

Molecular Interplay Between Ulcerative Colitis and Nonspecific Orbital Inflammation: Insights
from Integrated Gene Expression Analysis and Machine Learning Approaches

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Appendix 1

DEGs linked to NSOI

Table S1. DEGs linked to NSOI.

id	logFC	AveExpr	P.Value	adj.P.Val
PEX19	-1.346922405	5.313274338	4.22E-24	9.14E-20
HLF	-1.901892931	4.456445723	5.25E-23	5.69E-19
GULP1	-1.133049689	3.408039302	4.74E-22	3.35E-18
PGRMC2	-1.642261187	3.920000347	6.20E-22	3.35E-18
FAXDC2	-1.35747775	5.041668539	5.23E-21	2.26E-17
MGST1	-2.238725129	4.85116665	2.11E-20	7.26E-17
Clorf198	-1.465303594	6.263436506	2.35E-20	7.26E-17
ANGPT1	-1.153547986	3.311956104	2.93E-20	7.93E-17
TUSC1	-1.685871084	5.496755049	5.47E-20	1.23E-16
TGFBR3	-2.272082813	5.286734533	5.68E-20	1.23E-16
HNMT	-1.075062651	4.10038052	1.11E-19	2.09E-16
CYB5A	-1.310060788	4.824209659	1.16E-19	2.09E-16
LARP6	-1.205647752	4.354315317	1.96E-19	3.27E-16
STXBP1	-1.87825361	4.59274839	4.17E-19	6.45E-16
ADH1B	-2.714177533	4.251497947	4.71E-19	6.80E-16
MXRA7	-1.261317664	5.105311502	8.76E-19	1.18E-15
PGM1	-1.691505094	5.596089129	1.24E-18	1.59E-15
CACHD1	-1.2318112	4.466240744	1.36E-18	1.63E-15
LOC284825	-1.965430398	3.244446679	1.44E-18	1.65E-15
ADH5	-1.382538866	5.188237059	1.77E-18	1.91E-15
PHYH	-1.83069758	4.442053449	2.99E-18	2.94E-15
CAV2	-1.845086215	4.819776034	4.83E-18	4.36E-15
SSPN	-1.166776108	4.322063451	5.30E-18	4.59E-15
CHRD1	-2.4939908	5.94327908	5.62E-18	4.68E-15
GHR	-2.795877137	3.889996857	5.85E-18	4.69E-15
PRDX6	-1.504067459	6.654628329	6.15E-18	4.75E-15
TSKU	-2.001162062	5.745303973	7.29E-18	5.26E-15
HADH	-1.345683363	4.795853661	7.33E-18	5.26E-15
FAM213A	-1.446389965	5.251316197	7.54E-18	5.26E-15
TMEM100	-1.752462984	2.853094704	8.00E-18	5.41E-15
THSD4	-1.234811464	3.781965517	9.81E-18	6.44E-15

FKBP1B	-1.296591629	3.013703455	1.49E-17	9.49E-15
NTRK2	-1.563274818	4.59895616	1.64E-17	1.01E-14
LRN4CL	-2.542083091	4.707819805	1.83E-17	1.10E-14
THRB	-1.036847658	3.901273232	2.07E-17	1.21E-14
APCDD1	-1.896988098	5.915671959	2.19E-17	1.22E-14
FMO3	-1.367318258	3.048833895	2.20E-17	1.22E-14
OLFML2A	-1.856159469	5.4688284	2.59E-17	1.40E-14
ADIPOR2	-1.04585593	5.599462001	2.71E-17	1.43E-14
ATXN1L	-1.540673103	5.135740578	2.80E-17	1.45E-14
ITGB5	-1.128373241	4.748498564	3.07E-17	1.54E-14
NGFRAP1	-1.596654057	6.64028862	3.33E-17	1.64E-14
SLC24A3	-1.489403066	4.368362469	3.83E-17	1.80E-14
C2orf40	-2.465717684	4.648947467	4.13E-17	1.90E-14
SLC17A9	1.07314378	5.642248113	4.81E-17	2.17E-14
AKAP12	-1.268216241	3.887652197	4.99E-17	2.20E-14
C2orf76	-1.030696597	3.22488543	8.05E-17	3.49E-14
TIMP4	-2.448850458	4.010299557	8.23E-17	3.50E-14
BC022047	-1.775777503	4.651942484	9.03E-17	3.69E-14
GPR146	-1.166601601	5.955826814	1.28E-16	5.03E-14
CDR1	-2.494245179	6.179794158	1.43E-16	5.52E-14
GPAM	-2.712940101	4.130533475	1.55E-16	5.89E-14
CFH	-2.044484589	5.462750158	1.74E-16	6.49E-14
RNF11	-1.968500907	3.589076431	2.16E-16	7.79E-14
AMOTL2	-1.782157654	5.35540193	2.23E-16	7.92E-14
OMD	-1.983265288	3.924457609	2.38E-16	8.20E-14
LINC01133	-1.006238413	3.274467948	2.39E-16	8.20E-14
ENPP6	-1.769467862	2.952727354	2.48E-16	8.28E-14
TCF7L1	-1.632229609	6.087154486	2.49E-16	8.28E-14
PCDH18	-1.808840491	5.560932664	2.72E-16	8.89E-14
WLS	-1.441121127	5.131490449	2.75E-16	8.89E-14
RNASE4	-1.788835397	5.109015851	2.88E-16	9.18E-14
PLSCR4	-1.705786881	2.895189238	3.40E-16	1.05E-13
SH3D19	-1.672449945	5.804860036	3.81E-16	1.16E-13
PPAP2B	-2.180149961	6.612946345	3.88E-16	1.17E-13
LEPR	-2.819452771	4.149217723	4.86E-16	1.44E-13
ALDH2	-2.008688618	7.145116275	5.39E-16	1.54E-13
CCDC23	-1.36767189	4.959462625	5.40E-16	1.54E-13
PLIN1	-4.414047995	6.766876957	5.83E-16	1.64E-13
SNX21	-1.107767584	4.315622591	6.42E-16	1.78E-13
MAGI2-AS3	-1.218415256	3.210398705	6.83E-16	1.87E-13
PBX1	-1.639650936	6.463432111	7.09E-16	1.92E-13
CAT	-1.31643793	5.2967694	7.31E-16	1.95E-13
MEST	-2.576135398	3.933513576	7.56E-16	2.00E-13

IGFBP6	-2.546942325	6.959957184	7.73E-16	2.02E-13
PPP1R1A	-2.537564563	5.8033746	8.81E-16	2.24E-13
LIMD2	1.241555522	7.558789326	9.65E-16	2.40E-13
LINC00094	-1.268978687	4.7165899	9.66E-16	2.40E-13
ADIPOQ	-4.208020702	4.605127099	1.09E-15	2.66E-13
F8	-1.485393106	3.996202435	1.10E-15	2.66E-13
ALDH3A2	-1.02729547	5.498017391	1.12E-15	2.66E-13
ZBP1	1.245611418	5.763250831	1.16E-15	2.74E-13
PRKAR2B	-2.334102491	3.058207454	1.65E-15	3.81E-13
IGHM	2.708926715	7.940703974	1.70E-15	3.86E-13
CAB39L	-1.174823944	4.9517854	1.71E-15	3.86E-13
OLFML1	-2.002024072	3.341196646	1.73E-15	3.86E-13
ZNF704	-1.010335869	4.266266972	1.90E-15	4.15E-13
CPE	-1.684851291	4.771562752	1.97E-15	4.23E-13
IGLL3P	2.098719666	8.630825634	2.10E-15	4.45E-13
PCOLCE2	-2.230045429	3.296285761	2.19E-15	4.61E-13
HPGDS	-1.378977143	4.295595806	2.25E-15	4.68E-13
FAM127B	-1.066155352	5.195164199	2.38E-15	4.90E-13
PPL	-2.038937111	6.444334653	2.93E-15	5.88E-13
MAMDC2	-2.346693197	3.342506938	3.65E-15	7.13E-13
GPC6	-1.245238415	4.413151874	4.44E-15	8.58E-13
USP53	-1.246460951	3.3921256	5.48E-15	1.01E-12
GSTM3	-1.385876428	4.748463638	6.29E-15	1.14E-12
THRSP	-2.272957195	5.043589185	6.42E-15	1.16E-12
CIDEC	-3.415541172	6.24971043	6.81E-15	1.22E-12
NDN	-1.138797665	5.566426718	7.01E-15	1.24E-12
CORO2B	-1.422471985	4.504386417	7.29E-15	1.28E-12
SEPT11	-1.347803954	4.140997432	8.88E-15	1.55E-12
AQPEP	-1.708536911	2.754947942	9.09E-15	1.57E-12
LYVE1	-2.920011323	5.664270463	9.26E-15	1.59E-12
GBE1	-1.533009434	2.983219098	9.36E-15	1.60E-12
CYSTM1	-1.181305357	6.807071202	9.71E-15	1.64E-12
DEF6	1.163595129	6.542391948	1.13E-14	1.86E-12
TUBB2A	-2.230846744	4.341156788	1.15E-14	1.89E-12
CDO1	-1.339388787	3.458349391	1.37E-14	2.18E-12
TNMD	-1.522707904	3.044711464	1.52E-14	2.40E-12
NTAN1	-1.100286355	5.153422303	1.58E-14	2.47E-12
MN1	-2.216193965	5.280345762	1.85E-14	2.84E-12
MAOA	-2.198329286	5.385941871	1.92E-14	2.92E-12
TRHDE-AS1	-2.113527774	3.2558261	1.95E-14	2.95E-12
UGDH	-1.438763539	4.210616162	2.01E-14	3.02E-12
EPHX1	-1.595552188	7.466946167	2.07E-14	3.09E-12
BNIP3L	-1.475548538	6.662112052	2.12E-14	3.15E-12

GNG12	-1.054419846	5.862736579	2.16E-14	3.15E-12
ALDH6A1	-1.026499105	4.584937302	2.20E-14	3.20E-12
SMIM3	-1.887486092	4.727042047	2.29E-14	3.28E-12
S100B	-1.120797687	3.294390738	2.33E-14	3.32E-12
NECAB1	-1.355278837	2.249003956	2.38E-14	3.34E-12
IGSF10	-1.23491807	4.005913648	2.42E-14	3.36E-12
FTO	-1.257443272	7.159644055	2.68E-14	3.65E-12
NEK7	-1.272093894	3.171281059	2.68E-14	3.65E-12
TMEM255A	-1.33700738	2.077681471	2.73E-14	3.69E-12
NPR3	-2.141156426	3.688892735	2.76E-14	3.71E-12
PPAP2A	-1.520096859	5.791832893	3.00E-14	4.02E-12
AR	-1.370517578	4.221567957	3.26E-14	4.34E-12
ADAMTS5	-1.632831669	3.089275022	3.29E-14	4.34E-12
SEPT10	-1.262013041	4.089970773	3.46E-14	4.51E-12
SCARA5	-1.675052722	6.000832813	3.74E-14	4.85E-12
PARVA	-1.05745194	5.122378484	3.78E-14	4.87E-12
KLB	-1.640560069	2.545437672	4.32E-14	5.51E-12
FABP4	-3.077529117	5.751986396	4.41E-14	5.59E-12
AOC3	-2.841914153	4.713624428	5.16E-14	6.42E-12
EAPP	-1.225717433	5.469165383	5.64E-14	6.90E-12
EFHD1	-1.576297376	6.414527894	6.15E-14	7.47E-12
PNMA1	-1.110410207	4.621359873	6.17E-14	7.47E-12
FAM127A	-1.321662708	7.2900977	6.36E-14	7.61E-12
VIT	-2.198342838	5.173424484	6.78E-14	7.99E-12
NFIA	-1.113835697	4.928932127	7.93E-14	9.18E-12
NDNF	-2.370086306	4.532445134	8.58E-14	9.83E-12
TCIRG1	1.015881537	6.884777628	9.02E-14	1.03E-11
GSTM5	-1.616813312	5.267678886	1.03E-13	1.16E-11
YAP1	-1.376318155	5.554197027	1.06E-13	1.18E-11
ZFYVE21	-1.084133281	5.487559362	1.08E-13	1.20E-11
C4orf3	-1.074642699	6.265491363	1.09E-13	1.21E-11
RUNX1-IT1	1.281488546	5.05663736	1.22E-13	1.34E-11
CYBRD1	-1.873434168	6.479844216	1.24E-13	1.35E-11
ACACB	-1.494754148	6.216319644	1.31E-13	1.41E-11
IGLC1	1.941418994	7.86919441	1.36E-13	1.45E-11
EHBP1	-1.451456723	5.916643666	1.36E-13	1.45E-11
SORBS1	-1.395725747	5.610656673	1.39E-13	1.46E-11
PLAT	-2.301554388	4.74388668	1.40E-13	1.47E-11
RORB	-1.176305165	2.49192975	1.48E-13	1.55E-11
AOX1	-1.99431064	5.349159701	1.65E-13	1.71E-11
RBMS3	-1.12224817	3.788388015	1.68E-13	1.73E-11
MZB1	1.507275693	7.125199431	1.80E-13	1.83E-11
SDPR	-1.233859014	3.750730108	1.93E-13	1.94E-11

OLFM2	-1.763864191	4.340777362	2.02E-13	2.02E-11
FERMT2	-1.243164577	6.163662104	2.07E-13	2.05E-11
ARHGAP21	-1.096164928	5.259120624	2.08E-13	2.05E-11
SUCLA2	-1.497250243	3.797340445	2.23E-13	2.18E-11
AVPI1	-1.18365138	5.342939917	2.43E-13	2.37E-11
EPB41L1	-1.136508436	5.506188314	2.47E-13	2.40E-11
KDSR	-1.013997207	3.466955807	3.16E-13	3.02E-11
CNRIP1	-1.581776864	4.344170647	3.33E-13	3.17E-11
ACAP1	1.179419278	6.678615939	3.49E-13	3.30E-11
HCAR1	-1.281682972	3.789937016	3.54E-13	3.33E-11
SVIL	-1.016993264	5.254959235	3.58E-13	3.36E-11
AXL	-1.329574107	5.741261107	3.72E-13	3.47E-11
GAS1	-1.506835118	5.442757476	3.92E-13	3.64E-11
EID1	-1.216927276	5.818830776	3.95E-13	3.64E-11
ZAP70	1.101928205	5.451030527	3.95E-13	3.64E-11
PKD4	-1.874794131	4.73541063	4.01E-13	3.68E-11
SLC2A10	-1.287970403	3.223819746	4.21E-13	3.83E-11
SESTD1	-1.310292048	5.730577978	4.27E-13	3.87E-11
ABL1	-1.037114177	7.611459103	4.35E-13	3.92E-11
MTURN	-1.210929226	5.352405162	4.45E-13	4.00E-11
EPDR1	-1.874163022	3.724216444	4.76E-13	4.21E-11
MRAP	-1.482475001	3.776073139	4.83E-13	4.25E-11
RP11-524D16__A.3	-1.441668785	3.289569643	4.86E-13	4.26E-11
MFAP4	-2.06403993	7.09258567	5.13E-13	4.46E-11
BOK	-1.789223444	5.21246852	5.41E-13	4.69E-11
FGFBP2	-1.508378423	2.972664364	5.48E-13	4.72E-11
SYNC	-1.237531833	3.345036689	5.70E-13	4.84E-11
CPED1	-1.309510792	4.329278474	5.89E-13	4.98E-11
ALDH1A1	-1.425617998	5.130829588	6.01E-13	5.06E-11
YWHAG	-1.638277859	5.86861932	6.51E-13	5.42E-11
ASPA	-1.380590389	3.868348527	6.78E-13	5.62E-11
HEBP1	-1.232055312	5.587693129	6.99E-13	5.78E-11
PDGFD	-1.74723778	5.025349302	7.02E-13	5.78E-11
FGF10	-1.273162528	3.52956116	7.50E-13	6.13E-11
CD34	-1.765257248	6.84845916	7.69E-13	6.26E-11
AKR1C3	-2.016328669	5.085094386	7.75E-13	6.29E-11
LEPROT	-1.186422502	5.004196012	7.89E-13	6.35E-11
SEMA3G	-1.585508725	5.958432293	8.46E-13	6.78E-11
NTN4	-1.520624775	4.911165286	8.79E-13	6.98E-11
RPS27L	-1.125261156	4.274925326	8.80E-13	6.98E-11
ZNF423	-1.804527351	4.93405478	9.00E-13	7.12E-11
ADH1C	-1.24015834	3.620815306	9.25E-13	7.23E-11
VKORC1L1	-1.18851215	4.990251821	9.40E-13	7.29E-11

LHFP	-1.096441445	4.638884535	9.87E-13	7.63E-11
SC5D	-1.092673334	4.707824332	9.93E-13	7.66E-11
ACSL1	-1.77027688	6.70737912	1.00E-12	7.70E-11
SBF2	-1.021439734	3.735406901	1.15E-12	8.74E-11
MIAT	1.102445042	5.113004415	1.23E-12	9.29E-11
PCYOX1	-1.408689127	5.227784166	1.26E-12	9.45E-11
CRNDE	-1.464882453	4.362898888	1.27E-12	9.48E-11
GNAI1	-1.099666102	2.657920905	1.51E-12	1.12E-10
IGK	1.702632804	8.408920275	1.56E-12	1.15E-10
CAV1	-2.417365412	7.104218278	1.58E-12	1.15E-10
BEX4	-1.342469052	4.059833178	1.70E-12	1.24E-10
TMC6	1.012545638	6.136343194	1.74E-12	1.26E-10
ANO6	-1.206257108	4.373737189	1.94E-12	1.38E-10
WASF3	-1.047630402	3.301150384	2.00E-12	1.42E-10
CRYBG3	-1.142913571	4.930418861	2.06E-12	1.46E-10
ADAM19	1.058918721	5.41694508	2.06E-12	1.46E-10
PAM	-1.395211389	5.761957524	2.13E-12	1.50E-10
ADIRF	-1.837646573	8.304380961	2.18E-12	1.53E-10
PLA2G16	-1.32376438	5.466092819	2.21E-12	1.54E-10
C15orf61	-1.219650473	4.169618105	2.33E-12	1.60E-10
SGCG	-2.288378104	3.435415513	2.37E-12	1.61E-10
CD79A	1.511906089	7.086980696	2.57E-12	1.71E-10
DNMBP	-1.241626231	5.036144666	2.60E-12	1.73E-10
HSPB6	-3.057178917	8.03293906	2.75E-12	1.81E-10
IGKC	1.767398691	6.457977124	2.76E-12	1.82E-10
EBF1	-1.773808355	4.786327183	2.80E-12	1.84E-10
PJA1	-1.016813839	5.236751302	2.98E-12	1.95E-10
ITGB2-AS1	1.230483234	5.825168488	3.20E-12	2.08E-10
LPL	-2.843866128	5.637432422	3.41E-12	2.21E-10
RBP4	-1.631134248	4.723338796	3.45E-12	2.23E-10
CYB5R3	-1.257052621	7.882272037	3.54E-12	2.28E-10
CETN2	-1.290114693	5.414155559	3.67E-12	2.34E-10
LINC01140	-1.056847653	5.027837881	3.96E-12	2.51E-10
OGN	-2.208503291	4.432107433	4.02E-12	2.55E-10
MYH10	-1.248441926	4.614982907	4.05E-12	2.56E-10
ECI2	-1.09761436	5.295690068	4.19E-12	2.64E-10
FHL1	-2.538464668	6.379870416	4.25E-12	2.67E-10
PTPRCAP	1.391791033	7.157964904	4.58E-12	2.84E-10
TPRG1	-1.314405674	3.929528619	4.67E-12	2.89E-10
G0S2	-2.848134546	6.790937784	4.70E-12	2.90E-10
SLC29A1	-1.038125263	6.703112469	4.96E-12	3.03E-10
SLC19A3	-1.486391146	3.051951517	4.98E-12	3.04E-10
DIAPH2	-1.066787232	4.905678426	5.00E-12	3.04E-10

PIM2	1.33376005	5.874375393	5.09E-12	3.07E-10
IGLJ3	1.468078731	6.287649009	5.29E-12	3.17E-10
TMEM132C	-1.757526255	4.244153098	5.43E-12	3.24E-10
MT1M	-1.60492149	4.555310842	5.62E-12	3.33E-10
FMO2	-1.807530201	6.229504376	5.67E-12	3.36E-10
ZCCHC24	-1.219207897	5.849718556	5.71E-12	3.36E-10
LINC00657	-1.486970677	5.24525721	5.92E-12	3.47E-10
TNS1	-1.56983591	7.510357201	6.59E-12	3.83E-10
MAN1A1	-1.383596262	4.139000851	7.25E-12	4.17E-10
TMEM200B	-1.386927543	4.700298932	7.37E-12	4.22E-10
ABHD14B	-1.05187318	5.860517983	7.43E-12	4.25E-10
TBC1D10C	1.683829758	6.396828197	8.00E-12	4.50E-10
MARC1	-1.282607014	4.545197366	8.34E-12	4.68E-10
NDFIP1	-1.340132354	5.817085069	8.51E-12	4.76E-10
DDR2	-1.567932782	6.281215929	9.02E-12	4.99E-10
CSTA	-2.106129271	6.990319998	9.13E-12	5.04E-10
SDC2	-1.436263006	5.759093475	9.58E-12	5.25E-10
CD36	-2.1713186	4.916225051	1.00E-11	5.43E-10
ZFHX4	-1.207704704	4.047003675	1.04E-11	5.61E-10
MFAP5	-1.796449525	4.969518673	1.04E-11	5.63E-10
ACKR3	-1.040024726	4.331396618	1.06E-11	5.72E-10
RSPO3	-1.438110984	4.633829679	1.09E-11	5.83E-10
RAMP2	-1.493842822	6.746999756	1.10E-11	5.84E-10
CAP2	-1.314747988	3.757243807	1.13E-11	6.00E-10
EXTL2	-1.268786567	4.077787311	1.26E-11	6.54E-10
GPR124	-1.53700859	6.228545986	1.26E-11	6.54E-10
SNX7	-1.082055628	4.475992981	1.32E-11	6.84E-10
RAB33B	-1.070909404	3.344301208	1.39E-11	7.09E-10
SCP2	-1.489636641	5.445489041	1.45E-11	7.40E-10
ZNF521	-1.458553286	4.329531738	1.53E-11	7.76E-10
GYG2	-1.724124216	4.912377997	1.81E-11	8.96E-10
ZNF667-AS1	-1.156492266	5.378439599	1.82E-11	9.02E-10
TMC8	1.08157622	5.742109285	1.86E-11	9.15E-10
VTI1B	-1.002630128	5.366423117	1.87E-11	9.16E-10
SUCLG2	-1.29357088	3.787184155	1.88E-11	9.21E-10
ARMCX1	-1.209734498	4.661274419	2.04E-11	9.91E-10
CFD	-2.261000812	7.756813477	2.27E-11	1.10E-09
RRAS	-1.129632133	6.406433432	2.29E-11	1.11E-09
LIMA1	-1.189717426	6.399361442	2.39E-11	1.15E-09
FKBP9	-1.168274508	7.592815468	2.50E-11	1.19E-09
LYRM5	-1.425715498	4.060971765	2.59E-11	1.23E-09
ACADL	-1.080497033	3.369445695	2.67E-11	1.26E-09
GALNT15	-1.004841134	4.135203559	2.83E-11	1.32E-09

AX747826	1.203923112	4.367338232	3.73E-11	1.70E-09
HIF3A	-1.070582109	4.632962112	4.00E-11	1.81E-09
PKD2	-1.447702233	3.884286584	4.03E-11	1.82E-09
EYA1	-1.213391524	3.226533532	4.11E-11	1.86E-09
TSPYL5	-1.296070438	3.845251281	4.13E-11	1.86E-09
ZFPM2	-1.392558299	3.074998396	4.30E-11	1.93E-09
TJP1	-1.117670882	5.233801257	4.41E-11	1.97E-09
PCK1	-2.150163325	3.15014784	4.45E-11	1.98E-09
PDE3B	-1.114624483	3.633828661	4.68E-11	2.07E-09
OSR2	-1.490722642	6.396591131	4.75E-11	2.09E-09

Appendix 2

DEGs linked to UC

Table S2. DEGs linked to UC.

id	logFC	AveExpr	t	P.Value	adj.P.Val	B
CDKN2BAS	-2.5406471 34	3.7401120 52	-26.809404 47	5.62E-10 3	1.12E-9 8	224.04471 82
CAPN13	-2.1144772 88	3.455007	-25.564018 45	1.51E-96	1.51E-9 2	209.35127 28
RBM24	-1.7494539 18	2.8430311 6	-24.803018 32	1.32E-92	8.77E-8 9	200.34346 59
ST6GAL2	-1.4127959 96	3.2420707 05	-24.198978 19	1.79E-89	8.91E-8 6	193.18395 45
LOC1001333 19	-2.1206926 4	3.8658366 05	-23.440273 35	1.54E-85	5.12E-8 2	184.18627 38
LOC389023	-2.5843988 96	3.1191458 71	-23.170233 99	3.88E-84	1.10E-8 0	180.98404 66
TIGD6	-1.2540941 49	3.5594308 26	-23.120658 24	7.01E-84	1.75E-8 0	180.39623 53
HOXD10	-2.7805408 14	4.4268832 84	-23.085323 28	1.07E-83	2.35E-8 0	179.97729 3
SLC6A19	-1.9641732 76	3.9121284 62	-23.077178 25	1.18E-83	2.35E-8 0	179.88072 54

IGKV1D-13	2.14900971 2	11.796423 69	22.4337873	2.54E-80	4.22E-7 7	172.25652 8
GHR	-2.3069381 03	3.4058465 82	-22.374635 52	5.15E-80	7.89E-7 7	171.55607 94
LOC1002934 40	2.49430493 7	11.413095 07	22.1153197 1	1.13E-78	1.61E-7 5	168.48670 27
IGKV3-20	3.13926298 1	10.579206 6	22.0149564 5	3.74E-78	4.97E-7 5	167.29940 18
CNTN3	-1.2549642 03	2.7090353 93	-21.816758 03	3.97E-77	4.94E-7 4	164.95590 49
LOC1002877 23	2.12089950 1	11.831309 46	21.7189707 6	1.27E-76	1.49E-7 3	163.80030 53
IGLV2-23	2.37704002 1	11.779666 29	21.7036107 9	1.52E-76	1.69E-7 3	163.61882 97
VDLR	-1.2239374 67	3.3280721 17	-21.098677 34	2.01E-73	2.01E-7 0	156.48164 61
DPP10	-1.0433870 34	2.8873822 67	-21.074149 37	2.69E-73	2.55E-7 0	156.19271 63
CLDN8	-5.9684206 25	3.9016534 24	-20.753285 97	1.21E-71	1.09E-6 8	152.41687 14
CCL11	3.88947911	9.1891122 73	20.4091049 1	7.06E-70	5.86E-6 7	148.37526 26
RNF125	-1.6449638 24	3.9747098 84	-20.317177 92	2.09E-69	1.66E-6 6	147.29745 99
IFITM3	1.78365427 3	11.236973 71	20.2642324 3	3.90E-69	2.99E-6 6	146.67703 62
PNLIPRP2	-1.8131629 45	3.1171093 72	-20.194327 77	8.90E-69	6.33E-6 6	145.85827 11
LOC1002936	2.33224460	10.104749	20.1534540	1.44E-68	9.89E-6	145.37974

79	3	4	3		6	22
LOC652493	2.20685875 3	11.225953 79	20.1221918 7	2.08E-68	1.38E-6 5	145.01384 66
IGLV1-44	1.41029796 4	8.9198419 04	20.1113952 6	2.36E-68	1.52E-6 5	144.88750 34
IGKC	1.91816266 1	12.227801 68	20.0325706 4	5.98E-68	3.72E-6 5	143.96542 77
THRB	-2.0735957 56	4.4867831 46	-19.935786 95	1.87E-67	1.13E-6 4	142.83410 29
BTG3	-1.0506773 15	5.3294432 02	-19.578309 79	1.24E-65	7.29E-6 3	138.66391 16
LOC1002905 57	3.11703048 5	10.622669 02	19.4739203 6	4.23E-65	2.41E-6 2	137.44879 93
SRM	2.01796296 8	8.1597996 44	19.3878883	1.16E-64	6.41E-6 2	136.44832 35
SLC2A12	-1.0120257 53	3.9037635 72	-19.312515 12	2.80E-64	1.51E-6 1	135.57252 73
GPBP1L1	-1.0015653 99	7.2346445 44	-19.264246 27	4.92E-64	2.58E-6 1	135.01203 26
MYH15	-1.5508731 75	4.4974104 72	-19.118838 93	2.69E-63	1.37E-6 0	133.32533 32
ABCB1	-2.5700575 11	4.4311596 45	-18.989036 37	1.22E-62	6.08E-6 0	131.82194 86
C2	1.40439113 4	5.7139979 85	18.8987341 3	3.50E-62	1.70E-5 9	130.77738 44
IGLJ3	2.73399773 6	10.714726 09	18.8774958 3	4.48E-62	2.12E-5 9	130.53187 33
CDC14A	-1.2244601 01	4.5040912 76	-18.856659 81	5.70E-62	2.64E-5 9	130.29107 31

IMPDH1	1.41952902 3	6.0087196 24	18.4133302 7	9.77E-60	4.33E-5 7	125.18234 2
FAM196A	-1.4491917 98	3.1764482 18	-18.360135 31	1.81E-59	7.83E-5 7	124.57133 19
C19orf10	1.40416489 3	8.2340576 06	18.3334850 5	2.46E-59	1.04E-5 6	124.26538 75
RUNDC3B	-1.5834164 35	3.7681635 06	-18.244808 49	6.85E-59	2.79E-5 6	123.24819 62
AKAP9	-1.3921595 6	5.3248083 29	-18.154864 5	1.93E-58	7.70E-5 6	122.21776 57
HOXD11	-2.2658507 78	3.9956414 24	-18.150024 99	2.05E-58	7.99E-5 6	122.16236 02
ARPC1B	1.21687262 6	8.5003790 25	18.0847642 3	4.34E-58	1.63E-5 5	121.41559 75
PPARGC1A	-2.4496077 54	4.6833286 49	-17.992433 62	1.26E-57	4.55E-5 5	120.36030 62
IFITM1	1.78840473 2	10.266738 72	17.9637694 9	1.75E-57	6.21E-5 5	120.03298 63
NTRK2	-1.1139828 09	3.5269846 27	-17.936145 19	2.40E-57	8.23E-5 5	119.71767 46
ANO5	-2.3287711 96	3.8723151 99	-17.920759 58	2.86E-57	9.66E-5 5	119.54211 63
TTPA	-1.2013852 29	3.4049344 69	-17.794284 97	1.22E-56	4.06E-5 4	118.10055 08
BST2	2.35212649 4	6.9897602 32	17.7460374 8	2.12E-56	6.94E-5 4	117.55137 56
NBEAL1	-1.1320718 34	4.7690882 51	-17.680839 39	4.48E-56	1.44E-5 3	116.80993 34
IFITM2	1.94575984	10.423202	17.6542097	6.08E-56	1.92E-5	116.50732

	6	79	2		3	15
RPS6KA6	-1.3560702	3.6175204 82	-17.482629 49	4.32E-55	1.32E-5 2	114.56071 99
TNNC1	-1.3145493 8	4.1118316 64	-17.402309 56	1.08E-54	3.25E-5 2	113.65141 34
PLVAP	2.06283664 2	8.7819402 39	17.3386036 8	2.23E-54	6.62E-5 2	112.93109 29
CHPT1	-1.7118420 69	5.3398092 49	-17.262070 45	5.32E-54	1.54E-5 1	112.06680 03
S100A11	1.24003423 9	11.013648	17.1625570 8	1.65E-53	4.62E-5 1	110.94476 25
C1orf161	-1.4766879 96	3.2267987 75	-17.073978 93	4.49E-53	1.23E-5 0	109.94773 69
CHPF	1.71586615 7	7.5916025 04	17.0345951 6	7.02E-53	1.88E-5 0	109.50496 47
MGC29506	3.46140526 9	8.9138573 41	17.0338057 8	7.08E-53	1.88E-5 0	109.49609 35
LPCAT1	1.97202807 5	7.4450476 73	17.0277235 7	7.58E-53	1.99E-5 0	109.42774 44
UGT2A3	-3.6440137 63	3.4549149 29	-16.973892 04	1.39E-52	3.61E-5 0	108.82315 32
FAM82A1	-1.3810060 29	4.2859868 39	-16.893145 06	3.47E-52	8.86E-5 0	107.91743 58
GK5	-1.3437446 53	4.6340082 28	-16.875452 01	4.24E-52	1.07E-4 9	107.71916 63
CYGB	1.33549351 9	6.0625973 93	16.8349329 3	6.69E-52	1.67E-4 9	107.26536 5
AKAP7	-1.6685398 77	5.6688791 8	-16.814792 09	8.40E-52	2.07E-4 9	107.03992 82

TSEN2	-1.2860302 69	5.0082316	-16.807031 68	9.17E-52	2.23E-4 9	106.95308 96
ISG20	2.0346731	9.3775642 5	16.7030273 5	2.96E-51	7.09E-4 9	105.79058 31
GNPTAB	-1.0466128 82	6.1637103 88	-16.667198 68	4.42E-51	1.05E-4 8	105.39067 27
LOC1002896 32	-1.4923982 13	4.2414067 92	-16.612562 31	8.17E-51	1.91E-4 8	104.78139 91
MGAT1	1.05798071 1	7.8636096 48	16.5914696 3	1.04E-50	2.40E-4 8	104.54636 9
LOC1001301 75	-1.5480135 08	5.6624481 08	-16.574835 89	1.25E-50	2.86E-4 8	104.36109 62
TNFAIP8L1	1.25312373	6.7134725 65	16.4757771 9	3.78E-50	8.57E-4 8	103.25907 91
PREB	1.05810711 3	7.8876426 22	16.4562736 9	4.71E-50	1.05E-4 7	103.04237 67
LOC1002895 50	-1.2782591 27	3.5949919 42	-16.376013 82	1.15E-49	2.53E-4 7	102.15156 68
C1R	2.46600512 8	9.1845921 27	16.3726002 5	1.20E-49	2.60E-4 7	102.11371 37
ATP8A1	-1.2142600 48	4.9564840 19	-16.331131 36	1.91E-49	4.04E-4 7	101.65408 84
MOSC2	-1.3163705 23	5.1130674 79	-16.309994 18	2.41E-49	5.06E-4 7	101.41997 26
ODF3B	1.34573963 9	6.1798296 54	16.3060565 2	2.52E-49	5.18E-4 7	101.37637 1
FAM5C	-1.4957034 56	3.0581378 66	-16.304956 37	2.55E-49	5.19E-4 7	101.36418 97
UQCRC2	-1.1238024	7.5678996	-16.234658	5.59E-49	1.12E-4	100.58644

	26	24	3		6	01
ABCA5	-1.9279963 13	5.9452561 99	-16.208380 52	7.48E-49	1.49E-4 6	100.29602 64
LOC1001294 06	-1.5680712 27	3.2814222 01	-16.161296 9	1.26E-48	2.49E-4 6	99.776103 2
ABCC1	1.33443667 2	7.8094309 17	16.1332353 9	1.73E-48	3.37E-4 6	99.466496 55
CD81	1.42182086 9	8.9279876 73	16.1010907 8	2.47E-48	4.77E-4 6	99.112084 72
SLC13A2	-1.6237096 77	4.3205820 45	-16.085131 85	2.94E-48	5.64E-4 6	98.936226 05
VPS13A	-1.3583310 72	5.3417566 57	-16.000397 88	7.53E-48	1.43E-4 5	98.003593 74
SYCP3	-1.5793553 93	4.7652053 93	-15.994381 11	8.05E-48	1.51E-4 5	97.937439 81
GPX1	1.18201491 1	9.2886163 42	15.9811902 1	9.32E-48	1.73E-4 5	97.792439 59
IL15RA	1.64383003 5	7.5072061 69	15.9347342 2	1.56E-47	2.87E-4 5	97.282134 8
TIMP1	2.65915931 7	10.418430 5	15.8986575 2	2.32E-47	4.24E-4 5	96.886232 21
LOC553103	-1.2069597 05	4.4243378 91	-15.863891 43	3.41E-47	6.12E-4 5	96.505036 35
STOM	1.46492105 2	7.4861492 39	15.8588003	3.61E-47	6.41E-4 5	96.449240 94
MAP3K15	-1.1560350 94	4.1679954 67	-15.856078 77	3.72E-47	6.55E-4 5	96.419417 68
ACVR2A	-1.4248471 31	5.8288028 44	-15.795098 42	7.28E-47	1.26E-4 4	95.751694 37

NR5A2	-1.6743206 71	4.9199316 57	-15.791538 82	7.57E-47	1.30E-4 4	95.712748 18
PXDN	2.53276310 2	7.8361544 55	15.7240195 2	1.59E-46	2.69E-4 4	94.974652 91
SYT17	-1.051696	4.8712399 34	-15.718514 87	1.69E-46	2.83E-4 4	94.914532 55
IP6K2	-1.1696589 57	7.3439441 4	-15.632031 14	4.38E-46	7.21E-4 4	93.971065 85
SHMT2	1.13783015 4	8.2082511 8	15.5793886 6	7.80E-46	1.26E-4 3	93.397788 05
ZNF91	-1.8749896 62	6.9313239 67	-15.538833 66	1.22E-45	1.94E-4 3	92.956669 16
SH3GL1	1.01121976 6	7.8944654 7	15.5232100 9	1.44E-45	2.28E-4 3	92.786853 57
ZNF763	-1.0346826 48	4.5165021 66	-15.519703 61	1.50E-45	2.33E-4 3	92.748750 49
COL18A1	2.65940095	8.4298429 15	15.5017572 6	1.83E-45	2.82E-4 3	92.553790 71
TRPM6	-3.4258301 8	4.3976122 92	-15.477229 86	2.39E-45	3.66E-4 3	92.287484 93
IYD	-2.3517665 59	3.9842741 45	-15.475901 46	2.42E-45	3.68E-4 3	92.273066 75
C4orf48	1.82577208 2	10.555350 73	15.4409488 9	3.55E-45	5.35E-4 3	91.893877 98
PECAM1	2.38291964 6	9.1812894 28	15.3887042 6	6.28E-45	9.06E-4 3	91.327743 83
ENG	2.22448718 3	7.9406116 88	15.3879317 1	6.33E-45	9.07E-4 3	91.319378 19
MIF	1.20065051	9.5256703	15.3560826	8.96E-45	1.27E-4	90.974647

		63	7		2	14
ABCA11P	-1.1281382	4.0819873 93	-15.348067 26	9.78E-45	1.38E-4 2	90.887935 29
ADD3	-1.2856389 45	7.7925814 6	-15.336961 23	1.10E-44	1.55E-4 2	90.767819 53
C21orf88	-1.5298963 66	4.2788198 83	-15.307621 16	1.52E-44	2.12E-4 2	90.450668 17
CDC25B	1.52573490 2	8.0982835 79	15.2887338 9	1.87E-44	2.56E-4 2	90.246639 18
NCRNA0008 1	-1.2728085 86	6.9382072 67	-15.281036 65	2.03E-44	2.77E-4 2	90.16352
PDCD4	-1.6967837 72	7.4853663 03	-15.236755 96	3.28E-44	4.33E-4 2	89.68569
HOXD13	-1.8547815 71	3.7420991 19	-15.224724 74	3.74E-44	4.90E-4 2	89.555961 77
IGKV4-1	2.64193996 1	11.141141 53	15.1505487 1	8.37E-44	1.09E-4 1	88.757098 33
SDF2L1	1.40956596 7	7.8900934 95	15.0946554 5	1.53E-43	1.97E-4 1	88.156225 54
CCDC14	-1.1649984 5	5.2176980 81	-15.087879 34	1.65E-43	2.11E-4 1	88.083443 96
IRAK1	1.01061933 4	8.3862114 67	15.0873186 8	1.66E-43	2.11E-4 1	88.077422 67
COL6A3	2.69576517	9.7427889 93	15.0516122 2	2.44E-43	3.08E-4 1	87.694138 86
TMEM20	-1.0385885 52	3.6279402 86	-15.047828 64	2.54E-43	3.19E-4 1	87.653547 5
C21orf116	-1.1927892 27	3.3511683 22	-15.043354 52	2.67E-43	3.32E-4 1	87.605553 49

NAPEPLD	-1.2697910 79	5.5149696 26	-15.037536 51	2.84E-43	3.52E-4 1	87.543152 61
C13orf15	1.88354594 7	5.9318798 48	15.0274253 4	3.17E-43	3.88E-4 1	87.434730 26
MLLT3	-1.6639781 4	4.9170353 23	-15.000825 73	4.23E-43	5.13E-4 1	87.149651 33
SRPR	1.13280818 5	8.7819037 55	14.9895106 8	4.78E-43	5.70E-4 1	87.028449 14
GPR125	-1.7544561 46	5.4361800 45	-14.979230 26	5.34E-43	6.33E-4 1	86.918363 66
CD74	1.48738688 1	10.551564 75	14.9476399 6	7.50E-43	8.79E-4 1	86.580290 37
BCKDK	1.19766096 4	7.2147603 69	14.9432097 3	7.87E-43	9.17E-4 1	86.532903 61
LEAP2	-1.7314756 17	4.5220583 07	-14.925631 1	9.51E-43	1.10E-4 0	86.344938 46
DENND4C	-1.2007914 19	5.1491727 2	-14.924584 24	9.62E-43	1.11E-4 0	86.333747 6
ZDHHC23	-1.6973297 59	5.1826530 37	-14.894782 55	1.33E-42	1.50E-4 0	86.015313 12
SLAMF7	2.36179487 5	9.0643522 2	14.8938340 8	1.34E-42	1.51E-4 0	86.005183 08
EFEMP2	1.67037956 9	6.8259681 48	14.8694484 5	1.74E-42	1.94E-4 0	85.744833 5
SIAE	-1.4457602 82	5.5114571 39	-14.867708 83	1.77E-42	1.96E-4 0	85.726267 83
DERL3	2.71897044 2	7.6416409 09	14.8364936 4	2.48E-42	2.72E-4 0	85.393293 06
MOBKL2B	-1.2567409	5.5903024	-14.763375	5.44E-42	5.79E-4	84.614545

	65	49	76		0	52
COL4A1	2.85804428 1	8.9798567 85	14.7624439 8	5.49E-42	5.82E-4 0	84.604632 46
WARS	2.33725012 1	9.0725953 62	14.7606450 1	5.60E-42	5.90E-4 0	84.585494 35
HAVCR1	-2.2793047 19	4.2086842 8	-14.696138 21	1.12E-41	1.16E-3 9	83.899933 24
SMARCB1	1.65164232 7	8.5678935 09	14.6810187 9	1.31E-41	1.34E-3 9	83.739441 84
CCL2	2.72420445 2	10.213383 73	14.6499737 8	1.83E-41	1.86E-3 9	83.410133 66
FAM189A1	-1.1601944 53	4.1674681 66	-14.619074 27	2.55E-41	2.56E-3 9	83.082680 16
CYAT1	3.08886728 7	8.9618672 56	14.5838096	3.71E-41	3.71E-3 9	82.709348 73
LOC642776	-1.2351824 56	3.3888126 24	-14.569634 4	4.31E-41	4.28E-3 9	82.559397 21
TPH1	-2.9865660 33	5.2576238 86	-14.539895 26	5.92E-41	5.84E-3 9	82.245018 67
ZNF711	-1.5380094 33	4.2881419 02	-14.538075 89	6.04E-41	5.93E-3 9	82.225795 19
LOC284889	1.06871418 8	9.8564677 49	14.5269783 6	6.80E-41	6.64E-3 9	82.108562 54
SATB2	-2.6548175 84	5.0711802 92	-14.501429 59	8.92E-41	8.58E-3 9	81.838824 48
COL6A1	2.43128006 8	8.2787997 37	14.5000559 4	9.05E-41	8.67E-3 9	81.824327 89
SPON2	2.64880806 8	7.6891007 64	14.4962118 4	9.43E-41	8.94E-3 9	81.783763 39

USP12	-1.1035363 91	6.8213423 58	-14.486784 51	1.04E-40	9.70E-3 9	81.684302 97
GAB1	-1.0678652 69	5.0858523 99	-14.475358 9	1.18E-40	1.09E-3 8	81.563800 04
IGLV3-19	3.05708096 9	10.178504 3	14.4546387 9	1.47E-40	1.34E-3 8	81.345381 9
FUT8	1.63681690 9	7.3784011 49	14.4378387 2	1.75E-40	1.59E-3 8	81.168392 07
SDC3	1.09368689	7.0997907 59	14.4268218 7	1.97E-40	1.78E-3 8	81.052380 24
ILDR1	-1.1231871 94	4.5922654 5	-14.378300 86	3.30E-40	2.94E-3 8	80.541922 31
KIAA1715	-1.5689749 86	5.0600845 67	-14.368000 26	3.68E-40	3.27E-3 8	80.433659 03
SELM	2.06362673 9	7.9043384 03	14.3470347 6	4.59E-40	4.03E-3 8	80.213414 99
C1QC	1.61034355 7	9.5872977 46	14.3076860 1	6.96E-40	6.05E-3 8	79.800458 68
FXYD5	1.87813538 1	9.0755566 43	14.3056007 6	7.11E-40	6.16E-3 8	79.778589 27
FAM101B	1.66906478 9	6.8904561 56	14.2964725 4	7.84E-40	6.76E-3 8	79.682872 97
FTSJ1	1.06183011 2	6.7142141 95	14.2916399 1	8.25E-40	7.08E-3 8	79.632210 82
FMO4	-1.2780360 95	3.4737395 23	-14.272483 39	1.01E-39	8.59E-3 8	79.431465 21
PDZK1P1	-1.0235620 03	4.2190853 73	-14.269532 35	1.04E-39	8.83E-3 8	79.400551 85
COL5A1	2.41653729	7.7974021	14.2638839	1.11E-39	9.33E-3	79.341390

	4	56	1		8	46
GRK5	1.10453374 4	6.3019691 38	14.2434610 9	1.37E-39	1.15E-3 7	79.127575 19
PCOLCE	2.56730768	8.3408832 9	14.2124654 6	1.90E-39	1.59E-3 7	78.803344 93
FKBP11	1.62686535 3	8.1410262 79	14.1928192 9	2.34E-39	1.95E-3 7	78.598009 02
LOC149703	-1.0896755 8	4.0296203 61	-14.135927 34	4.26E-39	3.50E-3 7	78.004152 94
ECM1	1.78923770 1	7.4213561 08	14.1110072 8	5.53E-39	4.51E-3 7	77.744387 92
DCPS	1.31259163 1	6.9803856 04	14.1047988 7	5.90E-39	4.80E-3 7	77.679706 01
ZNF593	1.50573369 8	7.9155810 03	14.1035067 7	5.98E-39	4.84E-3 7	77.666246 13
HLA-DRB1	1.16693982	11.040100 72	14.0911347 5	6.81E-39	5.47E-3 7	77.537395 45
CRELD2	1.18747366	9.2650111 67	14.0879214	7.05E-39	5.64E-3 7	77.503938 31
RAVER2	-1.5972881 97	4.6642178 72	-14.067266 62	8.75E-39	6.94E-3 7	77.288969 83
COTL1	1.35882896 1	7.9351418 95	14.0527994 6	1.02E-38	8.05E-3 7	77.138490 59
KLHL8	-1.0765995 2	4.5341622 05	-14.048477 63	1.07E-38	8.39E-3 7	77.093551 81
SLC36A1	-1.4150880 49	6.6270979 74	-14.047243 77	1.08E-38	8.46E-3 7	77.080723 24
APLNR	2.53603397 2	7.2178432 86	14.0392768 8	1.17E-38	9.09E-3 7	76.997903 78

IGL@	1.97719376 3	9.6543857 54	14.0254869 1	1.36E-38	1.04E-3 6	76.854604 47
TMEM98	-1.6046763 1	6.2695269 36	-14.023796 91	1.38E-38	1.06E-3 6	76.837047 38
SLC22A5	-2.1047706 7	6.2651081 77	-14.001197 47	1.75E-38	1.33E-3 6	76.602364 95
LOC344887	-1.2880572 21	3.7750347 3	-13.995379 55	1.86E-38	1.41E-3 6	76.541978 85
IGLV6-57	2.78670395 7	9.5417362 7	13.9816728 1	2.14E-38	1.62E-3 6	76.399760 16
UBE2L6	1.53499490 4	9.2019865 28	13.9757935 3	2.28E-38	1.72E-3 6	76.338778 54
SLC30A4	-1.0936191 35	5.2610814 17	-13.951289 47	2.95E-38	2.20E-3 6	76.084749 72
OXR1	-1.0201670 04	6.4648681 8	-13.949160 98	3.01E-38	2.24E-3 6	76.062694 34
FLJ32063	-2.2913929 21	4.5540459 29	-13.926697 59	3.81E-38	2.81E-3 6	75.830029 13
C1QB	1.63950265 4	9.1185189 76	13.8992602 7	5.07E-38	3.69E-3 6	75.546095 2
BLVRA	1.38254356 7	6.6237335 06	13.8885473 7	5.67E-38	4.11E-3 6	75.435307 75
APOL1	2.20987469 1	8.5180295 06	13.8103241 8	1.28E-37	9.07E-3 6	74.627638 44
C6orf129	1.14565590 3	7.2958576 48	13.7963662 3	1.48E-37	1.04E-3 5	74.483757 08
PLCE1	-1.1829089 93	5.0313811 73	-13.767401 93	2.00E-37	1.40E-3 5	74.185408 19
GCOM1	-1.4774846	5.3663172	-13.766310	2.02E-37	1.41E-3	74.174182

	43	23	6		5	92
TCIRG1	1.30096268 3	9.5553927 14	13.7463193 2	2.49E-37	1.71E-3 5	73.968458 06
SCN9A	-1.1425261 15	3.5121236 24	-13.741729 15	2.61E-37	1.79E-3 5	73.921242 9
PIGN	-1.1402788 44	5.0923097 17	-13.740560 05	2.64E-37	1.81E-3 5	73.909218 62
LAMB2	1.97571869 2	7.7671387 8	13.7265164 5	3.06E-37	2.07E-3 5	73.764819 2
OLFM4	3.75888480 4	11.596325 7	13.7164950 6	3.39E-37	2.29E-3 5	73.661822 09
CHN2	-1.3523853 67	5.0365554 9	-13.713618 27	3.49E-37	2.35E-3 5	73.632262 26
TGFBI	2.01899635 3	9.5546219 52	13.7048112 7	3.83E-37	2.57E-3 5	73.541786 9
BGN	3.0846726	7.8386579 71	13.6602107	6.07E-37	4.06E-3 5	73.084048 35
VWF	2.22752853 7	7.2982627 54	13.6544329 3	6.44E-37	4.28E-3 5	73.024805 63
ZNF141	-1.1050649 85	5.6614028 14	-13.646882 1	6.97E-37	4.61E-3 5	72.947401 71
PRAF2	1.36035950 6	6.7481735 91	13.6298556 8	8.31E-37	5.48E-3 5	72.772942 45
RAMP2	2.25855300 5	7.2087444 38	13.5932968 9	1.21E-36	7.96E-3 5	72.398719 36
CASD1	-1.0311060 72	4.2284333 64	-13.577311 59	1.43E-36	9.33E-3 5	72.235250 69
LOC440993	-1.4759159 71	5.1839546 09	-13.564872 1	1.62E-36	1.05E-3 4	72.108109 84

HLA-DMA	1.54954356	9.1127793 85	13.5554547 6	1.79E-36	1.15E-3 4	72.011896 99
ORAI1	1.14132760 5	6.7008588 76	13.5382311 6	2.14E-36	1.36E-3 4	71.836019 07
ARHGAP42	-1.0360149 25	4.4144106 27	-13.516588 09	2.67E-36	1.68E-3 4	71.615173 94
USP30	-1.1059564 86	5.3698172 93	-13.512729	2.78E-36	1.74E-3 4	71.575814 82
BACE2	1.51743290 9	9.1530638 89	13.4909655 4	3.47E-36	2.16E-3 4	71.353955 96
IGKV1-5	1.31102663 1	5.0317977 89	13.4762419 1	4.04E-36	2.50E-3 4	71.203965 8
C1S	2.11000724 1	8.4847315 21	13.4656689 4	4.50E-36	2.77E-3 4	71.096310 48
KIAA1468	-1.2695357 85	5.7713490 14	-13.464623 51	4.55E-36	2.79E-3 4	71.085668 19
VANGL2	-1.5581547 54	4.9175087 18	-13.451877 73	5.19E-36	3.17E-3 4	70.955952 02
RPS6KA2	1.12151891 2	6.7370277 08	13.4480340 8	5.40E-36	3.28E-3 4	70.916846 87
APOE	1.591987	8.3022727 88	13.4442310 6	5.61E-36	3.40E-3 4	70.878160 73
ELTD1	2.54555238 4	6.5589659 42	13.4340047	6.23E-36	3.74E-3 4	70.774161 35
KIAA1984	-1.9065597 2	4.0038425 03	-13.412295 19	7.79E-36	4.63E-3 4	70.553516 9
LOC1001295 00	1.82006629 5	7.6140443 49	13.4078108 4	8.15E-36	4.83E-3 4	70.507963 26
ZDHHC7	-1.0418645	7.2764728	-13.385797	1.02E-35	5.97E-3	70.284459

	11	11	6		4	13
MTM1	-2.1112448 29	5.1277254 2	-13.378390 37	1.10E-35	6.42E-3 4	70.209295 05
ZNF137	-1.2924764 22	4.3242051 66	-13.375734 72	1.13E-35	6.57E-3 4	70.182352 38
SYTL1	1.29176548	6.5965754 6	13.3699557	1.20E-35	6.95E-3 4	70.123731 48
COL1A1	1.98913010 1	8.5586901 13	13.3690806 3	1.21E-35	7.00E-3 4	70.114856 12
MAN2B1	1.06077868 7	9.1706609 67	13.3661831 2	1.25E-35	7.19E-3 4	70.085470 44
SERPING1	2.15542156 6	8.2421932 09	13.3490286 3	1.49E-35	8.49E-3 4	69.911562 69
ZYX	1.36518975 1	7.7479272 25	13.3254540 6	1.89E-35	1.06E-3 3	69.672759 67
PIM2	2.48932095	7.9893733 7	13.2914244 6	2.68E-35	1.50E-3 3	69.328439 24
PPP2R3A	-1.1817201 12	4.7505237 49	-13.275479 88	3.15E-35	1.74E-3 3	69.167266 49
LOC1001336 60	-1.1876309 63	4.3448883 88	-13.267447 65	3.42E-35	1.89E-3 3	69.086112 63
MST1P9	-1.8577382 83	4.6140890 12	-13.231632 24	4.93E-35	2.71E-3 3	68.724564 91
PLEKHO2	1.63955895 5	7.2439861 7	13.2282331 3	5.10E-35	2.80E-3 3	68.690278 5
CSF1R	1.42490637 3	7.9349342 34	13.2222635 7	5.42E-35	2.96E-3 3	68.630075 43
KIAA1949	1.98127383 7	8.1289717 58	13.2094357 4	6.17E-35	3.35E-3 3	68.500755 28

SHKBP1	1.15862823 4	8.3185636 77	13.2079010 6	6.27E-35	3.39E-3 3	68.485288 33
IGHM	2.48333277 4	9.8921257 24	13.2025852 3	6.62E-35	3.57E-3 3	68.431720 98
LOXL2	1.27228501 8	5.6826836 32	13.2021901	6.64E-35	3.58E-3 3	68.427739 68
SLC15A3	1.61536831 1	6.3842589 52	13.1634004 5	9.85E-35	5.23E-3 3	68.037210 4
PEA15	1.33135338 1	8.7628079 07	13.1430268	1.21E-34	6.37E-3 3	67.832335 28
SLC26A2	-4.4963550 68	6.8684945 64	-13.126698 46	1.43E-34	7.43E-3 3	67.668261 19
PRKACB	-1.2837119 18	6.9988873 43	-13.126297 07	1.44E-34	7.44E-3 3	67.664229 2
SNAPC3	-1.1848898 03	6.2458194 19	-13.105195 68	1.78E-34	9.15E-3 3	67.452358 07
MANF	1.10198655 1	9.3254881 16	13.0795605 2	2.30E-34	1.17E-3 2	67.195209 92
RGS5	2.15150689 4	7.2774647 06	13.0711613	2.51E-34	1.26E-3 2	67.111015 34
LOC1001310 15	-1.3805480 14	3.8290014 86	-13.068181 6	2.58E-34	1.30E-3 2	67.081153 55
KIAA0831	-1.0396289 06	5.9907001 66	-13.065664 82	2.65E-34	1.33E-3 2	67.055933 87
FANK1	-1.1145475 95	4.0476560 15	-13.061231 33	2.77E-34	1.38E-3 2	67.011513 8
RRN3	-1.1923787 15	5.6668053 11	-13.041431 04	3.39E-34	1.68E-3 2	66.813229 63
TEAD4	1.54557263	6.0842387	13.0397188	3.44E-34	1.70E-3	66.796090

	1	18	4		2	87
TMEM158	2.78740775 6	7.2724663 59	13.0271494 6	3.91E-34	1.92E-3 2	66.670311 24
PRDX4	1.46634001 9	9.2056060 94	13.0150281 5	4.42E-34	2.15E-3 2	66.549077 25
BLCAP	-1.2232601 81	8.5863744 99	-13.002126 04	5.03E-34	2.45E-3 2	66.420100 78
LOC151878	-1.2175663 79	4.5085672 29	-12.964314 88	7.37E-34	3.54E-3 2	66.042517 93
SLC22A4	-1.4870121 28	4.2279327 93	-12.955290 84	8.07E-34	3.85E-3 2	65.952491 66
UBE2S	1.46453622 1	6.5089595 91	12.9359967 8	9.80E-34	4.67E-3 2	65.760123 02
EHD2	1.65294188 9	7.1321002 55	12.9279827 7	1.06E-33	5.05E-3 2	65.680266 29
TBXAS1	1.10837562 9	6.6420436 63	12.9235067 4	1.11E-33	5.27E-3 2	65.635675 94
LOC1002889 39	-1.1536387 23	4.6155878 57	-12.913665 34	1.23E-33	5.79E-3 2	65.537665 2
TPST2	1.73076523 3	7.5236216 25	12.9132643 1	1.23E-33	5.80E-3 2	65.533672 19
TSPAN11	1.89062375 7	8.1812079 6	12.9119007 4	1.25E-33	5.86E-3 2	65.520095 85
C1QA	1.29765292	8.1636786 57	12.8703914 5	1.89E-33	8.83E-3 2	65.107182 64
WDR52	-1.1417528 74	4.4642488 28	-12.853417 82	2.24E-33	1.04E-3 1	64.938546 98
RPL22L1	1.29551287 7	8.8478100 81	12.8037924 8	3.69E-33	1.69E-3 1	64.446211 88

WDR54	1.05563032 1	6.0358613 84	12.7675069 1	5.30E-33	2.40E-3 1	64.086884 86
AEBP1	1.97419357 8	9.7528699 15	12.7612218 1	5.64E-33	2.55E-3 1	64.024702 25
LOC340184	-2.1572966 9	5.3794085 48	-12.754465 29	6.03E-33	2.73E-3 1	63.957874 53
LOC151877	-1.2434201 67	5.3092436 63	-12.742348 27	6.81E-33	3.06E-3 1	63.838075 85
LOC285758	-1.1775511 08	4.6814618 47	-12.725873 66	8.03E-33	3.58E-3 1	63.675295 69
DOK2	1.04899094 6	6.5471589 74	12.7091260 4	9.48E-33	4.23E-3 1	63.509937 8
PLTP	1.88518383 7	6.9318968 99	12.6872025 4	1.18E-32	5.22E-3 1	63.293658 67
RNF152	-1.9916898 18	3.9621185 71	-12.650125 76	1.71E-32	7.48E-3 1	62.928363 49
NID1	1.36633711 2	6.3469126 5	12.6363534 2	1.96E-32	8.54E-3 1	62.792824 94
IGHG1	1.13000980 3	5.4364321 97	12.6267410 4	2.15E-32	9.37E-3 1	62.698275 06
ERMP1	-1.2284687 91	6.8808504 96	-12.625372 86	2.18E-32	9.48E-3 1	62.684820 59
DEPDC7	-1.1967653 09	3.2450115 14	-12.624964 64	2.19E-32	9.50E-3 1	62.680806 36
ELMO1	1.98664810 9	6.0427086 58	12.6227466 8	2.24E-32	9.69E-3 1	62.658997 36
TAP1	1.16811446 4	9.3145173 11	12.6223758 5	2.25E-32	9.70E-3 1	62.655351 27
TLN2	-1.0732648	4.7544612	-12.615734	2.40E-32	1.03E-3	62.590065

	51		9		0	34
LYZ	1.15254031 8	11.191452 52	12.6091570 8	2.56E-32	1.10E-3 0	62.525419 07
MAD2L2	1.14635348 7	6.8531922 86	12.5847928 8	3.26E-32	1.38E-3 0	62.286134 47
KIAA1737	-1.5184751 56	5.4197199 22	-12.579395 24	3.44E-32	1.46E-3 0	62.233158 63
SRI	-1.5136281 26	7.8518929 37	-12.569438 88	3.80E-32	1.60E-3 0	62.135474 21
VAMP5	1.24438863 7	7.1764414 53	12.5471361 8	4.73E-32	1.98E-3 0	61.916814 7
PLEKHO1	1.34673008	7.8483638 46	12.5401237 4	5.07E-32	2.12E-3 0	61.848108 84
CXCL1	3.76302975 3	9.8213442 87	12.5386652 9	5.15E-32	2.15E-3 0	61.833822 14
ADA	1.58291419 3	5.8264258 63	12.5181070 8	6.30E-32	2.62E-3 0	61.632537 11
WFS1	1.46706782 8	7.8916365 2	12.5166180 7	6.40E-32	2.65E-3 0	61.617965 44
PCDH18	1.21628875 4	7.4166819	12.4923616 7	8.13E-32	3.35E-3 0	61.380728 04
APOL3	1.73068030 2	6.4982459 89	12.4861692 9	8.64E-32	3.55E-3 0	61.320205 9
PRLR	-1.4914495 14	4.3963325 31	-12.476913 09	9.47E-32	3.87E-3 0	61.229770 74
NBPF1	-1.2022177 05	5.3449473 11	-12.472131 12	9.92E-32	4.04E-3 0	61.183064 81
GRAMD3	-1.2535619 57	5.1271178 91	-12.452326 75	1.21E-31	4.87E-3 0	60.989742

Appendix 3

Analysis of enrichment

Table S3a. Analysis of GO.

ONTOLOGY	ID	Description	GeneRatio	pvalue	qvalue
BP	GO:0009615	response to virus	10/78	7.64E-06	0.010265725
BP	GO:1903131	mononuclear cell differentiation	10/78	2.79E-05	0.015132354
BP	GO:0050900	leukocyte migration	9/78	3.84E-05	0.015132354
BP	GO:0007159	leukocyte cell-cell adhesion	9/78	5.84E-05	0.015132354
BP	GO:0030098	lymphocyte differentiation	9/78	6.65E-05	0.015132354
BP	GO:0030595	leukocyte chemotaxis	7/78	6.76E-05	0.015132354
BP	GO:0070661	leukocyte proliferation	8/78	0.000103414	0.01934585
BP	GO:0002407	dendritic cell chemotaxis	3/78	0.000171688	0.01934585
BP	GO:0019730	antimicrobial humoral response	5/78	0.000186626	0.01934585
BP	GO:0050851	antigen receptor-mediated signaling pathway	6/78	0.000198078	0.01934585
BP	GO:1990266	neutrophil migration	5/78	0.00020086	0.01934585
BP	GO:0071674	mononuclear cell migration	6/78	0.000203468	0.01934585
BP	GO:0019221	cytokine-mediated signaling pathway	9/78	0.0002117	0.01934585
BP	GO:0002253	activation of immune response	9/78	0.000221463	0.01934585
BP	GO:0030217	T cell differentiation	7/78	0.000261686	0.01934585
BP	GO:0045619	regulation of lymphocyte	6/78	0.000264002	0.01934585

		differentiation			
BP	GO:009038 2	phagosome maturation	3/78	0.00026488 4	0.01934585
BP	GO:005160 7	defense response to virus	7/78	0.00027796 7	0.01934585
BP	GO:014054 6	defense response to symbiont	7/78	0.00028357 2	0.01934585
BP	GO:004665 1	lymphocyte proliferation	7/78	0.00029505 5	0.01934585
BP	GO:005085 3	B cell receptor signaling pathway	4/78	0.00030615 9	0.01934585
BP	GO:006032 6	cell chemotaxis	7/78	0.00033176 7	0.01934585
BP	GO:003294 3	mononuclear cell proliferation	7/78	0.00033822 7	0.01934585
BP	GO:003633 6	dendritic cell migration	3/78	0.00035275 9	0.01934585
BP	GO:190210 5	regulation of leukocyte differentiation	7/78	0.00037914 6	0.01934585
BP	GO:004557 7	regulation of B cell differentiation	3/78	0.00038573 3	0.01934585
BP	GO:000275 7	immune response-activating signaling pathway	8/78	0.00038888 8	0.01934585
BP	GO:003018 3	B cell differentiation	5/78	0.00045779 7	0.02196047 6
BP	GO:009753 0	granulocyte migration	5/78	0.00050022 3	0.02316820 9
BP	GO:002260 4	regulation of cell morphogenesis	6/78	0.00056949 5	0.02456145 5
BP	GO:007009 8	chemokine-mediated signaling pathway	4/78	0.00057846 5	0.02456145 5
BP	GO:000276 4	immune response-regulating signaling pathway	8/78	0.00058516 3	0.02456145 5
BP	GO:005087 0	positive regulation of T cell activation	6/78	0.00062000 2	0.02472074 5
BP	GO:005123 5	maintenance of location	7/78	0.00062576 8	0.02472074 5
BP	GO:199086 8	response to chemokine	4/78	0.00079441 7	0.02963967
BP	GO:199086 9	cellular response to chemokine	4/78	0.00079441 7	0.02963967
BP	GO:190262	regulation of	3/78	0.00088491	0.03212383

	2	neutrophil migration		6	1
BP	GO:190303 9	positive regulation of leukocyte cell-cell adhesion	6/78	0.00100033 1	0.03317022
BP	GO:005086 3	regulation of T cell activation	7/78	0.00101682 1	0.03317022
BP	GO:190210 7	positive regulation of leukocyte differentiation	5/78	0.00105313 3	0.03317022
BP	GO:190370 8	positive regulation of hemopoiesis	5/78	0.00105313 3	0.03317022
BP	GO:004211 3	B cell activation	6/78	0.00105826	0.03317022
BP	GO:003059 3	neutrophil chemotaxis	4/78	0.00106191 5	0.03317022
BP	GO:004558 2	positive regulation of T cell differentiation	4/78	0.00143215 3	0.04371833 9
BP	GO:000242 9	immune response-activating cell surface receptor signaling pathway	6/78	0.00167514 9	0.04936583 8
BP	GO:007267 6	lymphocyte migration	4/78	0.00172389 8	0.04936583 8
BP	GO:004645 9	short-chain fatty acid metabolic process	2/78	0.00175693 7	0.04936583 8
BP	GO:190370 6	regulation of hemopoiesis	7/78	0.00176417 1	0.04936583 8
BP	GO:000268 8	regulation of leukocyte chemotaxis	4/78	0.00193987 6	0.05226590 2
BP	GO:004209 8	T cell proliferation	5/78	0.00200798 4	0.05226590 2
BP	GO:004562 1	positive regulation of lymphocyte differentiation	4/78	0.00217392 1	0.05226590 2
BP	GO:005086 4	regulation of B cell activation	4/78	0.00217392 1	0.05226590 2
BP	GO:005120 9	release of sequestered calcium ion into cytosol	4/78	0.00217392 1	0.05226590 2
BP	GO:001072 0	positive regulation of cell development	7/78	0.00221270 8	0.05226590 2
BP	GO:005128 3	negative regulation of sequestering of calcium ion	4/78	0.00223534 4	0.05226590 2

BP	GO:007162 1	granulocyte chemotaxis	4/78	0.00223534 4	0.05226590 2
BP	GO:002240 9	positive regulation of cell-cell adhesion	6/78	0.00227607 2	0.05226590 2
BP	GO:005128 2	regulation of sequestering of calcium ion	4/78	0.00236176 5	0.05226590 2
BP	GO:005125 1	positive regulation of lymphocyte activation	6/78	0.00249603 4	0.05226590 2
BP	GO:000315 9	morphogenesis of an endothelium	2/78	0.00253934 5	0.05226590 2
BP	GO:002155 4	optic nerve development	2/78	0.00253934 5	0.05226590 2
BP	GO:004321 7	myelin maintenance	2/78	0.00253934 5	0.05226590 2
BP	GO:006026 3	regulation of respiratory burst	2/78	0.00253934 5	0.05226590 2
BP	GO:006115 4	endothelial tube morphogenesis	2/78	0.00253934 5	0.05226590 2
BP	GO:000276 8	immune response-regulating cell surface receptor signaling pathway	6/78	0.0025728	0.05226590 2
BP	GO:005120 8	sequestering of calcium ion	4/78	0.00262923 3	0.05226590 2
BP	GO:000257 3	myeloid leukocyte differentiation	5/78	0.00264606 4	0.05226590 2
BP	GO:000268 5	regulation of leukocyte migration	5/78	0.00264606 4	0.05226590 2
BP	GO:000836 0	regulation of cell shape	4/78	0.00269921 4	0.05254305 7
BP	GO:005092 0	regulation of chemotaxis	5/78	0.00279995 7	0.05372548 3
BP	GO:007055 5	response to interleukin-1	4/78	0.00291681 5	0.05504995 7
BP	GO:005165 1	maintenance of location in cell	5/78	0.00296024 1	0.05504995 7
BP	GO:003806 1	NIK/NF-kappaB signaling	4/78	0.00299193 9	0.05504995 7
BP	GO:005092 1	positive regulation of chemotaxis	4/78	0.00306837 7	0.05569344 6
BP	GO:000254 8	monocyte chemotaxis	3/78	0.00329685 7	0.05757423 2
BP	GO:007267	T cell migration	3/78	0.00329685	0.05757423

	8			7	2
BP	GO:0050670	regulation of lymphocyte proliferation	5/78	0.003300592	0.057574232
BP	GO:0002687	positive regulation of leukocyte migration	4/78	0.003387492	0.058043463
BP	GO:0097529	myeloid leukocyte migration	5/78	0.003420067	0.058043463
BP	GO:1901739	regulation of myoblast fusion	2/78	0.003457134	0.058043463
BP	GO:0032944	regulation of mononuclear cell proliferation	5/78	0.003542629	0.058744573
BP	GO:0006959	humoral immune response	5/78	0.003996554	0.065463457
BP	GO:0045785	positive regulation of cell adhesion	7/78	0.004054772	0.065616859
BP	GO:1903861	positive regulation of dendrite extension	2/78	0.004142512	0.066238656
BP	GO:0043087	regulation of GTPase activity	6/78	0.004225032	0.066763347
BP	GO:0090023	positive regulation of neutrophil chemotaxis	2/78	0.004885536	0.076302858
BP	GO:0051279	regulation of release of sequestered calcium ion into cytosol	3/78	0.004943083	0.076314256
BP	GO:0002696	positive regulation of leukocyte activation	6/78	0.005004568	0.076385514
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	6/78	0.005068633	0.076494091
BP	GO:0070665	positive regulation of leukocyte proliferation	4/78	0.005214348	0.077818808
BP	GO:1903859	regulation of dendrite extension	2/78	0.005278356	0.077908416
BP	GO:0070663	regulation of leukocyte proliferation	5/78	0.005353319	0.078156013
BP	GO:0014072	response to isoquinoline alkaloid	2/78	0.006106003	0.08454976
BP	GO:0043278	response to morphine	2/78	0.006106003	0.08454976
BP	GO:0060219	camera-type eye photoreceptor cell differentiation	2/78	0.006106003	0.08454976
BP	GO:007026	pyroptosis	2/78	0.00610600	0.08454976

	9			3	
BP	GO:007162 4	positive regulation of granulocyte chemotaxis	2/78	0.00610600 3	0.08454976
BP	GO:005086 7	positive regulation of cell activation	6/78	0.00617787 1	0.084672
BP	GO:004663 1	alpha-beta T cell activation	4/78	0.00627318 7	0.08510991 1
BP	GO:005082 9	defense response to Gram-negative bacterium	3/78	0.00640253 5	0.08599615 3
BP	GO:001099 6	response to auditory stimulus	2/78	0.00654058 8	0.08612786 3
BP	GO:009002 5	regulation of monocyte chemotaxis	2/78	0.00654058 8	0.08612786 3
BP	GO:000244 3	leukocyte mediated immunity	6/78	0.00671515 6	0.0875681
BP	GO:004558 0	regulation of T cell differentiation	4/78	0.00691902 5	0.08855785
BP	GO:006014 2	regulation of syncytium formation by plasma membrane fusion	2/78	0.00698885 2	0.08855785
BP	GO:009014 0	regulation of mitochondrial fission	2/78	0.00698885 2	0.08855785
BP	GO:004212 9	regulation of T cell proliferation	4/78	0.00732691 7	0.09197389 3
BP	GO:000269 0	positive regulation of leukocyte chemotaxis	3/78	0.00764874	0.09512468 5
BP	GO:000236 6	leukocyte activation involved in immune response	5/78	0.00806856 1	0.09942523 7
BP	GO:004838 4	retinoic acid receptor signaling pathway	2/78	0.00841453 8	0.10149195 7
BP	GO:000226 3	cell activation involved in immune response	5/78	0.00852223 7	0.10149195 7
BP	GO:000244 9	lymphocyte mediated immunity	5/78	0.00852223 7	0.10149195 7
BP	GO:003010 1	natural killer cell activation	3/78	0.00855368 8	0.10149195 7
BP	GO:000687 4	intracellular calcium ion homeostasis	5/78	0.00887391 9	0.10149195 7
BP	GO:004246 2	eye photoreceptor cell development	2/78	0.00891633 9	0.10149195 7

BP	GO:009002 2	regulation of neutrophil chemotaxis	2/78	0.00891633 9	0.10149195 7
BP	GO:190262 4	positive regulation of neutrophil migration	2/78	0.00891633 9	0.10149195 7
BP	GO:200040 6	positive regulation of T cell migration	2/78	0.00891633 9	0.10149195 7
BP	GO:004210 2	positive regulation of T cell proliferation	3/78	0.00976986 1	0.11027282 7
BP	GO:000246 0	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	5/78	0.00986072	0.11037086 3
BP	GO:009748 4	dendrite extension	2/78	0.00995909 8	0.11055075
BP	GO:009755 3	calcium ion transmembrane import into cytosol	4/78	0.01010999 4	0.11130588 8
BP	GO:004274 2	defense response to bacterium	5/78	0.01024951 7	0.11192454 5
BP	GO:003817 9	neurotrophin signaling pathway	2/78	0.01049982 6	0.11373325 8
BP	GO:190122 2	regulation of NIK/NF-kappaB signaling	3/78	0.01108188 6	0.11907778 5
BP	GO:000762 3	circadian rhythm	4/78	0.01117100 7	0.11908274 6
BP	GO:000228 5	lymphocyte activation involved in immune response	4/78	0.01135455 3	0.12008628 4
BP	GO:004573 0	respiratory burst	2/78	0.01161940 8	0.12098217 2
BP	GO:006039 0	regulation of SMAD protein signal transduction	2/78	0.01161940 8	0.12098217 2
BP	GO:005507 4	calcium ion homeostasis	5/78	0.01205645 9	0.12456714 2
BP	GO:000026 6	mitochondrial fission	2/78	0.01219803 7	0.12506785 7
BP	GO:003571 0	CD4-positive, alpha-beta T cell activation	3/78	0.01249107 9	0.12626033 9

BP	GO:001604 2	lipid catabolic process	5/78	0.01250234 6	0.12626033 9
BP	GO:000961 2	response to mechanical stimulus	4/78	0.01269402 7	0.12630694 6
BP	GO:005128 1	positive regulation of release of sequestered calcium ion into cytosol	2/78	0.01278907 3	0.12630694 6
BP	GO:200040 3	positive regulation of lymphocyte migration	2/78	0.01278907 3	0.12630694 6
BP	GO:000604 0	amino sugar metabolic process	2/78	0.01339240 7	0.13130012 3
BP	GO:000228 6	T cell activation involved in immune response	3/78	0.01368914 6	0.13323684 6
BP	GO:004424 2	cellular lipid catabolic process	4/78	0.01413084	0.13654640 1
BP	GO:007167 5	regulation of mononuclear cell migration	3/78	0.01462926 4	0.13746725 7
BP	GO:003083 5	negative regulation of actin filament depolymerization	2/78	0.01463552 3	0.13746725 7
BP	GO:004302 9	T cell homeostasis	2/78	0.01463552 3	0.13746725 7
BP	GO:200051 6	positive regulation of CD4-positive, alpha-beta T cell activation	2/78	0.01463552 3	0.13746725 7
BP	GO:003476 5	regulation of monoatomic ion transmembrane transport	6/78	0.01506737 8	0.13957042 1
BP	GO:190406 2	regulation of monoatomic cation transmembrane transport	5/78	0.01507072 7	0.13957042 1
BP	GO:003057 4	collagen catabolic process	2/78	0.01527508 6	0.13957042 1
BP	GO:003129 5	T cell costimulation	2/78	0.01527508 6	0.13957042 1
BP	GO:000283 2	negative regulation of response to biotic stimulus	3/78	0.01560520 6	0.14162334 6

BP	GO:004278 9	mRNA transcription by RNA polymerase II	2/78	0.01592650 7	0.14261209 2
BP	GO:199009 0	cellular response to nerve growth factor stimulus	2/78	0.01592650 7	0.14261209 2
BP	GO:000175 4	eye photoreceptor cell differentiation	2/78	0.01658967 9	0.14659578
BP	GO:003129 4	lymphocyte costimulation	2/78	0.01658967 9	0.14659578
BP	GO:200011 6	regulation of cysteine-type endopeptidase activity	4/78	0.01682680 9	0.14676545 5
BP	GO:002240 7	regulation of cell-cell adhesion	6/78	0.01697868 8	0.14676545 5
BP	GO:000752 0	myoblast fusion	2/78	0.01726449 4	0.14676545 5
BP	GO:004246 1	photoreceptor cell development	2/78	0.01726449 4	0.14676545 5
BP	GO:199008 9	response to nerve growth factor	2/78	0.01726449 4	0.14676545 5
BP	GO:200040 4	regulation of T cell migration	2/78	0.01726449 4	0.14676545 5
BP	GO:003158 9	cell-substrate adhesion	5/78	0.01740208 1	0.14700466 9
BP	GO:000929 9	mRNA transcription	2/78	0.01935773 7	0.16250310 6
BP	GO:000696 8	cellular defense response	2/78	0.02007806 6	0.16518152
BP	GO:000715 7	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	2/78	0.02007806 6	0.16518152
BP	GO:004508 8	regulation of innate immune response	5/78	0.02016871 5	0.16518152
BP	GO:007099 7	neuron death	5/78	0.02016871 5	0.16518152
BP	GO:003083 4	regulation of actin filament depolymerization	2/78	0.02080951 2	0.16837626 4
BP	GO:007162 2	regulation of granulocyte chemotaxis	2/78	0.02080951 2	0.16837626 4
BP	GO:005145 2	intracellular pH reduction	2/78	0.02155197 1	0.17333952 2

BP	GO:0031529	ruffle organization	2/78	0.022305342	0.178330928
BP	GO:0042552	myelination	3/78	0.022625681	0.178956425
BP	GO:0016064	immunoglobulin mediated immune response	3/78	0.023035549	0.178956425
BP	GO:0050671	positive regulation of lymphocyte proliferation	3/78	0.023035549	0.178956425
BP	GO:2000107	negative regulation of leukocyte apoptotic process	2/78	0.023069522	0.178956425
BP	GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	4/78	0.023135642	0.178956425
BP	GO:0051402	neuron apoptotic process	4/78	0.023425776	0.178956425
BP	GO:0007272	ensheathment of neurons	3/78	0.023449463	0.178956425
BP	GO:0008366	axon ensheathment	3/78	0.023449463	0.178956425
BP	GO:0043388	positive regulation of DNA binding	2/78	0.023844409	0.180099517
BP	GO:0045667	regulation of osteoblast differentiation	3/78	0.02386742	0.180099517
BP	GO:0019724	B cell mediated immunity	3/78	0.024289422	0.180417256
BP	GO:0032946	positive regulation of mononuclear cell proliferation	3/78	0.024289422	0.180417256
BP	GO:0001894	tissue homeostasis	4/78	0.024608512	0.180417256
BP	GO:0060249	anatomical structure homeostasis	4/78	0.024608512	0.180417256
BP	GO:0030042	actin filament depolymerization	2/78	0.024629904	0.180417256
BP	GO:0008064	regulation of actin polymerization or depolymerization	3/78	0.024715467	0.180417256
BP	GO:0001961	positive regulation of cytokine-mediated signaling pathway	2/78	0.025425905	0.183730239
BP	GO:005192	regulation of calcium	4/78	0.02551897	0.18373023

	4	ion transport		2	9
BP	GO:001082 1	regulation of mitochondrion organization	3/78	0.02557968 4	0.18373023 9
BP	GO:003083 2	regulation of actin filament length	3/78	0.02601785 3	0.18588343 1
BP	GO:002154 5	cranial nerve development	2/78	0.02623231 4	0.18642402 1
BP	GO:004566 8	negative regulation of osteoblast differentiation	2/78	0.02704903 2	0.19021529 4
BP	GO:006004 2	retina morphogenesis in camera-type eye	2/78	0.02704903 2	0.19021529 4
BP	GO:006004 1	retina development in camera-type eye	3/78	0.02735658 4	0.19102967 7
BP	GO:000076 8	syncytium formation by plasma membrane fusion	2/78	0.02787596 1	0.19102967 7
BP	GO:002261 7	extracellular matrix disassembly	2/78	0.02787596 1	0.19102967 7
BP	GO:004653 0	photoreceptor cell differentiation	2/78	0.02787596 1	0.19102967 7
BP	GO:014025 3	cell-cell fusion	2/78	0.02787596 1	0.19102967 7
BP	GO:006144 8	connective tissue development	4/78	0.02837164 4	0.19343957 9
BP	GO:003273 1	positive regulation of interleukin-1 beta production	2/78	0.02871300 2	0.19477826 2
BP	GO:001973 1	antibacterial humoral response	2/78	0.02956006	0.19655360 5
BP	GO:004650 3	glycerolipid catabolic process	2/78	0.02956006	0.19655360 5
BP	GO:004824 7	lymphocyte chemotaxis	2/78	0.02956006	0.19655360 5
BP	GO:005091 8	positive chemotaxis	2/78	0.02956006	0.19655360 5
BP	GO:005072 7	regulation of inflammatory response	5/78	0.02988555 8	0.19773903 1
BP	GO:000694 9	syncytium formation	2/78	0.03128384	0.20497139 6
BP	GO:006076 0	positive regulation of response to cytokine stimulus	2/78	0.03128384	0.20497139 6

BP	GO:005149 4	negative regulation of cytoskeleton organization	3/78	0.03159023 3	0.20569740 7
BP	GO:003009 9	myeloid cell differentiation	5/78	0.03179525 2	0.20569740 7
BP	GO:000195 9	regulation of cytokine-mediated signaling pathway	3/78	0.03208070 6	0.20569740 7
BP	GO:004863 9	positive regulation of developmental growth	3/78	0.03208070 6	0.20569740 7
BP	GO:190122 4	positive regulation of NIK/NF-kappaB signaling	2/78	0.03216037	0.20569740 7
BP	GO:200040 1	regulation of lymphocyte migration	2/78	0.03304653 6	0.20954306 9
BP	GO:190290 4	negative regulation of supramolecular fiber organization	3/78	0.03307364 7	0.20954306 9
BP	GO:004557 6	mast cell activation	2/78	0.03394224 2	0.21403657 5
BP	GO:000700 9	plasma membrane organization	3/78	0.03459297 8	0.2156938
BP	GO:000724 9	I-kappaB kinase/NF-kappaB signaling	4/78	0.03462900 3	0.2156938
BP	GO:003051 4	negative regulation of BMP signaling pathway	2/78	0.03484739 6	0.2156938
BP	GO:190188 0	negative regulation of protein depolymerization	2/78	0.03484739 6	0.2156938
BP	GO:005105 6	regulation of small GTPase mediated signal transduction	4/78	0.03649897 6	0.22155813 3
BP	GO:000226 0	lymphocyte homeostasis	2/78	0.03668567 5	0.22155813 3
BP	GO:004663 5	positive regulation of alpha-beta T cell activation	2/78	0.03668567 5	0.22155813 3
BP	GO:007167 7	positive regulation of mononuclear cell migration	2/78	0.03668567 5	0.22155813 3
BP	GO:004866 0	regulation of smooth muscle cell	3/78	0.03773884 9	0.22155813 3

		proliferation			
BP	GO:006075 9	regulation of response to cytokine stimulus	3/78	0.03827699 3	0.22155813 3
BP	GO:004851 1	rhythmic process	4/78	0.03842657 1	0.22155813 3
BP	GO:003273 2	positive regulation of interleukin-1 production	2/78	0.03856064	0.22155813 3
BP	GO:004512 3	cellular extravasation	2/78	0.03856064	0.22155813 3
BP	GO:004566 1	regulation of myoblast differentiation	2/78	0.03856064	0.22155813 3
BP	GO:005095 4	sensory perception of mechanical stimulus	3/78	0.03936508 3	0.22155813 3
BP	GO:001082 2	positive regulation of mitochondrion organization	2/78	0.03951165 2	0.22155813 3
BP	GO:004866 2	negative regulation of smooth muscle cell proliferation	2/78	0.03951165 2	0.22155813 3
BP	GO:004865 9	smooth muscle cell proliferation	3/78	0.03991501 7	0.22155813 3
BP	GO:004226 7	natural killer cell mediated cytotoxicity	2/78	0.04047156 5	0.22155813 3
BP	GO:000229 1	T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell	1/78	0.04113229 3	0.22155813 3
BP	GO:000610 4	succinyl-CoA metabolic process	1/78	0.04113229 3	0.22155813 3
BP	GO:000962 9	response to gravity	1/78	0.04113229 3	0.22155813 3
BP	GO:001088 7	negative regulation of cholesterol storage	1/78	0.04113229 3	0.22155813 3
BP	GO:004213 5	neurotransmitter catabolic process	1/78	0.04113229 3	0.22155813 3
BP	GO:004562 5	regulation of T-helper 1 cell differentiation	1/78	0.04113229 3	0.22155813 3
BP	GO:007086 2	negative regulation of protein exit from endoplasmic reticulum	1/78	0.04113229 3	0.22155813 3
BP	GO:190546 1	positive regulation of vascular associated	1/78	0.04113229 3	0.22155813 3

		smooth muscle cell apoptotic process			
BP	GO:200056 3	positive regulation of CD4-positive, alpha-beta T cell proliferation	1/78	0.04113229 3	0.22155813 3
BP	GO:200065 9	regulation of interleukin-1-mediated signaling pathway	1/78	0.04113229 3	0.22155813 3
BP	GO:000340 7	neural retina development	2/78	0.04144028 9	0.22155813 3
BP	GO:200051 4	regulation of CD4-positive, alpha-beta T cell activation	2/78	0.04144028 9	0.22155813 3
BP	GO:000681 6	calcium ion transport	5/78	0.04215385	0.22155813 3
BP	GO:004315 4	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	2/78	0.04241773 5	0.22155813 3
BP	GO:004582 4	negative regulation of innate immune response	2/78	0.04241773 5	0.22155813 3
BP	GO:004340 5	regulation of MAP kinase activity	3/78	0.04329661 6	0.22155813 3
BP	GO:005189 6	regulation of protein kinase B signaling	3/78	0.04329661 6	0.22155813 3
BP	GO:190316 9	regulation of calcium ion transmembrane transport	3/78	0.04329661 6	0.22155813 3
BP	GO:000222 8	natural killer cell mediated immunity	2/78	0.04340381 5	0.22155813 3
BP	GO:005068 8	regulation of defense response to virus	2/78	0.04340381 5	0.22155813 3
BP	GO:001972 2	calcium-mediated signaling	3/78	0.04387381 5	0.22155813 3
BP	GO:000189 5	retina homeostasis	2/78	0.04439844 2	0.22155813 3
BP	GO:000229 2	T cell differentiation involved in immune response	2/78	0.04439844 2	0.22155813 3
BP	GO:004324	negative regulation of	2/78	0.04439844	0.22155813

	2	protein-containing complex disassembly		2	3
BP	GO:0002831	regulation of response to biotic stimulus	5/78	0.044856567	0.221558133
BP	GO:0002158	osteoclast proliferation	1/78	0.045152487	0.221558133
BP	GO:0002604	regulation of dendritic cell antigen processing and presentation	1/78	0.045152487	0.221558133
BP	GO:0006703	estrogen biosynthetic process	1/78	0.045152487	0.221558133
BP	GO:0014745	negative regulation of muscle adaptation	1/78	0.045152487	0.221558133
BP	GO:0033632	regulation of cell-cell adhesion mediated by integrin	1/78	0.045152487	0.221558133
BP	GO:0033860	regulation of NAD(P)H oxidase activity	1/78	0.045152487	0.221558133
BP	GO:0033869	nucleoside bisphosphate catabolic process	1/78	0.045152487	0.221558133
BP	GO:0034031	ribonucleoside bisphosphate catabolic process	1/78	0.045152487	0.221558133
BP	GO:0034034	purine nucleoside bisphosphate catabolic process	1/78	0.045152487	0.221558133
BP	GO:0042118	endothelial cell activation	1/78	0.045152487	0.221558133
BP	GO:0043320	natural killer cell degranulation	1/78	0.045152487	0.221558133
BP	GO:0045060	negative thymic T cell selection	1/78	0.045152487	0.221558133
BP	GO:0046349	amino sugar biosynthetic process	1/78	0.045152487	0.221558133
BP	GO:0071492	cellular response to UV-A	1/78	0.045152487	0.221558133
BP	GO:0097250	mitochondrial respirasome assembly	1/78	0.045152487	0.221558133
BP	GO:0043299	leukocyte degranulation	2/78	0.04540153	0.221558133
BP	GO:0050848	regulation of calcium-mediated	2/78	0.046412991	0.221558133

		signaling			
BP	GO:006184 4	antimicrobial humoral immune response mediated by antimicrobial peptide	2/78	0.04641299 1	0.22155813 3
BP	GO:000815 4	actin polymerization or depolymerization	3/78	0.04681763	0.22155813 3
BP	GO:000975 5	hormone-mediated signaling pathway	3/78	0.04681763	0.22155813 3
BP	GO:004312 3	positive regulation of I-kappaB kinase/NF-kappaB signaling	3/78	0.04681763	0.22155813 3
BP	GO:003043 3	ubiquitin-dependent ERAD pathway	2/78	0.04743274	0.22155813 3
BP	GO:000255 1	mast cell chemotaxis	1/78	0.04915604	0.22155813 3
BP	GO:000264 5	positive regulation of tolerance induction	1/78	0.04915604	0.22155813 3
BP	GO:001933 6	phenol-containing compound catabolic process	1/78	0.04915604	0.22155813 3
BP	GO:003129 3	membrane protein intracellular domain proteolysis	1/78	0.04915604	0.22155813 3
BP	GO:003818 0	nerve growth factor signaling pathway	1/78	0.04915604	0.22155813 3
BP	GO:004244 7	hormone catabolic process	1/78	0.04915604	0.22155813 3
BP	GO:004338 0	regulation of memory T cell differentiation	1/78	0.04915604	0.22155813 3
BP	GO:004338 3	negative T cell selection	1/78	0.04915604	0.22155813 3
BP	GO:004654 9	retinal cone cell development	1/78	0.04915604	0.22155813 3
BP	GO:005154 9	positive regulation of keratinocyte migration	1/78	0.04915604	0.22155813 3
BP	GO:006022 1	retinal rod cell differentiation	1/78	0.04915604	0.22155813 3
BP	GO:006039 4	negative regulation of pathway-restricted SMAD protein phosphorylation	1/78	0.04915604	0.22155813 3
BP	GO:007268	T cell extravasation	1/78	0.04915604	0.22155813

	3				3
BP	GO:009704 8	dendritic cell apoptotic process	1/78	0.04915604	0.22155813 3
BP	GO:009955 0	trans-synaptic signaling, modulating synaptic transmission	1/78	0.04915604	0.22155813 3
BP	GO:190015 2	negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	1/78	0.04915604	0.22155813 3
BP	GO:190417 7	regulation of adipose tissue development	1/78	0.04915604	0.22155813 3
BP	GO:200050 8	regulation of dendritic cell chemotaxis	1/78	0.04915604	0.22155813 3
BP	GO:200066 8	regulation of dendritic cell apoptotic process	1/78	0.04915604	0.22155813 3
BP	GO:009858 6	cellular response to virus	2/78	0.04949676 2	0.22234771 5
BP	GO:003166 7	response to nutrient levels	5/78	0.04983287 7	0.22247805 6
BP	GO:000190 6	cell killing	3/78	0.04985705 3	0.22247805 6
CC	GO:000989 7	external side of plasma membrane	11/79	1.12E-06	0.00014874 8
CC	GO:003558 0	specific granule lumen	4/79	0.00011602 7	0.00769440 1
CC	GO:003067 0	phagocytic vesicle membrane	4/79	0.00028250 1	0.00792760 1
CC	GO:003477 4	secretory granule lumen	7/79	0.00032685 8	0.00792760 1
CC	GO:006020 5	cytoplasmic vesicle lumen	7/79	0.00034563 6	0.00792760 1
CC	GO:003198 3	vesicle lumen	7/79	0.00035863	0.00792760 1
CC	GO:004258 1	specific granule	5/79	0.00048073 8	0.00891878 5
CC	GO:007082 0	tertiary granule	5/79	0.00053795 8	0.00891878 5
CC	GO:000177 2	immunological synapse	3/79	0.00070091 4	0.01032925 4
CC	GO:001981 4	immunoglobulin complex	4/79	0.00096842 1	0.01253857 5

CC	GO:0042105	alpha-beta T cell receptor complex	2/79	0.001039906	0.012538575
CC	GO:0000153	cytoplasmic ubiquitin ligase complex	2/79	0.001225756	0.013547831
CC	GO:1904724	tertiary granule lumen	3/79	0.001439	0.014681294
CC	GO:0045335	phagocytic vesicle	4/79	0.002578455	0.024427468
CC	GO:0031252	cell leading edge	6/79	0.007267784	0.064262508
CC	GO:0030666	endocytic vesicle membrane	4/79	0.008248242	0.068373583
CC	GO:0005796	Golgi lumen	3/79	0.009132134	0.070092098
CC	GO:0030667	secretory granule membrane	5/79	0.009512499	0.070092098
CC	GO:0072562	blood microparticle	3/79	0.020688198	0.144416232
CC	GO:0101003	ficolin-1-rich granule membrane	2/79	0.025375655	0.16828066
CC	GO:0005775	vacuolar lumen	3/79	0.034613871	0.198909457
CC	GO:0101002	ficolin-1-rich granule	3/79	0.039219321	0.198909457
CC	GO:0000220	vacuolar proton-transporting V-type ATPase, V0 domain	1/79	0.039755142	0.198909457
CC	GO:0044224	juxtaparanode region of axon	1/79	0.039755142	0.198909457
CC	GO:0071735	IgG immunoglobulin complex	1/79	0.039755142	0.198909457
CC	GO:0071745	IgA immunoglobulin complex	1/79	0.039755142	0.198909457
CC	GO:0098802	plasma membrane signaling receptor complex	4/79	0.040492282	0.198909457
CC	GO:0030062	mitochondrial tricarboxylic acid cycle enzyme complex	1/79	0.043643769	0.199604897
CC	GO:0033270	paranode region of axon	1/79	0.043643769	0.199604897
CC	GO:0033179	proton-transporting V-type ATPase, V0	1/79	0.047516848	0.20342959

		domain			
CC	GO:0030027	lamellipodium	3/79	0.048723631	0.20342959
MF	GO:0008009	chemokine activity	3/79	0.001223337	0.215648375
MF	GO:0046965	nuclear retinoid X receptor binding	2/79	0.001849233	0.215648375
MF	GO:0045236	CXCR chemokine receptor binding	2/79	0.002672165	0.215648375
MF	GO:0042379	chemokine receptor binding	3/79	0.003985486	0.229543107
MF	GO:0042974	nuclear retinoic acid receptor binding	2/79	0.004740564	0.229543107
MF	GO:0003785	actin monomer binding	2/79	0.006877255	0.252699569
MF	GO:0004896	cytokine receptor activity	3/79	0.007306314	0.252699569
MF	GO:0031406	carboxylic acid binding	4/79	0.010858759	0.278204106
MF	GO:0043177	organic acid binding	4/79	0.013214593	0.278204106
MF	GO:0003823	antigen binding	3/79	0.014344074	0.278204106
MF	GO:0017124	SH3 domain binding	3/79	0.01601716	0.278204106
MF	GO:0004879	nuclear receptor activity	2/79	0.016726054	0.278204106
MF	GO:0098531	ligand-activated transcription factor activity	2/79	0.016726054	0.278204106
MF	GO:0030695	GTPase regulator activity	6/79	0.019743691	0.278204106
MF	GO:0060589	nucleoside-triphosphatase regulator activity	6/79	0.019743691	0.278204106
MF	GO:0002020	protease binding	3/79	0.021670919	0.278204106
MF	GO:0140375	immune receptor activity	3/79	0.022916501	0.278204106
MF	GO:0017022	myosin binding	2/79	0.036535231	0.278204106
MF	GO:0004252	serine-type endopeptidase activity	3/79	0.036927066	0.278204106
MF	GO:0003779	actin binding	5/79	0.039070097	0.278204106

MF	GO:000379 6	lysozyme activity	1/79	0.04219452 3	0.27820410 6
MF	GO:000495 4	prostanoid receptor activity	1/79	0.04219452 3	0.27820410 6
MF	GO:000495 5	prostaglandin receptor activity	1/79	0.04219452 3	0.27820410 6
MF	GO:001845 5	alcohol dehydrogenase [NAD(P)+] activity	1/79	0.04219452 3	0.27820410 6
MF	GO:003498 7	immunoglobulin receptor binding	1/79	0.04219452 3	0.27820410 6
MF	GO:004312 1	neurotrophin binding	1/79	0.04219452 3	0.27820410 6
MF	GO:004320 8	glycosphingolipid binding	1/79	0.04219452 3	0.27820410 6
MF	GO:004633 2	SMAD binding	2/79	0.04342634 7	0.27820410 6
MF	GO:003203 6	myosin heavy chain binding	1/79	0.04631602 4	0.27820410 6
MF	GO:003451 1	U3 snoRNA binding	1/79	0.04631602 4	0.27820410 6
MF	GO:004260 8	T cell receptor binding	1/79	0.04631602 4	0.27820410 6
MF	GO:000823 6	serine-type peptidase activity	3/79	0.04863351 7	0.27820410 6

Table S3b. Analysis of KEGG.

ID	Description	GeneRatio	BgRatio	pvalue	qvalue
hsa04670	Leukocyte transendothelial migration	5/44	115/8772	0.000256305	0.032105527
hsa04060	Cytokine-cytokine receptor interaction	7/44	297/8772	0.000620247	0.038847044
hsa04657	IL-17 signaling pathway	4/44	94/8772	0.001209412	0.047649826
hsa04061	Viral protein interaction with cytokine and cytokine receptor	4/44	100/8772	0.001521591	0.047649826
hsa04062	Chemokine signaling pathway	5/44	192/8772	0.002590427	0.064897009
hsa04623	Cytosolic DNA-sensing pathway	3/44	83/8772	0.008183292	0.170844158
hsa00020	Citrate cycle (TCA cycle)	2/44	30/8772	0.00978462	0.174799761
hsa04970	Salivary secretion	3/44	93/8772	0.011163682	0.174799761
hsa00350	Tyrosine metabolism	2/44	36/8772	0.013904142	0.193123722
hsa05340	Primary immunodeficiency	2/44	38/8772	0.01541744	0.193123722
hsa00620	Pyruvate metabolism	2/44	47/8772	0.023043327	0.262407269
hsa04810	Regulation of actin cytoskeleton	4/44	229/8772	0.027172877	0.283646695
hsa04370	VEGF signaling pathway	2/44	59/8772	0.035121895	0.338421502
hsa00010	Glycolysis / Gluconeogenesis	2/44	67/8772	0.044261533	0.389744494
hsa05416	Viral myocarditis	2/44	69/8772	0.046671084	0.389744494

Appendix 4

DEG Identification of PPI

Table S4. DEG Identification of PPI

#node1	node2	neighborhood_on_chromosome	gene_fusion	phylogenetic_cooccurrence	homology
ADH1C	PCK1	0	0	0	0
ADH1C	MAOA	0	0	0	0
AIM2	CXCL10	0	0	0	0
AIM2	ZBP1	0	0	0	0
ARHGA P9	CORO1 A	0	0	0	0
ARHGA P9	RAC2	0	0	0	0
ARHGA P9	CYTIP	0	0	0	0
ARHGA P9	FGD3	0	0	0	0
ARHGA P9	ITGAL	0	0	0	0
ARHGA P9	TBC1D1 0C	0	0	0	0
CCL19	CD79A	0	0	0	0
CCL19	GZMK	0	0	0	0
CCL19	MMP7	0	0	0	0
CCL19	CD27	0	0	0	0
CCL19	NTRK2	0	0	0	0
CCL19	CXCL10	0	0	0	0
CCL19	MMP9	0	0	0	0
CCL19	IL21R	0	0	0	0
CCL19	SELL	0	0	0	0
CCL19	CXCL9	0	0	0	0
CCL19	CXCR4	0	0	0	0
CD27	CORO1 A	0	0	0	0

CD27	CD79A	0	0	0	0
CD27	GZMK	0	0	0	0
CD27	CXCL9	0	0	0	0
CD27	SLAMF7	0	0	0	0
CD27	PTPRCAP	0	0	0	0
CD27	ITGAL	0	0	0	0
CD27	FCRL5	0	0	0	0
CD27	CXCL10	0	0	0	0
CD27	IL21R	0	0	0	0
CD27	CXCR4	0	0	0	0
CD27	CD3E	0	0	0	0
CD27	SELL	0	0	0	0
CD3E	CORO1A	0	0	0	0
CD3E	CD79A	0	0	0	0
CD3E	GZMK	0	0	0	0
CD3E	LYZ	0	0	0	0
CD3E	CXCL10	0	0	0	0
CD3E	PTPRCAP	0	0	0	0
CD3E	ITGAL	0	0	0	0
CD3E	CXCR4	0	0	0	0
CD3E	CXCL9	0	0	0	0
CD3E	SELL	0	0	0	0
CD79A	GZMK	0	0	0	0
CD79A	CXCR4	0	0	0	0
CD79A	IL21R	0	0	0.275	0
CD79A	PTPRCAP	0	0	0	0
CD79A	LYZ	0	0	0	0
CD79A	CXCL10	0	0	0	0
CD79A	RHOH	0	0	0	0
CD79A	FCRL5	0	0	0	0
CD79A	CXCL9	0	0	0	0
CHI3L1	MMP7	0	0	0	0
CHI3L1	CXCL10	0	0	0	0
CHI3L1	MMP9	0	0	0	0
CHI3L1	LCN2	0	0	0	0
CORO1A	LYZ	0	0	0	0
CORO1	TBC1D1	0	0	0	0

A	0C				
CORO1 A	SELL	0	0	0	0
CORO1 A	ITGAL	0	0	0	0
CORO1 A	PTPRC AP	0	0.042	0	0
CORO1 A	RHOH	0	0	0	0
CORO1 A	RAC2	0	0	0	0
CORO1 A	FGD3	0	0	0	0
CXCL1 0	GZMK	0	0	0	0
CXCL1 0	MMP7	0	0	0	0
CXCL1 0	PPARG	0	0	0	0
CXCL1 0	ITGAL	0	0	0	0
CXCL1 0	ZBP1	0	0	0	0
CXCL1 0	LCN2	0	0	0	0
CXCL1 0	SELL	0	0	0	0
CXCL1 0	IL21R	0	0	0	0
CXCL1 0	ISG20	0	0	0	0
CXCL1 0	MMP9	0	0	0	0
CXCL1 0	CXCR4	0	0	0	0
CXCL1 0	CXCL9	0	0	0	0.856
CXCL9	GZMK	0	0	0	0
CXCL9	SLAMF 8	0	0	0	0
CXCL9	ISG20	0	0	0	0
CXCL9	IL21R	0	0	0	0
CXCL9	SLAMF	0	0	0	0

	7				
CXCL9	LCN2	0	0	0	0
CXCL9	SELL	0	0	0	0
CXCL9	MMP9	0	0	0	0
CXCL9	CXCR4	0	0	0	0
CXCR4	RAC2	0	0	0	0
CXCR4	MMP7	0	0	0	0
CXCR4	CYTIP	0	0	0	0
CXCR4	PPARG	0	0	0	0
CXCR4	IL21R	0	0	0	0
CXCR4	ITGAL	0	0	0	0
CXCR4	MMP9	0	0	0	0
CXCR4	RHOH	0	0	0	0
CXCR4	SUCLG 2	0	0	0	0
CXCR4	SELL	0	0	0	0
CYTIP	KLHL6	0	0	0	0
CYTIP	RHOH	0	0	0	0
DERL3	FAM8A 1	0	0	0	0
DERL3	FCRL5	0	0	0	0
DMBT1	LYZ	0	0	0	0
DMBT1	PDZK1I P1	0	0	0	0
DMBT1	MUC5B	0	0	0	0
FCRL5	SLAMF 7	0	0	0	0
GZMK	SLAMF 7	0	0	0	0
GZMK	ITGAL	0	0	0	0
GZMK	MMP9	0	0	0	0
GZMK	PTPRC AP	0	0	0	0
GZMK	SELL	0	0	0	0
IKZF3	KLHL6	0	0	0	0
IKZF3	P2RY8	0	0	0	0
IKZF3	SLAMF 7	0	0	0	0
IKZF3	RHOH	0	0	0	0
IL21R	SELL	0	0	0	0
ITGAL	RAC2	0	0	0	0
ITGAL	TBC1D1 0C	0	0	0	0

ITGAL	SELL	0	0	0	0
KCNA3	NTRK2	0	0	0	0
LCN2	OLFM4	0	0	0	0
LCN2	MMP7	0	0	0	0
LCN2	LYZ	0	0	0	0
LCN2	PPARG	0	0	0	0
LCN2	PDZK1I P1	0	0	0	0
LCN2	MMP9	0	0	0	0
LCN2	MUC5B	0	0	0	0
LYZ	OLFM4	0	0	0	0
MAOA	NTRK2	0	0	0	0
MAOA	PPARG	0	0	0	0
MMP7	OLFM4	0	0	0	0
MMP7	NTRK2	0	0	0	0
MMP7	MMP9	0	0	0	0.803
MMP9	RAC2	0	0	0	0
MMP9	PPARG	0	0	0	0
MMP9	TBC1D1 0C	0	0	0	0
MMP9	SELL	0	0	0	0
MUC5B	PDZK1I P1	0	0	0	0
MXI1	PDZK1I P1	0	0	0	0
NRIP1	PPARG	0	0	0	0
NRIP1	PCK1	0	0	0	0
NRIP1	THRB	0	0	0	0
P2RY8	TBC1D1 0C	0	0	0	0
PCK1	PPARG	0	0	0	0
PRDX6	SUCLG 2	0.055	0	0	0
PTPRC AP	TBC1D1 0C	0	0	0	0
RAC2	SELL	0	0	0	0
SLAMF 7	SLAMF 8	0	0	0	0.597

Appendix 5

Analysis of enrichment

Table S5a. Analysis of GO.

ONTOLOGY	ID	Description	BgRatio	pvalue	qvalue
BP	GO:0070098	chemokine-mediated signaling pathway	91/18614	1.10E-07	1.21E-05
BP	GO:1990868	response to chemokine	99/18614	1.54E-07	1.21E-05
BP	GO:1990869	cellular response to chemokine	99/18614	1.54E-07	1.21E-05
BP	GO:0050900	leukocyte migration	393/18614	9.45E-07	5.54E-05
BP	GO:0030595	leukocyte chemotaxis	241/18614	5.41E-06	0.000254189
BP	GO:0060326	cell chemotaxis	312/18614	1.50E-05	0.000587462
BP	GO:0030593	neutrophil chemotaxis	107/18614	2.15E-05	0.000632733
BP	GO:1990266	neutrophil migration	128/18614	3.68E-05	0.000632733
BP	GO:0051209	release of sequestered calcium ion into cytosol	130/18614	3.85E-05	0.000632733
BP	GO:0051283	negative regulation of sequestering of calcium ion	131/18614	3.94E-05	0.000632733
BP	GO:0071621	granulocyte chemotaxis	131/18614	3.94E-05	0.000632733
BP	GO:0003159	morphogenesis of an endothelium	18/18614	3.96E-05	0.000632733
BP	GO:0061154	endothelial tube morphogenesis	18/18614	3.96E-05	0.000632733
BP	GO:0051282	regulation of sequestering of calcium ion	133/18614	4.13E-05	0.000632733
BP	GO:0009615	response to virus	408/18614	4.30E-05	0.000632733
BP	GO:00512	sequestering of calcium	137/18614	4.51E-05	0.0006327

	08	ion	4		33
BP	GO:0007159	leukocyte cell-cell adhesion	415/18614	4.60E-05	0.000632733
BP	GO:0030098	lymphocyte differentiation	422/18614	4.91E-05	0.000632733
BP	GO:0050921	positive regulation of chemotaxis	143/18614	5.12E-05	0.000632733
BP	GO:1901739	regulation of myoblast fusion	21/18614	5.43E-05	0.000636784
BP	GO:0006816	calcium ion transport	455/18614	6.58E-05	0.000708087
BP	GO:0097530	granulocyte migration	156/18614	6.64E-05	0.000708087
BP	GO:1903131	mononuclear cell differentiation	474/18614	7.72E-05	0.000787735
BP	GO:0002407	dendritic cell chemotaxis	26/18614	8.38E-05	0.000820073
BP	GO:0019221	cytokine-mediated signaling pathway	492/18614	8.92E-05	0.000837659
BP	GO:0060142	regulation of syncytium formation by plasma membrane fusion	30/18614	0.000112096	0.001012041
BP	GO:0036336	dendritic cell migration	33/18614	0.000135944	0.00115625
BP	GO:0097553	calcium ion transmembrane import into cytosol	201/18614	0.000140765	0.00115625
BP	GO:0071674	mononuclear cell migration	202/18614	0.000142846	0.00115625
BP	GO:0050920	regulation of chemotaxis	230/18614	0.000209576	0.001595017
BP	GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	41/18614	0.000210642	0.001595017
BP	GO:0051651	maintenance of location in cell	233/18614	0.000217735	0.001597203
BP	GO:0097529	myeloid leukocyte migration	241/18614	0.000240499	0.0016763
BP	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation	44/18614	0.0002428	0.0016763
BP	GO:0031295	T cell costimulation	45/18614	0.000254021	0.001703657
BP	GO:00508	positive regulation of T	249/1861	0.0002647	0.0017263

	70	cell activation	4	58	47
BP	GO:0031294	lymphocyte costimulation	47/18614	0.000277211	0.001758693
BP	GO:0007520	myoblast fusion	48/18614	0.000289181	0.001786353
BP	GO:0051924	regulation of calcium ion transport	266/18614	0.000321468	0.001934879
BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	273/18614	0.000346931	0.002035939
BP	GO:2000107	negative regulation of leukocyte apoptotic process	56/18614	0.000393899	0.002255187
BP	GO:0030217	T cell differentiation	300/18614	0.00045732	0.002472804
BP	GO:0006874	intracellular calcium ion homeostasis	303/18614	0.000470823	0.002472804
BP	GO:0000768	syncytium formation by plasma membrane fusion	62/18614	0.000482846	0.002472804
BP	GO:0140253	cell-cell fusion	62/18614	0.000482846	0.002472804
BP	GO:0046651	lymphocyte proliferation	306/18614	0.000484581	0.002472804
BP	GO:0048247	lymphocyte chemotaxis	64/18614	0.000514469	0.002531668
BP	GO:0032943	mononuclear cell proliferation	313/18614	0.000517686	0.002531668
BP	GO:0006949	syncytium formation	66/18614	0.000547075	0.002594746
BP	GO:0022409	positive regulation of cell-cell adhesion	321/18614	0.00055727	0.002594746
BP	GO:1901224	positive regulation of NIK/NF-kappaB signaling	67/18614	0.000563746	0.002594746
BP	GO:0051251	positive regulation of lymphocyte activation	327/18614	0.000588204	0.002605153
BP	GO:0055074	calcium ion homeostasis	327/18614	0.000588204	0.002605153
BP	GO:0002548	monocyte chemotaxis	71/18614	0.000632883	0.002751128
BP	GO:0046635	positive regulation of alpha-beta T cell activation	72/18614	0.000650779	0.002777486
BP	GO:00456	regulation of myoblast	74/18614	0.0006873	0.0028054

	61	differentiation		03	3
BP	GO:19040 62	regulation of monoatomic cation transmembrane transport	346/1861 4	0.0006934 04	0.0028054 3
BP	GO:00512 35	maintenance of location	347/1861 4	0.0006992 52	0.0028054 3
BP	GO:00706 61	leukocyte proliferation	348/1861 4	0.0007051 32	0.0028054 3
BP	GO:20005 14	regulation of CD4-positive, alpha-beta T cell activation	77/18614	0.0007439 17	0.0029104 11
BP	GO:00431 54	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	78/18614	0.0007632 75	0.0029371 91
BP	GO:00705 88	calcium ion transmembrane transport	360/1861 4	0.0007781 85	0.0029462 68
BP	GO:00512 79	regulation of release of sequestered calcium ion into cytosol	82/18614	0.0008431 33	0.0030924 14
BP	GO:00618 44	antimicrobial humoral immune response mediated by antimicrobial peptide	82/18614	0.0008431 33	0.0030924 14
BP	GO:00026 96	positive regulation of leukocyte activation	377/1861 4	0.0008897 38	0.0031260 39
BP	GO:00508 63	regulation of T cell activation	377/1861 4	0.0008897 38	0.0031260 39
BP	GO:19030 37	regulation of leukocyte cell-cell adhesion	378/1861 4	0.0008966	0.0031260 39
BP	GO:00985 86	cellular response to virus	85/18614	0.0009055 7	0.0031260 39
BP	GO:00508 67	positive regulation of cell activation	394/1861 4	0.0010110 54	0.0034018 65
BP	GO:20001 06	regulation of leukocyte apoptotic process	90/18614	0.0010144 57	0.0034018 65
BP	GO:20001 17	negative regulation of cysteine-type endopeptidase activity	91/18614	0.0010369 57	0.0034283 38
BP	GO:19044 27	positive regulation of calcium ion transmembrane transport	93/18614	0.0010826 76	0.0035297 77
BP	GO:00463	positive regulation of	95/18614	0.0011293	0.0036315

	30	JNK cascade		54	21
BP	GO:0002690	positive regulation of leukocyte chemotaxis	96/18614	0.001153053	0.00365762
BP	GO:0010959	regulation of metal ion transport	423/18614	0.0012415	0.003885678
BP	GO:0010720	positive regulation of cell development	432/18614	0.001319251	0.004074695
BP	GO:0042102	positive regulation of T cell proliferation	105/18614	0.001377071	0.004198042
BP	GO:0045445	myoblast differentiation	110/18614	0.001509837	0.004486259
BP	GO:1901222	regulation of NIK/NF-kappaB signaling	110/18614	0.001509837	0.004486259
BP	GO:0046634	regulation of alpha-beta T cell activation	114/18614	0.001620303	0.00475431
BP	GO:0035710	CD4-positive, alpha-beta T cell activation	115/18614	0.001648508	0.004777353
BP	GO:0045582	positive regulation of T cell differentiation	116/18614	0.001676948	0.004800507
BP	GO:0071887	leukocyte apoptotic process	117/18614	0.001705623	0.004823767
BP	GO:0034765	regulation of monoatomic ion transmembrane transport	478/18614	0.001765039	0.004932377
BP	GO:0045785	positive regulation of cell adhesion	482/18614	0.001807752	0.004992305
BP	GO:0072676	lymphocyte migration	122/18614	0.001852516	0.005056438
BP	GO:0022407	regulation of cell-cell adhesion	491/18614	0.001906235	0.005143259
BP	GO:0002688	regulation of leukocyte chemotaxis	126/18614	0.001974236	0.005207034
BP	GO:0019730	antimicrobial humoral response	126/18614	0.001974236	0.005207034
BP	GO:0014902	myotube differentiation	127/18614	0.002005249	0.005230065
BP	GO:0032874	positive regulation of stress-activated MAPK cascade	129/18614	0.002067972	0.005276405
BP	GO:0051928	positive regulation of calcium ion transport	129/18614	0.002067972	0.005276405
BP	GO:0045621	positive regulation of lymphocyte	130/18614	0.002099682	0.005299706

		differentiation			
BP	GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	131/18614	0.002131624	0.005323092
BP	GO:0003158	endothelium development	137/18614	0.002328135	0.005752622
BP	GO:0046328	regulation of JNK cascade	139/18614	0.002395485	0.005857382
BP	GO:0007189	adenylate cyclase-activating G protein-coupled receptor signaling pathway	140/18614	0.002429506	0.005879325
BP	GO:0038061	NIK/NF-kappaB signaling	142/18614	0.002498236	0.00598396
BP	GO:0050671	positive regulation of lymphocyte proliferation	145/18614	0.002603052	0.006172043
BP	GO:0002687	positive regulation of leukocyte migration	147/18614	0.002674075	0.006277038
BP	GO:0032946	positive regulation of mononuclear cell proliferation	148/18614	0.002709929	0.006298219
BP	GO:1904064	positive regulation of cation transmembrane transport	152/18614	0.002855625	0.006571769
BP	GO:0030183	B cell differentiation	153/18614	0.002892618	0.006592272
BP	GO:0008037	cell recognition	155/18614	0.002967286	0.006697417
BP	GO:0010951	negative regulation of endopeptidase activity	160/18614	0.003157922	0.007059816
BP	GO:0070665	positive regulation of leukocyte proliferation	166/18614	0.003394134	0.007516306
BP	GO:0007254	JNK cascade	170/18614	0.003556104	0.007801389
BP	GO:0034767	positive regulation of monoatomic ion transmembrane transport	175/18614	0.003763599	0.008105095
BP	GO:0046631	alpha-beta T cell activation	175/18614	0.003763599	0.008105095
BP	GO:0045580	regulation of T cell differentiation	180/18614	0.003976663	0.008486085
BP	GO:0009266	response to temperature stimulus	183/18614	0.004107165	0.008547525
BP	GO:00421	regulation of T cell	183/18614	0.0041071	0.0085475

	29	proliferation	4	65	25
BP	GO:1902107	positive regulation of leukocyte differentiation	184/18614	0.004151108	0.008547525
BP	GO:1903708	positive regulation of hemopoiesis	184/18614	0.004151108	0.008547525
BP	GO:1903169	regulation of calcium ion transmembrane transport	186/18614	0.004239656	0.008653943
BP	GO:0019722	calcium-mediated signaling	187/18614	0.004284261	0.008669603
BP	GO:0032872	regulation of stress-activated MAPK cascade	193/18614	0.004556513	0.009141721
BP	GO:0070302	regulation of stress-activated protein kinase signaling cascade	196/18614	0.0046956	0.009340934
BP	GO:0050851	antigen receptor-mediated signaling pathway	201/18614	0.004931779	0.009728321
BP	GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	204/18614	0.005076099	0.009929562
BP	GO:0045625	regulation of T-helper 1 cell differentiation	10/18614	0.005360624	0.01031423
BP	GO:2000563	positive regulation of CD4-positive, alpha-beta T cell proliferation	10/18614	0.005360624	0.01031423
BP	GO:0045619	regulation of lymphocyte differentiation	212/18614	0.005470483	0.010440031
BP	GO:0042098	T cell proliferation	213/18614	0.005520752	0.010450999
BP	GO:0009612	response to mechanical stimulus	215/18614	0.005621936	0.010557403
BP	GO:0002604	regulation of dendritic cell antigen processing and presentation	11/18614	0.005895262	0.010644885
BP	GO:0033632	regulation of cell-cell adhesion mediated by integrin	11/18614	0.005895262	0.010644885
BP	GO:0042118	endothelial cell activation	11/18614	0.005895262	0.010644885
BP	GO:00450	negative thymic T cell	11/18614	0.0058952	0.0106448

	60	selection		62	85
BP	GO:00714 92	cellular response to UV-A	11/18614	0.0058952 62	0.0106448 85
BP	GO:00712 22	cellular response to lipopolysaccharide	224/1861 4	0.0060878 7	0.0109087 59
BP	GO:00025 73	myeloid leukocyte differentiation	227/1861 4	0.0062470 23	0.0109130 65
BP	GO:00026 85	regulation of leukocyte migration	227/1861 4	0.0062470 23	0.0109130 65
BP	GO:00026 45	positive regulation of tolerance induction	12/18614	0.0064296 4	0.0109130 65
BP	GO:00433 83	negative T cell selection	12/18614	0.0064296 4	0.0109130 65
BP	GO:00515 49	positive regulation of keratinocyte migration	12/18614	0.0064296 4	0.0109130 65
BP	GO:00970 48	dendritic cell apoptotic process	12/18614	0.0064296 4	0.0109130 65
BP	GO:20006 68	regulation of dendritic cell apoptotic process	12/18614	0.0064296 4	0.0109130 65
BP	GO:00432 70	positive regulation of monoatomic ion transport	231/1861 4	0.0064621 99	0.0109130 65
BP	GO:00071 88	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	234/1861 4	0.0066258 03	0.0109942 76
BP	GO:20001 16	regulation of cysteine-type endopeptidase activity	234/1861 4	0.0066258 03	0.0109942 76
BP	GO:00347 64	positive regulation of transmembrane transport	235/1861 4	0.0066807 6	0.0109942 76
BP	GO:00104 66	negative regulation of peptidase activity	236/1861 4	0.0067359 29	0.0109942 76
BP	GO:00514 03	stress-activated MAPK cascade	237/1861 4	0.0067913 07	0.0109942 76
BP	GO:00712 19	cellular response to molecule of bacterial origin	237/1861 4	0.0067913 07	0.0109942 76
BP	GO:00506 70	regulation of lymphocyte proliferation	239/1861 4	0.0069026 96	0.0110980 62
BP	GO:00026 64	regulation of T cell tolerance induction	13/18614	0.0069637 61	0.0111200 76
BP	GO:00329 44	regulation of mononuclear cell	243/1861 4	0.0071279 92	0.0113054 21

		proliferation			
BP	GO:0031098	stress-activated protein kinase signaling cascade	245/18614	0.007241896	0.011408992
BP	GO:0045059	positive thymic T cell selection	14/18614	0.007497622	0.011478189
BP	GO:0051547	regulation of keratinocyte migration	14/18614	0.007497622	0.011478189
BP	GO:0061043	regulation of vascular wound healing	14/18614	0.007497622	0.011478189
BP	GO:0070141	response to UV-A	14/18614	0.007497622	0.011478189
BP	GO:0006959	humoral immune response	250/18614	0.00753031	0.011478189
BP	GO:0097305	response to alcohol	252/18614	0.007647132	0.011581055
BP	GO:0001768	establishment of T cell polarity	15/18614	0.008031226	0.011782653
BP	GO:0001771	immunological synapse formation	15/18614	0.008031226	0.011782653
BP	GO:0002468	dendritic cell antigen processing and presentation	15/18614	0.008031226	0.011782653
BP	GO:0002517	T cell tolerance induction	15/18614	0.008031226	0.011782653
BP	GO:0050966	detection of mechanical stimulus involved in sensory perception of pain	15/18614	0.008031226	0.011782653
BP	GO:0071216	cellular response to biotic stimulus	264/18614	0.008365443	0.012104359
BP	GO:0001767	establishment of lymphocyte polarity	16/18614	0.008564571	0.012104359
BP	GO:0010819	regulation of T cell chemotaxis	16/18614	0.008564571	0.012104359
BP	GO:0045579	positive regulation of B cell differentiation	16/18614	0.008564571	0.012104359
BP	GO:1901741	positive regulation of myoblast fusion	16/18614	0.008564571	0.012104359
BP	GO:2000696	regulation of epithelial cell differentiation involved in kidney development	16/18614	0.008564571	0.012104359
BP	GO:0070663	regulation of leukocyte proliferation	268/18614	0.008611464	0.012104359

BP	GO:00336 31	cell-cell adhesion mediated by integrin	17/18614	0.0090976 58	0.0124373 77
BP	GO:00973 96	response to interleukin-17	17/18614	0.0090976 58	0.0124373 77
BP	GO:00973 98	cellular response to interleukin-17	17/18614	0.0090976 58	0.0124373 77
BP	GO:20012 67	regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	17/18614	0.0090976 58	0.0124373 77
BP	GO:00421 13	B cell activation	276/1861 4	0.0091133 07	0.0124373 77
BP	GO:00432 17	myelin maintenance	18/18614	0.0096304 87	0.0129921 27
BP	GO:00509 65	detection of temperature stimulus involved in sensory perception of pain	18/18614	0.0096304 87	0.0129921 27
BP	GO:00199 32	second-messenger-medi ated signaling	292/1861 4	0.0101558 56	0.0136225 92
BP	GO:00511 46	striated muscle cell differentiation	297/1861 4	0.0104921 83	0.0139937 61
BP	GO:00025 77	regulation of antigen processing and presentation	20/18614	0.0106953 72	0.0140256 86
BP	GO:00026 43	regulation of tolerance induction	20/18614	0.0106953 72	0.0140256 86
BP	GO:00515 46	keratinocyte migration	20/18614	0.0106953 72	0.0140256 86
BP	GO:00024 29	immune response-activating cell surface receptor signaling pathway	302/1861 4	0.0108334 84	0.0141278 76
BP	GO:00516 07	defense response to virus	303/1861 4	0.0109023 39	0.0141391 19
BP	GO:01405 46	defense response to symbiont	304/1861 4	0.0109713 91	0.0141504 93
BP	GO:00450 63	T-helper 1 cell differentiation	21/18614	0.0112274 28	0.0142458 97
BP	GO:00717 31	response to nitric oxide	21/18614	0.0112274 28	0.0142458 97
BP	GO:00900 26	positive regulation of monocyte chemotaxis	21/18614	0.0112274 28	0.0142458 97

BP	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	311/18614	0.011460283	0.014376685
BP	GO:0033630	positive regulation of cell adhesion mediated by integrin	22/18614	0.011759226	0.014376685
BP	GO:0035739	CD4-positive, alpha-beta T cell proliferation	22/18614	0.011759226	0.014376685
BP	GO:0045061	thymic T cell selection	22/18614	0.011759226	0.014376685
BP	GO:0045624	positive regulation of T-helper cell differentiation	22/18614	0.011759226	0.014376685
BP	GO:0050961	detection of temperature stimulus involved in sensory perception	22/18614	0.011759226	0.014376685
BP	GO:2000561	regulation of CD4-positive, alpha-beta T cell proliferation	22/18614	0.011759226	0.014376685
BP	GO:1902105	regulation of leukocyte differentiation	319/18614	0.012030792	0.014632488
BP	GO:0010560	positive regulation of glycoprotein biosynthetic process	23/18614	0.012290767	0.014645156
BP	GO:0061042	vascular wound healing	23/18614	0.012290767	0.014645156
BP	GO:1900120	regulation of receptor binding	23/18614	0.012290767	0.014645156
BP	GO:1903861	positive regulation of dendrite extension	23/18614	0.012290767	0.014645156
BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	329/18614	0.012761451	0.014915762
BP	GO:0034695	response to prostaglandin E	24/18614	0.01282205	0.014915762
BP	GO:0060143	positive regulation of syncytium formation by plasma membrane fusion	24/18614	0.01282205	0.014915762
BP	GO:00702	negative regulation of T	24/18614	0.0128220	0.0149157

	33	cell apoptotic process		5	62
BP	GO:0045861	negative regulation of proteolysis	330/18614	0.012835582	0.014915762
BP	GO:0060562	epithelial tube morphogenesis	334/18614	0.013134029	0.014997412
BP	GO:0052548	regulation of endopeptidase activity	336/18614	0.013284406	0.014997412
BP	GO:0016048	detection of temperature stimulus	25/18614	0.013353077	0.014997412
BP	GO:0045662	negative regulation of myoblast differentiation	25/18614	0.013353077	0.014997412
BP	GO:0046641	positive regulation of alpha-beta T cell proliferation	25/18614	0.013353077	0.014997412
BP	GO:0048714	positive regulation of oligodendrocyte differentiation	25/18614	0.013353077	0.014997412
BP	GO:0090023	positive regulation of neutrophil chemotaxis	25/18614	0.013353077	0.014997412
BP	GO:0046629	gamma-delta T cell activation	26/18614	0.013883846	0.01518244
BP	GO:0140374	antiviral innate immune response	26/18614	0.013883846	0.01518244
BP	GO:1901623	regulation of lymphocyte chemotaxis	26/18614	0.013883846	0.01518244
BP	GO:1903020	positive regulation of glycoprotein metabolic process	26/18614	0.013883846	0.01518244
BP	GO:1903859	regulation of dendrite extension	26/18614	0.013883846	0.01518244
BP	GO:0032496	response to lipopolysaccharide	345/18614	0.013970568	0.01518244
BP	GO:0051346	negative regulation of hydrolase activity	345/18614	0.013970568	0.01518244
BP	GO:0045765	regulation of angiogenesis	349/18614	0.014280478	0.015310321
BP	GO:0010818	T cell chemotaxis	27/18614	0.014414358	0.015310321
BP	GO:0032753	positive regulation of interleukin-4 production	27/18614	0.014414358	0.015310321
BP	GO:0062149	detection of stimulus involved in sensory perception of pain	27/18614	0.014414358	0.015310321
BP	GO:00902	positive regulation of	27/18614	0.0144143	0.0153103

	00	release of cytochrome c from mitochondria		58	21
BP	GO:1901342	regulation of vasculature development	355/18614	0.014751017	0.015522351
BP	GO:0014072	response to isoquinoline alkaloid	28/18614	0.014944614	0.015522351
BP	GO:0043278	response to morphine	28/18614	0.014944614	0.015522351
BP	GO:0050951	sensory perception of temperature stimulus	28/18614	0.014944614	0.015522351
BP	GO:0071624	positive regulation of granulocyte chemotaxis	28/18614	0.014944614	0.015522351
BP	GO:0010996	response to auditory stimulus	29/18614	0.015474612	0.015931849
BP	GO:0090025	regulation of monocyte chemotaxis	29/18614	0.015474612	0.015931849
BP	GO:0002237	response to molecule of bacterial origin	366/18614	0.015631242	0.016022831
BP	GO:0002507	tolerance induction	30/18614	0.016004354	0.016263253
BP	GO:0002825	regulation of T-helper 1 type immune response	30/18614	0.016004354	0.016263253
BP	GO:0071276	cellular response to cadmium ion	31/18614	0.01653384	0.016728885
BP	GO:0034694	response to prostaglandin	32/18614	0.017063068	0.017043961
BP	GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	32/18614	0.017063068	0.017043961
BP	GO:0060055	angiogenesis involved in wound healing	32/18614	0.017063068	0.017043961
BP	GO:0050901	leukocyte tethering or rolling	33/18614	0.017592041	0.017497882
BP	GO:0032743	positive regulation of interleukin-2 production	34/18614	0.018120758	0.017576898
BP	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	34/18614	0.018120758	0.017576898
BP	GO:0045577	regulation of B cell differentiation	34/18614	0.018120758	0.017576898
BP	GO:0090022	regulation of neutrophil chemotaxis	34/18614	0.018120758	0.017576898
BP	GO:1902624	positive regulation of neutrophil migration	34/18614	0.018120758	0.017576898

BP	GO:2000406	positive regulation of T cell migration	34/18614	0.018120758	0.017576898
BP	GO:0032633	interleukin-4 production	35/18614	0.018649218	0.01779536
BP	GO:0032673	regulation of interleukin-4 production	35/18614	0.018649218	0.01779536
BP	GO:0045879	negative regulation of smoothened signaling pathway	35/18614	0.018649218	0.01779536
BP	GO:0050974	detection of mechanical stimulus involved in sensory perception	35/18614	0.018649218	0.01779536
BP	GO:0090218	positive regulation of lipid kinase activity	36/18614	0.019177422	0.018151804
BP	GO:0097484	dendrite extension	36/18614	0.019177422	0.018151804
BP	GO:0042692	muscle cell differentiation	410/18614	0.01937506	0.018265223
BP	GO:0033280	response to vitamin D	37/18614	0.019705371	0.018502306
BP	GO:1903706	regulation of hemopoiesis	415/18614	0.019822625	0.018538248
BP	GO:0043368	positive T cell selection	38/18614	0.020233063	0.018698604
BP	GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	38/18614	0.020233063	0.018698604
BP	GO:0070229	negative regulation of lymphocyte apoptotic process	38/18614	0.020233063	0.018698604
BP	GO:0030099	myeloid cell differentiation	421/18614	0.020365557	0.018747241
BP	GO:0002757	immune response-activating signaling pathway	423/18614	0.020547947	0.018841251
BP	GO:0052547	regulation of peptidase activity	425/18614	0.020731042	0.018888582
BP	GO:0070232	regulation of T cell apoptotic process	39/18614	0.0207605	0.018888582
BP	GO:0050850	positive regulation of calcium-mediated signaling	40/18614	0.021287682	0.019219243
BP	GO:19011	positive regulation of	40/18614	0.0212876	0.0192192

	86	ERBB signaling pathway		82	43
BP	GO:0150077	regulation of neuroinflammatory response	41/18614	0.021814608	0.019544626
BP	GO:2000403	positive regulation of lymphocyte migration	41/18614	0.021814608	0.019544626
BP	GO:0043551	regulation of phosphatidylinositol 3-kinase activity	42/18614	0.022341278	0.019864853
BP	GO:0045622	regulation of T-helper cell differentiation	42/18614	0.022341278	0.019864853
BP	GO:0032735	positive regulation of interleukin-12 production	43/18614	0.022867694	0.019954982
BP	GO:0043507	positive regulation of JUN kinase activity	43/18614	0.022867694	0.019954982
BP	GO:0045663	positive regulation of myoblast differentiation	43/18614	0.022867694	0.019954982
BP	GO:0045687	positive regulation of glial cell differentiation	43/18614	0.022867694	0.019954982
BP	GO:0048713	regulation of oligodendrocyte differentiation	43/18614	0.022867694	0.019954982
BP	GO:0002764	immune response-regulating signaling pathway	450/18614	0.023078585	0.020064423
BP	GO:0009314	response to radiation	452/18614	0.023271052	0.020157097
BP	GO:0046640	regulation of alpha-beta T cell proliferation	44/18614	0.023393854	0.020188968
BP	GO:0030574	collagen catabolic process	45/18614	0.023919759	0.020417632
BP	GO:0097028	dendritic cell differentiation	45/18614	0.023919759	0.020417632
BP	GO:1902622	regulation of neutrophil migration	45/18614	0.023919759	0.020417632
BP	GO:0008038	neuron recognition	46/18614	0.02444541	0.020715662
BP	GO:0042088	T-helper 1 type immune response	46/18614	0.02444541	0.020715662
BP	GO:0016339	calcium-dependent cell-cell adhesion via plasma membrane cell	47/18614	0.024970805	0.020934171

		adhesion molecules			
BP	GO:0046633	alpha-beta T cell proliferation	47/18614	0.024970805	0.020934171
BP	GO:0090199	regulation of release of cytochrome c from mitochondria	47/18614	0.024970805	0.020934171
BP	GO:0035850	epithelial cell differentiation involved in kidney development	48/18614	0.025495946	0.021147837
BP	GO:0035987	endodermal cell differentiation	48/18614	0.025495946	0.021147837
BP	GO:2000404	regulation of T cell migration	48/18614	0.025495946	0.021147837
BP	GO:0033628	regulation of cell adhesion mediated by integrin	49/18614	0.026020833	0.021507212
BP	GO:0001819	positive regulation of cytokine production	489/18614	0.026953658	0.022106895
BP	GO:0045058	T cell selection	51/18614	0.027069842	0.022106895
BP	GO:1904707	positive regulation of vascular associated smooth muscle cell proliferation	51/18614	0.027069842	0.022106895
BP	GO:0002253	activation of immune response	495/18614	0.027572317	0.022106895
BP	GO:0043410	positive regulation of MAPK cascade	495/18614	0.027572317	0.022106895
BP	GO:0006968	cellular defense response	52/18614	0.027593965	0.022106895
BP	GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	52/18614	0.027593965	0.022106895
BP	GO:0046638	positive regulation of alpha-beta T cell differentiation	52/18614	0.027593965	0.022106895
BP	GO:0048013	ephrin receptor signaling pathway	52/18614	0.027593965	0.022106895
BP	GO:0048260	positive regulation of receptor-mediated endocytosis	53/18614	0.028117835	0.022298283
BP	GO:0050982	detection of mechanical stimulus	53/18614	0.028117835	0.022298283

BP	GO:00716 22	regulation of granulocyte chemotaxis	53/18614	0.0281178 35	0.0222982 83
BP	GO:00094 09	response to cold	54/18614	0.0286414 5	0.0223362 24
BP	GO:00308 57	negative regulation of epithelial cell differentiation	54/18614	0.0286414 5	0.0223362 24
BP	GO:00435 50	regulation of lipid kinase activity	54/18614	0.0286414 5	0.0223362 24
BP	GO:00466 86	response to cadmium ion	54/18614	0.0286414 5	0.0223362 24
BP	GO:19046 45	response to amyloid-beta	54/18614	0.0286414 5	0.0223362 24
BP	GO:00433 70	regulation of CD4-positive, alpha-beta T cell differentiation	55/18614	0.0291648 11	0.0226690 59
BP	GO:00019 54	positive regulation of cell-matrix adhesion	56/18614	0.0296879 19	0.0228486 83
BP	GO:00105 59	regulation of glycoprotein biosynthetic process	56/18614	0.0296879 19	0.0228486 83
BP	GO:00702 31	T cell apoptotic process	56/18614	0.0296879 19	0.0228486 83
BP	GO:00017 06	endoderm formation	57/18614	0.0302107 72	0.0228760 69
BP	GO:00075 66	embryo implantation	57/18614	0.0302107 72	0.0228760 69
BP	GO:00103 32	response to gamma radiation	57/18614	0.0302107 72	0.0228760 69
BP	GO:00433 88	positive regulation of DNA binding	57/18614	0.0302107 72	0.0228760 69
BP	GO:00617 56	leukocyte adhesion to vascular endothelial cell	57/18614	0.0302107 72	0.0228760 69
BP	GO:00018 36	release of cytochrome c from mitochondria	58/18614	0.0307333 73	0.0230487 38
BP	GO:00302 25	macrophage differentiation	58/18614	0.0307333 73	0.0230487 38
BP	GO:00610 05	cell differentiation involved in kidney development	58/18614	0.0307333 73	0.0230487 38
BP	GO:00019 61	positive regulation of cytokine-mediated signaling pathway	59/18614	0.0312557 19	0.0232179 39
BP	GO:00702	regulation of	59/18614	0.0312557	0.0232179

	28	lymphocyte apoptotic process		19	39
BP	GO:2001258	negative regulation of cation channel activity	59/18614	0.031255719	0.023217939
BP	GO:0022029	telencephalon cell migration	61/18614	0.032299653	0.023917724
BP	GO:0022617	extracellular matrix disassembly	62/18614	0.03282124	0.024001103
BP	GO:0043506	regulation of JUN kinase activity	62/18614	0.03282124	0.024001103
BP	GO:0090303	positive regulation of wound healing	62/18614	0.03282124	0.024001103
BP	GO:1903018	regulation of glycoprotein metabolic process	62/18614	0.03282124	0.024001103
BP	GO:0032623	interleukin-2 production	63/18614	0.033342574	0.024156576
BP	GO:0032663	regulation of interleukin-2 production	63/18614	0.033342574	0.024156576
BP	GO:0032731	positive regulation of interleukin-1 beta production	63/18614	0.033342574	0.024156576
BP	GO:0021885	forebrain cell migration	64/18614	0.033863655	0.024234901
BP	GO:0032615	interleukin-12 production	64/18614	0.033863655	0.024234901
BP	GO:0032655	regulation of interleukin-12 production	64/18614	0.033863655	0.024234901
BP	GO:0050918	positive chemotaxis	64/18614	0.033863655	0.024234901
BP	GO:1905330	regulation of morphogenesis of an epithelium	65/18614	0.034384483	0.024532842
BP	GO:0060760	positive regulation of response to cytokine stimulus	66/18614	0.034905059	0.024828798
BP	GO:0034605	cellular response to heat	67/18614	0.035425382	0.025122786
BP	GO:2000401	regulation of lymphocyte migration	68/18614	0.035945452	0.025414825
BP	GO:0014015	positive regulation of gliogenesis	69/18614	0.03646527	0.025627971
BP	GO:00420	T-helper cell	69/18614	0.0364652	0.0256279

	93	differentiation		7	71
BP	GO:00148 23	response to activity	70/18614	0.0369848 36	0.0259155 33
BP	GO:00022 94	CD4-positive, alpha-beta T cell differentiation involved in immune response	71/18614	0.0375041 49	0.0261234 59
BP	GO:00726 78	T cell migration	71/18614	0.0375041 49	0.0261234 59
BP	GO:00022 87	alpha-beta T cell activation involved in immune response	72/18614	0.0380232 11	0.0261743 36
BP	GO:00022 93	alpha-beta T cell differentiation involved in immune response	72/18614	0.0380232 11	0.0261743 36
BP	GO:00099 88	cell-cell recognition	72/18614	0.0380232 11	0.0261743 36
BP	GO:00716 77	positive regulation of mononuclear cell migration	72/18614	0.0380232 11	0.0261743 36
BP	GO:00466 37	regulation of alpha-beta T cell differentiation	73/18614	0.0385420 21	0.0264538 95
BP	GO:00327 32	positive regulation of interleukin-1 production	74/18614	0.0390605 78	0.0266539 44
BP	GO:00451 23	cellular extravasation	74/18614	0.0390605 78	0.0266539 44
BP	GO:00108 22	positive regulation of mitochondrion organization	75/18614	0.0395788 84	0.0268515 1
BP	GO:00420 58	regulation of epidermal growth factor receptor signaling pathway	75/18614	0.0395788 84	0.0268515 1
BP	GO:01500 76	neuroinflammatory response	76/18614	0.0400969 39	0.0270466 35
BP	GO:19030 36	positive regulation of response to wounding	76/18614	0.0400969 39	0.0270466 35
BP	GO:00327 29	positive regulation of type II interferon production	77/18614	0.0406147 42	0.0271617 56
BP	GO:00456 85	regulation of glial cell differentiation	77/18614	0.0406147 42	0.0271617 56
BP	GO:00508 53	B cell receptor signaling pathway	77/18614	0.0406147 42	0.0271617 56
BP	GO:00022	T cell differentiation	80/18614	0.0421666	0.0280398

	92	involved in immune response		43	43
BP	GO:00702 27	lymphocyte apoptotic process	80/18614	0.0421666 43	0.0280398 43
BP	GO:00508 48	regulation of calcium-mediated signaling	82/18614	0.0431999 88	0.0285651 51
BP	GO:19011 84	regulation of ERBB signaling pathway	82/18614	0.0431999 88	0.0285651 51
BP	GO:00074 92	endoderm development	83/18614	0.0437162 84	0.0287446 01
BP	GO:00508 71	positive regulation of B cell activation	83/18614	0.0437162 84	0.0287446 01
BP	GO:00330 77	T cell differentiation in thymus	86/18614	0.0452636 68	0.0296789 12
BP	GO:00085 89	regulation of smoothened signaling pathway	87/18614	0.0457789 62	0.0297673 38
BP	GO:00320 92	positive regulation of protein binding	87/18614	0.0457789 62	0.0297673 38
BP	GO:00336 27	cell adhesion mediated by integrin	87/18614	0.0457789 62	0.0297673 38
BP	GO:00324 13	negative regulation of ion transmembrane transporter activity	88/18614	0.0462940 05	0.0299363 87
BP	GO:00332 73	response to vitamin	88/18614	0.0462940 05	0.0299363 87
BP	GO:00433 67	CD4-positive, alpha-beta T cell differentiation	89/18614	0.0468087 99	0.0301861 25
BP	GO:00346 44	cellular response to UV	93/18614	0.0488654 72	0.0314261
BP	GO:19047 05	regulation of vascular associated smooth muscle cell proliferation	95/18614	0.0498923 1	0.0319988 07
CC	GO:00098 97	external side of plasma membrane	426/1951 8	2.04E-08	2.79E-07
CC	GO:00421 05	alpha-beta T cell receptor complex	12/19518	0.0061325 99	0.0375916 68
CC	GO:00057 70	late endosome	296/1951 8	0.0095183 3	0.0375916 68
CC	GO:00988 02	plasma membrane signaling receptor complex	319/1951 8	0.0109883 34	0.0375916 68
CC	GO:00017	immunological synapse	43/19518	0.0218187	0.0597145

	72			92	89
CC	GO:19047 24	tertiary granule lumen	55/19518	0.0278307 96	0.0634737 46
CC	GO:00057 71	multivesicular body	67/19518	0.0338095 25	0.0660938 08
MF	GO:00080 09	chemokine activity	49/18369	2.11E-06	5.78E-05
MF	GO:00423 79	chemokine receptor binding	74/18369	7.38E-06	0.0001009 9
MF	GO:00452 36	CXCR chemokine receptor binding	18/18369	4.06E-05	0.0003705 93
MF	GO:00051 25	cytokine activity	235/1836 9	0.0002321 39	0.0015883 21
MF	GO:00051 26	cytokine receptor binding	270/1836 9	0.0003491 3	0.0019110 29
MF	GO:00016 64	G protein-coupled receptor binding	289/1836 9	0.0004261 22	0.0019437 15
MF	GO:00480 18	receptor ligand activity	497/1836 9	0.0020499 15	0.0080147 06
MF	GO:00082 01	heparin binding	168/1836 9	0.0035657 14	0.0110971 44
MF	GO:00042 52	serine-type endopeptidase activity	170/1836 9	0.0036492 53	0.0110971 44
MF	GO:00082 36	serine-type peptidase activity	190/1836 9	0.0045348 13	0.0117504 7
MF	GO:00171 71	serine hydrolase activity	194/1836 9	0.0047227 85	0.0117504 7
MF	GO:00432 08	glycosphingolipid binding	10/18369	0.0054319 65	0.0123886 92
MF	GO:00426 08	T cell receptor binding	11/18369	0.0059736 98	0.0125762 07
MF	GO:00055 39	glycosaminoglycan binding	232/1836 9	0.0066856 3	0.0128747 77
MF	GO:00086 03	cAMP-dependent protein kinase regulator activity	13/18369	0.0070563 68	0.0128747 77
MF	GO:00704 92	oligosaccharide binding	15/18369	0.0081379 76	0.0139202 23
MF	GO:19016 81	sulfur compound binding	269/1836 9	0.0088973 02	0.0143238 3
MF	GO:00430 27	cysteine-type endopeptidase inhibitor activity involved in apoptotic process	21/18369	0.0113764 42	0.0163050 93

MF	GO:00199 56	chemokine binding	22/18369	0.0119152 61	0.0163050 93
MF	GO:00336 91	sialic acid binding	22/18369	0.0119152 61	0.0163050 93
MF	GO:00016 37	G protein-coupled chemoattractant receptor activity	25/18369	0.0135301 3	0.0168317 4
MF	GO:00049 50	chemokine receptor activity	25/18369	0.0135301 3	0.0168317 4
MF	GO:00466 25	sphingolipid binding	28/18369	0.0151426 23	0.0178802 38
MF	GO:00518 61	glycolipid binding	29/18369	0.0156795 93	0.0178802 38
MF	GO:00302 96	protein tyrosine kinase activator activity	34/18369	0.0183604 95	0.0200999 1
MF	GO:00420 56	chemoattractant activity	39/18369	0.0210348 23	0.0218298 32
MF	GO:00041 75	endopeptidase activity	428/1836 9	0.0215359 69	0.0218298 32
MF	GO:00430 28	cysteine-type endopeptidase regulator activity involved in apoptotic process	43/18369	0.0231695 63	0.0226469 41
MF	GO:00150 26	coreceptor activity	48/18369	0.0258320 95	0.0243787 47
MF	GO:00480 20	CCR chemokine receptor binding	50/18369	0.0268952 78	0.0245360 43
MF	GO:00301 59	signaling receptor complex adaptor activity	52/18369	0.0279574 16	0.0246822 69
MF	GO:00048 69	cysteine-type endopeptidase inhibitor activity	54/18369	0.0290185 11	0.0248184 63
MF	GO:00055 18	collagen binding	66/18369	0.0353632 18	0.0293283 47
MF	GO:00170 22	myosin binding	70/18369	0.0374698 13	0.0301614 6
MF	GO:00016 18	virus receptor activity	77/18369	0.0411463 95	0.0316793 94
MF	GO:01402 72	exogenous protein binding	78/18369	0.0416705 88	0.0316793 94
MF	GO:00355 91	signaling adaptor activity	83/18369	0.0442876 86	0.0327590 28
MF	GO:00048 96	cytokine receptor activity	92/18369	0.0489822 57	0.0351036 3

Table S5b. Analysis of KEGG.

ID	Description	GeneRatio	BgRatio	pvalue	qvalue
hsa04061	Viral protein interaction with cytokine and cytokine receptor	4 月 9 日	100/8772	1.92E-06	6.66E-05
hsa04060	Cytokine-cytokine receptor interaction	5 月 9 日	297/8772	4.85E-06	8.42E-05
hsa04062	Chemokine signaling pathway	4 月 9 日	192/8772	2.57E-05	0.000297831
hsa05340	Primary immunodeficiency	2 月 9 日	38/8772	0.00064538	0.005604618
hsa04657	IL-17 signaling pathway	2 月 9 日	94/8772	0.003894766	0.025079008
hsa04620	Toll-like receptor signaling pathway	2 月 9 日	108/8772	0.005110179	0.025079008
hsa04668	TNF signaling pathway	2 月 9 日	114/8772	0.005678351	0.025079008
hsa04670	Leukocyte transendothelial migration	2 月 9 日	115/8772	0.005775772	0.025079008
hsa05169	Epstein-Barr virus infection	2 月 9 日	202/8772	0.017076129	0.06500265
hsa05170	Human immunodeficiency virus 1 infection	2 月 9 日	212/8772	0.018712884	0.06500265
hsa05219	Bladder cancer	1 月 9 日	41/8772	0.041306215	0.13044068
hsa04672	Intestinal immune network for IgA production	1 月 9 日	49/8772	0.049186746	0.142382687

Appendix 6

Gene regulatory networks

Table 6. Gene regulatory networks.

Entity 1	Entity 2	Weight	Network group	Network	
CXCL9	CXCL10	0.027576016	Co-expression	Wang-Maris-2006	
CD79A	CD3E	0.021439591	Co-expression	Wang-Maris-2006	
GZMK	CD3E	0.018368779	Co-expression	Wang-Maris-2006	
GZMK	CXCL9	0.019503657	Co-expression	Wang-Maris-2006	
GZMK	CCL19	0.01618638	Co-expression	Wang-Maris-2006	
CD27	CD3E	0.012935489	Co-expression	Wang-Maris-2006	
CD27	CCL19	0.015270154	Co-expression	Wang-Maris-2006	
CD27	CD79A	0.014181419	Co-expression	Wang-Maris-2006	
CD27	GZMK	0.0131663	Co-expression	Wang-Maris-2006	
SELL	CD3E	0.014967633	Co-expression	Wang-Maris-2006	
SELL	CCL19	0.012926118	Co-expression	Wang-Maris-2006	
SELL	CD79A	0.017198157	Co-expression	Wang-Maris-2006	
SELL	GZMK	0.011555683	Co-expression	Wang-Maris-2006	
SELL	CD27	0.012249365	Co-expression	Wang-Maris-2006	
CXCL11	CXCL10	0.026501197	Co-expression	Wang-Maris-2006	
CXCL11	CXCL9	0.026518384	Co-expression	Wang-Maris-2006	
CD247	CD3E	0.018089892	Co-expression	Wang-Maris-2006	
CD247	CXCL9	0.013338995	Co-expression	Wang-Maris-2006	
CD247	CCL19	0.016162567	Co-expression	Wang-Maris-2006	
CD247	CD79A	0.014797314	Co-expression	Wang-Maris-2006	
CD247	GZMK	0.015650151	Co-expression	Wang-Maris-2006	
CD247	CD27	0.014280867	Co-expression	Wang-Maris-2006	
CD247	SELL	0.013930772	Co-expression	Wang-Maris-2006	
CD3D	CD3E	0.014366075	Co-expression	Wang-Maris-2006	
CD3D	CCL19	0.015589681	Co-expression	Wang-Maris-2006	
CD3D	CD79A	0.012305325	Co-expression	Wang-Maris-2006	
CD3D	GZMK	0.013261133	Co-expression	Wang-Maris-2006	
CD3D	CD27	0.012771437	Co-expression	Wang-Maris-2006	
CD3D	SELL	0.012642901	Co-expression	Wang-Maris-2006	
CD3D	CD247	0.014020314	Co-expression	Wang-Maris-2006	
CD3G	CCL19	0.0173163	Co-expression	Wang-Maris-2006	
CD3G	GZMK	0.016420906	Co-expression	Wang-Maris-2006	
CD3G	CD27	0.013918649	Co-expression	Wang-Maris-2006	
CD3G	SELL	0.014692183	Co-expression	Wang-Maris-2006	
CD3G	CD247	0.01678739	Co-expression	Wang-Maris-2006	

CD3G	CD3D	0.01538538	Co-expression	Wang-Maris-2006	
CCL21	CCL19	0.021823285	Co-expression	Wang-Maris-2006	
CCL21	CD79A	0.019763695	Co-expression	Wang-Maris-2006	
CCL21	CD27	0.014475848	Co-expression	Wang-Maris-2006	
CCL21	SELL	0.01321316	Co-expression	Wang-Maris-2006	
CCL21	CD247	0.013920764	Co-expression	Wang-Maris-2006	
CCL21	CD3D	0.01371663	Co-expression	Wang-Maris-2006	
CCL21	CD3G	0.015954554	Co-expression	Wang-Maris-2006	
CCL5	CXCL10	0.018103655	Co-expression	Wang-Maris-2006	
CCL5	CXCL9	0.027344452	Co-expression	Wang-Maris-2006	
CCL5	GZMK	0.025909867	Co-expression	Wang-Maris-2006	
CCL5	CD27	0.014444218	Co-expression	Wang-Maris-2006	
CCL5	CD247	0.015168726	Co-expression	Wang-Maris-2006	
CCL5	CD3D	0.012679914	Co-expression	Wang-Maris-2006	
GZMA	CXCL10	0.019231252	Co-expression	Wang-Maris-2006	
GZMA	CXCL9	0.023870775	Co-expression	Wang-Maris-2006	
GZMA	GZMK	0.023087377	Co-expression	Wang-Maris-2006	
GZMA	CXCL11	0.018522426	Co-expression	Wang-Maris-2006	
GZMA	CD247	0.015348025	Co-expression	Wang-Maris-2006	
GZMA	CD3D	0.01236316	Co-expression	Wang-Maris-2006	
GZMA	CD3G	0.016516253	Co-expression	Wang-Maris-2006	
GZMA	CCL5	0.02838688	Co-expression	Wang-Maris-2006	
CD79B	CD3E	0.013525307	Co-expression	Wang-Maris-2006	
CD79B	CCL19	0.013857274	Co-expression	Wang-Maris-2006	
CD79B	CD79A	0.015250171	Co-expression	Wang-Maris-2006	
CD79B	GZMK	0.013223798	Co-expression	Wang-Maris-2006	
CD79B	CD27	0.011824127	Co-expression	Wang-Maris-2006	
CD79B	SELL	0.011457166	Co-expression	Wang-Maris-2006	
CD79B	CD247	0.011875679	Co-expression	Wang-Maris-2006	
CD79B	CD3D	0.011595935	Co-expression	Wang-Maris-2006	
CD79B	CD3G	0.01361335	Co-expression	Wang-Maris-2006	
CD79B	CCL21	0.014791765	Co-expression	Wang-Maris-2006	
IL2RB	CXCL10	0.013703891	Co-expression	Wang-Maris-2006	
IL2RB	CXCL9	0.016718296	Co-expression	Wang-Maris-2006	
IL2RB	CCL19	0.013936936	Co-expression	Wang-Maris-2006	
IL2RB	CD79A	0.013337142	Co-expression	Wang-Maris-2006	
IL2RB	GZMK	0.015422817	Co-expression	Wang-Maris-2006	
IL2RB	CD27	0.011741382	Co-expression	Wang-Maris-2006	
IL2RB	CXCL11	0.014288055	Co-expression	Wang-Maris-2006	
IL2RB	CD247	0.012748633	Co-expression	Wang-Maris-2006	
IL2RB	CD3D	0.01048073	Co-expression	Wang-Maris-2006	
IL2RB	CD3G	0.012482227	Co-expression	Wang-Maris-2006	
IL2RB	CCL21	0.012403141	Co-expression	Wang-Maris-2006	

IL2RB	CCL5	0.019566258	Co-expression	Wang-Maris-2006	
IL2RB	GZMA	0.017791316	Co-expression	Wang-Maris-2006	
IL2RB	CD79B	0.010506865	Co-expression	Wang-Maris-2006	
JCHAIN	CXCL10	0.020036617	Co-expression	Wang-Maris-2006	
JCHAIN	CXCL9	0.0279185	Co-expression	Wang-Maris-2006	
JCHAIN	GZMK	0.01665866	Co-expression	Wang-Maris-2006	
JCHAIN	CD27	0.013539185	Co-expression	Wang-Maris-2006	
JCHAIN	CXCL11	0.019893775	Co-expression	Wang-Maris-2006	
JCHAIN	CCL5	0.023211485	Co-expression	Wang-Maris-2006	
JCHAIN	GZMA	0.019462738	Co-expression	Wang-Maris-2006	
JCHAIN	IL2RB	0.015805462	Co-expression	Wang-Maris-2006	
LCK	CD3E	0.02422701	Co-expression	Wang-Maris-2006	
LCK	GZMK	0.017062789	Co-expression	Wang-Maris-2006	
LCK	CD27	0.013427493	Co-expression	Wang-Maris-2006	
LCK	SELL	0.015817083	Co-expression	Wang-Maris-2006	
LCK	CD247	0.016365878	Co-expression	Wang-Maris-2006	
LCK	CD3D	0.015217649	Co-expression	Wang-Maris-2006	
LCK	CD3G	0.018914921	Co-expression	Wang-Maris-2006	
LCK	CCL21	0.015454858	Co-expression	Wang-Maris-2006	
LCK	CD79B	0.013343019	Co-expression	Wang-Maris-2006	
TRAT1	CD3E	0.02222182	Co-expression	Wang-Maris-2006	
TRAT1	CCL19	0.018833844	Co-expression	Wang-Maris-2006	
TRAT1	GZMK	0.020280179	Co-expression	Wang-Maris-2006	
TRAT1	CD27	0.016940014	Co-expression	Wang-Maris-2006	
TRAT1	SELL	0.015261708	Co-expression	Wang-Maris-2006	
TRAT1	CD247	0.017527852	Co-expression	Wang-Maris-2006	
TRAT1	CD3D	0.016620098	Co-expression	Wang-Maris-2006	
TRAT1	CD79B	0.015078186	Co-expression	Wang-Maris-2006	
TRAT1	IL2RB	0.015981173	Co-expression	Wang-Maris-2006	
STAT1	CXCL10	0.02325975	Co-expression	Wang-Maris-2006	
STAT1	CXCL9	0.016688563	Co-expression	Wang-Maris-2006	
STAT1	CXCL11	0.022227637	Co-expression	Wang-Maris-2006	
CD8A	CD3E	0.018285612	Co-expression	Wang-Maris-2006	
CD8A	CCL19	0.02101431	Co-expression	Wang-Maris-2006	
CD8A	GZMK	0.02185485	Co-expression	Wang-Maris-2006	
CD8A	CD27	0.014954403	Co-expression	Wang-Maris-2006	
CD8A	SELL	0.012468442	Co-expression	Wang-Maris-2006	
CD8A	CD247	0.0166262	Co-expression	Wang-Maris-2006	
CD8A	CD3D	0.015746549	Co-expression	Wang-Maris-2006	
CD8A	CD3G	0.020871136	Co-expression	Wang-Maris-2006	
CD8A	CCL5	0.02117148	Co-expression	Wang-Maris-2006	
CD8A	GZMA	0.020244474	Co-expression	Wang-Maris-2006	
CD8A	CD79B	0.012455688	Co-expression	Wang-Maris-2006	

CD8A	IL2RB	0.014109829	Co-expression	Wang-Maris-2006	
CD8A	LCK	0.018337116	Co-expression	Wang-Maris-2006	
CD8A	TRAT1	0.022471936	Co-expression	Wang-Maris-2006	
CD69	CD3E	0.014316722	Co-expression	Wang-Maris-2006	
CD69	GZMK	0.014708173	Co-expression	Wang-Maris-2006	
CD69	CD27	0.01076655	Co-expression	Wang-Maris-2006	
CD69	SELL	0.011809817	Co-expression	Wang-Maris-2006	
CD69	CD247	0.011783074	Co-expression	Wang-Maris-2006	
CD69	CD3D	0.011823009	Co-expression	Wang-Maris-2006	
CD69	CD79B	0.01155238	Co-expression	Wang-Maris-2006	
CD69	LCK	0.016217548	Co-expression	Wang-Maris-2006	
CD69	TRAT1	0.018672219	Co-expression	Wang-Maris-2006	
CD69	CD8A	0.014725908	Co-expression	Wang-Maris-2006	
POU2AF1	CXCL9	0.01389945	Co-expression	Wang-Maris-2006	
POU2AF1	CD79A	0.01867383	Co-expression	Wang-Maris-2006	
POU2AF1	GZMK	0.01404518	Co-expression	Wang-Maris-2006	
POU2AF1	CD27	0.014423166	Co-expression	Wang-Maris-2006	
POU2AF1	SELL	0.013048315	Co-expression	Wang-Maris-2006	
POU2AF1	CD247	0.012956338	Co-expression	Wang-Maris-2006	
POU2AF1	CD3D	0.012815938	Co-expression	Wang-Maris-2006	
POU2AF1	CD3G	0.014711105	Co-expression	Wang-Maris-2006	
POU2AF1	CCL21	0.016466102	Co-expression	Wang-Maris-2006	
POU2AF1	CD79B	0.014267252	Co-expression	Wang-Maris-2006	
POU2AF1	IL2RB	0.012099805	Co-expression	Wang-Maris-2006	
POU2AF1	JCHAIN	0.021014862	Co-expression	Wang-Maris-2006	
POU2AF1	LCK	0.015686626	Co-expression	Wang-Maris-2006	
POU2AF1	TRAT1	0.01564035	Co-expression	Wang-Maris-2006	
POU2AF1	CD69	0.012631361	Co-expression	Wang-Maris-2006	
LTB	CD3E	0.015938375	Co-expression	Wang-Maris-2006	
LTB	CCL19	0.022825314	Co-expression	Wang-Maris-2006	
LTB	CD79A	0.015025198	Co-expression	Wang-Maris-2006	
LTB	GZMK	0.014647751	Co-expression	Wang-Maris-2006	
LTB	CD27	0.015872363	Co-expression	Wang-Maris-2006	
LTB	SELL	0.015226449	Co-expression	Wang-Maris-2006	
LTB	CD247	0.01784119	Co-expression	Wang-Maris-2006	
LTB	CD3D	0.01576144	Co-expression	Wang-Maris-2006	
LTB	CD3G	0.017507473	Co-expression	Wang-Maris-2006	
LTB	CCL21	0.017839	Co-expression	Wang-Maris-2006	
LTB	CD79B	0.013292138	Co-expression	Wang-Maris-2006	
LTB	IL2RB	0.013491571	Co-expression	Wang-Maris-2006	
LTB	LCK	0.015201217	Co-expression	Wang-Maris-2006	
LTB	TRAT1	0.020525305	Co-expression	Wang-Maris-2006	
LTB	CD8A	0.01831065	Co-expression	Wang-Maris-2006	

LTB	POU2AF1	0.013377057	Co-expression	Wang-Maris-2006	
ITGAL	CXCL10	0.009573601	Co-expression	Wang-Maris-2006	
ITGAL	CD3E	0.012041593	Co-expression	Wang-Maris-2006	
ITGAL	CXCL9	0.010405866	Co-expression	Wang-Maris-2006	
ITGAL	CCL19	0.010053695	Co-expression	Wang-Maris-2006	
ITGAL	CD79A	0.011535995	Co-expression	Wang-Maris-2006	
ITGAL	GZMK	0.011683311	Co-expression	Wang-Maris-2006	
ITGAL	CD27	0.009522268	Co-expression	Wang-Maris-2006	
ITGAL	SELL	0.009812091	Co-expression	Wang-Maris-2006	
ITGAL	CXCL11	0.010504913	Co-expression	Wang-Maris-2006	
ITGAL	CD247	0.0107134	Co-expression	Wang-Maris-2006	
ITGAL	CD3D	0.009306426	Co-expression	Wang-Maris-2006	
ITGAL	CD3G	0.011739682	Co-expression	Wang-Maris-2006	
ITGAL	CCL21	0.010620886	Co-expression	Wang-Maris-2006	
ITGAL	CCL5	0.0128287	Co-expression	Wang-Maris-2006	
ITGAL	GZMA	0.013379218	Co-expression	Wang-Maris-2006	
ITGAL	CD79B	0.009271394	Co-expression	Wang-Maris-2006	
ITGAL	IL2RB	0.01027069	Co-expression	Wang-Maris-2006	
ITGAL	JCHAIN	0.010073965	Co-expression	Wang-Maris-2006	
ITGAL	LCK	0.011761925	Co-expression	Wang-Maris-2006	
ITGAL	TRAT1	0.011878272	Co-expression	Wang-Maris-2006	
ITGAL	STAT1	0.009283154	Co-expression	Wang-Maris-2006	
ITGAL	CD8A	0.011453235	Co-expression	Wang-Maris-2006	
ITGAL	CD69	0.009099326	Co-expression	Wang-Maris-2006	
ITGAL	POU2AF1	0.01066261	Co-expression	Wang-Maris-2006	
ITGAL	LTB	0.010553623	Co-expression	Wang-Maris-2006	
CXCL9	CXCL10	0.016749116	Co-expression	Ramaswamy-Golub-2001	
CCL19	CXCL9	0.017374769	Co-expression	Ramaswamy-Golub-2001	
MMP9	CXCL10	0.015973877	Co-expression	Ramaswamy-Golub-2001	
MMP9	CXCL9	0.013855047	Co-expression	Ramaswamy-Golub-2001	
MMP9	CCL19	0.018014994	Co-expression	Ramaswamy-Golub-2001	
CD79A	CXCR4	0.013466583	Co-expression	Ramaswamy-Golub-2001	
GZMK	CXCL9	0.021979468	Co-expression	Ramaswamy-Golub-2001	
GZMK	CCL19	0.023908323	Co-expression	Ramaswamy-Golub-2001	
GZMK	MMP9	0.014100867	Co-expression	Ramaswamy-Golub-2001	

Appendix 7

MiRNA and LncRNA

Table 8a. Gene-miRNA.

Gene	miRNA	miRanda	miRDB	TargetScan	Sum
CXCR4	hsa-miR-622	1	1	1	3
CXCL9	hsa-miR-146a-3p	1	1	1	3
GZMK	hsa-miR-3163	1	1	1	3
SELL	hsa-miR-92a-2-5p	1	1	1	3
CXCR4	hsa-miR-548d-3p	1	1	1	3
GZMK	hsa-miR-145-3p	1	1	1	3
MMP9	hsa-miR-3065-5p	1	1	1	3
GZMK	hsa-miR-499a-3p	1	1	1	3
CXCL10	hsa-miR-4291	1	1	1	3
CD79A	hsa-miR-486-3p	1	1	1	3
CXCL9	hsa-miR-4321	1	1	1	3
CXCR4	hsa-miR-139-5p	1	1	1	3
CXCL9	hsa-miR-4307	1	1	1	3
CXCL10	hsa-miR-570-3p	1	1	1	3
CXCL10	hsa-miR-3153	1	1	1	3
CXCL9	hsa-miR-9-5p	1	1	1	3
CXCR4	hsa-miR-548a-3p	1	1	1	3
CD79A	hsa-miR-661	1	1	1	3
CXCL9	hsa-miR-297	1	1	1	3
CXCL10	hsa-miR-27b-5p	1	1	1	3
CXCL10	hsa-miR-4252	1	1	1	3
SELL	hsa-miR-3190-3p	1	1	1	3
CXCL9	hsa-miR-185-5p	1	1	1	3
CD79A	hsa-miR-663b	1	1	1	3
CXCL9	hsa-miR-452-5p	1	1	1	3
SELL	hsa-miR-1276	1	1	1	3
CXCR4	hsa-miR-548g-3p	1	1	1	3
CXCL9	hsa-miR-2052	1	1	1	3
CD27	hsa-miR-214-3p	1	1	1	3
CXCR4	hsa-miR-206	1	1	1	3
CD3E	hsa-miR-582-5p	1	1	1	3
CXCL9	hsa-miR-381-3p	1	1	1	3
CXCL9	hsa-miR-3188	1	1	1	3

SELL	hsa-miR-186-5p	1	1	1	3
SELL	hsa-miR-3126-5p	1	1	1	3
CXCL9	hsa-miR-4289	1	1	1	3
CD27	hsa-miR-3199	1	1	1	3
CD79A	hsa-miR-1915-3p	1	1	1	3
CXCR4	hsa-miR-613	1	1	1	3
CD3E	hsa-miR-2355-5p	1	1	1	3
CD27	hsa-miR-1291	1	1	1	3
CXCL10	hsa-miR-30b-3p	1	1	1	3
CXCL9	hsa-miR-320e	1	1	1	3
CD3E	hsa-miR-615-5p	1	1	1	3
CXCL10	hsa-miR-1276	1	1	1	3
SELL	hsa-miR-204-5p	1	1	1	3
SELL	hsa-miR-1236-3p	1	1	1	3
CD3E	hsa-miR-424-5p	1	1	1	3
CXCL10	hsa-miR-411-3p	1	1	1	3
GZMK	hsa-miR-379-5p	1	1	1	3
SELL	hsa-miR-211-5p	1	1	1	3
CXCL9	hsa-miR-331-3p	1	1	1	3
CXCL10	hsa-miR-296-5p	1	1	1	3
CD79A	hsa-miR-4266	1	1	1	3
CXCL9	hsa-miR-205-3p	1	1	1	3
MMP9	hsa-miR-149-5p	1	1	1	3
CD79A	hsa-miR-637	1	1	1	3
CXCL9	hsa-miR-3190-3p	1	1	1	3
CXCR4	hsa-miR-3120-3p	1	1	1	3
CD27	hsa-miR-509-5p	1	1	1	3
CD79A	hsa-miR-1275	1	1	1	3
CXCL9	hsa-miR-671-5p	1	1	1	3
CXCL10	hsa-let-7g-3p	1	1	1	3
SELL	hsa-miR-4289	1	1	1	3
CXCL9	hsa-miR-607	1	1	1	3
SELL	hsa-miR-570-3p	1	1	1	3
CXCL9	hsa-miR-4267	1	1	1	3
CXCR4	hsa-miR-373-3p	1	1	1	3
CD79A	hsa-miR-1291	1	1	1	3
CXCL9	hsa-miR-103b	1	1	1	3
CXCL9	hsa-miR-551b-5p	1	1	1	3
CXCL9	hsa-miR-4316	1	1	1	3
CXCL9	hsa-miR-4329	1	1	1	3
CXCR4	hsa-miR-185-5p	1	1	1	3
CD3E	hsa-miR-497-5p	1	1	1	3
SELL	hsa-miR-4279	1	1	1	3

SELL	hsa-miR-1909-3p	1	1	1	3
CXCR4	hsa-miR-1-3p	1	1	1	3
CXCL9	hsa-miR-548g-3p	1	1	1	3
CXCR4	hsa-miR-302c-5p	1	1	1	3
CXCL10	hsa-miR-646	1	1	1	3
CXCL9	hsa-miR-30c-2-3p	1	1	1	3
CD3E	hsa-miR-195-5p	1	1	1	3
MMP9	hsa-miR-3123	1	1	1	3
CXCL10	hsa-miR-135b-3p	1	1	1	3
SELL	hsa-miR-143-3p	1	1	1	3
CD3E	hsa-miR-16-5p	1	1	1	3
CXCL10	hsa-miR-155-3p	1	1	1	3
SELL	hsa-miR-575	1	1	1	3
CD3E	hsa-miR-221-5p	1	1	1	3
CXCL9	hsa-miR-4320	1	1	1	3
GZMK	hsa-miR-590-3p	1	1	1	3
CXCR4	hsa-miR-9-5p	1	1	1	3
CXCR4	hsa-miR-548x-3p	1	1	1	3
GZMK	hsa-miR-634	1	1	1	3
CXCL10	hsa-miR-297	1	1	1	3
CD79A	hsa-miR-885-3p	1	1	1	3
CXCL9	hsa-miR-3153	1	1	1	3
CD79A	hsa-miR-625-5p	1	1	1	3
CXCL10	hsa-miR-379-3p	1	1	1	3
CD3E	hsa-miR-4278	1	1	1	3
GZMK	hsa-miR-3148	1	1	1	3
CXCL9	hsa-miR-4330	1	1	1	3
CXCL9	hsa-miR-92a-1-5p	1	1	1	3
CD27	hsa-miR-509-3-5p	1	1	1	3
CXCL9	hsa-miR-2115-5p	1	1	1	3
CXCL9	hsa-miR-543	1	1	1	3
SELL	hsa-miR-637	1	1	1	3
CXCL9	hsa-miR-1293	1	1	1	3
CXCR4	hsa-miR-3135a	1	1	1	3
SELL	hsa-miR-423-5p	1	1	1	3
CD3E	hsa-miR-3202	1	1	1	3
CXCL10	hsa-let-7a-2-3p	1	1	1	3
CD27	hsa-miR-193a-5p	1	1	1	3
CXCL9	hsa-miR-624-3p	1	1	1	3
CXCR4	hsa-miR-588	1	1	1	3
CXCL9	hsa-miR-3174	1	1	1	3
CXCL9	hsa-miR-573	1	1	1	3
GZMK	hsa-miR-711	1	1	1	3

CXCL9	hsa-miR-16-1-3p	1	1	1	3
CXCL10	hsa-miR-4251	1	1	1	3
GZMK	hsa-miR-4276	1	1	1	3
CXCL9	hsa-miR-4255	1	1	1	3
CXCL9	hsa-miR-33a-3p	1	1	1	3
SELL	hsa-miR-4325	1	1	1	3
CXCL9	hsa-miR-300	1	1	1	3
CXCR4	hsa-miR-4282	1	1	1	3
CD3E	hsa-miR-485-5p	1	1	1	3
CXCL10	hsa-miR-466	1	1	1	3
SELL	hsa-miR-3157-5p	1	1	1	3
SELL	hsa-miR-105-5p	1	1	1	3
CD3E	hsa-miR-1207-5p	1	1	1	3
SELL	hsa-miR-4261	1	1	1	3
CD3E	hsa-miR-4270	1	1	1	3

Table 8b. Gene-lncRNA.

miRNA	lncRNA
hsa-miR-615-5p	MUC2
hsa-miR-570-3p	RP11-10J21.4
hsa-miR-221-5p	LINC01043
hsa-miR-214-3p	LA16c-306A4.2
hsa-miR-92a-1-5p	MUC2
hsa-miR-671-5p	RP5-894D12.5
hsa-miR-671-5p	RP1-34P24.3
hsa-miR-221-5p	RP5-894D12.5
hsa-miR-615-5p	PAX8-AS1
hsa-miR-30b-3p	C10orf91
hsa-miR-423-5p	C10orf91
hsa-miR-149-5p	LINC01043
hsa-miR-193a-5p	MUC2
hsa-miR-1-3p	LINC01043
hsa-miR-146a-3p	FAM74A1
hsa-miR-146a-3p	RP11-830F9.6
hsa-miR-486-3p	C10orf91
hsa-miR-193a-5p	CTB-60B18.18
hsa-miR-185-5p	CTC-265F19.1
hsa-miR-423-5p	PAX8-AS1
hsa-miR-185-5p	AC092657.2
hsa-miR-186-5p	RP11-99L13.2
hsa-miR-296-5p	RP11-14P20.1
hsa-miR-146a-3p	FAM74A7
hsa-miR-221-5p	LL22NC03-2H8.4
hsa-miR-624-3p	RP11-333E1.2
hsa-miR-499a-3p	RP4-737E23.2
hsa-miR-2355-5p	RP11-54O7.17
hsa-miR-146a-3p	FAM74A6
hsa-miR-214-3p	RP4-539M6.22
hsa-miR-185-5p	AATBC
hsa-miR-624-3p	AC011718.2
hsa-miR-543	RP11-429B14.4
hsa-miR-186-5p	MIR325HG
hsa-miR-1207-5p	C10orf91
hsa-miR-625-5p	RP11-394A14.2
hsa-miR-1207-5p	RP11-618K13.2
hsa-miR-92a-1-5p	RP11-13K12.1
hsa-miR-423-5p	RP11-627G23.1
hsa-miR-1236-3p	RP11-717I24.1
hsa-miR-622	RP13-507P19.2

hsa-miR-149-5p	RP11-394A14.2
hsa-miR-30b-3p	MUC2
hsa-miR-625-5p	AATBC
hsa-miR-1207-5p	LINC00265
hsa-miR-1207-5p	RP11-333E1.2
hsa-miR-625-5p	RP3-470B24.5
hsa-miR-193a-5p	HCG22
hsa-miR-622	CTC-459F4.1
hsa-miR-499a-3p	RP11-210M15.1
hsa-miR-486-3p	RP11-94C24.13
hsa-miR-1207-5p	AP001476.4
hsa-miR-1207-5p	RP4-539M6.22
hsa-miR-185-5p	RP11-384K6.6
hsa-miR-499a-3p	FAM182A
hsa-miR-671-5p	CTD-2561B21.7
hsa-miR-185-5p	FLJ35934
hsa-miR-1-3p	RP3-470B24.5
hsa-miR-625-5p	LINC00173
hsa-miR-663b	RP11-54O7.17
hsa-miR-615-5p	COL4A2-AS2
hsa-miR-885-3p	LINC00689
hsa-miR-499a-3p	CH507-216K13.2
hsa-miR-1236-3p	LINC00689
hsa-miR-885-3p	RP4-697K14.15
hsa-miR-16-1-3p	CTD-3099C6.5
hsa-miR-1236-3p	LINC00940
hsa-miR-186-5p	LINC00613
hsa-miR-671-5p	RP5-1029F21.3
hsa-miR-185-5p	RP11-269G24.6
hsa-miR-423-5p	FLJ35934
hsa-miR-671-5p	RP11-762H8.5
hsa-miR-297	CTA-929C8.6
hsa-miR-1207-5p	RP11-680F20.6
hsa-miR-30b-3p	LINCMD1
hsa-miR-186-5p	DYX1C1-CCPG1
hsa-miR-30b-3p	RP11-153F5.7
hsa-miR-625-5p	AC006019.3
hsa-miR-214-3p	TTLL10-AS1
hsa-miR-145-3p	AC011284.3
hsa-let-7a-2-3p	AC011718.2
hsa-miR-214-3p	AC015849.16
hsa-miR-1207-5p	RP11-867G23.4
hsa-miR-30b-3p	AC011284.3

hsa-miR-214-3p	TMEM9B-AS1
hsa-miR-186-5p	RP11-154D6.1
hsa-miR-185-5p	CTA-280A3.2
hsa-miR-139-5p	AC015849.16
hsa-miR-185-5p	RP11-159D12.10
hsa-miR-186-5p	RP11-22A3.2
hsa-miR-590-3p	LINC00240
hsa-miR-185-5p	LINC00265
hsa-miR-221-5p	RP11-244H3.1
hsa-miR-186-5p	SFTPD-AS1
hsa-miR-423-5p	SRRM2-AS1
hsa-miR-1207-5p	LINC00969
hsa-miR-615-5p	RP11-32B5.8
hsa-miR-423-5p	RP11-14P20.1
hsa-miR-16-1-3p	RP11-50B3.4
hsa-miR-625-5p	RP11-186N15.3
hsa-miR-146a-3p	LINC00689
hsa-miR-1207-5p	H19
hsa-miR-1207-5p	RP5-1142A6.2
hsa-miR-423-5p	RP11-186N15.3
hsa-miR-590-3p	AC005614.3
hsa-miR-625-5p	VPS9D1-AS1
hsa-miR-331-3p	RP11-44M6.7
hsa-miR-543	AC113607.3
hsa-miR-1236-3p	RP11-798K23.1
hsa-miR-139-5p	RP11-231D20.2
hsa-miR-499a-3p	ZNF883
hsa-miR-30b-3p	TTLL10-AS1
hsa-miR-615-5p	RP11-54O7.17
hsa-miR-1236-3p	RP11-91K11.2
hsa-miR-885-3p	LINC01070
hsa-miR-2355-5p	RP11-161M6.2
hsa-miR-30b-3p	RP11-94C24.13
hsa-miR-885-3p	CTA-390C10.9
hsa-miR-1236-3p	RP11-23J9.4
hsa-miR-590-3p	RP11-762H8.4
hsa-miR-186-5p	RP1-288H2.2
hsa-miR-485-5p	AP001626.2
hsa-miR-214-3p	CTC-242N15.1
hsa-miR-296-5p	LINC00896
hsa-miR-671-5p	LINC00689
hsa-miR-186-5p	AC124997.1
hsa-miR-149-5p	CTD-2008P7.3

hsa-miR-1207-5p	LINC01168
hsa-miR-1-3p	GNG12-AS1
hsa-miR-590-3p	AC006548.28
hsa-miR-30b-3p	RP11-244B22.11
hsa-miR-590-3p	AC093639.1
hsa-miR-1207-5p	AC000095.11
hsa-miR-485-5p	LINC00265
hsa-miR-214-3p	NR2F1-AS1
hsa-miR-625-5p	RP11-394A14.4
hsa-miR-186-5p	CTD-2410N18.4
hsa-miR-214-3p	CTC-321K16.1
hsa-miR-186-5p	AJ003147.8
hsa-miR-296-5p	C1QTNF9B-AS1
hsa-miR-2355-5p	LA16c-306A4.2
hsa-miR-9-5p	RP11-397O4.1
hsa-miR-186-5p	CTD-3046C4.1
hsa-miR-186-5p	RP11-227H15.4
hsa-miR-297	AC084219.4
hsa-miR-185-5p	SSTR5-AS1
hsa-miR-885-3p	TTLL10-AS1
hsa-miR-186-5p	LINC00662
hsa-miR-423-5p	RP11-394A14.2
hsa-miR-590-3p	CTD-2561J22.5
hsa-miR-30b-3p	RP11-480I12.10
hsa-miR-186-5p	CTB-181F24.1
hsa-miR-485-5p	RP11-384K6.6
hsa-miR-486-3p	RP4-539M6.22
hsa-miR-485-5p	AC138035.2
hsa-miR-590-3p	LA16c-60D12.2
hsa-miR-185-5p	RP11-458F8.4
hsa-miR-1207-5p	MIRLET7BHG
hsa-miR-214-3p	LINC01304
hsa-miR-186-5p	SNHG14
hsa-miR-590-3p	RP11-638L3.1
hsa-miR-423-5p	HP09025
hsa-miR-509-3-5p	RP3-470B24.5
hsa-miR-92a-2-5p	CTD-2619J13.14
hsa-miR-143-3p	LL22NC03-2H8.5

