.00228904	
bta-miR-503-3p	0.448917001	0.00286355	
bta-miR-34a	0.440810896	0.003479881	
bta-miR-148a	0.440586277	0.003498496	
bta-miR-503-5p	0.4105405	0.00692328	
bta-miR-100	0.401843325	0.008342789	
bta-miR-6522	0.397692421	0.009104186	
bta-miR-150	0.395513097	0.009527291	
bta-miR-411a	0.384075236	0.012035066	
bta-miR-2285t	0.380786739	0.01285268	

bta-miR-184	0.379419183	0.013206351
bta-miR-6518	0.376910193	0.01387675
bta-miR-664	0.367452445	0.016669644
bta-miR-885	0.36180422	0.018553661
bta-miR-452	0.360277695	0.019092561
bta-miR-195	0.356646902	0.020427397
bta-miR-335	0.35651172	0.02047857
bta-miR-497	0.35321329	0.021760906
bta-miR-10b	0.350373642	0.022918076
bta-miR-760-3p	0.336398975	0.029387768
bta-miR-23b-3p	0.32727637	0.034375801
bta-miR-1246	0.316455021	0.041173768
bta-let-7e	0.311786419	0.044426646
bta-let-7c	0.307271222	0.047768042
bta-miR-2454-5p	0.307147411	0.047862451
bta-miR-99b	0.304428905	0.049973662
bta-miR-215	0.304071928	0.050256385
bta-miR-222	0.302441557	0.051564061
bta-miR-146a	0.297809227	0.055429521
bta-miR-451	0.296457792	0.056599956
bta-miR-1388-3p	0.293620701	0.059121425
bta-miR-380-3p	0.277190784	0.075535992
bta-miR-2411-3p	0.267842378	0.086359312
bta-miR-221	0.266570168	0.087920909
bta-miR-2347	0.246817419	0.115077329
bta-miR-29c	0.240300061	0.125304505
bta-miR-138	0.23599549	0.132423568
bta-miR-196b	0.235784399	0.132780269
bta-miR-126-5p	0.233164557	0.137267006
bta-miR-2436-3p	0.231490616	0.14019209
bta-miR-181c	0.223316793	0.155140287
bta-miR-2344	0.220609396	0.16033929
bta-miR-98	0.215738825	0.170009111
bta-miR-2350	0.213190092	0.175233628
bta-miR-2284x	0.201854965	0.199865691
bta-miR-421	0.201493315	0.200689668
bta-miR-149-5p	0.193523407	0.219456572
bta-miR-125b	0.191340147	0.224802281
bta-miR-6524	0.184519861	0.242075413
bta-miR-151-5p	0.18400968	0.243402635
bta-miR-129-3p	0.176398227	0.263788396
bta-miR-27a-3p	0.169361036	0.283616456
bta-miR-210	0.16074485	0.309182227
bta-miR-6521	0.157845223	0.318105248
bta-miR-455-3p	0.151142942	0.33934423
bta-miR-760-5p	0.146830919	0.353460167
bta-miR-190a	0.14383183	0.363485377

bta-miR-126-3p	0.141255255	0.372233389
bta-miR-3613	0.139610992	0.377881033
bta-miR-2289	0.139290076	0.378989192
bta-miR-2355-5p	0.13599317	0.390484805
bta-miR-188	0.133343932	0.39986807
bta-miR-1940	0.130152129	0.411344437
bta-miR-145	0.128618279	0.416925706
bta-miR-2411-5p	0.128430486	0.417611973
bta-miR-208b	0.125836756	0.427155723
bta-miR-181d	0.124615169	0.431692599
bta-miR-1434-5p	0.116981352	0.46064486
bta-miR-193a-5p	0.114514288	0.470219797
bta-miR-296	0.113025332	0.476049342
bta-miR-2398	0.112101779	0.47968428
bta-miR-410	0.108930855	0.49227451
bta-miR-1434-3p	0.107778674	0.496891119
bta-miR-24	0.106821226	0.500744275
bta-miR-2331-5p	0.098914138	0.533138244
bta-miR-2483-5p	0.095983199	0.545399228
bta-miR-6527	0.092246262	0.561224472
bta-miR-2419-3p	0.090838997	0.567238851
bta-miR-1307	0.089428461	0.573296845
bta-miR-1296	0.088911905	0.575522713
bta-miR-671	0.087898041	0.579902893
bta-miR-362-3p	0.086874611	0.584339589
bta-miR-92b	0.083507393	0.599042966
bta-miR-2447	0.083086321	0.600892917
bta-miR-378b	0.074534927	0.63898566
bta-miR-2320-5p	0.07221027	0.649506953
bta-miR-30d	0.065247312	0.681418809
bta-miR-532	0.062856456	0.692507572
bta-miR-2448-3p	0.060909016	0.701586985
bta-miR-330	0.054815255	0.730258193
bta-miR-2419-5p	0.052403901	0.741707104
bta-miR-2388-3p	0.051909937	0.744059302
bta-miR-139	0.051387698	0.746548641
bta-miR-2450a	0.04335411	0.785148636
bta-miR-660	0.039595104	0.803392372
bta-miR-2370-3p	0.038467703	0.808884653
bta-miR-6119-3p	0.037439238	0.813902881
bta-miR-149-3p	0.036689552	0.817565497
bta-miR-32	0.035973712	0.82106634
bta-miR-1249	0.035671775	0.822544003
bta-miR-2425-3p	0.034412929	0.828711216
bta-miR-345-3p	0.033254119	0.834397336
bta-miR-23a	0.031353289	0.843742389
bta-miR-132	0.031117146	0.84490484

bta-miR-25	0.028060593	0.859979737
bta-miR-193a-3p	0.023209511	0.884004238
bta-let-7b/bta-miR-3596	0.020187461	0.89902409
bta-miR-362-5p	0.016696357	0.916418255
bta-miR-301b	0.015947957	0.920152394
bta-miR-340	0.015124041	0.92426528
bta-let-7i	0.012417893	0.937787175
bta-miR-16a	0.010725923	0.946250514
bta-miR-2903	0.007102071	0.964395714
bta-miR-2468	0.0015315	0.992319904
bta-miR-324	-0.006530678	0.96725862
bta-miR-33b	-0.007287239	0.96346804
bta-miR-374b	-0.008160815	0.959092174
bta-miR-6520	-0.008617679	0.956804144
bta-miR-2349	-0.008872866	0.955526284
bta-miR-6531	-0.01076706	0.946044672
bta-miR-449a	-0.019042786	0.904722603
bta-miR-2285q	-0.019784759	0.901028296
bta-miR-374a	-0.022550514	0.887276279
bta-miR-2320-3p	-0.023169231	0.884204185
bta-miR-369-3p	-0.025296767	0.873653448
bta-miR-2346	-0.029139226	0.854654034
bta-miR-378	-0.031583404	0.842609922
bta-let-7g	-0.034189617	0.829806315
bta-miR-2417	-0.035143023	0.825133151
bta-miR-326	-0.038184666	0.810264943
bta-miR-2316	-0.038536096	0.80855121
bta-miR-28	-0.039320074	0.804731365
bta-miR-2431-3p	-0.040749638	0.797777569
bta-miR-1343-5p	-0.044428771	0.779953283
bta-miR-2478	-0.048339242	0.761129666
bta-miR-449b	-0.04968153	0.754698996
bta-miR-197	-0.053148223	0.738167124
bta-miR-2368-3p	-0.06180531	0.697403072
bta-miR-363	-0.062234317	0.695403582
bta-miR-2339	-0.06431292	0.685744784
bta-miR-16b	-0.067392921	0.671523474
bta-miR-2454-3p	-0.070555304	0.657038602
bta-miR-2448-5p	-0.070854086	0.655676354
bta-miR-2323	-0.071982883	0.65053976
bta-miR-2409	-0.073736395	0.642592038
bta-miR-505	-0.07394619	0.641643762
bta-miR-6120-3p	-0.075902318	0.632829231
bta-miR-22-5p	-0.07599112	0.632430258
bta-miR-19a	-0.077187054	0.627067145
bta-miR-22-3p/bta-miR-3600	-0.077558514	0.625405183
bta-miR-2431-5p	-0.077934846	0.62372329

bta-miR-2397-3p	-0.079813647	0.615354934
bta-miR-185	-0.082304471	0.604334486
bta-miR-1468	-0.083553209	0.598841826
bta-miR-2410	-0.090068382	0.570544842
bta-miR-2465	-0.092233877	0.561277275
bta-miR-186	-0.09260834	0.559681837
bta-miR-2319a	-0.093466027	0.556035571
bta-miR-2400	-0.094825201	0.550280283
bta-miR-6523	-0.102799858	0.51709269
bta-miR-2284w	-0.103644343	0.513637622
bta-miR-155	-0.103804213	0.512984843
bta-miR-769	-0.104776417	0.509024132
bta-miR-425-5p	-0.105187372	0.507354571
bta-let-7a-5p	-0.109421324	0.490316013
bta-miR-2285h	-0.114032496	0.472101939
bta-miR-6517	-0.116312188	0.463231542
bta-miR-4286	-0.116684035	0.461793193
bta-miR-2389	-0.118208475	0.455921626
bta-miR-331	-0.118590618	0.454456116
bta-miR-30e-5p	-0.128254731	0.418254828
bta-miR-6525	-0.12830146	0.418083853
bta-miR-6123	-0.131642755	0.405961557
bta-miR-2469	-0.133478632	0.399387856
bta-miR-3432	-0.136253379	0.389570178
bta-miR-2336	-0.138134216	0.382996422
bta-miR-6529	-0.138821438	0.380610905
bta-miR-2284i	-0.139075658	0.379730671
bta-miR-2483-3p	-0.141980917	0.369757012
bta-miR-1839	-0.142932608	0.366524266
bta-miR-181b	-0.145824497	0.35680547
bta-miR-6533	-0.149478942	0.344749773
bta-miR-2449	-0.154338062	0.329112382
bta-miR-2332	-0.155461629	0.32556055
bta-miR-26a/bta-miR-26c	-0.156786807	0.321402329
bta-miR-484	-0.160502524	0.309921781
bta-miR-2425-5p	-0.163058721	0.302177076
bta-miR-425-3p	-0.164480389	0.297923831
bta-miR-502b	-0.16667567	0.291432097
bta-miR-874	-0.166775382	0.291139423
bta-miR-378c	-0.16714313	0.290061659
bta-miR-33a	-0.168030926	0.287470446
bta-miR-30b-5p	-0.175148009	0.26724204
bta-miR-2898	-0.180437927	0.252832134
bta-miR-677	-0.183878364	0.243745042
bta-miR-328	-0.189022772	0.23057354
bta-miR-2397-5p	-0.189965451	0.228213764
bta-miR-345-5p	-0.190171105	0.227701164

bta-miR-2443	-0.190177063	0.227686325
bta-miR-27a-5p	-0.192131537	0.22285432
bta-miR-21-3p	-0.192540168	0.221853064
bta-miR-342	-0.19524747	0.215297711
bta-miR-147	-0.196487628	0.212340133
bta-miR-23b-5p	-0.198206577	0.208287578
bta-miR-2357	-0.198645246	0.207262078
bta-miR-219-5p	-0.204668397	0.193536683
bta-miR-128	-0.205600528	0.191471361
bta-miR-192	-0.206359492	0.189801283
bta-miR-29b	-0.206616062	0.18923905
bta-miR-2318	-0.207757098	0.186752952
bta-miR-103	-0.209045721	0.183973296
bta-miR-2424	-0.212692005	0.176267943
bta-miR-130a	-0.21799414	0.16548053
bta-miR-1271	-0.219721176	0.162072217
bta-miR-6119-5p	-0.221230594	0.159135356
bta-miR-301a	-0.223102448	0.155547348
bta-miR-1306	-0.223641999	0.154524178
bta-miR-101	-0.226514883	0.149158918
bta-miR-2328-5p	-0.227880826	0.14665647
bta-miR-423-3p	-0.231036753	0.140993069
bta-miR-6530	-0.234168773	0.135534082
bta-let-7f	-0.236026014	0.132372048
bta-miR-491	-0.236317029	0.131881606
bta-let-7a	-0.237188979	0.130420231
bta-miR-2446	-0.238928374	0.127541181
bta-miR-2313-5p	-0.242228801	0.122209415
bta-miR-361	-0.246666243	0.115307168
bta-miR-21-5p	-0.2481323	0.113092845
bta-miR-10a	-0.249720416	0.110730688
bta-miR-2402	-0.250367439	0.109779127
bta-miR-292	-0.25543691	0.102537364
bta-miR-34b	-0.260564514	0.095590258
bta-miR-30b-3p	-0.265827604	0.088842453
bta-miR-423-5p	-0.267375579	0.086929771
bta-let-7d	-0.271157629	0.082391119
bta-miR-15a	-0.271558545	0.081921043
bta-miR-744	-0.274483632	0.078554395
bta-miR-1343-3p	-0.275354864	0.077572866
bta-miR-142-3p	-0.280337861	0.072142358
bta-miR-18a	-0.284649111	0.067689611
bta-miR-212	-0.286402518	0.065942087
bta-miR-2285b	-0.286545256	0.065801416
bta-miR-146b	-0.28667658	0.065672205
bta-miR-20b	-0.291129551	0.061408649
bta-miR-877	-0.291285488	0.061263441

bta-miR-545-3p	-0.300441478	0.053205528
bta-miR-34c	-0.301249349	0.052537525
bta-miR-2484	-0.301436325	0.052383886
bta-miR-500	-0.303619741	0.050616364
bta-miR-2376	-0.30560126	0.049054176
bta-miR-2313-3p	-0.312977774	0.043577383
bta-miR-19b	-0.319581621	0.039105818
bta-miR-1291	-0.32922953	0.033253141
bta-miR-1277	-0.336373768	0.029400677
bta-miR-2285v	-0.336401296	0.02938658
bta-miR-142-5p	-0.340555344	0.027322485
bta-miR-449c	-0.341304711	0.02696326
bta-miR-191	-0.352113528	0.022203124
bta-miR-338	-0.353990857	0.021452712
bta-miR-454	-0.35543769	0.020888974
bta-miR-194	-0.360429585	0.019038357
bta-miR-652	-0.365270004	0.017377515
bta-miR-93	-0.366134548	0.017094128
bta-miR-2415-3p	-0.371445372	0.015437496
bta-miR-2440	-0.37173612	0.01535087
bta-miR-339a	-0.372520651	0.015119176
bta-miR-17-5p	-0.382026526	0.012539049
bta-miR-2457	-0.398639524	0.008925401
bta-miR-130b	-0.400629264	0.008559597
bta-miR-2299-5p	-0.404503816	0.007884139
bta-miR-2284z	-0.405299157	0.007751316
bta-miR-2353	-0.407910146	0.007328742
bta-miR-30c	-0.411088881	0.006841234
bta-miR-106a	-0.424385316	0.005093219
bta-miR-181a	-0.427543344	0.004740333
bta-miR-2285k	-0.438127356	0.003708044
bta-miR-107	-0.445169175	0.003135454
bta-miR-92a	-0.4483553	0.002902934
bta-miR-628	-0.458698281	0.002249024
bta-miR-18b	-0.460153865	0.002168297
bta-miR-545-5p	-0.460371471	0.002156451
bta-miR-2388-5p	-0.460992369	0.002122963
bta-miR-223	-0.468278072	0.001762925
bta-miR-140	-0.473714902	0.001530556
bta-miR-26b	-0.481188509	0.001255501
bta-miR-187	-0.494619514	0.000869463
bta-miR-2299-3p	-0.510869568	0.00054613
bta-miR-106b	-0.515514763	0.000476101
bta-miR-20a	-0.521658047	0.00039588
bta-miR-26a	-0.56005634	0.000114915
bta-miR-935	-0.565032982	9.68E-05
bta-miR-17-3p	-0.57775536	6.16E-05

bta-miR-15b	-0.637616978	5.59E-06
bta-miR-148b	-0.648377783	3.43E-06

miRNA_id	MEblue	MEblue
bta-miR-200a	0.928817336	7.62E-19
bta-miR-182	0.893636358	1.68E-15
bta-miR-429	0.874820089	3.66E-14
bta-miR-200b	0.870454822	6.96E-14
bta-miR-205	0.863049728	1.97E-13
bta-miR-30a-5p	0.855615079	5.28E-13
bta-miR-141	0.83547703	5.91E-12
bta-miR-29a	0.790749317	4.66E-10
bta-miR-200c	0.790041799	4.95E-10
bta-miR-183	0.770615478	2.39E-09
bta-miR-450b	0.752136142	9.33E-09
bta-miR-375	0.73037795	4.02E-08
bta-miR-127	0.722821996	6.46E-08
bta-miR-99a-5p	0.721902097	6.84E-08
bta-miR-31	0.713835057	1.11E-07
bta-miR-125a	0.676352344	8.82E-07
bta-miR-504	0.673715817	1.01E-06
bta-miR-193b	0.66306478	1.71E-06
bta-miR-143	0.651044877	3.03E-06

Supplementary File S12: The generated molecular interactome for the construction of integrated

STRING database PPI network

#node1	node2	experimentally_determined_interaction	combined_score
ABCA3	JAK1	0.052	0.436
ABCA3	SLC6A9	0	0.462
ABCA3	LOC515755	0	0.462
ABCA3	QKI	0	0.742
ABCA7	PTK2B	0	0.488
ABCA7	CASS4	0	0.609
ABCA7	PSEN1	0	0.539
ABCA7	INPP5D	0	0.597
ABCA7	LOC100138951	0	0.669
ABHD13	APRT	0	0.449
ABHD13	POLR2A	0	0.468
ABHD13	ZDHHC2	0	0.481
ABHD13	LIG4	0	0.493
ABHD13	LIPM	0	0.674
ABI1	RHOG	0.126	0.489
ABI1	ELMO2	0	0.537
ABI1	GRB2	0.052	0.401
ABI1	PIK3CA	0	0.642
ABI1	JAK2	0.158	0.44
ABI1	PIK3R6	0	0.62
ABI1	ITGA9	0.138	0.498
ABI1	VASP	0.242	0.671
ABI1	FNBP1	0.191	0.615
ABI1	RIPK2	0.158	0.419
ABI1	ROCK1	0.158	0.574
ABI1	CRKL	0.052	0.58
ABI1	DIAPH2	0.12	0.665
ABT1	EIF4A1	0.164	0.434
ABT1	ISG20L2	0.455	0.772
ABT1	PI4K2A	0	0.592
ABT1	RPS9	0	0.441
ABT1	ESF1	0.925	0.99
ABT1	XRN2	0.42	0.433
ABT1	RCL1	0	0.481
ABT1	DDX5	0.164	0.52
ABT1	NOP9	0	0.573
ABT1	TFB1M	0	0.574
ABT1	ISG20	0.232	0.665
ABT1	GTPBP4	0	0.689
ABT1	LTV1	0	0.769
ABT1	NOM1	0.762	0.838
ABT1	KRR1	0.925	0.984

ABTB1	STK19	0	0.632
ABTB1	CARS	0.433	0.433
ABTB1	FBXO9	0	0.403
ABTB1	HOMEZ	0	0.424
ABTB1	LENG8	0	0.497
ABTB2	NDRG1	0	0.48
ABTB2	SAMSN1	0	0.465
ABTB2	CD99	0	0.41
ABTB2	KDM7A	0	0.543
ABTB2	SIDT2	0	0.559
ABTB2	MYBPH	0	0.632
ACSL4	DGAT2	0	0.501
ACSL4	ELOVL5	0.041	0.411
ACSL4	AGPAT6	0.046	0.586
ACSL4	MBOAT1	0	0.506
ACSL4	AGPAT9	0.046	0.594
ACSL4	LPCAT2	0.046	0.487
ACSL4	ACSL5	0.114	0.723
ACSL4	TBXAS1	0.057	0.422
ACSL4	AMMECR1	0	0.585
ACSL5	DGAT2	0	0.794
ACSL5	CYP4V2	0.057	0.499
ACSL5	ELOVL5	0	0.401
ACSL5	AGPAT6	0.046	0.535
ACSL5	CASP7	0.055	0.44
ACSL5	DTX3L	0	0.432
ACSL5	TAPBPL	0	0.422
ACSL5	AGPAT9	0.046	0.509
ACSL5	SRGN	0	0.643
ACSL5	LPCAT2	0.046	0.488
ACSL5	DCAF11	0	0.423
ACSL5	TCF7L2	0	0.463
ACTA2	KAT2B	0.163	0.585
ACTA2	HCLS1	0.146	0.631
ACTA2	CORO6	0.296	0.433
ACTA2	IL1B	0	0.426
ACTA2	EPC1	0.431	0.469
ACTA2	CALM1	0.316	0.445
ACTA2	CREBBP	0.163	0.518
ACTA2	JUN	0.055	0.627
ACTA2	TPM4	0.405	0.574
ACTA2	SLC16A12	0	0.47
ACTA2	IRF5	0	0.502
ACTA2	KAT5	0.399	0.525
ACTA2	PTK2B	0.06	0.556
ACTA2	CASP7	0.161	0.422
ACTA2	EHBP1L1	0.257	0.508

ACTA2	UBXN7	0.254	0.552
ACTA2	PIK3CA	0.164	0.638
ACTA2	PTPRC	0.058	0.533
ACTA2	KAT8	0.394	0.518
ACTA2	MEF2A	0.07	0.435
ACTA2	NF1	0.051	0.558
ACTA2	BCAR1	0.044	0.611
ACTA2	CORO2A	0.296	0.433
ACTA2	RELA	0.073	0.568
ACTA2	SERPINE1	0	0.459
ACTA2	SNAI1	0	0.483
ACTA2	CAPN2	0.053	0.403
ACTA2	CD44	0.045	0.411
ACTA2	ITGAV	0.041	0.419
ACTA2	COTL1	0.322	0.421
ACTA2	TNF	0.079	0.433
ACTA2	ARF6	0.12	0.448
ACTA2	ITGB7	0.08	0.463
ACTA2	VASP	0.158	0.474
ACTA2	CORO1A	0.296	0.478
ACTA2	IRF1	0	0.495
ACTA2	CNN2	0.257	0.51
ACTA2	ARID4A	0.443	0.511
ACTA2	ARID4B	0.443	0.511
ACTA2	IRF7	0	0.514
ACTA2	ELN	0	0.534
ACTA2	GTF2B	0.045	0.537
ACTA2	HIP1R	0.389	0.551
ACTA2	TGFBR1	0.093	0.571
ACTA2	DAAM2	0.43	0.58
ACTA2	DIAPH2	0.078	0.583
ACTA2	CRKL	0.044	0.586
ACTA2	ARHGEF6	0.043	0.592
ACTA2	LIMK2	0.093	0.602
ACTA2	LAMB3	0	0.609
ACTA2	FLT4	0.043	0.639
ACTA2	VEGFA	0	0.645
ACTA2	PXN	0.055	0.668
ACTA2	AVIL	0.334	0.669
ACTA2	ZYX	0.089	0.689
ACTA2	MYSM1	0.525	0.719
ACTA2	POLR2A	0.43	0.74
ACTA2	GSN	0.501	0.871
ACTB	PRKAA1	0.078	0.452
ACTB	CSF1	0.174	0.535
ACTB	RHOG	0.158	0.404
ACTB	MYD88	0	0.513

ACTB	RET	0.052	0.411
ACTB	KAT2B	0.163	0.709
ACTB	HCLS1	0.146	0.612
ACTB	CXCR4	0	0.45
ACTB	CORO6	0.296	0.433
ACTB	IL1B	0	0.71
ACTB	BCL6	0.082	0.414
ACTB	EPC1	0.431	0.469
ACTB	CALM1	0.257	0.455
ACTB	EIF2C2	0.114	0.429
ACTB	NFKBIB	0.119	0.508
ACTB	TAGLN2	0.223	0.405
ACTB	TUBA4A	0.156	0.433
ACTB	JAK1	0.093	0.533
ACTB	NCF1	0.164	0.526
ACTB	RBPJ	0.12	0.401
ACTB	CREBBP	0.163	0.788
ACTB	JUN	0.055	0.866
ACTB	ALAS1	0	0.426
ACTB	TNFRSF1A	0.043	0.407
ACTB	FOS	0.044	0.639
ACTB	RAF1	0.093	0.406
ACTB	TPM4	0.405	0.579
ACTB	IRF5	0	0.673
ACTB	CREB1	0	0.552
ACTB	KAT5	0.534	0.672
ACTB	PTK2B	0.06	0.554
ACTB	MAP1LC3A	0.054	0.62
ACTB	ACTG1	0.76	0.891
ACTB	TLR4	0.123	0.638
ACTB	STAT6	0.045	0.41
ACTB	RPS9	0.042	0.53
ACTB	SOD2	0	0.509
ACTB	CASP7	0.161	0.67
ACTB	IL10	0	0.659
ACTB	EHBP1L1	0.257	0.495
ACTB	NOS2	0.069	0.519
ACTB	UBXN7	0.254	0.552
ACTB	IKBKB	0.093	0.541
ACTB	TLR2	0.123	0.565
ACTB	EDN1	0	0.461
ACTB	FRMD4A	0.125	0.424
ACTB	CDKN1A	0	0.587
ACTB	SOCS3	0	0.463
ACTB	ATF3	0.081	0.472
ACTB	RAP1B	0.12	0.413
ACTB	PIK3CA	0.164	0.69

ACTB	EZH2	0.051	0.43
ACTB	IRF2	0	0.638
ACTB	PTPRC	0.058	0.686
ACTB	ICAM1	0	0.538
ACTB	IL1A	0	0.42
ACTB	KAT8	0.394	0.544
ACTB	MEF2A	0.07	0.455
ACTB	CFLAR	0.161	0.526
ACTB	TYK2	0.093	0.426
ACTB	NF1	0.051	0.726
ACTB	BCAR1	0.054	0.549
ACTB	JAK2	0.093	0.616
ACTB	CORO2A	0.296	0.433
ACTB	SLC1A2	0	0.434
ACTB	ITGA5	0.041	0.432
ACTB	RELA	0.081	0.819
ACTB	SIRT1	0.087	0.569
ACTB	PTGS2	0	0.616
ACTB	PKNOX1	0.174	0.566
ACTB	SERPINE1	0	0.443
ACTB	SNAI1	0	0.548
ACTB	ISG15	0.14	0.457
ACTB	VEGFC	0	0.47
ACTB	IL6	0	0.734
ACTB	MCL1	0.079	0.462
ACTB	COTL1	0.466	0.609
ACTB	LAMB3	0	0.544
ACTB	AVIL	0.334	0.669
ACTB	PPARD	0.069	0.463
ACTB	HDAC4	0.156	0.405
ACTB	ARHGEF6	0.043	0.43
ACTB	ZYX	0.081	0.613
ACTB	TGFBR1	0.093	0.42
ACTB	PXN	0.055	0.687
ACTB	TLR9	0.123	0.469
ACTB	CDKN1B	0	0.535
ACTB	ARID4A	0.443	0.511
ACTB	ITGB7	0.08	0.505
ACTB	VASP	0.204	0.491
ACTB	CXCL8	0	0.462
ACTB	GSN	0.354	0.809
ACTB	ITGAV	0.041	0.444
ACTB	CYBB	0.081	0.579
ACTB	NFKB1	0.119	0.583
ACTB	AIF1	0.2	0.633
ACTB	SMG1	0.164	0.425
ACTB	CNN2	0.223	0.651

ACTB	CASP4	0.161	0.488
ACTB	IRAK4	0.093	0.414
ACTB	STAT3	0.045	0.694
ACTB	HIP1R	0.389	0.551
ACTB	MYSM1	0.525	0.719
ACTB	H3F3A	0.258	0.508
ACTB	CHD1	0.164	0.415
ACTB	TNF	0.087	0.786
ACTB	SMAD7	0.06	0.408
ACTB	HCK	0.16	0.408
ACTB	PSEN1	0	0.416
ACTB	CLIC4	0.217	0.429
ACTB	MX1	0.107	0.437
ACTB	IL18	0	0.443
ACTB	CORO1A	0.296	0.45
ACTB	HK2	0.119	0.459
ACTB	ROCK1	0.152	0.461
ACTB	CAPN2	0.053	0.505
ACTB	BCL2L11	0	0.508
ACTB	ARID4B	0.443	0.511
ACTB	ARF6	0.12	0.513
ACTB	DIAPH2	0.078	0.515
ACTB	LAMP1	0.055	0.529
ACTB	FLT4	0.043	0.537
ACTB	CRKL	0.044	0.55
ACTB	STAT4	0.045	0.55
ACTB	XIAP	0.055	0.551
ACTB	MDM2	0.081	0.554
ACTB	DDIT3	0.042	0.563
ACTB	DAAM2	0.43	0.58
ACTB	STAT1	0.078	0.592
ACTB	LIMK2	0.093	0.618
ACTB	LOC100297725	0.258	0.631
ACTB	CD44	0.045	0.644
ACTB	LRRK2	0.463	0.647
ACTB	LMNB1	0.233	0.654
ACTB	KRAS	0.12	0.673
ACTB	GTF2B	0.045	0.677
ACTB	IRF1	0	0.704
ACTB	VEGFA	0	0.726
ACTB	IRF7	0	0.755
ACTB	POLR2A	0.646	0.933
ACTG1	KAT2B	0.163	0.683
ACTG1	HCLS1	0.146	0.918
ACTG1	CORO6	0.296	0.492
ACTG1	EPC1	0.431	0.469
ACTG1	CALM1	0.257	0.474

ACTG1	TAGLN2	0.223	0.945
ACTG1	JAK1	0.093	0.409
ACTG1	CREBBP	0.163	0.703
ACTG1	JUN	0.055	0.709
ACTG1	FOS	0.044	0.48
ACTG1	TPM4	0.405	0.807
ACTG1	IRF5	0	0.606
ACTG1	CREB1	0	0.432
ACTG1	KAT5	0.471	0.596
ACTG1	PTK2B	0.06	0.532
ACTG1	LOC541180	0.115	0.403
ACTG1	TMSB4X	0.203	0.405
ACTG1	TRAF2	0.347	0.41
ACTG1	LOC100297725	0.218	0.411
ACTG1	ARHGEF6	0.043	0.43
ACTG1	CORO2A	0.296	0.433
ACTG1	PPIF	0.069	0.44
ACTG1	DNM2	0.139	0.442
ACTG1	AIF1	0.2	0.442
ACTG1	FLT4	0.043	0.443
ACTG1	STAT3	0.045	0.443
ACTG1	MEF2A	0.07	0.455
ACTG1	CASP4	0.161	0.456
ACTG1	ROCK1	0.152	0.458
ACTG1	ARF6	0.12	0.46
ACTG1	IL10	0	0.466
ACTG1	LMNB1	0.233	0.467
ACTG1	JAK2	0.093	0.472
ACTG1	CORO1A	0.296	0.475
ACTG1	LAMB3	0	0.49
ACTG1	EHBP1L1	0.257	0.495
ACTG1	ARID4A	0.443	0.511
ACTG1	ARID4B	0.443	0.511
ACTG1	CAPN2	0.053	0.512
ACTG1	IL6	0	0.513
ACTG1	DIAPH2	0.078	0.515
ACTG1	KAT8	0.394	0.518
ACTG1	CRKL	0.044	0.52
ACTG1	BCAR1	0.052	0.548
ACTG1	UBXN7	0.254	0.552
ACTG1	VEGFA	0	0.558
ACTG1	PIK3CA	0.164	0.569
ACTG1	DAAM2	0.43	0.58
ACTG1	HIP1R	0.389	0.592
ACTG1	IRF2	0	0.593
ACTG1	TNF	0.079	0.594
ACTG1	COTL1	0.47	0.601

ACTG1	KDM3A	0	0.612
ACTG1	IRF1	0	0.616
ACTG1	LIMK2	0.093	0.618
ACTG1	LRRK2	0.489	0.624
ACTG1	IRF7	0	0.654
ACTG1	GTF2B	0.045	0.658
ACTG1	NF1	0.051	0.66
ACTG1	CNN2	0.223	0.66
ACTG1	AVIL	0.334	0.669
ACTG1	FMNL3	0.165	0.683
ACTG1	ITGA9	0.041	0.685
ACTG1	RELA	0.078	0.709
ACTG1	ITGAV	0.041	0.713
ACTG1	PXN	0.055	0.73
ACTG1	ITGA5	0.041	0.745
ACTG1	MYSM1	0.525	0.749
ACTG1	POLR2A	0.464	0.837
ACTG1	ITGB7	0.08	0.89
ACTG1	VASP	0.336	0.893
ACTG1	CASP7	0.161	0.901
ACTG1	MANF	0	0.901
ACTG1	GSN	0.334	0.903
ACTG1	PLEK	0	0.936
ACTG1	ZYX	0.081	0.942
ACVR1B	HIVEP1	0.208	0.509
ACVR1B	PPP1R15A	0.044	0.645
ACVR1B	CREBBP	0.129	0.422
ACVR1B	GRB2	0.163	0.572
ACVR1B	PPM1D	0.158	0.441
ACVR1B	TAB2	0.156	0.684
ACVR1B	ITGA5	0.12	0.419
ACVR1B	ACVRL1	0.184	0.65
ACVR1B	PML	0.067	0.579
ACVR1B	VDR	0.1	0.4
ACVR1B	DAXX	0.055	0.579
ACVR1B	IL13RA1	0.044	0.407
ACVR1B	ITGAV	0.12	0.68
ACVR1B	PTPN6	0.101	0.525
ACVR1B	SMURF1	0.465	0.802
ACVR1B	PIK3R5	0	0.419
ACVR1B	TEC	0.453	0.472
ACVR1B	CD44	0.209	0.483
ACVR1B	XIAP	0.164	0.797
ACVR1B	SMAD7	0.47	0.88
ACVRL1	PPM1D	0.158	0.441
ACVRL1	TAB2	0.156	0.469
ACVRL1	VEGFA	0	0.41

ACVRL1	SMURF1	0.184	0.418
ACVRL1	ID1	0	0.431
ACVRL1	TGFBR1	0.257	0.719
ACVRL1	SMAD7	0.297	0.879
ADAM17	IL1B	0	0.403
ADAM17	SEMA4D	0	0.467
ADAM17	RHBDF2	0.441	0.818
ADAM17	RBPJ	0	0.504
ADAM17	TNFRSF1A	0.113	0.63
ADAM17	PLEK	0	0.459
ADAM17	ICAM1	0	0.431
ADAM17	MAD2L2	0.078	0.461
ADAM17	ITGA5	0.164	0.488
ADAM17	IL6	0	0.583
ADAM17	TFPI2	0.093	0.408
ADAM17	MMP25	0.046	0.512
ADAM17	NFIX	0	0.515
ADAM17	IL6R	0	0.496
ADAM17	CXCL8	0	0.417
ADAM17	PRKCB	0	0.62
ADAM17	HBEGF	0	0.709
ADAM17	TNFRSF1B	0.113	0.786
ADAM17	TNF	0.078	0.912
ADAM17	PSEN1	0.079	0.649
ADAM17	DLL1	0.16	0.797
ADAM17	SELL	0	0.61
ADAM17	CD44	0	0.488
ADAM19	HBEGF	0	0.423
ADAM19	PRKCB	0	0.464
ADAM19	ITGAV	0.087	0.539
ADAM19	MAD2L2	0.125	0.562
ADAM19	DLL1	0.046	0.566
ADAM19	ITGA9	0.071	0.599
ADAM19	SDC4	0	0.607
ADAP1	MXD1	0	0.424
ADAP1	PTK2B	0.136	0.463
ADAP1	PLEK	0	0.408
ADAP1	MXD4	0	0.481
ADAP1	CRLF3	0.042	0.45
ADAP1	GPR146	0	0.692
ADAP1	ARF6	0.142	0.787
ADAR	EIF2C2	0.113	0.484
ADAR	STAT2	0	0.729
ADAR	HPSE	0	0.554
ADAR	PML	0.055	0.4
ADAR	IRF1	0	0.404
ADAR	PARP9	0	0.416

ADAR	IFIT2	0.117	0.421
ADAR	DHX58	0	0.424
ADAR	SFPQ	0	0.425
ADAR	IFNAR1	0	0.433
ADAR	PARP12	0	0.472
ADAR	TNFRSF1B	0	0.475
ADAR	ALKBH1	0	0.478
ADAR	HERC6	0.043	0.491
ADAR	MX2	0	0.525
ADAR	ISG20	0	0.537
ADAR	IRF9	0	0.548
ADAR	MOV10	0.158	0.549
ADAR	MX1	0	0.562
ADAR	RNF213	0	0.569
ADAR	ISG15	0	0.591
ADAR	ZBP1	0	0.594
ADAR	RSAD2	0	0.606
ADAR	STAT1	0	0.655
ADAR	IFIT3	0.459	0.688
ADAR	DDX58	0	0.69
ADAR	IRF7	0	0.719
ADAR	ZNFX1	0.12	0.721
ADAR	IFIH1	0	0.733
ADAR	OAS2	0.406	0.777
ADAR	TRANK1	0	0.8
ADCY4	GNG4	0.046	0.72
ADCY4	GCH1	0	0.608
ADCY4	EDN1	0	0.612
ADCY4	PDE4B	0.157	0.863
ADCY4	PRKCD	0.06	0.869
ADCY4	IL1A	0	0.506
ADCY4	MOCS1	0	0.621
ADCY4	FITM1	0	0.427
ADCY4	TCF7L2	0.044	0.526
ADCY4	KRAS	0.124	0.533
ADCY4	PRKCB	0.046	0.612
ADCY4	ENTPD1	0	0.676
ADORA2A	SLC6A2	0.055	0.404
ADORA2A	LPAR3	0	0.8
ADORA2A	FOS	0	0.505
ADORA2A	ADORA2B	0.143	0.828
ADORA2A	CSF2RB	0	0.65
ADORA2A	ZSWIM6	0	0.452
ADORA2A	SAG	0	0.588
ADORA2A	P2RY6	0	0.424
ADORA2A	TNF	0	0.429
ADORA2A	ENTPD1	0	0.766

ADORA2B	LPAR3	0	0.8
ADORA2B	IL6	0	0.4
ADORA2B	P2RY6	0	0.412
ADORA2B	CECR1	0.071	0.527
ADORA2B	NFKB1	0.061	0.559
ADORA2B	ZSWIM7	0	0.584
ADORA2B	PANX1	0	0.584
ADORA2B	SLC9A3R1	0.12	0.596
ADORA2B	ENTPD1	0	0.648
ADORA2B	CSF2RB	0	0.65
AEBP2	PHF1	0	0.695
AEBP2	SYAP1	0	0.594
AEBP2	PCGF5	0.055	0.796
AEBP2	FXR2	0.057	0.638
AEBP2	EZH2	0.933	0.992
AEBP2	JARID2	0.962	0.998
AEBP2	NFIX	0.078	0.684
AEBP2	RYBP	0.071	0.673
AEBP2	LOC100297725	0.078	0.432
AEBP2	KDM6B	0.209	0.739
AFF4	ELL	0.764	0.971
AFF4	CCNT1	0.947	0.998
AFF4	HEXIM1	0.432	0.827
AFF4	HIPK3	0.045	0.403
AFF4	BRWD3	0	0.403
AFF4	NF1	0	0.416
AFF4	SEMA7A	0	0.426
AFF4	EPG5	0	0.507
AFF4	NIPBL	0	0.512
AFF4	UBR1	0	0.512
AFF4	XRN1	0	0.521
AFF4	SMG1	0.057	0.522
AFF4	ARL5B	0.072	0.528
AFF4	MEF2A	0	0.589
AFF4	RC3H2	0	0.831
AFF4	MED13	0	0.927
AGPAT6	DGAT2	0	0.775
AGPAT6	INSIG1	0	0.618
AGPAT6	SWT1	0	0.416
AGPAT6	SPTLC2	0.08	0.417
AGPAT6	LPCAT2	0.055	0.434
AGPAT6	GOLGA7	0	0.517
AGPAT6	XDH	0	0.518
AGPAT6	LPIN2	0.069	0.549
AGPAT6	SLC37A1	0	0.667
AGPAT6	AGPAT9	0	0.804
AGPAT6	CDS2	0	0.921

AGPAT6	MBOAT1	0.158	0.975
AGPAT9	DGAT2	0	0.603
AGPAT9	SLC39A8	0	0.504
AGPAT9	CDS2	0	0.921
AGPAT9	TNFAIP6	0	0.452
AGPAT9	MBOAT1	0.158	0.975
AGPAT9	LPCAT2	0.055	0.422
AGTRAP	PHC2	0	0.412
AGTRAP	LIG4	0	0.426
AGTRAP	UBE2D1	0	0.465
AGTRAP	FBXO9	0	0.517
AIF1	CSF1	0	0.426
AIF1	IL1B	0	0.702
AIF1	FOS	0.118	0.446
AIF1	CREB1	0.053	0.414
AIF1	TLR4	0.071	0.562
AIF1	CD53	0.042	0.629
AIF1	IL10	0	0.58
AIF1	NOS2	0	0.4
AIF1	TLR2	0.071	0.47
AIF1	CCR5	0.055	0.463
AIF1	ATF3	0.118	0.456
AIF1	PTPRC	0.045	0.674
AIF1	IL1A	0	0.427
AIF1	SLC1A2	0	0.404
AIF1	CCR2	0.055	0.408
AIF1	PTGS2	0	0.46
AIF1	IL6	0	0.67
AIF1	TSPO	0	0.585
AIF1	CYBB	0.168	0.578
AIF1	FCGR3A	0	0.446
AIF1	FCER1G	0	0.449
AIF1	LAPTM5	0	0.455
AIF1	IL18	0	0.472
AIF1	HCK	0.093	0.493
AIF1	SELPLG	0	0.512
AIF1	CNP	0.073	0.531
AIF1	PSEN1	0.077	0.549
AIF1	TMEM119	0	0.596
AIF1	TNF	0	0.682
AKIRIN2	PSPC1	0	0.425
AKIRIN2	MAP2K3	0.135	0.435
AKIRIN2	UBE2D1	0	0.502
AKIRIN2	CLK2	0	0.597
AKIRIN2	ZNF292	0.045	0.609
AKIRIN2	NFKB2	0.337	0.673
AKIRIN2	NFKB1	0.337	0.673

ALAS1	BACH1	0	0.453
ALAS1	SLC25A37	0	0.462
ALCAM	CD80	0	0.412
ALCAM	RFK	0	0.414
ALCAM	CD5	0	0.453
ALCAM	CD14	0	0.468
ALCAM	CD38	0	0.469
ALCAM	ITGA5	0	0.479
ALCAM	CD164	0	0.484
ALCAM	CXCR4	0	0.582
ALCAM	ITGAV	0	0.611
ALCAM	SDCBP	0	0.633
ALCAM	ICAM1	0	0.665
ALCAM	PTPRC	0	0.88
ALCAM	CD44	0	0.901
ALDH2	UPB1	0	0.925
ALDH2	TKT	0.478	0.629
ALDH2	LAP3	0.218	0.487
ALDH2	GLS	0.044	0.627
ALDH2	PTGS2	0.182	0.403
ALDH2	PDXK	0	0.434
ALDH2	CD44	0	0.475
ALDH3B1	UPB1	0	0.914
ALDH3B1	TKT	0.184	0.408
ALDH3B1	FCGR2B	0	0.499
ALDH3B1	LOC100138951	0	0.499
ALKBH1	WTAP	0	0.551
ALKBH1	HIST1H2AJ	0	0.41
ALKBH1	HIST3H2A	0	0.41
ALKBH1	CWC22	0	0.421
ALKBH1	TET2	0	0.451
ALKBH1	MOV10	0	0.659
ALOX5AP	SLA	0	0.426
ALOX5AP	CSF2RB	0	0.459
ALOX5AP	LCP2	0	0.621
ALOX5AP	PLEK	0	0.574
ALOX5AP	PTPRC	0	0.4
ALOX5AP	PTGS2	0	0.403
ALOX5AP	SRGN	0	0.405
ALOX5AP	COTL1	0	0.457
ALOX5AP	LTB4R	0	0.464
ALOX5AP	IGSF6	0	0.503
ALOX5AP	LAPTM5	0	0.516
ALOX5AP	PLA2G4A	0	0.566
ALPK1	MALT1	0	0.454
ALPL	LAP3	0	0.4
ALPL	GCH1	0	0.9

ALPL	SLC20A1	0	0.443
ALPL	DUSP11	0	0.412
ALPL	ELN	0	0.431
ALPL	GGT5	0	0.502
ALPL	ENPP2	0	0.53
ALYREF	EIF4A1	0.219	0.698
ALYREF	DDX19B	0.218	0.467
ALYREF	YRDC	0	0.49
ALYREF	PAPOLG	0	0.474
ALYREF	THOC2	0.763	0.993
ALYREF	SAT1	0	0.418
ALYREF	SUPT6H	0	0.436
ALYREF	WDR77	0.113	0.438
ALYREF	SWT1	0.114	0.441
ALYREF	TRA2A	0.21	0.472
ALYREF	SRRM2	0.426	0.481
ALYREF	NOP9	0	0.49
ALYREF	SFPQ	0.053	0.495
ALYREF	XRN2	0.129	0.508
ALYREF	ETF1	0	0.511
ALYREF	SF3B1	0.402	0.53
ALYREF	XRN1	0.164	0.53
ALYREF	DDX17	0.334	0.54
ALYREF	DDX5	0.399	0.548
ALYREF	HNRNPF	0.337	0.66
ALYREF	SRSF5	0.352	0.68
ALYREF	HNRNPH1	0.336	0.685
ALYREF	DDX39A	0.668	0.971
ALYREF	NXF1	0.436	0.993
ALYREF	DDX39B	0.819	0.999
AMMECR1	MREG	0	0.533
AMPD3	APRT	0.161	0.894
AMPD3	PSMA2	0	0.499
AMPD3	C4A	0.41	0.47
AMPD3	UPP1	0	0.405
AMPD3	FGR	0	0.405
AMPD3	PNP	0	0.669
AMPD3	SLC2A9	0	0.43
AMPD3	FAM3B	0	0.442
AMPD3	LOC790312	0	0.503
AMPD3	RUFY4	0	0.569
AMPD3	CECR1	0	0.728
ANKFY1	SNX10	0.349	0.492
ANKFY1	REC8	0.055	0.588
ANKFY1	CREBBP	0.12	0.487
ANKFY1	WARS	0.501	0.519
ANKFY1	LAP3	0.452	0.452

ANKFY1	TSPAN31	0.042	0.578
ANKFY1	VMP1	0	0.672
ANKFY1	TBC1D2B	0.06	0.558
ANKFY1	NAMPT	0.502	0.502
ANKFY1	DDA1	0.451	0.451
ANKFY1	PLAGL2	0.116	0.528
ANKFY1	ZNFX1	0.093	0.424
ANKFY1	SMG1	0.171	0.413
ANKFY1	DCAF11	0.455	0.455
ANKFY1	POGZ	0.116	0.467
ANKFY1	PHLDB1	0	0.578
ANKFY1	ARF6	0.106	0.428
ANKFY1	PARP3	0.073	0.608
ANKFY1	DCBLD1	0	0.612
ANKFY1	DCUN1D3	0.042	0.636
ANKRD12	JMJD1C	0	0.428
ANKRD12	ZCCHC6	0	0.4
ANKRD12	STAM2	0	0.488
ANKRD12	SLFN12L	0	0.401
ANKRD12	SMG1	0	0.42
ANKRD12	ARID4A	0	0.43
ANKRD12	ING5	0	0.456
ANKRD12	PIK3AP1	0	0.511
ANKRD12	ZNF292	0	0.515
ANKRD12	ARID4B	0	0.527
ANKRD12	BIN2	0	0.587
ANKRD12	ROCK1	0.042	0.637
ANKRD12	THOC2	0	0.694
ANKRD12	NIPBL	0	0.874
ANKRD13A	USP25	0	0.416
ANKRD13A	NEK6	0	0.586
ANKRD2	FOXS1	0.072	0.664
ANKRD2	SIK1	0.081	0.422
ANKRD2	RELA	0.192	0.42
ANKRD2	TM6SF1	0	0.534
ANKRD22	CDKN2D	0	0.417
ANKRD22	LIPM	0.116	0.544
ANKRD22	RGS2	0.079	0.472
ANKRD22	PDXK	0	0.512
ANKRD22	TMEM156	0	0.596
ANKRD44	CDK17	0.316	0.446
ANKRD44	TNFRSF1A	0.043	0.517
ANKRD44	CASP7	0.218	0.429
ANKRD44	CFLAR	0.218	0.429
ANKRD44	PPP4C	0.137	0.434
ANKRD44	DOPEY2	0	0.541
ANKRD44	TRAF7	0.16	0.408

ANKRD44	RGS2	0.163	0.444
ANKRD44	SMG1	0.211	0.423
ANKRD44	CASP4	0.218	0.429
ANKRD44	RNF213	0	0.402
ANKRD44	TNF	0.053	0.492
ANKRD44	LRRK2	0.161	0.527
ANTXR2	SERINC2	0	0.412
ANXA3	TM9SF4	0	0.42
ANXA3	CD82	0.042	0.434
ANXA3	CD81	0.042	0.511
AOAH	ARHGAP31	0	0.427
AOAH	OVCA2	0	0.513
AOAH	IGSF6	0	0.409
AOAH	LTB	0	0.452
AOAH	GRAMD4	0	0.412
APOBEC3A	LOC616948	0	0.452
APOBEC3A	ATP5F1	0.52	0.792
APOBEC3A	MX2	0.055	0.405
APOBEC3A	LTBR	0	0.454
APOBEC3A	MOV10	0.084	0.534
APOL3	HIVEP1	0	0.41
APOL3	PLAUR	0	0.456
APOL3	F5	0	0.499
APOL3	C4A	0	0.51
APOL3	IL6	0	0.511
APOL3	RHBDF2	0	0.553
APRT	NDRG1	0.423	0.422
APRT	PSTPIP1	0.134	0.435
APRT	RPIA	0	0.44
APRT	DNAJC1	0	0.482
APRT	TOP1	0	0.507
APRT	PPIF	0.5	0.51
APRT	DPYD	0	0.56
APRT	PPA1	0	0.61
APRT	CECR1	0.257	0.696
APRT	UPP1	0	0.755
APRT	PDE4B	0	0.9
APRT	ENTPD1	0	0.904
APRT	LOC790312	0	0.988
APRT	PNP	0	0.995
ARAP1	RHOG	0.142	0.571
ARAP1	ARL4A	0.142	0.441
ARAP1	GRB2	0.346	0.475
ARAP1	RAP1B	0.142	0.618
ARAP1	PLEK	0	0.509
ARAP1	PSTPIP1	0.045	0.528
ARAP1	PXK	0	0.422

ARAP1	SERINC2	0	0.426
ARAP1	CRKL	0.114	0.401
ARAP1	ARL5B	0.142	0.422
ARAP1	KRAS	0.142	0.543
ARAP1	ARF6	0.142	0.695
ARF6	RHOG	0.071	0.45
ARF6	ARL4A	0.097	0.414
ARF6	IQSEC1	0.296	0.939
ARF6	IPCEF1	0.128	0.668
ARF6	ELMO2	0.124	0.434
ARF6	RABGEF1	0.129	0.407
ARF6	VAV1	0.157	0.41
ARF6	GRB2	0.093	0.427
ARF6	LGR6	0.12	0.474
ARF6	CYTH1	0.447	0.983
ARF6	EHBP1L1	0.081	0.577
ARF6	ITGA2B	0	0.612
ARF6	FRMD4A	0.114	0.663
ARF6	PIK3CA	0.158	0.659
ARF6	PLEK	0.043	0.642
ARF6	FLOT1	0.072	0.463
ARF6	TIAM2	0.161	0.75
ARF6	MCF2L2	0.158	0.429
ARF6	RAB27A	0	0.568
ARF6	ITGA5	0	0.671
ARF6	PLXNA4	0.156	0.431
ARF6	RABGAP1L	0.152	0.513
ARF6	MST1R	0.258	0.679
ARF6	ITGA9	0	0.648
ARF6	ARHGEF6	0.114	0.554
ARF6	PXN	0.128	0.85
ARF6	RND1	0.071	0.401
ARF6	ITGB7	0.06	0.527
ARF6	LOC785769	0.161	0.45
ARF6	SDCBP	0.081	0.573
ARF6	ITGAV	0	0.616
ARF6	USP32	0.093	0.783
ARF6	GALNT11	0	0.513
ARF6	SAG	0.118	0.653
ARF6	HIP1R	0	0.424
ARF6	CYTH4	0.269	0.937
ARF6	PLXNA1	0.156	0.463
ARF6	TTC19	0	0.404
ARF6	DNM2	0.07	0.745
ARF6	DAAM2	0.161	0.401
ARF6	USP15	0.072	0.636
ARF6	SLC2A3	0.045	0.492

ARF6	SLC2A1	0.045	0.498
ARF6	KRAS	0.079	0.446
ARF6	PREX1	0.161	0.45
ARF6	RASA2	0.08	0.416
ARF6	LAMP1	0	0.578
ARF6	BIN2	0.114	0.56
ARF6	TNFAIP2	0.055	0.462
ARF6	TBC1D10A	0.152	0.76
ARF6	HCK	0.124	0.445
ARF6	SLC2A9	0.045	0.415
ARGLU1	HNRNPH1	0	0.58
ARGLU1	NXF1	0	0.474
ARGLU1	SRSF5	0.107	0.537
ARGLU1	FBXO9	0	0.588
ARGLU1	SRRM2	0	0.431
ARGLU1	DDX5	0	0.444
ARGLU1	FNBP4	0	0.695
ARHGAP15	RHOG	0.456	0.971
ARHGAP15	ERBB2IP	0.042	0.554
ARHGAP15	ARL4A	0.257	0.498
ARHGAP15	NCF1	0.242	0.556
ARHGAP15	VAV1	0.456	0.689
ARHGAP15	MICU1	0	0.414
ARHGAP15	FGD3	0.317	0.424
ARHGAP15	CPB2	0.391	0.41
ARHGAP15	NCF4	0.242	0.557
ARHGAP15	RAP1B	0.257	0.534
ARHGAP15	SH3PXD2B	0.242	0.529
ARHGAP15	LCP2	0	0.406
ARHGAP15	PLEK	0	0.436
ARHGAP15	TIAM2	0.408	0.559
ARHGAP15	PTPRC	0.042	0.62
ARHGAP15	CD48	0	0.456
ARHGAP15	DIRAS3	0.257	0.432
ARHGAP15	RHOH	0.456	0.749
ARHGAP15	RRAD	0.257	0.432
ARHGAP15	FGD2	0.317	0.445
ARHGAP15	ARHGAP35	0.453	0.639
ARHGAP15	PRICKLE3	0.425	0.541
ARHGAP15	REM2	0.257	0.432
ARHGAP15	ARHGEF6	0.339	0.571
ARHGAP15	SRGAP2	0.452	0.491
ARHGAP15	PXN	0.352	0.475
ARHGAP15	RND1	0.456	0.716
ARHGAP15	LOC785769	0.408	0.559
ARHGAP15	PSTPIP1	0.42	0.547
ARHGAP15	BCR	0.299	0.409

ARHGAP15	DAAM2	0.218	0.417
ARHGAP15	HIPK3	0.316	0.441
ARHGAP15	TAGAP	0	0.439
ARHGAP15	KRAS	0.257	0.432
ARHGAP15	PREX1	0.408	0.653
ARHGAP15	CDC42SE2	0	0.426
ARHGAP15	PSTPIP2	0.42	0.506
ARHGAP15	MAML2	0	0.469
ARHGAP15	ARL5B	0.257	0.488
ARHGAP17	RIC1	0	0.639
ARHGAP17	TRIP10	0.395	0.693
ARHGAP17	PARD3	0.113	0.48
ARHGAP17	RAP1GAP2	0	0.468
ARHGAP17	FNBP1	0.296	0.44
ARHGAP17	SLC9A3R1	0.121	0.66
ARHGAP31	ARHGAP35	0.161	0.471
ARHGAP31	RBPJ	0	0.504
ARHGAP31	RNF19A	0	0.535
ARHGAP31	EOGT	0	0.54
ARHGAP31	RLF	0.054	0.715
ARHGAP35	RHOG	0.219	0.956
ARHGAP35	BMX	0.093	0.489
ARHGAP35	ARL4A	0.149	0.481
ARHGAP35	VAV1	0	0.667
ARHGAP35	GRB2	0.218	0.706
ARHGAP35	PTK2B	0.055	0.639
ARHGAP35	IRAK2	0.164	0.409
ARHGAP35	FGD3	0.218	0.486
ARHGAP35	FRMD4A	0.042	0.499
ARHGAP35	PRKCD	0	0.758
ARHGAP35	RAP1B	0.149	0.412
ARHGAP35	MCF2L2	0	0.499
ARHGAP35	FGR	0.093	0.446
ARHGAP35	BCAR1	0	0.478
ARHGAP35	RHOH	0.219	0.558
ARHGAP35	TPC3	0	0.402
ARHGAP35	ARID4B	0	0.419
ARHGAP35	VASP	0	0.439
ARHGAP35	PTPN6	0.042	0.441
ARHGAP35	LIMK2	0.219	0.454
ARHGAP35	ARHGEF6	0	0.456
ARHGAP35	SRGAP2	0.453	0.48
ARHGAP35	ARL5B	0.149	0.481
ARHGAP35	IRAK4	0.164	0.535
ARHGAP35	PXN	0.136	0.545
ARHGAP35	ARHGEF2	0.093	0.657
ARHGAP35	KRAS	0.149	0.664

ARHGAP35	ARHGEF1	0.093	0.719
ARHGAP35	ROCK1	0.08	0.726
ARHGAP35	RND1	0.219	0.79
ARHGEF1	RHOG	0.218	0.533
ARHGEF1	GRB2	0.045	0.449
ARHGEF1	PTK2B	0	0.517
ARHGEF1	PLEK	0	0.487
ARHGEF1	MCF2L2	0	0.453
ARHGEF1	JAK2	0.081	0.427
ARHGEF1	RHOH	0.218	0.458
ARHGEF1	RND1	0.218	0.446
ARHGEF1	ROCK1	0.093	0.534
ARHGEF1	PREX1	0.123	0.553
ARHGEF1	CD44	0.113	0.687
ARHGEF2	RHOG	0.218	0.545
ARHGEF2	GRIPAP1	0	0.411
ARHGEF2	MARK3	0.219	0.475
ARHGEF2	RHOH	0.218	0.468
ARHGEF2	BOLA-DQA5	0	0.412
ARHGEF2	FMNL3	0.081	0.561
ARHGEF2	ARHGEF6	0.257	0.567
ARHGEF2	PXN	0.182	0.576
ARHGEF2	RND1	0.218	0.446
ARHGEF2	SERINC2	0	0.41
ARHGEF2	PSTPIP2	0.159	0.426
ARHGEF2	UGCG	0.449	0.449
ARHGEF2	NOD1	0.045	0.643
ARHGEF6	RHOG	0.162	0.457
ARHGEF6	ERBB2IP	0.258	0.491
ARHGEF6	HCLS1	0	0.577
ARHGEF6	PLCG2	0	0.435
ARHGEF6	VAV1	0.311	0.466
ARHGEF6	PTK2B	0	0.627
ARHGEF6	FGD3	0.203	0.537
ARHGEF6	RAP1GAP	0	0.459
ARHGEF6	PLEK	0	0.444
ARHGEF6	MARK3	0	0.453
ARHGEF6	RHOH	0.162	0.437
ARHGEF6	RELA	0	0.451
ARHGEF6	RND1	0.162	0.428
ARHGEF6	SRGAP2	0.184	0.439
ARHGEF6	ITGB7	0	0.525
ARHGEF6	LRRK2	0.343	0.679
ARHGEF6	KRAS	0.114	0.863
ARHGEF6	PXN	0.353	0.916
ARID3B	GAB2	0	0.464
ARID3B	RBPJ	0.338	0.532

ARID3B	NFE2L3	0	0.455
ARID3B	LGR6	0	0.52
ARID3B	FRMD4A	0	0.405
ARID3B	NACC2	0.077	0.446
ARID3B	FAM134C	0	0.449
ARID3B	MEGF9	0	0.493
ARID3B	MYSM1	0.439	0.558
ARID4A	SP3	0.158	0.42
ARID4A	KAT2B	0.335	0.504
ARID4A	STRA8	0.433	0.503
ARID4A	EPC1	0.44	0.625
ARID4A	ZCCHC6	0	0.543
ARID4A	RPIA	0	0.457
ARID4A	CREBBP	0.335	0.451
ARID4A	ARIH2	0	0.407
ARID4A	KAT5	0.392	0.509
ARID4A	HDAC11	0.454	0.547
ARID4A	UBXN7	0.168	0.405
ARID4A	THOC2	0	0.641
ARID4A	ING5	0.508	0.597
ARID4A	KMT2E	0.2	0.453
ARID4A	PIK3CA	0.258	0.419
ARID4A	KAT8	0.392	0.528
ARID4A	MEF2A	0.08	0.422
ARID4A	JARID2	0.222	0.43
ARID4A	GTPBP4	0	0.635
ARID4A	NIPBL	0	0.862
ARID4A	PHF12	0.52	0.703
ARID4A	LOC507820	0.164	0.451
ARID4A	TET2	0.331	0.461
ARID4A	HDAC4	0.454	0.508
ARID4A	GGT5	0	0.534
ARID4A	BAZ1A	0.335	0.409
ARID4A	MPHOSPH8	0.112	0.458
ARID4A	KDM6B	0.333	0.461
ARID4A	H3F3A	0.392	0.463
ARID4A	LOC613345	0.392	0.463
ARID4A	BAZ2A	0.335	0.491
ARID4A	LOC100297725	0.392	0.502
ARID4A	NACC2	0.158	0.539
ARID4A	KDM5A	0.222	0.578
ARID4A	ZBTB12	0.158	0.582
ARID4A	CHD1	0.413	0.667
ARID4A	MYSM1	0.491	0.721
ARID4A	ARID4B	0.113	0.88
ARID4A	HIST3H2A	0.18	0.915
ARID4B	KAT2B	0.335	0.608

ARID4B	STRA8	0.442	0.575
ARID4B	EPC1	0.44	0.624
ARID4B	JMJD1C	0	0.517
ARID4B	ZCCHC6	0	0.441
ARID4B	CREBBP	0.335	0.455
ARID4B	MYLIP	0	0.564
ARID4B	KAT5	0.392	0.509
ARID4B	HDAC11	0.454	0.494
ARID4B	UBXN7	0.168	0.436
ARID4B	THOC2	0	0.659
ARID4B	SF3B1	0	0.584
ARID4B	ING5	0.508	0.597
ARID4B	KMT2E	0.2	0.698
ARID4B	PIK3CA	0.258	0.401
ARID4B	PAN3	0	0.421
ARID4B	KAT8	0.392	0.598
ARID4B	ATXN7	0	0.431
ARID4B	RRAD	0.055	0.421
ARID4B	WDR77	0.072	0.428
ARID4B	GTPBP4	0	0.419
ARID4B	NIPBL	0	0.897
ARID4B	PHF12	0.52	0.819
ARID4B	TET2	0.331	0.557
ARID4B	HDAC4	0.454	0.557
ARID4B	GGT5	0	0.407
ARID4B	BAZ1A	0.335	0.44
ARID4B	KDM5A	0.222	0.609
ARID4B	NACC2	0.158	0.538
ARID4B	SMG1	0.258	0.533
ARID4B	USP36	0	0.443
ARID4B	MYSM1	0.491	0.774
ARID4B	H3F3A	0.392	0.516
ARID4B	CHD1	0.413	0.746
ARID4B	BAZ2A	0.335	0.592
ARID4B	HIPK3	0.124	0.445
ARID4B	LOC613345	0.392	0.463
ARID4B	ZNF292	0.158	0.494
ARID4B	LOC100297725	0.392	0.495
ARID4B	KDM6B	0.333	0.508
ARID4B	CREBRF	0	0.515
ARID4B	USP34	0	0.64
ARID5A	EMR3	0	0.411
ARID5A	CSRNP1	0	0.454
ARID5A	CREBBP	0.403	0.422
ARID5A	RARG	0.45	0.461
ARID5A	ZC3H12A	0	0.551
ARID5A	TBL1X	0.459	0.472

ARID5A	ZNF263	0.077	0.441
ARID5A	MYSM1	0.439	0.558
ARID5A	ATXN1	0.123	0.509
ARID5A	ZFP36	0.087	0.424
ARIH2	TNFRSF1A	0.395	0.518
ARIH2	TNF	0.356	0.405
ARIH2	UBXN7	0	0.412
ARIH2	RBCK1	0.295	0.413
ARIH2	DIXDC1	0	0.433
ARIH2	7-Mar	0	0.493
ARIH2	CYLD	0.474	0.63
ARIH2	UBE2L6	0.761	0.787
ARL14EP	SETDB1	0.76	0.878
ARL14EP	KRR1	0	0.589
ARL14EP	PLXNA4	0	0.457
ARL14EP	LMNB1	0	0.447
ARL4A	RHOG	0.058	0.501
ARL4A	CYTH4	0.169	0.426
ARL4A	SRGAP2	0.129	0.432
ARL4A	BFAR	0	0.47
ARL4A	TRIP10	0.129	0.492
ARL4A	ELMO2	0.124	0.519
ARL4A	FRMD4A	0.114	0.613
ARL4A	CYTH1	0.169	0.615
ARL5B	GOSR1	0.093	0.602
ARL5B	CYTH1	0.169	0.446
ARL5B	CACHD1	0.042	0.531
ARL5B	PLEKHM2	0.041	0.641
ARL5B	CYTH4	0.169	0.4
ARL5B	LAMP1	0	0.535
ARL5B	DUSP11	0	0.452
ARL5B	RHBDD2	0	0.417
ARRDC2	SEMA4D	0.042	0.404
ARRDC2	HECW2	0.312	0.411
ARRDC2	SMURF1	0.312	0.411
ARRDC2	SAG	0.091	0.481
ARRDC2	FRMD4A	0	0.518
ARRDC4	MLXIP	0	0.479
ARRDC4	CARS	0	0.537
ARRDC4	MCTP2	0	0.519
ARRDC4	KLF10	0.054	0.403
ARRDC4	BTG3	0	0.408
ARRDC4	HECW2	0.312	0.411
ARRDC4	SMURF1	0.312	0.411
ARRDC4	SAG	0.091	0.48
ATAD1	MAP1LC3A	0.136	0.405
ATAD1	NCLN	0	0.427

ATAD1	IFIT2	0.079	0.438
ATAD1	ISG15	0.184	0.459
ATAD1	HERC6	0.06	0.625
ATAD1	UBXN7	0.659	0.684
ATF3	DDIT4	0	0.426
ATF3	NR4A1	0.129	0.719
ATF3	KAT2B	0.114	0.466
ATF3	PPP1R15A	0	0.9
ATF3	NFE2	0.115	0.59
ATF3	NR4A2	0.129	0.511
ATF3	CSRNP1	0	0.473
ATF3	CREBBP	0.184	0.534
ATF3	JUN	0.923	0.999
ATF3	NFE2L3	0.115	0.475
ATF3	FOS	0.114	0.86
ATF3	STAT2	0.121	0.454
ATF3	IRF5	0	0.493
ATF3	CREB1	0.079	0.846
ATF3	NFKB2	0.163	0.48
ATF3	TLR4	0.046	0.431
ATF3	STAT6	0.121	0.401
ATF3	CDKN1A	0	0.547
ATF3	SOCS3	0	0.615
ATF3	DUSP2	0.152	0.4
ATF3	SMAD7	0.118	0.4
ATF3	ID1	0	0.405
ATF3	TRAF1	0.253	0.405
ATF3	MKNK1	0	0.418
ATF3	ZFP36	0	0.431
ATF3	ETS2	0.044	0.434
ATF3	KLF10	0.077	0.436
ATF3	TRIB1	0.158	0.438
ATF3	IER3	0	0.458
ATF3	SLC2A1	0	0.468
ATF3	BACH2	0.115	0.471
ATF3	IRF2	0	0.474
ATF3	GTF2B	0	0.497
ATF3	IRF9	0	0.497
ATF3	BATF3	0.438	0.503
ATF3	DUSP5	0.152	0.507
ATF3	CXCL8	0	0.508
ATF3	NFKB1	0.163	0.549
ATF3	STAT1	0.211	0.561
ATF3	PTGS2	0	0.574
ATF3	HERPUD1	0	0.586
ATF3	EGR3	0.077	0.596
ATF3	FOSL2	0.115	0.601

ATF3	IRF7	0	0.603
ATF3	GADD45B	0	0.611
ATF3	IL6	0	0.631
ATF3	RELA	0.157	0.633
ATF3	IRF1	0	0.647
ATF3	EGR2	0.077	0.648
ATF3	NFE2L2	0.124	0.663
ATF3	TNF	0	0.673
ATF3	KLF7	0.077	0.694
ATF3	STAT3	0.218	0.694
ATF3	CREM	0.079	0.719
ATF3	MAFF	0.136	0.729
ATF3	ATF4	0.463	0.893
ATF3	BTG2	0	0.893
ATF3	MDM2	0.759	0.904
ATF3	KLF6	0.077	0.905
ATF3	JUNB	0.435	0.921
ATF3	DDIT3	0.764	0.959
ATF4	PPP1R15A	0	0.972
ATF4	CREBBP	0.674	0.946
ATF4	JUN	0.67	0.867
ATF4	FOS	0.763	0.867
ATF4	CREB1	0.174	0.918
ATF4	CCNT1	0	0.454
ATF4	CAMK1D	0.156	0.649
ATF4	MAP3K5	0	0.481
ATF4	SLC38A2	0	0.539
ATF4	MAPKAPK2	0	0.804
ATF4	EDEM1	0	0.562
ATF4	CREM	0.152	0.678
ATF4	MAPKAPK3	0	0.804
ATF4	HERPUD1	0	0.605
ATF4	BCL2L11	0	0.406
ATF4	CASP4	0	0.517
ATF4	HDAC4	0	0.631
ATF4	PRKCB	0	0.637
ATF4	FOSL2	0.184	0.707
ATF4	MKNK1	0	0.806
ATF4	CRTC2	0	0.825
ATF4	NFE2L2	0.764	0.925
ATF4	DDIT3	0.649	0.993
ATG16L1	RB1CC1	0.924	0.998
ATG16L1	NLRP3	0	0.643
ATG16L1	IL1B	0	0.42
ATG16L1	RAB3D	0.164	0.408
ATG16L1	WDR45	0	0.552
ATG16L1	RIPK2	0.043	0.411

ATG16L1	TBC1D14	0	0.416
ATG16L1	NLRC4	0	0.416
ATG16L1	EPG5	0	0.422
ATG16L1	DRAM1	0	0.423
ATG16L1	TNF	0	0.434
ATG16L1	IL10	0	0.452
ATG16L1	TLR4	0.137	0.456
ATG16L1	LRRK2	0.108	0.485
ATG16L1	SNAP29	0	0.487
ATG16L1	IL18	0	0.489
ATG16L1	RAB37	0.084	0.533
ATG16L1	CPB2	0	0.552
ATG16L1	VMP1	0	0.556
ATG16L1	STK38L	0	0.593
ATG16L1	TLR2	0.432	0.615
ATG16L1	OPTN	0.113	0.631
ATG16L1	LAMP1	0	0.707
ATG16L1	CALCOCO2	0.114	0.724
ATG16L1	MEFV	0.113	0.808
ATG16L1	ATG16L2	0.113	0.837
ATG16L1	MAP1LC3A	0.218	0.847
ATG16L1	GABARAPL1	0.392	0.968
ATG16L1	NOD1	0.218	0.971
ATG16L1	NOD2	0.432	0.997
ATG16L2	RB1CC1	0.572	0.952
ATG16L2	FAM46A	0	0.404
ATG16L2	MAP1LC3A	0.218	0.437
ATG16L2	IKBKB	0.109	0.454
ATG16L2	DRAM1	0	0.412
ATG16L2	GABARAPL1	0.218	0.647
ATG16L2	IL17REL	0	0.669
ATP11B	PPP4R2	0	0.408
ATP11B	MCF2L2	0	0.662
ATP11B	HLX	0	0.447
ATP11B	PTBP3	0	0.41
ATP11B	UBR1	0.041	0.419
ATP1A1	KCNJ15	0	0.533
ATP1A1	TPT1	0.391	0.4
ATP1A1	SLC8A1	0.439	0.523
ATP1A1	KCNK9	0	0.553
ATP5F1	C17orf80	0	0.613
ATP5F1	NCLN	0	0.412
ATP5F1	IL2RG	0	0.427
ATP5F1	FAM105A	0	0.434
ATP5F1	TSPO	0.435	0.44
ATP5F1	TARS	0	0.443
ATP5F1	TIMM17A	0	0.474

ATP5F1	KDM5A	0	0.531
ATP5F1	JARID2	0	0.531
ATP5F1	KDM6B	0.064	0.543
ATP5F1	ATP6V1E1	0	0.613
ATP5F1	PPA1	0	0.734
ATP6V1E1	TTC33	0.4	0.406
ATP6V1E1	TCIRG1	0.528	0.9
ATP6V1E1	UPB1	0.588	0.588
ATP6V1E1	PPA1	0	0.728
ATP6V1E1	DMXL2	0.361	0.563
ATP6V1E1	BID	0	0.514
ATP8B4	SIRPB1	0	0.537
ATP8B4	LOC617909	0	0.499
ATXN1	FAM46A	0.124	0.476
ATXN1	RBPJ	0.164	0.934
ATXN1	KAT5	0.211	0.943
ATXN1	PTPRC	0.055	0.4
ATXN1	CD48	0	0.639
ATXN1	ATXN7	0	0.822
ATXN1	SIRT1	0	0.412
ATXN1	HDAC4	0.113	0.541
ATXN1	PQBP1	0.119	0.709
ATXN1	PIM3	0	0.414
ATXN7	KAT2B	0.641	0.776
ATXN7	CREBBP	0.266	0.413
ATXN7	NRDE2	0	0.571
ATXN7	USP3	0.453	0.566
ATXN7	PRICKLE3	0	0.405
ATXN7	PTPRG	0.077	0.416
ATXN7	SMG1	0.276	0.432
ATXN7	TAF5L	0.524	0.661
ATXN7	ATXN7L3	0.764	0.958
ATXN7L3	USP42	0	0.556
ATXN7L3	KAT2B	0.764	0.894
ATXN7L3	JMJD1C	0	0.414
ATXN7L3	USP3	0.642	0.771
ATXN7L3	PLAGL2	0.076	0.432
ATXN7L3	SDC3	0	0.456
ATXN7L3	TAF5L	0.682	0.881
AVIL	PIK3CA	0.055	0.449
AVIL	SCARF1	0.174	0.58
AVIL	TRPM5	0	0.412
B3GNT3	UAP1	0	0.413
B3GNT3	ST3GAL3	0	0.554
B3GNT3	B4GALT4	0	0.949
B3GNT3	FUT4	0	0.966
B3GNT3	LFNG	0	0.544

B4GALT4	ST3GAL3	0	0.502
B4GALT4	RNASE10	0	0.66
B4GALT4	FUT4	0	0.934
B4GALT5	TMEM165	0	0.601
B4GALT5	SPTLC2	0	0.541
B4GALT5	SPTSSA	0	0.692
B4GALT5	UGCG	0	0.947
BACH1	KLHL8	0.2	0.416
BACH1	JUN	0.184	0.55
BACH1	FOSL2	0.115	0.414
BACH1	VAT1L	0	0.416
BACH1	KLHL5	0.2	0.416
BACH1	CREM	0.08	0.453
BACH1	CREB1	0.115	0.543
BACH1	JUNB	0.184	0.55
BACH1	HIAT1	0	0.639
BACH1	MAFF	0.44	0.737
BACH2	PRDM1	0.116	0.722
BACH2	BCL6	0.127	0.409
BACH2	KLHL8	0.2	0.416
BACH2	JUN	0.184	0.641
BACH2	FOS	0.115	0.516
BACH2	CREB1	0.055	0.475
BACH2	KLHL5	0.2	0.416
BACH2	PTPN2	0	0.486
BACH2	BATF3	0.217	0.59
BACH2	JUNB	0.184	0.557
BACH2	CREM	0.055	0.401
BACH2	VAT1L	0	0.416
BACH2	PTPN22	0	0.443
BACH2	IL2RA	0	0.4
BACH2	FOSL2	0.121	0.539
BACH2	MAML2	0	0.554
BACH2	BATF	0.115	0.74
BACH2	MAFF	0.414	0.824
BATF	PRDM1	0	0.637
BATF	BCL6	0.077	0.703
BATF	NFE2	0.115	0.587
BATF	PPP4R2	0	0.414
BATF	CREBBP	0.184	0.469
BATF	JUN	0.438	0.922
BATF	STAT2	0.121	0.453
BATF	IRF5	0	0.467
BATF	CREB1	0.079	0.41
BATF	STAT6	0.121	0.555
BATF	IL10	0.174	0.457
BATF	IFI35	0.113	0.57

BATF	POU2F2	0.08	0.518
BATF	STAT5B	0.121	0.466
BATF	IRF2	0	0.466
BATF	BATF2	0	0.822
BATF	BATF3	0.114	0.839
BATF	JUNB	0.889	0.971
BATF	RELA	0.157	0.584
BATF	IL6	0	0.562
BATF	CREM	0.079	0.511
BATF	STAT3	0.121	0.729
BATF	STAT5A	0.121	0.442
BATF	GTF2B	0	0.421
BATF	TRAF1	0.253	0.449
BATF	IRF7	0	0.453
BATF	STAT4	0.121	0.457
BATF	IRF9	0	0.474
BATF	EGR2	0.077	0.479
BATF	TNF	0	0.487
BATF	STAT1	0.121	0.568
BATF	IRF1	0	0.636
BATF	DDIT3	0.762	0.824
BATF2	CREBBP	0.184	0.44
BATF2	JUN	0.42	0.78
BATF2	GBP4	0	0.403
BATF2	CREB1	0.079	0.408
BATF2	IRF2	0	0.503
BATF2	LOC507055	0	0.447
BATF2	RELA	0.157	0.447
BATF2	IRF9	0	0.457
BATF2	PHF11	0.046	0.462
BATF2	GBP2	0	0.465
BATF2	STAT1	0.121	0.487
BATF2	IRF7	0	0.501
BATF2	NABP1	0	0.537
BATF2	JUNB	0.42	0.597
BATF2	IRF1	0	0.775
BATF2	BATF3	0	0.822
BATF3	CREBBP	0.184	0.44
BATF3	JUN	0.666	0.955
BATF3	FOS	0	0.711
BATF3	IRF5	0	0.47
BATF3	IRF2	0	0.538
BATF3	PTPRC	0	0.45
BATF3	CD40	0	0.4
BATF3	IRF9	0	0.405
BATF3	STAT1	0.121	0.421
BATF3	CREM	0.079	0.431

BATF3	CIITA	0	0.443
BATF3	TNF	0	0.46
BATF3	IL6	0	0.461
BATF3	IRF7	0	0.493
BATF3	IRF1	0	0.527
BATF3	RELA	0.157	0.53
BATF3	DDIT3	0.431	0.573
BATF3	JUNB	0.651	0.758
BATF3	XCR1	0	0.801
BAZ1A	CTBP2	0.184	0.415
BAZ1A	JUN	0.219	0.411
BAZ1A	MIER1	0.043	0.64
BAZ1A	RARG	0.133	0.446
BAZ1A	KAT8	0.218	0.495
BAZ1A	JUNB	0.219	0.411
BAZ1A	RARA	0.133	0.446
BAZ1A	RELA	0.218	0.425
BAZ1A	MIER3	0.043	0.436
BAZ1A	MXD4	0.158	0.534
BAZ1A	CNOT7	0.055	0.608
BAZ1A	POLR2A	0.168	0.422
BAZ1A	BRF2	0.218	0.471
BAZ1A	TAF5L	0.165	0.498
BAZ1A	DOK3	0	0.536
BAZ1A	GTF2B	0.218	0.566
BAZ1A	MYSM1	0.401	0.67
BAZ1A	CHD1	0.165	0.805
BAZ2A	SETDB1	0.122	0.566
BAZ2A	CTBP2	0.254	0.517
BAZ2A	JUN	0.219	0.411
BAZ2A	SUPT6H	0.219	0.415
BAZ2A	KPNA1	0.093	0.467
BAZ2A	JUNB	0.219	0.411
BAZ2A	RELA	0.218	0.425
BAZ2A	PCMTD1	0.062	0.488
BAZ2A	ZFAT	0.121	0.449
BAZ2A	MYSM1	0.401	0.683
BAZ2A	UBTF	0.156	0.765
BAZ2A	CHD1	0.165	0.491
BAZ2A	SRRM2	0.06	0.677
BAZ2A	IRF1	0.16	0.423
BAZ2A	LOC100297725	0.163	0.432
BAZ2A	GTF2B	0.218	0.446
BAZ2A	BRF2	0.218	0.471
BAZ2A	MPHOSPH8	0.161	0.476
BAZ2A	TCF7L2	0.159	0.561
BCAR1	CSF1	0	0.651

BCAR1	RHOG	0.05	0.522
BCAR1	BMX	0.184	0.67
BCAR1	RET	0	0.671
BCAR1	CXCR4	0	0.644
BCAR1	JAK1	0.184	0.535
BCAR1	ELMO2	0	0.92
BCAR1	PTPN12	0.764	0.981
BCAR1	JUN	0	0.453
BCAR1	VAV1	0	0.585
BCAR1	GRB2	0.763	0.968
BCAR1	GTF2H1	0	0.517
BCAR1	PTK2B	0.762	0.997
BCAR1	PTPN1	0.764	0.949
BCAR1	EHBP1L1	0.044	0.416
BCAR1	ITGAL	0.051	0.723
BCAR1	PRKCD	0.1	0.698
BCAR1	RAP1B	0.043	0.678
BCAR1	PIK3CA	0	0.644
BCAR1	PTPN2	0.397	0.722
BCAR1	TYK2	0.184	0.466
BCAR1	FGR	0.184	0.722
BCAR1	TGFBR1	0.119	0.401
BCAR1	TEC	0.184	0.413
BCAR1	PTPRG	0.171	0.417
BCAR1	PTPN5	0.171	0.421
BCAR1	RND1	0.05	0.461
BCAR1	STAT3	0.052	0.474
BCAR1	CAPN2	0	0.493
BCAR1	KRAS	0.043	0.494
BCAR1	VEGFC	0	0.499
BCAR1	RHOH	0.05	0.52
BCAR1	PTPN22	0.312	0.54
BCAR1	JAK3	0.184	0.558
BCAR1	VASP	0	0.56
BCAR1	PTPN6	0.157	0.624
BCAR1	MST1R	0.119	0.632
BCAR1	PRKCB	0	0.663
BCAR1	FLT4	0	0.69
BCAR1	VEGFA	0	0.696
BCAR1	JAK2	0.184	0.717
BCAR1	ITGA9	0.055	0.742
BCAR1	HCK	0.184	0.774
BCAR1	ITGA5	0.067	0.814
BCAR1	ITGB7	0.114	0.845
BCAR1	LYN	0.264	0.846
BCAR1	ITGAV	0.113	0.894
BCAR1	SH2D3C	0.926	0.957

BCAR1	RAPGEF1	0.159	0.957
BCAR1	ZYX	0.114	0.979
BCAR1	CRKL	0.8	0.993
BCAR1	PXN	0.764	0.998
BCL2A1	DKK4	0	0.512
BCL2A1	RIPK2	0.064	0.405
BCL2A1	SAMSN1	0	0.405
BCL2A1	CSF2RB	0	0.406
BCL2A1	CREM	0	0.411
BCL2A1	SRGN	0	0.413
BCL2A1	NMI	0	0.427
BCL2A1	PLEK	0	0.431
BCL2A1	CD40	0	0.432
BCL2A1	NAIP	0.082	0.458
BCL2A1	XIAP	0.082	0.465
BCL2A1	HCK	0.064	0.468
BCL2A1	IRF1	0	0.469
BCL2A1	TNFSF10	0	0.481
BCL2A1	CASP7	0.219	0.484
BCL2A1	IER3	0.055	0.484
BCL2A1	PTPRC	0	0.499
BCL2A1	C5AR1	0	0.51
BCL2A1	TRAF1	0.045	0.511
BCL2A1	CREB1	0	0.512
BCL2A1	IL2RG	0	0.537
BCL2A1	CD53	0	0.563
BCL2A1	TNF	0.053	0.563
BCL2A1	CD69	0	0.576
BCL2A1	STAT3	0.06	0.58
BCL2A1	CXCL8	0	0.59
BCL2A1	IL1B	0	0.601
BCL2A1	NFKB2	0.052	0.624
BCL2A1	POU2F2	0.055	0.626
BCL2A1	CFLAR	0.219	0.666
BCL2A1	BIRC2	0.082	0.679
BCL2A1	CCL20	0	0.68
BCL2A1	CASP4	0.219	0.686
BCL2A1	LCP2	0	0.69
BCL2A1	MCL1	0	0.698
BCL2A1	RELA	0.055	0.718
BCL2A1	BIRC3	0.082	0.745
BCL2A1	NFKB1	0.052	0.783
BCL2A1	BID	0.935	0.968
BCL2A1	BCL2L11	0.935	0.988
BCL2L11	PPP1R15A	0	0.544
BCL2L11	BCL6	0	0.532
BCL2L11	JUN	0	0.723

BCL2L11	RAF1	0.055	0.476
BCL2L11	CREB1	0	0.405
BCL2L11	CASP7	0	0.757
BCL2L11	CDKN1A	0	0.553
BCL2L11	MAP3K5	0	0.588
BCL2L11	PIK3CA	0	0.42
BCL2L11	FAS	0	0.551
BCL2L11	CFLAR	0	0.718
BCL2L11	SIRT1	0	0.437
BCL2L11	MCL1	0.926	0.999
BCL2L11	CDKN1B	0	0.551
BCL2L11	TNFSF10	0	0.447
BCL2L11	CASP4	0	0.613
BCL2L11	STAT3	0	0.62
BCL2L11	BIRC3	0	0.41
BCL2L11	TNF	0	0.598
BCL2L11	BID	0.164	0.924
BCL2L11	KRAS	0	0.589
BCL2L11	DDIT3	0	0.929
BCL2L11	MDM2	0	0.563
BCL2L11	FASLG	0	0.423
BCL2L11	CD44	0	0.405
BCL2L11	LOC100297725	0	0.454
BCL2L11	BIRC2	0	0.59
BCL2L11	XIAP	0	0.75
BCL2L15	PRICKLE3	0	0.406
BCL2L15	TARS	0	0.422
BCL2L15	PTPN22	0	0.437
BCL2L15	FAM105A	0	0.453
BCL2L15	RAB3GAP1	0	0.453
BCL2L15	RNASE10	0	0.512
BCL3	IL1B	0	0.44
BCL3	SAMSN1	0	0.42
BCL3	JUN	0.113	0.492
BCL3	TNFRSF1A	0.043	0.42
BCL3	NFKB2	0.764	0.93
BCL3	CYLD	0.471	0.948
BCL3	IKBKB	0.08	0.522
BCL3	SOCS3	0.042	0.702
BCL3	BIRC3	0.093	0.402
BCL3	RND1	0.08	0.43
BCL3	PVRL2	0	0.443
BCL3	IGSF6	0	0.476
BCL3	CD40	0	0.477
BCL3	JUNB	0.044	0.5
BCL3	TNF	0.053	0.504
BCL3	CRISPLD2	0	0.528

BCL3	IKBKE	0	0.53
BCL3	SBNO2	0.069	0.559
BCL3	STAT3	0.113	0.611
BCL3	RELB	0.229	0.842
BCL3	RELA	0.192	0.876
BCL3	NFKB1	0.764	0.987
BCL6	MYD88	0.07	0.409
BCL6	PRDM1	0.113	0.427
BCL6	CXCR4	0.045	0.508
BCL6	MCL1	0.043	0.405
BCL6	CD80	0	0.409
BCL6	STAT5B	0.093	0.412
BCL6	DDIT3	0.078	0.415
BCL6	S1PR2	0	0.419
BCL6	RELA	0.098	0.42
BCL6	STAT5A	0.093	0.421
BCL6	RARA	0.093	0.424
BCL6	RBPJ	0.127	0.424
BCL6	TLR4	0.055	0.426
BCL6	SOCS3	0	0.436
BCL6	FOS	0.077	0.448
BCL6	IL7R	0	0.451
BCL6	IL2RB	0	0.453
BCL6	ICOSLG	0	0.457
BCL6	IL6	0.045	0.461
BCL6	SOCS1	0	0.463
BCL6	SLAMF1	0	0.492
BCL6	RHOH	0.06	0.528
BCL6	ZBTB17	0.408	0.533
BCL6	KLF6	0	0.534
BCL6	TEC	0.072	0.536
BCL6	STAT6	0.093	0.541
BCL6	STAT1	0.093	0.542
BCL6	CD69	0.055	0.546
BCL6	IL2RA	0	0.554
BCL6	TNF	0.043	0.558
BCL6	EZH2	0.161	0.56
BCL6	VAV1	0.057	0.562
BCL6	CREBBP	0.184	0.563
BCL6	FAS	0	0.568
BCL6	CD44	0	0.569
BCL6	IL10	0.053	0.58
BCL6	CXCL13	0	0.593
BCL6	FCGR2C	0	0.602
BCL6	GRB2	0.071	0.63
BCL6	DAPP1	0.072	0.632
BCL6	BCR	0	0.633

BCL6	HBEGF	0.218	0.634
BCL6	SELL	0.055	0.636
BCL6	PIK3CA	0.06	0.637
BCL6	CD38	0	0.647
BCL6	CD40	0	0.647
BCL6	PLCG2	0	0.651
BCL6	INPP5D	0.069	0.662
BCL6	LYN	0.072	0.67
BCL6	CTBP2	0.479	0.681
BCL6	STAT3	0.113	0.682
BCL6	GTF2B	0.457	0.694
BCL6	CD72	0.055	0.697
BCL6	CD5	0	0.707
BCL6	FCGR2B	0	0.71
BCL6	PPARD	0.132	0.773
BCL6	SIRT1	0.211	0.775
BCL6	PTPRC	0.045	0.826
BCL6	JUN	0.139	0.837
BCL6	HDAC4	0.218	0.861
BCL6	BCOR	0.924	0.999
BCOR	PCGF5	0.354	0.411
BCOR	EZH2	0.113	0.613
BCOR	RARA	0.079	0.496
BCOR	SIRT1	0.174	0.809
BCOR	TET2	0	0.606
BCOR	HDAC4	0.113	0.584
BCOR	PQBP1	0.113	0.46
BCOR	NABP1	0	0.499
BCOR	RYBP	0.764	0.964
BCOR	POGZ	0.164	0.41
BCOR	CHD1	0.045	0.454
BCOR	ZBTB17	0.164	0.413
BCOR	ETV6	0	0.55
BCR	RHOG	0.219	0.42
BCR	PLCG2	0.055	0.653
BCR	JAK1	0.114	0.565
BCR	VAV1	0.078	0.505
BCR	GRB2	0.777	0.994
BCR	DAPP1	0	0.631
BCR	PIK3CA	0.165	0.68
BCR	STAT5B	0	0.861
BCR	PTPRC	0.08	0.643
BCR	JAK2	0.114	0.758
BCR	PAM	0	0.532
BCR	RARA	0	0.472
BCR	RHOH	0.219	0.42
BCR	RND1	0.219	0.42

BCR	LYN	0.114	0.753
BCR	INPP5D	0.113	0.66
BCR	PTPN6	0.122	0.443
BCR	SMG1	0.093	0.492
BCR	JAK3	0.114	0.547
BCR	KRAS	0.156	0.423
BCR	TEC	0.114	0.547
BCR	HCK	0.435	0.61
BCR	STAT5A	0	0.84
BCR	CRKL	0.432	0.909
BFAR	GTF2H1	0	0.41
BFAR	UBXN7	0	0.414
BFAR	SERTAD1	0	0.485
BFAR	CFLAR	0.062	0.444
BFAR	ZC3H12A	0	0.519
BFAR	TARS	0	0.575
BHLHE40	DDIT4	0	0.423
BHLHE40	CTBP2	0.205	0.437
BHLHE40	RBPJ	0.108	0.483
BHLHE40	SIRT1	0.184	0.411
BHLHE40	JUNB	0	0.413
BHLHE40	STAT1	0.07	0.421
BHLHE40	TRIB1	0	0.427
BHLHE40	TBL1X	0	0.491
BHLHE40	STAT3	0.113	0.63
BID	NAIP	0	0.5
BID	TNFRSF1A	0.119	0.742
BID	RIPK1	0	0.697
BID	CASP7	0.161	0.667
BID	MAP3K5	0	0.69
BID	TRAF2	0.093	0.683
BID	FAS	0.433	0.889
BID	CFLAR	0.161	0.688
BID	MLKL	0	0.406
BID	TRAF3	0.093	0.518
BID	MCL1	0.923	0.972
BID	DAXX	0	0.696
BID	RIPK3	0	0.444
BID	TNFSF10	0	0.748
BID	TRAF7	0.093	0.427
BID	LTB	0.06	0.41
BID	CASP4	0.161	0.521
BID	NOD2	0	0.436
BID	BIRC3	0	0.581
BID	TNF	0.086	0.742
BID	RNF41	0.093	0.405
BID	TNFSF14	0	0.428

BID	RIPK2	0	0.504
BID	MPHOSPH8	0	0.512
BID	FASLG	0.06	0.527
BID	TRAF1	0.093	0.603
BID	XIAP	0	0.619
BID	BIRC2	0	0.66
BID	CAPN2	0.428	0.895
BIN2	FYB	0	0.687
BIN2	STAM2	0.042	0.447
BIN2	MX2	0.318	0.636
BIN2	LCP2	0	0.505
BIN2	COTL1	0.259	0.524
BIN2	PIK3AP1	0	0.427
BIN2	INPP5D	0.159	0.635
BIN2	PSTPIP1	0.257	0.464
BIN2	DNM2	0.318	0.746
BIN2	MX1	0.318	0.636
BIRC2	MYD88	0.158	0.467
BIRC2	TNFRSF1A	0.653	0.991
BIRC2	NFKB2	0.122	0.605
BIRC2	IRAK2	0.339	0.484
BIRC2	TLR4	0.158	0.429
BIRC2	CYLD	0	0.66
BIRC2	RIPK1	0.639	0.991
BIRC2	CASP7	0.433	0.986
BIRC2	IKBKB	0.257	0.57
BIRC2	NLRC4	0.347	0.543
BIRC2	MAP3K5	0	0.648
BIRC2	IKBKE	0.257	0.489
BIRC2	TRAF2	0.764	0.994
BIRC2	FAS	0	0.728
BIRC2	CFLAR	0.295	0.899
BIRC2	XAF1	0.184	0.459
BIRC2	JAK2	0.132	0.42
BIRC2	MLKL	0.158	0.692
BIRC2	TAB2	0.061	0.915
BIRC2	TRAF3	0.473	0.994
BIRC2	RELA	0.317	0.855
BIRC2	MCL1	0.082	0.726
BIRC2	LTBR	0.205	0.558
BIRC2	RBCK1	0.087	0.867
BIRC2	RIPK3	0.158	0.945
BIRC2	TNFSF10	0.051	0.416
BIRC2	TRAF7	0.184	0.46
BIRC2	NFKB1	0.162	0.631
BIRC2	CD40	0.501	0.87
BIRC2	CASP4	0.295	0.651

BIRC2	NOD2	0.093	0.447
BIRC2	STAT3	0.096	0.404
BIRC2	TNFRSF1B	0.087	0.736
BIRC2	TNF	0.59	0.943
BIRC2	TRAF1	0.761	0.984
BIRC2	MDM2	0.149	0.493
BIRC2	TANK	0.34	0.54
BIRC2	MALT1	0.087	0.539
BIRC2	FASLG	0.157	0.451
BIRC2	LOC100297725	0.17	0.409
BIRC2	LRRK2	0.183	0.42
BIRC2	RELB	0	0.645
BIRC2	RIPK2	0.413	0.691
BIRC2	DDX3X	0.07	0.849
BIRC2	UBE2D1	0.648	0.85
BIRC2	XIAP	0.483	0.96
BIRC3	MYD88	0.158	0.495
BIRC3	NFKBIB	0.093	0.445
BIRC3	JUN	0	0.443
BIRC3	TNFRSF1A	0.653	0.949
BIRC3	NFKB2	0.122	0.752
BIRC3	IRAK2	0.339	0.625
BIRC3	TLR4	0.158	0.437
BIRC3	RIPK1	0.639	0.943
BIRC3	CASP7	0.433	0.906
BIRC3	IKBKB	0.257	0.606
BIRC3	NLRC4	0.347	0.562
BIRC3	MAP3K5	0	0.596
BIRC3	IKBKE	0.257	0.521
BIRC3	TRAF2	0.764	0.943
BIRC3	FAS	0	0.675
BIRC3	CFLAR	0.295	0.888
BIRC3	IER3	0.087	0.522
BIRC3	MAP3K8	0	0.436
BIRC3	JAK2	0.132	0.42
BIRC3	TAB2	0.061	0.672
BIRC3	TRAF3	0.473	0.878
BIRC3	RELA	0.317	0.836
BIRC3	MCL1	0.082	0.53
BIRC3	LTBR	0.205	0.511
BIRC3	TGFBR1	0.161	0.429
BIRC3	RIPK3	0.158	0.457
BIRC3	TNFSF10	0.051	0.567
BIRC3	TRAF7	0.184	0.422
BIRC3	CXCL8	0	0.514
BIRC3	NFKB1	0.162	0.782
BIRC3	LTB	0.157	0.477

BIRC3	CD40	0.501	0.882
BIRC3	CASP4	0.295	0.77
BIRC3	IRAK4	0.132	0.403
BIRC3	CCL20	0	0.432
BIRC3	GADD45B	0	0.41
BIRC3	FASLG	0.157	0.42
BIRC3	LRRK2	0.183	0.438
BIRC3	NOD1	0.093	0.448
BIRC3	IRF1	0.165	0.495
BIRC3	TANK	0.34	0.537
BIRC3	NFKBIE	0.093	0.572
BIRC3	MALT1	0.087	0.575
BIRC3	RELB	0	0.616
BIRC3	RIPK2	0.413	0.749
BIRC3	XIAP	0.483	0.791
BIRC3	TNFRSF1B	0.087	0.821
BIRC3	UBE2D1	0.648	0.843
BIRC3	TNF	0.59	0.929
BIRC3	TRAF1	0.761	0.964
BLZF1	HOMEZ	0	0.403
BLZF1	GRIPAP1	0	0.463
BLZF1	DAPP1	0	0.48
BLZF1	DOPEY2	0	0.485
BLZF1	UBAP1	0	0.572
BLZF1	STARD3	0	0.592
BMX	STAT4	0.236	0.4
BMX	IL2RB	0.175	0.407
BMX	CSF2RB	0.193	0.41
BMX	RAPGEF1	0.161	0.415
BMX	PPP4C	0.125	0.42
BMX	SH3BP2	0.115	0.428
BMX	IFNAR1	0.218	0.428
BMX	IL6	0.045	0.431
BMX	CRKL	0.184	0.431
BMX	STAT6	0.236	0.44
BMX	STAT1	0.236	0.45
BMX	PTPN12	0.139	0.454
BMX	PLA2G4A	0.127	0.46
BMX	LCP2	0.209	0.465
BMX	MST1R	0.225	0.468
BMX	IL10RA	0.205	0.475
BMX	PLEK	0	0.483
BMX	PLCG2	0.138	0.485
BMX	GRB2	0.257	0.498
BMX	MYD88	0.178	0.626
BMX	PTK2B	0.219	0.667
BMX	TNFRSF1B	0.078	0.709

BMX	STAT3	0.764	0.898
BOLA	PSMB8	0	0.514
BOLA	JUN	0	0.544
BOLA	VAV1	0.043	0.506
BOLA	IL2RG	0	0.525
BOLA	PSMB9	0	0.511
BOLA	RAP1B	0.043	0.501
BOLA	PIK3CA	0.053	0.797
BOLA	LCP2	0	0.508
BOLA	BOLA-DMA	0.044	0.404
BOLA	BOLA-DRB3	0.043	0.409
BOLA	C6orf106	0	0.485
BOLA	SNAP29	0	0.507
BOLA	IL2RA	0	0.519
BOLA	LAMP1	0.043	0.541
BOLA	IL2RB	0	0.546
BOLA	CD80	0	0.568
BOLA	TAPBPL	0.179	0.586
BOLA	LOC512672	0	0.601
BOLA	TAP1	0.129	0.719
BOLA	TAPBP	0.422	0.978
BOLA-DMA	PSMB8	0	0.522
BOLA-DMA	CD274	0	0.571
BOLA-DMA	PSMB9	0	0.556
BOLA-DMA	LCP2	0	0.43
BOLA-DMA	BOLA-DRA	0.931	0.99
BOLA-DMA	BOLA-DMB	0.965	0.999
BOLA-DMA	BOLA-DRB3	0.604	0.972
BOLA-DMA	TAPBPL	0	0.426
BOLA-DMA	BOLA-DQA5	0.45	0.821
BOLA-DMA	ENSBTAP00000019939	0.45	0.827
BOLA-DMA	CD74	0.415	0.965
BOLA-DMA	BOLA-NC1	0.044	0.411
BOLA-DMA	TAPBP	0.115	0.475
BOLA-DMA	FCER1G	0	0.549
BOLA-DMA	CD80	0	0.55
BOLA-DMA	CIITA	0	0.619
BOLA-DMB	PSMB8	0	0.731
BOLA-DMB	CD53	0.052	0.472
BOLA-DMB	PSMB9	0	0.779
BOLA-DMB	BOLA-DRA	0.938	0.998
BOLA-DMB	FCER1G	0	0.423
BOLA-DMB	CIITA	0	0.429
BOLA-DMB	LAPTM5	0	0.441
BOLA-DMB	TAPBP	0	0.492
BOLA-DMB	FCGR3A	0	0.579
BOLA-DMB	TAP1	0	0.631

BOLA-DMB	BOLA-DQA5	0.463	0.882
BOLA-DMB	ENSBTAP00000019939	0.463	0.891
BOLA-DMB	CD74	0.078	0.965
BOLA-DMB	BOLA-DRB3	0.296	0.969
BOLA-DQA5	FYB	0	0.538
BOLA-DQA5	INTS6	0	0.41
BOLA-DQA5	VAV1	0	0.565
BOLA-DQA5	STAT6	0	0.554
BOLA-DQA5	LCP2	0	0.56
BOLA-DQA5	PTPRC	0.045	0.614
BOLA-DQA5	BOLA-DRA	0	0.814
BOLA-DQA5	BOLA-DRB3	0.501	0.915
BOLA-DQA5	STAT4	0	0.401
BOLA-DQA5	PSTPIP2	0	0.518
BOLA-DQA5	CD80	0	0.598
BOLA-DQA5	ENSBTAP00000019939	0	0.603
BOLA-DQA5	CD74	0.639	0.979
BOLA-DRA	FYB	0	0.681
BOLA-DRA	PSMB8	0	0.582
BOLA-DRA	VAV1	0	0.666
BOLA-DRA	STAT6	0	0.666
BOLA-DRA	CD53	0.045	0.483
BOLA-DRA	PRKCD	0	0.46
BOLA-DRA	PSMB9	0	0.481
BOLA-DRA	LCP2	0	0.699
BOLA-DRA	PTPRC	0.045	0.817
BOLA-DRA	LYN	0	0.414
BOLA-DRA	PTPN22	0.042	0.435
BOLA-DRA	PTPN6	0.042	0.461
BOLA-DRA	TAPBP	0.156	0.468
BOLA-DRA	FCGR3A	0	0.507
BOLA-DRA	STAT1	0	0.508
BOLA-DRA	FCER1G	0	0.53
BOLA-DRA	LAPTM5	0	0.619
BOLA-DRA	SH3BP2	0	0.62
BOLA-DRA	CIITA	0	0.651
BOLA-DRA	CD80	0	0.728
BOLA-DRA	ENSBTAP00000019939	0	0.832
BOLA-DRA	BOLA-DRB3	0.763	0.997
BOLA-DRA	CD74	0.761	0.999
BOLA-DRB3	FYB	0	0.612
BOLA-DRB3	PSMB8	0	0.404
BOLA-DRB3	VAV1	0	0.632
BOLA-DRB3	STAT6	0.045	0.603
BOLA-DRB3	PRKCD	0	0.427
BOLA-DRB3	LCP2	0	0.655
BOLA-DRB3	PTPRC	0	0.742

BOLA-DRB3	BOLA-NC1	0.043	0.423
BOLA-DRB3	PTPN6	0	0.433
BOLA-DRB3	CIITA	0	0.445
BOLA-DRB3	STAT4	0.045	0.472
BOLA-DRB3	PTPN22	0	0.592
BOLA-DRB3	CD80	0	0.676
BOLA-DRB3	ENSBTAP00000019939	0.501	0.938
BOLA-DRB3	CD74	0.162	0.992
BOLA-NC1	PSMB8	0	0.419
BOLA-NC1	JUN	0	0.536
BOLA-NC1	VAV1	0.043	0.506
BOLA-NC1	IL2RG	0	0.513
BOLA-NC1	RAP1B	0.043	0.501
BOLA-NC1	PIK3CA	0.053	0.797
BOLA-NC1	LCP2	0	0.522
BOLA-NC1	SNAP29	0	0.507
BOLA-NC1	C6orf106	0	0.513
BOLA-NC1	IL2RA	0	0.519
BOLA-NC1	LAMP1	0.043	0.527
BOLA-NC1	IL2RB	0	0.553
BOLA-NC1	CD80	0	0.571
BOLA-NC1	TAP1	0.129	0.71
BOLA-NC1	TAPBP	0.422	0.777
BRAF	RET	0.16	0.441
BRAF	RAF1	0.776	0.915
BRAF	GRB2	0.163	0.573
BRAF	CD274	0.042	0.416
BRAF	KSR1	0.44	0.832
BRAF	SHOC2	0.218	0.62
BRAF	EDN1	0	0.504
BRAF	RAP1B	0.529	0.829
BRAF	PIK3CA	0.122	0.742
BRAF	MAP2K3	0.102	0.656
BRAF	NF1	0.122	0.517
BRAF	DIRAS3	0.245	0.481
BRAF	MCL1	0.139	0.462
BRAF	PXN	0.117	0.459
BRAF	INPP5D	0.076	0.419
BRAF	PRKCB	0.093	0.654
BRAF	SAG	0.16	0.457
BRAF	STAT3	0.147	0.414
BRAF	ETV6	0.352	0.404
BRAF	FCGR2C	0.087	0.426
BRAF	FCGR2B	0.087	0.426
BRAF	XIAP	0.315	0.472
BRAF	DNM2	0.093	0.493
BRAF	FCER1G	0.12	0.509

BRAF	KRAS	0.762	0.979
BRF2	KAT2B	0.218	0.422
BRF2	POLR2C	0.413	0.535
BRF2	CREBBP	0.218	0.422
BRF2	JUN	0.116	0.444
BRF2	UBXN7	0.395	0.632
BRF2	JUNB	0.116	0.444
BRF2	RELA	0.127	0.516
BRF2	SNAPC1	0	0.849
BRF2	IRF1	0	0.438
BRF2	POLR2A	0.395	0.632
BRWD3	MAP3K2	0.045	0.589
BRWD3	UBXN7	0.609	0.881
BRWD3	SH3BGRL	0	0.636
BRWD3	NIPBL	0	0.408
BRWD3	MYSM1	0.158	0.451
BRWD3	SMG1	0.169	0.486
BRWD3	MED13	0.045	0.556
BRWD3	CUL4A	0.505	0.607
BRWD3	RC3H2	0.045	0.638
BRWD3	UBR1	0.468	0.8
BTBD1	LOC616948	0.07	0.606
BTBD1	LOC516599	0.07	0.475
BTBD1	TOP1	0.218	0.699
BTBD1	TAB2	0	0.407
BTBD11	FRYL	0	0.414
BTBD11	TSPAN2	0	0.513
BTBD11	PRR5L	0	0.637
BTG1	HCLS1	0	0.414
BTG1	CNOT7	0.79	0.909
BTG2	NR4A1	0	0.849
BTG2	PPP1R15A	0	0.528
BTG2	JUN	0	0.828
BTG2	FOS	0	0.873
BTG2	CDKN1A	0	0.523
BTG2	IER3	0	0.445
BTG2	JUNB	0	0.693
BTG2	KLF6	0	0.815
BTG2	DUSP5	0	0.429
BTG2	GADD45B	0	0.444
BTG2	MDM2	0	0.465
BTG2	KIAA0247	0	0.489
BTG2	KLF7	0	0.657
BTG2	CNOT7	0.66	0.93
BTG3	C1H21orf91	0	0.412
BTG3	PI4K2A	0	0.461
BTG3	CNOT7	0.689	0.769

BTG3	NIPAL4	0	0.632
BTG3	IL13RA1	0	0.633
C15orf48	SAMSN1	0	0.418
C15orf48	FAM129A	0	0.412
C17orf80	VPS4B	0	0.406
C18orf8	ORAOV1	0	0.403
C18orf8	EPG5	0	0.62
C19orf26	MIDN	0	0.418
C19orf26	SBNO2	0	0.62
C1H21orf91	GPR4	0	0.474
C1H21orf91	PNRC1	0	0.535
C1H21orf91	EIF4E3	0	0.56
C1H21orf91	PPTC7	0	0.601
C1RL	CDADC1	0	0.591
C1RL	C4A	0.159	0.708
C1RL	C3	0.159	0.415
C1RL	FCAR	0	0.406
C1RL	FCN1	0.07	0.572
C3	IL1B	0.137	0.448
C3	CD46	0.761	0.927
C3	TLR4	0.08	0.406
C3	IL10	0.156	0.47
C3	C4A	0	0.858
C3	CFB	0.761	0.987
C3	PTX3	0.184	0.474
C3	MYBPH	0	0.403
C3	IL6	0	0.411
C3	SERPING1	0	0.624
C3	GSN	0	0.443
C3	CXCL8	0	0.465
C3	GPR77	0.13	0.488
C3	TNF	0	0.496
C3	F12	0.16	0.607
C3	C5AR1	0.124	0.613
C3	ELANE	0.219	0.65
C3	SELP	0.082	0.68
C3	CFD	0.357	0.962
C3orf38	USPL1	0	0.512
C4A	PHF1	0	0.426
C4A	CD46	0.44	0.893
C4A	STK19	0	0.55
C4A	IL10	0.156	0.41
C4A	C5AR1	0.124	0.448
C4A	SRGN	0	0.468
C4A	CD40	0	0.574
C4A	GPR77	0.13	0.587
C4A	IL6	0	0.591

C4A	ELANE	0.219	0.631
C4A	F5	0	0.658
C4A	CFD	0.315	0.709
C4A	SERPING1	0	0.752
C4A	CFB	0.391	0.833
C5AR1	IL1B	0	0.471
C5AR1	FYB	0	0.498
C5AR1	CD46	0	0.464
C5AR1	TLR4	0	0.87
C5AR1	ITGAL	0	0.417
C5AR1	CFB	0	0.446
C5AR1	TLR2	0	0.789
C5AR1	LOC506364	0	0.557
C5AR1	CSF2RB	0	0.605
C5AR1	LCP2	0	0.574
C5AR1	PLEK	0	0.596
C5AR1	PTPRC	0	0.572
C5AR1	IL6	0	0.508
C5AR1	TREM1	0	0.471
C5AR1	IGSF6	0	0.66
C5AR1	CCR1	0.042	0.504
C5AR1	CXCL8	0	0.461
C5AR1	TNF	0	0.453
C5AR1	CYTH4	0	0.487
C5AR1	SAG	0.055	0.491
C5AR1	LOC100138951	0	0.581
C5AR1	MPEG1	0	0.632
C5AR1	PTAFR	0	0.645
C5AR1	FCGR2B	0	0.671
C6H4orf32	MIER1	0	0.675
C6H4orf32	TAPT1	0	0.41
C6H4orf32	LYSMD3	0	0.47
C6H4orf32	GRK6	0	0.588
C6orf106	NUDT3	0	0.462
C7H19orf43	DDX5	0.398	0.414
C7H19orf43	DDX17	0.413	0.428
C7H19orf43	TFIP11	0.45	0.462
C7H19orf66	UBE2L6	0	0.453
C7H19orf66	MOV10	0	0.414
C7H19orf66	IRF9	0	0.421
CA4	MAP1LC3A	0	0.417
CA4	SLC4A2	0.156	0.613
CA4	MARK3	0	0.416
CA5B	SYAP1	0	0.641
CA5B	PM20D2	0.053	0.533
CABYR	SPATA6	0	0.778
CABYR	CFAP69	0	0.707

CABYR	7-Mar	0	0.405
CABYR	SLC24A3	0	0.465
CACHD1	PTPN9	0.042	0.533
CALCOCO2	RB1CC1	0.41	0.89
CALCOCO2	EIF2C2	0	0.513
CALCOCO2	COPZ1	0	0.685
CALCOCO2	MAP1LC3A	0.432	0.735
CALCOCO2	TAB2	0.071	0.419
CALCOCO2	SNAP29	0	0.425
CALCOCO2	ISG20	0	0.522
CALCOCO2	LAMP1	0	0.579
CALCOCO2	IKBKE	0.493	0.618
CALCOCO2	SRGN	0	0.621
CALCOCO2	DCAF11	0	0.712
CALCOCO2	DTX3L	0	0.718
CALCOCO2	TAPBPL	0	0.757
CALCOCO2	OPTN	0.053	0.901
CALCOCO2	GABARAPL1	0.351	0.95
CALM1	FAS	0.397	0.403
CALM1	CAMK1D	0.391	0.507
CALM1	RYR1	0.431	0.518
CALM1	MARCKS	0.484	0.53
CALM1	GTPBP1	0	0.539
CALM1	NOS2	0.491	0.556
CALM1	ITPR2	0.118	0.563
CALM1	PPP4C	0.163	0.58
CAMK1D	CREB1	0.157	0.878
CAMK1D	TCF7L2	0	0.42
CAMK1D	HDAC4	0.158	0.498
CAMK1D	ZFAND6	0	0.505
CAMK1D	HHEX	0	0.506
CAMK1D	MEF2A	0.094	0.6
CAMK1D	CREM	0.126	0.66
CAPN2	NFE2L3	0.042	0.537
CAPN2	MB21D2	0	0.45
CAPN2	PTK2B	0	0.689
CAPN2	PTPN1	0.121	0.483
CAPN2	FRMD4A	0.093	0.774
CAPN2	PIK3CA	0	0.463
CAPN2	IL1A	0.055	0.803
CAPN2	PTPN2	0.121	0.463
CAPN2	ZYX	0.045	0.602
CAPN2	PXN	0	0.697
CAPN2	ITGB7	0.098	0.42
CAPN2	PROSC	0.453	0.453
CAPN2	SRI	0.294	0.5
CAPN2	CRKL	0	0.523

CARS	WARS	0	0.747
CARS	LAP3	0	0.468
CARS	LIG4	0	0.425
CARS	TSFM	0.055	0.435
CARS	PROSC	0.436	0.527
CARS	RANBP2	0	0.618
CARS	RHBDD1	0	0.632
CARS	TARS	0	0.728
CARS	SARS	0.218	0.962
CASP4	EIF4A1	0.054	0.593
CASP4	MYD88	0.116	0.632
CASP4	NLRP3	0.073	0.935
CASP4	IL1B	0.45	0.926
CASP4	NAIP	0.295	0.76
CASP4	RABGEF1	0.119	0.505
CASP4	TNFRSF1A	0.157	0.64
CASP4	IL1R1	0	0.543
CASP4	NLRC5	0.068	0.5
CASP4	CD274	0	0.486
CASP4	IRAK2	0.106	0.428
CASP4	TLR4	0.093	0.688
CASP4	IL1R2	0	0.73
CASP4	RIPK1	0.126	0.541
CASP4	CD53	0.042	0.518
CASP4	IL10	0	0.487
CASP4	CFB	0.055	0.45
CASP4	IKBKB	0.136	0.48
CASP4	TLR2	0.093	0.636
CASP4	IFIH1	0	0.703
CASP4	NLRC4	0.589	0.957
CASP4	PSMB9	0	0.446
CASP4	MAP3K5	0.05	0.495
CASP4	DTX3L	0	0.618
CASP4	IL1A	0.08	0.464
CASP4	IKBKE	0.136	0.432
CASP4	TRAF2	0.119	0.583
CASP4	FAS	0.258	0.655
CASP4	CFLAR	0	0.507
CASP4	XAF1	0	0.413
CASP4	PANX1	0.161	0.587
CASP4	MLKL	0.126	0.55
CASP4	UBA7	0.071	0.433
CASP4	TRAF3	0.119	0.429
CASP4	RELA	0	0.517
CASP4	ISG15	0.09	0.484
CASP4	IL6	0	0.573
CASP4	PARP14	0	0.689

CASP4	PTBP3	0.045	0.468
CASP4	DAXX	0.055	0.43
CASP4	TLR9	0.093	0.524
CASP4	RIPK3	0.126	0.631
CASP4	TNFSF10	0.218	0.716
CASP4	MEFV	0.08	0.655
CASP4	IL1RN	0.11	0.484
CASP4	CXCL8	0	0.466
CASP4	NFKB1	0.119	0.462
CASP4	TANK	0	0.401
CASP4	PARP3	0.203	0.408
CASP4	IFNAR1	0	0.412
CASP4	LRRK2	0.219	0.418
CASP4	STAT1	0.045	0.431
CASP4	TRAF1	0.119	0.441
CASP4	IRAK4	0.106	0.46
CASP4	DDX58	0	0.539
CASP4	PARP9	0	0.568
CASP4	NLRP12	0.073	0.644
CASP4	NOD1	0.159	0.654
CASP4	RIPK2	0.159	0.655
CASP4	DDIT3	0.045	0.699
CASP4	XIAP	0.295	0.706
CASP4	TNF	0.068	0.729
CASP4	NOD2	0.218	0.733
CASP4	IL18	0.172	0.929
CASP7	EIF4A1	0.054	0.64
CASP7	MYD88	0.116	0.493
CASP7	IL1B	0.184	0.573
CASP7	NAIP	0.295	0.623
CASP7	JUN	0.077	0.402
CASP7	TNFRSF1A	0.218	0.718
CASP7	NFKB2	0.119	0.413
CASP7	IL1R2	0	0.416
CASP7	RIPK1	0.126	0.489
CASP7	STAT1	0.114	0.402
CASP7	NFKB1	0.119	0.405
CASP7	SMG1	0.123	0.408
CASP7	ROCK1	0.184	0.412
CASP7	LOC100297725	0.041	0.423
CASP7	KRAS	0.075	0.425
CASP7	IKBKB	0.136	0.432
CASP7	STAT3	0.045	0.436
CASP7	CDKN1A	0.132	0.438
CASP7	LRRK2	0.219	0.443
CASP7	RELA	0	0.445
CASP7	GSN	0.064	0.446

CASP7	LMNB1	0.158	0.447
CASP7	TRAF2	0.119	0.448
CASP7	MLKL	0.126	0.467
CASP7	TRAF1	0.119	0.468
CASP7	TOP1	0.138	0.473
CASP7	RIPK3	0.126	0.479
CASP7	NLRC4	0.216	0.49
CASP7	PTBP3	0.045	0.494
CASP7	MAP3K5	0.05	0.494
CASP7	PANX1	0.113	0.498
CASP7	MDM2	0.163	0.504
CASP7	ITGB7	0	0.506
CASP7	DDIT3	0.045	0.52
CASP7	IL18	0.093	0.554
CASP7	RIPK2	0.126	0.601
CASP7	TNF	0.086	0.694
CASP7	DAXX	0.055	0.699
CASP7	TNFSF10	0.218	0.706
CASP7	MCL1	0.219	0.74
CASP7	FAS	0.258	0.862
CASP7	PARP3	0.203	0.883
CASP7	XIAP	0.929	0.999
CASS4	SLC13A3	0	0.449
CASS4	GAB2	0	0.42
CASS4	PTK2B	0.042	0.576
CASS4	LOC100138951	0	0.403
CASS4	INPP5D	0.301	0.762
CBLN3	MTMR7	0	0.417
CBLN3	DRAXIN	0	0.534
CC2D2A	ZNF259	0	0.516
CC2D2A	RAB3GAP1	0	0.524
CC2D2A	NIN	0	0.58
CCDC146	SLCO3A1	0	0.565
CCDC146	TPM4	0	0.469
CCDC19	CLIC5	0	0.517
CCDC19	STOML3	0	0.617
CCDC69	FAM129A	0	0.65
CCDC69	CRISPLD2	0	0.42
CCDC82	POU2F2	0	0.487
CCL20	CSF1	0	0.433
CCL20	MYD88	0	0.4
CCL20	CXCR4	0.054	0.822
CCL20	IL1B	0	0.933
CCL20	IL23A	0	0.476
CCL20	LOC515976	0.054	0.685
CCL20	TLR4	0	0.589
CCL20	IL1R2	0	0.425

CCL20	IL10	0	0.681
CCL20	NOS2	0	0.833
CCL20	CFB	0	0.476
CCL20	TLR2	0	0.594
CCL20	CCR5	0.054	0.826
CCL20	CXCL13	0	0.675
CCL20	ICAM1	0	0.648
CCL20	IL1A	0	0.867
CCL20	ZC3H12A	0	0.45
CCL20	CCR2	0.054	0.82
CCL20	CCL8	0.06	0.617
CCL20	PTGS2	0	0.522
CCL20	IL6	0	0.766
CCL20	IL15	0	0.52
CCL20	CXCL16	0	0.464
CCL20	RND1	0	0.698
CCL20	CCR1	0.054	0.768
CCL20	CXCL8	0.08	0.92
CCL20	XCR1	0.054	0.772
CCL20	NFKB1	0	0.572
CCL20	CD40	0	0.442
CCL20	NOD2	0.045	0.41
CCL20	STAT1	0	0.419
CCL20	S100A12	0	0.422
CCL20	TRAF1	0.055	0.426
CCL20	STAT3	0	0.465
CCL20	TNFAIP2	0	0.48
CCL20	RELB	0	0.492
CCL20	IL17RC	0	0.52
CCL20	IL18	0	0.551
CCL20	IRF1	0	0.591
CCL20	LOC529196	0.054	0.622
CCL20	NFKBIE	0	0.683
CCL20	CXCR2	0.054	0.83
CCL20	CXCR1	0.054	0.83
CCL20	TNF	0	0.875
CCL8	CSF1	0	0.401
CCL8	CXCR4	0.081	0.882
CCL8	IL1B	0	0.508
CCL8	PLCG2	0	0.478
CCL8	JUN	0	0.532
CCL8	FOS	0	0.514
CCL8	IL12B	0	0.41
CCL8	LOC515976	0.081	0.415
CCL8	IL10	0	0.485
CCL8	EDN1	0	0.595
CCL8	CCR5	0.334	0.963

CCL8	MX2	0	0.628
CCL8	CXCL13	0.071	0.465
CCL8	IL1A	0	0.413
CCL8	FGR	0	0.592
CCL8	JUNB	0	0.4
CCL8	CCR2	0.334	0.982
CCL8	IRF1	0	0.412
CCL8	SAG	0.042	0.415
CCL8	IL15	0	0.419
CCL8	IL6	0	0.454
CCL8	KRAS	0	0.5
CCL8	SERPINB2	0	0.505
CCL8	LOC281376	0	0.505
CCL8	PPARD	0	0.517
CCL8	CXCL16	0	0.54
CCL8	TNF	0	0.588
CCL8	HCK	0	0.59
CCL8	MX1	0	0.593
CCL8	CXCL8	0.087	0.756
CCL8	CXCR1	0.081	0.773
CCL8	CXCR2	0.081	0.779
CCL8	XCR1	0.081	0.801
CCL8	LOC529196	0.334	0.94
CCL8	CCR1	0.334	0.982
CCNJL	CDK17	0.388	0.636
CCNJL	CDKN1A	0.315	0.658
CCNJL	PARM1	0	0.609
CCNJL	E2F2	0.337	0.685
CCNJL	CDKN1B	0.315	0.658
CCNJL	E2F3	0.337	0.685
CCNJL	STK38L	0.136	0.43
CCNJL	FZR1	0.44	0.511
CCNJL	MDM2	0.134	0.481
CCNL1	DUSP16	0.053	0.706
CCNL1	CDK17	0.218	0.47
CCNL1	DDX5	0.043	0.407
CCNL1	POLR2A	0.217	0.421
CCNL1	PPP1R3B	0.052	0.427
CCNL1	MED13	0.316	0.441
CCNL1	GTF2H1	0.405	0.493
CCNL1	TFIP11	0.046	0.633
CCNL1	HIAT1	0	0.639
CCNL1	CLK1	0.055	0.796
CCNL2	CDK17	0.218	0.47
CCNL2	MED13	0.316	0.441
CCNL2	HIAT1	0	0.441
CCNL2	FMNL1	0.456	0.456

CCNL2	SF3B1	0	0.459
CCNL2	SRSF5	0.137	0.476
CCNL2	GTF2H1	0.405	0.493
CCNL2	STK19	0	0.513
CCNL2	GPCPD1	0	0.665
CCNT1	KAT2B	0.157	0.596
CCNT1	CXCR4	0	0.532
CCNT1	USPL1	0	0.449
CCNT1	CDK17	0.218	0.59
CCNT1	ELL	0.216	0.818
CCNT1	CREBBP	0.157	0.44
CCNT1	GTF2H1	0.405	0.492
CCNT1	MYSM1	0	0.408
CCNT1	LOC100297725	0.055	0.428
CCNT1	GLS	0	0.428
CCNT1	XRN1	0	0.429
CCNT1	KDM5A	0.052	0.441
CCNT1	DDX5	0.049	0.453
CCNT1	RANBP2	0	0.461
CCNT1	RLF	0.071	0.502
CCNT1	RC3H2	0	0.541
CCNT1	UBXN7	0.306	0.578
CCNT1	PML	0.426	0.621
CCNT1	SMG1	0.044	0.637
CCNT1	GTF2B	0.138	0.652
CCNT1	CIITA	0.114	0.654
CCNT1	POLR2A	0.306	0.728
CCNT1	MED13	0.316	0.766
CCNT1	HEXIM1	0.934	0.998
CCR1	CXCR4	0.218	0.706
CCR1	IL1B	0.042	0.478
CCR1	PLCG2	0.071	0.494
CCR1	JUN	0.042	0.539
CCR1	IL10RA	0	0.495
CCR1	TLR4	0.053	0.527
CCR1	CD53	0.055	0.452
CCR1	IL10	0	0.586
CCR1	ITGAL	0	0.408
CCR1	TLR2	0.053	0.48
CCR1	EDN1	0.079	0.628
CCR1	CCR5	0	0.635
CCR1	CXCL13	0.055	0.831
CCR1	LCP2	0	0.422
CCR1	PTPRC	0.045	0.53
CCR1	LOC504773	0	0.641
CCR1	ICAM1	0	0.507
CCR1	JAK2	0.129	0.699

CCR1	CCR2	0	0.587
CCR1	CD80	0	0.488
CCR1	CXCL16	0	0.72
CCR1	IL13RA1	0	0.41
CCR1	CD300A	0	0.416
CCR1	TNFRSF1B	0	0.455
CCR1	IL18	0	0.459
CCR1	HCK	0.08	0.526
CCR1	IL1RN	0	0.543
CCR1	CD40	0.121	0.597
CCR1	TNF	0	0.617
CCR1	JAK3	0.116	0.698
CCR1	GRK6	0.053	0.733
CCR1	CXCR1	0	0.743
CCR1	LOC529196	0	0.805
CCR1	PTAFR	0	0.818
CCR1	CXCL8	0.078	0.898
CCR2	CSF1	0	0.664
CCR2	MYD88	0	0.536
CCR2	CXCR4	0.34	0.766
CCR2	IL1B	0.042	0.6
CCR2	PLCG2	0.071	0.474
CCR2	CD69	0.042	0.479
CCR2	JUN	0.042	0.671
CCR2	IL10RA	0	0.427
CCR2	IL1R1	0	0.491
CCR2	CD274	0	0.437
CCR2	TLR4	0.053	0.755
CCR2	STAT6	0.053	0.424
CCR2	IL10	0	0.741
CCR2	NOS2	0	0.486
CCR2	ITGAL	0	0.453
CCR2	TLR2	0.053	0.6
CCR2	EDN1	0.079	0.669
CCR2	CXCL13	0.055	0.824
CCR2	PTPRC	0.045	0.829
CCR2	ICAM1	0	0.617
CCR2	JAK2	0.162	0.745
CCR2	SLC9A3R1	0.12	0.414
CCR2	VEGFA	0	0.417
CCR2	IL15	0	0.425
CCR2	SELP	0.042	0.427
CCR2	CD74	0.042	0.441
CCR2	CD44	0	0.497
CCR2	IL18	0	0.497
CCR2	STAT1	0.07	0.499
CCR2	FCGR3A	0	0.542

CCR2	SAG	0	0.546
CCR2	IL6	0	0.56
CCR2	STAT3	0.162	0.593
CCR2	LOC529196	0	0.599
CCR2	FCGR2B	0	0.608
CCR2	CD80	0	0.647
CCR2	SELL	0.042	0.657
CCR2	CD40	0.121	0.667
CCR2	CXCL16	0	0.709
CCR2	JAK3	0.116	0.722
CCR2	GRK6	0.053	0.729
CCR2	TNF	0	0.76
CCR2	CXCL8	0.078	0.88
CCR5	CSF1	0	0.487
CCR5	CXCR4	0.34	0.769
CCR5	IL1B	0.042	0.458
CCR5	PLCG2	0.071	0.49
CCR5	CD69	0.042	0.706
CCR5	GNG4	0.065	0.678
CCR5	JUN	0.042	0.655
CCR5	LOC616948	0	0.474
CCR5	IL10RA	0	0.486
CCR5	CD274	0	0.478
CCR5	TLR4	0.053	0.607
CCR5	CD53	0.055	0.459
CCR5	IL10	0	0.714
CCR5	ITGAL	0	0.521
CCR5	IL2RG	0	0.5
CCR5	TLR2	0.053	0.567
CCR5	EDN1	0.079	0.657
CCR5	TLR9	0.053	0.403
CCR5	ICAM3	0	0.404
CCR5	SLC9A3R1	0.12	0.414
CCR5	IL7R	0	0.455
CCR5	IL6	0	0.498
CCR5	CD44	0	0.498
CCR5	IL18	0	0.5
CCR5	STAT3	0.162	0.507
CCR5	STAT1	0.07	0.523
CCR5	FCGR2B	0	0.531
CCR5	IL2RB	0	0.532
CCR5	SAG	0	0.546
CCR5	FCGR3A	0	0.566
CCR5	LOC529196	0	0.598
CCR5	IL15	0	0.611
CCR5	FAS	0	0.613
CCR5	LOC504773	0	0.631

CCR5	ICAM1	0	0.632
CCR5	CD38	0	0.667
CCR5	CD80	0	0.677
CCR5	SELL	0.042	0.695
CCR5	CXCL16	0	0.72
CCR5	GRK6	0.053	0.729
CCR5	CD40	0.121	0.73
CCR5	JAK3	0.116	0.732
CCR5	PTPRC	0.045	0.749
CCR5	TNF	0	0.75
CCR5	JAK2	0.162	0.753
CCR5	PPIF	0.055	0.802
CCR5	CXCL13	0.055	0.836
CCR5	CXCL8	0.078	0.912
CD101	CD82	0.127	0.412
CD101	RNF24	0	0.532
CD101	SLC45A4	0	0.584
CD101	CD81	0.127	0.402
CD101	SLC28A3	0	0.412
CD14	CSF1	0	0.541
CD14	MYD88	0	0.897
CD14	IL1B	0	0.604
CD14	CD69	0	0.448
CD14	IRAK2	0.042	0.459
CD14	TLR4	0.201	0.999
CD14	IL10	0	0.656
CD14	NOS2	0	0.408
CD14	ITGAL	0	0.452
CD14	TLR2	0.408	0.986
CD14	PTPRC	0	0.762
CD14	ICAM1	0.051	0.508
CD14	ITGA5	0	0.457
CD14	VCAN	0	0.659
CD14	IL6	0	0.64
CD14	LRRK2	0.079	0.408
CD14	ITGB7	0.055	0.437
CD14	LIMK2	0.042	0.441
CD14	SELP	0	0.446
CD14	FUT4	0	0.457
CD14	ITGAV	0	0.465
CD14	SELL	0	0.474
CD14	CD40	0	0.478
CD14	LOC100138951	0.06	0.51
CD14	FCGR2B	0	0.512
CD14	HCK	0	0.537
CD14	ITGA9	0	0.562
CD14	CD80	0	0.564

CD14	CD44	0	0.588
CD14	CXCL8	0	0.657
CD14	IRAK4	0.042	0.664
CD14	TLR9	0.164	0.675
CD14	FCGR2C	0	0.676
CD14	FCER1G	0	0.678
CD14	FCGR3A	0	0.711
CD14	TNF	0	0.718
CD14	TIRAP	0	0.725
CD164	CXCR4	0.113	0.706
CD164	RNF24	0	0.41
CD164	SLC45A4	0	0.476
CD164	EDEM1	0	0.535
CD164	KIAA1033	0	0.406
CD164	CD44	0	0.418
CD164	CD97	0	0.467
CD1D	CD69	0	0.722
CD1D	CD274	0	0.485
CD1D	TLR4	0	0.483
CD1D	IL10	0	0.712
CD1D	TLR2	0	0.482
CD1D	PTPRC	0.079	0.648
CD1D	ICAM1	0	0.427
CD1D	CD38	0	0.529
CD1D	CD5	0	0.825
CD1D	CD74	0.06	0.74
CD1D	IL2RB	0	0.676
CD1D	CD80	0	0.685
CD1D	TLR9	0	0.401
CD1D	IL15	0	0.536
CD1D	CD40	0	0.685
CD1D	FCGR2B	0	0.57
CD1D	LAMP1	0	0.437
CD1D	NCR1	0	0.481
CD1D	IL18	0	0.482
CD1D	TNF	0	0.608
CD1D	CD44	0	0.647
CD1D	SELL	0	0.684
CD244	CD69	0	0.578
CD244	SLAMF1	0	0.4
CD244	ENTPD1	0	0.408
CD244	IL7R	0	0.416
CD244	LCP2	0	0.417
CD244	TNF	0	0.437
CD244	IL15	0	0.453
CD244	INPP5D	0.437	0.472
CD244	FCGR3A	0	0.483

CD244	CD274	0	0.493
CD244	LAMP1	0	0.534
CD244	SLAMF8	0	0.542
CD244	SH3BP2	0.071	0.553
CD244	SELL	0	0.553
CD244	PTPRC	0.113	0.564
CD244	IL2RB	0	0.573
CD244	ITGAL	0	0.586
CD244	EZH2	0	0.633
CD244	NCR1	0	0.764
CD244	CD48	0	0.814
CD274	CSF1	0	0.564
CD274	MYD88	0	0.437
CD274	CXCR4	0	0.502
CD274	IL1B	0	0.535
CD274	CD69	0	0.704
CD274	PSMB8	0	0.461
CD274	JAK1	0.042	0.501
CD274	IL10RA	0	0.418
CD274	GBP2	0	0.41
CD274	CXCR1	0	0.411
CD274	CXCR2	0	0.417
CD274	IL2RA	0	0.421
CD274	CD74	0	0.427
CD274	STAT6	0	0.438
CD274	CIITA	0	0.44
CD274	PARP14	0	0.446
CD274	PTGS2	0	0.447
CD274	IL18	0	0.448
CD274	IL2RB	0	0.45
CD274	KTN1	0	0.453
CD274	IKBKE	0.042	0.454
CD274	IL7R	0	0.457
CD274	IFNAR1	0	0.462
CD274	PIK3CA	0.045	0.467
CD274	RIPK1	0.042	0.469
CD274	CD5	0	0.481
CD274	FAS	0	0.491
CD274	TLR2	0	0.492
CD274	TLR9	0	0.496
CD274	TNFSF9	0	0.499
CD274	NCR1	0	0.539
CD274	JAK2	0.042	0.541
CD274	CXCL8	0	0.551
CD274	TAPBP	0	0.563
CD274	CD38	0	0.565
CD274	LAMP1	0	0.568

CD274	LOC100138951	0	0.569
CD274	TLR4	0	0.578
CD274	VEGFA	0	0.578
CD274	IRF1	0	0.615
CD274	KRAS	0	0.617
CD274	ENTPD1	0	0.62
CD274	ICAM1	0	0.626
CD274	IL6	0	0.627
CD274	CD47	0	0.633
CD274	TNFRSF18	0	0.642
CD274	IL15	0	0.645
CD274	FCGR2B	0	0.647
CD274	FCGR3A	0	0.667
CD274	CD44	0	0.673
CD274	SELL	0	0.682
CD274	LGALS9	0	0.685
CD274	STAT3	0	0.701
CD274	TNF	0	0.788
CD274	PTPRC	0.045	0.789
CD274	STAT1	0	0.791
CD274	CD40	0	0.821
CD274	IL10	0	0.841
CD274	CD80	0.923	0.999
CD300A	TLR4	0	0.533
CD300A	RNF24	0	0.469
CD300A	SLC45A4	0	0.497
CD300A	TRIM35	0	0.422
CD300A	CD72	0	0.4
CD300A	INPP5D	0.174	0.426
CD300A	FCER1G	0.079	0.561
CD300A	LAIR1	0	0.644
CD37	VAV1	0	0.411
CD37	ITGAL	0.12	0.51
CD37	TSPAN31	0	0.437
CD37	ZDHHC18	0.042	0.41
CD37	MYSM1	0.078	0.417
CD37	CD74	0	0.421
CD37	LAPTM5	0	0.444
CD37	CORO1A	0	0.459
CD38	PRDM1	0	0.624
CD38	CXCR4	0	0.776
CD38	CD69	0	0.763
CD38	VAV1	0	0.446
CD38	CD46	0	0.608
CD38	LOC784222	0	0.408
CD38	IL10	0	0.643
CD38	RYR1	0	0.811

CD38	ITGAL	0	0.471
CD38	LCP2	0	0.463
CD38	PTPRC	0	0.819
CD38	ICAM1	0	0.498
CD38	FAS	0	0.698
CD38	PNP	0	0.915
CD38	LYN	0.093	0.4
CD38	CXCL8	0	0.403
CD38	CD47	0	0.42
CD38	NCR1	0	0.425
CD38	TLR9	0	0.429
CD38	IL2RB	0	0.429
CD38	FUT4	0	0.473
CD38	FCGR2B	0	0.501
CD38	IL15	0	0.505
CD38	LAMP1	0	0.511
CD38	CD81	0.044	0.511
CD38	IL6	0	0.514
CD38	IL7R	0	0.53
CD38	ENTPD1	0	0.645
CD38	TNF	0	0.649
CD38	SELL	0	0.673
CD38	CD40	0	0.696
CD38	CD80	0	0.703
CD38	CD44	0	0.728
CD38	FCGR3A	0.12	0.743
CD38	SIRT1	0	0.767
CD38	CD5	0	0.798
CD38	LOC100138951	0	0.811
CD38	PRKCB	0	0.819
CD38	LOC790312	0	0.909
CD38	NAMPT	0	0.949
CD40	CSF1	0	0.534
CD40	MYD88	0	0.763
CD40	PRDM1	0	0.539
CD40	CXCR4	0.121	0.671
CD40	IL1B	0	0.719
CD40	IL4R	0.113	0.498
CD40	NFKBIB	0	0.471
CD40	CD69	0	0.763
CD40	JAK1	0.093	0.701
CD40	NAIP	0.234	0.577
CD40	JUN	0	0.498
CD40	TNFRSF1A	0	0.737
CD40	MAP3K2	0.218	0.55
CD40	IL23A	0	0.495
CD40	STAT2	0	0.536

CD40	SOCS1	0	0.402
CD40	OLR1	0	0.49
CD40	IL12B	0	0.473
CD40	IRF5	0	0.469
CD40	IL10RA	0	0.421
CD40	IL1R1	0	0.437
CD40	NFKB2	0	0.784
CD40	LOC515976	0.121	0.563
CD40	TLR4	0	0.834
CD40	STAT6	0	0.679
CD40	RIPK1	0.162	0.432
CD40	IL10	0	0.9
CD40	LGALS9	0	0.453
CD40	NOS2	0	0.447
CD40	F3	0	0.411
CD40	ITGAL	0	0.595
CD40	IKBKB	0.576	0.811
CD40	IL2RG	0	0.415
CD40	TLR2	0	0.774
CD40	CXCL13	0	0.499
CD40	PIK3CA	0.113	0.652
CD40	STAT5B	0	0.655
CD40	PTPRC	0	0.828
CD40	ICAM1	0	0.779
CD40	IL1A	0	0.546
CD40	IKBKE	0.257	0.519
CD40	TRAF2	0.963	0.999
CD40	CD72	0	0.424
CD40	MAP3K8	0.113	0.403
CD40	TYK2	0.093	0.436
CD40	JAK2	0.093	0.815
CD40	TRAF3	0.967	0.999
CD40	CD5	0	0.685
CD40	RELA	0	0.932
CD40	PTGS2	0	0.42
CD40	ICOSLG	0	0.58
CD40	IL6	0	0.763
CD40	IL12A	0	0.532
CD40	CD74	0	0.574
CD40	TNFRSF18	0	0.624
CD40	ICAM3	0	0.44
CD40	PIK3R6	0	0.631
CD40	CD80	0	0.948
CD40	TLR9	0	0.828
CD40	IL15	0	0.693
CD40	TRAF7	0.345	0.732
CD40	ICAM2	0	0.46

CD40	PTPN22	0	0.443
CD40	CXCL8	0	0.71
CD40	IL7R	0	0.437
CD40	XCR1	0.121	0.518
CD40	LYN	0.093	0.676
CD40	NFKB1	0	0.802
CD40	CIITA	0	0.407
CD40	VEGFA	0	0.414
CD40	LOC281376	0	0.414
CD40	SERPINB2	0	0.414
CD40	LOC100138951	0	0.425
CD40	CD81	0	0.429
CD40	DDIT3	0	0.436
CD40	DDX58	0	0.443
CD40	PIK3R5	0	0.463
CD40	CD47	0	0.463
CD40	ENTPD1	0	0.469
CD40	CXCR1	0.121	0.47
CD40	IRF1	0	0.47
CD40	LAMP1	0	0.47
CD40	NFKBIE	0	0.473
CD40	RIPK2	0.162	0.474
CD40	CXCR2	0.121	0.49
CD40	NOD2	0	0.508
CD40	SELP	0	0.516
CD40	IRF7	0	0.53
CD40	IL2RA	0	0.533
CD40	FCGR2C	0	0.539
CD40	IRAK4	0.093	0.542
CD40	RNF41	0.345	0.578
CD40	XIAP	0.234	0.599
CD40	TNFSF9	0	0.604
CD40	FCGR3A	0	0.607
CD40	TNFSF13B	0	0.621
CD40	STAT4	0	0.623
CD40	STAT5A	0	0.644
CD40	IL18	0	0.67
CD40	TANK	0.113	0.693
CD40	SELL	0	0.704
CD40	CD44	0	0.707
CD40	STAT1	0	0.746
CD40	STAT3	0	0.776
CD40	FCGR2B	0	0.84
CD40	JAK3	0.093	0.897
CD40	TNF	0	0.908
CD40	RELB	0	0.91
CD40	TRAF1	0.753	0.985

CD44	CSF1	0	0.482
CD44	HYAL1	0.054	0.704
CD44	HYAL2	0.113	0.945
CD44	MYD88	0	0.504
CD44	PRDM1	0	0.453
CD44	CXCR4	0	0.896
CD44	IL1B	0	0.585
CD44	EIF2C2	0	0.422
CD44	CD69	0.079	0.873
CD44	JAK1	0.157	0.455
CD44	JUN	0	0.458
CD44	GRB2	0	0.599
CD44	IL1R1	0	0.421
CD44	CD82	0.08	0.502
CD44	PTK2B	0	0.431
CD44	TLR4	0	0.943
CD44	IL10	0	0.738
CD44	LGALS9	0.162	0.822
CD44	ITGAL	0.054	0.699
CD44	TNFAIP6	0	0.401
CD44	IL2RG	0	0.422
CD44	SLAMF1	0	0.415
CD44	TLR2	0	0.87
CD44	EZH2	0	0.41
CD44	TIAM2	0.466	0.624
CD44	PTPRC	0.204	0.916
CD44	ICAM1	0	0.914
CD44	FAS	0	0.65
CD44	JAK2	0.157	0.585
CD44	S100A8	0	0.641
CD44	PLAUR	0	0.519
CD44	CD5	0	0.695
CD44	ITGA5	0.06	0.555
CD44	PTGS2	0	0.482
CD44	SERPINE1	0	0.412
CD44	SNAI1	0	0.644
CD44	VCAN	0.163	0.971
CD44	IL6	0	0.66
CD44	MST1R	0.211	0.523
CD44	CD74	0.433	0.994
CD44	TNFRSF18	0	0.566
CD44	ICAM3	0	0.509
CD44	TSPAN2	0.08	0.439
CD44	IL2RB	0	0.719
CD44	MMP25	0.053	0.654
CD44	ITGA9	0.08	0.482
CD44	SRGN	0.078	0.849

CD44	TGFBR1	0.274	0.736
CD44	CD80	0	0.715
CD44	PXN	0	0.686
CD44	IL15	0	0.588
CD44	ICAM2	0	0.529
CD44	CXCL8	0	0.68
CD44	ITGAV	0.06	0.698
CD44	IL7R	0	0.647
CD44	LYN	0.157	0.65
CD44	IL2RA	0	0.629
CD44	STAT3	0.113	0.975
CD44	HBEGF	0.113	0.744
CD44	FCGR2B	0	0.702
CD44	LOC281376	0	0.44
CD44	SERPINB2	0	0.442
CD44	FCGR3A	0	0.486
CD44	SLC9A3R1	0	0.514
CD44	TNF	0	0.776
CD44	SDC3	0	0.413
CD44	KRAS	0.07	0.687
CD44	DLL1	0	0.434
CD44	DDIT3	0	0.663
CD44	LAMP1	0.053	0.548
CD44	SELL	0.079	0.904
CD44	SELP	0.21	0.872
CD44	ENTPD1	0	0.469
CD44	FCGR2C	0	0.498
CD44	ELN	0	0.472
CD44	CXCR2	0	0.805
CD44	FUT4	0	0.46
CD44	CD47	0	0.643
CD44	IL18	0	0.4
CD44	LOC100297725	0	0.41
CD44	NCR1	0	0.465
CD44	STAT1	0.06	0.489
CD44	LOC100138951	0	0.587
CD44	CD81	0.08	0.631
CD44	CXCR1	0	0.673
CD44	ROCK1	0.074	0.69
CD44	VEGFA	0.055	0.693
CD44	SDC4	0	0.703
CD46	RBMS1	0	0.448
CD46	RAPGEF1	0	0.405
CD46	CD81	0.103	0.407
CD46	CD97	0	0.41
CD46	ENTPD1	0	0.45
CD46	IL10	0	0.476

CD46	IFNAR1	0	0.479
CD46	CD47	0	0.48
CD46	CD80	0	0.495
CD46	SERPING1	0	0.568
CD46	MYBPH	0	0.632
CD46	SLAMF1	0	0.822
CD47	CXCR4	0	0.409
CD47	NLRP3	0	0.548
CD47	TLR4	0.052	0.497
CD47	SIRPB2	0.318	0.655
CD47	IL10	0	0.417
CD47	ITGAL	0.054	0.481
CD47	SIRPA	0.641	0.994
CD47	ITGA2B	0.054	0.723
CD47	SIRPB1	0.641	0.815
CD47	PTPRC	0	0.595
CD47	ICAM1	0	0.513
CD47	ICAM4	0	0.513
CD47	FAS	0.078	0.407
CD47	CD5	0	0.448
CD47	ITGA5	0.056	0.597
CD47	ITGA9	0.054	0.516
CD47	ITGB7	0.069	0.501
CD47	ITGAV	0.078	0.842
CD47	CD97	0.134	0.484
CD47	FCGR2B	0	0.435
CD47	DCSTAMP	0	0.478
CD47	TNF	0	0.459
CD47	OCSTAMP	0	0.423
CD47	FAM134C	0.407	0.407
CD47	VEGFA	0	0.465
CD47	LOC100138951	0	0.492
CD47	NLRP12	0	0.499
CD47	CD81	0.148	0.517
CD48	CD53	0	0.788
CD48	SELL	0	0.431
CD5	CXCR4	0	0.479
CD5	CD69	0.071	0.81
CD5	VAV1	0.113	0.492
CD5	NFKB2	0	0.505
CD5	IL10	0	0.695
CD5	ITGAL	0	0.632
CD5	SIRPA	0	0.426
CD5	IL2RG	0	0.462
CD5	SLAMF1	0	0.535
CD5	CXCL13	0	0.408
CD5	LCP2	0	0.413

CD5	PTPRC	0.046	0.836
CD5	FAS	0	0.574
CD5	CD72	0.218	0.92
CD5	PAF1	0	0.412
CD5	DDIT3	0	0.414
CD5	FCGR2C	0	0.422
CD5	IL15	0	0.467
CD5	FUT4	0	0.491
CD5	IL6	0	0.498
CD5	FCGR3A	0	0.553
CD5	IL2RA	0	0.555
CD5	TNF	0	0.573
CD5	IL7R	0	0.593
CD5	IL2RB	0	0.599
CD5	FCGR2B	0	0.627
CD5	CD80	0	0.645
CD5	NCR1	0	0.653
CD5	LOC100138951	0	0.679
CD5	SELL	0.071	0.717
CD53	CD69	0	0.434
CD53	SAMSN1	0	0.419
CD53	NCF1	0	0.422
CD53	IL10RA	0	0.514
CD53	CLK2	0	0.4
CD53	CD74	0	0.402
CD53	SELL	0	0.406
CD53	CLEC5A	0	0.407
CD53	CHI3L2	0.073	0.407
CD53	LAT2	0	0.431
CD53	IL2RG	0	0.44
CD53	PLEK	0	0.444
CD53	FCGR3A	0	0.452
CD53	ITGAL	0.12	0.453
CD53	IGSF8	0.166	0.468
CD53	PTPN6	0.048	0.472
CD53	SIRPB1	0	0.51
CD53	LOC617909	0	0.53
CD53	TMEM156	0	0.54
CD53	LCP2	0	0.558
CD53	CORO1A	0	0.697
CD53	SRGN	0	0.718
CD53	PTAFR	0	0.731
CD53	FCER1G	0	0.733
CD53	PTPRC	0.059	0.856
CD53	LAPTM5	0	0.907
CD55	LOC100300051	0	0.479
CD55	FCN1	0	0.401

CD55	CD97	0	0.479
CD69	MYD88	0	0.419
CD69	PRDM1	0	0.526
CD69	CXCR4	0.042	0.642
CD69	IL1B	0	0.508
CD69	PTPN6	0.126	0.4
CD69	VAV1	0	0.409
CD69	SERPINB2	0.055	0.411
CD69	LOC281376	0.055	0.411
CD69	ITGB7	0	0.412
CD69	LOC515976	0.042	0.419
CD69	LOC100138951	0	0.423
CD69	PTPN22	0.159	0.425
CD69	CD74	0.05	0.431
CD69	JAK1	0.06	0.434
CD69	STAT5A	0.042	0.438
CD69	JAK2	0.06	0.447
CD69	STAT4	0.042	0.462
CD69	STAT6	0.042	0.462
CD69	STAT5B	0.042	0.464
CD69	STAT3	0.042	0.502
CD69	FCGR2C	0	0.528
CD69	IL6	0	0.533
CD69	LCP2	0	0.534
CD69	IL2RG	0	0.551
CD69	STAT1	0.042	0.564
CD69	ENTPD1	0.042	0.566
CD69	TLR9	0.045	0.581
CD69	DDIT3	0	0.592
CD69	TLR2	0.045	0.605
CD69	TNFRSF18	0	0.619
CD69	TLR4	0.045	0.631
CD69	IL18	0	0.631
CD69	CXCL8	0.042	0.636
CD69	ICAM1	0	0.639
CD69	IL7R	0	0.642
CD69	FCGR2B	0	0.707
CD69	ITGAL	0	0.716
CD69	FCGR3A	0	0.731
CD69	FAS	0	0.734
CD69	IL15	0	0.743
CD69	IL2RA	0	0.748
CD69	IL2RB	0	0.755
CD69	LAMP1	0.054	0.757
CD69	NCR1	0	0.76
CD69	IL10	0	0.763
CD69	CD80	0	0.791

CD69	TNF	0	0.811
CD69	JAK3	0.06	0.812
CD69	PTPRC	0.126	0.868
CD69	SELL	0	0.907
CD72	SEMA4D	0.218	0.93
CD72	PLCG2	0.045	0.718
CD72	GRB2	0.078	0.688
CD72	ITGAL	0	0.404
CD72	PTPRC	0.126	0.46
CD72	RFK	0	0.426
CD72	TRIB1	0	0.461
CD72	TEC	0.06	0.537
CD72	CD74	0.05	0.547
CD72	FCRL5	0	0.573
CD72	LYN	0.168	0.776
CD72	PTPN6	0.126	0.894
CD74	CXCR4	0.113	0.938
CD74	PSMB8	0	0.609
CD74	NLRC5	0	0.455
CD74	TLR4	0.052	0.479
CD74	IL10	0	0.478
CD74	ITGAL	0.044	0.499
CD74	TLR2	0.052	0.406
CD74	PSMB9	0	0.481
CD74	PTPRC	0.055	0.609
CD74	ICAM1	0	0.403
CD74	ENSBTAP00000019939	0.639	0.978
CD74	SDC4	0	0.404
CD74	LAMP1	0	0.41
CD74	PLAGL2	0	0.418
CD74	TMEM119	0	0.424
CD74	PSME2	0	0.435
CD74	CYTH4	0	0.456
CD74	FCER1G	0	0.458
CD74	CXCL8	0	0.478
CD74	ITGB7	0.045	0.498
CD74	HERPUD1	0	0.512
CD74	CD80	0	0.512
CD74	LAPTM5	0	0.543
CD74	TAPBP	0	0.543
CD74	TNF	0	0.62
CD74	CIITA	0	0.774
CD74	CXCR1	0.084	0.83
CD74	CXCR2	0.113	0.954
CD80	CSF1	0	0.589
CD80	MYD88	0	0.681
CD80	CXCR4	0	0.539

CD80	IL1B	0	0.664
CD80	FYB	0	0.606
CD80	IL4R	0	0.573
CD80	JAK1	0	0.492
CD80	TNFRSF1A	0	0.413
CD80	IL23A	0	0.493
CD80	GRB2	0	0.692
CD80	IL12B	0	0.498
CD80	IL10RA	0	0.441
CD80	TLR4	0	0.795
CD80	STAT6	0	0.431
CD80	IL10	0	0.885
CD80	LGALS9	0	0.436
CD80	NOS2	0	0.486
CD80	LOC616942	0	0.548
CD80	ITGAL	0	0.647
CD80	SIRPA	0	0.592
CD80	TLR2	0	0.759
CD80	PRKCD	0	0.544
CD80	CSF2RB	0	0.676
CD80	PIK3CA	0	0.643
CD80	LCP2	0	0.689
CD80	PLEK	0	0.498
CD80	MR1	0	0.522
CD80	PTPRC	0	0.9
CD80	ICAM1	0	0.843
CD80	IL1A	0	0.449
CD80	FAS	0	0.618
CD80	TYK2	0	0.448
CD80	JAK2	0	0.494
CD80	ICOSLG	0	0.652
CD80	IL6	0	0.738
CD80	ENSBTAP00000019939	0	0.621
CD80	IL12A	0	0.586
CD80	TNFRSF18	0	0.603
CD80	ICAM3	0	0.498
CD80	IL2RB	0	0.503
CD80	XCR1	0	0.406
CD80	STAT4	0	0.407
CD80	CD81	0	0.423
CD80	SERPINB2	0	0.425
CD80	LOC281376	0	0.425
CD80	MPEG1	0	0.426
CD80	DDX58	0	0.43
CD80	VEGFA	0	0.43
CD80	IFNAR1	0	0.431
CD80	JAK3	0	0.451

CD80	PTPN22	0	0.477
CD80	CIITA	0	0.481
CD80	IRF7	0	0.481
CD80	DDIT3	0	0.497
CD80	LOC100138951	0	0.499
CD80	IL7R	0	0.517
CD80	NCR1	0	0.533
CD80	FCER1G	0	0.542
CD80	ENTPD1	0	0.543
CD80	LAMP1	0	0.543
CD80	STAT1	0	0.555
CD80	FCGR2C	0	0.555
CD80	STAT3	0	0.557
CD80	PTPN6	0	0.568
CD80	IL2RA	0	0.57
CD80	IL18	0	0.627
CD80	FCGR3A	0	0.668
CD80	CXCL8	0	0.685
CD80	IL15	0	0.695
CD80	TLR9	0	0.711
CD80	SELL	0	0.767
CD80	FCGR2B	0	0.769
CD80	TNFSF9	0	0.825
CD80	TNF	0	0.892
CD81	CXCR4	0.055	0.439
CD81	EIF2C2	0	0.41
CD81	ITGAL	0.12	0.451
CD81	ITGA2B	0.12	0.458
CD81	FLOT1	0	0.747
CD81	IGSF8	0.504	0.895
CD81	FLOT2	0	0.482
CD81	PTPRC	0.059	0.605
CD81	ICAM1	0	0.669
CD81	VPS4B	0	0.615
CD81	XRN1	0	0.512
CD81	RAB27A	0	0.589
CD81	ITGA5	0.12	0.542
CD81	ICAM3	0	0.4
CD81	ITGA9	0.12	0.584
CD81	ITGB7	0.184	0.554
CD81	IFITM3	0.158	0.478
CD81	SDCBP	0.043	0.588
CD81	ITGAV	0.12	0.578
CD81	IRAK4	0.071	0.44
CD81	TNF	0	0.468
CD81	LAMP1	0.113	0.59
CD81	KYNU	0	0.433

CD82	ITGAL	0.12	0.401
CD82	TAB2	0	0.405
CD82	ICAM1	0	0.427
CD82	ITGAV	0.124	0.465
CD82	ITGA5	0.124	0.473
CD82	TSPAN31	0	0.484
CD82	RAB27A	0	0.511
CD82	LAMP1	0.113	0.52
CD82	FLOT1	0	0.6
CD82	IGSF8	0.166	0.734
CD97	RPS9	0	0.513
CD97	GRK6	0	0.579
CD99	PLXNA4	0	0.4
CD99	ICAM2	0	0.533
CD99	ICAM1	0	0.787
CDADC1	ELL	0	0.418
CDADC1	CMPK2	0	0.443
CDADC1	ENTPD1	0	0.479
CDADC1	TOP1	0	0.484
CDADC1	UPP1	0	0.645
CDC42SE2	ELMO2	0	0.448
CDC42SE2	DNASE1L1	0	0.414
CDC42SE2	FNBP4	0	0.487
CDH10	MST1R	0.07	0.405
CDH10	FBXO40	0	0.405
CDH10	LIMK2	0.062	0.442
CDH10	KRR1	0	0.452
CDH10	5-Sep	0	0.498
CDK17	PPP4C	0.159	0.4
CDK17	RALGDS	0	0.403
CDK17	FRAT2	0	0.412
CDK17	POLR2A	0.314	0.435
CDK17	NFKBID	0.16	0.436
CDK17	UBXN7	0.314	0.441
CDK17	GPCPD1	0.295	0.443
CDK17	LYN	0.257	0.45
CDK17	PLK3	0.219	0.457
CDK17	MDM2	0.054	0.475
CDK17	E2F2	0.218	0.494
CDK17	E2F3	0.218	0.494
CDK17	FZR1	0.48	0.591
CDK17	CDKN1A	0.444	0.717
CDK17	CDKN1B	0.43	0.735
CDK17	TDRD7	0.433	0.786
CDKN1A	SP3	0.057	0.653
CDKN1A	KAT2B	0.127	0.464
CDKN1A	RBPJ	0	0.401

CDKN1A	CREBBP	0.477	0.857
CDKN1A	JUN	0.113	0.809
CDKN1A	KPNA3	0.158	0.435
CDKN1A	CREB1	0	0.74
CDKN1A	TGFBR1	0.117	0.407
CDKN1A	SERPINE1	0	0.411
CDKN1A	XIAP	0	0.417
CDKN1A	MYSM1	0.162	0.418
CDKN1A	VEGFA	0	0.423
CDKN1A	RND1	0.124	0.429
CDKN1A	KPNA1	0.158	0.435
CDKN1A	CXCL8	0	0.439
CDKN1A	RELA	0.218	0.447
CDKN1A	HDAC4	0.121	0.459
CDKN1A	TNF	0	0.469
CDKN1A	SIRT1	0.051	0.474
CDKN1A	SESN2	0	0.48
CDKN1A	CUL4A	0.295	0.486
CDKN1A	STAT1	0.182	0.489
CDKN1A	DDIT3	0.09	0.497
CDKN1A	GADD45B	0.218	0.505
CDKN1A	MCL1	0	0.507
CDKN1A	JUNB	0.06	0.542
CDKN1A	EZH2	0.055	0.544
CDKN1A	SMAD7	0.123	0.561
CDKN1A	NFE2L2	0.113	0.614
CDKN1A	KRAS	0.103	0.64
CDKN1A	LOC100297725	0.073	0.65
CDKN1A	CDKN2D	0.044	0.657
CDKN1A	E2F2	0.055	0.779
CDKN1A	E2F3	0.055	0.805
CDKN1A	STAT3	0.764	0.891
CDKN1A	CDKN1B	0.439	0.91
CDKN1A	LYN	0.117	0.918
CDKN1A	JAK2	0.117	0.936
CDKN1A	MAP3K5	0.113	0.945
CDKN1A	MDM2	0.764	0.958
CDKN1B	KAT2B	0.127	0.418
CDKN1B	CREBBP	0.258	0.71
CDKN1B	JUN	0.06	0.652
CDKN1B	GRB2	0.435	0.718
CDKN1B	KPNA3	0.433	0.703
CDKN1B	CREB1	0	0.542
CDKN1B	CDKN2D	0.044	0.744
CDKN1B	KPNA1	0.317	0.761
CDKN1B	JAK2	0.211	0.952
CDKN1B	JUNB	0.06	0.485

CDKN1B	ITGA5	0	0.447
CDKN1B	CREM	0	0.431
CDKN1B	E2F2	0.055	0.573
CDKN1B	CREBL2	0	0.422
CDKN1B	EMP1	0	0.425
CDKN1B	SMAD7	0.123	0.461
CDKN1B	STAT3	0.182	0.555
CDKN1B	E2F3	0.055	0.603
CDKN1B	KRAS	0.103	0.614
CDKN1B	ITGAV	0	0.628
CDKN1B	MDM2	0.316	0.629
CDKN1B	CUL4A	0.761	0.818
CDKN1B	LYN	0.117	0.921
CDKN2AIP	KDM4A	0	0.4
CDKN2AIP	DOM3Z	0	0.421
CDKN2AIP	USP18	0	0.468
CDKN2AIP	XRN1	0.453	0.548
CDKN2AIP	XRN2	0.762	0.892
CDKN2D	PGS1	0	0.431
CDKN2D	RELB	0.229	0.428
CDKN2D	E2F3	0.093	0.465
CDKN2D	FZR1	0.087	0.481
CDKN2D	E2F2	0.093	0.51
CDKN2D	MDM2	0.121	0.716
CDS2	NAB1	0	0.467
CDS2	PGS1	0	0.993
CDS2	ELOVL5	0	0.415
CDS2	FAR2	0	0.577
CDS2	LPCAT2	0	0.673
CDS2	SPRYD3	0	0.737
CDS2	LPIN2	0	0.753
CDS2	DGKD	0	0.759
CDS2	MBOAT1	0	0.975
CECR1	ISG20L2	0	0.453
CECR1	RPIA	0	0.568
CECR1	PNP	0	0.988
CECR1	GTPBP4	0	0.602
CECR1	WDR4	0	0.405
CECR1	ISG20	0	0.513
CECR1	LOC790312	0	0.969
CEP120	CEP83	0	0.671
CEP120	RICTOR	0	0.407
CEP120	CEP76	0	0.616
CEP120	CEP192	0.043	0.56
CEP120	NDEL1	0	0.505
CEP120	TACC3	0	0.583
CEP120	NIN	0	0.685

CEP192	FAM46A	0.428	0.428
CEP192	PLK3	0.417	0.481
CEP192	NIN	0.053	0.42
CEP192	TACC3	0	0.452
CEP192	SEH1L	0.049	0.663
CEP76	FAM107B	0	0.639
CEP76	NIN	0	0.404
CEP76	SEH1L	0	0.444
CEP76	PTPN2	0	0.508
CEP83	TTC33	0	0.639
CEP83	PPP4R2	0	0.513
CEP83	RAB3IP	0	0.402
CEP83	CHD1	0	0.411
CEP83	NIN	0	0.534
CFAP69	SPATA6	0	0.857
CFAP69	PM20D2	0	0.453
CFB	SOD2	0	0.407
CFB	F3	0.125	0.418
CFB	PLAUR	0.144	0.407
CFB	TNF	0.042	0.435
CFB	CHI3L1	0	0.444
CFB	PSMB9	0.135	0.446
CFB	CXCL8	0	0.459
CFB	GSN	0	0.479
CFB	F5	0.119	0.486
CFB	SERPING1	0.121	0.705
CFB	CFD	0.357	0.95
CFD	PSMA2	0	0.499
CFD	RETN	0	0.766
CFD	FGL2	0.07	0.429
CFD	FGR	0.055	0.413
CFD	PLAUR	0.144	0.598
CFD	SERPINE1	0.121	0.556
CFD	SERPING1	0.121	0.586
CFD	F5	0.119	0.46
CFD	FCN1	0.07	0.502
CFLAR	IL1B	0.184	0.644
CFLAR	NAIP	0.295	0.595
CFLAR	JUN	0.077	0.438
CFLAR	TNFRSF1A	0.157	0.795
CFLAR	RAF1	0.344	0.518
CFLAR	MAP4K4	0.12	0.433
CFLAR	NFKB2	0.119	0.43
CFLAR	CYLD	0.081	0.439
CFLAR	RIPK1	0.569	0.964
CFLAR	IKBKB	0.136	0.555
CFLAR	TOP1	0.138	0.433

CFLAR	MAP3K5	0.113	0.549
CFLAR	FAM107B	0	0.632
CFLAR	IKBKE	0.136	0.412
CFLAR	TRAF2	0.294	0.806
CFLAR	FAS	0.569	0.966
CFLAR	TNFSF14	0.139	0.4
CFLAR	SMG1	0.123	0.412
CFLAR	XAF1	0	0.416
CFLAR	TRAF3	0.119	0.421
CFLAR	MDM2	0.163	0.43
CFLAR	IL18	0.093	0.46
CFLAR	RELA	0	0.555
CFLAR	FASLG	0.174	0.578
CFLAR	NFKB1	0.119	0.602
CFLAR	MLKL	0.126	0.646
CFLAR	TNF	0.086	0.716
CFLAR	MCL1	0.219	0.741
CFLAR	DAXX	0.113	0.772
CFLAR	RIPK2	0.126	0.773
CFLAR	RIPK3	0.126	0.783
CFLAR	XIAP	0.295	0.882
CFLAR	TRAF1	0.439	0.909
CFLAR	TNFSF10	0.764	0.941
CHD1	TTC33	0.093	0.464
CHD1	SETDB1	0.138	0.659
CHD1	KAT2B	0.348	0.663
CHD1	JMJD1C	0	0.523
CHD1	SAFB	0.087	0.546
CHD1	PPP4R2	0	0.426
CHD1	KAT5	0.184	0.421
CHD1	UBXN7	0.262	0.582
CHD1	TOP1	0.12	0.803
CHD1	THOC2	0.086	0.404
CHD1	SUPT6H	0.688	0.895
CHD1	KMT2E	0.184	0.486
CHD1	PIK3CA	0.161	0.509
CHD1	EZH2	0.138	0.515
CHD1	NF1	0.093	0.405
CHD1	SIRT1	0.166	0.454
CHD1	MIER3	0.157	0.731
CHD1	NIPBL	0.184	0.739
CHD1	USP25	0.115	0.427
CHD1	PAF1	0.665	0.75
CHD1	KDM5A	0.158	0.577
CHD1	SMG1	0.161	0.452
CHD1	SLC8B1	0.046	0.417
CHD1	MYSM1	0.401	0.621

CHD1	POGZ	0.131	0.438
CHD1	H3F3A	0.351	0.616
CHD1	MBD2	0.167	0.435
CHD1	HIST3H2A	0.162	0.435
CHD1	LOC613345	0.351	0.463
CHD1	MPHOSPH8	0.258	0.516
CHD1	GTF2B	0.08	0.541
CHD1	POLR2A	0.219	0.631
CHD1	LOC100297725	0.351	0.711
CHD1	RANBP2	0.079	0.862
CHI3L1	IL6	0	0.465
CHI3L1	OSM	0	0.457
CHIC2	RIOK3	0	0.494
CHIC2	KDM8	0	0.41
CHIC2	ETV6	0	0.534
CHM	RAB3GAP1	0	0.405
CHM	HERC5	0.424	0.447
CHM	HERC6	0.424	0.447
CHM	KRAS	0.178	0.469
CHM	GZF1	0	0.513
CHM	EPG5	0.688	0.728
CHMP2A	PHF1	0	0.417
CHMP2A	STAM2	0	0.547
CHMP2A	ZC3H12C	0	0.546
CHMP2A	VPS37A	0.164	0.801
CHMP2A	VPS4B	0.763	0.948
CHMP2A	MLKL	0.055	0.625
CHMP2A	UBAP1	0	0.418
CHMP2A	ISG15	0.098	0.548
CHP1	TMEM165	0	0.513
CHP1	TMBIM4	0	0.585
CHP1	STK17A	0.411	0.519
CHP1	STK17B	0.477	0.64
CHP1	TNIP2	0.042	0.417
CHP1	LRRK2	0.157	0.473
CHRNE	PTK2B	0	0.586
CHRNE	MARCKSL1	0	0.425
CHST11	CHST15	0	0.981
CHST11	CSGALNACT2	0	0.717
CHST11	CHSY1	0	0.697
CHST11	ZC3H12C	0	0.518
CHST11	VCAN	0	0.436
CHST11	SRGN	0	0.496
CHST15	IQSEC1	0	0.483
CHST15	SLC7A5	0	0.412
CHST15	CYTH1	0	0.414
CHST15	SPTLC2	0	0.479

CHST15	SRGN	0	0.526
CHST15	CHSY1	0	0.578
CHST15	CSGALNACT2	0	0.641
CHSY1	CSGALNACT2	0.053	0.923
CHSY1	EOGT	0	0.416
CHSY1	VCAN	0	0.423
CHSY1	TBC1D2B	0	0.44
CIITA	PRDM1	0	0.482
CIITA	PSMB8	0.042	0.435
CIITA	NAIP	0.093	0.825
CIITA	PTPN12	0	0.406
CIITA	CREBBP	0.08	0.689
CIITA	NLRC5	0	0.498
CIITA	CREB1	0	0.954
CIITA	IL10	0	0.402
CIITA	NLRC4	0.097	0.61
CIITA	PSMB9	0	0.451
CIITA	CSF2RB	0	0.667
CIITA	LCP2	0	0.621
CIITA	PTPRC	0	0.552
CIITA	IL2RB	0	0.645
CIITA	TAPBP	0	0.433
CIITA	MEFV	0.042	0.522
CIITA	PTPN22	0	0.675
CIITA	IL7R	0	0.609
CIITA	XCR1	0	0.593
CIITA	IL18	0	0.404
CIITA	RIPK2	0.097	0.406
CIITA	TNFSF13B	0	0.423
CIITA	TNF	0	0.518
CIITA	STAT1	0	0.536
CIITA	IRF1	0	0.566
CIITA	P2RY8	0	0.582
CLCN7	CSF1	0	0.403
CLCN7	TCIRG1	0	0.859
CLCN7	KCNJ15	0	0.416
CLCN7	SNX10	0	0.712
CLCN7	OSTM1	0.486	0.958
CLCN7	RNF13	0.465	0.478
CLCN7	SLC4A2	0	0.629
CLCN7	DCSTAMP	0	0.454
CLCN7	LAMP1	0.045	0.492
CLCN7	CLN3	0	0.512
CLEC5A	TLR2	0.045	0.437
CLEC5A	SIRPB1	0	0.605
CLEC5A	GPR84	0.042	0.599
CLEC5A	TREM1	0	0.517

CLEC5A	LOC617909	0	0.651
CLEC5A	PTAFR	0	0.402
CLEC5A	FCER1G	0.046	0.723
CLIC4	HIVEP2	0	0.687
CLIC4	HIVEP1	0	0.435
CLIC4	EMILIN2	0	0.481
CLIC4	UAP1	0.405	0.415
CLIC4	CLIC5	0.764	0.889
CLIC4	TXNDC16	0.075	0.478
CLIC4	GABRR2	0	0.54
CLIC4	CRKL	0.436	0.448
CLIC5	PSMA2	0.078	0.556
CLIC5	SHROOM4	0	0.533
CLIC5	UAP1	0.405	0.415
CLIC5	GABRR2	0	0.54
CLIP1	TUBA4A	0.335	0.446
CLIP1	GRIPAP1	0	0.515
CLIP1	SMG1	0.14	0.461
CLIP1	CNN2	0	0.461
CLIP1	DNAH17	0.219	0.511
CLIP1	NDEL1	0.074	0.563
CLIP1	NIN	0.045	0.635
CLK1	HNRNPH1	0.06	0.407
CLK1	FNBP4	0	0.411
CLK1	NXF1	0	0.424
CLK1	CLK2	0.434	0.479
CLK1	CLK3	0.478	0.497
CLK1	SRSF5	0.184	0.526
CLK1	N4BP1	0	0.535
CLK1	TRA2A	0.425	0.74
CLK1	SF3B1	0.218	0.883
CLK1	CLK4	0	0.99
CLK2	CLK3	0.764	0.784
CLK2	TRA2A	0.434	0.591
CLK2	DDX5	0.129	0.415
CLK2	UBE2D1	0.093	0.466
CLK2	SNIP1	0.666	0.679
CLK3	SRSF5	0.184	0.416
CLK3	SRSF12	0.294	0.432
CLK3	SNIP1	0.418	0.442
CLK3	SRRM2	0.438	0.478
CLK3	CLK4	0.478	0.519
CLK3	STK38L	0.131	0.538
CLK3	TRA2A	0.52	0.569
CLK3	WDR4	0	0.571
CLK4	SF3B1	0.218	0.478
CLK4	SRSF5	0.184	0.668

CLK4	TRA2A	0.303	0.559
CLK4	CWC22	0.124	0.428
CLK4	LYSMD3	0	0.529
CLN3	LRP10	0	0.489
CLN3	KCTD7	0	0.697
CLN3	MFSD6L	0	0.514
CLN3	LAMP1	0	0.538
CMIP	HIVEP2	0	0.467
CMIP	SLC16A6	0	0.412
CMIP	SLC37A1	0	0.469
CMIP	RASGEF1B	0	0.619
CMPK2	STAT2	0	0.447
CMPK2	DPYD	0	0.421
CMPK2	IFIH1	0	0.625
CMPK2	UPP1	0	0.527
CMPK2	MX2	0	0.854
CMPK2	PNPT1	0	0.44
CMPK2	PARP10	0	0.504
CMPK2	IFIT3	0	0.834
CMPK2	XAF1	0	0.406
CMPK2	UBE2L6	0	0.448
CMPK2	OAS2	0	0.449
CMPK2	ISG15	0	0.706
CMPK2	GBP5	0	0.481
CMPK2	STOML1	0	0.446
CMPK2	RSAD2	0	0.973
CMPK2	PARP12	0	0.563
CMPK2	PARP14	0	0.555
CMPK2	USP18	0	0.83
CMPK2	FCRL6	0	0.431
CMPK2	EPSTI1	0	0.822
CMPK2	IRF9	0	0.412
CMPK2	ZNFX1	0	0.559
CMPK2	PARP9	0	0.616
CMPK2	STAT1	0	0.627
CMPK2	DDX58	0	0.654
CMPK2	IRF7	0	0.702
CMPK2	HERC6	0	0.718
CMPK2	DHX58	0	0.735
CMPK2	IFIT2	0	0.775
CMPK2	MX1	0	0.886
CMPK2	ENTPD1	0	0.905
CMTR1	DOM3Z	0	0.72
CMTR1	IFIH1	0	0.407
CNN2	PPP4R2	0	0.424
CNN2	IQSEC1	0	0.467
CNN2	TPM4	0.204	0.453

CNN2	EHBP1L1	0.16	0.428
CNN2	PLEK	0	0.417
CNN2	COTL1	0.26	0.432
CNN2	ZYX	0.356	0.507
CNN2	ELN	0	0.412
CNOT7	EIF2C2	0.491	0.591
CNOT7	MIER1	0	0.618
CNOT7	PAPD4	0	0.432
CNOT7	PAN3	0	0.525
CNOT7	TRIM35	0.093	0.469
CNOT7	XRN2	0	0.503
CNOT7	XRN1	0	0.619
CNOT7	TP53RK	0	0.457
CNOT7	STAT1	0.113	0.49
CNOT7	RC3H2	0.431	0.659
CNOT7	ZFP36	0.385	0.838
CNP	GALC	0	0.598
CNP	SLFN12L	0	0.469
COPZ1	ST3GAL3	0	0.412
COPZ1	PPP1R3B	0	0.415
COPZ1	GPR84	0	0.447
COPZ1	HM13	0	0.456
COPZ1	N4BP1	0	0.467
COPZ1	SEC24B	0.117	0.469
COPZ1	SF3B1	0.428	0.482
COPZ1	SRPR	0	0.493
CORO1A	RHOG	0.045	0.48
CORO1A	HCLS1	0.055	0.479
CORO1A	STK4	0	0.407
CORO1A	VAV1	0	0.507
CORO1A	GCH1	0	0.469
CORO1A	IL2RG	0	0.476
CORO1A	PTPRC	0.042	0.513
CORO1A	PPP4C	0.055	0.501
CORO1A	COTL1	0.045	0.532
CORO1A	ITGB7	0	0.449
CORO1A	RFK	0	0.5
CORO1A	PTPN6	0	0.584
CORO1A	LTB	0	0.44
CORO1A	PSTPIP1	0	0.494
CORO1A	CYTH4	0	0.678
CORO1A	FCER1G	0	0.419
CORO1A	FMNL1	0.054	0.545
CORO1A	LAT2	0	0.638
CORO1A	LAPTM5	0	0.883
CORO2A	STEAP2	0	0.413
CORO2A	SLC39A8	0	0.464

CORO2A	GCH1	0	0.469
CORO2A	DAPP1	0	0.65
CORO2A	XPO6	0	0.611
CORO2A	TESK1	0.12	0.523
CORO2A	DIAPH2	0	0.428
CORO2A	RFK	0	0.461
CORO2A	RFWD2	0.162	0.593
CORO6	ZBTB17	0	0.441
CORO6	CRKL	0.046	0.447
CORO6	RFK	0	0.461
CORO6	GCH1	0	0.469
CORO6	GSN	0	0.593
COTL1	PSMA2	0	0.532
COTL1	TAGLN2	0.26	0.438
COTL1	GRB2	0.055	0.539
COTL1	LOC541180	0.072	0.568
COTL1	LCP2	0	0.587
COTL1	SH3BGRL	0.114	0.499
COTL1	FGR	0.066	0.465
COTL1	HCK	0.066	0.427
COTL1	EFHD2	0	0.434
COTL1	CRKL	0	0.435
COTL1	FCER1G	0	0.436
COTL1	LAPTM5	0	0.515
COTL1	HIP1R	0.571	0.719
CPB2	LAP3	0	0.651
CPB2	RASGEF1B	0.423	0.422
CPB2	F3	0	0.532
CPB2	SERPINE1	0	0.576
CPB2	UBE2B	0	0.586
CPB2	KYNU	0	0.607
CPB2	KMO	0	0.609
CPB2	F12	0	0.754
CREB1	NR4A1	0	0.516
CREB1	MYD88	0	0.405
CREB1	RET	0	0.68
CREB1	KAT2B	0.18	0.729
CREB1	IL1B	0	0.549
CREB1	NFE2	0.055	0.58
CREB1	PLCG2	0	0.561
CREB1	SNX15	0.176	0.402
CREB1	JAK1	0.049	0.424
CREB1	NR4A2	0	0.56
CREB1	CREBBP	0.963	0.999
CREB1	JUN	0.261	0.96
CREB1	MAP3K2	0	0.407
CREB1	FOS	0.161	0.953

CREB1	STAT2	0.054	0.496
CREB1	RAF1	0.049	0.493
CREB1	GRB2	0	0.766
CREB1	EGR2	0.08	0.409
CREB1	FMR1	0	0.42
CREB1	KAT5	0.113	0.433
CREB1	NF1	0	0.438
CREB1	STAT5B	0.054	0.439
CREB1	EGR3	0.08	0.443
CREB1	RELB	0	0.456
CREB1	NFIX	0.093	0.462
CREB1	PPARD	0.157	0.466
CREB1	IRF1	0	0.466
CREB1	STAT4	0.054	0.467
CREB1	VASP	0	0.47
CREB1	PSEN1	0	0.479
CREB1	CREBL2	0.174	0.483
CREB1	STAT5A	0.054	0.489
CREB1	RELA	0	0.496
CREB1	XPO6	0.112	0.498
CREB1	NFKB1	0.135	0.507
CREB1	CXCL8	0	0.532
CREB1	JAK2	0.049	0.551
CREB1	PDE4B	0	0.566
CREB1	STAT6	0.054	0.573
CREB1	DDIT3	0.201	0.587
CREB1	IL10	0	0.587
CREB1	SIK1	0	0.59
CREB1	MCL1	0	0.602
CREB1	TLR4	0	0.615
CREB1	IL6	0	0.615
CREB1	MAPKAPK3	0.067	0.617
CREB1	NOS2	0	0.633
CREB1	PTGS2	0	0.634
CREB1	LOC100297725	0.055	0.647
CREB1	KRAS	0.124	0.652
CREB1	PRKCB	0.055	0.652
CREB1	STAT1	0.054	0.664
CREB1	JUNB	0.138	0.664
CREB1	HDAC4	0.174	0.665
CREB1	TNF	0	0.679
CREB1	CREM	0.218	0.684
CREB1	GTF2B	0	0.707
CREB1	FOSL2	0.079	0.733
CREB1	PIK3CA	0.045	0.748
CREB1	EDN1	0	0.753
CREB1	SIRT1	0.113	0.761

CREB1	STAT3	0.113	0.765
CREB1	MAPKAPK2	0.078	0.786
CREB1	NFE2L2	0.055	0.79
CREB1	VEGFA	0.093	0.791
CREB1	CRTC2	0.836	0.998
CREBBP	SETDB1	0.122	0.523
CREBBP	SENP3	0.296	0.425
CREBBP	SP3	0.496	0.624
CREBBP	NR4A1	0.22	0.792
CREBBP	KAT2B	0.849	0.996
CREBBP	MXD1	0.164	0.452
CREBBP	GMEB1	0.184	0.437
CREBBP	IL1B	0	0.725
CREBBP	EPC1	0.157	0.479
CREBBP	NFKBIB	0.12	0.429
CREBBP	JAK1	0.125	0.507
CREBBP	NR1H2	0.26	0.759
CREBBP	CTBP2	0.204	0.76
CREBBP	TLE4	0.086	0.63
CREBBP	RBPJ	0.218	0.972
CREBBP	NR4A2	0.219	0.673
CREBBP	PHF11	0.386	0.4
CREBBP	SMG1	0.209	0.402
CREBBP	IL1A	0	0.403
CREBBP	KRAS	0.08	0.409
CREBBP	LIMK2	0.157	0.414
CREBBP	IRAK2	0.157	0.42
CREBBP	RBM43	0.093	0.424
CREBBP	SERTAD1	0.257	0.424
CREBBP	NIPBL	0.08	0.425
CREBBP	ZMIZ2	0.119	0.43
CREBBP	MCL1	0.078	0.432
CREBBP	KDM6B	0.201	0.433
CREBBP	FOXN3	0.218	0.434
CREBBP	TGFBR1	0.129	0.434
CREBBP	USP34	0.095	0.44
CREBBP	JAK3	0.125	0.441
CREBBP	GADD45B	0	0.443
CREBBP	NOS2	0	0.464
CREBBP	TAL1	0.296	0.466
CREBBP	MNT	0.164	0.47
CREBBP	H3F3A	0.351	0.471
CREBBP	MXD4	0.164	0.479
CREBBP	FOSL2	0.184	0.485
CREBBP	ZMIZ1	0.119	0.488
CREBBP	JAK2	0.125	0.491
CREBBP	UBTF	0.158	0.492

CREBBP	TFEC	0.106	0.5
CREBBP	TYK2	0.125	0.502
CREBBP	IKBKE	0.264	0.508
CREBBP	SP110	0.11	0.512
CREBBP	KAT8	0.218	0.515
CREBBP	FOXJ2	0.218	0.529
CREBBP	PIK3CA	0.209	0.53
CREBBP	HES4	0.139	0.534
CREBBP	POGZ	0.163	0.535
CREBBP	PIAS2	0.129	0.537
CREBBP	PARP3	0.21	0.54
CREBBP	DDIT3	0.258	0.548
CREBBP	E2F3	0.219	0.563
CREBBP	E2F2	0.219	0.568
CREBBP	EZH2	0.165	0.586
CREBBP	HDAC11	0.184	0.601
CREBBP	PIAS1	0.214	0.617
CREBBP	EDN1	0	0.617
CREBBP	DDX17	0.218	0.623
CREBBP	TLE3	0.114	0.627
CREBBP	SP140L	0.11	0.628
CREBBP	SMAD7	0.334	0.632
CREBBP	VEGFA	0.157	0.635
CREBBP	KLF5	0.41	0.645
CREBBP	SUPT6H	0.478	0.654
CREBBP	NMI	0.113	0.665
CREBBP	SNAI1	0.163	0.678
CREBBP	MYSM1	0.401	0.679
CREBBP	IRF2	0.081	0.681
CREBBP	TBL1X	0.165	0.689
CREBBP	DDX5	0.218	0.691
CREBBP	UBXN7	0.258	0.694
CREBBP	CXCL8	0.163	0.706
CREBBP	SNIP1	0.161	0.712
CREBBP	RARG	0.224	0.712
CREBBP	LOC100297725	0.351	0.72
CREBBP	NFKB2	0.377	0.721
CREBBP	HDAC4	0.184	0.726
CREBBP	IKBKB	0.499	0.741
CREBBP	NFE2L2	0.432	0.743
CREBBP	NLK	0.218	0.744
CREBBP	SKIL	0	0.747
CREBBP	MAX	0.296	0.75
CREBBP	ZBTB17	0.345	0.76
CREBBP	UBE2D1	0.432	0.772
CREBBP	RARA	0.224	0.781
CREBBP	JUNB	0.43	0.784

CREBBP	KAT5	0.218	0.796
CREBBP	VDR	0.437	0.8
CREBBP	TNF	0.08	0.817
CREBBP	DAXX	0.218	0.82
CREBBP	IRF5	0.435	0.828
CREBBP	POLR2A	0.342	0.83
CREBBP	NUP98	0.218	0.836
CREBBP	PML	0.639	0.863
CREBBP	PPARD	0.298	0.863
CREBBP	EGR2	0.163	0.866
CREBBP	IRF1	0.465	0.896
CREBBP	MEF2A	0.543	0.905
CREBBP	STAT4	0.258	0.909
CREBBP	FOS	0.641	0.91
CREBBP	MAML2	0.113	0.912
CREBBP	CREM	0.59	0.913
CREBBP	EGR3	0.399	0.914
CREBBP	SIRT1	0.493	0.917
CREBBP	NFKB1	0.502	0.921
CREBBP	ETS2	0.771	0.932
CREBBP	STAT5A	0.258	0.941
CREBBP	STAT5B	0.258	0.943
CREBBP	CRTC2	0.116	0.955
CREBBP	GTF2B	0.814	0.965
CREBBP	MDM2	0.763	0.969
CREBBP	TCF7L2	0.644	0.982
CREBBP	STAT3	0.501	0.983
CREBBP	JUN	0.764	0.983
CREBBP	STAT6	0.763	0.986
CREBBP	IRF7	0.113	0.992
CREBBP	STAT2	0.926	0.993
CREBBP	RELA	0.929	0.995
CREBBP	STAT1	0.947	0.996
CREBL2	SAFB	0	0.482
CREBL2	ELL	0	0.412
CREBL2	CYP4F2	0	0.471
CREBL2	CREM	0.152	0.425
CREBL2	ETV6	0	0.587
CREBL2	SEH1L	0	0.587
CREBL2	CREBRF	0.504	0.819
CREBRF	SKIL	0	0.465
CREBRF	FAM129A	0	0.433
CREBRF	SMG1	0.157	0.44
CREBRF	HIPK3	0	0.585
CRELD2	DNAJB11	0.456	0.952
CRELD2	HM13	0	0.502
CRELD2	LAMB3	0	0.473

CRELD2	HERPUD1	0	0.715
CRELD2	DDX39A	0	0.41
CRELD2	DDIT3	0	0.41
CRELD2	MANF	0	0.988
CREM	KAT2B	0.18	0.423
CREM	STRA8	0	0.41
CREM	NFE2	0.055	0.455
CREM	PLCG2	0	0.428
CREM	SNX15	0.176	0.439
CREM	JUN	0.184	0.823
CREM	FOS	0.218	0.82
CREM	GRB2	0	0.605
CREM	NOS2	0	0.435
CREM	RARG	0.157	0.403
CREM	EDN1	0	0.523
CREM	PIK3CA	0.045	0.474
CREM	XPO6	0.112	0.498
CREM	IER3	0	0.41
CREM	MAPKAPK2	0.055	0.432
CREM	JUNB	0.138	0.607
CREM	RARA	0.157	0.403
CREM	TSPAN2	0	0.523
CREM	MAPKAPK3	0.055	0.432
CREM	SFPQ	0	0.445
CREM	FOSL2	0.079	0.482
CREM	VEGFA	0.077	0.513
CREM	FOXN3	0.119	0.54
CREM	NFE2L2	0.055	0.57
CRISPLD2	FAM129A	0	0.436
CRKL	RHOG	0	0.418
CRKL	RET	0.3	0.687
CRKL	RASGRP2	0.352	0.628
CRKL	SAMSN1	0.055	0.427
CRKL	GAB2	0.432	0.879
CRKL	JAK1	0.184	0.721
CRKL	DOK2	0.16	0.68
CRKL	ELMO2	0.392	0.808
CRKL	PTPN12	0.093	0.402
CRKL	STAT2	0.157	0.4
CRKL	SOCS1	0.262	0.758
CRKL	RAF1	0.176	0.544
CRKL	DUSP6	0.045	0.42
CRKL	GRB2	0.465	0.841
CRKL	PRKAB1	0	0.424
CRKL	PTK2B	0.258	0.837
CRKL	PTPN1	0.093	0.706
CRKL	IKBKB	0.127	0.729

CRKL	5-Sep	0.042	0.44
CRKL	SOCS3	0.139	0.734
CRKL	RAP1B	0	0.79
CRKL	PIK3CA	0.068	0.695
CRKL	LCP2	0	0.708
CRKL	STAT5B	0.317	0.742
CRKL	PLEK	0	0.457
CRKL	SH2B2	0	0.822
CRKL	PTPN2	0.093	0.629
CRKL	TYK2	0.184	0.706
CRKL	FGR	0.184	0.534
CRKL	JAK2	0.184	0.751
CRKL	S100A8	0	0.412
CRKL	GAB3	0	0.411
CRKL	ITGA5	0	0.46
CRKL	MST1R	0.163	0.656
CRKL	ZYX	0	0.732
CRKL	PXN	0.564	0.983
CRKL	ITGB7	0.055	0.547
CRKL	VASP	0.082	0.742
CRKL	ITGAV	0	0.512
CRKL	LYN	0.184	0.685
CRKL	PTPN5	0.093	0.46
CRKL	PTPN6	0.218	0.759
CRKL	SNAP29	0	0.615
CRKL	JAK3	0.184	0.692
CRKL	PRKCB	0	0.427
CRKL	STAT3	0.157	0.463
CRKL	PLXNA1	0.07	0.46
CRKL	RAPGEF1	0.935	0.999
CRKL	STAT5A	0.317	0.753
CRKL	FLT4	0.334	0.618
CRKL	KRAS	0	0.469
CRKL	RASGEF1B	0.352	0.606
CRKL	HCK	0.206	0.692
CRKL	RIPK2	0.127	0.471
CRKL	PIK3R5	0	0.672
CRLF3	MIER1	0	0.641
CRLF3	RSAD2	0	0.518
CRLF3	PARP12	0	0.632
CRLF3	HERC5	0	0.401
CRLF3	HERC6	0	0.401
CRLF3	TRAF7	0	0.403
CRLF3	PARP11	0	0.632
CRTC2	PRKAA1	0.15	0.851
CRTC2	PRKAB1	0	0.806
CRTC2	SIK1	0.338	0.911

CRTC2	PPP4C	0.12	0.834
CRTC2	MARK3	0.203	0.469
CRTC2	SIRT1	0	0.427
CRTC2	SIK3	0.268	0.895
CSF1	ITGAL	0	0.401
CSF1	PTPRG	0	0.413
CSF1	PTPN12	0	0.413
CSF1	IRF1	0	0.413
CSF1	RELB	0	0.413
CSF1	LOC100138951	0	0.416
CSF1	JAK2	0.174	0.418
CSF1	CXCR1	0	0.418
CSF1	JUN	0	0.419
CSF1	IL1RN	0	0.423
CSF1	IL1R1	0	0.423
CSF1	ITGA9	0	0.423
CSF1	TMEM119	0	0.431
CSF1	IRF5	0	0.433
CSF1	NLRP3	0	0.436
CSF1	ITGB7	0	0.436
CSF1	PTPRJ	0	0.437
CSF1	PTPN22	0	0.448
CSF1	NOS2	0	0.453
CSF1	CXCR2	0	0.465
CSF1	PTGS2	0	0.482
CSF1	OCSTAMP	0	0.507
CSF1	ITGA5	0	0.508
CSF1	STAT6	0	0.516
CSF1	FCGR2B	0	0.57
CSF1	STAT1	0	0.574
CSF1	CXCR4	0	0.582
CSF1	STAT3	0	0.594
CSF1	PTPN1	0	0.616
CSF1	IL1A	0	0.618
CSF1	IL18	0	0.62
CSF1	PTPN2	0	0.622
CSF1	RET	0.336	0.624
CSF1	TLR2	0	0.625
CSF1	ICAM1	0.11	0.652
CSF1	MYD88	0.174	0.655
CSF1	IL15	0	0.663
CSF1	DCSTAMP	0	0.663
CSF1	VEGFA	0	0.677
CSF1	KRAS	0	0.678
CSF1	TLR4	0	0.686
CSF1	IL1B	0	0.692
CSF1	CXCL8	0	0.702

CSF1	ITGAV	0	0.703
CSF1	PTPRC	0	0.726
CSF1	IL6	0	0.765
CSF1	IL10	0	0.816
CSF1	TNF	0.078	0.848
CSF1	FLT4	0.336	0.855
CSF2RB	RET	0.084	0.533
CSF2RB	RASGRP2	0	0.432
CSF2RB	FYB	0	0.68
CSF2RB	GAB2	0	0.62
CSF2RB	JAK1	0.77	0.964
CSF2RB	PTPN12	0.121	0.54
CSF2RB	RABGEF1	0	0.564
CSF2RB	IL23A	0	0.608
CSF2RB	STAT2	0.16	0.707
CSF2RB	GRB2	0	0.882
CSF2RB	IL12B	0	0.609
CSF2RB	IL10RA	0	0.406
CSF2RB	TLR4	0	0.665
CSF2RB	STAT6	0.16	0.593
CSF2RB	IL10	0	0.67
CSF2RB	NCF4	0.055	0.654
CSF2RB	IKBKB	0.093	0.656
CSF2RB	IL2RG	0.439	0.903
CSF2RB	IL7R	0	0.403
CSF2RB	IL6R	0	0.413
CSF2RB	GPR77	0	0.414
CSF2RB	RASGEF1B	0	0.414
CSF2RB	RAPGEF1	0	0.414
CSF2RB	LYST	0	0.441
CSF2RB	TREM1	0	0.452
CSF2RB	IGSF6	0	0.456
CSF2RB	SLC37A1	0	0.481
CSF2RB	TEC	0.193	0.486
CSF2RB	STAT4	0.16	0.493
CSF2RB	IKBKE	0.093	0.498
CSF2RB	HCK	0.193	0.515
CSF2RB	HBEGF	0	0.518
CSF2RB	FCER1G	0	0.553
CSF2RB	TFEC	0	0.56
CSF2RB	EPSTI1	0	0.565
CSF2RB	FGR	0.193	0.567
CSF2RB	IL12A	0	0.6
CSF2RB	IL2RA	0	0.617
CSF2RB	FGL2	0	0.628
CSF2RB	GPR65	0	0.642
CSF2RB	P2RY8	0	0.646

CSF2RB	PIK3CA	0.113	0.653
CSF2RB	CYTH4	0	0.663
CSF2RB	OSM	0	0.663
CSF2RB	IL6	0	0.672
CSF2RB	MPEG1	0	0.68
CSF2RB	IL2RB	0	0.702
CSF2RB	IL15	0	0.705
CSF2RB	PTPN22	0.121	0.71
CSF2RB	STAT1	0.16	0.713
CSF2RB	INPP5D	0.051	0.714
CSF2RB	STAT5B	0.16	0.721
CSF2RB	LCP2	0	0.723
CSF2RB	STAT5A	0.16	0.731
CSF2RB	STAT3	0.203	0.74
CSF2RB	PLEK	0	0.744
CSF2RB	PTPN6	0.427	0.774
CSF2RB	TYK2	0.193	0.79
CSF2RB	PTPRC	0.121	0.8
CSF2RB	IL13RA1	0.433	0.811
CSF2RB	LYN	0.193	0.818
CSF2RB	KRAS	0	0.926
CSF2RB	JAK3	0.566	0.94
CSF2RB	JAK2	0.795	0.993
CSGALNACT2	SDC4	0	0.465
CSRNP1	PPP1R16B	0	0.416
CSRNP1	PPP1R15A	0	0.486
CSRNP1	SLCO3A1	0	0.414
CSRNP1	EMR3	0	0.421
CSRNP1	FOXS1	0	0.403
CSRNP1	INPP1	0	0.431
CSRNP1	RASSF2	0	0.445
CSRNP2	NAB1	0	0.47
CSRNP2	TMBIM4	0	0.466
CSRNP2	PLEKHO2	0	0.735
CSRNP2	IL20RA	0	0.512
CSRNP2	ST6GALNAC4	0	0.513
CSRNP2	GPR84	0	0.558
CTBP2	KAT2B	0.218	0.517
CTBP2	MXD1	0.042	0.412
CTBP2	HIVEP1	0.337	0.432
CTBP2	MNT	0.042	0.412
CTBP2	PRKCB	0	0.412
CTBP2	MAX	0.042	0.412
CTBP2	MXD4	0.042	0.412
CTBP2	RARA	0.12	0.416
CTBP2	PKNOX1	0.145	0.419
CTBP2	RARG	0.12	0.435

CTBP2	E2F3	0.042	0.438
CTBP2	E2F2	0.042	0.438
CTBP2	POR	0.114	0.459
CTBP2	HERC5	0.055	0.478
CTBP2	HERC6	0.055	0.478
CTBP2	UBA7	0	0.502
CTBP2	SIRT1	0	0.503
CTBP2	SMAD7	0.163	0.52
CTBP2	NOS2	0.122	0.533
CTBP2	HDAC4	0.148	0.538
CTBP2	UBE2B	0.055	0.556
CTBP2	SNAI1	0.325	0.592
CTBP2	CTDSP2	0.044	0.597
CTBP2	PPARD	0.12	0.624
CTBP2	HIC1	0.432	0.733
CTBP2	TLE3	0.257	0.763
CTBP2	HES4	0.658	0.799
CTBP2	TLE4	0.257	0.807
CTBP2	TGIF1	0.442	0.835
CTBP2	TCF7L2	0.163	0.903
CTBP2	RBPJ	0.129	0.961
CTDSP2	ZSWIM4	0	0.44
CTDSP2	LPIN2	0.335	0.487
CTDSP2	ZFAND6	0.052	0.514
CTDSP2	TIMM17A	0.295	0.407
CTDSP2	IL17REL	0	0.456
CTIF	LRCH1	0	0.633
CTIF	DDX19B	0.595	0.615
CTIF	DOM3Z	0	0.414
CTIF	NOM1	0	0.408
CTIF	MIF4GD	0.741	0.784
CUL4A	UBXN7	0.467	0.762
CUL4A	TRAF2	0.318	0.411
CUL4A	TRAF3	0.318	0.411
CUL4A	UBE2G1	0.184	0.476
CUL4A	ISG15	0.218	0.452
CUL4A	FBXO9	0.347	0.442
CUL4A	DDA1	0.646	0.875
CUL4A	TRAF7	0.483	0.694
CUL4A	TRAF1	0.318	0.411
CUL4A	RNF41	0.318	0.411
CUL4A	HIST1H2AJ	0.045	0.413
CUL4A	MPHOSPH8	0.165	0.421
CUL4A	UBE2B	0.184	0.423
CUL4A	HIST3H2A	0.045	0.425
CUL4A	LOC100297725	0.116	0.454
CUL4A	UBE2D1	0.184	0.465

CUL4A	DCUN1D3	0.295	0.508
CUL4A	MDM2	0.218	0.596
CUL4A	DCAF12	0.232	0.597
CUL4A	RFWD2	0.668	0.76
CUL4A	DCAF11	0.764	0.949
CWC22	USPL1	0	0.565
CWC22	FRG1	0.736	0.758
CWC22	ESF1	0	0.834
CWC22	DHX8	0.763	0.883
CWC22	THOC2	0.309	0.618
CWC22	SF3B1	0.852	0.983
CWC22	SUPT6H	0	0.642
CWC22	XPO6	0	0.418
CWC22	SRSF5	0.122	0.85
CWC22	TFIP11	0.257	0.635
CWC22	SDE2	0.76	0.765
CWC22	SNIP1	0.893	0.931
CWC22	WAC	0.217	0.473
CWC22	SMG1	0.07	0.538
CWC22	RANBP2	0.257	0.592
CWC22	SRRM2	0.757	0.884
CXCL13	CXCR4	0.055	0.936
CXCL13	IL1B	0	0.451
CXCL13	LOC515976	0.055	0.509
CXCL13	TLR4	0	0.424
CXCL13	IL10	0	0.628
CXCL13	SELL	0	0.451
CXCL13	CXCL16	0	0.468
CXCL13	IL6	0	0.481
CXCL13	ICAM1	0	0.499
CXCL13	CXCL8	0.055	0.508
CXCL13	PTPRC	0	0.518
CXCL13	LTB	0	0.575
CXCL13	LTBR	0	0.632
CXCL13	TNF	0	0.649
CXCL13	LOC529196	0.055	0.665
CXCL13	TNFSF13B	0	0.694
CXCL13	XCR1	0.055	0.792
CXCL13	CXCR1	0.055	0.918
CXCL13	CXCR2	0.055	0.933
CXCL16	CXCR4	0	0.764
CXCL16	IL1B	0	0.453
CXCL16	TNF	0	0.418
CXCL16	CXCL8	0	0.541
CXCL16	XCR1	0	0.626
CXCL16	LOC529196	0	0.642
CXCL16	CXCR2	0	0.779

CXCL16	CXCR1	0	0.782
CXCL8	MYD88	0	0.789
CXCL8	CXCR4	0.078	0.915
CXCL8	NLRP3	0	0.684
CXCL8	IL1B	0	0.96
CXCL8	JAK1	0	0.544
CXCL8	NCF1	0	0.465
CXCL8	LPAR3	0.078	0.884
CXCL8	JUN	0.098	0.935
CXCL8	TNFRSF1A	0	0.618
CXCL8	FOS	0	0.543
CXCL8	IL23A	0	0.48
CXCL8	STAT2	0	0.581
CXCL8	SOCS1	0	0.441
CXCL8	OLR1	0.042	0.418
CXCL8	RETN	0	0.557
CXCL8	IL12B	0	0.692
CXCL8	IL1R1	0	0.704
CXCL8	LITAF	0	0.524
CXCL8	PLAU	0	0.623
CXCL8	NFKB2	0	0.571
CXCL8	LOC515976	0.078	0.545
CXCL8	IRAK2	0	0.508
CXCL8	TLR4	0	0.91
CXCL8	STAT6	0	0.597
CXCL8	IL1R2	0	0.417
CXCL8	S100A9	0	0.518
CXCL8	SOD2	0	0.573
CXCL8	IL10	0	0.94
CXCL8	NOS2	0	0.62
CXCL8	F3	0	0.665
CXCL8	ITGAL	0	0.468
CXCL8	TNFAIP6	0.162	0.923
CXCL8	IKBKB	0	0.567
CXCL8	TLR2	0	0.91
CXCL8	EDN1	0	0.601
CXCL8	IFIH1	0	0.585
CXCL8	NLRC4	0	0.527
CXCL8	SOCS3	0	0.601
CXCL8	MX2	0	0.506
CXCL8	PTX3	0	0.53
CXCL8	PTPRC	0.042	0.703
CXCL8	LOC504773	0	0.445
CXCL8	ICAM1	0	0.887
CXCL8	IL1A	0	0.864
CXCL8	MAP2K3	0	0.496
CXCL8	FAS	0	0.412

CXCL8	MAP3K8	0	0.459
CXCL8	TYK2	0	0.411
CXCL8	FGR	0	0.65
CXCL8	JAK2	0	0.647
CXCL8	S100A8	0	0.665
CXCL8	PLAUR	0	0.565
CXCL8	TRAF3	0	0.41
CXCL8	RELA	0.496	0.984
CXCL8	SIRT1	0	0.434
CXCL8	PTGS2	0	0.887
CXCL8	SERPINE1	0	0.716
CXCL8	ISG15	0	0.538
CXCL8	VEGFC	0	0.594
CXCL8	IL6	0	0.958
CXCL8	IL12A	0.075	0.494
CXCL8	OSM	0	0.55
CXCL8	MMP25	0.055	0.704
CXCL8	TREM1	0	0.589
CXCL8	TLR9	0	0.699
CXCL8	IL15	0	0.836
CXCL8	IL6R	0	0.609
CXCL8	TNFSF10	0	0.413
CXCL8	VASP	0	0.654
CXCL8	IL1RN	0	0.778
CXCL8	IL2RA	0	0.401
CXCL8	TNFRSF1B	0	0.41
CXCL8	IFNAR1	0	0.412
CXCL8	IL17RC	0	0.413
CXCL8	ZFP36	0	0.414
CXCL8	GRK6	0	0.421
CXCL8	TRAF1	0	0.432
CXCL8	RIPK2	0	0.435
CXCL8	KRAS	0	0.459
CXCL8	TIRAP	0	0.468
CXCL8	LOC100297725	0	0.47
CXCL8	CYBB	0	0.5
CXCL8	ELANE	0	0.508
CXCL8	IRAK4	0	0.511
CXCL8	DNM2	0	0.526
CXCL8	SAA2	0	0.53
CXCL8	ELN	0	0.531
CXCL8	HBEGF	0	0.544
CXCL8	FCGR2B	0	0.564
CXCL8	FCGR3A	0	0.565
CXCL8	IRF7	0	0.611
CXCL8	IRF1	0	0.62
CXCL8	S100A12	0	0.638

CXCL8	SELL	0.042	0.639
CXCL8	DDX58	0	0.652
CXCL8	LOC529196	0.078	0.653
CXCL8	SELP	0.042	0.668
CXCL8	RELB	0	0.673
CXCL8	MX1	0	0.673
CXCL8	LYN	0	0.675
CXCL8	NOD1	0	0.697
CXCL8	NOD2	0	0.703
CXCL8	STAT1	0	0.711
CXCL8	XCR1	0.078	0.742
CXCL8	HCK	0	0.758
CXCL8	STAT3	0	0.761
CXCL8	VEGFA	0	0.869
CXCL8	IL18	0	0.895
CXCL8	TNF	0	0.909
CXCL8	NFKB1	0	0.927
CXCL8	SDC3	0.046	0.931
CXCL8	CXCR2	0.69	0.999
CXCL8	CXCR1	0.69	0.999
CXCR1	MYD88	0	0.413
CXCR1	IL1B	0.042	0.558
CXCR1	NFE2	0	0.714
CXCR1	EMR3	0	0.426
CXCR1	TGM3	0	0.788
CXCR1	IL1R1	0	0.47
CXCR1	TLR4	0.053	0.602
CXCR1	S100A9	0	0.46
CXCR1	IL10	0	0.619
CXCR1	ITGAL	0	0.43
CXCR1	TLR2	0.053	0.607
CXCR1	PTPRC	0.045	0.604
CXCR1	ICAM1	0	0.596
CXCR1	IL1A	0	0.41
CXCR1	FGR	0.051	0.656
CXCR1	JAK2	0.051	0.734
CXCR1	IL6	0	0.469
CXCR1	TREM1	0	0.637
CXCR1	VASP	0.084	0.893
CXCR1	IL1RN	0	0.623
CXCR1	LYN	0.051	0.638
CXCR1	JAK3	0.051	0.66
CXCR1	SAG	0	0.439
CXCR1	STAT3	0.053	0.581
CXCR1	FCGR3A	0	0.424
CXCR1	SLC9A3R1	0.12	0.622
CXCR1	TNF	0	0.713

CXCR1	DNM2	0.051	0.432
CXCR1	SDS	0	0.418
CXCR1	SELL	0.042	0.594
CXCR1	CXCR2	0.078	0.521
CXCR1	HCK	0.051	0.709
CXCR1	GRK6	0	0.775
CXCR1	IL18	0	0.416
CXCR1	VEGFA	0	0.548
CXCR2	MYD88	0	0.431
CXCR2	IL1B	0.042	0.596
CXCR2	IL1R1	0	0.47
CXCR2	TLR4	0.053	0.603
CXCR2	IL10	0	0.629
CXCR2	ITGAL	0	0.42
CXCR2	TLR2	0.053	0.608
CXCR2	PTPRC	0.045	0.619
CXCR2	ICAM1	0	0.606
CXCR2	IL1A	0	0.442
CXCR2	FGR	0.051	0.588
CXCR2	JAK2	0.051	0.734
CXCR2	IL6	0	0.557
CXCR2	VASP	0.113	0.927
CXCR2	IL1RN	0	0.416
CXCR2	LYN	0.051	0.581
CXCR2	JAK3	0.051	0.659
CXCR2	SAG	0	0.599
CXCR2	STAT3	0.053	0.601
CXCR2	FCGR3A	0	0.402
CXCR2	SLC9A3R1	0.12	0.716
CXCR2	TNF	0	0.713
CXCR2	DNM2	0.051	0.432
CXCR2	KRAS	0.046	0.418
CXCR2	SELL	0.042	0.549
CXCR2	SELP	0.042	0.407
CXCR2	ELANE	0.095	0.427
CXCR2	IL18	0	0.43
CXCR2	VEGFA	0	0.574
CXCR2	HCK	0.051	0.62
CXCR2	GRK6	0	0.793
CXCR4	PRDM1	0.045	0.421
CXCR4	SDC3	0	0.401
CXCR4	SOCS3	0.113	0.41
CXCR4	FUT4	0	0.414
CXCR4	SOCS1	0.164	0.424
CXCR4	FCGR2B	0	0.431
CXCR4	IL18	0	0.432
CXCR4	FLT4	0.052	0.438

CXCR4	ITGAV	0	0.443
CXCR4	LOC516599	0	0.45
CXCR4	IL15	0	0.455
CXCR4	FAS	0	0.462
CXCR4	HERC6	0.055	0.462
CXCR4	HERC5	0.055	0.462
CXCR4	PLAUR	0	0.462
CXCR4	JUN	0.042	0.467
CXCR4	LOC100138951	0	0.479
CXCR4	PTGS2	0.053	0.486
CXCR4	KRAS	0.046	0.513
CXCR4	MMP25	0.045	0.515
CXCR4	SELP	0.042	0.53
CXCR4	ITGAL	0	0.543
CXCR4	LOC616948	0	0.548
CXCR4	SMURF1	0.258	0.556
CXCR4	IL1B	0.042	0.561
CXCR4	VEGFC	0	0.567
CXCR4	SSH2	0.043	0.568
CXCR4	DNM2	0.051	0.571
CXCR4	JAK1	0.078	0.611
CXCR4	PIK3R6	0	0.621
CXCR4	IL6	0	0.632
CXCR4	SELL	0.042	0.646
CXCR4	STAT5A	0.07	0.65
CXCR4	PLCG2	0.071	0.652
CXCR4	GNG4	0.065	0.657
CXCR4	PTK2B	0.08	0.669
CXCR4	LOC529196	0.218	0.669
CXCR4	STAT5B	0.07	0.67
CXCR4	IL10	0	0.672
CXCR4	TLR4	0.053	0.686
CXCR4	LYN	0.051	0.689
CXCR4	PXN	0	0.69
CXCR4	ICAM1	0	0.691
CXCR4	PIK3CA	0.123	0.708
CXCR4	STAT2	0.078	0.753
CXCR4	VAV1	0.078	0.754
CXCR4	EDN1	0.079	0.756
CXCR4	SAG	0	0.772
CXCR4	TNF	0	0.787
CXCR4	STAT1	0.078	0.794
CXCR4	VEGFA	0	0.824
CXCR4	GRK6	0.069	0.869
CXCR4	STAT3	0.078	0.876
CXCR4	SDC4	0.078	0.878
CXCR4	TLR2	0.408	0.908

CXCR4	JAK3	0.113	0.921
CXCR4	JAK2	0.113	0.963
CXCR4	PTPRC	0.203	0.964
CXorf65	IL2RG	0	0.564
CYBB	MYD88	0	0.553
CYBB	NLRP3	0	0.534
CYBB	IL1B	0	0.617
CYBB	NCF1	0.078	0.999
CYBB	OLR1	0	0.542
CYBB	TLR4	0.071	0.707
CYBB	SOD2	0	0.549
CYBB	PTPN1	0	0.402
CYBB	IL10	0	0.538
CYBB	SLC7A5	0.416	0.416
CYBB	NOS2	0	0.55
CYBB	NCF4	0.046	0.981
CYBB	TLR2	0.071	0.891
CYBB	EDN1	0	0.534
CYBB	PRKCD	0	0.856
CYBB	NRROS	0.174	0.603
CYBB	PLEK	0	0.46
CYBB	PTPRC	0	0.673
CYBB	ICAM1	0	0.542
CYBB	RAB27A	0	0.486
CYBB	XDH	0	0.596
CYBB	PTGS2	0.086	0.536
CYBB	IL6	0	0.588
CYBB	NAMPT	0	0.817
CYBB	RIPK3	0.08	0.819
CYBB	IGSF6	0	0.46
CYBB	NFE2L2	0	0.42
CYBB	SELL	0	0.439
CYBB	STAT1	0.069	0.439
CYBB	SRI	0	0.493
CYBB	HCK	0.08	0.521
CYBB	TNF	0	0.693
CYLD	MYD88	0.113	0.487
CYLD	PRDM1	0	0.424
CYLD	TNFRSF1A	0.617	0.949
CYLD	STAT2	0.114	0.452
CYLD	NFKB2	0.134	0.441
CYLD	STAT4	0.114	0.409
CYLD	LTBR	0	0.412
CYLD	TNIP1	0	0.413
CYLD	USP3	0	0.417
CYLD	MYSM1	0	0.427
CYLD	NOD2	0.16	0.43

CYLD	MALT1	0	0.431
CYLD	RBCK1	0.055	0.432
CYLD	STAT5A	0.114	0.438
CYLD	STAT5B	0.114	0.44
CYLD	ISG15	0.347	0.448
CYLD	USP32	0	0.449
CYLD	RELA	0	0.449
CYLD	DHX58	0.073	0.45
CYLD	TANK	0	0.45
CYLD	STAT6	0.114	0.452
CYLD	HCK	0.133	0.456
CYLD	LRRK2	0.219	0.461
CYLD	FASLG	0.165	0.493
CYLD	TRIM25	0.069	0.493
CYLD	RIPK2	0.219	0.503
CYLD	TRIM38	0.069	0.504
CYLD	LTB	0.165	0.522
CYLD	RELB	0	0.53
CYLD	USP36	0	0.554
CYLD	RNF41	0.31	0.572
CYLD	IKBKB	0.212	0.575
CYLD	TAB2	0.047	0.581
CYLD	USP25	0	0.582
CYLD	IFIH1	0.08	0.582
CYLD	STAT3	0.174	0.584
CYLD	USP15	0	0.593
CYLD	TRAF7	0.35	0.63
CYLD	THOC2	0	0.66
CYLD	STAT1	0.114	0.7
CYLD	TRAF1	0.31	0.75
CYLD	MLKL	0.219	0.792
CYLD	OPTN	0.218	0.813
CYLD	RIPK3	0.219	0.829
CYLD	TRAF3	0.31	0.835
CYLD	TNF	0.445	0.882
CYLD	DDX58	0.113	0.926
CYLD	IKBKE	0.432	0.939
CYLD	TRAF2	0.432	0.975
CYLD	RIPK1	0.763	0.994
CYP27B1	VDR	0.139	0.82
CYP27B1	PPIF	0	0.485
CYP27B1	EMP1	0	0.421
CYP4F2	PLA2G4A	0	0.654
CYP4F2	PTGS2	0.043	0.734
CYP4F2	KMO	0.159	0.432
CYP4F2	R3HDM4	0.263	0.448
CYP4F2	POR	0.081	0.551

CYP4V2	KMO	0.159	0.432
CYP4V2	R3HDM4	0.263	0.448
CYP4V2	SCLY	0	0.466
CYP4V2	FRG1	0	0.551
CYP4V2	POR	0.081	0.681
CYTH1	IPCEF1	0.453	0.732
CYTH1	NPEPPS	0	0.402
CYTH1	RASSF5	0	0.406
CYTH1	VMP1	0	0.414
CYTH1	RAB11FIP1	0	0.422
CYTH1	PLEK	0	0.591
CYTH1	PIK3CA	0.07	0.646
CYTH1	CYTH4	0	0.816
CYTH1	FRMD4A	0.357	0.835
CYTH4	RHOG	0.143	0.414
CYTH4	FYB	0	0.614
CYTH4	SLC2A6	0	0.501
CYTH4	IQSEC1	0.461	0.515
CYTH4	IPCEF1	0.218	0.496
CYTH4	TLR4	0.043	0.586
CYTH4	IL2RG	0	0.586
CYTH4	PIK3CA	0.07	0.637
CYTH4	LCP2	0	0.688
CYTH4	PLEK	0	0.792
CYTH4	PTPRC	0	0.693
CYTH4	SLC24A3	0	0.523
CYTH4	MCTP2	0	0.449
CYTH4	IL2RB	0	0.479
CYTH4	RND1	0.143	0.428
CYTH4	IGSF6	0	0.586
CYTH4	PTPN22	0	0.594
CYTH4	PTPN6	0	0.654
CYTH4	LAPTM5	0	0.407
CYTH4	DDX58	0	0.428
CYTH4	SIGLEC5	0	0.494
CYTH4	P2RY8	0	0.598
CYTH4	MPEG1	0	0.651
DAAM2	RHOG	0.249	0.427
DAAM2	ZNF668	0.055	0.421
DAAM2	RAP1B	0.161	0.434
DAAM2	SH3PXD2B	0.121	0.436
DAAM2	GRTP1	0.132	0.41
DAAM2	RHOH	0.249	0.427
DAAM2	FMNL3	0.33	0.466
DAAM2	RND1	0.249	0.427
DAAM2	PSTPIP1	0.642	0.778
DAAM2	FMNL1	0.463	0.595

DAAM2	ROCK1	0.07	0.455
DAAM2	DIAPH2	0.257	0.716
DAAM2	PSTPIP2	0.642	0.778
DAGLB	TXNDC16	0	0.637
DAPP1	PLCG2	0.078	0.653
DAPP1	SLC39A8	0	0.429
DAPP1	GABRR2	0	0.432
DAPP1	PLEK	0	0.448
DAPP1	DOPEY2	0	0.495
DAPP1	INPP5D	0.115	0.496
DAPP1	PSTPIP1	0	0.524
DAPP1	SH3BP2	0	0.545
DAPP1	FGR	0.045	0.623
DAPP1	PIK3CA	0	0.631
DAPP1	PLBD1	0	0.669
DAPP1	HCK	0.045	0.674
DAPP1	LYN	0.078	0.938
DAXX	SETDB1	0.211	0.718
DAXX	SENP3	0.115	0.404
DAXX	PSMB8	0	0.494
DAXX	TNFRSF1A	0.113	0.845
DAXX	LOC616948	0.158	0.414
DAXX	LOC516599	0.158	0.414
DAXX	RIPK1	0.113	0.42
DAXX	PIAS2	0	0.448
DAXX	PSMB9	0	0.536
DAXX	MAP3K5	0.784	0.998
DAXX	ETS2	0.275	0.559
DAXX	TRIM25	0.158	0.432
DAXX	MAP2K3	0	0.677
DAXX	FAS	0.835	0.993
DAXX	MLKL	0.096	0.464
DAXX	RELA	0.432	0.467
DAXX	SP110	0.158	0.67
DAXX	PML	0.928	0.991
DAXX	USP18	0.218	0.633
DAXX	TAPBP	0	0.545
DAXX	TRIM21	0.158	0.403
DAXX	MEFV	0.158	0.411
DAXX	RASSF2	0.325	0.423
DAXX	LRRK2	0.096	0.438
DAXX	TRIM8	0.158	0.443
DAXX	USP34	0.16	0.457
DAXX	RIPK3	0.184	0.493
DAXX	PIAS1	0	0.568
DAXX	LOC613345	0.573	0.624
DAXX	RIPK2	0.096	0.649

DAXX	RASSF5	0.5	0.67
DAXX	USP25	0.218	0.687
DAXX	SP140L	0.158	0.776
DAXX	TNFRSF1B	0	0.825
DAXX	LOC100297725	0.573	0.842
DAXX	H3F3A	0.573	0.904
DAXX	TGFBR1	0.055	0.923
DAXX	RASSF1	0.807	0.932
DAXX	MDM2	0.838	0.987
DAZAP2	FAM46A	0.079	0.462
DAZAP2	PCGF5	0	0.491
DAZAP2	PTPN9	0	0.586
DCAF11	PRKCD	0.045	0.421
DCAF11	DTX3L	0	0.678
DCAF11	MAEA	0	0.467
DCAF11	TAPBPL	0	0.576
DCAF11	DDA1	0.482	0.816
DCAF11	SRGN	0	0.646
DCAF11	SELP	0	0.42
DCAF11	DYSF	0.059	0.421
DCAF11	KDM6B	0.494	0.57
DCAF11	DCAF12	0	0.746
DCAF12	VEZF1	0	0.459
DCAF12	LOC541180	0	0.409
DCAF12	DOPEY2	0	0.53
DCAF12	DDA1	0.093	0.735
DCAF12	PPTC7	0	0.597
DCAF12	FNBP4	0	0.589
DCAF12	LAT2	0	0.493
DCBLD1	KPNA3	0	0.554
DCBLD1	TSPAN31	0	0.66
DCBLD1	KPNA1	0	0.459
DCBLD1	PLAGL2	0	0.56
DCBLD1	RNF213	0	0.424
DCBLD1	PHLDB1	0	0.665
DCBLD1	NUP210	0	0.569
DCBLD1	DCUN1D3	0	0.702
DCSTAMP	TCIRG1	0	0.498
DCSTAMP	FOS	0	0.536
DCSTAMP	OCSTAMP	0	0.952
DCUN1D3	TSPAN31	0	0.681
DCUN1D3	SOCS3	0	0.6
DCUN1D3	FBXO40	0	0.6
DCUN1D3	PLAGL2	0	0.561
DCUN1D3	FBXL3	0	0.6
DCUN1D3	PHLDB1	0	0.681
DDA1	TRIB1	0	0.41

DDA1	RFWD2	0.389	0.692
DDIT3	DDIT4	0	0.511
DDIT3	PRDM1	0.119	0.451
DDIT3	PPP1R15A	0	0.891
DDIT3	JUN	0.218	0.886
DDIT3	FOS	0.764	0.898
DDIT3	MAP4K4	0	0.447
DDIT3	FUS	0.113	0.704
DDIT3	PLK3	0	0.412
DDIT3	IL10	0.12	0.563
DDIT3	TSPAN31	0	0.412
DDIT3	MAP3K5	0	0.596
DDIT3	PTPRC	0	0.67
DDIT3	TRAF2	0.068	0.49
DDIT3	FAS	0.046	0.429
DDIT3	JUNB	0.2	0.524
DDIT3	EDEM1	0	0.654
DDIT3	PTGS2	0.047	0.4
DDIT3	IL6	0.058	0.516
DDIT3	MCL1	0.045	0.484
DDIT3	KLF6	0.078	0.429
DDIT3	HERPUD1	0	0.719
DDIT3	NFE2L2	0.124	0.903
DDIT3	STAT3	0.093	0.446
DDIT3	FOSL2	0.201	0.465
DDIT3	GADD45B	0	0.492
DDIT3	TNF	0	0.579
DDIT3	PTAFR	0	0.633
DDIT3	MANF	0	0.412
DDIT3	NCR1	0	0.414
DDIT3	MDM2	0.085	0.455
DDIT3	XIAP	0	0.47
DDIT3	SESN2	0	0.595
DDIT3	SELL	0	0.65
DDIT4	SLC2A1	0	0.427
DDIT4	DUSP5	0	0.496
DDIT4	SESN2	0	0.54
DDIT4	NDRG1	0	0.559
DDX17	FRYL	0	0.418
DDX17	STAU1	0.132	0.51
DDX17	KAT2B	0.127	0.69
DDX17	EIF2C2	0.265	0.478
DDX17	RBM47	0.497	0.521
DDX17	FXR2	0.403	0.566
DDX17	FUS	0.763	0.839
DDX17	ESF1	0.218	0.564
DDX17	DHX8	0.16	0.622

DDX17	THOC2	0.217	0.423
DDX17	NUP98	0.136	0.623
DDX17	HNRNPF	0.296	0.468
DDX17	SF3B1	0.271	0.752
DDX17	HNRNPH1	0.341	0.569
DDX17	NXF1	0.257	0.466
DDX17	PAN3	0.086	0.407
DDX17	EIF6	0.165	0.442
DDX17	XRN1	0.164	0.547
DDX17	KRR1	0.169	0.519
DDX17	FMR1	0.403	0.554
DDX17	GTPBP4	0.226	0.812
DDX17	IK	0.046	0.414
DDX17	SFPQ	0.296	0.507
DDX17	DDX5	0.764	0.805
DDX17	SMG1	0.119	0.534
DDX17	SRRM2	0.296	0.687
DDX17	QKI	0.165	0.407
DDX17	RASA2	0	0.409
DDX17	POLR2A	0.316	0.427
DDX17	NOM1	0.202	0.509
DDX17	NOP9	0.114	0.656
DDX17	DDX3X	0.518	0.739
DDX19B	XPO6	0.309	0.444
DDX19B	PHACTR2	0	0.553
DDX19B	NUP98	0.222	0.623
DDX19B	NXF1	0.394	0.769
DDX19B	MIF4GD	0.759	0.779
DDX39A	ISG20L2	0.08	0.535
DDX39A	FUS	0.158	0.414
DDX39A	UBXN7	0.16	0.416
DDX39A	DHX8	0.258	0.755
DDX39A	THOC2	0.675	0.908
DDX39A	HNRNPF	0.138	0.525
DDX39A	SF3B1	0.258	0.55
DDX39A	SUPT6H	0.071	0.47
DDX39A	NXF1	0.212	0.632
DDX39A	EIF6	0.165	0.454
DDX39A	XRN2	0.164	0.441
DDX39A	XRN1	0.164	0.417
DDX39A	SRSF5	0.197	0.441
DDX39A	TRA2A	0.236	0.464
DDX39A	WDR77	0.093	0.482
DDX39A	MOV10	0.161	0.511
DDX39A	GTPBP4	0.226	0.415
DDX39A	WAC	0.208	0.426
DDX39A	SRSF12	0.236	0.434

DDX39A	POLR2A	0.16	0.436
DDX39A	LMNB1	0.4	0.469
DDX39A	MANF	0	0.575
DDX39A	DDX39B	0.792	0.81
DDX39A	ETF1	0.041	0.812
DDX39B	UBXN7	0.16	0.416
DDX39B	DHX8	0.258	0.702
DDX39B	THOC2	0.683	0.959
DDX39B	NUP98	0.125	0.415
DDX39B	HNRNPF	0.138	0.823
DDX39B	SF3B1	0.258	0.651
DDX39B	SUPT6H	0.071	0.47
DDX39B	HNRNPH1	0.138	0.464
DDX39B	NXF1	0.212	0.922
DDX39B	XRN2	0.164	0.482
DDX39B	XRN1	0.164	0.492
DDX39B	SRSF5	0.197	0.444
DDX39B	TRA2A	0.236	0.503
DDX39B	MOV10	0.161	0.568
DDX39B	SFPQ	0.079	0.658
DDX39B	WAC	0.208	0.426
DDX39B	SMG1	0.119	0.428
DDX39B	SRRM2	0.158	0.412
DDX39B	SAFB2	0	0.42
DDX39B	RANBP2	0.179	0.426
DDX39B	SRSF12	0.236	0.434
DDX39B	POLR2A	0.16	0.436
DDX39B	LMNB1	0.4	0.458
DDX39B	MX1	0.055	0.472
DDX3X	EIF4A1	0.5	0.657
DDX3X	EIF2C2	0.294	0.648
DDX3X	EIF1	0.129	0.478
DDX3X	FUS	0.68	0.745
DDX3X	IRAK2	0.07	0.49
DDX3X	PAPOLG	0.091	0.426
DDX3X	IFIH1	0.093	0.543
DDX3X	DHX8	0.16	0.532
DDX3X	THOC2	0.217	0.405
DDX3X	NUP98	0.125	0.456
DDX3X	SF3B1	0.258	0.463
DDX3X	NXF1	0.126	0.683
DDX3X	IKBKE	0.389	0.687
DDX3X	XRN1	0.259	0.706
DDX3X	FMR1	0.183	0.456
DDX3X	SARS	0	0.439
DDX3X	MOV10	0.161	0.551
DDX3X	GTPBP4	0.226	0.81

DDX3X	E2F2	0.182	0.415
DDX3X	TBL1X	0.093	0.601
DDX3X	DDX5	0.518	0.698
DDX3X	SMG1	0.119	0.422
DDX3X	E2F3	0.182	0.415
DDX3X	MYSM1	0.207	0.648
DDX3X	RANBP2	0.179	0.487
DDX3X	LMNB1	0.257	0.422
DDX3X	TRIM21	0.157	0.467
DDX3X	USP34	0.184	0.538
DDX3X	DHX58	0.07	0.597
DDX3X	DDX58	0.093	0.766
DDX5	STAU1	0.132	0.48
DDX5	KAT2B	0.127	0.523
DDX5	EIF2C2	0.265	0.537
DDX5	RBM47	0.497	0.521
DDX5	PSPC1	0.217	0.428
DDX5	FXR2	0.403	0.559
DDX5	FUS	0.763	0.814
DDX5	ESF1	0.218	0.564
DDX5	DHX8	0.16	0.729
DDX5	NUP98	0.136	0.483
DDX5	HNRNPF	0.413	0.618
DDX5	SF3B1	0.402	0.794
DDX5	HNRNPH1	0.343	0.769
DDX5	NXF1	0.257	0.508
DDX5	TRIM25	0.08	0.4
DDX5	EIF6	0.165	0.43
DDX5	XRN2	0.164	0.546
DDX5	KRR1	0.169	0.548
DDX5	SRSF5	0.128	0.463
DDX5	FMR1	0.403	0.602
DDX5	TRA2A	0.218	0.455
DDX5	GTPBP4	0.226	0.832
DDX5	SFPQ	0.389	0.615
DDX5	LTV1	0.042	0.511
DDX5	NOM1	0.202	0.509
DDX5	POLR2A	0.435	0.527
DDX5	RASA2	0	0.539
DDX5	SRRM2	0.417	0.605
DDX5	NOP9	0.114	0.656
DDX58	MYD88	0	0.778
DDX58	NLRP3	0	0.696
DDX58	IL1B	0	0.564
DDX58	JAK1	0.046	0.951
DDX58	STAT2	0.052	0.812
DDX58	SOCS1	0	0.543

DDX58	LOC616948	0.134	0.634
DDX58	IRF5	0	0.574
DDX58	IL1R1	0	0.414
DDX58	GBP4	0.079	0.582
DDX58	NLRC5	0.113	0.847
DDX58	IRAK2	0.046	0.419
DDX58	TLR4	0.041	0.728
DDX58	STAT6	0.052	0.413
DDX58	RIPK1	0.046	0.745
DDX58	IL10	0	0.549
DDX58	IFI35	0	0.718
DDX58	IKBKB	0.093	0.513
DDX58	TLR2	0.041	0.684
DDX58	IFIH1	0	0.978
DDX58	NLRC4	0	0.56
DDX58	DHX8	0.055	0.46
DDX58	MX2	0	0.981
DDX58	IFIT3	0.113	0.931
DDX58	DTX3L	0	0.865
DDX58	TRIM25	0.928	0.999
DDX58	IRF2	0	0.468
DDX58	IKBKE	0.161	0.738
DDX58	TRAF2	0.064	0.839
DDX58	XRN2	0.119	0.432
DDX58	XAF1	0	0.775
DDX58	TYK2	0.046	0.498
DDX58	JAK2	0.046	0.431
DDX58	UBA7	0.077	0.653
DDX58	UBE2L6	0.064	0.553
DDX58	TRAF3	0.113	0.919
DDX58	OAS2	0	0.81
DDX58	ISG15	0.159	0.989
DDX58	IL6	0	0.554
DDX58	IFNAR2	0	0.536
DDX58	SP110	0.134	0.641
DDX58	RSAD2	0	0.953
DDX58	PARP12	0.121	0.702
DDX58	PARP14	0	0.728
DDX58	USP18	0	0.912
DDX58	TLR9	0.041	0.707
DDX58	TRIM38	0.134	0.46
DDX58	IFITM3	0	0.678
DDX58	EPSTI1	0	0.611
DDX58	MEFV	0.134	0.533
DDX58	ZNFX1	0.077	0.401
DDX58	HERC6	0.043	0.788
DDX58	NOD2	0.046	0.756

DDX58	IRAK4	0.046	0.467
DDX58	TIRAP	0	0.449
DDX58	STAT3	0.052	0.486
DDX58	PARP9	0	0.946
DDX58	IFNAR1	0	0.76
DDX58	RNF213	0	0.541
DDX58	TNF	0	0.697
DDX58	MX1	0	0.951
DDX58	IRF1	0	0.738
DDX58	TANK	0	0.591
DDX58	IRF9	0	0.817
DDX58	IFIT2	0.045	0.917
DDX58	ZBP1	0	0.66
DDX58	GBP2	0.079	0.442
DDX58	HERC5	0.043	0.826
DDX58	NOD1	0.046	0.646
DDX58	STAT1	0.113	0.901
DDX58	RIPK2	0.046	0.428
DDX58	SDC4	0	0.551
DDX58	IL18	0	0.609
DDX58	ISG20	0	0.666
DDX58	TRIM21	0.134	0.694
DDX58	DHX58	0.113	0.901
DDX58	IRF7	0	0.965
DEDD2	RB1CC1	0	0.405
DEDD2	INPP5D	0	0.426
DEDD2	DNAJB12	0	0.468
DEDD2	GADD45B	0	0.47
DEDD2	NOD1	0	0.499
DEDD2	SNAPC1	0	0.518
DEDD2	DGKD	0	0.624
DENND3	VEZF1	0.045	0.416
DENND3	NCLN	0	0.632
DENND3	RNF19A	0	0.632
DENND3	DENND5A	0.486	0.641
DENND5A	SLC8A1	0	0.414
DENND5A	SIPA1L1	0	0.601
DGAT2	LPCAT2	0	0.505
DGAT2	INSIG1	0	0.556
DGAT2	DGKD	0	0.714
DGAT2	LPIN2	0.072	0.925
DGKD	PLCG2	0	0.743
DGKD	MBOAT1	0	0.69
DGKD	INPP5D	0	0.806
DGKD	SAG	0	0.405
DGKD	RNF41	0	0.461
DHRS3	FAM46A	0	0.517

DHX58	MYD88	0	0.516
DHX58	NLRP3	0	0.4
DHX58	STAT2	0.052	0.714
DHX58	GBP4	0.071	0.43
DHX58	NLRC5	0.073	0.64
DHX58	IFI35	0	0.594
DHX58	TLR2	0.041	0.428
DHX58	IFIH1	0.113	0.941
DHX58	DHX8	0.055	0.583
DHX58	MX2	0	0.908
DHX58	PARP10	0	0.562
DHX58	IFIT3	0.073	0.789
DHX58	DTX3L	0	0.586
DHX58	TRIM25	0.49	0.898
DHX58	IKBKE	0.122	0.63
DHX58	XAF1	0	0.495
DHX58	UBA7	0.077	0.872
DHX58	UBE2L6	0.064	0.621
DHX58	TRAF3	0.113	0.653
DHX58	MOV10	0.077	0.454
DHX58	OAS2	0	0.638
DHX58	ISG15	0.159	0.964
DHX58	RSAD2	0	0.95
DHX58	PARP12	0.113	0.786
DHX58	PARP14	0	0.714
DHX58	USP18	0	0.89
DHX58	TLR9	0.041	0.556
DHX58	IFITM3	0	0.598
DHX58	EPSTI1	0	0.756
DHX58	ZNFX1	0.077	0.578
DHX58	HERC6	0.043	0.465
DHX58	NOD2	0.046	0.491
DHX58	PARP9	0	0.846
DHX58	IFNAR1	0	0.534
DHX58	RNF213	0	0.829
DHX58	MX1	0	0.895
DHX58	IRF1	0	0.57
DHX58	IRF9	0	0.703
DHX58	IFIT2	0.045	0.74
DHX58	ZBP1	0	0.514
DHX58	GBP2	0.071	0.409
DHX58	HERC5	0.043	0.462
DHX58	NOD1	0.046	0.428
DHX58	STAT1	0.073	0.754
DHX58	TRIM21	0.134	0.756
DHX58	ISG20	0	0.482
DHX58	IRF7	0	0.936

DHX8	EIF4A1	0.16	0.719
DHX8	STAU1	0.093	0.497
DHX8	EIF2C2	0.156	0.473
DHX8	ESF1	0.401	0.484
DHX8	IFIH1	0.055	0.511
DHX8	SMG1	0.045	0.431
DHX8	SNIP1	0.339	0.467
DHX8	IK	0.458	0.472
DHX8	KRR1	0.401	0.567
DHX8	NOM1	0.401	0.608
DHX8	PNPT1	0	0.635
DHX8	SF3B1	0.335	0.662
DHX8	SDE2	0.67	0.686
DHX8	MOV10	0.459	0.74
DHX8	TFIP11	0.504	0.749
DHX8	SRRM2	0.67	0.805
DIAPH2	RHOG	0.296	0.518
DIAPH2	RHOH	0.296	0.526
DIAPH2	FMNL3	0.339	0.564
DIAPH2	RND1	0.296	0.513
DIAPH2	FMNL1	0.337	0.757
DIAPH2	ROCK1	0.218	0.479
DIRAS3	RABGEF1	0.134	0.471
DIRAS3	RAF1	0.245	0.621
DIRAS3	GRB2	0.133	0.402
DIRAS3	PIK3CA	0.201	0.469
DIRAS3	NF1	0.303	0.468
DIRAS3	RALGDS	0.219	0.422
DIRAS3	MST1R	0.258	0.472
DIRAS3	SMG1	0.268	0.482
DIRAS3	RASSF1	0.156	0.505
DIRAS3	FNBP1	0.129	0.507
DIRAS3	RASSF2	0.156	0.543
DIRAS3	STAT3	0.113	0.689
DIXDC1	SEMA7A	0	0.403
DIXDC1	ECE1	0	0.414
DIXDC1	NDEL1	0.163	0.762
DKK4	DRAXIN	0	0.422
DKK4	LRP10	0.185	0.51
DLL1	RBPJ	0.294	0.894
DLL1	PTPRC	0.071	0.421
DLL1	HES4	0.121	0.592
DLL1	SDCBP	0.073	0.535
DLL1	OLFM4	0.042	0.418
DLL1	DNM2	0.053	0.526
DLL1	PSEN1	0.451	0.818
DLL1	HIC1	0.049	0.478

DLL1	NUMB	0.209	0.667
DLL1	LFNG	0.355	0.764
DMXL2	TCIRG1	0.208	0.463
DMXL2	UPB1	0	0.513
DMXL2	GRAMD1A	0	0.441
DMXL2	LRRFIP1	0	0.48
DMXL2	NOS2	0	0.434
DMXL2	RAB3GAP1	0.517	0.775
DMXL2	HEATR5B	0	0.423
DMXL2	PPIF	0.053	0.41
DMXL2	OTUD4	0	0.474
DNAH17	NDEL1	0.212	0.575
DNAJB11	DNAJC1	0.161	0.405
DNAJB11	TARS	0	0.448
DNAJB11	HM13	0	0.449
DNAJB11	RC3H2	0.045	0.457
DNAJB11	GRB2	0.148	0.462
DNAJB11	HERPUD1	0	0.488
DNAJB11	EDEM1	0.125	0.526
DNAJB11	TP53INP2	0	0.54
DNAJB11	MANF	0	0.986
DNAJB12	6-Mar	0.051	0.431
DNAJB12	TTC19	0.156	0.664
DNAJB6	TXNDC16	0.119	0.513
DNAJC1	ZNF259	0	0.42
DNAJC1	MIER1	0	0.445
DNAJC1	FAM107B	0	0.586
DNAJC1	WDR55	0	0.693
DNAJC1	LPCAT2	0	0.422
DNASE1L1	LRP10	0	0.441
DNM2	HCLS1	0.304	0.903
DNM2	VAV1	0.078	0.84
DNM2	RAF1	0.093	0.574
DNM2	GRB2	0.862	0.982
DNM2	RYR1	0.081	0.434
DNM2	PLEK	0	0.548
DNM2	FLOT1	0	0.465
DNM2	FLOT2	0	0.447
DNM2	FGR	0.093	0.608
DNM2	TRIP10	0.231	0.427
DNM2	GPR84	0.051	0.503
DNM2	GJB2	0	0.406
DNM2	LYN	0.093	0.425
DNM2	FNBP1	0.448	0.622
DNM2	PSTPIP1	0.218	0.548
DNM2	SAG	0	0.507
DNM2	HIP1R	0.152	0.752

DNM2	DYSF	0.078	0.755
DNM2	NUMB	0	0.401
DNM2	FLT4	0.07	0.445
DNM2	LAMP1	0	0.454
DNM2	NDEL1	0	0.472
DNM2	LRRK2	0.316	0.554
DNM2	VEGFA	0	0.64
DNM2	HCK	0.113	0.714
DNM2	SDC4	0	0.809
DOK2	RET	0.483	0.812
DOK2	HCLS1	0	0.502
DOK2	IL4R	0.078	0.64
DOK2	PTPRE	0.119	0.457
DOK2	JAK1	0.149	0.694
DOK2	FGR	0.149	0.4
DOK2	PTPRC	0.119	0.415
DOK2	LYN	0.173	0.432
DOK2	PTPN1	0.119	0.436
DOK2	VAV1	0.054	0.441
DOK2	LCP2	0	0.448
DOK2	PLEK	0	0.474
DOK2	FCER1G	0	0.538
DOK2	PTPN6	0.234	0.564
DOK2	GRB2	0.218	0.607
DOK2	JAK2	0.149	0.617
DOK2	IL2RA	0	0.62
DOK2	IL2RB	0	0.648
DOK2	TEC	0.149	0.655
DOK2	IL2RG	0	0.666
DOK2	HCK	0.529	0.692
DOK2	KRAS	0	0.72
DOK2	INPP5D	0.477	0.721
DOK2	JAK3	0.149	0.724
DOK3	RHOG	0.045	0.44
DOK3	GRB2	0.246	0.921
DOK3	NFAM1	0	0.516
DOK3	PTPN1	0.119	0.433
DOK3	LOC506364	0	0.532
DOK3	PLEK	0	0.513
DOK3	SIRPB1	0	0.502
DOK3	RIOK3	0	0.441
DOK3	PTPRC	0.119	0.471
DOK3	LOC617909	0	0.535
DOK3	INPP5D	0.257	0.789
DOK3	PTPN6	0.234	0.491
DOK3	FCGR2B	0.093	0.67
DOK3	FCER1G	0	0.646

DOK3	LOC100138951	0	0.519
DOM3Z	NUDT3	0	0.48
DOM3Z	STK19	0	0.518
DOM3Z	DUSP11	0	0.823
DOM3Z	XRN1	0.634	0.937
DOM3Z	XRN2	0.925	0.989
DOPEY2	ETF1	0	0.411
DOPEY2	RNF213	0.077	0.425
DPYD	UPB1	0.218	0.971
DPYD	TKT	0.219	0.451
DPYD	TMEM120A	0	0.534
DPYD	LOC790312	0	0.943
DPYD	PNP	0	0.943
DPYD	UPP1	0	0.997
DRAM1	EPG5	0	0.489
DRAM1	NMI	0	0.427
DRAM1	MPEG1	0	0.421
DRAM1	GABARAPL1	0	0.425
DRAM1	SESN2	0	0.545
DTX3L	USP42	0	0.469
DTX3L	IFIH1	0	0.927
DTX3L	MX2	0	0.634
DTX3L	PSMB9	0	0.418
DTX3L	SUPT6H	0	0.513
DTX3L	IFIT2	0	0.402
DTX3L	DYSF	0	0.402
DTX3L	TRIM38	0	0.41
DTX3L	IRF9	0	0.481
DTX3L	EPSTI1	0	0.481
DTX3L	IFITM3	0	0.493
DTX3L	TRIM21	0	0.52
DTX3L	TAPBPL	0	0.537
DTX3L	UBE2D1	0.409	0.564
DTX3L	HERC6	0.046	0.569
DTX3L	XAF1	0	0.602
DTX3L	SRGN	0	0.62
DTX3L	STAT1	0.218	0.626
DTX3L	UBE2L6	0.112	0.65
DTX3L	RSAD2	0	0.7
DTX3L	PARP12	0	0.702
DTX3L	USP18	0	0.781
DTX3L	RNF213	0	0.823
DTX3L	MX1	0	0.826
DTX3L	ISG15	0	0.861
DTX3L	UBA7	0	0.886
DTX3L	PARP14	0.238	0.979
DTX3L	PARP9	0.761	0.998

DUSP11	PPM1M	0	0.4
DUSP11	PAPOLG	0	0.71
DUSP11	UBXN7	0.659	0.762
DUSP11	RNF144B	0	0.533
DUSP11	XRN2	0.119	0.768
DUSP11	XRN1	0.157	0.838
DUSP11	DUSP5	0	0.677
DUSP11	POLR2A	0.659	0.762
DUSP16	LRRK2	0.206	0.415
DUSP16	PPP1R3B	0.118	0.534
DUSP16	DUSP5	0	0.598
DUSP16	DUSP6	0.041	0.635
DUSP16	DUSP2	0	0.641
DUSP2	DUSP6	0	0.66
DUSP2	DUSP5	0	0.633
DUSP2	SNRK	0	0.522
DUSP5	NR4A2	0	0.41
DUSP5	JUN	0.133	0.44
DUSP5	FOS	0.152	0.591
DUSP5	DUSP6	0	0.597
DUSP5	PPARD	0.067	0.504
DUSP5	PTPN22	0.088	0.484
DUSP5	PTPN5	0.088	0.439
DUSP5	TNIP3	0	0.404
DUSP5	SNRK	0	0.602
DUSP6	PTPRE	0.088	0.625
DUSP6	JUN	0.103	0.433
DUSP6	FOS	0.119	0.477
DUSP6	RAF1	0.119	0.517
DUSP6	EGR2	0.055	0.427
DUSP6	MAPKAPK2	0	0.428
DUSP6	PTPN22	0.088	0.433
DUSP6	PTPN5	0.121	0.463
DUSP6	SPRED2	0	0.481
DUSP6	GRB2	0	0.481
DUSP6	SPRED1	0	0.497
DUSP6	KRAS	0.218	0.673
DYSF	KAT5	0	0.475
DYSF	RYR1	0	0.448
DYSF	MX2	0.078	0.404
DYSF	SRGN	0	0.414
DYSF	FAM65B	0.473	0.671
DYSF	MX1	0.078	0.419
DYSF	FLT4	0	0.517
DYSF	VEGFA	0	0.528
E2F2	KAT2B	0.165	0.509
E2F2	RABGEF1	0.07	0.608

E2F2	ELF1	0	0.622
E2F2	ETV3	0.067	0.509
E2F2	EZH2	0.143	0.521
E2F2	MEF2A	0	0.513
E2F2	STK40	0	0.517
E2F2	ELK4	0.067	0.413
E2F2	HDAC4	0.12	0.459
E2F2	TGFBR1	0.076	0.494
E2F2	MDM2	0.115	0.635
E2F2	RYBP	0.218	0.872
E2F2	E2F3	0	0.925
E2F3	SP3	0.093	0.416
E2F3	KAT2B	0.165	0.509
E2F3	EIF2C2	0.08	0.415
E2F3	TDRD7	0.151	0.446
E2F3	ELF1	0	0.622
E2F3	ETV3	0.067	0.506
E2F3	PIK3CA	0.135	0.409
E2F3	EZH2	0.143	0.541
E2F3	MEF2A	0	0.548
E2F3	SIRT1	0.158	0.593
E2F3	PTBP3	0	0.493
E2F3	HDAC4	0.12	0.521
E2F3	ELK4	0.067	0.409
E2F3	KRAS	0	0.454
E2F3	MDM2	0.115	0.704
E2F3	RYBP	0.218	0.761
ECE1	EDN1	0.078	0.814
ECE1	HYPK	0	0.632
EDEM1	PPP1R15A	0	0.61
EDEM1	WARS	0	0.423
EDEM1	6-Mar	0	0.426
EDEM1	HERPUD1	0	0.788
EDN1	IL1B	0	0.618
EDN1	JAK1	0	0.463
EDN1	NCF1	0	0.447
EDN1	JUN	0	0.783
EDN1	FOS	0	0.422
EDN1	SOCS1	0	0.447
EDN1	RAF1	0	0.644
EDN1	OLR1	0	0.401
EDN1	PLAU	0	0.47
EDN1	TLR4	0	0.454
EDN1	FFAR2	0	0.6
EDN1	KSR1	0	0.452
EDN1	IL10	0	0.457
EDN1	NOS2	0	0.458

EDN1	F3	0	0.647
EDN1	SERPINB2	0	0.411
EDN1	LOC281376	0	0.414
EDN1	MMP25	0	0.417
EDN1	PTX3	0	0.432
EDN1	STAT3	0	0.446
EDN1	ROCK1	0	0.464
EDN1	HBEGF	0	0.491
EDN1	VEGFC	0	0.498
EDN1	GRK6	0	0.499
EDN1	SELP	0	0.524
EDN1	ELN	0	0.526
EDN1	FRMD4A	0	0.527
EDN1	JAK3	0	0.538
EDN1	JUNB	0	0.546
EDN1	PPARD	0	0.599
EDN1	LOC529196	0.079	0.603
EDN1	PTGS2	0	0.626
EDN1	SLC9A3R1	0	0.633
EDN1	ICAM1	0	0.641
EDN1	SAG	0	0.646
EDN1	HCAR3	0.079	0.68
EDN1	IL6	0	0.68
EDN1	GHSR	0.079	0.691
EDN1	JAK2	0	0.694
EDN1	KRAS	0	0.697
EDN1	TNF	0	0.716
EDN1	SERPINE1	0	0.773
EDN1	VEGFA	0	0.776
EFHD2	LYN	0.054	0.567
EFHD2	ZBTB17	0	0.546
EFHD2	KIAA1033	0	0.414
EFHD2	LRRK2	0.211	0.703
EGR2	NAB1	0.157	0.766
EGR2	NR4A1	0.073	0.679
EGR2	NR4A2	0.073	0.499
EGR2	JUN	0.139	0.655
EGR2	FOS	0.077	0.764
EGR2	LITAF	0.041	0.401
EGR2	NAB2	0.479	0.974
EGR2	PIAS2	0.162	0.478
EGR2	EZH2	0.161	0.413
EGR2	JUNB	0.139	0.514
EGR2	KLF6	0	0.412
EGR2	IL2RB	0	0.409
EGR2	EGR3	0	0.926
EGR2	FOSL2	0.077	0.417

EGR2	GADD45B	0	0.4
EGR2	TNF	0.043	0.415
EGR3	NAB1	0.164	0.794
EGR3	NR4A1	0.073	0.655
EGR3	NR4A2	0.073	0.473
EGR3	JUN	0.139	0.729
EGR3	FOS	0.077	0.939
EGR3	NAB2	0.161	0.821
EGR3	JUNB	0.337	0.669
EGR3	FOSL2	0.171	0.479
EGR3	FOXJ2	0.093	0.527
EHBP1L1	TPM4	0.295	0.503
EHBP1L1	PTK2B	0.161	0.503
EHBP1L1	SDC4	0	0.404
EHBP1L1	ITGB7	0.125	0.422
EHBP1L1	ZYX	0.157	0.48
EHBP1L1	MARK3	0.067	0.495
EHBP1L1	PXN	0.297	0.559
EHBP1L1	RAB8B	0.493	0.687
EIF1	EIF4A1	0.538	0.94
EIF1	S100A8	0	0.4
EIF1	EIF4E3	0	0.442
EIF1	PPP1R15B	0	0.477
EIF1	ZNF668	0.054	0.498
EIF1	EIF6	0	0.505
EIF1	RPS9	0.69	0.749
EIF2C2	SETDB1	0.124	0.546
EIF2C2	STAU1	0.388	0.722
EIF2C2	NRDE2	0.075	0.418
EIF2C2	ZCCHC6	0.207	0.419
EIF2C2	RBM47	0.165	0.44
EIF2C2	SFPQ	0.055	0.501
EIF2C2	SIRT1	0.078	0.531
EIF2C2	RC3H2	0.407	0.55
EIF2C2	EZH2	0.124	0.573
EIF2C2	LRRK2	0.239	0.573
EIF2C2	UBXN7	0.485	0.58
EIF2C2	MPHOSPH8	0.462	0.602
EIF2C2	POLR2A	0.491	0.605
EIF2C2	QKI	0.242	0.63
EIF2C2	FAM107B	0	0.632
EIF2C2	XRN2	0.219	0.673
EIF2C2	FXR2	0.428	0.697
EIF2C2	ZNFX1	0.452	0.72
EIF2C2	XRN1	0.18	0.784
EIF2C2	MOV10	0.218	0.884
EIF2C2	FMR1	0.46	0.894

EIF4A1	SENP3	0.101	0.686
EIF4A1	XRN2	0.164	0.439
EIF4A1	TPT1	0.087	0.449
EIF4A1	PTBP3	0.044	0.509
EIF4A1	FMR1	0.159	0.514
EIF4A1	XRN1	0.164	0.526
EIF4A1	GTPBP4	0.226	0.528
EIF4A1	SRSF12	0.258	0.54
EIF4A1	TRA2A	0.258	0.551
EIF4A1	PSMB9	0.479	0.554
EIF4A1	NOM1	0.202	0.644
EIF4A1	ETF1	0.041	0.656
EIF4A1	EIF4E3	0.184	0.701
EIF4A1	EIF6	0.165	0.708
EIF4A1	RPS9	0.67	0.785
EIF4A1	MKNK1	0	0.786
EIF4E3	PPP4R2	0	0.426
EIF4E3	PPTC7	0	0.512
EIF4E3	SMG1	0.093	0.48
EIF4E3	MKNK1	0.258	0.518
EIF6	RPS9	0.266	0.62
EIF6	XRN1	0.068	0.443
EIF6	ETF1	0	0.487
EIF6	MOV10	0	0.581
EIF6	RCL1	0	0.598
EIF6	GTPBP4	0.925	0.974
ELANE	IL1B	0.055	0.474
ELANE	TLR4	0.053	0.495
ELANE	F3	0.125	0.478
ELANE	PADI4	0	0.484
ELANE	PLAUR	0.144	0.68
ELANE	IL6	0	0.452
ELANE	SERPING1	0.121	0.408
ELANE	MS4A3	0	0.58
ELANE	TCN1	0	0.445
ELANE	OLFM4	0	0.415
ELANE	TNF	0.055	0.555
ELANE	ELN	0.078	0.647
ELF1	JUNB	0.12	0.463
ELK3	JUN	0.184	0.406
ELK3	KRAS	0.093	0.461
ELK4	HIVEP2	0.058	0.408
ELK4	JUN	0.184	0.533
ELK4	FOS	0.078	0.405
ELK4	KCTD7	0.043	0.486
ELK4	ZNF263	0.058	0.531
ELK4	HIVEP3	0.058	0.423

ELK4	RC3H2	0	0.507
ELK4	RASA2	0	0.475
ELL	USPL1	0.164	0.575
ELL	NFKB2	0	0.43
ELMO2	RHOG	0.759	0.998
ELMO2	PTK2B	0	0.44
ELMO2	SH2B2	0	0.494
ELMO2	LYN	0.046	0.556
ELMO2	FGR	0.046	0.561
ELMO2	SLC4A7	0	0.568
ELMO2	HCK	0.084	0.642
ELN	HYAL2	0	0.506
ELN	IL1B	0	0.459
ELN	IL10	0	0.418
ELN	PTPRC	0	0.47
ELN	ICAM1	0	0.47
ELN	SERPINE1	0	0.48
ELN	VCAN	0	0.89
ELN	IL6	0	0.508
ELN	TGM2	0	0.431
ELN	MMP25	0.053	0.742
ELN	TNF	0	0.622
ELN	FCN1	0.093	0.506
ELN	VEGFA	0	0.543
ELOVL5	MBOAT1	0	0.587
EMP1	ICAM1	0	0.455
EMP3	MAP3K8	0	0.4
EMP3	KCNT1	0	0.447
EMP3	GSN	0	0.612
EMP3	STOM	0	0.673
EMR3	FCGR2C	0	0.433
EMR3	FCAR	0	0.45
EMR3	IGSF6	0	0.52
ENPP2	LPAR3	0.041	0.869
ENPP2	GPR132	0	0.418
ENPP2	GPCPD1	0	0.403
ENPP2	GPR87	0.041	0.584
ENPP2	PLA2G4A	0	0.731
ENPP2	GPR4	0	0.465
ENPP2	SDC4	0	0.45
3TAP0000001	FYB	0	0.538
3TAP0000001	PSMB8	0	0.567
3TAP0000001	VAV1	0	0.562
3TAP0000001	STAT6	0	0.554
3TAP0000001	PSMB9	0	0.552
3TAP0000001	LCP2	0	0.562
3TAP0000001	PTPRC	0.045	0.613

3TAP0000001	TAP1	0	0.402
3TAP0000005	LOC514257	0	0.407
ENTPD1	IL1B	0	0.412
ENTPD1	IL10	0	0.681
ENTPD1	GCH1	0	0.804
ENTPD1	F3	0	0.477
ENTPD1	ITGAL	0	0.552
ENTPD1	PDE4B	0	0.715
ENTPD1	PTPRC	0	0.598
ENTPD1	MOCS1	0	0.804
ENTPD1	PANX1	0	0.679
ENTPD1	IL6	0	0.409
ENTPD1	TNFRSF18	0	0.69
ENTPD1	TFPI2	0	0.641
ENTPD1	PARP14	0	0.517
ENTPD1	IL27	0	0.412
ENTPD1	IL7R	0	0.509
ENTPD1	IL2RA	0	0.466
ENTPD1	TNF	0	0.558
ENTPD1	SELL	0.042	0.568
ENTPD1	P2RY6	0	0.545
EOGT	RBPJ	0	0.432
EOGT	NPEPPS	0	0.515
EPC1	SMG1	0.306	0.423
EPC1	KIAA0232	0	0.531
EPC1	EZH2	0.162	0.585
EPC1	KAT8	0.511	0.645
EPC1	ING5	0.665	0.807
EPC1	KAT5	0.861	0.971
EPG5	RB1CC1	0	0.438
EPG5	WDR45	0	0.701
EPG5	VMP1	0	0.708
EPG5	GABARAPL1	0.06	0.431
EPG5	MED13	0	0.431
EPG5	RC3H2	0	0.499
EPG5	SMG1	0	0.525
EPG5	KDM5A	0	0.642
EPG5	SNAP29	0	0.842
EPSTI1	FYB	0	0.557
EPSTI1	KLHL5	0	0.476
EPSTI1	IFIH1	0	0.701
EPSTI1	MX2	0	0.813
EPSTI1	LCP2	0	0.593
EPSTI1	UBA7	0	0.519
EPSTI1	MOV10	0	0.595
EPSTI1	ISG15	0	0.512
EPSTI1	RSAD2	0	0.689

EPSTI1	PARP12	0	0.504
EPSTI1	PARP14	0	0.552
EPSTI1	USP18	0	0.831
EPSTI1	HERC6	0.046	0.405
EPSTI1	ZBP1	0	0.414
EPSTI1	MPEG1	0	0.438
EPSTI1	RNF213	0	0.515
EPSTI1	ZNFX1	0	0.536
EPSTI1	HERC5	0.046	0.565
EPSTI1	PARP9	0	0.606
EPSTI1	MX1	0	0.748
ERAP2	ICOSLG	0	0.405
ERAP2	FNBP1	0	0.406
ERAP2	PSMB8	0.046	0.423
ERAP2	SLC2A3	0.078	0.432
ERAP2	SLC2A1	0.078	0.432
ERAP2	TRIP10	0	0.438
ERAP2	LAP3	0.134	0.483
ERAP2	TAPBP	0	0.535
ERAP2	TAPBPL	0	0.551
ERAP2	LAMP1	0	0.635
ERAP2	GGT5	0	0.67
ERBB2IP	FRYL	0	0.433
ERBB2IP	SLC9A3R1	0.07	0.401
ERBB2IP	LGR6	0.402	0.402
ERBB2IP	THOC2	0.044	0.404
ERBB2IP	SF3B1	0.218	0.439
ERBB2IP	JMJD1C	0	0.442
ERBB2IP	STXBP3	0.055	0.444
ERBB2IP	PAN3	0	0.455
ERBB2IP	PARD3	0.093	0.471
ERBB2IP	WAC	0.157	0.489
ERBB2IP	MED12L	0	0.491
ERBB2IP	LRCH1	0.461	0.496
ERBB2IP	LMNB1	0.06	0.496
ERBB2IP	KRAS	0.336	0.522
ERBB2IP	NIPBL	0	0.838
ERBB2IP	NOD2	0.121	0.911
ESF1	NFE2L3	0	0.497
ESF1	TFIP11	0	0.442
ESF1	GSN	0	0.459
ESF1	TAPT1	0	0.461
ESF1	TRIP10	0	0.518
ESF1	TFB1M	0	0.565
ESF1	THOC2	0	0.593
ESF1	RIOK3	0	0.595
ESF1	NIPBL	0	0.608

ESF1	RCL1	0.453	0.667
ESF1	NOP9	0.12	0.8
ESF1	LTV1	0	0.811
ESF1	KRR1	0.184	0.847
ESF1	GTPBP4	0.452	0.889
ESF1	NOM1	0.762	0.894
ESYT2	GRAMD1A	0	0.422
ESYT2	MKNK1	0.053	0.453
ETF1	PSMA2	0	0.421
ETF1	RPS9	0.67	0.839
ETF1	PIAS2	0	0.522
ETF1	XRN1	0	0.458
ETF1	SMG9	0	0.635
ETF1	SARS	0	0.45
ETF1	MARK3	0	0.424
ETF1	TARS	0	0.493
ETF1	GTPBP4	0	0.794
ETF1	SMG1	0.92	0.969
ETF1	SNAPC1	0	0.513
ETF1	WDR4	0	0.756
ETF1	HRH2	0	0.515
ETNK1	PGS1	0.085	0.456
ETNK1	FAM46A	0	0.43
ETNK1	WWC2	0	0.4
ETNK1	ZDHHC2	0	0.425
ETNK1	GPR146	0	0.465
ETNK1	PROSC	0	0.469
ETNK1	IPMK	0.055	0.495
ETNK1	PIH1D1	0	0.777
ETNK1	GPCPD1	0	0.925
ETS2	HIVEP2	0.058	0.517
ETS2	HIVEP1	0.058	0.438
ETS2	IL4R	0	0.576
ETS2	JAK1	0.069	0.606
ETS2	JUN	0.478	0.891
ETS2	FOS	0.113	0.835
ETS2	RAF1	0.257	0.453
ETS2	NFKB2	0.342	0.444
ETS2	STAT6	0.064	0.66
ETS2	IL2RG	0	0.573
ETS2	IRF1	0	0.408
ETS2	KLF7	0.058	0.425
ETS2	HIVEP3	0.058	0.429
ETS2	MEF2A	0.136	0.438
ETS2	STAT5A	0.07	0.444
ETS2	STAT5B	0.07	0.454
ETS2	STAT3	0.043	0.476

ETS2	KLF10	0.058	0.478
ETS2	KLF5	0.058	0.49
ETS2	JAK3	0.069	0.493
ETS2	JAK2	0.069	0.517
ETS2	RFWD2	0.44	0.524
ETS2	STAT1	0.043	0.527
ETS2	NFKB1	0.342	0.542
ETS2	ETV6	0.418	0.57
ETS2	JUNB	0.184	0.599
ETS2	KRAS	0.352	0.756
ETV3	HIVEP2	0.058	0.468
ETV3	HIVEP1	0.058	0.54
ETV3	JUN	0.184	0.415
ETV3	MCEMP1	0	0.414
ETV3	JUNB	0.184	0.411
ETV3	TRIB1	0.095	0.415
ETV3	RNF13	0	0.457
ETV3	PHLDB1	0	0.482
ETV3	KLF7	0.058	0.483
ETV3	HIVEP3	0.058	0.51
ETV3	HDAC4	0.054	0.527
ETV3	SBNO2	0	0.614
ETV6	HIVEP2	0.055	0.417
ETV6	HIVEP1	0.055	0.4
ETV6	SOCS1	0.218	0.403
ETV6	RAF1	0.352	0.404
ETV6	TAL1	0	0.461
ETV6	KAT5	0.211	0.4
ETV6	EZH2	0.065	0.53
ETV6	NF1	0	0.43
ETV6	JAK2	0.112	0.667
ETV6	RARA	0.09	0.404
ETV6	KLF6	0.055	0.467
ETV6	TET2	0	0.582
ETV6	HIVEP3	0.055	0.517
ETV6	JAK3	0.112	0.412
ETV6	KRAS	0.418	0.627
ETV6	P2RY8	0	0.563
EVA1C	PDXK	0	0.412
EZH2	SETDB1	0	0.828
EZH2	STAU1	0	0.511
EZH2	PRDM1	0.113	0.501
EZH2	PHF1	0.867	0.977
EZH2	KDM4A	0.079	0.54
EZH2	VAV1	0.435	0.891
EZH2	FOS	0.079	0.418
EZH2	PCGF5	0.136	0.405

EZH2	KAT5	0.129	0.464
EZH2	HDAC11	0.159	0.413
EZH2	KMT2E	0.142	0.585
EZH2	PIK3CA	0.08	0.436
EZH2	MCL1	0	0.404
EZH2	NF1	0	0.41
EZH2	KAT8	0.129	0.413
EZH2	JAK3	0.072	0.416
EZH2	KLF5	0.161	0.438
EZH2	MPHOSPH8	0.218	0.438
EZH2	KDM3A	0.052	0.45
EZH2	LMNB1	0.042	0.496
EZH2	RYBP	0.069	0.504
EZH2	STAT5A	0.055	0.533
EZH2	SUV420H2	0	0.543
EZH2	HDAC4	0.159	0.548
EZH2	KRAS	0.052	0.553
EZH2	STAT5B	0.055	0.572
EZH2	H3F3A	0.218	0.575
EZH2	JAK2	0.113	0.588
EZH2	HIC1	0.161	0.597
EZH2	SUV420H1	0	0.601
EZH2	HIST3H2A	0.158	0.602
EZH2	HIST1H2AJ	0.157	0.603
EZH2	RELB	0.113	0.635
EZH2	TET2	0.043	0.756
EZH2	MDM2	0.211	0.769
EZH2	KDM5A	0.402	0.777
EZH2	SIRT1	0.274	0.858
EZH2	SNAI1	0.432	0.877
EZH2	KDM6B	0.468	0.878
EZH2	LOC100297725	0.218	0.904
EZH2	STAT3	0.113	0.912
EZH2	RELA	0.357	0.971
EZH2	JARID2	0.927	0.995
F12	RBPJ	0.294	0.439
F12	F3	0.125	0.659
F12	F13A1	0	0.493
F12	FGL2	0.158	0.523
F12	PLAUR	0.16	0.506
F12	SERPINE1	0.121	0.469
F12	MST1R	0.219	0.462
F12	SERPING1	0.121	0.862
F12	F5	0.119	0.637
F12	PSEN1	0.216	0.444
F12	KYNU	0	0.499
F12	KMO	0	0.506

F13A1	F5	0	0.405
F13A1	FCN1	0.157	0.454
F13A1	FGL2	0.157	0.483
F13A1	ITGA9	0	0.62
F3	IL1B	0	0.542
F3	PLAU	0.125	0.619
F3	TLR4	0	0.516
F3	IL10	0	0.467
F3	PTGS2	0	0.455
F3	ITGA2B	0	0.513
F3	FGL2	0	0.534
F3	VEGFA	0	0.539
F3	IL6	0	0.605
F3	TNF	0	0.69
F3	ICAM1	0	0.703
F3	TFPI2	0	0.76
F3	F5	0	0.775
F3	SERPINE1	0	0.82
F3	SELP	0	0.838
F5	RHBDF2	0	0.471
F5	SERPING1	0.129	0.423
FAIM3	YIPF4	0	0.634
FAIM3	ITM2C	0	0.749
FAIM3	MTMR7	0	0.499
FAIM3	MARCKSL1	0	0.583
FAM102A	FYB	0	0.616
FAM102A	FGR	0	0.478
FAM102A	MCTP2	0	0.507
FAM102A	PCMTD1	0	0.404
FAM102A	HCK	0	0.428
FAM102A	SKAP2	0.163	0.68
FAM105A	IL2RG	0	0.422
FAM105A	PIAS2	0	0.448
FAM105A	PTGS2	0	0.522
FAM105A	TARS	0	0.503
FAM105A	PTPN9	0	0.632
FAM107B	STOM	0	0.408
FAM107B	TNFAIP8	0	0.424
FAM107B	LPCAT2	0	0.519
FAM129A	MCTP2	0	0.42
FAM134C	MAP1LC3A	0.438	0.452
FAM134C	6-Mar	0	0.448
FAM13B	SIRT1	0.044	0.421
FAM13B	SLC4A7	0	0.657
FAM167B	PCDH17	0	0.47
FAM167B	FCRL6	0	0.528
FAM3B	IGSF10	0	0.469

FAM3B	SLC2A9	0	0.461
FAM43A	SCLY	0	0.619
FAM43A	RASSF2	0	0.516
FAM46A	PSMA2	0	0.422
FAM46A	SLAMF8	0	0.41
FAM46A	PHACTR2	0	0.414
FAM46A	IL13RA1	0	0.441
FAM46A	ZDHHC2	0	0.476
FAM46A	PROSC	0	0.491
FAM46A	USP32	0.042	0.597
FAM65B	RASGRP2	0	0.515
FAM65B	THEMIS2	0	0.405
FAM8A1	MBOAT1	0	0.683
FAM8A1	TRIM8	0	0.405
FAS	IL1B	0	0.458
FAS	PLCG2	0.08	0.406
FAS	JAK1	0.132	0.408
FAS	NAIP	0	0.532
FAS	TMBIM1	0.07	0.572
FAS	TNFRSF1A	0.119	0.962
FAS	STAT2	0	0.479
FAS	SLC16A12	0	0.416
FAS	PLK3	0	0.414
FAS	TLR4	0	0.434
FAS	TMBIM4	0.07	0.526
FAS	STAT6	0	0.489
FAS	RIPK1	0.214	0.863
FAS	IL10	0	0.593
FAS	ITGAL	0	0.46
FAS	IKBKB	0.055	0.685
FAS	FRMD4A	0.131	0.441
FAS	MAP3K5	0.435	0.839
FAS	PIK3CA	0	0.625
FAS	STAT5B	0	0.636
FAS	PTPRC	0.093	0.723
FAS	ICAM1	0	0.52
FAS	IKBKE	0.055	0.459
FAS	MAP2K3	0	0.621
FAS	IL18	0	0.402
FAS	TRAF1	0.067	0.413
FAS	IL2RA	0	0.438
FAS	JAK2	0.132	0.449
FAS	TNFSF14	0.21	0.452
FAS	IL7R	0	0.46
FAS	FCGR3A	0	0.461
FAS	STAT4	0	0.463
FAS	LAMP1	0	0.47

FAS	TLR9	0	0.475
FAS	IL2RB	0	0.511
FAS	SMPDL3B	0	0.512
FAS	IL6	0	0.529
FAS	IL15	0	0.532
FAS	FCGR2B	0	0.532
FAS	LYN	0.132	0.543
FAS	MLKL	0.093	0.559
FAS	HIPK3	0.211	0.565
FAS	MCL1	0	0.582
FAS	STAT1	0	0.606
FAS	RIPK3	0.093	0.612
FAS	TEC	0.132	0.615
FAS	STAT3	0	0.619
FAS	NMI	0	0.634
FAS	STAT5A	0	0.639
FAS	RIPK2	0.093	0.682
FAS	XIAP	0	0.703
FAS	SELL	0	0.705
FAS	TNFSF10	0.21	0.762
FAS	TNF	0.113	0.802
FAS	FASLG	0.174	0.968
FASLG	JUN	0.054	0.554
FASLG	TNFRSF1A	0.317	0.734
FASLG	RIPK1	0.093	0.737
FASLG	IL10	0	0.448
FASLG	NOS2	0	0.444
FASLG	MAP3K5	0	0.409
FASLG	PTPRC	0.053	0.456
FASLG	TRAF2	0.133	0.753
FASLG	JUNB	0.054	0.443
FASLG	TAB2	0.158	0.441
FASLG	RELA	0.136	0.502
FASLG	TNFSF10	0.055	0.682
FASLG	FNBP1	0	0.497
FASLG	JAK3	0.093	0.4
FASLG	TNFRSF1B	0.348	0.659
FASLG	TANK	0.246	0.535
FASLG	XIAP	0.157	0.539
FBRS	PCGF5	0.764	0.91
FBRS	JARID2	0	0.467
FBRS	RYBP	0.764	0.893
FBXL3	MIER1	0	0.424
FBXL3	STXBP3	0	0.425
FBXL3	SOCS3	0	0.499
FBXL3	LOC541180	0.046	0.651
FBXL3	SIK1	0.061	0.424

FBXL3	FBXO9	0.158	0.554
FBXL3	RNF19A	0.08	0.565
FBXL3	MYCBP2	0	0.479
FBXO38	SF3B1	0	0.4
FBXO38	SH3BGRL	0	0.559
FBXO38	KLF7	0.113	0.804
FBXO40	SOCS3	0	0.499
FBXO40	LOC541180	0	0.6
FBXO40	FBXO9	0	0.512
FBXO40	IKZF5	0	0.564
FBXO40	RFWD2	0	0.632
FBXO9	PHC2	0	0.592
FBXO9	HEXIM1	0	0.424
FBXO9	ZMIZ1	0	0.457
FBXO9	TRIM21	0.549	0.558
FCAR	RPS9	0	0.528
FCAR	SIRPB1	0	0.51
FCAR	ICAM3	0	0.468
FCAR	LOC617909	0	0.499
FCAR	FCGR2B	0.043	0.481
FCAR	FCGR2C	0.043	0.552
FCAR	FCER1G	0.113	0.584
FCAR	LENG8	0	0.711
FCER1G	HCLS1	0	0.677
FCER1G	RASGRP2	0	0.488
FCER1G	FYB	0	0.593
FCER1G	IL4R	0	0.472
FCER1G	PLCG2	0.078	0.798
FCER1G	GAB2	0.071	0.76
FCER1G	JUN	0	0.638
FCER1G	VAV1	0.093	0.822
FCER1G	FOS	0	0.649
FCER1G	RAF1	0.12	0.624
FCER1G	GRB2	0.051	0.769
FCER1G	IL10RA	0	0.404
FCER1G	PTK2B	0	0.601
FCER1G	TLR4	0	0.448
FCER1G	KSR1	0.12	0.456
FCER1G	IL2RG	0	0.662
FCER1G	TLR2	0	0.412
FCER1G	PRKCD	0.164	0.474
FCER1G	PIK3CA	0	0.927
FCER1G	LCP2	0	0.859
FCER1G	PLEK	0	0.429
FCER1G	SIRPB1	0	0.559
FCER1G	PTPRC	0.057	0.527
FCER1G	FGR	0.12	0.658

FCER1G	JAK2	0.174	0.416
FCER1G	JUNB	0	0.471
FCER1G	PLA2G4A	0	0.625
FCER1G	SH3BP2	0	0.583
FCER1G	IL2RB	0	0.504
FCER1G	KLRG2	0.046	0.807
FCER1G	LOC617909	0	0.561
FCER1G	LYN	0.12	0.966
FCER1G	INPP5D	0.053	0.817
FCER1G	PTPN6	0.057	0.707
FCER1G	IL2RA	0	0.578
FCER1G	JAK3	0.156	0.45
FCER1G	FCGR2B	0	0.857
FCER1G	FCGR3A	0.072	0.968
FCER1G	SELP	0.046	0.4
FCER1G	RASGEF1B	0	0.415
FCER1G	TNF	0	0.417
FCER1G	LAIR1	0	0.433
FCER1G	LAMP1	0	0.435
FCER1G	SELL	0.046	0.5
FCER1G	PTAFR	0	0.585
FCER1G	LAPTM5	0.055	0.596
FCER1G	TEC	0.12	0.645
FCER1G	LAT2	0	0.776
FCER1G	HCK	0.12	0.78
FCER1G	FCGR2C	0	0.917
FCER1G	NCR1	0.123	0.98
FCGR2B	RHOG	0	0.502
FCGR2B	MYD88	0	0.481
FCGR2B	IL1B	0	0.485
FCGR2B	TAGLN2	0	0.426
FCGR2B	RAF1	0.087	0.61
FCGR2B	GRB2	0.051	0.571
FCGR2B	TLR4	0	0.677
FCGR2B	IL10	0	0.756
FCGR2B	ITGAL	0	0.603
FCGR2B	TLR2	0	0.608
FCGR2B	LOC506364	0	0.581
FCGR2B	FGL2	0	0.776
FCGR2B	PTPRC	0.083	0.944
FCGR2B	ICAM1	0	0.541
FCGR2B	FGR	0.12	0.413
FCGR2B	IL6	0	0.543
FCGR2B	IL2RB	0	0.431
FCGR2B	TLR9	0	0.664
FCGR2B	IL15	0	0.515
FCGR2B	IL7R	0	0.438

FCGR2B	LYN	0.435	0.833
FCGR2B	INPP5D	0.674	0.953
FCGR2B	IL2RA	0	0.485
FCGR2B	IL18	0	0.435
FCGR2B	FCGR3A	0	0.449
FCGR2B	LAMP1	0	0.484
FCGR2B	HCK	0.12	0.495
FCGR2B	PTAFR	0	0.562
FCGR2B	NCR1	0.043	0.601
FCGR2B	FCGR2C	0.52	0.683
FCGR2B	TNF	0	0.727
FCGR2B	LOC100138951	0	0.743
FCGR2B	SELL	0	0.768
FCGR2C	IL1B	0	0.548
FCGR2C	TAGLN2	0	0.405
FCGR2C	RAF1	0.087	0.524
FCGR2C	TLR4	0	0.54
FCGR2C	SIRPB2	0	0.414
FCGR2C	IL10	0	0.575
FCGR2C	ITGAL	0	0.446
FCGR2C	IL2RG	0	0.431
FCGR2C	SLAMF1	0	0.429
FCGR2C	TLR2	0	0.507
FCGR2C	ITGA2B	0	0.45
FCGR2C	PTX3	0	0.505
FCGR2C	FGL2	0	0.556
FCGR2C	PTPRC	0.083	0.679
FCGR2C	IL6	0	0.503
FCGR2C	TLR9	0	0.59
FCGR2C	IL15	0	0.537
FCGR2C	IGSF6	0	0.421
FCGR2C	IL7R	0	0.429
FCGR2C	LYN	0.315	0.667
FCGR2C	INPP5D	0.474	0.898
FCGR2C	PTPN6	0.184	0.458
FCGR2C	IL2RA	0	0.57
FCGR2C	FCGR3A	0	0.894
FCGR2C	TNF	0	0.541
FCGR2C	SELL	0	0.524
FCGR2C	NCR1	0.043	0.518
FCGR2C	HCK	0.12	0.519
FCGR3A	IL1B	0	0.472
FCGR3A	VAV1	0	0.499
FCGR3A	TLR4	0	0.547
FCGR3A	IL10	0	0.671
FCGR3A	ITGAL	0.042	0.663
FCGR3A	SIRPA	0	0.496

FCGR3A	IL2RG	0	0.457
FCGR3A	TLR2	0	0.532
FCGR3A	PIK3CA	0.043	0.588
FCGR3A	LCP2	0.055	0.494
FCGR3A	PTPRC	0.072	0.836
FCGR3A	ICAM1	0	0.439
FCGR3A	PLA2G4A	0	0.483
FCGR3A	IL6	0	0.452
FCGR3A	IL2RB	0	0.435
FCGR3A	IL15	0	0.639
FCGR3A	IL7R	0	0.479
FCGR3A	LYN	0.079	0.858
FCGR3A	FUT4	0	0.42
FCGR3A	IL18	0	0.433
FCGR3A	LAMP1	0	0.642
FCGR3A	LOC100138951	0	0.667
FCGR3A	TNF	0	0.674
FCGR3A	NCR1	0.07	0.698
FCGR3A	SELL	0	0.793
FCGR3A	HCK	0.079	0.928
FCN1	PSMA2	0	0.499
FCN1	LOC407171	0.055	0.413
FCN1	FFAR2	0.093	0.466
FCN1	PTX3	0.538	0.826
FCN1	FGR	0.045	0.468
FCN1	S100A8	0.043	0.606
FCN1	TAPBPL	0	0.663
FCN1	SERPING1	0.07	0.433
FCN1	SAT1	0	0.515
FCN1	TREM1	0	0.562
FCN1	SBNO2	0	0.4
FCN1	SDC4	0	0.514
FCN1	S100A12	0.055	0.722
FCRL5	SNX20	0	0.57
FCRL5	PTPN22	0.046	0.437
FCRL6	PLCG2	0.045	0.408
FCRL6	METRNL	0	0.587
FCRL6	TIAM2	0	0.416
FCRL6	PLA2G4A	0	0.5
FCRL6	SLAMF8	0	0.565
FCRL6	MS4A3	0	0.471
FCRL6	PIK3AP1	0	0.523
FFAR2	PTGS2	0	0.42
FFAR2	TNF	0.042	0.421
FFAR2	LPIN2	0	0.466
FFAR2	IL10	0	0.468
FFAR2	MMP25	0	0.512

FFAR2	GPR84	0	0.762
FGD2	TCIRG1	0	0.426
FGD2	RHOG	0.157	0.467
FGD2	TLE4	0	0.47
FGD2	TAGAP	0	0.444
FGD2	USP15	0	0.494
FGD3	RHOG	0.157	0.931
FGD3	PPP1R16B	0.052	0.549
FGD3	RASGEF1B	0.39	0.41
FGL2	PSMA2	0	0.516
FGL2	FYB	0	0.621
FGL2	LCP2	0	0.542
FGL2	SERPING1	0.07	0.466
FGL2	MPEG1	0	0.495
FGL2	PTPRC	0.08	0.588
FGR	PSMA2	0.043	0.501
FGR	HCLS1	0.166	0.508
FGR	RASGRP2	0.161	0.479
FGR	IL1B	0.054	0.403
FGR	FYB	0.198	0.533
FGR	IL4R	0.136	0.447
FGR	PLCG2	0.138	0.729
FGR	NCF1	0.079	0.452
FGR	VAV1	0.093	0.629
FGR	STAT2	0.236	0.507
FGR	RAF1	0.175	0.496
FGR	GRB2	0.257	0.504
FGR	IL10RA	0.205	0.564
FGR	PTK2B	0.219	0.945
FGR	LOC515976	0.051	0.516
FGR	STAT6	0.236	0.544
FGR	IL10	0.054	0.401
FGR	IL2RG	0.133	0.443
FGR	SLA	0.065	0.713
FGR	SOCS3	0.207	0.448
FGR	PRKCD	0.131	0.69
FGR	PIK3CA	0.129	0.748
FGR	LCP2	0.209	0.713
FGR	STAT5B	0.236	0.609
FGR	PLEK	0	0.52
FGR	PTPRC	0.133	0.459
FGR	ITGB7	0.122	0.403
FGR	SERPINE1	0	0.418
FGR	PTPN22	0.139	0.427
FGR	IFNAR1	0.218	0.428
FGR	STAT1	0.236	0.435
FGR	IL2RB	0.175	0.456

FGR	SELL	0.06	0.462
FGR	PLA2G4A	0.127	0.471
FGR	S100A12	0.042	0.471
FGR	S100A8	0.042	0.475
FGR	PTPN6	0.219	0.498
FGR	MST1R	0.225	0.514
FGR	TEC	0	0.524
FGR	STAT5A	0.236	0.597
FGR	KRAS	0.141	0.677
FGR	LYN	0.093	0.695
FGR	PIK3R5	0	0.708
FGR	PIK3R6	0	0.714
FGR	PXN	0.099	0.74
FGR	STAT3	0.236	0.781
FGR	HCK	0	0.818
FITM1	LPIN2	0	0.499
FITM1	GPR4	0	0.477
FLCN	PRKAA1	0.164	0.498
FLCN	FNIP1	0.763	0.999
FLCN	PRKAB1	0	0.416
FLCN	IPMK	0	0.4
FLCN	MOB3C	0	0.404
FLCN	MOB3A	0	0.512
FLCN	SESN2	0	0.513
FLCN	SEH1L	0	0.701
FLOT1	PSMB8	0	0.457
FLOT1	RAF1	0.052	0.587
FLOT1	S100A9	0	0.508
FLOT1	KSR1	0.052	0.421
FLOT1	TSPAN2	0	0.47
FLOT1	VPS4B	0	0.563
FLOT1	LAMP1	0.103	0.612
FLOT1	STOM	0	0.613
FLOT1	FLOT2	0.848	0.977
FLOT2	SUPT6H	0	0.408
FLOT2	STOML1	0	0.448
FLOT2	STOM	0	0.62
FLT4	RET	0.456	0.577
FLT4	PLCG2	0.395	0.718
FLT4	RAF1	0.16	0.598
FLT4	GRB2	0.457	0.942
FLT4	PTK2B	0.206	0.622
FLT4	PTPN1	0.106	0.571
FLT4	NOS2	0	0.495
FLT4	PIK3CA	0.334	0.914
FLT4	PTPRC	0.106	0.51
FLT4	PTPN2	0.106	0.571

FLT4	ITGA5	0.08	0.748
FLT4	VEGFC	0.929	0.999
FLT4	ITGA9	0.054	0.705
FLT4	PXN	0.055	0.733
FLT4	ITGAV	0.06	0.582
FLT4	STAT3	0.165	0.463
FLT4	PTPRJ	0.157	0.723
FLT4	ROCK1	0.125	0.505
FLT4	TEC	0.463	0.53
FLT4	KRAS	0.215	0.56
FLT4	SDC4	0	0.596
FLT4	VEGFA	0.661	0.993
FMNL1	FMNL3	0.438	0.478
FMNL1	FNBP1	0.052	0.511
FMNL1	OSBPL2	0	0.524
FMNL3	SAMD4B	0	0.497
FMNL3	SIRPB2	0	0.453
FMNL3	ROCK1	0.077	0.403
FMNL3	FNBP1	0.052	0.413
FMNL3	ZMIZ2	0	0.484
FMNL3	VASP	0	0.523
FMR1	STAU1	0.234	0.631
FMR1	FXR2	0.923	0.984
FMR1	FUS	0.218	0.578
FMR1	NXF1	0	0.42
FMR1	XRN1	0	0.476
FMR1	MYCBP2	0.307	0.403
FMR1	ROCK1	0.173	0.437
FMR1	MOV10	0.109	0.596
FMR1	PQBP1	0.411	0.606
FNBP1	RHOG	0.206	0.42
FNBP1	NPEPPS	0	0.406
FNBP1	SRGAP2	0	0.565
FNBP1	SLC2A1	0.056	0.411
FNBP1	SLC2A3	0.056	0.411
FNBP1	PSTPIP2	0.097	0.482
FNBP1	PSTPIP1	0.097	0.532
FNBP1	GABARAPL1	0.42	0.534
FNBP1	FNBP4	0	0.747
FNBP4	SF3B1	0	0.745
FNBP4	HNRNPH1	0	0.518
FNBP4	KIAA0226L	0	0.515
FNBP4	SRGAP2	0	0.412
FNBP4	PPTC7	0	0.557
FNBP4	LAT2	0	0.465
FNBP4	MYSM1	0	0.497
FNBP4	SRRM2	0	0.524

FNIP1	PRKAA1	0.113	0.554
FNIP1	SLCO4A1	0	0.419
FNIP1	OGFR	0	0.431
FNIP1	MAP3K5	0.462	0.461
FNIP1	PRKAB1	0.113	0.474
FNIP1	SEH1L	0	0.489
FNIP1	GTPBP4	0	0.507
FNIP1	XRN1	0	0.516
FNIP1	SNAPC1	0	0.677
FOS	NR4A1	0.129	0.811
FOS	RET	0	0.492
FOS	KAT2B	0.114	0.5
FOS	IL1B	0	0.58
FOS	NFE2	0.115	0.464
FOS	NR4A2	0.129	0.626
FOS	LPAR3	0	0.693
FOS	JUN	0.969	0.999
FOS	SERPINE1	0	0.401
FOS	TGFBR1	0.067	0.401
FOS	HDAC4	0.17	0.405
FOS	RARA	0.131	0.411
FOS	HBEGF	0	0.412
FOS	VEGFA	0.093	0.419
FOS	MDM2	0.162	0.421
FOS	NFKB2	0.064	0.432
FOS	SMAD7	0.118	0.436
FOS	JAK2	0.067	0.439
FOS	GHSR	0	0.45
FOS	NF1	0.079	0.454
FOS	IER3	0	0.457
FOS	POLR2A	0.113	0.458
FOS	IRF5	0	0.46
FOS	GADD45B	0	0.471
FOS	STAT2	0.121	0.473
FOS	TRAF3	0.253	0.474
FOS	IL10	0.093	0.478
FOS	STAT6	0.121	0.484
FOS	TLR4	0.046	0.488
FOS	MAFF	0.136	0.507
FOS	TEC	0.067	0.537
FOS	IRF7	0	0.538
FOS	GTF2B	0	0.542
FOS	NFKB1	0.078	0.554
FOS	KLF6	0.077	0.559
FOS	STAT4	0.121	0.564
FOS	IL1R2	0.067	0.567
FOS	IRF2	0	0.571

FOS	SOCS3	0	0.58
FOS	SIRT1	0.211	0.588
FOS	KLF10	0.077	0.589
FOS	PTGS2	0	0.596
FOS	POR	0	0.623
FOS	IRF1	0	0.627
FOS	KRAS	0.117	0.655
FOS	RFWD2	0.666	0.666
FOS	LYN	0.067	0.669
FOS	IRF9	0	0.676
FOS	STK40	0.687	0.687
FOS	STAT5A	0.121	0.701
FOS	STAT5B	0.121	0.71
FOS	ZFP36	0	0.723
FOS	NFE2L2	0.115	0.763
FOS	TCF7L2	0.459	0.795
FOS	IL6	0	0.84
FOS	TNF	0	0.853
FOS	PRKCB	0	0.859
FOS	STAT1	0.515	0.864
FOS	STAT3	0.219	0.864
FOS	RELA	0.416	0.881
FOS	FOSL2	0	0.929
FOS	JUNB	0.784	0.999
FOSL2	NR4A1	0.129	0.499
FOSL2	KAT2B	0.114	0.453
FOSL2	NFE2	0.115	0.434
FOSL2	JUN	0.764	0.998
FOSL2	STAT6	0.121	0.415
FOSL2	IRF2	0	0.451
FOSL2	JUNB	0.764	0.996
FOSL2	RELA	0.157	0.574
FOSL2	IL6	0	0.514
FOSL2	KLF6	0.077	0.469
FOSL2	STK40	0.763	0.767
FOSL2	NFE2L2	0.124	0.43
FOSL2	MAFF	0.136	0.444
FOSL2	STAT3	0.121	0.511
FOSL2	TRIB1	0.539	0.554
FOSL2	IRF7	0	0.408
FOSL2	STAT1	0.121	0.419
FOSL2	IRF1	0	0.427
FOSL2	RFWD2	0.438	0.438
FOSL2	TNF	0	0.47
FOSL2	SIPA1L1	0	0.514
FOXJ2	SENP2	0.052	0.428
FOXJ2	SIRT1	0.271	0.418

FOXJ2	U2AF1L4	0	0.47
FOXN3	KCNJ15	0	0.512
FOXN3	RARG	0.12	0.408
FOXN3	RARA	0.12	0.408
FOXN3	SIRT1	0.271	0.523
FOXN3	PKNOX1	0.057	0.403
FOXN3	RFWD2	0.073	0.403
FOXRED1	ZNF263	0	0.52
FOXS1	NFE2L3	0	0.406
FOXS1	MX2	0.051	0.661
FOXS1	SIRT1	0.271	0.407
FOXS1	TAP1	0	0.496
FOXS1	UBA7	0.075	0.596
FOXS1	USP18	0.089	0.681
FOXS1	ZNFX1	0.048	0.694
FRAT1	RGS10	0.053	0.44
FRAT1	RGS2	0.053	0.44
FRAT1	FRAT2	0	0.828
FRAT2	XRN2	0	0.447
FRAT2	IKZF5	0	0.41
FREM1	HIVEP2	0	0.449
FREM1	ITGA5	0	0.554
FREM1	HIVEP3	0	0.42
FREM1	RNF41	0	0.451
FRG1	SRRM2	0.46	0.471
FRG1	SUV420H1	0	0.616
FRMD4A	NFE2L3	0	0.597
FRMD4A	PTK2B	0.079	0.46
FRMD4A	PARD3	0.165	0.457
FRMD4A	SLC16A7	0	0.534
FRYL	MAP3K8	0.212	0.433
FRYL	MYSM1	0	0.462
FRYL	GALNT11	0	0.487
FRYL	MYCBP2	0	0.514
FRYL	NIPBL	0	0.515
FRYL	STK4	0	0.523
FRYL	TET2	0	0.555
FRYL	SMG1	0.042	0.59
FRYL	STK38L	0.663	0.849
FUS	RBM47	0.656	0.719
FUS	PSPC1	0.464	0.668
FUS	FXR2	0.218	0.443
FUS	RELA	0.119	0.421
FUS	TAF5L	0.438	0.447
FUS	MOV10	0.113	0.454
FUS	HNRNPH1	0.317	0.456
FUS	SRSF12	0.214	0.539

FUS	UBXN7	0.39	0.557
FUS	OPTN	0.053	0.579
FUS	SFPQ	0.741	0.879
FUT4	PTPRC	0.045	0.543
FUT4	ST3GAL3	0	0.663
FUT4	SELPLG	0.16	0.412
FUT4	SELL	0.042	0.469
FUT4	SELP	0.078	0.77
FUT4	ST6GALNAC6	0	0.621
FUT4	LOC100138951	0	0.646
FXR2	STAU1	0.218	0.404
FXR2	PQBP1	0.403	0.469
FXR2	TRAF2	0.053	0.469
FXR2	NFIX	0	0.612
FXR2	KDM6B	0.071	0.647
FYB	TTC33	0	0.514
FYB	ZYX	0	0.412
FYB	KDM4A	0	0.414
FYB	TEC	0.198	0.419
FYB	ITGAL	0	0.421
FYB	PTK2B	0	0.422
FYB	IL7R	0	0.429
FYB	INPP5D	0.115	0.458
FYB	IGSF6	0	0.462
FYB	PTPN12	0	0.525
FYB	LYN	0.198	0.574
FYB	HCK	0.198	0.576
FYB	P2RY8	0	0.615
FYB	IL2RB	0	0.631
FYB	VAV1	0	0.639
FYB	MPEG1	0	0.659
FYB	PTPN22	0	0.708
FYB	GRB2	0.142	0.734
FYB	PTPN6	0	0.749
FYB	VASP	0.121	0.781
FYB	PLEK	0	0.786
FYB	ITGA5	0	0.8
FYB	PTPRC	0	0.866
FYB	SKAP2	0.418	0.869
FYB	LCP2	0.84	0.999
FZR1	REC8	0.073	0.488
FZR1	PLK3	0.45	0.867
FZR1	MAD2L2	0.432	0.912
GAB2	IL4R	0	0.412
GAB2	PLCG2	0.113	0.929
GAB2	PTPN9	0.154	0.405
GAB2	PLXNA4	0.055	0.418

GAB2	PLXNA1	0.055	0.436
GAB2	TARM1	0	0.465
GAB2	INPP5D	0.078	0.472
GAB2	PIK3AP1	0	0.493
GAB2	STAT5A	0	0.529
GAB2	STAT5B	0	0.544
GAB2	RAP1B	0.044	0.561
GAB2	IL6	0	0.623
GAB2	JAK3	0.054	0.654
GAB2	JAK1	0.054	0.676
GAB2	IL2RA	0	0.699
GAB2	MST1R	0.114	0.706
GAB2	KRAS	0.07	0.709
GAB2	RAPGEF1	0	0.715
GAB2	JAK2	0.054	0.718
GAB2	TRAF2	0	0.802
GAB2	PTPN6	0.467	0.803
GAB2	HCK	0.054	0.934
GAB2	PIK3CA	0.075	0.942
GAB2	LYN	0.113	0.942
GAB2	GRB2	0.95	0.999
GAB3	GRB2	0.113	0.711
GAB3	PLEK	0	0.435
GAB3	MEF2A	0	0.423
GABARAPL1	RB1CC1	0.657	0.873
GABARAPL1	TUBA4A	0.294	0.518
GABARAPL1	WDR45	0	0.582
GABARAPL1	GOSR1	0.093	0.423
GABARAPL1	TP53INP2	0.153	0.865
GABARAPL1	VMP1	0	0.418
GABARAPL1	SIRT1	0.219	0.528
GABARAPL1	ISG15	0.124	0.455
GABARAPL1	OPTN	0.347	0.933
GABARAPL1	LYST	0.418	0.493
GABARAPL1	SNAP29	0	0.414
GABARAPL1	LAMP1	0.111	0.57
GABARAPL1	R3HDM4	0.407	0.407
GABARAPL1	LMNB1	0.084	0.561
GADD45B	NR4A1	0	0.512
GADD45B	PPP1R15A	0	0.43
GADD45B	JUN	0	0.543
GADD45B	IFI35	0	0.402
GADD45B	SERTAD1	0	0.436
GADD45B	MAP2K3	0.158	0.693
GADD45B	IER3	0	0.445
GADD45B	JUNB	0	0.411
GALC	UGCG	0	0.922

GALNT11	PRODH	0	0.46
GANC	LAP3	0.218	0.649
GANC	GGT5	0	0.409
GANC	SIDT2	0	0.632
GANC	HK2	0	0.698
GBP2	PSMB8	0.046	0.557
GBP2	GBP4	0.055	0.638
GBP2	IFI35	0	0.523
GBP2	IFIH1	0.131	0.593
GBP2	MX2	0	0.427
GBP2	IFIT3	0.042	0.566
GBP2	IRF2	0	0.417
GBP2	OAS2	0	0.512
GBP2	ISG15	0.045	0.555
GBP2	RSAD2	0	0.606
GBP2	PARP14	0	0.472
GBP2	USP18	0	0.422
GBP2	LOC512486	0	0.635
GBP2	MX1	0	0.629
GBP2	IRF1	0	0.705
GBP2	IRF9	0	0.465
GBP2	LOC507055	0.055	0.7
GBP2	IFIT2	0.042	0.577
GBP2	ZBP1	0	0.435
GBP2	ISG20	0	0.41
GBP2	TRIM21	0	0.415
GBP2	IRF7	0.12	0.572
GBP2	STAT1	0	0.66
GBP4	PSMB8	0.046	0.457
GBP4	STAT2	0	0.4
GBP4	SERPING1	0	0.406
GBP4	ZBP1	0	0.412
GBP4	TRIM21	0	0.417
GBP4	IRF2	0	0.418
GBP4	TNFSF10	0	0.441
GBP4	IFITM3	0	0.446
GBP4	IRF9	0	0.463
GBP4	ISG20	0	0.498
GBP4	LOC512486	0.055	0.518
GBP4	PARP14	0	0.53
GBP4	HERC5	0.055	0.585
GBP4	USP18	0	0.616
GBP4	IFI35	0	0.618
GBP4	IRF7	0.126	0.626
GBP4	OAS2	0	0.629
GBP4	IFIT2	0.042	0.63
GBP4	MX2	0	0.64

GBP4	STAT1	0	0.644
GBP4	ISG15	0.045	0.681
GBP4	IFIT3	0.042	0.7
GBP4	MX1	0	0.708
GBP4	IRF1	0	0.726
GBP4	RSAD2	0	0.747
GBP4	IFIH1	0.093	0.764
GBP5	NLRP3	0	0.762
GBP5	IFI35	0	0.404
GBP5	IFIH1	0.06	0.716
GBP5	MX2	0	0.609
GBP5	SH3PXD2B	0	0.412
GBP5	IFIT3	0.042	0.481
GBP5	PHF11	0	0.423
GBP5	ISG15	0.045	0.562
GBP5	SP110	0	0.431
GBP5	MX1	0	0.444
GBP5	HERC6	0.055	0.471
GBP5	ISG20	0	0.522
GBP5	USP18	0	0.532
GBP5	IRF7	0.093	0.545
GBP5	STAT1	0	0.569
GBP5	IFIT2	0.042	0.641
GBP5	IRF1	0	0.65
GBP5	RSAD2	0	0.718
GBP5	LOC511531	0.043	0.788
GBP6	IFI35	0	0.428
GBP6	IFIT3	0.042	0.618
GBP6	ISG15	0.045	0.513
GBP6	RSAD2	0	0.566
GBP6	USP18	0	0.413
GBP6	ISG20	0	0.424
GBP6	MX1	0	0.44
GBP6	STAT1	0	0.446
GBP6	IRF1	0	0.471
GBP6	IFIT2	0.042	0.562
GCH1	PNKD	0	0.419
GCH1	SOD2	0	0.538
GCH1	PNP	0	0.41
GCH1	RFK	0	0.478
GCH1	XDH	0	0.609
GCH1	MOCS1	0	0.956
GDI1	RAB3D	0.258	0.424
GDI1	RABGEF1	0.08	0.473
GDI1	RAB8B	0.675	0.829
GDI1	LRRK2	0.087	0.428
GDI1	RAB3GAP1	0	0.477

GGT5	LAP3	0	0.934
GGT5	GLS	0	0.803
GGT5	TTYH2	0	0.406
GGT5	NPEPPS	0	0.593
GGT5	GPX3	0	0.721
GHSR	SAG	0	0.472
GJB2	PANX1	0	0.83
GLS	TKT	0	0.431
GLS	SLC7A5	0	0.536
GLS	KYNU	0	0.414
GLS	KRAS	0.046	0.422
GLS	SLC16A3	0	0.489
GLS	SLC38A2	0	0.52
GLS	HK2	0	0.537
GLS	SLC1A2	0	0.556
GLS	SLC1A5	0	0.871
GMEB1	PKNOX1	0	0.461
GNG4	PRKAA1	0	0.6
GNG4	KCNJ15	0.116	0.526
GNG4	PLCG2	0	0.735
GNG4	PTGER2	0.065	0.65
GNG4	NFE2L3	0	0.418
GNG4	RRAD	0.042	0.469
GNG4	KCNK17	0	0.589
GNG4	PRKAB1	0	0.6
GNG4	PDCL	0.055	0.614
GNG4	PREX1	0.107	0.627
GNG4	KRAS	0.042	0.667
GNG4	PIK3R5	0.046	0.675
GNG4	PIK3CA	0.044	0.721
GNG4	PIK3R6	0.044	0.742
GNG4	PRKCB	0.086	0.77
GNG4	LPAR3	0.065	0.825
GOLGA7	USP3	0	0.585
GOLGA7	SPTSSA	0	0.756
GOLGA7	ZDHHC18	0.153	0.473
GOLGA7	ZDHHC2	0.12	0.506
GOSR1	TMEM165	0	0.758
GOSR1	SEC24B	0.087	0.432
GOSR1	STX11	0.296	0.469
GOSR1	MDM2	0	0.476
GOSR1	UGCG	0	0.522
GOSR1	TAPT1	0	0.552
GOSR1	SNAP29	0.218	0.775
GOSR1	STX6	0.756	0.919
GPBP1	RRAD	0	0.403
GPBP1	PLEKHA4	0	0.424

GPBP1	GTF2B	0.174	0.525
GPBP1	PNRC1	0	0.586
GPBP1	TNIP3	0	0.632
GPR132	GPR65	0	0.429
GPR132	P2RY8	0	0.43
GPR141	LOC518134	0	0.478
GPR146	MS4A7	0	0.668
GPR146	NMUR2	0	0.468
GPR146	PARP11	0	0.47
GPR31	GPR84	0	0.405
GPR4	ZNF408	0	0.47
GPR65	PTPN12	0.042	0.475
GPR65	LCP2	0	0.633
GPR65	PLEK	0	0.581
GPR65	PTPRC	0.045	0.518
GPR65	RNF13	0.041	0.4
GPR65	LYST	0.051	0.475
GPR65	IGSF6	0	0.63
GPR65	PTPN22	0.042	0.7
GPR65	IL7R	0	0.417
GPR65	PSTPIP1	0	0.599
GPR65	TAGAP	0	0.45
GPR65	PSTPIP2	0	0.443
GPR65	P2RY8	0	0.618
GPR77	ZSWIM4	0	0.4
GPR77	TLR4	0	0.426
GPR77	PLEK	0	0.434
GPR77	TREM1	0	0.41
GPR77	IGSF6	0	0.588
GPR77	SAG	0.055	0.65
GPR77	MPEG1	0	0.47
GPR84	IRG1	0	0.493
GPR84	SIRPB1	0	0.499
GPR84	RIN2	0	0.403
GPR84	INPP5D	0	0.457
GPR84	LOC617909	0	0.512
GPR84	PTAFR	0	0.535
GPR84	HCAR3	0	0.659
GPR87	LPAR3	0	0.775
GPR87	RNF144B	0	0.633
GPR87	MOCS1	0	0.412
GPR87	NIPAL4	0	0.493
GPR97	MMP25	0	0.408
GPR97	RALGDS	0	0.4
GPX3	SOD2	0.399	0.925
GPX3	PRDX5	0.12	0.528
GPX3	SELK	0	0.74

GRAMD1A	IL6R	0	0.465
GRAMD4	SLCO3A1	0	0.416
GRAMD4	INPP1	0	0.469
GRAMD4	SLC37A1	0	0.51
GRAMD4	ZNF408	0	0.535
GRAMD4	SWT1	0	0.663
GRB2	RET	0.663	0.975
GRB2	RASGRP2	0.398	0.607
GRB2	IL4R	0	0.655
GRB2	PLCG2	0.764	0.904
GRB2	PTPRE	0.537	0.868
GRB2	JAK1	0.257	0.931
GRB2	PTPN12	0.427	0.764
GRB2	JUN	0	0.473
GRB2	TNFRSF1A	0.218	0.648
GRB2	VAV1	0.924	0.978
GRB2	STAT2	0.053	0.541
GRB2	SOCS1	0.218	0.906
GRB2	RAF1	0.163	0.665
GRB2	REM2	0.133	0.402
GRB2	RRAD	0.133	0.402
GRB2	SH3BP2	0.113	0.402
GRB2	STOML1	0	0.404
GRB2	STOML3	0	0.404
GRB2	STOM	0	0.404
GRB2	GSN	0.045	0.405
GRB2	ITGA2B	0.203	0.432
GRB2	ROCK1	0.163	0.433
GRB2	TESK1	0.163	0.435
GRB2	PLXNA4	0.159	0.439
GRB2	PLXNA1	0.159	0.439
GRB2	ITGAV	0.07	0.445
GRB2	ITGA5	0.07	0.465
GRB2	SMG1	0.173	0.483
GRB2	SIRPA	0.08	0.485
GRB2	STAT4	0.053	0.49
GRB2	LRRK2	0.314	0.498
GRB2	PTPRJ	0.165	0.499
GRB2	PTPN5	0.258	0.503
GRB2	RAP1B	0.133	0.515
GRB2	TNF	0	0.521
GRB2	STAT5A	0.053	0.526
GRB2	SHOC2	0.073	0.534
GRB2	PTPRG	0.258	0.546
GRB2	SOCS3	0.08	0.549
GRB2	TYK2	0.257	0.559
GRB2	PTPRC	0.201	0.562

GRB2	MX1	0.316	0.57
GRB2	MX2	0.316	0.57
GRB2	KSR1	0.163	0.572
GRB2	PTPN22	0.318	0.572
GRB2	STAT6	0.053	0.575
GRB2	STAT5B	0.053	0.585
GRB2	RASGEF1B	0.398	0.588
GRB2	SSH2	0	0.593
GRB2	PLEK	0	0.6
GRB2	STAT1	0.053	0.615
GRB2	ITGB7	0.045	0.626
GRB2	IL6R	0	0.628
GRB2	IL2RG	0.053	0.643
GRB2	IL15	0	0.652
GRB2	PSEN1	0.08	0.661
GRB2	VEGFC	0	0.665
GRB2	ZFYVE28	0	0.669
GRB2	IL2RB	0.113	0.702
GRB2	IL6	0	0.707
GRB2	VEGFA	0	0.736
GRB2	PRKCD	0.069	0.737
GRB2	S100A8	0.098	0.737
GRB2	SH2B2	0.336	0.738
GRB2	TGFBR1	0.163	0.758
GRB2	PTPN6	0.447	0.76
GRB2	HCK	0.257	0.764
GRB2	RAPGEF1	0.479	0.802
GRB2	THEMIS2	0.589	0.849
GRB2	HBEGF	0	0.854
GRB2	STAT3	0.113	0.859
GRB2	PTPN2	0.352	0.866
GRB2	TEC	0.257	0.891
GRB2	IL2RA	0	0.895
GRB2	PXN	0.113	0.896
GRB2	LYN	0.257	0.906
GRB2	LAT2	0.435	0.921
GRB2	JAK3	0.309	0.926
GRB2	INPP5D	0.773	0.934
GRB2	PIK3CA	0.456	0.94
GRB2	PTPN1	0.513	0.94
GRB2	MST1R	0.648	0.943
GRB2	KRAS	0.338	0.946
GRB2	JAK2	0.452	0.976
GRB2	PTK2B	0.763	0.978
GRB2	LCP2	0.865	0.999
GRIPAP1	RALGDS	0	0.464
GRIPAP1	TRPC5	0	0.513

GRK6	HPCAL1	0.046	0.487
GRK6	MIDN	0	0.467
GRK6	PXN	0	0.504
GRK6	XCR1	0	0.642
GRK6	SAG	0.157	0.489
GRK6	LTB4R	0.078	0.416
GRK6	LOC529196	0.053	0.733
GRTP1	PPP1R16B	0.045	0.66
GRTP1	MXD1	0	0.512
GRTP1	RABGEF1	0.045	0.423
GRTP1	RASA4	0	0.426
GRTP1	TMEM119	0	0.414
GRTP1	RABGAP1L	0	0.419
GRTP1	RHBDD2	0	0.534
GRTP1	STK10	0	0.578
GRTP1	RAB8B	0.317	0.593
GRTP1	PLBD1	0	0.757
GSN	NDRG1	0	0.548
GSN	ITPR2	0	0.4
GSN	TPM4	0	0.423
GSN	PTK2B	0.113	0.645
GSN	PIK3CA	0.113	0.741
GSN	RBM18	0.453	0.453
GSN	PXN	0.113	0.648
GSN	VASP	0.078	0.48
GSN	STOM	0	0.487
GTF2B	KAT2B	0.218	0.824
GTF2B	POLR2C	0.854	0.951
GTF2B	JUN	0.158	0.775
GTF2B	IRF5	0	0.646
GTF2B	GTF2H1	0.67	0.807
GTF2B	RPS9	0.079	0.618
GTF2B	UBXN7	0.763	0.95
GTF2B	RARG	0.079	0.598
GTF2B	SUPT6H	0	0.528
GTF2B	IRF2	0	0.72
GTF2B	XRN2	0	0.465
GTF2B	NF1	0	0.668
GTF2B	JUNB	0.158	0.688
GTF2B	RARA	0.079	0.675
GTF2B	SARS	0	0.403
GTF2B	RELA	0.218	0.833
GTF2B	SRPR	0	0.414
GTF2B	VDR	0.079	0.732
GTF2B	PPARD	0.079	0.446
GTF2B	MYSM1	0.093	0.565
GTF2B	UBTF	0.078	0.457

GTF2B	MED13	0	0.604
GTF2B	ZNF143	0.12	0.48
GTF2B	LOC100297725	0.079	0.522
GTF2B	IRF7	0	0.638
GTF2B	IRF1	0	0.725
GTF2B	POLR2A	0.928	0.99
GTF2H1	POLR2C	0.761	0.796
GTF2H1	MDM2	0	0.405
GTF2H1	PLEK	0	0.416
GTF2H1	SERTAD1	0	0.47
GTF2H1	UBXN7	0.556	0.623
GTF2H1	POLR2A	0.926	0.947
GTPBP1	POLR2C	0	0.663
GTPBP1	TMBIM4	0	0.512
GTPBP1	LAMP1	0	0.636
GTPBP4	USP42	0	0.607
GTPBP4	ISG20L2	0.052	0.531
GTPBP4	RPIA	0	0.659
GTPBP4	RPS9	0.221	0.416
GTPBP4	UBXN7	0.184	0.606
GTPBP4	IGBP1	0	0.41
GTPBP4	NXF1	0.114	0.461
GTPBP4	RNF13	0	0.465
GTPBP4	KRR1	0.042	0.782
GTPBP4	TRA2A	0.144	0.466
GTPBP4	TIMM17A	0	0.433
GTPBP4	NOM1	0	0.469
GTPBP4	ISG20	0.052	0.487
GTPBP4	RANBP2	0	0.512
GTPBP4	POLR2A	0.184	0.556
GTPBP4	WDR4	0	0.583
GTPBP4	TFB1M	0	0.599
GTPBP4	USP36	0	0.607
GTPBP4	RCL1	0	0.768
GTPBP4	NOP9	0.12	0.834
GTPBP4	LTV1	0	0.979
GUCD1	OSTM1	0	0.416
GUCD1	SRRM2	0	0.42
H3F3A	SETDB1	0.317	0.417
H3F3A	KAT2B	0.447	0.528
H3F3A	KDM4A	0.441	0.526
H3F3A	SUPT6H	0.296	0.431
H3F3A	MORC3	0.425	0.424
H3F3A	KDM5A	0.31	0.453
H3F3A	MPHOSPH8	0.4	0.45
H3F3A	HIST1H2AJ	0.218	0.451
H3F3A	HIST3H2A	0.301	0.542

H3F3A	KDM6B	0.451	0.544
HBEGF	RET	0	0.542
HBEGF	IL1B	0	0.401
HBEGF	JAK1	0	0.502
HBEGF	STAT2	0	0.459
HBEGF	STAT6	0	0.49
HBEGF	PIK3CA	0	0.85
HBEGF	STAT5B	0	0.62
HBEGF	JAK2	0	0.82
HBEGF	PLA2G4A	0	0.553
HBEGF	PTGS2	0	0.536
HBEGF	IL6	0	0.406
HBEGF	MMP25	0.053	0.908
HBEGF	ITGB7	0	0.411
HBEGF	TNFSF10	0	0.422
HBEGF	JAK3	0	0.6
HBEGF	STAT3	0	0.611
HBEGF	STAT4	0	0.452
HBEGF	STAT1	0	0.48
HBEGF	TNF	0	0.498
HBEGF	VEGFA	0	0.547
HBEGF	STAT5A	0	0.617
HBEGF	LRRK2	0	0.642
HCK	MYD88	0.178	0.424
HCK	RET	0.453	0.516
HCK	HCLS1	0.166	0.51
HCK	TM9SF4	0.045	0.645
HCK	IL1B	0.054	0.461
HCK	PLCG2	0.295	0.8
HCK	PTPRE	0.133	0.406
HCK	JAK1	0	0.645
HCK	NCF1	0.079	0.484
HCK	PTPN12	0.139	0.404
HCK	JUN	0.125	0.426
HCK	LOC407171	0.054	0.552
HCK	VAV1	0.093	0.759
HCK	STAT2	0.236	0.542
HCK	IL10RA	0.205	0.61
HCK	PTK2B	0.219	0.947
HCK	THEMIS2	0.05	0.62
HCK	STAT6	0.236	0.542
HCK	S100A9	0.042	0.495
HCK	IL10	0.054	0.417
HCK	ITGAL	0.08	0.449
HCK	IL2RG	0.133	0.447
HCK	SLA	0.065	0.753
HCK	TLR2	0.093	0.474

HCK	SOCS3	0.207	0.462
HCK	PRKCD	0.131	0.714
HCK	PIK3CA	0.411	0.817
HCK	LCP2	0.209	0.64
HCK	STAT5B	0.236	0.619
HCK	PLEK	0	0.609
HCK	PTPRC	0.133	0.898
HCK	JAK2	0	0.519
HCK	S100A8	0.042	0.507
HCK	PLA2G4A	0.127	0.46
HCK	IL6	0.045	0.694
HCK	MST1R	0.225	0.484
HCK	PIK3R6	0	0.702
HCK	IL2RB	0.175	0.437
HCK	PXN	0.099	0.762
HCK	PLAGL2	0.072	0.528
HCK	IL6R	0.054	0.627
HCK	ITGB7	0.122	0.552
HCK	IL1RN	0.047	0.414
HCK	LYN	0.053	0.953
HCK	INPP5D	0.471	0.704
HCK	PTPN6	0.219	0.581
HCK	JAK3	0	0.505
HCK	SAG	0.149	0.584
HCK	STAT3	0.236	0.821
HCK	IFNAR1	0.218	0.428
HCK	RAPGEF1	0.203	0.638
HCK	PTPRJ	0.101	0.407
HCK	STAT5A	0.236	0.6
HCK	TNF	0.093	0.435
HCK	PTAFR	0.054	0.529
HCK	KRAS	0.141	0.693
HCK	TEC	0.08	0.54
HCK	LAPTM5	0	0.401
HCK	S100A12	0.042	0.473
HCK	STAT1	0.236	0.507
HCK	LAT2	0	0.521
HCK	PIK3R5	0	0.69
HCLS1	PLEK	0	0.402
HCLS1	JAK3	0.166	0.405
HCLS1	MEGF9	0	0.414
HCLS1	TYK2	0.166	0.422
HCLS1	RHOH	0	0.428
HCLS1	TEC	0.166	0.442
HCLS1	NCF4	0.066	0.45
HCLS1	ORAOV1	0	0.45
HCLS1	PTPRC	0.086	0.456

HCLS1	SLA	0	0.478
HCLS1	NCF1	0.08	0.51
HCLS1	ITGAL	0	0.514
HCLS1	ITGB7	0	0.517
HCLS1	LCP2	0	0.523
HCLS1	LAMB3	0	0.585
HCLS1	VAV1	0	0.591
HCLS1	PTK2B	0.12	0.619
HCLS1	SDC3	0.08	0.661
HCLS1	LAPTM5	0	0.719
HCLS1	PXN	0.253	0.74
HCLS1	LYN	0.589	0.922
HDAC11	KAT2B	0.184	0.663
HDAC11	RBPJ	0.218	0.434
HDAC11	NUP210L	0	0.406
HDAC11	KAT5	0.239	0.676
HDAC11	STAT3	0.16	0.419
HDAC11	KDM7A	0.104	0.434
HDAC11	MEF2A	0.184	0.438
HDAC11	NUP210	0	0.458
HDAC11	RELA	0.219	0.465
HDAC11	PHF12	0.394	0.511
HDAC11	RANBP2	0.173	0.526
HDAC11	MPHOSPH8	0.411	0.565
HDAC11	KAT8	0.239	0.595
HDAC11	LOC100297725	0.162	0.623
HDAC11	HDAC4	0.124	0.655
HDAC11	HIST1H2AJ	0.158	0.782
HDAC11	HIST3H2A	0.158	0.831
HDAC11	SIRT1	0.204	0.892
HDAC4	SETDB1	0.159	0.421
HDAC4	KAT2B	0.296	0.614
HDAC4	TUBA4A	0.219	0.43
HDAC4	RBPJ	0.218	0.523
HDAC4	NUP210L	0	0.605
HDAC4	KAT5	0.239	0.633
HDAC4	KAT8	0.239	0.629
HDAC4	MEF2A	0.69	0.963
HDAC4	SIK1	0.165	0.427
HDAC4	RELA	0.219	0.535
HDAC4	SIRT1	0.314	0.954
HDAC4	SIK3	0.165	0.69
HDAC4	PHF12	0.394	0.545
HDAC4	MBD2	0.219	0.434
HDAC4	KDM6B	0.227	0.435
HDAC4	HIC1	0.121	0.454
HDAC4	TBL1X	0.311	0.481

HDAC4	TNF	0.174	0.492
HDAC4	STAT3	0.16	0.5
HDAC4	MPHOSPH8	0.411	0.601
HDAC4	NUP210	0	0.636
HDAC4	STAT1	0.16	0.684
HDAC4	LOC100297725	0.162	0.728
HDAC4	HIST1H2AJ	0.158	0.739
HDAC4	HIST3H2A	0.158	0.785
HDAC4	RANBP2	0.173	0.789
HDAC4	RELB	0.042	0.794
HEATR5B	KIAA1033	0	0.74
HECA	SNX20	0	0.64
HECA	SELPLG	0	0.411
HECA	SELP	0	0.668
HECA	SELL	0	0.725
HECW2	ZSWIM4	0.069	0.555
HECW2	PAPOLG	0.045	0.538
HECW2	UBXN7	0.565	0.688
HECW2	PPM1D	0.08	0.54
HECW2	UBE2L6	0.335	0.457
HECW2	STK17B	0.052	0.68
HECW2	NDFIP2	0.399	0.541
HECW2	UBE2G1	0.219	0.446
HECW2	TAPT1	0	0.412
HECW2	ZSWIM6	0.113	0.731
HECW2	PSTPIP2	0.045	0.413
HECW2	TRANK1	0	0.426
HECW2	POLR2A	0.4	0.493
HEG1	RAP1B	0.46	0.528
HEG1	PTPRJ	0	0.539
HERC5	STAT2	0.043	0.406
HERC5	IFIH1	0.043	0.814
HERC5	MX2	0.145	0.749
HERC5	IFIT3	0.121	0.837
HERC5	TRIM25	0.054	0.566
HERC5	XAF1	0	0.518
HERC5	UBA7	0.078	0.902
HERC5	UBE2L6	0.219	0.827
HERC5	OAS2	0	0.583
HERC5	ISG15	0.165	0.869
HERC5	RSAD2	0	0.832
HERC5	PARP14	0.048	0.571
HERC5	USP18	0.163	0.889
HERC5	ZNFX1	0.044	0.522
HERC5	PARP9	0.048	0.649
HERC5	UBE2B	0.158	0.561
HERC5	MX1	0.145	0.804

HERC5	IRF9	0	0.485
HERC5	IFIT2	0.121	0.787
HERC5	ZBP1	0	0.496
HERC5	TRIM21	0.054	0.493
HERC5	ISG20	0	0.507
HERC5	STAT1	0.043	0.643
HERC5	IRF7	0.042	0.693
HERC6	ZSWIM4	0.043	0.413
HERC6	NLRC5	0.055	0.409
HERC6	IFIH1	0.043	0.77
HERC6	MX2	0.145	0.738
HERC6	IFIT3	0.121	0.687
HERC6	XAF1	0	0.638
HERC6	UBA7	0.078	0.784
HERC6	UBE2L6	0.219	0.798
HERC6	OAS2	0	0.537
HERC6	ISG15	0.165	0.785
HERC6	RSAD2	0	0.85
HERC6	PARP12	0.045	0.668
HERC6	PARP14	0.048	0.569
HERC6	USP18	0.163	0.848
HERC6	ZNFX1	0.044	0.807
HERC6	PLSCR2	0	0.476
HERC6	IRF9	0	0.499
HERC6	UBE2B	0.158	0.561
HERC6	STAT1	0.043	0.562
HERC6	RNF213	0	0.641
HERC6	IRF7	0.042	0.657
HERC6	PARP9	0.048	0.685
HERC6	IFIT2	0.121	0.744
HERC6	MX1	0.145	0.746
HERPUD1	PPP1R15A	0	0.62
HERPUD1	STEAP3	0	0.458
HERPUD1	MANF	0	0.416
HES4	JAK1	0.079	0.442
HES4	TLE4	0.761	0.875
HES4	RBPJ	0.108	0.773
HES4	JAK2	0.079	0.442
HES4	SIRT1	0.46	0.692
HES4	JAK3	0.079	0.442
HES4	STAT3	0.164	0.618
HES4	TLE3	0.761	0.895
HEXIM1	SFPQ	0.204	0.408
HEXIM1	PQBP1	0	0.43
HEXIM1	POLR2A	0	0.596
HHEX	JUN	0.201	0.625
HHEX	WSB1	0.073	0.42

HHEX	TAL1	0	0.499
HHEX	TLE3	0.078	0.52
HHEX	TCF7L2	0	0.632
HIAT1	SLC46A2	0	0.519
HIC1	NFKBIB	0.093	0.636
HIC1	OVCA2	0	0.404
HIC1	SIRT1	0.763	0.965
HIC1	RASSF1	0	0.585
HIC1	STAT3	0.218	0.584
HIC1	MNT	0.081	0.414
HIGD1A	RLF	0	0.729
HIGD1A	LYSMD3	0	0.557
HIPK3	TLE4	0.451	0.535
HIPK3	WSB1	0.093	0.442
HIPK3	PPM1D	0.079	0.421
HIPK3	SRSF5	0.212	0.648
HIPK3	TAB2	0	0.688
HIPK3	NLK	0.155	0.603
HIPK3	PML	0.393	0.475
HIPK3	TLE3	0.451	0.535
HIPK3	QKI	0	0.403
HIPK3	SUV420H1	0.049	0.413
HIPK3	RASSF5	0.155	0.852
HIST1H2AJ	KAT5	0.218	0.486
HIST1H2AJ	JARID2	0.16	0.498
HIST1H2AJ	WDR77	0.184	0.412
HIST1H2AJ	RYBP	0.048	0.48
HIST1H2AJ	MYSM1	0.219	0.517
HIST1H2AJ	LOC100297725	0.218	0.837
HIST3H2A	KAT5	0.258	0.517
HIST3H2A	JARID2	0.16	0.507
HIST3H2A	WDR77	0.255	0.471
HIST3H2A	TBL1X	0.139	0.91
HIST3H2A	RYBP	0.055	0.483
HIST3H2A	MYSM1	0.219	0.508
HIST3H2A	LOC613345	0.301	0.466
HIST3H2A	LOC100297725	0.301	0.864
HIVEP1	SMAD7	0.102	0.406
HIVEP1	PHACTR2	0.072	0.415
HIVEP1	TGFBR1	0.208	0.509
HIVEP2	IK	0	0.451
HIVEP2	LCP2	0	0.463
HK2	PRKAA1	0.219	0.424
HK2	MXD1	0	0.518
HK2	TKT	0	0.877
HK2	LAP3	0	0.454
HK2	SOD2	0	0.425

HK2	PFKFB4	0.056	0.795
HK2	VPS4B	0	0.452
HK2	MAP3K8	0	0.528
HK2	HK3	0.437	0.459
HK2	PPIF	0	0.558
HK2	SLC16A3	0	0.632
HK2	SLC2A3	0.054	0.713
HK2	SLC2A1	0.054	0.757
HK2	KRAS	0.046	0.488
HK3	SLC2A6	0.046	0.441
HK3	RPIA	0	0.568
HK3	TKT	0	0.403
HK3	MAP3K8	0	0.51
HK3	TMEM150B	0	0.406
HLX	TLE4	0.395	0.411
HLX	PSMB9	0	0.635
HLX	KIAA0247	0	0.481
HLX	STAT4	0	0.7
HM13	IGSF10	0.044	0.507
HM13	ID1	0	0.421
HM13	TAPBP	0	0.425
HM13	6-Mar	0.113	0.46
HM13	PSEN1	0.042	0.461
HM13	TAPBPL	0	0.632
HM13	MANF	0	0.77
HNRNPF	ZNF614	0.045	0.438
HNRNPF	KAT5	0.184	0.401
HNRNPF	KDM3A	0	0.41
HNRNPF	SRRM2	0.35	0.447
HNRNPF	PNPT1	0.15	0.457
HNRNPF	HNRNPH1	0.385	0.53
HNRNPF	SF3B1	0.352	0.545
HNRNPF	SRSF5	0.117	0.57
HNRNPF	SFPQ	0.055	0.718
HNRNPH1	SAFB	0	0.401
HNRNPH1	SF3B1	0.345	0.94
HNRNPH1	SFPQ	0.08	0.559
HNRNPH1	TRA2A	0.181	0.596
HNRNPH1	SRRM2	0.337	0.612
HNRNPH1	SRSF5	0.117	0.787
HPCAL1	NAIP	0.084	0.531
HPCAL1	MAP3K2	0.07	0.438
HPCAL1	VAT1L	0.049	0.439
HPCAL1	POLR2A	0	0.468
HPCAL1	LRP10	0	0.674
HPSE	RETN	0	0.509
HPSE	SDC3	0	0.409

HPSE	SDC4	0	0.41
HPSE	TCF7L2	0	0.412
HSD11B1	LONRF3	0.093	0.454
HSD11B1	VPS4B	0.067	0.407
HSD17B1	MLXIP	0	0.514
HSD17B1	MXD4	0	0.426
HSH2D	TMEM140	0	0.497
HSH2D	LTB4R	0	0.426
HYAL1	TNFAIP6	0	0.429
HYAL1	VCAN	0	0.513
HYAL2	PLA2G4A	0	0.422
HYAL2	TNFAIP6	0	0.457
HYAL2	PTPRC	0.053	0.477
HYAL2	VCAN	0	0.508
HYAL2	MST1R	0.078	0.695
HYLS1	PKNOX1	0	0.414
HYPK	RNF114	0	0.471
HYPK	PSEN1	0	0.635
ICAM1	MYD88	0	0.568
ICAM1	NLRP3	0	0.401
ICAM1	IL1B	0	0.84
ICAM1	PLCG2	0	0.828
ICAM1	NCF1	0	0.444
ICAM1	JUN	0	0.527
ICAM1	TNFRSF1A	0	0.518
ICAM1	STAT2	0	0.403
ICAM1	OLR1	0	0.613
ICAM1	IL1R1	0	0.48
ICAM1	NFKB2	0	0.468
ICAM1	TLR4	0	0.804
ICAM1	STAT6	0	0.424
ICAM1	SOD2	0	0.426
ICAM1	IL10	0	0.768
ICAM1	NOS2	0	0.563
ICAM1	ITGAL	0.126	0.998
ICAM1	IKBKB	0	0.499
ICAM1	TLR2	0	0.709
ICAM1	ITGA2B	0.126	0.583
ICAM1	SOCS3	0	0.484
ICAM1	LCP2	0	0.431
ICAM1	PTPRC	0	0.769
ICAM1	PXN	0	0.406
ICAM1	IL1RN	0	0.407
ICAM1	ITGA9	0.126	0.422
ICAM1	SELPLG	0	0.424
ICAM1	ITGB7	0.125	0.429
ICAM1	LAMP1	0	0.433

ICAM1	JAK2	0	0.467
ICAM1	TLR9	0	0.472
ICAM1	LTBR	0	0.494
ICAM1	TRAF1	0	0.513
ICAM1	NFKB1	0	0.534
ICAM1	ITGA5	0.126	0.545
ICAM1	MMP25	0	0.552
ICAM1	IL1A	0	0.556
ICAM1	IRF1	0	0.586
ICAM1	STAT1	0	0.592
ICAM1	IL15	0	0.594
ICAM1	ITGAV	0.126	0.601
ICAM1	RELB	0	0.609
ICAM1	IL18	0	0.612
ICAM1	RELA	0.174	0.622
ICAM1	STAT3	0	0.652
ICAM1	SERPINE1	0	0.693
ICAM1	VEGFA	0	0.697
ICAM1	PTGS2	0	0.712
ICAM1	SELL	0	0.773
ICAM1	ICAM3	0	0.82
ICAM1	IL6	0	0.832
ICAM1	KRAS	0	0.868
ICAM1	SELP	0	0.875
ICAM1	TNF	0	0.922
ICAM2	ITGAL	0.518	0.978
ICAM2	ITGA2B	0.162	0.412
ICAM2	PTPRC	0	0.433
ICAM2	ITGA5	0.162	0.402
ICAM2	MST1R	0	0.51
ICAM2	ITGB7	0.184	0.535
ICAM2	VEGFA	0	0.4
ICAM2	ITGAV	0.162	0.461
ICAM2	TNF	0	0.519
ICAM2	SELL	0.042	0.614
ICAM2	SELP	0.042	0.691
ICAM3	TLR4	0	0.419
ICAM3	IL10	0	0.454
ICAM3	ITGAL	0.926	0.998
ICAM3	TLR2	0	0.426
ICAM3	ITGA2B	0.162	0.471
ICAM3	PTPRC	0	0.407
ICAM3	ITGA5	0.162	0.4
ICAM3	MST1R	0	0.51
ICAM3	SELP	0.042	0.4
ICAM3	TNF	0	0.426
ICAM3	SELL	0.042	0.48

ICAM3	ITGB7	0.184	0.569
ICAM4	S1PR2	0	0.58
ICAM4	ITGA9	0.126	0.431
ICAM4	ITGA5	0.126	0.456
ICAM4	MAEA	0	0.556
ICAM4	ITGAV	0.126	0.72
ICAM5	S1PR2	0	0.517
ICAM5	ITGAL	0.759	0.925
ICAM5	STARD8	0	0.41
ICAM5	PSEN1	0.113	0.662
ICOSLG	IL10	0	0.481
ICOSLG	TNFSF9	0	0.466
ICOSLG	KLRG2	0	0.62
ICOSLG	TAPBP	0	0.633
ID1	RAP1B	0.043	0.8
ID1	SMAD7	0.082	0.561
IER3	NR4A1	0	0.436
IER3	NFKBID	0	0.47
IER3	ZC3H12A	0.078	0.566
IER3	MAP3K8	0	0.429
IER3	ZFP36	0	0.487
IER3	MCL1	0.068	0.543
IER3	RELA	0.113	0.692
IFI35	PSMB8	0	0.618
IFI35	STAT2	0.053	0.689
IFI35	SOCS1	0	0.49
IFI35	PSME1	0	0.403
IFI35	STAT4	0.053	0.426
IFI35	STAT3	0.053	0.429
IFI35	SOCS3	0	0.456
IFI35	TAPBP	0	0.462
IFI35	USP25	0	0.475
IFI35	LOC507055	0	0.492
IFI35	SP110	0.045	0.506
IFI35	PARP14	0	0.511
IFI35	RBCK1	0	0.523
IFI35	IL2RG	0	0.532
IFI35	IL2RA	0	0.55
IFI35	PARP12	0	0.583
IFI35	PARP9	0	0.599
IFI35	OAS2	0	0.606
IFI35	XAF1	0	0.628
IFI35	IRF1	0	0.631
IFI35	RNF213	0	0.631
IFI35	ZBP1	0	0.638
IFI35	TRIM21	0.113	0.655
IFI35	IFIT2	0	0.69

IFI35	UBA7	0.042	0.695
IFI35	RSAD2	0	0.702
IFI35	IFITM3	0	0.707
IFI35	PSMB9	0	0.713
IFI35	ISG20	0	0.719
IFI35	MX2	0	0.725
IFI35	IRF9	0	0.735
IFI35	USP18	0	0.736
IFI35	IFIH1	0	0.76
IFI35	UBE2L6	0.054	0.845
IFI35	PSME2	0	0.849
IFI35	MX1	0	0.85
IFI35	IRF7	0.135	0.87
IFI35	ISG15	0	0.883
IFI35	STAT1	0.053	0.899
IFI35	IFIT3	0	0.903
IFI35	NMI	0.554	0.935
IFIH1	MYD88	0	0.722
IFIH1	NLRP3	0	0.55
IFIH1	IL1B	0	0.504
IFIH1	TMEM140	0	0.53
IFIH1	JAK1	0.046	0.537
IFIH1	STAT2	0.052	0.765
IFIH1	SOCS1	0	0.478
IFIH1	LOC616948	0.134	0.54
IFIH1	IRF5	0	0.578
IFIH1	NLRC5	0.113	0.806
IFIH1	TLR4	0.041	0.66
IFIH1	RIPK1	0.046	0.454
IFIH1	IL10	0	0.456
IFIH1	LGALS9	0	0.433
IFIH1	TLR2	0.041	0.622
IFIH1	LOC511531	0.131	0.411
IFIH1	PLSCR2	0	0.413
IFIH1	IL2RA	0	0.416
IFIH1	LOC512486	0.131	0.418
IFIH1	STAT4	0.052	0.422
IFIH1	MEFV	0.134	0.436
IFIH1	NLRC4	0	0.437
IFIH1	IL6	0	0.467
IFIH1	IL18	0	0.483
IFIH1	LOC507055	0.093	0.499
IFIH1	SP110	0.134	0.502
IFIH1	IFNAR2	0	0.503
IFIH1	PTPN2	0.055	0.514
IFIH1	IRF2	0	0.545
IFIH1	UBE2L6	0.064	0.552

IFIH1	TYK2	0.046	0.56
IFIH1	NOD1	0.046	0.564
IFIH1	TANK	0	0.566
IFIH1	NMI	0	0.615
IFIH1	ZNFX1	0.077	0.622
IFIH1	RBM43	0	0.624
IFIH1	TRIM38	0.134	0.625
IFIH1	PTPN22	0.055	0.63
IFIH1	TNF	0	0.641
IFIH1	PSMB9	0	0.644
IFIH1	NOD2	0.046	0.656
IFIH1	MORC3	0	0.659
IFIH1	IKBKE	0.135	0.678
IFIH1	TLR9	0.041	0.692
IFIH1	ZBP1	0	0.695
IFIH1	IFITM3	0	0.7
IFIH1	XAF1	0	0.731
IFIH1	ISG20	0	0.738
IFIH1	IRF9	0	0.746
IFIH1	IFNAR1	0	0.761
IFIH1	IRF1	0	0.774
IFIH1	RNF213	0	0.775
IFIH1	OAS2	0	0.776
IFIH1	TRIM21	0.134	0.801
IFIH1	TRAF3	0.08	0.852
IFIH1	UBA7	0.077	0.868
IFIH1	PARP12	0.121	0.893
IFIH1	STAT1	0.08	0.922
IFIH1	IFIT3	0.08	0.925
IFIH1	IFIT2	0.045	0.926
IFIH1	TRIM25	0.66	0.931
IFIH1	IRF7	0	0.94
IFIH1	USP18	0	0.943
IFIH1	MX2	0	0.949
IFIH1	PARP14	0	0.952
IFIH1	PARP9	0	0.953
IFIH1	MX1	0	0.964
IFIH1	ISG15	0.159	0.971
IFIH1	RSAD2	0	0.975
IFIT2	PSMB8	0.121	0.407
IFIT2	STAT2	0.045	0.722
IFIT2	MX2	0	0.882
IFIT2	IFIT3	0.764	0.969
IFIT2	TRIM25	0.045	0.411
IFIT2	XAF1	0.042	0.704
IFIT2	UBA7	0.078	0.5
IFIT2	UBE2L6	0.126	0.487

IFIT2	OAS2	0.406	0.881
IFIT2	ISG15	0.162	0.943
IFIT2	RSAD2	0.156	0.958
IFIT2	PARP12	0	0.626
IFIT2	PARP14	0.054	0.615
IFIT2	USP18	0.148	0.867
IFIT2	TNFSF10	0	0.408
IFIT2	IFITM3	0	0.698
IFIT2	ZNFX1	0.093	0.654
IFIT2	PARP9	0.054	0.63
IFIT2	IFNAR1	0	0.632
IFIT2	RNF213	0	0.529
IFIT2	TNF	0	0.437
IFIT2	MX1	0	0.923
IFIT2	IRF1	0	0.703
IFIT2	IRF9	0	0.694
IFIT2	LOC507055	0.042	0.511
IFIT2	TRIM21	0.045	0.41
IFIT2	ISG20	0	0.814
IFIT2	IRF7	0	0.848
IFIT2	STAT1	0.045	0.859
IFIT3	PSMB8	0.121	0.469
IFIT3	STAT2	0.045	0.794
IFIT3	NLRC5	0.055	0.412
IFIT3	LGALS9	0.412	0.541
IFIT3	MX2	0	0.854
IFIT3	TNFSF10	0	0.422
IFIT3	ZNFX1	0.093	0.436
IFIT3	PLSCR2	0	0.448
IFIT3	IKBKE	0.113	0.498
IFIT3	LOC507055	0.042	0.521
IFIT3	UBA7	0.078	0.525
IFIT3	IFNAR1	0	0.551
IFIT3	TRIM21	0.045	0.565
IFIT3	ZBP1	0	0.617
IFIT3	SP110	0.045	0.619
IFIT3	UBE2L6	0.126	0.649
IFIT3	IFITM3	0	0.667
IFIT3	PARP12	0	0.67
IFIT3	IRF1	0	0.687
IFIT3	RNF213	0	0.69
IFIT3	ISG20	0	0.759
IFIT3	PARP9	0.157	0.767
IFIT3	XAF1	0.042	0.786
IFIT3	PARP14	0.054	0.848
IFIT3	OAS2	0.407	0.874
IFIT3	IRF9	0	0.876

IFIT3	STAT1	0.045	0.92
IFIT3	IRF7	0	0.934
IFIT3	USP18	0.148	0.937
IFIT3	MX1	0	0.953
IFIT3	ISG15	0.162	0.96
IFIT3	RSAD2	0.463	0.966
IFITM3	STAT2	0.053	0.605
IFITM3	MX2	0	0.621
IFITM3	IRF2	0	0.47
IFITM3	XAF1	0	0.454
IFITM3	UBA7	0	0.699
IFITM3	OAS2	0	0.505
IFITM3	ISG15	0	0.895
IFITM3	RSAD2	0	0.857
IFITM3	PARP12	0	0.57
IFITM3	USP18	0	0.544
IFITM3	RNF213	0	0.502
IFITM3	IRF1	0	0.557
IFITM3	IFNAR1	0	0.587
IFITM3	STAT1	0.053	0.603
IFITM3	ISG20	0	0.626
IFITM3	IRF9	0	0.707
IFITM3	IRF7	0	0.716
IFITM3	MX1	0	0.885
IFNAR1	MYD88	0	0.697
IFNAR1	IL1B	0	0.457
IFNAR1	JAK1	0.218	0.997
IFNAR1	IL23A	0	0.612
IFNAR1	STAT2	0.764	0.999
IFNAR1	SOCS1	0.113	0.882
IFNAR1	IL12B	0	0.612
IFNAR1	IRF5	0	0.668
IFNAR1	IL10RA	0.06	0.608
IFNAR1	IL1R1	0	0.466
IFNAR1	TLR4	0	0.639
IFNAR1	STAT6	0.296	0.823
IFNAR1	RIPK1	0.174	0.527
IFNAR1	PTPN1	0.041	0.92
IFNAR1	IL10	0.206	0.922
IFNAR1	TLR2	0	0.528
IFNAR1	SOCS3	0.055	0.841
IFNAR1	MX2	0	0.607
IFNAR1	STAT5B	0.296	0.673
IFNAR1	TRIM25	0	0.535
IFNAR1	IRF2	0	0.542
IFNAR1	PTPRC	0.078	0.57
IFNAR1	IKBKE	0.093	0.515

IFNAR1	TRAF2	0	0.486
IFNAR1	TYK2	0.947	0.999
IFNAR1	JAK2	0.218	0.968
IFNAR1	UBA7	0.073	0.412
IFNAR1	IFNGR2	0	0.871
IFNAR1	TRAF3	0	0.467
IFNAR1	OAS2	0	0.538
IFNAR1	ISG15	0	0.801
IFNAR1	IL6	0	0.779
IFNAR1	IL12A	0	0.665
IFNAR1	IFNAR2	0.931	0.999
IFNAR1	RSAD2	0	0.674
IFNAR1	OSM	0	0.604
IFNAR1	USP18	0.061	0.741
IFNAR1	TLR9	0	0.673
IFNAR1	IL15	0	0.744
IFNAR1	RIPK3	0.093	0.443
IFNAR1	LYN	0.218	0.457
IFNAR1	JAK3	0.218	0.936
IFNAR1	NOD2	0	0.48
IFNAR1	IRAK4	0.093	0.42
IFNAR1	STAT3	0.296	0.845
IFNAR1	TEC	0.218	0.428
IFNAR1	IL18	0	0.482
IFNAR1	ISG20	0	0.533
IFNAR1	TNF	0	0.654
IFNAR1	STAT5A	0.296	0.657
IFNAR1	IRF1	0	0.752
IFNAR1	MX1	0	0.788
IFNAR1	IRF7	0	0.841
IFNAR1	STAT4	0.296	0.857
IFNAR1	IRF9	0	0.987
IFNAR1	STAT1	0.296	0.99
IFNAR2	JAK1	0.218	0.997
IFNAR2	VAV1	0	0.481
IFNAR2	IL23A	0	0.61
IFNAR2	STAT2	0.759	0.998
IFNAR2	SOCS1	0	0.42
IFNAR2	IL12B	0	0.639
IFNAR2	STAT6	0.259	0.74
IFNAR2	IL10	0	0.787
IFNAR2	MX2	0	0.419
IFNAR2	STAT5B	0.259	0.65
IFNAR2	MAP3K8	0	0.428
IFNAR2	TYK2	0.093	0.995
IFNAR2	JAK2	0.157	0.94
IFNAR2	IFNGR2	0.306	0.974

IFNAR2	ISG15	0	0.604
IFNAR2	IL6	0	0.709
IFNAR2	IL12A	0	0.6
IFNAR2	RSAD2	0	0.435
IFNAR2	TNF	0	0.517
IFNAR2	IRF1	0	0.559
IFNAR2	IRF7	0	0.565
IFNAR2	MX1	0	0.579
IFNAR2	OSM	0	0.608
IFNAR2	STAT5A	0.259	0.637
IFNAR2	IL15	0	0.682
IFNAR2	STAT3	0.259	0.684
IFNAR2	IL20RA	0.306	0.686
IFNAR2	STAT4	0.259	0.687
IFNAR2	USP18	0.389	0.879
IFNAR2	JAK3	0.157	0.927
IFNAR2	IRF9	0.216	0.931
IFNAR2	IL10RB	0.538	0.938
IFNAR2	STAT1	0.274	0.961
IFNGR2	JAK1	0.294	0.991
IFNGR2	IL23A	0	0.6
IFNGR2	STAT2	0.159	0.683
IFNGR2	IL12B	0	0.727
IFNGR2	IL10RA	0.06	0.566
IFNGR2	STAT6	0.159	0.53
IFNGR2	IL10	0.206	0.862
IFNGR2	PIK3CA	0.042	0.664
IFNGR2	STAT5B	0.159	0.437
IFNGR2	TYK2	0.158	0.865
IFNGR2	JAK2	0.502	0.992
IFNGR2	STAT5A	0.159	0.419
IFNGR2	ISG15	0	0.432
IFNGR2	STAT3	0.159	0.508
IFNGR2	IRF1	0	0.539
IFNGR2	OSM	0	0.6
IFNGR2	IL12A	0	0.6
IFNGR2	STAT4	0.159	0.633
IFNGR2	IL15	0	0.647
IFNGR2	IRF9	0	0.664
IFNGR2	IL6	0	0.674
IFNGR2	STAT1	0.159	0.777
IFNGR2	KRAS	0.042	0.8
IFNGR2	JAK3	0.351	0.809
IGBP1	PPP4R2	0.424	0.671
IGBP1	SUPT6H	0	0.42
IGBP1	TIMM17A	0	0.432
IGBP1	RNF13	0	0.497

IGBP1	SMG1	0.394	0.584
IGBP1	PPP4C	0.765	0.884
IGSF6	MS4A7	0	0.464
IGSF6	TLR4	0	0.639
IGSF6	LCP2	0	0.706
IGSF6	PLEK	0	0.616
IGSF6	IGSF8	0	0.467
IGSF6	IL13RA1	0	0.437
IGSF6	MPEG1	0	0.474
IGSF8	ITGAV	0	0.411
IGSF8	ITGA9	0	0.512
IK	TOP1	0.409	0.424
IK	THOC2	0.402	0.415
IK	SF3B1	0.67	0.737
IK	LCP2	0	0.524
IK	TFIP11	0.421	0.674
IK	SNIP1	0.453	0.474
IK	WDR55	0	0.609
IKBKB	MYD88	0.178	0.859
IKBKB	RB1CC1	0.214	0.463
IKBKB	IL1B	0.047	0.642
IKBKB	NFKBIB	0.675	0.99
IKBKB	JUN	0.113	0.617
IKBKB	TNFRSF1A	0.924	0.997
IKBKB	MAP3K2	0.215	0.58
IKBKB	MAP4K4	0.08	0.656
IKBKB	IL1R1	0.08	0.75
IKBKB	NLRC5	0.211	0.74
IKBKB	NFKB2	0.733	0.948
IKBKB	IRAK2	0.082	0.689
IKBKB	TLR4	0.093	0.847
IKBKB	RIPK1	0.218	0.952
IKBKB	IL10	0.054	0.51
IKBKB	VCPIP1	0.161	0.45
IKBKB	RICTOR	0.16	0.454
IKBKB	NOS2	0.12	0.446
IKBKB	RIPK3	0.139	0.41
IKBKB	SOCS3	0.123	0.443
IKBKB	MLKL	0.139	0.443
IKBKB	KRAS	0.124	0.449
IKBKB	RBCK1	0.174	0.451
IKBKB	LTB	0.093	0.458
IKBKB	IKBKE	0.218	0.461
IKBKB	PTGS2	0.084	0.493
IKBKB	TRAF7	0.183	0.498
IKBKB	PPM1D	0.158	0.507
IKBKB	SBNO2	0	0.512

IKBKB	STAT1	0.147	0.516
IKBKB	ZDHHC18	0.051	0.526
IKBKB	TRIM21	0.218	0.559
IKBKB	TLR9	0.093	0.568
IKBKB	STAT3	0.147	0.579
IKBKB	XIAP	0.257	0.59
IKBKB	IL6	0	0.608
IKBKB	OPTN	0.479	0.614
IKBKB	PRKCD	0.344	0.632
IKBKB	SH2D3C	0.042	0.634
IKBKB	IRF7	0.174	0.645
IKBKB	IL1A	0	0.678
IKBKB	TNFSF10	0.051	0.694
IKBKB	TRAF3	0.183	0.711
IKBKB	TANK	0.478	0.717
IKBKB	RIPK2	0.139	0.755
IKBKB	TIRAP	0.093	0.76
IKBKB	TLR2	0.093	0.794
IKBKB	PRKCB	0.439	0.798
IKBKB	TRAF1	0.385	0.813
IKBKB	MAP3K8	0.08	0.856
IKBKB	RELB	0.054	0.862
IKBKB	NFKBIE	0.08	0.917
IKBKB	IRAK4	0.14	0.942
IKBKB	TNF	0.502	0.943
IKBKB	MALT1	0.113	0.949
IKBKB	TAB2	0.156	0.968
IKBKB	TRAF2	0.764	0.988
IKBKB	NFKB1	0.764	0.996
IKBKB	RELA	0.838	0.996
IKBKE	MYD88	0.178	0.819
IKBKE	IL1B	0.047	0.459
IKBKE	NFKBIB	0	0.531
IKBKE	JUN	0.093	0.448
IKBKE	TNFRSF1A	0.435	0.763
IKBKE	MAP3K2	0.215	0.459
IKBKE	STAT2	0.147	0.544
IKBKE	SOCS1	0.123	0.447
IKBKE	MAP4K4	0.08	0.428
IKBKE	IRF5	0.078	0.496
IKBKE	IL1R1	0.08	0.543
IKBKE	NFKB2	0.046	0.476
IKBKE	IRAK2	0.082	0.594
IKBKE	TLR4	0.093	0.669
IKBKE	RIPK1	0.435	0.677
IKBKE	IL10	0.054	0.564
IKBKE	VCPIP1	0.161	0.45

IKBKE	TLR2	0.093	0.587
IKBKE	PRKCD	0.159	0.432
IKBKE	PPM1D	0.158	0.466
IKBKE	TRIM25	0.055	0.555
IKBKE	IL1A	0	0.572
IKBKE	NOD1	0.083	0.401
IKBKE	NFKBIE	0	0.413
IKBKE	RIPK2	0.139	0.415
IKBKE	MX1	0.093	0.418
IKBKE	STAT3	0.147	0.421
IKBKE	XIAP	0.257	0.429
IKBKE	TRAF7	0.183	0.433
IKBKE	PRKCB	0.219	0.446
IKBKE	ISG15	0.127	0.479
IKBKE	RIPK3	0.139	0.481
IKBKE	IL6	0	0.481
IKBKE	IRAK4	0.082	0.485
IKBKE	PELI1	0.15	0.486
IKBKE	MALT1	0.073	0.517
IKBKE	NFKB1	0.046	0.534
IKBKE	RNF41	0.183	0.543
IKBKE	STAT1	0.147	0.576
IKBKE	TLR9	0.093	0.625
IKBKE	TIRAP	0.093	0.627
IKBKE	SEMA7A	0.055	0.637
IKBKE	TRAF1	0.416	0.644
IKBKE	RELB	0.048	0.668
IKBKE	TNFSF10	0.051	0.683
IKBKE	TAB2	0.156	0.695
IKBKE	TRAF2	0.626	0.803
IKBKE	RELA	0.408	0.824
IKBKE	OPTN	0.76	0.836
IKBKE	ZBP1	0.156	0.869
IKBKE	TNF	0.768	0.941
IKBKE	IRF7	0.131	0.962
IKBKE	TANK	0.764	0.991
IKBKE	TRAF3	0.764	0.991
IKZF5	SHOC2	0.055	0.622
IL10	MYD88	0	0.863
IL10	PRDM1	0	0.548
IL10	NLRP3	0	0.709
IL10	IL1B	0	0.953
IL10	IL4R	0	0.83
IL10	JAK1	0.054	0.913
IL10	NCF1	0	0.403
IL10	JUN	0	0.577
IL10	TNFRSF1A	0	0.593

IL10	IL23A	0	0.668
IL10	STAT2	0.12	0.691
IL10	SOCS1	0	0.671
IL10	RETN	0	0.604
IL10	IL12B	0	0.769
IL10	IRF5	0	0.565
IL10	IL10RA	0.953	0.999
IL10	IL1R1	0	0.678
IL10	LITAF	0	0.674
IL10	NFKB2	0.07	0.472
IL10	IL15RA	0	0.674
IL10	LOC515976	0	0.499
IL10	IRAK2	0.116	0.441
IL10	TLR4	0.116	0.908
IL10	STAT6	0.12	0.793
IL10	IL1R2	0	0.444
IL10	S100A9	0	0.43
IL10	TRAF3	0	0.408
IL10	ZFP36	0	0.41
IL10	SIRPA	0	0.41
IL10	ISG15	0	0.414
IL10	SIRT1	0	0.422
IL10	PTX3	0	0.425
IL10	LYN	0.054	0.438
IL10	TNFSF13B	0	0.456
IL10	SAA2	0	0.47
IL10	LGALS9	0	0.47
IL10	ITGAL	0	0.473
IL10	STAT5A	0.12	0.475
IL10	TIRAP	0	0.476
IL10	TNFRSF1B	0	0.477
IL10	MX1	0	0.484
IL10	NLRC4	0	0.485
IL10	RELB	0	0.49
IL10	STAT5B	0.12	0.495
IL10	PSME1	0	0.517
IL10	NFE2L2	0	0.518
IL10	NFKB1	0.055	0.518
IL10	OSM	0	0.523
IL10	RELA	0	0.526
IL10	LOC100138951	0	0.543
IL10	IL2RB	0	0.555
IL10	LOC281376	0	0.555
IL10	SERPINB2	0	0.555
IL10	IRF7	0	0.557
IL10	SERPINE1	0	0.558
IL10	SELP	0	0.558

IL10	TREM1	0	0.569
IL10	MMP25	0	0.586
IL10	NCR1	0	0.586
IL10	TNFAIP6	0	0.588
IL10	LAMP1	0	0.589
IL10	NOD1	0	0.593
IL10	IL27	0	0.595
IL10	IRAK4	0.152	0.609
IL10	IRF1	0	0.636
IL10	MAP3K5	0	0.676
IL10	STAT4	0.12	0.678
IL10	TNFRSF18	0	0.692
IL10	IL22RA2	0	0.7
IL10	TYK2	0.054	0.702
IL10	NOD2	0	0.702
IL10	IL1RN	0	0.71
IL10	IL13RA1	0	0.715
IL10	IL12A	0	0.738
IL10	JAK3	0.054	0.739
IL10	SOCS3	0	0.742
IL10	SELL	0	0.763
IL10	PTGS2	0	0.77
IL10	IL2RG	0	0.776
IL10	NOS2	0	0.777
IL10	TLR9	0.055	0.809
IL10	IL7R	0	0.815
IL10	STAT1	0.12	0.82
IL10	VEGFA	0	0.824
IL10	PTPRC	0	0.827
IL10	IL6R	0	0.835
IL10	JAK2	0.054	0.843
IL10	IL1A	0	0.844
IL10	IL15	0	0.874
IL10	IL2RA	0	0.893
IL10	IL18	0	0.895
IL10	TLR2	0.055	0.899
IL10	IL20RA	0.206	0.904
IL10	STAT3	0.211	0.94
IL10	IL6	0	0.953
IL10	TNF	0	0.954
IL10	IL10RB	0.48	0.992
IL10RA	IL1B	0	0.458
IL10RA	IL4R	0	0.638
IL10RA	JAK1	0.926	0.998
IL10RA	IL23A	0	0.671
IL10RA	STAT2	0.114	0.586
IL10RA	IL12B	0	0.6

IL10RA	IL18	0	0.419
IL10RA	TLR2	0	0.42
IL10RA	SELL	0	0.42
IL10RA	IL7R	0	0.424
IL10RA	IL1A	0	0.426
IL10RA	NCF4	0	0.428
IL10RA	IRAK4	0.12	0.437
IL10RA	IL1RN	0	0.455
IL10RA	TEC	0.205	0.459
IL10RA	LTB	0	0.462
IL10RA	TLR4	0	0.481
IL10RA	LAPTM5	0	0.491
IL10RA	LYN	0.205	0.494
IL10RA	TNFRSF1B	0	0.495
IL10RA	IL1R1	0	0.519
IL10RA	IL2RB	0	0.519
IL10RA	IL13RA1	0	0.522
IL10RA	THEMIS2	0	0.529
IL10RA	IL2RG	0	0.532
IL10RA	SOCS3	0	0.546
IL10RA	STAT4	0.114	0.546
IL10RA	IL20RA	0.06	0.553
IL10RA	PTPRC	0	0.585
IL10RA	STAT6	0.114	0.597
IL10RA	IL6R	0	0.613
IL10RA	TNF	0	0.614
IL10RA	MAP3K5	0	0.624
IL10RA	OSM	0	0.65
IL10RA	IL12A	0	0.665
IL10RA	STAT5A	0.114	0.712
IL10RA	STAT5B	0.114	0.714
IL10RA	IL15	0	0.758
IL10RA	IL6	0	0.766
IL10RA	STAT1	0.114	0.829
IL10RA	JAK2	0.475	0.925
IL10RA	JAK3	0.475	0.928
IL10RA	STAT3	0.174	0.932
IL10RA	TYK2	0.205	0.982
IL10RA	IL10RB	0.093	0.992
IL10RB	JAK1	0.093	0.98
IL10RB	TNFRSF1A	0.065	0.411
IL10RB	IL23A	0	0.627
IL10RB	STAT2	0.159	0.617
IL10RB	IL12B	0	0.611
IL10RB	IL1R1	0	0.472
IL10RB	STAT6	0.159	0.428
IL10RB	IL2RG	0	0.428

IL10RB	PLEKHO2	0	0.496
IL10RB	STAT5B	0.159	0.479
IL10RB	TYK2	0.093	0.967
IL10RB	JAK2	0.093	0.856
IL10RB	IL6	0	0.713
IL10RB	IL12A	0	0.617
IL10RB	IL20RA	0	0.862
IL10RB	OSM	0	0.604
IL10RB	IL15	0	0.689
IL10RB	IL13RA1	0	0.419
IL10RB	LYN	0.093	0.402
IL10RB	IL1RN	0	0.422
IL10RB	STAT5A	0.159	0.427
IL10RB	STAT4	0.159	0.497
IL10RB	IRF9	0	0.643
IL10RB	STAT1	0.159	0.675
IL10RB	STAT3	0.159	0.677
IL10RB	JAK3	0.093	0.849
IL12A	MYD88	0	0.486
IL12A	IL1B	0	0.778
IL12A	IL4R	0	0.626
IL12A	JAK1	0	0.575
IL12A	IL23A	0	0.889
IL12A	STAT2	0	0.44
IL12A	SOCS1	0	0.692
IL12A	IL12B	0.935	0.998
IL12A	NFKB2	0	0.618
IL12A	IL15RA	0	0.623
IL12A	TLR4	0	0.541
IL12A	STAT6	0	0.714
IL12A	NOS2	0	0.749
IL12A	IL2RG	0	0.626
IL12A	TLR2	0	0.5
IL12A	SOCS3	0	0.488
IL12A	STAT5B	0	0.573
IL12A	TYK2	0	0.702
IL12A	JAK2	0	0.726
IL12A	IL6	0	0.558
IL12A	IL15	0	0.41
IL12A	IL1RN	0	0.428
IL12A	TLR9	0	0.473
IL12A	IRF1	0	0.474
IL12A	IL18	0	0.532
IL12A	NFKB1	0	0.533
IL12A	STAT5A	0	0.573
IL12A	JAK3	0	0.574
IL12A	IL20RA	0	0.6

IL12A	IL22RA2	0	0.6
IL12A	IL13RA1	0	0.629
IL12A	IL7R	0	0.63
IL12A	IL6R	0	0.66
IL12A	RELB	0	0.671
IL12A	IL2RA	0	0.674
IL12A	STAT4	0	0.682
IL12A	TNF	0	0.701
IL12A	IL27	0	0.757
IL12A	STAT3	0	0.76
IL12A	STAT1	0	0.782
IL12B	IL1B	0	0.796
IL12B	IL4R	0	0.6
IL12B	JAK1	0	0.503
IL12B	IL23A	0.948	0.991
IL12B	STAT2	0	0.422
IL12B	TLR4	0	0.412
IL12B	POR	0	0.437
IL12B	TLR2	0	0.469
IL12B	IL18	0	0.552
IL12B	JAK3	0	0.555
IL12B	IL13RA1	0	0.6
IL12B	LITAF	0	0.6
IL12B	IL7R	0	0.6
IL12B	IL15RA	0	0.6
IL12B	IL6	0	0.605
IL12B	IL20RA	0	0.611
IL12B	NFKB2	0	0.612
IL12B	SOCS3	0	0.624
IL12B	IL6R	0	0.628
IL12B	IL15	0	0.631
IL12B	STAT4	0	0.634
IL12B	STAT3	0	0.634
IL12B	NFKB1	0	0.635
IL12B	IL2RA	0	0.635
IL12B	IL2RG	0	0.637
IL12B	RELA	0.113	0.641
IL12B	JAK2	0	0.641
IL12B	IL22RA2	0	0.642
IL12B	STAT6	0	0.647
IL12B	STAT1	0	0.689
IL12B	TYK2	0	0.695
IL12B	NOS2	0	0.729
IL12B	TNF	0	0.756
IL13RA1	IL4R	0.927	0.998
IL13RA1	JAK1	0.054	0.91
IL13RA1	IL23A	0	0.612

IL13RA1	STAT2	0	0.5
IL13RA1	SOCS1	0	0.715
IL13RA1	IL15RA	0	0.411
IL13RA1	STAT6	0	0.846
IL13RA1	SOCS3	0	0.476
IL13RA1	STAT5B	0	0.512
IL13RA1	TYK2	0.113	0.945
IL13RA1	JAK2	0.054	0.947
IL13RA1	IL6	0	0.684
IL13RA1	OSM	0	0.641
IL13RA1	IL15	0	0.708
IL13RA1	ITGAV	0	0.42
IL13RA1	NIPAL4	0	0.459
IL13RA1	STAT5A	0	0.497
IL13RA1	STAT1	0	0.527
IL13RA1	STAT3	0	0.598
IL13RA1	JAK3	0.054	0.903
IL15	MYD88	0	0.492
IL15	IL1B	0	0.733
IL15	IL4R	0	0.762
IL15	JAK1	0	0.821
IL15	IL23A	0	0.41
IL15	STAT2	0.042	0.508
IL15	SOCS1	0	0.417
IL15	IL1R1	0	0.444
IL15	IL15RA	0.954	0.999
IL15	TLR4	0	0.662
IL15	STAT6	0.042	0.568
IL15	IL2RG	0.803	0.991
IL15	TLR2	0	0.565
IL15	SOCS3	0	0.403
IL15	LCP2	0	0.567
IL15	STAT5B	0.045	0.526
IL15	PTPRC	0	0.69
IL15	IL1A	0	0.659
IL15	TYK2	0	0.421
IL15	JAK2	0	0.587
IL15	IL6	0	0.74
IL15	IL20RA	0	0.61
IL15	IL2RB	0.937	0.993
IL15	IL22RA2	0	0.671
IL15	TLR9	0	0.537
IL15	LOC100138951	0	0.406
IL15	IRF7	0	0.432
IL15	IL1RN	0	0.436
IL15	TNFSF13B	0	0.443
IL15	TNFSF10	0	0.465

IL15	STAT4	0.042	0.469
IL15	STAT5A	0.045	0.507
IL15	IRF1	0	0.531
IL15	STAT3	0.042	0.605
IL15	STAT1	0.042	0.629
IL15	TNFSF9	0	0.65
IL15	VEGFA	0	0.674
IL15	SELL	0	0.679
IL15	LAMP1	0	0.698
IL15	IL6R	0	0.731
IL15	NCR1	0	0.757
IL15	JAK3	0	0.862
IL15	IL7R	0	0.868
IL15	TNF	0	0.882
IL15	IL2RA	0	0.906
IL15	IL18	0	0.942
IL15RA	JAK1	0.042	0.655
IL15RA	IL23A	0	0.623
IL15RA	SP110	0	0.41
IL15RA	IL7R	0	0.421
IL15RA	IL1RN	0	0.429
IL15RA	IL2RA	0	0.495
IL15RA	OSM	0	0.635
IL15RA	JAK2	0.042	0.651
IL15RA	IL6	0	0.657
IL15RA	TYK2	0.042	0.66
IL15RA	JAK3	0.042	0.687
IL15RA	IL2RB	0.926	0.982
IL15RA	IL2RG	0.926	0.992
IL17RC	IL18R1	0	0.508
IL17RC	TRAF3	0	0.562
IL17RC	IL6	0	0.407
IL17RC	IL20RA	0	0.551
IL17RC	TNF	0	0.409
IL17REL	RHBDF2	0	0.651
IL17REL	NCF4	0	0.468
IL17REL	PPP1R3B	0	0.45
IL17REL	RELT	0	0.589
IL17REL	SUSD2	0	0.553
IL17REL	RNF213	0	0.517
IL17REL	TNIP3	0	0.479
IL17REL	ZMIZ2	0	0.663
IL18	MYD88	0	0.822
IL18	IL18R1	0.926	0.999
IL18	NLRP3	0	0.915
IL18	IL1B	0	0.908
IL18	NAIP	0	0.579

IL18	JUN	0	0.879
IL18	TNFRSF1A	0	0.427
IL18	IL23A	0	0.518
IL18	STAT2	0	0.645
IL18	IL1R1	0.276	0.944
IL18	NLRC5	0	0.443
IL18	LITAF	0	0.517
IL18	NFKB2	0	0.602
IL18	TLR4	0	0.83
IL18	STAT6	0	0.652
IL18	IL1R2	0.276	0.693
IL18	NOS2	0	0.514
IL18	IL2RG	0	0.419
IL18	TLR2	0	0.765
IL18	NLRC4	0	0.883
IL18	STAT5B	0	0.466
IL18	PTPRC	0	0.568
IL18	IL1A	0	0.729
IL18	PANX1	0	0.506
IL18	RELA	0	0.945
IL18	PTGS2	0	0.597
IL18	IL6	0	0.823
IL18	IL2RB	0	0.415
IL18	TLR9	0	0.681
IL18	MEFV	0	0.756
IL18	IL1RN	0	0.602
IL18	NFKB1	0	0.948
IL18	IL2RA	0	0.43
IL18	NOD2	0	0.698
IL18	IRAK4	0.044	0.531
IL18	TIRAP	0	0.432
IL18	STAT3	0	0.714
IL18	STAT5A	0	0.464
IL18	TNF	0	0.898
IL18	IRF1	0	0.579
IL18	LAMP1	0	0.586
IL18	IL1RAP	0	0.448
IL18	SELL	0	0.491
IL18	IL18RAP	0.807	0.996
IL18	STAT4	0	0.779
IL18	NOD1	0	0.678
IL18	STAT1	0	0.736
IL18	NCR1	0	0.666
IL18	IRF7	0	0.531
IL18	VEGFA	0	0.586
IL18R1	MYD88	0.311	0.698
IL18R1	TXNDC16	0	0.41

IL18R1	TAGAP	0	0.412
IL18R1	IL2RB	0	0.437
IL18R1	STAT3	0.071	0.457
IL18R1	STAT5B	0.071	0.458
IL18R1	IL7R	0	0.461
IL18R1	STAT5A	0.071	0.469
IL18R1	STAT6	0.071	0.473
IL18R1	STAT1	0.071	0.487
IL18R1	JUNB	0	0.495
IL18R1	NFKB2	0	0.517
IL18R1	IL1RN	0.16	0.525
IL18R1	IL2RA	0	0.536
IL18R1	IL1B	0.16	0.605
IL18R1	IL1A	0.184	0.617
IL18R1	IL20RA	0	0.632
IL18R1	JUN	0	0.636
IL18R1	RELA	0	0.655
IL18R1	IL1RAP	0.344	0.656
IL18R1	NFKB1	0	0.675
IL18R1	STAT4	0.071	0.744
IL18R1	IL18RAP	0.67	0.981
IL18RAP	MYD88	0.311	0.75
IL18RAP	IL1B	0.16	0.568
IL18RAP	RPIA	0	0.632
IL18RAP	NFKB2	0	0.543
IL18RAP	STAT6	0.071	0.414
IL18RAP	STAT5B	0.071	0.424
IL18RAP	IL1A	0.184	0.624
IL18RAP	VNN2	0	0.432
IL18RAP	PTPN22	0	0.441
IL18RAP	IL1RN	0.16	0.484
IL18RAP	NFKB1	0	0.613
IL18RAP	IL2RA	0	0.405
IL18RAP	NOD2	0	0.423
IL18RAP	STAT3	0.071	0.456
IL18RAP	STAT5A	0.071	0.433
IL18RAP	TAGAP	0	0.555
IL18RAP	IL1RAP	0.344	0.666
IL18RAP	STAT1	0.071	0.453
IL18RAP	STAT4	0.071	0.696
IL1A	MYD88	0	0.873
IL1A	NLRP3	0	0.475
IL1A	IL1B	0	0.997
IL1A	JUN	0	0.492
IL1A	TNFRSF1A	0	0.452
IL1A	MAP3K2	0	0.462
IL1A	MAP4K4	0	0.664

IL1A	IL1R1	0.201	0.992
IL1A	NFKB2	0.043	0.46
IL1A	IRAK2	0	0.746
IL1A	TLR4	0	0.745
IL1A	IL1R2	0.431	0.99
IL1A	RIPK1	0	0.487
IL1A	NOS2	0	0.431
IL1A	TLR2	0	0.656
IL1A	PTPRC	0	0.447
IL1A	RELA	0	0.402
IL1A	MX1	0	0.405
IL1A	TRAF2	0	0.406
IL1A	TNFRSF1B	0	0.41
IL1A	TNFSF10	0	0.418
IL1A	TNIP1	0	0.42
IL1A	TLR9	0	0.425
IL1A	STAT1	0	0.427
IL1A	SERPINE1	0	0.429
IL1A	TREM1	0	0.437
IL1A	TRAF3	0	0.451
IL1A	MLKL	0	0.452
IL1A	STAT3	0	0.469
IL1A	RELB	0	0.471
IL1A	RIPK3	0	0.479
IL1A	TNFSF9	0	0.48
IL1A	TNIP3	0	0.503
IL1A	RIPK2	0	0.527
IL1A	VEGFA	0	0.527
IL1A	NFKB1	0.043	0.572
IL1A	RND1	0	0.572
IL1A	IRF1	0	0.582
IL1A	MAP3K8	0	0.635
IL1A	MAPKAPK3	0	0.647
IL1A	NFKBIE	0.078	0.653
IL1A	SP140L	0	0.661
IL1A	TRAF1	0	0.663
IL1A	MAPKAPK2	0	0.673
IL1A	OSM	0	0.716
IL1A	IRAK4	0	0.733
IL1A	MEFV	0	0.764
IL1A	PTGS2	0	0.77
IL1A	IL1RN	0	0.913
IL1A	TNF	0	0.939
IL1A	IL6	0	0.941
IL1A	IL1RAP	0.078	0.972
IL1B	MYD88	0	0.947
IL1B	NLRP3	0	0.972

IL1B	NAIP	0	0.401
IL1B	NAMPT	0	0.402
IL1B	STAT2	0	0.408
IL1B	S100A12	0	0.41
IL1B	TNFSF10	0	0.411
IL1B	LYN	0.113	0.416
IL1B	KRAS	0	0.416
IL1B	IRF5	0	0.433
IL1B	LIMK2	0.061	0.435
IL1B	STAT4	0	0.435
IL1B	TRAF7	0.08	0.438
IL1B	SAA2	0	0.447
IL1B	PSEN1	0	0.45
IL1B	TNFAIP6	0	0.45
IL1B	XDH	0	0.45
IL1B	PTX3	0	0.455
IL1B	MX1	0	0.458
IL1B	MAP3K5	0	0.462
IL1B	SOCS1	0	0.462
IL1B	IL7R	0	0.464
IL1B	PLAU	0	0.466
IL1B	ISG15	0.042	0.469
IL1B	MLKL	0.081	0.475
IL1B	S100A8	0	0.475
IL1B	LOC281376	0	0.478
IL1B	TNFRSF1B	0	0.484
IL1B	SERPINB2	0	0.486
IL1B	TIRAP	0	0.489
IL1B	ZC3H12A	0.113	0.49
IL1B	IL23A	0	0.507
IL1B	RETN	0	0.508
IL1B	IL6R	0	0.512
IL1B	RIPK2	0.081	0.514
IL1B	NCF1	0	0.518
IL1B	IL2RA	0	0.52
IL1B	SELL	0	0.521
IL1B	LOC515976	0.042	0.525
IL1B	MAP3K8	0	0.527
IL1B	STAT6	0	0.528
IL1B	SOD2	0	0.53
IL1B	SIRT1	0	0.532
IL1B	RIPK1	0.174	0.532
IL1B	RIPK3	0.174	0.537
IL1B	RND1	0	0.539
IL1B	PANX1	0	0.553
IL1B	TREM1	0	0.566
IL1B	NFE2L2	0	0.571

IL1B	IRF7	0	0.579
IL1B	TRAF2	0.08	0.59
IL1B	NOD1	0	0.591
IL1B	SELP	0	0.599
IL1B	RELB	0	0.601
IL1B	SERPINE1	0	0.614
IL1B	TRAF3	0.159	0.615
IL1B	SOCS3	0	0.622
IL1B	NFKBIB	0	0.625
IL1B	JAK1	0.054	0.657
IL1B	JAK3	0.054	0.659
IL1B	PIK3CA	0	0.667
IL1B	NOD2	0	0.668
IL1B	LITAF	0	0.67
IL1B	TRAF1	0.08	0.673
IL1B	PTPRC	0.042	0.686
IL1B	MMP25	0.078	0.692
IL1B	TLR9	0	0.702
IL1B	TNFRSF1A	0	0.704
IL1B	VEGFA	0	0.705
IL1B	IRF1	0	0.71
IL1B	STAT1	0	0.715
IL1B	TYK2	0.054	0.725
IL1B	NFKBIE	0	0.73
IL1B	NFKB2	0	0.768
IL1B	IRG1	0	0.776
IL1B	IRAK2	0.061	0.776
IL1B	IL1RN	0	0.782
IL1B	STAT3	0	0.782
IL1B	NLRC4	0	0.79
IL1B	OSM	0	0.798
IL1B	JAK2	0.054	0.808
IL1B	NOS2	0	0.822
IL1B	IRAK4	0.08	0.833
IL1B	MEFV	0	0.875
IL1B	TLR2	0	0.884
IL1B	TLR4	0	0.894
IL1B	PTGS2	0	0.904
IL1B	JUN	0	0.943
IL1B	TNF	0	0.966
IL1B	IL6	0	0.972
IL1B	RELA	0.055	0.976
IL1B	NFKB1	0	0.977
IL1B	IL1R2	0.759	0.996
IL1B	IL1RAP	0.948	0.998
IL1B	IL1R1	0.931	0.999
IL1R1	MYD88	0.876	0.999

IL1R1	NLRP3	0	0.676
IL1R1	IL4R	0	0.422
IL1R1	JUN	0	0.513
IL1R1	TNFRSF1A	0.045	0.784
IL1R1	MAP3K2	0.055	0.495
IL1R1	STAT2	0.093	0.412
IL1R1	MAP4K4	0	0.657
IL1R1	IL7R	0	0.413
IL1R1	RNF41	0.157	0.414
IL1R1	PTPRC	0	0.418
IL1R1	STAT6	0.093	0.43
IL1R1	MLKL	0.08	0.434
IL1R1	RIPK3	0.08	0.454
IL1R1	TAB2	0	0.462
IL1R1	TNIP2	0	0.463
IL1R1	NOD2	0	0.478
IL1R1	TNFRSF1B	0	0.48
IL1R1	TRAF7	0.157	0.487
IL1R1	RIPK2	0.08	0.5
IL1R1	LIMK2	0.236	0.506
IL1R1	PTGS2	0	0.506
IL1R1	NLRC4	0	0.507
IL1R1	STAT1	0.093	0.517
IL1R1	TRAF2	0.157	0.518
IL1R1	TRAF1	0.157	0.558
IL1R1	TRAF3	0.157	0.594
IL1R1	IL6R	0	0.605
IL1R1	TLR9	0	0.616
IL1R1	TIRAP	0	0.624
IL1R1	IL6	0	0.644
IL1R1	RIPK1	0.08	0.65
IL1R1	NFKB2	0	0.66
IL1R1	STAT3	0.174	0.672
IL1R1	RELA	0	0.735
IL1R1	NFKB1	0	0.739
IL1R1	TLR2	0	0.75
IL1R1	TLR4	0	0.806
IL1R1	TNF	0	0.837
IL1R1	IL1R2	0	0.868
IL1R1	IRAK2	0.236	0.91
IL1R1	IRAK4	0.584	0.99
IL1R1	IL1RAP	0.952	0.997
IL1R1	IL1RN	0.926	0.998
IL1R2	MYD88	0.311	0.687
IL1R2	LONRF3	0	0.472
IL1R2	JUN	0	0.4
IL1R2	TNFRSF1A	0.045	0.454

IL1R2	MAP4K4	0	0.58
IL1R2	TLR4	0	0.429
IL1R2	TRAF3	0.116	0.402
IL1R2	IL6	0	0.404
IL1R2	TNFRSF1B	0	0.411
IL1R2	IL7R	0	0.416
IL1R2	SOCS3	0	0.428
IL1R2	TNF	0	0.45
IL1R2	LTB4R	0	0.471
IL1R2	TBC1D8	0	0.585
IL1R2	IL1RAP	0.926	0.964
IL1R2	IL1RN	0.16	0.97
IL1RAP	MYD88	0.217	0.953
IL1RAP	NFKB2	0	0.572
IL1RAP	IRAK2	0.149	0.762
IL1RAP	TRAF2	0.055	0.407
IL1RAP	TRAF3	0.113	0.443
IL1RAP	RELA	0	0.635
IL1RAP	TRAF7	0.055	0.407
IL1RAP	IL1RN	0.238	0.954
IL1RAP	NFKB1	0	0.653
IL1RAP	IRAK4	0.203	0.853
IL1RAP	RNF41	0.055	0.407
IL1RAP	TRAF1	0.055	0.407
IL1RAP	LIMK2	0.149	0.521
IL1RN	MYD88	0	0.739
IL1RN	NLRP3	0	0.401
IL1RN	NFKB2	0	0.445
IL1RN	IRAK2	0.047	0.692
IL1RN	TLR4	0	0.491
IL1RN	S100A9	0	0.421
IL1RN	TNFAIP6	0	0.444
IL1RN	TLR2	0	0.48
IL1RN	SOCS3	0	0.438
IL1RN	S100A8	0	0.467
IL1RN	RELA	0.113	0.554
IL1RN	PTGS2	0	0.496
IL1RN	IL6	0	0.727
IL1RN	TREM1	0	0.427
IL1RN	KLRG2	0	0.512
IL1RN	TNFSF13B	0	0.41
IL1RN	IRF7	0	0.414
IL1RN	LIMK2	0.047	0.423
IL1RN	S100A12	0	0.45
IL1RN	NFKB1	0	0.468
IL1RN	IRAK4	0.047	0.649
IL1RN	TNF	0	0.665

IL20RA	JAK1	0.093	0.702
IL20RA	IL23A	0	0.6
IL20RA	STAT2	0.159	0.411
IL20RA	TYK2	0.093	0.698
IL20RA	JAK2	0.093	0.664
IL20RA	IL6	0	0.645
IL20RA	IRF9	0	0.445
IL20RA	IL2RB	0	0.562
IL20RA	STAT1	0.159	0.567
IL20RA	OSM	0	0.6
IL20RA	STAT3	0.159	0.612
IL20RA	JAK3	0.093	0.705
IL22RA2	KCNJ15	0	0.461
IL22RA2	JAK1	0	0.617
IL22RA2	IL23A	0	0.611
IL22RA2	RNF19B	0	0.414
IL22RA2	TYK2	0	0.649
IL22RA2	JAK2	0	0.6
IL22RA2	SPTSSA	0	0.632
IL22RA2	IL6	0	0.634
IL22RA2	OSM	0	0.63
IL22RA2	RNF19A	0	0.632
IL22RA2	JAK3	0	0.635
IL23A	IL4R	0	0.626
IL23A	JAK1	0	0.534
IL23A	STAT2	0	0.468
IL23A	TLR4	0	0.478
IL23A	SOCS1	0	0.479
IL23A	TLR2	0	0.481
IL23A	STAT6	0	0.503
IL23A	NFKB2	0	0.519
IL23A	IL6	0	0.528
IL23A	JAK3	0	0.537
IL23A	STAT5A	0	0.583
IL23A	STAT5B	0	0.583
IL23A	IL2RG	0	0.616
IL23A	NFKB1	0	0.631
IL23A	IL7R	0	0.637
IL23A	SOCS3	0	0.671
IL23A	IL2RA	0	0.672
IL23A	IL6R	0	0.686
IL23A	TNF	0	0.691
IL23A	STAT4	0	0.703
IL23A	RELA	0.174	0.709
IL23A	STAT1	0	0.741
IL23A	IL27	0	0.764
IL23A	STAT3	0	0.801

IL23A	TYK2	0	0.936
IL23A	JAK2	0	0.937
IL27	JAK1	0	0.675
IL27	STAT2	0	0.699
IL27	STAT6	0	0.484
IL27	STAT5B	0	0.572
IL27	TYK2	0	0.672
IL27	JAK2	0	0.667
IL27	IL6R	0	0.461
IL27	JAK3	0	0.536
IL27	STAT5A	0	0.572
IL27	STAT4	0	0.666
IL27	STAT3	0	0.749
IL27	STAT1	0	0.792
IL2RA	PRDM1	0	0.445
IL2RA	IL4R	0	0.664
IL2RA	JAK1	0	0.946
IL2RA	STAT2	0.12	0.559
IL2RA	SOCS1	0	0.715
IL2RA	STAT6	0.12	0.628
IL2RA	LOC616942	0	0.519
IL2RA	IL2RG	0	0.985
IL2RA	SOCS3	0	0.709
IL2RA	PRKCD	0	0.457
IL2RA	PIK3CA	0	0.612
IL2RA	STAT5B	0.162	0.959
IL2RA	MR1	0	0.498
IL2RA	PTPRC	0	0.707
IL2RA	PTPN2	0	0.562
IL2RA	TYK2	0	0.768
IL2RA	JAK2	0	0.943
IL2RA	IL6	0	0.797
IL2RA	TNFRSF18	0	0.637
IL2RA	OSM	0	0.619
IL2RA	NMI	0	0.62
IL2RA	IL2RB	0.204	0.98
IL2RA	PTPN22	0	0.736
IL2RA	IL7R	0	0.696
IL2RA	PTPN6	0	0.481
IL2RA	TNFRSF1B	0	0.418
IL2RA	SDS	0	0.421
IL2RA	SERPINB2	0	0.426
IL2RA	LOC281376	0	0.426
IL2RA	NCR1	0	0.457
IL2RA	TNF	0	0.653
IL2RA	STAT4	0.12	0.664
IL2RA	KRAS	0	0.665

IL2RA	SELL	0	0.715
IL2RA	STAT1	0.12	0.771
IL2RA	STAT3	0.12	0.798
IL2RA	STAT5A	0.162	0.951
IL2RA	JAK3	0	0.977
IL2RB	PRDM1	0	0.445
IL2RB	IL4R	0	0.448
IL2RB	STAM2	0	0.621
IL2RB	JAK1	0.764	0.976
IL2RB	PTPN12	0.042	0.497
IL2RB	STAT2	0.121	0.614
IL2RB	SOCS1	0.218	0.759
IL2RB	NLRC5	0	0.485
IL2RB	PTK2B	0	0.641
IL2RB	THEMIS2	0	0.406
IL2RB	STAT6	0.121	0.573
IL2RB	LOC616942	0	0.533
IL2RB	ITGAL	0	0.619
IL2RB	IL2RG	0.935	0.998
IL2RB	SOCS3	0.119	0.735
IL2RB	PRKCD	0	0.462
IL2RB	PIK3CA	0	0.643
IL2RB	LCP2	0	0.702
IL2RB	STAT5B	0.165	0.816
IL2RB	MR1	0	0.505
IL2RB	PTPRC	0.042	0.82
IL2RB	TYK2	0.175	0.522
IL2RB	JAK2	0.418	0.821
IL2RB	RHOH	0	0.434
IL2RB	KDM3A	0	0.412
IL2RB	TNFRSF18	0	0.504
IL2RB	RND1	0	0.404
IL2RB	TEC	0.175	0.421
IL2RB	LAMP1	0	0.422
IL2RB	RASGEF1B	0	0.422
IL2RB	IL6R	0	0.423
IL2RB	LYN	0.175	0.458
IL2RB	INPP5D	0	0.494
IL2RB	TNF	0	0.514
IL2RB	PTPN6	0.06	0.546
IL2RB	STAT4	0.121	0.555
IL2RB	KRAS	0	0.652
IL2RB	NCR1	0	0.69
IL2RB	PRKCB	0	0.711
IL2RB	PTPN22	0.042	0.744
IL2RB	SELL	0	0.765
IL2RB	STAT1	0.121	0.773

IL2RB	STAT5A	0.165	0.788
IL2RB	STAT3	0.121	0.855
IL2RB	IL7R	0	0.895
IL2RB	JAK3	0.418	0.942
IL2RG	RHOG	0	0.424
IL2RG	RASGRP2	0	0.427
IL2RG	IL4R	0.934	0.998
IL2RG	JAK1	0.219	0.987
IL2RG	STAT2	0.053	0.598
IL2RG	SOCS1	0	0.714
IL2RG	PTK2B	0	0.647
IL2RG	THEMIS2	0	0.42
IL2RG	TLR4	0	0.489
IL2RG	STAT6	0.053	0.961
IL2RG	LOC616942	0	0.513
IL2RG	ITGAL	0	0.615
IL2RG	RND1	0	0.406
IL2RG	PTPN22	0.06	0.409
IL2RG	TEC	0.133	0.432
IL2RG	TNFSF13B	0	0.435
IL2RG	PRKCD	0	0.439
IL2RG	LYN	0.133	0.443
IL2RG	TARS	0	0.451
IL2RG	TNF	0	0.463
IL2RG	NCR1	0	0.466
IL2RG	STAT4	0.053	0.47
IL2RG	ITGA9	0	0.47
IL2RG	RASGEF1B	0	0.484
IL2RG	MR1	0	0.488
IL2RG	RHOH	0	0.516
IL2RG	MCL1	0	0.517
IL2RG	SELL	0	0.536
IL2RG	NMI	0	0.636
IL2RG	ITGA2B	0	0.639
IL2RG	PIK3CA	0	0.642
IL2RG	MPEG1	0	0.65
IL2RG	PRKCB	0	0.655
IL2RG	OSM	0	0.671
IL2RG	LCP2	0	0.674
IL2RG	KRAS	0	0.678
IL2RG	SOCS3	0	0.692
IL2RG	PTPN6	0.06	0.692
IL2RG	INPP5D	0	0.706
IL2RG	IL6	0	0.729
IL2RG	STAT1	0.078	0.772
IL2RG	PTPRC	0.093	0.821
IL2RG	TYK2	0.133	0.829

IL2RG	STAT5A	0.07	0.943
IL2RG	STAT5B	0.07	0.948
IL2RG	STAT3	0.053	0.951
IL2RG	JAK2	0.296	0.963
IL2RG	IL7R	0.165	0.974
IL2RG	JAK3	0.432	0.996
IL4R	LYN	0.136	0.4
IL4R	TREM1	0	0.441
IL4R	TNF	0	0.477
IL4R	PTPRC	0.121	0.489
IL4R	IL6R	0	0.53
IL4R	SOCS3	0.095	0.577
IL4R	STAT4	0.219	0.587
IL4R	STAT2	0.219	0.614
IL4R	IL7R	0	0.621
IL4R	PIK3CA	0.046	0.622
IL4R	OSM	0	0.638
IL4R	PTPN6	0.235	0.653
IL4R	INPP5D	0.113	0.654
IL4R	STAT1	0.219	0.684
IL4R	STAT3	0.219	0.707
IL4R	SOCS1	0.095	0.727
IL4R	IL6	0	0.749
IL4R	STAT5B	0.219	0.76
IL4R	STAT5A	0.219	0.768
IL4R	TYK2	0.136	0.789
IL4R	JAK2	0.229	0.957
IL4R	JAK3	0.229	0.969
IL4R	JAK1	0.442	0.973
IL4R	STAT6	0.661	0.994
IL6	MYD88	0	0.829
IL6	NLRP3	0	0.637
IL6	NFKBIB	0.045	0.514
IL6	PTPRE	0	0.621
IL6	JAK1	0.07	0.977
IL6	NCF1	0	0.473
IL6	JUN	0	0.977
IL6	TNFRSF1A	0	0.61
IL6	VAV1	0	0.71
IL6	STAT2	0.114	0.825
IL6	SOCS1	0	0.768
IL6	OLR1	0	0.417
IL6	RETN	0	0.75
IL6	IRF5	0	0.443
IL6	LITAF	0	0.642
IL6	PLAU	0	0.412
IL6	NFKB2	0.045	0.61

IL6	LOC515976	0	0.495
IL6	IRAK2	0	0.445
IL6	TLR4	0	0.932
IL6	STAT6	0.114	0.833
IL6	RIPK1	0	0.412
IL6	SOD2	0	0.445
IL6	PTPN1	0	0.436
IL6	NOS2	0	0.788
IL6	ITGAL	0	0.406
IL6	TNFAIP6	0	0.47
IL6	PIAS2	0	0.449
IL6	TLR2	0	0.849
IL6	NLRC4	0	0.407
IL6	SOCS3	0	0.967
IL6	PTX3	0	0.549
IL6	STAT5B	0.114	0.737
IL6	PTPRC	0	0.862
IL6	MAP2K3	0	0.682
IL6	ZC3H12A	0.113	0.437
IL6	MAP3K8	0	0.442
IL6	TYK2	0.045	0.925
IL6	JAK2	0.055	0.988
IL6	JUNB	0	0.669
IL6	XDH	0	0.424
IL6	SLC1A2	0	0.439
IL6	RELA	0.113	0.968
IL6	SIRT1	0	0.608
IL6	PTGS2	0	0.903
IL6	SERPINE1	0	0.739
IL6	SNAI1	0	0.42
IL6	ISG15	0	0.418
IL6	VEGFC	0	0.47
IL6	RIPK2	0	0.4
IL6	MST1R	0	0.405
IL6	PSME1	0	0.414
IL6	TNFSF13B	0	0.414
IL6	TGFBR1	0	0.415
IL6	PPARD	0	0.416
IL6	RAPGEF1	0	0.422
IL6	TARM1	0	0.435
IL6	VDR	0	0.439
IL6	RASGEF1B	0	0.441
IL6	LOC100138951	0	0.448
IL6	MEFV	0	0.451
IL6	TREM1	0	0.455
IL6	NCR1	0	0.458
IL6	SAA2	0	0.459

IL6	NOD1	0	0.459
IL6	MX1	0	0.464
IL6	LOC281376	0	0.481
IL6	SERPINB2	0	0.485
IL6	TIRAP	0	0.491
IL6	LYN	0.045	0.5
IL6	TNFRSF1B	0	0.51
IL6	MCL1	0	0.519
IL6	PTPN6	0	0.53
IL6	IRAK4	0	0.545
IL6	IRF1	0	0.549
IL6	NAMPT	0	0.555
IL6	NFE2L2	0	0.557
IL6	RELB	0	0.559
IL6	NOD2	0	0.579
IL6	IRF7	0	0.584
IL6	KRAS	0	0.587
IL6	SELL	0	0.587
IL6	SELP	0	0.598
IL6	MMP25	0	0.636
IL6	PIAS1	0	0.67
IL6	STAT5A	0.114	0.736
IL6	IL7R	0	0.764
IL6	OSM	0.113	0.773
IL6	STAT4	0.114	0.782
IL6	VEGFA	0	0.783
IL6	TLR9	0	0.809
IL6	NFKB1	0.045	0.917
IL6	JAK3	0.055	0.92
IL6	STAT1	0.114	0.942
IL6	TNF	0	0.945
IL6	STAT3	0.174	0.969
IL6	IL6R	0.95	0.999
IL6R	PLCG2	0	0.8
IL6R	PTPRE	0	0.62
IL6R	JAK1	0.113	0.966
IL6R	TNFRSF1A	0	0.558
IL6R	VAV1	0	0.632
IL6R	STAT2	0.06	0.547
IL6R	SOCS1	0	0.514
IL6R	TLR4	0	0.401
IL6R	STAT6	0.06	0.613
IL6R	PIAS2	0	0.449
IL6R	SOCS3	0	0.93
IL6R	STAT5B	0.06	0.54
IL6R	PTPRC	0	0.591
IL6R	MAP2K3	0	0.578

IL6R	TYK2	0.054	0.916
IL6R	JAK2	0.075	0.969
IL6R	OSM	0	0.79
IL6R	ZMIZ1	0	0.445
IL6R	TNFRSF1B	0	0.452
IL6R	PTPN6	0	0.504
IL6R	STAT5A	0.06	0.53
IL6R	STAT4	0.06	0.597
IL6R	PIAS1	0	0.64
IL6R	TNF	0.07	0.686
IL6R	STAT1	0.06	0.798
IL6R	JAK3	0.075	0.953
IL6R	STAT3	0.113	0.987
IL7R	PRDM1	0	0.519
IL7R	JAK1	0.201	0.966
IL7R	SOCS1	0.12	0.513
IL7R	LOC515976	0	0.535
IL7R	ITGAL	0	0.451
IL7R	SLAMF1	0	0.571
IL7R	LCP2	0	0.681
IL7R	STAT5B	0.07	0.487
IL7R	PTPRC	0	0.776
IL7R	TYK2	0.114	0.697
IL7R	JAK2	0.163	0.898
IL7R	TNFRSF18	0	0.528
IL7R	OSM	0	0.669
IL7R	PTPN22	0	0.658
IL7R	LAMP1	0	0.401
IL7R	STAT5A	0.07	0.404
IL7R	STAT3	0.078	0.495
IL7R	NCR1	0	0.53
IL7R	P2RY8	0	0.622
IL7R	TNF	0	0.627
IL7R	SELL	0	0.732
IL7R	JAK3	0.203	0.95
ING5	KAT5	0.505	0.806
ING5	PHF12	0.138	0.411
ING5	TRPC5	0	0.491
ING5	RELA	0.311	0.572
ING5	KAT8	0.505	0.586
ING5	LOC100297725	0.317	0.654
INPP1	PLCG2	0	0.656
INPP1	INPP4A	0	0.938
INPP1	SLC37A1	0	0.409
INPP1	RASSF2	0	0.42
INPP1	SWT1	0	0.58
INPP1	INPP5D	0	0.903

INPP4A	SNX10	0	0.401
INPP4A	PI4K2A	0	0.557
INPP4A	PIK3R5	0	0.59
INPP4A	MTMR7	0	0.682
INPP4A	MTMR3	0	0.97
INPP4A	INPP5D	0	0.993
INPP5D	PLCG2	0.13	0.499
INPP5D	JAK1	0.135	0.686
INPP5D	PTPN12	0.072	0.526
INPP5D	VAV1	0	0.424
INPP5D	SOCS1	0	0.434
INPP5D	RAF1	0.076	0.605
INPP5D	PTK2B	0.045	0.509
INPP5D	SLAMF1	0.506	0.576
INPP5D	SUPT6H	0.398	0.43
INPP5D	PIK3CA	0.045	0.911
INPP5D	LCP2	0.123	0.649
INPP5D	PTPRC	0.072	0.499
INPP5D	IPMK	0	0.917
INPP5D	JAK2	0.135	0.74
INPP5D	SH3BP2	0	0.433
INPP5D	MST1R	0.215	0.653
INPP5D	PTPN22	0.072	0.576
INPP5D	LYN	0.135	0.629
INPP5D	TREML2	0	0.402
INPP5D	KRAS	0.093	0.443
INPP5D	SAG	0	0.449
INPP5D	LOC100138951	0	0.455
INPP5D	MPEG1	0	0.472
INPP5D	P2RY8	0	0.494
INPP5D	LAIR1	0	0.508
INPP5D	TEC	0.135	0.515
INPP5D	SELPLG	0	0.532
INPP5D	PSTPIP1	0.174	0.559
INPP5D	PRKCB	0	0.666
INPP5D	PTPN6	0.118	0.736
INPP5D	JAK3	0.135	0.738
INSIG1	XDH	0	0.412
INTS6	KPNA3	0	0.455
INTS6	STK17B	0	0.492
INTS6	NABP1	0.212	0.562
INTS6	POLR2A	0.492	0.637
IPCEF1	PTAFR	0	0.41
IPCEF1	SLC6A9	0	0.476
IPCEF1	PSTPIP2	0	0.595
IPMK	PLCG2	0.079	0.765
IPMK	LMTK2	0	0.469

IPMK	MYSM1	0.044	0.431
IQSEC1	PFKFB4	0	0.404
IQSEC1	IRAK2	0.462	0.461
IQSEC1	ZYX	0	0.469
IQSEC1	ZC3H12C	0.461	0.473
IQSEC1	MYCBP2	0.06	0.479
IQSEC1	PLXNA1	0	0.506
IRAK2	MYD88	0.953	0.999
IRAK2	TNFRSF1A	0.13	0.548
IRAK2	SOCS1	0.123	0.411
IRAK2	MAP4K4	0.08	0.461
IRAK2	IRF5	0.175	0.511
IRAK2	RELA	0.121	0.401
IRAK2	PPM1D	0.158	0.413
IRAK2	ROCK1	0.219	0.414
IRAK2	RIPK2	0.165	0.415
IRAK2	ZC3H12A	0.296	0.43
IRAK2	TRAF7	0.219	0.432
IRAK2	RIPK1	0.165	0.444
IRAK2	TRAF2	0.219	0.444
IRAK2	TATDN2	0	0.484
IRAK2	STAT1	0.147	0.489
IRAK2	IRF7	0.158	0.5
IRAK2	ZC3H12C	0.47	0.511
IRAK2	RELB	0.044	0.541
IRAK2	TNF	0.093	0.571
IRAK2	TLR9	0.184	0.643
IRAK2	TRAF1	0.219	0.666
IRAK2	PELI1	0.327	0.67
IRAK2	TRAF3	0.219	0.686
IRAK2	TAB2	0.259	0.81
IRAK2	TLR2	0.184	0.866
IRAK2	TLR4	0.184	0.892
IRAK2	TIRAP	0.597	0.964
IRAK2	IRAK4	0.936	0.996
IRAK4	PIM1	0.123	0.427
IRAK4	MYD88	0.962	0.999
IRAK4	NLRP3	0.049	0.421
IRAK4	JUN	0.093	0.466
IRAK4	TNFRSF1A	0.152	0.583
IRAK4	MAP3K2	0.124	0.504
IRAK4	STAT2	0.147	0.446
IRAK4	SOCS1	0.123	0.539
IRAK4	MAP4K4	0.08	0.527
IRAK4	IRF5	0.294	0.743
IRAK4	TLR4	0.274	0.989
IRAK4	STAT6	0.147	0.463

IRAK4	RIPK1	0.165	0.419
IRAK4	S100A9	0.042	0.494
IRAK4	TLR2	0.184	0.947
IRAK4	PPM1D	0.158	0.413
IRAK4	TRAF2	0.219	0.885
IRAK4	MAPKAPK2	0.093	0.51
IRAK4	S100A8	0.042	0.529
IRAK4	TAB2	0.49	0.983
IRAK4	TRAF3	0.219	0.863
IRAK4	RELA	0.121	0.506
IRAK4	RSAD2	0.203	0.42
IRAK4	TLR9	0.184	0.852
IRAK4	RIPK3	0.165	0.413
IRAK4	TRAF7	0.219	0.465
IRAK4	NFKB1	0.093	0.557
IRAK4	PELI1	0.764	0.921
IRAK4	NOD2	0.06	0.565
IRAK4	PIM3	0.123	0.411
IRAK4	LRRK2	0.252	0.425
IRAK4	RNF41	0.219	0.43
IRAK4	ROCK1	0.219	0.432
IRAK4	RELB	0.044	0.433
IRAK4	TRAF1	0.219	0.463
IRAK4	STAT3	0.159	0.465
IRAK4	NOD1	0.06	0.47
IRAK4	TANK	0.134	0.472
IRAK4	STAT1	0.147	0.512
IRAK4	S100A12	0.042	0.558
IRAK4	RIPK2	0.165	0.609
IRAK4	TNF	0.093	0.713
IRAK4	IRF7	0.219	0.973
IRAK4	TIRAP	0.422	0.989
IRF1	MYD88	0.357	0.865
IRF1	KAT2B	0.435	0.79
IRF1	PSMB8	0	0.715
IRF1	JAK1	0.054	0.678
IRF1	JUN	0	0.921
IRF1	STAT2	0.262	0.855
IRF1	SOCS1	0	0.65
IRF1	IRF5	0	0.713
IRF1	NLRC5	0	0.651
IRF1	NFKB2	0.064	0.589
IRF1	TLR4	0	0.6
IRF1	STAT6	0.262	0.757
IRF1	NOS2	0	0.434
IRF1	UBXN7	0.141	0.626
IRF1	TLR2	0	0.553

IRF1	IRG1	0	0.417
IRF1	SOCS3	0	0.588
IRF1	MX2	0	0.599
IRF1	PSMB9	0	0.786
IRF1	STAT5B	0.262	0.559
IRF1	TRIM25	0.068	0.478
IRF1	IRF2	0.113	0.696
IRF1	XAF1	0.113	0.519
IRF1	MAP3K8	0	0.438
IRF1	TYK2	0.054	0.605
IRF1	JAK2	0.054	0.625
IRF1	JUNB	0	0.624
IRF1	UBA7	0	0.456
IRF1	RARA	0	0.497
IRF1	UBE2L6	0.069	0.406
IRF1	TRAF3	0.055	0.423
IRF1	RELA	0.078	0.862
IRF1	PTGS2	0	0.497
IRF1	OAS2	0	0.626
IRF1	ISG15	0.051	0.784
IRF1	RSAD2	0	0.754
IRF1	PARP14	0	0.607
IRF1	USP18	0	0.632
IRF1	TAPBP	0	0.49
IRF1	LOC512486	0	0.557
IRF1	TLR9	0	0.536
IRF1	RND1	0	0.428
IRF1	NFKB1	0.078	0.698
IRF1	STAT3	0.262	0.872
IRF1	PARP9	0	0.462
IRF1	LOC511531	0	0.488
IRF1	UBTF	0	0.416
IRF1	STAT5A	0.262	0.545
IRF1	TNF	0	0.759
IRF1	NFKBIE	0.043	0.506
IRF1	TRAF1	0.055	0.429
IRF1	MX1	0	0.778
IRF1	TRIM21	0.068	0.411
IRF1	TNFAIP2	0	0.458
IRF1	RELB	0	0.593
IRF1	ISG20	0	0.69
IRF1	LOC507055	0	0.691
IRF1	POLR2A	0.162	0.692
IRF1	TAP1	0	0.725
IRF1	STAT4	0.262	0.743
IRF1	IRF9	0.119	0.743
IRF1	IRF7	0	0.785

IRF1	PSME2	0	0.825
IRF1	MDM2	0.432	0.892
IRF1	STAT1	0.764	0.993
IRF2	KAT2B	0.218	0.761
IRF2	PRDM1	0.209	0.429
IRF2	NR1H2	0	0.435
IRF2	JUN	0	0.698
IRF2	STAT2	0.053	0.659
IRF2	IRF5	0	0.714
IRF2	TAL1	0	0.465
IRF2	STAT6	0.053	0.452
IRF2	TLR2	0	0.461
IRF2	MX2	0	0.423
IRF2	NMI	0	0.404
IRF2	NFKB1	0.113	0.414
IRF2	LOC507055	0	0.416
IRF2	UBTF	0.047	0.419
IRF2	ISG20	0	0.48
IRF2	TYK2	0	0.49
IRF2	MYSM1	0	0.562
IRF2	JUNB	0	0.581
IRF2	RSAD2	0	0.595
IRF2	MX1	0	0.597
IRF2	ISG15	0	0.598
IRF2	MDM2	0.113	0.619
IRF2	STAT1	0.078	0.709
IRF2	IRF7	0	0.744
IRF2	RELA	0.113	0.757
IRF5	MYD88	0.465	0.956
IRF5	KAT2B	0.117	0.646
IRF5	ISG20L2	0	0.412
IRF5	JAK1	0.071	0.401
IRF5	NR1H2	0.055	0.406
IRF5	JUN	0	0.71
IRF5	STAT2	0	0.621
IRF5	SOCS1	0	0.477
IRF5	ISG20	0	0.406
IRF5	RSAD2	0	0.429
IRF5	MX1	0	0.444
IRF5	PXK	0	0.469
IRF5	UBTF	0	0.475
IRF5	TNIP1	0	0.482
IRF5	TRIM21	0.113	0.486
IRF5	MYSM1	0.051	0.495
IRF5	TRAF3	0.114	0.497
IRF5	TLR2	0	0.542
IRF5	PTPN22	0	0.55

IRF5	JUNB	0	0.556
IRF5	NOD2	0	0.557
IRF5	LYN	0.071	0.567
IRF5	ISG15	0.093	0.592
IRF5	STAT6	0	0.595
IRF5	TYK2	0.071	0.598
IRF5	TLR4	0	0.627
IRF5	STAT4	0	0.662
IRF5	TLR9	0	0.663
IRF5	STAT1	0	0.711
IRF5	TNF	0.113	0.715
IRF5	IRF7	0	0.733
IRF5	RELA	0.113	0.902
IRF7	MYD88	0.538	0.994
IRF7	KAT2B	0.078	0.636
IRF7	PSMB8	0	0.416
IRF7	JAK1	0.078	0.605
IRF7	JUN	0	0.847
IRF7	STAT2	0	0.924
IRF7	SOCS1	0.113	0.662
IRF7	LOC616948	0.069	0.514
IRF7	NLRC5	0	0.497
IRF7	TLR4	0	0.709
IRF7	STAT6	0	0.556
IRF7	RIPK1	0.078	0.452
IRF7	TLR2	0	0.688
IRF7	SOCS3	0.113	0.553
IRF7	MX2	0	0.881
IRF7	PSMB9	0	0.401
IRF7	PARP10	0	0.538
IRF7	TRIM25	0.069	0.786
IRF7	XAF1	0	0.653
IRF7	TYK2	0.078	0.617
IRF7	JUNB	0	0.577
IRF7	UBA7	0	0.692
IRF7	UBE2L6	0	0.697
IRF7	TRAF3	0.257	0.905
IRF7	RELA	0	0.787
IRF7	OAS2	0	0.79
IRF7	ISG15	0	0.965
IRF7	SP110	0.069	0.576
IRF7	RSAD2	0.174	0.965
IRF7	NMI	0.211	0.503
IRF7	PARP12	0	0.527
IRF7	PARP14	0	0.703
IRF7	USP18	0	0.932
IRF7	TLR9	0	0.818

IRF7	TRIM38	0.069	0.429
IRF7	ZNFX1	0	0.493
IRF7	NFKB1	0	0.439
IRF7	NOD2	0	0.528
IRF7	TIRAP	0	0.53
IRF7	STAT3	0	0.525
IRF7	PARP9	0	0.708
IRF7	RNF213	0	0.552
IRF7	TNF	0	0.71
IRF7	TRAF1	0.257	0.492
IRF7	MX1	0	0.96
IRF7	TANK	0.113	0.588
IRF7	SMAD7	0.06	0.443
IRF7	IRF9	0	0.792
IRF7	PIAS1	0.07	0.511
IRF7	TAP1	0	0.438
IRF7	STAT4	0	0.592
IRF7	LOC507055	0.126	0.555
IRF7	ZBP1	0	0.954
IRF7	STAT1	0	0.962
IRF7	TRIM21	0.128	0.709
IRF7	POLR2A	0	0.627
IRF7	ISG20	0	0.79
IRF9	MYD88	0	0.466
IRF9	PSMB8	0	0.489
IRF9	JAK1	0	0.965
IRF9	STAT2	0.937	0.999
IRF9	SOCS1	0	0.487
IRF9	NLRC5	0	0.422
IRF9	STAT6	0.389	0.956
IRF9	SOCS3	0	0.407
IRF9	MX2	0	0.694
IRF9	PNPT1	0	0.432
IRF9	PSMB9	0	0.436
IRF9	STAT5B	0.389	0.924
IRF9	PARP10	0	0.44
IRF9	TRIM25	0	0.417
IRF9	XAF1	0	0.769
IRF9	TYK2	0	0.979
IRF9	JAK2	0	0.498
IRF9	UBA7	0	0.73
IRF9	UBE2L6	0.042	0.536
IRF9	OAS2	0	0.718
IRF9	ISG15	0	0.907
IRF9	RSAD2	0	0.743
IRF9	PARP12	0	0.64
IRF9	PARP14	0	0.637

IRF9	USP18	0	0.87
IRF9	TLR9	0	0.42
IRF9	STAT3	0.389	0.955
IRF9	PARP9	0	0.614
IRF9	RNF213	0	0.411
IRF9	STAT5A	0.389	0.924
IRF9	TNF	0	0.404
IRF9	MX1	0	0.917
IRF9	PSME2	0	0.459
IRF9	ZBP1	0	0.414
IRF9	LOC507055	0	0.44
IRF9	TRIM21	0	0.484
IRF9	ISG20	0	0.586
IRF9	STAT4	0.389	0.956
IRF9	STAT1	0.463	0.998
IRG1	STAT3	0	0.448
IRG1	STX11	0	0.482
IRG1	TNF	0	0.557
IRG1	ZC3H12A	0	0.561
ISG15	MYD88	0.093	0.577
ISG15	PSMA2	0.393	0.408
ISG15	PSMB8	0.35	0.589
ISG15	JAK1	0.125	0.874
ISG15	STAT2	0.06	0.791
ISG15	SOCS1	0.045	0.547
ISG15	LOC616948	0.148	0.551
ISG15	MAP1LC3A	0.124	0.431
ISG15	TLR4	0.093	0.508
ISG15	STAT6	0.06	0.436
ISG15	RPS9	0.459	0.492
ISG15	LGALS9	0	0.472
ISG15	UBXN7	0.661	0.704
ISG15	TLR2	0.093	0.414
ISG15	MX2	0.146	0.991
ISG15	PSMB9	0.403	0.69
ISG15	PARP10	0.117	0.557
ISG15	TRIM25	0.148	0.774
ISG15	XAF1	0	0.807
ISG15	TYK2	0.125	0.624
ISG15	JAK2	0.125	0.41
ISG15	UBA7	0.764	0.998
ISG15	UBE2L6	0.275	0.886
ISG15	TRAF3	0.215	0.617
ISG15	UBE2G1	0.357	0.46
ISG15	OAS2	0	0.836
ISG15	LOC511531	0.045	0.404
ISG15	PML	0.148	0.404

ISG15	TAP1	0.076	0.405
ISG15	TNFSF10	0	0.423
ISG15	UBE2B	0.317	0.437
ISG15	PSME2	0.052	0.445
ISG15	SP110	0.148	0.484
ISG15	MDM2	0.253	0.489
ISG15	TLR9	0.093	0.509
ISG15	LOC507055	0.045	0.51
ISG15	PLSCR2	0	0.512
ISG15	STAT4	0.06	0.54
ISG15	MYSM1	0.451	0.581
ISG15	ZNFX1	0.055	0.607
ISG15	ZBP1	0	0.637
ISG15	TNF	0.137	0.676
ISG15	TRIM21	0.148	0.697
ISG15	PARP12	0.043	0.748
ISG15	ISG20	0.043	0.841
ISG15	RNF213	0	0.844
ISG15	PARP9	0	0.883
ISG15	PARP14	0	0.886
ISG15	STAT1	0.06	0.946
ISG15	RSAD2	0	0.986
ISG15	MX1	0.146	0.992
ISG15	USP18	0.906	0.998
ISG20	STAT2	0	0.605
ISG20	MX2	0	0.844
ISG20	PAN3	0.412	0.534
ISG20	TRIM25	0	0.43
ISG20	UBE2L6	0	0.414
ISG20	OAS2	0	0.686
ISG20	RSAD2	0	0.767
ISG20	USP18	0	0.629
ISG20	RCL1	0	0.475
ISG20	TNFSF10	0	0.428
ISG20	MX1	0	0.777
ISG20	STAT1	0	0.652
ISG20L2	USPL1	0	0.501
ISG20L2	STAT2	0	0.416
ISG20L2	LTV1	0	0.45
ISG20L2	XRN2	0	0.48
ISG20L2	RCL1	0	0.491
ISG20L2	TRIM8	0	0.499
ISG20L2	PAN3	0.412	0.534
ISG20L2	USP32	0	0.625
ITGA2B	RASGRP2	0.052	0.418
ITGA2B	JAK1	0.08	0.651
ITGA2B	TAL1	0	0.419

ITGA2B	PTK2B	0.145	0.681
ITGA2B	PTPN1	0.113	0.658
ITGA2B	SLAMF1	0	0.523
ITGA2B	MST1R	0.127	0.41
ITGA2B	LOC100138951	0	0.451
ITGA2B	PTPN2	0.113	0.57
ITGA2B	STAT5B	0.045	0.613
ITGA2B	STAT5A	0.045	0.613
ITGA2B	JAK2	0.08	0.639
ITGA2B	PIK3CA	0	0.643
ITGA2B	PXN	0.123	0.66
ITGA2B	JAK3	0.08	0.679
ITGA2B	PTPRC	0.113	0.679
ITGA2B	RAP1B	0.042	0.688
ITGA2B	SELP	0	0.694
ITGA2B	ITGB7	0.419	0.757
ITGA5	VAV1	0	0.405
ITGA5	PLAU	0.042	0.727
ITGA5	PTK2B	0.224	0.942
ITGA5	PTPRC	0.115	0.468
ITGA5	PLAUR	0.054	0.709
ITGA5	KRAS	0.07	0.401
ITGA5	TSPAN2	0.12	0.401
ITGA5	MMP25	0.069	0.405
ITGA5	TGM2	0	0.477
ITGA5	SAT1	0.12	0.49
ITGA5	ZYX	0.051	0.504
ITGA5	TGFBR1	0.12	0.508
ITGA5	VEGFC	0	0.517
ITGA5	ROCK1	0.073	0.518
ITGA5	MST1R	0.127	0.525
ITGA5	VEGFA	0	0.593
ITGA5	SDC4	0.115	0.635
ITGA5	SERPINE1	0	0.685
ITGA5	VASP	0	0.776
ITGA5	PXN	0.166	0.79
ITGA5	SKAP2	0	0.816
ITGA5	LAMB3	0.093	0.848
ITGA5	ITGB7	0.349	0.96
ITGA9	PLAU	0.042	0.402
ITGA9	PTK2B	0.167	0.555
ITGA9	PLAUR	0.054	0.439
ITGA9	VEGFC	0	0.825
ITGA9	MST1R	0.127	0.474
ITGA9	TGM2	0	0.623
ITGA9	LAMB3	0.093	0.8
ITGA9	SDC4	0.115	0.534

ITGA9	VASP	0	0.603
ITGA9	VEGFA	0	0.615
ITGA9	SAT1	0.201	0.876
ITGA9	PXN	0.26	0.899
ITGA9	ITGB7	0.671	0.979
ITGAL	VAV1	0	0.572
ITGAL	PTK2B	0.145	0.885
ITGAL	TLR4	0.055	0.436
ITGAL	LAMP1	0	0.406
ITGAL	MST1R	0.127	0.41
ITGAL	TLR2	0.055	0.413
ITGAL	LCP2	0	0.417
ITGAL	PXN	0.123	0.42
ITGAL	SELPLG	0	0.485
ITGAL	ITGAV	0	0.49
ITGAL	SIRPA	0	0.492
ITGAL	PLAUR	0.054	0.506
ITGAL	NCR1	0	0.563
ITGAL	SELP	0	0.591
ITGAL	TNF	0	0.63
ITGAL	ITGB7	0.334	0.806
ITGAL	RAP1B	0.042	0.826
ITGAL	SELL	0	0.859
ITGAL	RASSF5	0.078	0.865
ITGAL	PTPRC	0.113	0.95
ITGAV	VAV1	0	0.422
ITGAV	PLAU	0.042	0.731
ITGAV	PTK2B	0.413	0.822
ITGAV	PIK3CA	0	0.663
ITGAV	SH2B2	0	0.447
ITGAV	PTPRC	0.115	0.628
ITGAV	PLAUR	0.054	0.802
ITGAV	SERPINE1	0	0.74
ITGAV	VEGFC	0	0.528
ITGAV	MST1R	0.127	0.512
ITGAV	TGM2	0	0.501
ITGAV	LAMB3	0.093	0.83
ITGAV	SAT1	0.12	0.49
ITGAV	ZYX	0.051	0.482
ITGAV	TGFBR1	0.12	0.862
ITGAV	PXN	0.219	0.723
ITGAV	ITGB7	0.349	0.958
ITGAV	VASP	0	0.651
ITGAV	KRAS	0.054	0.407
ITGAV	SELP	0	0.411
ITGAV	STAT1	0.113	0.647
ITGAV	ROCK1	0.073	0.679

ITGAV	SDC4	0.115	0.709
ITGAV	VEGFA	0	0.717
ITGB7	VAV1	0.055	0.445
ITGB7	PTK2B	0.408	0.81
ITGB7	PTPN1	0.166	0.423
ITGB7	RAP1B	0.114	0.481
ITGB7	PIK3CA	0.043	0.416
ITGB7	PTPRC	0.158	0.557
ITGB7	PTPN2	0.166	0.423
ITGB7	PLAUR	0.069	0.453
ITGB7	SERPINE1	0	0.406
ITGB7	VEGFC	0.121	0.459
ITGB7	MST1R	0.269	0.558
ITGB7	TGM2	0.141	0.57
ITGB7	MMP25	0.113	0.448
ITGB7	LAMB3	0.122	0.823
ITGB7	ZYX	0.067	0.648
ITGB7	PXN	0.257	0.906
ITGB7	PTPN6	0.134	0.403
ITGB7	PTPN22	0.159	0.443
ITGB7	SELL	0	0.454
ITGB7	SDC4	0.122	0.491
ITGB7	VEGFA	0.121	0.492
ITGB7	SELP	0	0.495
ITGB7	VASP	0	0.639
ITGB7	PRKCB	0.122	0.746
ITM2C	TMEM140	0	0.534
ITM2C	ITPR2	0.115	0.446
ITPR2	PLCG2	0.12	0.917
ITPR2	MTMR3	0	0.406
ITPR2	PIK3AP1	0.163	0.414
ITPR2	UBXN7	0	0.54
ITPR2	ORAI2	0.12	0.585
ITPR2	PRKCB	0	0.823
ITPR2	PSEN1	0.12	0.871
JAK1	MYD88	0.178	0.646
JAK1	STAM2	0.184	0.938
JAK1	PLCG2	0.138	0.573
JAK1	PTPRE	0.133	0.666
JAK1	TRIM25	0.055	0.404
JAK1	RAF1	0.24	0.428
JAK1	MDM2	0.218	0.443
JAK1	RSAD2	0.065	0.443
JAK1	MST1R	0.225	0.468
JAK1	LCP2	0.209	0.474
JAK1	PLA2G4A	0.127	0.48
JAK1	TEC	0.127	0.482

JAK1	RAP1B	0.141	0.488
JAK1	TRAF3	0.121	0.492
JAK1	TLR4	0.093	0.494
JAK1	PXN	0.099	0.495
JAK1	SH2B2	0.406	0.513
JAK1	PRKCD	0.131	0.523
JAK1	QKI	0.159	0.531
JAK1	RELB	0.044	0.533
JAK1	NFKB2	0.055	0.541
JAK1	NOS2	0.12	0.542
JAK1	VEGFA	0	0.545
JAK1	PTPRC	0.173	0.554
JAK1	JUN	0.125	0.56
JAK1	MCL1	0.064	0.569
JAK1	MAP2K3	0.102	0.593
JAK1	PIAS2	0.114	0.594
JAK1	NFKB1	0.07	0.601
JAK1	USP18	0.081	0.605
JAK1	UGCG	0.045	0.613
JAK1	RELA	0.121	0.623
JAK1	NMI	0.045	0.636
JAK1	PLAUR	0.113	0.65
JAK1	MAP3K5	0.067	0.651
JAK1	PTPN22	0.139	0.651
JAK1	PRKCB	0.093	0.658
JAK1	TNFRSF1A	0.218	0.68
JAK1	TNF	0.093	0.69
JAK1	MX1	0.093	0.698
JAK1	VAV1	0.12	0.707
JAK1	PTK2B	0.219	0.746
JAK1	PIAS1	0.114	0.764
JAK1	KRAS	0.141	0.808
JAK1	OSM	0	0.819
JAK1	PIK3CA	0.129	0.899
JAK1	PTPN6	0.219	0.903
JAK1	MX2	0.093	0.937
JAK1	JAK2	0.159	0.939
JAK1	JAK3	0.203	0.94
JAK1	TYK2	0.203	0.94
JAK1	STAT4	0.236	0.98
JAK1	PTPN2	0.405	0.983
JAK1	PTPN1	0.405	0.985
JAK1	STAT6	0.236	0.989
JAK1	SOCS1	0.676	0.992
JAK1	STAT5B	0.661	0.992
JAK1	STAT5A	0.661	0.992
JAK1	STAT2	0.236	0.993

JAK1	SOCS3	0.494	0.996
JAK1	STAT1	0.447	0.997
JAK1	STAT3	0.764	0.999
JAK2	MYD88	0.178	0.682
JAK2	RET	0.172	0.685
JAK2	STAM2	0.157	0.925
JAK2	PLCG2	0.138	0.916
JAK2	PTPRE	0.133	0.557
JAK2	PTPN12	0.139	0.441
JAK2	JUN	0.125	0.605
JAK2	TNFRSF1A	0.218	0.835
JAK2	VAV1	0.218	0.642
JAK2	STAT2	0.236	0.992
JAK2	SOCS1	0.926	0.999
JAK2	RAF1	0.264	0.493
JAK2	PTK2B	0.219	0.645
JAK2	NFKB2	0.054	0.696
JAK2	TLR4	0.093	0.674
JAK2	STAT6	0.236	0.992
JAK2	PTPN1	0.763	0.986
JAK2	NOS2	0.12	0.756
JAK2	PIAS2	0.119	0.495
JAK2	TLR2	0.093	0.428
JAK2	SOCS3	0.925	0.999
JAK2	PRKCD	0.131	0.489
JAK2	RAP1B	0.141	0.642
JAK2	MAP3K5	0.113	0.592
JAK2	PIK3CA	0.129	0.968
JAK2	LCP2	0.209	0.547
JAK2	STAT5B	0.736	0.997
JAK2	SH2B2	0.457	0.903
JAK2	PTPRC	0.173	0.596
JAK2	PTPN2	0.451	0.973
JAK2	MAP2K3	0.102	0.442
JAK2	TYK2	0.144	0.937
JAK2	NF1	0.122	0.465
JAK2	LOC100297725	0.07	0.412
JAK2	QKI	0.159	0.418
JAK2	PLAUR	0.093	0.437
JAK2	TRAF3	0.121	0.449
JAK2	PTGS2	0.084	0.459
JAK2	PRKCB	0.093	0.468
JAK2	MST1R	0.225	0.488
JAK2	MDM2	0.157	0.491
JAK2	PLA2G4A	0.127	0.521
JAK2	WDR77	0.071	0.526
JAK2	UGCG	0.045	0.538

JAK2	NMI	0.046	0.551
JAK2	XIAP	0.132	0.553
JAK2	MX1	0.093	0.574
JAK2	PIK3R6	0	0.62
JAK2	XCR1	0.051	0.637
JAK2	PIAS1	0.119	0.65
JAK2	VEGFA	0	0.657
JAK2	PIK3R5	0	0.669
JAK2	LOC529196	0.129	0.678
JAK2	TET2	0	0.678
JAK2	RELB	0.044	0.68
JAK2	TEC	0.218	0.692
JAK2	PXN	0.099	0.708
JAK2	MCL1	0.064	0.73
JAK2	TNF	0.093	0.73
JAK2	RELA	0.121	0.739
JAK2	NFKB1	0.054	0.761
JAK2	OSM	0	0.831
JAK2	LYN	0.113	0.843
JAK2	KRAS	0.141	0.867
JAK2	PTPN6	0.219	0.934
JAK2	JAK3	0.203	0.936
JAK2	STAT4	0.236	0.982
JAK2	STAT5A	0.736	0.995
JAK2	STAT1	0.796	0.996
JAK2	STAT3	0.894	0.999
JAK3	MYD88	0.178	0.512
JAK3	STAM2	0.157	0.947
JAK3	PLCG2	0.138	0.632
JAK3	PTPRE	0.133	0.524
JAK3	JUN	0.125	0.479
JAK3	VAV1	0.163	0.607
JAK3	STAT2	0.236	0.979
JAK3	SOCS1	0.667	0.977
JAK3	RAF1	0.264	0.411
JAK3	PTK2B	0.219	0.773
JAK3	NFKB2	0.054	0.64
JAK3	STAT6	0.236	0.985
JAK3	PTPN1	0.451	0.751
JAK3	NOS2	0.12	0.557
JAK3	PIAS2	0.119	0.484
JAK3	SOCS3	0.662	0.979
JAK3	PRKCD	0.131	0.429
JAK3	RAP1B	0.141	0.517
JAK3	MAP3K5	0.072	0.504
JAK3	PIK3CA	0.129	0.907
JAK3	LCP2	0.209	0.523

JAK3	STAT5B	0.736	0.994
JAK3	SH2B2	0.457	0.555
JAK3	PTPRC	0.156	0.577
JAK3	PTPN2	0.451	0.971
JAK3	MAP2K3	0.102	0.456
JAK3	TYK2	0.144	0.709
JAK3	PLA2G4A	0.127	0.462
JAK3	TRAF3	0.121	0.564
JAK3	RELA	0.121	0.621
JAK3	WDR55	0	0.403
JAK3	MST1R	0.225	0.468
JAK3	MCL1	0.064	0.479
JAK3	OSM	0	0.734
JAK3	NMI	0.053	0.645
JAK3	PIK3R6	0	0.547
JAK3	PXN	0.099	0.567
JAK3	XCR1	0.051	0.637
JAK3	NFKB1	0.054	0.665
JAK3	PTPN6	0.219	0.91
JAK3	QKI	0.159	0.404
JAK3	VEGFA	0	0.432
JAK3	PIAS1	0.119	0.513
JAK3	TNF	0.093	0.532
JAK3	TEC	0.163	0.595
JAK3	RELB	0.044	0.61
JAK3	UGCG	0.045	0.613
JAK3	PRKCB	0.093	0.644
JAK3	LOC529196	0.116	0.669
JAK3	KRAS	0.141	0.77
JAK3	STAT4	0.236	0.963
JAK3	STAT1	0.578	0.968
JAK3	STAT5A	0.736	0.993
JAK3	STAT3	0.652	0.996
JARID2	SETDB1	0.164	0.809
JARID2	PHF1	0.179	0.688
JARID2	SUPT6H	0.184	0.403
JARID2	KDM7A	0.132	0.416
JARID2	RYBP	0	0.418
JARID2	KDM3A	0.045	0.447
JARID2	NEK6	0	0.464
JARID2	KDM8	0	0.555
JARID2	PHF12	0.476	0.575
JARID2	KDM6B	0.051	0.613
JARID2	LOC100297725	0.257	0.698
JMJD1C	TET2	0	0.403
JMJD1C	MYCBP2	0.296	0.429
JMJD1C	KDM8	0	0.431

JMJD1C	SF3B1	0	0.455
JMJD1C	MOCS1	0	0.456
JMJD1C	KDM5A	0.045	0.459
JMJD1C	KDM6B	0.055	0.486
JMJD1C	RYBP	0	0.518
JMJD1C	KDM7A	0	0.542
JMJD1C	PHF1	0	0.552
JMJD1C	KDM4A	0	0.657
JMJD1C	KMT2E	0	0.785
JMJD1C	NIPBL	0	0.9
JUN	SP3	0.139	0.4
JUN	NR4A1	0.105	0.694
JUN	MYD88	0	0.653
JUN	RET	0.14	0.58
JUN	KAT2B	0.318	0.82
JUN	MXD1	0.126	0.485
JUN	PPP1R15A	0	0.59
JUN	NFE2	0.184	0.614
JUN	NFKBIB	0.044	0.548
JUN	NR1H2	0.148	0.713
JUN	NR4A2	0.105	0.477
JUN	LPAR3	0.042	0.622
JUN	RIPK1	0.093	0.4
JUN	TRAF7	0.312	0.402
JUN	TAB2	0	0.403
JUN	SOD2	0	0.408
JUN	MAPKAPK2	0.053	0.413
JUN	MXD4	0.126	0.415
JUN	MNT	0.126	0.427
JUN	XIAP	0	0.429
JUN	TIRAP	0	0.432
JUN	MAX	0.126	0.433
JUN	VAV1	0.113	0.434
JUN	TYK2	0.125	0.436
JUN	KLF10	0.139	0.448
JUN	ZFP36	0	0.449
JUN	MMP25	0.093	0.456
JUN	SERPINE1	0	0.46
JUN	TNFRSF1A	0	0.463
JUN	MCL1	0	0.471
JUN	TGFBR1	0.116	0.473
JUN	MAP4K4	0.265	0.478
JUN	PXN	0	0.479
JUN	RAF1	0.121	0.48
JUN	RELB	0	0.481
JUN	SOCS3	0	0.484
JUN	MAFF	0.158	0.488

JUN	MR1	0	0.493
JUN	VEGFC	0.085	0.5
JUN	RARA	0.148	0.503
JUN	LOC529196	0.042	0.512
JUN	LOC616942	0	0.516
JUN	TOP1	0.119	0.525
JUN	VDR	0.148	0.526
JUN	TLR2	0	0.542
JUN	TRAF2	0.113	0.542
JUN	MAP2K3	0	0.546
JUN	NFE2L3	0.184	0.55
JUN	MDM2	0.042	0.554
JUN	SNAI1	0	0.564
JUN	STAT5A	0.164	0.568
JUN	SMAD7	0.163	0.573
JUN	MYSM1	0.165	0.576
JUN	STAT2	0.162	0.578
JUN	TGM2	0	0.58
JUN	NFKB2	0.044	0.608
JUN	TEC	0.125	0.61
JUN	UBXN7	0.21	0.612
JUN	STAT5B	0.164	0.619
JUN	MAP3K5	0	0.62
JUN	STAT6	0.162	0.639
JUN	TLR4	0	0.644
JUN	PTGS2	0	0.657
JUN	POR	0	0.663
JUN	NFKB1	0.044	0.67
JUN	KLF5	0.139	0.67
JUN	POLR2A	0.156	0.721
JUN	LYN	0.125	0.73
JUN	MEF2A	0.055	0.746
JUN	KLF7	0.139	0.75
JUN	KRAS	0.265	0.752
JUN	TCF7L2	0	0.773
JUN	RFWD2	0.764	0.774
JUN	PPARD	0.148	0.776
JUN	NOS2	0	0.777
JUN	STAT4	0.162	0.801
JUN	STAT1	0.162	0.803
JUN	VEGFA	0.162	0.812
JUN	PML	0.761	0.813
JUN	SIRT1	0.658	0.882
JUN	STAT3	0.162	0.921
JUN	KLF6	0.139	0.923
JUN	RELA	0.257	0.932
JUN	NFE2L2	0.639	0.962

JUN	JUNB	0.397	0.967
JUN	TNF	0.054	0.985
JUNB	NR4A1	0.105	0.551
JUNB	KAT2B	0.318	0.713
JUNB	MXD1	0.126	0.415
JUNB	PPP1R15A	0	0.414
JUNB	NFE2	0.184	0.57
JUNB	NR1H2	0.148	0.441
JUNB	NR4A2	0.128	0.425
JUNB	NFE2L3	0.184	0.55
JUNB	STAT2	0.162	0.408
JUNB	NFKB2	0.044	0.415
JUNB	STAT6	0.162	0.46
JUNB	UBXN7	0.21	0.612
JUNB	SOCS3	0	0.511
JUNB	SH3PXD2B	0	0.412
JUNB	SERTAD1	0	0.439
JUNB	MEF2A	0.055	0.439
JUNB	SSH2	0.133	0.444
JUNB	ZC3H12A	0	0.403
JUNB	NFKB1	0.044	0.4
JUNB	TRAF7	0.312	0.402
JUNB	KLF10	0.139	0.407
JUNB	MNT	0.126	0.415
JUNB	MXD4	0.126	0.415
JUNB	MAX	0.126	0.415
JUNB	UBTF	0.132	0.417
JUNB	RND1	0.138	0.445
JUNB	SMAD7	0.163	0.46
JUNB	STAT1	0.162	0.46
JUNB	MED11	0.12	0.465
JUNB	STK40	0.438	0.471
JUNB	TRIB1	0.206	0.486
JUNB	STAT4	0.162	0.502
JUNB	MAFF	0.158	0.529
JUNB	NFE2L2	0.184	0.55
JUNB	RFWD2	0.439	0.552
JUNB	STAT3	0.162	0.554
JUNB	MYSM1	0.165	0.576
JUNB	VEGFA	0.124	0.582
JUNB	POLR2A	0.156	0.586
JUNB	TNF	0.054	0.588
JUNB	RELA	0.165	0.664
JUNB	ZFP36	0	0.858
KAT2B	SETDB1	0.122	0.438
KAT2B	TFEC	0.156	0.403
KAT2B	UBTF	0.12	0.445

KAT2B	KMT2E	0.208	0.447
KAT2B	ZBTB17	0.121	0.452
KAT2B	SUPT6H	0.219	0.492
KAT2B	MXD4	0.273	0.493
KAT2B	KDM6B	0.175	0.501
KAT2B	MXD1	0.273	0.51
KAT2B	TACC3	0.093	0.522
KAT2B	LOC613345	0.447	0.528
KAT2B	MNT	0.273	0.557
KAT2B	USP3	0.451	0.558
KAT2B	UBE2B	0.079	0.566
KAT2B	LOC100297725	0.447	0.612
KAT2B	MAX	0.273	0.642
KAT2B	UBXN7	0.219	0.673
KAT2B	MEF2A	0.16	0.724
KAT2B	RARG	0.337	0.734
KAT2B	RELA	0.218	0.76
KAT2B	RARA	0.489	0.797
KAT2B	TAF5L	0.639	0.806
KAT2B	RBPJ	0.257	0.819
KAT2B	KAT8	0.432	0.835
KAT2B	POLR2A	0.342	0.839
KAT2B	MAML2	0.046	0.846
KAT2B	KAT5	0.432	0.856
KAT2B	MYSM1	0.48	0.9
KAT2B	SIRT1	0.352	0.904
KAT2B	MDM2	0.76	0.925
KAT5	SETDB1	0.129	0.467
KAT5	KDM4A	0.257	0.497
KAT5	PHF12	0.218	0.404
KAT5	MNT	0.16	0.408
KAT5	STAT3	0.113	0.422
KAT5	SMG1	0.219	0.435
KAT5	KDM6B	0.296	0.436
KAT5	NMI	0.113	0.509
KAT5	ZNF668	0.124	0.558
KAT5	PLA2G4A	0.35	0.625
KAT5	RELA	0.113	0.658
KAT5	LOC100297725	0.257	0.741
KAT5	MAX	0.274	0.748
KAT5	SIRT1	0.489	0.861
KAT5	MDM2	0.759	0.982
KAT8	KDM4A	0.257	0.427
KAT8	PHF12	0.218	0.427
KAT8	SMG1	0.219	0.448
KAT8	KDM6B	0.296	0.476
KAT8	MAX	0.16	0.498

KAT8	LOC100297725	0.257	0.613
KAT8	MDM2	0.295	0.667
KAT8	SIRT1	0.444	0.793
KCNJ15	TRPM5	0	0.42
KCNJ15	KCNK17	0	0.655
KCNJ2	SLC8A1	0	0.479
KCNK17	SLC38A2	0.055	0.413
KCNK17	SLC24A3	0	0.674
KCNK17	KCNK9	0	0.705
KCNK9	SLC24A3	0	0.518
KCNT1	PLEK	0	0.438
KCNT1	STOM	0	0.48
KCP	TTYH2	0	0.649
KCTD7	RABGEF1	0.044	0.488
KDM3A	SETDB1	0.052	0.513
KDM3A	KDM4A	0	0.795
KDM3A	PHC2	0.486	0.502
KDM3A	STAT6	0.434	0.455
KDM3A	KMT2E	0	0.416
KDM3A	KDM8	0	0.417
KDM3A	LOC100297725	0.047	0.515
KDM3A	MYCBP2	0.549	0.577
KDM3A	TRANK1	0.584	0.584
KDM3A	KDM5A	0.045	0.755
KDM3A	KDM7A	0	0.765
KDM3A	KDM6B	0.078	0.767
KDM4A	SETDB1	0.079	0.602
KDM4A	LOC613345	0.441	0.454
KDM4A	KDM8	0	0.455
KDM4A	KDM5A	0.159	0.458
KDM4A	KMT2E	0.125	0.502
KDM4A	LPAR3	0	0.523
KDM4A	KDM7A	0.121	0.698
KDM4A	LOC100297725	0.441	0.81
KDM4A	KDM6B	0.159	0.818
KDM5A	SETDB1	0.164	0.713
KDM5A	MXD1	0.164	0.411
KDM5A	PHF1	0.179	0.471
KDM5A	RBPJ	0.39	0.789
KDM5A	UBXN7	0.128	0.401
KDM5A	NUP98	0	0.763
KDM5A	SUPT6H	0.184	0.495
KDM5A	KMT2E	0.162	0.545
KDM5A	PHF12	0.764	0.89
KDM5A	TET2	0	0.433
KDM5A	TBL1X	0.059	0.471
KDM5A	RANBP2	0.055	0.417

KDM5A	SP140L	0.114	0.428
KDM5A	USP34	0.054	0.438
KDM5A	MYSM1	0.133	0.489
KDM5A	LOC100297725	0.31	0.68
KDM5A	KDM6B	0.051	0.703
KDM5A	KDM7A	0.132	0.768
KDM5A	RC3H2	0.054	0.787
KDM5A	SMG1	0.045	0.834
KDM6B	SETDB1	0.296	0.608
KDM6B	PHF1	0.179	0.486
KDM6B	POLR2C	0.158	0.48
KDM6B	RBPJ	0.461	0.576
KDM6B	WSB1	0.494	0.57
KDM6B	LOC515976	0.055	0.474
KDM6B	RPS9	0.143	0.431
KDM6B	UBXN7	0.258	0.498
KDM6B	SUPT6H	0.275	0.778
KDM6B	KMT2E	0.336	0.652
KDM6B	SIRT1	0.119	0.433
KDM6B	PTGS2	0	0.431
KDM6B	PHF12	0.476	0.637
KDM6B	NFIX	0.072	0.607
KDM6B	KDM8	0	0.422
KDM6B	STAT3	0.121	0.41
KDM6B	KDM7A	0.218	0.748
KDM6B	LOC100297725	0.451	0.818
KDM6B	POLR2A	0.258	0.504
KDM6B	LOC613345	0.451	0.475
KDM7A	SETDB1	0.16	0.448
KDM7A	PPP1R3B	0	0.475
KDM7A	XRN1	0.172	0.443
KDM7A	KDM8	0	0.428
KDM7A	SMG1	0.081	0.404
KDM7A	RYBP	0.404	0.447
KDM7A	MYSM1	0.139	0.43
KDM7A	MPHOSPH8	0.309	0.409
KDM7A	SUV420H1	0	0.424
KDM7A	LOC100297725	0.257	0.482
KDM8	MYSM1	0	0.419
KHNYN	TRIM25	0.045	0.484
KHNYN	MARK3	0	0.428
KHNYN	XRN1	0	0.495
KIAA0226L	SF3B1	0	0.634
KIAA0226L	PARP11	0	0.528
KIAA0226L	TBC1D14	0	0.589
KIAA0226L	RASSF2	0	0.646
KIAA0226L	SP140L	0	0.925

KIAA1033	UBR1	0	0.896
KIAA1033	U2AF1L4	0	0.545
KIAA1033	MYSM1	0.07	0.407
KIAA1147	RIC1	0	0.683
KIAA1147	SNAP29	0	0.41
KLF10	NR4A2	0.073	0.426
KLF10	PPM1D	0.046	0.487
KLF10	RELA	0.098	0.42
KLF10	SMAD7	0.102	0.524
KLF10	KLF5	0	0.608
KLF10	KLF6	0	0.696
KLF17	KLF6	0	0.411
KLF17	KLF5	0	0.6
KLF5	RARG	0.317	0.605
KLF5	RARA	0.483	0.794
KLF5	KLF6	0	0.656
KLF5	NFKB1	0.184	0.555
KLF5	STAT3	0.093	0.494
KLF5	KLF7	0	0.586
KLF6	SP2	0	0.428
KLF6	RELA	0.113	0.426
KLF7	ZBTB2	0	0.4
KLF7	NFIX	0.078	0.481
KLHL5	NFE2	0.2	0.418
KLHL5	NFE2L3	0.2	0.435
KLHL5	SAMD4B	0	0.426
KLHL5	MYCBP2	0	0.412
KLHL5	NFE2L2	0.2	0.416
KLHL5	RASA2	0	0.48
KLHL5	TMEM156	0	0.686
KLHL8	NFE2	0.2	0.416
KLHL8	NFE2L3	0.2	0.416
KLHL8	NFE2L2	0.2	0.416
KLHL8	VCPIP1	0	0.666
KMO	XDH	0	0.47
KMO	MOCOS	0	0.473
KMO	KYNU	0	0.999
KMT2E	SETDB1	0.142	0.627
KMT2E	SF3B1	0	0.447
KMT2E	SRRM2	0	0.421
KMT2E	TET2	0	0.428
KMT2E	PCMTD1	0	0.459
KMT2E	SIRT1	0.386	0.463
KMT2E	POGZ	0.12	0.485
KMT2E	SP140L	0.053	0.49
KMT2E	ZNF292	0.12	0.492
KMT2E	LOC100297725	0.317	0.513

KMT2E	SUV420H1	0	0.553
KMT2E	NIPBL	0	0.607
KMT2E	PPIF	0.436	0.661
KMT2E	TBL1X	0.76	0.881
KPNA1	SENP3	0.399	0.491
KPNA1	SENP2	0.399	0.491
KPNA1	STAT2	0.138	0.636
KPNA1	KPNA3	0.4	0.955
KPNA1	NUP210L	0	0.525
KPNA1	NUP98	0.316	0.539
KPNA1	XPO6	0.295	0.511
KPNA1	PTPN2	0.069	0.401
KPNA1	UBTF	0.163	0.415
KPNA1	R3HCC1L	0	0.436
KPNA1	STAT4	0.138	0.465
KPNA1	NUP210	0	0.525
KPNA1	MDM2	0.113	0.574
KPNA1	STAT3	0.203	0.697
KPNA1	NFKB1	0.079	0.816
KPNA1	RELA	0.161	0.833
KPNA1	RANBP2	0.405	0.844
KPNA1	STAT1	0.759	0.944
KPNA3	SENP3	0.399	0.491
KPNA3	SENP2	0.399	0.496
KPNA3	LRCH1	0.042	0.571
KPNA3	RNF213	0	0.408
KPNA3	MPHOSPH8	0.347	0.408
KPNA3	TGM2	0.08	0.414
KPNA3	XPO6	0.295	0.457
KPNA3	MED11	0	0.496
KPNA3	STAT3	0.138	0.515
KPNA3	NUP210L	0	0.516
KPNA3	NUP210	0	0.516
KPNA3	NUP98	0.316	0.531
KPNA3	NFKB1	0.117	0.842
KPNA3	RANBP2	0.405	0.851
KPNA3	RELA	0.257	0.877
KRAS	PRKAA1	0.119	0.46
KRAS	PIM1	0.119	0.672
KRAS	RET	0.257	0.871
KRAS	RASGRP2	0.218	0.894
KRAS	PLCG2	0.142	0.446
KRAS	NCF1	0.165	0.401
KRAS	RABGEF1	0.164	0.58
KRAS	MAP3K2	0.571	0.798
KRAS	VAV1	0.157	0.765
KRAS	SOCS1	0.053	0.597

KRAS	RAF1	0.847	0.998
KRAS	LLGL1	0.409	0.51
KRAS	RASA4	0.198	0.843
KRAS	PLAU	0.055	0.404
KRAS	PTK2B	0.043	0.659
KRAS	TLR4	0.12	0.408
KRAS	KSR1	0.432	0.782
KRAS	PTPN1	0.137	0.413
KRAS	RICTOR	0.114	0.504
KRAS	SHOC2	0.751	0.984
KRAS	SOCS3	0.053	0.722
KRAS	PRKCD	0.165	0.62
KRAS	RAP1GAP	0.184	0.517
KRAS	SH3PXD2B	0.165	0.429
KRAS	PIK3CA	0.45	0.998
KRAS	LCP2	0	0.43
KRAS	STAT5B	0.12	0.465
KRAS	PLEK	0.043	0.553
KRAS	TIAM2	0.212	0.757
KRAS	PTPRC	0.093	0.562
KRAS	MAP2K3	0.069	0.467
KRAS	XRN1	0.06	0.447
KRAS	TYK2	0.141	0.412
KRAS	NF1	0.685	0.995
KRAS	RHOH	0.181	0.427
KRAS	TRAF3	0.06	0.409
KRAS	SLC1A5	0.156	0.415
KRAS	RELA	0	0.476
KRAS	SIRT1	0.046	0.43
KRAS	PTGS2	0.078	0.517
KRAS	SERPINE1	0	0.448
KRAS	SNAI1	0	0.534
KRAS	MST1R	0.258	0.694
KRAS	MCL1	0.054	0.591
KRAS	PIK3R6	0	0.93
KRAS	MMP25	0	0.404
KRAS	RASSF2	0.156	0.465
KRAS	TET2	0.042	0.449
KRAS	SRGAP2	0.129	0.405
KRAS	TGFBR1	0.124	0.573
KRAS	PXN	0.128	0.589
KRAS	RND1	0.181	0.53
KRAS	NFE2L2	0.055	0.402
KRAS	SPRED2	0.492	0.721
KRAS	LOC785769	0.329	0.532
KRAS	VASP	0.174	0.435
KRAS	PIK3AP1	0.393	0.514

KRAS	LYN	0.165	0.538
KRAS	SMG1	0.268	0.51
KRAS	PRKCB	0.06	0.932
KRAS	RASSF1	0.352	0.964
KRAS	SAG	0.055	0.453
KRAS	STAT3	0.072	0.779
KRAS	RALGDS	0.512	0.998
KRAS	RAPGEF1	0.218	0.58
KRAS	STAT5A	0.12	0.431
KRAS	TNF	0.046	0.617
KRAS	SLC2A1	0.055	0.43
KRAS	LOC100297725	0.042	0.469
KRAS	ROCK1	0.16	0.485
KRAS	XIAP	0.105	0.541
KRAS	STAT1	0.072	0.543
KRAS	RIN2	0.162	0.546
KRAS	PREX1	0.329	0.56
KRAS	LRRK2	0.264	0.573
KRAS	TEC	0.141	0.591
KRAS	PIM3	0.119	0.642
KRAS	MDM2	0.043	0.673
KRAS	VEGFA	0	0.685
KRAS	SPRED1	0.67	0.867
KRAS	PIK3R5	0	0.868
KRAS	RASSF5	0.43	0.946
KRAS	RASA2	0.258	0.95
KRR1	RPS9	0.764	0.866
KRR1	RIOK3	0.391	0.634
KRR1	KYNU	0	0.409
KRR1	WDR4	0	0.433
KRR1	MRPS15	0.418	0.495
KRR1	TFB1M	0.345	0.639
KRR1	NOP9	0.042	0.796
KRR1	RCL1	0.789	0.97
KRR1	LTV1	0.539	0.977
KRR1	NOM1	0.925	0.98
KSR1	RABGEF1	0.153	0.44
KSR1	RAF1	0.44	0.959
KSR1	MOB3C	0	0.412
KSR1	RAPGEF1	0.129	0.419
KSR1	MX1	0.113	0.422
KSR1	PPM1D	0.158	0.422
KSR1	SIRT1	0.08	0.423
KSR1	RALGDS	0.064	0.427
KSR1	SUPT6H	0.051	0.431
KSR1	RAP1B	0.245	0.457
KSR1	SAG	0.16	0.49

KSR1	SHOC2	0.093	0.575
KSR1	MARK3	0.489	0.647
KTN1	PTPN6	0	0.56
KTN1	PROSC	0	0.491
KTN1	RANBP2	0.069	0.414
KYNU	SAMSN1	0	0.782
KYNU	SIRT1	0.41	0.484
KYNU	NAMPT	0.133	0.474
KYNU	MOCOS	0	0.454
LAIR1	RPS9	0	0.55
LAIR1	SLAMF8	0	0.462
LAIR1	PTPN6	0.413	0.675
LAIR1	LENG8	0	0.666
LAMB3	PTK2B	0	0.559
LAMB3	SLC24A3	0	0.547
LAMB3	USP15	0	0.4
LAMB3	ZYX	0	0.412
LAMB3	PXN	0	0.711
LAMP1	RB1CC1	0	0.488
LAMP1	NLRP3	0	0.41
LAMP1	RABGEF1	0	0.425
LAMP1	MAP1LC3A	0.114	0.689
LAMP1	TLR4	0	0.469
LAMP1	TLR2	0	0.424
LAMP1	SIRPB1	0	0.516
LAMP1	PTPRC	0	0.636
LAMP1	VPS37A	0	0.449
LAMP1	RAB27A	0	0.613
LAMP1	TFEC	0.165	0.406
LAMP1	TSPAN2	0.113	0.455
LAMP1	OPTN	0	0.432
LAMP1	LYST	0.08	0.416
LAMP1	TLR9	0	0.467
LAMP1	LOC617909	0	0.499
LAMP1	STX6	0	0.529
LAMP1	SNAP29	0.044	0.585
LAMP1	TNF	0.055	0.75
LAMP1	STX11	0	0.412
LAMP1	LRRK2	0.08	0.475
LAMP1	LAPTM5	0.114	0.501
LAMP1	SELL	0.054	0.673
LAMP1	NCR1	0	0.754
LAP3	RPIA	0.532	0.543
LAP3	WARS	0.452	0.562
LAP3	PSME2	0	0.402
LAP3	NAMPT	0.455	0.455
LAP3	STAT1	0	0.54

LAP3	TAPT1	0	0.721
LAP3	NPEPPS	0.134	0.795
LAP3	PRODH	0	0.9
LAPTM5	NCF1	0.242	0.492
LAPTM5	VAV1	0	0.462
LAPTM5	NCF4	0.463	0.629
LAPTM5	SLA	0	0.421
LAPTM5	LCP2	0	0.524
LAPTM5	PLEK	0	0.689
LAPTM5	PTPRC	0	0.701
LAPTM5	SRGN	0	0.524
LAPTM5	TNFRSF1B	0	0.405
LAPTM5	SERINC2	0	0.469
LAPTM5	SDC3	0	0.545
LAPTM5	LAT2	0	0.553
LAT2	PLCG2	0.158	0.709
LAT2	VAV1	0	0.557
LAT2	LCP2	0	0.828
LAT2	PPTC7	0	0.467
LAT2	LYN	0	0.776
LAT2	SLC9A3R1	0	0.465
LAT2	TREML2	0	0.447
LCP2	RHOG	0	0.438
LCP2	NDRG1	0	0.45
LCP2	SLC2A6	0	0.539
LCP2	PLCG2	0.513	0.989
LCP2	PTPN12	0.11	0.509
LCP2	MAP3K2	0	0.43
LCP2	VAV1	0.772	0.999
LCP2	NLRC5	0	0.408
LCP2	PTK2B	0	0.435
LCP2	THEMIS2	0.093	0.44
LCP2	TLR4	0	0.649
LCP2	LOC616942	0	0.508
LCP2	PRKCD	0.08	0.567
LCP2	RAP1B	0	0.846
LCP2	PIK3CA	0	0.683
LCP2	LOC529196	0	0.409
LCP2	TYK2	0.209	0.411
LCP2	SELL	0	0.416
LCP2	SKAP2	0.123	0.422
LCP2	RIPK3	0.121	0.436
LCP2	PSTPIP2	0	0.444
LCP2	RHOH	0	0.475
LCP2	SH3BP2	0	0.478
LCP2	MR1	0	0.502
LCP2	SRGN	0	0.509

LCP2	TREM1	0	0.534
LCP2	TAGAP	0	0.6
LCP2	P2RY8	0	0.639
LCP2	LYN	0.209	0.651
LCP2	MPEG1	0	0.678
LCP2	PSTPIP1	0	0.68
LCP2	PTPN22	0.11	0.742
LCP2	PLEK	0	0.833
LCP2	TEC	0.209	0.902
LCP2	PTPN6	0.24	0.952
LCP2	PTPRC	0.11	0.961
LENG8	RPS9	0	0.665
LENG8	SFPQ	0	0.473
LENG8	NCR1	0	0.49
LENG8	TRANK1	0	0.491
LFNG	RBPJ	0	0.554
LGALS9	RIPK1	0.105	0.445
LGALS9	PARP12	0	0.414
LGALS9	ST6GALNAC4	0	0.422
LGALS9	TNF	0.052	0.446
LGALS9	PARP14	0	0.476
LGALS9	RNF213	0	0.518
LGALS9	MX1	0	0.592
LGALS9	UBA7	0	0.664
LGALS9	MX2	0	0.675
LGALS9	USP18	0	0.705
LGALS9	PTPRC	0.06	0.747
LGALS9	RSAD2	0.427	0.788
LGR6	PRR7	0	0.476
LIG4	POLB	0.224	0.819
LIG4	MAD2L2	0	0.59
LIG4	RHBDD1	0	0.455
LIG4	MDM2	0	0.469
LIG4	SMG1	0.218	0.622
LIG4	PARP3	0.218	0.713
LIMK2	MYD88	0.52	0.709
LIMK2	5-Sep	0	0.541
LIMK2	PPM1D	0.158	0.413
LIMK2	SSH2	0.415	0.793
LIMK2	TAB2	0.259	0.512
LIMK2	PELI1	0.327	0.569
LIMK2	TIRAP	0.219	0.527
LIMK2	PLXNA1	0.093	0.433
LIMK2	LRRK2	0.252	0.404
LIMK2	ROCK1	0.501	0.971
LIPM	MBOAT1	0	0.404
LIPM	R3HCC1L	0	0.488

LITAF	TNF	0	0.401
LITAF	TLR4	0	0.423
LITAF	SMURF1	0.429	0.454
LITAF	NOS2	0	0.522
LITAF	STAT6	0.211	0.738
LLGL1	RHBDD2	0	0.422
LLGL1	SNAP29	0.356	0.496
LLGL1	PARD3	0.271	0.544
LLGL1	NUMB	0.352	0.603
LMNB1	SAMSN1	0	0.402
LMNB1	SYNE3	0	0.534
LMNB1	NUP98	0.257	0.577
LMNB1	SIRT1	0.045	0.474
LMNB1	NFE2L2	0.075	0.514
LMNB1	TNF	0.07	0.428
LMNB1	NUP210	0	0.407
LMNB1	RANBP2	0.055	0.494
LMNB1	LRRK2	0.218	0.455
LMNB1	LOC100297725	0.064	0.658
LMTK2	PPP4C	0.161	0.433
LMTK2	OPTN	0	0.435
LMTK2	ZDHHC18	0	0.459
.OC10013895	RHOG	0	0.499
.OC10013895	TLR4	0.128	0.525
.OC10013895	SLAMF1	0	0.571
.OC10013895	SOCS3	0.062	0.483
.OC10013895	PTPRC	0.08	0.907
.OC10013895	TNF	0	0.481
.OC10013895	PTAFR	0	0.504
.OC10013895	TMEM119	0	0.422
.OC10013895	SELL	0	0.491
.OC10013895	NCR1	0	0.428
.OC10029772	SETDB1	0.317	0.81
.OC10029772	PLK3	0.136	0.436
.OC10029772	SUPT6H	0.296	0.431
.OC10029772	MORC3	0.425	0.454
.OC10029772	PADI4	0.046	0.591
.OC10029772	RELA	0.046	0.493
.OC10029772	SIRT1	0.219	0.77
.OC10029772	MCL1	0	0.465
.OC10029772	TET2	0.044	0.471
.OC10029772	STAT3	0.046	0.642
.OC10029772	UBTF	0.114	0.407
.OC10029772	TNF	0	0.586
.OC10029772	MDM2	0.055	0.465
.OC10029772	SUV420H1	0.127	0.454
.OC10029772	MPHOSPH8	0.4	0.557

.OC10029772	STAT1	0.055	0.477
.OC10029772	XIAP	0.17	0.511
.OC10029772	POLR2A	0.165	0.443
LOC281376	PLAU	0.171	0.915
LOC281376	TLR4	0	0.474
LOC281376	PTPRC	0	0.442
LOC281376	PLAUR	0.051	0.866
LOC281376	SERPINE1	0	0.86
LOC281376	SELL	0.055	0.413
LOC281376	TNF	0	0.576
LOC281376	SERPINB2	0	0.816
LOC407171	TREM1	0	0.414
LOC506364	RHOG	0	0.511
LOC506364	TLR4	0.209	0.705
LOC506364	ST3GAL3	0	0.414
LOC506364	SIRPB1	0	0.506
LOC506364	LOC617909	0	0.54
LOC506364	PTPRC	0.08	0.668
LOC507055	PSMB8	0.046	0.499
LOC507055	OAS2	0	0.5
LOC507055	RSAD2	0	0.572
LOC507055	MX1	0	0.624
LOC507055	STAT1	0	0.581
LOC507820	SENP3	0.452	0.71
LOC507820	USPL1	0	0.448
LOC507820	SENP2	0.452	0.667
LOC507820	PARP8	0	0.518
LOC507820	MIER1	0	0.605
LOC507820	RICTOR	0	0.488
LOC507820	UBXN7	0.159	0.403
LOC507820	SHOC2	0.045	0.53
LOC507820	PIAS2	0.148	0.581
LOC507820	XRN1	0.312	0.406
LOC507820	RANBP2	0.127	0.476
LOC507820	PIAS1	0.148	0.692
LOC511531	RSAD2	0	0.461
LOC511531	LOC512486	0	0.833
LOC511531	STAT1	0	0.495
LOC512486	PARP14	0	0.43
LOC512486	PARP9	0	0.423
LOC512486	STAT1	0	0.51
LOC512672	TAPBP	0	0.824
LOC514257	STRA8	0	0.512
LOC515333	SLCO4A1	0	0.48
LOC515676	RBPJ	0.294	0.413
LOC515676	PSEN1	0.216	0.439
LOC515755	SLC7A5	0.143	0.494

LOC515755	SLC1A5	0	0.457
LOC515976	STAT1	0.053	0.403
LOC515976	NCR1	0.051	0.408
LOC515976	SERPINE1	0.055	0.415
LOC515976	MX2	0.051	0.423
LOC515976	STAT3	0.053	0.483
LOC515976	SELL	0.042	0.489
LOC515976	PTPRC	0.045	0.537
LOC515976	TNF	0	0.548
LOC516599	LOC616948	0	0.808
LOC518134	MS4A7	0	0.449
LOC518134	NCF4	0	0.446
LOC518134	PTPRC	0.045	0.447
LOC529196	PLCG2	0.071	0.474
LOC541180	RICTOR	0.132	0.412
LOC541180	SOCS3	0	0.6
LOC541180	SIK1	0.081	0.569
LOC613345	SUPT6H	0.296	0.431
LOC613345	MORC3	0.425	0.424
LOC613345	MPHOSPH8	0.4	0.45
LOC616942	VAV1	0.043	0.506
LOC616942	TAPBP	0.422	0.45
LOC616942	PIK3CA	0.053	0.514
LOC616948	STAT1	0.055	0.401
LOC616948	MDM2	0.118	0.464
LOC616948	PNRC1	0	0.465
LOC616948	RANBP2	0.073	0.482
LOC616948	RSAD2	0	0.528
LOC616948	MX1	0.042	0.53
LOC616948	TAB2	0.087	0.627
LOC616948	MX2	0.042	0.629
LOC616948	PML	0	0.765
LOC617909	SIRPA	0	0.442
LOC617909	SIRPB1	0	0.597
LOC617909	PTAFR	0	0.534
LOC618664	SAMD4B	0	0.689
LOC784222	MORC3	0	0.738
LOC785769	RHOG	0.242	0.421
LOC785769	NCF1	0.392	0.492
LOC785769	NCF4	0.392	0.496
LOC785769	RAP1B	0.452	0.668
LOC785769	SH3PXD2B	0.571	0.707
LOC785769	RHOH	0.242	0.4
LOC790312	UPP1	0	0.946
LOC790312	PNP	0	0.903
LOC790312	XDH	0	0.987
LOC790312	SIRT1	0.052	0.766

LOC790312	NAMPT	0	0.918
LONRF3	PCDH17	0.073	0.487
LONRF3	MAP4K4	0	0.493
LONRF3	MST1R	0.08	0.498
LONRF3	TBC1D8	0	0.564
LONRF3	UBXN7	0.169	0.577
LPAR3	MYBPH	0	0.414
LPAR3	PIK3CA	0.052	0.488
LPAR3	NFKB2	0.061	0.517
LPAR3	PTK2B	0.042	0.524
LPAR3	PPARD	0.043	0.558
LPAR3	ST3GAL3	0	0.591
LPAR3	PLA2G4A	0	0.593
LPAR3	RELA	0.044	0.613
LPAR3	LYN	0.051	0.616
LPAR3	NFKB1	0.061	0.62
LPAR3	PIK3R5	0.042	0.643
LPAR3	PIK3R6	0	0.658
LPCAT2	PLA2G4A	0	0.816
LPCAT2	MBOAT1	0.158	0.419
LPIN2	SLC10A1	0	0.404
LPIN2	PSTPIP1	0	0.456
LPIN2	PSTPIP2	0	0.516
LPIN2	MBOAT1	0	0.747
LRCH1	TNFAIP6	0.051	0.43
LRCH1	STK4	0.044	0.467
LRCH1	PTPN1	0.131	0.484
LRP10	PI4K2A	0	0.616
LRP10	MRPS15	0	0.416
LRRFIP1	MYD88	0.211	0.6
LRRFIP1	UPB1	0	0.467
LRRFIP1	ZBP1	0	0.414
LRRFIP1	MLKL	0	0.475
LRRFIP1	RIPK1	0	0.512
LRRFIP1	PLBD1	0	0.631
LRRK2	MYD88	0.418	0.737
LRRK2	NAIP	0.183	0.459
LRRK2	NR4A2	0.069	0.406
LRRK2	TNFRSF1A	0.298	0.621
LRRK2	MAP3K2	0.236	0.44
LRRK2	TLR4	0.143	0.435
LRRK2	RILPL2	0	0.556
LRRK2	MAP3K5	0.072	0.477
LRRK2	PPM1D	0.219	0.437
LRRK2	TRAF2	0.219	0.534
LRRK2	MAP2K3	0.432	0.694
LRRK2	RAB8B	0.311	0.431

LRRK2	TAB2	0.35	0.615
LRRK2	TRAF3	0.219	0.436
LRRK2	RELA	0.177	0.412
LRRK2	NLK	0.295	0.547
LRRK2	OPTN	0.167	0.442
LRRK2	LYST	0.078	0.457
LRRK2	TRAF7	0.25	0.483
LRRK2	NOD2	0.116	0.678
LRRK2	TIRAP	0.174	0.446
LRRK2	TNF	0.235	0.657
LRRK2	RNF41	0.219	0.436
LRRK2	PSEN1	0.12	0.575
LRRK2	TRAF1	0.219	0.482
LRRK2	PDP1	0.218	0.413
LRRK2	TANK	0.134	0.46
LRRK2	MALT1	0.12	0.494
LRRK2	XIAP	0.183	0.478
LTB	TNFRSF1A	0.317	0.798
LTB	NFKB2	0.045	0.507
LTB	PTPRC	0.053	0.405
LTB	TRAF2	0.133	0.751
LTB	TAB2	0.158	0.474
LTB	TRAF3	0.133	0.463
LTB	RELA	0.136	0.672
LTB	LTBR	0.759	0.992
LTB	RELT	0	0.525
LTB	TRAF1	0.133	0.479
LTB	TANK	0.246	0.529
LTB	RELB	0	0.729
LTB	TNFSF14	0.124	0.758
LTB	TNF	0.655	0.763
LTB	TNFRSF1B	0.348	0.765
LTB	TNFSF13B	0	0.808
LTB4R	PADI4	0	0.41
LTB4R	SAG	0	0.414
LTBR	TNFRSF1A	0	0.869
LTBR	NFKB2	0.113	0.566
LTBR	PTPRC	0	0.406
LTBR	TRAF2	0.854	0.98
LTBR	TRAF3	0.813	0.996
LTBR	RELA	0	0.601
LTBR	RIPK2	0	0.403
LTBR	TNFSF10	0.21	0.45
LTBR	NFKB1	0.08	0.493
LTBR	RELB	0	0.745
LTBR	TRAF1	0.589	0.749
LTBR	TNFSF13B	0	0.769

LTBR	TNF	0.461	0.847
LTBR	TNFSF14	0.472	0.985
LTV1	RPS9	0.801	0.841
LTV1	RIOK3	0	0.838
LTV1	XPO6	0.344	0.551
LTV1	PTPN22	0	0.418
LTV1	MRPS15	0.44	0.483
LTV1	PHACTR2	0	0.516
LTV1	RCL1	0	0.534
LTV1	TFB1M	0.264	0.606
LTV1	NOP9	0	0.757
LTV1	NOM1	0	0.765
LYN	MYD88	0.178	0.499
LYN	PPP1R15A	0.113	0.652
LYN	NFKBIB	0.054	0.462
LYN	PLCG2	0.492	0.878
LYN	MAP3K2	0.12	0.446
LYN	VAV1	0.093	0.89
LYN	STAT2	0.236	0.459
LYN	RAF1	0.175	0.656
LYN	PTK2B	0.3	0.951
LYN	NFKB2	0.054	0.548
LYN	THEMIS2	0.05	0.59
LYN	TLR4	0.093	0.686
LYN	STAT6	0.236	0.472
LYN	SLA	0.065	0.669
LYN	TLR2	0.093	0.64
LYN	SOCS3	0.207	0.401
LYN	PRKCD	0.131	0.779
LYN	RAP1B	0.141	0.49
LYN	PIK3CA	0.14	0.936
LYN	STAT5B	0.236	0.769
LYN	SH2B2	0.184	0.7
LYN	PTPRC	0.203	0.976
LYN	PLA2G4A	0.127	0.703
LYN	SH3BP2	0.115	0.643
LYN	MST1R	0.225	0.476
LYN	PIK3R6	0	0.682
LYN	PXN	0.099	0.871
LYN	PTPN22	0.139	0.442
LYN	STAT4	0.236	0.438
LYN	TNF	0.113	0.453
LYN	SKAP2	0.296	0.463
LYN	SPRED1	0.121	0.544
LYN	PTPN6	0.219	0.574
LYN	NFKB1	0.054	0.642
LYN	PIK3R5	0	0.677

LYN	TEC	0.203	0.702
LYN	STAT1	0.236	0.75
LYN	STAT5A	0.236	0.771
LYN	STAT3	0.236	0.816
LYN	PRKCB	0.218	0.881
LYSMD1	SARS	0	0.465
LYSMD3	SMG1	0	0.616
LYST	TNFRSF1A	0.204	0.67
LYST	MAP1LC3A	0.295	0.44
LYST	PLEK	0	0.533
LYST	VPS4B	0	0.43
LYST	RAB27A	0	0.686
LYST	TRAF7	0.075	0.411
LYST	RIPK3	0.055	0.414
LYST	MYCBP2	0	0.442
LYST	MPEG1	0.128	0.484
LYST	TNF	0	0.52
LYST	PTPN6	0	0.523
LYST	XIAP	0	0.54
LYST	STX11	0.074	0.687
MAD2L2	TUBA4A	0.048	0.667
MAD2L2	POGZ	0.764	0.809
MAEA	TMBIM4	0	0.538
MAEA	ZFAND3	0	0.42
MAEA	TAPT1	0	0.426
MAEA	SPRYD3	0.687	0.834
MAFF	PPP1R15A	0	0.406
MAFF	NFE2	0.302	0.937
MAFF	NFE2L3	0.406	0.772
MAFF	NFKBID	0.127	0.406
MAFF	ZC3H12A	0	0.442
MAFF	RND1	0	0.559
MAFF	NFE2L2	0.764	0.95
MAFF	NFKBIE	0.127	0.534
MALT1	RIPK1	0.174	0.583
MALT1	TRAF2	0.225	0.568
MALT1	ZC3H12A	0	0.409
MALT1	TAB2	0.218	0.536
MALT1	TRAF3	0.225	0.872
MALT1	RIPK3	0.12	0.453
MALT1	TRAF7	0.225	0.476
MALT1	RC3H2	0	0.459
MALT1	SRRM2	0	0.407
MALT1	RNF41	0.225	0.472
MALT1	TRAF1	0.225	0.535
MALT1	RASSF5	0	0.411
MALT1	RELB	0.113	0.483

MALT1	RIPK2	0.12	0.536
MAML2	RBPJ	0.113	0.976
MAML2	MIF4GD	0	0.405
MAML2	QKI	0	0.537
MANF	RET	0.071	0.405
MANF	TAGLN2	0	0.9
MANF	YRDC	0	0.444
MANF	PLEK	0	0.9
MANF	SELK	0	0.499
MAP1LC3A	RB1CC1	0.534	0.786
MAP1LC3A	VEZF1	0.052	0.414
MAP1LC3A	RUFY4	0.316	0.414
MAP1LC3A	TNF	0	0.43
MAP1LC3A	SRRD	0	0.478
MAP1LC3A	UBA7	0.258	0.48
MAP1LC3A	VMP1	0	0.524
MAP1LC3A	SIRT1	0.158	0.528
MAP1LC3A	OPTN	0.347	0.702
MAP2K3	MYD88	0	0.403
MAP2K3	TNFRSF1A	0	0.677
MAP2K3	MAP3K2	0.113	0.547
MAP2K3	RAF1	0.102	0.546
MAP2K3	PTK2B	0	0.634
MAP2K3	NFKB2	0.042	0.428
MAP2K3	TLR4	0.086	0.405
MAP2K3	RIPK1	0.168	0.937
MAP2K3	RAP1B	0.046	0.825
MAP2K3	MAP3K5	0.508	0.969
MAP2K3	PPM1D	0.062	0.527
MAP2K3	TRAF2	0.081	0.931
MAP2K3	RIPK3	0.168	0.4
MAP2K3	TRAF7	0.081	0.405
MAP2K3	RIPK2	0.168	0.454
MAP2K3	MLKL	0.168	0.456
MAP2K3	TRAF1	0.081	0.584
MAP2K3	TRAF3	0.081	0.665
MAP2K3	TNF	0	0.762
MAP2K3	TAB2	0	0.943
MAP3K2	MYD88	0	0.554
MAP3K2	TNFRSF1A	0	0.603
MAP3K2	RELB	0	0.413
MAP3K2	MAP3K8	0.157	0.416
MAP3K2	RASA2	0	0.418
MAP3K2	PDP1	0.137	0.428
MAP3K2	STK38L	0.391	0.448
MAP3K2	TNFRSF1B	0	0.455
MAP3K2	SMURF1	0.207	0.462

MAP3K2	PPM1D	0.168	0.479
MAP3K2	UBXN7	0.219	0.481
MAP3K2	TANK	0.069	0.485
MAP3K2	RELA	0	0.486
MAP3K2	TGFBR1	0.12	0.489
MAP3K2	MAP3K5	0.078	0.499
MAP3K2	TRAF1	0.162	0.515
MAP3K2	TRAF7	0.2	0.53
MAP3K2	TAB2	0	0.543
MAP3K2	TNF	0	0.544
MAP3K2	TRAF2	0.162	0.592
MAP3K2	RIPK1	0.12	0.622
MAP3K2	RAP1B	0.215	0.664
MAP3K2	XIAP	0.251	0.664
MAP3K2	MAP4K4	0.052	0.678
MAP3K5	PPP1R15A	0	0.439
MAP3K5	TNFRSF1A	0	0.775
MAP3K5	SOCS1	0.439	0.789
MAP3K5	RAF1	0.164	0.587
MAP3K5	MAP4K4	0	0.693
MAP3K5	TLR4	0	0.465
MAP3K5	RIPK1	0.072	0.702
MAP3K5	PGAM5	0.211	0.442
MAP3K5	RNF41	0.164	0.425
MAP3K5	PLEK	0	0.447
MAP3K5	MLKL	0.072	0.464
MAP3K5	TRAF7	0.164	0.469
MAP3K5	TRAF3	0.164	0.53
MAP3K5	XIAP	0	0.555
MAP3K5	SAG	0.158	0.709
MAP3K5	TNF	0	0.843
MAP3K5	TRAF1	0.404	0.86
MAP3K5	TRAF2	0.784	0.997
MAP3K8	RAF1	0.15	0.423
MAP3K8	MAP4K4	0.053	0.654
MAP3K8	NFKB2	0.574	0.828
MAP3K8	TRAF2	0.435	0.552
MAP3K8	TNF	0	0.468
MAP3K8	ZNF655	0.08	0.491
MAP3K8	TRAF1	0.275	0.493
MAP3K8	STK38L	0.386	0.516
MAP3K8	RND1	0.053	0.595
MAP3K8	RELA	0.745	0.799
MAP3K8	TNIP2	0.641	0.894
MAP3K8	NFKB1	0.838	0.994
MAP4K4	MYD88	0	0.645
MAP4K4	TNFRSF1A	0	0.64

MAP4K4	RASA2	0	0.442
MAP4K4	RIPK2	0.128	0.483
MAP4K4	TRAF1	0.161	0.584
MAP4K4	TCF7L2	0.157	0.609
MAP4K4	TANK	0	0.616
MAP4K4	TBC1D8	0	0.632
MAP4K4	TLR4	0.052	0.655
MAP4K4	RIPK1	0.128	0.661
MAP4K4	TRAF3	0.161	0.703
MAP4K4	TAB2	0.078	0.715
MAP4K4	TNF	0	0.717
MAP4K4	TRAF2	0.161	0.782
MAPKAPK2	RIPK3	0.093	0.407
MAPKAPK2	TNF	0	0.753
MAPKAPK2	MAPKAPK3	0	0.821
MAPKAPK2	ZFP36	0.12	0.905
MAPKAPK3	RILPL2	0	0.523
MAPKAPK3	PIK3R6	0	0.412
MAPKAPK3	WAC	0	0.401
MAPKAPK3	TNF	0	0.647
3-Mar	UAP1	0	0.408
3-Mar	UBE2J2	0.336	0.513
3-Mar	7-Mar	0	0.614
3-Mar	STX6	0.349	0.778
6-Mar	MYLIP	0	0.432
6-Mar	RNF19B	0	0.57
6-Mar	UBE2G1	0.113	0.432
6-Mar	UBE2J2	0.642	0.862
6-Mar	USP25	0.119	0.429
6-Mar	RNF175	0	0.414
6-Mar	UBR1	0.353	0.708
6-Mar	TRIM21	0	0.481
7-Mar	NLRP3	0.093	0.424
7-Mar	SPATA6	0	0.412
7-Mar	UBR1	0.218	0.408
7-Mar	UBE2J2	0.336	0.513
MARCKS	PLEK	0	0.48
MARCKS	PRKCB	0.24	0.775
MARCKSL1	SMPDL3B	0	0.404
MARCKSL1	PRKCB	0.121	0.437
MARK3	PIM1	0.44	0.553
MARK3	PARD3	0.199	0.416
MAX	PIM1	0.113	0.641
MAX	MXD1	0.97	0.996
MAX	PIK3CA	0.159	0.586
MAX	NF1	0.042	0.491
MAX	RELA	0.158	0.51

MAX	MXD4	0.685	0.792
MAX	PML	0.121	0.644
MAX	TRIB1	0.105	0.401
MAX	TRAF7	0.258	0.415
MAX	PIM3	0.105	0.596
MAX	MNT	0.66	0.726
MAX	ZBTB17	0.113	0.933
MB21D2	ZCCHC6	0	0.518
MB21D2	POGZ	0.042	0.424
MB21D2	PAPOLG	0	0.639
MBD2	WDR77	0.218	0.816
MBD2	SNAI1	0.073	0.586
MBD2	UBTF	0.078	0.905
MBD2	TACC3	0.093	0.477
MBOAT1	STARD3	0	0.641
MBOAT1	TNFSF10	0	0.416
MBOAT1	TATDN2	0	0.65
MCEMP1	RETN	0	0.487
MCF2L2	RHOG	0.228	0.488
MCF2L2	RND1	0.228	0.429
MCF2L2	RHOH	0.228	0.441
MCL1	PRKAA1	0.459	0.459
MCL1	STAT2	0.06	0.534
MCL1	RAF1	0.139	0.565
MCL1	PRKAB1	0.397	0.408
MCL1	STAT6	0.06	0.589
MCL1	PIK3CA	0.08	0.521
MCL1	STAT5B	0.06	0.479
MCL1	TPT1	0.158	0.598
MCL1	RELA	0.055	0.518
MCL1	SIRT1	0	0.496
MCL1	NMI	0	0.421
MCL1	TNFSF10	0	0.459
MCL1	STAT5A	0.06	0.467
MCL1	VEGFA	0	0.588
MCL1	TNF	0.053	0.589
MCL1	STAT1	0.06	0.664
MCL1	MDM2	0.119	0.683
MCL1	STAT3	0.06	0.865
MCL1	XIAP	0.082	0.879
MCTP2	SLCO3A1	0	0.497
MCTP2	MEF2A	0	0.404
MCTP2	ZFAT	0	0.616
MDM2	NFKBIB	0.121	0.415
MDM2	PIAS2	0.157	0.703
MDM2	PIK3CA	0.046	0.683
MDM2	PPM1D	0.113	0.883

MDM2	TRIM25	0.118	0.409
MDM2	NF1	0	0.52
MDM2	RELA	0.124	0.441
MDM2	SIRT1	0.12	0.617
MDM2	PTGS2	0.164	0.452
MDM2	SNAI1	0.218	0.428
MDM2	PML	0.764	0.899
MDM2	USP18	0.258	0.547
MDM2	PPIF	0.108	0.546
MDM2	RASSF2	0.157	0.456
MDM2	USP25	0.258	0.587
MDM2	ZMIZ1	0.113	0.533
MDM2	NFKB1	0.121	0.448
MDM2	SMG1	0.06	0.532
MDM2	RASSF1	0.274	0.857
MDM2	TRIM8	0.118	0.555
MDM2	SAG	0.307	0.747
MDM2	STAT3	0	0.542
MDM2	RYBP	0.113	0.462
MDM2	USP15	0.113	0.476
MDM2	UBE2B	0.164	0.726
MDM2	RFWD2	0.113	0.435
MDM2	SESN2	0.046	0.418
MDM2	USP34	0.184	0.435
MDM2	VEGFA	0.093	0.446
MDM2	ZMIZ2	0.113	0.523
MDM2	RANBP2	0.218	0.742
MDM2	XIAP	0.35	0.762
MDM2	PIAS1	0.218	0.779
MDM2	NUMB	0.517	0.858
MDM2	RASSF5	0.211	0.962
MDM2	UBE2D1	0.983	0.997
MED11	MED30	0.761	0.946
MED11	MED12L	0.503	0.606
MED12L	MED30	0.504	0.634
MED12L	PRKCD	0	0.405
MED12L	RAB37	0	0.485
MED12L	SUPT6H	0	0.609
MED12L	MED13	0.728	0.977
MED13	MED30	0.503	0.962
MED13	UBXN7	0.148	0.561
MED13	SUPT6H	0	0.483
MED13	XRN1	0	0.514
MED13	NF1	0	0.516
MED13	NIPBL	0.042	0.521
MED13	TBL1X	0.069	0.537
MED13	SMG1	0.201	0.709

MED13	UBR1	0	0.713
MED13	RC3H2	0	0.831
MED13	MYSM1	0	0.438
MED13	ZNF292	0.113	0.445
MED13	SMAD7	0	0.474
MED13	XIAP	0	0.516
MEF2A	PRKAA1	0.078	0.523
MEF2A	NR4A1	0	0.593
MEF2A	NR4A2	0	0.439
MEF2A	VEZF1	0.079	0.474
MEF2A	TAL1	0.07	0.46
MEF2A	PTK2B	0.457	0.501
MEF2A	UBXN7	0	0.439
MEF2A	POLR2A	0	0.517
MEF2A	SRGAP2	0	0.521
MEF2A	SIRT1	0.08	0.598
MEF2A	NIPBL	0	0.69
MEFV	MYD88	0.045	0.436
MEFV	NLRP3	0.093	0.446
MEFV	NAIP	0.042	0.55
MEFV	PTPN12	0.051	0.482
MEFV	TNFRSF1A	0	0.443
MEFV	NLRC5	0.042	0.502
MEFV	TLR4	0.052	0.447
MEFV	TLR2	0.052	0.428
MEFV	NLRC4	0	0.818
MEFV	TRIM25	0	0.562
MEFV	PML	0	0.587
MEFV	RIPK2	0.072	0.461
MEFV	TRIM8	0	0.476
MEFV	ZBP1	0	0.525
MEFV	TNF	0	0.558
MEFV	NOD1	0.042	0.567
MEFV	NOD2	0.042	0.649
MEFV	NLRP12	0.093	0.659
MEFV	PSTPIP2	0.259	0.723
MEFV	PSTPIP1	0.435	0.907
MEGF9	STX11	0	0.638
METRNL	PIK3AP1	0	0.424
METRNL	NAMPT	0	0.439
METRNL	SRGAP2	0	0.659
MICU1	RYR1	0	0.423
MICU1	ORAI2	0	0.499
MICU1	PPIF	0	0.564
MICU1	SLC8B1	0	0.885
MIDN	5-Sep	0	0.537
MIDN	SBNO2	0	0.424

MIER1	SP3	0.079	0.452
MIER1	SHOC2	0	0.512
MIER1	SRRD	0	0.65
MIER3	RC3H2	0	0.468
MIER3	ST6GALNAC4	0	0.469
MIER3	UBE2J2	0	0.486
MIF4GD	PLSCR2	0	0.471
MKNK1	TDRD7	0	0.483
MKNK1	PLA2G4A	0.078	0.749
MKNK1	TNIP2	0.046	0.461
MKNK1	SLC2A1	0	0.45
MLKL	MYD88	0.178	0.607
MLKL	NLRP3	0.049	0.918
MLKL	NAIP	0.158	0.523
MLKL	TNFRSF1A	0.298	0.787
MLKL	TLR4	0.093	0.536
MLKL	RIPK1	0.113	0.803
MLKL	PGAM5	0.158	0.981
MLKL	PPM1D	0.219	0.532
MLKL	VPS4B	0.079	0.615
MLKL	TRAF2	0.184	0.629
MLKL	RELA	0.14	0.403
MLKL	TNFRSF1B	0.055	0.411
MLKL	PPIF	0.071	0.426
MLKL	TRAF1	0.184	0.442
MLKL	TANK	0.134	0.453
MLKL	TNFSF10	0.093	0.536
MLKL	NLK	0.295	0.582
MLKL	XIAP	0.158	0.601
MLKL	TAB2	0.35	0.676
MLKL	ZBP1	0.158	0.734
MLKL	TNF	0.219	0.788
MLKL	RIPK3	0.937	0.993
MLXIP	PRKAA1	0	0.534
MLXIP	MXD1	0	0.632
MLXIP	PARP8	0	0.487
MLXIP	NINJ1	0	0.416
MLXIP	TRIB1	0	0.44
MLXIP	PRKAB1	0	0.53
MLXIP	MNT	0	0.535
MLXIP	MXD4	0	0.535
MMP25	PLAU	0.159	0.759
MMP25	TLR4	0.045	0.498
MMP25	STAT6	0.045	0.416
MMP25	NOS2	0	0.41
MMP25	PTPRC	0.044	0.417
MMP25	PLAUR	0.184	0.613

MMP25	PTGS2	0	0.669
MMP25	SERPINE1	0.093	0.667
MMP25	VEGFC	0.045	0.466
MMP25	VCAN	0.069	0.428
MMP25	OSM	0	0.512
MMP25	SDC4	0	0.406
MMP25	PSEN1	0	0.411
MMP25	STAT1	0.045	0.414
MMP25	PXN	0	0.447
MMP25	STAT3	0.045	0.636
MMP25	VEGFA	0.051	0.709
MMP25	TNF	0.067	0.754
MNT	MXD1	0.113	0.74
MNT	PIK3CA	0.159	0.436
MNT	OVCA2	0	0.471
MNT	RELA	0.158	0.521
MNT	MXD4	0	0.79
MNT	TRAF7	0.258	0.415
MNT	TLE3	0.116	0.413
MOB3A	STK4	0.337	0.405
MOB3A	STK3	0.337	0.405
MOB3A	ZNF292	0.067	0.53
MOB3A	STK38L	0.346	0.733
MOB3C	STK4	0.337	0.405
MOB3C	TNIP2	0	0.468
MOB3C	STK3	0.337	0.405
MOB3C	ZNF292	0.067	0.429
MOB3C	STK38L	0.346	0.668
MOCOS	PLAU	0.123	0.407
MOCOS	PRDX5	0	0.527
MOCOS	SCLY	0	0.723
MOCOS	MOCS1	0.14	0.685
MOCOS	UBA7	0	0.411
MOCOS	XDH	0	0.77
MOCOS	STK17B	0	0.452
MOCOS	RASSF2	0	0.434
MOCOS	RNF41	0	0.579
MOCOS	PROSC	0	0.818
MOCS1	SCLY	0	0.433
MOCS1	UBA7	0	0.436
MOCS1	SH3BP2	0	0.499
MOCS1	XDH	0	0.69
MORC3	RNF213	0	0.412
MORC3	TRIM21	0.042	0.457
MOV10	SENP3	0.405	0.405
MOV10	ZCCHC6	0.155	0.565
MOV10	MX2	0	0.438

MOV10	RAP1B	0.257	0.4
MOV10	TRIM25	0.055	0.43
MOV10	XRN1	0.257	0.679
MOV10	TFIP11	0.418	0.418
MOV10	MX1	0	0.409
MOV10	RNF122	0.043	0.422
MOV10	RSAD2	0.213	0.446
MOV10	SLFN12L	0	0.485
MPEG1	TLR4	0	0.636
MPEG1	PLEK	0	0.719
MPEG1	PTPRC	0	0.712
MPEG1	PTPN6	0	0.723
MPEG1	P2RY8	0	0.58
MPHOSPH8	SETDB1	0.351	0.757
MPHOSPH8	TDRD7	0.12	0.548
MPHOSPH8	UBXN7	0.434	0.482
MPHOSPH8	TOP1	0.093	0.513
MPHOSPH8	RELA	0.192	0.413
MPHOSPH8	SIRT1	0.392	0.557
MPHOSPH8	NIPBL	0.484	0.613
MPHOSPH8	NUDT3	0.044	0.411
MPHOSPH8	SMG1	0.218	0.41
MPHOSPH8	POGZ	0.387	0.669
MPHOSPH8	RELB	0.317	0.435
MPHOSPH8	POLR2A	0.434	0.466
MR1	VAV1	0.042	0.515
MR1	PIK3CA	0.053	0.492
MR1	TAPBP	0.394	0.423
MR1	SLC46A2	0	0.512
MREG	RAB27A	0	0.524
MRPS15	POLR2C	0.263	0.472
MRPS15	RPS9	0.427	0.873
MRPS15	SOD2	0.679	0.739
MRPS15	TPT1	0.317	0.547
MRPS15	TARS	0.401	0.535
MRPS15	TSFM	0	0.466
MRPS15	RCL1	0.392	0.411
MRPS15	TFB1M	0.351	0.445
MS4A3	SAMSN1	0	0.544
MS4A3	TCN1	0	0.527
MST1R	RHOG	0.258	0.517
MST1R	RET	0.459	0.594
MST1R	RASGRP2	0.184	0.568
MST1R	SEMA4D	0.257	0.526
MST1R	PLCG2	0.257	0.691
MST1R	SAMSN1	0.21	0.616
MST1R	PTPN12	0.201	0.522

MST1R	PTPN1	0.219	0.621
MST1R	SLAMF1	0.116	0.445
MST1R	RAP1B	0.258	0.488
MST1R	PIK3CA	0.122	0.673
MST1R	PCDH17	0.07	0.405
MST1R	PTPN2	0.219	0.569
MST1R	SEMA7A	0.257	0.428
MST1R	TYK2	0.225	0.468
MST1R	S100A8	0.042	0.516
MST1R	PLAUR	0.055	0.608
MST1R	RHOH	0.258	0.517
MST1R	RRAD	0.258	0.481
MST1R	REM2	0.258	0.472
MST1R	STAT3	0.159	0.474
MST1R	TEC	0.225	0.48
MST1R	RASGEF1B	0.184	0.511
MST1R	PTPN22	0.201	0.522
MST1R	PTPN5	0.201	0.522
MST1R	PTPRG	0.201	0.532
MST1R	RND1	0.258	0.553
MST1R	SPRYD3	0.093	0.581
MST1R	RAPGEF1	0.184	0.615
MST1R	PTPRJ	0.295	0.7
MST1R	PTPN6	0.409	0.72
MTMR3	PI4K2A	0	0.658
MTMR3	PLCG2	0	0.756
MTMR3	VMP1	0	0.403
MTMR3	RCL1	0	0.405
MTMR3	MTMR7	0.486	0.555
MTMR3	PLEKHA4	0	0.699
MTMR7	SLCO3A1	0	0.484
MTMR7	PI4K2A	0	0.688
MTMR7	PLCG2	0	0.695
MTMR7	TEX2	0	0.413
MTMR7	RASA2	0	0.47
MX1	MYD88	0	0.494
MX1	VAV1	0.046	0.601
MX1	STAT2	0	0.802
MX1	SOCS1	0	0.544
MX1	RAF1	0.093	0.425
MX1	TLR4	0.113	0.476
MX1	SLAMF1	0	0.418
MX1	SOCS3	0	0.431
MX1	MX2	0	0.951
MX1	PSMB9	0	0.417
MX1	TRIM25	0.042	0.502
MX1	PTPRC	0.055	0.532

MX1	XAF1	0	0.828
MX1	TYK2	0.093	0.675
MX1	UBA7	0.053	0.885
MX1	UBE2L6	0.055	0.576
MX1	OAS2	0	0.877
MX1	SP110	0.05	0.609
MX1	RSAD2	0	0.983
MX1	PARP12	0	0.722
MX1	PARP14	0	0.766
MX1	USP18	0.114	0.974
MX1	TLR9	0.113	0.517
MX1	TNFSF10	0	0.409
MX1	ZNFX1	0	0.544
MX1	SAG	0	0.448
MX1	STAT3	0	0.472
MX1	PARP9	0	0.885
MX1	PLSCR2	0	0.543
MX1	RNF213	0	0.84
MX1	TNF	0	0.616
MX1	STAT4	0	0.444
MX1	VEGFA	0	0.478
MX1	SDC4	0	0.487
MX1	ZBP1	0	0.557
MX1	TRIM21	0.042	0.598
MX1	STAT1	0	0.947
MX2	TNFRSF1A	0	0.409
MX2	STAT2	0	0.681
MX2	RAF1	0.093	0.402
MX2	WARS	0	0.437
MX2	NLRC5	0	0.405
MX2	RBM43	0.055	0.407
MX2	TNF	0	0.409
MX2	TYK2	0.093	0.412
MX2	VEGFA	0	0.414
MX2	SP110	0.05	0.415
MX2	NMI	0	0.446
MX2	SAG	0	0.448
MX2	SDC4	0	0.463
MX2	RANBP2	0.051	0.487
MX2	UBE2L6	0.055	0.502
MX2	ZBP1	0	0.52
MX2	PLEKHA4	0.064	0.663
MX2	XAF1	0	0.671
MX2	PARP9	0	0.691
MX2	PARP14	0	0.745
MX2	TRIM21	0.042	0.772
MX2	STAT1	0	0.819

MX2	OAS2	0	0.831
MX2	PARP12	0	0.839
MX2	UBA7	0.053	0.842
MX2	ZNFX1	0	0.843
MX2	RNF213	0	0.866
MX2	USP18	0.114	0.964
MX2	RSAD2	0	0.977
MXD1	TRAF7	0.258	0.415
MXD1	TET2	0.054	0.43
MXD1	PIK3CA	0.159	0.436
MXD1	PIAS2	0.116	0.454
MXD1	RELA	0.158	0.51
MXD1	ZFYVE28	0	0.537
MXD1	RHBDD2	0	0.64
MXD4	PIK3CA	0.159	0.436
MXD4	RELA	0.158	0.523
MXD4	TRAF7	0.258	0.415
MXD4	RGS2	0.045	0.436
MXD4	ZFYVE28	0	0.724
MYBPH	TLR4	0	0.455
MYBPH	SLAMF1	0	0.764
MYBPH	TLR2	0	0.522
MYBPH	PPP1R15B	0	0.519
MYCBP2	POGZ	0.055	0.429
MYCBP2	USP34	0.119	0.541
MYCBP2	TRANK1	0.549	0.585
MYD88	SAA2	0	0.404
MYD88	STAT5A	0	0.404
MYD88	STAT5B	0	0.425
MYD88	SELL	0	0.429
MYD88	STAT4	0	0.454
MYD88	PTX3	0	0.456
MYD88	NFKBIB	0	0.458
MYD88	RSAD2	0	0.49
MYD88	RELB	0	0.499
MYD88	PPM1D	0	0.516
MYD88	TANK	0.174	0.518
MYD88	TEC	0.178	0.534
MYD88	TYK2	0.178	0.548
MYD88	PTPRC	0	0.554
MYD88	PELI1	0.218	0.57
MYD88	TRAF7	0.27	0.577
MYD88	SOCS3	0.055	0.579
MYD88	STAT6	0	0.585
MYD88	NOS2	0	0.596
MYD88	STAT2	0	0.606
MYD88	RIPK3	0.178	0.607

MYD88	NFKB2	0	0.611
MYD88	PTGS2	0	0.627
MYD88	TNFRSF1A	0	0.636
MYD88	RNF41	0.27	0.638
MYD88	TRAF2	0.27	0.649
MYD88	SOCS1	0.055	0.65
MYD88	S100A12	0	0.652
MYD88	TRAF1	0.27	0.661
MYD88	TNIP1	0.471	0.665
MYD88	NLRC4	0	0.67
MYD88	S100A8	0	0.672
MYD88	PIK3AP1	0.211	0.673
MYD88	RELA	0	0.682
MYD88	S100A9	0	0.704
MYD88	RIPK1	0.178	0.712
MYD88	PTK2B	0.113	0.715
MYD88	STAT3	0	0.72
MYD88	STAT1	0	0.731
MYD88	NFKB1	0	0.751
MYD88	NLRP3	0	0.757
MYD88	NOD1	0	0.761
MYD88	NOD2	0	0.773
MYD88	RIPK2	0.178	0.805
MYD88	TNF	0	0.91
MYD88	TAB2	0	0.923
MYD88	TRAF3	0.754	0.984
MYD88	TLR2	0.758	0.988
MYD88	TIRAP	0.837	0.991
MYD88	TLR4	0.937	0.996
MYD88	TLR9	0.459	0.999
MYLIP	NR1H2	0.051	0.546
MYLIP	RNF19B	0	0.41
MYLIP	PROSC	0	0.449
MYLIP	ZDHHC2	0	0.602
MYLIP	UBE2D1	0.941	0.963
MYSM1	PSMA2	0.557	0.801
MYSM1	USPL1	0	0.524
MYSM1	PSMB8	0.489	0.804
MYSM1	NR1H2	0.262	0.41
MYSM1	PRKAB1	0.068	0.405
MYSM1	VCPIP1	0	0.462
MYSM1	UBXN7	0.295	0.724
MYSM1	THOC2	0	0.604
MYSM1	USP3	0.045	0.567
MYSM1	PSMB9	0.552	0.874
MYSM1	SUPT6H	0.07	0.469
MYSM1	PAN3	0	0.4

MYSM1	XRN1	0.092	0.547
MYSM1	NF1	0	0.681
MYSM1	UBA7	0.165	0.462
MYSM1	NIPBL	0.054	0.683
MYSM1	TET2	0.137	0.678
MYSM1	PLAGL2	0.148	0.458
MYSM1	USP25	0.044	0.518
MYSM1	OTUD4	0	0.557
MYSM1	USP32	0.132	0.514
MYSM1	SMG1	0.132	0.916
MYSM1	UBR1	0	0.664
MYSM1	RC3H2	0.093	0.81
MYSM1	ROCK1	0.138	0.404
MYSM1	UBTF	0.141	0.417
MYSM1	USP15	0.132	0.45
MYSM1	ZNF292	0.148	0.477
MYSM1	USP34	0.044	0.55
MYSM1	POLR2A	0.295	0.623
MYSM1	XIAP	0.121	0.847
N4BP1	RIPK1	0.056	0.434
N4BP1	RNF19B	0	0.667
N4BP1	RAP1B	0	0.457
N4BP1	TRIM25	0.079	0.533
N4BP1	RAB11FIP1	0	0.769
N4BP1	NDFIP2	0	0.474
N4BP1	USP25	0	0.526
N4BP1	RNF213	0	0.517
N4BP2L2	RBM47	0	0.561
N4BP2L2	PARP11	0	0.631
NAB1	STAT2	0	0.41
NAB1	PSMA2	0.459	0.459
NAB1	PLEKHO2	0	0.533
NAB2	STAT2	0	0.414
NAB2	RASSF5	0	0.458
NAB2	NXF1	0	0.476
NAB2	SWT1	0	0.481
NAB2	STAT6	0	0.579
NABP1	YIPF4	0.054	0.632
NABP1	ZNFX1	0	0.433
NACC2	QKI	0.045	0.529
NAIP	NLRP3	0	0.785
NAIP	PTPRC	0.051	0.402
NAIP	TRAF3	0.184	0.405
NAIP	TNFRSF1B	0.06	0.458
NAIP	TAB2	0.061	0.508
NAIP	TRAF1	0.184	0.515
NAIP	RIPK2	0.158	0.518

NAIP	XAF1	0.184	0.519
NAIP	SMPDL3B	0	0.524
NAIP	ROCK1	0.132	0.526
NAIP	RELA	0.164	0.55
NAIP	TNF	0.209	0.594
NAIP	TNFRSF1A	0.294	0.655
NAIP	NLRC5	0.093	0.689
NAIP	NOD1	0.093	0.715
NAIP	NLRC4	0.764	0.976
NAMPT	UPB1	0	0.41
NAMPT	WARS	0.452	0.452
NAMPT	RETN	0	0.66
NAMPT	TLR4	0.042	0.573
NAMPT	PNP	0	0.94
NAMPT	SIRT1	0.082	0.984
NAMPT	SERPINE1	0	0.509
NAMPT	VNN2	0	0.41
NAMPT	TNF	0	0.573
NAPSA	SARS	0.594	0.597
NCF1	RHOG	0.295	0.504
NCF1	PTGS2	0	0.406
NCF1	VAV1	0	0.427
NCF1	OLR1	0	0.428
NCF1	TLR2	0.042	0.429
NCF1	PXN	0.161	0.432
NCF1	RND1	0.295	0.446
NCF1	NOS2	0	0.458
NCF1	RHOH	0.295	0.469
NCF1	TIAM2	0.392	0.492
NCF1	TLR4	0.042	0.528
NCF1	PREX1	0.392	0.561
NCF1	XDH	0	0.566
NCF1	PTAFR	0	0.606
NCF1	TNF	0	0.659
NCF1	PLA2G4A	0.408	0.692
NCF1	NCF4	0.107	0.902
NCF1	PRKCD	0.436	0.934
NCF1	PRKCB	0.764	0.966
NCF4	RHOG	0.295	0.499
NCF4	SAMSN1	0.463	0.536
NCF4	XDH	0	0.444
NCF4	RND1	0.295	0.446
NCF4	RHOH	0.295	0.466
NCF4	SLC37A1	0	0.481
NCF4	TIAM2	0.392	0.492
NCF4	PREX1	0.392	0.518
NCF4	PRKCD	0.134	0.844

NCF4	PRKCB	0.238	0.847
NCLN	VEZF1	0	0.436
NCLN	ZBTB17	0	0.596
NCR1	RPS9	0	0.476
NCR1	PTPRC	0.082	0.783
NCR1	PVRL2	0	0.571
NCR1	TNF	0	0.627
NCR1	SELL	0	0.675
NDEL1	PDE4B	0	0.588
NDEL1	TACC3	0.117	0.777
NDEL1	NIN	0.045	0.465
NDFIP2	PSMA2	0	0.434
NDFIP2	STEAP2	0	0.432
NDFIP2	THEMIS2	0	0.468
NDFIP2	SMURF1	0.399	0.576
NDRG1	NR4A1	0.113	0.442
NDRG1	SLC2A1	0	0.427
NDRG1	RICTOR	0	0.5
NDRG1	STK38L	0	0.634
NEK6	NLRP3	0.495	0.518
NEK6	NLRP12	0.495	0.495
NF1	SP3	0	0.405
NF1	RET	0	0.671
NF1	NR1H2	0	0.467
NF1	RAF1	0.122	0.483
NF1	WSB1	0	0.456
NF1	RICTOR	0.093	0.416
NF1	UBXN7	0.131	0.647
NF1	SHOC2	0.044	0.425
NF1	RAP1B	0.303	0.468
NF1	PIK3CA	0	0.711
NF1	UBR1	0	0.409
NF1	VASP	0.322	0.415
NF1	RARA	0	0.424
NF1	SMG1	0	0.429
NF1	SDC3	0.164	0.45
NF1	STAT3	0.089	0.462
NF1	REM2	0.303	0.468
NF1	RRAD	0.303	0.468
NF1	RASGEF1B	0.192	0.495
NF1	TET2	0	0.556
NF1	POLR2A	0.211	0.713
NF1	NFIX	0	0.8
NF1	SPRED2	0.529	0.834
NF1	SPRED1	0.753	0.946
NFAM1	PDXK	0	0.469
NFAM1	TNFSF13B	0	0.539

NFE2	VAT1L	0	0.416
NFE2	TAL1	0	0.47
NFE2	S100A9	0	0.637
NFE2L2	NLRP3	0	0.465
NFE2L2	TLR4	0	0.434
NFE2L2	SOD2	0	0.65
NFE2L2	NOS2	0	0.579
NFE2L2	PGAM5	0.138	0.405
NFE2L2	RARA	0.113	0.513
NFE2L2	SIRT1	0.043	0.627
NFE2L2	PTGS2	0	0.588
NFE2L2	POR	0	0.661
NFE2L2	SAT1	0	0.531
NFE2L2	VAT1L	0	0.416
NFE2L2	STAT3	0.124	0.459
NFE2L2	PTPN22	0	0.54
NFE2L2	TNF	0	0.589
NFE2L2	PRKCB	0.079	0.64
NFE2L3	VAT1L	0	0.416
NFIX	NR1H2	0.067	0.437
NFIX	PPP1R3B	0	0.416
NFIX	XRN1	0	0.4
NFIX	PSEN1	0	0.707
NFKB1	NLRP3	0	0.858
NFKB1	NFKBIB	0.764	0.985
NFKB1	TNFRSF1A	0.043	0.789
NFKB1	RAF1	0.042	0.812
NFKB1	NFKB2	0.487	0.942
NFKB1	TLR4	0.077	0.926
NFKB1	STAT6	0.113	0.45
NFKB1	RIPK1	0.078	0.743
NFKB1	NOS2	0.055	0.454
NFKB1	NFKBID	0.397	0.546
NFKB1	TLR2	0.077	0.925
NFKB1	RNF19B	0.057	0.51
NFKB1	SOCS3	0.113	0.514
NFKB1	POU2F2	0.069	0.655
NFKB1	PRKCD	0.119	0.717
NFKB1	PIK3CA	0.124	0.723
NFKB1	STAT5B	0.087	0.577
NFKB1	NRROS	0.077	0.469
NFKB1	TRAF2	0.093	0.723
NFKB1	TYK2	0.054	0.685
NFKB1	TNIP1	0.437	0.733
NFKB1	TAB2	0.113	0.529
NFKB1	TRAF3	0.093	0.534
NFKB1	RELA	0.997	0.999

NFKB1	SIRT1	0.211	0.869
NFKB1	PTGS2	0.07	0.529
NFKB1	TNIP2	0.762	0.966
NFKB1	TLR9	0.077	0.423
NFKB1	RND1	0.08	0.48
NFKB1	TNFRSF1B	0.045	0.408
NFKB1	NOD2	0.045	0.414
NFKB1	XIAP	0.093	0.462
NFKB1	RIPK2	0.069	0.554
NFKB1	STAT5A	0.087	0.555
NFKB1	PRKCB	0.13	0.584
NFKB1	STAT1	0.071	0.689
NFKB1	STAT4	0.071	0.7
NFKB1	NLRP12	0	0.811
NFKB1	ROCK1	0.072	0.812
NFKB1	STAT3	0.391	0.817
NFKB1	TRAF1	0.093	0.83
NFKB1	NFKBIE	0.218	0.921
NFKB1	TNF	0.053	0.977
NFKB1	RELB	0.957	0.992
NFKB2	NFKBIB	0.764	0.916
NFKB2	TNFRSF1A	0.043	0.739
NFKB2	PTK2B	0	0.418
NFKB2	PTGS2	0.054	0.403
NFKB2	XIAP	0.093	0.414
NFKB2	TNFRSF1B	0.045	0.42
NFKB2	STAT5B	0.071	0.43
NFKB2	STAT5A	0.071	0.437
NFKB2	PRKCD	0.119	0.47
NFKB2	TAB2	0.08	0.471
NFKB2	PIK3CA	0.124	0.473
NFKB2	PRKCB	0.12	0.479
NFKB2	TNFAIP2	0.118	0.498
NFKB2	NFKBIE	0.162	0.507
NFKB2	TNFSF13B	0.046	0.507
NFKB2	NFKBID	0.353	0.513
NFKB2	STAT1	0.071	0.521
NFKB2	POU2F2	0.069	0.548
NFKB2	TLR2	0.077	0.557
NFKB2	STAT3	0.231	0.614
NFKB2	TLR4	0.077	0.627
NFKB2	STAT4	0.071	0.637
NFKB2	TYK2	0.054	0.64
NFKB2	NRROS	0.077	0.645
NFKB2	TRAF2	0.093	0.66
NFKB2	RIPK1	0.069	0.66
NFKB2	TRAF3	0.093	0.685

NFKB2	TNIP1	0.276	0.737
NFKB2	TRAF1	0.093	0.794
NFKB2	TNIP2	0.473	0.848
NFKB2	TNF	0.053	0.849
NFKB2	RELA	0.873	0.991
NFKB2	RELB	0.956	0.999
NFKBIB	NOS2	0.055	0.412
NFKBIB	TXNDC16	0.08	0.441
NFKBIB	PTGS2	0	0.443
NFKBIB	TRAF3	0.093	0.456
NFKBIB	TNFRSF1A	0.043	0.46
NFKBIB	TRAF2	0.093	0.495
NFKBIB	TNIP2	0.134	0.497
NFKBIB	TLR4	0.077	0.525
NFKBIB	TNF	0.053	0.663
NFKBIB	NFKBID	0	0.669
NFKBIB	RELB	0.229	0.813
NFKBIB	NFKBIE	0	0.895
NFKBIB	RELA	0.924	0.998
NFKBID	SLC13A5	0	0.415
NFKBID	STARD8	0	0.41
NFKBID	TNFAIP2	0.118	0.474
NFKBID	TNF	0.053	0.486
NFKBID	RC3H2	0.079	0.488
NFKBID	ZC3H12A	0.113	0.584
NFKBID	RELA	0.192	0.722
NFKBID	RELB	0.229	0.803
NFKBIE	ZNF614	0.093	0.408
NFKBIE	TNFRSF1A	0.043	0.404
NFKBIE	RIPK1	0.069	0.493
NFKBIE	ZC3H12A	0.042	0.467
NFKBIE	TRAF3	0.093	0.415
NFKBIE	RELA	0.435	0.969
NFKBIE	RND1	0.08	0.69
NFKBIE	TNF	0.053	0.709
NFKBIE	TNFAIP2	0.118	0.446
NFKBIE	TRAF1	0.093	0.653
NFKBIE	RELB	0.488	0.917
NGP	S100A9	0	0.572
NIN	NIPBL	0	0.495
NIN	TACC3	0	0.479
NINJ1	PARP8	0	0.423
NIPAL4	PI4K2A	0	0.582
NIPAL4	SNAP29	0	0.424
NIPBL	SP3	0	0.405
NIPBL	ZCCHC6	0.093	0.58
NIPBL	REC8	0.75	0.883

NIPBL	UBXN7	0	0.411
NIPBL	THOC2	0	0.872
NIPBL	SF3B1	0	0.799
NIPBL	PAN3	0.164	0.92
NIPBL	SUV420H1	0	0.431
NIPBL	XIAP	0	0.435
NIPBL	TGFBR1	0.072	0.441
NIPBL	UBR1	0.071	0.456
NIPBL	ZNF292	0	0.614
NIPBL	RANBP2	0	0.644
NIPBL	ROCK1	0.072	0.768
NIPBL	WAC	0	0.819
NIPBL	SMG1	0	0.873
NIPBL	USP34	0	0.915
NLK	SETDB1	0	0.781
NLK	TLE4	0.093	0.667
NLK	RIPK1	0.295	0.548
NLK	PPM1D	0	0.524
NLK	TAB2	0.113	0.712
NLK	PRICKLE3	0.258	0.426
NLK	RIPK3	0.295	0.546
NLK	RIPK2	0.295	0.548
NLK	SMAD7	0.231	0.557
NLK	TLE3	0.12	0.628
NLK	TCF7L2	0.798	0.985
NLRC4	NLRP3	0.093	0.868
NLRC4	NLRC5	0.097	0.741
NLRC4	TLR4	0	0.675
NLRC4	TLR2	0	0.688
NLRC4	XIAP	0.347	0.439
NLRC4	RIPK2	0	0.496
NLRC4	TLR9	0	0.512
NLRC4	NOD2	0.218	0.545
NLRC4	NLRP12	0.093	0.628
NLRC4	TNF	0	0.654
NLRC4	NOD1	0.113	0.853
NLRC4	PRKCD	0.174	0.871
NLRC5	NLRP3	0	0.423
NLRC5	PSMB8	0.042	0.596
NLRC5	RNF19A	0.081	0.434
NLRC5	RIPK2	0.097	0.448
NLRC5	TAPBP	0	0.509
NLRC5	PSMB9	0	0.625
NLRC5	TAP1	0	0.862
NLRP12	RELA	0	0.82
NLRP3	PSTPIP1	0	0.4
NLRP3	STAT3	0	0.431

NLRP3	PTPRC	0	0.435
NLRP3	STAT1	0	0.469
NLRP3	TRAF3	0	0.472
NLRP3	RIPK2	0.049	0.473
NLRP3	PTPN22	0	0.49
NLRP3	PTGS2	0	0.527
NLRP3	RIPK3	0.049	0.578
NLRP3	TLR9	0	0.636
NLRP3	PANX1	0	0.73
NLRP3	TLR2	0	0.764
NLRP3	TNF	0	0.828
NLRP3	RELA	0	0.838
NLRP3	TLR4	0	0.869
NMI	PSMB8	0	0.434
NMI	STAT2	0.06	0.681
NMI	SOCS1	0	0.625
NMI	STAT6	0.113	0.531
NMI	SOCS3	0	0.618
NMI	PSMB9	0	0.484
NMI	STAT5B	0.087	0.753
NMI	UBE2L6	0.054	0.573
NMI	PML	0.045	0.48
NMI	PARP14	0	0.411
NMI	STAT4	0.113	0.447
NMI	STAT3	0.113	0.447
NMI	PTPN6	0	0.494
NMI	PARP9	0	0.506
NMI	USP18	0	0.581
NMI	STAT1	0.113	0.694
NMI	STAT5A	0.087	0.753
NMUR2	RASA4	0	0.59
NOD1	RSPRY1	0	0.449
NOD1	TLR4	0.045	0.834
NOD1	RIPK1	0.097	0.463
NOD1	TLR2	0.045	0.875
NOD1	S100A8	0	0.424
NOD1	TRAF3	0.058	0.56
NOD1	TLR9	0.045	0.707
NOD1	OLFM4	0.211	0.567
NOD1	TNF	0	0.678
NOD1	RIPK2	0.764	0.987
NOD2	SNX20	0	0.428
NOD2	TLR4	0.045	0.891
NOD2	RIPK1	0.113	0.515
NOD2	TLR2	0.045	0.961
NOD2	SOCS3	0.174	0.479
NOD2	TRAF3	0.058	0.408

NOD2	RELA	0.113	0.437
NOD2	OAS2	0	0.742
NOD2	RBCK1	0.432	0.573
NOD2	TLR9	0.045	0.792
NOD2	RIPK3	0.097	0.43
NOD2	PSTPIP1	0	0.404
NOD2	TIRAP	0	0.444
NOD2	STAT1	0	0.465
NOD2	TRIM8	0.071	0.488
NOD2	XIAP	0.389	0.69
NOD2	TNF	0	0.736
NOD2	RIPK2	0.764	0.992
NOM1	SENP3	0	0.547
NOM1	WDR55	0	0.636
NOM1	UBTF	0	0.659
NOM1	NOP9	0	0.847
NOP9	RCL1	0	0.74
NOP9	TFB1M	0.084	0.584
NOS2	TLR4	0	0.706
NOS2	STAT6	0	0.483
NOS2	PTPN6	0.122	0.404
NOS2	PRKCD	0.055	0.446
NOS2	PRKCB	0.053	0.489
NOS2	STAT3	0	0.508
NOS2	SLC9A3R1	0.113	0.548
NOS2	PPARD	0.091	0.559
NOS2	PTPRC	0.072	0.586
NOS2	STAT1	0	0.592
NOS2	TLR2	0	0.6
NOS2	VEGFA	0	0.679
NOS2	TYK2	0.12	0.761
NOS2	PTGS2	0.174	0.844
NOS2	RELA	0.482	0.86
NOS2	TNF	0	0.936
NPEPPS	SCLY	0.483	0.495
NPEPPS	TRIP10	0	0.406
NPEPPS	SLC2A3	0.073	0.413
NPEPPS	SLC2A1	0.073	0.435
NPEPPS	SRGAP2	0	0.553
NR1H2	NR4A1	0.231	0.464
NR1H2	SLC10A1	0	0.481
NR1H2	TESK1	0.093	0.434
NR1H2	NUDT3	0.044	0.445
NR1H2	TNF	0	0.467
NR1H2	NR4A2	0.231	0.495
NR1H2	SIRT1	0.211	0.552
NR1H2	PPARD	0.253	0.684

NR1H2	RELA	0.164	0.715
NR4A1	RARG	0.231	0.404
NR4A1	VDR	0.231	0.405
NR4A1	PPARD	0.231	0.406
NR4A1	SIK1	0	0.474
NR4A1	RELA	0.211	0.544
NR4A2	RGS2	0.046	0.485
NRDE2	PAPD4	0	0.422
NRDE2	ZNFX1	0	0.538
NRDE2	PAPOLG	0	0.585
NRDE2	ZNF331	0	0.692
NRDE2	TFIP11	0.843	0.856
NRROS	PTK2B	0.044	0.593
NRROS	SLAMF8	0	0.557
NUB1	TGIF1	0.436	0.46
NUDT3	RPS9	0.423	0.439
NUDT3	PDXK	0	0.524
NUDT3	OTUD4	0	0.429
NUMB	RBPJ	0.129	0.628
NUMB	TRAF2	0.167	0.438
NUMB	TAB2	0.158	0.427
NUMB	TRAF3	0.167	0.418
NUMB	PARD3	0.334	0.878
NUMB	TRAF7	0.261	0.474
NUMB	SLC9A3R1	0.218	0.415
NUMB	RNF41	0.167	0.405
NUMB	TRAF1	0.167	0.405
NUMB	SMURF1	0.16	0.479
NUP210	NUP210L	0	0.81
NUP210	NUP98	0.688	0.897
NUP210	XPO6	0	0.534
NUP210	SFPQ	0.44	0.44
NUP210	SEH1L	0.214	0.571
NUP210	RANBP2	0	0.872
NUP210L	TBL1X	0	0.438
NUP210L	XPO6	0	0.514
NUP210L	SEH1L	0.163	0.543
NUP210L	RAB8B	0	0.792
NUP210L	RANBP2	0	0.812
NUP210L	NUP98	0.688	0.902
NUP98	TOP1	0	0.501
NUP98	POGZ	0.093	0.402
NUP98	RARA	0.242	0.469
NUP98	SUPT6H	0	0.513
NUP98	XPO6	0.489	0.653
NUP98	NXF1	0.764	0.944
NUP98	RANBP2	0.329	0.97

NUP98	SEH1L	0.928	0.994
NXF1	THOC2	0.156	0.803
NXF1	SUPT6H	0.129	0.553
NXF1	XPO6	0.218	0.409
NXF1	XRN1	0.042	0.512
NXF1	SWT1	0	0.533
NXF1	WDR77	0.055	0.536
NXF1	SEH1L	0.641	0.782
NXF1	SRSF5	0.257	0.794
NXF1	RANBP2	0.764	0.888
OAS2	STAT2	0	0.638
OAS2	TRIM25	0	0.48
OAS2	XAF1	0	0.516
OAS2	RNF213	0	0.47
OAS2	PARP12	0	0.5
OAS2	SLFN12L	0	0.579
OAS2	PARP9	0.412	0.613
OAS2	USP18	0	0.625
OAS2	PARP14	0.408	0.647
OAS2	STAT1	0	0.724
OAS2	RSAD2	0.411	0.887
OCSTAMP	TCIRG1	0	0.468
OCSTAMP	S1PR4	0	0.564
OCSTAMP	SBNO2	0	0.513
OLFM4	PCDH17	0	0.471
OLFM4	TCN1	0	0.472
OLR1	TNF	0	0.582
OLR1	SCARF1	0	0.61
OLR1	TLR4	0.045	0.653
OLR1	TLR2	0.045	0.69
OPTN	RB1CC1	0.053	0.454
OPTN	TUBA4A	0	0.442
OPTN	RIPK1	0.759	0.831
OPTN	RAB8B	0.556	0.78
OPTN	TNIP1	0.532	0.719
OPTN	TNF	0.218	0.421
OPTN	TANK	0	0.865
ORAI2	RYR1	0	0.419
ORAI2	TRPC5	0.055	0.585
ORAI2	SLC8B1	0	0.596
ORAOV1	YRDC	0	0.498
ORAOV1	SLC4A7	0	0.403
OSBPL2	RPS9	0	0.468
OSBPL2	SPTLC2	0.042	0.402
OSGEP	SRPR	0	0.401
OSGEP	POLR2A	0	0.405
OSGEP	SELL	0	0.444

OSGEP	SDS	0	0.448
OSGEP	YRDC	0	0.947
OSGEP	TP53RK	0.924	0.998
OSM	STAT2	0	0.495
OSM	STAT6	0	0.568
OSM	SOCS3	0	0.555
OSM	PTPRC	0	0.403
OSM	TYK2	0	0.786
OSM	VEGFA	0	0.408
OSM	STAT4	0	0.468
OSM	STAT1	0	0.653
OSM	TNF	0	0.657
OSM	STAT3	0	0.783
OSTM1	TCIRG1	0	0.762
OSTM1	SNX10	0	0.715
OSTM1	RILPL2	0	0.568
OSTM1	PARP14	0	0.411
OSTM1	TFEC	0	0.416
OSTM1	SRRM2	0	0.455
OTUD4	VCPIP1	0.042	0.601
OTUD4	RAB3GAP1	0	0.404
OTUD4	PDXK	0	0.508
OTUD4	USP25	0.053	0.455
OTUD4	USP34	0.064	0.432
OTUD4	RC3H2	0.343	0.473
OTUD4	SMG1	0	0.543
OTUD4	PARP11	0.053	0.652
P2RY6	PANX1	0	0.67
P2RY8	RGS10	0	0.424
P2RY8	S1PR2	0	0.533
P2RY8	PLEK	0	0.624
P2RY8	PTPRC	0	0.658
P2RY8	TREM1	0	0.42
P2RY8	TBL1X	0	0.452
P2RY8	PTPN22	0	0.586
P2RY8	PSTPIP1	0	0.401
PADI4	TAL1	0	0.513
PADI4	USP15	0	0.413
PADI4	TRAF1	0	0.421
PADI4	PTPN22	0	0.781
PAF1	POLR2C	0.763	0.801
PAF1	UBXN7	0.762	0.775
PAF1	SUPT6H	0.692	0.733
PAF1	POLR2A	0.948	0.952
PALM2	STX11	0	0.416
PALM2	PTBP3	0	0.416
PAN3	TREX1	0.412	0.522

PAN3	WAC	0.048	0.407
PAN3	PRR7	0	0.451
PAN3	RC3H2	0.262	0.53
PAN3	USP34	0	0.532
PAN3	XRN1	0	0.568
PAN3	SMG1	0	0.657
PAN3	TCF7L2	0	0.699
PANX1	TRPM5	0	0.704
PAPD4	RC3H2	0	0.436
PAPD4	XRN1	0.093	0.461
PAPD4	QKI	0.078	0.485
PAPD4	PAPOLG	0.06	0.661
PAPD4	XRN2	0.093	0.734
PAPOLG	ZCCHC6	0.06	0.78
PAPOLG	TLR4	0	0.512
PAPOLG	WAC	0	0.416
PAPOLG	XRN2	0.093	0.527
PAPOLG	USP34	0	0.542
PAPOLG	SRSF5	0.258	0.544
PAPOLG	XRN1	0.071	0.576
PAPOLG	RFK	0	0.586
PAPOLG	TRA2A	0.164	0.673
PAPOLG	WDR77	0.674	0.771
PAQR8	PPP4R2	0	0.642
PAQR8	SIDT2	0	0.586
PARD3	TIAM2	0.219	0.563
PARD3	PVRL2	0.055	0.803
PARM1	SLC24A3	0	0.424
PARP10	PARP8	0	0.678
PARP10	PML	0	0.412
PARP10	PARP9	0.06	0.471
PARP10	PARP12	0	0.525
PARP10	PARP14	0.113	0.528
PARP10	UBA7	0	0.656
PARP10	PARP3	0	0.766
PARP11	PARP8	0	0.671
PARP11	RSAD2	0	0.499
PARP11	RNF166	0.425	0.438
PARP11	RNF114	0.513	0.524
PARP11	PARP3	0	0.726
PARP11	SP140L	0	0.515
PARP12	POLB	0	0.447
PARP12	ZSWIM4	0	0.4
PARP12	PARP8	0	0.627
PARP12	STAT2	0	0.411
PARP12	ZC3H12C	0.128	0.402
PARP12	TRIM25	0.219	0.55

PARP12	XAF1	0	0.696
PARP12	UBA7	0	0.663
PARP12	UBE2L6	0	0.549
PARP12	RSAD2	0	0.888
PARP12	RC3H2	0.131	0.472
PARP12	ZBP1	0	0.6
PARP12	PARP3	0	0.702
PARP12	PARP14	0	0.725
PARP12	STAT1	0	0.725
PARP12	TRIM21	0.073	0.728
PARP12	RNF213	0	0.754
PARP12	USP18	0.055	0.88
PARP12	ZNFX1	0.054	0.915
PARP12	PARP9	0	0.939
PARP14	PARP8	0	0.562
PARP14	STAT2	0.093	0.655
PARP14	STAT6	0.211	0.832
PARP14	PSMB9	0	0.412
PARP14	XAF1	0	0.403
PARP14	UBA7	0	0.67
PARP14	UBE2L6	0.042	0.407
PARP14	RSAD2	0.465	0.882
PARP14	TRIM21	0.042	0.435
PARP14	ZNFX1	0.098	0.519
PARP14	ZBP1	0	0.698
PARP14	PARP3	0.163	0.704
PARP14	USP18	0.048	0.789
PARP14	STAT1	0.093	0.81
PARP14	RNF213	0	0.926
PARP14	PARP9	0.487	0.977
PARP3	POLB	0.161	0.451
PARP3	PHF1	0	0.426
PARP3	PARP8	0	0.814
PARP3	TOP1	0.258	0.48
PARP3	TIPARP	0	0.544
PARP3	SBNO2	0	0.411
PARP3	PARP9	0.163	0.741
PARP8	ZFAT	0	0.415
PARP8	PARP9	0	0.635
PARP9	PSMB8	0	0.525
PARP9	STAT2	0.113	0.57
PARP9	PSMB9	0	0.438
PARP9	SUPT6H	0.06	0.424
PARP9	XAF1	0	0.75
PARP9	TIPARP	0	0.668
PARP9	UBA7	0	0.821
PARP9	UBE2L6	0.042	0.597

PARP9	RSAD2	0.205	0.817
PARP9	USP18	0.048	0.886
PARP9	TRIM38	0.042	0.418
PARP9	ZNFX1	0.098	0.578
PARP9	ZBP1	0	0.453
PARP9	TAP1	0	0.459
PARP9	RNF213	0	0.702
PARP9	TRIM21	0.042	0.726
PARP9	STAT1	0.218	0.882
PCGF5	PHC2	0.438	0.638
PCGF5	RCL1	0	0.407
PCGF5	UBE2D1	0.255	0.41
PCGF5	THEMIS2	0	0.461
PCGF5	XIAP	0	0.689
PCGF5	RYBP	0.764	0.954
PCMTD1	RB1CC1	0	0.464
PCMTD1	SMG1	0	0.491
PDE4B	SLC25A19	0	0.416
PDE4B	TNF	0	0.411
PDE4B	SAG	0.13	0.423
PDP1	SLC25A19	0	0.663
PDP1	RPIA	0	0.408
PDP1	TAB2	0.158	0.409
PDP1	PPTC7	0.159	0.836
PDXK	PSMA2	0	0.499
PDXK	SARS	0	0.576
PDXK	USP25	0	0.418
PDXK	WDR4	0	0.447
PDXK	PROSC	0	0.562
PDXK	ZNF295	0	0.599
PELI1	RIPK1	0.129	0.464
PELI1	SERTAD1	0	0.476
PELI1	TRAF2	0.158	0.411
PELI1	TAB2	0	0.764
PELI1	TRAF3	0.158	0.585
PELI1	TRAF7	0.158	0.443
PELI1	RNF41	0.158	0.411
PELI1	RIPK2	0.129	0.416
PELI1	TRAF1	0.158	0.425
PELI1	PSME1	0	0.465
PELI1	PSME2	0	0.468
PFKFB4	PRKAA1	0.07	0.667
PFKFB4	TKT	0	0.436
PFKFB4	PRKAB1	0.065	0.66
PFKFB4	SLC2A3	0	0.494
PFKFB4	SLC2A1	0	0.495
PGAM5	RIPK1	0.113	0.709

PGAM5	PPIF	0	0.405
PGAM5	RNF126	0	0.573
PGAM5	RIPK3	0.113	0.797
PGS1	POR	0	0.425
PGS1	TSFM	0	0.623
PHACTR2	PPM1M	0	0.457
PHACTR2	ZNF331	0.072	0.606
PHC2	RYBP	0	0.469
PHC2	TRANK1	0.486	0.485
PHF1	PSEN1	0	0.523
PHF1	PHF11	0.161	0.693
PHF11	UBE2L6	0.08	0.42
PHF12	UBXN7	0.114	0.434
PHF12	SUPT6H	0	0.536
PHF12	POLR2A	0.12	0.491
PHLDB1	TSPAN31	0	0.614
PHLDB1	PLEK	0	0.448
PHLDB1	TBC1D2B	0	0.416
PHLDB1	STK10	0	0.418
PHLDB1	PLAGL2	0.045	0.524
PI4K2A	PLCG2	0	0.653
PI4K2A	PIK3R6	0	0.947
PIAS1	SETDB1	0.347	0.509
PIAS1	SENP3	0.132	0.584
PIAS1	SENP2	0.132	0.4
PIAS1	SAFB	0.093	0.415
PIAS1	STAT2	0.257	0.924
PIAS1	SOCS1	0	0.571
PIAS1	STAT6	0.257	0.82
PIAS1	PTPN1	0.113	0.733
PIAS1	PIAS2	0.393	0.438
PIAS1	TOP1	0.46	0.606
PIAS1	STAT5B	0.294	0.846
PIAS1	PTPN2	0.079	0.726
PIAS1	TYK2	0.078	0.506
PIAS1	RELA	0.257	0.431
PIAS1	STAT3	0.417	0.915
PIAS1	STAT5A	0.294	0.85
PIAS1	UBE2B	0.205	0.521
PIAS1	RANBP2	0.049	0.783
PIAS1	STAT4	0.257	0.903
PIAS1	STAT1	0.764	0.988
PIAS2	SETDB1	0.347	0.466
PIAS2	SENP3	0.132	0.514
PIAS2	STAT2	0.257	0.798
PIAS2	STAT6	0.257	0.778
PIAS2	PTPN1	0.079	0.526

PIAS2	SHOC2	0.042	0.508
PIAS2	UBE2B	0.205	0.475
PIAS2	PTPN2	0.079	0.526
PIAS2	RELA	0.257	0.544
PIAS2	TOP1	0.46	0.582
PIAS2	RANBP2	0.049	0.752
PIAS2	STAT5A	0.294	0.816
PIAS2	STAT5B	0.294	0.816
PIAS2	STAT1	0.411	0.819
PIAS2	STAT4	0.257	0.888
PIAS2	STAT3	0.417	0.895
PIH1D1	POLR2C	0.764	0.769
PIH1D1	SUPT6H	0.435	0.449
PIH1D1	SHISA5	0	0.467
PIH1D1	SMG1	0.093	0.44
PIH1D1	WDR4	0	0.519
PIH1D1	POLR2A	0.617	0.744
PIK3AP1	RET	0.396	0.522
PIK3AP1	PIK3CA	0	0.853
PIK3AP1	PIK3R6	0	0.48
PIK3AP1	SNRK	0	0.41
PIK3CA	PRKAA1	0.125	0.427
PIK3CA	RET	0.207	0.886
PIK3CA	PLCG2	0.212	0.755
PIK3CA	VAV1	0	0.671
PIK3CA	RAF1	0.122	0.9
PIK3CA	PTK2B	0.124	0.698
PIK3CA	TLR4	0.13	0.846
PIK3CA	PTPN1	0.12	0.713
PIK3CA	RICTOR	0.388	0.819
PIK3CA	SOCS3	0.093	0.579
PIK3CA	PRKCD	0.161	0.934
PIK3CA	RAP1B	0.201	0.868
PIK3CA	TRAF7	0.104	0.408
PIK3CA	STAT1	0.113	0.414
PIK3CA	RHOH	0.158	0.43
PIK3CA	TIAM2	0.051	0.431
PIK3CA	ROCK1	0.122	0.443
PIK3CA	SLC2A9	0	0.444
PIK3CA	RANBP2	0.219	0.447
PIK3CA	REM2	0.201	0.451
PIK3CA	TGFBR1	0.122	0.461
PIK3CA	VDR	0.078	0.488
PIK3CA	SIRT1	0.118	0.552
PIK3CA	TEC	0.129	0.572
PIK3CA	PLEK	0	0.578
PIK3CA	SLC2A1	0	0.582

PIK3CA	PTPN2	0.12	0.6
PIK3CA	SMG1	0.219	0.609
PIK3CA	UGCG	0	0.628
PIK3CA	ZYX	0.055	0.63
PIK3CA	SLC2A3	0	0.636
PIK3CA	TNFSF10	0	0.637
PIK3CA	PXN	0	0.68
PIK3CA	VEGFC	0	0.698
PIK3CA	RELA	0.113	0.708
PIK3CA	VEGFA	0	0.736
PIK3CA	PTPN6	0.161	0.81
PIK3CA	STAT3	0.109	0.811
PIK3CA	TRAF2	0.055	0.84
PIK3CA	TYK2	0.129	0.857
PIK3CA	PREX1	0.051	0.865
PIK3CA	PIK3R6	0.338	0.962
PIK3CA	PIK3R5	0.409	0.964
PIK3R5	PRKAA1	0	0.412
PIK3R5	PTPN1	0	0.587
PIK3R5	PLEK	0	0.476
PIK3R5	SH2B2	0	0.709
PIK3R5	PIK3R6	0.174	0.897
PIK3R5	PTPN6	0	0.458
PIM1	SOCS3	0.063	0.414
PIM1	ZBTB17	0.121	0.444
PIM1	PRKAB1	0.397	0.652
PIM3	PRKAB1	0.397	0.652
PIM3	SOCS3	0.063	0.519
PIM3	SIK1	0.211	0.404
PIM3	SUSD2	0	0.488
PION	SPTSSA	0	0.45
PION	PSEN1	0.211	0.627
PKD1L3	TRPM5	0	0.715
PKNOX1	PROSC	0	0.41
PLA2G4A	PLCG2	0	0.881
PLA2G4A	PTGER2	0	0.453
PLA2G4A	TYK2	0.127	0.49
PLA2G4A	TNF	0	0.454
PLA2G4A	TEC	0.127	0.464
PLA2G4A	PRKCB	0.093	0.647
PLA2G4A	PPARD	0.045	0.689
PLA2G4A	PTGS2	0	0.902
PLAGL2	TM9SF4	0.08	0.77
PLAGL2	PLCG2	0	0.488
PLAGL2	TSPAN31	0	0.521
PLAU	SERPING1	0.171	0.448
PLAU	SERPINB4	0.171	0.452

PLAU	TYK2	0.055	0.488
PLAU	PTGS2	0.045	0.499
PLAU	TNF	0	0.508
PLAU	VEGFA	0	0.541
PLAU	UBE2B	0	0.638
PLAU	SERPINB2	0.171	0.92
PLAU	SERPINE1	0.948	0.999
PLAU	PLAUR	0.953	0.999
PLAUR	TLR4	0	0.407
PLAUR	TYK2	0.203	0.588
PLAUR	STAT3	0	0.411
PLAUR	TNF	0	0.432
PLAUR	VEGFA	0	0.508
PLAUR	SELL	0	0.676
PLAUR	SERPINB2	0.051	0.866
PLAUR	SERPINE1	0.051	0.985
PLBD1	PPP1R16B	0.055	0.462
PLBD1	TKT	0.4	0.435
PLBD1	RRAD	0	0.448
PLBD1	STK10	0	0.662
PLCG2	S1PR4	0	0.519
PLCG2	RET	0.343	0.609
PLCG2	RASGRP2	0.218	0.455
PLCG2	TYK2	0.138	0.405
PLCG2	RAP1B	0.142	0.41
PLCG2	STAT1	0	0.412
PLCG2	STOML1	0	0.43
PLCG2	STAT3	0	0.447
PLCG2	PTPRC	0.062	0.455
PLCG2	PLEK	0	0.489
PLCG2	RAPGEF1	0.218	0.491
PLCG2	SELP	0.071	0.516
PLCG2	STAT5A	0	0.535
PLCG2	VEGFA	0	0.549
PLCG2	STAT5B	0	0.563
PLCG2	PTPN6	0.218	0.649
PLCG2	VAV1	0.17	0.675
PLCG2	PTK2B	0.253	0.734
PLCG2	PRKCD	0.078	0.877
PLCG2	SH3BP2	0.272	0.935
PLCG2	TEC	0.295	0.94
PLCG2	PRKCB	0.157	0.948
PLEK	RHOG	0.054	0.519
PLEK	TAGLN2	0	0.9
PLEK	VAV1	0	0.744
PLEK	TLR4	0	0.673
PLEK	RICTOR	0	0.587

PLEK	TAGAP	0	0.417
PLEK	SH2B2	0	0.423
PLEK	PLEKHA4	0	0.479
PLEK	ROCK1	0	0.492
PLEK	VASP	0	0.505
PLEK	PREX1	0	0.507
PLEK	PXN	0	0.631
PLEK	PTPRC	0	0.785
PLEKHA4	UBA7	0.073	0.532
PLEKHA4	PPP1R15B	0	0.632
PLEKHA4	USP18	0.061	0.627
PLEKHO2	ST6GALNAC4	0	0.589
PLK3	RASGRP2	0.046	0.411
PLK3	TUBA4A	0.175	0.41
PLK3	REC8	0.404	0.583
PLK3	RAF1	0.068	0.842
PLK3	TBC1D2B	0.257	0.4
PLK3	RASGEF1B	0.046	0.512
PLK3	TPT1	0.054	0.555
PLK3	PSTPIP1	0.21	0.586
PLK3	PSTPIP2	0.21	0.586
PLSCR2	XKR8	0	0.622
PLSCR2	RSAD2	0	0.505
PLSCR2	TLR9	0	0.587
PLSCR2	STAT1	0	0.432
PLXNA1	SEMA4D	0.257	0.864
PLXNA1	SEMA7A	0.257	0.579
PLXNA1	PLXNA4	0	0.905
PLXNA1	RND1	0.353	0.964
PLXNA4	SEMA4D	0.257	0.814
PLXNA4	SEMA7A	0.257	0.769
PLXNA4	RND1	0.353	0.937
PML	SKIL	0.471	0.543
PML	RARG	0.488	0.672
PML	TRIM25	0	0.722
PML	TRIM35	0.063	0.549
PML	RARA	0.764	0.985
PML	SIRT1	0.165	0.833
PML	SP110	0.262	0.699
PML	TRIM38	0	0.561
PML	SMURF1	0.054	0.567
PML	TGFBR1	0.078	0.626
PML	SMAD7	0.127	0.648
PML	TRIM8	0	0.674
PML	TRIM21	0.063	0.728
PML	SP140L	0.341	0.787
PNP	TAGLN2	0.053	0.429

PNP	UPP1	0	0.962
PNP	PNRC1	0	0.514
PNP	SIRT1	0.052	0.766
PNP	XDH	0	0.991
PNPT1	PROSC	0	0.405
PNPT1	XRN2	0	0.448
PNPT1	RBM43	0	0.468
PNPT1	TSFM	0.045	0.473
PNPT1	XRN1	0	0.493
POGZ	SETDB1	0.161	0.434
POGZ	RHBDD1	0	0.515
POLR2A	SETDB1	0.182	0.411
POLR2A	POLR2C	0.997	0.999
POLR2A	RPS9	0.258	0.603
POLR2A	UBXN7	0	0.459
POLR2A	RARG	0.12	0.616
POLR2A	POU2F2	0.053	0.605
POLR2A	USP3	0.296	0.423
POLR2A	SUPT6H	0.926	0.987
POLR2A	XRN2	0.39	0.749
POLR2A	XRN1	0.16	0.414
POLR2A	SRSF5	0.338	0.405
POLR2A	RARA	0.12	0.654
POLR2A	RELA	0.114	0.663
POLR2A	VDR	0.434	0.586
POLR2A	TGFBR1	0.042	0.437
POLR2A	WAC	0.316	0.406
POLR2A	TRAF7	0.069	0.433
POLR2A	SNAPC1	0	0.6
POLR2A	WDR4	0	0.415
POLR2A	UBTF	0.156	0.453
POLR2A	UBE2B	0.392	0.631
POLR2A	SMURF1	0.535	0.678
POLR2A	SAFB2	0.065	0.408
POLR2C	XRN2	0.041	0.41
POLR2C	XRN1	0.045	0.449
POLR2C	TOP1	0	0.531
POLR2C	SNAPC1	0	0.641
POLR2C	POU2F2	0.055	0.65
POLR2C	TSFM	0	0.712
POLR2C	RPS9	0.344	0.825
POLR2C	UBXN7	0.461	0.889
POLR2C	SUPT6H	0.764	0.891
POR	RELA	0.218	0.568
POR	VDR	0.091	0.417
POR	PTPN6	0.122	0.404
POR	VEGFA	0	0.458

POR	TBXAS1	0.081	0.507
POU2F2	SNAPC1	0	0.6
POU2F2	RELA	0.055	0.672
PPA1	TARS	0	0.429
PPA1	UBR1	0.217	0.459
PPARD	TLE4	0.167	0.649
PPARD	RAF1	0.121	0.52
PPARD	RETN	0	0.464
PPARD	STAT6	0.152	0.486
PPARD	RELA	0.164	0.682
PPARD	SIRT1	0.312	0.721
PPARD	PTGS2	0.045	0.462
PPARD	STAT3	0.119	0.428
PPARD	TLE3	0.167	0.651
PPARD	TNF	0	0.747
PPIF	RIPK1	0.071	0.401
PPIF	SOD2	0.431	0.721
PPIF	XPO6	0.046	0.417
PPIF	SIRT1	0.114	0.427
PPIF	RIPK3	0.071	0.466
PPIF	TSPO	0	0.622
PPIF	SLC8B1	0	0.627
PPIF	TBL1X	0.68	0.818
PPIF	STAT3	0.042	0.876
PPM1D	PPM1M	0	0.661
PPM1D	TNFRSF1A	0	0.432
PPM1D	RIPK1	0.219	0.419
PPM1D	RIPK2	0.219	0.419
PPM1D	TGFBR1	0.158	0.441
PPM1D	RIPK3	0.219	0.454
PPM1D	TNF	0.136	0.483
PPM1D	SESN2	0	0.509
PPM1D	PPP4C	0.392	0.565
PPM1D	TAB2	0.27	0.627
PPM1D	PPTC7	0.073	0.639
PPM1M	PPTC7	0	0.523
PPP1R15A	ZFP36	0	0.478
PPP1R15A	SHOC2	0	0.54
PPP1R15A	PPP1R3B	0	0.541
PPP1R15A	TGFBR1	0.044	0.705
PPP1R15A	PPP4C	0.258	0.799
PPP1R15A	SMAD7	0.113	0.927
PPP1R16B	STK10	0.046	0.469
PPP1R16B	ROCK1	0.16	0.512
PPP1R3B	SHOC2	0.042	0.549
PPP1R3B	ST3GAL3	0	0.423
PPP1R3B	TRIB1	0.051	0.438

PPP1R3B	PPP4C	0.209	0.682
PPP4C	PPP4R2	0.925	0.976
PPP4C	SHOC2	0.158	0.754
PPP4C	PRKCD	0.156	0.407
PPP4C	SUPT6H	0.07	0.414
PPP4C	PSEN1	0.042	0.411
PPP4R2	TTC33	0	0.678
PPP4R2	SUPT6H	0	0.479
PPP4R2	XRN1	0	0.479
PPTC7	TAB2	0.158	0.445
PPTC7	UBE2J2	0.046	0.633
PQBP1	TREX1	0	0.577
PQBP1	WDR77	0.404	0.453
PRDM1	TNF	0	0.404
PRDM1	WDR77	0	0.418
PRDM1	STRA8	0	0.469
PRDM1	SELL	0	0.524
PRDM1	PTPRC	0	0.534
PRDM1	STAT3	0.113	0.59
PRDX5	SOD2	0.119	0.879
PRDX5	VNN2	0.211	0.434
PRDX5	SLC4A2	0.459	0.481
PREX1	RHOG	0.242	0.724
PREX1	RICTOR	0.218	0.581
PREX1	RAP1B	0.452	0.668
PREX1	SH3PXD2B	0.571	0.714
PREX1	RHOH	0.242	0.435
PREX1	RND1	0.242	0.439
PRICKLE3	SIRT1	0.053	0.404
PRKAA1	TTC33	0.055	0.514
PRKAA1	RICTOR	0	0.407
PRKAA1	SIRT1	0.093	0.673
PRKAA1	SESN2	0	0.707
PRKAA1	RB1CC1	0.043	0.921
PRKAA1	PRKAB1	0.944	0.999
PRKAB1	RB1CC1	0	0.912
PRKAB1	SNAP29	0	0.469
PRKAB1	TRIB1	0.397	0.652
PRKAB1	STK40	0.397	0.652
PRKAB1	SESN2	0	0.748
PRKCB	RET	0.045	0.5
PRKCB	SKIL	0	0.447
PRKCB	RAF1	0.093	0.926
PRKCB	PTK2B	0	0.643
PRKCB	RICTOR	0.079	0.605
PRKCB	RARG	0.055	0.415
PRKCB	PRKCD	0.116	0.826

PRKCB	STAT5B	0	0.579
PRKCB	RARA	0.055	0.415
PRKCB	RELA	0	0.719
PRKCB	RBCK1	0.763	0.802
PRKCB	STAT1	0.05	0.406
PRKCB	STAT3	0	0.435
PRKCB	STAT5A	0	0.579
PRKCB	SDC4	0.166	0.643
PRKCB	SLC9A3R1	0.184	0.857
PRKCD	RHOG	0.259	0.45
PRKCD	VAV1	0.08	0.698
PRKCD	STAT2	0.157	0.401
PRKCD	RAF1	0.131	0.93
PRKCD	PTK2B	0.44	0.816
PRKCD	RBCK1	0	0.404
PRKCD	SMG1	0.223	0.416
PRKCD	RHOH	0.259	0.432
PRKCD	RND1	0.259	0.432
PRKCD	TIAM2	0.138	0.457
PRKCD	TIRAP	0.164	0.497
PRKCD	SDC4	0.078	0.651
PRKCD	RELA	0	0.68
PRKCD	STAT3	0.203	0.849
PRKCD	STAT1	0.764	0.962
PRODH	SDS	0	0.423
PROSC	SCLY	0	0.6
PROSC	RAB11FIP1	0	0.779
PROSC	ZDHHC2	0	0.538
PRR5L	RICTOR	0.527	0.889
PRR5L	SBNO2	0	0.43
PRR5L	ZFP36	0.073	0.473
PSEN1	RBPJ	0.184	0.694
PSEN1	TRAF2	0.163	0.416
PSEN1	TRAF3	0.163	0.416
PSEN1	TFPI2	0.174	0.445
PSEN1	TRAF7	0.262	0.552
PSEN1	TNF	0	0.518
PSEN1	SDC3	0	0.616
PSEN1	RNF41	0.163	0.427
PSEN1	TRAF1	0.163	0.416
PSEN1	SRI	0.162	0.438
PSMA2	TNFAIP6	0	0.499
PSMA2	SLA	0	0.513
PSMA2	S100A12	0	0.537
PSMA2	S100A8	0	0.605
PSMA2	PSME1	0.513	0.712
PSMA2	PSME2	0.672	0.795

PSMA2	PSMB8	0.964	0.998
PSMA2	PSMB9	0.965	0.999
PSMB8	TAP2	0.068	0.753
PSMB8	UBE2G1	0.081	0.418
PSMB8	XAF1	0	0.42
PSMB8	TAPBPL	0	0.456
PSMB8	UBA7	0.078	0.564
PSMB8	STAT1	0	0.752
PSMB8	PSME2	0.461	0.887
PSMB8	TAPBP	0	0.898
PSMB8	PSME1	0.461	0.928
PSMB8	TAP1	0.071	0.953
PSMB8	PSMB9	0.945	0.999
PSMB9	TAP2	0.068	0.741
PSMB9	TNF	0	0.407
PSMB9	TRIM21	0.044	0.411
PSMB9	TAPBPL	0	0.45
PSMB9	UBA7	0.115	0.563
PSMB9	STAT1	0	0.786
PSMB9	TAPBP	0	0.834
PSMB9	PSME1	0.503	0.891
PSMB9	PSME2	0.67	0.964
PSMB9	TAP1	0.071	0.982
PSME1	UBE2G1	0.053	0.529
PSME1	TAPBPL	0	0.44
PSME1	TAPBP	0	0.565
PSME1	TAP1	0	0.404
PSME1	TNF	0	0.901
PSME1	PSME2	0.764	0.995
PSME2	TXNDC16	0.053	0.474
PSME2	TAPBPL	0	0.478
PSME2	TAPBP	0	0.603
PSME2	STAT1	0	0.407
PSME2	TAP1	0	0.54
PSPC1	SAFB	0.156	0.43
PSPC1	SAFB2	0.156	0.412
PSPC1	TRA2A	0.165	0.482
PSPC1	TET2	0	0.49
PSPC1	XRN2	0.058	0.591
PSPC1	SFPQ	0.934	0.943
PSTPIP1	PTPN12	0.928	0.994
PSTPIP1	ZC3H12A	0	0.537
PSTPIP1	SUV420H2	0.162	0.479
PSTPIP1	PVRL2	0	0.43
PSTPIP1	PXN	0.454	0.733
PSTPIP1	PTPN22	0.507	0.784
PSTPIP1	PTPN6	0.12	0.424

PSTPIP2	PTPN12	0.691	0.842
PSTPIP2	SRGAP2	0.097	0.579
PSTPIP2	PXN	0.454	0.666
PSTPIP2	TAPT1	0	0.475
PSTPIP2	PTPN22	0.47	0.62
PSTPIP2	STEAP4	0	0.432
PSTPIP2	TRANK1	0	0.47
PTAFR	TLR4	0	0.575
PTAFR	SLA	0	0.429
PTAFR	TLR2	0	0.421
PTAFR	SIRPB1	0	0.51
PTAFR	PTPRC	0	0.428
PTAFR	TBXAS1	0	0.404
PTAFR	TNF	0	0.439
PTBP3	ZCCHC6	0.051	0.658
PTBP3	UBXN7	0.122	0.415
PTBP3	ST3GAL3	0	0.4
PTBP3	QKI	0.557	0.604
PTGER2	PTX3	0	0.427
PTGER2	TXNDC16	0	0.538
PTGER2	PTGS2	0.053	0.693
PTGS2	STAT2	0	0.475
PTGS2	TLR4	0	0.784
PTGS2	STAT6	0	0.497
PTGS2	SOD2	0	0.527
PTGS2	TNFAIP6	0	0.701
PTGS2	TLR2	0	0.683
PTGS2	SOCS3	0	0.438
PTGS2	PTX3	0	0.527
PTGS2	PTPRC	0.13	0.529
PTGS2	RELA	0	0.499
PTGS2	SIRT1	0	0.5
PTGS2	SBNO2	0	0.407
PTGS2	ZFP36	0	0.41
PTGS2	STAT4	0	0.422
PTGS2	TRAF1	0	0.424
PTGS2	VEGFC	0	0.434
PTGS2	SLC2A1	0	0.563
PTGS2	SERPINE1	0	0.563
PTGS2	RELB	0	0.568
PTGS2	STAT1	0	0.616
PTGS2	STAT3	0	0.7
PTGS2	VEGFA	0	0.774
PTGS2	TNF	0	0.88
PTGS2	TBXAS1	0.043	0.995
PTK2B	RHOG	0.05	0.419
PTK2B	RET	0.541	0.792

PTK2B	RB1CC1	0.113	0.593
PTK2B	TM9SF4	0	0.478
PTK2B	PTPRE	0.125	0.515
PTK2B	PTPN12	0.204	0.719
PTK2B	VAV1	0.113	0.812
PTK2B	STAT2	0.161	0.498
PTK2B	RAF1	0.136	0.414
PTK2B	TEC	0.219	0.412
PTK2B	PTPRC	0.125	0.413
PTK2B	STAT4	0.161	0.417
PTK2B	SKAP2	0.117	0.419
PTK2B	PTPN22	0.125	0.423
PTK2B	SRI	0	0.429
PTK2B	PTPN1	0.125	0.435
PTK2B	VEGFC	0	0.436
PTK2B	TYK2	0.219	0.483
PTK2B	STAT6	0.161	0.503
PTK2B	ROCK1	0.136	0.542
PTK2B	SDC4	0	0.566
PTK2B	SOCS3	0.494	0.603
PTK2B	STAT1	0.348	0.633
PTK2B	ZYX	0.055	0.671
PTK2B	RAP1B	0.043	0.677
PTK2B	PTPN5	0.125	0.679
PTK2B	VEGFA	0	0.693
PTK2B	RAPGEF1	0.053	0.697
PTK2B	STAT5B	0.161	0.718
PTK2B	STAT5A	0.161	0.722
PTK2B	STAT3	0.296	0.77
PTK2B	PTPN6	0.339	0.772
PTK2B	PXN	0.943	0.999
PTMS	SRPR	0	0.414
PTPN1	STAM2	0.213	0.512
PTPN1	PTPRE	0.316	0.409
PTPN1	STAT2	0.158	0.936
PTPN1	STAT6	0.158	0.67
PTPN1	RAPGEF1	0.128	0.471
PTPN1	VEGFA	0.055	0.611
PTPN1	SOCS3	0.079	0.622
PTPN1	SH2B2	0	0.654
PTPN1	STAT5B	0.164	0.714
PTPN1	STAT5A	0.164	0.724
PTPN1	STAT1	0.317	0.759
PTPN1	STAT3	0.4	0.839
PTPN1	TYK2	0.139	0.972
PTPN12	STAT4	0.158	0.426
PTPN12	STAT3	0.158	0.437

PTPN12	SKAP2	0.218	0.449
PTPN12	VASP	0.119	0.48
PTPN12	PTPRC	0.167	0.482
PTPN12	RAPGEF1	0.128	0.502
PTPN12	PXN	0.574	0.974
PTPN2	PTPRE	0.463	0.537
PTPN2	STAT2	0.158	0.792
PTPN2	STAT6	0.158	0.894
PTPN2	SOCS3	0.079	0.458
PTPN2	STAT5B	0.164	0.905
PTPN2	TAGAP	0	0.467
PTPN2	PTPRJ	0.463	0.5
PTPN2	PTPRG	0.463	0.526
PTPN2	VEGFA	0.055	0.646
PTPN2	STAT4	0.158	0.781
PTPN2	STAT5A	0.164	0.912
PTPN2	TYK2	0.139	0.945
PTPN2	STAT1	0.467	0.955
PTPN2	STAT3	0.639	0.976
PTPN22	STAT2	0.158	0.413
PTPN22	STAT6	0.158	0.438
PTPN22	PTPRC	0.167	0.699
PTPN22	TYK2	0.139	0.486
PTPN22	TRAF3	0.113	0.696
PTPN22	PXN	0.219	0.435
PTPN22	PXK	0	0.428
PTPN22	PTPN6	0.157	0.45
PTPN22	STAT3	0.158	0.458
PTPN22	TAGAP	0	0.472
PTPN22	SKAP2	0.41	0.49
PTPN22	STAT1	0.158	0.526
PTPN22	TRAF1	0.048	0.611
PTPN22	STAT4	0.158	0.721
PTPN6	RASGRP2	0.293	0.51
PTPN6	VAV1	0.06	0.539
PTPN6	STAT2	0.218	0.495
PTPN6	SOCS1	0.162	0.473
PTPN6	THEMIS2	0.205	0.429
PTPN6	STAT6	0.218	0.527
PTPN6	SIRPA	0.412	0.608
PTPN6	SLAMF1	0.235	0.445
PTPN6	SOCS3	0.162	0.509
PTPN6	RAP1B	0.162	0.406
PTPN6	STAT5B	0.218	0.527
PTPN6	SIRPB1	0.412	0.589
PTPN6	PTPRC	0.156	0.814
PTPN6	TYK2	0.219	0.888

PTPN6	SH3BP2	0.128	0.615
PTPN6	TGFBR1	0.101	0.45
PTPN6	PXN	0.139	0.512
PTPN6	SPRED2	0.119	0.571
PTPN6	VASP	0.119	0.613
PTPN6	VEGFA	0.044	0.435
PTPN6	STAT4	0.218	0.489
PTPN6	RAPGEF1	0.293	0.496
PTPN6	RIPK2	0.101	0.503
PTPN6	RASGEF1B	0.293	0.507
PTPN6	TARM1	0.257	0.528
PTPN6	STAT5A	0.218	0.535
PTPN6	STAT1	0.218	0.565
PTPN6	STAT3	0.218	0.589
PTPN9	USP42	0	0.412
PTPN9	ZNF614	0.045	0.438
PTPN9	STK17A	0.078	0.448
PTPN9	STK17B	0.078	0.434
PTPN9	USP36	0	0.412
PTPRC	RHOG	0.093	0.422
PTPRC	SEMA4D	0.435	0.802
PTPRC	TNFRSF1A	0.045	0.4
PTPRC	VAV1	0.174	0.87
PTPRC	STAT2	0.117	0.46
PTPRC	SOCS1	0.079	0.4
PTPRC	TAL1	0	0.424
PTPRC	TLR4	0.131	0.741
PTPRC	STAT6	0.117	0.589
PTPRC	SIRPA	0.146	0.485
PTPRC	SLAMF1	0.113	0.699
PTPRC	TLR2	0.131	0.658
PTPRC	STAT5B	0.117	0.474
PTPRC	SIGLEC5	0.08	0.413
PTPRC	TYK2	0.133	0.413
PTPRC	TAGAP	0	0.429
PTPRC	SERPINB2	0	0.443
PTPRC	VEGFC	0.044	0.444
PTPRC	RHOH	0.093	0.445
PTPRC	SIRT1	0	0.461
PTPRC	STAT5A	0.117	0.469
PTPRC	XCR1	0.045	0.471
PTPRC	TMEM119	0	0.493
PTPRC	STAT4	0.117	0.508
PTPRC	TLR9	0.131	0.583
PTPRC	TNFRSF18	0	0.587
PTPRC	SELP	0.126	0.634
PTPRC	STAT1	0.117	0.663

PTPRC	VEGFA	0.044	0.708
PTPRC	STAT3	0.117	0.754
PTPRC	TNF	0.053	0.857
PTPRC	SELL	0.126	0.934
PTPRE	SIRPB2	0.146	0.453
PTPRE	RNF24	0.045	0.547
PTPRE	PTPRG	0.483	0.562
PTPRE	PTPRJ	0.483	0.573
PTPRE	TYK2	0.133	0.662
PTPRG	STK10	0	0.405
PTPRG	ST3GAL3	0	0.406
PTPRG	PTPRJ	0.483	0.523
PTPRG	RASA2	0.118	0.426
PTPRG	SLC39A13	0	0.527
PTPRJ	SDCBP	0.076	0.661
PTPRJ	VEGFA	0.06	0.659
PTX3	TNFAIP6	0.164	0.941
PTX3	VNN2	0	0.42
PTX3	VEGFA	0	0.423
PTX3	VCAN	0	0.426
PTX3	TNF	0	0.465
PTX3	SERPINE1	0	0.547
PTX3	SELP	0.059	0.806
PXK	SP3	0	0.535
PXK	XK	0	0.513
PXN	RHOG	0.184	0.606
PXN	RET	0.078	0.656
PXN	RBPJ	0	0.48
PXN	RAF1	0.162	0.461
PXN	RICTOR	0.093	0.579
PXN	RILPL2	0	0.449
PXN	SF3B1	0	0.41
PXN	RAP1B	0.128	0.7
PXN	SUPT6H	0	0.513
PXN	RHOH	0.184	0.521
PXN	VEGFC	0	0.52
PXN	ZYX	0.161	0.809
PXN	SDC4	0.078	0.537
PXN	RND1	0.184	0.546
PXN	ROCK1	0.085	0.576
PXN	RAPGEF1	0.106	0.69
PXN	VASP	0	0.754
PXN	VEGFA	0	0.827
PXN	STAT3	0.045	0.866
QKI	RBM47	0.184	0.402
QKI	TRA2A	0.213	0.405
QKI	WDR77	0.443	0.455

QKI	UBE2G1	0.043	0.469
R3HCC1L	TBL1X	0	0.469
RAB11FIP1	STAU1	0	0.454
RAB11FIP1	VMP1	0	0.613
RAB11FIP1	TIPARP	0	0.405
RAB11FIP1	TAGAP	0	0.454
RAB27A	SYTL3	0.433	0.879
RAB27A	TSPAN2	0	0.52
RAB27A	TBC1D10A	0	0.523
RAB27A	STX11	0.046	0.688
RAB37	RILPL2	0	0.412
RAB3D	RAB3IP	0.166	0.43
RAB3D	STX11	0.052	0.445
RAB3D	VCPIP1	0	0.461
RAB3GAP1	RABGEF1	0	0.485
RAB3GAP1	UBXN7	0	0.471
RAB3GAP1	TBC1D2B	0	0.465
RAB3GAP1	RAB3IP	0	0.617
RAB3IP	RABGEF1	0	0.413
RAB3IP	RAB8B	0.478	0.731
RAB3IP	STOM	0	0.414
RAB3IP	STK38L	0.121	0.437
RAB3IP	TBC1D10A	0.055	0.526
RAB8B	RABGEF1	0.071	0.531
RAB8B	STXBP3	0.331	0.653
RAB8B	RILPL2	0.218	0.575
RAB8B	RAP1B	0.329	0.502
RAB8B	SH3PXD2B	0.085	0.419
RAB8B	TNFAIP2	0.296	0.402
RAB8B	RABGAP1L	0.162	0.41
RAB8B	SNAP29	0.205	0.412
RABGAP1L	RABGEF1	0.051	0.458
RABGEF1	RIC1	0	0.424
RABGEF1	STK4	0.41	0.425
RABGEF1	TBC1D2B	0.045	0.436
RABGEF1	STK3	0.41	0.44
RABGEF1	RRAD	0.134	0.471
RABGEF1	RAP1B	0.134	0.471
RABGEF1	REM2	0.134	0.526
RAF1	RET	0.16	0.609
RAF1	STK4	0.402	0.484
RAF1	RICTOR	0.16	0.412
RAF1	SPRED1	0.121	0.453
RAF1	VEGFA	0	0.454
RAF1	REM2	0.245	0.467
RAF1	SAG	0.16	0.487
RAF1	STK3	0.402	0.501

RAF1	RALGDS	0.087	0.585
RAF1	STAT3	0.147	0.603
RAF1	XIAP	0.518	0.691
RAF1	RELA	0.121	0.851
RAF1	SHOC2	0.389	0.949
RAF1	RAP1B	0.661	0.972
RALGDS	SPATA6	0	0.403
RALGDS	RASA4	0	0.522
RALGDS	RAP1GAP	0.093	0.641
RALGDS	RAP1B	0.425	0.983
RALGDS	RRAD	0.219	0.548
RALGDS	REM2	0.219	0.402
RALGDS	UBTF	0	0.412
RALGDS	TNF	0	0.552
RALGDS	RASSF5	0	0.666
RANBP2	SENP3	0.181	0.491
RANBP2	USPL1	0	0.483
RANBP2	SOD2	0.431	0.451
RANBP2	SF3B1	0.257	0.418
RANBP2	TRIM35	0.073	0.424
RANBP2	XPO6	0.473	0.857
RANBP2	UBE2L6	0.27	0.514
RANBP2	UBE2G1	0.219	0.664
RANBP2	TBL1X	0.323	0.471
RANBP2	USP32	0.072	0.445
RANBP2	SMG1	0.219	0.664
RANBP2	UBE2B	0.219	0.468
RANBP2	UBE2D1	0.219	0.475
RANBP2	USP34	0.071	0.543
RANBP2	SEH1L	0.218	0.553
RAP1B	RHOG	0.181	0.403
RAP1B	RET	0.114	0.615
RAP1B	RASGRP2	0.562	0.986
RAP1B	VAV1	0.157	0.534
RAP1B	RAP1GAP	0.65	0.975
RAP1B	RHOH	0.181	0.405
RAP1B	RND1	0.181	0.428
RAP1B	SMG1	0.268	0.482
RAP1B	RASSF1	0.157	0.485
RAP1B	TRAF3	0.06	0.492
RAP1B	RASA2	0.123	0.515
RAP1B	VASP	0.174	0.525
RAP1B	SH3PXD2B	0.335	0.631
RAP1B	RAP1GAP2	0.5	0.731
RAP1B	SIPA1L1	0.184	0.862
RAP1B	RAPGEF1	0.275	0.867
RAP1B	RASSF5	0.184	0.959

RAP1GAP	RET	0	0.492
RAP1GAP	RASA2	0	0.439
RAP1GAP	RAP1GAP2	0.458	0.491
RAP1GAP	RAPGEF1	0	0.511
RAP1GAP2	RASGRP2	0	0.457
RAP1GAP2	TP53INP2	0	0.424
RAPGEF1	RET	0.157	0.409
RAPGEF1	SH2B2	0	0.62
RAPGEF1	RND1	0.164	0.471
RAPGEF1	TAGAP	0	0.434
RAPGEF1	RASSF5	0	0.462
RARA	TLE4	0.263	0.424
RARA	RARG	0.431	0.789
RARA	STAT5B	0.119	0.474
RARA	TLE3	0.263	0.424
RARA	SIRT1	0.211	0.472
RARA	RELA	0.164	0.484
RARA	TRIB1	0.058	0.526
RARA	VDR	0	0.665
RARG	TLE4	0.263	0.424
RARG	RELA	0.164	0.407
RARG	TLE3	0.263	0.424
RARG	SIRT1	0.16	0.438
RARG	TCF7L2	0.408	0.488
RARG	ZBTB12	0.093	0.511
RARG	ZNF408	0.093	0.516
RARG	VDR	0	0.66
RASA2	USP42	0	0.457
RASA2	SHOC2	0	0.594
RASA4	5-Sep	0	0.44
RASA4	TMEM119	0	0.522
RASA4	TAGAP	0	0.632
RASA4	RRAD	0.123	0.636
RASGEF1B	TBC1D2B	0.159	0.491
RASGEF1B	RRAD	0.218	0.459
RASGEF1B	REM2	0.218	0.424
RASGEF1B	SRGAP2	0.45	0.461
RASGEF1B	SLC37A1	0	0.598
RASGEF1B	VEGFA	0	0.403
RASGRP2	RASSF5	0	0.543
RASSF1	STK4	0.657	0.967
RASSF1	TNFRSF1A	0.078	0.546
RASSF1	RASSF2	0.178	0.436
RASSF1	ZSWIM6	0	0.418
RASSF1	RASSF5	0.219	0.851
RASSF1	STK3	0.657	0.959
RASSF2	STK4	0.65	0.802

RASSF2	SLA	0	0.465
RASSF2	STK17B	0	0.507
RASSF2	SP140L	0	0.493
RASSF2	RASSF5	0.355	0.53
RASSF2	RNF41	0	0.639
RASSF2	STK3	0.65	0.944
RASSF5	STK4	0.767	0.98
RASSF5	STK3	0.767	0.825
RASSF5	SKAP2	0	0.437
RB1CC1	TRAF2	0.211	0.4
RB1CC1	RICTOR	0	0.425
RB1CC1	VMP1	0	0.528
RB1CC1	WDR45	0	0.533
RB1CC1	SMG1	0	0.577
RB1CC1	RFWD2	0.113	0.753
RBCK1	TNFRSF1A	0.763	0.841
RBCK1	RIPK1	0.218	0.905
RBCK1	TSPAN31	0	0.47
RBCK1	TRAF2	0.294	0.766
RBCK1	UBE2L6	0.43	0.65
RBCK1	TAB2	0.113	0.499
RBCK1	TRAF1	0.439	0.529
RBCK1	TNF	0.766	0.824
RBCK1	XIAP	0.069	0.825
RBM43	TMEM140	0	0.753
RBM43	RNF144B	0	0.632
RBM43	SIRT1	0.093	0.528
RBM43	USP18	0.045	0.412
RBM43	ZNFX1	0.045	0.51
RBM43	RNF213	0	0.555
RBM43	TRANK1	0	0.58
RBM47	SIK1	0	0.422
RBM47	TMEM156	0	0.489
RBM47	SRSF12	0.163	0.615
RBMS1	SLC44A3	0	0.41
RBPJ	TLE4	0.251	0.583
RBPJ	TCF7L2	0.161	0.49
RBPJ	TLE3	0.251	0.578
RBPJ	XRN1	0	0.598
RBPJ	ZFP36	0.47	0.63
RBPJ	TBL1X	0.078	0.637
RC3H2	UBXN7	0	0.516
RC3H2	ZC3H12C	0	0.625
RC3H2	ZC3H12A	0	0.585
RC3H2	XRN1	0.082	0.88
RC3H2	TIPARP	0	0.431
RC3H2	SMG1	0	0.846

RC3H2	UBR1	0	0.912
RC3H2	VEGFA	0	0.402
RC3H2	USP34	0.07	0.54
RCL1	RPS9	0.764	0.854
RCL1	XRN2	0	0.692
RCL1	SYNGR2	0	0.431
RCL1	TFB1M	0.265	0.575
REC8	STRA8	0	0.738
RELA	SP3	0.113	0.62
RELA	TNFRSF1A	0	0.847
RELA	STAT2	0.238	0.658
RELA	SOCS1	0.515	0.804
RELA	TLR4	0.054	0.923
RELA	STAT6	0.238	0.655
RELA	RIPK1	0.14	0.769
RELA	SOD2	0	0.725
RELA	UBXN7	0.079	0.593
RELA	TLR2	0.054	0.894
RELA	SOCS3	0.218	0.434
RELA	STAT5B	0.238	0.628
RELA	XPO6	0	0.553
RELA	TRAF2	0	0.762
RELA	TYK2	0.121	0.713
RELA	TRAF3	0	0.722
RELA	VDR	0.164	0.402
RELA	UBTF	0.055	0.407
RELA	RIPK3	0.14	0.445
RELA	SAG	0.123	0.463
RELA	TGM2	0.218	0.465
RELA	SMG1	0.08	0.509
RELA	TRAF7	0.055	0.513
RELA	RIPK2	0.14	0.519
RELA	STAT5A	0.238	0.64
RELA	XIAP	0.164	0.731
RELA	STAT4	0.238	0.782
RELA	TRAF1	0	0.787
RELA	TNIP2	0.429	0.818
RELA	STAT1	0.336	0.837
RELA	ROCK1	0.121	0.845
RELA	RELB	0.764	0.96
RELA	STAT3	0.759	0.99
RELA	TNF	0.274	0.991
RELA	SIRT1	0.489	0.995
RELB	TNFRSF1A	0	0.478
RELB	TLR4	0	0.625
RELB	RIPK1	0.044	0.416
RELB	TLR2	0	0.515

RELB	TRAF2	0	0.523
RELB	ZC3H12A	0	0.414
RELB	TYK2	0.044	0.672
RELB	TNIP1	0	0.407
RELB	TAB2	0	0.457
RELB	TRAF3	0	0.72
RELB	SIRT1	0	0.631
RELB	TNIP2	0.218	0.413
RELB	STAT3	0.114	0.602
RELB	TNFRSF1B	0	0.414
RELB	TNF	0	0.827
RELB	TRAF1	0	0.708
RELB	TNFAIP2	0	0.449
RELB	STAT1	0.061	0.512
RELB	XIAP	0	0.483
RELB	TNFSF13B	0	0.523
RELT	TRAF1	0.113	0.507
RELT	SUSD2	0	0.544
REM2	SMG1	0.268	0.482
RET	SSH2	0.115	0.415
RET	SHOC2	0.115	0.419
RET	SDC4	0	0.444
RET	STAT5A	0.165	0.477
RET	STAT5B	0.165	0.497
RET	VEGFC	0.219	0.507
RET	TEC	0.453	0.524
RET	SDC3	0.042	0.534
RET	STAT1	0.165	0.549
RET	VEGFA	0.219	0.713
RET	STAT3	0.596	0.853
RETN	SOCS3	0	0.441
RETN	SERPINE1	0	0.752
RETN	TNF	0	0.765
RETN	TLR4	0	0.954
RFK	SMNDC1	0	0.434
RFK	TNFRSF1A	0.473	0.799
RFK	YIPF4	0	0.456
RFWD2	TLE4	0.042	0.776
RFWD2	STK40	0.764	0.788
RFWD2	TRIB1	0.787	0.908
RGS10	TNIP2	0	0.412
RGS10	TANK	0	0.518
RGS2	VNN2	0	0.698
RHBDD1	RHBDF2	0	0.64
RHBDD1	STEAP3	0	0.51
RHBDD1	STEAP4	0	0.409
RHBDD1	RHBDD2	0	0.752

RHBDD2	RHBDF2	0	0.429
RHBDD2	VNN2	0	0.436
RHBDF2	RNF213	0	0.419
RHBDF2	SLC2A9	0	0.501
RHBDF2	SMPDL3B	0	0.568
RHBDF2	ZMIZ2	0	0.599
RHOG	TRIP10	0.206	0.41
RHOG	SRGAP2	0.206	0.414
RHOG	TNF	0.05	0.414
RHOG	ZYX	0.125	0.435
RHOG	SH3PXD2B	0.295	0.446
RHOG	VASP	0.157	0.461
RHOG	SDC4	0	0.535
RHOG	ROCK1	0.21	0.548
RHOG	TIAM2	0.242	0.661
RHOG	VAV1	0.227	0.759
RHOG	TAGAP	0.133	0.921
RHOH	VAV1	0.227	0.695
RHOH	SH3PXD2B	0.295	0.446
RHOH	TIAM2	0.242	0.444
RHOH	TRIP10	0.206	0.409
RHOH	TREML2	0	0.469
RHOH	ROCK1	0.21	0.522
RHOH	TMEM156	0	0.547
RIC1	SMG1	0.056	0.416
RIC1	XRN1	0.121	0.432
RIC1	TAPT1	0	0.472
RIC1	SYS1	0.345	0.677
RICTOR	ZNF259	0	0.412
RICTOR	SHOC2	0	0.407
RICTOR	ROCK1	0.16	0.439
RICTOR	SIRT1	0.218	0.612
RICTOR	SMG1	0.752	0.932
RIN2	RYR1	0	0.41
RIN2	XRN2	0	0.688
RIN2	SLC24A3	0	0.672
RIOK3	SF3B1	0	0.52
RIOK3	ZFAND6	0	0.477
RIOK3	WDR77	0.126	0.588
RIPK1	TNFRSF1A	0.997	0.999
RIPK1	TLR4	0.174	0.684
RIPK1	STAT3	0.147	0.43
RIPK1	TRAF7	0.184	0.438
RIPK1	TLR9	0.093	0.442
RIPK1	RNF41	0.184	0.453
RIPK1	TIRAP	0.093	0.457
RIPK1	TLR2	0.093	0.46

RIPK1	TNFRSF1B	0.113	0.707
RIPK1	STAT1	0.147	0.778
RIPK1	TANK	0.174	0.844
RIPK1	TRAF3	0.184	0.852
RIPK1	TNFSF10	0.218	0.923
RIPK1	XIAP	0.184	0.933
RIPK1	TRAF1	0.654	0.944
RIPK1	ZBP1	0.539	0.957
RIPK1	TNF	0.935	0.993
RIPK1	TAB2	0.759	0.995
RIPK1	RIPK3	0.965	0.995
RIPK1	TRAF2	0.926	0.998
RIPK2	TNFRSF1A	0.298	0.699
RIPK2	TLR4	0.093	0.534
RIPK2	TLR2	0.093	0.572
RIPK2	TRAF2	0.388	0.729
RIPK2	TAB2	0.35	0.719
RIPK2	TRAF3	0.184	0.762
RIPK2	TNFSF10	0.093	0.549
RIPK2	VASP	0.121	0.514
RIPK2	TNFRSF1B	0.055	0.466
RIPK2	TNF	0.219	0.64
RIPK2	TRAF1	0.225	0.574
RIPK2	TANK	0.134	0.497
RIPK2	STAT4	0.147	0.675
RIPK2	STAT1	0.147	0.422
RIPK2	XIAP	0.682	0.924
RIPK3	TNFRSF1A	0.298	0.875
RIPK3	TLR4	0.093	0.607
RIPK3	TLR2	0.093	0.434
RIPK3	TRAF2	0.184	0.919
RIPK3	TAB2	0.35	0.698
RIPK3	TRAF3	0.184	0.429
RIPK3	STOML1	0.079	0.661
RIPK3	TANK	0.134	0.453
RIPK3	TRAF1	0.184	0.464
RIPK3	TNFRSF1B	0.055	0.471
RIPK3	TNFSF10	0.093	0.53
RIPK3	XIAP	0.158	0.617
RIPK3	TNF	0.219	0.798
RIPK3	ZBP1	0.158	0.978
RLF	UPB1	0	0.47
RLF	TAB2	0	0.56
RLF	ZNF292	0	0.653
RND1	SEMA4D	0.06	0.618
RND1	VAV1	0.227	0.612
RND1	SH3PXD2B	0.295	0.446

RND1	TIAM2	0.242	0.435
RND1	SERTAD1	0.045	0.462
RND1	SEMA7A	0.06	0.426
RND1	TRIP10	0.206	0.499
RND1	RRAD	0.181	0.458
RND1	SLCO4A1	0	0.408
RND1	SRGAP2	0.206	0.43
RND1	SDC4	0	0.406
RND1	ROCK1	0.21	0.629
RNF114	RNF19B	0.055	0.677
RNF114	XAF1	0.437	0.54
RNF114	TNIP1	0	0.448
RNF114	UBE2L6	0.119	0.405
RNF114	USP36	0	0.417
RNF114	RNF213	0	0.486
RNF114	UBE2D1	0.459	0.466
RNF122	SSFA2	0	0.636
RNF122	UBXN7	0.495	0.519
RNF126	UBXN7	0.495	0.519
RNF126	UBE2D1	0.394	0.446
RNF126	UBR1	0.124	0.596
RNF126	STOML1	0.043	0.618
RNF13	TRIM25	0.042	0.41
RNF13	UBE2D1	0.296	0.451
RNF13	SLC24A3	0	0.521
RNF144B	RNF41	0.121	0.482
RNF144B	UBE2L6	0.43	0.515
RNF144B	RRAD	0.05	0.587
RNF166	TRIM25	0.042	0.438
RNF19A	UBE2L6	0.43	0.609
RNF19A	SIK3	0	0.465
RNF19A	TRIM38	0.08	0.478
RNF19B	USP18	0.043	0.42
RNF19B	UBE2B	0.177	0.458
RNF19B	USP25	0.043	0.491
RNF19B	RNF213	0	0.641
RNF19B	UBE2L6	0.43	0.67
RNF213	ZSWIM4	0	0.418
RNF213	STAT2	0	0.441
RNF213	XAF1	0	0.544
RNF213	UBA7	0	0.824
RNF213	RSAD2	0	0.864
RNF213	USP18	0	0.886
RNF213	USP25	0	0.451
RNF213	ZNFX1	0	0.764
RNF213	ZBP1	0	0.445
RNF213	ZMIZ2	0	0.479

RNF213	TRANK1	0	0.524
RNF213	STAT1	0	0.581
RNF213	TRIM21	0	0.704
RNF24	SLC16A6	0	0.601
RNF24	SLC16A12	0	0.598
RNF24	RSPRY1	0.081	0.711
RNF24	UBXN7	0.495	0.534
RNF24	SLC25A37	0	0.524
RNF24	TRPC5	0.067	0.528
RNF24	SLC2A9	0	0.593
RNF24	SLC28A3	0	0.625
RNF24	SLC45A4	0	0.762
RNF41	TNFRSF1A	0.296	0.565
RNF41	STK17B	0.045	0.562
RNF41	TAB2	0.348	0.581
RNF41	TIRAP	0.218	0.608
RNF41	TNFRSF1B	0.219	0.486
RNF41	TNF	0.184	0.406
RNF41	XIAP	0.184	0.409
RNF41	TANK	0.219	0.584
RNF41	UBE2D1	0.219	0.732
ROCK1	THOC2	0.059	0.405
ROCK1	TNFAIP8	0.45	0.45
ROCK1	VASP	0.121	0.432
ROCK1	STAT3	0.147	0.543
ROCK1	TNF	0.093	0.456
ROCK1	XIAP	0.132	0.472
ROCK1	VEGFA	0	0.696
RPIA	TKT	0.672	0.999
RPS9	XRN2	0.207	0.414
RPS9	XRN1	0.455	0.48
RPS9	SOD2	0.487	0.573
RPS9	UBXN7	0.258	0.603
RPS9	TFB1M	0.403	0.652
RPS9	TSFM	0	0.699
RPS9	TPT1	0.6	0.896
RRAD	SHROOM4	0	0.491
RRAD	SRGAP2	0.129	0.426
RRAD	SMG1	0.268	0.482
RSAD2	TMEM140	0	0.554
RSAD2	STAT2	0	0.721
RSAD2	SOCS1	0	0.424
RSAD2	TRIM25	0	0.702
RSAD2	XAF1	0	0.858
RSAD2	UBA7	0	0.825
RSAD2	UBE2L6	0	0.52
RSAD2	TNF	0	0.409

RSAD2	STAT4	0	0.421
RSAD2	ZBP1	0	0.45
RSAD2	TNFSF10	0	0.593
RSAD2	TRIM21	0	0.642
RSAD2	ZNFX1	0.156	0.763
RSAD2	STAT1	0	0.88
RSAD2	USP18	0	0.972
RSPRY1	SNX20	0.046	0.833
RUFY4	TMBIM1	0	0.658
RUFY4	TNFAIP2	0	0.43
RYBP	ZFYVE28	0	0.493
RYR1	ZNF655	0.051	0.422
RYR1	SRI	0.158	0.558
RYR1	TSFM	0	0.586
S100A12	TLR4	0.042	0.914
S100A12	S100A9	0.995	0.999
S100A12	TLR2	0.042	0.626
S100A12	S100A8	0.661	0.997
S100A12	VNN2	0	0.58
S100A12	TIRAP	0	0.637
S100A12	SAA2	0	0.524
S100A12	TNF	0	0.466
S100A12	SERPINB4	0	0.492
S100A8	TLR4	0.042	0.839
S100A8	S100A9	0.936	0.999
S100A8	TLR2	0.042	0.55
S100A8	TGFBR1	0.042	0.468
S100A9	TLR4	0.042	0.912
S100A9	SDS	0	0.41
S100A9	TOP1	0.398	0.415
S100A9	TNF	0	0.418
S100A9	TREM1	0	0.449
S100A9	TLR2	0.042	0.523
S100A9	TIRAP	0	0.627
SAA2	TLR4	0	0.509
SAA2	TLR2	0	0.441
SAA2	TNF	0	0.591
SAFB	SFPQ	0.156	0.414
SAFB	SAFB2	0.447	0.905
SAFB2	THOC2	0	0.506
SAG	TUBA4A	0.999	0.999
SAG	TRAF3	0.158	0.592
SAG	SLC9A3R1	0.055	0.554
SAMD4B	STAU1	0	0.404
SAMD4B	SKAP2	0	0.468
SAMD4B	WDR77	0.093	0.51
SAMSN1	TGM3	0	0.547

SARS	WARS	0.16	0.803
SARS	TARS	0.218	0.963
SAT1	SCLY	0	0.51
SAT1	SLC46A2	0	0.485
SAT1	SH2D3C	0	0.403
SAT1	TBC1D8	0	0.488
SBNO2	SEMA4D	0	0.413
SBNO2	SNX20	0	0.426
SCARA5	STEAP3	0	0.479
SCARA5	SCARF1	0	0.482
SCARA5	SCARF2	0	0.555
SCARF1	TLR2	0	0.53
SCARF2	SPATA6	0	0.518
SCARF2	SRI	0	0.41
SCLY	UBA7	0.157	0.431
SCLY	SELK	0	0.45
SCLY	ZNF331	0	0.484
SCLY	ZNF143	0	0.509
SCNN1D	STARD3	0	0.448
SCYL3	UBR1	0	0.403
SDC3	VCAN	0	0.464
SDC3	SDCBP	0.111	0.552
SDC3	SDC4	0.215	0.762
SDC4	VCAN	0	0.527
SDC4	TFPI2	0.046	0.411
SDC4	TGM2	0	0.728
SDC4	SRGN	0	0.47
SDC4	SDCBP	0.926	0.99
SDE2	UBXN7	0	0.538
SDE2	SRSF5	0.433	0.433
SDE2	SRRM2	0.694	0.696
SDS	SPTLC2	0.073	0.822
SEC24B	SYS1	0.219	0.701
SEC24B	STXBP3	0.397	0.515
SEC24B	TAB2	0	0.511
SEC24B	TAPT1	0	0.626
SEH1L	TNFAIP8	0	0.598
SEH1L	SESN2	0	0.91
SELL	VAV1	0	0.459
SELL	TLR4	0.045	0.649
SELL	STAT6	0.042	0.486
SELL	TLR2	0.045	0.59
SELL	VCAN	0.12	0.69
SELL	TNFRSF18	0	0.713
SELL	TLR9	0.045	0.502
SELL	STAT3	0.042	0.575
SELL	SELPLG	0.054	0.782

SELL	SERPINB2	0.055	0.413
SELL	TNF	0	0.802
SELL	STAT4	0.042	0.421
SELL	STAT1	0.042	0.529
SELP	TLR4	0.045	0.639
SELP	TLR2	0.045	0.452
SELP	SERPINE1	0.055	0.606
SELP	VCAN	0.12	0.768
SELP	VASP	0	0.469
SELP	STAT3	0.042	0.466
SELP	SELPLG	0.161	0.883
SELP	TNF	0	0.726
SELP	VEGFA	0	0.519
SELPLG	VCAN	0	0.512
SEMA4D	VEGFA	0.045	0.499
SEMA7A	VAT1L	0	0.411
SEMA7A	SMPDL3B	0	0.42
SENP2	SMNDC1	0	0.511
SENP2	ST6GALNAC4	0	0.469
SENP2	TBC1D8	0.043	0.532
SENP2	ZDHHC2	0	0.536
SENP2	UBXN7	0.159	0.538
SENP2	U2AF1L4	0	0.665
SENP3	USPL1	0	0.431
SENP3	UBXN7	0.159	0.525
5-Sep	TMEM119	0	0.426
5-Sep	ZFAND6	0	0.467
5-Sep	XIAP	0.479	0.594
SERINC2	STOML3	0.064	0.498
SERPINB2	TLR4	0	0.473
SERPINB2	SERPINE1	0	0.859
SERPINB2	TNF	0	0.575
SERPINE1	STAU1	0.045	0.44
SERPINE1	TLR4	0	0.5
SERPINE1	SIRT1	0.045	0.407
SERPINE1	VCAN	0	0.423
SERPINE1	TGM2	0.045	0.431
SERPINE1	STAT3	0.043	0.49
SERPINE1	SNAI1	0	0.509
SERPINE1	TFPI2	0.08	0.527
SERPINE1	TGFBR1	0	0.613
SERPINE1	VEGFA	0	0.653
SERPINE1	SMAD7	0.053	0.71
SERPINE1	TNF	0	0.742
SERPING1	ZDHHC18	0	0.4
SERTAD1	SLC25A19	0	0.416
SERTAD1	XIAP	0.389	0.554

SETDB1	SIRT1	0.124	0.427
SETDB1	SUV420H2	0	0.606
SETDB1	SUV420H1	0	0.773
SF3B1	SMNDC1	0.764	0.886
SF3B1	THOC2	0	0.452
SF3B1	USP34	0	0.407
SF3B1	SRSF12	0.346	0.431
SF3B1	TFIP11	0	0.475
SF3B1	SFPQ	0.419	0.542
SF3B1	WAC	0.123	0.566
SF3B1	XPO6	0	0.579
SF3B1	TRA2A	0.346	0.62
SF3B1	SRSF5	0.275	0.661
SF3B1	SUPT6H	0	0.76
SF3B1	U2AF1L4	0.752	0.877
SF3B1	SRRM2	0.763	0.895
SF3B1	SNIP1	0.93	0.967
SFPQ	TOP1	0.218	0.404
SFPQ	XRN2	0.054	0.489
SFPQ	SRSF5	0.138	0.403
SH2B2	SIRPB1	0	0.485
SH2D3C	TIPARP	0	0.405
SH2D3C	TNFSF10	0	0.474
SH3BGRL	STEAP4	0	0.401
SH3BP2	VAV1	0.745	0.932
SH3PXD2B	TIAM2	0.392	0.492
SHISA5	SRI	0.119	0.439
SHOC2	SLC30A1	0	0.408
SHOC2	SPRED1	0.042	0.554
SIK1	TRIB1	0.211	0.431
SIK1	SMAD7	0.045	0.443
SIK3	TSPAN31	0	0.412
SIPA1L1	SRGAP2	0.045	0.435
SIRPA	XCR1	0	0.542
SIRPA	SIRPB1	0	0.824
SIRT1	TLR4	0.046	0.479
SIRT1	SOD2	0.055	0.822
SIRT1	TOP1	0.111	0.506
SIRT1	TBL1X	0.331	0.407
SIRT1	VDR	0.117	0.439
SIRT1	VEGFA	0	0.472
SIRT1	SUV420H1	0	0.534
SIRT1	SMAD7	0.211	0.554
SIRT1	TNF	0	0.705
SIRT1	STAT3	0.113	0.759
SKIL	TXNDC16	0	0.403
SKIL	TGFBR1	0.12	0.485

SKIL	SMURF1	0.211	0.539
SKIL	TGIF1	0	0.588
SKIL	SMAD7	0.332	0.857
SLA	VAV1	0.113	0.438
SLAMF1	VAV1	0	0.481
SLAMF1	TAGAP	0	0.411
SLAMF8	TAGLN2	0	0.509
SLC10A1	SLC22A1	0	0.512
SLC10A1	SLCO4A1	0	0.632
SLC13A3	TSPAN31	0.042	0.469
SLC13A5	SLC20A1	0.121	0.431
SLC13A5	STARD8	0	0.57
SLC16A12	SLC22A3	0.055	0.414
SLC16A12	SLC2A9	0	0.456
SLC16A12	SLC28A3	0	0.465
SLC16A12	SLC2A1	0	0.59
SLC16A12	SLC45A4	0	0.639
SLC16A3	SLC1A5	0	0.539
SLC16A3	SLC2A1	0	0.722
SLC16A3	SLC2A3	0	0.731
SLC16A6	SLC2A9	0	0.41
SLC16A6	SLC28A3	0	0.482
SLC16A6	SLC45A4	0	0.638
SLC16A7	SLCO3A1	0	0.41
SLC16A7	STEAP1	0	0.467
SLC16A7	SLC2A1	0	0.46
SLC16A7	SLC2A3	0	0.511
SLC1A2	SLC7A5	0.054	0.86
SLC1A2	SLC38A2	0.056	0.887
SLC1A2	TNF	0	0.448
SLC1A2	SLC2A3	0	0.552
SLC1A2	SLC2A1	0	0.595
SLC1A5	SLC6A9	0	0.506
SLC1A5	SLC7A5	0.054	0.835
SLC1A5	SLC38A2	0.056	0.813
SLC1A5	SLC2A3	0	0.539
SLC1A5	SLC2A1	0	0.586
SLC20A1	SLC7A5	0	0.457
SLC20A1	SLC22A3	0	0.429
SLC20A1	SLC37A1	0	0.507
SLC22A1	SLCO3A1	0	0.402
SLC22A1	SLC2A1	0.051	0.519
SLC22A1	SLC2A9	0.051	0.52
SLC22A1	SLC22A3	0	0.814
SLC22A1	SLC44A3	0	0.873
SLC22A3	SLCO3A1	0	0.431
SLC22A3	SLC6A2	0	0.421

SLC22A3	YRDC	0	0.514
SLC22A3	SLC7A5	0.156	0.464
SLC22A3	SLCO4A1	0	0.448
SLC22A3	SLC44A3	0	0.806
SLC24A3	SLC7A5	0	0.418
SLC25A37	STEAP3	0	0.436
SLC25A37	SLC45A4	0	0.542
SLC28A3	SLC45A4	0	0.665
SLC28A3	SLC39A13	0	0.472
SLC28A3	SLC2A9	0.047	0.478
SLC2A1	SLC7A5	0.055	0.704
SLC2A1	SLC38A2	0	0.472
SLC2A1	TRIP10	0.056	0.47
SLC2A1	TNF	0	0.438
SLC2A1	VEGFA	0	0.637
SLC2A1	STOM	0.113	0.713
SLC2A3	SLC38A2	0	0.641
SLC2A3	TRIP10	0.056	0.599
SLC2A3	STOM	0.107	0.443
SLC2A9	SLC45A4	0	0.604
SLC2A9	ZC3H12C	0	0.645
SLC2A9	SMPDL3B	0	0.487
SLC30A1	SLC39A8	0.131	0.66
SLC30A1	SLC39A13	0.121	0.661
SLC37A1	UAP1	0.515	0.515
SLC37A1	WDR4	0	0.404
SLC37A1	SWT1	0	0.59
SLC38A2	SLC6A9	0	0.518
SLC38A2	SLC7A5	0.057	0.765
SLC39A8	STEAP2	0.045	0.4
SLC39A8	SLC44A3	0	0.417
SLC44A3	SLC46A2	0	0.478
SLC46A2	TBC1D8	0	0.498
SLC4A7	SLC9A3R1	0.113	0.662
SLC6A2	TSPO	0	0.49
SLC6A2	YRDC	0	0.534
SLC6A9	SLC7A5	0.143	0.488
SLC8A1	SLC8B1	0	0.487
SLC8A1	TAGAP	0	0.512
SLC8B1	USP25	0	0.454
SLC8B1	STOM	0	0.412
SLC9A3R1	TRPC5	0.201	0.663
SLC9A3R1	TGM2	0.411	0.423
SLC9A3R1	TBC1D10A	0.509	0.816
SLCO4A1	SOCS3	0	0.414
SMAD7	TAB2	0.113	0.914
SMAD7	SNAI1	0.079	0.509

SMAD7	SNIP1	0.06	0.439
SMAD7	TGFBR1	0.932	0.999
SMAD7	STAT3	0.046	0.465
SMAD7	TNF	0	0.496
SMAD7	USP15	0.218	0.827
SMAD7	TGIF1	0.154	0.518
SMAD7	SMURF1	0.825	0.986
SMAD7	STAT1	0.046	0.425
SMAD7	XIAP	0	0.642
SMG1	USPL1	0	0.585
SMG1	THOC2	0.053	0.556
SMG1	XRN1	0	0.835
SMG1	SMG9	0.946	0.994
SMG1	TET2	0	0.538
SMG1	ZNF292	0.093	0.463
SMG1	STK38L	0.175	0.498
SMG1	USP34	0.055	0.922
SMG9	XRN1	0	0.724
SMNDC1	VCAN	0	0.416
SMNDC1	ZDHHC2	0	0.424
SMNDC1	U2AF1L4	0.688	0.905
SMPDL3B	TNFRSF1A	0.051	0.528
SMPDL3B	UPP1	0	0.426
SMPDL3B	WDR55	0	0.403
SMPDL3B	TNF	0	0.48
SMURF1	TAL1	0.043	0.436
SMURF1	UBXN7	0.565	0.679
SMURF1	TRIM25	0.06	0.527
SMURF1	UBE2L6	0.335	0.527
SMURF1	UBE2G1	0.219	0.446
SMURF1	TGFBR1	0.688	0.923
SMURF1	USP25	0.412	0.569
SMURF1	USP15	0.165	0.552
SMURF1	UBE2D1	0.317	0.69
SNAI1	VEGFA	0	0.419
SNAI1	ZBTB17	0.459	0.473
SNAI1	TGFBR1	0.08	0.477
SNAI1	TNF	0.113	0.502
SNAI1	STAT3	0	0.64
SNAP29	STXBP3	0.314	0.7
SNAP29	SYTL3	0.159	0.401
SNAP29	STX6	0.644	0.917
SNAP29	STX11	0.257	0.62
SNAPC1	SUPT6H	0	0.642
SNAPC1	UBTF	0	0.445
SNIP1	TRA2A	0.433	0.446
SNIP1	SWT1	0	0.434

SNIP1	ST3GAL3	0	0.444
SNIP1	WAC	0.489	0.502
SNIP1	SRRM2	0.934	0.947
SNRK	XRN2	0	0.499
SNX10	TCIRG1	0	0.7
SNX10	WLS	0.158	0.422
SNX10	SNX20	0	0.697
SNX15	UBAP1	0	0.426
SNX20	STOM	0	0.412
SOCS1	VAV1	0.492	0.929
SOCS1	STAT2	0.173	0.92
SOCS1	TEC	0.218	0.4
SOCS1	TAB2	0	0.47
SOCS1	USP18	0	0.485
SOCS1	TLR2	0.044	0.546
SOCS1	ZBTB17	0	0.565
SOCS1	TLR4	0.044	0.661
SOCS1	TNF	0	0.692
SOCS1	STAT4	0.173	0.695
SOCS1	TIRAP	0.268	0.72
SOCS1	TRIM8	0.219	0.792
SOCS1	STAT6	0.173	0.798
SOCS1	SOCS3	0	0.87
SOCS1	STAT1	0.173	0.898
SOCS1	STAT5A	0.173	0.898
SOCS1	STAT5B	0.173	0.919
SOCS1	STAT3	0.173	0.942
SOCS1	TYK2	0.218	0.995
SOCS3	VAV1	0.148	0.42
SOCS3	STAT2	0.173	0.968
SOCS3	TLR4	0.044	0.645
SOCS3	STAT6	0.173	0.806
SOCS3	TLR2	0.044	0.6
SOCS3	TEC	0.207	0.406
SOCS3	SYNGR2	0	0.541
SOCS3	STAT4	0.173	0.715
SOCS3	TNF	0	0.726
SOCS3	STAT5A	0.173	0.923
SOCS3	STAT1	0.173	0.943
SOCS3	STAT5B	0.173	0.943
SOCS3	TYK2	0.207	0.984
SOCS3	STAT3	0.173	0.986
SOD2	XDH	0	0.4
SOD2	SRPR	0	0.407
SOD2	STAT3	0	0.434
SOD2	TNF	0	0.628
SP110	WARS	0.116	0.517

SP110	XAF1	0	0.57
SP110	UBE2L6	0.093	0.418
SP110	STAT1	0.055	0.647
SP140L	STK17B	0.093	0.581
SP2	WAC	0	0.495
SP3	WAC	0	0.42
SPATA6	TBC1D14	0	0.416
SPATA6	ZFAND3	0	0.452
SPATA6	TEX2	0	0.456
SPRED1	TESK1	0.128	0.579
SPRED2	TESK1	0.161	0.43
SPRED2	VASP	0	0.422
SPTLC2	SPTSSA	0.084	0.988
SPTLC2	UGCG	0.073	0.632
SPTSSA	UGCG	0	0.636
SRGAP2	VAV1	0.453	0.502
SRGAP2	SSH2	0.042	0.441
SRGN	TAB2	0	0.447
SRGN	TAPBPL	0	0.64
SRGN	VCAN	0.159	0.556
SRI	STOM	0	0.409
SRPR	WARS	0	0.413
SRRM2	SRSF5	0.297	0.619
SRRM2	TRA2A	0.306	0.754
SRSF12	SRSF5	0.296	0.418
SRSF12	TRA2A	0.491	0.547
SRSF5	UBXN7	0.338	0.473
SRSF5	XRN1	0.275	0.46
SRSF5	U2AF1L4	0.243	0.43
SRSF5	WAC	0.245	0.503
SRSF5	TRA2A	0.458	0.594
SSFA2	TEX2	0	0.53
SSH2	TESK1	0.119	0.418
ST6GALNAC4	WDR55	0	0.418
ST6GALNAC4	U2AF1L4	0	0.517
STAM2	ZFAND6	0	0.418
STAM2	UBAP1	0	0.632
STAM2	TYK2	0.115	0.862
STARD3	STARD8	0	0.406
STARD3	TSPO	0	0.506
STAT1	TNFRSF1A	0.113	0.758
STAT1	STAT2	0.768	0.969
STAT1	TLR4	0.084	0.724
STAT1	TLR2	0.084	0.686
STAT1	STAT5B	0.236	0.755
STAT1	TRIM25	0.055	0.587
STAT1	TRAF2	0.045	0.68

STAT1	XAF1	0	0.598
STAT1	TYK2	0.236	0.974
STAT1	UBA7	0.093	0.663
STAT1	UBE2L6	0.053	0.71
STAT1	TRAF3	0.045	0.655
STAT1	VDR	0.119	0.433
STAT1	USP18	0.078	0.877
STAT1	TAPBP	0	0.407
STAT1	TLR9	0.084	0.629
STAT1	TNFSF10	0	0.469
STAT1	ZMIZ1	0.257	0.441
STAT1	STAT3	0.792	0.924
STAT1	STAT5A	0.236	0.756
STAT1	TNF	0	0.937
STAT1	TRAF1	0.045	0.655
STAT1	TAP1	0	0.57
STAT1	ZBP1	0	0.529
STAT1	ZMIZ2	0.257	0.412
STAT1	TRIM21	0.174	0.574
STAT1	VEGFA	0.132	0.582
STAT2	TNFRSF1A	0.06	0.459
STAT2	ZMIZ2	0.257	0.412
STAT2	ZMIZ1	0.257	0.412
STAT2	UBA7	0.093	0.452
STAT2	TLR9	0.084	0.486
STAT2	TLR2	0.084	0.508
STAT2	TRIM25	0.055	0.557
STAT2	TRAF3	0.045	0.593
STAT2	TLR4	0.084	0.594
STAT2	TNF	0	0.757
STAT2	STAT4	0	0.833
STAT2	STAT5A	0	0.852
STAT2	USP18	0.184	0.853
STAT2	STAT5B	0	0.854
STAT2	STAT6	0.113	0.887
STAT2	STAT3	0.211	0.946
STAT2	TYK2	0.236	0.994
STAT3	TKT	0.054	0.464
STAT3	TNFRSF1A	0.06	0.653
STAT3	TLR4	0.084	0.759
STAT3	STAT6	0.045	0.866
STAT3	TLR2	0.084	0.662
STAT3	STAT5B	0.236	0.944
STAT3	TYK2	0.236	0.992
STAT3	TRAF3	0.045	0.402
STAT3	VEGFC	0.093	0.448
STAT3	TGFBR1	0.147	0.468

STAT3	TLR9	0.084	0.509
STAT3	ZMIZ1	0.257	0.412
STAT3	TRIM8	0.055	0.459
STAT3	ZMIZ2	0.257	0.412
STAT3	XIAP	0.096	0.653
STAT3	VEGFA	0.244	0.86
STAT3	TNF	0	0.896
STAT3	STAT4	0.078	0.927
STAT3	STAT5A	0.236	0.944
STAT4	TNFRSF1A	0.06	0.453
STAT4	TLR4	0.084	0.586
STAT4	STAT6	0	0.858
STAT4	TLR2	0.084	0.482
STAT4	STAT5B	0	0.831
STAT4	TYK2	0.236	0.964
STAT4	TNIP1	0	0.429
STAT4	TLR9	0.084	0.457
STAT4	ZMIZ1	0.257	0.412
STAT4	STAT5A	0	0.833
STAT4	TNF	0	0.725
STAT4	TRAF1	0.045	0.574
STAT4	ZMIZ2	0.257	0.412
STAT5A	TNFRSF1A	0.06	0.437
STAT5A	STAT6	0	0.833
STAT5A	STAT5B	0	0.812
STAT5A	TYK2	0.236	0.946
STAT5A	ZMIZ1	0.257	0.436
STAT5A	TEC	0.236	0.436
STAT5A	ZMIZ2	0.257	0.443
STAT5A	TNF	0	0.561
STAT5B	TNFRSF1A	0.06	0.437
STAT5B	STAT6	0	0.824
STAT5B	ZMIZ2	0.257	0.412
STAT5B	TEC	0.236	0.436
STAT5B	ZMIZ1	0.257	0.436
STAT5B	TNF	0	0.591
STAT5B	TYK2	0.236	0.948
STAT6	TNFRSF1A	0.06	0.487
STAT6	TLR4	0.084	0.655
STAT6	TLR9	0.084	0.404
STAT6	ZMIZ1	0.257	0.412
STAT6	ZMIZ2	0.257	0.412
STAT6	VEGFA	0.132	0.414
STAT6	TET2	0.054	0.461
STAT6	TLR2	0.084	0.559
STAT6	TNF	0	0.802
STAT6	TYK2	0.236	0.97

STAU1	TDRD7	0	0.609
STEAP1	STEAP2	0	0.838
STEAP3	TPT1	0.07	0.477
STEAP4	TNFAIP2	0	0.419
STK10	STRA8	0.446	0.446
STK17B	TNFAIP8	0	0.546
STK3	STK4	0	0.803
STK3	WWC2	0.219	0.517
STK38L	TP53RK	0	0.405
STK4	XIAP	0.253	0.411
STK4	WWC2	0.219	0.517
STK40	TRIB1	0.764	0.801
STOM	TRPC5	0.13	0.5
STOM	SYTL3	0	0.412
STOML1	TRPC5	0.13	0.48
STOML1	STOML3	0.161	0.439
STOML3	TRPC5	0.13	0.534
STX11	STXBP3	0.264	0.643
STX11	SYTL3	0.219	0.417
STX11	STX6	0.387	0.73
STX6	STXBP3	0.264	0.553
STXBP3	TNFAIP2	0.411	0.577
SUPT6H	UBXN7	0.763	0.93
SUPT6H	TOP1	0	0.487
SUPT6H	USP32	0	0.475
SUPT6H	XRN2	0	0.48
SUPT6H	XRN1	0	0.493
SUPT6H	XDH	0	0.519
SUPT6H	XPO6	0	0.537
SUPT6H	UBTF	0.06	0.79
SUSD2	TMBIM1	0	0.409
SUV420H1	WAC	0	0.406
SUV420H1	UGCG	0.458	0.491
SUV420H1	USP34	0	0.414
SWT1	THOC2	0.157	0.468
SWT1	XRN2	0	0.512
SWT1	XRN1	0	0.467
SYNGR2	TMEM165	0	0.441
SYS1	TAPBPL	0	0.617
SYTL3	ZMIZ1	0	0.706
TAB2	TNFRSF1A	0.435	0.883
TAB2	TLR4	0.115	0.555
TAB2	TLR2	0.115	0.403
TAB2	TRIM25	0.08	0.435
TAB2	TRAF2	0.759	0.993
TAB2	TRIM8	0.08	0.441
TAB2	TRIM21	0.08	0.441

TAB2	TAPBPL	0	0.519
TAB2	TRIM38	0.113	0.541
TAB2	TIRAP	0.055	0.553
TAB2	TRAF7	0.348	0.637
TAB2	TGFBR1	0.156	0.746
TAB2	XIAP	0.093	0.756
TAB2	WAC	0	0.764
TAB2	TRAF1	0.447	0.846
TAB2	TNF	0.469	0.891
TAB2	TRAF3	0.348	0.963
TACC3	VASP	0.093	0.407
TAF5L	UBXN7	0.241	0.455
TAF5L	USP3	0.42	0.531
TAF5L	UBE2D1	0.12	0.43
TAGAP	TIPARP	0	0.512
TAGLN2	TPM4	0.12	0.448
TANK	TNFRSF1A	0.435	0.859
TANK	ZC3H12C	0.219	0.502
TANK	TRAF2	0.824	0.942
TANK	ZC3H12A	0.407	0.775
TANK	TRAF3	0.764	0.996
TANK	TRAF7	0.219	0.519
TANK	TNFRSF1B	0	0.688
TANK	TNF	0.763	0.923
TANK	TRAF1	0.767	0.989
TAP1	TAP2	0.923	0.993
TAP1	UBA7	0.059	0.506
TAP1	TAPBPL	0	0.635
TAP1	TAPBP	0.791	0.989
TAP2	TAPBP	0.429	0.98
TAPBP	UBA7	0	0.449
TAPBP	TAPBPL	0	0.59
TAPBPL	THEMIS2	0	0.503
TAPBPL	UBA7	0	0.44
TAPBPL	TRIM21	0	0.414
TAPT1	TBC1D14	0	0.429
TAPT1	TRANK1	0	0.483
TARS	WARS	0	0.88
TBC1D2B	ZNFX1	0	0.486
TBC1D2B	ZNF263	0.045	0.528
TBC1D8	TBC1D9	0.518	0.527
TBC1D8	U2AF1L4	0	0.591
TBC1D8	ZDHHC2	0	0.43
TBL1X	TLE4	0.042	0.492
TBL1X	TMSB4X	0	0.425
TBL1X	TLE3	0.042	0.587
TBL1X	TCF7L2	0.273	0.797

TCF7L2	TLE4	0.753	0.948
TCF7L2	WLS	0	0.523
TCF7L2	TLE3	0.753	0.944
TDRD10	TDRD7	0	0.461
TEC	VAV1	0.203	0.577
TESK1	TFEC	0.052	0.439
TET2	VDR	0	0.589
TET2	U2AF1L4	0	0.412
TFIP11	THOC2	0.401	0.4
TGFBR1	VDR	0.1	0.4
TGFBR1	VEGFA	0	0.404
TGFBR1	TNF	0.093	0.435
TGFBR1	TMEM119	0	0.485
TGFBR1	USP15	0.432	0.564
TGFBR1	XIAP	0.191	0.892
TGM2	TNF	0	0.414
THEMIS2	VAV1	0	0.425
THEMIS2	VNN2	0	0.408
THOC2	ZCCHC6	0	0.406
THOC2	WTAP	0.5	0.551
THOC2	XRN2	0	0.4
TIAM2	WSB1	0.461	0.578
TIRAP	TLR4	0.769	0.999
TIRAP	TLR2	0.231	0.993
TIRAP	YIPF4	0	0.4
TIRAP	TRAF2	0.218	0.528
TIRAP	TRAF3	0.218	0.779
TIRAP	TLR9	0.231	0.968
TIRAP	TRAF7	0.218	0.486
TIRAP	TNFSF9	0.211	0.473
TIRAP	TRAF1	0.218	0.591
TIRAP	TNF	0	0.623
TKT	UBE2D1	0.407	0.42
TLE3	TLE4	0.39	0.4
TLR2	TNFRSF1A	0	0.593
TLR2	TLR4	0	0.881
TLR2	VEGFA	0	0.403
TLR2	TRAF2	0.134	0.406
TLR2	TNFSF13B	0	0.411
TLR2	TRAF1	0.134	0.471
TLR2	TNFSF10	0	0.489
TLR2	TRAF3	0.134	0.651
TLR2	TREM1	0	0.761
TLR2	TLR9	0	0.88
TLR2	VCAN	0.064	0.929
TLR2	TNF	0.041	0.939
TLR4	TNFRSF1A	0	0.667

TLR4	TNFSF13B	0	0.438
TLR4	TNFSF10	0	0.445
TLR4	TRAF2	0.134	0.47
TLR4	TRAF1	0.134	0.525
TLR4	VCAN	0.064	0.527
TLR4	VEGFA	0	0.545
TLR4	XDH	0	0.679
TLR4	TNFSF9	0.113	0.76
TLR4	TREM1	0	0.835
TLR4	TLR9	0	0.881
TLR4	TRAF3	0.184	0.924
TLR4	TNF	0.041	0.932
TLR9	TNFRSF1A	0	0.408
TLR9	TYK2	0.093	0.4
TLR9	TRAF3	0.134	0.71
TLR9	VCAN	0.064	0.411
TLR9	TNFSF13B	0	0.462
TLR9	ZBP1	0	0.507
TLR9	TNF	0.041	0.865
TM9SF4	TMEM165	0	0.414
TMBIM1	TP53I11	0	0.41
TMEM140	TRANK1	0	0.667
TMEM140	ZNFX1	0	0.682
TMEM165	UGCG	0	0.593
TNF	TNFRSF1A	0.997	0.999
TNF	VCPIP1	0.268	0.562
TNF	TNFAIP6	0	0.661
TNF	TRAF2	0.818	0.982
TNF	TYK2	0.093	0.537
TNF	XDH	0	0.521
TNF	TNIP1	0.488	0.672
TNF	TRAF3	0.184	0.843
TNF	VEGFC	0	0.51
TNF	TNIP2	0.424	0.548
TNF	TNFRSF18	0	0.544
TNF	VDR	0	0.621
TNF	TREM1	0	0.575
TNF	TSPO	0	0.434
TNF	TNFSF10	0.055	0.809
TNF	TRAF7	0.184	0.559
TNF	TNFRSF1B	0.955	0.999
TNF	TNIP3	0.159	0.463
TNF	TNFSF13B	0	0.533
TNF	TNFSF9	0.081	0.572
TNF	ZFP36	0.064	0.607
TNF	XIAP	0.209	0.839
TNF	VEGFA	0	0.882

TNF	TRAF1	0.519	0.948
TNFAIP2	TNFAIP6	0	0.432
TNFAIP2	ZC3H12A	0	0.442
TNFAIP2	TNIP1	0	0.491
TNFAIP2	TNFAIP8	0	0.495
TNFAIP2	TRAF1	0	0.541
TNFAIP2	TNIP3	0	0.546
TNFRSF18	TNFRSF1A	0	0.517
TNFRSF18	TRAF1	0.219	0.467
TNFRSF18	TNFSF9	0	0.635
TNFRSF1A	TNIP2	0.508	0.559
TNFRSF1A	TNFSF9	0	0.632
TNFRSF1A	TRAF7	0.296	0.677
TNFRSF1A	TNFSF10	0	0.686
TNFRSF1A	VCPIP1	0.452	0.707
TNFRSF1A	TNIP1	0.644	0.744
TNFRSF1A	XIAP	0.294	0.766
TNFRSF1A	TRAF3	0.296	0.844
TNFRSF1A	TNFRSF1B	0.113	0.959
TNFRSF1A	TRAF1	0.66	0.964
TNFRSF1A	TRAF2	0.928	0.998
TNFRSF1B	TRAF2	0.768	0.993
TNFRSF1B	TRAF3	0.219	0.833
TNFRSF1B	TRAF7	0.219	0.519
TNFRSF1B	XIAP	0.06	0.492
TNFRSF1B	TRAF1	0.594	0.969
TNFSF10	TRAF2	0.113	0.88
TNFSF10	XAF1	0	0.544
TNFSF10	TRAF3	0.055	0.46
TNFSF10	XIAP	0.051	0.543
TNFSF10	TRAF1	0.08	0.629
TNFSF13B	TRAF2	0	0.849
TNFSF13B	TRAF3	0	0.769
TNFSF13B	TRAF1	0	0.605
TNFSF13B	TNFSF14	0	0.702
TNFSF14	TRAF2	0.113	0.715
TNFSF14	TRAF3	0.113	0.462
TNFSF14	TNFSF9	0	0.402
TNFSF9	TRAF2	0.078	0.694
TNFSF9	TRAF3	0.051	0.424
TNFSF9	TRAF7	0.051	0.403
TNFSF9	TRAF1	0.078	0.707
TNFSF9	TNIP3	0	0.479
TNIP1	TRAF3	0.113	0.536
TNIP1	TRAF1	0.113	0.647
TNIP1	TNIP2	0.071	0.71
TNIP2	TNIP3	0.054	0.633

TNIP3	ZMIZ2	0	0.41
TOP1	ZCCHC6	0.218	0.418
TOP1	ZMIZ2	0.428	0.551
TOP1	ZMIZ1	0.428	0.551
TOP1	XRN2	0.077	0.559
TP53I11	TP53INP2	0	0.67
TP53I11	TP53RK	0	0.556
TP53INP2	TP53RK	0	0.518
TP53INP2	VMP1	0	0.898
TP53RK	YRDC	0	0.652
TRAF1	TRAF2	0.97	0.997
TRAF1	TRAF3	0.451	0.819
TRAF1	TRAF7	0.042	0.74
TRAF1	XIAP	0.184	0.68
TRAF2	UBE2D1	0.219	0.404
TRAF2	USP25	0.14	0.461
TRAF2	ZFAND6	0.659	0.659
TRAF2	XIAP	0.184	0.85
TRAF2	TRAF3	0.756	0.982
TRAF3	TRIM25	0.046	0.651
TRAF3	TYK2	0.121	0.45
TRAF3	UBE2D1	0.219	0.414
TRAF3	XIAP	0.184	0.523
TRAF3	USP25	0.14	0.616
TRAF3	TRAF7	0.042	0.629
TRAF7	UBE2L6	0.313	0.537
TRAF7	UBE2G1	0.345	0.626
TRAF7	USP36	0.163	0.429
TRAF7	XIAP	0.184	0.476
TRAF7	UBE2B	0.313	0.517
TRAF7	UBE2D1	0.313	0.566
TRANK1	ZNFX1	0	0.718
TREM1	TREML2	0	0.795
TRIB1	ZNF259	0	0.485
TRIM21	XAF1	0.045	0.509
TRIM21	UBA7	0.055	0.729
TRIM21	UBE2L6	0.093	0.412
TRIM21	USP18	0.107	0.852
TRIM21	TRIM38	0	0.411
TRIM21	ZNFX1	0.055	0.525
TRIM21	TRIM8	0.071	0.686
TRIM21	UBE2D1	0.218	0.503
TRIM25	WARS	0.535	0.586
TRIM25	XRN1	0.07	0.497
TRIM25	UBA7	0.055	0.575
TRIM25	UBE2L6	0.113	0.582
TRIM25	USP18	0.107	0.591

TRIM25	USP15	0.113	0.658
TRIM25	UBE2D1	0.948	0.982
TRIM38	TRIM8	0	0.586
TRIM8	USP32	0.08	0.427
TSPAN2	TSPAN31	0.049	0.454
TSPAN31	USP25	0	0.404
TTC19	ZSWIM7	0	0.74
TYK2	VAV1	0.113	0.662
TYK2	USP18	0.081	0.414
U2AF1L4	ZDHHC2	0.044	0.594
UBA7	XAF1	0	0.507
UBA7	UBE2D1	0.34	0.514
UBA7	UBE2J2	0.405	0.523
UBA7	ZNFX1	0.042	0.603
UBA7	UBE2G1	0.527	0.706
UBA7	UBE2B	0.489	0.813
UBA7	ZBP1	0	0.845
UBA7	UBE2L6	0.309	0.949
UBA7	USP18	0.162	0.962
UBAP1	VPS37A	0.764	0.94
UBAP1	UBE2G1	0	0.475
UBE2B	UBXN7	0.665	0.753
UBE2B	ZMIZ1	0.205	0.44
UBE2B	UBR1	0.676	0.891
UBE2B	ZMIZ2	0.205	0.44
UBE2B	UBE2D1	0.404	0.514
UBE2D1	UBXN7	0.35	0.407
UBE2D1	UBE2L6	0.124	0.463
UBE2D1	UBR1	0.226	0.609
UBE2D1	XIAP	0.682	0.771
UBE2J2	UBXN7	0	0.414
UBE2L6	UBXN7	0.436	0.445
UBE2L6	USP18	0.127	0.888
UBR1	UBXN7	0.522	0.844
UBR1	XRN1	0	0.697
UBR1	USP32	0	0.417
UBR1	XIAP	0	0.592
UBTF	UBXN7	0.156	0.465
UBTF	ZNF143	0.114	0.514
UBXN7	ZNF259	0.648	0.656
UBXN7	VCPIP1	0.118	0.634
UBXN7	WDR77	0.241	0.401
UBXN7	USP3	0.296	0.421
UBXN7	USP18	0.22	0.471
UBXN7	USP25	0.22	0.471
UBXN7	WAC	0.316	0.525
UBXN7	USP34	0.419	0.529

UBXN7	XRN1	0.16	0.533
UBXN7	XRN2	0.297	0.653
UPB1	UPP1	0	0.566
UPP1	YRDC	0.114	0.545
UPP1	XDH	0	0.457
USP15	VCPIP1	0	0.407
USP15	USP3	0.184	0.451
USP15	ZYX	0.042	0.42
USP15	USP25	0.158	0.77
USP18	XAF1	0	0.715
USP18	ZBP1	0	0.561
USP18	ZNFX1	0.144	0.855
USP25	VCPIP1	0	0.474
USP25	USP32	0.158	0.434
USP25	WDR4	0	0.459
USP25	USP36	0	0.467
USP3	VCPIP1	0	0.429
USP32	VCPIP1	0	0.485
USP32	USP34	0.122	0.417
USP34	WAC	0	0.767
USP34	ZNF292	0.106	0.554
VASP	ZYX	0.559	0.997
VAV1	ZYX	0.093	0.745
VCAN	VEGFA	0	0.564
VCPIP1	WAC	0.218	0.473
VEGFA	XIAP	0	0.469
VEZF1	WDR4	0	0.53
VEZF1	WAC	0	0.545
WDR77	XRN2	0.051	0.439
XAF1	ZBP1	0	0.513
XAF1	XIAP	0.652	0.979
XK	XKR8	0	0.757
XPO6	XRN2	0.12	0.424
XPO6	XRN1	0.12	0.474
XRN1	ZCCHC6	0.093	0.692
XRN1	XRN2	0.924	0.987
XRN1	ZFP36	0.184	0.659
XRN2	ZNFX1	0.257	0.465
ZFAND3	ZFAND6	0	0.659
ZFAND3	ZMIZ2	0	0.44
ZNFX1	ZSWIM4	0	0.481

immunoregulatory network behind bovine mastitis

WGCNA hub mRNAs-lncRNAs network

hub_lncRNA	hub_mRNA
CDC42SE1	SH2D3C
CDC42SE1	RASA2
CDC42SE1	NAMPT
CDC42SE1	ARHGAP35
CDC42SE1	PLBD1
CDC42SE1	TLE3
CDC42SE1	GPR84
CDC42SE1	PREX1
CDC42SE1	TNFRSF18
CDC42SE1	SHFL
CDC42SE1	IL20RA
CDC42SE1	TMEM156
CDC42SE1	TREML2
CDC42SE1	BTG2
CDC42SE1	BOLA-DMA
CDC42SE1	ICAM3
CDC42SE1	STEAP1
CDC42SE1	SP110
CDC42SE1	USB1
CDC42SE1	STOML1
CDC42SE1	MFSD14A
CDC42SE1	PML
CDC42SE1	SIPA1L1
CDC42SE1	AMPD3
CDC42SE1	TFPI2
CDC42SE1	LIG4
CDC42SE1	UBE2J2
CDC42SE1	CLCN7
CDC42SE1	PARM1
CDC42SE1	ADAP1
CDC42SE1	TSPAN2
CDC42SE1	STK40
CDC42SE1	PHF12
CDC42SE1	LRRC63
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CDC42SE1	RSAD2
CDC42SE1	UGCG
CDC42SE1	ZNF143
CDC42SE1	PRICKLE3
CDC42SE1	TMEM120A
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CDC42SE1	PHLDB1
CDC42SE1	C1RL
CDC42SE1	TGM2
CDC42SE1	RBM43
CDC42SE1	BRWD3
CDC42SE1	LRRK2
CDC42SE1	SERPING1
CDC42SE1	COTL1
CDC42SE1	SFPQ
CDC42SE1	PIK3R6
CDC42SE1	IL2RB
CDC42SE1	DGAT2
CDC42SE1	VNN2
CDC42SE1	RBM18
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CDC42SE1	REM2
CDC42SE1	SLCO4A1
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CDC42SE1	RNF122
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CDC42SE1	CACHD1
CDC42SE1	RELT
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CDC42SE1	AVIL
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CDC42SE1	POR
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CDC42SE1	RIPK3
CDC42SE1	DDX5
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CDC42SE1	CTIF
CDC42SE1	ARHGEF1
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CDC42SE1	ACSL4
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CDC42SE1	LOC112441484
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CDC42SE1	RFK
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CDC42SE1	SBNO2
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CDC42SE1	C5AR1
CDC42SE1	CASP4
CDC42SE1	IL2RA
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CDC42SE1	SNAPC1
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CDC42SE1	U2AF1L4
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CDC42SE1	BRF2
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CDC42SE1	RABGAP1L
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PRKAA1	CDC42SE1
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SENP3	CDC42SE1
EIF4A1	CDC42SE1
FRYL	CDC42SE1
RANBP2	CDC42SE1
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ARHGAP31	CDC42SE1
ARID4B	CDC42SE1
POLB	CDC42SE1
DKK4	CDC42SE1
STAU1	CDC42SE1
NAB1	CDC42SE1
PARP11	CDC42SE1

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ATP11B	CDC42SE1
TCIRG1	CDC42SE1
UBAP1	CDC42SE1
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BMX	CDC42SE1
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ERBIN	CDC42SE1
HYAL1	CDC42SE1
HYAL2	CDC42SE1
GTF2B	CDC42SE1
NR4A1	CDC42SE1
ZFAND3	CDC42SE1
SMNDC1	CDC42SE1
MYD88	CDC42SE1
RET	CDC42SE1
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APRT	CDC42SE1
PPP1R16B	CDC42SE1
PARP3	CDC42SE1
OTULINL	CDC42SE1
PGS1	CDC42SE1
NDRG1	CDC42SE1
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KCNJ15	CDC42SE1
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RASGRP2	CDC42SE1
MTMR3	CDC42SE1

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CORO6	CDC42SE1
GALC	CDC42SE1
ADAM17	CDC42SE1
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GMEB1	CDC42SE1
USPL1	CDC42SE1
KMT5B	CDC42SE1
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GPR31	CDC42SE1
FBXO40	CDC42SE1
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MOB3A	CDC42SE1
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HLX	CDC42SE1
ETV6	CDC42SE1
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OAS2	CDC42SE1
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HES4	CDC42SE1
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TAPBPL	CDC42SE1
VEGFC	CDC42SE1
ISG20	CDC42SE1
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SCYL3	CDC42SE1
NLK	CDC42SE1
MYRFL	CDC42SE1
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ICOSLG	CDC42SE1
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ABCA3	CDC42SE1
VCAN	CDC42SE1
GTPBP4	CDC42SE1
IL6	CDC42SE1
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PARD3	CDC42SE1
FSD2	CDC42SE1
CD14	CDC42SE1
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WDR55	CDC42SE1
MST1R	CDC42SE1
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SDC4	CDC42SE1
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MCL1	CDC42SE1
KLF6	CDC42SE1
RMC1	CDC42SE1
MXD4	CDC42SE1
IFNAR2	CDC42SE1
CD74	CDC42SE1
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LTBR	CDC42SE1
NECTIN2	CDC42SE1

hub mRNAs-miRNAs and hub lncRNAs-miRNAs network

miRNAs	hub_mRNAs/lncRNAs
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bta-miR-1388-5p	IL2RB
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bta-miR-3431	CXCR1
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bta-miR-3431	ABI1
bta-miR-3431	CD69
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bta-miR-3431	SPTSSA
bta-miR-3431	LCP2
bta-miR-3431	STAT2
bta-miR-3431	RUBCNL
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bta-miR-3431	CHI3L1
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bta-miR-3431	NOD1
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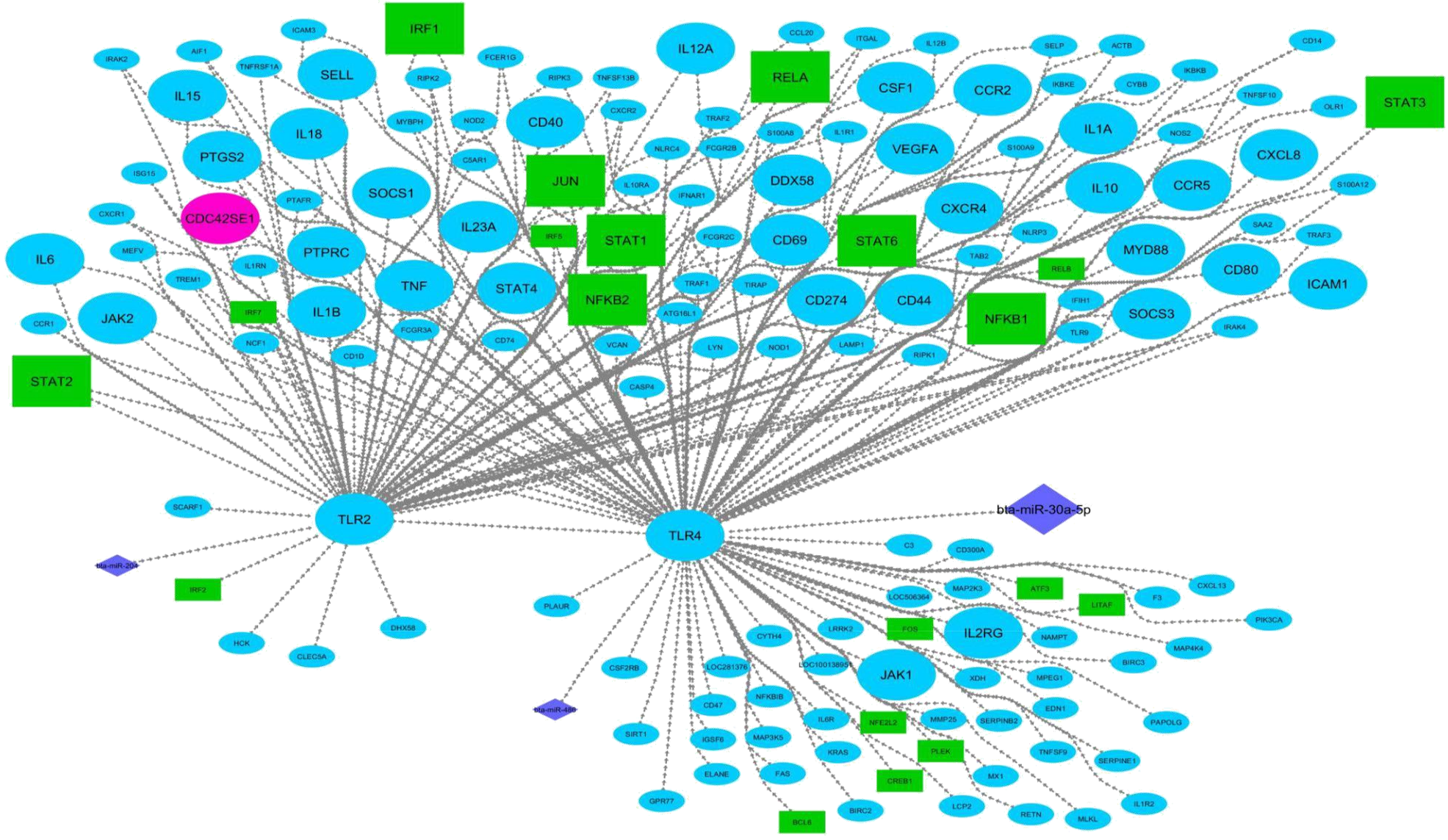
bta-miR-3431	IRF5
bta-miR-3431	ANKRD13A
bta-miR-3431	PLEKHO2
bta-miR-3431	ZMIZ2
bta-miR-3431	SDC3
bta-miR-3431	TTYH2
bta-miR-3431	GNG4
bta-miR-3431	OTULINL
bta-miR-3431	TP53INP2
bta-miR-3431	DIXDC1

turquoise RNA-seq-based module

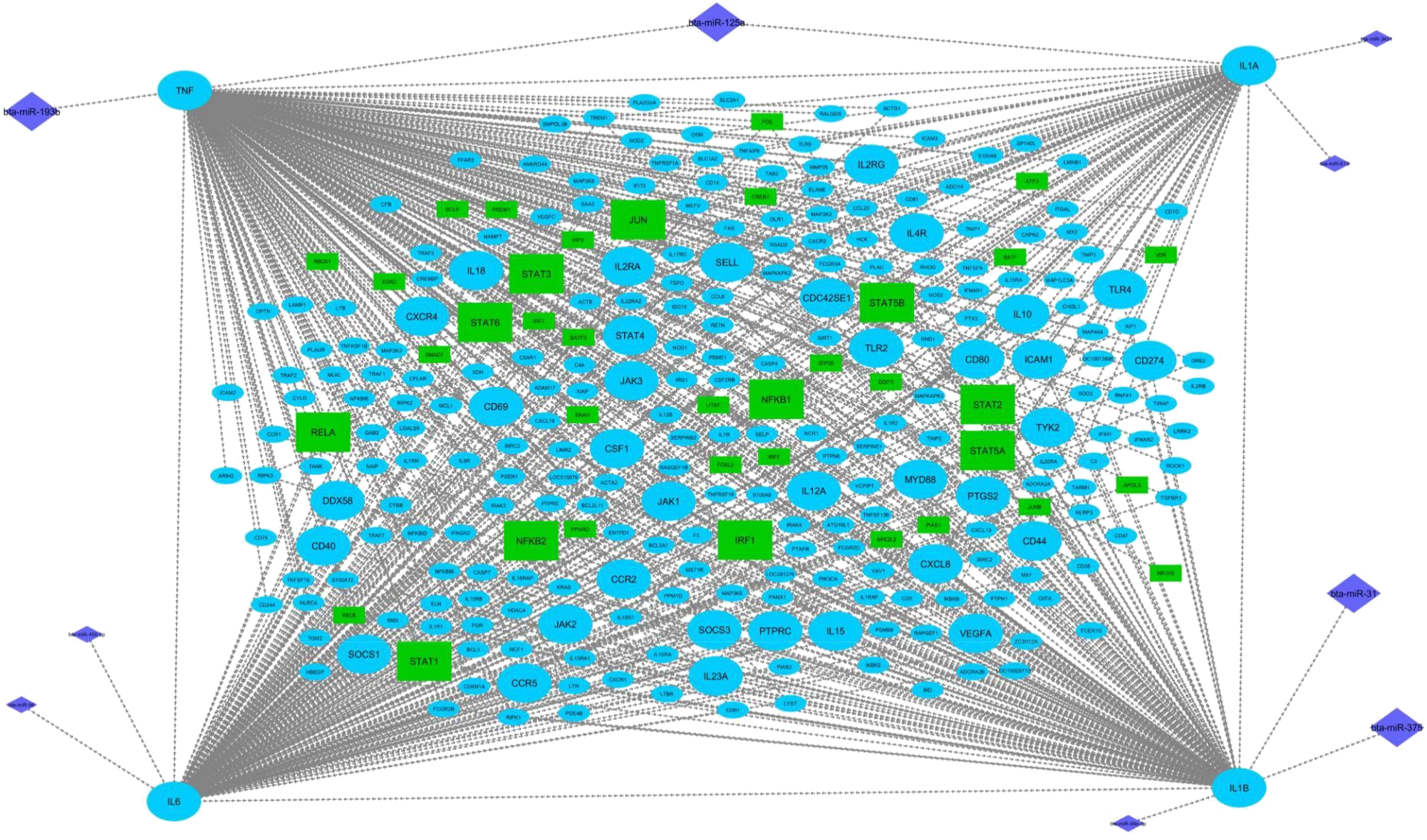
Hub-hub RNAs	Category
CDC42SE1	LncRNA
TNF	Protein_coding
IL6	Protein_coding
IL10	Protein_coding
STAT3	Transcription_factor
IL15	Protein_coding
CD40	Protein_coding
STAT1	Transcription_factor
IL1B	Protein_coding
TLR4	Protein_coding
CXCL8	Protein_coding
ICAM1	Protein_coding
TLR2	Protein_coding
PTPRC	Protein_coding
CD274	Protein_coding
CD80	Protein_coding
CD44	Protein_coding
IL18	Protein_coding
CCR2	Protein_coding
CXCR4	Protein_coding
JAK2	Protein_coding
CD69	Protein_coding
SELL	Protein_coding
STAT2	Transcription_factor
STAT6	Transcription_factor
JAK1	Protein_coding
TYK2	Protein_coding
JAK3	Protein_coding
STAT5B	Transcription_factor
STAT5A	Transcription_factor
IL4R	Protein_coding
IL12A	Protein_coding
IL23A	Protein_coding
STAT4	Transcription_factor
IL2RG	Protein_coding
CSF1	Protein_coding
SOCS1	Protein_coding
IL2RA	Protein_coding
VEGFA	Protein_coding
MYD88	Protein_coding
CCR5	Protein_coding
SOCS3	Protein_coding

RELA	Transcription_factor
NFKB1	Transcription_factor
JUN	Transcription_factor
IL1A	Protein_coding
NFKB2	Transcription_factor
IRF1	Transcription_factor
PTGS2	Protein_coding
DDX58	Protein_coding

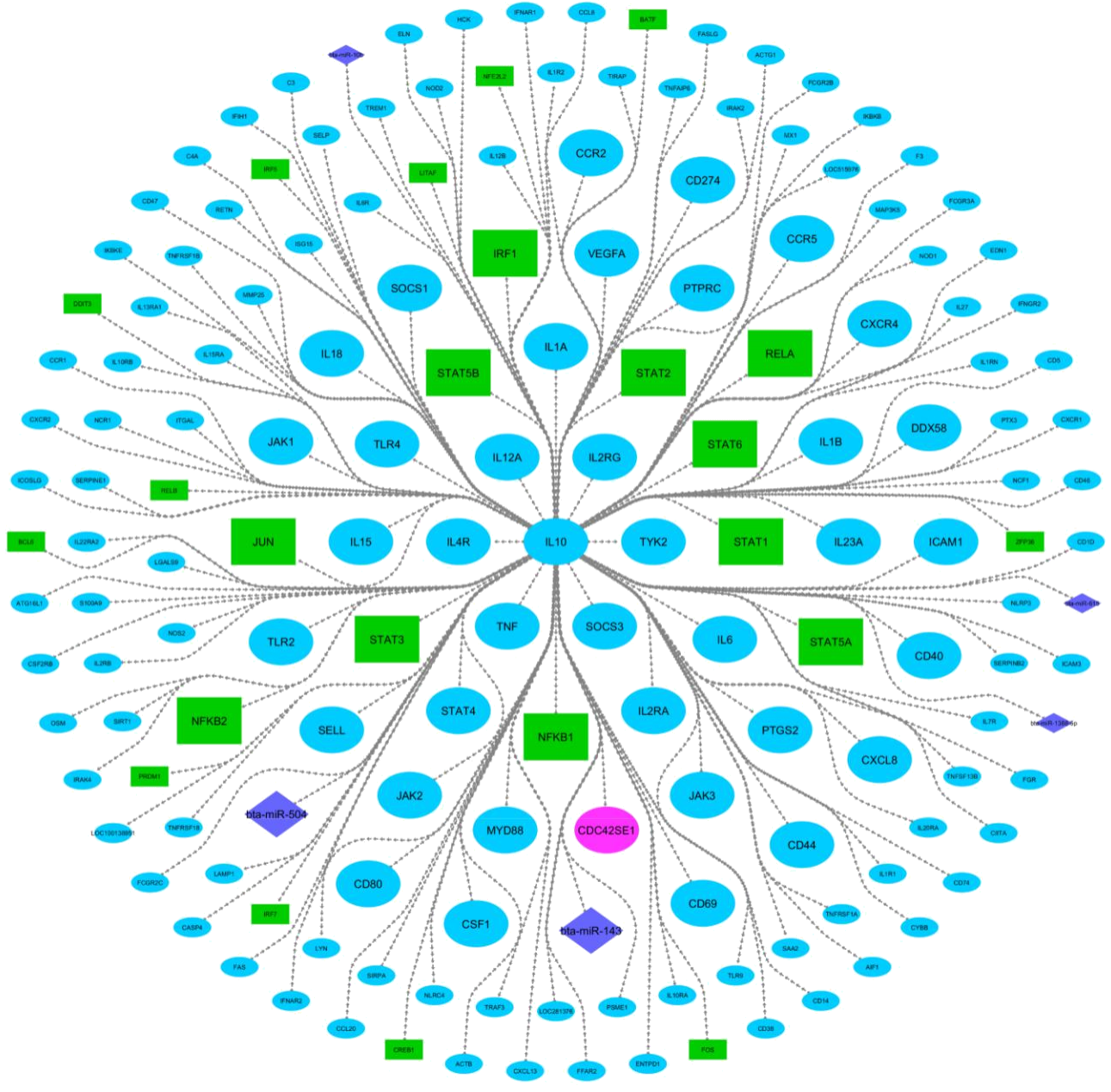
Supplementary File S13: The sub-networks of important inflammatory hub-hub genes during mastitis.



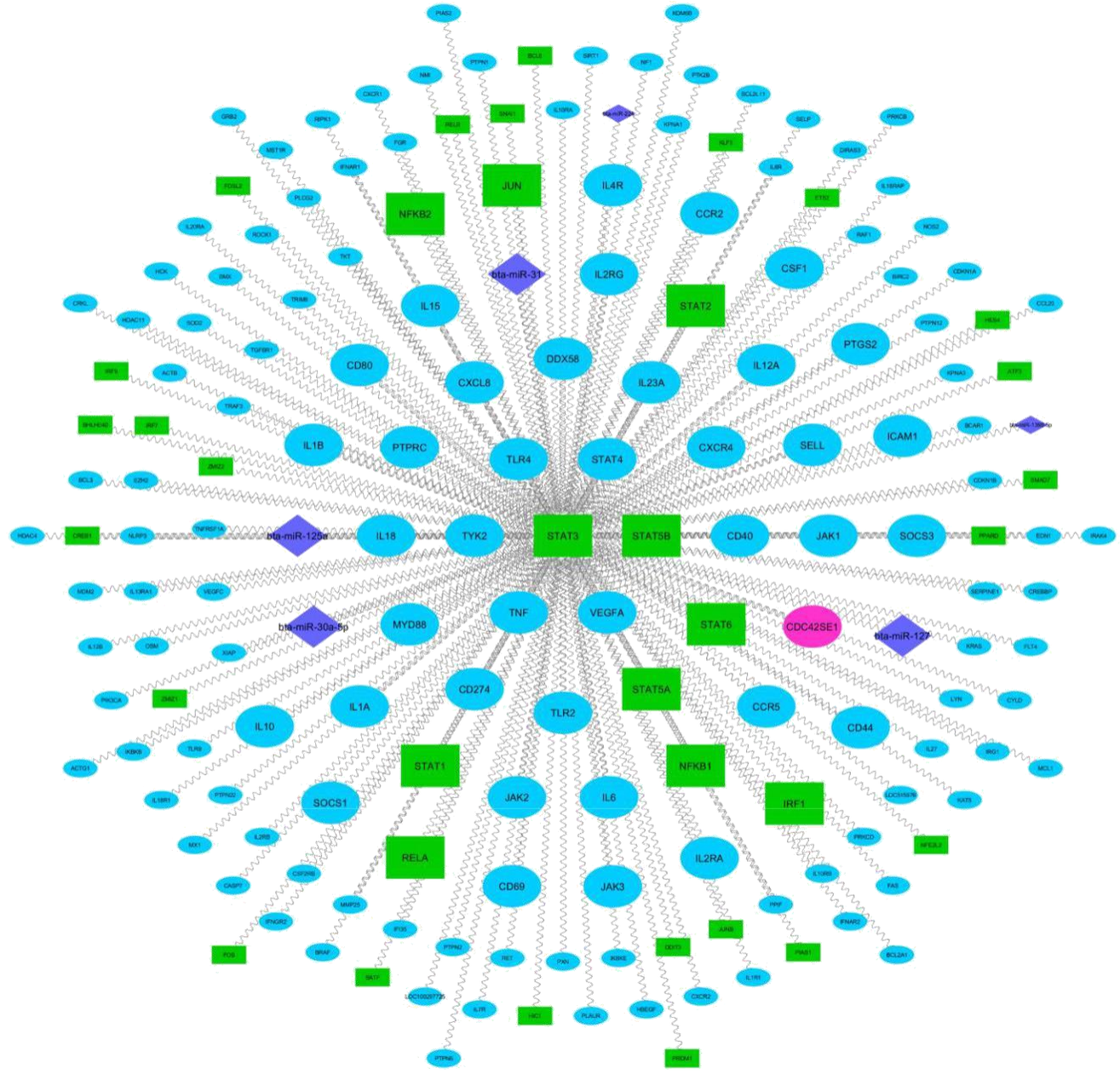
The constructed integrated regulatory sub-network related to *TLR2*, and *TLR4* hub-hub genes. Small circles and rectangles represent hub genes and hub transcription factors (TFs) of the turquoise RNA-seq-based module, respectively. Small diamonds represent regulatory miRNAs of the blue miRNA-seq-based module. On the other hand, large circles and rectangles represent hub-hub genes and hub-hub TFs of the turquoise RNA-seq-based module, respectively. large diamonds represent hub miRNAs of the blue miRNA-seq-based module. Additionally, the large pink octagon represents the only hub-hub lncRNA in the turquoise RNA-seq-based module. Cytoscape software (version 3.7.1) (https://cytoscape.org/) was used to generate this figure.



The constructed integrated regulatory sub-network related to *IL1A*, *IL1B*, *IL6*, and *TNF* hub-hub genes. Small circles and rectangles represent hub genes and hub transcription factors (TFs) of the turquoise RNA-seq-based module, respectively. Small diamonds represent regulatory miRNAs of the blue miRNA-seq-based module. On the other hand, large circles and rectangles represent hub-hub genes and hub-hub TFs of the turquoise RNA-seq-based module, respectively. large diamonds represent hub miRNAs of the blue miRNA-seq-based module. Cytoscape software (version 3.7.1) (https://cytoscape.org/) was used to generate this figure.



The constructed integrated regulatory sub-network related to *IL10* hub-hub gene. Small circles and rectangles represent hub genes and hub transcription factors (TFs) of the turquoise RNA-seq-based module, respectively. Small diamonds represent regulatory miRNAs of the blue miRNA-seq-based module. On the other hand, large circles and rectangles represent hub-hub genes and hub-hub TFs of the turquoise RNA-seq-based module, respectively. large diamonds represent hub miRNAs of the blue miRNA-seq-based module. Additionally, the large pink octagon represents the only hub-hub lncRNA in the turquoise RNA-seq-based module. Cytoscape software (version 3.7.1) (https://cytoscape.org/) was used to generate this figure.



The constructed integrated regulatory sub-network related to *STAT3* hub-hub transcription factor (TF). Small circles and rectangles represent hub genes and hub TFs of the turquoise RNA-seq-based module, respectively. Small diamonds represent regulatory miRNAs of the blue miRNA-seq-based module. On the other hand, large circles and rectangles represent hub-hub genes and hub-hub TFs of the turquoise RNA-seq-based module, respectively. large diamonds represent hub miRNAs of the blue miRNA-seq-based module. Additionally, the large pink octagon represents the only hub-hub lncRNA in the turquoise RNA-seq-based module. Cytoscape software (version 3.7.1) (https://cytoscape.org/) was used to generate this figure.