

Supplementary Table1. The 32 Immune-related genes

GSE20907	logFC	GSE45006	logFC	Merged
(54genes)		(246genes)		(32genes)
Cxcl10	-1.2787665	Tnfrsf12a	6.342416075	Agt
Fabp3	-0.8533805	S100a8	6.449887975	Fabp3
S1pr1	-0.7049235	Vgf	3.927269	S1pr1
Crabp1	-0.69395625	Ifitm1	6.471016775	Lgmn
Htr1a	-0.643363	Ccl2	10.75071248	Fcer1g
Agt	-0.62975975	Slpi	9.1036857	Plxnb2
S100a10	0.59725275	S100a9	8.47528155	Grn
Ctsb	0.60175125	Lcn2	9.03615005	Ctsb
Tlr4	0.608656	Procr	3.20508845	Tyrobp
Masp1	0.62046025	S100a11	4.041319925	Lyn
Igfl	0.6614585	Cd14	7.99560965	Vim
Lgmn	0.684163	Il33	3.256177175	Ptprc
Ptpn6	0.7164675	Ccl7	8.50031865	Ifi30
Tnfrsf1a	0.71673475	Nfkbiz	1.801046125	S100a6
Cxcl14	0.745693	S100a10	2.48176325	Stat3
Lbp	0.75857	Psme2	1.201062675	Tlr4
Lyn	0.76091125	Hck	5.20229815	Tlr2
Btk	0.764564	Fgf11	1.293145275	Tnfrsf1a
Fcer1g	0.764785	Sema6d	-1.689940475	Lcp2
Csfl	0.7719825	Il1rap	3.08946795	Gmfg
Fas	0.77857625	Hbegf	4.629345175	Ptpn6
Plxnb2	0.808006	Sdc1	4.3658326	Pf4
Stat3	0.89481825	Psmid8	1.414512075	S100a10
Ifngr1	0.904202	Agt	-2.04543665	Cybb
Tyrobp	0.91357225	Plaur	2.063822875	C3ar1
Blnk	0.927294	Cxcl1	3.847685925	Fcgr2b
Cd14	0.93145425	Ppp4c	1.188742675	Fcgr3a
Il7r	0.95615475	Fgf9	-2.438577775	S100a11
Cd48	0.96100275	Nr3c2	-2.034369475	Hmox1
Csf2rb	0.976506	Il17ra	2.291617925	Cd14
Pf4	0.97877625	Trh	4.891422575	Lcn2
Grn	1.0047535	Il4r	2.839389625	Ccl2
Gmfg	1.00501475	Ctsl	1.809824375	
C3ar1	1.04268	S1pr1	-0.91352675	
Fcgr3a	1.04685875	Psmid13	1.294113425	
Calca	1.050444	Manf	1.069527225	
Lcp2	1.07543225	Psmid4	0.691910525	
Tlr2	1.081872	Fabp4	4.7274115	
Ptprc	1.146709	Cntf	0.869650475	
S100a11	1.16122675	Ccr1	4.40856085	
Ifi30	1.17754575	Tinag11	4.3139559	
Csflr	1.1874865	Plscr1	0.807753725	
Cd4	1.2452205	Apln	2.809090775	
Hmox1	1.28778375	Aimp1	1.174861525	
S100a6	1.33800075	Trim27	1.3381952	
C3	1.35432925	Akt3	-1.113971575	
Tlr7	1.4228225	Fos	1.605887625	
Cybb	1.55334625	Tnfrsf1a	2.08701965	

Fcgr2b	1.6608785	Psmc3	0.747
Vim	1.7911145	Hmox1	7.922289275
Ccl2	1.81522025	Ogfr	0.789169775
Lcn2	1.8365455	Fabp3	-1.82476425
Hest	2.01355625	Gmfg	2.169749125
Cxcl13	2.27547575	Cdk4	1.651369575
		Igf1	-4.3842781
		Map2k2	0.765441725
		Fabp5	1.096780225
		Rbp4	-5.06851475
		Plau	3.26074835
		Nfatc2	-0.8194059
		Socs3	4.6727609
		Lgmn	0.7774691
		Ndrg1	-1.466900875
		Ifngr2	1.341651325
		Psmd7	0.6098554
		Kitlg	0.95636095
		Jun	1.60644515
		Sema3b	-1.6571691
		Nfkbib	1.217195675
		Sort1	-1.09392505
		Stat3	1.7934193
		Bid	0.8699807
		Csk	0.8512712
		Fgfl2	-0.9194011
		Nr2f1	-0.97389495
		Pgr	-0.7564067
		Angptl4	3.877828875
		Fcgr2b	2.750865525
		Sema3c	2.192754175
		Chga	-1.646750175
		Tac1	3.524948475
		Cmtm5	-0.6883895
		Fgf13	-1.119129
		Psmd3	0.813119725
		Cmtm7	1.470789775
		Kcnh2	-0.87291375
		Slc22a17	-0.73598045
		Ctss	-1.116066925
		Psmd5	0.90869195
		Nras	1.042122325
		Gal	3.8492663
		Casp3	1.9271854
		Il1r2	5.0581961
		Mdk	-0.90262405
		Cxcl2	4.54579085
		S100a13	-0.97841965
		Zyx	1.534475825
		Psmd14	0.784229625
		Hdac1	1.2330456

Mapt	-1.113871725
C3ar1	2.6168613
Rbp1	5.617855775
Flt1	1.255837475
Cx3cl1	-1.512034675
Inhbb	-1.8783907
Vegfb	-1.102308775
Ptn	-1.81431
Irf9	1.1238387
Adcyap1r1	-1.342854825
Il18	1.128884125
C3	-2.03126085
Trhr	-1.16749705
Furin	1.161774775
Nfkbia	1.561294525
Vav1	2.4587238
Sdc3	-1.1026628
Bmp4	-1.6495149
S100a6	1.7212402
Irf3	1.316868975
Thra	-0.697226725
Ucn2	3.359089325
Rabep1	-0.60130485
Tlr2	1.9641849
Esrrg	-2.64442475
Cmtm6	1.5700987
Nampt	1.141506225
Ednrb	-1.11760045
Pik3r3	-1.1579597
S100a1	-0.695144425
Bcl10	1.1362543
Fgfr3	-0.869297475
Nfya	0.74505765
Fabp7	-1.210403375
Ptgds	-1.733037175
Tfrc	0.9315101
Rasgrp3	-1.432559025
Vtn	-4.85518335
Icam1	2.633755975
Bcl3	0.888013475
Rac2	2.226035625
Tgfb2	-1.063020125
Map2k1	0.599491175
Aplnr	-1.263341775
Rhoa	1.004070575
Igf2	-1.15432775
Eed	0.895777475
Adrm1	0.65509575
Lyn	1.2070316
Il6r	1.0640093
Lrsam1	-0.940591375

Pak2	0.629685075
Colec12	-3.93460165
Cblb	2.312739075
Nrg1	-1.089506625
Fgfr1	1.011826375
Inhba	1.374820475
Ltbr	1.889511125
Vim	1.266482825
Adm	1.2842977
Ifi30	1.633259125
Bmp1	0.745281475
Ccl4	2.254940325
Tnfrsf11b	-2.644151775
Cspg5	-1.655204375
Mapk14	0.7796278
Bmp2	3.5561686
Adrb2	-0.830843375
Tgfb3	2.9169843
Hdgf	1.38090305
Lcp2	2.112134125
Fyn	0.742468975
Fgf1	-1.2591427
Ngfr	1.17533485
Tlr4	1.949129825
Gbp2	1.150594875
Bdnf	1.045547925
Ltbp3	-1.15049995
Tgfbr2	0.8947434
Cck	-0.652489975
Cmtm3	1.13227055
Sh3bp2	1.400317175
Ptgs2	1.89113165
Ap3b1	0.648305425
Ptpn6	2.4274416
Bst2	1.380615
Akt2	0.7831182
Raf1	0.6857794
Bmp6	-1.836321225
Clefl	1.652384875
Pf4	2.43515005
Ebi3	0.6217301
Prkca	-0.654240825
Il6	3.19100695
Fcgr3a	2.90463375
Psm1	0.6392132
Ctsb	0.9497628
Chgb	-0.888653375
Fgr	2.46702445
Csf3r	2.514020825
Bmpr1a	-1.0956696
Plxnb2	0.832789275

Ccl3	2.592917325
Irf1	0.9241385
Cat	-0.715960075
Il11	2.377157125
Sdc4	0.591322725
Pdgfra	-1.495722775
Angpt1	-0.817076275
Itgal	0.900448
Tgfbr1	-1.400005325
Cdh1	-0.5879394
Vip	2.544718425
Ccl27	-0.735739375
Rsad2	2.381131
Cybb	2.5797895
Calca	-0.68611695
Fgf2	1.088115725
Itgb2	2.20607185
Cxcl3	0.754549075
Olr1	1.819337675
Rfx5	-0.766311725
Flt3	-0.810755725
Pmp2	0.86633475
Tyrobp	1.06885245
Ptpnc	1.5982528
Mmp12	1.733187175
Shc1	1.1002178
Aen	0.74445825
Pak4	1.095406425
Gm	0.90292515
Pdyn	1.750274975
Ctse	-0.65439725
Crh	2.221238275
Fcer1g	0.79637105
Ltb	1.6298249
Tgfb1	1.248357475
Adipor2	0.888427125
Nr2f2	-1.05064205
Il10rb	1.14826265
Tapbp	0.79440715
Irf7	1.065586375
Cldn4	1.1166138
Rela	0.8796661
Psmb8	1.186608075
Il1b	1.742730375
Cd4	-0.839647875

Supplementary Table2. The details for actual gene IDs and GO descriptions

ONTOLO GY	ID	Description	GeneRat io	BgRatio	pvalue	p.adjust	qvalue	geneID	Cou nt
BP	GO:00421 19	neutrophil activation	14/32	498/186 70	2.34E-14	4.54E-11	2.08E-11	FCER1G/GRN/CTSB/TYROBP/PTPRC/TLR2/GMFG/PTPN6/CYBB/C3AR1/FCGR2B/S100A11/CD14/LCN2	14
BP	GO:00433 12	neutrophil degranulation	13/32	485/186 70	4.63E-13	3.22E-10	1.48E-10	FCER1G/GRN/CTSB/TYROBP/PTPRC/TLR2/GMFG/PTPN6/CYBB/C3AR1/S100A11/CD14/LCN2	13
BP	GO:00022 83	neutrophil activation involved in immune response	13/32	488/186 70	5.01E-13	3.22E-10	1.48E-10	FCER1G/GRN/CTSB/TYROBP/PTPRC/TLR2/GMFG/PTPN6/CYBB/C3AR1/S100A11/CD14/LCN2	13
BP	GO:00024 46	neutrophil mediated immunity	13/32	499/186 70	6.65E-13	3.22E-10	1.48E-10	FCER1G/GRN/CTSB/TYROBP/PTPRC/TLR2/GMFG/PTPN6/CYBB/C3AR1/S100A11/CD14/LCN2	13
BP	GO:00327 60	positive regulation of tumor necrosis factor production	8/32	86/1867 0	1.40E-12	5.41E-10	2.49E-10	FCER1G/TYROBP/PTPRC/TLR4/TLR2/PF4/CYBB/CD14	8
BP	GO:19035 57	positive regulation of tumor necrosis factor superfamily cytokine production	8/32	88/1867 0	1.69E-12	5.45E-10	2.50E-10	FCER1G/TYROBP/PTPRC/TLR4/TLR2/PF4/CYBB/CD14	8
BP	GO:00326 80	regulation of tumor necrosis factor production	9/32	160/186 70	4.71E-12	1.18E-09	5.43E-10	FCER1G/TYROBP/PTPRC/TLR4/TLR2/PTPN6/PF4/CYBB/CD14	9
BP	GO:00326 40	tumor necrosis factor production	9/32	163/186 70	5.57E-12	1.18E-09	5.43E-10	FCER1G/TYROBP/PTPRC/TLR4/TLR2/PTPN6/PF4/CYBB/CD14	9
BP	GO:19035 55	regulation of tumor necrosis factor superfamily cytokine production	9/32	163/186 70	5.57E-12	1.18E-09	5.43E-10	FCER1G/TYROBP/PTPRC/TLR4/TLR2/PTPN6/PF4/CYBB/CD14	9
BP	GO:00026 83	negative regulation of immune system process	12/32	463/186 70	6.76E-12	1.18E-09	5.43E-10	FCER1G/GRN/TYROBP/LYN/PTPRC/TLR4/PTPN6/PF4/FCGR2B/HMOX1/CD14/CCL2	12
BP	GO:00018 19	positive regulation of cytokine production	12/32	464/186 70	6.94E-12	1.18E-09	5.43E-10	AGT/FCER1G/TYROBP/PTPRC/STAT3/TLR4/TLR2/PF4/CYBB/C3AR1/HMOX1/CD14	12
BP	GO:00717 06	tumor necrosis factor superfamily cytokine production	9/32	168/186 70	7.32E-12	1.18E-09	5.43E-10	FCER1G/TYROBP/PTPRC/TLR4/TLR2/PTPN6/PF4/CYBB/CD14	9
BP	GO:00712 19	cellular response to molecule of bacterial origin	9/32	212/186 70	5.92E-11	8.83E-09	4.06E-09	LYN/VIM/TLR4/TLR2/PF4/FCGR2B/CD14/LCN2/CCL2	9
BP	GO:00712 16	cellular response to biotic stimulus	9/32	236/186 70	1.54E-10	2.13E-08	9.80E-09	LYN/VIM/TLR4/TLR2/PF4/FCGR2B/CD14/LCN2/CCL2	9
BP	GO:00069 09	phagocytosis	10/32	369/186 70	3.53E-10	4.56E-08	2.10E-08	FCER1G/TYROBP/LYN/PTPRC/TLR4/TLR2/FCGR2B/FCGR3A/CD14/CCL2	10
BP	GO:00421 08	positive regulation of cytokine biosynthetic process	6/32	67/1867 0	1.43E-09	1.73E-07	7.96E-08	TYROBP/PTPRC/STAT3/TLR4/CYBB/HMOX1	6

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BP	GO:00712	cellular response to lipopolysaccharide	8/32	205/186 70	1.55E-09	1.76E-07	8.10E-08	LYN/VIM/TLR4/TLR2/PF4/CD14/LCN2/CCL2	8
BP	GO:00321	positive regulation of response to external stimulus	9/32	323/186 70	2.46E-09	2.56E-07	1.18E-07	AGT/S1PR1/LGMN/FCER1G/GRN/TLR4/TLR2/TNFRSF1A/C3AR1	9
BP	GO:00450	regulation of innate immune response	10/32	452/186 70	2.51E-09	2.56E-07	1.18E-07	LGMN/FCER1G/GRN/CTSB/LYN/TLR4/TLR2/PTPN6/FCGR2B/CD14	10
BP	GO:00022	response to molecule of bacterial origin	9/32	343/186 70	4.15E-09	4.02E-07	1.85E-07	LYN/VIM/TLR4/TLR2/PF4/FCGR2B/CD14/LCN2/CCL2	9
BP	GO:00507	regulation of inflammatory response	10/32	485/186 70	4.93E-09	4.55E-07	2.09E-07	AGT/FCER1G/GRN/LYN/PTPRC/TLR4/TLR2/TNFRSF1A/C3AR1/FCGR2B	10
BP	GO:00421	macrophage activation	6/32	95/1867 0	1.20E-08	1.06E-06	4.88E-07	GRN/TYROBP/PTPRC/TLR4/TLR2/FCGR2B	6
BP	GO:00026	negative regulation of leukocyte activation	7/32	175/186 70	1.56E-08	1.31E-06	6.03E-07	GRN/TYROBP/LYN/PTPRC/PTPN6/FCGR2B/HMOX1	7
BP	GO:00326	regulation of interleukin-10 production	5/32	52/1867 0	2.62E-08	2.11E-06	9.71E-07	FCER1G/TYROBP/TLR4/TLR2/FCGR2B	5
BP	GO:00326	interleukin-10 production	5/32	55/1867 0	3.49E-08	2.69E-06	1.24E-06	FCER1G/TYROBP/TLR4/TLR2/FCGR2B	5
BP	GO:00420	regulation of cytokine biosynthetic process	6/32	114/186 70	3.61E-08	2.69E-06	1.24E-06	TYROBP/PTPRC/STAT3/TLR4/CYBB/HMOX1	6
BP	GO:00508	negative regulation of cell activation	7/32	199/186 70	3.78E-08	2.71E-06	1.25E-06	GRN/TYROBP/LYN/PTPRC/PTPN6/FCGR2B/HMOX1	7
BP	GO:00027	regulation of leukocyte mediated immunity	7/32	201/186 70	4.05E-08	2.80E-06	1.29E-06	FCER1G/LYN/PTPRC/TLR4/PTPN6/FCGR2B/HMOX1	7
BP	GO:19012	regulation of neuron death	8/32	313/186 70	4.23E-08	2.83E-06	1.30E-06	LGMN/GRN/TYROBP/STAT3/TLR4/FCGR2B/HMOX1/CCL2	8
BP	GO:00316	lipopolysaccharide-mediated signaling pathway	5/32	58/1867 0	4.58E-08	2.96E-06	1.36E-06	LYN/TLR4/TLR2/CD14/CCL2	5
BP	GO:00026	regulation of immune effector process	9/32	458/186 70	5.05E-08	3.16E-06	1.45E-06	FCER1G/GRN/LYN/PTPRC/TLR4/PTPN6/C3AR1/FCGR2B/HMOX1	9
BP	GO:00420	cytokine biosynthetic process	6/32	123/186 70	5.70E-08	3.41E-06	1.57E-06	TYROBP/PTPRC/STAT3/TLR4/CYBB/HMOX1	6
BP	GO:00308	regulation of B cell proliferation	5/32	61/1867 0	5.93E-08	3.41E-06	1.57E-06	TYROBP/LYN/PTPRC/TLR4/FCGR2B	5
BP	GO:00421	cytokine metabolic process	6/32	124/186 70	5.98E-08	3.41E-06	1.57E-06	TYROBP/PTPRC/STAT3/TLR4/CYBB/HMOX1	6
BP	GO:00324	response to lipopolysaccharide	8/32	330/186 70	6.36E-08	3.52E-06	1.62E-06	LYN/VIM/TLR4/TLR2/PF4/CD14/LCN2/CCL2	8
BP	GO:00714	cellular response to external stimulus	8/32	339/186 70	7.83E-08	4.22E-06	1.94E-06	AGT/LYN/PTPRC/TLR4/TNFRSF1A/CYBB/HMOX1/LCN2	8
BP	GO:00305	leukocyte chemotaxis	7/32	224/186 70	8.50E-08	4.45E-06	2.05E-06	S1PR1/LGMN/FCER1G/LYN/PF4/C3AR1/CCL2	7

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BP	GO:00709 97	neuron death	8/32	348/186 70	9.57E-08	4.88E-06	2.24E-06	LGMN/GRN/TYROBP/STAT3/TLR4/FCGR2B/HMOX1/CCL2	8
BP	GO:00509 00	leukocyte migration	9/32	499/186 70	1.05E-07	5.22E-06	2.40E-06	S1PR1/LGMN/FCER1G/LYN/PTPN6/PF4/C3AR1/HMOX1/CCL2	9
BP	GO:00506 63	cytokine secretion	7/32	240/186 70	1.36E-07	6.59E-06	3.03E-06	AGT/LYN/TLR4/TLR2/LCP2/FCGR2B/CD14	7
BP	GO:00022 24	toll-like receptor signaling pathway	6/32	146/186 70	1.58E-07	7.48E-06	3.43E-06	LGMN/CTSB/LYN/TLR4/TLR2/CD14	6
BP	GO:00507 77	negative regulation of immune response	6/32	150/186 70	1.86E-07	8.57E-06	3.93E-06	GRN/LYN/PTPRC/PTPN6/FCGR2B/HMOX1	6
BP	GO:00326 75	regulation of interleukin-6 production	6/32	152/186 70	2.01E-07	8.99E-06	4.13E-06	FCER1G/TYROBP/STAT3/TLR4/TLR2/PTPN6	6
BP	GO:00301 68	platelet activation	6/32	153/186 70	2.09E-07	8.99E-06	4.13E-06	FCER1G/LYN/TLR4/LCP2/PTPN6/PF4	6
BP	GO:00507 29	positive regulation of inflammatory response	6/32	153/186 70	2.09E-07	8.99E-06	4.13E-06	AGT/FCER1G/GRN/TLR4/TLR2/TNFRSF1A	6
BP	GO:00072 59	JAK-STAT cascade	6/32	156/186 70	2.34E-07	9.86E-06	4.53E-06	AGT/LYN/PTPRC/STAT3/TNFRSF1A/CCL2	6
BP	GO:00326 35	interleukin-6 production	6/32	161/186 70	2.82E-07	1.16E-05	5.34E-06	FCER1G/TYROBP/STAT3/TLR4/TLR2/PTPN6	6
BP	GO:19021 05	regulation of leukocyte differentiation	7/32	272/186 70	3.18E-07	1.28E-05	5.90E-06	TYROBP/LYN/PTPRC/TLR4/PTPN6/PF4/FCGR2B	7
BP	GO:00976 96	STAT cascade	6/32	166/186 70	3.38E-07	1.34E-05	6.14E-06	AGT/LYN/PTPRC/STAT3/TNFRSF1A/CCL2	6
BP	GO:00300 99	myeloid cell differentiation	8/32	416/186 70	3.74E-07	1.45E-05	6.66E-06	FCER1G/TYROBP/LYN/STAT3/TLR4/TLR2/PTPN6/PF4	8
BP	GO:00420 63	gliogenesis	7/32	290/186 70	4.90E-07	1.86E-05	8.55E-06	GRN/LYN/VIM/STAT3/TLR4/TLR2/CCL2	7
BP	GO:00703 91	response to lipoteichoic acid	3/32	10/1867 0	5.44E-07	1.99E-05	9.14E-06	TLR4/TLR2/CD14	3
BP	GO:00712 23	cellular response to lipoteichoic acid	3/32	10/1867 0	5.44E-07	1.99E-05	9.14E-06	TLR4/TLR2/CD14	3
BP	GO:00421 00	B cell proliferation	5/32	95/1867 0	5.54E-07	1.99E-05	9.14E-06	TYROBP/LYN/PTPRC/TLR4/FCGR2B	5
BP	GO:00327 55	positive regulation of interleukin-6 production	5/32	96/1867 0	5.84E-07	2.04E-05	9.35E-06	FCER1G/TYROBP/STAT3/TLR4/TLR2	5
BP	GO:00027 58	innate immune response-activating signal transduction	7/32	298/186 70	5.88E-07	2.04E-05	9.35E-06	LGMN/FCER1G/CTSB/LYN/TLR4/TLR2/CD14	7
BP	GO:00508 64	regulation of B cell activation	6/32	184/186 70	6.18E-07	2.10E-05	9.66E-06	TYROBP/LYN/PTPRC/TLR4/PTPN6/FCGR2B	6
BP	GO:00507 64	regulation of phagocytosis	5/32	98/1867 0	6.47E-07	2.16E-05	9.93E-06	FCER1G/PTPRC/TLR2/FCGR2B/CCL2	5
BP	GO:00603	cell chemotaxis	7/32	304/186	6.72E-07	2.21E-05	1.01E-05	S1PR1/LGMN/FCER1G/LYN/PF4/C3AR1/CCL2	7

Supplementary Table2. The details for actual gene IDs and GO descriptions

	26			70						
		regulation of humoral								
BP	GO:00029	immune response	3/32	11/1867	7.48E-07	2.42E-05	1.11E-05	PTPRC/PTPN6/FCGR2B		3
	23	mediated by circulating immunoglobulin		0						
		pattern recognition								
BP	GO:00022	receptor signaling pathway	6/32	197/186	9.22E-07	2.90E-05	1.33E-05	LGMN/CTSB/LYN/TLR4/TLR2/CD14		6
	21			70						
		activation of innate immune response								
BP	GO:00022		7/32	319/186	9.28E-07	2.90E-05	1.33E-05	LGMN/FCER1G/CTSB/LYN/TLR4/TLR2/CD14		7
	18			70						
		immune response-activating cell surface receptor signaling pathway								
BP	GO:00024		8/32	473/186	9.86E-07	3.03E-05	1.39E-05	FCER1G/LYN/PTPRC/LCP2/PTPN6/C3AR1/FCGR2B/FCGR3A		8
	29			70						
		regulation of hemopoiesis								
BP	GO:19037		8/32	475/186	1.02E-06	3.08E-05	1.42E-05	TYROBP/LYN/PTPRC/STAT3/TLR4/PTPN6/PF4/FCGR2B		8
	06			70						
		regulation of leukocyte degranulation								
BP	GO:00433		4/32	46/1867	1.10E-06	3.29E-05	1.51E-05	FCER1G/LYN/FCGR2B/HMOX1		4
	00			0						
		myeloid leukocyte differentiation								
BP	GO:00025		6/32	204/186	1.13E-06	3.32E-05	1.53E-05	FCER1G/TYROBP/LYN/TLR4/TLR2/PF4		6
	73			70						
		regulation of lymphocyte proliferation								
BP	GO:00506		6/32	208/186	1.27E-06	3.63E-05	1.67E-05	TYROBP/LYN/PTPRC/TLR4/PTPN6/FCGR2B		6
	70			70						
		regulation of mononuclear cell proliferation								
BP	GO:00329		6/32	209/186	1.30E-06	3.63E-05	1.67E-05	TYROBP/LYN/PTPRC/TLR4/PTPN6/FCGR2B		6
	44			70						
		microglial cell activation								
BP	GO:00017		4/32	48/1867	1.31E-06	3.63E-05	1.67E-05	GRN/TYROBP/PTPRC/TLR2		4
	74			0						
		leukocyte activation involved in inflammatory response								
BP	GO:00022		4/32	48/1867	1.31E-06	3.63E-05	1.67E-05	GRN/TYROBP/PTPRC/TLR2		4
	69			0						
		myeloid leukocyte migration								
BP	GO:00975		6/32	210/186	1.34E-06	3.66E-05	1.68E-05	LGMN/FCER1G/LYN/PF4/C3AR1/CCL2		6
	29			70						
		negative regulation of leukocyte mediated immunity								
BP	GO:00027		4/32	49/1867	1.43E-06	3.84E-05	1.76E-05	PTPRC/PTPN6/FCGR2B/HMOX1		4
	04			0						
		glial cell development								
BP	GO:00217		5/32	116/186	1.50E-06	3.97E-05	1.82E-05	GRN/LYN/VIM/TLR4/TLR2		5
	82			70						
		glial cell differentiation								
BP	GO:00100		6/32	218/186	1.66E-06	4.28E-05	1.97E-05	GRN/LYN/VIM/STAT3/TLR4/TLR2		6
	01			70						
		regulation of B cell mediated immunity								
BP	GO:00027		4/32	51/1867	1.68E-06	4.28E-05	1.97E-05	FCER1G/PTPRC/PTPN6/FCGR2B		4
	12			0						
		regulation of immunoglobulin mediated immune response								
BP	GO:00028		4/32	51/1867	1.68E-06	4.28E-05	1.97E-05	FCER1G/PTPRC/PTPN6/FCGR2B		4
	89			0						

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00026	negative regulation of immune effector process	5/32	120/186 70	1.77E-06	4.45E-05	2.04E-05	GRN/PTPRC/PTPN6/FCGR2B/HMOX1	5
BP	GO:00706	regulation of leukocyte proliferation	6/32	222/186 70	1.85E-06	4.60E-05	2.11E-05	TYROBP/LYN/PTPRC/TLR4/PTPN6/FCGR2B	6
BP	GO:00069	humoral immune response	7/32	356/186 70	1.93E-06	4.72E-05	2.17E-05	PTPRC/PTPN6/PF4/C3AR1/FCGR2B/LCN2/CCL2	7
BP	GO:00971	extrinsic apoptotic signaling pathway	6/32	224/186 70	1.95E-06	4.72E-05	2.17E-05	AGT/PTPRC/TNFRSF1A/PF4/HMOX1/LCN2	6
BP	GO:00517	positive regulation of nitric-oxide synthase biosynthetic process	3/32	15/1867 0	2.05E-06	4.91E-05	2.26E-05	TLR4/TLR2/CCL2	3
BP	GO:00028	regulation of myeloid leukocyte mediated immunity	4/32	55/1867 0	2.28E-06	5.33E-05	2.45E-05	FCER1G/LYN/FCGR2B/HMOX1	4
BP	GO:00430	regulation of macrophage activation	4/32	55/1867 0	2.28E-06	5.33E-05	2.45E-05	GRN/PTPRC/TLR4/FCGR2B	4
BP	GO:00308	negative regulation of B cell proliferation	3/32	16/1867 0	2.52E-06	5.75E-05	2.64E-05	TYROBP/LYN/FCGR2B	3
BP	GO:00430	negative regulation of macrophage activation	3/32	16/1867 0	2.52E-06	5.75E-05	2.64E-05	GRN/PTPRC/FCGR2B	3
BP	GO:00619	glial cell activation	4/32	58/1867 0	2.83E-06	6.37E-05	2.93E-05	GRN/TYROBP/PTPRC/TLR2	4
BP	GO:00026	positive regulation of leukocyte activation	7/32	380/186 70	2.97E-06	6.55E-05	3.01E-05	FCER1G/TYROBP/LYN/PTPRC/TLR4/PTPN6/CCL2	7
BP	GO:00380	Fc receptor signaling pathway	6/32	241/186 70	2.97E-06	6.55E-05	3.01E-05	FCER1G/LYN/PTPRC/LCP2/FCGR2B/FCGR3A	6
BP	GO:00450	positive regulation of innate immune response	7/32	381/186 70	3.02E-06	6.59E-05	3.03E-05	LGMN/FCER1G/CTSB/LYN/TLR4/TLR2/CD14	7
BP	GO:00457	regulation of angiogenesis	7/32	383/186 70	3.13E-06	6.74E-05	3.10E-05	AGT/GRN/STAT3/PF4/CYBB/C3AR1/HMOX1	7
BP	GO:19016	cellular response to peptide	7/32	385/186 70	3.24E-06	6.83E-05	3.14E-05	AGT/LGMN/LYN/VIM/STAT3/TLR4/FCGR2B	7
BP	GO:00455	mast cell activation	4/32	60/1867 0	3.24E-06	6.83E-05	3.14E-05	FCER1G/LYN/LCP2/HMOX1	4
BP	GO:00464	regulation of JAK-STAT cascade	5/32	137/186 70	3.40E-06	7.08E-05	3.25E-05	AGT/LYN/PTPRC/STAT3/TNFRSF1A	5
BP	GO:00027	regulation of production of molecular mediator of immune response	5/32	139/186 70	3.65E-06	7.52E-05	3.45E-05	FCER1G/PTPRC/TLR4/FCGR2B/HMOX1	5
BP	GO:00508	positive regulation of cell activation	7/32	394/186 70	3.77E-06	7.70E-05	3.54E-05	FCER1G/TYROBP/LYN/PTPRC/TLR4/PTPN6/CCL2	7
BP	GO:00380	Fc-gamma receptor signaling pathway	5/32	142/186 70	4.05E-06	8.18E-05	3.75E-05	FCER1G/LYN/PTPRC/FCGR2B/FCGR3A	5
BP	GO:00507	regulation of	6/32	256/186	4.21E-06	8.42E-05	3.87E-05	AGT/LYN/PTPRC/STAT3/TNFRSF1A/PTPN6	6

Supplementary Table2. The details for actual gene IDs and GO descriptions

	30	peptidyl-tyrosine phosphorylation		70							
		regulation of antigen		65/1867							
BP	GO:00508	receptor-mediated signaling pathway	4/32	0	4.47E-06	8.78E-05	4.03E-05	LYN/PTPRC/PTPN6/FCGR2B			4
	54										
		Fc receptor mediated		145/186							
BP	GO:00024	stimulatory signaling pathway	5/32	70	4.48E-06	8.78E-05	4.03E-05	FCER1G/LYN/PTPRC/FCGR2B/FCGR3A			5
	31										
		regulation of STAT		146/186							
BP	GO:19048	cascade	5/32	70	4.64E-06	8.99E-05	4.13E-05	AGT/LYN/PTPRC/STAT3/TNFRSF1A			5
	92										
		positive regulation of		20/1867							
BP	GO:00425	tumor necrosis factor biosynthetic process	3/32	0	5.11E-06	9.62E-05	4.42E-05	TYROBP/TLR4/CYBB			3
	35										
		nitric-oxide synthase		20/1867							
BP	GO:00517	biosynthetic process	3/32	0	5.11E-06	9.62E-05	4.42E-05	TLR4/TLR2/CCL2			3
	67										
		regulation of nitric-oxide		20/1867							
BP	GO:00517	synthase biosynthetic process	3/32	0	5.11E-06	9.62E-05	4.42E-05	TLR4/TLR2/CCL2			3
	69										
		positive regulation of		153/186		0.0001080					
BP	GO:00458	endocytosis	5/32	70	5.83E-06	58	4.96E-05	FCER1G/PTPRC/FCGR2B/CD14/CCL2			5
	07										
		regulation of vasculature		422/186		0.0001080					
BP	GO:19013	development	7/32	70	5.92E-06	58	4.96E-05	AGT/GRN/STAT3/PF4/CYBB/C3AR1/HMOX1			7
	42										
		lymphocyte proliferation		272/186		0.0001080					
BP	GO:00466		6/32	70	5.96E-06	58	4.96E-05	TYROBP/LYN/PTPRC/TLR4/PTPN6/FCGR2B			6
	51										
		regulation of toll-like		70/1867		0.0001080					
BP	GO:00341	receptor signaling pathway	4/32	0	6.02E-06	58	4.96E-05	LYN/TLR4/TLR2/CD14			4
	21										
		positive regulation of		70/1867		0.0001080					
BP	GO:00507	phagocytosis	4/32	0	6.02E-06	58	4.96E-05	FCER1G/PTPRC/FCGR2B/CCL2			4
	66										
		mononuclear cell		274/186		0.0001106					
BP	GO:00329	proliferation	6/32	70	6.22E-06	54	5.08E-05	TYROBP/LYN/PTPRC/TLR4/PTPN6/FCGR2B			6
	43										
		production of molecular		72/1867		0.0001187					
BP	GO:00025	mediator involved in inflammatory response	4/32	0	6.74E-06	55	5.45E-05	FCER1G/GRN/LYN/TLR4			4
	32										
		negative regulation of		73/1867		0.0001232					
BP	GO:00329	mononuclear cell proliferation	4/32	0	7.12E-06	48	5.66E-05	TYROBP/LYN/PTPN6/FCGR2B			4
	45										
		negative regulation of		73/1867		0.0001232					
BP	GO:00506	lymphocyte proliferation	4/32	0	7.12E-06	48	5.66E-05	TYROBP/LYN/PTPN6/FCGR2B			4
	72										
		regulation of endocytosis		281/186		0.0001233					
BP	GO:00301		6/32	70	7.19E-06	1	5.66E-05	FCER1G/PTPRC/TLR2/FCGR2B/CD14/CCL2			6
	00										
		regulation of		74/1867		0.0001278					
BP	GO:00326	interleukin-8 production	4/32	0	7.52E-06	51	5.87E-05	PTPRC/TLR4/TLR2/CD14			4
	77										
		reactive oxygen species		284/186		0.0001287					
BP	GO:00725		6/32	70	7.64E-06	59	5.91E-05	AGT/TYROBP/STAT3/TLR4/TLR2/CYBB			6

Supplementary Table2. The details for actual gene IDs and GO descriptions

	93	metabolic process		70		46				
BP	GO:01500	neuroinflammatory response	4/32	75/1867	7.93E-06	0.0001317	6.05E-05	GRN/TYROBP/PTPRC/TLR2		4
	76			0		19				
BP	GO:00024	production of molecular mediator of immune response	6/32	286/186	7.95E-06	0.0001317	6.05E-05	FCER1G/PTPRC/TLR4/TLR2/FCGR2B/HMOX1		6
	40			70		19				
BP	GO:00019	cell killing	5/32	168/186	9.19E-06	0.0001510	6.94E-05	TYROBP/PTPRC/PTPN6/PF4/FCGR2B		5
	06			70		83				
BP	GO:00706	negative regulation of leukocyte proliferation	4/32	78/1867	9.27E-06	0.0001511	6.94E-05	TYROBP/LYN/PTPN6/FCGR2B		4
	64			0		09				
BP	GO:00018	negative regulation of cytokine production	6/32	296/186	9.67E-06	0.0001562	7.18E-05	TYROBP/PTPRC/TLR4/PTPN6/FCGR2B/HMOX1		6
	18			70		31				
BP	GO:00706	leukocyte proliferation	6/32	298/186	1.00E-05	0.0001609	7.39E-05	TYROBP/LYN/PTPRC/TLR4/PTPN6/FCGR2B		6
	61			70		96				
BP	GO:00487	astrocyte differentiation	4/32	81/1867	1.08E-05	0.0001712	7.87E-05	GRN/VIM/STAT3/TLR4		4
	08			0		98				
BP	GO:00421	T cell activation	7/32	464/186	1.10E-05	0.0001733	7.96E-05	FCER1G/LYN/PTPRC/STAT3/PTPN6/FCGR2B/CCL2		7
	10			70		21				
		antigen processing and presentation of exogenous peptide antigen								
BP	GO:00024	presentation of exogenous peptide antigen	5/32	175/186	1.12E-05	0.0001752	8.05E-05	LGMN/FCER1G/IFI30/CYBB/FCGR2B		5
	78			70		66				
BP	GO:00326	interleukin-8 production	4/32	82/1867	1.13E-05	0.0001755	8.06E-05	PTPRC/TLR4/TLR2/CD14		4
	37			0		49				
BP	GO:00421	B cell activation	6/32	310/186	1.26E-05	0.0001935	8.89E-05	TYROBP/LYN/PTPRC/TLR4/PTPN6/FCGR2B		6
	13			70		06				
BP	GO:00713	cellular response to interferon-gamma	5/32	180/186	1.28E-05	0.0001961	9.01E-05	VIM/IFI30/TLR4/TLR2/CCL2		5
	46			70		4				
		lymphocyte activation involved in immune response								
BP	GO:00022	involved in immune response	5/32	181/186	1.32E-05	0.0001998	9.18E-05	FCER1G/PTPRC/STAT3/TLR4/FCGR2B		5
	85			70		95				
		antigen processing and presentation of exogenous antigen								
BP	GO:00198	presentation of exogenous antigen	5/32	182/186	1.36E-05	0.0002037	9.36E-05	LGMN/FCER1G/IFI30/CYBB/FCGR2B		5
	84			70		02				
BP	GO:00703	ERK1 and ERK2 cascade	6/32	317/186	1.43E-05	0.0002128	9.78E-05	AGT/LYN/PTPRC/TLR4/PTPN6/CCL2		6
	71			70		74				
BP	GO:00512	regulation of lymphocyte activation	7/32	485/186	1.46E-05	0.0002168	9.96E-05	TYROBP/LYN/PTPRC/TLR4/PTPN6/FCGR2B/CCL2		7
	49			70		08				
		positive regulation of cytosolic calcium ion concentration								
BP	GO:00072	positive regulation of cytosolic calcium ion concentration	6/32	319/186	1.48E-05	0.0002172	9.98E-05	AGT/S1PR1/LYN/PTPRC/PTPN6/C3AR1		6
	04			70		53				
		positive regulation of JAK-STAT cascade								
BP	GO:00464	positive regulation of JAK-STAT cascade	4/32	89/1867	1.57E-05	0.0002283	0.0001048	AGT/LYN/STAT3/TNFRSF1A		4
	27			0		93	94			
BP	GO:00480	antigen processing and	5/32	189/186	1.63E-05	0.0002351	0.0001080	LGMN/FCER1G/IFI30/CYBB/FCGR2B		5

Supplementary Table2. The details for actual gene IDs and GO descriptions

	02	presentation of peptide antigen	70	93	17				
BP	GO:00716	mononuclear cell migration	4/32	90/1867	1.64E-05	0.0002351	0.0001080	LGMN/LYN/C3AR1/CCL2	4
BP	GO:00607	regulation of response to cytokine stimulus	5/32	190/186	1.67E-05	0.0002378	0.0001092	PTPRC/TLR4/TLR2/TNFRSF1A/PTPN6	5
BP	GO:00507	positive regulation of peptidyl-tyrosine phosphorylation	5/32	192/186	1.75E-05	0.0002474	0.0001136	AGT/LYN/PTPRC/STAT3/TNFRSF1A	5
BP	GO:19048	positive regulation of STAT cascade	4/32	92/1867	1.79E-05	0.0002474	0.0001136	AGT/LYN/STAT3/TNFRSF1A	4
BP	GO:00427	defense response to bacterium	6/32	330/186	1.79E-05	0.0002474	0.0001136	FCER1G/GRN/TLR4/TLR2/TNFRSF1A/LCN2	6
BP	GO:00508	negative regulation of B cell activation	3/32	30/1867	1.80E-05	0.0002474	0.0001136	TYROBP/LYN/FCGR2B	3
BP	GO:00610	myeloid leukocyte cytokine production	3/32	30/1867	1.80E-05	0.0002474	0.0001136	FCER1G/TLR4/HMOX1	3
BP	GO:00512	positive regulation of lymphocyte activation	6/32	334/186	1.92E-05	0.0002618	0.0001202	TYROBP/LYN/PTPRC/TLR4/PTPN6/CCL2	6
BP	GO:00026	regulation of leukocyte migration	5/32	196/186	1.94E-05	0.0002618	0.0001202	LGMN/LYN/C3AR1/HMOX1/CCL2	5
BP	GO:19012	positive regulation of neuron death	4/32	94/1867	1.94E-05	0.0002618	0.0001202	GRN/TYROBP/TLR4/FCGR2B	4
BP	GO:00075	blood coagulation	6/32	336/186	1.98E-05	0.0002624	0.0001205	FCER1G/LYN/TLR4/LCP2/PTPN6/PF4	6
BP	GO:00105	regulation of platelet activation	3/32	31/1867	1.99E-05	0.0002624	0.0001205	FCER1G/LYN/TLR4	3
BP	GO:00433	regulation of mast cell degranulation	3/32	31/1867	1.99E-05	0.0002624	0.0001205	FCER1G/LYN/HMOX1	3
BP	GO:00343	response to interferon-gamma	5/32	199/186	2.08E-05	0.0002731	0.0001254	VIM/IFI30/TLR4/TLR2/CCL2	5
BP	GO:00075	hemostasis	6/32	341/186	2.16E-05	0.0002805	0.0001288	FCER1G/LYN/TLR4/LCP2/PTPN6/PF4	6
BP	GO:00508	coagulation	6/32	342/186	2.19E-05	0.0002816	0.0001293	FCER1G/LYN/TLR4/LCP2/PTPN6/PF4	6
BP	GO:00330	regulation of mast cell activation involved in immune response	3/32	32/1867	2.19E-05	0.0002816	0.0001293	FCER1G/LYN/HMOX1	3
BP	GO:00198	antigen processing and presentation of exogenous peptide antigen via MHC class II	4/32	98/1867	2.29E-05	0.0002924	0.0001343	LGMN/FCER1G/IFI30/FCGR2B	4
BP	GO:00457	positive regulation of angiogenesis	5/32	204/186	2.35E-05	0.0002976	0.0001367	GRN/STAT3/CYBB/C3AR1/HMOX1	5

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:19012	negative regulation of neuron death	5/32	208/186	2.58E-05	0.0003230	0.0001483	LGMN/GRN/STAT3/HMOX1/CCL2	5
	15			70		29	58		
BP	GO:00024	antigen processing and presentation of peptide antigen via MHC class II	4/32	101/186	2.58E-05	0.0003230	0.0001483	LGMN/FCER1G/IFI30/FCGR2B	4
	95			70		29	58		
BP	GO:00425	tumor necrosis factor biosynthetic process	3/32	34/1867	2.64E-05	0.0003251	0.0001493	TYROBP/TLR4/CYBB	3
	33			0		12	15		
BP	GO:00425	regulation of tumor necrosis factor biosynthetic process	3/32	34/1867	2.64E-05	0.0003251	0.0001493	TYROBP/TLR4/CYBB	3
	34			0		12	15		
BP	GO:00023	cytokine production involved in immune response	4/32	102/186	2.68E-05	0.0003251	0.0001493	FCER1G/TLR4/TLR2/HMOX1	4
	67			70		12	15		
BP	GO:00025	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	4/32	102/186	2.68E-05	0.0003251	0.0001493	LGMN/FCER1G/IFI30/FCGR2B	4
	04			70		12	15		
BP	GO:00435	regulation of neuron apoptotic process	5/32	210/186	2.70E-05	0.0003251	0.0001493	LGMN/GRN/TYROBP/HMOX1/CCL2	5
	23			70		12	15		
BP	GO:00507	regulation of cytokine secretion	5/32	210/186	2.70E-05	0.0003251	0.0001493	LYN/TLR4/TLR2/FCGR2B/CD14	5
	07			70		12	15		
BP	GO:00514	regulation of cytosolic calcium ion concentration	6/32	357/186	2.79E-05	0.0003339	0.0001533	AGT/S1PR1/LYN/PTPRC/PTPN6/C3AR1	6
	80			70		14	57		
BP	GO:00341	toll-like receptor 4 signaling pathway	3/32	35/1867	2.88E-05	0.0003425	0.0001573	LYN/TLR4/CD14	3
	42			0		91	42		
BP	GO:00305	neutrophil chemotaxis	4/32	104/186	2.90E-05	0.0003425	0.0001573	FCER1G/PF4/C3AR1/CCL2	4
	93			70		91	42		
BP	GO:00024	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	6/32	361/186	2.97E-05	0.0003489	0.0001602	FCER1G/PTPRC/STAT3/TLR4/PTPN6/FCGR2B	6
	60			70		9	81		
BP	GO:00181	peptidyl-tyrosine phosphorylation	6/32	363/186	3.06E-05	0.0003578	0.0001643	AGT/LYN/PTPRC/STAT3/TNFRSF1A/PTPN6	6
	08			70		01	27		
BP	GO:00026	positive regulation of immune effector process	5/32	216/186	3.09E-05	0.0003581	0.0001644	FCER1G/LYN/PTPRC/TLR4/HMOX1	5
	99			70		52	89		
BP	GO:00027	MyD88-dependent toll-like receptor signaling pathway	3/32	36/1867	3.14E-05	0.0003581	0.0001644	TLR4/TLR2/CD14	3
	55			0		52	89		
BP	GO:00327	positive regulation of interleukin-10 production	3/32	36/1867	3.14E-05	0.0003581	0.0001644	FCER1G/TLR4/TLR2	3
	33			0		52	89		

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00425	superoxide anion generation	3/32	36/1867 0	3.14E-05	0.0003581 52	0.0001644 89	AGT/TYROBP/CYBB	3
BP	GO:00509	regulation of chemotaxis	5/32	217/186 70	3.16E-05	0.0003581 52	0.0001644 89	S1PR1/LGMN/LYN/C3AR1/CCL2	5
BP	GO:00182	peptidyl-tyrosine modification	6/32	366/186 70	3.21E-05	0.0003616 16	0.0001660 8	AGT/LYN/PTPRC/STAT3/TNFRSF1A/PTPN6	6
BP	GO:00019	leukocyte mediated cytotoxicity	4/32	107/186 70	3.24E-05	0.0003631 87	0.0001668 01	TYROBP/PTPRC/PTPN6/FCGR2B	4
BP	GO:00027	negative regulation of lymphocyte mediated immunity	3/32	38/1867 0	3.70E-05	0.0004127 86	0.0001895 8	PTPRC/PTPN6/FCGR2B	3
BP	GO:00198	antigen processing and presentation	5/32	226/186 70	3.84E-05	0.0004249 64	0.0001951 74	LGMN/FCER1G/IFI30/CYBB/FCGR2B	5
BP	GO:00026	regulation of leukocyte chemotaxis	4/32	114/186 70	4.15E-05	0.0004568 28	0.0002098 08	LGMN/LYN/C3AR1/CCL2	4
BP	GO:19040	positive regulation of vasculature development	5/32	230/186 70	4.17E-05	0.0004568 28	0.0002098 08	GRN/STAT3/CYBB/C3AR1/HMOX1	5
BP	GO:00028	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3/32	40/1867 0	4.33E-05	0.0004714 79	0.0002165 37	PTPRC/PTPN6/FCGR2B	3
BP	GO:00027	regulation of myeloid leukocyte differentiation	4/32	117/186 70	4.60E-05	0.0004982 48	0.0002288 31	TYROBP/LYN/TLR4/PF4	4
BP	GO:00341	negative regulation of toll-like receptor signaling pathway	3/32	41/1867 0	4.66E-05	0.0005024 64	0.0002307 67	LYN/TLR4/CD14	3
BP	GO:19902	neutrophil migration	4/32	118/186 70	4.76E-05	0.0005094 21	0.0002339 62	FCER1G/PF4/C3AR1/CCL2	4
BP	GO:00514	neuron apoptotic process	5/32	239/186 70	5.01E-05	0.0005316 25	0.0002441 6	LGMN/GRN/TYROBP/HMOX1/CCL2	5
BP	GO:00330	regulation of mast cell activation	3/32	42/1867 0	5.02E-05	0.0005316 25	0.0002441 6	FCER1G/LYN/HMOX1	3
BP	GO:19046	cellular response to amyloid-beta	3/32	43/1867 0	5.39E-05	0.0005677 29	0.0002607 42	LGMN/TLR4/FCGR2B	3
BP	GO:19034	reactive oxygen species biosynthetic process	4/32	122/186 70	5.42E-05	0.0005677 39	0.0002607 46	AGT/STAT3/TLR4/CYBB	4
BP	GO:00716	granulocyte chemotaxis	4/32	123/186 70	5.59E-05	0.0005829 68	0.0002677 4	FCER1G/PF4/C3AR1/CCL2	4
BP	GO:00140	astrocyte development	3/32	44/1867 0	5.77E-05	0.0005987 99	0.0002750 11	GRN/VIM/TLR4	3

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00028	negative regulation of adaptive immune response	3/32	45/1867	6.18E-05	0.0006374	0.0002927	PTPRC/PTPN6/FCGR2B	3
BP	GO:00456	regulation of myeloid cell differentiation	5/32	251/186	6.32E-05	0.0006479	0.0002976	TYROBP/LYN/STAT3/TLR4/PF4	5
BP	GO:00105	positive regulation of endothelial cell migration	4/32	128/186	6.53E-05	0.0006665	0.0003061	AGT/LGMN/GRN/HMOX1	4
BP	GO:00716	regulation of mononuclear cell migration	3/32	46/1867	6.60E-05	0.0006703	0.0003078	LGMN/LYN/C3AR1	3
BP	GO:00508	B cell receptor signaling pathway	4/32	129/186	6.73E-05	0.0006799	0.0003122	LYN/PTPRC/PTPN6/FCGR2B	4
BP	GO:00433	mast cell degranulation	3/32	47/1867	7.05E-05	0.0007078	0.0003250	FCER1G/LYN/HMOX1	3
BP	GO:00022	mast cell activation involved in immune response	3/32	48/1867	7.51E-05	0.0007502	0.0003445	FCER1G/LYN/HMOX1	3
BP	GO:00029	regulation of humoral immune response	4/32	134/186	7.81E-05	0.0007761	0.0003564	PTPRC/PTPN6/C3AR1/FCGR2B	4
BP	GO:00024	mast cell mediated immunity	3/32	49/1867	7.99E-05	0.0007861	0.0003610	FCER1G/LYN/HMOX1	3
BP	GO:00327	positive regulation of interleukin-8 production	3/32	49/1867	7.99E-05	0.0007861	0.0003610	TLR4/TLR2/CD14	3
BP	GO:00434	response to peptide hormone	6/32	436/186	8.48E-05	0.0008306	0.0003814	AGT/FABP3/LYN/STAT3/TLR2/CYBB	6
BP	GO:00316	cellular response to extracellular stimulus	5/32	268/186	8.61E-05	0.0008388	0.0003852	LYN/PTPRC/CYBB/HMOX1/LCN2	5
BP	GO:00072	I-kappaB kinase/NF-kappaB signaling	5/32	269/186	8.76E-05	0.0008493	0.0003901	TLR4/TLR2/TNFRSF1A/HMOX1/CD14	5
BP	GO:00024	immune response-regulating cell surface receptor signaling pathway	4/32	139/186	9.00E-05	0.0008637	0.0003966	LYN/PTPRC/FCGR2B/FCGR3A	4
BP	GO:00380	involved in phagocytosis Fc-gamma receptor signaling pathway	4/32	139/186	9.00E-05	0.0008637	0.0003966	LYN/PTPRC/FCGR2B/FCGR3A	4
BP	GO:00975	involved in phagocytosis granulocyte migration	4/32	141/186	9.51E-05	0.0009084	0.0004172	FCER1G/PF4/C3AR1/CCL2	4
BP	GO:00028	regulation of adaptive immune response based on somatic recombination of	4/32	145/186	0.0001059	0.0010073	0.0004626	FCER1G/PTPRC/PTPN6/FCGR2B	4

Supplementary Table2. The details for actual gene IDs and GO descriptions

		immune receptors built								
		from immunoglobulin								
		superfamily domains								
BP	GO:19046	response to amyloid-beta	3/32	54/1867	0.0001069	0.0010111	0.0004643			
	45			0	04	51	92	LGMMN/TLR4/FCGR2B		3
BP	GO:00458	positive regulation of	4/32	146/186	0.0001088	0.0010195	0.0004682			
	34	lipid metabolic process		70	39	1	31	AGT/FABP3/LYN/TNFRSF1A		4
BP	GO:00512	negative regulation of	4/32	146/186	0.0001088	0.0010195	0.0004682			
	50	lymphocyte activation		70	39	1	31	TYROBP/LYN/PTPN6/FCGR2B		4
BP	GO:00068	cellular calcium ion	6/32	458/186	0.0001111	0.0010318	0.0004738			
	74	homeostasis		70	68	17	84	AGT/S1PR1/LYN/PTPRC/PTPN6/C3AR1		6
BP	GO:00022	myeloid cell homeostasis	4/32	147/186	0.0001117	0.0010318	0.0004738			
	62			70	49	17	84	FCER1G/LYN/STAT3/HMOX1		4
BP	GO:00435	negative regulation of	4/32	147/186	0.0001117	0.0010318	0.0004738			
	24	neuron apoptotic process		70	49	17	84	LGMMN/GRN/HMOX1/CCL2		4
BP	GO:00027	regulation of lymphocyte	4/32	149/186	0.0001177	0.0010768	0.0004945			
	06	mediated immunity		70	39	66	73	FCER1G/PTPRC/PTPN6/FCGR2B		4
BP	GO:00510	positive regulation of	4/32	149/186	0.0001177	0.0010768	0.0004945			
	92	NF-kappaB transcription factor activity		70	39	66	73	AGT/STAT3/TLR4/TLR2		4
BP	GO:00423	negative regulation of	6/32	468/186	0.0001251	0.0011390	0.0005231			
	26	phosphorylation		70	22	22	19	LYN/PTPRC/STAT3/TLR4/GMFG/PTPN6		6
BP	GO:00027	negative regulation of B	2/32	10/1867	0.0001269	0.0011451	0.0005259			
	13	cell mediated immunity		0	8	84	5	PTPN6/FCGR2B		2
BP	GO:00028	negative regulation of	2/32	10/1867	0.0001269	0.0011451	0.0005259			
	90	immunoglobulin mediated immune response		0	8	84	5	PTPN6/FCGR2B		2
BP	GO:00550	calcium ion homeostasis	6/32	471/186	0.0001295	0.0011631	0.0005341			
	74			70	69	25	89	AGT/S1PR1/LYN/PTPRC/PTPN6/C3AR1		6
BP	GO:00327	positive regulation of	3/32	58/1867	0.0001323	0.0011827	0.0005432			
	22	chemokine production		0	7	88	2	TLR4/TLR2/HMOX1		3
BP	GO:19037	negative regulation of	4/32	155/186	0.0001371	0.0012139	0.0005575			
	07	hemopoiesis		70	08	39	27	LYN/TLR4/PF4/FCGR2B		4
BP	GO:20012	regulation of extrinsic	4/32	155/186	0.0001371	0.0012139	0.0005575			
	36	apoptotic signaling pathway		70	08	39	27	AGT/PTPRC/PF4/HMOX1		4
BP	GO:00703	regulation of ERK1 and	5/32	300/186	0.0001461	0.0012881	0.0005916			
	72	ERK2 cascade		70	54	48	09	LYN/PTPRC/TLR4/PTPN6/CCL2		5
BP	GO:00028	regulation of adaptive	4/32	160/186	0.0001549	0.0013222	0.0006072			
	19	immune response		70	33	28	61	FCER1G/PTPRC/PTPN6/FCGR2B		4
BP	GO:19033	regulation of regulated	4/32	160/186	0.0001549	0.0013222	0.0006072			
	05	secretory pathway		70	33	28	61	FCER1G/LYN/FCGR2B/HMOX1		4
BP	GO:00028	negative regulation of	2/32	11/1867	0.0001550	0.0013222	0.0006072			
								FCGR2B/HMOX1		2

Supplementary Table2. The details for actual gene IDs and GO descriptions

	87	myeloid leukocyte mediated immunity	0	32	28	61			
BP	GO:00324	detection of molecule of bacterial origin	2/32	11/1867	0.0001550	0.0013222	0.0006072	TLR4/TLR2	2
	90		0	32	28	61			
BP	GO:00702	extracellular matrix constituent secretion	2/32	11/1867	0.0001550	0.0013222	0.0006072	AGT/TNFRSF1A	2
	78		0	32	28	61			
BP	GO:19025	regulation of neutrophil activation	2/32	11/1867	0.0001550	0.0013222	0.0006072	GRN/FCGR2B	2
	63		0	32	28	61			
BP	GO:19052	regulation of aspartic-type peptidase activity	2/32	11/1867	0.0001550	0.0013222	0.0006072	GRN/LYN	2
	45		0	32	28	61			
BP	GO:19030	regulation of leukocyte cell-cell adhesion	5/32	304/186	0.0001554	0.0013222	0.0006072	LYN/PTPRC/PTPN6/FCGR2B/CCL2	5
	37		70	76	28	61			
BP	GO:00725	cellular divalent inorganic cation homeostasis	6/32	493/186	0.0001661	0.0014070	0.0006462	AGT/S1PR1/LYN/PTPRC/PTPN6/C3AR1	6
	03		70	71	14	01			
BP	GO:00508	regulation of T cell activation	5/32	314/186	0.0001807	0.0015240	0.0006999	LYN/PTPRC/PTPN6/FCGR2B/CCL2	5
	63		70	8	52	53			
BP	GO:00029	negative regulation of humoral immune response	2/32	12/1867	0.0001858	0.0015298	0.0007026	PTPN6/FCGR2B	2
	21		0	39	2	02			
BP	GO:00360	response to macrophage colony-stimulating factor	2/32	12/1867	0.0001858	0.0015298	0.0007026	TLR4/TLR2	2
	05		0	39	2	02			
BP	GO:00360	cellular response to macrophage colony-stimulating factor stimulus	2/32	12/1867	0.0001858	0.0015298	0.0007026	TLR4/TLR2	2
	06		0	39	2	02			
BP	GO:00603	regulation of Fc receptor mediated stimulatory signaling pathway	2/32	12/1867	0.0001858	0.0015298	0.0007026	LYN/PTPRC	2
	68		0	39	2	02			
BP	GO:00025	monocyte chemotaxis	3/32	65/1867	0.0001858	0.0015298	0.0007026	LGMN/LYN/CCL2	3
	48		0	64	2	02			
BP	GO:00508	antigen receptor-mediated signaling pathway	5/32	316/186	0.0001861	0.0015298	0.0007026	LYN/PTPRC/LCP2/PTPN6/FCGR2B	5
	51		70	98	2	02			
BP	GO:00507	negative regulation of inflammatory response	4/32	169/186	0.0001911	0.0015639	0.0007182	GRN/PTPRC/TNFRSF1A/FCGR2B	4
	28		70	63	87	94			
BP	GO:00106	positive regulation of epithelial cell migration	4/32	171/186	0.0001999	0.0016292	0.0007482	AGT/LGMN/GRN/HMOX1	4
	34		70	78	34	6			
BP	GO:00466	response to antibiotic	5/32	327/186	0.0002182	0.0017506	0.0008040	STAT3/CYBB/HMOX1/CD14/LCN2	5
	77		70	56	29	13			
BP	GO:00022	macrophage activation involved in immune response	2/32	13/1867	0.0002193	0.0017506	0.0008040	GRN/TYROBP	2
	81		0	93	29	13			

Supplementary Table2. The details for actual gene IDs and GO descriptions

		regulation of acute								
BP	GO:00028	inflammatory response	2/32	13/1867	0.0002193	0.0017506	0.0008040		FCER1G/FCGR2B	2
	64	to antigenic stimulus		0	93	29	13			
BP	GO:00433	negative regulation of	2/32	13/1867	0.0002193	0.0017506	0.0008040		FCGR2B/HMOX1	2
	01	leukocyte degranulation		0	93	29	13			
BP	GO:00905	inflammatory response	2/32	13/1867	0.0002193	0.0017506	0.0008040		GRN/HMOX1	2
	94	to wounding		0	93	29	13			
BP	GO:00615	myeloid cell	3/32	70/1867	0.0002315	0.0018402	0.0008451		TYROBP/TLR2/PTPN6	3
	15	development		0	75	6	78			
BP	GO:19030	regulation of response to	4/32	179/186	0.0002381	0.0018851	0.0008657		FCER1G/GRN/LYN/TLR4	4
	34	wounding		70	96	48	94			
BP	GO:00425	positive regulation of	3/32	71/1867	0.0002415	0.0019036	0.0008742		LYN/STAT3/TNFRSF1A	3
	31	tyrosine phosphorylation		0	1	11	73			
		of STAT protein								
BP	GO:00071	leukocyte cell-cell	5/32	337/186	0.0002509	0.0019697	0.0009046		LYN/PTPRC/PTPN6/FCGR2B/CCL2	5
	59	adhesion		70	11	01	26			
BP	GO:00453	regulation of MHC class	2/32	14/1867	0.0002556	0.0019830	0.0009107		TLR4/PF4	2
	46	II biosynthetic process		0	84	88	75			
		JAK-STAT cascade								
BP	GO:00603	involved in growth	2/32	14/1867	0.0002556	0.0019830	0.0009107		LYN/STAT3	2
	97	hormone signaling		0	84	88	75			
		pathway								
BP	GO:00985	detection of other	2/32	14/1867	0.0002556	0.0019830	0.0009107		TLR4/TLR2	2
	43	organism		0	84	88	75			
BP	GO:00023	B cell activation	3/32	73/1867	0.0002622	0.0020174	0.0009265		PTPRC/TLR4/FCGR2B	3
	12	involved in immune		0	01	88	74			
		response								
BP	GO:00068	superoxide metabolic	3/32	73/1867	0.0002622	0.0020174	0.0009265		AGT/TYROBP/CYBB	3
	01	process		0	01	88	74			
BP	GO:00434	negative regulation of	4/32	184/186	0.0002646	0.0020279	0.0009313		LYN/PTPRC/TLR4/PTPN6	4
	09	MAPK cascade		70		01	56			
BP	GO:19037	positive regulation of	4/32	185/186	0.0002701	0.0020620	0.0009470		TYROBP/PTPRC/STAT3/PF4	4
	08	hemopoiesis		70	23	82	54			
BP	GO:00324	lysosome localization	3/32	74/1867	0.0002729	0.0020674	0.0009495		FCER1G/LYN/HMOX1	3
	18			0	62	73	3			
BP	GO:00703	negative regulation of	3/32	74/1867	0.0002729	0.0020674	0.0009495		LYN/PTPRC/TLR4	3
	73	ERK1 and ERK2		0	62	73	3			
		cascade								
BP	GO:00341	toll-like receptor 2	2/32	15/1867	0.0002947	0.0021978	0.0010093		LYN/TLR2	2
	34	signaling pathway		0	05	17	94			
BP	GO:00453	MHC class II	2/32	15/1867	0.0002947	0.0021978	0.0010093		TLR4/PF4	2
	42	biosynthetic process		0	05	17	94			
BP	GO:00454	positive regulation of	2/32	15/1867	0.0002947	0.0021978	0.0010093		TYROBP/STAT3	2
	10	interleukin-6		0	05	17	94			

Supplementary Table2. The details for actual gene IDs and GO descriptions

		biosynthetic process								
BP	GO:20004	positive regulation of interleukin-8 secretion	2/32	15/1867	0.0002947	0.0021978	0.0010093	TLR2/CD14		2
	84			0	05	17	94			
BP	GO:00324	positive regulation of type I interferon production	3/32	77/1867	0.0003069	0.0022630	0.0010393	TLR4/TLR2/CD14		3
	81			0	49	16	37			
BP	GO:00486	response to axon injury	3/32	77/1867	0.0003069	0.0022630	0.0010393	GRN/TYROBP/LYN		3
	78			0	49	16	37			
BP	GO:19012	positive regulation of NIK/NF-kappaB signaling	3/32	77/1867	0.0003069	0.0022630	0.0010393	TLR4/TLR2/CD14		3
	24			0	49	16	37			
BP	GO:00300	lymphocyte differentiation	5/32	353/186	0.0003107	0.0022824	0.0010482	FCER1G/PTPRC/STAT3/PTPN6/FCGR2B		5
	98			70	6	37	57			
BP	GO:00019	regulation of leukocyte mediated cytotoxicity	3/32	78/1867	0.0003188	0.0023330	0.0010715	TYROBP/PTPRC/FCGR2B		3
	10			0	56	6	06			
BP	GO:20003	regulation of reactive oxygen species metabolic process	4/32	195/186	0.0003300	0.0023863	0.0010959	AGT/TYROBP/STAT3/TLR4		4
	77			70	18	16	66			
BP	GO:00301	regulation of blood coagulation	3/32	79/1867	0.0003310	0.0023863	0.0010959	FCER1G/LYN/TLR4		3
	93			0	57	16	66			
BP	GO:00425	antigen processing and presentation of exogenous peptide antigen via MHC class I	3/32	79/1867	0.0003310	0.0023863	0.0010959	FCER1G/IFI30/CYBB		3
	90			0	57	16	66			
BP	GO:00712	cellular response to mechanical stimulus	3/32	79/1867	0.0003310	0.0023863	0.0010959	AGT/TLR4/TNFRSF1A		3
	60			0	57	16	66			
BP	GO:00109	positive regulation of peptidase activity	4/32	197/186	0.0003430	0.0024581	0.0011289	LGMMN/GRN/LYN/STAT3		4
	52			70	51	33	49			
BP	GO:19000	regulation of hemostasis	3/32	80/1867	0.0003435	0.0024581	0.0011289	FCER1G/LYN/TLR4		3
	46			0	55	33	49			
BP	GO:00321	negative regulation of response to external stimulus	5/32	365/186	0.0003623	0.0025830	0.0011863	GRN/PTPRC/TNFRSF1A/FCGR2B/CCL2		5
	02			70	41	1	02			
BP	GO:00326	regulation of chemokine production	3/32	82/1867	0.0003694	0.0026145	0.0012007	TLR4/TLR2/HMOX1		3
	42			0	57	17	72			
BP	GO:00462	nitric oxide metabolic process	3/32	82/1867	0.0003694	0.0026145	0.0012007	AGT/TLR4/TLR2		3
	09			0	57	17	72			
BP	GO:00508	positive regulation of T cell activation	4/32	202/186	0.0003772	0.0026599	0.0012216	LYN/PTPRC/PTPN6/CCL2		4
	70			70	48	45	35			
BP	GO:00107	positive regulation of macrophage derived foam cell differentiation	2/32	17/1867	0.0003808	0.0026662	0.0012245	AGT/PF4		2
	44			0	96	75	42			
BP	GO:00506	hydrogen peroxide biosynthetic process	2/32	17/1867	0.0003808	0.0026662	0.0012245	STAT3/CYBB		2
	65			0	96	75	42			

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00425	regulation of tyrosine phosphorylation of STAT protein	3/32	83/1867	0.0003828	0.0026704	0.0012264	LYN/STAT3/TNFRSF1A	3
BP	GO:00027	regulation of cytokine production involved in immune response	3/32	84/1867	0.0003965	0.0027463	0.0012613	FCER1G/TLR4/HMOX1	3
BP	GO:00508	regulation of coagulation	3/32	84/1867	0.0003965	0.0027463	0.0012613	FCER1G/LYN/TLR4	3
BP	GO:20010	reactive nitrogen species metabolic process	3/32	85/1867	0.0004106	0.0028334	0.0013013	AGT/TLR4/TLR2	3
BP	GO:00072	tyrosine phosphorylation of STAT protein	3/32	86/1867	0.0004249	0.0029020	0.0013328	LYN/STAT3/TNFRSF1A	3
BP	GO:00019	negative regulation of leukocyte mediated cytotoxicity	2/32	18/1867	0.0004280	0.0029020	0.0013328	PTPRC/FCGR2B	2
BP	GO:00072	I-kappaB phosphorylation	2/32	18/1867	0.0004280	0.0029020	0.0013328	TLR4/TLR2	2
BP	GO:00326	negative regulation of interleukin-10 production	2/32	18/1867	0.0004280	0.0029020	0.0013328	TYROBP/FCGR2B	2
BP	GO:01500	negative regulation of neuroinflammatory response	2/32	18/1867	0.0004280	0.0029020	0.0013328	GRN/PTPRC	2
BP	GO:00140	positive regulation of phosphatidylinositol 3-kinase signaling	3/32	87/1867	0.0004396	0.0029701	0.0013641	AGT/LYN/PTPN6	3
BP	GO:00313	positive regulation of cell projection organization	5/32	383/186	0.0004515	0.0030404	0.0013963	AGT/PLXNB2/GRN/LYN/LCN2	5
BP	GO:00326	chemokine production	3/32	89/1867	0.0004699	0.0031411	0.0014426	TLR4/TLR2/HMOX1	3
BP	GO:00027	negative regulation of T cell mediated immunity	2/32	19/1867	0.0004778	0.0031411	0.0014426	PTPRC/FCGR2B	2
BP	GO:00029	positive regulation of humoral immune response	2/32	19/1867	0.0004778	0.0031411	0.0014426	PTPRC/FCGR2B	2
BP	GO:00329	positive regulation of superoxide anion generation	2/32	19/1867	0.0004778	0.0031411	0.0014426	AGT/TYROBP	2
BP	GO:00610	positive regulation of myeloid leukocyte cytokine production involved in immune response	2/32	19/1867	0.0004778	0.0031411	0.0014426	FCER1G/TLR4	2
BP	GO:00985	detection of external	2/32	19/1867	0.0004778	0.0031411	0.0014426	TLR4/TLR2	2

Supplementary Table2. The details for actual gene IDs and GO descriptions

	81	biotic stimulus		0	97	61	44		
BP	GO:20000	positive regulation of protein localization to cell surface	2/32	19/1867	0.0004778	0.0031411	0.0014426	FCER1G/TYROBP	2
	10			0	97	61	44		
BP	GO:00171	regulation of exocytosis	4/32	217/186	0.0004944	0.0032392	0.0014876	FCER1G/LYN/FCGR2B/HMOX1	4
	57			70	84	07	73		
BP	GO:00456	negative regulation of myeloid cell differentiation	3/32	91/1867	0.0005015	0.0032518	0.0014934	LYN/TLR4/PF4	3
	38			0	41	55	83		
BP	GO:00456	positive regulation of myeloid cell differentiation	3/32	91/1867	0.0005015	0.0032518	0.0014934	TYROBP/STAT3/PF4	3
	39			0	41	55	83		
BP	GO:00160	immunoglobulin mediated immune response	4/32	218/186	0.0005031	0.0032518	0.0014934	FCER1G/PTPRC/PTPN6/FCGR2B	4
	64			70	24	55	83		
BP	GO:19030	positive regulation of leukocyte cell-cell adhesion	4/32	218/186	0.0005031	0.0032518	0.0014934	LYN/PTPRC/PTPN6/CCL2	4
	39			70	24	55	83		
BP	GO:00025	acute inflammatory response	4/32	220/186	0.0005207	0.0033544	0.0015405	FCER1G/STAT3/C3AR1/FCGR2B	4
	26			70	24	34	94		
BP	GO:00197	B cell mediated immunity	4/32	221/186	0.0005296	0.0033943	0.0015589	FCER1G/PTPRC/PTPN6/FCGR2B	4
	24			70	88	94	46		
BP	GO:19039	regulation of microglial cell activation	2/32	20/1867	0.0005304	0.0033943	0.0015589	GRN/PTPRC	2
	78			0	29	94	46		
BP	GO:19035	positive regulation of secretion by cell	5/32	399/186	0.0005440	0.0034703	0.0015938	AGT/FCER1G/TLR4/TLR2/CD14	5
	32			70	87	47	29		
BP	GO:00027	positive regulation of production of molecular mediator of immune response	3/32	95/1867	0.0005687	0.0035956	0.0016513	FCER1G/PTPRC/TLR4	3
	02			0	85	3	68		
BP	GO:00224	regulation of cell-cell adhesion	5/32	403/186	0.0005692	0.0035956	0.0016513	LYN/PTPRC/PTPN6/FCGR2B/CCL2	5
	07			70	93	3	68		
BP	GO:00457	positive regulation of cell adhesion	5/32	403/186	0.0005692	0.0035956	0.0016513	LYN/PTPRC/PTPN6/S100A10/CCL2	5
	85			70	93	3	68		
BP	GO:00024	acute inflammatory response to antigenic stimulus	2/32	21/1867	0.0005856	0.0036681	0.0016846	FCER1G/FCGR2B	2
	38			0	36	56	77		
BP	GO:00170	antibiotic biosynthetic process	2/32	21/1867	0.0005856	0.0036681	0.0016846	STAT3/CYBB	2
	00			0	36	56	77		
BP	GO:00024	antigen processing and presentation of peptide antigen via MHC class I	3/32	96/1867	0.0005864	0.0036681	0.0016846	FCER1G/IFI30/CYBB	3
	74			0	51	56	77		
BP	GO:00303	osteoclast differentiation	3/32	97/1867	0.0006044	0.0037624	0.0017279	FCER1G/TYROBP/TLR4	3
	16			0	65	21	71		

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00105	regulation of endothelial cell migration	4/32	229/186	0.0006054	0.0037624	0.0017279	AGT/LGMN/GRN/HMOX1	4
	94			70	03	21	71		
BP	GO:00313	regulation of cell killing	3/32	98/1867	0.0006228	0.0038583	0.0017720	TYROBP/PTPRC/FCGR2B	3
	41			0	29	56	31		
BP	GO:00313	negative regulation of cell killing	2/32	22/1867	0.0006435	0.0039486	0.0018134	PTPRC/FCGR2B	2
	42			0	11	32	92		
BP	GO:00329	regulation of superoxide anion generation	2/32	22/1867	0.0006435	0.0039486	0.0018134	AGT/TYROBP	2
	28			0	11	32	92		
BP	GO:00507	negative regulation of phagocytosis	2/32	22/1867	0.0006435	0.0039486	0.0018134	TLR2/FCGR2B	2
	65			0	11	32	92		
		phospholipase							
BP	GO:00072	C-activating G protein-coupled receptor signaling pathway	3/32	100/186	0.0006606	0.0040408	0.0018558	AGT/S1PR1/C3AR1	3
	00			70	2	29	35		
BP	GO:00064	negative regulation of protein kinase activity	4/32	235/186	0.0006670	0.0040671	0.0018679	LYN/PTPRC/GMFG/PTPN6	4
	69			70	28	91	42		
BP	GO:00486	positive regulation of smooth muscle cell proliferation	3/32	101/186	0.0006800	0.0041206	0.0018925	AGT/S1PR1/HMOX1	3
	61			70	53	96	16		
BP	GO:19034	regulation of reactive oxygen species biosynthetic process	3/32	101/186	0.0006800	0.0041206	0.0018925	AGT/STAT3/TLR4	3
	26			70	53	96	16		
BP	GO:20003	positive regulation of reactive oxygen species metabolic process	3/32	102/186	0.0006998	0.0042274	0.0019415	AGT/TYROBP/TLR4	3
	79			70	47	25	34		
BP	GO:00095	detection of biotic stimulus	2/32	23/1867	0.0007040	0.0042395	0.0019471	TLR4/TLR2	2
	95			0	44	7	11		
BP	GO:00313	negative regulation of defense response	4/32	239/186	0.0007105	0.0042520	0.0019528	GRN/PTPRC/TNFRSF1A/FCGR2B	4
	48			70	09	87	6		
BP	GO:00330	muscle cell proliferation	4/32	239/186	0.0007105	0.0042520	0.0019528	AGT/S1PR1/STAT3/HMOX1	4
	02			70	09	87	6		
BP	GO:19021	negative regulation of leukocyte differentiation	3/32	103/186	0.0007200	0.0042956	0.0019728	LYN/TLR4/FCGR2B	3
	06			70	06	65	74		
BP	GO:00510	positive regulation of secretion	5/32	428/186	0.0007473	0.0044450	0.0020415	AGT/FCER1G/TLR4/TLR2/CD14	5
	47			70	44	9	01		
BP	GO:00019	negative regulation of protein phosphorylation	5/32	429/186	0.0007552	0.0044783	0.0020567	LYN/PTPRC/TLR4/GMFG/PTPN6	5
	33			70	42	3	67		
BP	GO:00028	regulation of inflammatory response to antigenic stimulus	2/32	24/1867	0.0007672	0.0045080	0.0020704	FCER1G/FCGR2B	2
	61			0	27	39	11		
BP	GO:00315	membrane raft organization	2/32	24/1867	0.0007672	0.0045080	0.0020704	PTPRC/S100A10	2
	79			0	27	39	11		
BP	GO:00603	growth hormone receptor signaling pathway	2/32	24/1867	0.0007672	0.0045080	0.0020704	LYN/STAT3	2
	96			0	27	39	11		

Supplementary Table2. The details for actual gene IDs and GO descriptions

		regulation of								
BP	GO:00510	DNA-binding	5/32	432/186	0.0007793	0.0045652	0.0020966			
	90	transcription factor		70	13	19	72	AGT/STAT3/TLR4/TLR2/HMOX1		5
		activity								
		T cell activation								
BP	GO:00022	involved in immune	3/32	106/186	0.0007826	0.0045712	0.0020994			
	86	response		70	95	19	28	FCER1G/STAT3/FCGR2B		3
		homeostasis of number								
BP	GO:00488	of cells	4/32	246/186	0.0007913	0.0046080	0.0021163			
	72			70	85	95	64	FCER1G/LYN/STAT3/HMOX1		4
		calcium ion transport								
BP	GO:00068		5/32	434/186	0.0007956	0.0046192	0.0021214			
	16			70	77	15	71	AGT/LYN/PTPRC/PTPN6/CCL2		5
		modulation of chemical								
BP	GO:00508	synaptic transmission	5/32	436/186	0.0008122	0.0047016	0.0021593			
	04			70	98	29	21	AGT/LGMN/TYROBP/STAT3/CCL2		5
		regulation of								
BP	GO:00991	trans-synaptic signaling	5/32	437/186	0.0008207	0.0047361	0.0021751			
	77			70	05	53	78	AGT/LGMN/TYROBP/STAT3/CCL2		5
		cellular response to								
BP	GO:00713	growth hormone	2/32	25/1867	0.0008330	0.0047508	0.0021819			
	78	stimulus		0	51	39	22	LYN/STAT3		2
		regulation of monocyte								
BP	GO:00900	chemotaxis	2/32	25/1867	0.0008330	0.0047508	0.0021819			
	25			0	51	39	22	LGMN/LYN		2
		negative regulation of								
BP	GO:19033	regulated secretory	2/32	25/1867	0.0008330	0.0047508	0.0021819			
	06	pathway		0	51	39	22	FCGR2B/HMOX1		2
		regulation of								
BP	GO:20004	interleukin-8 secretion	2/32	25/1867	0.0008330	0.0047508	0.0021819			
	82			0	51	39	22	TLR2/CD14		2
		regulation of calcium ion								
BP	GO:00519	transport	4/32	254/186	0.0008915	0.0050696	0.0023283			
	24			70	7	6	47	AGT/LYN/PTPN6/CCL2		4
		positive regulation of								
BP	GO:00224	cell-cell adhesion	4/32	255/186	0.0009046	0.0051292	0.0023557			
	09			70	93	41	11	LYN/PTPRC/PTPN6/CCL2		4
		G protein-coupled								
		receptor signaling								
BP	GO:00071	pathway, coupled to	4/32	256/186	0.0009179	0.0051892	0.0023832			
	87	cyclic nucleotide second		70	53	44	69	AGT/S1PR1/PF4/CCL2		4
		messenger								
		negative regulation of								
BP	GO:00336	kinase activity	4/32	257/186	0.0009313	0.0052496	0.0024110			
	73			70	49	7	21	LYN/PTPRC/GMFG/PTPN6		4
		regulation of peptidase								
BP	GO:00525	activity	5/32	452/186	0.0009548	0.0053663	0.0024645			
	47			70	11	13	91	AGT/LGMN/GRN/LYN/STAT3		5
		positive regulation of								
		DNA-binding								
BP	GO:00510	transcription factor	4/32	261/186	0.0009863	0.0055273	0.0025385			
	91	activity		70	19	76	63	AGT/STAT3/TLR4/TLR2		4
		regulation of								
BP	GO:19012	NIK/NF-kappaB	3/32	117/186	0.0010419		0.0026621			
	22	signaling		70	77		18	TLR4/TLR2/CD14		3

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00454	regulation of interleukin-6 biosynthetic process	2/32	28/1867	0.0010462	0.0026621	0.0057964	0.0026621	TYROBP/STAT3	2
	08			0	82		18			
BP	GO:00508	antigen receptor-mediated signaling pathway	2/32	28/1867	0.0010462	0.0026621	0.0057964	0.0026621	PTPN6/FCGR2B	2
	58			0	82		18			
BP	GO:19907	response to angiotensin	2/32	28/1867	0.0010462	0.0026621	0.0057964	0.0026621	AGT/CYBB	2
	76			0	82		18			
BP	GO:00356	TRIF-dependent toll-like receptor signaling pathway	2/32	29/1867	0.0011225	0.0061488	0.0028239	0.0028239	TLR4/CD14	2
	66			0	83	37	82			
BP	GO:00422	interleukin-6 biosynthetic process	2/32	29/1867	0.0011225	0.0061488	0.0028239	0.0028239	TYROBP/STAT3	2
	26			0	83	37	82			
BP	GO:00508	regulation of B cell receptor signaling pathway	2/32	29/1867	0.0011225	0.0061488	0.0028239	0.0028239	LYN/FCGR2B	2
	55			0	83	37	82			
BP	GO:00726	interleukin-8 secretion	2/32	29/1867	0.0011225	0.0061488	0.0028239	0.0028239	TLR2/CD14	2
	06			0	83	37	82			
BP	GO:00328	response to insulin	4/32	272/186	0.0011492	0.0062771	0.0028829	0.0028829	AGT/FABP3/LYN/TLR2	4
	68			70	49	67	2			
BP	GO:00507	regulation of protein secretion	5/32	472/186	0.0011583	0.0063089	0.0028975	0.0028975	LYN/TLR4/TLR2/FCGR2B/CD14	5
	08			70	18	3	08			
BP	GO:00435	endothelial cell migration	4/32	273/186	0.0011649	0.0063272	0.0029059	0.0029059	AGT/LGMN/GRN/HMOX1	4
	42			70	42	33	14			
BP	GO:00341	erythrocyte homeostasis	3/32	122/186	0.0011757	0.0063504	0.0029165	0.0029165	LYN/STAT3/HMOX1	3
	01			70	69	64	84			
BP	GO:00435	muscle adaptation	3/32	122/186	0.0011757	0.0063504	0.0029165	0.0029165	AGT/TNFRSF1A/HMOX1	3
	00			70	69	64	84			
BP	GO:00507	positive regulation of neurogenesis	5/32	474/186	0.0011803	0.0063572	0.0029197	0.0029197	AGT/PLXNB2/GRN/LYN/TLR2	5
	69			70	12	93	2			
BP	GO:00107	regulation of macrophage derived foam cell differentiation	2/32	30/1867	0.0012014	0.0064355	0.0029556	0.0029556	AGT/PF4	2
	43			0	82	63	67			
BP	GO:00327	positive regulation of interferon-beta production	2/32	30/1867	0.0012014	0.0064355	0.0029556	0.0029556	TLR4/TLR2	2
	28			0	82	63	67			
BP	GO:00140	regulation of phosphatidylinositol 3-kinase signaling	3/32	124/186	0.0012321	0.0065637	0.0030145	0.0030145	AGT/LYN/PTPN6	3
	66			70	8	28	29			
BP	GO:00512	release of sequestered calcium ion into cytosol	3/32	124/186	0.0012321	0.0065637	0.0030145	0.0030145	LYN/PTPRC/PTPN6	3
	09			70	8	28	29			
BP	GO:00454	response to ethanol	3/32	125/186	0.0012610	0.0066989	0.0030766	0.0030766	STAT3/CYBB/CD14	3
	71			70	15	27	22			

Supplementary Table2. The details for actual gene IDs and GO descriptions

		positive regulation of cytosolic calcium ion concentration involved								
BP	GO:00514	in phospholipase C-activating G protein-coupled signaling pathway	2/32	31/1867	0.0012829	0.0067609	0.0031051	S1PR1/C3AR1		2
	82			0	71	8	22			
BP	GO:00347	regulation of ion transmembrane transport	5/32	483/186	0.0012831	0.0067609	0.0031051	AGT/LYN/PTPN6/CYBB/CCL2		5
	65			70	57	8	22			
BP	GO:00708	divalent metal ion transport	5/32	483/186	0.0012831	0.0067609	0.0031051	AGT/LYN/PTPRC/PTPN6/CCL2		5
	38			70	57	8	22			
BP	GO:00324	regulation of type I interferon production	3/32	126/186	0.0012902	0.0067617	0.0031054	TLR4/TLR2/CD14		3
	79			70	73	29	65			
BP	GO:00512	negative regulation of sequestering of calcium ion	3/32	126/186	0.0012902	0.0067617	0.0031054	LYN/PTPRC/PTPN6		3
	83			70	73	29	65			
BP	GO:00109	positive regulation of neuron projection development	4/32	281/186	0.0012959	0.0067732	0.0031107	AGT/PLXNB2/GRN/LYN		4
	76			70	57	08	38			
BP	GO:00025	platelet degranulation	3/32	128/186	0.0013500	0.0069994	0.0032146	FCER1G/LYN/PF4		3
	76			70	68	17	29			
BP	GO:00326	type I interferon production	3/32	128/186	0.0013500	0.0069994	0.0032146	TLR4/TLR2/CD14		3
	06			70	68	17	29			
BP	GO:00512	regulation of sequestering of calcium ion	3/32	128/186	0.0013500	0.0069994	0.0032146	LYN/PTPRC/PTPN6		3
	82			70	68	17	29			
BP	GO:00725	divalent inorganic cation transport	5/32	489/186	0.0013553	0.0070079	0.0032185	AGT/LYN/PTPRC/PTPN6/CCL2		5
	11			70	26	41	43			
BP	GO:00513	negative regulation of transferase activity	4/32	285/186	0.0013651	0.0070310	0.0032291	LYN/PTPRC/GMFG/PTPN6		4
	48			70	96	08	38			
BP	GO:00550	response to lipoprotein particle	2/32	32/1867	0.0013670	0.0070310	0.0032291	FCER1G/TLR4		2
	94			0	4	08	38			
BP	GO:00071	negative regulation of cell adhesion	4/32	289/186	0.0014369	0.0073594	0.0033800	PLXNB2/PTPRC/PTPN6/FCGR2B		4
	62			70	89	98	04			
BP	GO:00301	B cell differentiation	3/32	131/186	0.0014429	0.0073594	0.0033800	PTPRC/PTPN6/FCGR2B		3
	83			70	92	98	04			
BP	GO:00512	sequestering of calcium ion	3/32	131/186	0.0014429	0.0073594	0.0033800	LYN/PTPRC/PTPN6		3
	08			70	92	98	04			
BP	GO:00019	regulation of T cell mediated cytotoxicity	2/32	33/1867	0.0014536	0.0073594	0.0033800	PTPRC/FCGR2B		2
	14			0	81	98	04			
BP	GO:00027	MyD88-independent toll-like receptor signaling pathway	2/32	33/1867	0.0014536	0.0073594	0.0033800	TLR4/CD14		2
	56			0	81	98	04			
BP	GO:19018	positive regulation of cell junction assembly	2/32	33/1867	0.0014536	0.0073594	0.0033800	AGT/S100A10		2
	90			0	81	98	04			

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00106	regulation of epithelial cell migration	4/32	291/186	0.0014738	0.0074422	0.0034179	AGT/LGMN/GRN/HMOX1	4
	32			70	59	21	96		
BP	GO:00109	regulation of neuron projection development	5/32	499/186	0.0014822	0.0074651	0.0034285	AGT/PLXNB2/GRN/LYN/VIM	5
	75			70	52	61	31		
BP	GO:00027	regulation of peptide secretion	5/32	500/186	0.0014954	0.0075119	0.0034500	LYN/TLR4/TLR2/FCGR2B/CD14	5
	91			70	12	28	1		
BP	GO:00328	positive regulation of organic acid transport	2/32	34/1867	0.0015428	0.0076709	0.0035230	AGT/FABP3	2
	92			0	86	15	28		
BP	GO:00433	positive T cell selection	2/32	34/1867	0.0015428	0.0076709	0.0035230	PTPRC/STAT3	2
	68			0	86	15	28		
BP	GO:00459	negative regulation of exocytosis	2/32	34/1867	0.0015428	0.0076709	0.0035230	FCGR2B/HMOX1	2
	20			0	86	15	28		
BP	GO:00714	cellular response to lipoprotein particle stimulus	2/32	34/1867	0.0015428	0.0076709	0.0035230	FCER1G/TLR4	2
	02			0	86	15	28		
BP	GO:00509	positive regulation of chemotaxis	3/32	135/186	0.0015730	0.0078007	0.0035826	S1PR1/LGMN/C3AR1	3
	21			70	2	31	49		
BP	GO:00027	negative regulation of production of molecular mediator of immune response	2/32	35/1867	0.0016346	0.0080446	0.0036946	FCGR2B/HMOX1	2
	01			0	47	2	6		
BP	GO:00327	positive regulation of interleukin-12 production	2/32	35/1867	0.0016346	0.0080446	0.0036946	TLR4/TLR2	2
	35			0	47	2	6		
BP	GO:00987	bone cell development	2/32	35/1867	0.0016346	0.0080446	0.0036946	TYROBP/PTPN6	2
	51			0	47	2	6		
BP	GO:00345	cellular response to oxidative stress	4/32	302/186	0.0016885	0.0082889	0.0038068	TLR4/CYBB/HMOX1/LCN2	4
	99			70	68	44	71		
BP	GO:00507	positive regulation of cytokine secretion	3/32	139/186	0.0017101	0.0083527	0.0038361	TLR4/TLR2/CD14	3
	15			70	86	71	85		
BP	GO:00706	positive regulation of leukocyte proliferation	3/32	139/186	0.0017101	0.0083527	0.0038361	LYN/PTPRC/TLR4	3
	65			70	86	71	85		
BP	GO:00107	macrophage derived foam cell differentiation	2/32	36/1867	0.0017289	0.0083811	0.0038491	AGT/PF4	2
	42			0	54	05	98		
BP	GO:00900	foam cell differentiation	2/32	36/1867	0.0017289	0.0083811	0.0038491	AGT/PF4	2
	77			0	54	05	98		
BP	GO:00903	regulation of superoxide metabolic process	2/32	36/1867	0.0017289	0.0083811	0.0038491	AGT/TYROBP	2
	22			0	54	05	98		
BP	GO:00975	calcium ion transmembrane import into cytosol	3/32	140/186	0.0017456	0.0084407	0.0038765	LYN/PTPRC/PTPN6	3
	53			70	09	38	85		
BP	GO:00027	positive regulation of B cell mediated immunity	2/32	37/1867	0.0018258	0.0087412	0.0040146	FCER1G/PTPRC	2
	14			0		97	24		
BP	GO:00028	positive regulation of	2/32	37/1867	0.0018258	0.0087412	0.0040146	FCER1G/PTPRC	2

Supplementary Table2. The details for actual gene IDs and GO descriptions

	91	immunoglobulin mediated immune response	0	97	24				
BP	GO:00457	respiratory burst	2/32	37/1867	0.0018258	0.0087412	0.0040146	GRN/CYBB	2
	30			0	97	24			
BP	GO:00712	cellular response to cadmium ion	2/32	37/1867	0.0018258	0.0087412	0.0040146	CYBB/HMOX1	2
	76			0	97	24			
BP	GO:19021	positive regulation of leukocyte differentiation	3/32	144/186	0.0018918	0.0090354	0.0041497	TYROBP/PTPRC/PF4	3
	07			70	95	31	11		
BP	GO:00346	response to tumor necrosis factor	4/32	312/186	0.0019018	0.0090608	0.0041613	TNFRSF1A/CD14/LCN2/CCL2	4
	12			70	95	7	94		
BP	GO:00482	macrophage chemotaxis	2/32	38/1867	0.0019251	0.0091257	0.0041911	C3AR1/CCL2	2
	46			0	75	18	77		
BP	GO:00604	response to growth hormone	2/32	38/1867	0.0019251	0.0091257	0.0041911	LYN/STAT3	2
	16			0	75	18	77		
BP	GO:00076	learning	3/32	145/186	0.0019296	0.0091257	0.0041911	AGT/LGMN/TLR2	3
	12			70	26	18	77		
BP	GO:00310	stress-activated protein kinase signaling cascade	4/32	315/186	0.0019693	0.0092910	0.0042671	AGT/LYN/TLR4/FCGR2B	4
	98			70	83	81	23		
BP	GO:00140	phosphatidylinositol 3-kinase signaling	3/32	148/186	0.0020456	0.0096040	0.0044108	AGT/LYN/PTPN6	3
	65			70	33	72	71		
BP	GO:00610	regulation of wound healing	3/32	148/186	0.0020456	0.0096040	0.0044108	FCER1G/LYN/TLR4	3
	41			70	33	72	71		
		humoral immune response mediated by circulating immunoglobulin							
BP	GO:00024	response mediated by circulating immunoglobulin	3/32	150/186	0.0021253	0.0099349	0.0045628	PTPRC/PTPN6/FCGR2B	3
	55			70	37	6	38		
		negative regulation of cytokine biosynthetic process							
BP	GO:00420	negative regulation of cytokine biosynthetic process	2/32	40/1867	0.0021314	0.0099349	0.0045628	TYROBP/PTPRC	2
	36			0	82	6	38		
		regulation of protein localization to cell surface							
BP	GO:20000	regulation of protein localization to cell surface	2/32	40/1867	0.0021314	0.0099349	0.0045628	FCER1G/TYROBP	2
	08			0	82	6	38		
		positive regulation of B cell proliferation							
BP	GO:00308	positive regulation of B cell proliferation	2/32	41/1867	0.0022383	0.0103585	0.0047574	PTPRC/TLR4	2
	90			0	97	94	01		
		regulation of neuroinflammatory response							
BP	GO:01500	regulation of neuroinflammatory response	2/32	41/1867	0.0022383	0.0103585	0.0047574	GRN/PTPRC	2
	77			0	97	94	01		
		regulation of extracellular matrix organization							
BP	GO:19030	regulation of extracellular matrix organization	2/32	41/1867	0.0022383	0.0103585	0.0047574	AGT/TNFRSF1A	2
	53			0	97	94	01		
		neurotransmitter metabolic process							
BP	GO:00421	neurotransmitter metabolic process	3/32	153/186	0.0022484	0.0103805	0.0047674	AGT/TLR4/TLR2	3
	33			70	85	07	65		
BP	GO:00512	maintenance of location	4/32	330/186	0.0023319	0.0107403	0.0049327	LYN/PTPRC/PTPN6/LCN2	4

Supplementary Table2. The details for actual gene IDs and GO descriptions

	35		70	66	37	24			
BP	GO:00970	dendritic cell differentiation	2/32	42/1867	0.0023478	0.0107621	0.0049427	LYN/FCGR2B	2
BP	GO:20012	regulation of neuron migration	2/32	42/1867	0.0023478	0.0107621	0.0049427	PLXNB2/STAT3	2
BP	GO:00454	positive regulation of nitric oxide biosynthetic process	2/32	43/1867	0.0024597	0.0112390	0.0051617	AGT/TLR4	2
BP	GO:00604	calcium ion transport into cytosol	3/32	158/186	0.0024634	0.0112390	0.0051617	LYN/PTPRC/PTPN6	3
BP	GO:00026	regulation of acute inflammatory response	3/32	159/186	0.0025079	0.0114150	0.0052426	FCER1G/C3AR1/FCGR2B	3
BP	GO:00434	regulation of MAP kinase activity	4/32	337/186	0.0025160	0.0114251	0.0052472	LYN/PTPRC/TLR4/PTPN6	4
BP	GO:00140	oligodendrocyte development	2/32	44/1867	0.0025740	0.0115804	0.0053185	LYN/TLR2	2
BP	GO:00302	macrophage differentiation	2/32	44/1867	0.0025740	0.0115804	0.0053185	TLR2/PF4	2
BP	GO:00702	necroptotic process	2/32	44/1867	0.0025740	0.0115804	0.0053185	TLR4/CD14	2
BP	GO:19044	positive regulation of nitric oxide metabolic process	2/32	44/1867	0.0025740	0.0115804	0.0053185	AGT/TLR4	2
BP	GO:19040	regulation of cation transmembrane transport	4/32	342/186	0.0026534	0.0119098	0.0054698	AGT/LYN/PTPN6/CCL2	4
BP	GO:00011	response to acid chemical	4/32	343/186	0.0026815	0.0120081	0.0055149	FABP3/LYN/TLR2/CYBB	4
BP	GO:19002	regulation of long-term synaptic potentiation	2/32	45/1867	0.0026909	0.0120224	0.0055215	LGMN/TYROBP	2
BP	GO:00024	inflammatory response to antigenic stimulus	2/32	46/1867	0.0028102	0.0124692	0.0057267	FCER1G/FCGR2B	2
BP	GO:00336	regulation of cell adhesion mediated by integrin	2/32	46/1867	0.0028102	0.0124692	0.0057267	LYN/PTPN6	2
BP	GO:00432	apoptotic cell clearance	2/32	46/1867	0.0028102	0.0124692	0.0057267	TYROBP/CCL2	2
BP	GO:00106	epithelial cell migration	4/32	351/186	0.0029137	0.0128915	0.0059207	AGT/LGMN/GRN/HMOX1	4
BP	GO:00508	positive regulation of synaptic transmission	3/32	168/186	0.0029306	0.0128915	0.0059207	LGMN/TYROBP/CCL2	3
BP	GO:00450	T cell selection	2/32	47/1867	0.0029320	0.0128915	0.0059207	PTPRC/STAT3	2
BP	GO:00456	regulation of erythrocyte differentiation	2/32	47/1867	0.0029320	0.0128915	0.0059207	LYN/STAT3	2

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00024	lymphocyte mediated immunity	4/32	352/186	0.0029437	0.0129137	0.0059309	FCER1G/PTPRC/PTPN6/FCGR2B	4
	49			70	17	29			
BP	GO:00380	Fc-epsilon receptor signaling pathway	3/32	169/186	0.0029801	0.0130146	0.0059772	FCER1G/LYN/LCP2	3
	95			70	45	42	47		
BP	GO:00486	regulation of smooth muscle cell proliferation	3/32	169/186	0.0029801	0.0130146	0.0059772	AGT/S1PR1/HMOX1	3
	60			70	45	42	47		
BP	GO:00901	epithelium migration	4/32	354/186	0.0030042	0.0130905	0.0060121	AGT/LGMN/GRN/HMOX1	4
	32			70	84	76	21		
BP	GO:00027	negative regulation of myeloid leukocyte differentiation	2/32	48/1867	0.0030562	0.0131689	0.0060481	LYN/TLR4	2
	62			0	34	72	26		
BP	GO:00326	regulation of interferon-beta production	2/32	48/1867	0.0030562	0.0131689	0.0060481	TLR4/TLR2	2
	48			0	34	72	26		
BP	GO:01010	vascular endothelial cell proliferation	2/32	48/1867	0.0030562	0.0131689	0.0060481	STAT3/CCL2	2
	23			0	34	72	26		
BP	GO:19037	positive regulation of phospholipid metabolic process	2/32	48/1867	0.0030562	0.0131689	0.0060481	FABP3/LYN	2
	27			0	34	72	26		
BP	GO:19055	regulation of vascular endothelial cell proliferation	2/32	48/1867	0.0030562	0.0131689	0.0060481	STAT3/CCL2	2
	62			0	34	72	26		
BP	GO:00486	smooth muscle cell proliferation	3/32	171/186	0.0030807	0.0132156	0.0060695	AGT/S1PR1/HMOX1	3
	59			70	07	88	81		
BP	GO:00604	cytosolic calcium ion transport	3/32	171/186	0.0030807	0.0132156	0.0060695	LYN/PTPRC/PTPN6	3
	01			70	07	88	81		
BP	GO:00019	T cell mediated cytotoxicity	2/32	49/1867	0.0031828	0.0134770	0.0061896	PTPRC/FCGR2B	2
	13			0	88	7	26		
BP	GO:00026	negative regulation of leukocyte migration	2/32	49/1867	0.0031828	0.0134770	0.0061896	HMOX1/CCL2	2
	86			0	88	7	26		
BP	GO:00973	programmed necrotic cell death	2/32	49/1867	0.0031828	0.0134770	0.0061896	TLR4/CD14	2
	00			0	88	7	26		
BP	GO:20012	positive regulation of extrinsic apoptotic signaling pathway	2/32	49/1867	0.0031828	0.0134770	0.0061896	AGT/PTPRC	2
	38			0	88	7	26		
BP	GO:00016	temperature homeostasis	3/32	173/186	0.0031833	0.0134770	0.0061896	STAT3/TLR4/LCN2	3
	59			70	41	7	26		
BP	GO:00703	positive regulation of stress-activated protein kinase signaling cascade	3/32	173/186	0.0031833	0.0134770	0.0061896	LYN/TLR4/FCGR2B	3
	04			70	41	7	26		
BP	GO:00901	tissue migration	4/32	360/186	0.0031911	0.0134805	0.0061912	AGT/LGMN/GRN/HMOX1	4
	30			70	16	55	27		
BP	GO:00458	positive regulation of proteolysis	4/32	363/186	0.0032874	0.0138573	0.0063642	LGMN/GRN/LYN/STAT3	4
	62			70	57	45	76		

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00326	interferon-beta production	2/32	50/1867	0.0033119	0.0139002	0.0063839	TLR4/TLR2	2
	08			0	72	45	78		
BP	GO:19037	positive regulation of anion transport	2/32	50/1867	0.0033119	0.0139002	0.0063839	AGT/FABP3	2
	93			0	72	45	78		
BP	GO:00100	response to metal ion	4/32	364/186	0.0033200	0.0139038	0.0063856	LGMN/CYBB/HMOX1/CD14	4
	38			70	08	8	48		
BP	GO:00019	regulation of endothelial cell proliferation	3/32	176/186	0.0033412	0.0139324	0.0063987	STAT3/HMOX1/CCL2	3
	36			70	06	72	79		
BP	GO:00094	response to heat	3/32	176/186	0.0033412	0.0139324	0.0063987	LYN/HMOX1/CD14	3
	08			70	06	72	79		
BP	GO:00019	regulation of cytokine-mediated signaling pathway	3/32	177/186	0.0033948	0.0141259	0.0064876	PTPRC/TNFRSF1A/PTPN6	3
	59			70	79	03	17		
BP	GO:00481	positive regulation of fibroblast proliferation	2/32	51/1867	0.0034434		0.0065630	AGT/S100A6	2
	46			0	78		27		
BP	GO:00109	positive regulation of endopeptidase activity	3/32	178/186	0.0034490		0.0065630	LGMN/LYN/STAT3	3
	50			70	8		27		
BP	GO:00356	cellular response to drug	4/32	369/186	0.0034860	0.0144126	0.0066192	VIM/CYBB/HMOX1/LCN2	4
	90			70	86	24	99		
BP	GO:00456	positive regulation of neuron differentiation	4/32	371/186	0.0035540	0.0146624	0.0067340	AGT/PLXNB2/GRN/LYN	4
	66			70	8	69	46		
BP	GO:00327	positive regulation of interleukin-1 beta production	2/32	52/1867	0.0035773	0.0147273	0.0067638	TYROBP/TLR4	2
	31			0	98	36	37		
BP	GO:00480	phosphatidylinositol-me diated signaling	3/32	181/186	0.0036148	0.0148500	0.0068202	AGT/LYN/PTPN6	3
	15			70	7	69	05		
BP	GO:00327	negative regulation of interleukin-6 production	2/32	53/1867	0.0037137	0.0151545	0.0069600	TLR4/PTPN6	2
	15			0	24	57	47		
BP	GO:00507	negative regulation of peptidyl-tyrosine phosphorylation	2/32	53/1867	0.0037137	0.0151545	0.0069600	PTPRC/PTPN6	2
	32			0	24	57	47		
BP	GO:19055	macrophage migration	2/32	53/1867	0.0037137	0.0151545	0.0069600	C3AR1/CCL2	2
	17			0	24	57	47		
BP	GO:00380	NIK/NF-kappaB signaling	3/32	183/186	0.0037280	0.0151545	0.0069600	TLR4/TLR2/CD14	3
	61			70	68	57	47		
BP	GO:00431	I-kappaB kinase/NF-kappaB signaling	3/32	183/186	0.0037280	0.0151545	0.0069600	TLR4/TNFRSF1A/HMOX1	3
	23			70	68	57	47		
BP	GO:00480	inositol lipid-mediated signaling	3/32	184/186	0.0037854	0.0153557	0.0070524	AGT/LYN/PTPN6	3
	17			70	74	18	35		
BP	GO:00506	regulation of epithelial cell proliferation	4/32	378/186	0.0037991	0.0153792	0.0070632	GRN/STAT3/HMOX1/CCL2	4
	78			70	98	16	26		
BP	GO:00027	positive regulation of	2/32	54/1867	0.0038524	0.0154977	0.0071176	FCER1G/TLR4	2

Supplementary Table2. The details for actual gene IDs and GO descriptions

	20	cytokine production involved in immune response		0	48	12	48			
BP	GO:00027	63	positive regulation of myeloid leukocyte differentiation	2/32	54/1867	0.0038524	0.0154977	0.0071176	TYROBP/PF4	2
BP	GO:00326	55	regulation of interleukin-12 production	2/32	54/1867	0.0038524	0.0154977	0.0071176	TLR4/TLR2	2
BP	GO:00481	67	regulation of synaptic plasticity	3/32	187/186	0.0039609	0.0159011	0.0073029	AGT/LGMN/TYROBP	3
BP	GO:00019	12	positive regulation of leukocyte mediated cytotoxicity	2/32	56/1867	0.0041370	0.0164886	0.0075727	TYROBP/PTPRC	2
BP	GO:00312	95	T cell costimulation	2/32	56/1867	0.0041370	0.0164886	0.0075727	LYN/PTPN6	2
BP	GO:00326	15	interleukin-12 production	2/32	56/1867	0.0041370	0.0164886	0.0075727	TLR4/TLR2	2
BP	GO:00712	48	cellular response to metal ion	3/32	190/186	0.0041412	0.0164886	0.0075727	LGMN/CYBB/HMOX1	3
BP	GO:00019	35	endothelial cell proliferation	3/32	191/186	0.0042025	0.0166981	0.0076689	STAT3/HMOX1/CCL2	3
BP	GO:00312	94	lymphocyte costimulation	2/32	57/1867	0.0042829	0.0168450	0.0077364	LYN/PTPN6	2
BP	GO:00427	43	hydrogen peroxide metabolic process	2/32	57/1867	0.0042829	0.0168450	0.0077364	STAT3/CYBB	2
BP	GO:00435	25	positive regulation of neuron apoptotic process	2/32	57/1867	0.0042829	0.0168450	0.0077364	GRN/TYROBP	2
BP	GO:00607	60	positive regulation of response to cytokine stimulus	2/32	57/1867	0.0042829	0.0168450	0.0077364	TLR4/TLR2	2
BP	GO:19034	28	positive regulation of reactive oxygen species biosynthetic process	2/32	57/1867	0.0042829	0.0168450	0.0077364	AGT/TLR4	2
BP	GO:00109	59	regulation of metal ion transport	4/32	394/186	0.0044022	0.0172793	0.0079359	AGT/LYN/PTPN6/CCL2	4
BP	GO:00327	32	positive regulation of interleukin-1 production	2/32	59/1867	0.0045817	0.0178393	0.0081931	TYROBP/TLR4	2
BP	GO:00328	90	regulation of organic acid transport	2/32	59/1867	0.0045817	0.0178393	0.0081931	AGT/FABP3	2
BP	GO:00705	27	platelet aggregation	2/32	59/1867	0.0045817	0.0178393	0.0081931	LYN/PTPN6	2
BP	GO:00977	55	positive regulation of blood vessel diameter	2/32	59/1867	0.0045817	0.0178393	0.0081931	AGT/HMOX1	2

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00068	cellular iron ion homeostasis	2/32	61/1867	0.0048899	0.0189831	0.0087183	HMOX1/LCN2	2
	79			0	75	19	94		
BP	GO:20012	regulation of apoptotic signaling pathway	4/32	406/186	0.0048950	0.0189831	0.0087183	AGT/PTPRC/PF4/HMOX1	4
	33			70	8	19	94		
BP	GO:00508	T cell receptor signaling pathway	3/32	202/186	0.0049125	0.0190129	0.0087320	PTPRC/LCP2/PTPN6	3
	52			70	78	52	96		
BP	GO:00508	synapse organization	4/32	408/186	0.0049806	0.0192381	0.0088355	LGMN/PLXNB2/TLR2/FCGR2B	4
	08			70	85	43	19		
BP	GO:00326	interleukin-2 production	2/32	62/1867	0.0050475	0.0194192	0.0089186	FCER1G/PTPRC	2
	23			0	91	04	76		
BP	GO:00702	necrotic cell death	2/32	62/1867	0.0050475	0.0194192	0.0089186	TLR4/CD14	2
	65			0	91	04	76		
BP	GO:00192	regulation of lipid metabolic process	4/32	410/186	0.0050672	0.0194564	0.0089357	AGT/FABP3/LYN/TNFRSF1A	4
	16			70	96	11	64		
BP	GO:00506	positive regulation of epithelial cell proliferation	3/32	206/186	0.0051876	0.0197988	0.0090930	GRN/STAT3/HMOX1	3
	79			70	85	35	29		
BP	GO:00026	regulation of immunoglobulin production	2/32	63/1867	0.0052075	0.0197988	0.0090930	PTPRC/FCGR2B	2
	37			0	33	35	29		
BP	GO:00075	excretion	2/32	63/1867	0.0052075	0.0197988	0.0090930	AGT/HMOX1	2
	88			0	33	35	29		
BP	GO:00343	protein localization to cell surface	2/32	63/1867	0.0052075	0.0197988	0.0090930	FCER1G/TYROBP	2
	94			0	33	35	29		
BP	GO:00466	response to cadmium ion	2/32	63/1867	0.0052075	0.0197988	0.0090930	CYBB/HMOX1	2
	86			0	33	35	29		
BP	GO:00456	regulation of osteoclast differentiation	2/32	64/1867	0.0053697	0.0203757	0.0093580	TYROBP/TLR4	2
	70			0	92	87	06		
BP	GO:00096	response to mechanical stimulus	3/32	210/186	0.0054719	0.0207228	0.0095174	AGT/TLR4/TNFRSF1A	3
	12			70	47	62	08		
BP	GO:00327	positive regulation of interferon-gamma production	2/32	65/1867	0.0055343	0.0208751	0.0095873	TLR4/CD14	2
	29			0	61	35	42		
BP	GO:00726	T cell migration	2/32	65/1867	0.0055343	0.0208751	0.0095873	S1PR1/CCL2	2
	78			0	61	35	42		
BP	GO:19035	negative regulation of secretion by cell	3/32	211/186	0.0055444	0.0208751	0.0095873	TNFRSF1A/FCGR2B/HMOX1	3
	31			70	53	35	42		
BP	GO:00400	regulation of multicellular organism growth	2/32	66/1867	0.0057012	0.0213823	0.0098203	LGMN/STAT3	2
	14			0	32	78	04		
BP	GO:00454	regulation of nitric oxide biosynthetic process	2/32	66/1867	0.0057012	0.0213823	0.0098203	AGT/TLR4	2
	28			0	32	78	04		
BP	GO:00525	regulation of endopeptidase activity	4/32	425/186	0.0057495	0.0215218	0.0098843	AGT/LGMN/LYN/STAT3	4
	48			70	23	63	66		

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00703	positive regulation of ERK1 and ERK2 cascade	3/32	215/186	0.0058402	0.0218194	0.0100210	PTPRC/TLR4/CCL2	3
	74			70	79	61	44		
BP	GO:00603	bone development	3/32	217/186	0.0059916	0.0222992	0.0102413	TYROBP/PTPRC/PTPN6	3
	48			70	9	07	77		
BP	GO:00712	cellular response to inorganic substance	3/32	217/186	0.0059916	0.0222992	0.0102413	LGMN/CYBB/HMOX1	3
	41			70	9	07	77		
BP	GO:00022	T cell differentiation involved in immune response	2/32	68/1867	0.0060418	0.0223145	0.0102484	FCER1G/STAT3	2
	92			0	49	61	29		
BP	GO:00313	positive regulation of cell killing	2/32	68/1867	0.0060418	0.0223145	0.0102484	TYROBP/PTPRC	2
	43			0	49	61	29		
BP	GO:00336	cell adhesion mediated by integrin	2/32	68/1867	0.0060418	0.0223145	0.0102484	LYN/PTPN6	2
	27			0	49	61	29		
BP	GO:00458	negative regulation of endocytosis	2/32	68/1867	0.0060418	0.0223145	0.0102484	TLR2/FCGR2B	2
	06			0	49	61	29		
BP	GO:00506	epithelial cell proliferation	4/32	434/186	0.0061871	0.0228077	0.0104749	GRN/STAT3/HMOX1/CCL2	4
	73			70	33	02	14		
BP	GO:00027	regulation of T cell mediated immunity	2/32	70/1867	0.0063915	0.0234721	0.0107800	PTPRC/FCGR2B	2
	09			0	78	03	54		
BP	GO:00327	negative regulation of tumor necrosis factor production	2/32	70/1867	0.0063915	0.0234721	0.0107800	TLR4/PTPN6	2
	20			0	78	03	54		
BP	GO:00192	transmission of nerve impulse	2/32	72/1867	0.0067503	0.0246032	0.0112995	AGT/S1PR1	2
	26			0	59	82	72		
BP	GO:00380	signal transduction in absence of ligand	2/32	72/1867	0.0067503	0.0246032	0.0112995	PF4/LCN2	2
	34			0	59	82	72		
BP	GO:00971	extrinsic apoptotic signaling pathway in absence of ligand	2/32	72/1867	0.0067503	0.0246032	0.0112995	PF4/LCN2	2
	92			0	59	82	72		
BP	GO:19035	negative regulation of tumor necrosis factor superfamily cytokine production	2/32	72/1867	0.0067503	0.0246032	0.0112995	TLR4/PTPN6	2
	56			0	59	82	72		
BP	GO:00069	response to oxidative stress	4/32	451/186	0.0070735	0.0257329	0.0118183	TLR4/CYBB/HMOX1/LCN2	4
	79			70	67	18	81		
BP	GO:00140	positive regulation of gliogenesis	2/32	74/1867	0.0071181	0.0257500	0.0118262	LYN/TLR2	2
	15			0	28	95	7		
BP	GO:00316	cellular response to nutrient	2/32	74/1867	0.0071181	0.0257500	0.0118262	CYBB/HMOX1	2
	70			0	28	95	7		
BP	GO:19030	positive regulation of response to wounding	2/32	74/1867	0.0071181	0.0257500	0.0118262	GRN/TLR4	2
	36			0	28	95	7		
BP	GO:00973	response to alcohol	3/32	233/186	0.0072882	0.0263163	0.0120863	STAT3/CYBB/CD14	3
	05			70	22	18	19		

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00106	regulation of cardiac muscle hypertrophy	2/32	75/1867	0.0073053	0.0263291	0.0120922	AGT/TNFRSF1A	2
	11			0	65	86	3		
BP	GO:00016	ameboidal-type cell migration	4/32	461/186	0.0076325	0.0273695	0.0125700	AGT/LGMN/GRN/HMOX1	4
	67			70	81	34	31		
BP	GO:00316	cellular response to nutrient levels	3/32	237/186	0.0076363	0.0273695	0.0125700	CYBB/HMOX1/LCN2	3
	69			70	68	34	31		
BP	GO:00431	regulation of I-kappaB kinase/NF-kappaB signaling	3/32	237/186	0.0076363	0.0273695	0.0125700	TLR4/TNFRSF1A/HMOX1	3
	22			70	68	34	31		
BP	GO:00068	nitric oxide biosynthetic process	2/32	77/1867	0.0076865	0.0274983	0.0126292	AGT/TLR4	2
	09			0	02	89	1		
BP	GO:00510	negative regulation of secretion	3/32	238/186	0.0077249	0.0275849	0.0126689	TNFRSF1A/FCGR2B/HMOX1	3
	48			70	25	52	66		
BP	GO:00703	regulation of stress-activated protein kinase signaling cascade	3/32	239/186	0.0078140	0.0278520	0.0127916	LYN/TLR4/FCGR2B	3
	02			70	91	63	43		
BP	GO:00030	muscle system process	4/32	465/186	0.0078641	0.0278833	0.0128060	AGT/VIM/TNFRSF1A/HMOX1	4
	12			70	61	41	08		
BP	GO:00083	associative learning	2/32	78/1867	0.0078803	0.0278833	0.0128060	AGT/LGMN	2
	06			0	87	41	08		
BP	GO:00147	regulation of muscle hypertrophy	2/32	78/1867	0.0078803	0.0278833	0.0128060	AGT/TNFRSF1A	2
	43			0	87	41	08		
BP	GO:00434	negative regulation of MAP kinase activity	2/32	78/1867	0.0078803	0.0278833	0.0128060	LYN/PTPN6	2
	07			0	87	41	08		
BP	GO:00302	T cell differentiation	3/32	240/186	0.0079038	0.0279154	0.0128207	FCER1G/PTPRC/STAT3	3
	17			70	68	84	7		
BP	GO:00550	iron ion homeostasis	2/32	79/1867	0.0080764	0.0284732	0.0130769	HMOX1/LCN2	2
	72			0	74	41	32		
BP	GO:00092	response to temperature stimulus	3/32	243/186	0.0081768	0.0287748	0.0132154	LYN/HMOX1/CD14	3
	66			70	76	86	69		
BP	GO:00970	dendritic spine organization	2/32	80/1867	0.0082747	0.0290140	0.0133252	LGMN/FCGR2B	2
	61			0	54	09	91		
BP	GO:01400	exocytic process	2/32	80/1867	0.0082747	0.0290140	0.0133252	FCER1G/LYN	2
	29			0	54	09	91		
BP	GO:00341	homotypic cell-cell adhesion	2/32	81/1867	0.0084752	0.0296632	0.0136234	LYN/PTPN6	2
	09			0	19	68	76		
BP	GO:00972	cellular response to toxic substance	3/32	247/186	0.0085494	0.0298693	0.0137181	CYBB/HMOX1/LCN2	3
	37			70	99	32	16		
BP	GO:00512	regulation of release of sequestered calcium ion into cytosol	2/32	82/1867	0.0086778	0.0302632	0.0138990	LYN/PTPN6	2
	79			0	63	68	39		
BP	GO:00430	regulation of GTPase activity	4/32	479/186	0.0087112	0.0303252	0.0139275	S1PR1/PLXNB2/S100A10/CCL2	4
	87			70	86	86	22		
BP	GO:00481	regulation of fibroblast	2/32	83/1867	0.0088826	0.0308112	0.0141507	AGT/S100A6	2

Supplementary Table2. The details for actual gene IDs and GO descriptions

	45	proliferation		0	78	93	31		
BP	GO:20001	regulation of leukocyte	2/32	83/1867	0.0088826	0.0308112	0.0141507	FCER1G/LYN	2
	06	apoptotic process		0	78	93	31		
BP	GO:00105	negative regulation of	2/32	84/1867	0.0090896	0.0312579	0.0143558	STAT3/HMOX1	2
	07	autophagy		0	56	49	67		
BP	GO:00468	positive regulation of lipid biosynthetic	2/32	84/1867	0.0090896	0.0312579	0.0143558	FABP3/TNFRSF1A	2
	89	process		0	56	49	67		
BP	GO:00481	fibroblast proliferation	2/32	84/1867	0.0090896	0.0312579	0.0143558	AGT/S100A6	2
	44			0	56	49	67		
BP	GO:00514	regulation of stress fiber	2/32	84/1867	0.0090896	0.0312579	0.0143558	S1PR1/S100A10	2
	92	assembly		0	56	49	67		
BP	GO:00488	multicellular organismal	4/32	485/186	0.0090920	0.0312579	0.0143558	S1PR1/STAT3/TLR4/LCN2	4
	71	homeostasis		70	49	49	67		
BP	GO:19047	regulation of vascular smooth muscle cell	2/32	85/1867	0.0092987	0.0318557	0.0146304	AGT/HMOX1	2
	05	proliferation		0	9	47	18		
BP	GO:19908	vascular smooth muscle	2/32	85/1867	0.0092987	0.0318557	0.0146304	AGT/HMOX1	2
	74	cell proliferation		0	9	47	18		
BP	GO:00076	learning or memory	3/32	256/186	0.0094241	0.0322283	0.0148015	AGT/LGMN/TLR2	3
	11			70	84	83	59		
BP	GO:00017	leukocyte homeostasis	2/32	86/1867	0.0095100	0.0322378	0.0148058	FCER1G/LYN	2
	76			0	71	11	89		
BP	GO:00086	extrinsic apoptotic signaling pathway via death domain receptors	2/32	86/1867	0.0095100	0.0322378	0.0148058	TNFRSF1A/HMOX1	2
	25			0	71	11	89		
BP	GO:00301	natural killer cell	2/32	86/1867	0.0095100	0.0322378	0.0148058	TYROBP/PTPRC	2
	01	activation		0	71	11	89		
BP	GO:00602	long-term synaptic	2/32	86/1867	0.0095100	0.0322378	0.0148058	LGMN/TYROBP	2
	91	potentiation		0	71	11	89		
BP	GO:00705	response to fatty acid	2/32	86/1867	0.0095100	0.0322378	0.0148058	FABP3/TLR2	2
	42			0	71	11	89		
BP	GO:00026	positive regulation of leukocyte chemotaxis	2/32	87/1867	0.0097234	0.0329037	0.0151117	LGMN/C3AR1	2
	90			0	93	58	39		
BP	GO:00726	protein localization to plasma membrane	3/32	260/186	0.0098291	0.0331130	0.0152078	FCER1G/TNFRSF1A/S100A10	3
	59			70	89	84	77		
BP	GO:01100	regulation of actin filament organization	3/32	261/186	0.0099320	0.0331130	0.0152078	S1PR1/GMFG/S100A10	3
	53			70	13	84	77		
BP	GO:00341	regulation of tissue remodeling	2/32	88/1867	0.0099390	0.0331130	0.0152078	AGT/S1PR1	2
	03			0	48	84	77		
BP	GO:00610	regulation of protein tyrosine kinase activity	2/32	88/1867	0.0099390	0.0331130	0.0152078	AGT/PTPRC	2
	97			0	48	84	77		
BP	GO:00700	chemokine-mediated signaling pathway	2/32	88/1867	0.0099390	0.0331130	0.0152078	PF4/CCL2	2
	98			0	48	84	77		

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:01060	neuron projection	2/32	88/1867	0.0099390	0.0331130	0.0152078	LGMN/FCGR2B	2
	27	organization		0	48	84	77		
BP	GO:19018	regulation of cell	2/32	88/1867	0.0099390	0.0331130	0.0152078	AGT/S100A10	2
	88	junction assembly		0	48	84	77		
BP	GO:19037	regulation of phospholipid metabolic process	2/32	88/1867	0.0099390	0.0331130	0.0152078	FABP3/LYN	2
	25			0	48	84	77		
BP	GO:19040	regulation of epithelial cell apoptotic process	2/32	88/1867	0.0099390	0.0331130	0.0152078	HMOX1/CCL2	2
	35			0	48	84	77		
BP	GO:00158	monoamine transport	2/32	90/1867	0.0103765	0.0344522	0.0158228	AGT/FCER1G	2
	44			0	28	06	97		
BP	GO:00326	regulation of interleukin-1 beta production	2/32	90/1867	0.0103765	0.0344522	0.0158228	TYROBP/TLR4	2
	51			0	28	06	97		
BP	GO:00507	positive regulation of protein secretion	3/32	268/186	0.0106694	0.0353643	0.0162418	TLR4/TLR2/CD14	3
	14			70	87	34	1		
BP	GO:19011	regulation of ERBB signaling pathway	2/32	93/1867	0.0110485	0.0365582	0.0167901	AGT/LGMN	2
	84			0	61	92	6		
BP	GO:00432	positive regulation of ion transport	3/32	275/186	0.0114381	0.0377828	0.0173525	AGT/FABP3/CCL2	3
	70			70	3	52	65		
BP	GO:00440	regulation of anion transport	2/32	95/1867	0.0115070	0.0378814	0.0173978	AGT/FABP3	2
	70			0	37	01	26		
BP	GO:01100	regulation of actomyosin structure organization	2/32	95/1867	0.0115070	0.0378814	0.0173978	S1PR1/S100A10	2
	20			0	37	01	26		
BP	GO:00106	regulation of muscle cell apoptotic process	2/32	96/1867	0.0117393	0.0385155	0.0176890	AGT/HMOX1	2
	60			0	9	29	63		
BP	GO:00302	megakaryocyte differentiation	2/32	96/1867	0.0117393	0.0385155	0.0176890	PTPN6/PF4	2
	19			0	9	29	63		
BP	GO:00322	regulation of actin filament bundle assembly	2/32	97/1867	0.0119738	0.0390205	0.0179209	S1PR1/S100A10	2
	31			0	1	33	96		
BP	GO:00487	oligodendrocyte differentiation	2/32	97/1867	0.0119738	0.0390205	0.0179209	LYN/TLR2	2
	09			0	1	33	96		
BP	GO:19908	response to chemokine	2/32	97/1867	0.0119738	0.0390205	0.0179209	PF4/CCL2	2
	68			0	1	33	96		
BP	GO:19908	cellular response to chemokine	2/32	97/1867	0.0119738	0.0390205	0.0179209	PF4/CCL2	2
	69			0	1	33	96		
BP	GO:00300	contractile actin filament bundle assembly	2/32	98/1867	0.0122102	0.0396578	0.0182137	S1PR1/S100A10	2
	38			0	89	72	07		
BP	GO:00431	stress fiber assembly	2/32	98/1867	0.0122102	0.0396578	0.0182137	S1PR1/S100A10	2
	49			0	89	72	07		
BP	GO:00028	positive regulation of adaptive immune response based on	2/32	100/186	0.0126893	0.0410730	0.0188636	FCER1G/PTPRC	2
	24			70	95	15	41		

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00028	positive regulation of adaptive immune response	2/32	105/186	0.0139226	0.0437165	0.0200777	FCER1G/PTPRC	2
	21			70	9	59	44		
BP	GO:00550	cardiac muscle tissue growth	2/32	105/186	0.0139226	0.0437165	0.0200777	AGT/S1PR1	2
	17			70	9	59	44		
BP	GO:00508	cognition	3/32	296/186	0.0139333	0.0437165	0.0200777	AGT/LGMN/TLR2	3
	90			70	85	59	44		
BP	GO:00024	T cell mediated immunity	2/32	106/186	0.0141753	0.0442609	0.0203277	PTPRC/FCGR2B	2
	56			70	82	76	79		
BP	GO:00033	cardiac muscle hypertrophy	2/32	106/186	0.0141753	0.0442609	0.0203277	AGT/TNFRSF1A	2
	00			70	82	76	79		
BP	GO:00421	neurotransmitter biosynthetic process	2/32	106/186	0.0141753	0.0442609	0.0203277	AGT/TLR4	2
	36			70	82	76	79		
BP	GO:00435	regulation of muscle adaptation	2/32	107/186	0.0144300	0.0449837	0.0206597	AGT/TNFRSF1A	2
	02			70	69	67	36		
BP	GO:00156	ammonium transport	2/32	108/186	0.0146867	0.0455641	0.0209262	FCER1G/LYN	2
	96			70	43	5	89		
BP	GO:00300	cellular monovalent inorganic cation homeostasis	2/32	108/186	0.0146867	0.0455641	0.0209262	AGT/GRN	2
	04			70	43	5	89		
BP	GO:00469	cellular transition metal ion homeostasis	2/32	108/186	0.0146867	0.0455641	0.0209262	HMOX1/LCN2	2
	16			70	43	5	89		
BP	GO:00148	striated muscle hypertrophy	2/32	109/186	0.0149453	0.0462925	0.0212608	AGT/TNFRSF1A	2
	97			70	96	3	13		
BP	GO:00148	muscle hypertrophy	2/32	111/186	0.0154686	0.0476846	0.0219001	AGT/TNFRSF1A	2
	96			70	16	53	75		
BP	GO:00726	lymphocyte migration	2/32	111/186	0.0154686	0.0476846	0.0219001	S1PR1/CCL2	2
	76			70	16	53	75		
BP	GO:19040	epithelial cell apoptotic process	2/32	111/186	0.0154686	0.0476846	0.0219001	HMOX1/CCL2	2
	19			70	16	53	75		
BP	GO:00019	positive regulation of endothelial cell proliferation	2/32	112/186	0.0157331	0.0482699	0.0221689	STAT3/HMOX1	2
	38			70	68	57	87		
BP	GO:00508	negative regulation of T cell activation	2/32	112/186	0.0157331	0.0482699	0.0221689	PTPN6/FCGR2B	2
	68			70	68	57	87		
BP	GO:00604	heart growth	2/32	112/186	0.0157331	0.0482699	0.0221689	AGT/S1PR1	2
	19			70	68	57	87		
BP	GO:19907	protein localization to cell periphery	3/32	311/186	0.0158917	0.0486795	0.0223571	FCER1G/TNFRSF1A/S100A10	3
	78			70	82	67	1		
BP	GO:00022	stimulatory C-type lectin receptor signaling pathway	2/32	113/186	0.0159996	0.0487788	0.0224027	FCER1G/LYN	2
	23			70	71	72	18		
BP	GO:00326	interferon-gamma production	2/32	113/186	0.0159996	0.0487788	0.0224027	TLR4/CD14	2
	09			70	71	72	18		

Supplementary Table2. The details for actual gene IDs and GO descriptions

BP	GO:00432	response to amino acid	2/32	113/186	0.0159996	0.0487788	0.0224027	LYN/CYBB	2
	00			70	71	72	18		
BP	GO:00066	icosanoid metabolic	2/32	114/186	0.0162681	0.0493076	0.0226455	TLR2/TNFRSF1A	2
	90	process		70	2	12	52		
BP	GO:00302	erythrocyte	2/32	114/186	0.0162681	0.0493076	0.0226455	LYN/STAT3	2
	18	differentiation		70	2	12	52		
BP	GO:00454	endothelial cell	2/32	114/186	0.0162681	0.0493076	0.0226455	S1PR1/TNFRSF1A	2
	46	differentiation		70	2	12	52		
BP	GO:00519	negative regulation of nervous system development	3/32	315/186	0.0164390	0.0493076	0.0226455	VIM/STAT3/TLR2	3
	61			70	43	12	52		
BP	GO:00705	calcium ion	3/32	315/186	0.0164390	0.0493076	0.0226455	LYN/PTPRC/PTPN6	3
	88	transmembrane transport		70	43	12	52		
BP	GO:00326	interleukin-1 production	2/32	115/186	0.0165385	0.0493076	0.0226455	TYROBP/TLR4	2
	12			70	06	12	52		
BP	GO:00329	collagen metabolic	2/32	115/186	0.0165385	0.0493076	0.0226455	CTSB/VIM	2
	63	process		70	06	12	52		
BP	GO:00068	receptor-mediated	3/32	316/186	0.0165775	0.0493076	0.0226455	FCER1G/FCGR2B/CD14	3
	98	endocytosis		70	1	12	52		
		innate immune response							
BP	GO:00022	activating cell surface	2/32	116/186	0.0168108	0.0493076	0.0226455	FCER1G/LYN	2
	20	receptor signaling pathway		70	23	12	52		
BP	GO:00018	serotonin secretion	1/32	10/1867	0.0170122	0.0493076	0.0226455	FCER1G	1
	20			0	7	12	52		
BP	GO:00033	sphingosine-1-phosphate receptor signaling pathway	1/32	10/1867	0.0170122	0.0493076	0.0226455	S1PR1	1
	76			0	7	12	52		
BP	GO:00158	arginine transport	1/32	10/1867	0.0170122	0.0493076	0.0226455	AGT	1
	09			0	7	12	52		
BP	GO:00326	interleukin-18	1/32	10/1867	0.0170122	0.0493076	0.0226455	TLR2	1
	21	production		0	7	12	52		
BP	GO:00332	leptin-mediated	1/32	10/1867	0.0170122	0.0493076	0.0226455	STAT3	1
	10	signaling pathway		0	7	12	52		
BP	GO:00341	regulation of toll-like receptor 2 signaling pathway	1/32	10/1867	0.0170122	0.0493076	0.0226455	LYN	1
	35			0	7	12	52		
BP	GO:00343	regulation of glial cell apoptotic process	1/32	10/1867	0.0170122	0.0493076	0.0226455	CCL2	1
	50			0	7	12	52		
BP	GO:00427	drinking behavior	1/32	10/1867	0.0170122	0.0493076	0.0226455	AGT	1
	56			0	7	12	52		
BP	GO:00445	long-chain fatty acid	1/32	10/1867	0.0170122	0.0493076	0.0226455	FABP3	1
	39	import		0	7	12	52		
BP	GO:00453	positive regulation of	1/32	10/1867	0.0170122	0.0493076	0.0226455	TLR4	1

Supplementary Table2. The details for actual gene IDs and GO descriptions

	48	MHC class II biosynthetic process	0	7	12	52			
BP	GO:0048304	positive regulation of isotype switching to IgG isotypes	1/32	10/1867	0.0170122	0.0493076	0.0226455	PTPRC	1
BP	GO:0051014	actin filament severing	1/32	10/1867	0.0170122	0.0493076	0.0226455	GMFG	1
BP	GO:0071104	response to interleukin-9	1/32	10/1867	0.0170122	0.0493076	0.0226455	STAT3	1
BP	GO:0071281	cellular response to iron ion	1/32	10/1867	0.0170122	0.0493076	0.0226455	HMOX1	1
BP	GO:0090154	positive regulation of sphingolipid biosynthetic process	1/32	10/1867	0.0170122	0.0493076	0.0226455	TNFRSF1A	1
BP	GO:0097048	dendritic cell apoptotic process	1/32	10/1867	0.0170122	0.0493076	0.0226455	LYN	1
BP	GO:0140052	cellular response to oxidised low-density lipoprotein particle stimulus	1/32	10/1867	0.0170122	0.0493076	0.0226455	TLR4	1
BP	GO:1900426	positive regulation of defense response to bacterium	1/32	10/1867	0.0170122	0.0493076	0.0226455	GRN	1
BP	GO:1903332	regulation of protein folding	1/32	10/1867	0.0170122	0.0493076	0.0226455	GRN	1
BP	GO:1903789	regulation of amino acid transmembrane transport	1/32	10/1867	0.0170122	0.0493076	0.0226455	AGT	1
BP	GO:1990822	basic amino acid transmembrane transport	1/32	10/1867	0.0170122	0.0493076	0.0226455	AGT	1
BP	GO:2000304	positive regulation of ceramide biosynthetic process	1/32	10/1867	0.0170122	0.0493076	0.0226455	TNFRSF1A	1
BP	GO:2000425	regulation of apoptotic cell clearance	1/32	10/1867	0.0170122	0.0493076	0.0226455	CCL2	1
BP	GO:2000668	regulation of dendritic cell apoptotic process	1/32	10/1867	0.0170122	0.0493076	0.0226455	LYN	1
CC	GO:0045121	membrane raft	9/32	315/19717	1.23E-09	6.72E-08	3.81E-08	S1PR1/LYN/PTPRC/TLR2/TNFRSF1A/LCP2/S100A10/HMOX1/CD14	9
CC	GO:0098857	membrane microdomain	9/32	316/19717	1.26E-09	6.72E-08	3.81E-08	S1PR1/LYN/PTPRC/TLR2/TNFRSF1A/LCP2/S100A10/HMOX1/CD14	9
CC	GO:0098589	membrane region	9/32	328/19717	1.75E-09	6.72E-08	3.81E-08	S1PR1/LYN/PTPRC/TLR2/TNFRSF1A/LCP2/S100A10/HMOX1/CD14	9
CC	GO:0030667	secretory granule membrane	7/32	298/19717	4.09E-07	1.18E-05	6.67E-06	FCER1G/TYROBP/PTPRC/TLR2/CYBB/C3AR1/CD14	7

Supplementary Table2. The details for actual gene IDs and GO descriptions

CC	GO:00098	external side of plasma membrane	7/32	393/197 17	2.59E-06	5.97E-05	3.39E-05	S1PR1/FCER1G/PTPRC/TLR4/FCGR2B/FCGR3A/CD14	7
CC	GO:00347	secretory granule lumen	6/32	321/197 17	1.13E-05	0.0002159	0.0001225	GRN/GMFG/PTPN6/PF4/S100A11/LCN2	6
CC	GO:00602	cytoplasmic vesicle lumen	6/32	338/197 17	1.51E-05	0.0002207	0.0001252	GRN/GMFG/PTPN6/PF4/S100A11/LCN2	6
CC	GO:00319	vesicle lumen	6/32	339/197 17	1.54E-05	0.0002207	0.0001252	GRN/GMFG/PTPN6/PF4/S100A11/LCN2	6
CC	GO:00425	specific granule	4/32	160/197 17	0.0001257	0.0016074	0.0009122	PTPN6/CYBB/C3AR1/LCN2	4
CC	GO:00057	vacuolar lumen	4/32	172/197 17	0.0001661	0.0019108	0.0010844	LGMN/GRN/CTSB/IFI30	4
CC	GO:00620	collagen-containing extracellular matrix	5/32	406/197 17	0.0004598	0.0042961	0.0024380	AGT/CTSB/S100A6/PF4/S100A10	5
CC	GO:00360	endolysosome	2/32	20/197 7	0.0004760	0.0042961	0.0024380	LGMN/CTSB	2
CC	GO:00432	lysosomal lumen	3/32	95/197 7	0.0004856	0.0042961	0.0024380	LGMN/CTSB/IFI30	3
CC	GO:00453	phagocytic vesicle	3/32	132/197 17	0.0012621	0.0103675	0.0058836	VIM/TLR2/CYBB	3
CC	GO:00319	endosome lumen	2/32	34/197 7	0.0013858	0.0106251	0.0060298	LGMN/CTSB	2
CC	GO:00098	cytoplasmic side of plasma membrane	3/32	154/197 17	0.0019628	0.0141076	0.0080061	LYN/PTPRC/S100A6	3
CC	GO:00708	tertiary granule	3/32	164/197 17	0.0023474	0.0152587	0.0086594	FCER1G/PTPN6/CYBB	3
CC	GO:00198	extrinsic component of plasma membrane	3/32	165/197 17	0.0023883	0.0152587	0.0086594	LYN/S100A6/S100A10	3
CC	GO:00985	cytoplasmic side of membrane	3/32	178/197 17	0.0029599	0.0179156	0.0101672	LYN/PTPRC/S100A6	3
CC	GO:01010	ficolin-1-rich granule	3/32	185/197 17	0.0032998	0.0189738	0.0107677	FCER1G/CTSB/GMFG	3
CC	GO:00355	specific granule lumen	2/32	62/197 7	0.0045411	0.0248682	0.0141128	PTPN6/LCN2	2
CC	GO:00059	cell-cell junction	4/32	459/197 17	0.0062214	0.0312068	0.0177100	LYN/LCP2/PTPN6/S100A11	4
CC	GO:00708	tertiary granule membrane	2/32	73/197 7	0.0062413	0.0312068	0.0177100	FCER1G/CYBB	2
CC	GO:00306	phagocytic vesicle membrane	2/32	76/197 7	0.0067481	0.0323349	0.0183502	TLR2/CYBB	2
CC	GO:00312	extrinsic component of cytoplasmic side of plasma membrane	2/32	91/197 7	0.0095506	0.0422430	0.0239731	LYN/S100A6	2
CC	GO:00355	specific granule	2/32	91/197 7	0.0095506	0.0422430	0.0239731	CYBB/C3AR1	2

Supplementary Table2. The details for actual gene IDs and GO descriptions

	79	membrane		7	06	63	8		
CC	GO:00198	extrinsic component of	3/32	295/197	0.0119345	0.0490170	0.0278174		
	98	membrane		17	88	57	6	LYN/S100A6/S100A10	3
CC	GO:00988	plasma membrane	3/32	295/197	0.0119345	0.0490170	0.0278174		
	02	receptor complex		17	88	57	6	LYN/TLR2/PTPN6	3
MF	GO:00198	IgG binding	3/32	11/1769		0.0001123			
	64			7	8.77E-07		6.47E-05	FCER1G/FCGR2B/FCGR3A	3
MF	GO:00083	signaling pattern recognition receptor	3/32	20/1769		0.0002980	0.0001715		
	29	activity		7	6.00E-06			TLR4/TLR2/CD14	3
MF	GO:00381	pattern recognition receptor activity	3/32	21/1769		0.0002980	0.0001715		
	87			7	6.99E-06			TLR4/TLR2/CD14	3
MF	GO:00198	immunoglobulin binding	3/32	24/1769		0.0003389	0.0001951		
	65			7	1.06E-05			FCER1G/FCGR2B/FCGR3A	3
MF	GO:00015	lipopolysaccharide binding	3/32	35/1769		0.0008651	0.0004980		
	30			7	3.38E-05			TLR4/TLR2/CD14	3
MF	GO:00016	G protein-coupled receptor binding	5/32	280/176	0.0001357	0.0025830	0.0014869		
	64			97	51	54	56	AGT/S1PR1/STAT3/PF4/CCL2	5
MF	GO:00717	lipopeptide binding	2/32	10/1769	0.0001412	0.0025830	0.0014869		
	23			7	61	54	56	TLR2/CD14	2
MF	GO:00423	chemokine receptor binding	3/32	66/1769	0.0002274	0.0036391	0.0020949		
	79			7	47	48	04	STAT3/PF4/CCL2	3
MF	GO:00445	S100 protein binding	2/32	15/1769	0.0003277	0.0045179			
	48			7	52	61	0.0026008	S100A6/S100A11	2
MF	GO:00015	amyloid-beta binding	3/32	78/1769	0.0003726	0.0045179			
	40			7	04	61	0.0026008	TLR4/TLR2/FCGR2B	3
MF	GO:00050	transmembrane receptor protein tyrosine phosphatase activity	2/32	17/1769	0.0004235	0.0045179			
	01			7	59	61	0.0026008	PTPRC/PTPN6	2
MF	GO:00191	transmembrane receptor protein phosphatase activity	2/32	17/1769	0.0004235	0.0045179			
	98			7	59	61	0.0026008	PTPRC/PTPN6	2
MF	GO:00466	sphingolipid binding	2/32	23/1769	0.0007826	0.0077058	0.0044359		
	25			7	25	45	31	S1PR1/LYN	2
MF	GO:00480	receptor ligand activity	5/32	482/176	0.0016095	0.0147163	0.0084715		
	18			97	96	08	59	AGT/GRN/GMFG/PF4/CCL2	5
MF	GO:00422	peptide binding	4/32	295/176	0.0018830	0.0153637	0.0088442		
	77			97	89	07	39	TLR4/TLR2/FCGR2B/CD14	4
MF	GO:00433	proteoglycan binding	2/32	36/1769	0.0019204	0.0153637	0.0088442		
	94			7	63	07	39	CTSB/PTPRC	2
MF	GO:00480	CCR chemokine receptor binding	2/32	43/1769	0.0027310	0.0205631	0.0118373		
	20			7	39	2	22	STAT3/CCL2	2
MF	GO:00080	growth factor activity	3/32	163/176	0.0031273	0.0222391	0.0128021		
	83			97	79	4	36	AGT/GRN/GMFG	3

Supplementary Table2. The details for actual gene IDs and GO descriptions

MF	GO:0008009	chemokine activity	2/32	49/1769	0.0035327	0.0237481	0.0136707	PF4/CCL2	2
				7	55	1	87		
MF	GO:0033218	amide binding	4/32	356/176	0.0037106	0.0237481	0.0136707	TLR4/TLR2/FCGR2B/CD14	4
				97	42	1	87		
MF	GO:0048306	calcium-dependent protein binding	2/32	61/1769	0.0054236	0.0330586	0.0190304	S100A6/S100A11	2
				7	88	69	84		
MF	GO:0005125	cytokine activity	3/32	220/176	0.0072070	0.0419320	0.0241385	GRN/PF4/CCL2	3
				97	67	28	03		
MF	GO:0005539	glycosaminoglycan binding	3/32	229/176	0.0080439	0.0447661	0.0257699	PTPRC/TLR2/PF4	3
				97	15	35	79		

Supplementary Table3. The details for actual gene IDs per pathway

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa05152	Tuberculosis	7/28	180/8102	1.90E-06	0.000206814	0.000117837	FCER1G/TLR4/TLR2/TNFRSF1A/FCGR2B/FCGR3A/CD14	7
hsa05140	Leishmaniasis	5/28	77/8102	5.63E-06	0.000288306	0.000164269	TLR4/TLR2/PTPN6/CYBB/FCGR3A	5
	Coronavirus							
hsa05171	disease - COVID-19	7/28	232/8102	1.02E-05	0.000288306	0.000164269	STAT3/TLR4/TLR2/TNFRSF1A/CYBB/C3AR1/CCL2	7
hsa04145	Phagosome	6/28	152/8102	1.06E-05	0.000288306	0.000164269	TLR4/TLR2/CYBB/FCGR2B/FCGR3A/CD14	6
hsa04380	Osteoclast differentiation	5/28	128/8102	6.68E-05	0.001355675	0.000772427	TYROBP/TNFRSF1A/LCP2/FCGR2B/FCGR3A	5
	Natural killer							
hsa04650	cell mediated cytotoxicity	5/28	131/8102	7.46E-05	0.001355675	0.000772427	FCER1G/TYROBP/LCP2/PTPN6/FCGR3A	5
hsa05132	Salmonella infection	6/28	249/8102	0.000169173	0.002634273	0.001500938	PTPRC/TLR4/TLR2/TNFRSF1A/S100A10/CD14	6
	PD-L1 expression and							
hsa05235	PD-1 checkpoint pathway in cancer	4/28	89/8102	0.000227737	0.003102916	0.001767958	STAT3/TLR4/TLR2/PTPN6	4
	Fc gamma							
hsa04666	R-mediated phagocytosis	4/28	97/8102	0.000317096	0.003759384	0.002141996	LYN/PTPRC/FCGR2B/FCGR3A	4
	AGE-RAGE signaling							
hsa04933	pathway in diabetic complications	4/28	100/8102	0.000356316	0.003759384	0.002141996	AGT/STAT3/CYBB/CCL2	4
hsa05142	Chagas disease	4/28	102/8102	0.000384324	0.003759384	0.002141996	TLR4/TLR2/TNFRSF1A/CCL2	4
	NF-kappa B							
hsa04064	signaling pathway	4/28	104/8102	0.000413877	0.003759384	0.002141996	LYN/TLR4/TNFRSF1A/CD14	4
	HIF-1							
hsa04066	signaling pathway	4/28	109/8102	0.00049484	0.004149044	0.002364013	STAT3/TLR4/CYBB/HMOX1	4
hsa05145	Toxoplasmosis	4/28	112/8102	0.00054852	0.004270621	0.002433285	STAT3/TLR4/TLR2/TNFRSF1A	4
hsa05144	Malaria	3/28	50/8102	0.000649963	0.004723061	0.002691073	TLR4/TLR2/CCL2	3
hsa05134	Legionellosis	3/28	57/8102	0.000954732	0.006504109	0.003705866	TLR4/TLR2/CD14	3
hsa05162	Measles	4/28	139/8102	0.001233546	0.007909206	0.004506452	STAT3/TLR4/TLR2/FCGR2B	4
hsa05321	Inflammatory bowel disease	3/28	65/8102	0.001399151	0.008472636	0.00482748	STAT3/TLR4/TLR2	3
	Fc epsilon RI							
hsa04664	signaling pathway	3/28	68/8102	0.001594226	0.009145825	0.005211045	FCER1G/LYN/LCP2	3
hsa04217	Necroptosis	4/28	159/8102	0.002025205	0.011037365	0.006288793	STAT3/TLR4/TNFRSF1A/CYBB	4
hsa04612	Antigen	3/28	78/8102	0.002364818	0.012274533	0.006993698	LGMN/CTSB/IFI30	3

	processing and presentation							
	B cell receptor							
hsa04662	signaling pathway	3/28	82/8102	0.002727597	0.013514003	0.007699915	LYN/PTPN6/FCGR2B	3
	NOD-like receptor							
hsa04621	signaling pathway	4/28	181/8102	0.003242997	0.015368985	0.008756833	CTSB/TLR4/CYBB/CCL2	4
	Neutrophil							
hsa04613	extracellular trap formation	4/28	190/8102	0.003860696	0.016803265	0.009574048	TLR4/TLR2/CYBB/FCGR3A	4
	Rheumatoid arthritis							
hsa05323	Chemokine signaling pathway	3/28	93/8102	0.003896623	0.016803265	0.009574048	TLR4/TLR2/CCL2	3
	Chemokine signaling pathway							
hsa04062	Staphylococcus aureus infection	4/28	192/8102	0.004008118	0.016803265	0.009574048	LYN/STAT3/PF4/CCL2	4
	Staphylococcus aureus infection							
hsa05150	Viral protein interaction	3/28	96/8102	0.00426085	0.017201208	0.009800785	C3AR1/FCGR2B/FCGR3A	3
	Viral protein interaction							
hsa04061	with cytokine and cytokine receptor	3/28	100/8102	0.004777846	0.017609731	0.01003355	TNFRSF1A/PF4/CCL2	3
	Epstein-Barr virus infection							
hsa05169	Epstein-Barr virus infection	4/28	202/8102	0.00480309	0.017609731	0.01003355	LYN/VIM/STAT3/TLR2	4
	Amoebiasis							
hsa05146	Amoebiasis	3/28	102/8102	0.005050002	0.017609731	0.01003355	TLR4/TLR2/CD14	3
	Proteoglycans in cancer							
hsa05205	Proteoglycans in cancer	4/28	205/8102	0.005060947	0.017609731	0.01003355	STAT3/TLR4/TLR2/PTPN6	4
	Toll-like receptor signaling pathway							
hsa04620	Toll-like receptor signaling pathway	3/28	104/8102	0.005331387	0.017609731	0.01003355	TLR4/TLR2/CD14	3
	T cell receptor							
hsa04660	signaling pathway	3/28	104/8102	0.005331387	0.017609731	0.01003355	PTPRC/LCP2/PTPN6	3
	Insulin resistance							
hsa04931	Insulin resistance	3/28	108/8102	0.005922192	0.018985851	0.010817626	AGT/STAT3/TNFRSF1A	3
	Sphingolipid							
hsa04071	signaling pathway	3/28	119/8102	0.007744419	0.024118333	0.013741976	S1PR1/FCER1G/TNFRSF1A	3
	Platelet activation							
hsa04611	Platelet activation	3/28	124/8102	0.008670932	0.025601705	0.014587162	FCER1G/LYN/LCP2	3
	Ferroptosis							
hsa04216	Ferroptosis	2/28	41/8102	0.008690487	0.025601705	0.014587162	CYBB/HMOX1	2
	Yersinia infection							
hsa05135	Yersinia infection	3/28	137/8102	0.011376126	0.03263152	0.018592561	TLR4/LCP2/CCL2	3

Fluid shear							
hsa05418	stress and	3/28	139/8102	0.011830964	0.033066027	0.018840131 TNFRSF1A/HMOX1/CCL2	3
atherosclerosis							
hsa05161	Hepatitis B	3/28	162/8102	0.017821347	0.048563169	0.027669985 STAT3/TLR4/TLR2	3

Supplementary Table4. Expression profile

GSE114426

Groups	Control	Control	Control	SCI	SCI	SCI
Samples	GSM3141545	GSM3141546	GSM3141547	GSM3141548	GSM3141549	GSM3141550
hsa_circ_0026646	6.423415612	5.950242761	6.154757261	7.276096435	6.634162375	7.732994944

GSE19890

Groups	Control	Control	Control	Control	Control	SCI	SCI	SCI	SCI	SCI
Samples	GSM497216	GSM497217	GSM497218	GSM497219	GSM497220	GSM497211	GSM497212	GSM497213	GSM497214	GSM497215
hsa-miR-331-3p	8.158	8.3795	8.04975	7.92725	8.12225	7.596	6.80175	7.56375	7.47925	7.59675

GSE45006

Groups	Control	Control	Control	Control	SCI	SCI	SCI	SCI
Samples	GSM1095725	GSM1095726	GSM1095727	GSM1095728	GSM1095741	GSM1095742	GSM1095743	GSM1095744
Plxnb2	7.9741355	8.7951538	8.2742306	8.8863489	9.2038751	9.2631006	9.5621571	9.2318931

GSE20907

Groups	Control	Control	Control	Control	SCI	SCI	SCI	SCI
Samples	GSM523055	GSM523056	GSM523057	GSM523058	GSM523051	GSM523052	GSM523053	GSM523054
Plxnb2	7.390165946	7.485844923	6.32288032	7.26818668	8.124178088	8.191373537	7.543543905	7.840006371