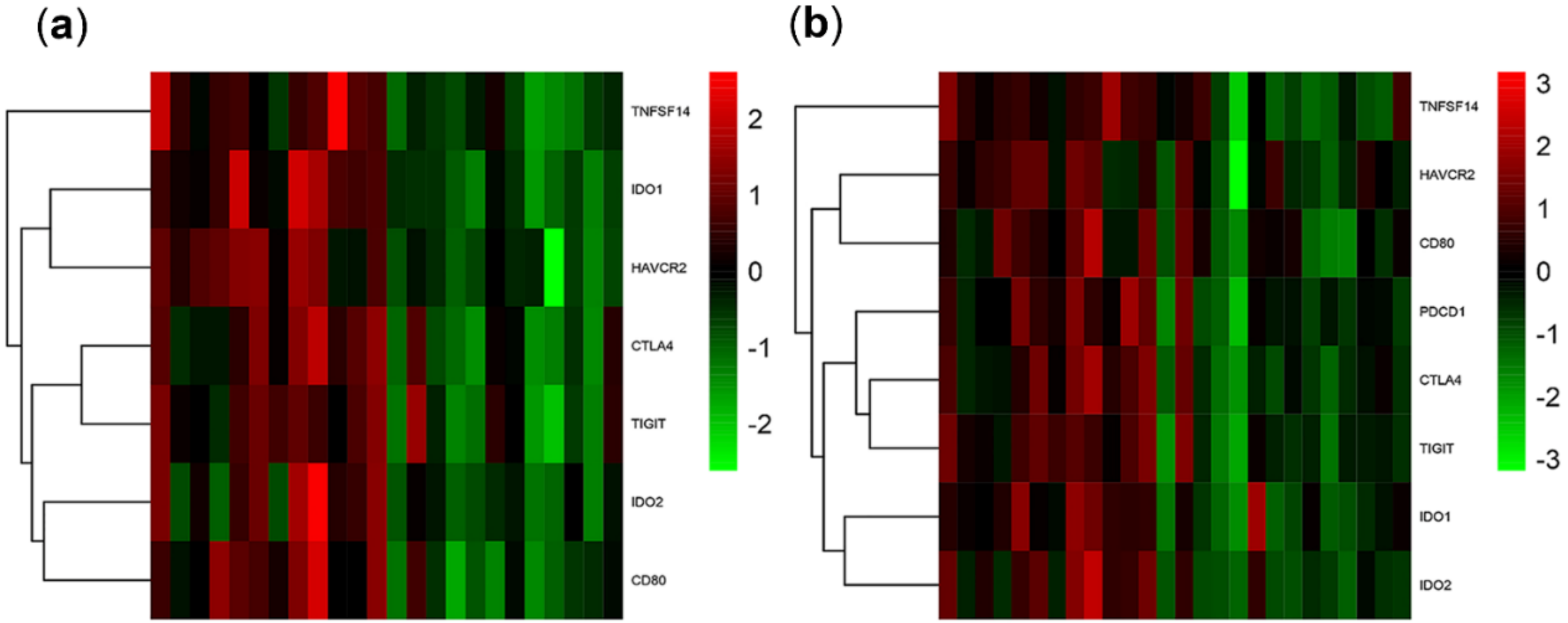
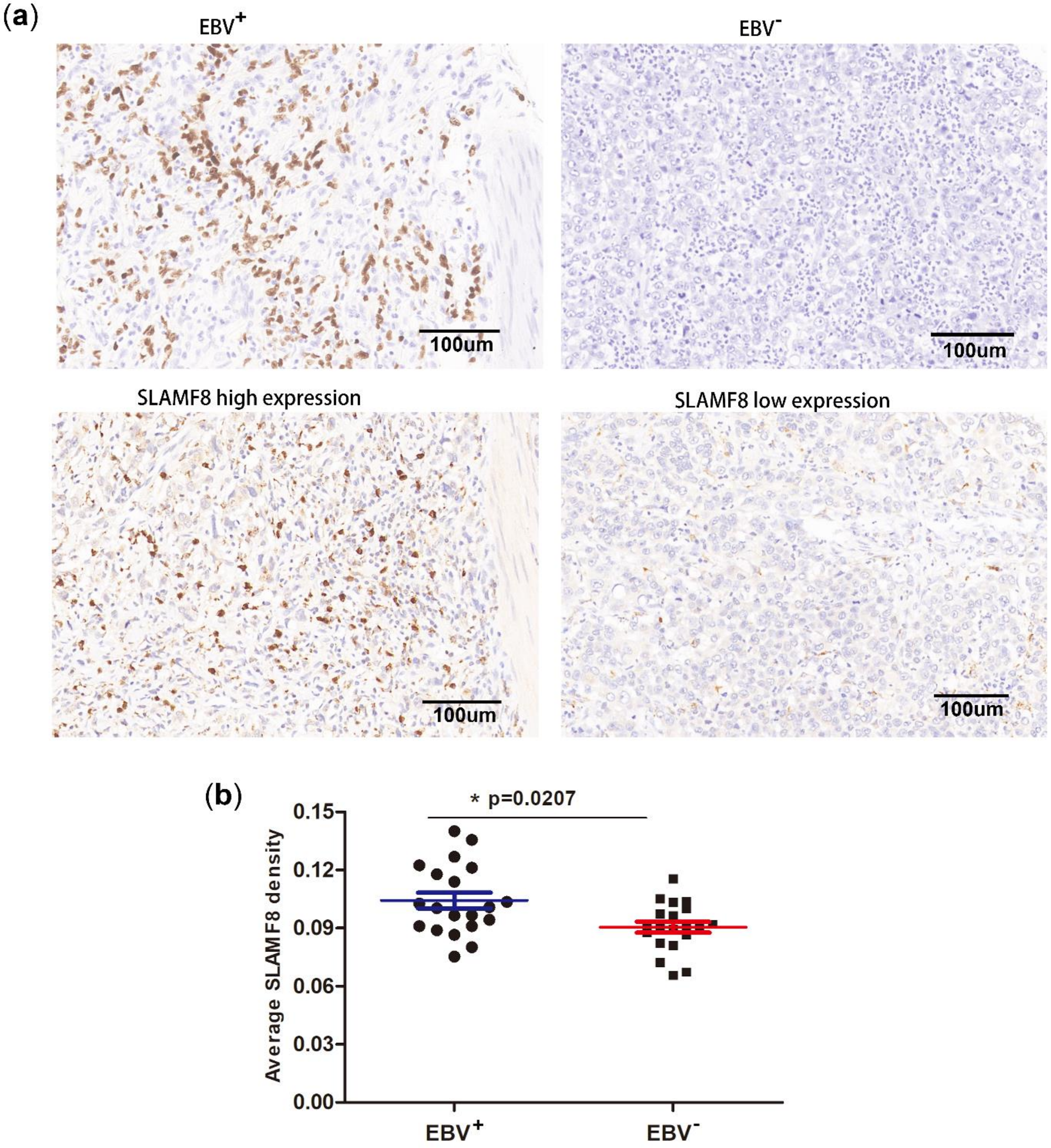


Supplementary figure 1: Differential expression analysis for 7 immune checkpoint gene, along with *PDCD1*, contained in 788-gene signature specific for EBV infection in GC.

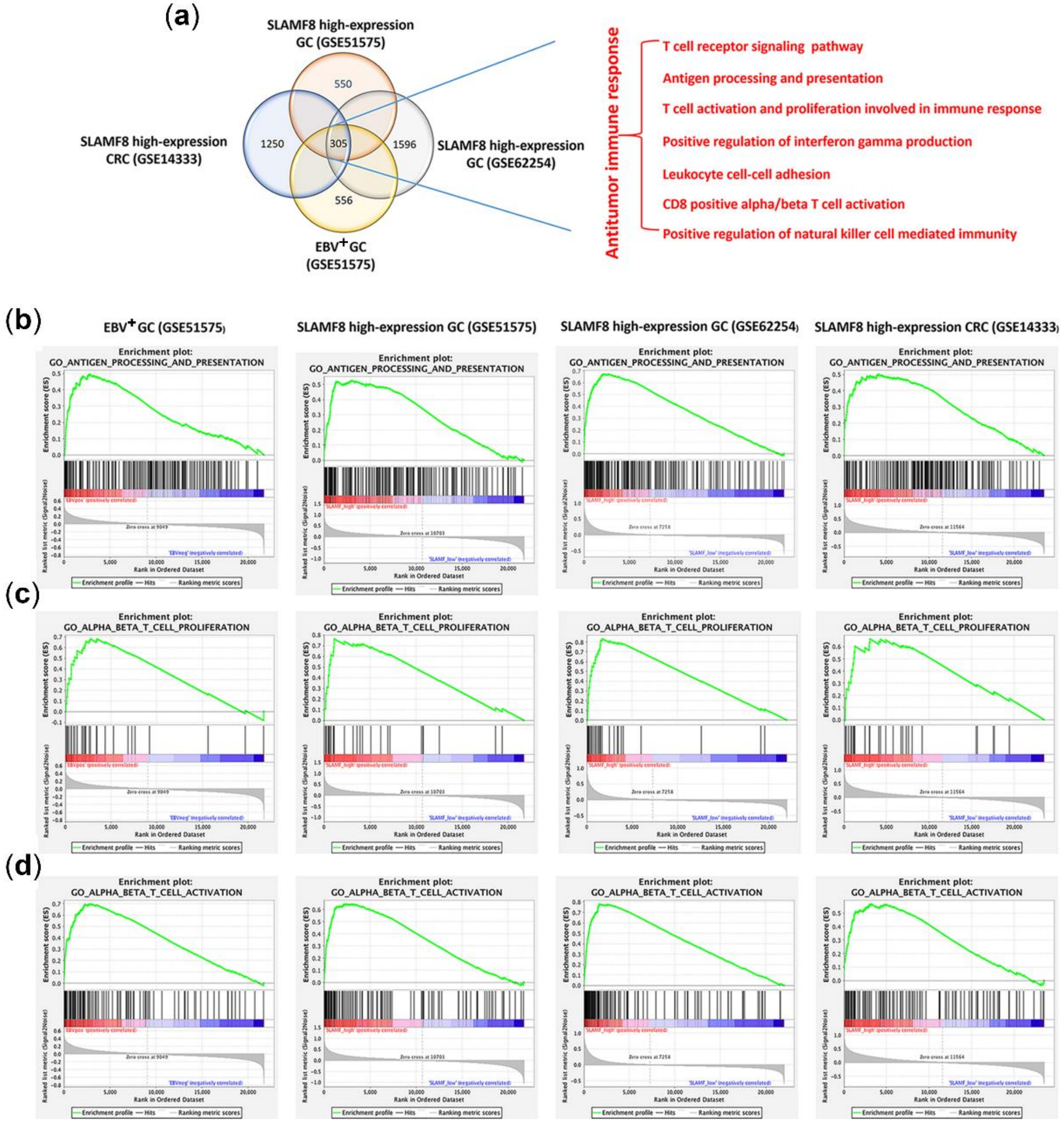
The differential expression of 7 immune checkpoint genes included in EBV related gene signature. Analysis were performed between EBV+ GC tissues and adjacent normal tissues **(a)**;

The differential expression of *PDCD1*, in addition to the 7 immune checkpoint genes, between EBV$^+$ and EBV$^-$ GC tissues **(b)**.



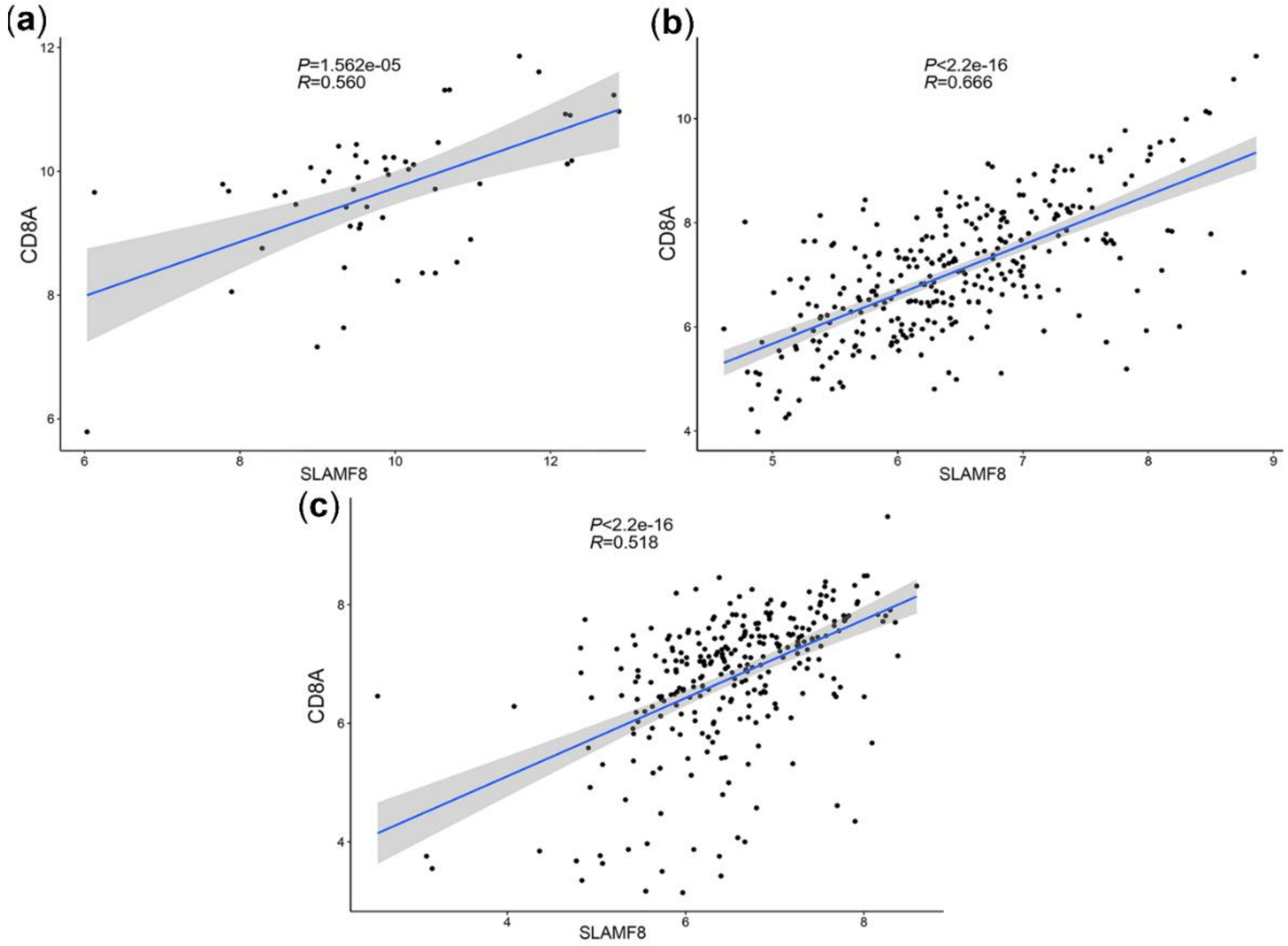
Supplementary figure2: The expression of SLAMF8 in EBV positive and negative GC tissues.

Representative image of IHC staining of *SLAMF8* in EBER positive (n=20) and negative GC tissues (n=20) with scale bar of 100μm **(a)**; Comparison of SLAMF8 expression between EBER positive and negative GC tissues by IHC staining **(b)**. Data are from one experiment that is representative of three separate experiments.



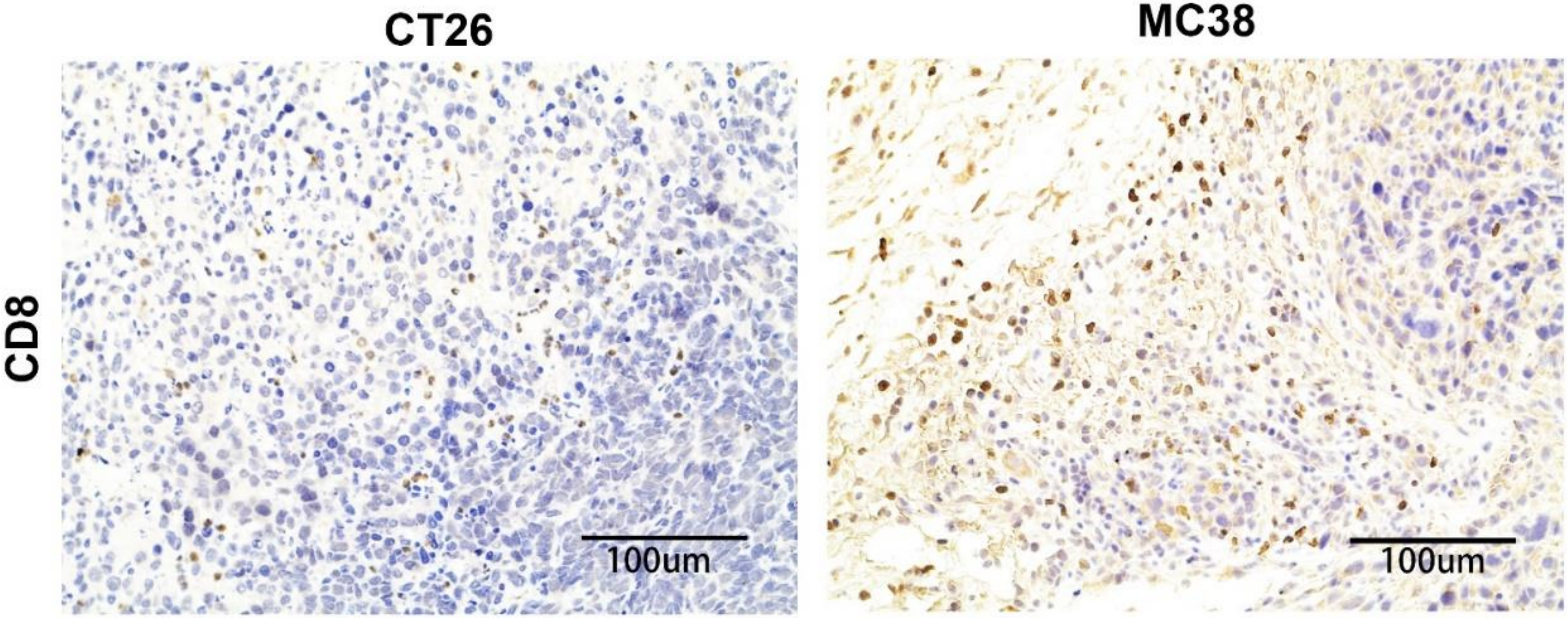
Supplementary figure 3: High-expression *SLAMF8* GI cancers may enrich the pathways involved in antitumor immune response.

Using transcriptome data from GEO database for GSEA analysis, we identified number of pathways enriched in *SLAMF8* high-expression GI cancer tissues (GSE62254 and GSE51575 for GC and GSE14333 for CRC) and EBV^{+} GC (GSE51575), and found that the enriched pathways contained pathways including **(a)**, antigen presentation **(b)**, T cells proliferation **(c)** and activation **(d)** pathways.



Supplementary figure 4: Correlation of *SLAMF8* with *CD8* mRNA expression in public GEO database.

The correlation of *SLAMF8* and *CD8A* mRNA expression in GSE51575 **(a)** and GSE62254 **(b)** datasets of GC tissues, and GSE14333 **(c)** dataset of CRC tissues.



Supplementary figure 5: The amount of CD8$^+$ T cells in CT26 and MC38 tumors

Representative image of IHC staining of pre-therapeutic CD8 in murine tumor tissues established by CT26 CRC cell line **(a)** and MC38 CRC cell line **(b)** with scale bar of 100μm. Data are from one experiment that is representative of three separate experiments.

Supplementary table 1: a 788-gene signature that was potentially involved in immune response against gastric cancer induced by EBV infection.

gensymbolpos	logFC	AveExpr	t	P.Value	adj.P.Val	B
RGN	-4.4576197	7.563354124	-13.13731616	7.59E-13	4.13E-09	19.15074968
CDKN1C	-2.8944618	10.76131169	-11.32259017	1.96E-11	4.26E-08	16.11682916
A_33_P3220911	2.38518576	13.74079917	11.04199058	3.35E-11	6.61E-08	15.61153805
TPD52L1	-3.9732307	7.707187139	-10.86960052	4.67E-11	6.78E-08	15.29603086
BCL2L10	-1.8818199	5.623533936	-9.786057711	4.11E-10	2.79E-07	13.22157472
BST2	2.38379055	13.11549176	9.637632839	5.60E-10	3.51E-07	12.92481248
NCRNA00087	-1.5281076	8.031775813	-9.633414449	5.65E-10	3.51E-07	12.91633293
IL8	3.40766488	7.450233651	9.112545918	1.71E-09	7.64E-07	11.84993327
C9orf24	-2.6045356	7.865929234	-8.950341511	2.43E-09	9.76E-07	11.50994034
LOC100291656	-2.0532025	6.582419881	-8.943554202	2.47E-09	9.76E-07	11.49563138
VLDLR	-1.5660941	6.302322625	-8.906943683	2.68E-09	1.04E-06	11.41833524
MTSS1	-1.8258071	7.422844849	-8.791065447	3.45E-09	1.21E-06	11.17241138
FNDC5	-3.3690757	5.828017788	-8.676917987	4.44E-09	1.46E-06	10.92827367
CTF1	-2.006424	7.79793681	-8.647199039	4.75E-09	1.50E-06	10.86440364
HSPH1	1.27111603	12.19599744	8.622486837	5.02E-09	1.53E-06	10.81119708
IFI30	1.82759405	15.17934993	8.595813428	5.32E-09	1.57E-06	10.75366942
PCOLCE2	-4.3542485	6.922878879	-8.586070111	5.44E-09	1.57E-06	10.73263009
HAPLN3	2.37367449	11.89908022	8.576929113	5.55E-09	1.57E-06	10.71287898
OBSL1	-2.1155925	7.693814206	-8.266455221	1.12E-08	2.61E-06	10.0349089
CXCL10	4.17915087	9.645611988	8.227314056	1.22E-08	2.80E-06	9.948457372
AP3B2	-1.1148596	4.570701783	-8.208773066	1.27E-08	2.86E-06	9.907429273
SNTA1	-2.0142653	6.814500767	-8.156355901	1.44E-08	3.15E-06	9.791173456
PDE9A	-2.1057649	6.843922283	-8.104038426	1.62E-08	3.31E-06	9.674748257
LOC388588	-2.4431597	8.420743928	-7.978701121	2.16E-08	4.27E-06	9.394245631
KCNJ12	-2.9943633	6.349758364	-7.973328713	2.19E-08	4.29E-06	9.38217252
CXCL9	4.01492332	12.3927015	7.964446937	2.23E-08	4.34E-06	9.362204053
PHGDH	-3.0888271	8.761732192	-7.934920833	2.39E-08	4.56E-06	9.295741832
SLC4A3	-1.5622434	5.699902291	-7.896099768	2.62E-08	4.95E-06	9.208169799
CDH19	-1.9054224	5.532525701	-7.823627136	3.10E-08	5.57E-06	9.044119553
DNASE1	-2.6311296	8.674247306	-7.733878808	3.82E-08	6.70E-06	8.839943816
IL18BP	2.06620303	7.963582989	7.629415276	4.89E-08	7.86E-06	8.600879013
C12orf34	-2.4817055	8.555294619	-7.627109465	4.91E-08	7.86E-06	8.595585117
IL8RBP	2.91388163	7.195426961	7.626479486	4.92E-08	7.86E-06	8.594138624

DIRAS3	-1.6077998	5.558640555	-7.579074619	5.50E-08	8.36E-06	8.4851355
CRABP1	-1.9809284	5.816155387	-7.572782499	5.59E-08	8.43E-06	8.470644098
RIMS4	-2.2096678	6.361689834	-7.476007435	7.03E-08	9.85E-06	8.247077972
CCNJL	-2.5632526	6.307042627	-7.471168119	7.11E-08	9.90E-06	8.235864809
ARHGEF4	-1.813844	6.315995383	-7.452962932	7.42E-08	1.01E-05	8.19365312
FCGR1B	3.01478808	9.676182174	7.448040195	7.51E-08	1.01E-05	8.182231223
CBLN1	-1.2134403	4.109254599	-7.437687672	7.70E-08	1.02E-05	8.158200238
ATCAY	-1.1138755	4.470290925	-7.434226034	7.76E-08	1.02E-05	8.150161606
ZNF287	-1.1966095	5.109613709	-7.433388925	7.78E-08	1.02E-05	8.148217424
MGC5566	2.55526979	6.757831731	7.393610007	8.55E-08	1.09E-05	8.055721844
TCP11L2	-1.0947212	7.233926203	-7.389227052	8.64E-08	1.09E-05	8.045517356
DCBLD2	-1.4917675	7.067905134	-7.369475966	9.06E-08	1.13E-05	7.999500368
AMH	1.91326715	6.642828299	7.368251295	9.09E-08	1.13E-05	7.996645347
GFRA2	-1.8558171	8.21863652	-7.316158507	1.03E-07	1.26E-05	7.875017512
PLA2G7	3.03964204	9.814353322	7.275345442	1.14E-07	1.34E-05	7.779472752
CRNKL1	1.03197928	7.880234335	7.268665996	1.15E-07	1.34E-05	7.763814859
SOBP	-1.556744	6.227449392	-7.237967682	1.24E-07	1.43E-05	7.691776161
ATF5	1.10592341	9.08986423	7.12283141	1.64E-07	1.76E-05	7.420485922
STAT1	1.81689059	11.74465476	7.106358766	1.71E-07	1.81E-05	7.381530859
UBE2L6	1.31209342	11.55517015	7.106113865	1.71E-07	1.81E-05	7.380951446
C2CD4B	-3.2886148	9.644457219	-7.082046765	1.81E-07	1.89E-05	7.323972927
WNT6	-2.1125903	7.671896472	-7.063687779	1.89E-07	1.94E-05	7.280458106
GBP5	2.97574941	10.89151139	6.981348226	2.31E-07	2.31E-05	7.084765098
APOC1	3.61057954	11.88019256	6.908049839	2.77E-07	2.59E-05	6.909838275
PARP14	1.28388243	11.44323574	6.901240115	2.81E-07	2.61E-05	6.893552712
UBD	2.90945003	15.26456805	6.897534383	2.84E-07	2.63E-05	6.884687973
RASSF10	-1.6386975	6.234710453	-6.873896855	3.01E-07	2.77E-05	6.828102881
HEJ1	1.06999752	12.27365854	6.87082399	3.03E-07	2.78E-05	6.82074177
PID1	-2.8779971	8.356511667	-6.859942316	3.11E-07	2.84E-05	6.794665118
MORN5	-1.1727607	4.544840595	-6.84250085	3.25E-07	2.91E-05	6.752838264
AMBP	-2.3638469	6.362039638	-6.816751837	3.46E-07	3.01E-05	6.691020619
TMEM25	-2.029771	7.484021348	-6.811030563	3.51E-07	3.04E-05	6.677274111
C10orf81	2.07416464	8.063152111	6.774927277	3.84E-07	3.25E-05	6.590436903
MST1	-2.2037316	11.67485696	-6.76381628	3.94E-07	3.30E-05	6.563680485
C13orf35	1.05553981	4.510060816	6.76087215	3.97E-07	3.31E-05	6.556588223

PC	-1.1842014	9.896038853	-6.747578698	4.11E-07	3.39E-05	6.524551978
ULK2	-1.4373722	7.561919004	-6.731360034	4.27E-07	3.51E-05	6.485437473
CA4	-1.9635075	5.928497268	-6.711121518	4.49E-07	3.64E-05	6.436584222
EFR3B	-1.1531167	6.323253589	-6.673125141	4.94E-07	3.93E-05	6.344734386
LTB4R	1.1441526	6.669651244	6.664541863	5.04E-07	3.97E-05	6.323962171
tcag7.873	1.4256654	12.229897	6.660294565	5.10E-07	3.99E-05	6.313680172
C19orf28	1.41264877	8.943596765	6.656038405	5.15E-07	4.00E-05	6.303374599
RFX6	-2.6475982	5.122838115	-6.648966353	5.24E-07	4.04E-05	6.286246127
CYS1	-2.3230461	6.718308581	-6.634933422	5.43E-07	4.17E-05	6.252241147
IDO1	4.09481482	11.58477047	6.619633717	5.64E-07	4.28E-05	6.215140365
GBP4	1.89407642	12.40051347	6.603303244	5.87E-07	4.40E-05	6.175510109
CCDC89	-1.4078812	5.649784571	-6.594616705	6.00E-07	4.48E-05	6.154417358
BAIAP3	-1.6595963	5.414232933	-6.54523968	6.78E-07	4.90E-05	6.03435529
THNSL2	-2.4668583	7.730906011	-6.530179836	7.04E-07	5.07E-05	5.997681552
PART1	-1.0950456	4.878038894	-6.522209501	7.18E-07	5.14E-05	5.978261834
SERPINE1	1.83714039	6.230151994	6.521896544	7.19E-07	5.14E-05	5.977499168
TMEM61	-3.1582993	7.926468974	-6.509018252	7.42E-07	5.26E-05	5.946105672
NTF3	-1.6155514	6.654577876	-6.508848923	7.42E-07	5.26E-05	5.945692774
OSBPL3	1.29040989	9.993395384	6.496177919	7.66E-07	5.37E-05	5.914786222
SLC7A2	-2.9367945	8.15800252	-6.438812077	8.84E-07	5.98E-05	5.774639179
PPP3CA	-1.0631504	9.953191228	-6.435109802	8.93E-07	6.00E-05	5.765581942
HMGCS2	-3.8969093	8.07225075	-6.430901113	9.02E-07	6.01E-05	5.755283998
TNFSF13B	1.51536579	10.51460734	6.424857675	9.16E-07	6.09E-05	5.74049336
CYP39A1	-1.2679418	5.280499438	-6.420747486	9.25E-07	6.13E-05	5.730431864
ZNF480	-1.7429813	7.596905305	-6.394906585	9.87E-07	6.37E-05	5.667132988
ENST00000287912	1.19164749	8.013786247	6.387265662	1.01E-06	6.41E-05	5.648402293
EPB41L4B	-1.3014447	7.401388964	-6.377731987	1.03E-06	6.53E-05	5.625022994
CD300LF	2.11643235	7.457585065	6.363636774	1.07E-06	6.69E-05	5.590439726
LOC154092	1.53252882	4.526520664	6.350598139	1.10E-06	6.85E-05	5.558430026
VAV3	-1.7482693	9.892396988	-6.350074198	1.10E-06	6.85E-05	5.55714338
CREB3L4	-1.5968751	10.31060108	-6.349608773	1.11E-06	6.85E-05	5.556000409
SCG2	-2.138421	5.986791989	-6.345196893	1.12E-06	6.91E-05	5.545164759
GM2A	1.43810396	11.23956646	6.284820178	1.30E-06	7.82E-05	5.39667389
CLGN	-1.5433447	5.346180461	-6.25781648	1.39E-06	8.28E-05	5.330138933
KCNJ2	2.06165065	8.837316428	6.248984312	1.43E-06	8.36E-05	5.30836105

CAMK2N2	2.89860314	9.107650413	6.235312813	1.48E-06	8.55E-05	5.27463505
CAPS	-1.9497291	8.306114162	-6.233290738	1.48E-06	8.55E-05	5.269645226
PLK1S1	-1.2105154	9.680612417	-6.231745269	1.49E-06	8.55E-05	5.265831233
MANEAL	1.23375256	8.776551506	6.231199388	1.49E-06	8.55E-05	5.264484023
ZC4H2	-1.9344373	9.19581362	-6.22629913	1.51E-06	8.60E-05	5.252389046
MAGI2	-1.0387935	5.858292224	-6.225545162	1.51E-06	8.60E-05	5.250527865
DCDC2	-2.18822	6.09309942	-6.22120525	1.53E-06	8.61E-05	5.239813619
CBS	-2.644146	10.46414939	-6.207801622	1.58E-06	8.86E-05	5.20671127
SMARCA1	-2.1072416	8.559177121	-6.191789853	1.65E-06	9.13E-05	5.167144337
MSX2	1.76231521	5.728119302	6.18505342	1.67E-06	9.22E-05	5.150490268
ZNF577	-1.213652	7.052524276	-6.178976651	1.70E-06	9.33E-05	5.135463222
CTSB	1.14947384	12.76695735	6.171963029	1.73E-06	9.41E-05	5.118114968
CHIC1	-1.0498058	5.842258594	-6.166805588	1.75E-06	9.50E-05	5.105354928
TBX1	-1.4654553	6.805620639	-6.165693639	1.76E-06	9.50E-05	5.102603513
SALL2	-1.9937904	7.525371663	-6.164216793	1.77E-06	9.50E-05	5.098949009
SYT12	-1.5627566	5.973205675	-6.142126288	1.87E-06	9.90E-05	5.044260083
FAM172A	-1.2551647	10.07714306	-6.12925105	1.93E-06	0.000101437	5.012363496
CCL3	2.13280247	11.75467095	6.127642976	1.94E-06	0.000101437	5.008378603
RAB6B	-1.8977594	5.279652011	-6.114695931	2.00E-06	0.000103574	4.976286182
CITED4	-2.0020738	12.17944912	-6.102156342	2.07E-06	0.000105415	4.945188594
MOGAT1	-2.027049	5.592707064	-6.101233874	2.07E-06	0.000105415	4.942900333
ENST00000369310	2.64047313	7.794359351	6.08968768	2.13E-06	0.000107793	4.914252229
FAM189A1	-1.8423789	5.731547204	-6.084408814	2.16E-06	0.000108994	4.901150293
IRX5	-2.8575541	8.195524925	-6.069035459	2.25E-06	0.000112034	4.862979466
GK	1.39571938	7.37693986	6.060618399	2.30E-06	0.000113762	4.842071304
FAM50B	-1.8262951	8.551483736	-6.056002784	2.32E-06	0.000114452	4.830603246
APOC2	2.71490484	7.122226961	6.01776956	2.56E-06	0.000123273	4.735533496
GBP1	2.11479899	10.06842536	6.013714933	2.59E-06	0.000123273	4.725443623
LAMP3	2.31823819	10.03197185	6.007921552	2.63E-06	0.000124316	4.711024337
SVOP	-1.9887917	5.066939586	-6.005733182	2.64E-06	0.000124739	4.70557687
MID2	-1.6743116	7.138293344	-6.001980982	2.67E-06	0.000125664	4.696235602
OR8B3	1.45281653	5.347520378	6.000802858	2.67E-06	0.000125768	4.693302353
ACADM	-1.1905949	9.567806292	-5.962546754	2.95E-06	0.000136248	4.597987256
C2	1.43590072	9.867141349	5.961829874	2.95E-06	0.000136248	4.596199929
KYNU	1.57580322	8.74158129	5.956415081	2.99E-06	0.00013785	4.582698319

HAVCR2	1.92688164	7.562414414	5.937266556	3.14E-06	0.000143729	4.534931862
PCMTD1	1.50150424	5.008655271	5.936742172	3.15E-06	0.000143729	4.533623335
KIAA1324L	-1.7451036	6.627989079	-5.929750257	3.20E-06	0.000145383	4.516173715
SLCO4A1	1.96758425	10.06669929	5.929230639	3.21E-06	0.000145383	4.514876745
LOC100289258	1.00169655	15.77809177	5.928984622	3.21E-06	0.000145383	4.514262678
GGT7	-1.4165834	7.10323884	-5.926833299	3.23E-06	0.00014588	4.50889268
TMEM120A	-1.08667	10.90753837	-5.922891226	3.26E-06	0.000146168	4.499051706
BAIAP2	-1.5518222	7.988334558	-5.922727886	3.26E-06	0.000146168	4.498643916
ENST00000382464	1.00870648	8.286133075	5.921205144	3.28E-06	0.000146168	4.494842178
CD300A	1.09201573	7.733943487	5.916912605	3.31E-06	0.000147028	4.484124201
PDE4A	-1.0440669	8.066662262	-5.916504561	3.31E-06	0.000147028	4.483105283
SYT7	-1.8309845	6.079480528	-5.907230525	3.39E-06	0.000149687	4.459943485
CXCL11	3.39509619	9.20911225	5.907101028	3.40E-06	0.000149687	4.459620018
TAP1	1.72258392	14.84613873	5.897816544	3.48E-06	0.000151593	4.436424839
NCKAP5	-1.6933655	6.124207272	-5.897417905	3.48E-06	0.000151593	4.435428768
LRRN1	-1.2931651	5.049171586	-5.876611214	3.67E-06	0.00015829	4.383421401
GALNTL1	-2.7792565	7.643108542	-5.872693962	3.71E-06	0.000159568	4.373626063
RNF180	-1.4323811	5.578383602	-5.863179338	3.80E-06	0.000163177	4.349828949
OR4X2	1.09884623	5.624172334	5.851498756	3.91E-06	0.000167139	4.320604534
PRPH2	-1.3288211	5.91029998	-5.846246679	3.97E-06	0.000168739	4.30746045
SGK2	-2.1706629	9.213830663	-5.839491982	4.04E-06	0.000170099	4.290552608
C22orf36	-2.5006612	8.441107786	-5.83563821	4.08E-06	0.000171374	4.280904516
F2RL2	2.59849719	8.00875218	5.824616178	4.19E-06	0.000174929	4.253303882
SEMA6A	-1.6404922	5.509429366	-5.810666192	4.35E-06	0.000179232	4.21835761
LOC284242	1.26904101	6.284225411	5.801602155	4.45E-06	0.000182753	4.195643081
GLA	1.16797435	11.99502263	5.795370418	4.52E-06	0.000183959	4.180022639
SLC25A21	-1.4693207	5.37640358	-5.792188255	4.56E-06	0.000184087	4.172045096
CABC1	-1.3679688	9.717253817	-5.782037044	4.68E-06	0.000188594	4.146591293
ADM	-1.7851936	11.08631042	-5.758216805	4.97E-06	0.000196476	4.086832344
NACAD	-1.1029958	5.843325448	-5.75156786	5.06E-06	0.000199281	4.070144266
FPR3	1.75437814	10.64496249	5.751283895	5.06E-06	0.000199281	4.069431475
BARX1	-1.6144144	6.78100022	-5.737278908	5.25E-06	0.000205465	4.034269647
ICAM1	2.27930382	10.4631707	5.732160041	5.32E-06	0.00020707	4.021414313
LOC100128593	1.14591865	6.439782721	5.73084007	5.33E-06	0.000207398	4.018099077
ZNF232	1.13682106	8.887417676	5.723162644	5.44E-06	0.000210036	3.99881398

NLRC5	1.07729571	7.973632183	5.721769652	5.46E-06	0.000210036	3.995314435
A_24_P68222	1.09789021	7.816328288	5.717610958	5.52E-06	0.000211919	3.984865931
PRICKLE1	-1.6526257	8.062148196	-5.714947985	5.56E-06	0.000212723	3.9781747
CRAT	-1.7356721	12.52434526	-5.71476576	5.56E-06	0.000212723	3.977716806
MLYCD	-1.4541809	7.484437341	-5.712882439	5.59E-06	0.00021338	3.972984269
ENTPD3	-3.3711814	6.417541133	-5.698312512	5.80E-06	0.000219599	3.936363461
NINL	-1.4808288	8.245795846	-5.690001077	5.93E-06	0.000222793	3.915466376
CENPK	1.78358313	7.533333408	5.681185029	6.06E-06	0.000225565	3.893295304
DUXA	1.11011221	5.049229091	5.672165001	6.20E-06	0.000229684	3.870605696
SGEF	-1.7464461	6.22159367	-5.66853463	6.26E-06	0.000231054	3.861472032
PPIAL4A	1.01474313	14.87498409	5.66553506	6.31E-06	0.000232122	3.853924723
CCL3L3	1.7940387	8.108619282	5.665427422	6.31E-06	0.000232122	3.853653881
SLAMF8	1.994987	10.55464263	5.664631559	6.32E-06	0.000232205	3.851651278
BMP7	-1.7174642	7.198551689	-5.657140343	6.45E-06	0.000234657	3.832799278
KRTAP11.1	1.113061	5.901020189	5.656637038	6.46E-06	0.000234657	3.831532551
TIAM2	-1.4304545	9.654140513	-5.653859106	6.50E-06	0.000235394	3.824540698
DTX2	1.18388289	9.810234594	5.653476956	6.51E-06	0.000235394	3.823578813
SLC16A2	-2.0355678	7.935035954	-5.651940668	6.54E-06	0.000235935	3.819711825
LOC100133478	1.98051028	7.392507597	5.649965964	6.57E-06	0.000236499	3.814741066
C6orf168	-1.3246898	4.718288404	-5.641551955	6.71E-06	0.00024034	3.793558268
KLK10	1.97969528	5.60590722	5.634548173	6.83E-06	0.000243703	3.775922221
TNNC2	-1.6462542	6.747393839	-5.627295158	6.96E-06	0.000246493	3.757655182
SYT17	-1.384092	7.325596189	-5.62344244	7.03E-06	0.00024742	3.747950542
CTSD	1.07619729	13.02050389	5.623321969	7.04E-06	0.00024742	3.747647073
TMEM52	-1.6908467	8.471645864	-5.621527413	7.07E-06	0.000248165	3.743126407
NMI	1.0306586	11.29984726	5.619294	7.11E-06	0.000249196	3.737499928
ENST00000455537	-1.3095457	4.624654022	-5.616691476	7.16E-06	0.000249769	3.730943165
MED29	1.08530103	6.751236793	5.616532527	7.16E-06	0.000249769	3.730542697
IGSF6	2.26481142	8.901511331	5.611334962	7.26E-06	0.000251926	3.717446661
OPN1SW	1.22223269	5.37227652	5.610594148	7.27E-06	0.000252005	3.715579931
TTLL7	-1.3798163	5.662486904	-5.597479159	7.52E-06	0.000258615	3.682526471
ISPD	-1.2818987	5.082191025	-5.59481277	7.57E-06	0.00025919	3.675805086
LOC732419	1.04531797	7.016140286	5.592051267	7.63E-06	0.000260613	3.668843468
A_33_P3332581	-1.0384393	4.100837814	-5.584191107	7.78E-06	0.00026388	3.649025762
CHI3L1	3.64220236	9.526205651	5.579912965	7.87E-06	0.000265873	3.638237728

TDGF1	-2.4658358	6.989638616	-5.579466464	7.88E-06	0.000265873	3.637111736
CAMK2B	-1.4213166	5.128506146	-5.578281585	7.90E-06	0.000266274	3.634123636
SLC38A6	1.40327363	5.840788719	5.570457041	8.06E-06	0.000269618	3.614389059
INSM1	-2.4521679	5.378825702	-5.566979901	8.14E-06	0.000270581	3.605618025
ENST00000390027	-1.4904152	5.105256999	-5.565781876	8.16E-06	0.000270581	3.602595854
SLC15A1	-4.8372556	6.637348349	-5.54983175	8.50E-06	0.000279638	3.562351363
OR8B8	1.14698615	7.305673218	5.546178819	8.59E-06	0.000281439	3.553132339
AMIGO1	-1.7732357	6.932343205	-5.544031929	8.63E-06	0.000282578	3.54771379
KBTBD11	-2.6781365	9.780712231	-5.538839346	8.75E-06	0.000284255	3.534607072
TMEM136	-1.2998638	8.391078033	-5.537864039	8.77E-06	0.000284547	3.532145099
WFDC2	-4.5039631	9.138740827	-5.535763395	8.82E-06	0.000285639	3.526842243
FERMT1	1.87095037	11.02482954	5.535228001	8.83E-06	0.000285639	3.525490658
TNRC4	-1.4734922	5.513954912	-5.534344346	8.85E-06	0.000285867	3.523259858
NDRG4	-1.654618	8.243832159	-5.533335227	8.88E-06	0.000286188	3.520712266
DACT2	-1.8976573	5.572963219	-5.530180451	8.95E-06	0.000287678	3.512747431
LRRC49	-1.2977213	7.604081379	-5.521229398	9.16E-06	0.000292957	3.490145645
SUMO1P3	1.07890388	8.600449453	5.520602725	9.17E-06	0.000292957	3.488563096
IL2RA	2.03519085	7.068821981	5.510497982	9.41E-06	0.000298639	3.463042298
SMO	-1.2182678	8.664417371	-5.499683566	9.68E-06	0.000304968	3.435722722
IFITM1	1.93782046	13.8927283	5.49601201	9.77E-06	0.000306989	3.426446079
GJB2	1.6858955	10.01903385	5.494898237	9.80E-06	0.00030743	3.423631844
SELE	1.69346873	5.827789859	5.482303357	1.01E-05	0.000314889	3.391802874
GGT1	-1.2919514	8.634034743	-5.470692607	1.04E-05	0.00032357	3.362453272
C16orf45	-1.6051198	9.167104175	-5.460489205	1.07E-05	0.000328462	3.33665519
FILIP1L	-1.0667355	7.83418219	-5.445741634	1.11E-05	0.000335742	3.29935803
WARS	2.03479728	12.73521145	5.430349841	1.16E-05	0.000346841	3.260419646
ABCC6P1	-2.6511988	6.496712873	-5.428086644	1.17E-05	0.0003478	3.254693164
CXCL16	1.2055683	10.78629654	5.411739904	1.22E-05	0.00035944	3.213324043
TLE6	1.32084537	6.92412359	5.391168494	1.28E-05	0.000374133	3.161244938
NFAM1	1.62199589	8.947302222	5.384860923	1.30E-05	0.000377748	3.145272502
MLF1	-1.2606378	6.201595882	-5.38402089	1.31E-05	0.000377748	3.143145174
ZNF683	2.07769492	9.842594824	5.383889401	1.31E-05	0.000377748	3.142812185
GCOM1	-1.2496702	8.506888968	-5.380582997	1.32E-05	0.000378953	3.134438604
C19orf46	-1.8704957	9.205956169	-5.374432717	1.34E-05	0.000383933	3.118861467
NPW	-1.5181888	5.554222232	-5.372726023	1.35E-05	0.000384216	3.114538526

CAND2	-1.2554908	6.769144321	-5.368673348	1.36E-05	0.000386272	3.10427284
CHRNB2	-1.0677277	5.131363563	-5.368649604	1.36E-05	0.000386272	3.104212693
CTSZ	1.15599266	10.4955358	5.364074803	1.38E-05	0.000388347	3.092623531
CNTFR	-1.5452058	4.834030038	-5.358987966	1.39E-05	0.000392489	3.079736146
ARL4D	-1.2262145	6.003806075	-5.357444558	1.40E-05	0.000392808	3.07582573
IRF1	1.43820957	10.85463608	5.357180465	1.40E-05	0.000392808	3.075156607
PBX1	-1.3834042	8.370713109	-5.350262483	1.43E-05	0.00039701	3.057627664
OR9A1P	1.65096092	4.973181275	5.331464965	1.50E-05	0.000410894	3.009987592
TEKT2	-1.5461995	5.915683984	-5.305686693	1.60E-05	0.000433338	2.944631556
ZNF605	-1.9020663	8.575133933	-5.305224925	1.60E-05	0.000433338	2.943460582
CTSC	1.33821698	9.632170913	5.301712462	1.62E-05	0.000435772	2.934553234
TMEM44	1.18039409	8.046597053	5.291329909	1.66E-05	0.000444299	2.908221006
HLA.DRB1	1.51593165	15.47712422	5.285594953	1.69E-05	0.000449865	2.893674224
ANGPTL7	-1.6615769	4.385494084	-5.283135953	1.70E-05	0.000451642	2.887436558
SLC6A8	-2.6946805	7.543678578	-5.281418456	1.71E-05	0.000452774	2.8830797
CD47	1.14909605	12.49678276	5.2788781	1.72E-05	0.000453842	2.876635255
APCDD1	-2.407496	8.70575728	-5.278629521	1.72E-05	0.000453842	2.876004642
TRIM63	-1.6916834	4.960095508	-5.278452163	1.72E-05	0.000453842	2.875554702
ENST00000367555	1.38290999	7.786421561	5.275874721	1.73E-05	0.000455354	2.86901589
PNMT	-1.1515942	4.846678812	-5.270798072	1.75E-05	0.000459614	2.856136016
GGTLC1	-1.8995577	9.294680028	-5.267470779	1.77E-05	0.000461381	2.847693888
MXI1	-1.1276335	8.291843536	-5.256679828	1.82E-05	0.000469441	2.820311931
DPY19L1P1	1.18666248	7.269233753	5.255398795	1.82E-05	0.000469892	2.817061044
SLC47A1	1.25667934	5.655319771	5.250006679	1.85E-05	0.000475402	2.803376793
LOC100131432	1.13219962	6.630351239	5.244789433	1.88E-05	0.000480475	2.790135364
NR4A1	1.87393494	5.540898111	5.244315599	1.88E-05	0.000480475	2.78893272
ADIPOR2	-1.0469033	11.45615633	-5.239405112	1.90E-05	0.000484702	2.776468915
CASP1	1.51896139	12.20266482	5.238942154	1.90E-05	0.000484702	2.775293792
PGM2	1.04951672	9.720706793	5.234277466	1.93E-05	0.000489475	2.763453041
CHGB	-2.9071839	6.371192648	-5.223753098	1.98E-05	0.000500726	2.736735538
CLEC7A	1.38066484	5.454242174	5.221773517	1.99E-05	0.000502728	2.731709704
TNFSF14	1.50861649	8.333746931	5.21833026	2.01E-05	0.000505492	2.722967534
B3GALNT1	-1.0927469	8.552673558	-5.212497914	2.04E-05	0.000507934	2.70815878
ENPP3	-1.5751307	5.602916952	-5.211009478	2.05E-05	0.000509322	2.704379361
ABHD8	-1.3476075	10.540149	-5.208589279	2.06E-05	0.000510788	2.698233872

SCIN	-3.2376625	7.761169153	-5.202440458	2.09E-05	0.000515869	2.682619664
SLC37A2	1.15804042	7.187628453	5.202428596	2.09E-05	0.000515869	2.68258954
LOC145216	1.14982454	7.166872356	5.198274331	2.12E-05	0.000519361	2.672039616
WNK4	-1.3969127	7.624509039	-5.193983642	2.14E-05	0.000522249	2.661142693
AASS	-1.535098	7.057486641	-5.189363696	2.17E-05	0.000526796	2.649408954
NPL	1.41926497	7.475262733	5.184518851	2.19E-05	0.00053229	2.637103344
GDF1	-1.0627064	5.140111605	-5.180109402	2.22E-05	0.000535271	2.625903027
PLTP	-1.6287708	10.35194908	-5.168508188	2.29E-05	0.000546423	2.596432488
SLC25A27	-1.577414	5.68442029	-5.161183453	2.33E-05	0.000554735	2.577823578
GZMB	2.06594925	11.65072231	5.161029512	2.33E-05	0.000554735	2.577432467
MYOT	-1.0320957	4.828691867	-5.156816177	2.36E-05	0.000559438	2.566727579
PRKY	1.00725509	8.766409661	5.146696894	2.42E-05	0.000570847	2.541015472
F10	-2.1504875	7.40640755	-5.145923031	2.43E-05	0.00057138	2.539049054
LOC148189	-1.1057495	7.157203269	-5.143395882	2.44E-05	0.00057369	2.53262736
IL27RA	1.42160823	9.803088116	5.142222323	2.45E-05	0.00057369	2.529645195
FOXD3	-1.139747	4.630370353	-5.142114498	2.45E-05	0.00057369	2.529371197
SERHL2	-1.3233191	6.806001924	-5.141484967	2.45E-05	0.00057369	2.52777146
MAPT	-2.0052359	5.600647027	-5.138844822	2.47E-05	0.000576397	2.521062341
DHDPSL	1.16891837	5.59315999	5.132800242	2.51E-05	0.000582862	2.50570125
TXNDC3	1.49485705	6.158738865	5.125621115	2.56E-05	0.000589691	2.487455805
COL22A1	2.10301065	6.311333743	5.125595182	2.56E-05	0.000589691	2.487389895
FAM13A	-1.6307366	9.773120222	-5.121868847	2.58E-05	0.000592932	2.477919097
LOC100288921	-1.3514399	5.324070445	-5.113300125	2.64E-05	0.000602368	2.456139768
TMEM62	1.08116331	9.218314418	5.106478887	2.69E-05	0.000609951	2.438800907
CAND1	1.22229391	9.615036708	5.09782669	2.75E-05	0.000620803	2.416806521
ADAMTS18	1.46830785	5.042669803	5.096360815	2.76E-05	0.000622534	2.41308003
PPP1R9A	-2.6157704	6.929795493	-5.090858622	2.80E-05	0.000628922	2.399092175
GZMH	1.65357547	10.95225707	5.086305918	2.83E-05	0.000634468	2.387517689
RAB42	1.75694803	8.022562939	5.078270887	2.89E-05	0.000643268	2.367089005
ENST00000360201	-1.3549034	6.86007547	-5.075270227	2.92E-05	0.000645682	2.359459661
TIMM8A	1.03693969	9.902064258	5.074233389	2.93E-05	0.000646773	2.356823403
CDRT8	1.19910294	5.096018508	5.071860648	2.94E-05	0.000649015	2.350790419
UGT3A1	1.01405044	5.639699918	5.068543336	2.97E-05	0.000653785	2.342355578
FAM169A	1.25576972	8.14637453	5.067424447	2.98E-05	0.000654535	2.339510563
CERK	-1.2789019	9.008494657	-5.067327494	2.98E-05	0.000654535	2.33926404

CRHR2	1.01212562	5.238219235	5.055089266	3.08E-05	0.000671023	2.308144334
C15orf52	-1.5754587	10.54319835	-5.054413249	3.08E-05	0.000671534	2.306425268
PKDREJ	-1.1887319	5.222903208	-5.051440866	3.10E-05	0.000674732	2.298866606
LOC729897	1.15998126	5.217398571	5.047103498	3.14E-05	0.000681731	2.287836588
WIPF3	-1.4276288	5.891954898	-5.046380453	3.15E-05	0.000682337	2.285997843
PCDH20	-2.2611789	5.060980919	-5.03656809	3.23E-05	0.000692214	2.261043645
CD80	1.15236152	5.568775945	5.028089742	3.30E-05	0.000700886	2.239480926
ENST00000395354	1.30360317	6.463289561	5.027781566	3.30E-05	0.000700886	2.238697134
NPY1R	-1.2726423	4.879006421	-5.020046469	3.37E-05	0.000711707	2.219023834
ITGAX	1.77928108	9.040445992	5.019452434	3.37E-05	0.000712119	2.217512944
ETNK2	-1.1108706	5.551056543	-5.013567763	3.43E-05	0.000720346	2.202545437
PCDHA11	-1.4487681	5.297966723	-5.009461665	3.46E-05	0.000727406	2.192101441
FCGR3A	2.17804124	11.88735887	5.008149756	3.48E-05	0.000729197	2.188764516
VSTM2L	-1.5540711	5.690283897	-5.00718672	3.48E-05	0.000730328	2.186314958
PSMB9	1.1514573	13.68116901	5.001675209	3.54E-05	0.000738776	2.17229581
LOC100129509	1.27118521	4.950714945	4.996246507	3.59E-05	0.000745024	2.158486979
PRLR	-1.3113346	5.560258304	-4.991063485	3.63E-05	0.0007507	2.145302801
PDZRN3	-2.1925137	7.183910968	-4.990642557	3.64E-05	0.0007507	2.144232065
SLC25A18	-1.6977163	4.539307367	-4.989986666	3.64E-05	0.000750842	2.142563639
FBXO22OS	1.87314168	6.785844559	4.986366843	3.68E-05	0.000754398	2.133355622
LOC100128916	1.00033158	6.123366233	4.985211421	3.69E-05	0.000755964	2.130416463
TNFAIP3	1.42509337	10.1185153	4.980782134	3.73E-05	0.00076136	2.119149147
ENST00000382123	1.17392093	5.573408888	4.98068787	3.73E-05	0.00076136	2.118909354
ENST00000372315	1.04093098	5.545219783	4.974106147	3.80E-05	0.00077311	2.102166321
DEPDC6	-1.5532874	10.53761365	-4.96426655	3.90E-05	0.000787749	2.077135078
MNX1	1.06106148	10.28350825	4.957656092	3.97E-05	0.000797346	2.060318174
LILRA4	1.26851133	7.83213369	4.952678462	4.02E-05	0.000802584	2.047654988
IFI44	1.02078028	11.78744956	4.948165472	4.07E-05	0.000810612	2.036173739
ZNF134	-1.1169781	6.652325784	-4.94722326	4.08E-05	0.000811865	2.033776697
PON3	-2.2728975	8.028893862	-4.945434921	4.09E-05	0.00081492	2.029227048
GGT3P	-1.2267857	7.538851565	-4.921276506	4.36E-05	0.00085646	1.967765312
AGRN	1.10648983	10.43467275	4.921184531	4.36E-05	0.00085646	1.967531314
PPP1R2P3	1.11154459	5.953374494	4.897976479	4.64E-05	0.000892277	1.90848635
JAKMIP1	1.25743365	6.91607468	4.895984304	4.66E-05	0.000894558	1.903417938
CCL4	1.61145903	11.40093905	4.892110619	4.71E-05	0.000902143	1.893562676

C12orf53	-1.5651052	4.842886256	-4.892078387	4.71E-05	0.000902143	1.893480674
CXCL1	2.17677979	11.08965792	4.885479531	4.79E-05	0.000913808	1.876692199
HRASLS	-1.2967141	5.582943367	-4.883798498	4.81E-05	0.000917027	1.872415415
ENTPD8	-3.9960155	9.617827517	-4.878310287	4.88E-05	0.000927348	1.858452678
MGAT5B	-1.2434196	5.531125702	-4.878181949	4.88E-05	0.000927348	1.858126172
C15orf53	1.00474127	4.830439787	4.861048961	5.10E-05	0.000958913	1.81453824
MAGI3	-1.0511364	9.901793985	-4.859471604	5.13E-05	0.00096155	1.810525359
IRS2	-1.825997	9.072982691	-4.857601449	5.15E-05	0.000962603	1.805767601
SCN3B	-1.5451932	6.343949138	-4.849599074	5.26E-05	0.000975404	1.785409416
TMEFF2	-1.0119718	5.002516144	-4.833176274	5.49E-05	0.001008636	1.743630827
SCN7A	-1.0992134	4.713460566	-4.826276309	5.59E-05	0.001020193	1.726078364
TTC25	-1.1610772	5.61585264	-4.82547553	5.60E-05	0.001021474	1.724041331
ADAMTS17	-1.3747177	5.959610095	-4.820287837	5.68E-05	0.001031626	1.710844943
SLC4A11	1.40058122	9.572867328	4.820092081	5.68E-05	0.001031626	1.710346986
RP11.431O22.2	1.07117113	13.34129821	4.816200893	5.74E-05	0.001038705	1.700448806
UPK1B	-3.4396524	5.766043932	-4.791638792	6.12E-05	0.001086795	1.637972965
C4orf40	1.82208961	5.05849955	4.788639895	6.17E-05	0.001093689	1.630345512
GNGT2	1.27300427	6.966477226	4.788284385	6.17E-05	0.001093689	1.629441308
RUNX1	1.06166785	8.644693577	4.787466271	6.19E-05	0.001094248	1.627360525
RPL23AP64	1.16727362	5.868275938	4.783875935	6.25E-05	0.001102776	1.618229009
LOC644662	-1.4393503	5.077263341	-4.778855765	6.33E-05	0.001112829	1.605461212
PDE8B	-1.5947123	7.646867929	-4.776951344	6.36E-05	0.001115484	1.600617794
C1QC	1.58471261	10.17617166	4.776577375	6.37E-05	0.001115484	1.599666703
RGS1	1.89488237	12.05028419	4.773863227	6.41E-05	0.001120387	1.592764053
GOLSYN	-1.8521167	8.540001407	-4.772923365	6.43E-05	0.001121157	1.590373812
HYLS1	-1.6740047	7.908867745	-4.767189305	6.52E-05	0.001133531	1.575791346
NUDT16	-1.2260508	9.449273708	-4.765089041	6.56E-05	0.001137064	1.57045023
LASS1	-1.2321578	5.849002822	-4.759462318	6.66E-05	0.001151166	1.556141436
LAP3	1.35762316	12.42701719	4.754296924	6.75E-05	0.001163121	1.543006274
HSPB3	-1.1700039	4.444049306	-4.741702094	6.97E-05	0.00119429	1.510980674
LOC100128219	1.11767093	5.826208201	4.738905351	7.03E-05	0.001199482	1.503869634
SRMS	1.22255157	6.994433451	4.7367972	7.06E-05	0.001203278	1.498509519
DYNC2H1	-1.1387179	6.800457405	-4.725925598	7.27E-05	0.001225497	1.470869152
GUCY2G	1.301634	5.860690402	4.72379635	7.31E-05	0.001231386	1.465455957
FCGR2A	1.35464293	10.20125304	4.720982311	7.36E-05	0.001236647	1.458301963

APOE	2.17832004	15.84921253	4.715287912	7.47E-05	0.001247491	1.443825896
NHS	1.00645276	8.163945465	4.714619815	7.49E-05	0.001247957	1.442127536
LOC340357	1.44740136	5.859160454	4.712469908	7.53E-05	0.001250954	1.43666235
CD226	1.03639961	5.812400314	4.710342761	7.57E-05	0.001256013	1.431255124
SLC22A2	1.08839739	4.925997847	4.709925503	7.58E-05	0.001256425	1.430194463
ANXA2	1.60133906	12.05414554	4.702630169	7.72E-05	0.001278678	1.411650527
ATP2C1	1.06508059	9.932153117	4.701313591	7.75E-05	0.001281137	1.408304062
PF4	-1.8215546	7.379139232	-4.698008994	7.82E-05	0.001289316	1.39990466
SCO2	1.27656226	11.41993747	4.696326667	7.85E-05	0.00129304	1.395628738
LTK	-1.4333172	11.01675728	-4.69508358	7.88E-05	0.001294004	1.392469264
BATF2	1.66199963	10.45885099	4.694884867	7.88E-05	0.001294004	1.391964212
HOXA4	-1.5081971	6.987541893	-4.691587462	7.95E-05	0.001302612	1.383583612
C19orf59	1.49115298	5.879036154	4.690074681	7.98E-05	0.001302612	1.379738856
TBX21	1.05754881	7.783957835	4.690046613	7.98E-05	0.001302612	1.379667522
TFEC	1.70210363	7.340914753	4.687882355	8.03E-05	0.001307062	1.374167134
SLC27A6	-1.479156	4.763533597	-4.687057889	8.05E-05	0.001308903	1.372071811
PRKAB2	-1.3691218	9.176797417	-4.684329171	8.10E-05	0.001314343	1.365137098
APOBEC3H	1.17196842	6.497927367	4.678417352	8.23E-05	0.001327886	1.350113579
LOC729970	-1.1765745	7.730007978	-4.676246908	8.28E-05	0.001333466	1.344598133
DKFZP564C152	-1.9692	10.53780991	-4.675026085	8.30E-05	0.001334737	1.341495882
C21orf88	-1.114129	8.069820551	-4.672432267	8.36E-05	0.001341399	1.334904829
MOCS1	-1.5188569	6.913453791	-4.668855755	8.44E-05	0.001348498	1.325816996
ADAMTS14	1.67207913	7.394007407	4.666186135	8.50E-05	0.001354957	1.319033787
HTRA4	2.3130232	6.81699109	4.664093131	8.54E-05	0.001358245	1.313715839
CCDC122	-1.5543835	6.827910479	-4.661912376	8.59E-05	0.001362542	1.308175065
WTIP	-1.3028594	9.979209004	-4.659372611	8.65E-05	0.001370271	1.301722304
NAP1L5	-1.4234746	7.472773663	-4.657289065	8.70E-05	0.001374752	1.296428799
C9orf122	-2.4247639	6.528704739	-4.652799644	8.80E-05	0.001385949	1.285023309
MMP25	1.05006408	7.591465964	4.646577428	8.94E-05	0.001403602	1.269216615
ENST00000378898	-1.0188509	5.366522745	-4.642487624	9.04E-05	0.001413746	1.258827677
LRRC3B	-1.0329585	4.865004039	-4.642359214	9.04E-05	0.001413746	1.258501497
LOC285972	1.14067935	6.033762911	4.639684253	9.11E-05	0.001421523	1.251706844
ENST00000400419	1.09028678	4.563956443	4.639071992	9.12E-05	0.001422184	1.250151675
ELOVL7	1.13267357	8.418498579	4.63046987	9.33E-05	0.00144418	1.228303206
LILRB4	1.25660768	8.068831158	4.626663612	9.42E-05	0.001453876	1.218636493

TM4SF4	-3.8941436	7.412091187	-4.618445506	9.63E-05	0.001473523	1.197766726
LOC650157	1.14018529	6.142594778	4.611044565	9.82E-05	0.001493031	1.178974135
HIST1H1A	-1.2095593	7.868430967	-4.609982874	9.84E-05	0.001495961	1.176278432
ZP1	-1.0210756	5.864097227	-4.608977591	9.87E-05	0.001496759	1.17372599
IFI44L	1.69446431	10.10049155	4.603142501	0.000100204	0.001510287	1.158911243
HCN4	-1.4139556	4.941562905	-4.579687888	0.000106542	0.001586015	1.099375037
C6orf174	-1.3645946	6.561207701	-4.574664557	0.00010795	0.001602593	1.086626811
ENST00000318291	-1.0528182	8.241878418	-4.574292781	0.000108055	0.001603056	1.085683358
STX19	-2.3524422	8.851666916	-4.565447002	0.000110584	0.001636012	1.063237135
APOL3	1.03403134	8.864397111	4.560710267	0.000111962	0.001648628	1.051218975
VPS37D	-1.1792046	8.816484219	-4.55423975	0.000113872	0.001669966	1.03480336
SOCS3	1.51903337	10.77670741	4.553824953	0.000113995	0.00167065	1.033751085
LOC645722	-1.0111449	8.172179053	-4.550302566	0.00011505	0.00168044	1.024815656
RENBP	1.5034595	6.635963961	4.538638432	0.000118612	0.001718609	0.995230529
C4BPA	2.55890109	6.887033726	4.533925012	0.000120083	0.001730685	0.983277061
ENST00000373544	1.51811724	9.755695925	4.53285163	0.00012042	0.001734398	0.98055505
PRAM1	1.29755602	8.683576358	4.531023149	0.000120997	0.001741553	0.975918296
LDHB	-1.4060025	13.57426297	-4.530255102	0.00012124	0.001742745	0.973970691
FAM110A	1.04021635	12.46653762	4.527294899	0.000122182	0.001750443	0.966464493
LOC400743	1.03271968	5.335440866	4.526432622	0.000122457	0.001752133	0.964278092
SOX9	1.09729281	8.582990986	4.524650483	0.000123029	0.001758753	0.959759385
NCF2	1.56545512	8.772211622	4.523435306	0.000123421	0.00176127	0.956678327
PRUNE2	-1.2011337	6.456685689	-4.523224486	0.000123489	0.00176127	0.956143803
ZNF75A	-1.1348743	9.567795647	-4.522848926	0.00012361	0.001761664	0.955191597
GOLT1A	-2.4764525	7.108791199	-4.521909525	0.000123914	0.001762549	0.952809838
FLJ35024	-1.1403691	4.618039906	-4.514927223	0.000126196	0.001787968	0.935108217
GNA15	1.26263922	7.758037267	4.511784023	0.000127237	0.001798665	0.927140309
EMR2	1.63203351	8.17824511	4.506032662	0.000129164	0.001819344	0.912562052
HEBP1	-1.2529432	11.85407119	-4.504783996	0.000129586	0.001824109	0.909397216
VRK2	1.14386308	9.011899578	4.503116397	0.000130152	0.001829702	0.905170683
SLC6A10P	-1.2740595	8.577745483	-4.490741508	0.00013443	0.001874084	0.873810907
TUB	-1.2532658	4.996817277	-4.487724701	0.000135494	0.001887706	0.866167074
CCR1	1.35323944	9.134493001	4.486729237	0.000135847	0.001890103	0.863644922
LEPREL2	-1.306547	11.8123058	-4.480762188	0.000137981	0.001910118	0.84852764
DDRGK1	1.0191924	10.1945318	4.479707338	0.000138362	0.001912214	0.845855416

PPAP2B	-1.3902836	11.19381778	-4.476831538	0.000139406	0.00192127	0.838570529
GCNT2	-1.0182732	5.801560041	-4.467010304	0.000143029	0.001959089	0.813695067
DKK1	3.51954415	7.841748063	4.466357513	0.000143273	0.001960894	0.81204185
LOC646993	1.31017075	6.781828628	4.465928041	0.000143434	0.00196186	0.810954211
ENST00000382794	-1.1361979	4.612315161	-4.462988989	0.00014454	0.00196909	0.803511316
KCNB1	-1.3904713	4.957233899	-4.461069416	0.000145266	0.001973415	0.798650425
TMEM63C	-1.2459848	7.379563392	-4.459890916	0.000145714	0.001976874	0.795666239
ISG15	1.36680265	13.43695642	4.45753416	0.000146614	0.00198338	0.789698718
CD84	1.37049488	7.389630621	4.457361715	0.00014668	0.00198338	0.789262084
F11	-1.2050819	5.645409346	-4.457202116	0.000146741	0.00198338	0.788857977
TTC14	-1.3348411	8.218729937	-4.456235456	0.000147112	0.001985983	0.786410415
BMPR1B	-1.3147873	4.431901303	-4.451868763	0.0001488	0.002000304	0.77535471
APOA1	-3.7450608	6.812624226	-4.450955419	0.000149155	0.002000481	0.77304242
TPPP2	-1.0551811	5.066916993	-4.449386385	0.000149768	0.00200558	0.769070248
LNX1	-1.452355	8.220495537	-4.44723932	0.00015061	0.002014377	0.763634964
ENST00000400702	1.49086833	6.719521584	4.446626975	0.000150851	0.002016361	0.762084863
RBBP8	1.05638455	9.890627096	4.443150977	0.000152227	0.002029208	0.753286083
KRTAP23.1	1.16777553	6.020346151	4.437411305	0.000154526	0.002052858	0.738758831
STX11	1.0783567	7.124217139	4.434352873	0.000155766	0.002065534	0.731018663
S1PR3	-1.4899359	9.59352918	-4.431588651	0.000156894	0.00207923	0.724023554
LILRB3	1.25620713	9.581654797	4.430964104	0.00015715	0.002081355	0.722443145
GRIN3A	1.5602421	7.447692515	4.429412292	0.000157788	0.002085039	0.718516408
PRKCQ	1.28655726	7.230139213	4.427150613	0.000158723	0.002094528	0.712793672
MAGED1	-1.505719	11.27871252	-4.421266672	0.000161181	0.002116678	0.697906974
ACOX2	-1.6328892	8.120562338	-4.418490143	0.000162354	0.002125658	0.690882944
C6orf186	-1.1392465	4.44751786	-4.40552632	0.000167943	0.002186981	0.658093626
ADRA1B	-1.1013982	6.157860175	-4.399963928	0.000170399	0.002207582	0.644027993
LCP2	1.14056173	10.57086547	4.398844744	0.000170898	0.00220984	0.641198152
FCER1G	1.00579423	11.86674388	4.398321048	0.000171132	0.002211284	0.639874023
TTTY13	1.02917957	5.583283903	4.393921734	0.000173108	0.002225677	0.628751363
ENHO	-1.1007038	7.244905034	-4.3923783	0.000173807	0.00222863	0.624849445
ENST00000421344	1.04634793	7.430049152	4.388751283	0.000175461	0.002244533	0.615680692
CXCL3	2.56578947	10.07953866	4.388318311	0.000175659	0.002245749	0.61458624
KRBA1	-1.3080444	10.37728708	-4.384563197	0.000177389	0.002261218	0.605094703
LOC100129555	-1.4678081	6.434357034	-4.382346435	0.000178418	0.002271674	0.599491994

GHSR	1.19355574	7.08918392	4.381195097	0.000178955	0.002275844	0.596582202
MXRA7	-1.1528763	8.705655381	-4.377579097	0.000180652	0.002292058	0.587444017
KRTAP13.2	1.12682897	4.93443682	4.376176157	0.000181315	0.002296444	0.583898813
HSPB2	-1.6767632	9.105242416	-4.371796952	0.000183399	0.00231609	0.572833511
CSRP2	-1.5240482	11.5995105	-4.369069153	0.000184709	0.002328576	0.565941625
RNF213	1.20071199	8.331836952	4.359131655	0.000189561	0.002375204	0.540838568
NELL1	-1.165221	5.500134366	-4.356809294	0.000190713	0.002384901	0.53497307
C3orf55	-2.4645906	6.216140013	-4.348470324	0.000194908	0.002427576	0.513914849
PSAT1	1.61118861	11.13678835	4.346853283	0.000195731	0.002430677	0.509831955
MYO1F	1.10350332	11.06859445	4.340147279	0.000199185	0.002465282	0.492901886
PRSS8	-1.0914089	15.06131886	-4.338317623	0.000200138	0.002471479	0.488283288
LAIR1	1.12810199	9.701580345	4.330916139	0.000204039	0.00250825	0.469602277
CTLA4	1.72714598	7.656729344	4.329444784	0.000204824	0.002515048	0.465889134
PSD3	-1.2204681	7.891031364	-4.327108954	0.000206075	0.002521372	0.459994718
ZNF347	-1.1025569	6.994705649	-4.327047261	0.000206108	0.002521372	0.459839043
TNFRSF4	1.13966534	8.543205581	4.326968216	0.000206151	0.002521372	0.459639582
ENST00000344149	-1.0757546	5.298524412	-4.321834505	0.000208929	0.002544139	0.446686289
ENTPD5	-1.1981067	7.48433612	-4.321190059	0.00020928	0.002545327	0.445060378
FAM47E	-1.3024602	7.757275839	-4.314718041	0.000212842	0.002579981	0.428733502
HECW2	1.37816417	7.809718147	4.312578932	0.000214032	0.002590076	0.423337913
MBIP	-1.0390325	9.62140168	-4.303675523	0.000219058	0.00263476	0.400884234
FAH	-1.4076098	8.619717737	-4.299613832	0.00022139	0.002654015	0.390643065
SYCE2	1.17986212	5.810480278	4.299398788	0.000221514	0.002654015	0.390100889
APOL4	1.00634834	7.849214495	4.292558214	0.000225499	0.002695814	0.372856145
IGSF9	-1.1039711	12.06557506	-4.289001815	0.000227598	0.002708995	0.36389214
SAMSN1	1.21523761	9.219920989	4.284939949	0.00023002	0.002727593	0.353655357
MUC16	1.02719082	4.882674717	4.28469893	0.000230165	0.002727593	0.353047981
FOXD4	1.22071104	6.605080488	4.283772569	0.000230721	0.00272972	0.350713559
A2LD1	-1.5068034	8.40338649	-4.28234907	0.000231579	0.002737606	0.347126492
HSD17B12	-1.6071341	11.51924029	-4.282247899	0.00023164	0.002737606	0.346871558
C6orf225	-1.3984908	6.490335461	-4.278389702	0.00023398	0.002761897	0.337150189
CHST4	2.02594279	7.375910937	4.275875168	0.000235518	0.00277439	0.330815071
IL9R	1.18260482	6.875698139	4.275195589	0.000235935	0.002776989	0.329103028
CCL20	2.64771099	10.57528375	4.26729054	0.000240845	0.002818804	0.309190963
PRO0628	1.13552455	8.230527551	4.26550673	0.000241966	0.002828886	0.304698448

OLFML2B	1.02465915	7.714790338	4.263206689	0.000243421	0.0028413	0.298906214
PLAG1	-1.572929	8.104522073	-4.262057974	0.00024415	0.002845231	0.296013553
SCAMP5	-1.0891273	9.394913488	-4.255789654	0.000248169	0.002878175	0.280230858
TUBB4	1.15030825	5.835311154	4.253990457	0.000249334	0.00289015	0.275701379
CHRNA1	1.2577965	4.910660489	4.252085213	0.000250575	0.002900139	0.270905235
TRIM2	-1.2980687	10.28091188	-4.250366498	0.000251699	0.002910316	0.266578922
ZNF512B	-1.3002159	9.061241628	-4.250297936	0.000251744	0.002910316	0.266406343
KCNMB4	-1.3568532	7.985948623	-4.248628652	0.00025284	0.002918337	0.262204714
SCG5	-2.3276932	8.059215718	-4.245512381	0.0002549	0.002934323	0.25436164
SIGLECP3	-1.0383083	6.391938581	-4.242306313	0.000257037	0.002955568	0.246293465
C1QTNF4	1.71501412	7.037743637	4.234285465	0.000262461	0.003007025	0.226112761
FDXR	1.1241727	12.86244703	4.23389208	0.00026273	0.00300852	0.225123142
DUSP5P	1.6938745	5.516680696	4.232305298	0.000263817	0.00301462	0.221131493
KLHDC7B	1.36544737	8.015641143	4.23154558	0.00026434	0.003017671	0.219220454
DSEL	-1.1221159	5.777955086	-4.231512974	0.000264362	0.003017671	0.219138437
CTSS	1.37529272	9.159636448	4.227062813	0.000267442	0.003041091	0.207945321
RAMP1	-2.1354577	11.56063566	-4.226671371	0.000267715	0.003041565	0.206960848
KRTAP12.2	1.02697966	6.901597298	4.22317109	0.000270165	0.003059804	0.198158286
C5AR1	1.27802157	7.763748592	4.222181321	0.000270862	0.003066099	0.195669404
GGTLC2	-1.2370949	8.745605037	-4.2171777	0.000274412	0.003096609	0.183088643
PYROXD2	-1.287878	7.764440381	-4.216702065	0.000274752	0.003098122	0.181892861
CCDC21	1.94896055	7.862430269	4.214977125	0.000275988	0.003107898	0.177556408
GBP2	1.04206282	11.20844835	4.214664826	0.000276212	0.003107898	0.176771325
RBM24	-1.2336342	4.016175242	-4.211961978	0.000278162	0.003117878	0.169977076
HOXA5	-1.0183692	7.972522823	-4.203714856	0.000284195	0.003166156	0.14925024
TYROBP	1.25445578	13.68251582	4.202547744	0.000285059	0.003172284	0.146317553
PEG10	-1.0269622	5.087216928	-4.200454085	0.000286616	0.003181463	0.141056989
VANGL2	-1.0943173	5.608424728	-4.19765989	0.000288707	0.003199769	0.134036902
C15orf26	1.35456809	4.931388155	4.19578947	0.000290115	0.003210463	0.129338112
PTK7	-1.2193198	7.25354591	-4.194960411	0.000290741	0.003213065	0.127255492
OAS2	1.16136664	9.440748243	4.186207474	0.000297435	0.003263229	0.105271954
TLR8	1.59826187	6.431881587	4.18295383	0.000299962	0.003285979	0.097102141
CRTAC1	-1.246435	5.432697052	-4.18074126	0.000301693	0.00329663	0.091547033
C2orf84	-1.1655026	5.377226317	-4.17977752	0.00030245	0.003303241	0.08912752
LOC100131544	1.44350342	6.868173052	4.178644048	0.000303343	0.003311326	0.086282005

C1QA	1.51530224	11.47784328	4.177746389	0.000304052	0.003315733	0.084028575
CEP78	1.03750096	9.021589313	4.176768897	0.000304825	0.003322503	0.081574828
hCG_1776018	-1.7066965	5.569605305	-4.176149146	0.000305317	0.003324526	0.080019149
NOL3	-1.0067389	10.94401615	-4.175637305	0.000305723	0.003327286	0.07873437
PRKAG2	-1.1377043	9.952641138	-4.170815425	0.00030958	0.003357489	0.066632205
NFATC4	-1.0741235	6.498914677	-4.169531503	0.000310615	0.003367033	0.063410156
EPOR	-1.1271944	6.953693564	-4.167268931	0.000312447	0.00338015	0.057732554
VPS13D	-1.1903701	7.153058886	-4.16660258	0.000312989	0.003380961	0.056060539
MPHOSPH6	1.03082533	8.293414182	4.165367499	0.000313995	0.003390147	0.052961582
PLOD2	-1.2603699	9.767785291	-4.16491519	0.000314364	0.0033909	0.051826726
GBE1	-1.1437622	9.640768729	-4.155032709	0.000322543	0.003458383	0.02703654
MCOLN3	-1.0065838	4.883349302	-4.150620728	0.000326262	0.003486618	0.015972345
CLDN16	1.00993759	5.323187893	4.148402885	0.000328147	0.003501201	0.010411289
TMEM151B	-1.0959728	7.852321291	-4.145038787	0.000331028	0.003518199	0.001977076
NKX2.2	-1.0531592	4.411676961	-4.141536061	0.000334053	0.003543346	-0.006803428
PXMP4	-1.0835555	8.781413717	-4.138891277	0.000336356	0.003562556	-0.013432418
RHBDF2	1.07779371	11.72950772	4.138483484	0.000336713	0.00356298	-0.014454462
SPRR2C	1.66889091	6.771988459	4.136632078	0.000338336	0.003571339	-0.019094376
CDH16	2.94628917	6.95209617	4.13431281	0.00034038	0.003583005	-0.024906312
MAPK10	-1.1159228	5.638407981	-4.133681412	0.000340938	0.00358662	-0.026488453
KRTAP4.2	1.8099639	6.456383428	4.132325291	0.000342141	0.003597532	-0.029886447
P2RX7	1.38238627	6.760309993	4.131369386	0.000342992	0.003602988	-0.032281513
C1QB	1.58869764	13.87728887	4.125034089	0.000348681	0.0036504	-0.04815241
TNFRSF9	1.67659382	6.868158597	4.121815335	0.000351607	0.003670427	-0.056214224
C1orf194	-1.3195876	5.659995858	-4.120972358	0.000352377	0.003674938	-0.058325388
MYEF2	-1.3598657	5.849374224	-4.117454469	0.00035561	0.00370155	-0.067134808
C4BPB	-2.2813273	7.914648894	-4.114122576	0.000358699	0.003717679	-0.075477209
ENST00000424686	1.33480326	13.82658109	4.111841339	0.00036083	0.003732638	-0.08118827
KLK12	-2.187081	6.107877312	-4.108052501	0.000364395	0.00375879	-0.090672325
GALNT14	-1.9466049	7.660154998	-4.105593234	0.000366729	0.003781062	-0.096827402
ENST00000329043	1.46649777	5.870438025	4.104595123	0.00036768	0.003787275	-0.099325291
DEPDC7	-1.4771583	6.252303811	-4.098340462	0.000373696	0.003832223	-0.114975761
LAMC2	1.74194369	10.36671388	4.092762449	0.000379143	0.003877785	-0.12892939
CDH10	-1.259683	4.962738143	-4.090041326	0.000381829	0.003890607	-0.135735106
RTN4RL1	-1.2746465	6.607071115	-4.089679302	0.000382187	0.003890614	-0.136640487

C2CD4A	1.75869473	8.098328159	4.088223385	0.000383633	0.003903506	-0.140281429
KLHDC9	-1.1172523	9.065410469	-4.085717622	0.000386135	0.003923668	-0.146547244
MIPOL1	-1.5300677	6.200787523	-4.083960976	0.000387898	0.003937683	-0.150939411
PNPLA1	-1.4488448	4.816730019	-4.079795612	0.000392111	0.003973027	-0.161352714
OPALIN	1.25635322	5.068551813	4.065220009	0.000407212	0.004091702	-0.197775388
PTCRA	1.41187469	6.885028156	4.063541159	0.000408988	0.004107647	-0.201969022
C10orf116	-3.1390927	12.61080206	-4.062681905	0.0004099	0.004114904	-0.20411524
IFIT3	1.15291454	10.67509488	4.058425965	0.000414446	0.004147135	-0.214744302
JAG1	1.38554585	10.34243303	4.052719648	0.00042062	0.004191545	-0.228992216
GNLY	1.6146318	9.403897006	4.049109557	0.000424573	0.00422319	-0.238004105
ENST00000380640	1.12813273	5.349789184	4.048235748	0.000425535	0.00422889	-0.240185159
MAPRE3	-1.0227484	5.536131052	-4.035356194	0.000439971	0.004346513	-0.272322109
SLC7A4	-1.7820584	6.29132867	-4.034053284	0.000441458	0.004357242	-0.275571981
LOC388948	1.03840279	6.378587232	4.029940483	0.000446184	0.004391926	-0.285829227
SLC15A3	1.08038757	11.49974311	4.027883441	0.000448567	0.004411384	-0.290958658
VASH1	1.04308939	11.04749936	4.027453717	0.000449067	0.004414297	-0.292030149
NAP1L2	-1.2714183	5.175342992	-4.026512602	0.000450162	0.004421067	-0.294376681
VEPH1	-1.1539596	6.295048217	-4.025123837	0.000451783	0.004432985	-0.297839163
C10orf58	-1.4222381	9.576939813	-4.024559629	0.000452444	0.004437461	-0.299245781
OR10P1	1.03533738	5.912141391	4.021006811	0.000456624	0.004469759	-0.308102339
HRH3	1.13283127	6.790423886	4.014515731	0.00046436	0.004535914	-0.324279343
BMP4	-1.6430131	7.654617612	-4.012153786	0.000467207	0.004555534	-0.330164426
A_33_P3327300	1.16009681	5.478584954	4.011524449	0.000467969	0.004560913	-0.331732379
MACC1	1.00294538	8.634373168	4.008267847	0.000471929	0.004591273	-0.339845179
CNR1	-2.0128191	6.178409966	-4.006638281	0.000473923	0.004606547	-0.343904218
CD68	1.11707256	11.56706587	4.004360814	0.000476724	0.004631699	-0.349576521
CD74	1.25778183	11.24081861	3.997924789	0.000484727	0.004682245	-0.365602573
CLCF1	1.16453793	7.495321505	3.995178935	0.000488182	0.004707121	-0.372438256
LOC339751	2.3469019	6.47235571	3.995037815	0.00048836	0.004707121	-0.372789541
SGCG	-1.1746692	4.73769451	-3.993612058	0.000490164	0.00472094	-0.376338484
LOC100130905	1.54163769	7.458460623	3.986895176	0.000498752	0.004787478	-0.393054305
PACSIN1	-1.7833718	7.977142449	-3.98397613	0.00050253	0.004806433	-0.400316864
LRTM2	-1.0193914	4.223000216	-3.982653127	0.000504252	0.004814541	-0.403608109
GRK4	-1.0062463	5.65718344	-3.98213784	0.000504924	0.00481739	-0.40488993
SIGLEC7	1.02759834	6.429800192	3.978441769	0.000509771	0.004855111	-0.414083185

LOC646548	-1.0411597	4.936472348	-3.974964823	0.000514373	0.004892572	-0.422729739
NOV	-1.5800706	7.810647835	-3.974855053	0.000514519	0.004892572	-0.423002691
CCDC148	1.06463984	5.277359057	3.974264546	0.000515304	0.00489562	-0.424471007
FAM26F	1.6532043	10.65246034	3.974210982	0.000515376	0.00489562	-0.424604193
A_33_P3226439	-1.1078335	8.292705655	-3.968992705	0.000522373	0.004940965	-0.437577539
WNK2	-1.4491184	7.949028633	-3.968955508	0.000522423	0.004940965	-0.437670002
TSPAN7	-1.8586788	7.44491944	-3.963048491	0.000530457	0.005001715	-0.452351155
SMTNL2	-1.0244375	4.353753592	-3.954976696	0.000541633	0.005085031	-0.472404862
SLMO1	1.20742212	7.914834501	3.95425423	0.000542644	0.005090602	-0.474199333
A_33_P3364869	1.09523108	10.10932566	3.954051384	0.000542929	0.005090602	-0.474703151
PTPN13	-1.3922154	7.540168795	-3.953602004	0.000543559	0.005092118	-0.475819276
KCNH6	-1.0813876	5.360236361	-3.950857436	0.000547425	0.005117307	-0.482635356
NCRNA00164	1.23436328	6.907141339	3.950204125	0.000548349	0.005119549	-0.484257688
HCK	1.15399681	8.385398837	3.950188411	0.000548372	0.005119549	-0.484296707
ENST00000342354	1.12122367	5.249606401	3.948432354	0.000550864	0.005136197	-0.488657128
FOXF2	-1.3341974	7.3792076	-3.94446723	0.000556532	0.005169816	-0.49850124
ZNF256	-1.0413882	7.5628118	-3.944412722	0.00055661	0.005169816	-0.498636551
PCDH7	1.73101347	8.78417074	3.942845779	0.000558866	0.005176842	-0.502526141
GPR4	1.05212684	7.749435919	3.94282384	0.000558898	0.005176842	-0.502580597
GPM6B	-1.2734482	6.1187314	-3.940234131	0.000562647	0.005201432	-0.509008214
BDH1	-1.9868415	10.39234775	-3.939396289	0.000563865	0.005203839	-0.51108752
ADAMDEC1	2.09535466	7.679347866	3.938271453	0.000565504	0.005216754	-0.513878919
PLA2G2A	3.8809909	9.155415137	3.935133505	0.000570103	0.005245537	-0.521665115
ME1	-1.8196574	7.944717949	-3.933513294	0.000572491	0.005261111	-0.525684803
NEFM	-1.050037	4.830362869	-3.932804144	0.00057354	0.00526852	-0.527444061
HAND1	1.03652942	4.69093792	3.931487578	0.000575492	0.005282972	-0.530710006
SLC46A1	-1.7501532	8.100640694	-3.924989377	0.000585222	0.005355455	-0.546826168
FAM115C	1.19028897	6.76908884	3.923864887	0.000586922	0.005366494	-0.549614394
MAPK4	-1.0146022	4.680765407	-3.916881995	0.000597588	0.005434303	-0.566924727
DNAH14	-1.2546031	6.236324091	-3.914789401	0.000600822	0.005450026	-0.572110812
AGTR1	-1.4347169	4.662890187	-3.914529452	0.000601225	0.005451405	-0.572755001
TRIMP1	1.19544443	6.546530358	3.907382005	0.000612407	0.005529727	-0.590463458
ATP6V0D2	1.33005346	5.494232025	3.905506583	0.000615375	0.00554898	-0.595108747
FLJ31183	-1.251826	5.353514968	-3.905389592	0.00061556	0.00554898	-0.595398508
C2orf61	1.11618253	5.66203377	3.90512312	0.000615983	0.005550491	-0.596058493

ProSAPiP1	-1.515859	8.388236043	-3.900980865	0.000622595	0.005584601	-0.606316492
ZBED2	1.56352553	6.795106758	3.899782026	0.000624522	0.005594955	-0.609284858
HMGA2	1.0152836	7.548397179	3.897313534	0.000628507	0.005621392	-0.615396253
HLA.DMB	1.21353417	13.88089179	3.892155476	0.000636916	0.005675581	-0.628163433
BHLHE40	1.18178638	9.722447411	3.890409174	0.000639788	0.005696502	-0.632484961
C16orf90	1.06678077	6.063664368	3.888629422	0.000642728	0.005715655	-0.636888797
TSPAN5	-1.4348023	9.025819608	-3.881921005	0.00065393	0.005789216	-0.653483869
SLC44A4	-2.8237325	10.607906	-3.881744311	0.000654228	0.005789492	-0.653920875
SOD3	-1.5013837	13.24033568	-3.880395261	0.000656505	0.005804914	-0.657257255
DAG1	1.03385602	10.4613658	3.879760238	0.000657579	0.005809687	-0.658827653
LRRC25	1.07206716	8.226920781	3.876921518	0.000662404	0.005835703	-0.665846998
IL27	1.01477559	6.84586925	3.869744866	0.000674756	0.005925309	-0.68358731
C17orf66	1.29582524	5.337983035	3.864687803	0.000683595	0.005983593	-0.696083342
AOX1	-1.7131387	6.803556989	-3.861533043	0.000689168	0.006022665	-0.703876761
PLCXD1	-1.0281639	9.075800869	-3.860178141	0.000691574	0.006034462	-0.707223394
RAB31	1.06439307	10.58128851	3.857507534	0.000696343	0.006063425	-0.713819001
LPA	1.14619792	5.782960142	3.855601961	0.000699765	0.006083474	-0.718524519
OR4N4	-1.0576067	5.296983842	-3.853976353	0.000702697	0.006099109	-0.722538256
FGF14	-1.2448954	5.070952576	-3.852034961	0.000706215	0.006117526	-0.727331141
TCEAL7	-1.3145267	6.163104829	-3.847521724	0.00071446	0.006161023	-0.738471067
CKLF	1.12618202	10.28558	3.847215465	0.000715023	0.006161897	-0.739226882
PCDHA5	1.55602378	6.418658621	3.842671073	0.000723427	0.006213918	-0.750440226
GPR113	1.05947642	5.323320488	3.842560561	0.000723632	0.006213918	-0.750712873
ENST00000304890	1.1696689	6.033252322	3.842164202	0.00072437	0.006217035	-0.751690732
SSBP2	-1.0504963	8.791165628	-3.840866558	0.000726791	0.006225169	-0.754891975
XAGE1D	-1.1826521	4.744540303	-3.840629476	0.000727234	0.006225169	-0.755476819
LOC731223	1.02924875	7.160892249	3.840278168	0.000727891	0.006225889	-0.756343424
NAT8B	-1.6199104	7.067054563	-3.834610428	0.000738573	0.006294086	-0.770321854
VIPR1	-1.9275946	7.174412767	-3.834407521	0.000738958	0.006294086	-0.77082219
SLC1A7	-1.7689708	7.668422967	-3.833971495	0.000739787	0.006294424	-0.771897339
PTPN21	-1.0337221	8.518856211	-3.832464728	0.000742657	0.006301398	-0.775612477
SGCE	-1.6085143	9.503169772	-3.827690385	0.000751825	0.006355565	-0.787381842
FAM174A	-1.4511147	8.765730219	-3.825500506	0.000756067	0.006380334	-0.792778937
TMEM150C	-1.2351031	6.298618354	-3.822681623	0.000761562	0.006420396	-0.799725101
C9orf98	1.42108695	7.962427401	3.812245946	0.000782248	0.006554118	-0.825428905

KHNYN	-1.0809999	11.46793492	-3.811616336	0.000783514	0.006558938	-0.826979106
LONRF3	-1.1829307	7.813013722	-3.811539222	0.000783669	0.006558938	-0.827168966
LOC100293193	1.41660058	9.152202656	3.80909018	0.000788612	0.006592188	-0.833198243
HPDL	1.941191	10.67361866	3.808165876	0.000790485	0.00660277	-0.835473519
CYBB	1.12258977	11.13862669	3.805948828	0.000794997	0.006629146	-0.840930452
ALDOC	-1.582635	7.873323478	-3.803778479	0.000799438	0.006639826	-0.846271648
CACNA1A	-1.1045376	7.645434927	-3.802170352	0.000802744	0.006648292	-0.850228718
IGSF10	-1.3069482	4.917585602	-3.79945915	0.000808349	0.006687726	-0.856899113
SLC16A10	-1.4733973	5.858949183	-3.798256039	0.000810848	0.006703301	-0.859858742
FBXO27	-1.1439829	5.885054283	-3.789144846	0.000830024	0.006815168	-0.882264178
THY1	1.52818666	12.00082196	3.781471548	0.000846519	0.006896297	-0.901122738
HRCT1	-1.5502048	6.958257878	-3.781448682	0.000846569	0.006896297	-0.901178922
PCNX	1.09943792	10.18251287	3.779345565	0.000851146	0.006926305	-0.906345957
SIGLEC1	1.26447105	6.86823207	3.778220501	0.000853604	0.006930231	-0.909109755
HLA.DRA	1.23012718	14.34206922	3.776038824	0.000858391	0.006953513	-0.914468577
SPRR1B	1.71914855	6.20193236	3.77545264	0.000859682	0.006961374	-0.915908272
CIDEC	-1.9639119	9.114733131	-3.77520245	0.000860233	0.006961928	-0.916522731
MRAP	-1.3357467	4.930153101	-3.772119221	0.000867058	0.007002179	-0.924094177
HS3ST2	1.96029977	6.189815772	3.766978546	0.000878555	0.007073504	-0.936714399
CRYBG3	-1.0251863	9.235303374	-3.766898069	0.000878737	0.007073504	-0.936911932
F2R	1.21528758	8.148148057	3.765288296	0.000882368	0.007094854	-0.940862915
TMEM217	1.02178024	6.105870077	3.761291821	0.000891448	0.007154629	-0.950669798
LOC100131733	1.02590201	11.18813022	3.760659912	0.000892892	0.00716093	-0.952220172
DHCR24	-1.2007748	11.60723675	-3.759626479	0.000895259	0.007172801	-0.954755526
TAP2	1.12708141	9.217988787	3.759581227	0.000895363	0.007172801	-0.954866542
NGFRAP1	-1.5932743	12.51944088	-3.758749546	0.000897272	0.007185448	-0.956906787
PRKAB1	-1.0302907	8.880493683	-3.755524984	0.000904712	0.007229049	-0.964816003
ROR2	-1.0830944	6.499230279	-3.755224161	0.000905409	0.007229304	-0.965553769
ZMYND12	-1.0676693	7.386163283	-3.752231287	0.000912374	0.007260707	-0.972892898
JAK2	1.20411902	9.93634792	3.751429934	0.000914248	0.007265181	-0.974857708
FAM110C	-1.6157056	7.53566753	-3.743674896	0.000932578	0.007370419	-0.993866117
CCDC85A	-1.5963058	5.535536512	-3.741431249	0.000937948	0.007402093	-0.99936353
HMOX1	1.18405299	12.10307602	3.7408561	0.00093933	0.007410304	-1.000772621
PVALB	-1.0793151	6.22597753	-3.740252702	0.000940781	0.007419062	-1.00225086
PAQR5	-2.2212742	7.816706411	-3.738213953	0.000945701	0.007449755	-1.007245012

SLC16A6	1.05713831	6.511233969	3.731893962	0.000961115	0.007543834	-1.022721807
C7orf29	1.05347735	10.36081035	3.722000939	0.000985739	0.007700953	-1.046933916
C3orf43	1.19597554	5.669343834	3.71928437	0.000992608	0.007743483	-1.053579296
NPDC1	-1.6092411	13.21153032	-3.717083625	0.000998207	0.007775998	-1.058961853
RASSF4	1.05423267	10.36240451	3.716373086	0.001000021	0.007784551	-1.060699489
ABAT	-1.1018624	9.933431437	-3.708420088	0.001020551	0.007913185	-1.080142341
SRPK3	-1.0792009	6.524410381	-3.706013662	0.001026844	0.007952726	-1.086023063
LOC100133920	1.0385383	5.163139808	3.705925003	0.001027077	0.007952726	-1.086239703
PLXDC2	1.21137198	8.734242993	3.705216927	0.001028936	0.007960639	-1.087969853
LOC100130274	1.08264693	6.969638039	3.705103038	0.001029235	0.007960639	-1.088248126
DYSF	1.16030581	7.708262912	3.704857155	0.001029882	0.007962807	-1.088848903
CLEC4A	1.11946724	8.71715021	3.703532943	0.001033371	0.007981266	-1.09208421
SYPL2	-1.111628	5.786965781	-3.70256961	0.001035916	0.007995244	-1.094437614
FAM117A	-1.2107346	10.56131877	-3.701749964	0.001038087	0.008006311	-1.096439855
FYB	1.21379893	9.992919699	3.69783915	0.001048506	0.008069483	-1.105991512
IDO2	1.39131457	5.775853616	3.696636119	0.001051731	0.008084027	-1.10892918
TBCEL	-1.0454327	7.934379768	-3.688562585	0.00107363	0.008196008	-1.128636785
TMEM132C	-1.3054683	4.880498384	-3.685985412	0.001080714	0.008229933	-1.134925098
CDCA7L	-1.042332	8.511408637	-3.68387444	0.00108655	0.008257021	-1.140074933
KRT6A	1.45961219	5.379500544	3.670526828	0.001124175	0.008504288	-1.172617402
ZIM2	1.0020294	5.516586171	3.66916362	0.001128089	0.008527958	-1.175939071
NR2E1	-1.0378788	4.835760344	-3.662683534	0.001146876	0.008645922	-1.191723867
PRKD1	-1.1366348	6.051601851	-3.662520627	0.001147352	0.008646513	-1.192120584
MYOM2	-1.2360865	6.983232526	-3.661070458	0.0011516	0.008666504	-1.195651874
SLC16A9	-1.7971885	6.699465901	-3.658688278	0.001158611	0.008713233	-1.201451797
HLA.DPA1	1.28814459	14.91883863	3.656401362	0.001165381	0.008752034	-1.207018733
LY6K	-1.7060908	6.494856414	-3.649287476	0.001186689	0.008875255	-1.224329151
MEP1B	-2.5627738	5.575691243	-3.647275244	0.001192785	0.008917778	-1.229223756
CHIT1	1.11131097	8.921037761	3.645875234	0.001197044	0.008936552	-1.232628701
TM6SF2	-1.4946508	6.953264176	-3.641780283	0.001209588	0.009000061	-1.242585738
PHGR1	-4.2132998	13.75845205	-3.636704417	0.001225315	0.009085974	-1.254923256
ZDBF2	-1.5518401	6.199460901	-3.631862671	0.001240502	0.009182929	-1.266686897
NTS	-1.648361	5.250508566	-3.628919187	0.001249826	0.009236215	-1.273836156
FMO1	1.43384619	6.93233298	3.627652624	0.001253858	0.00925029	-1.276911899
OR6K2	1.38491766	6.418587607	3.622115584	0.001271638	0.009333932	-1.290354315

LOC642666	1.89043732	5.60632323	3.614896212	0.00129519	0.009471137	-1.307871582
PLP1	-1.4012738	5.743695019	-3.612961644	0.001301573	0.009502312	-1.312563849
TOM1L1	-1.098412	10.28967019	-3.611885913	0.001305135	0.009520477	-1.315172687
SCGB1D2	-1.1734048	4.562290111	-3.611813682	0.001305375	0.009520477	-1.315347852
DAPK2	-1.2506035	8.930777141	-3.61156196	0.00130621	0.009523372	-1.315958284
F8	1.5181314	7.087376941	3.611010981	0.00130804	0.009533516	-1.317294376
MMAB	-1.2037863	7.139212012	-3.610719268	0.00130901	0.0095342	-1.318001738
HEYL	1.43706451	8.539297526	3.607123781	0.001321022	0.009597199	-1.326718831
LOC100134937	-1.1450754	7.279146956	-3.60516643	0.001327606	0.00963734	-1.331463214
C11orf53	-2.0448545	7.771513112	-3.60073963	0.001342616	0.009725766	-1.34219031
CBX6	-1.1920917	11.63439669	-3.600388124	0.001343815	0.009725766	-1.343041912
SULT1A2	-1.233947	11.70119509	-3.599821398	0.00134575	0.009730052	-1.344414876
LOC389332	-2.8008394	6.884432191	-3.59839257	0.001350641	0.009758829	-1.347876091
TIGIT	1.27685937	7.428615508	3.596872606	0.001355863	0.009781146	-1.351557607
G0S2	-1.889152	11.4478232	-3.596249639	0.001358009	0.009789379	-1.353066362
KRTAP10.9	1.01318652	6.944900103	3.594127931	0.001365343	0.009826874	-1.358204282
CCL18	2.38013803	12.43819871	3.593275938	0.001368299	0.00983745	-1.360267197
MGC13005	1.56526181	7.381980102	3.589161059	0.001382663	0.009911213	-1.370228341
CGREF1	-2.3819307	7.231196691	-3.586555767	0.001391833	0.009963803	-1.376533288
TMPRSS4	1.82434519	10.44591486	3.585476241	0.001395651	0.00998784	-1.379145378

Supplementary table 2. The relationship between module expression and clinical characteristics of GC patients

Variable	**CCGs module expression**						***P* [a]**
	Low (N=100)		**Medium (N=100)**		**High (N=100)**		
	No.	**%**	**No.**	**%**	**No.**	**%**	
Age							0.157
<60	29	27.36	42	39.62	35	33.02	
≥60	71	36.60	58	29.90	65	33.51	
Sex							0.788
Female	31	30.69	35	34.65	35	34.65	
Male	69	34.67	65	32.66	65	32.66	
EBV status							**1.105e-06**
Positive	0	0.00	2	11.11	16	88.88	
Negative	91	35.41	91	35.41	75	29.18	
T stage							0.163
2	68	36.56	61	32.80	57	30.65	
3	21	23.08	34	37.36	36	39.56	
4	9	42.86	5	23.81	7	33.33	
N stage							0.379
0	12	31.58	9	23.68	17	44.74	
1	48	36.64	48	36.64	35	26.72	
2	23	28.75	28	35.00	29	36.25	
3	17	33.33	15	29.41	19	37.25	
M stage							**0.033** [b]
0	97	35.53	89	32.60	87	31.87	
1	3	11.11	11	40.74	13	48.15	
Lauren							**0.0002** [b]
Intestinal	66	45.21	41	28.08	39	26.71	
Diffuse	27	20.15	54	40.30	53	39.55	
Mixed	7	41.18	3	17.65	7	41.18	
Indeterminate	0	0.00	1	50.00	1	50.00	

Abbreviations: CCG, consistent co-expression genes; Lauren, Lauren classification; GC, gastric cancer.

Note: [a] $P<0.05$ was considered as significant; and $0.1>P>0.05$ was considered as boundary significant.

[b] Fisher's exact test.

The statistically significant results were marked in **bold**.

Supplementary table 3. The impact of mRNA expression levels of module or *SLAMF8* on GC patients' survival

SLAMF8 expression	**Univariate analysis**		**Multivariate analysis**		**CCGs module expression**	**Univariate analysis**		**Multivariate analysis** [b]	
	HR (95%CI)	***P***	**HR (95%CI)**	***P***		**HR (95%CI)**	***P*** [a]	**HR (95%CI)**	***P***
Low	1.00 (Reference)		1.00 (Reference)	Low	Low	1.00 (Reference)		1.00 (Reference)	
Medium	0.80 (0.66-0.98)	0.028	0.68 (0.45-1.05)	0.080	Medium	0.96 (0.66-1.40)	0.825	0.80 (0.52-1.25)	0.330
High	**0.64 (0.43-0.95)**	**0.027**	**0.50 (0.31-0.79)**	**0.004**	**High**	**0.74 (0.49-1.10)**	**0.131**	**0.56 (0.35-0.92)**	**0.021**
Trend				**0.003**					**0.018**

Abbreviation: GC, gastric cancer; CCG, consistent co-expression genes

Note: [a] All *P* value were calculated from Cox proportional hazards regression analysis. $P<0.05$ was considered as significant; and $0.1>P>0.05$ was considered as boundary significant.

[b] Adjust for age, sex, Lauren classification, pathologic TNM stage, EBV status and adjuvant treatment.

The statistically significant results were marked in **bold**.

Supplementary table 4: High-expression SLAMF8 GI cancers may enrich the pathways involved in antitumor immune response.

High-expression *SLAMF8* vs. low-expression *SLAMF8* gastric cancer tissues (GSE51575)

NAME	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	RANK.AT.MAX	LEADING.EDGE
GO_DOUBLE_STRANDED_RNA_BINDING	67	0.467236	1.672284	0.028736	0.168964	0.927	7431	tags=60%, list=34%, signal=90%
GO_T_CELL_RECEPTOR_SIGNALING_PATHWAY	171	0.535854	1.657666	0.041016	0.14619	0.942	4947	tags=40%, list=23%, signal=52%
GO_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	212	0.583773	1.662842	0.038462	0.152928	0.939	2988	tags=34%, list=14%, signal=40%
GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	41	0.643962	1.736948	0.003914	0.228686	0.819	3914	tags=44%, list=18%, signal=53%
GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	349	0.552287	1.644021	0.037624	0.137786	0.951	2988	tags=33%, list=14%, signal=38%
GO_FC_RECEPTOR_SIGNALING_PATHWAY	172	0.447083	1.619786	0.045726	0.13758	0.967	4956	tags=35%, list=23%, signal=45%
GO_NEGATIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	27	0.762306	1.675931	0.005639	0.178565	0.925	1275	tags=41%, list=6%, signal=43%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	65	0.650576	1.791706	0	0.387076	0.679	5323	tags=52%, list=24%, signal=69%
GO_ALPHA_BETA_T_CELL_DIFFERENTIATION	97	0.636863	1.666487	0.020677	0.153047	0.937	2951	tags=49%, list=14%, signal=57%
GO_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	36	0.727104	1.632334	0.015414	0.134016	0.956	1275	tags=36%, list=6%, signal=38%
GO_T_HELPER_1_TYPE_IMMUNE_RESPONSE	41	0.703003	1.634092	0.011494	0.135976	0.956	2917	tags=59%, list=13%, signal=67%
GO_NEGATIVE_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	20	0.762535	1.598214	0.017893	0.141404	0.98	1275	tags=40%, list=6%, signal=42%
GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	93	0.665913	1.705225	0.005769	0.202523	0.89	2951	tags=48%, list=14%, signal=56%
GO_RESPONSE_TO_TYPE_I_INTERFERON	83	0.64012	1.745469	0.015267	0.281605	0.799	3725	tags=48%, list=17%, signal=58%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	58	0.663015	1.608101	0.019194	0.142386	0.972	2951	tags=53%, list=14%, signal=62%

GO_ALPHA_BETA_T_CELL_ACTIVATION	129	0.644528	1.655476	0.01711	0.147859	0.943	2951	tags=48%, list=14%, signal=55%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	139	0.628029	1.671682	0.009862	0.168808	0.929	2246	tags=40%, list=10%, signal=45%
GO_NATURAL_KILLER_CELL_ACTIVATION	70	0.628578	1.742537	0.001931	0.262159	0.804	1792	tags=33%, list=8%, signal=36%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	45	0.640741	1.605087	0.009728	0.142809	0.976	2951	tags=51%, list=14%, signal=59%
GO_NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_KINASE_ACTIVITY	44	0.634397	1.648452	0.015414	0.141561	0.947	2963	tags=43%, list=14%, signal=50%
GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	71	0.665356	1.660691	0.011561	0.15035	0.941	3139	tags=56%, list=14%, signal=66%
GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	161	0.643853	1.745157	0	0.263288	0.799	2951	tags=43%, list=14%, signal=49%
GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	295	0.641077	1.678417	0.005837	0.186258	0.921	2659	tags=46%, list=12%, signal=51%
GO_T_CELL_ACTIVATION	428	0.609767	1.697589	0.005929	0.192147	0.9	2262	tags=38%, list=10%, signal=42%
GO_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	57	0.730172	1.652262	0.011321	0.145856	0.944	2077	tags=46%, list=10%, signal=50%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	90	0.65334	1.614403	0.017476	0.139523	0.969	2226	tags=47%, list=10%, signal=52%
GO_LYMPHOCYTE_DIFFERENTIATION	330	0.595905	1.664713	0.009921	0.15288	0.939	2712	tags=39%, list=12%, signal=44%
GO_DEFENSE_RESPONSE_TO_VIRUS	216	0.619116	1.794858	0.003922	0.408072	0.663	3452	tags=40%, list=16%, signal=47%
GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	41	0.706329	1.753255	0.002	0.312143	0.778	2620	tags=44%, list=12%, signal=50%
GO_POSITIVE_REGULATION_OF_INTERFERON_ALPHA_PRODUCTION	21	0.677428	1.570643	0.038835	0.149827	0.989	5572	tags=62%, list=26%, signal=83%
GO_RESPONSE_TO_VIRUS	293	0.57097	1.736362	0.003937	0.224221	0.819	3493	tags=39%, list=16%, signal=45%
GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	60	0.676287	1.658423	0.003891	0.146004	0.941	3139	tags=53%, list=14%, signal=62%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	30	0.708637	1.854336	0	1	0.467	1060	tags=27%, list=5%, signal=28%

GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	86	0.649942	1.661529	0.009634	0.151949	0.941	2951	tags=50%, list=14%, signal=58%
GO_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	32	0.629212	1.552107	0.043053	0.158403	0.992	1111	tags=34%, list=5%, signal=36%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	202	0.676791	1.65264	0.001996	0.147196	0.944	2259	tags=47%, list=10%, signal=52%
GO_INTERFERON_GAMMA_PRODUCTION	102	0.679368	1.620991	0.015534	0.136934	0.964	2226	tags=49%, list=10%, signal=54%
GO_ACTIVATED_T_CELL_PROLIFERATION	39	0.576155	1.607167	0.011881	0.142201	0.973	2036	tags=31%, list=9%, signal=34%
GO_CELLULAR_RESPONSE_TO_INTERFERON_BETA	19	0.784348	1.841141	0	0.557828	0.53	599	tags=32%, list=3%, signal=32%
GO_ACTIVATION_OF_INNATE_IMMUNE_RESPONSE	288	0.456736	1.545998	0.046653	0.159748	0.993	5110	tags=42%, list=24%, signal=54%
GO_MYD88_INDEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	32	0.597825	1.635912	0.02947	0.136223	0.956	3762	tags=34%, list=17%, signal=42%
GO_INTERFERON_ALPHA_PRODUCTION	29	0.689032	1.62663	0.019084	0.136234	0.962	2801	tags=41%, list=13%, signal=47%
GO_T_CELL_DIFFERENTIATION	226	0.617476	1.685026	0.009728	0.184682	0.914	2712	tags=42%, list=12%, signal=48%
GO_POSITIVE_REGULATION_OF_INTERFERON_BETA_PRODUCTION	30	0.603305	1.701191	0.011538	0.194224	0.897	5572	tags=53%, list=26%, signal=72%
GO_T_CELL_PROLIFERATION	169	0.622033	1.706032	0	0.20723	0.89	2259	tags=38%, list=10%, signal=43%
GO_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PROCESS	30	0.674022	1.57796	0.032505	0.145866	0.988	2035	tags=43%, list=9%, signal=48%
GO_RESPONSE_TO_INTERFERON_ALPHA	20	0.744673	1.551279	0.014315	0.15806	0.992	3018	tags=60%, list=14%, signal=70%
GO_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	85	0.682202	1.660675	0.005725	0.149342	0.941	2951	tags=52%, list=14%, signal=60%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	357	0.506282	1.620014	0.023576	0.137821	0.965	3432	tags=33%, list=16%, signal=39%
GO_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	65	0.674108	1.643087	0.015385	0.137681	0.952	3139	tags=55%, list=14%, signal=65%
GO_LEUKOCYTE_DIFFERENTIATION	483	0.557242	1.651578	0.007968	0.142553	0.944	2980	tags=37%, list=14%, signal=42%

GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	26	0.695444	1.53512	0.039548	0.166197	0.993	2917	tags=65%, list=13%, signal=75%
GO_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	60	0.568754	1.574513	0.027613	0.1466	0.988	2181	tags=33%, list=10%, signal=37%
GO_POSITIVE_REGULATION_OF_HEMOPOIESIS	174	0.584335	1.657524	0.006061	0.145468	0.942	3762	tags=47%, list=17%, signal=57%
GO_POSITIVE_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	19	0.747776	1.58361	0.01341	0.145859	0.986	2659	tags=68%, list=12%, signal=78%
GO_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	110	0.535268	1.648135	0.009823	0.140417	0.947	2380	tags=32%, list=11%, signal=36%
GO_ADAPTIVE_IMMUNE_RESPONSE	360	0.670422	1.712724	0.003781	0.215094	0.874	3092	tags=50%, list=14%, signal=57%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	33	0.709069	1.686116	0.007767	0.186476	0.914	1387	tags=36%, list=6%, signal=39%
GO_PHAGOCYTOSIS	244	0.518121	1.630926	0.017928	0.134238	0.958	2232	tags=32%, list=10%, signal=35%
GO_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	256	0.587823	1.669792	0.007921	0.166623	0.932	2246	tags=36%, list=10%, signal=39%
GO_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	144	0.592573	1.566533	0.038153	0.153127	0.989	1602	tags=36%, list=7%, signal=39%
GO_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	472	0.540505	1.701238	0.011696	0.196978	0.897	3436	tags=36%, list=16%, signal=42%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION	200	0.526552	1.75989	0.007921	0.352187	0.769	3046	tags=29%, list=14%, signal=33%
GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	232	0.630871	1.667789	0.011561	0.15828	0.936	2422	tags=43%, list=11%, signal=48%
GO_REGULATION_OF_T_CELL_ACTIVATION	292	0.647371	1.69573	0.001996	0.193919	0.902	2259	tags=42%, list=10%, signal=46%
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	425	0.584386	1.691284	0.007813	0.188449	0.909	2226	tags=32%, list=10%, signal=35%
GO_REGULATION_OF_HEMOPOIESIS	411	0.517847	1.667312	0.006048	0.155347	0.936	2988	tags=31%, list=14%, signal=35%
GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	236	0.637768	1.675806	0.001961	0.176961	0.925	2280	tags=44%, list=10%, signal=48%

GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	191	0.621286	1.659109	0.009881	0.148943	0.941	3092	tags=45%, list=14%, signal=52%
GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	59	0.726944	1.652257	0.013233	0.144955	0.944	2226	tags=54%, list=10%, signal=60%
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	23	0.721825	1.605185	0.017717	0.143212	0.976	1387	tags=39%, list=6%, signal=42%
GO_IMMUNOLOGICAL_SYNAPSE	34	0.758648	1.695442	0.011278	0.186894	0.903	1701	tags=41%, list=8%, signal=45%
GO_POSITIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	486	0.480173	1.675935	0.013972	0.180359	0.925	3344	tags=28%, list=15%, signal=33%
GO_T_CELL_MEDIATED_IMMUNITY	90	0.668253	1.723569	0	0.22703	0.857	1749	tags=41%, list=8%, signal=45%
GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	37	0.757347	1.552845	0.021154	0.158586	0.992	2680	tags=65%, list=12%, signal=74%
GO_REGULATION_OF_MACROPHAGE_MIGRATION	35	0.647091	1.63291	0.005929	0.13505	0.956	1990	tags=37%, list=9%, signal=41%
GO_LEUKOCYTE_CELL_CELL_ADHESION	311	0.621727	1.616395	0.015968	0.139394	0.968	2259	tags=41%, list=10%, signal=45%
GO_CYTOKINE_SECRETION	213	0.610559	1.61639	0.015474	0.138848	0.968	2077	tags=40%, list=10%, signal=44%
GO_LYMPHOCYTE_MEDIATED_IMMUNITY	226	0.655432	1.705111	0.005814	0.199548	0.89	2108	tags=42%, list=10%, signal=46%
GO_RESPONSE_TO_INTERFERON_GAMMA	176	0.614366	1.672355	0.007937	0.170389	0.927	3073	tags=46%, list=14%, signal=53%
GO_CD8_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	21	0.757175	1.599962	0.009653	0.142147	0.98	2236	tags=62%, list=10%, signal=69%
GO_SYNCYTIUM_FORMATION	48	0.592116	1.668541	0.016822	0.162141	0.934	2770	tags=35%, list=13%, signal=41%
GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	357	0.596355	1.670183	0.005941	0.16885	0.932	3163	tags=42%, list=15%, signal=48%
GO_MYOBLAST_FUSION	36	0.584878	1.609542	0.027726	0.141783	0.971	2770	tags=36%, list=13%, signal=41%
GO_REGULATION_OF_LYMPHOCYTE_ACTIVATION	391	0.623001	1.681151	0.004	0.184226	0.917	2259	tags=39%, list=10%, signal=43%
GO_LEUKOCYTE_PROLIFERATION	269	0.586043	1.625038	0.015873	0.136793	0.963	2312	tags=38%, list=11%, signal=41%

GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	188	0.55472	1.547922	0.047431	0.15983	0.993	3143	tags=39%, list=14%, signal=45%
GO_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	85	0.694952	1.687499	0.001942	0.18778	0.913	2259	tags=48%, list=10%, signal=54%
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	53	0.639712	1.715147	0.003976	0.226511	0.872	2380	tags=36%, list=11%, signal=40%
GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	82	0.620637	1.622987	0.023211	0.137991	0.964	1148	tags=37%, list=5%, signal=38%
GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	35	0.739347	1.599006	0.007828	0.141576	0.98	2951	tags=63%, list=14%, signal=73%
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	65	0.711503	1.604395	0.01378	0.142239	0.976	2108	tags=57%, list=10%, signal=63%
GO_INTERLEUKIN_12_PRODUCTION	54	0.697462	1.669918	0.003795	0.167903	0.932	2226	tags=50%, list=10%, signal=56%
GO_REGULATION_OF_LEUKOCYTE_MIGRATION	176	0.577243	1.539436	0.045187	0.162467	0.993	2232	tags=36%, list=10%, signal=40%
GO_INTERLEUKIN_8_SECRETION	28	0.665304	1.549334	0.021526	0.158964	0.992	1427	tags=43%, list=7%, signal=46%
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	180	0.652107	1.693103	0.001976	0.186785	0.905	3139	tags=49%, list=14%, signal=57%
GO_T_CELL_MIGRATION	61	0.72474	1.676006	0.00198	0.182017	0.925	2014	tags=51%, list=9%, signal=56%
GO_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	50	0.61928	1.57531	0.033932	0.146725	0.988	2620	tags=40%, list=12%, signal=45%
GO_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	162	0.536259	1.649265	0.023576	0.143722	0.947	4014	tags=41%, list=18%, signal=50%
GO_LYMPHOCYTE_HOMEOSTASIS	61	0.648387	1.754054	0.001916	0.324515	0.777	2704	tags=36%, list=12%, signal=41%
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	249	0.544997	1.561676	0.036072	0.153674	0.991	2424	tags=34%, list=11%, signal=38%
GO_FC_RECEPTOR_MEDIATED_STIMULATORY_SIGNALING_PATHWAY	80	0.502192	1.624398	0.01996	0.136574	0.963	3821	tags=35%, list=18%, signal=42%
GO_LYMPHOCYTE_MIGRATION	101	0.687346	1.595362	0.019646	0.142233	0.98	2014	tags=48%, list=9%, signal=52%
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	45	0.757258	1.668146	0	0.161481	0.934	3139	tags=64%, list=14%, signal=75%

GO_LEUKOCYTE_MEDIATED_CYTOTOXICITY	94	0.670961	1.667716	0.009747	0.157177	0.936	1897	tags=46%, list=9%, signal=50%
GO_INTERLEUKIN_8_PRODUCTION	75	0.595735	1.543537	0.033865	0.162144	0.993	1427	tags=31%, list=7%, signal=33%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	70	0.591493	1.726731	0.001969	0.222534	0.845	6739	tags=64%, list=31%, signal=93%
GO_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	160	0.63558	1.649375	0.007984	0.144371	0.947	2226	tags=41%, list=10%, signal=45%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	125	0.624584	1.619692	0.009766	0.137171	0.967	3602	tags=53%, list=17%, signal=63%
GO_REGULATION_OF_T_CELL_DIFFERENTIATION	129	0.661295	1.665499	0.005894	0.152543	0.938	2226	tags=44%, list=10%, signal=49%
GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	29	0.748337	1.576903	0.013861	0.146158	0.988	2951	tags=66%, list=14%, signal=76%
GO_REGULATION_OF_LYMPHOCYTE_MIGRATION	55	0.689108	1.69555	0.003831	0.189128	0.902	2014	tags=44%, list=9%, signal=48%
GO_T_CELL_SELECTION	46	0.750541	1.646313	0.009416	0.137883	0.947	4197	tags=72%, list=19%, signal=89%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	121	0.623584	1.613673	0.019608	0.138965	0.969	1990	tags=38%, list=9%, signal=42%
GO_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	55	0.64547	1.607776	0.03876	0.141834	0.972	2226	tags=40%, list=10%, signal=44%
GO_NEGATIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	20	0.752734	1.609297	0.004082	0.141593	0.971	1700	tags=40%, list=8%, signal=43%
GO_INTERLEUKIN_1_BETA_PRODUCTION	83	0.622144	1.533827	0.034884	0.16784	0.994	1575	tags=43%, list=7%, signal=47%
GO_REGULATION_OF_CELL_KILLING	86	0.684438	1.641583	0.015385	0.138433	0.952	2680	tags=52%, list=12%, signal=59%
GO_POSITIVE_REGULATION_OF_CYTOKINE_SECRETION	130	0.579451	1.55734	0.033074	0.156184	0.992	2035	tags=36%, list=9%, signal=40%
GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	408	0.555341	1.621046	0.01006	0.137441	0.964	2077	tags=32%, list=10%, signal=35%
GO_REGULATION_OF_SYNCYTIUM_FORMATION_BY_PLASMA_MEMBRANE_FUSION	26	0.729529	1.632993	0.01341	0.135542	0.956	465	tags=31%, list=2%, signal=31%
GO_NIK_NF_KAPPAB_SIGNALING	154	0.485864	1.637969	0.014028	0.138134	0.954	4947	tags=38%, list=23%, signal=48%

GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	91	0.529362	1.742364	0.011881	0.254226	0.804	6739	tags=58%, list=31%, signal=84%
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	20	0.832431	1.529116	0.019493	0.171089	0.994	2514	tags=70%, list=12%, signal=79%
GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	72	0.643796	1.631347	0.032755	0.134262	0.958	3030	tags=50%, list=14%, signal=58%
GO_POSITIVE_REGULATION_OF_CELL_ADHESION	372	0.524638	1.516244	0.038229	0.180509	0.997	2586	tags=34%, list=12%, signal=38%
GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PROCESS	20	0.794877	1.71824	0.001919	0.227315	0.864	1148	tags=45%, list=5%, signal=47%
GO_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	199	0.49506	1.677346	0.003992	0.182839	0.923	2580	tags=29%, list=12%, signal=32%
GO_POSITIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	25	0.729097	1.699722	0.005792	0.194898	0.899	1840	tags=40%, list=8%, signal=44%
GO_I_KAPPAB_PHOSPHORYLATION	18	0.720468	1.654744	0.001931	0.148209	0.943	4705	tags=61%, list=22%, signal=78%
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	23	0.817612	1.512059	0.036538	0.184622	0.997	1294	tags=61%, list=6%, signal=65%
GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_INVOLVED_IN_INFLAMMATORY_RESPONSE	64	0.557946	1.504455	0.042254	0.188977	0.998	1148	tags=27%, list=5%, signal=28%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	43	0.757691	1.63672	0.013619	0.137141	0.955	2108	tags=60%, list=10%, signal=67%
GO_REGULATION_OF_MAST_CELL_ACTIVATION	36	0.608929	1.551067	0.035573	0.157617	0.992	2620	tags=39%, list=12%, signal=44%
GO_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	23	0.584108	1.530758	0.044574	0.170442	0.994	1990	tags=30%, list=9%, signal=33%
GO_INTERLEUKIN_1_PRODUCTION	96	0.604986	1.520069	0.044574	0.177688	0.996	2324	tags=45%, list=11%, signal=50%
GO_NEGATIVE_REGULATION_OF_EXOCYTOSIS	28	0.692518	1.667625	0.007984	0.15603	0.936	2068	tags=32%, list=10%, signal=35%
GO_MHC_PROTEIN_BINDING	27	0.751244	1.600268	0.029412	0.142762	0.98	1060	tags=52%, list=5%, signal=54%
GO_T_CELL_MEDIATED_CYTOTOXICITY	35	0.710116	1.672631	0.007828	0.171495	0.926	2108	tags=51%, list=10%, signal=57%
GO_POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	67	0.768965	1.847391	0	0.675251	0.493	1553	tags=45%, list=7%, signal=48%

GO_CELLULAR_DEFENSE_RESPONSE	49	0.718718	1.636794	0.011472	0.137665	0.955	1227	tags=47%, list=6%, signal=50%
GO_REGULATION_OF_T_CELL_MIGRATION	40	0.689454	1.676333	0	0.183084	0.924	1869	tags=43%, list=9%, signal=46%
GO_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY	154	0.507805	1.649515	0.021739	0.144946	0.946	5298	tags=45%, list=24%, signal=60%
GO_RESPIRATORY_BURST	30	0.763634	1.645026	0.001946	0.138351	0.949	2141	tags=53%, list=10%, signal=59%
GO_MYELOID_LEUKOCYTE_DIFFERENTIATION	194	0.526718	1.635197	0.011928	0.136834	0.956	3762	tags=40%, list=17%, signal=48%
GO_DENDRITIC_CELL_DIFFERENTIATION	37	0.712	1.644301	0.009728	0.138079	0.951	2659	tags=51%, list=12%, signal=58%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	90	0.728478	1.695708	0.001969	0.191359	0.902	3602	tags=63%, list=17%, signal=76%
GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	34	0.708638	1.659369	0.001961	0.149613	0.941	3436	tags=62%, list=16%, signal=73%
GO_LEUKOCYTE_ACTIVATION_INVOLVED_IN_INFLAMMATORY_RESPONSE	43	0.743805	1.562629	0.015656	0.155018	0.991	1165	tags=51%, list=5%, signal=54%
GO_TYPE_I_INTERFERON_PRODUCTION	119	0.589848	1.818684	0.001976	0.427165	0.606	5855	tags=48%, list=27%, signal=65%
GO_INTERLEUKIN_2_PRODUCTION	63	0.659841	1.622658	0.009766	0.137271	0.964	1667	tags=41%, list=8%, signal=45%
GO_REGULATION_OF_CELL_CELL_ADHESION	367	0.576465	1.604828	0.01002	0.142685	0.976	2280	tags=36%, list=10%, signal=40%
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	56	0.735077	1.668852	0	0.164262	0.934	3139	tags=59%, list=14%, signal=69%
GO_RESPONSE_TO_AMYLOID_BETA	47	0.637475	1.561687	0.026104	0.15406	0.991	1183	tags=30%, list=5%, signal=31%
GO_INTERFERON_BETA_PRODUCTION	48	0.582404	1.721311	0.005871	0.228245	0.86	5572	tags=52%, list=26%, signal=70%
GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	132	0.670852	1.668999	0.001988	0.166822	0.934	3139	tags=53%, list=14%, signal=62%
GO_RESPONSE_TO_INTERFERON_BETA	27	0.772964	1.785216	0	0.383432	0.699	2355	tags=52%, list=11%, signal=58%
GO_CELL_KILLING	148	0.566326	1.578983	0.02277	0.145301	0.988	2680	tags=39%, list=12%, signal=44%

GO_MYD88_DEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	32	0.729719	1.584935	0.033138	0.145727	0.984	1390	tags=44%, list=6%, signal=47%
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	451	0.506731	1.569983	0.040777	0.149952	0.989	3272	tags=34%, list=15%, signal=39%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	116	0.696066	1.715748	0.005917	0.229474	0.871	3092	tags=52%, list=14%, signal=60%
GO_POSITIVE_REGULATION_OF_MACROPHAGE_ACTIVATION	21	0.696343	1.559372	0.022556	0.155115	0.992	2620	tags=52%, list=12%, signal=60%
GO_POSITIVE_REGULATION_OF_CELL_KILLING	56	0.743797	1.71187	0.001923	0.213628	0.876	2108	tags=52%, list=10%, signal=57%
GO_B_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	68	0.642114	1.648377	0.009921	0.140826	0.947	4771	tags=56%, list=22%, signal=71%
GO_LEUKOCYTE_HOMEOSTASIS	81	0.671093	1.728475	0.001965	0.234102	0.837	2704	tags=40%, list=12%, signal=45%
GO_INTERLEUKIN_10_PRODUCTION	50	0.777316	1.647994	0	0.139055	0.947	1492	tags=52%, list=7%, signal=56%
GO_FICOLIN_1_RICH_GRANULE_MEMBRANE	56	0.619805	1.689659	0.017613	0.187799	0.911	1899	tags=34%, list=9%, signal=37%
GO_REGULATION_OF_MYOBLAST_FUSION	20	0.74135	1.638447	0.005693	0.138191	0.954	1792	tags=40%, list=8%, signal=44%
GO_LEUKOCYTE_MIGRATION	402	0.564321	1.570929	0.021912	0.149912	0.989	2173	tags=35%, list=10%, signal=38%
GO_LEUKOCYTE_CHEMOTAXIS	194	0.622202	1.595452	0.015873	0.142571	0.98	2077	tags=43%, list=10%, signal=47%
GO_PHAGOCYTIC_CUP	24	0.664571	1.592329	0.025896	0.141975	0.981	3487	tags=58%, list=16%, signal=69%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	33	0.687373	1.567614	0.013566	0.152155	0.989	1148	tags=42%, list=5%, signal=45%
GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	203	0.609616	1.649255	0.005917	0.142904	0.947	2312	tags=41%, list=11%, signal=45%
GO_VIRAL_GENOME_REPLICATION	113	0.523149	1.645398	0.027505	0.13859	0.949	2910	tags=32%, list=13%, signal=37%
GO_POSITIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR_ACTIVITY	144	0.512094	1.558875	0.040404	0.15509	0.992	3492	tags=34%, list=16%, signal=40%
GO_MACROPHAGE_ACTIVATION	87	0.658847	1.62848	0.013462	0.136671	0.962	1165	tags=39%, list=5%, signal=41%

GO_OSTEOCLAST_DIFFERENTIATION	91	0.52933	1.587034	0.01222	0.145938	0.983	3648	tags=42%, list=17%, signal=50%
GO_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	18	0.752606	1.58284	0.011811	0.145743	0.986	2014	tags=56%, list=9%, signal=61%
GO_POSITIVE_REGULATION_OF_T_CELL_MIGRATION	29	0.748188	1.707908	0	0.205792	0.886	1869	tags=48%, list=9%, signal=53%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	16	0.810801	1.582621	0.007547	0.145649	0.986	2026	tags=63%, list=9%, signal=69%
GO_B_CELL_PROLIFERATION	84	0.618715	1.516039	0.046512	0.180494	0.997	3602	tags=49%, list=17%, signal=58%
GO_REGULATION_OF_B_CELL_RECEPTOR_SIGNALING_PATHWAY	24	0.780802	1.589691	0.001916	0.144051	0.983	2077	tags=58%, list=10%, signal=64%
GO_T_CELL_CYTOKINE_PRODUCTION	40	0.660812	1.614714	0.016162	0.140194	0.969	3602	tags=52%, list=17%, signal=63%
GO_ANTIGEN_BINDING	35	0.699988	1.640808	0.012	0.138937	0.952	3073	tags=63%, list=14%, signal=73%
GO_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	54	0.744015	1.622508	0.013487	0.136905	0.964	1758	tags=50%, list=8%, signal=54%
GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	146	0.646475	1.65964	0.004024	0.150189	0.941	3602	tags=53%, list=17%, signal=63%
GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	93	0.696237	1.708679	0.001953	0.20737	0.886	3602	tags=58%, list=17%, signal=69%
GO_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	27	0.749614	1.666462	0.005792	0.151913	0.937	1041	tags=48%, list=5%, signal=51%
GO_POSITIVE_REGULATION_OF_MACROPHAGE_MIGRATION	20	0.767491	1.666819	0.007767	0.153686	0.936	3516	tags=60%, list=16%, signal=72%
GO_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	63	0.665917	1.641935	0.006	0.138625	0.952	1749	tags=43%, list=8%, signal=46%
GO_INTERLEUKIN_6_PRODUCTION	134	0.588348	1.562414	0.029821	0.154542	0.991	2226	tags=40%, list=10%, signal=45%
GO_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	52	0.697602	1.741231	0	0.242438	0.808	1823	tags=42%, list=8%, signal=46%
GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	198	0.56716	1.745954	0.00396	0.2909	0.797	3452	tags=41%, list=16%, signal=49%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	54	0.644087	1.597146	0.009542	0.142043	0.98	1148	tags=39%, list=5%, signal=41%

GO_PHOSPHATIDYLINOSITOL_3_4_BISPHOSPHATE_BINDING	24	0.620163	1.742027	0.007874	0.247575	0.806	955	tags=21%, list=4%, signal=22%
GO_MACROPHAGE_MIGRATION	47	0.596808	1.577267	0.017751	0.146074	0.988	2014	tags=36%, list=9%, signal=40%
GO_INTERLEUKIN_4_PRODUCTION	34	0.70805	1.575716	0.019724	0.146542	0.988	1041	tags=44%, list=5%, signal=46%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	49	0.632772	1.542038	0.04008	0.162185	0.993	1427	tags=33%, list=7%, signal=35%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MIGRATION	36	0.737191	1.668915	0	0.165548	0.934	1869	tags=47%, list=9%, signal=52%
GO_CELL_CHEMOTAXIS	264	0.583531	1.54934	0.037624	0.159335	0.992	2077	tags=39%, list=10%, signal=43%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_SECRETION	16	0.742549	1.502181	0.037255	0.189794	0.999	1427	tags=56%, list=7%, signal=60%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	79	0.641457	1.646462	0	0.138351	0.947	1990	tags=41%, list=9%, signal=44%
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	84	0.61215	1.757298	0.001957	0.327894	0.772	1823	tags=32%, list=8%, signal=35%
GO_T_CELL_HOMEOSTASIS	38	0.631626	1.705438	0.003854	0.205335	0.89	2026	tags=29%, list=9%, signal=32%
GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	80	0.663989	1.579221	0.026052	0.145335	0.988	3139	tags=51%, list=14%, signal=60%
GO_NEGATIVE_REGULATION_OF_B_CELL_PROLIFERATION	16	0.843428	1.727295	0	0.232093	0.843	2077	tags=56%, list=10%, signal=62%
GO_MYELOID_CELL_DIFFERENTIATION	355	0.464557	1.632773	0.01002	0.133971	0.956	3762	tags=33%, list=17%, signal=40%
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS	225	0.508756	1.680739	0.006085	0.183092	0.919	4196	tags=38%, list=19%, signal=46%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	22	0.752042	1.622675	0.005825	0.137843	0.964	1041	tags=50%, list=5%, signal=52%
GO_B_CELL_HOMEOSTASIS	28	0.665912	1.602981	0.029183	0.142255	0.976	4459	tags=50%, list=21%, signal=63%
GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	55	0.651572	1.589706	0.029528	0.144478	0.983	2355	tags=49%, list=11%, signal=55%
GO_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	27	0.730886	1.62155	0.015748	0.137226	0.964	2108	tags=59%, list=10%, signal=66%

GO_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	129	0.607851	1.59724	0.02	0.142386	0.98	3139	tags=45%, list=14%, signal=52%
GO_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	100	0.627285	1.634112	0.007722	0.136582	0.956	2077	tags=40%, list=10%, signal=44%
GO_B_CELL_MEDIATED_IMMUNITY	107	0.621184	1.618552	0.00947	0.137273	0.968	2053	tags=40%, list=9%, signal=44%
GO_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	213	0.625709	1.698394	0.001957	0.195597	0.899	2226	tags=38%, list=10%, signal=41%
GO_SPECIFIC_GRANULE_MEMBRANE	83	0.638533	1.632775	0.009901	0.134592	0.956	2158	tags=39%, list=10%, signal=43%
GO_RESPONSE_TO_CHEMOKINE	85	0.712135	1.604035	0.009634	0.14174	0.976	2014	tags=49%, list=9%, signal=54%
GO_B_CELL_ACTIVATION	224	0.587612	1.601377	0.021569	0.142573	0.978	3400	tags=41%, list=16%, signal=48%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	31	0.718526	1.583031	0.021318	0.145886	0.986	3092	tags=55%, list=14%, signal=64%
GO_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	145	0.452543	1.498655	0.02544	0.192897	0.999	2077	tags=29%, list=10%, signal=32%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	54	0.662697	1.673528	0.006098	0.173046	0.926	4014	tags=56%, list=18%, signal=68%
GO_POSITIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	40	0.499346	1.466152	0.042636	0.215539	1	1081	tags=23%, list=5%, signal=24%
GO_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	95	0.576637	1.673937	0.004	0.173848	0.926	1335	tags=25%, list=6%, signal=27%
GO_CYTOKINE_METABOLIC_PROCESS	114	0.654664	1.777672	0	0.392539	0.718	1553	tags=37%, list=7%, signal=39%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	18	0.812361	1.564506	0.009671	0.153668	0.989	1111	tags=61%, list=5%, signal=64%
GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	15	0.795992	1.541588	0.013619	0.162098	0.993	2014	tags=67%, list=9%, signal=73%
GO_REGULATION_OF_B_CELL_PROLIFERATION	60	0.636772	1.526316	0.033074	0.173241	0.995	3602	tags=55%, list=17%, signal=66%
GO_NEGATIVE_REGULATION_OF_VIRAL_LIFE_CYCLE	77	0.579488	1.579899	0.031683	0.144792	0.988	3600	tags=49%, list=17%, signal=59%
GO_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	73	0.598652	1.826392	0.001942	0.447535	0.575	5827	tags=49%, list=27%, signal=67%

GO_T_CELL_APOPTOTIC_PROCESS	47	0.684316	1.745239	0.001873	0.272434	0.799	1418	tags=32%, list=7%, signal=34%
GO_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	85	0.567208	1.677666	0.002008	0.185821	0.921	2580	tags=35%, list=12%, signal=40%
GO_MYELOID_LEUKOCYTE_MIGRATION	184	0.609361	1.585081	0.019724	0.145929	0.984	2158	tags=41%, list=10%, signal=45%
GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	181	0.657419	1.711707	0	0.206543	0.876	2077	tags=41%, list=10%, signal=45%
GO_PROTEIN_AUTOPHOSPHORYLATION	223	0.374869	1.483751	0.028283	0.204879	0.999	2711	tags=24%, list=12%, signal=27%
GO_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	317	0.544006	1.53313	0.039216	0.168592	0.994	2226	tags=34%, list=10%, signal=38%
GO_T_CELL_RECEPTOR_COMPLEX	17	0.807172	1.551909	0.046296	0.158296	0.992	1701	tags=65%, list=8%, signal=70%
GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_SUPERFAMILY_BINDING	42	0.697434	1.710937	0.005929	0.204747	0.877	2236	tags=45%, list=10%, signal=50%
GO_REGULATION_OF_MYOTUBE_DIFFERENTIATION	48	0.584307	1.667805	0.001919	0.159551	0.936	3400	tags=40%, list=16%, signal=47%
GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	86	0.599371	1.541512	0.036437	0.161846	0.993	3092	tags=45%, list=14%, signal=53%
GO_REGULATORY_T_CELL_DIFFERENTIATION	28	0.855135	1.653422	0	0.146691	0.943	1667	tags=75%, list=8%, signal=81%
GO_NEGATIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	17	0.762996	1.652374	0.002041	0.146642	0.944	1275	tags=47%, list=6%, signal=50%
GO_POSITIVE_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	70	0.628253	1.663686	0.001972	0.153605	0.939	1335	tags=29%, list=6%, signal=30%
GO_MYELOID_DENDRITIC_CELL_ACTIVATION	26	0.82026	1.683927	0.00198	0.182743	0.914	2369	tags=65%, list=11%, signal=73%
GO_REGULATION_OF_T_CELL_CYTOKINE_PRODUCTION	30	0.694568	1.559095	0.024096	0.155176	0.992	3092	tags=53%, list=14%, signal=62%
GO_POSITIVE_REGULATION_OF_PHAGOCYTOSIS	65	0.601504	1.576884	0.016	0.145766	0.988	2729	tags=45%, list=13%, signal=51%
GO_INTERLEUKIN_1_SECRETION	55	0.599248	1.472741	0.042969	0.212651	0.999	1213	tags=38%, list=6%, signal=40%
GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	34	0.70559	1.712989	0.003968	0.218617	0.874	2068	tags=47%, list=10%, signal=52%

GO_POSITIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	19	0.775929	1.528425	0.031068	0.171084	0.994	1962	tags=58%, list=9%, signal=64%
GO_LYMPHOCYTE_CHEMOTAXIS	56	0.748544	1.612056	0.007813	0.140202	0.971	2014	tags=57%, list=9%, signal=63%
GO_GLIAL_CELL_ACTIVATION	51	0.704474	1.583692	0.015534	0.146159	0.986	1165	tags=45%, list=5%, signal=48%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	16	0.812378	1.585309	0.00578	0.14606	0.983	2035	tags=63%, list=9%, signal=69%
GO_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	41	0.679039	1.611812	0.011561	0.140014	0.971	2077	tags=44%, list=10%, signal=48%
GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	66	0.536887	1.535395	0.029644	0.166515	0.993	2077	tags=29%, list=10%, signal=32%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	83	0.596875	1.560501	0.031746	0.154266	0.992	2226	tags=36%, list=10%, signal=40%
GO_ALPHA_BETA_T_CELL_PROLIFERATION	30	0.763289	1.647083	0.003868	0.139814	0.947	1111	tags=47%, list=5%, signal=49%
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	137	0.668741	1.765317	0	0.347583	0.754	2077	tags=42%, list=10%, signal=47%
GO_THYMIC_T_CELL_SELECTION	21	0.743312	1.567529	0.02907	0.151879	0.989	1019	tags=43%, list=5%, signal=45%
GO_INTERLEUKIN_2_BIOSYNTHETIC_PROCESS	23	0.755652	1.64689	0.005671	0.139309	0.947	1431	tags=52%, list=7%, signal=56%
GO_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	34	0.563466	1.849898	0.001976	0.974251	0.48	2390	tags=26%, list=11%, signal=30%
GO_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	21	0.7397	1.563044	0.023256	0.154803	0.991	1553	tags=48%, list=7%, signal=51%
GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	30	0.650789	1.480014	0.042945	0.207921	0.999	1492	tags=37%, list=7%, signal=39%
GO_NEGATIVE_REGULATION_OF_VIRAL_PROCESS	93	0.572498	1.637013	0.012	0.138062	0.955	3600	tags=45%, list=17%, signal=54%
GO_SH2_DOMAIN_BINDING	35	0.599715	1.524776	0.02686	0.174139	0.995	2935	tags=34%, list=14%, signal=40%
GO_IMMUNOGLOBULIN_PRODUCTION	98	0.592497	1.593983	0.021359	0.14227	0.98	3918	tags=44%, list=18%, signal=53%
GO_GRANULOCYTE_MIGRATION	122	0.64776	1.587267	0.021739	0.146576	0.983	2068	tags=44%, list=10%, signal=49%

GO_REGULATION_OF_PHAGOCYTOSIS	87	0.56558	1.594719	0.005952	0.142235	0.98	2203	tags=40%, list=10%, signal=45%
GO_LEUKOCYTE_APOPTOTIC_PROCESS	101	0.640109	1.71478	0.005859	0.218393	0.873	2077	tags=35%, list=10%, signal=38%
GO_POSITIVE_REGULATION_OF_CHEMOTAXIS	126	0.566594	1.532692	0.027944	0.168917	0.994	1990	tags=35%, list=9%, signal=38%
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	50	0.590516	1.573114	0.007859	0.148055	0.989	3306	tags=44%, list=15%, signal=52%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	111	0.616475	1.633141	0.001988	0.136589	0.956	2068	tags=38%, list=10%, signal=42%
GO_DEFENSE_RESPONSE_TO_BACTERIUM	209	0.434721	1.409884	0.032946	0.258066	1	2514	tags=29%, list=12%, signal=32%
GO_CYTOKINE_PRODUCTION_INVOLVED_IN_INFLAMMATORY_RESPONSE	42	0.623174	1.564865	0.01996	0.154757	0.989	1148	tags=29%, list=5%, signal=30%
GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	43	0.67693	1.584709	0.013917	0.145584	0.984	3602	tags=60%, list=17%, signal=72%
GO_REGULATION_OF_VIRAL_LIFE_CYCLE	134	0.509807	1.626468	0.02729	0.135898	0.962	3452	tags=35%, list=16%, signal=41%
GO_LYMPHOCYTE_APOPTOTIC_PROCESS	70	0.65084	1.739605	0	0.240517	0.813	2077	tags=34%, list=10%, signal=38%
GO_PURINERGIC_RECEPTOR_ACTIVITY	25	0.659924	1.479237	0.048263	0.208839	0.999	2232	tags=56%, list=10%, signal=62%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	33	0.844374	1.651867	0	0.142991	0.944	1148	tags=58%, list=5%, signal=61%
GO_ACUTE_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	18	0.782743	1.564792	0.006085	0.153622	0.989	774	tags=44%, list=4%, signal=46%
GO_POSITIVE_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL	36	0.639342	1.562154	0.00996	0.154543	0.991	3306	tags=47%, list=15%, signal=56%
GO_POSITIVE_REGULATION_OF_MONOCYTE_CHEMOTAXIS	17	0.766396	1.529833	0.025194	0.171062	0.994	1636	tags=59%, list=8%, signal=64%
GO_NEUTROPHIL_MIGRATION	102	0.697523	1.596986	0.015905	0.141743	0.98	2014	tags=49%, list=9%, signal=54%
GO_POSITIVE_REGULATION_OF_JNK_CASCADE	124	0.445748	1.488026	0.04142	0.20145	0.999	3092	tags=27%, list=14%, signal=32%
GO_REGULATION_OF_MONOCYTE_CHEMOTAXIS	23	0.749101	1.516487	0.029014	0.180488	0.997	2077	tags=57%, list=10%, signal=62%

GO_TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	79	0.502347	1.489096	0.031008	0.201486	0.999	2648	tags=38%, list=12%, signal=43%
GO_MONONUCLEAR_CELL_MIGRATION	80	0.703346	1.611646	0.015595	0.139726	0.971	2158	tags=50%, list=10%, signal=55%
GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	140	0.598235	1.618858	0.002016	0.137282	0.968	2514	tags=41%, list=12%, signal=46%
GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	44	0.607749	1.543108	0.024145	0.162067	0.993	1275	tags=34%, list=6%, signal=36%
GO_NEUROINFLAMMATORY_RESPONSE	63	0.687638	1.588274	0.011719	0.145606	0.983	1897	tags=49%, list=9%, signal=54%
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS_WITHIN_A_TISSUE	27	0.645225	1.673373	0.006061	0.171667	0.926	3516	tags=48%, list=16%, signal=57%
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT	228	0.425793	1.413653	0.048387	0.255828	1	3306	tags=32%, list=15%, signal=37%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	15	0.777744	1.587115	0.017341	0.146296	0.983	1758	tags=60%, list=8%, signal=65%
GO_DEFENSE_RESPONSE_TO_GRAM_POSITIVE_BACTERIUM	78	0.465921	1.398109	0.032567	0.268418	1	2236	tags=33%, list=10%, signal=37%
GO_MONOCYTE_CHEMOTAXIS	59	0.741498	1.582009	0.013619	0.145767	0.986	2077	tags=56%, list=10%, signal=62%
GO_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	159	0.548803	1.539863	0.016	0.162553	0.993	2068	tags=31%, list=10%, signal=34%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	23	0.660505	1.493925	0.030181	0.196846	0.999	1209	tags=43%, list=6%, signal=46%
GO_POSITIVE_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	22	0.706162	1.517436	0.023346	0.179368	0.997	1636	tags=50%, list=8%, signal=54%
GO_POSITIVE_REGULATION_OF_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	87	0.489641	1.432507	0.038986	0.243151	1	2980	tags=41%, list=14%, signal=48%
GO_REGULATION_OF_CHEMOTAXIS	191	0.51561	1.477487	0.049801	0.211061	0.999	2231	tags=31%, list=10%, signal=35%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	46	0.674911	1.645003	0.001976	0.137637	0.949	2026	tags=48%, list=9%, signal=53%
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	112	0.473982	1.497458	0.00994	0.194063	0.999	3306	tags=36%, list=15%, signal=42%
GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	31	0.605547	1.445945	0.036	0.234851	1	3535	tags=55%, list=16%, signal=65%

GO_NEGATIVE_REGULATION_OF_HEMOPOIESIS	132	0.476585	1.48807	0.034343	0.201736	0.999	2077	tags=29%, list=10%, signal=32%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	95	0.543435	1.580779	0.013944	0.143908	0.988	2077	tags=36%, list=10%, signal=39%
GO_VITAMIN_D_METABOLIC_PROCESS	22	0.553086	1.461212	0.04845	0.217894	1	1234	tags=27%, list=6%, signal=29%

High-expression *SLAMF8* vs. low-expression *SLAMF8* gastric cancer tissues (GSE62254)

NAME	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	RANK.AT.MAX	LEADING.EDGE
GO_DOUBLE_STRANDED_RNA_BINDING	71	0.59326	1.955017	0	0.016286	0.299	1423	tags=20%, list=6%, signal=21%
GO_T_CELL_RECEPTOR_SIGNALING_PATHWAY	177	0.718104	2.07907	0	0.023697	0.096	2591	tags=36%, list=12%, signal=40%
GO_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	226	0.755765	1.99388	0	0.018044	0.217	2518	tags=42%, list=11%, signal=46%
GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	41	0.743664	1.939196	0	0.0165	0.343	1748	tags=37%, list=8%, signal=40%
GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	367	0.725011	1.996541	0	0.01894	0.212	1910	tags=34%, list=9%, signal=37%
GO_FC_RECEPTOR_SIGNALING_PATHWAY	176	0.678946	2.124753	0	0.04496	0.058	3318	tags=34%, list=15%, signal=39%
GO_NEGATIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	28	0.851966	1.749407	0	0.028585	0.928	1610	tags=50%, list=7%, signal=54%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	64	0.74106	1.951909	0	0.016281	0.305	2547	tags=45%, list=12%, signal=51%
GO_ALPHA_BETA_T_CELL_DIFFERENTIATION	95	0.767748	1.827434	0	0.0222	0.71	2640	tags=58%, list=12%, signal=66%
GO_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	38	0.813637	1.789642	0	0.024708	0.837	2348	tags=53%, list=11%, signal=59%
GO_T_HELPER_1_TYPE_IMMUNE_RESPONSE	41	0.83013	1.819502	0	0.022679	0.729	1794	tags=61%, list=8%, signal=66%

GO_NEGATIVE_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	20	0.827348	1.717477	0	0.033052	0.968	1610	tags=45%, list=7%, signal=49%
GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	100	0.782252	1.921796	0	0.016603	0.399	1878	tags=45%, list=9%, signal=49%
GO_RESPONSE_TO_TYPE_I_INTERFERON	88	0.778059	1.928884	0	0.016733	0.371	2449	tags=49%, list=11%, signal=55%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	58	0.788274	1.767791	0	0.026695	0.882	1699	tags=53%, list=8%, signal=58%
GO_ALPHA_BETA_T_CELL_ACTIVATION	125	0.77952	1.824684	0	0.022315	0.717	1699	tags=50%, list=8%, signal=54%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	143	0.746741	1.886988	0	0.018935	0.508	2493	tags=50%, list=11%, signal=56%
GO_NATURAL_KILLER_CELL_ACTIVATION	77	0.746862	2.004396	0	0.018379	0.199	1984	tags=34%, list=9%, signal=37%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	45	0.77487	1.780283	0	0.025283	0.852	1699	tags=51%, list=8%, signal=55%
GO_NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_KINASE_ACTIVITY	45	0.691924	1.813227	0	0.022943	0.76	2587	tags=40%, list=12%, signal=45%
GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	69	0.785206	1.842485	0	0.021272	0.666	2624	tags=61%, list=12%, signal=69%
GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	168	0.763967	2.023399	0	0.018187	0.167	2348	tags=45%, list=11%, signal=50%
GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	305	0.775334	1.901967	0	0.017312	0.454	1787	tags=46%, list=8%, signal=49%
GO_T_CELL_ACTIVATION	432	0.747336	1.991544	0	0.017888	0.221	1794	tags=39%, list=8%, signal=42%
GO_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	61	0.819349	1.797942	0	0.023534	0.813	1843	tags=52%, list=8%, signal=57%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	91	0.798044	1.858897	0	0.019753	0.609	2002	tags=56%, list=9%, signal=61%
GO_LYMPHOCYTE_DIFFERENTIATION	336	0.730655	1.947066	0	0.016482	0.32	2860	tags=46%, list=13%, signal=53%
GO_DEFENSE_RESPONSE_TO_VIRUS	218	0.73019	1.983906	0	0.017648	0.235	2547	tags=43%, list=12%, signal=48%
GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	42	0.797907	1.802652	0	0.023376	0.796	2493	tags=52%, list=11%, signal=59%

GO_POSITIVE_REGULATION_OF_INTERFERON_ALPHA_PRODUCTION	22	0.835511	1.756272	0	0.02752	0.911	1461	tags=45%, list=7%, signal=49%
GO_RESPONSE_TO_VIRUS	295	0.705234	1.990985	0	0.017436	0.222	2567	tags=39%, list=12%, signal=44%
GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	60	0.777516	1.867116	0	0.019006	0.578	1878	tags=53%, list=9%, signal=58%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	30	0.708149	1.877816	0	0.018767	0.544	2860	tags=37%, list=13%, signal=42%
GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	83	0.774985	1.847208	0	0.021269	0.649	1693	tags=51%, list=8%, signal=55%
GO_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	32	0.791045	1.868744	0	0.019178	0.574	1984	tags=47%, list=9%, signal=51%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	203	0.78428	1.924573	0	0.016716	0.39	1843	tags=49%, list=8%, signal=53%
GO_INTERFERON_GAMMA_PRODUCTION	100	0.826651	1.880726	0	0.018798	0.527	1835	tags=55%, list=8%, signal=60%
GO_ACTIVATED_T_CELL_PROLIFERATION	39	0.735605	1.911369	0	0.016556	0.421	1693	tags=38%, list=8%, signal=42%
GO_CELLULAR_RESPONSE_TO_INTERFERON_BETA	18	0.866009	1.764844	0	0.026811	0.89	835	tags=39%, list=4%, signal=40%
GO_ACTIVATION_OF_INNATE_IMMUNE_RESPONSE	290	0.689124	2.075543	0	0.020247	0.1	2773	tags=36%, list=13%, signal=40%
GO_MYD88_INDEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	32	0.757867	1.797119	0	0.023704	0.817	1683	tags=34%, list=8%, signal=37%
GO_INTERFERON_ALPHA_PRODUCTION	29	0.846866	1.809526	0	0.023308	0.771	1461	tags=48%, list=7%, signal=52%
GO_T_CELL_DIFFERENTIATION	226	0.754506	1.920971	0	0.01639	0.4	1878	tags=42%, list=9%, signal=45%
GO_POSITIVE_REGULATION_OF_INTERFERON_BETA_PRODUCTION	30	0.760581	1.8028	0	0.023398	0.796	1744	tags=37%, list=8%, signal=40%
GO_T_CELL_PROLIFERATION	172	0.75633	1.989193	0	0.017241	0.226	1794	tags=42%, list=8%, signal=45%
GO_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PROCESS	28	0.858437	1.688591	0	0.037116	0.99	718	tags=39%, list=3%, signal=41%
GO_RESPONSE_TO_INTERFERON_ALPHA	20	0.857017	1.718355	0	0.032905	0.968	1922	tags=60%, list=9%, signal=66%

GO_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	83	0.793679	1.850895	0	0.02091	0.638	1699	tags=54%, list=8%, signal=59%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	361	0.705319	2.066495	0	0.020998	0.109	2591	tags=37%, list=12%, signal=41%
GO_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	65	0.79352	1.804832	0	0.023347	0.792	1878	tags=54%, list=9%, signal=59%
GO_LEUKOCYTE_DIFFERENTIATION	492	0.698004	1.963433	0	0.01726	0.279	2508	tags=39%, list=11%, signal=44%
GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	26	0.872198	1.759716	0	0.027029	0.905	1794	tags=77%, list=8%, signal=84%
GO_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	61	0.728227	1.78146	0	0.025214	0.849	2503	tags=44%, list=11%, signal=50%
GO_POSITIVE_REGULATION_OF_HEMOPOIESIS	178	0.705672	1.936022	0	0.016707	0.35	2659	tags=46%, list=12%, signal=51%
GO_POSITIVE_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	19	0.895768	1.728396	0	0.031311	0.957	1794	tags=84%, list=8%, signal=92%
GO_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	110	0.676643	1.849218	0	0.02103	0.646	2986	tags=44%, list=14%, signal=50%
GO_ADAPTIVE_IMMUNE_RESPONSE	375	0.802703	1.923011	0	0.016641	0.395	2002	tags=51%, list=9%, signal=55%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	32	0.78512	1.793445	0	0.024017	0.829	2547	tags=56%, list=12%, signal=64%
GO_PHAGOCYTOSIS	244	0.728161	1.940916	0	0.016514	0.337	2111	tags=38%, list=10%, signal=42%
GO_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	259	0.719716	1.957875	0	0.016549	0.292	2503	tags=44%, list=11%, signal=49%
GO_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	139	0.787494	1.817686	0	0.02268	0.739	1787	tags=43%, list=8%, signal=47%
GO_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	475	0.71857	2.079365	0	0.024802	0.094	2591	tags=39%, list=12%, signal=43%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION	198	0.672086	2.093362	0	0.024053	0.083	2130	tags=29%, list=10%, signal=32%
GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	240	0.784206	1.924668	0	0.016808	0.39	2394	tags=51%, list=11%, signal=56%

GO_REGULATION_OF_T_CELL_ACTIVATION	291	0.759037	1.99052	0	0.017159	0.223	1878	tags=43%, list=9%, signal=46%
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	421	0.734962	1.996229	0	0.018569	0.212	1855	tags=37%, list=8%, signal=39%
GO_REGULATION_OF_HEMOPOIESIS	421	0.654756	2.075563	0	0.021512	0.1	2379	tags=33%, list=11%, signal=36%
GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	239	0.744603	1.927715	0	0.016548	0.378	1878	tags=45%, list=9%, signal=48%
GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	189	0.767986	1.927852	0	0.016648	0.378	1984	tags=44%, list=9%, signal=48%
GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	57	0.858161	1.800882	0	0.023555	0.804	1835	tags=63%, list=8%, signal=69%
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	22	0.780808	1.804955	0.002045	0.02338	0.792	2547	tags=59%, list=12%, signal=67%
GO_IMMUNOLOGICAL_SYNAPSE	35	0.797977	1.771566	0	0.026406	0.875	1602	tags=40%, list=7%, signal=43%
GO_POSITIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	494	0.660645	2.133885	0	0.05398	0.05	2663	tags=32%, list=12%, signal=36%
GO_T_CELL_MEDIATED_IMMUNITY	93	0.784674	1.903693	0	0.01713	0.449	1984	tags=47%, list=9%, signal=52%
GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	36	0.823817	1.706575	0	0.034345	0.974	2348	tags=56%, list=11%, signal=62%
GO_REGULATION_OF_MACROPHAGE_MIGRATION	35	0.781408	1.676999	0	0.039437	0.993	1463	tags=46%, list=7%, signal=49%
GO_LEUKOCYTE_CELL_CELL_ADHESION	313	0.754614	1.940054	0	0.016574	0.34	1878	tags=45%, list=9%, signal=48%
GO_CYTOKINE_SECRETION	217	0.751916	1.858196	0	0.019853	0.61	1844	tags=44%, list=8%, signal=47%
GO_LYMPHOCYTE_MEDIATED_IMMUNITY	235	0.791206	1.939942	0	0.01643	0.34	2002	tags=46%, list=9%, signal=50%
GO_RESPONSE_TO_INTERFERON_GAMMA	166	0.781386	1.950556	0	0.016333	0.308	2774	tags=58%, list=13%, signal=66%

GO_CD8_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	19	0.848101	1.589159	0.004228	0.063196	1	2420	tags=68%, list=11%, signal=77%
GO_SYNCYTIUM_FORMATION	50	0.704486	1.942645	0	0.016592	0.334	2493	tags=38%, list=11%, signal=43%
GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	360	0.742376	1.959976	0	0.017553	0.29	2566	tags=45%, list=12%, signal=50%
GO_MYOBLAST_FUSION	37	0.69498	1.894916	0	0.018179	0.476	2493	tags=38%, list=11%, signal=43%
GO_REGULATION_OF_LYMPHOCYTE_ACTIVATION	398	0.755279	1.976847	0	0.017815	0.249	1787	tags=41%, list=8%, signal=44%
GO_LEUKOCYTE_PROLIFERATION	280	0.752767	1.971418	0	0.018249	0.264	1794	tags=40%, list=8%, signal=43%
GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	190	0.738759	1.924092	0	0.016693	0.394	1982	tags=40%, list=9%, signal=44%
GO_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	87	0.804347	1.886301	0	0.018748	0.509	1693	tags=48%, list=8%, signal=52%
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	54	0.704477	1.833127	0	0.022172	0.694	2986	tags=48%, list=14%, signal=56%
GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	79	0.818294	1.765371	0	0.026949	0.89	1787	tags=47%, list=8%, signal=51%
GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	35	0.841239	1.726328	0	0.031595	0.96	1693	tags=63%, list=8%, signal=68%
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	66	0.811243	1.746319	0	0.02889	0.93	1949	tags=53%, list=9%, signal=58%
GO_INTERLEUKIN_12_PRODUCTION	56	0.83612	1.787054	0	0.024841	0.84	1835	tags=54%, list=8%, signal=58%
GO_REGULATION_OF_LEUKOCYTE_MIGRATION	183	0.752287	1.830642	0	0.022243	0.701	2129	tags=47%, list=10%, signal=52%
GO_INTERLEUKIN_8_SECRETION	30	0.836872	1.691705	0	0.036717	0.985	1694	tags=50%, list=8%, signal=54%
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	183	0.793738	1.965742	0	0.017769	0.277	1984	tags=46%, list=9%, signal=51%
GO_T_CELL_MIGRATION	61	0.839423	1.839955	0	0.02138	0.672	1787	tags=57%, list=8%, signal=62%

GO_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	51	0.794797	1.833282	0	0.022184	0.694	1861	tags=47%, list=8%, signal=51%
GO_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	159	0.695834	2.027518	0	0.018326	0.158	2646	tags=40%, list=12%, signal=45%
GO_LYMPHOCYTE_HOMEOSTASIS	61	0.739533	1.953599	0	0.016463	0.302	2691	tags=46%, list=12%, signal=52%
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	251	0.714429	1.945353	0	0.016525	0.329	2348	tags=41%, list=11%, signal=46%
GO_FC_RECEPTOR_MEDIATED_STIMULATORY_SIGNALING_PATHWAY	83	0.700023	1.928083	0	0.016873	0.377	3284	tags=42%, list=15%, signal=49%
GO_LYMPHOCYTE_MIGRATION	100	0.820289	1.815523	0	0.022802	0.747	1787	tags=55%, list=8%, signal=60%
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	44	0.827268	1.810852	0	0.023126	0.767	1878	tags=61%, list=9%, signal=67%
GO_LEUKOCYTE_MEDIATED_CYTOTOXICITY	96	0.78362	1.812567	0	0.022982	0.763	1949	tags=46%, list=9%, signal=50%
GO_INTERLEUKIN_8_PRODUCTION	74	0.763168	1.823548	0	0.022404	0.72	1694	tags=39%, list=8%, signal=42%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	68	0.747054	2.061956	0	0.017683	0.111	2234	tags=29%, list=10%, signal=33%
GO_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	162	0.758995	1.957642	0	0.016464	0.292	2073	tags=47%, list=9%, signal=51%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	127	0.778547	1.912256	0	0.016568	0.421	1735	tags=45%, list=8%, signal=48%
GO_REGULATION_OF_T_CELL_DIFFERENTIATION	131	0.76304	1.913832	0	0.016586	0.42	2073	tags=48%, list=9%, signal=53%
GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	29	0.852513	1.712143	0	0.033668	0.971	1693	tags=66%, list=8%, signal=71%
GO_REGULATION_OF_LYMPHOCYTE_MIGRATION	58	0.783609	1.805821	0	0.023349	0.786	1787	tags=47%, list=8%, signal=51%
GO_T_CELL_SELECTION	47	0.80924	1.710598	0	0.033773	0.973	2640	tags=62%, list=12%, signal=70%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	123	0.79414	1.851023	0	0.020972	0.638	2129	tags=50%, list=10%, signal=55%
GO_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	56	0.77814	1.885409	0	0.018687	0.511	2537	tags=52%, list=12%, signal=58%

GO_NEGATIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	21	0.789089	1.643194	0.00404	0.046879	1	1704	tags=43%, list=8%, signal=46%
GO_INTERLEUKIN_1_BETA_PRODUCTION	82	0.789092	1.738878	0	0.029428	0.941	1748	tags=54%, list=8%, signal=58%
GO_REGULATION_OF_CELL_KILLING	87	0.793013	1.781918	0	0.025232	0.849	2348	tags=51%, list=11%, signal=56%
GO_POSITIVE_REGULATION_OF_CYTOKINE_SECRETION	128	0.76589	1.786933	0	0.024773	0.84	1941	tags=45%, list=9%, signal=49%
GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	409	0.704167	1.96605	0	0.017927	0.276	2503	tags=41%, list=11%, signal=45%
GO_REGULATION_OF_SYNCYTIUM_FORMATION_BY_PLASMA_MEMBRANE_FUSION	27	0.783439	1.773433	0	0.026265	0.87	2493	tags=52%, list=11%, signal=58%
GO_NIK_NF_KAPPAB_SIGNALING	156	0.657684	2.135638	0	0.07848	0.049	2891	tags=32%, list=13%, signal=37%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	89	0.703419	2.045506	0	0.017724	0.132	2234	tags=30%, list=10%, signal=34%
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	19	0.894618	1.628814	0	0.050755	1	1262	tags=53%, list=6%, signal=56%
GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	70	0.773314	1.815929	0	0.022797	0.747	2234	tags=56%, list=10%, signal=62%
GO_POSITIVE_REGULATION_OF_CELL_ADHESION	376	0.679959	1.911566	0	0.016627	0.421	2099	tags=38%, list=10%, signal=41%
GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PROCESS	20	0.906751	1.696208	0	0.035772	0.983	718	tags=45%, list=3%, signal=46%
GO_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	208	0.614475	1.932516	0	0.016662	0.359	2986	tags=36%, list=14%, signal=41%
GO_POSITIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	26	0.736571	1.712023	0	0.033654	0.971	1693	tags=38%, list=8%, signal=42%
GO_I_KAPPAB_PHOSPHORYLATION	18	0.836097	1.868993	0	0.019271	0.572	1748	tags=39%, list=8%, signal=42%
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	22	0.86151	1.61853	0	0.054254	1	1809	tags=55%, list=8%, signal=59%
GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_INVOLVED_IN_INFLAMMATORY_RESPONSE	63	0.739126	1.814857	0	0.022816	0.748	2547	tags=44%, list=12%, signal=50%

GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	44	0.825352	1.674626	0	0.039883	0.993	1949	tags=55%, list=9%, signal=60%
GO_REGULATION_OF_MAST_CELL_ACTIVATION	38	0.749776	1.725015	0	0.031824	0.96	2167	tags=47%, list=10%, signal=52%
GO_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	24	0.780567	1.691406	0.002045	0.036738	0.985	798	tags=33%, list=4%, signal=35%
GO_INTERLEUKIN_1_PRODUCTION	95	0.779269	1.772164	0	0.026378	0.873	1748	tags=52%, list=8%, signal=56%
GO_NEGATIVE_REGULATION_OF_EXOCYTOSIS	28	0.745422	1.69772	0	0.035498	0.981	1704	tags=36%, list=8%, signal=39%
GO_MHC_PROTEIN_BINDING	23	0.835355	1.652874	0.002062	0.044927	1	1189	tags=48%, list=5%, signal=51%
GO_T_CELL_MEDIATED_CYTOTOXICITY	37	0.76858	1.703915	0.002037	0.034582	0.975	1949	tags=51%, list=9%, signal=56%
GO_POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	66	0.839014	1.829462	0	0.022055	0.704	1537	tags=48%, list=7%, signal=52%
GO_CELLULAR_DEFENSE_RESPONSE	48	0.831501	1.671595	0	0.040551	0.994	1879	tags=56%, list=9%, signal=61%
GO_REGULATION_OF_T_CELL_MIGRATION	41	0.81156	1.810761	0	0.023093	0.769	2101	tags=51%, list=10%, signal=57%
GO_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY	150	0.592777	1.969041	0	0.018553	0.271	2547	tags=28%, list=12%, signal=31%
GO_RESPIRATORY_BURST	30	0.825143	1.712176	0	0.033699	0.971	2079	tags=50%, list=9%, signal=55%
GO_MYELOID_LEUKOCYTE_DIFFERENTIATION	196	0.664277	1.909455	0	0.016501	0.426	2503	tags=38%, list=11%, signal=43%
GO_DENDRITIC_CELL_DIFFERENTIATION	39	0.804437	1.868333	0	0.019164	0.575	2847	tags=59%, list=13%, signal=68%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	89	0.808073	1.865433	0	0.019237	0.585	1984	tags=49%, list=9%, signal=54%

GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	33	0.804379	1.814603	0	0.022833	0.749	1878	tags=58%, list=9%, signal=63%
GO_LEUKOCYTE_ACTIVATION_INVOLVED_IN_INFLAMMATORY_RESPONSE	42	0.887616	1.641745	0	0.047138	1	1463	tags=67%, list=7%, signal=71%
GO_TYPE_I_INTERFERON_PRODUCTION	119	0.689816	2.048374	0	0.017887	0.129	2547	tags=33%, list=12%, signal=37%
GO_INTERLEUKIN_2_PRODUCTION	62	0.767136	1.753969	0.00207	0.027728	0.916	1564	tags=47%, list=7%, signal=50%
GO_REGULATION_OF_CELL_CELL_ADHESION	375	0.692488	1.958907	0	0.016744	0.291	1878	tags=37%, list=9%, signal=40%
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	54	0.814371	1.815482	0	0.022737	0.747	1878	tags=59%, list=9%, signal=65%
GO_RESPONSE_TO_AMYLOID_BETA	45	0.822319	1.748974	0	0.028611	0.928	1536	tags=49%, list=7%, signal=52%
GO_INTERFERON_BETA_PRODUCTION	49	0.735619	1.898888	0	0.017545	0.46	2547	tags=41%, list=12%, signal=46%
GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	133	0.799937	1.949071	0	0.016264	0.312	1984	tags=47%, list=9%, signal=51%
GO_RESPONSE_TO_INTERFERON_BETA	26	0.865676	1.839537	0	0.02142	0.675	1941	tags=58%, list=9%, signal=63%
GO_CELL_KILLING	146	0.742431	1.855253	0	0.020381	0.619	2400	tags=41%, list=11%, signal=46%
GO_MYD88_DEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	35	0.850245	1.703173	0	0.034525	0.977	2284	tags=54%, list=10%, signal=60%
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	458	0.709903	2.015769	0	0.018143	0.178	2343	tags=36%, list=11%, signal=40%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	117	0.784342	1.922574	0	0.016561	0.396	1984	tags=44%, list=9%, signal=48%
GO_POSITIVE_REGULATION_OF_MACROPHAGE_ACTIVATION	22	0.820509	1.654143	0.002075	0.044616	1	1439	tags=55%, list=7%, signal=58%
GO_POSITIVE_REGULATION_OF_CELL_KILLING	57	0.808597	1.710659	0	0.033805	0.973	1949	tags=47%, list=9%, signal=52%

GO_B_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	67	0.766306	1.964694	0	0.017422	0.278	2344	tags=45%, list=11%, signal=50%
GO_LEUKOCYTE_HOMEOSTASIS	83	0.780179	1.889945	0	0.018841	0.496	2129	tags=47%, list=10%, signal=52%
GO_INTERLEUKIN_10_PRODUCTION	50	0.84242	1.769502	0	0.026575	0.879	1693	tags=56%, list=8%, signal=61%
GO_FICOLIN_1_RICH_GRANULE_MEMBRANE	57	0.789797	1.897648	0	0.017625	0.467	1794	tags=40%, list=8%, signal=44%
GO_REGULATION_OF_MYOBLAST_FUSION	20	0.770395	1.721433	0	0.032572	0.964	2493	tags=50%, list=11%, signal=56%
GO_LEUKOCYTE_MIGRATION	413	0.74811	1.870771	0	0.019234	0.563	2365	tags=48%, list=11%, signal=52%
GO_LEUKOCYTE_CHEMOTAXIS	200	0.798099	1.816334	0	0.022828	0.747	2101	tags=53%, list=10%, signal=58%
GO_PHAGOCYTIC_CUP	24	0.843301	1.727441	0	0.031315	0.958	2095	tags=63%, list=10%, signal=69%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	35	0.847839	1.776342	0	0.025866	0.864	1835	tags=51%, list=8%, signal=56%
GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	206	0.762026	1.931267	0	0.016503	0.363	1735	tags=42%, list=8%, signal=45%
GO_VIRAL_GENOME_REPLICATION	113	0.622485	1.93679	0	0.01678	0.349	2534	tags=33%, list=12%, signal=37%
GO_POSITIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR_ACTIVITY	143	0.712442	2.051414	0	0.018671	0.127	1861	tags=33%, list=8%, signal=36%
GO_MACROPHAGE_ACTIVATION	82	0.833666	1.743377	0	0.029126	0.936	2196	tags=59%, list=10%, signal=65%
GO_OSTEOCLAST_DIFFERENTIATION	94	0.672125	1.805594	0	0.02337	0.789	2503	tags=40%, list=11%, signal=45%
GO_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	18	0.877789	1.634011	0.004219	0.049017	1	999	tags=56%, list=5%, signal=58%
GO_POSITIVE_REGULATION_OF_T_CELL_MIGRATION	29	0.825386	1.721895	0.002096	0.032613	0.963	2640	tags=62%, list=12%, signal=70%

GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	17	0.863167	1.60176	0	0.05914	1	1693	tags=65%, list=8%, signal=70%
GO_B_CELL_PROLIFERATION	92	0.783837	1.898422	0	0.017588	0.466	1784	tags=37%, list=8%, signal=40%
GO_REGULATION_OF_B_CELL_RECEPTOR_SIGNALING_PATHWAY	26	0.843848	1.719784	0	0.032913	0.965	1555	tags=58%, list=7%, signal=62%
GO_T_CELL_CYTOKINE_PRODUCTION	40	0.820193	1.825456	0	0.022267	0.716	1878	tags=50%, list=9%, signal=55%
GO_ANTIGEN_BINDING	44	0.842617	1.715769	0	0.033157	0.969	1992	tags=66%, list=9%, signal=72%
GO_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	54	0.819454	1.781158	0	0.025177	0.849	2348	tags=52%, list=11%, signal=58%
GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	147	0.797555	1.959463	0	0.017421	0.291	1984	tags=50%, list=9%, signal=54%
GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	93	0.803633	1.875998	0	0.018622	0.551	1984	tags=52%, list=9%, signal=56%
GO_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	26	0.795327	1.67547	0.00211	0.039707	0.993	2503	tags=62%, list=11%, signal=69%
GO_POSITIVE_REGULATION_OF_MACROPHAGE_MIGRATION	20	0.870037	1.727502	0	0.03135	0.958	1463	tags=55%, list=7%, signal=59%
GO_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	65	0.792652	1.830283	0	0.022067	0.701	2394	tags=54%, list=11%, signal=60%
GO_INTERLEUKIN_6_PRODUCTION	139	0.758804	1.849522	0	0.021059	0.645	2225	tags=46%, list=10%, signal=51%
GO_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	51	0.792239	1.890717	0	0.018795	0.493	2348	tags=55%, list=11%, signal=61%
GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	195	0.686704	2.031096	0	0.018258	0.153	2348	tags=39%, list=11%, signal=43%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	52	0.817755	1.755902	0	0.027571	0.911	1530	tags=50%, list=7%, signal=54%
GO_PHOSPHATIDYLINOSITOL_3_4_BISPHOSPHATE_BINDING	26	0.680059	1.867987	0	0.019177	0.576	1548	tags=27%, list=7%, signal=29%
GO_MACROPHAGE_MIGRATION	46	0.773627	1.703446	0	0.034512	0.975	1463	tags=43%, list=7%, signal=46%

GO_INTERLEUKIN_4_PRODUCTION	33	0.768622	1.704076	0.002075	0.034622	0.975	2503	tags=61%, list=11%, signal=68%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	47	0.781344	1.71628	0	0.033071	0.968	1694	tags=45%, list=8%, signal=48%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MIGRATION	35	0.810504	1.714185	0.002096	0.033483	0.969	1787	tags=51%, list=8%, signal=56%
GO_CELL_CHEMOTAXIS	270	0.765652	1.828884	0	0.022113	0.705	2344	tags=50%, list=11%, signal=55%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_SECRETION	16	0.862207	1.508767	0.004167	0.100068	1	1694	tags=69%, list=8%, signal=74%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	82	0.805328	1.832708	0	0.022083	0.694	1693	tags=46%, list=8%, signal=50%
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	84	0.738638	1.977912	0	0.017919	0.247	2464	tags=44%, list=11%, signal=49%
GO_T_CELL_HOMEOSTASIS	38	0.683877	1.866767	0	0.01903	0.58	2691	tags=42%, list=12%, signal=48%
GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	79	0.803399	1.807855	0	0.023377	0.776	1941	tags=54%, list=9%, signal=59%
GO_NEGATIVE_REGULATION_OF_B_CELL_PROLIFERATION	16	0.849144	1.603886	0.002083	0.058684	1	1159	tags=50%, list=5%, signal=53%
GO_MYELOID_CELL_DIFFERENTIATION	368	0.603602	2.016002	0	0.018554	0.177	3010	tags=34%, list=14%, signal=39%
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS	232	0.649019	2.117239	0	0.032903	0.064	2483	tags=30%, list=11%, signal=34%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	21	0.823096	1.642053	0.004202	0.047082	1	1537	tags=57%, list=7%, signal=61%

GO_B_CELL_HOMEOSTASIS	28	0.770019	1.806259	0	0.023364	0.785	2691	tags=50%, list=12%, signal=57%
GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	52	0.714082	1.708888	0.002028	0.033889	0.974	1941	tags=44%, list=9%, signal=48%
GO_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	29	0.776513	1.657801	0.002008	0.043673	0.998	1949	tags=52%, list=9%, signal=57%
GO_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	128	0.762824	1.905876	0	0.016988	0.442	1982	tags=44%, list=9%, signal=48%
GO_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	104	0.779091	1.783816	0	0.025127	0.846	1693	tags=44%, list=8%, signal=48%
GO_B_CELL_MEDIATED_IMMUNITY	111	0.791582	1.885557	0	0.018752	0.51	2002	tags=45%, list=9%, signal=49%
GO_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	218	0.747262	1.909629	0	0.016635	0.424	1761	tags=40%, list=8%, signal=43%
GO_SPECIFIC_GRANULE_MEMBRANE	87	0.774442	1.887699	0	0.018985	0.504	3126	tags=59%, list=14%, signal=68%
GO_RESPONSE_TO_CHEMOKINE	88	0.842962	1.739819	0	0.029374	0.938	1863	tags=61%, list=8%, signal=67%
GO_B_CELL_ACTIVATION	238	0.742005	1.98591	0	0.017381	0.232	2952	tags=47%, list=13%, signal=53%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	30	0.836231	1.685204	0	0.037771	0.99	1564	tags=57%, list=7%, signal=61%
GO_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	152	0.673905	1.971729	0	0.018415	0.261	2510	tags=37%, list=11%, signal=41%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	51	0.768307	1.875774	0	0.018607	0.551	1941	tags=47%, list=9%, signal=51%
GO_POSITIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	39	0.649638	1.764525	0	0.026791	0.891	2492	tags=36%, list=11%, signal=40%
GO_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	99	0.695489	1.919913	0	0.016206	0.403	2891	tags=42%, list=13%, signal=49%
GO_CYTOKINE_METABOLIC_PROCESS	111	0.76819	1.883707	0	0.018628	0.518	1612	tags=41%, list=7%, signal=44%

GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	18	0.849835	1.644999	0	0.046317	1	1693	tags=72%, list=8%, signal=78%
GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	15	0.922282	1.609215	0	0.057138	1	999	tags=67%, list=5%, signal=70%
GO_REGULATION_OF_B_CELL_PROLIFERATION	60	0.810683	1.825183	0	0.022278	0.716	1159	tags=40%, list=5%, signal=42%
GO_NEGATIVE_REGULATION_OF_VIRAL_LIFE_CYCLE	74	0.700029	1.829505	0	0.022126	0.704	2038	tags=39%, list=9%, signal=43%
GO_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	74	0.690953	2.005027	0	0.01867	0.198	1744	tags=26%, list=8%, signal=28%
GO_T_CELL_APOPTOTIC_PROCESS	48	0.740908	1.843197	0	0.021438	0.662	2712	tags=48%, list=12%, signal=55%
GO_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	86	0.641631	1.880628	0	0.018723	0.527	2986	tags=42%, list=14%, signal=48%
GO_MYELOID_LEUKOCYTE_MIGRATION	190	0.791666	1.804069	0	0.023362	0.793	1904	tags=52%, list=9%, signal=56%
GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	182	0.73634	1.879466	0	0.018796	0.534	2079	tags=44%, list=9%, signal=48%
GO_PROTEIN_AUTOPHOSPHORYLATION	223	0.507402	1.92345	0	0.016739	0.395	2900	tags=24%, list=13%, signal=27%
GO_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	322	0.717051	1.886812	0	0.018869	0.508	2224	tags=41%, list=10%, signal=45%
GO_T_CELL_RECEPTOR_COMPLEX	21	0.839008	1.510183	0.008565	0.099402	1	1610	tags=57%, list=7%, signal=62%
GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_SUPERFAMILY_BINDING	41	0.714936	1.85461	0.004264	0.02035	0.62	2331	tags=41%, list=11%, signal=46%
GO_REGULATION_OF_MYOTUBE_DIFFERENTIATION	49	0.593265	1.673167	0.005882	0.040171	0.993	2121	tags=27%, list=10%, signal=29%
GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	85	0.757766	1.878069	0	0.018811	0.542	1982	tags=44%, list=9%, signal=48%

GO_REGULATORY_T_CELL_DIFFERENTIATION	28	0.856444	1.693619	0	0.03619	0.985	1641	tags=61%, list=7%, signal=66%
GO_NEGATIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	17	0.816996	1.732606	0.002088	0.030734	0.95	2348	tags=47%, list=11%, signal=53%
GO_POSITIVE_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	75	0.717609	1.899907	0	0.017542	0.457	2891	tags=45%, list=13%, signal=52%
GO_MYELOID_DENDRITIC_CELL_ACTIVATION	27	0.83214	1.811952	0	0.023025	0.765	2847	tags=70%, list=13%, signal=81%
GO_REGULATION_OF_T_CELL_CYTOKINE_PRODUCTION	30	0.839294	1.737343	0.002132	0.029693	0.944	1332	tags=53%, list=6%, signal=57%
GO_POSITIVE_REGULATION_OF_PHAGOCYTOSIS	63	0.772464	1.754077	0	0.027728	0.915	1794	tags=46%, list=8%, signal=50%
GO_INTERLEUKIN_1_SECRETION	53	0.755497	1.71733	0	0.033003	0.968	1713	tags=51%, list=8%, signal=55%
GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	31	0.76904	1.838379	0	0.021638	0.679	2493	tags=65%, list=11%, signal=73%
GO_POSITIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	21	0.832583	1.609012	0	0.05717	1	2142	tags=67%, list=10%, signal=74%
GO_LYMPHOCYTE_CHEMOTAXIS	52	0.844449	1.732362	0	0.030704	0.95	2216	tags=67%, list=10%, signal=75%
GO_GLIAL_CELL_ACTIVATION	49	0.875162	1.69767	0	0.035459	0.981	1463	tags=59%, list=7%, signal=63%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	16	0.88127	1.58078	0	0.066352	1	1512	tags=75%, list=7%, signal=80%
GO_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	43	0.824517	1.790381	0	0.024584	0.836	1159	tags=44%, list=5%, signal=47%
GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	70	0.614499	1.750618	0	0.028409	0.926	2342	tags=29%, list=11%, signal=32%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	89	0.770278	1.819478	0	0.022614	0.729	2351	tags=47%, list=11%, signal=53%
GO_ALPHA_BETA_T_CELL_PROLIFERATION	29	0.832186	1.705138	0	0.03433	0.974	1693	tags=66%, list=8%, signal=71%

GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	136	0.756201	1.920528	0	0.016186	0.4	1699	tags=43%, list=8%, signal=46%
GO_THYMIC_T_CELL_SELECTION	21	0.817989	1.654786	0	0.044462	0.999	1699	tags=48%, list=8%, signal=52%
GO_INTERLEUKIN_2_BIOSYNTHETIC_PROCESS	22	0.837284	1.631797	0.006641	0.049683	1	1541	tags=55%, list=7%, signal=59%
GO_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	36	0.580683	1.793584	0.002012	0.02407	0.827	1926	tags=22%, list=9%, signal=24%
GO_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	21	0.88374	1.558488	0	0.075637	1	878	tags=62%, list=4%, signal=64%
GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	30	0.813437	1.808866	0	0.023325	0.771	1530	tags=47%, list=7%, signal=50%
GO_NEGATIVE_REGULATION_OF_VIRAL_PROCESS	89	0.678502	1.877101	0	0.018856	0.547	2284	tags=37%, list=10%, signal=41%
GO_SH2_DOMAIN_BINDING	35	0.735767	1.859379	0	0.019706	0.606	2797	tags=43%, list=13%, signal=49%
GO_IMMUNOGLOBULIN_PRODUCTION	101	0.739307	1.944789	0	0.016399	0.329	2493	tags=41%, list=11%, signal=46%
GO_GRANULOCYTE_MIGRATION	128	0.818331	1.786576	0	0.024662	0.84	1904	tags=57%, list=9%, signal=62%
GO_REGULATION_OF_PHAGOCYTOSIS	86	0.760257	1.818115	0	0.022635	0.737	1794	tags=42%, list=8%, signal=45%
GO_LEUKOCYTE_APOPTOTIC_PROCESS	103	0.777835	1.869699	0	0.019203	0.569	1787	tags=44%, list=8%, signal=47%
GO_POSITIVE_REGULATION_OF_CHEMOTAXIS	130	0.755838	1.817303	0	0.022746	0.741	1863	tags=42%, list=8%, signal=45%
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	51	0.661767	1.699829	0	0.035225	0.98	2194	tags=35%, list=10%, signal=39%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	112	0.728414	1.915642	0	0.016255	0.415	1699	tags=40%, list=8%, signal=43%
GO_DEFENSE_RESPONSE_TO_BACTERIUM	209	0.672049	1.852704	0	0.020583	0.629	2776	tags=39%, list=13%, signal=44%

GO_CYTOKINE_PRODUCTION_INVOLVED_IN_INFLAMMATORY_RESPONSE	40	0.749268	1.78218	0	0.025278	0.849	2224	tags=40%, list=10%, signal=44%
GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	44	0.787339	1.767538	0	0.026711	0.883	2234	tags=57%, list=10%, signal=63%
GO_REGULATION_OF_VIRAL_LIFE_CYCLE	132	0.611931	1.883644	0	0.018533	0.518	2642	tags=33%, list=12%, signal=37%
GO_LYMPHOCYTE_APOPTOTIC_PROCESS	71	0.728088	1.890886	0	0.018857	0.491	2712	tags=44%, list=12%, signal=50%
GO_PURINERGIC_RECEPTOR_ACTIVITY	23	0.874581	1.66846	0	0.041179	0.995	895	tags=52%, list=4%, signal=54%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	32	0.851097	1.708075	0	0.034048	0.974	1693	tags=59%, list=8%, signal=64%
GO_ACUTE_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	19	0.856623	1.648338	0	0.045649	1	747	tags=42%, list=3%, signal=44%
GO_POSITIVE_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL	37	0.692906	1.678587	0.002041	0.038954	0.992	2194	tags=38%, list=10%, signal=42%
GO_POSITIVE_REGULATION_OF_MONOCYTE_CHEMOTAXIS	18	0.873965	1.64759	0.002012	0.04584	1	997	tags=56%, list=5%, signal=58%
GO_NEUTROPHIL_MIGRATION	107	0.838374	1.746261	0	0.028851	0.93	1863	tags=62%, list=8%, signal=67%
GO_POSITIVE_REGULATION_OF_JNK_CASCADE	131	0.570891	1.758142	0	0.027238	0.908	2891	tags=31%, list=13%, signal=35%
GO_REGULATION_OF_MONOCYTE_CHEMOTAXIS	24	0.847239	1.614016	0.002045	0.055591	1	1159	tags=54%, list=5%, signal=57%
GO_TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	81	0.717407	1.977988	0	0.018146	0.247	2510	tags=44%, list=11%, signal=50%
GO_MONONUCLEAR_CELL_MIGRATION	77	0.831299	1.761796	0	0.027062	0.9	1863	tags=57%, list=8%, signal=62%
GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	140	0.748506	1.95296	0	0.016251	0.303	2351	tags=50%, list=11%, signal=56%

GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	43	0.787939	1.88521	0	0.01862	0.513	1878	tags=47%, list=9%, signal=51%
GO_NEUROINFLAMMATORY_RESPONSE	61	0.881156	1.760387	0	0.027136	0.901	1463	tags=62%, list=7%, signal=67%
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS_WITHIN_A_TISSUE	29	0.660955	1.778674	0.002062	0.025467	0.857	2121	tags=31%, list=10%, signal=34%
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT	232	0.559044	1.691116	0.002008	0.036812	0.987	3000	tags=32%, list=14%, signal=37%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	15	0.848612	1.628079	0.002088	0.050871	1	2348	tags=73%, list=11%, signal=82%
GO_DEFENSE_RESPONSE_TO_GRAM_POSITIVE_BACTERIUM	69	0.695502	1.813331	0	0.022993	0.759	2721	tags=41%, list=12%, signal=46%
GO_MONOCYTE_CHEMOTAXIS	55	0.852848	1.678406	0	0.038963	0.992	1863	tags=65%, list=8%, signal=71%
GO_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	163	0.662148	1.918805	0	0.01625	0.407	1878	tags=34%, list=9%, signal=37%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	23	0.730447	1.551977	0.031621	0.079015	1	984	tags=39%, list=4%, signal=41%
GO_POSITIVE_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	23	0.855244	1.725974	0	0.031673	0.96	997	tags=48%, list=5%, signal=50%
GO_POSITIVE_REGULATION_OF_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	88	0.709538	1.854866	0	0.020385	0.619	3047	tags=51%, list=14%, signal=59%
GO_REGULATION_OF_CHEMOTAXIS	199	0.695545	1.827111	0	0.02222	0.711	1761	tags=33%, list=8%, signal=36%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	46	0.831702	1.8617	0	0.019669	0.599	2348	tags=59%, list=11%, signal=66%

GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	115	0.571194	1.630533	0.0019988	0.050135	1	2897	tags=34%, list=13%, signal=39%
GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	30	0.733026	1.605951	0.0019198	0.058043	1	2869	tags=43%, list=13%, signal=50%
GO_NEGATIVE_REGULATION_OF_HEMOPOIESIS	130	0.620958	1.861355	0	0.01972	0.6	2493	tags=32%, list=11%, signal=36%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	94	0.668702	1.86286	0	0.01955	0.596	2493	tags=39%, list=11%, signal=44%
GO_VITAMIN_D_METABOLIC_PROCESS	22	0.667356	1.517227	0.0154887	0.096468	1	2024	tags=36%, list=9%, signal=40%

High-expression *SLAMF8* vs. low-expression *SLAMF8* colorectal cancer tissues (GSE14333)

NAME	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	RANK.AT.MAX	LEADING.EDGE
GO_DOUBLE_STRANDED_RNA_BINDING	71	0.383642	1.753444	0.02686	0.068359	0.986	3337	tags=15%, list=14%, signal=18%
GO_T_CELL_RECEPTOR_SIGNALING_PATHWAY	177	0.49015	1.916435	0.0160644	0.069494	0.761	4220	tags=29%, list=18%, signal=36%
GO_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	226	0.528749	1.845068	0.0204492	0.058657	0.904	4232	tags=34%, list=18%, signal=41%
GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	41	0.597512	1.883927	0.0020833	0.06072	0.842	3812	tags=37%, list=16%, signal=44%

GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	367	0.51636	1.884659	0.0010331	0.061126	0.84	4747	tags=35%, list=20%, signal=43%
GO_FC_RECEPTOR_SIGNALING_PATHWAY	176	0.444502	1.981939	0.004132	0.101125	0.573	4979	tags=26%, list=21%, signal=33%
GO_NEGATIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	28	0.647988	1.757378	0.004107	0.068666	0.985	4828	tags=57%, list=21%, signal=72%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	64	0.53041	1.916082	0.004264	0.069166	0.761	3285	tags=33%, list=14%, signal=38%
GO_ALPHA_BETA_T_CELL_DIFFERENTIATION	95	0.489395	1.609541	0.046316	0.107697	1	5019	tags=42%, list=21%, signal=53%
GO_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	38	0.595375	1.775356	0.01626	0.068181	0.978	4106	tags=45%, list=17%, signal=54%
GO_T_HELPER_1_TYPE_IMMUNE_RESPONSE	41	0.581493	1.653433	0.0150021	0.0926	1	2727	tags=41%, list=12%, signal=47%
GO_NEGATIVE_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	20	0.556472	1.60799	0.040241	0.107877	1	4828	tags=50%, list=21%, signal=63%
GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	100	0.527208	1.719737	0.019108	0.074375	0.997	1290	tags=25%, list=5%, signal=26%

GO_RESPONSE_TO_TYPE_I_INTERFERON	88	0.528139	1.775453	0.040685	0.068324	0.978	3892	tags=33%, list=17%, signal=39%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	58	0.571468	1.746833	0.014614	0.068831	0.991	2983	tags=36%, list=13%, signal=41%
GO_ALPHA_BETA_T_CELL_ACTIVATION	125	0.567392	1.830541	0.006198	0.059295	0.92	3220	tags=37%, list=14%, signal=42%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	143	0.567369	1.881682	0	0.060426	0.851	4537	tags=43%, list=19%, signal=53%
GO_NATURAL_KILLER_CELL_ACTIVATION	77	0.559543	1.728608	0.008621	0.072389	0.993	4334	tags=40%, list=18%, signal=49%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	45	0.516947	1.628626	0.026749	0.100979	1	2801	tags=31%, list=12%, signal=35%
GO_NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_KINASE_ACTIVITY	45	0.572785	1.88713	0.00404	0.062042	0.835	912	tags=20%, list=4%, signal=21%
GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	69	0.513923	1.639782	0.030612	0.096635	1	5019	tags=45%, list=21%, signal=57%
GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	168	0.513866	1.820689	0.01222	0.060451	0.93	4723	tags=40%, list=20%, signal=50%
GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	305	0.615113	2.031769	0	0.15916	0.394	4362	tags=46%, list=19%, signal=56%

GO_T_CELL_ACTIVATION	432	0.555944	1.982338	0.002045	0.105793	0.572	4362	tags=40%, list=19%, signal=48%
GO_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	61	0.594571	1.78903	0.01006	0.065534	0.967	4405	tags=46%, list=19%, signal=56%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	91	0.60838	1.892767	0.008282	0.06136	0.823	4362	tags=47%, list=19%, signal=58%
GO_LYMPHOCYTE_DIFFERENTIATION	336	0.512893	1.849743	0.010438	0.058444	0.898	4723	tags=39%, list=20%, signal=48%
GO_DEFENSE_RESPONSE_TO_VIRUS	218	0.50743	1.885747	0.008547	0.061273	0.836	3673	tags=32%, list=16%, signal=37%
GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	42	0.686726	2.080969	0	0.2714	0.283	1621	tags=31%, list=7%, signal=33%
GO_POSITIVE_REGULATION_OF_INTERFERON_ALPHA_PRODUCTION	22	0.582119	1.645835	0.030612	0.096256	1	3673	tags=41%, list=16%, signal=48%
GO_RESPONSE_TO_VIRUS	295	0.508219	1.947244	0.006424	0.08376	0.671	3742	tags=31%, list=16%, signal=36%
GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	60	0.472705	1.563552	0.04888	0.125248	1	4909	tags=40%, list=21%, signal=50%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	30	0.628481	1.906292	0.006036	0.066249	0.783	3839	tags=33%, list=16%, signal=40%

GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	83	0.530324	1.735621	0.012397	0.071594	0.992	5019	tags=46%, list=21%, signal=58%
GO_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	32	0.662459	1.771591	0.004149	0.068617	0.98	5862	tags=63%, list=25%, signal=83%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	203	0.619851	1.979063	0.002079	0.101223	0.585	4423	tags=48%, list=19%, signal=58%
GO_INTERFERON_GAMMA_PRODUCTION	100	0.611245	1.802486	0.00823	0.063859	0.947	3092	tags=44%, list=13%, signal=50%
GO_ACTIVATED_T_CELL_PROLIFERATION	39	0.503599	1.524933	0.029167	0.140825	1	5911	tags=51%, list=25%, signal=68%
GO_CELLULAR_RESPONSE_TO_INTERFERON_BETA	18	0.630759	1.633326	0.039014	0.099806	1	3189	tags=44%, list=14%, signal=51%
GO_ACTIVATION_OF_INNATE_IMMUNE_RESPONSE	290	0.493433	2.009849	0.002096	0.124322	0.458	3892	tags=26%, list=17%, signal=31%
GO_MYD88_INDEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	32	0.522131	1.752095	0.018519	0.068576	0.986	3153	tags=22%, list=13%, signal=25%
GO_INTERFERON_ALPHA_PRODUCTION	29	0.626119	1.724703	0.012526	0.073341	0.994	3673	tags=45%, list=16%, signal=53%

GO_T_CELL_DIFFERENTIATION	226	0.528922	1.823678	0.0010571	0.060361	0.926	4558	tags=42%, list=19%, signal=51%
GO_POSITIVE_REGULATION_OF_INTERFERON_BETA_PRODUCTION	30	0.593329	1.857831	0.0040073	0.057779	0.889	4881	tags=40%, list=21%, signal=50%
GO_T_CELL_PROLIFERATION	172	0.578607	1.901161	0.0020062	0.064577	0.797	4294	tags=45%, list=18%, signal=54%
GO_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PROCESS	28	0.700841	1.736839	0.0083668	0.071074	0.992	3953	tags=57%, list=17%, signal=69%
GO_RESPONSE_TO_INTERFERON_ALPHA	20	0.642976	1.640341	0.02935	0.096542	1	2737	tags=35%, list=12%, signal=40%
GO_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	83	0.571025	1.802738	0.0012474	0.063928	0.947	4909	tags=48%, list=21%, signal=61%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	361	0.509011	1.991695	0.0021055	0.122188	0.541	3923	tags=28%, list=17%, signal=33%
GO_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	65	0.526346	1.64926	0.0032787	0.094461	1	1290	tags=26%, list=5%, signal=28%
GO_LEUKOCYTE_DIFFERENTIATION	492	0.48498	1.870467	0.0041755	0.059387	0.875	4362	tags=34%, list=19%, signal=41%

GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	26	0.619103	1.607067	0.0016701	0.108387	1	2727	tags=50%, list=12%, signal=56%
GO_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	61	0.528031	1.699452	0.0080645	0.078796	0.999	4511	tags=39%, list=19%, signal=49%
GO_POSITIVE_REGULATION_OF_HEMOPOIESIS	178	0.527321	1.893671	0	0.061329	0.821	4537	tags=38%, list=19%, signal=47%
GO_POSITIVE_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	19	0.675712	1.632503	0.0180036	0.099878	1	2727	tags=58%, list=12%, signal=65%
GO_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	110	0.480341	1.723573	0.0061355	0.073413	0.994	4537	tags=35%, list=19%, signal=44%
GO_ADAPTIVE_IMMUNE_RESPONSE	375	0.603362	1.909092	0.0081114	0.069302	0.776	4747	tags=50%, list=20%, signal=62%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	32	0.590207	1.863418	0	0.057001	0.884	3285	tags=44%, list=14%, signal=51%
GO_PHAGOCYTOSIS	244	0.579946	2.000153	0	0.13285	0.494	3483	tags=36%, list=15%, signal=41%
GO_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	259	0.522377	1.908355	0.0021114	0.066743	0.779	4537	tags=39%, list=19%, signal=48%
GO_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	139	0.654879	1.941725	0	0.076496	0.685	3953	tags=49%, list=17%, signal=58%
GO_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	475	0.519058	2.053773	0.00207	0.211872	0.341	4340	tags=31%, list=18%, signal=38%

GO_ANTIGEN_PROCESSING_AND_PRESENTATION	198	0.502073	2.212674	0.0020558	0.20959	0.087	4064	tags=23%, list=17%, signal=27%
GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	240	0.580635	1.87715	0.0040733	0.059839	0.865	4932	tags=49%, list=21%, signal=62%
GO_REGULATION_OF_T_CELL_ACTIVATION	291	0.578692	1.977132	0.0020533	0.097981	0.593	4362	tags=43%, list=19%, signal=53%
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	421	0.574911	2.009983	0	0.129422	0.458	3798	tags=37%, list=16%, signal=43%
GO_REGULATION_OF_HEMOPOIESIS	421	0.454115	1.950592	0.0021011	0.084778	0.663	4537	tags=30%, list=19%, signal=37%
GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	239	0.589185	1.99143	0	0.118755	0.542	4423	tags=44%, list=19%, signal=54%
GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	189	0.596565	2.017376	0	0.131928	0.437	2689	tags=33%, list=11%, signal=37%
GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	57	0.629001	1.779578	0.00616	0.067844	0.974	3092	tags=46%, list=13%, signal=52%
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	22	0.548	1.563311	0.0483190	0.125288	1	3069	tags=41%, list=13%, signal=47%
GO_IMMUNOLOGICAL_SYNAPSE	35	0.651923	1.758961	0.0241194	0.068468	0.985	5089	tags=54%, list=22%, signal=69%
GO_POSITIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	494	0.468012	2.03806	0	0.17161	0.382	3923	tags=25%, list=17%, signal=29%

GO_T_CELL_MEDIATED_IMMUNITY	93	0.613577	1.938337	0	0.077157	0.695	4275	tags=48%, list=18%, signal=59%
GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	36	0.701648	1.753554	0.00813	0.068477	0.986	3923	tags=58%, list=17%, signal=70%
GO_REGULATION_OF_MACROPHAGE_MIGRATION	35	0.645928	1.668615	0.016495	0.087813	1	2643	tags=43%, list=11%, signal=48%
GO_LEUKOCYTE_CELL_CELL_ADHESION	313	0.588336	1.984448	0	0.109311	0.564	4239	tags=43%, list=18%, signal=52%
GO_CYTOKINE_SECRETION	217	0.623457	1.945327	0	0.08173	0.675	3548	tags=44%, list=15%, signal=52%
GO_LYMPHOCYTE_MEDIATED_IMMUNITY	235	0.607805	1.91241	0.006073	0.070882	0.769	4275	tags=46%, list=18%, signal=56%
GO_RESPONSE_TO_INTERFERON_GAMMA	166	0.577902	1.974359	0.004057	0.09448	0.599	3402	tags=34%, list=14%, signal=39%
GO_CD8_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	19	0.711396	1.709825	0.010482	0.07694	0.998	4362	tags=58%, list=19%, signal=71%
GO_SYNCYTIUM_FORMATION	50	0.605592	1.786735	0	0.065923	0.969	1565	tags=30%, list=7%, signal=32%
GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	360	0.570686	1.978365	0.002012	0.099391	0.589	4281	tags=40%, list=18%, signal=48%
GO_MYOBLAST_FUSION	37	0.589702	1.678016	0.002053	0.084937	1	1565	tags=30%, list=7%, signal=32%

GO_REGULATION_OF_LYMPHOCYTE_ACTIVATION	398	0.586384	1.998357	0	0.129799	0.502	4362	tags=43%, list=19%, signal=52%
GO_LEUKOCYTE_PROLIFERATION	280	0.575534	1.895628	0	0.061736	0.817	4334	tags=45%, list=18%, signal=54%
GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	190	0.579545	1.963584	0	0.089149	0.624	4549	tags=42%, list=19%, signal=52%
GO_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	87	0.649425	1.866554	0.002033	0.057589	0.879	3035	tags=45%, list=13%, signal=51%
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	54	0.520849	1.703765	0.008264	0.078182	0.999	1698	tags=26%, list=7%, signal=28%
GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	79	0.672967	1.873587	0.002092	0.058673	0.872	3548	tags=49%, list=15%, signal=58%
GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	35	0.627699	1.778788	0.014374	0.067678	0.974	2645	tags=40%, list=11%, signal=45%
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	66	0.64233	1.772355	0.012448	0.068586	0.98	4275	tags=53%, list=18%, signal=65%
GO_INTERLEUKIN_12_PRODUCTION	56	0.701077	1.926458	0	0.071021	0.734	3673	tags=52%, list=16%, signal=61%
GO_REGULATION_OF_LEUKOCYTE_MIGRATION	183	0.60286	1.942392	0	0.079285	0.684	2829	tags=37%, list=12%, signal=42%
GO_INTERLEUKIN_8_SECRETION	30	0.73284	1.875587	0	0.058466	0.869	3305	tags=47%, list=14%, signal=54%
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	183	0.605721	1.973216	0	0.093297	0.602	4599	tags=48%, list=20%, signal=59%
GO_T_CELL_MIGRATION	61	0.724322	1.966808	0	0.095021	0.619	2508	tags=48%, list=11%, signal=53%

GO_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	51	0.642674	2.013018	0	0.131764	0.448	1621	tags=29%, list=7%, signal=32%
GO_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	159	0.496183	1.995088	0.002045	0.125725	0.523	4232	tags=33%, list=18%, signal=40%
GO_LYMPHOCYTE_HOMEOSTASIS	61	0.563441	1.851099	0.008602	0.058424	0.896	3955	tags=36%, list=17%, signal=43%
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	251	0.592826	1.983741	0	0.107325	0.569	3855	tags=40%, list=16%, signal=48%
GO_FC_RECEPTOR_MEDIATED_STIMULATORY_SIGNALING_PATHWAY	83	0.509124	1.903836	0.012552	0.064123	0.79	3387	tags=29%, list=14%, signal=34%
GO_LYMPHOCYTE_MIGRATION	100	0.661819	1.869935	0.002012	0.059384	0.875	2993	tags=46%, list=13%, signal=52%
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	44	0.53156	1.633093	0.028689	0.099715	1	4909	tags=45%, list=21%, signal=57%
GO_LEUKOCYTE_MEDIATED_CYTOTOXICITY	96	0.594458	1.784202	0.006224	0.066371	0.969	4275	tags=46%, list=18%, signal=56%
GO_INTERLEUKIN_8_PRODUCTION	74	0.628637	1.886038	0	0.061482	0.836	3305	tags=39%, list=14%, signal=45%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	68	0.5407	2.034859	0.002114	0.164181	0.388	1933	tags=15%, list=8%, signal=16%

GO_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	162	0.547855	1.899529	0.004124	0.063183	0.803	4909	tags=45%, list=21%, signal=57%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	127	0.634533	1.886504	0	0.061542	0.836	3035	tags=43%, list=13%, signal=49%
GO_REGULATION_OF_T_CELL_DIFFERENTIATION	131	0.534219	1.82347	0.010526	0.060234	0.926	4362	tags=42%, list=19%, signal=51%
GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	29	0.636804	1.755818	0.022965	0.068492	0.985	2645	tags=41%, list=11%, signal=47%
GO_REGULATION_OF_LYMPHOCYTE_MIGRATION	58	0.643304	1.877324	0	0.060429	0.864	2993	tags=40%, list=13%, signal=45%
GO_T_CELL_SELECTION	47	0.591107	1.584288	0.045549	0.116747	1	4533	tags=49%, list=19%, signal=60%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	123	0.666063	2.026164	0	0.149213	0.407	2722	tags=42%, list=12%, signal=48%
GO_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	56	0.604851	1.844236	0.002096	0.05828	0.906	2394	tags=36%, list=10%, signal=40%
GO_NEGATIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	21	0.676505	1.832148	0.002012	0.05986	0.918	2052	tags=33%, list=9%, signal=36%
GO_INTERLEUKIN_1_BETA_PRODUCTION	82	0.688958	1.936436	0.002024	0.074855	0.701	3548	tags=55%, list=15%, signal=64%

GO_REGULATION_OF_CELL_KILLING	87	0.636137	1.830969	0.0060085	0.059738	0.92	4275	tags=49%, list=18%, signal=60%
GO_POSITIVE_REGULATION_OF_CYTOKINE_SECRETION	128	0.627197	1.902245	0	0.064486	0.795	3548	tags=45%, list=15%, signal=52%
GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	409	0.540242	1.955147	0	0.086628	0.648	4723	tags=39%, list=20%, signal=48%
GO_REGULATION_OF_SYNCYTIUM_FORMATION_BY_PLASMA_MEMBRANE_FUSION	27	0.678339	1.702274	0.0021322	0.078219	0.999	1310	tags=41%, list=6%, signal=43%
GO_NIK_NF_KAPPAB_SIGNALING	156	0.441959	2.028258	0.0020004	0.154353	0.403	3264	tags=20%, list=14%, signal=23%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	89	0.503121	2.02274	0.0083668	0.132298	0.422	3892	tags=20%, list=17%, signal=24%
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	19	0.702196	1.623173	0.0342205	0.1028	1	3923	tags=58%, list=17%, signal=69%
GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	70	0.514441	1.772402	0.0259918	0.068751	0.98	3953	tags=34%, list=17%, signal=41%
GO_POSITIVE_REGULATION_OF_CELL_ADHESION	376	0.532868	1.944265	0	0.079178	0.678	4511	tags=39%, list=19%, signal=48%
GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PROCESS	20	0.706414	1.694775	0.0103331	0.080729	0.999	553	tags=40%, list=2%, signal=41%

GO_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	208	0.41527	1.754606	0.006061	0.068327	0.985	3855	tags=25%, list=16%, signal=29%
GO_POSITIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	26	0.545977	1.554348	0.044088	0.127963	1	5788	tags=50%, list=25%, signal=66%
GO_I_KAPPAB_PHOSPHORYLATION	18	0.653138	1.753719	0.020367	0.068533	0.986	2666	tags=33%, list=11%, signal=38%
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	22	0.706093	1.638585	0.022267	0.09699	1	3923	tags=59%, list=17%, signal=71%
GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_INVOLVED_IN_INFLAMMATORY_RESPONSE	63	0.549873	1.707486	0.008299	0.077206	0.999	2794	tags=32%, list=12%, signal=36%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	44	0.635764	1.676248	0.022587	0.085682	1	4275	tags=52%, list=18%, signal=64%
GO_REGULATION_OF_MAST_CELL_ACTIVATION	38	0.628639	1.899546	0	0.06364	0.803	2478	tags=32%, list=11%, signal=35%
GO_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	24	0.621815	1.567738	0.028926	0.12308	1	4315	tags=54%, list=18%, signal=66%
GO_INTERLEUKIN_1_PRODUCTION	95	0.66467	1.895147	0.002028	0.061298	0.818	3548	tags=53%, list=15%, signal=62%

GO_NEGATIVE_REGULATION_OF_EXOCYTOSIS	28	0.573507	1.709834	0.006024	0.077075	0.998	2052	tags=25%, list=9%, signal=27%
GO_MHC_PROTEIN_BINDING	23	0.845704	1.896395	0	0.06218	0.813	382	tags=39%, list=2%, signal=40%
GO_T_CELL_MEDIATED_CYTOTOXICITY	37	0.612745	1.754113	0.006198	0.068418	0.985	4275	tags=46%, list=18%, signal=56%
GO_POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	66	0.654222	1.879447	0	0.060579	0.86	4747	tags=56%, list=20%, signal=70%
GO_CELLULAR_DEFENSE_RESPONSE	48	0.763495	1.937914	0	0.076522	0.697	2564	tags=50%, list=11%, signal=56%
GO_REGULATION_OF_T_CELL_MIGRATION	41	0.662101	1.892315	0.003861	0.061214	0.823	2492	tags=37%, list=11%, signal=41%
GO_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY	150	0.396032	1.734128	0.012632	0.072147	0.992	4549	tags=29%, list=19%, signal=35%
GO_RESPIRATORY_BURST	30	0.693429	1.810416	0.006211	0.062349	0.943	2727	tags=40%, list=12%, signal=45%
GO_MYELOID_LEUKOCYTE_DIFFERENTIATION	196	0.476119	1.813922	0.002079	0.061619	0.937	3855	tags=30%, list=16%, signal=36%
GO_DENDRITIC_CELL_DIFFERENTIATION	39	0.695099	1.982121	0	0.103371	0.572	972	tags=28%, list=4%, signal=29%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	89	0.61552	1.852553	0.008114	0.058693	0.895	4549	tags=49%, list=19%, signal=61%

GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	33	0.523356	1.598148	0.0033932	0.112313	1	1290	tags=27%, list=5%, signal=29%
GO_LEUKOCYTE_ACTIVATION_INVOLVED_IN_INFLAMMATORY_RESPONSE	42	0.742282	1.778511	0	0.067254	0.974	2413	tags=55%, list=10%, signal=61%
GO_TYPE_I_INTERFERON_PRODUCTION	119	0.509189	2.049263	0.002088	0.182377	0.352	4941	tags=31%, list=21%, signal=39%
GO_INTERLEUKIN_2_PRODUCTION	62	0.652755	1.814285	0.006224	0.061652	0.937	3285	tags=45%, list=14%, signal=52%
GO_REGULATION_OF_CELL_CELL_ADHESION	375	0.531037	1.929867	0	0.071655	0.722	4238	tags=37%, list=18%, signal=44%
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	54	0.560987	1.730911	0.018947	0.072701	0.992	2645	tags=35%, list=11%, signal=40%
GO_RESPONSE_TO_AMYLOID_BETA	45	0.690976	1.855044	0	0.058557	0.891	4174	tags=56%, list=18%, signal=67%
GO_INTERFERON_BETA_PRODUCTION	49	0.577751	1.967324	0.002066	0.096467	0.618	4941	tags=35%, list=21%, signal=44%
GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	133	0.613178	1.895272	0.006061	0.061581	0.818	4599	tags=51%, list=20%, signal=63%
GO_RESPONSE_TO_INTERFERON_BETA	26	0.646143	1.768265	0.010504	0.067433	0.98	3189	tags=38%, list=14%, signal=44%

GO_CELL_KILLING	146	0.568462	1.765632	0.006148	0.068208	0.981	4278	tags=43%, list=18%, signal=52%
GO_MYD88_DEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	35	0.794742	1.921054	0	0.07185	0.751	3153	tags=51%, list=13%, signal=59%
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	458	0.497716	1.941706	0.002028	0.075528	0.685	4341	tags=31%, list=18%, signal=38%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	117	0.59547	1.92009	0.004065	0.070434	0.754	2645	tags=35%, list=11%, signal=39%
GO_POSITIVE_REGULATION_OF_MACROPHAGE_ACTIVATION	22	0.712065	1.780912	0	0.067507	0.972	3153	tags=50%, list=13%, signal=58%
GO_POSITIVE_REGULATION_OF_CELL_KILLING	57	0.64023	1.746535	0.014315	0.068865	0.991	4275	tags=49%, list=18%, signal=60%
GO_B_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	67	0.545324	1.746021	0.018145	0.068985	0.991	3916	tags=39%, list=17%, signal=46%
GO_LEUKOCYTE_HOMEOSTASIS	83	0.575811	1.862567	0.006356	0.056802	0.884	4251	tags=40%, list=18%, signal=48%
GO_INTERLEUKIN_10_PRODUCTION	50	0.752161	2.025252	0	0.14326	0.412	1948	tags=48%, list=8%, signal=52%
GO_FICOLIN_1_RICH_GRANULE_MEMBRANE	57	0.584689	1.750275	0.008214	0.06859	0.988	4331	tags=46%, list=18%, signal=56%

GO_REGULATION_OF_MYOBLAST_FUSION	20	0.661876	1.619583	0.017131	0.103929	1	1310	tags=40%, list=6%, signal=42%
GO_LEUKOCYTE_MIGRATION	413	0.581843	1.965646	0	0.092319	0.622	2924	tags=36%, list=12%, signal=40%
GO_LEUKOCYTE_CHEMOTAXIS	200	0.630229	1.864378	0.002062	0.057049	0.882	2924	tags=42%, list=12%, signal=48%
GO_PHAGOCYTIC_CUP	24	0.625792	1.663783	0.022044	0.089897	1	2852	tags=42%, list=12%, signal=47%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	35	0.675803	1.768622	0.00207	0.067726	0.98	2393	tags=43%, list=10%, signal=48%
GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	206	0.611642	1.900205	0	0.064231	0.8	4334	tags=49%, list=18%, signal=59%
GO_VIRAL_GENOME_REPLICATION	113	0.469629	1.959311	0.002105	0.087708	0.636	3189	tags=21%, list=14%, signal=24%
GO_POSITIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR_ACTIVITY	143	0.5071	1.954644	0.001984	0.08553	0.651	3539	tags=28%, list=15%, signal=33%
GO_MACROPHAGE_ACTIVATION	82	0.692112	1.860864	0	0.057418	0.884	4341	tags=60%, list=18%, signal=73%
GO_OSTEOCLAST_DIFFERENTIATION	94	0.503967	1.806591	0.001984	0.063086	0.945	4511	tags=37%, list=19%, signal=46%
GO_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	18	0.735554	1.74225	0.00409	0.069927	0.992	1789	tags=44%, list=8%, signal=48%

GO_POSITIVE_REGULATION_OF_T_CELL_MIGRATION	29	0.761823	1.877161	0.002041	0.060165	0.865	1554	tags=41%, list=7%, signal=44%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	17	0.824222	1.841381	0	0.058413	0.908	1290	tags=65%, list=5%, signal=68%
GO_B_CELL_PROLIFERATION	92	0.590112	1.769382	0.00616	0.068186	0.98	3196	tags=40%, list=14%, signal=46%
GO_REGULATION_OF_B_CELL_RECEPTOR_SIGNALING_PATHWAY	26	0.612265	1.557249	0.042254	0.127373	1	4405	tags=46%, list=19%, signal=57%
GO_T_CELL_CYTOKINE_PRODUCTION	40	0.616521	1.682396	0.00431	0.082835	0.999	3189	tags=48%, list=14%, signal=55%
GO_ANTIGEN_BINDING	44	0.690416	1.72892	0.008299	0.072669	0.993	4040	tags=59%, list=17%, signal=71%
GO_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	54	0.662679	1.751839	0.010288	0.068395	0.986	4909	tags=57%, list=21%, signal=72%
GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	147	0.579474	1.931096	0.004073	0.073958	0.717	4909	tags=50%, list=21%, signal=62%
GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	93	0.62381	1.945047	0.002066	0.080888	0.677	2801	tags=39%, list=12%, signal=44%
GO_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	26	0.648298	1.685297	0.01217	0.081788	0.999	2983	tags=42%, list=13%, signal=48%

GO_POSITIVE_REGULATION_OF_MACROPHAGE_MIGRATION	20	0.755584	1.691026	0	0.081041	0.999	2643	tags=65%, list=11%, signal=73%
GO_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	65	0.616653	1.829343	0.004141	0.059702	0.921	4275	tags=49%, list=18%, signal=60%
GO_INTERLEUKIN_6_PRODUCTION	139	0.629149	1.98872	0	0.114504	0.549	3548	tags=42%, list=15%, signal=50%
GO_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	51	0.627183	1.948698	0	0.085142	0.666	3908	tags=41%, list=17%, signal=49%
GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	195	0.497169	1.948146	0.002092	0.084303	0.669	3908	tags=30%, list=17%, signal=35%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	52	0.654685	1.754717	0.004149	0.068424	0.985	3548	tags=48%, list=15%, signal=56%
GO_PHOSPHATIDYLINOSITOL_3_4_BISPHOSPHATE_BINDING	26	0.483683	1.540555	0.034188	0.133996	1	3386	tags=27%, list=14%, signal=31%
GO_MACROPHAGE_MIGRATION	46	0.619902	1.660613	0.014286	0.09051	1	2722	tags=43%, list=12%, signal=49%
GO_INTERLEUKIN_4_PRODUCTION	33	0.671711	1.786138	0.00202	0.066035	0.969	2983	tags=45%, list=13%, signal=52%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	47	0.66382	1.909882	0.004141	0.070554	0.773	4902	tags=49%, list=21%, signal=62%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MIGRATION	35	0.758851	1.907721	0	0.066496	0.78	1554	tags=43%, list=7%, signal=46%

GO_CELL_CHEMOTAXIS	270	0.586707	1.841273	0.004167	0.05822	0.908	2722	tags=36%, list=12%, signal=40%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_SECRETION	16	0.770907	1.769643	0.006342	0.068221	0.98	1789	tags=44%, list=8%, signal=47%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	82	0.692237	1.959043	0	0.086372	0.636	2722	tags=45%, list=12%, signal=51%
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	84	0.535774	1.909543	0.002024	0.069529	0.773	3908	tags=33%, list=17%, signal=40%
GO_T_CELL_HOMEOSTASIS	38	0.548801	1.756751	0.010776	0.068652	0.985	2426	tags=26%, list=10%, signal=29%
GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	79	0.695878	1.928469	0	0.070442	0.728	4533	tags=62%, list=19%, signal=77%
GO_NEGATIVE_REGULATION_OF_B_CELL_PROLIFERATION	16	0.734367	1.715912	0.01222	0.075742	0.997	2499	tags=44%, list=11%, signal=49%
GO_MYELOID_CELL_DIFFERENTIATION	368	0.393076	1.800709	0.004065	0.063973	0.948	3239	tags=20%, list=14%, signal=23%
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS	232	0.463884	1.985807	0	0.110763	0.558	3955	tags=27%, list=17%, signal=32%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	21	0.679295	1.650391	0.008097	0.09402	1	2983	tags=48%, list=13%, signal=54%
GO_B_CELL_HOMEOSTASIS	28	0.570287	1.732911	0.02449	0.072451	0.992	3754	tags=32%, list=16%, signal=38%

GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	52	0.566007	1.789739	0.008282	0.065478	0.965	3492	tags=29%, list=15%, signal=34%
GO_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	29	0.653364	1.732421	0.008147	0.072262	0.992	2080	tags=38%, list=9%, signal=42%
GO_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	128	0.628819	1.975897	0	0.097337	0.596	4549	tags=48%, list=19%, signal=60%
GO_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	104	0.673402	1.931448	0.002045	0.074578	0.716	2722	tags=43%, list=12%, signal=49%
GO_B_CELL_MEDIATED_IMMUNITY	111	0.602822	1.845072	0.009728	0.058901	0.904	2938	tags=39%, list=12%, signal=44%
GO_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	218	0.558834	1.894193	0	0.061516	0.819	3291	tags=32%, list=14%, signal=37%
GO_SPECIFIC_GRANULE_MEMBRANE	87	0.590158	1.917644	0.004124	0.069324	0.759	1327	tags=24%, list=6%, signal=25%
GO_RESPONSE_TO_CHEMOKINE	88	0.689443	1.806724	0.002083	0.063239	0.945	2421	tags=47%, list=10%, signal=52%
GO_B_CELL_ACTIVATION	238	0.536521	1.867156	0.00611	0.058219	0.878	4549	tags=39%, list=19%, signal=48%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	30	0.705601	1.803561	0.006098	0.063679	0.947	2983	tags=50%, list=13%, signal=57%

GO_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	152	0.441949	1.674814	0.006303	0.086159	1	3798	tags=32%, list=16%, signal=38%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	51	0.591216	1.900367	0.004132	0.0646	0.8	4174	tags=39%, list=18%, signal=48%
GO_POSITIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	39	0.533957	1.60993	0.011952	0.107834	1	3883	tags=41%, list=17%, signal=49%
GO_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	99	0.524569	1.962118	0	0.088578	0.627	1922	tags=23%, list=8%, signal=25%
GO_CYTOKINE_METABOLIC_PROCESS	111	0.589876	1.87584	0	0.058695	0.867	3153	tags=39%, list=13%, signal=45%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	18	0.736754	1.729096	0.007905	0.072853	0.993	1290	tags=44%, list=5%, signal=47%
GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	15	0.755689	1.642909	0.006198	0.09615	1	1789	tags=53%, list=8%, signal=58%
GO_REGULATION_OF_B_CELL_PROLIFERATION	60	0.669057	1.851757	0.004158	0.05861	0.896	2801	tags=45%, list=12%, signal=51%
GO_NEGATIVE_REGULATION_OF_VIRAL_LIFE_CYCLE	74	0.510536	1.762204	0.014523	0.068734	0.982	3675	tags=27%, list=16%, signal=32%
GO_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	74	0.493459	1.94439	0.006289	0.080085	0.678	3673	tags=26%, list=16%, signal=30%

GO_T_CELL_APOPTOTIC_PROCESS	48	0.513928	1.749218	0.0012632	0.068387	0.989	3475	tags=29%, list=15%, signal=34%
GO_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	86	0.483132	1.77778	0.0062289	0.067479	0.976	2356	tags=24%, list=10%, signal=27%
GO_MYELOID_LEUKOCYTE_MIGRATION	190	0.633889	1.857782	0	0.057523	0.889	2924	tags=42%, list=12%, signal=48%
GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	182	0.600714	1.910591	0.0021055	0.070628	0.772	4362	tags=44%, list=19%, signal=54%
GO_PROTEIN_AUTOPHOSPHORYLATION	223	0.28812	1.387363	0.0418841	0.215689	1	1999	tags=11%, list=8%, signal=12%
GO_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	322	0.541392	1.891498	0	0.061307	0.825	3802	tags=34%, list=16%, signal=41%
GO_T_CELL_RECEPTOR_COMPLEX	21	0.735579	1.620389	0.0365585	0.103599	1	912	tags=48%, list=4%, signal=49%
GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_SUPERFAMILY_BINDING	41	0.460919	1.628771	0.002045	0.101137	1	4549	tags=32%, list=19%, signal=39%
GO_REGULATION_OF_MYOTUBE_DIFFERENTIATION	49	0.540352	1.642877	0.0101163	0.096035	1	2052	tags=27%, list=9%, signal=29%
GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	85	0.619927	1.993041	0	0.124034	0.533	4717	tags=48%, list=20%, signal=60%

GO_REGULATORY_T_CELL_DIFFERENTIATION	28	0.744641	1.781818	0.008639	0.067438	0.972	4315	tags=68%, list=18%, signal=83%
GO_NEGATIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	17	0.653706	1.521194	0.03719	0.142743	1	3714	tags=53%, list=16%, signal=63%
GO_POSITIVE_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	75	0.564514	2.024275	0	0.137378	0.414	1922	tags=25%, list=8%, signal=27%
GO_MYELOID_DENDRITIC_CELL_ACTIVATION	27	0.668017	1.724284	0.010638	0.073284	0.994	2770	tags=41%, list=12%, signal=46%
GO_REGULATION_OF_T_CELL_CYTOKINE_PRODUCTION	30	0.6596	1.731799	0.004193	0.072475	0.992	3189	tags=53%, list=14%, signal=62%
GO_POSITIVE_REGULATION_OF_PHAGOCYTOSIS	63	0.628592	1.850587	0.002049	0.058412	0.897	2976	tags=41%, list=13%, signal=47%
GO_INTERLEUKIN_1_SECRETION	53	0.660769	1.844477	0	0.058473	0.906	3548	tags=51%, list=15%, signal=60%
GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	31	0.586977	1.715101	0.012685	0.075899	0.998	4723	tags=45%, list=20%, signal=56%
GO_POSITIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	21	0.665158	1.658998	0.024145	0.090644	1	4232	tags=52%, list=18%, signal=64%
GO_LYMPHOCYTE_CHEMOTAXIS	52	0.698642	1.744175	0.006198	0.069588	0.991	2699	tags=54%, list=11%, signal=61%

GO_GLIAL_CELL_ACTIVATION	49	0.731852	1.8707	0	0.059542	0.875	2413	tags=49%, list=10%, signal=54%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	16	0.792028	1.741985	0	0.069776	0.992	3397	tags=69%, list=14%, signal=80%
GO_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	43	0.686775	1.73279	0	0.07223	0.992	2643	tags=51%, list=11%, signal=58%
GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	70	0.465051	1.506332	0.03212	0.150912	1	4366	tags=37%, list=19%, signal=45%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	89	0.629386	1.929888	0	0.072413	0.722	3548	tags=40%, list=15%, signal=47%
GO_ALPHA_BETA_T_CELL_PROLIFERATION	29	0.663897	1.739327	0.016194	0.070428	0.992	3053	tags=48%, list=13%, signal=55%
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	136	0.614635	1.904004	0	0.065048	0.789	1547	tags=29%, list=7%, signal=31%
GO_THYMIC_T_CELL_SELECTION	21	0.691895	1.641293	0.023529	0.096421	1	2983	tags=52%, list=13%, signal=60%
GO_INTERLEUKIN_2_BIOSYNTHETIC_PROCESS	22	0.679685	1.62855	0.034623	0.100889	1	2983	tags=55%, list=13%, signal=62%
GO_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	36	0.49156	1.658701	0.018789	0.090719	1	3474	tags=28%, list=15%, signal=33%
GO_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	21	0.821017	1.776144	0	0.0681	0.978	1789	tags=67%, list=8%, signal=72%
GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	30	0.667242	1.670147	0.012448	0.087356	1	1789	tags=40%, list=8%, signal=43%

GO_NEGATIVE_REGULATION_OF_VIRAL_PROCESS	89	0.499085	1.799775	0.006342	0.064274	0.949	3675	tags=25%, list=16%, signal=29%
GO_SH2_DOMAIN_BINDING	35	0.553236	1.790795	0.004193	0.065584	0.961	4902	tags=40%, list=21%, signal=50%
GO_IMMUNOGLOBULIN_PRODUCTION	101	0.564441	1.898503	0.002066	0.06283	0.806	2938	tags=32%, list=12%, signal=36%
GO_GRANULOCYTE_MIGRATION	128	0.663273	1.84254	0	0.058446	0.908	2397	tags=45%, list=10%, signal=50%
GO_REGULATION_OF_PHAGOCYTOSIS	86	0.601328	1.85689	0	0.057753	0.889	2727	tags=36%, list=12%, signal=41%
GO_LEUKOCYTE_APOPTOTIC_PROCESS	103	0.617217	2.044555	0	0.174599	0.364	3475	tags=35%, list=15%, signal=41%
GO_POSITIVE_REGULATION_OF_CHEMOTAXIS	130	0.637042	1.912386	0	0.070249	0.769	2319	tags=37%, list=10%, signal=41%
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	51	0.58719	1.713756	0	0.075999	0.998	4341	tags=53%, list=18%, signal=65%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	112	0.569803	1.848491	0.002083	0.05851	0.9	3220	tags=35%, list=14%, signal=40%
GO_DEFENSE_RESPONSE_TO_BACTERIUM	209	0.501471	1.640216	0.00611	0.09649	1	4352	tags=38%, list=19%, signal=46%
GO_CYTOKINE_PRODUCTION_INVOLVED_IN_INFLAMMATORY_RESPONSE	40	0.549462	1.58705	0.02459	0.116034	1	3153	tags=35%, list=13%, signal=40%
GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	44	0.645123	1.844745	0.002053	0.058569	0.904	2645	tags=41%, list=11%, signal=46%

GO_REGULATION_OF_VIRAL_LIFE_CYCLE	132	0.434954	1.848315	0.002114	0.058365	0.901	3675	tags=22%, list=16%, signal=26%
GO_LYMPHOCYTE_APOPTOTIC_PROCESS	71	0.567368	1.95873	0	0.085155	0.636	3475	tags=30%, list=15%, signal=35%
GO_PURINERGIC_RECEPTOR_ACTIVITY	23	0.645153	1.559038	0.044898	0.126636	1	3113	tags=57%, list=13%, signal=65%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	32	0.721205	1.899607	0.002004	0.064064	0.803	1948	tags=44%, list=8%, signal=48%
GO_ACUTE_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	19	0.739943	1.674321	0.00998	0.086229	1	2022	tags=47%, list=9%, signal=52%
GO_POSITIVE_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL	37	0.623136	1.705743	0	0.077818	0.999	4341	tags=54%, list=18%, signal=66%
GO_POSITIVE_REGULATION_OF_MONOCYTE_CHEMOTAXIS	18	0.767392	1.702185	0	0.078134	0.999	1859	tags=56%, list=8%, signal=60%
GO_NEUTROPHIL_MIGRATION	107	0.687986	1.846637	0	0.058831	0.902	2397	tags=48%, list=10%, signal=53%
GO_POSITIVE_REGULATION_OF_JNK_CASCADE	131	0.434873	1.688553	0.007905	0.081083	0.999	2678	tags=21%, list=11%, signal=24%
GO_REGULATION_OF_MONOCYTE_CHEMOTAXIS	24	0.764869	1.738063	0.002146	0.070701	0.992	1859	tags=54%, list=8%, signal=59%
GO_TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	81	0.488352	1.628887	0.010616	0.101189	1	5911	tags=54%, list=25%, signal=72%

GO_MONONUCLEAR_CELL_MIGRATION	77	0.696672	1.786079	0.002096	0.065864	0.969	2876	tags=52%, list=12%, signal=59%
GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	140	0.577044	1.930486	0	0.072732	0.719	3908	tags=39%, list=17%, signal=47%
GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	43	0.570313	1.650956	0.016461	0.093765	1	3714	tags=42%, list=16%, signal=50%
GO_NEUROINFLAMMATORY_RESPONSE	61	0.673164	1.79649	0	0.064531	0.951	4511	tags=61%, list=19%, signal=75%
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS_WITHIN_A_TISSUE	29	0.584606	1.760322	0.002033	0.06874	0.982	3305	tags=38%, list=14%, signal=44%
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT	232	0.477143	1.714267	0.002146	0.076114	0.998	5137	tags=46%, list=22%, signal=58%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	15	0.72288	1.632238	0.022587	0.099804	1	3256	tags=53%, list=14%, signal=62%
GO_DEFENSE_RESPONSE_TO_GRAM_POSITIVE_BACTERIUM	69	0.540607	1.608544	0.012474	0.107725	1	2917	tags=33%, list=12%, signal=38%
GO_MONOCYTE_CHEMOTAXIS	55	0.729532	1.759362	0.002101	0.068552	0.984	1876	tags=49%, list=8%, signal=53%
GO_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	163	0.521923	1.888374	0.00207	0.062212	0.832	4835	tags=39%, list=21%, signal=48%

GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	23	0.712968	1.72547	0.006048	0.073208	0.994	2051	tags=43%, list=9%, signal=48%
GO_POSITIVE_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	23	0.743045	1.731539	0	0.072481	0.992	1859	tags=52%, list=8%, signal=57%
GO_POSITIVE_REGULATION_OF_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	88	0.498726	1.660154	0.008299	0.090536	1	3953	tags=42%, list=17%, signal=50%
GO_REGULATION_OF_CHEMOTAXIS	199	0.566801	1.858888	0.004158	0.058108	0.885	2722	tags=33%, list=12%, signal=37%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	46	0.650234	1.764497	0.008163	0.068728	0.981	3714	tags=48%, list=16%, signal=57%
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	115	0.508148	1.728645	0.002008	0.07252	0.993	4341	tags=43%, list=18%, signal=53%
GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	30	0.587423	1.604732	0.014344	0.109044	1	1491	tags=37%, list=6%, signal=39%
GO_NEGATIVE_REGULATION_OF_HEMOPOIESIS	130	0.453729	1.749352	0.004158	0.068626	0.989	4799	tags=34%, list=20%, signal=42%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	94	0.504537	1.779453	0.002066	0.067714	0.974	4799	tags=39%, list=20%, signal=49%

GO_VITAMIN_D_METABOLIC_PROCESS	22	0.575765	1.549092	0.030181	0.130594	1	4511	tags=41%, list=19%, signal=51%

EBV(+) vs. EBV(-) gastric cancer tissues (GSE51575)

NAME	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	RANK.AT.MAX	LEADING.EDGE
GO_DOUBLE_STRANDED_RNA_BINDING	67	0.532143	2.07555	0	0.118608	0.075	1335	tags=21%, list=6%, signal=22%
GO_T_CELL_RECEPTOR_SIGNALING_PATHWAY	171	0.6057	2.068084	0	0.066787	0.081	2254	tags=27%, list=10%, signal=30%
GO_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	212	0.655218	2.016444	0	0.09044	0.141	2339	tags=35%, list=11%, signal=39%
GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	41	0.662911	1.975701	0	0.12449	0.229	2596	tags=41%, list=12%, signal=47%
GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	349	0.609736	1.974831	0	0.101337	0.233	2937	tags=36%, list=14%, signal=41%
GO_FC_RECEPTOR_SIGNALING_PATHWAY	172	0.478577	1.944169	0.006073	0.092807	0.308	2075	tags=20%, list=10%, signal=22%
GO_NEGATIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	27	0.812242	1.929389	0	0.091005	0.357	2239	tags=56%, list=10%, signal=62%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	65	0.623399	1.916685	0.00625	0.098472	0.398	3521	tags=42%, list=16%, signal=49%
GO_ALPHA_BETA_T_CELL_DIFFERENTIATION	97	0.699449	1.912125	0	0.095753	0.406	2847	tags=49%, list=13%, signal=57%
GO_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	36	0.769538	1.907191	0	0.095157	0.425	2159	tags=42%, list=10%, signal=46%
GO_T_HELPER_1_TYPE_IMMUNE_RESPONSE	41	0.771303	1.9044	0	0.091853	0.435	3008	tags=61%, list=14%, signal=71%

GO_NEGATIVE_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	20	0.809517	1.89716	0	0.095051	0.457	1886	tags=45%, list=9%, signal=49%
GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	93	0.689298	1.89236	0	0.096687	0.481	3170	tags=49%, list=15%, signal=58%
GO_RESPONSE_TO_TYPE_I_INTERFERON	83	0.656337	1.89105	0.007921	0.092699	0.484	2349	tags=41%, list=11%, signal=46%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	58	0.735926	1.889221	0	0.088889	0.487	2740	tags=55%, list=13%, signal=63%
GO_ALPHA_BETA_T_CELL_ACTIVATION	129	0.696362	1.888638	0	0.084711	0.49	2847	tags=52%, list=13%, signal=59%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	139	0.646592	1.882527	0	0.083264	0.512	2984	tags=44%, list=14%, signal=51%
GO_NATURAL_KILLER_CELL_ACTIVATION	70	0.64797	1.880601	0.002028	0.081306	0.517	1540	tags=40%, list=7%, signal=43%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	45	0.700164	1.879509	0	0.078576	0.52	2740	tags=51%, list=13%, signal=58%
GO_NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_KINASE_ACTIVITY	44	0.664984	1.875492	0	0.079667	0.528	3595	tags=50%, list=17%, signal=60%
GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	71	0.703661	1.875399	0	0.076512	0.528	3170	tags=54%, list=15%, signal=62%
GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	161	0.638088	1.875173	0.002045	0.073817	0.531	3008	tags=43%, list=14%, signal=50%
GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	295	0.641128	1.871428	0.001976	0.074893	0.542	2944	tags=46%, list=14%, signal=53%
GO_T_CELL_ACTIVATION	428	0.610333	1.861958	0	0.081683	0.574	3064	tags=44%, list=14%, signal=50%
GO_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	57	0.76958	1.859198	0	0.082267	0.587	2339	tags=53%, list=11%, signal=59%

GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	90	0.697315	1.852445	0	0.087073	0.607	2740	tags=50%, list=13%, signal=57%
GO_LYMPHOCYTE_DIFFERENTIATION	330	0.596995	1.844472	0.004	0.091501	0.634	2948	tags=41%, list=14%, signal=47%
GO_DEFENSE_RESPONSE_TO_VIRUS	216	0.587663	1.842569	0.004158	0.091415	0.643	3204	tags=41%, list=15%, signal=47%
GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	41	0.658022	1.842412	0.002049	0.088914	0.644	2339	tags=44%, list=11%, signal=49%
GO_POSITIVE_REGULATION_OF_INTERFERON_ALPHA_PRODUCTION	21	0.712938	1.839819	0.004115	0.089487	0.652	1198	tags=33%, list=6%, signal=35%
GO_RESPONSE_TO_VIRUS	293	0.552695	1.839111	0.002045	0.087719	0.654	3303	tags=38%, list=15%, signal=44%
GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	60	0.696276	1.83504	0	0.089871	0.666	3008	tags=50%, list=14%, signal=58%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	30	0.644294	1.834945	0.008147	0.087611	0.667	2698	tags=33%, list=12%, signal=38%
GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	86	0.667926	1.834328	0	0.084143	0.668	3170	tags=52%, list=15%, signal=61%
GO_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	32	0.713663	1.830459	0	0.083872	0.681	2741	tags=50%, list=13%, signal=57%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	202	0.667313	1.829509	0.002004	0.083033	0.684	2984	tags=50%, list=14%, signal=57%

GO_INTERFERON_GAMMA_PRODUCTION	102	0.701112	1.829297	0.002004	0.081587	0.686	3172	tags=58%, list=15%, signal=67%
GO_ACTIVATED_T_CELL_PROLIFERATION	39	0.638953	1.82811	0	0.079241	0.687	3172	tags=46%, list=15%, signal=54%
GO_CELLULAR_RESPONSE_TO_INTERFERON_BETA	19	0.714158	1.828074	0.006211	0.077604	0.687	990	tags=37%, list=5%, signal=39%
GO_ACTIVATION_OF_INNATE_IMMUNE_RESPONSE	288	0.492785	1.827737	0.004184	0.076396	0.687	3283	tags=31%, list=15%, signal=36%
GO_MYD88_INDEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	32	0.601914	1.826671	0.012371	0.075901	0.691	2251	tags=25%, list=10%, signal=28%
GO_INTERFERON_ALPHA_PRODUCTION	29	0.714405	1.822396	0.004149	0.073613	0.699	1198	tags=34%, list=6%, signal=36%
GO_T_CELL_DIFFERENTIATION	226	0.619099	1.816524	0.008333	0.07805	0.715	3008	tags=45%, list=14%, signal=51%
GO_POSITIVE_REGULATION_OF_INTERFERON_BETA_PRODUCTION	30	0.587582	1.814785	0.002058	0.078551	0.722	1198	tags=23%, list=6%, signal=25%
GO_T_CELL_PROLIFERATION	169	0.605301	1.813714	0	0.076811	0.725	3172	tags=47%, list=15%, signal=54%
GO_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PROCESS	30	0.743548	1.813475	0.006012	0.075804	0.727	2639	tags=57%, list=12%, signal=64%

GO_RESPONSE_TO_INTERFERON_ALPHA	20	0.802559	1.813431	0	0.074591	0.727	2958	tags=50%, list=14%, signal=58%
GO_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	85	0.70215	1.812802	0	0.074049	0.731	2740	tags=53%, list=13%, signal=60%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	357	0.519389	1.811001	0.00207	0.074529	0.736	2855	tags=31%, list=13%, signal=35%
GO_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	65	0.696255	1.810075	0	0.074065	0.738	3170	tags=52%, list=15%, signal=61%
GO_LEUKOCYTE_DIFFERENTIATION	483	0.549542	1.809998	0.004032	0.072967	0.738	3008	tags=37%, list=14%, signal=42%
GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	26	0.784888	1.806428	0	0.075277	0.746	3008	tags=69%, list=14%, signal=80%
GO_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	60	0.622047	1.806098	0.003984	0.074388	0.746	3112	tags=43%, list=14%, signal=50%
GO_POSITIVE_REGULATION_OF_HEMOPOIESIS	174	0.56977	1.806073	0.004115	0.073287	0.746	2984	tags=39%, list=14%, signal=44%
GO_POSITIVE_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	19	0.802101	1.805928	0.002083	0.072315	0.746	2740	tags=68%, list=13%, signal=78%
GO_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	110	0.551528	1.805397	0.002049	0.071775	0.747	4014	tags=43%, list=18%, signal=52%
GO_ADAPTIVE_IMMUNE_RESPONSE	360	0.669405	1.804561	0	0.071565	0.749	3008	tags=52%, list=14%, signal=60%

GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	33	0.681596	1.802333	0.008264	0.072543	0.756	3172	tags=48%, list=15%, signal=57%
GO_PHAGOCYTOSIS	244	0.530821	1.8009	0.006061	0.073	0.758	3172	tags=37%, list=15%, signal=43%
GO_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	256	0.572929	1.800725	0.00611	0.072157	0.758	3008	tags=39%, list=14%, signal=45%
GO_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	144	0.647568	1.800362	0.002092	0.071484	0.76	2740	tags=44%, list=13%, signal=51%
GO_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	472	0.524319	1.799777	0.002079	0.071097	0.762	3008	tags=33%, list=14%, signal=37%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION	200	0.497105	1.796585	0.008247	0.073207	0.769	2790	tags=24%, list=13%, signal=27%
GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	232	0.629235	1.792233	0.002041	0.075187	0.78	3008	tags=47%, list=14%, signal=54%
GO_REGULATION_OF_T_CELL_ACTIVATION	292	0.611557	1.787092	0.004049	0.077396	0.794	3064	tags=46%, list=14%, signal=53%
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	425	0.562649	1.784505	0.004107	0.078934	0.798	3213	tags=40%, list=15%, signal=45%

GO_REGULATION_OF_HEMOPOIESIS	411	0.493657	1.78205	0.006173	0.079482	0.806	3008	tags=30%, list=14%, signal=35%
GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	236	0.619326	1.781671	0.006135	0.078922	0.807	3172	tags=47%, list=15%, signal=54%
GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	191	0.607795	1.778337	0.004158	0.081026	0.812	2400	tags=39%, list=11%, signal=43%
GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	59	0.735751	1.777663	0.002024	0.080728	0.814	3172	tags=63%, list=15%, signal=73%
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	23	0.72683	1.775511	0.006	0.080614	0.815	3172	tags=61%, list=15%, signal=71%
GO_IMMUNOLOGICAL_SYNAPSE	34	0.753183	1.768777	0.005976	0.084469	0.826	1041	tags=41%, list=5%, signal=43%
GO_POSITIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	486	0.461857	1.765812	0.004175	0.08551	0.827	3896	tags=32%, list=18%, signal=38%
GO_T_CELL_MEDIATED_IMMUNITY	90	0.634361	1.763922	0.010373	0.085024	0.833	2980	tags=44%, list=14%, signal=51%
GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	37	0.786649	1.763025	0.00198	0.084973	0.833	1936	tags=59%, list=9%, signal=65%

GO_REGULATION_OF_MACROPHAGE_MIGRATION	35	0.678628	1.762488	0.002088	0.083866	0.833	2944	tags=54%, list=14%, signal=63%
GO_LEUKOCYTE_CELL_CELL_ADHESION	311	0.607091	1.760927	0.004032	0.084754	0.837	3172	tags=47%, list=15%, signal=54%
GO_CYTOKINE_SECRETION	213	0.618408	1.760452	0.004115	0.08435	0.837	3176	tags=47%, list=15%, signal=55%
GO_LYMPHOCYTE_MEDIATED_IMMUNITY	226	0.623315	1.75393	0.002053	0.089076	0.849	2464	tags=44%, list=11%, signal=49%
GO_RESPONSE_TO_INTERFERON_GAMMA	176	0.603542	1.753501	0.008475	0.088598	0.849	2439	tags=38%, list=11%, signal=43%
GO_CD8_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	21	0.774716	1.752461	0.00207	0.08813	0.851	2188	tags=62%, list=10%, signal=69%
GO_SYNCYTIUM_FORMATION	48	0.604808	1.752112	0.002033	0.087622	0.852	3519	tags=35%, list=16%, signal=42%
GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	357	0.5728	1.75154	0.006186	0.086617	0.853	3008	tags=41%, list=14%, signal=47%
GO_MYOBLAST_FUSION	36	0.624999	1.75114	0	0.086252	0.853	3519	tags=39%, list=16%, signal=46%

GO_REGULATION_OF_LYMPHOCYTE_ACTIVATION	391	0.58108	1.749263	0.010163	0.087223	0.855	2944	tags=42%, list=14%, signal=48%
GO_LEUKOCYTE_PROLIFERATION	269	0.582168	1.749237	0.006073	0.086494	0.855	3172	tags=45%, list=15%, signal=52%
GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	188	0.578198	1.748427	0.01006	0.086537	0.856	2711	tags=37%, list=12%, signal=42%
GO_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	85	0.677528	1.747109	0.002049	0.08716	0.858	3172	tags=55%, list=15%, signal=64%
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	53	0.60329	1.746511	0.010684	0.086975	0.858	4013	tags=45%, list=18%, signal=55%
GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	82	0.64123	1.745379	0.006289	0.087573	0.862	3406	tags=49%, list=16%, signal=58%
GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	35	0.755068	1.744388	0.002096	0.087781	0.862	2740	tags=63%, list=13%, signal=72%
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	65	0.712696	1.740307	0.006036	0.090354	0.872	2790	tags=57%, list=13%, signal=65%
GO_INTERLEUKIN_12_PRODUCTION	54	0.696942	1.739938	0.006173	0.090123	0.873	2944	tags=56%, list=14%, signal=64%

GO_REGULATION_OF_LEUKOCYTE_MIGRATION	176	0.611181	1.739868	0.0020053	0.089435	0.873	3234	tags=50%, list=15%, signal=58%
GO_INTERLEUKIN_8_SECRETION	28	0.701842	1.739168	0	0.088617	0.873	3489	tags=61%, list=16%, signal=72%
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	180	0.611164	1.73909	0.0040158	0.087972	0.873	2342	tags=41%, list=11%, signal=46%
GO_T_CELL_MIGRATION	61	0.706476	1.73721	0.0102225	0.088358	0.873	3172	tags=61%, list=15%, signal=71%
GO_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	50	0.605102	1.735227	0.0082999	0.088387	0.875	2339	tags=42%, list=11%, signal=47%
GO_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	162	0.513426	1.734185	0.0142228	0.088667	0.875	3453	tags=36%, list=16%, signal=42%
GO_LYMPHOCYTE_HOMEOSTASIS	61	0.611723	1.732582	0.0084033	0.089132	0.876	2339	tags=38%, list=11%, signal=42%
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	249	0.551638	1.73235	0.00611	0.088691	0.876	3172	tags=41%, list=15%, signal=48%
GO_FC_RECEPTOR_MEDIATED_STIMULATORY_SIGNALING_PATHWAY	80	0.490009	1.732124	0.0226344	0.088293	0.876	1775	tags=21%, list=8%, signal=23%

GO_LYMPHOCYTE_MIGRATION	101	0.699145	1.731363	0.008114	0.08845	0.878	2421	tags=52%, list=11%, signal=59%
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	45	0.720555	1.72789	0.004167	0.089381	0.882	3008	tags=56%, list=14%, signal=64%
GO_LEUKOCYTE_MEDIATED_CYTOTOXICITY	94	0.645264	1.726987	0.006098	0.089755	0.883	2188	tags=49%, list=10%, signal=54%
GO_INTERLEUKIN_8_PRODUCTION	75	0.620417	1.726975	0.002066	0.089129	0.883	3826	tags=51%, list=18%, signal=61%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	70	0.537368	1.726889	0.016327	0.088533	0.883	2555	tags=26%, list=12%, signal=29%
GO_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	160	0.599258	1.725773	0.010267	0.089109	0.886	3008	tags=44%, list=14%, signal=51%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	125	0.620684	1.724812	0.006211	0.089503	0.886	2740	tags=46%, list=13%, signal=52%
GO_REGULATION_OF_T_CELL_DIFFERENTIATION	129	0.622571	1.724585	0.010267	0.089104	0.886	2740	tags=46%, list=13%, signal=52%
GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	29	0.754175	1.724539	0.004149	0.088519	0.886	2740	tags=62%, list=13%, signal=71%

GO_REGULATION_OF_LYMPHOCYTE_MIGRATION	55	0.655742	1.722753	0.011976	0.089694	0.887	3234	tags=56%, list=15%, signal=66%
GO_T_CELL_SELECTION	46	0.73819	1.722177	0.005894	0.089629	0.887	2254	tags=57%, list=10%, signal=63%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	121	0.627913	1.720353	0.002075	0.089788	0.892	3222	tags=53%, list=15%, signal=62%
GO_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	55	0.627051	1.719611	0.012371	0.089964	0.893	3461	tags=40%, list=16%, signal=47%
GO_NEGATIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	20	0.71304	1.719377	0	0.089607	0.893	2065	tags=45%, list=10%, signal=50%
GO_INTERLEUKIN_1_BETA_PRODUCTION	83	0.664539	1.718675	0.006198	0.089809	0.893	2323	tags=51%, list=11%, signal=56%
GO_REGULATION_OF_CELL_KILLING	86	0.671233	1.716264	0.006173	0.09082	0.895	2790	tags=51%, list=13%, signal=58%
GO_POSITIVE_REGULATION_OF_CYTOKINE_SECRETION	130	0.595605	1.715394	0.004167	0.090609	0.898	3406	tags=45%, list=16%, signal=53%
GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	408	0.528804	1.713604	0.00813	0.092048	0.9	3064	tags=38%, list=14%, signal=43%
GO_REGULATION_OF_SYNCYTIUM_FORMATION_BY_PLASMA_MEMBRANE_FUSION	26	0.738185	1.71264	0	0.092451	0.9	2895	tags=50%, list=13%, signal=58%

GO_NIK_NF_KAPPAB_SIGNALING	154	0.455834	1.712259	0.018443	0.092245	0.9	3130	tags=22%, list=14%, signal=26%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	91	0.493832	1.711387	0.035789	0.092559	0.901	2555	tags=22%, list=12%, signal=25%
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	20	0.860364	1.710702	0.001984	0.092073	0.902	1090	tags=65%, list=5%, signal=68%
GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	72	0.638614	1.704809	0.010373	0.09329	0.911	2318	tags=42%, list=11%, signal=46%
GO_POSITIVE_REGULATION_OF_CELL_ADHESION	372	0.542566	1.702229	0.010373	0.094989	0.916	3229	tags=40%, list=15%, signal=47%
GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PROCESS	20	0.731927	1.702123	0.009843	0.09457	0.916	2639	tags=55%, list=12%, signal=63%
GO_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	199	0.462122	1.702103	0.008333	0.094046	0.916	2984	tags=29%, list=14%, signal=33%
GO_POSITIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	25	0.695878	1.70117	0.014228	0.093891	0.916	1305	tags=40%, list=6%, signal=43%
GO_I_KAPPAB_PHOSPHORYLATION	18	0.714063	1.700445	0.014989	0.094126	0.917	2175	tags=33%, list=10%, signal=37%

GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	23	0.851879	1.700028	0.004	0.094052	0.917	1090	tags=65%, list=5%, signal=69%
GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_INVOLVED_IN_INFLAMMATORY_RESPONSE	64	0.573841	1.697523	0.012048	0.095049	0.922	3826	tags=45%, list=18%, signal=55%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	43	0.753409	1.69715	0.008197	0.094929	0.922	1305	tags=51%, list=6%, signal=54%
GO_REGULATION_OF_MAST_CELL_ACTIVATION	36	0.603179	1.696913	0.01006	0.09465	0.922	3890	tags=53%, list=18%, signal=64%
GO_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	23	0.635588	1.695188	0.016293	0.095355	0.922	2944	tags=52%, list=14%, signal=60%
GO_INTERLEUKIN_1_PRODUCTION	96	0.64295	1.694339	0.004202	0.095772	0.922	2464	tags=47%, list=11%, signal=53%
GO_NEGATIVE_REGULATION_OF_EXOCYTOSIS	28	0.639229	1.693805	0.003984	0.095902	0.922	3606	tags=46%, list=17%, signal=56%
GO_MHC_PROTEIN_BINDING	27	0.746001	1.691088	0.010395	0.097806	0.924	1387	tags=52%, list=6%, signal=55%
GO_T_CELL_MEDIATED_CYTOTOXICITY	35	0.696986	1.690623	0.019397	0.097708	0.924	2790	tags=51%, list=13%, signal=59%

GO_POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	67	0.65781	1.689663	0.014228	0.096641	0.924	2254	tags=46%, list=10%, signal=51%
GO_CELLULAR_DEFENSE_RESPONSE	49	0.694775	1.688768	0.00625	0.097088	0.924	2937	tags=65%, list=14%, signal=75%
GO_REGULATION_OF_T_CELL_MIGRATION	40	0.651461	1.688088	0.008333	0.096827	0.925	3172	tags=55%, list=15%, signal=64%
GO_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY	154	0.468989	1.687174	0.02714	0.096744	0.928	3489	tags=29%, list=16%, signal=35%
GO_RESPIRATORY_BURST	30	0.722644	1.686566	0.01222	0.09703	0.929	3461	tags=50%, list=16%, signal=59%
GO_MYELOID_LEUKOCYTE_DIFFERENTIATION	194	0.495534	1.686534	0.010267	0.096597	0.929	2991	tags=34%, list=14%, signal=39%
GO_DENDRITIC_CELL_DIFFERENTIATION	37	0.680844	1.686317	0.008316	0.096316	0.93	2613	tags=54%, list=12%, signal=61%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	90	0.662857	1.685799	0.012397	0.096454	0.932	2790	tags=47%, list=13%, signal=53%
GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	34	0.659059	1.682898	0.010438	0.098181	0.935	3008	tags=47%, list=14%, signal=55%

GO_LEUKOCYTE_ACTIVATION_INVOLVED_IN_INFLAMMATORY_RESPONSE	43	0.738744	1.681784	0.006048	0.09886	0.936	1587	tags=49%, list=7%, signal=53%
GO_TYPE_I_INTERFERON_PRODUCTION	119	0.483092	1.680991	0.034694	0.099197	0.936	4343	tags=34%, list=20%, signal=43%
GO_INTERLEUKIN_2_PRODUCTION	63	0.630422	1.680667	0.004065	0.099052	0.936	2254	tags=43%, list=10%, signal=48%
GO_REGULATION_OF_CELL_CELL_ADHESION	367	0.545398	1.680177	0.014374	0.099119	0.937	3196	tags=41%, list=15%, signal=47%
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	56	0.684021	1.679877	0.002083	0.099016	0.938	2740	tags=54%, list=13%, signal=61%
GO_RESPONSE_TO_AMYLOID_BETA	47	0.640562	1.678387	0.008048	0.098721	0.94	3274	tags=45%, list=15%, signal=52%
GO_INTERFERON_BETA_PRODUCTION	48	0.509982	1.678049	0.018868	0.098614	0.942	1198	tags=19%, list=6%, signal=20%
GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	132	0.621522	1.678018	0.010417	0.09819	0.942	2790	tags=45%, list=13%, signal=51%
GO_RESPONSE_TO_INTERFERON_BETA	27	0.665993	1.676567	0.016736	0.098811	0.943	2175	tags=41%, list=10%, signal=45%

GO_CELL_KILLING	148	0.574832	1.675126	0.006263	0.099385	0.944	2790	tags=42%, list=13%, signal=48%
GO_MYD88_DEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	32	0.719706	1.674273	0.016529	0.099877	0.945	2251	tags=44%, list=10%, signal=49%
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	451	0.503873	1.673487	0.014831	0.099392	0.947	2984	tags=32%, list=14%, signal=36%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	116	0.625753	1.673474	0.012632	0.098969	0.947	2342	tags=39%, list=11%, signal=43%
GO_POSITIVE_REGULATION_OF_MACROPHAGE_ACTIVATION	21	0.732414	1.67267	0.014257	0.09937	0.948	2639	tags=57%, list=12%, signal=65%
GO_POSITIVE_REGULATION_OF_CELL_KILLING	56	0.70643	1.672203	0.014737	0.099536	0.948	2790	tags=55%, list=13%, signal=63%
GO_B_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	68	0.602735	1.670883	0.024048	0.100002	0.949	2464	tags=38%, list=11%, signal=43%
GO_LEUKOCYTE_HOMEOSTASIS	81	0.584732	1.670614	0.026157	0.099842	0.95	2723	tags=41%, list=13%, signal=46%
GO_INTERLEUKIN_10_PRODUCTION	50	0.712045	1.669795	0.008163	0.09989	0.952	3406	tags=62%, list=16%, signal=73%

GO_FICOLIN_1_RICH_GRANULE_MEMBRANE	56	0.560816	1.668633	0.026263	0.10033	0.953	2460	tags=32%, list=11%, signal=36%
GO_REGULATION_OF_MYOBLAST_FUSION	20	0.741889	1.666886	0.012146	0.101195	0.955	2895	tags=50%, list=13%, signal=58%
GO_LEUKOCYTE_MIGRATION	402	0.560099	1.666192	0.006224	0.100991	0.955	2780	tags=40%, list=13%, signal=45%
GO_LEUKOCYTE_CHEMOTAXIS	194	0.607626	1.664689	0.008163	0.100864	0.957	2944	tags=47%, list=14%, signal=54%
GO_PHAGOCYTIC_CUP	24	0.642135	1.66283	0.022	0.101999	0.958	2984	tags=50%, list=14%, signal=58%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	33	0.697868	1.660289	0.006122	0.104317	0.961	2944	tags=58%, list=14%, signal=66%
GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	203	0.56483	1.659729	0.020367	0.104418	0.961	3172	tags=46%, list=15%, signal=54%
GO_VIRAL_GENOME_REPLICATION	113	0.476013	1.659588	0.038934	0.104193	0.961	3204	tags=29%, list=15%, signal=34%
GO_POSITIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR_ACTIVITY	144	0.495156	1.65856	0.016667	0.103632	0.961	4369	tags=35%, list=20%, signal=43%

GO_MACROPHAGE_ACTIVATION	87	0.627719	1.658264	0.01227	0.103515	0.961	3418	tags=51%, list=16%, signal=60%
GO_OSTEOCLAST_DIFFERENTIATION	91	0.513336	1.655173	0.012448	0.105057	0.962	4164	tags=42%, list=19%, signal=51%
GO_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	18	0.738579	1.654954	0.008197	0.104464	0.962	1147	tags=39%, list=5%, signal=41%
GO_POSITIVE_REGULATION_OF_T_CELL_MIGRATION	29	0.685262	1.653475	0.014257	0.105532	0.965	3172	tags=62%, list=15%, signal=73%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	16	0.807768	1.653083	0.002101	0.104821	0.965	2921	tags=75%, list=13%, signal=87%
GO_B_CELL_PROLIFERATION	84	0.635145	1.653062	0.013834	0.104446	0.965	2464	tags=45%, list=11%, signal=51%
GO_REGULATION_OF_B_CELL_RECEPTOR_SIGNALING_PATHWAY	24	0.770522	1.652408	0.004057	0.104768	0.967	2339	tags=67%, list=11%, signal=75%
GO_T_CELL_CYTOKINE_PRODUCTION	40	0.636765	1.652314	0.01232	0.104483	0.967	2323	tags=38%, list=11%, signal=42%
GO_ANTIGEN_BINDING	35	0.669544	1.651225	0.016842	0.104776	0.967	2790	tags=57%, list=13%, signal=65%

GO_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	54	0.704037	1.65093	0.0014085	0.104337	0.968	1936	tags=56%, list=9%, signal=61%
GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	146	0.587119	1.65086	0.0016736	0.10405	0.968	3008	tags=42%, list=14%, signal=49%
GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	93	0.622303	1.650367	0.0019027	0.104151	0.968	2790	tags=41%, list=13%, signal=47%
GO_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	27	0.707242	1.646731	0.0014199	0.107134	0.969	2875	tags=63%, list=13%, signal=72%
GO_POSITIVE_REGULATION_OF_MACROPHAGE_MIGRATION	20	0.747323	1.645851	0.001875	0.107631	0.97	2944	tags=60%, list=14%, signal=69%
GO_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	63	0.626303	1.645507	0.002079	0.107633	0.97	2790	tags=43%, list=13%, signal=49%
GO_INTERLEUKIN_6_PRODUCTION	134	0.571424	1.645207	0.002521	0.10762	0.97	3418	tags=46%, list=16%, signal=55%
GO_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	52	0.614702	1.640846	0.0012397	0.110252	0.97	3319	tags=44%, list=15%, signal=52%
GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	198	0.49202	1.640808	0.0016293	0.10989	0.97	3481	tags=38%, list=16%, signal=45%

GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	54	0.623382	1.63948	0.014493	0.110657	0.97	2323	tags=41%, list=11%, signal=46%
GO_PHOSPHATIDYLINOSITOL_3_4_BISPHOSPHATE_BINDING	24	0.548267	1.639246	0.033333	0.110518	0.97	2922	tags=29%, list=13%, signal=34%
GO_MACROPHAGE_MIGRATION	47	0.592201	1.637127	0.018443	0.111995	0.97	2944	tags=47%, list=14%, signal=54%
GO_INTERLEUKIN_4_PRODUCTION	34	0.678796	1.637075	0.016032	0.111696	0.971	2875	tags=56%, list=13%, signal=64%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	49	0.6157	1.635631	0.02449	0.112971	0.972	3826	tags=51%, list=18%, signal=62%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MIGRATION	36	0.672357	1.635511	0.021359	0.112714	0.972	3172	tags=64%, list=15%, signal=75%
GO_CELL_CHEMOTAXIS	264	0.576952	1.635305	0.006198	0.112512	0.972	2944	tags=42%, list=14%, signal=48%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_SECRETION	16	0.753508	1.634012	0.014344	0.113659	0.973	3172	tags=69%, list=15%, signal=80%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	79	0.592868	1.63318	0.011834	0.113765	0.973	3083	tags=51%, list=14%, signal=59%

GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	84	0.528513	1.633117	0.030738	0.113486	0.973	3319	tags=38%, list=15%, signal=45%
GO_T_CELL_HOMEOSTASIS	38	0.575413	1.632854	0.025641	0.113412	0.973	2093	tags=32%, list=10%, signal=35%
GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	80	0.632357	1.631929	0.026	0.114021	0.973	2711	tags=46%, list=12%, signal=53%
GO_NEGATIVE_REGULATION_OF_B_CELL_PROLIFERATION	16	0.745988	1.628264	0.02686	0.116602	0.976	2464	tags=56%, list=11%, signal=63%
GO_MYELOID_CELL_DIFFERENTIATION	355	0.418781	1.626251	0.016427	0.117242	0.976	2991	tags=26%, list=14%, signal=30%
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS	225	0.438113	1.625164	0.018595	0.117344	0.976	2723	tags=27%, list=13%, signal=30%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	22	0.722226	1.624901	0.012146	0.117306	0.976	2323	tags=64%, list=11%, signal=71%
GO_B_CELL_HOMEOSTASIS	28	0.620491	1.622157	0.04499	0.119606	0.976	2339	tags=39%, list=11%, signal=44%
GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	55	0.603034	1.621507	0.036217	0.119957	0.976	3204	tags=45%, list=15%, signal=53%
GO_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	27	0.710552	1.621153	0.025478	0.119932	0.977	2790	tags=52%, list=13%, signal=59%

GO_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	129	0.569046	1.619851	0.0204922	0.121155	0.977	2711	tags=39%, list=12%, signal=44%
GO_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	100	0.593726	1.619711	0.0162933	0.120941	0.977	3083	tags=50%, list=14%, signal=58%
GO_B_CELL_MEDIATED_IMMUNITY	107	0.586216	1.619169	0.0224449	0.120693	0.977	2464	tags=44%, list=11%, signal=49%
GO_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	213	0.546571	1.61842	0.0206199	0.120742	0.977	3826	tags=42%, list=18%, signal=51%
GO_SPECIFIC_GRANULE_MEMBRANE	83	0.58851	1.617893	0.0303364	0.120913	0.979	2555	tags=31%, list=12%, signal=35%
GO_RESPONSE_TO_CHEMOKINE	85	0.680309	1.617713	0.0186334	0.120758	0.979	2780	tags=54%, list=13%, signal=62%
GO_B_CELL_ACTIVATION	224	0.543623	1.617311	0.0425966	0.120831	0.98	2593	tags=36%, list=12%, signal=40%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	31	0.675363	1.616585	0.0359288	0.121336	0.981	2723	tags=48%, list=13%, signal=55%
GO_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	145	0.456899	1.615501	0.006	0.121924	0.981	2984	tags=34%, list=14%, signal=40%

GO_POSITIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	54	0.580063	1.615101	0.028283	0.122027	0.981	3697	tags=43%, list=17%, signal=51%
GO_POSITIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	40	0.535194	1.614361	0.002028	0.122148	0.981	4274	tags=45%, list=20%, signal=56%
GO_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	95	0.514965	1.613052	0.029046	0.122413	0.981	3489	tags=29%, list=16%, signal=35%
GO_CYTOKINE_METABOLIC_PROCESS	114	0.546713	1.612755	0.028689	0.12203	0.981	3063	tags=44%, list=14%, signal=51%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	18	0.804215	1.612694	0.012422	0.121751	0.981	3461	tags=83%, list=16%, signal=99%
GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	15	0.783149	1.609693	0.014228	0.124516	0.983	1147	tags=47%, list=5%, signal=49%
GO_REGULATION_OF_B_CELL_PROLIFERATION	60	0.621963	1.60787	0.032129	0.12621	0.985	2464	tags=43%, list=11%, signal=49%
GO_NEGATIVE_REGULATION_OF_VIRAL_LIFE_CYCLE	77	0.54812	1.606765	0.028926	0.126758	0.985	3204	tags=43%, list=15%, signal=50%
GO_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	73	0.472138	1.606652	0.040404	0.126516	0.985	1335	tags=18%, list=6%, signal=19%

GO_T_CELL_APOPTOTIC_PROCESS	47	0.592546	1.606158	0.016701	0.126799	0.986	2421	tags=40%, list=11%, signal=45%
GO_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	85	0.489004	1.60547	0.018711	0.12712	0.986	2984	tags=33%, list=14%, signal=38%
GO_MYELOID_LEUKOCYTE_MIGRATION	184	0.582922	1.603419	0.022541	0.128837	0.987	3170	tags=45%, list=15%, signal=52%
GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	181	0.548694	1.602389	0.02439	0.129577	0.988	2980	tags=45%, list=14%, signal=52%
GO_PROTEIN_AUTOPHOSPHORYLATION	223	0.380361	1.598179	0.026369	0.132719	0.989	2990	tags=21%, list=14%, signal=24%
GO_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	317	0.521708	1.592622	0.022495	0.138495	0.989	3466	tags=39%, list=16%, signal=46%
GO_T_CELL_RECEPTOR_COMPLEX	17	0.816614	1.591983	0.013889	0.138538	0.99	2254	tags=71%, list=10%, signal=79%
GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_SUPERFAMILY_BINDING	42	0.60185	1.591682	0.036885	0.138507	0.99	4354	tags=50%, list=20%, signal=62%
GO_REGULATION_OF_MYOTUBE_DIFFERENTIATION	48	0.531148	1.591326	0.013592	0.138541	0.99	2895	tags=29%, list=13%, signal=34%

GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	86	0.561692	1.587644	0.022727	0.142164	0.991	2400	tags=35%, list=11%, signal=39%
GO_REGULATORY_T_CELL_DIFFERENTIATION	28	0.74057	1.587081	0.022312	0.142073	0.991	2186	tags=61%, list=10%, signal=67%
GO_NEGATIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	17	0.667494	1.587078	0.021696	0.141692	0.991	2188	tags=47%, list=10%, signal=52%
GO_POSITIVE_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	70	0.553181	1.586961	0.033195	0.141448	0.991	3057	tags=29%, list=14%, signal=33%
GO_MYELOID_DENDRITIC_CELL_ACTIVATION	26	0.700851	1.58645	0.03681	0.141749	0.991	2613	tags=62%, list=12%, signal=70%
GO_REGULATION_OF_T_CELL_CYTOKINE_PRODUCTION	30	0.667841	1.586172	0.02449	0.141297	0.991	2323	tags=43%, list=11%, signal=48%
GO_POSITIVE_REGULATION_OF_PHAGOCYTOSIS	65	0.567212	1.585233	0.020161	0.142067	0.992	3172	tags=46%, list=15%, signal=54%
GO_INTERLEUKIN_1_SECRETION	55	0.614199	1.585216	0.029228	0.14171	0.992	2323	tags=45%, list=11%, signal=51%
GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	34	0.588758	1.583031	0.030675	0.143417	0.992	2188	tags=47%, list=10%, signal=52%

GO_POSITIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	19	0.755182	1.582902	0.03272	0.14318	0.992	979	tags=47%, list=5%, signal=50%
GO_LYMPHOCYTE_CHEMOTAXIS	56	0.694839	1.582657	0.028398	0.143083	0.992	2421	tags=52%, list=11%, signal=58%
GO_GLIAL_CELL_ACTIVATION	51	0.654791	1.581665	0.030426	0.143926	0.992	1731	tags=43%, list=8%, signal=47%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	16	0.767695	1.579399	0.02449	0.145672	0.992	3535	tags=75%, list=16%, signal=90%
GO_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	41	0.629825	1.579095	0.017822	0.145665	0.992	2984	tags=54%, list=14%, signal=62%
GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	66	0.509074	1.577991	0.028283	0.145622	0.992	2466	tags=33%, list=11%, signal=37%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	83	0.556282	1.577892	0.039501	0.145385	0.992	3406	tags=43%, list=16%, signal=51%
GO_ALPHA_BETA_T_CELL_PROLIFERATION	30	0.681822	1.57627	0.028866	0.145284	0.992	3461	tags=70%, list=16%, signal=83%
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	137	0.544893	1.575841	0.035343	0.144348	0.992	2944	tags=46%, list=14%, signal=53%

GO_THYMIC_T_CELL_SELECTION	21	0.722722	1.575607	0.030242	0.14426	0.992	2254	tags=52%, list=10%, signal=58%
GO_INTERLEUKIN_2_BIOSYNTHETIC_PROCESS	23	0.680165	1.575528	0.022312	0.143973	0.992	2254	tags=52%, list=10%, signal=58%
GO_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	34	0.449661	1.572448	0.043478	0.146676	0.994	1202	tags=15%, list=6%, signal=16%
GO_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	21	0.723451	1.571554	0.029474	0.147165	0.994	1387	tags=48%, list=6%, signal=51%
GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	30	0.645357	1.570975	0.014768	0.147574	0.995	2921	tags=57%, list=13%, signal=65%
GO_NEGATIVE_REGULATION_OF_VIRAL_PROCESS	93	0.507962	1.569751	0.043121	0.148053	0.995	3204	tags=39%, list=15%, signal=45%
GO_SH2_DOMAIN_BINDING	35	0.558832	1.567668	0.044898	0.150348	0.995	2626	tags=31%, list=12%, signal=36%
GO_IMMUNOGLOBULIN_PRODUCTION	98	0.541153	1.56714	0.046559	0.1507	0.995	2464	tags=32%, list=11%, signal=36%
GO_GRANULOCYTE_MIGRATION	122	0.598001	1.565807	0.024793	0.15203	0.995	3406	tags=48%, list=16%, signal=57%

GO_REGULATION_OF_PHAGOCYTOSIS	87	0.530417	1.564345	0.027426	0.153613	0.995	2984	tags=43%, list=14%, signal=49%
GO_LEUKOCYTE_APOPTOTIC_PROCESS	101	0.534878	1.563196	0.041068	0.153987	0.995	2780	tags=39%, list=13%, signal=44%
GO_POSITIVE_REGULATION_OF_CHEMOTAXIS	126	0.547487	1.561407	0.02454	0.1559	0.995	3216	tags=43%, list=15%, signal=50%
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	50	0.564414	1.558949	0.020121	0.158088	0.996	2513	tags=40%, list=12%, signal=45%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	111	0.540662	1.558947	0.025316	0.157716	0.996	3064	tags=46%, list=14%, signal=53%
GO_DEFENSE_RESPONSE_TO_BACTERIUM	209	0.468984	1.558392	0.006122	0.158131	0.996	3835	tags=43%, list=18%, signal=51%
GO_CYTOKINE_PRODUCTION_INVOLVED_IN_INFLAMMATORY_RESPONSE	42	0.575466	1.557872	0.04829	0.158464	0.996	3826	tags=43%, list=18%, signal=52%
GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	43	0.615147	1.55733	0.046748	0.158107	0.996	2790	tags=42%, list=13%, signal=48%
GO_REGULATION_OF_VIRAL_LIFE_CYCLE	134	0.452043	1.550675	0.045643	0.164278	0.997	3204	tags=31%, list=15%, signal=36%

GO_LYMPHOCYTE_APOPTOTIC_PROCESS	70	0.545867	1.549659	0.032189	0.165285	0.997	2464	tags=37%, list=11%, signal=42%
GO_PURINERGIC_RECEPTOR_ACTIVITY	25	0.673012	1.548467	0.022088	0.166165	0.997	1731	tags=56%, list=8%, signal=61%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	33	0.713652	1.545691	0.044715	0.16782	0.997	3406	tags=64%, list=16%, signal=75%
GO_ACUTE_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	18	0.700452	1.542931	0.028112	0.170734	0.997	1763	tags=50%, list=8%, signal=54%
GO_POSITIVE_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL	36	0.589364	1.536248	0.030829	0.174799	0.997	2466	tags=39%, list=11%, signal=44%
GO_POSITIVE_REGULATION_OF_MONOCYTE_CHEMOTAXIS	17	0.739504	1.534826	0.032454	0.174953	0.997	1587	tags=59%, list=7%, signal=63%
GO_NEUTROPHIL_MIGRATION	102	0.622646	1.534672	0.035052	0.174778	0.997	3721	tags=54%, list=17%, signal=65%
GO_POSITIVE_REGULATION_OF_JNK_CASCADE	124	0.430747	1.533806	0.039337	0.175188	0.998	3470	tags=29%, list=16%, signal=34%
GO_REGULATION_OF_MONOCYTE_CHEMOTAXIS	23	0.714487	1.529388	0.034068	0.179402	0.998	2636	tags=65%, list=12%, signal=74%

GO_TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	79	0.486878	1.528263	0.0031683	0.180626	0.998	2984	tags=39%, list=14%, signal=45%
GO_MONONUCLEAR_CELL_MIGRATION	80	0.63763	1.527834	0.0040323	0.180513	0.998	2984	tags=50%, list=14%, signal=58%
GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	140	0.515637	1.525324	0.003527	0.183325	0.998	2984	tags=41%, list=14%, signal=47%
GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	44	0.551975	1.525016	0.003252	0.183346	0.998	2188	tags=41%, list=10%, signal=45%
GO_NEUROINFLAMMATORY_RESPONSE	63	0.60858	1.521846	0.0044807	0.186036	0.998	3303	tags=52%, list=15%, signal=62%
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS_WITHIN_A_TISSUE	27	0.539376	1.521634	0.0047131	0.185627	0.998	2200	tags=37%, list=10%, signal=41%
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT	228	0.435123	1.520519	0.0011719	0.185308	0.998	2698	tags=31%, list=12%, signal=35%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	15	0.711046	1.51966	0.0046748	0.185677	0.998	2711	tags=53%, list=12%, signal=61%
GO_DEFENSE_RESPONSE_TO_GRAM_POSITIVE_BACTERIUM	78	0.500116	1.515437	0.0012346	0.18825	0.998	2984	tags=33%, list=14%, signal=38%

GO_MONOCYTE_CHEMOTAXIS	59	0.683522	1.513854	0.0386977	0.188747	0.998	2780	tags=54%, list=13%, signal=62%
GO_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	159	0.48915	1.508935	0.0373444	0.194434	0.998	3064	tags=38%, list=14%, signal=44%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	23	0.628044	1.504912	0.0383844	0.197137	0.998	2188	tags=43%, list=10%, signal=48%
GO_POSITIVE_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	22	0.669835	1.503565	0.0409	0.197233	0.998	1587	tags=45%, list=7%, signal=49%
GO_POSITIVE_REGULATION_OF_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	87	0.486268	1.502135	0.0303364	0.199045	0.998	2984	tags=43%, list=14%, signal=49%
GO_REGULATION_OF_CHEMOTAXIS	191	0.489947	1.498151	0.0386977	0.203468	0.998	3234	tags=37%, list=15%, signal=43%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	46	0.571005	1.49647	0.0267749	0.204034	0.998	2188	tags=43%, list=10%, signal=48%
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	112	0.458319	1.492927	0.0236222	0.206657	0.998	2696	tags=32%, list=12%, signal=37%
GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	31	0.597164	1.488505	0.0263166	0.209971	0.998	3785	tags=58%, list=17%, signal=70%

GO_NEGATIVE_REGULATION_OF_HEMOPOIESIS	132	0.434857	1.483592	0.044025	0.214753	0.999	2339	tags=28%, list=11%, signal=31%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	95	0.469487	1.478162	0.048523	0.221122	0.999	3112	tags=38%, list=14%, signal=44%
GO_VITAMIN_D_METABOLIC_PROCESS	22	0.542598	1.422083	0.043651	0.275781	1	4070	tags=55%, list=19%, signal=67%