

Figure S1. The correlation of SBDGs in rosacea.

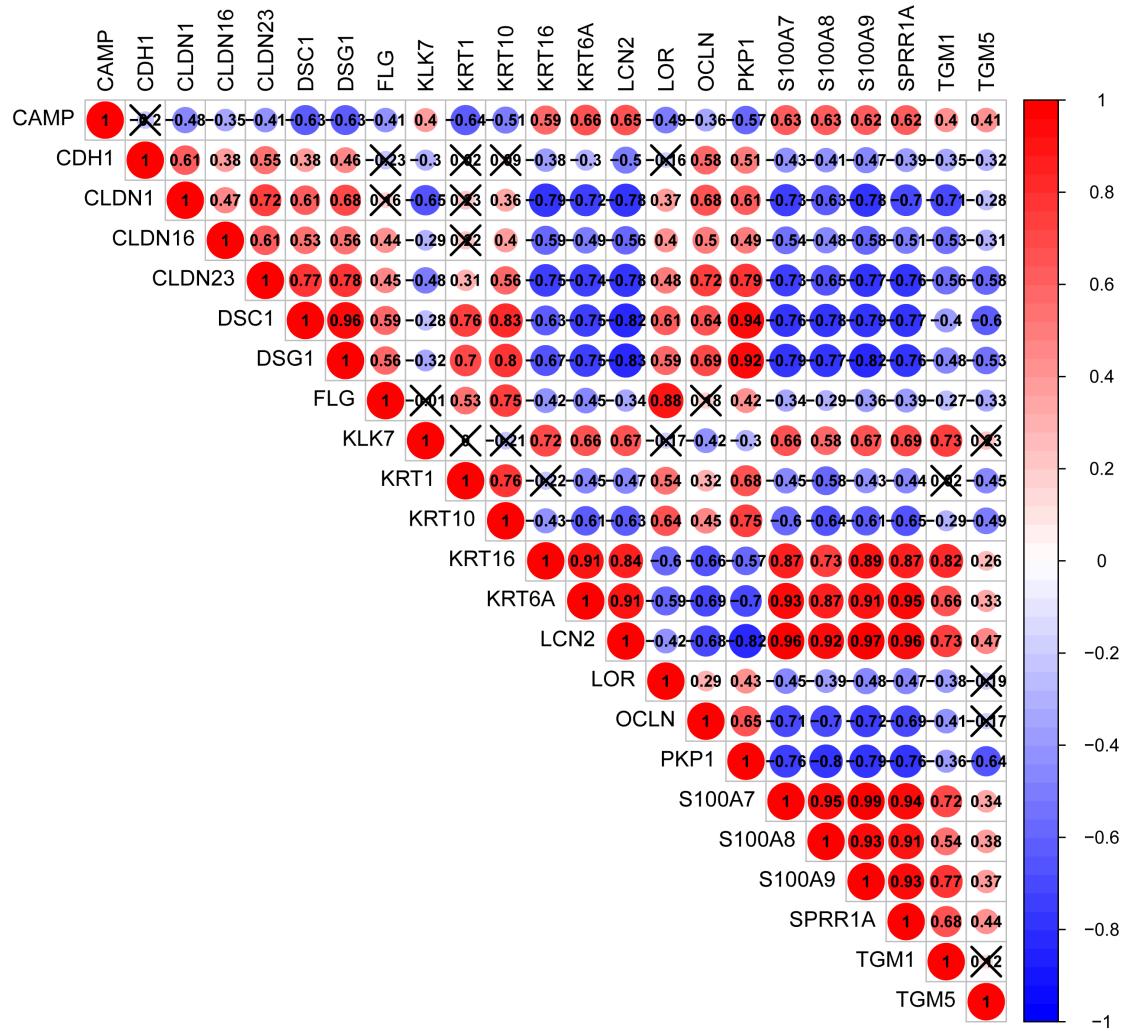


Figure S2. The immune cells in different subtypes of rosacea.

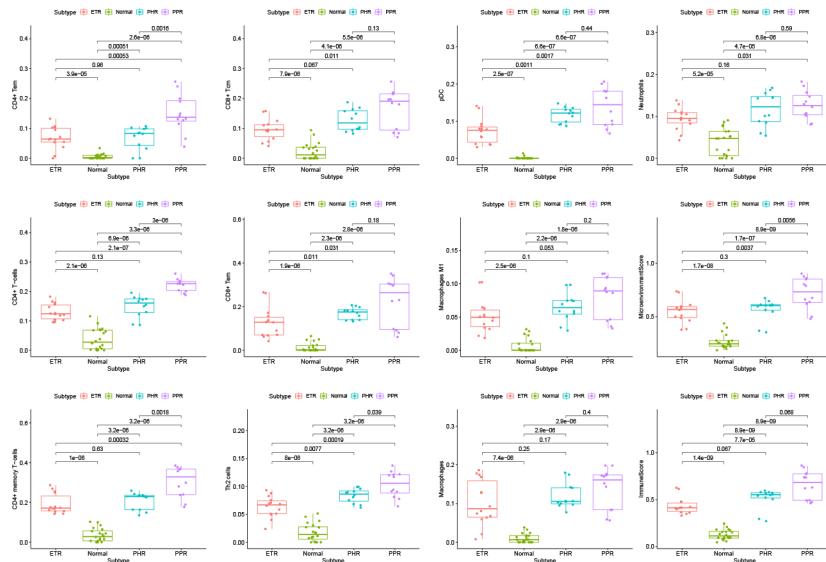


Figure S3. The 3 hub genes expression in rosacea was verified in Shih's study and epidermal transcriptome data.

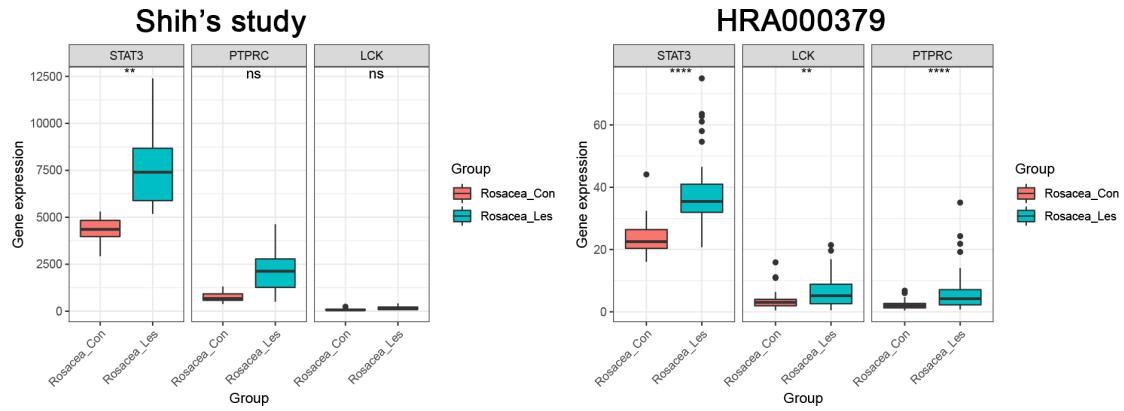


Figure S4. The expression and enrichment of STAT3-related genes in lightgreen. A, The expression of STAT3-related genes in rosacea and normal tissues. B, The expression of genes in 3 SBDs clusters. C, The heatmap of STAT3-related genes in 3 SBDs clusters. The enrichment of STAT3-related genes.

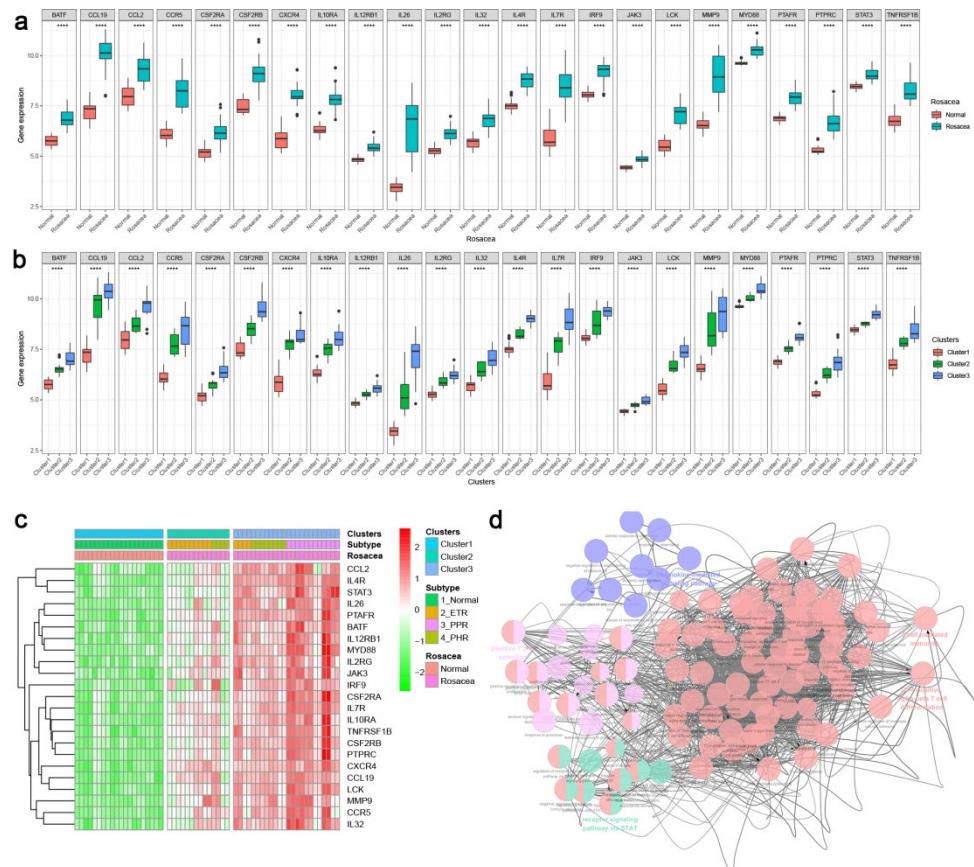


Figure S5. The KEGG analysis of genes from 3 subnetworks.

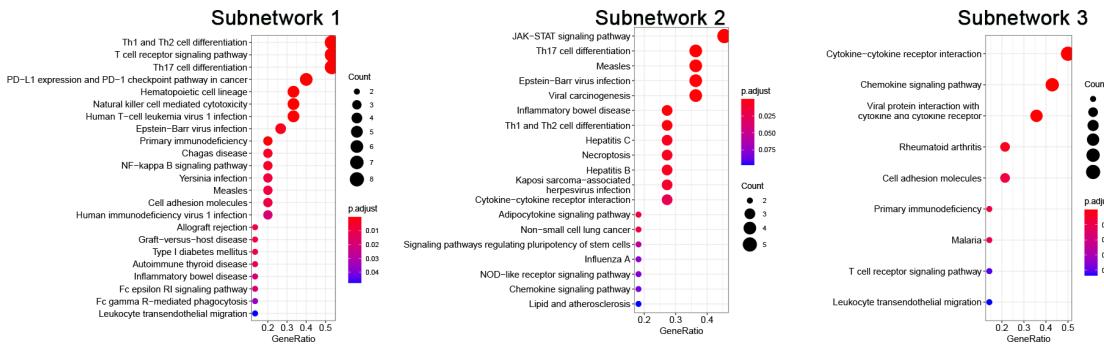
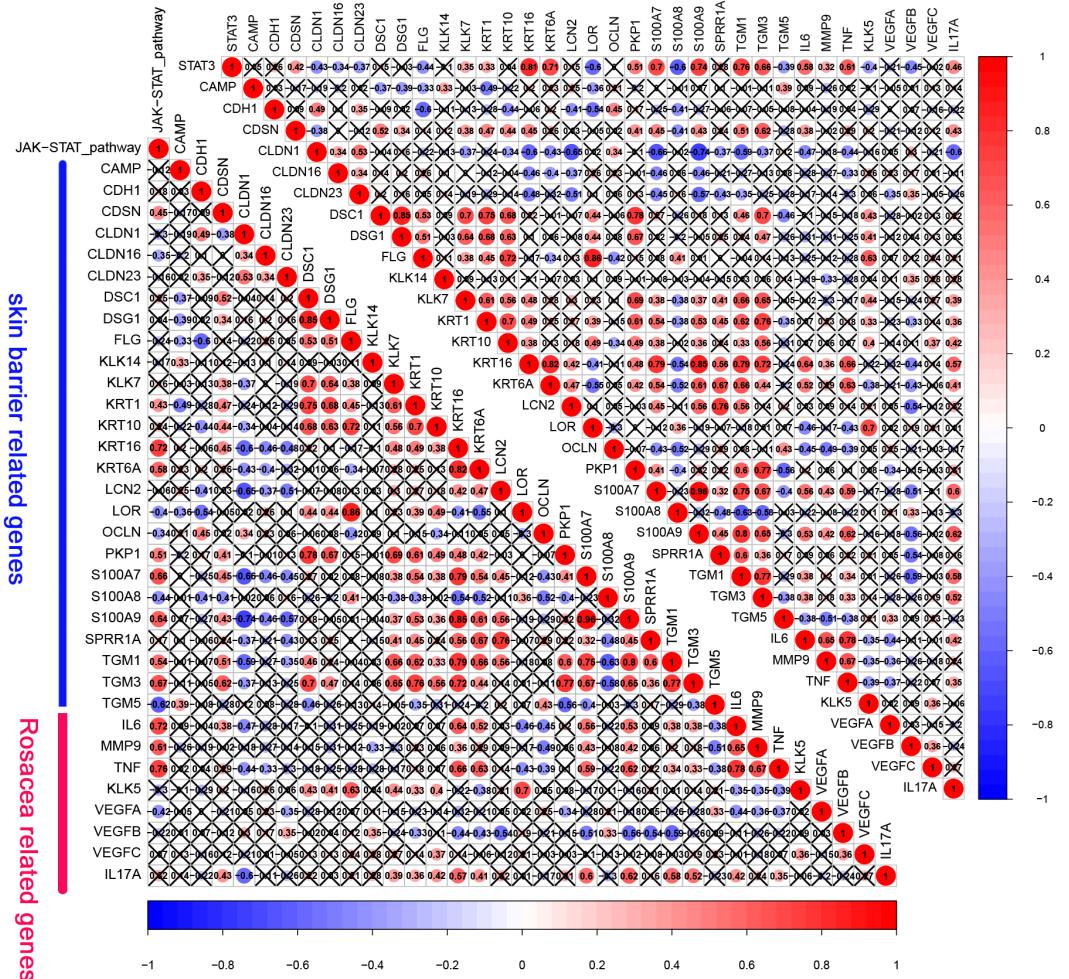


Figure S6. The correlation of SBDGs and rosacea related genes.



STAT3

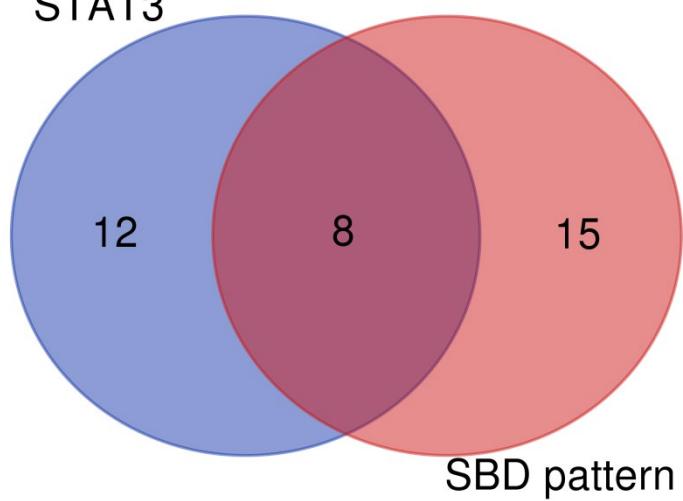


Table S1. The GO enrichment analysis of upregulated genes in cluster 3

BP_000493 positive regulation of peptide efflux	4
GO_000239 positive regulation of peptide efflux	4
GO_000239 acute inflammatory response to antigenic stimulus	4
GO_000239 negative regulation of cytokine production involved in immune response	4
GO_000430 iodide-containing compound metabolic process	4
GO_000430 iodide-containing compound metabolic process	4
GO_000972 aromatic amino acid family metabolic process	5
GO_190492 regulation of receptor signaling pathway via JAK-STAT	5
GO_003323 regulation of receptor signaling pathway	7
GO_000295 antigen processing and presentation of peptide antigen via MHC class II	8
GO_004865 positive regulation of smooth muscle cell proliferation	8
GO_000295 antigen processing and presentation of peptide antigen via MHC class II	8
GO_001496 regulation of phosphorylated 3-kinase signaling	9
GO_005730 regulation of peptide/protein phosphorylation	14
GO_000295 antigen processing and presentation of peptide antigen via MHC class II	14
GO_004093 helper-cell differentiation	5
GO_190428 positive regulation of reactive oxygen species biosynthetic process	6
GO_000295 antigen processing and presentation of peptide or polypeptide antigen via MHC class II	8
GO_000295 phosphatase C-activating G protein-coupled receptor signaling pathway	8
GO_000295 antigen processing and presentation of peptide antigen via MHC class II	8
GO_005957 positive regulation of antigen receptor-mediated signaling pathway	4
GO_007177 positive regulation of monocyte/macrophage migration	4
GO_000295 antigen processing and presentation of peptide antigen via MHC class II	3
GO_000249 dendritic cell antigen processing and presentation	3
GO_002517 cell telomere induction	3
GO_000295 antigen processing and presentation of peptide antigen via MHC class II	3
GO_003329 detection of molecule of bacterial origin	3
GO_004242 gamma delta T cell differentiation	3
GO_000295 antigen processing and presentation of peptide antigen via MHC class II	3
GO_005235 maintenance of location	16
GO_002765 platelet degranulation	9
GO_000295 antigen processing and adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	9
GO_004267 natural killer cell mediated cytotoxicity	6
GO_009023 positive regulation of MAPK cascade	5
GO_000277 negative regulation of lymphocyte mediated immunity	12
GO_000277 immunoglobulin production	5
GO_000277 positive regulation of reactive oxygen species metabolic process	6
GO_000295 regulation of cell surface receptor linked signal transduction	10
GO_002500 lymphocyte homeostasis	6
GO_000295 regulation of cell surface receptor linked signal transduction involved in immune response	6
GO_004416 0x0 cellular antimetabolic process	9
GO_003144 regulation of heterotypic cell-cell adhesion	4
GO_000295 cell adhesion	4
GO_190320 regulation of bone development	4
GO_003348 negative regulation of defense response	4
GO_000295 regulation of cell cycle/cell organization	17
GO_003635 MAPK-activated kinase signalling	11
GO_004628 regulation of JNK cascade	6
GO_002527 alpha-beta T cell activation involved in immune response	15
GO_000752 negative regulation of cell adhesion	15
GO_000295 establishment of lymphocyte polarity	3
GO_000295 regulation of cell surface receptor linked signal transduction	3
GO_003389 positive regulation of T cell differentiation in thymus	3
GO_002981 cell extrusion	3
GO_000295 positive regulation of cell differentiation	3
GO_003337 CD8-positive, alpha-beta T cell activation	4
GO_004263 0x0 regulation of T cell proliferation	6
GO_000295 regulation of cell migration	11
GO_007055 necrotic cell death	10
GO_004493 response to drug	4
GO_000295 regulation of adaptive immune response	9
GO_003389 positive regulation of immunoglobulin production	5
GO_003272 positive regulation of chemokine production	5
GO_000295 regulation of cell surface receptor linked signal transduction	5
GO_004516 regulation of keratinocyte differentiation	5
GO_009568 cellular response to virus	6
GO_000295 regulation of cell differentiation or depolarization	11
GO_003124 biomaterial tissue development	10
GO_011048 biomineralization	10
GO_000295 regulation of vascular endothelial growth factor production	10
GO_003944 positive regulation of blood coagulation	10
GO_003944 positive regulation of hemostasis	10
GO_000295 actin filament organization	19
GO_003594 protein localization to cell surface	6
GO_000295 regulation of cell length	11
GO_033987 endosomal cell differentiation	5
GO_000771 immunological synapse formation	3
GO_000295 regulation of cell surface receptor-mediated endocytosis	3
GO_005459 positive rhythmic T cell selection	3
GO_005179 regulation of killing of cells of other organism	3
GO_000295 regulation of cell surface receptor linked signal transduction	9
GO_003770 regulation of actin filament-based process	18
GO_003041 actin filament polymerization	4
GO_000295 regulation of cell surface receptor linked signal transduction	4
GO_005820 positive regulation of coagulation	4
GO_003722 integrin-12-mediated signaling pathway	5
GO_000295 regulation of receptor signaling pathway via JAK-STAT	7
GO_000598 arame metabolic process	9
GO_000295 regulation of immunoglobulin production	6
GO_000295 regulation of cell differentiation or depolarization	9
GO_001396 carbohydrate derivative catabolic process	11
GO_005124 regulation of calcium ion transport	10
GO_000295 regulation of cell surface receptor linked signal transduction	10
GO_003230 negative regulation of adaptive immune response	5
GO_003548 regulation of interferon-beta production	5
GO_000295 regulation of cell surface receptor linked signal transduction by integrin	5
GO_004625 regulation of receptor signaling pathway via JAK-STAT	9
GO_002467 genital centriole formation	3
GO_000295 regulation of cell differentiation or proliferation	3
GO_003323 regulation of integrin activation	3
GO_003440-like receptor Z signaling pathway	3
GO_000295 regulation of cell differentiation or proliferation	3
GO_005952 positive regulation of T cell receptor signaling pathway	3
GO_005144 positive regulation of membrane protein ectodomain proteolysis	3
GO_000295 regulation of cell surface receptor linked signal transduction	3
GO_007711 membrane vesicle organization	4
GO_003282 bone mineralization	8
GO_003724 positive regulation of p53-activated MAPK cascade	10
GO_007052 response to interleukin-12	5
GO_190305 negative regulation of response to wounding	7
GO_003589 negative regulation of T cell activation	8
GO_000295 regulation of cell surface receptor linked signal transduction	8
GO_000218 activation of innate immune response	9
GO_004397 regulation of CTPase activity	9
GO_000295 regulation of cell surface receptor linked signal transduction	9
GO_004649 positive regulation of apoptosis	4
GO_004649 positive regulation of p53 protein signal transduction	4
GO_005128 negative regulation of sequencing of calcium ion	5
GO_000295 regulation of cell surface receptor linked signal transduction	5
GO_003208 interferon-beta production	5
GO_007071 response to interleukin-10	5
GO_000295 regulation of cell differentiation or proliferation	5
GO_003323 regulation of integrin activation	3
GO_003440-like receptor Z signaling pathway	3
GO_000295 regulation of cell differentiation or proliferation	3
GO_005952 positive regulation of T cell receptor signaling pathway	3
GO_005144 positive regulation of membrane protein ectodomain proteolysis	3
GO_000295 regulation of cell differentiation or proliferation	3
GO_004395 positive regulation of muscle cell degeneration	3
GO_005128 sequencing of a metal ion	3
GO_003033 regulation of actin filament polymerization	13
GO_005673 epithelial cell proliferation	10
GO_000295 regulation of cell differentiation or proliferation	10
GO_003329 regulation of blood leukocyte differentiation	19
GO_190047 negative regulation of hemostasis	5
GO_005128 regulation of sequencing of calcium ion	5
GO_000295 regulation of cell differentiation or proliferation	4
GO_005959 negative regulation of S cell activation	4
GO_005959 positive regulation of S cell activation	4
GO_005958 positive regulation of synaptic transmission, glutamatergic	4
GO_000295 regulation of cell surface receptor linked signal transduction	5
GO_003248 positive regulation of type I interferon production	6
GO_190306 positive regulation of response to wounding	6
GO_000295 regulation of cell surface receptor linked signal transduction	6
GO_003525 positive regulation of rho protein signal transduction	15
GO_003590 purinic nucleotide receptor signaling pathway	4
GO_000295 negative regulation of cell surface receptor linked signal transduction	3
GO_000275 negative regulation of natural killer cell mediated immunity	3
GO_003889 negative regulation of S cell activation	3
GO_000295 regulation of cell differentiation or proliferation	3
GO_003331 cell adhesion mediated by integrin	3
GO_004754 multi-organismal cellular process	3
GO_000295 regulation of cell differentiation or proliferation	3
GO_007056 protein timerace	3
GO_200357 regulation of cyclin-type endopeptidase activity involved in apoptotic signaling pathway	3
GO_000295 regulation of cell differentiation or proliferation	3
GO_003218 lysosome location	8
GO_005793 stress-activated protein kinase signaling cascade	4
GO_000295 regulation of cyclin secretion	4
GO_005752 positive regulation of cyclin secretion	4
GO_003329 regulation of cyclin-dependent kinase activity	4
GO_003329 regulation of cyclin polymerization	4
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GO_003329 regulation of cyclin polymerization	4
GO_00	

MF
GO:0070932 oligosaccharide binding
GO:0032056 coenzyme activity
MF
GO:0043177 organic acid binding
MF
GO:0005164 tumor necrosis factor receptor binding
MF
GO:0031533 arylidene acyl transferase activity, transferring pentoyl groups
GO:0046911 peroxidase activity

3/412 151852 0.00481 0.08102 0.0041 SEL/SEL/SEL
5/412 491852 0.00412 0.08687 0.02945 CX365A/Y96TC44/CD35/CD86
5/412 2241852 0.00485 0.04078 0.03377 S100A9/PAF5/T002/CRAPII2/EL/EL/GLU/SEL/PA0X5AP/ST8SAA4/VCAN/FCN1/SIGLEC10
4/412 371852 0.00476 0.04078 0.03377 TNF/TNF91/STAT1/STAT1/INF51B
5/412 591852 0.00545 0.04199 0.004197 PAF1/TNF/PAF1/PP3/PAF9
5/412 5071852 0.00699 0.04059 0.03697 PCP1/PP2/PP2/PP4/PP5/PP6/PTG2

Table S2. The KEGG enrichment analysis of upregulated genes in cluster 3

ID	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	genelD	Count
hsa0510 Staphylococcus aureus infection	22/235	96/8091	2.30E-145	5.31E-12	4.04E-12	KRT16/PTAFL/CFI/FCGR3B/ITGA1/SELP/FPRI/FCGR2A/CFB/C3AR1/FPR3/C1QCA/CAM1/HLA-DRA/H-LA-DPA1/C1R/HLA-DMA/ITGB2/C1QAB/C1QB/HLA-DMB/C1S	22
hsa04060 Cytokine–cytokine receptor interaction	34/235	295/8091	3.25E-10	12.73E-10	2.86E-10	IL4R/L36G/CSF2BL/IL7R/CLL2/IL26/CXCL6/CSF2RA/CXCR1/CCR7/CXCR2/EB13/TNF/TNFRSF1B/IL21R/CXCL8/FA5/TNFRSF21/CD27/IL32/IL10RA/TNFSF10/IL6/CXCL13/IL12RB2/CCL7/CCR1/CCL19/CCR5/CCL4/TNFRSF17/TNFSF13B/IL22	34
hsa05523 Rheumatoid arthritis	18/235	93/8091	1.19E-10	9.13E-09	6.95E-09	CCL2/CXCL6/MMP1/ITGA1/CXCL1/TNF/CXCL8/IL6/CAM1/CTS1/HLA-DRA/H-LA-DPA1/H-LA-DMA/ITGB2/C86/HLA-DMB/TNFSF13B/MMP3	18
hsa04640 Hematopoietic cell lineage	17/235	99/8091	2.77E-09	1.50E-07	1.14E-07	IL4R/C2D4L/IR7/CSF2RA/CD3G/TNF/CD3D/CD2/L6/HLA-DRA/H-LA-DPA1/H-LA-DMA/CD38/C1D4/ITGA4/MSA41/HLA-DMB	17
hsa04061 Viral protein interaction with cytokine and cytokine receptor	17/235	100/8091	3.26E-09	2.12E-07	2.32E-07	CCL2/CXCL6/CXCL1/CCR7/CXCR2/IL10RA/TNFSF10/IL6/CXCL13/CCR1/CCR4/ITGA4/MSA41/HLA-DMB	17
hsa04514 Cell adhesion molecules	20/235	149/8091	9.20E-09	3.11E-07	2.36E-07	CDH3/SELE/ITGA1/SELI/ICOS/SELP/CD27/IL4NLY4/PTRC/CD2/VCAN/CAM1/HLA-DRA/CLDN7/HLA-DPA1/H-LA-DMA/ITGB2/CDB86/HLA-DMB	20
hsa04657 IL-17 signaling pathway	16/235	94/8091	9.42E-09	3.11E-07	2.36E-07	T100A9/S100A7/A/CLL2/CXCL6/MMP1/CXCL1/TNF/CXCL8/IL6/CAM1/CTS1/HLA-DRA/H-LA-DPA1/H-LA-DMA/ITGB2/C86/HLA-DMB/TNFSF13B/MMP3	16
hsa05171 Coronavirus disease - COVID-19	25/235	232/8091	1.22E-08	3.51E-07	2.67E-07	CLL2/MPP1/ITGA1/CXCL1/TNF/CXCL8/IL6/FOS1/IL2/PTGS2/MMP9/HMP3	25
hsa04610 Complement and coagulation cascades	15/235	85/8091	1.67E-08	4.28E-07	3.25E-07	SERPINB2A/C/CFB/PLAT/SERPINAL/C3AR1/F5/C1QC/THBD/C1R/PLAU/ITGB2/C1QAB/C1QB/C1S	15
hsa05321 Inflammatory bowel disease	13/235	65/8091	3.23E-08	7.46E-07	5.68E-07	IL4R/NOD2/IL2R2B/HLA-DRA/H-LA-DPA1/IL12RB2/HLA-DMA/STAT1/IL22	13
hsa05164 Influenza A	20/235	172/8091	1.08E-07	2.26E-06	1.72E-06	TMPRSS11D/TMPPSS4/IR7/CCL2/TNF/CXCL8/FAS/MX1/OAS2/TNFSF10/IL6/TLR7/MX2/CAM1/HLA-DRA/H-LA-DPA1/IRF9/HLA-DMA/HLA-DMB/STAT1	20
hsa05133 Pertussis	13/235	76/8091	2.26E-07	4.35E-06	3.31E-06	CXCL6/TNF/IRF8/CXCL8/IL6/C1QC/LY96/C1R/CD14/ITGB2/C1QAB/C1S	13
hsa05140 Leishmaniasis	13/235	77/8091	2.85E-07	4.71E-06	3.59E-06	FCGR2A/CYBB/IL6/HLA-DRA/H-LA-DPA1/H-LA-DMA/ITGB2/ITGA4/PTGS2/HLA-DMB/STAT1	13
hsa04062 Chemokine signaling pathway	20/235	192/8091	6.57E-07	1.08E-06	8.24E-06	RAC2/CCL2/CXCL6/LYN/CXCR6/CXCL1/CCR7/CXCR2/HCK/PREX1/CXCL13/CCL7/CCR1/CCL19/CCR5/CCL4/STAT1/FGR	20
hsa05417 Lipid and atherosclerosis	15/235	112/8091	7.23E-07	1.11E-06	8.48E-06	NOD2/MLK2/CXCL6/SELE/IRF8/CXCL1/TNF/CNFS1B/IL6/CAM1/BIRC3/PTGS2/MMP9/HMP3	15
hsa05152 Tuberculosis	21/235	215/8091	9.96E-07	1.33E-06	1.01E-05	IRF7/CCL2/HSPA6/NCFA/LYN/MMP1/SELE/CXCL1/SELE/TNF/CXCL8/FAS/IL6/CXCL13/SEL/TNF/CXCL8/IL6/Y96/CAM1/CD14/SOD2/MPP9/HMP3	21
hsa04672 Intestinal immune network for IgA production	10/235	180/8091	1.03E-06	1.35E-05	1.01E-05	NOD2/CLEC7A/FCGR8B/CORO1A/TNF/FCGR2A/TLR1/IL10RA/H-LA-DRA/FCER1G/HLA-DPA1/H-LA-DMA/CD14/CYP27B1/ITGB2/HLA-DMB/CTSS/STAT1	19
hsa04650 Natural killer cell mediated cytotoxicity	16/235	49/8091	1.07E-06	1.33E-05	1.01E-05	ICOS1/IL6/HLA-DRA/H-LA-DPA1/H-LA-DMA/ITGA4/CD86/IL2R2B/HLA-DMB/TNFSF13B	10
hsa04064 NFKappa B signaling pathway	14/235	131/8091	1.09E-06	1.33E-05	1.01E-05	RAC2/FCGR3B/LCK/ITGA1/GZMB/TNF/CD48/FAS/TNFSF10/MICB/CAM1/FCER1G/LCP2/D247/TYROB/ITGB2	16
hsa05332 Graft-versus-host disease	9/235	104/8091	1.16E-06	1.86E-05	1.41E-05	LYN/LCK/CXCL1/TNF/CXCL8/LY96/CAM1/BIRC3/PTGS2/MMP9/HMP3	14
hsa04659 Th17 cell differentiation	14/235	129/8091	1.25E-06	2.68E-05	2.04E-05	IL4R/CCL2/CD3G/EB13/IL21R/CD3D/IL6/HLA-DRA/H-LA-DPA1/H-LA-DMA/CD247/HLA-DMB/STAT1/IL22	14
hsa05169 Epstein-Barr virus infection	19/235	153/8091	5.83E-06	1.75E-05	1.47E-05	IRF7/TNF/CXCL8/TLR1/IL6/TLR7/Y96/CD14/TLR8/CLL2/MPP9/HMP3	19
hsa04621 NOD-like receptor signaling pathway	18/235	184/8091	5.97E-06	1.75E-05	4.37E-05	NOD2/CARD6/IRF7/F16/CCL2/AIM2/NAMP/TCXCL8/OAS2/CYBB/IL6/IRF9/BIRC3/GPBP1/STAT1/GBP2	18
hsa04145 Phagosome	16/235	152/8091	7.83E-06	7.24E-05	5.51E-05	CLECT7A/NCFA/FCGR8B/CORO1A/FCGR2A/CD86/IL2R2B/HLA-DMB/TNFSF17	16
hsa05330 Allograft rejection	8/235	38/8091	1.03E-05	9.19E-05	7.00E-05	GZMB/TNF/FAS/HLA-DRA/H-LA-DPA1/H-LA-DMA/CD14/ITGB2/TAP1/HLA-DMB/CTSS	8
hsa05144 Malaria	9/235	50/8091	1.12E-05	9.57E-05	7.28E-05	CCL2/SELE/IRF8/CXCL8/IL6/CAM1/ITGB2	9
hsa04658 Th1 and Th2 cell differentiation	12/235	92/8091	1.26E-05	0.000104	7.93E-05	NOD2/MLK2/CXCL6/SELE/IRF8/CXCL8/IL6/CAM1/BIRC3/PTGS2/MPP9/HMP3	12
hsa04940 Type I diabetes mellitus	8/235	12/8091	2.15E-05	0.000216	6.000164	GZMB/TNF/FAS/HLA-DRA/H-LA-DPA1/H-LA-DMA/CD86/HLA-DMB	8
hsa04620 TLR-like receptor signaling pathway	12/235	104/8091	4.42E-05	0.000341	0.000259	IRF7/TNF/CXCL8/TLR1/IL6/TLR7/Y96/CD14/TLR8/CLL2/CD86/STAT1	12
hsa05416 Viral myocarditis	9/235	60/8091	5.13E-05	0.000302	0.000291	RAC2/ITGA1/ICAM1/HLA-DRA/H-LA-DPA1/H-LA-DMA/ITGB2/CD86/HLA-DMB	9
hsa05143 African trypanosomiasis	7/235	37/8091	7.80E-05	0.000563	0.000428	SELE/TNF/APOL1/FAS/IL6/CAM1/CD01	7
hsa04670 Leukocyte transendothelial migration	12/235	114/8091	0.000109	0.000769	0.000583	RAC2/NCFA/FCGR3B/TNF/FCGR2A/CD3D/IL6/CAM1/CDLN7/ITGB2/ITGA4/MPP9	12
hsa04933 AGE-RAGE signaling pathway in diabetic complications	11/235	100/8091	0.000142	0.000968	0.000737	TCL2/COL4A1/SELE/TNF/CXCL8/CYBB/IL6/CAM1/CDLN7/ITGB2/ITGA4/MPP9	11
hsa05322 Systemic lupus erythematosus	13/235	136/8091	0.000153	0.000109	0.000768	FCGR3B/TNF/FCGR2A/C1QC/HLA-DRA/H-LA-DPA1/C1R/HLA-DMA/C1QAB/C1QB/HLA-DMB/CTSS	13
hsa05167 Kaposi's sarcoma-associated herpesvirus infection	16/235	149/8091	0.000157	0.001009	0.000769	FCGR3B/TNF/FCGR2A/C1QC/HLA-DRA/H-LA-DPA1/C1R/HLA-DMA/C1QAB/C1QB/HLA-DMB/CTSS	16
hsa05142 Chagas disease	11/235	102/8091	0.00017	0.001035	0.000788	CCL2/CD3G/CD3D/CXCL8/FAS/IL6/C10/CD27/CLQA/C1QB	11
hsa05146 Amoebiasis	11/235	102/8091	0.00017	0.001035	0.000788	SERPINB3/SELENINB13/COL4A1/CXCL1/TNF/CXCL8/SERPINB9/IL6/COL3A1/CD14/ITGB2	11
hsa05310 Asthma	6/235	31/8091	0.000225	0.001355	0.0001016	TNF/HLA-DRA/FCER1G/HLA-DPA1/H-LA-DMB	6
hsa04380 Osteoclast differentiation	12/235	128/8091	0.000328	0.001896	0.001443	NCFA/FCGR3B/LCK/TNF/FCGR2A/FOSL1/LILR2B/IRF9/LCP2/TYROB/LILR8/STAT1	12
hsa05145 Toxoplasmosis	11/235	112/8091	0.000389	0.001929	0.001657	HSPA16/IL10RA/LY96/HLA-DRA/H-LA-DPA1/H-LA-DMA/BIRC3/CCRS5/HLA-DMB/STAT1	11
hsa04612 Antigen processing and presentation	9/235	78/8091	0.000404	0.00221	0.001681	HSPA6/TNF/CTSL/HLA-DRA/H-LA-DPA1/H-LA-DMA/TAP1/HLA-DMB/CTSS	9
hsa05162 Measles	12/235	139/8091	0.000699	0.003740	0.002846	IRF7/TNF/CXCL1/HCK/PREX1/CXCL8/FAS/MICB/IL6/CAM1/IRF9/CCR1/CCR5/PTGS2/CD86/STAT1	12
hsa05340 Primary immunodeficiency	6/235	38/8091	0.000713	0.003743	0.002848	L7R/CCK/ICOS/PTRC/CD3D/STAT1	6
hsa05320 Autoimmune thyroid disease	7/235	53/8091	0.000787	0.004038	0.003073	GZMB/FAS/HLA-DRA/H-LA-DPA1/H-LA-DMA/CD86/HLA-DMB	7
hsa04660 T cell receptor signaling pathway	10/235	109/8091	0.000842	0.002449	0.003218	RASGRP1/LCK/ICOS/CD3G/TNF/PTPRC/CD3D/ITK/LCP2/CD247	10
hsa05134 Legionellosis	7/235	57/8091	0.001223	0.000611	0.004574	HSPA6/CXCL1/TNF/CXCL8/IL6/CD14/ITGB2	7
hsa04630 JAK-STAT signaling pathway	12/235	162/8091	0.002162	0.012572	0.009567	IL4R/CSF2RA/IL21R/L10RA/L6/IRF9/IL12RB2/STAT4/STAT1/IL22	12
hsa04613 Neutrophil extracellular trap formation	13/235	190/8091	0.003521	0.016598	0.012631	RAC2/CЛЕ7A/NCFA/FCGR3B/ITGA1/SELE/FPR1/FCGR2A/CYBB/TLR7/FPR3/TLR8/ITGB2	13
hsa05235 PD-1 expression and PD-1 checkpoint pathway in cancer	8/235	89/8091	0.004192	0.019369	0.014739	RASGRP1/LCK/CD3G/CD3D/CD27/CD40/IR7/CD247/STAT1	8
hsa05163 Human cyromegalovirus infection	14/235	229/8091	0.005229	0.026401	0.020091	EIF4EBP1/RAC2/CCL2/CXCR2/TNF/CXCL8/FAS/IL10RA/H-LA-DPA1/CCR1/CCR5/PTGS2	14
hsa05135 Yersinia infection	10/235	137/8091	0.006446	0.028636	0.021792	RAC2/CCL2/LCK/TNF/FCGR2A/CXCL8/L6/WIPF1/LCP2/CD247	10
hsa00380 Tryptophan metabolism	5/235	42/8091	0.007014	0.030573	0.032265	KYNU/TD02/L141/KMO/ID01	5
hsa05166 Human T-cell leukemia virus 1 infection	13/235	219/8091	0.011289	0.048292	0.036751C/ITGA1/CD3G/CD3D/IL6/CAM1/FOSL1/HLA-DRA/H-LA-DPA1/H-LA-DMA/ITGB2/HLA-DMB	13	
hsa04664 Fc epsilon RI signaling pathway	6/235	68/8091	0.013749	0.057745	0.043944	RAC2/LYN/TNF/ALOX5AP/FCER1G/LCP2	6
hsa04217 Necrosis	10/235	190/8091	0.017293	0.070306	0.053502	MILK/GLUL/TNF/FAS/CYBB/TNF/S10/IRF9/STAT1/BIRC3/STAT1	10
hsa04210 Apoptosis	9/235	136/8091	0.017348	0.070306	0.053502	CFZRB/GZMB/TNF/FAS/TNFSF10/CTSL/BCL2A1/BIRC3/CTSS	9
hsa05418 Fluid shear stress and atherosclerosis	9/235	139/8091	0.019721	0.078546	0.059773	RAC2/CCL2/SELE/TNF/PLAT/CAM1/CTSL/THBD/MMP9	9
hsa05170 Human immunodeficiency virus 1 infection	12/235	212/8091	0.020542	0.080426	0.061203	RAC2/CNB1/CD3G/TNF/TNFSF1B/CD3D/FAS/SAMHD1/B1ST2/CD247/TAP1/CCRS5	12
hsa05130 Pathogenic Escherichia coli infection	11/235	197/8091	0.028354	0.081964	0.083073	HCL51/TNF/MY016/NCKAP1L/FCGR2A/CXCL8/FAS/TNFSF10/IL6/CDLN7/WIPF1	11
hsa04974 Protein digestion and absorption	7/235	73/8091	0.029967	0.112983	0.085797	ATP1B1/COL15A1/COL52A/COL52A1/SLC7A7	7
hsa05219 Bladder cancer	4/235	41/8091	0.030324	0.112983	0.085797	TYMP/MMPI/CXCL8/MMP9	4
hsa04625 C-type lectin receptor signaling pathway	7/235	104/8091	0.031367	0.115013	0.087524	CLECT7A/TNF/L6/FCER1G/IRF9/PTGS2/STAT1	7
hsa05160 Hepatitis C	9/235	157/8091	0.039061	0.141057	0.107343	IRF7/TNF/FAS/MXO/A52/MX2/CDLN7/IRF9/STAT1	9
hsa05202 Transcriptional misregulation in cancer	10/235	192/8091	0.052925	0.188089	0.143134	GZMB/CXCL8/PLAT/L6/CD14/BCL2A1/BIRC3/CD86/MMP9/HMP9	10
hsa04666 Fc gamma R-mediated phagocytosis	6/235	97/8091	0.062634	0.219218	0.166824	RAC2/FCGR3B/LYN/HCK/FCGR2A/PTPRC	6
hsa04611 Platelet activation	7/235	124/8091	0.068956	0.237743	0.180921	RASGRP1/LYN/FCGR2A/FERMT3/FCER1G/COL3A1/LCP2	7
hsa00240 Pyrimidine metabolism	4/235	56/8091	0.078956	0.268217	0.204111	PNP/RRM2/TYMP/UPP1	4
hsa00760 Nicotinate and nicotinamide metabolism	3/235	35/8091	0.080224	0.268576	0.204385	PNP/NAMP/CD38	3
hsa00120 Primary bile acid biosynthesis	2/235	17/8091	0.085842	0.283279	0.215574	CYP7B1/CH25H	2
hsa04662 B cell receptor signaling pathway	5/235	82/8091	0.089582	0.291457	0.221797	RAC2/LYN/FITM1/LILR2B/LILR8	5
hsa04978 Mineral absorption	4/235	60/8091	0.096056	0.308180	0.234523	SLC5A1/ATP1B1/MT1E/MT2A	4
hsa05161 Hepatitis B	8/235	162/8091	0.099199	0.313902	0.238887	IRF7/TNF/CXCL8/FAS/IL6/STAT4/STAT1/MMP9	8
hsa00590 Arachidonic acid metabolism	4/235	61/8091	0.100583	0.313982	0.238938	ALOX12B/GPX2/PLA2G2A/PTG52	4
hsa00551 Glycosaminoglycan degradation	2/235	19/8091	0.103982	0.320263	0.243718	HYAL4/HPS	2
hsa05132 Salmonella infection	11/235	249/8091	0.109228	0.329778	0.250593	MILK/RHOH/TNF/NCKAP1L/PTPRC/CXCL8/TNFSF10/IL6/LY96/CD14/BIRC3	11
hsa04623 Cytosolic DNA-sensing pathway	2/235	63/8091	0.109262	0.329778	0.250593	IRF7/AM2/L6/C14	4
hsa00100 Steroid biosynthesis	2/235	20/8091	0.113408	0.335863	0.255589	CYP2A1/CYP2B1	2
hsa05221 Acute myeloid leukemia	4/235	67/8091	0.129717	0.379298	0.288643	EIF4EBP1/PIIM2/CD14/BCL2A1	4
hsa04622 RIG-I-like receptor signaling pathway	4/235	70/8091	0.145460	0.414820	0.315682	LYN/CXCL8/ISG15	4
hsa05120 Epithelial cell signaling in Helicobacter pylori infection	4/235	70/8091	0.145460	0.414820	0.315682	LYN/CXCL8/CXCR2/CXCL8	4
hsa00565 Ether lipid metabolism	3/235	49/8091	0.169567	0.477683	0.363514	LPCAT1/GPDP3/PLA2G2A	3

Table S3. The GO enrichment analysis of downregulated genes in cluster 3

ONTOLOGY ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	genelist	Count
BP	GO_0006631 fatty acid metabolic process	33/207	396/18866	8.50E-20	2.31E-16	1.62E-27	16 PHHY/GPAK/CYPA4/SLC27A6/CYP4F3/SLC25A17/NR1H3/HAC1/LI/PHP/GPAM/EC1/HAO2/SCD/PECR/FA2H/ACAT2/AACS/ECHD3/PPARG/ACSS2/PNPLA3/MSMO1/CRAT/ACSBG1/ABH5/GNPAT/INSIG1/ACSL1/ELOVL3/FADS2/DGAT2/MECR/AWAT1/LEP	33
BP	GO_0006606 alcohol metabolic process	24/207	385/18866	6.82E-12	9.28E-09	8.31E-08	16 PHHY/ACER1/GK5/APOE/GPAM/SCD/PECR/RBP4/FDPS/CYP39A1/DHCR7/ACAT2/DHCR24/GPD1/ACSS2/PMVK/MOGAT2/MSMO1/INSIG1/MVD/DGAT2/LEP/SOAT1	24
BP	GO_0008203 cholesterol metabolic process	16/207	153/18866	1.26E-11	1.14E-08	1.02E-08	08 CYP27A1/APOE/GPAM/SCD/FDPS/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/MVD/DGAT2/LEP/SOAT1	16
BP	GO_0006641 triglyceride metabolic process	14/207	110/18866	1.72E-11	1.14E-08	1.02E-08	08 CYP27A1/APOE/GK5/APOE/NR1H3/1PHP/GPAM/PNPLA3/MOGAT2/THRS/PPAR/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/MVD/DGAT2/LEP	14
BP	GO_1902652 secondary alcohol metabolic process	16/207	162/18866	3.02E-11	1.14E-08	1.02E-08	08 CYP27A1/APOE/GPAM/SCD/FDPS/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/MVD/DGAT2/LEP/SOAT1	16
BP	GO_0016042 lipid catabolic process	22/207	343/18866	3.12E-11	1.14E-08	1.02E-08	08 PHHY/CYP4F3/CYP27A1/ACER1/GK5/APOE/NR1H3/1PHP/GPAM/PNPLA3/MOGAT2/THRS/PPAR/CYP39A1/DHCR7/ACAT2/PLNI/GDPD1/PNPLA3/CRAT/ABHD5/SRD5A1/MECR/LEP	22
BP	GO_0016125 sterol metabolic process	16/207	169/18866	5.74E-11	2.11E-08	1.02E-08	08 CYP27A1/APOE/GPAM/SCD/FDPS/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/MVD/DGAT2/LEP/SOAT1	16
BP	GO_0006694 steroid biosynthetic process	17/207	197/18866	1.28E-11	2.11E-08	1.02E-08	08 CYP27A1/APOE/GA/PECR/DHCR24/PMVK/MSMO1/INSIG1/HSD3B1/MVD/DGAT2/SDR5A1/LEP	17
BP	GO_0008202 steroid metabolic process	21/207	332/18866	1.16E-10	3.52E-08	3.15E-08	08 CYP27A1/APOE/GA/PECR/DHRS2/GPM/SCD/FDPS/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/HSD3B1/MVD/DGAT2/SDR5A1/LEP	21
BP	GO_0044282 small molecule catabolic process	24/207	452/18866	1.90E-10	5.16E-08	4.86E-08	08 PHHY/CYP4F3/CYP27A1/ALD11G5/K/HAC1/HAO2/ARG2/PECR/CYP39A1/PPM1K/ACAT2/BCKDH/CRAT/HIBCH/ENO3/MECR/LEP	24
BP	GO_0006638 neutral lipid metabolic process	14/207	138/18866	3.76E-10	8.54E-08	7.64E-08	08 PNPLA4/GK5/APOE/NR1H3/1PHP/GPAM/PNPLA3/MOGAT2/THRS/PPAR/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/ACSL1/DGAT2	14
BP	GO_0006639 acyl/glycerol metabolic process	14/207	138/18866	3.76E-10	8.54E-08	7.64E-08	08 GAK5/APOE/NR1H3/1PHP/GPAM/PNPLA3/MOGAT2/THRS/PPAR/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/ACSL1/DGAT2	14
BP	GO_0006695 cholesterol biosynthetic process	11/207	75/18866	5.64E-10	1.10E-08	9.78E-08	08 APOE/GPAM/SCD/FDPS/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/MVD	11
BP	GO_1902653 secondary alcohol biosynthetic process	11/207	75/18866	5.64E-10	1.10E-08	9.78E-08	08 APOE/GPAM/SCD/FDPS/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/MVD	11
BP	GO_0044242 cellular lipid catabolic process	17/207	236/18866	1.04E-09	1.88E-08	1.76E-08	08 CYP27A1/APOE/GA/PECR/DHRS2/GPM/SCD/FDPS/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/HSD3B1/MVD/DGAT2/SDR5A1/LEP	17
BP	GO_0016126 sterol biosynthetic process	11/207	81/18866	1.32E-09	2.24E-08	2.11E-08	08 CYP27A1/APOE/GA/PECR/DHRS2/GPM/SCD/FDPS/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/MVD/DGAT2/SDR5A1/LEP	11
BP	GO_0019395 fatty acid oxidation	12/207	106/18866	1.97E-09	3.16E-08	2.783E-08	07 PHHY/CYP4F3/CYP27A1/ALD11G5/K/HAC1/HAO2/ARG2/PECR/CYP39A1/PPM1K/ACAT2/BCKDH/CRAT/HIBCH/ENO3/MECR/LEP	12
BP	GO_0034440 lipid oxidation	12/207	111/18866	3.37E-09	4.86E-08	4.735E-08	07 PHHY/CYP4F3/CYP27A1/HAC1/CLU/HAO2/PECR/ACAT2/PPARG/CRT/DGAT2/MECR/LEP	12
BP	GO_0055088 lipid homeostasis	14/207	163/18866	3.39E-09	4.86E-08	4.735E-08	09 APOE/APOE/TMEM97/NR1H3/GPAM/TL/CD1/CYP39A1/PPARG/CNPLA3/ITM2/BADH5/INSIG1/DGAT2/SOAT1	14
BP	GO_0046165 alcohol biosynthetic process	14/207	164/18866	3.67E-09	5.00E-08	4.735E-08	09 CYP27A1/APOE/GPAM/SCD/FDPS/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/MVD/LEP	14
BP	GO_0019216 regulation of lipid metabolic process	21/207	431/18866	1.26E-08	1.63E-06	1.04E-06	06 RORC/ACER1/GA/APOE/NR1H3/PEX11A/GPAM/SCD/FDPS/DHCR7/PSAP1/PPARG/PMVK/THRS/PPAR/CYP39A1/PPM1K/ACAT2/BCKDH/CRAT/HIBCH/MECR/LEP	21
BP	GO_0016054 organic acid catabolic process	17/207	282/18866	1.52E-08	1.80E-06	1.61E-06	06 PHHY/CYP4F3/ALD11J/HYK5/SLC25A17/HAC1/EC1/HAO2/PECR/PPM1K/ACAT2/BCKDH/CRAT/HIBCH/MECR/LEP	17
BP	GO_004395 carboxylic acid catabolic process	17/207	282/18866	1.52E-08	1.80E-06	1.61E-06	06 PHHY/CYP4F3/ALD11J/HYK5/SLC25A17/HAC1/EC1/HAO2/PECR/PPM1K/ACAT2/BCKDH/CRAT/HIBCH/MECR/LEP	17
BP	GO_0019432 triglyceride biosynthetic process	8/207	43/18866	1.91E-08	2.11E-06	1.89E-06	06 NR1H3/GPAM/PNPLA3/MOGAT2/THRS/PPAR/CNPLA3/DGAT2	8
BP	GO_0019915 lipid storage	10/207	81/18866	1.94E-08	2.11E-06	1.89E-06	06 MEST/APOE/NR1H3/PPARG/ACVR1C/PPM1K/ACAT2/BCKDH/CRAT/HIBCH/ENO3/MECR/LEP	10
BP	GO_0019218 regulation of steroid metabolic process	12/207	131/18866	2.24E-08	2.34E-06	2.02E-06	06 RORC/CGA/APOE/GPAM/SCD/FDPS/DHCR7/PPM1K/ACAT2/BCKDH/CRAT/HIBCH/ENO3/MECR/LEP	12
BP	GO_0009642 fatty acid catabolic process	11/207	114/18866	5.10E-08	5.15E-06	4.61E-06	06 PHHY/CYP4F3/SLC25A17/HAC1/EC1/HAO2/PECR/ACAT2/PPARG/CRT/DGAT2/MECR/LEP	11
BP	GO_0006654 phosphatidic acid biosynthetic process	8/207	49/18866	5.62E-08	5.15E-06	4.61E-06	06 AC6P/APGAT1/UPH/GPAM/APGAT3/PNPLA3/BADH5/GNPAT	8
BP	GO_0046890 regulation of lipid biosynthetic process	14/207	207/18866	6.14E-08	6.03E-06	5.61E-06	06 PHHY/CYP4F3/ALD11J/HYK5/SLC25A17/HAC1/EC1/HAO2/PECR/PPM1K/ACAT2/BCKDH/CRAT/HIBCH/MECR/LEP	14
BP	GO_0046460 neutral lipid biosynthetic process	8/207	51/18866	7.79E-08	6.63E-06	6.94E-06	06 NR1H3/GPAM/PNPLA3/MOGAT2/THRS/PPAR/CNPLA3/DGAT2	8
BP	GO_0046463 acyl/glycerol biosynthetic process	8/207	51/18866	7.79E-08	6.63E-06	6.94E-06	06 NR1H3/GPAM/PNPLA3/MOGAT2/THRS/PPAR/CNPLA3/DGAT2	8
BP	GO_0046473 phosphatidic acid metabolic process	8/207	51/18866	7.79E-08	6.63E-06	6.94E-06	06 AC6P/APGAT1/UPH/GPAM/APGAT3/PNPLA3/BADH5/GNPAT	8
BP	GO_0072330 monocarboxylic acid biosynthetic process	15/207	246/18866	9.19E-08	9.61E-06	8.99E-06	06 GPX4/SLC25A17/HAC1/EC1/HAO2/PECR/FA2H/CYP39A1/ACSS2/ACSBG1/INSIG1/ELOVL3/FADS2/MECR	15
BP	GO_0050810 regulation of steroid biosynthetic process	10/207	98/18866	1.23E-07	9.79E-06	8.82E-06	06 CGA/APOE/GPAM/SCD/FDPS/DHCR7/PPM1K/INSIG1/MVD/LEP	10
BP	GO_1901617 organic hydroxy compound biosynthetic process	15/207	258/18866	1.76E-07	1.37E-06	1.03E-06	05 CYP27A1/ACER1/APOE/GPAM/SCD/DPDS/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/MVD/LEP	15
BP	GO_0006637 acyl-CoA metabolic process	10/207	104/18866	2.17E-07	1.15E-06	1.03E-06	05 MPC2/GPAM/SCD/ACSS2/PMVK/ACSBG1/ACSL1/ELOVL3/MVD/DGAT2	10
BP	GO_0035384 esterol metabolic process	10/207	104/18866	2.17E-07	1.15E-06	1.03E-06	05 MPC2/GPAM/SCD/ACSS2/PMVK/ACSBG1/ACSL1/ELOVL3/MVD/DGAT2	10
BP	GO_0030258 lipid modification	15/207	271/18866	3.31E-07	2.36E-06	2.11E-06	05 PHHY/CYP4F3/SLC25A17/HAC1/EC1/HAO2/PECR/FA2H/ACAT2/PPARG/CRT/DGAT2/MECR/LEP	15
BP	GO_0046486 glycerolipid metabolic process	19/207	434/18866	3.38E-07	2.36E-06	2.11E-06	05 GPX4/SLC25A17/HAC1/EC1/HAO2/PECR/FA2H/ACAT2/PPARG/CNPLA3/DGAT2/THRS/PPAR/CNPLA3/DGAT2	19
BP	GO_0072329 monocarboxylic acid catabolic process	11/207	138/18866	3.63E-07	2.47E-06	2.21E-06	05 PHHY/CYP4F3/SLC25A17/HAC1/EC1/HAO2/PECR/ACAT2/CRAT/MECR/LEP	11
BP	GO_0016176 long-chain fatty acid metabolic process	10/207	113/18866	4.73E-07	3.11E-06	2.52E-06	05 GPX4/SLC25A17/HAC1/EC1/HAO2/PECR/ACAT2/CRAT/MECR/LEP	10
BP	GO_0006633 fatty acid biosynthetic process	12/207	173/18866	4.79E-07	3.11E-06	2.52E-06	05 GPX4/NR1H3/PPAR/CDC/PPCR/FA2H/CYP39A1/ACSBG1/INSIG1/ELOVL3/FADS2/MECR	12
BP	GO_0090181 regulation of cholesterol metabolic process	8/207	65/18866	5.42E-07	3.43E-06	3.07E-06	05 CYP27A1/ACER1/APOE/GPAM/SCD/DPDS/CYP39A1/DHCR7/ACAT2/DHCR24/PMVK/MSMO1/INSIG1/MVD/LEP	8
BP	GO_0045540 regulation of cholesterol biosynthetic process	7/207	50/18866	1.16E-06	07 01E-06	6.27E-06	05 APOE/GPAM/SCD/FDPS/DHCR7/PPM1K/INSIG1/MVD/DGAT2	7
BP	GO_0106118 regulation of sterol biosynthetic process	7/207	50/18866	1.16E-06	07 01E-06	6.27E-06	05 APOE/GPAM/SCD/FDPS/DHCR7/PPM1K/INSIG1/MVD/DGAT2	7
BP	GO_0045017 glycerolipid biosynthetic process	14/207	270/18866	1.79E-06	06 0.0106	9.61E-06	05 AC6P/APGAT1/UPH/GPAM/APGAT3/PNPLA3/MOGAT2/THRS/PPAR/CNPLA3/DGAT2	14
BP	GO_0023865 nucleoside bisphosphate metabolic process	10/207	138/18866	2.97E-06	06 0.00165	9.001E-06	00048 MPC2/GPAM/SCD/ACSS2/PMVK/ACSBG1/ACSL1/ELOVL3/MVD/DGAT2	10
BP	GO_0033875 ribonucleotide bisphosphate metabolic process	10/207	138/18866	2.97E-06	06 0.00165	9.001E-06	00048 MPC2/GPAM/SCD/ACSS2/PMVK/ACSBG1/ACSL1/ELOVL3/MVD/DGAT2	10
BP	GO_0024042 purine nucleoside bisphosphate metabolic process	10/207	138/18866	2.97E-06	06 0.00165	9.001E-06	00048 MPC2/GPAM/SCD/ACSS2/PMVK/ACSBG1/ACSL1/ELOVL3/MVD/DGAT2	10
BP	GO_0043394 carboxylic acid biosynthetic process	16/207	367/18866	3.13E-06	00 0.00321	5.62E-06	05 GPX4/CP127A6/PPAR/CNPLA3/MOGAT2/THRS/PPAR/CNPLA3/DGAT2/MECR	16
BP	GO_0016053 organic acid biosynthetic process	16/207	368/18866	3.24E-06	00 0.00173	5.62E-06	05 GPX4/CP27A1/PPAR/CNPLA3/MOGAT2/THRS/PPAR/CNPLA3/DGAT2	16
BP	GO_0006720 isoprenoid regulation	10/207	144/18866	4.36E-06	00 0.00228	6.002E-06	00024 PNLPA4/PHHY/APOE/PECR/FA2H/CYP39A1/ACSS2/ACSBG1/INSIG1/ELOVL3/FADS2	10
BP	GO_0090207 regulation of triglyceride metabolic process	6/207	43/18866	7.05E-06	00 0.00362	6.003E-06	00024 APCE/NR1H3/THRS/PPAR/CNPLA3/DGAT2/SDR5A1/LEP	6
BP	GO_0010876 lipid localization	17/207	440/18866	7.65E-06	00 0.00368	6.003E-06	00035 MEST/SLC25A17/HAC1/EC1/HAO2/PECR/FA2H/CYP39A1/ACSS2/ACSBG1/INSIG1/ELOVL3/FADS2/MECR	17
BP	GO_0006790 sulfur compound metabolic process	15/207	371/18866	1.57E-05	0.00777	0.00088	05 GPX4/GHR/GSTM3/MPC2/GPAM/SCD/ACSS2/PMVK/LHC5/ACSBG1/GNG/ACSL1/ELOVL3/MVD/DGAT2	15
BP	GO_0010883 regulation of lipid storage	6/207	52/18866	2.17E-05	0.00510	0.00044	05 MEST/SLC25A17/HAC1/EC1/HAO2/PECR/FA2H/CYP39A1/ACSS2/ACSBG1/INSIG1/ELOVL3/FADS2/MECR	6
BP	GO_0019058 fatty acid derivative metabolic process	10/207	175/18866	2.42E-05	0.00119	0.00100	05 GPX4/CP43/ACSS2/ACSBG1/ACSL1/ELOVL3/DGAT2/AWAT1	10
BP	GO_0035384 thioester biosynthetic process	6/207	53/18866	2.42E-05	0.00119	0.00100	05 MPC2/SCD/ACSS2/ACSBG1/ACSL1/ELOVL3	6
BP	GO_0017161 fatty-acyl-CoA biosynthetic process	6/207	53/18866	2.42E-05	0.00119	0.00100	05 MPC2/SCD/ACSS2/ACSBG1/ACSL1/ELOVL3	6
BP	GO_1902930 regulation of alcohol biosynthetic process	7/207	82/18866	3.28E-05	0.00148	0.00131	05 APCE/GPAM/SCD/FPDS/DHCR7/PPM1K/INSIG1/LEP	7
BP	GO_0042445 hormone metabolic process	11/207	221/18866	3.42E-05	0.00152	0.00135	05 PNLPA4/GHR/CGA/YD/DHRS2/RPB4/DHCR7/HSD3B1/DGAT2/SDR5A1/LEP	11
BP	GO_0007031 peroxisome organization	7/207	83/18866	3.55E-05	0.00159	0.00134	05 PHHY/HAC1/PECR/FA2H/CYP39A1/ACSS2/ACSBG1/INSIG1/ELOVL3/FADS2/MECR	7
BP	GO_0066444 phospholipid metabolic process	16/207	455/18866	4.46E-05	0.00193	0.00177	05 GPX4/GHR/GSTM3/MPC2/GPAM/SCD/ACSS2/PMVK/LHC5/ACSBG1/GNG/ACSL1/ELOVL3/MVD/DGAT2	16
BP	GO_0086544 phospholipid biosynthetic process	12/207	271/18866	4.73E-05	0.00203	0.00180	05 GPX4/CP127A6/PPAR/CNPLA3/MOGAT2/THRS/PPAR/CNPLA3/DGAT2/SDR5A1/MECR	12
BP	GO_0070542 response to fatty acid	7/207	41/18866	5.98E-05	0.002506	0.002243 CLDN1/SCDA/AC5C/PPARG/GNPA/TCG1/DGAT2/SDR5A1/LEP	7	
BP	GO_0035337 fatty-acyl-CoA metabolic process	5/207	22/18866	8.82E-05	0.003520	0.003161 GKS/APGAT2/LEP	5	
BP	GO_0010888 negative regulation of lipid storage	4/207	22/18866	8.82E-05	0.003520	0.003161 RORC/APRC/ABHD5/LEP	4	
BP	GO_0033866 nucleoside bisphosphate biosynthetic process	6/207	67/18866	9.28E-05	0.003589	0.003184 MPC2/SCD/ACSS2/ACSBG1/ACSL1/ELOVL3	6	
BP	GO_0034030 ribonucleotide bisphosphate biosynthetic process	6/207	67/18866	9.28E-05	0.003589	0.003184 MPC2/SCD/ACSS2/ACSBG1/ACSL1/ELOVL3	6	
BP	GO_0024033 purine nucleoside bisphosphate biosynthetic process	6/207	67/18866	9.28E-05	0.003589	0.003184 MPC2/SCD/ACSS2/ACSBG1/ACSL1/ELOVL3	6	
BP								

BP	GO:000684 acetyl-CoA metabolic process	4/207	38/18666 0.000776 0.019742 0.017668 MPC2/ACSS2/PMVK/MVD	4
BP	GO:0019433 triglyceride catabolic process	4/207	38/18666 0.000776 0.019742 0.017668 PNPLA4/LIPH/PNPLA3/ABHD5	4
BP	GO:0030730 sequestering of triglyceride	3/207	17/18666 0.00079 0.019742 0.017668 PPAR/GITM2/ABHD5	3
BP	GO:0046459 short-chain fatty acid metabolic process	3/207	17/18666 0.00079 0.019742 0.017668 PHYH/ACSS2/CRT	3
BP	GO:0055089 fatty acid homeostasis	3/207	17/18666 0.00079 0.019742 0.017668 APOE/GPAM/DGAT2	3
BP	GO:0055090 acyl/glycerol homeostasis	4/207	39/18666 0.000957 0.021028 0.018818 APOE/NR1H3/FITM2/DGAT2	4
BP	GO:0070328 triglyceride homeostasis	4/207	39/18666 0.000957 0.021028 0.018818 APOE/NR1H3/FITM2/DGAT2	4
BP	GO:0035338 long-chain fatty-acyl-CoA biosynthetic process	3/207	19/18666 0.00108 0.02694 0.024109 ACSBG1/ACSL1/ELOVL3	3
BP	GO:0010878 cholesterol storage	3/207	20/18666 0.001293 0.030981 0.027725 NR1H3/PPAR/SOAT1	3
BP	GO:0044727 sulfur compound biosynthetic process	8/207	192/18666 0.001297 0.030981 0.027725 GSTM3/MPC2/SCD/ACSS2/ACSBG1/OGN/ACSL1/ELOVL3	8
BP	GO:0046503 glycerolipid catabolic process	5/207	74/18666 0.001321 0.031287 0.027999 PNPLA4/LIPH/GDPDI/PNPLA3/ABHD5	5
BP	GO:0006869 lipid transport	12/207	393/18666 0.001386 0.03250 0.02909 SLC27A6/SLC25A17/APOE/ABC13/NR1H3/RBP4/PPARG/AQP9/THRSP/ACSL1/LEP/SOAT1	12
BP	GO:0015809 long-chain fatty acid transport	5/207	75/18666 0.001403 0.03266 0.029227 SLC27A6/APOE/PPARG/THRSP/ACSL1	5
BP	GO:1901616 organic hydroxy compound catabolic process	5/207	76/18666 0.001489 0.032969 0.03039 CYP4F3/CYP27A1/GKS/APOE/CYP39A1	5
BP	GO:0043651 linoleic acid metabolic process	3/207	21/18666 0.0014970 0.032989 0.03039 ACSL1/ELOVL3/FADS2	3
BP	GO:2000738 positive regulation of stem cell differentiation	3/207	21/18666 0.0014970 0.032989 0.03039 GATA8/FOXC1/RBM24	3
BP	GO:0016101 diterpenoid metabolic process	6/207	114/18666 0.001620 0.036311 0.032495 PKLR/MPC2/GPAM/SCD/ACSS2/PMVK/ACSBG1/EN03/ACSL1/ELOVL3/MVD/DGAT2	6
BP	GO:0062012 regulation of small molecule metabolic process	13/207	456/18666 0.0016340 0.036311 0.032495 PKLR/MPC2/GPAM/SCD/ACSS2/PMVK/ACSBG1/EN03/ACSL1/ELOVL3/MVD/DGAT2	13
BP	GO:0009150 purine ribonucleotide metabolic process	12/207	401/18666 0.001640 0.036311 0.032495 PKLR/MPC2/GPAM/SCD/ACSS2/PMVK/ACSBG1/EN03/ACSL1/ELOVL3/MVD/DGAT2	12
BP	GO:0009083 branched-chain amino acid catabolic process	3/207	22/18666 0.0017190 0.037744 0.03378 PPM1K/BCKDHB/HIBCH	3
BP	GO:0046942 carboxylic acid transport	11/207	350/18666 0.0017360 0.037844 SLC27A6/SLC1A6/SLC25A17/APOE/MPC2/SLC25A18/APOE/PMP2/PPAR/AQP9/THRSP/ACSL1/LEP	11
BP	GO:0015849 organic acid transport	11/207	353/18666 0.001856 0.039949 0.035751 SLC27A6/SLC1A6/SLC25A17/APOE/MPC2/SLC25A18/APOE/PMP2/PPAR/AQP9/THRSP/ACSL1/LEP	11
BP	GO:0046461 neutral lipid catabolic process	4/207	48/18666 0.001878 0.039949 0.035751 PNPLA4/LIPH/PNPLA3/ABHD5	4
BP	GO:0046464 acyl/glycerol catabolic process	4/207	48/18666 0.001878 0.039949 0.035751 PNPLA4/LIPH/PNPLA3/ABHD5	4
BP	GO:0034284 response to monosaccharide	8/207	207/18666 0.002083 0.043974 0.03935 CT5V/PKLR/MPC2/GPAM/AAC5/CPB2/ACVR1C/LEP	8
BP	GO:0090208 positive regulation of triglyceride metabolic process	3/207	24/18666 0.002223 0.046226 0.041369 NR1H3/ABHD5/DGAT2	3
BP	GO:0009259 ribonucleotide metabolic process	12/207	416/18666 0.002224 0.046226 0.041369 PKLR/MPC2/GPAM/SCD/ACSS2/PMVK/ACSBG1/EN03/ACSL1/ELOVL3/MVD/DGAT2	12
CC	GO:005777 peroxisome	12/215	137/19559 3.81E-08 4.80E-06 4.50E-06 PHYH/ISOCU/SLC25A17/HACL1/PEX11A/HAO2/PCR/XMP2/PMVK/CRAT/GNPAT/ACSL1	12
CC	GO:0042579 microbody	12/215	137/19559 3.81E-08 4.80E-06 4.50E-06 PHYH/ISOCU/SLC25A17/HACL1/PEX11A/HAO2/PCR/XMP2/PMVK/CRAT/GNPAT/ACSL1	12
CC	GO:005778 peroxisomal membrane	6/215	60/19559 5.02E-05 0.00316 0.00296 SLC25A17/PEX11A/PCR/XMP2/GNPAT/ACSL1	6
CC	GO:0031903 microbody membrane	6/215	60/19559 5.02E-05 0.00316 0.00296 SLC25A17/PEX11A/PCR/XMP2/GNPAT/ACSL1	6
CC	GO:005782 peroxisomal matrix	5/215	52/19559 0.00262 0.010986 0.001279 PHYH/HACL1/HAO2/CRAT/GNPAT	5
CC	GO:0031907 microbody lumen	5/215	52/19559 0.00262 0.010986 0.001279 PHYH/HACL1/HAO2/CRAT/GNPAT	5
CC	GO:0005811 lipid droplet	6/215	93/19559 0.000566 0.020386 0.019075 PNPLA4/PLIN4/PLINLA3/ABHD5/DGAT2	6
MF	GO:0008374 O-acyltransferase activity	11/205	50/18352 6.59E-12 2.86E-09 2.50E-09 AGPAT1/GPAM/AGPAT3/PNPLA3/MOGAT2/CRAT/ABHD5/GNPAT/DGAT2/AWAT1/SOAT1	11
MF	GO:0016411 acyl/glycerol O-acyltransferase activity	6/205	23/18352 1.56E-07 3.38E-05 2.95E-05 AGPAT1/AGPAT3/PNPLA3/MOGAT2/ABHD5/DGAT2	6
MF	GO:0016747 transferase activity, transferring acyl groups other than amino-acyl groups	14/205	229/18352 3.07E-07 3.74E-05 3.27E-05 AGPAT1/GPAM/ACAT2/CERS4/AGPAT3/PNPLA3/MOGAT2/CRAT/ABHD5/GNPAT/ELOVL3/DGAT2/AWAT1/SOAT1	14
MF	GO:0016405 CoA-ligase activity	6/205	26/18352 3.45E-07 3.74E-05 3.27E-05 SLC27A6/ACSS3/AACS/ACSS2/ACSBG1/ACSL1	6
MF	GO:0016878 acyl-thio ligase activity	6/205	30/18352 8.57E-07 7.44E-05 6.50E-05 SLC27A6/ACSS3/AACS/ACSS2/ACSBG1/ACSL1	6
MF	GO:0016746 transferase activity, transferring acyl groups	14/205	259/18352 1.35E-06 9.73E-05 8.50E-05 AGPAT1/GPAM/ACAT2/CERS4/AGPAT3/PNPLA3/MOGAT2/CRAT/ABHD5/GNPAT/ELOVL3/DGAT2/AWAT1/SOAT1	14
MF	GO:0016877 ligase activity, forming carbon-sulfur bonds	6/205	40/18352 5.05E-06 0.000313 0.000273 SLC27A6/ACSS3/AACS/ACSS2/ACSBG1/ACSL1	6
MF	GO:0016628 oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	5/205	26/18352 9.00E-06 0.000468 0.000426 PCR/DHCR24/SRD5A1/MECR	5
MF	GO:0003841 1-acylglycerol-3-phosphate O-acyltransferase activity	4/205	15/18352 1.87E-05 0.000904 0.000789 AGPAT1/AGPAT3/PNPLA3/MOGAT2/ABHD5/DGAT2	4
MF	GO:0042171 lysophosphatidic acid acyltransferase activity	4/205	17/18352 3.21E-05 0.001393 0.002127 AGPAT1/AGPAT3/PNPLA3/ABHD5	4
MF	GO:0016627 oxidoreductase activity, acting on the CH-CH group of donors	6/205	59/18352 4.97E-05 0.001858 0.001623 PCR/DHCR24/SRD5A1/MECR	6
MF	GO:0071617 lysophospholipid acyltransferase activity	4/205	19/18352 5.14E-05 0.001858 0.001623 AGPAT1/AGPAT3/PNPLA3/ABHD5	4
MF	GO:0016705 oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	9/205	162/18352 1.35E-06 9.73E-05 8.50E-05 AGPAT1/GPAM/ACAT2/CERS4/AGPAT3/PNPLA3/MOGAT2/CRAT/ABHD5/GNPAT/ELOVL3/DGAT2/AWAT1/SOAT1	9
MF	GO:0005496 steroid binding	7/205	106/18352 0.000186 0.005815 0.005077 PGRCM2/NR3C2/RORC/NR1H3/PGRCM1/INSIG1/SOAT1	7
MF	GO:0004467 long-chain fatty-acid-CoA ligase activity	3/205	165/18352 0.0005430 0.017434 0.012865 SLC27A6/ACSS3/TTL7/AAAC/ACSS2/HLC5/ACSBG1/ACSL1	3
MF	GO:0016874 ligase activity	8/205	165/18352 0.0005430 0.017434 0.012865 SLC27A6/ACSS3/TTL7/AAAC/ACSS2/HLC5/ACSBG1/ACSL1	8
MF	GO:0020037 heme binding	7/205	138/18352 0.0009240 0.028740 0.019973 PGRCM2/CYP4F3/CYP27A1/ABCB10/CYP5A/FA2H/CYP39A1/PGRCM1	7
MF	GO:0004497 monooxygenase activity	6/205	101/18352 0.0009490 0.028740 0.019973 CYP4F3/CYP27A1/CYP39A1/NLRP11/HEATR4/MSMO1/FADS2	6
MF	GO:003218 amide binding	12/205	381/18352 0.001236 0.028233 0.024652 GHR/CYRB1/TSV1/APOE/GSTM3/PGRCM1/DHCR24/PPARG/HLC5/PNPLA3/SRD5A1/SOAT1	12
MF	GO:0046906 tetrapyrrole binding	7/205	148/18352 0.001389 0.030134 0.026312 PGRCM2/CYP4F3/CYP27A1/CYP5A/FA2H/CYP39A1/PGRCM1	7
MF	GO:005506 iron ion binding	7/205	151/18352 0.001559 0.032211 0.028125 PHYH/CYP4F3/CYP27A1/ABCB10/CYP39A1/MSMO1	7
MF	GO:0015645 fatty acid ligase activity	3/205	22/18352 0.001809 0.035678 0.031152 SLC27A6/ACSBG1/ACSL1	3
MF	GO:0004987 nuclear receptor activity	4/205	52/18352 0.002692 0.048688 0.04251 NR3C2/RORC/NR1H3/PPARG	4
MF	GO:0098531 ligand-activated transcription factor activity	4/205	52/18352 0.002692 0.048688 0.04251 NR3C2/RORC/NR1H3/PPARG	4

Table S4. The KEGG enrichment analysis of downregulated genes in cluster 3

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	genelD	Count
hsa04146	Peroxisome	11/112	82/8091	1.34E-08	2.36E-06	2.17E-06	PHYH/SLC25A17/HACL1/PEX11A/HAO2/PECR/PXMP2/PMVK/CRAT/GNPAT/ACSL1	11
hsa03320	PPAR signaling pathway	10/112	76/8091	7.65E-08	6.73E-06	6.20E-06	SLC27A6/CYP27A1/NR1H3/PLIN4/SCD/PLIN1/PPARG/ACSBG1/ACSL1/FADS2	10
hsa01212	Fatty acid metabolism	7/112	57/8091	1.21E-05	0.000707	0.000651	SCD/ACAT2/ACSBG1/ACSL1/ELOVL3/FADS2/MECR	7
hsa00640	Propanoate metabolism	5/112	34/8091	9.39E-05	0.00413	0.003804	ACSS3/ACAT2/ACSS2/BCKDHB/HIBCH	5
hsa00100	Steroid biosynthesis	4/112	20/8091	0.000142	0.005001	0.004606	DHCR7/DHCR24/MSMO1/SOAT1	4
hsa00561	Glycerolipid metabolism	6/112	61/8091	0.000184	0.005279	0.004863	AGPAT1/GPAM/AGPAT3/PNPLA3/MOGAT2/DGAT2	6
hsa00900	Terpenoid backbone biosynthesis	4/112	22/8091	0.00021	0.005279	0.004863	FDPS/ACAT2/PMVK/MVD	4
hsa01200	Carbon metabolism	7/112	115/8091	0.001034	0.022755	0.020959	PKLR/HAO2/ACAT2/FBP2/ACSS2/HIBCH/ENO3	7
hsa00061	Fatty acid biosynthesis	3/112	18/8091	0.001811	0.035411	0.032616	ACSBG1/ACSL1/MECR	3
hsa00071	Fatty acid degradation	4/112	43/8091	0.002834	0.045339	0.04176	ECI1/ACAT2/ACSBG1/ACSL1	4
hsa04975	Fat digestion and absorption	4/112	43/8091	0.002834	0.045339	0.04176	AGPAT1/ACAT2/MOGAT2/DGAT2	4
hsa00280	Valine, leucine and isoleucine degradation	4/112	48/8091	0.004238	0.062154	0.057247	ACAT2/AACS/BCKDHB/HIBCH	4
hsa01040	Biosynthesis of unsaturated fatty acids	3/112	27/8091	0.00593	0.080283	0.073945	SCD/ELOVL3/FADS2	3
hsa00630	Glyoxylate and dicarboxylate metabolism	3/112	30/8091	0.007988	0.100417	0.092489	HAO2/ACAT2/ACSS2	3
hsa00410	beta-Alanine metabolism	3/112	31/8091	0.008756	0.102732	0.094622	CNDP1/UPB1/HIBCH	3
hsa00010	Glycolysis / Gluconeogenesis	4/112	67/8091	0.013668	0.150349	0.138479	PKLR/FBP2/ACSS2/ENO3	4
hsa00120	Primary bile acid biosynthesis	2/112	17/8091	0.022555	0.233512	0.215076	CYP27A1/CYP39A1	2
hsa00620	Pyruvate metabolism	3/112	47/8091	0.026942	0.263432	0.242635	PKLR/ACAT2/ACSS2	3
hsa00600	Sphingolipid metabolism	3/112	49/8091	0.030014	0.27802	0.256071	ACER1/PSAPL1/CERS4	3
hsa04979	Cholesterol metabolism	3/112	50/8091	0.031616	0.27822	0.256255	CYP27A1/APOE/SOAT1	3
hsa04923	Regulation of lipolysis in adipocytes	3/112	57/8091	0.044057	0.369239	0.340088	CGA/PLIN1/ABHD5	3
hsa00564	Glycerophospholipid metabolism	4/112	98/8091	0.046655	0.373237	0.343771	AGPAT1/GPAM/AGPAT3/GNPAT	4
hsa00062	Fatty acid elongation	2/112	27/8091	0.053247	0.407454	0.375287	ELOVL3/MECR	2
hsa00650	Butanoate metabolism	2/112	28/8091	0.056837	0.416804	0.383899	ACAT2/AACS	2
hsa04920	Adipocytokine signaling pathway	3/112	69/8091	0.070161	0.493932	0.454937	ACSBG1/ACSL1/LEP	3

Table S5. The GO enrichment analysis of key genes in lightgreen

ONTOLOGY ID	Description	GeneRatio	BgRatio	p-value	p-adjust value	genelist	Count
GO_0045110 T cell activation		45/208	483/18666	9.96E- 29	1.54E- 24	genelist	34
GO_0011899 negative cell-cell adhesion		34/208	483/18666	9.96E- 29	1.54E- 24	genelist	34
GO_0050638 regulation of T cell activation		33/208	483/18666	9.47E- 29	1.6E- 24	genelist	30
GO_0030217 T cell differentiation		26/208	253/18666	5.94E- 18	3.47E- 15	genelist	26
GO_0024499 positive regulation of cell-cell adhesion		27/208	279/18666	6.20E- 18	3.47E- 15	genelist	27
GO_1903039 positive regulation of leukocyte cell-cell adhesion		25/208	235/18666	1.92E- 17	5.45E- 14	genelist	25
GO_0002595 positive regulation of leukocyte activation		30/208	409/18666	1.48E- 16	16.53E- 13	genelist	30
GO_0002596 positive regulation of leukocyte differentiation		24/208	241/18666	1.48E- 16	16.53E- 13	genelist	31
GO_0050700 positive regulation of T cell activation		23/208	214/18666	2.00E- 16	14.94E- 13	genelist	23
GO_0050667 positive regulation of cell activation		30/208	421/18666	1.98E- 16	13.18E- 13	genelist	30
GO_1903037 regulation of leukocyte cell-cell adhesion		27/208	309/18666	1.82E- 16	10.18E- 13	genelist	27
GO_0003098 lymphocyte differentiation		22/208	209/18666	1.78E- 16	10.18E- 13	genelist	22
GO_0002597 immune response, local pathway		26/208	209/18666	1.75E- 16	10.18E- 13	genelist	26
GO_0050651 antigen receptor-mediated signaling pathway		25/208	225/18666	1.74E- 16	12.34E- 13	genelist	25
GO_0051251 positive regulation of lymphocyte activation		27/208	357/18666	1.10E- 15	5.57E- 12	genelist	27
GO_0045785 positive regulation of cell adhesion		28/208	409/18666	1.6E- 15	4.56E- 12	genelist	28
GO_0002429 immune response-activating cell surface receptor signaling pathway		29/208	481/18666	1.61E- 15	4.14E- 12	genelist	29
GO_0017571 immune response-regulating signal transduction		27/208	409/18666	1.58E- 15	4.14E- 12	genelist	27
GO_0071131 negative regulation of apoptotic process		26/208	409/18666	1.55E- 15	4.14E- 12	genelist	15
GO_0046551 alpha-beta T cell activation		15/208	146/18666	1.58E- 15	4.05E- 12	genelist	16
GO_0032943 mononuclear cell proliferation		21/208	283/18666	1.35E- 15	4.05E- 12	genelist	21
GO_0050767 regulation of lymphocyte proliferation		16/208	286/18666	1.38E- 15	4.05E- 12	genelist	21
GO_0002598 G-protein coupled receptor signaling pathway		20/208	309/18666	1.35E- 15	4.05E- 12	genelist	20
GO_0032944 regulation of mononuclear cell proliferation		18/208	221/18666	1.72E- 15	5.25E- 12	genelist	18
GO_0040298 cell proliferation		17/208	195/18666	6.69E- 15	11.61E- 12	genelist	17
GO_0051607 defense response to virus		19/208	259/18666	1.68E- 15	11.75E- 12	genelist	19
GO_2000010 negative regulation of leukocyte apoptotic process		10/208	49/18666	1.21E- 15	10.91E- 12	genelist	10
GO_0050652 alpha-beta T cell activation		10/208	44/18666	1.57E- 15	10.91E- 12	genelist	10
GO_0008193 negative regulation of cytokine production		24/208	44/18666	1.57E- 15	10.91E- 12	genelist	24
GO_2000105 regulation of leukocyte apoptotic process		19/208	86/18666	1.05E- 15	10.91E- 12	genelist	12
GO_0070663 regulation of leukocyte proliferation		21/208	240/18666	1.84E- 16	1.01E- 12	genelist	21
GO_0009151 response to virus		21/208	219/18666	1.05E- 16	1.01E- 12	genelist	18
GO_0042429 regulation of T cell proliferation		21/208	219/18666	1.05E- 16	1.01E- 12	genelist	20
GO_0001905 positive regulation of alpha-beta T cell activation		21/208	221/18666	1.05E- 16	1.01E- 12	genelist	19
GO_0034341 response to interferon-gamma		15/208	172/18666	1.93E- 16	10.61E- 12	genelist	15
GO_0043674 positive, alpha-beta T cell differentiation		15/208	202/18666	1.81E- 16	10.63E- 12	genelist	16
GO_0006353 negative regulation of alpha-beta T cell activation		10/208	49/18666	1.21E- 16	10.63E- 12	genelist	10
GO_0040454 T cell activation		10/208	44/18666	1.57E- 16	10.63E- 12	genelist	9
GO_0050671 positive regulation of lymphocyte proliferation		13/208	86/18666	1.56E- 16	10.63E- 12	genelist	13
GO_1902015 regulation of leukocyte differentiation		13/208	290/18666	1.38E- 16	10.63E- 12	genelist	13
GO_0032464 positive regulation of mononuclear cell proliferation		13/208	137/18666	1.39E- 16	10.63E- 12	genelist	13
GO_0043598 positive T cell selection		8/208	36/18666	4.43E- 09	4.26E- 09	genelist	8
GO_0001905 regulation of adaptive immune response		14/208	18/18666	1.54E- 09	4.26E- 09	genelist	14
GO_1902078 positive regulation of hemopoiesis		15/208	204/18666	6.32E- 09	4.05E- 09	genelist	15
GO_0000909 phagocytosis		20/208	38/18666	1.33E- 09	4.05E- 09	genelist	20
GO_0002583 negative regulation of immune system process		22/208	42/18666	1.35E- 09	4.05E- 09	genelist	22
GO_0046534 regulation of alpha-beta T cell activation		11/208	97/18666	9.76E- 10	4.05E- 09	genelist	11
GO_0002598 T cell activation		10/208	63/18666	1.64E- 10	4.05E- 09	genelist	10
GO_0040454 T cell activation		10/208	97/18666	1.37E- 10	4.05E- 09	genelist	9
GO_0050671 positive regulation of lymphocyte proliferation		13/208	139/18666	1.60E- 10	4.05E- 09	genelist	13
GO_1902015 regulation of leukocyte differentiation		13/208	286/18666	1.77E- 10	4.05E- 09	genelist	13
GO_0032464 positive regulation of mononuclear cell proliferation		13/208	219/18666	1.78E- 10	4.05E- 09	genelist	13
GO_0045119 regulation of lymphocyte differentiation		14/208	18/18666	1.39E- 10	4.05E- 09	genelist	14
GO_0040212 positive regulation of T cell proliferation		11/208	107/18666	1.50E- 10	4.05E- 09	genelist	11
GO_0001905 positive regulation of hematopoiesis		10/208	108/18666	1.32E- 10	4.05E- 09	genelist	10
GO_0020281 regulation of T cell differentiation		20/208	409/18666	1.32E- 10	4.05E- 09	genelist	20
GO_0000909 phagocytosis		11/208	108/18666	1.04E- 10	4.05E- 09	genelist	11
GO_1902076 regulation of hemopoiesis		12/208	49/18666	1.52E- 10	4.05E- 09	genelist	12
GO_0045852 positive regulation of T cell differentiation		13/208	150/18666	1.19E- 10	4.05E- 09	genelist	13
GO_0002598 negative regulation of T cell differentiation		13/208	407/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0002597 regulation of immune effector process		12/208	17/18666	1.25E- 10	4.05E- 09	genelist	12
GO_0045119 regulation of lymphocyte differentiation		14/208	18/18666	1.39E- 10	4.05E- 09	genelist	14
GO_0040295 regulation of protein kinase C signaling		11/208	18/18666	1.19E- 10	4.05E- 09	genelist	13
GO_0033462 cellular response to interferon-gamma		10/208	18/18666	1.17E- 10	4.05E- 09	genelist	10
GO_0019969 cellular response to chemoattractant		10/208	18/18666	1.17E- 10	4.05E- 09	genelist	10
GO_0071346 cellular response to interferon-gamma		13/208	18/18666	1.17E- 10	4.05E- 09	genelist	13
GO_0045119 positive regulation of alpha-beta T cell activation		13/208	18/18666	1.17E- 10	4.05E- 09	genelist	13
GO_0034341 response to interferon-gamma		13/208	18/18666	1.17E- 10	4.05E- 09	genelist	13
GO_0043674 positive, alpha-beta T cell differentiation		13/208	18/18666	1.17E- 10	4.05E- 09	genelist	13
GO_0002583 negative regulation of alpha-beta T cell activation		13/208	18/18666	1.17E- 10	4.05E- 09	genelist	13
GO_0046534 regulation of alpha-beta T cell activation		13/208	18/18666	1.17E- 10	4.05E- 09	genelist	13
GO_0040454 T cell activation		10/208	108/18666	1.57E- 10	4.05E- 09	genelist	17
GO_0050777 negative regulation of immune response		12/208	108/18666	1.57E- 10	4.05E- 09	genelist	12
GO_0045637 regulation of alpha-beta T cell differentiation		10/208	108/18666	1.57E- 10	4.05E- 09	genelist	10
GO_0000909 phagocyte mediated cytotoxicity		20/208	108/18666	1.57E- 10	4.05E- 09	genelist	20
GO_1902076 regulation of hemopoiesis		11/208	108/18666	1.57E- 10	4.05E- 09	genelist	11
GO_0045852 positive regulation of T cell differentiation		10/208	97/18666	9.76E- 10	4.05E- 09	genelist	10
GO_0002598 negative regulation of T cell differentiation		10/208	97/18666	9.76E- 10	4.05E- 09	genelist	10
GO_0002597 regulation of immune effector process		10/208	97/18666	9.76E- 10	4.05E- 09	genelist	10
GO_0032944 positive regulation of mononuclear cell proliferation		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0040295 regulation of T cell proliferation		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0001905 positive regulation of hematopoiesis		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0020281 regulation of T cell differentiation		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0000909 phagocytosis		20/208	108/18666	1.25E- 10	4.05E- 09	genelist	20
GO_1902075 regulation of hemopoiesis		11/208	108/18666	1.25E- 10	4.05E- 09	genelist	11
GO_0046534 regulation of alpha-beta T cell activation		11/208	97/18666	9.76E- 10	4.05E- 09	genelist	11
GO_0040454 T cell activation		10/208	97/18666	9.76E- 10	4.05E- 09	genelist	10
GO_0002598 negative regulation of T cell differentiation		10/208	97/18666	9.76E- 10	4.05E- 09	genelist	10
GO_0002597 regulation of immune effector process		10/208	97/18666	9.76E- 10	4.05E- 09	genelist	10
GO_0032944 positive regulation of mononuclear cell proliferation		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0040295 regulation of T cell proliferation		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0001905 positive regulation of hematopoiesis		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0020281 regulation of T cell differentiation		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0000909 phagocytosis		20/208	108/18666	1.25E- 10	4.05E- 09	genelist	20
GO_1902074 regulation of hemopoiesis		11/208	108/18666	1.25E- 10	4.05E- 09	genelist	11
GO_0046534 regulation of alpha-beta T cell activation		11/208	97/18666	9.76E- 10	4.05E- 09	genelist	11
GO_0040454 T cell activation		10/208	97/18666	9.76E- 10	4.05E- 09	genelist	10
GO_0002598 negative regulation of T cell differentiation		10/208	97/18666	9.76E- 10	4.05E- 09	genelist	10
GO_0002597 regulation of immune effector process		10/208	97/18666	9.76E- 10	4.05E- 09	genelist	10
GO_0032944 positive regulation of mononuclear cell proliferation		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0040295 regulation of T cell proliferation		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0001905 positive regulation of hematopoiesis		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0020281 regulation of T cell differentiation		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0000909 phagocytosis		20/208	108/18666	1.25E- 10	4.05E- 09	genelist	20
GO_1902073 regulation of hemopoiesis		11/208	108/18666	1.25E- 10	4.05E- 09	genelist	11
GO_0046534 regulation of alpha-beta T cell activation		11/208	97/18666	9.76E- 10	4.05E- 09	genelist	11
GO_0040454 T cell activation		10/208	97/18666	9.76E- 10	4.05E- 09	genelist	10
GO_0002598 negative regulation of T cell differentiation		10/208	97/18666	9.76E- 10	4.05E- 09	genelist	10
GO_0002597 regulation of immune effector process		10/208	97/18666	9.76E- 10	4.05E- 09	genelist	10
GO_0032944 positive regulation of mononuclear cell proliferation		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0040295 regulation of T cell proliferation		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0001905 positive regulation of hematopoiesis		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13
GO_0020281 regulation of T cell differentiation		13/208	108/18666	1.25E- 10	4.05E- 09	genelist	13

BP	G_004827/phagocyte chemotaxis	7/208	65/18666 7.25E-06 00005.0 00019/PKCD1/CBL/CL2/CKL16/[CKL11]/PRB13/CKL19	7
BP	G_004828/regulation of phagocytosis pathway	6/208	43/18666 7.25E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	10
BP	G_002022/regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	10/208	153/18666 7.25E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	10
BP	G_002022/regulation of lymphocyte mediated immunity	10/208	153/18666 7.25E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	10
BP	G_004512/defense response to protozoan	5/208	154/18666 8.26E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	5
BP	G_004513/cellular extravasation	5/208	154/18666 8.26E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	5
BP	G_004726/cell migration	5/208	154/18666 8.26E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	5
BP	G_004727/cell migration regulation by phagocytosis	5/208	154/18666 8.26E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	5
GO	G_002237/response to molecule of bacterial origin	5/208	154/18666 8.26E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	5
BP	G_0001562/response to protein	5/208	154/18666 8.26E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	5
GO	G_002825/regulation of T-helper 1 type immune response	5/208	154/18666 8.26E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	5
BP	G_004254/regulation of calcium ion concentration	17/208	35/18666 1.05E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	15
BP	G_0050564/regulation of B cell activation	17/208	35/18666 1.05E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	15
GO	G_001979/viral genome replication	17/208	35/18666 1.05E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	15
BP	G_007162/granulocyte chemotaxis	9/208	71/18666 1.17E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	9
GO	G_0002397/cell differentiation involved in immune response	9/208	71/18666 1.17E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	9
GO	G_007711/lymphangiogenesis/syntaxe formation	9/208	71/18666 1.17E-06 00005.0 00019/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	9
GO	G_003436/positive regulation of signal transduction	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_000220/negative regulation of adaptive immune response	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0019835/cytokine	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0002448/mast cell mediated hypersensitivity	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_003811.1/intervention in interleukin signaling pathway	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0040003/negative regulation of tumor necrosis factor production	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_001810/regulation of leukocyte mediated cytotoxicity	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0050866/negative regulation of cell activation	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_007029/negative regulation of lymphocyte apoptotic process	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0019257/regulation of tumor necrosis factor superfamily cytokine production	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_002023/3-myeloid leukocyte differentiation	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_009796/receptor signaling pathway via STAT	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0050905/regulation of defense response to virus	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_002222/regulation of receptor signaling pathway via NF-kappaB signaling	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_003456/response to interferon-beta	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_007153/cellular response to interleukin-4	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0051896/regulation of protein kinase B signaling	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0070734/positive regulation of ERK1 and ERK2 cascade	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0050959/positive regulation of receptor-mediated signaling pathway	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_002828/regulation of cytokine production	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0001818/negative regulation of cytokine production	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0043373/C34-positive alpha-1 beta 1 cell lineage commitment	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0046629/gamma-delta T cell activation	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0070722/negative regulation of cell apoptotic process	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0045230/natural killer cells	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0097529/myeloid leukocyte migration	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0026353/interleukin-4 production	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0050571/regulation of viral genome replication	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0045250/mast cell activation	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0038971/c receptor signaling pathway	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0072749-1/kgap3 kinase/NF-kappaB signaling pathway	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_00390 positive regulation of B cell proliferation	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0002605/phagocyte homeostasis	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_004824/negative regulation of innate immune response	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0070723/ERK1 and ERK2 cascade	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0028275/regulation of cell cycle progression	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0029689/negative regulation of immune effector process	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0023633/alpha-beta T cell lineage commitment	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0050911/regulation of defense response to virus by host	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0038937/c receptor signaling pathway	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0028213/regulation of receptor-mediated signaling pathway	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0072749-1/kgap3 kinase/NF-kappaB signaling	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_00390 positive regulation of B cell proliferation	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0070729/regulation of cytokine production	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_002828/regulation of immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0050777/regulation of neutrophilic respiratory response	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0023653/interleukin-6 production	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0026263-alpha/beta T cell lineage commitment	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0045061/thym T cell selection	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0034087/regulation of GTPase activity	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0020770/negative regulation of lymphocyte mediated immunity	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0098760/response to interleukin-1	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0098761/cellular response to interleukin-7	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0047269/regulation of phagocytosis	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0001911/negative regulation of leukocyte mediated cytotoxicity	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0002260/phagocyte homeostasis	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_004824/negative regulation of innate immune response	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0070725/regulation of receptor-mediated signaling pathway	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0028232/negative regulation of response to biotic stimulus	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_002828/regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0050778/regulation of defense response to virus by host	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0045230/regulation of cell adhesion	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_003814/regulation of protein-containing complex assembly	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0045241/regulation of T-cell differentiation	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0045242/regulation of T helper 1 cell differentiation	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0071114/response to interleukin-9	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0002557 positive regulation of antigen receptor-mediated signaling pathway	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0044338/positive regulation of cell killing	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_002715/regulation of natural killer cell mediated immunity	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0071762/negative regulation of cell adhesion	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0031334/positive regulation of protein-containing complex assembly	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0045241/regulation of T-cell differentiation	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0045242/regulation of cell adhesion mediated by integrin	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0044803/multi-organism membrane organization	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0150076/neuron inflammation response	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0055074/calculum ion homeostasis	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0020233/cell lineage commitment	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0045232/positive regulation of protein-containing complex assembly	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0045233/regulation of cell adhesion	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0044803/regulation of protein-containing complex assembly	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0044803/regulation of protein-containing complex assembly	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0051056/regulation of small GTPase mediated signal transduction	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0001768/establishment of T cell polarity	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
GO	G_0043383/negative T cell selection	13/208	239/18666 1.38E-06 00004.70005/HAVCR2/CL2/CKL16/[CKL11]/PRC/CKR7/CKL19	13
BP	G_0071047/positive regulation of adaptive immune response	13/208	239/18666 1.38E-06 00004.70005/HAVCR	

GO:001283-negative regulation of sequestration of calcium ion	7
GO:005659-negative regulation of antigen receptor-mediated signaling pathway	4
GO:0072538-T-helper 17 type immune response	4
GO:190202-positive regulation of neutrophil migration	4
GO:1903900-regulation of viral life cycle	8
GO:1903901-negative regulation of viral life cycle	6
GO:0072593-cellular division; inorganic cation homeostasis	15
GO:0000207-transporter activity, cation; calcium ion	7
GO:0325373-regulation of interleukin-4 production	4
GO:005669-negative regulation of B cell activation	4
GO:003589-G protein-coupled purinergic nucleotide receptor signaling pathway	3
GO:0000206-positive thymic T cell selection	3
GO:0007672-negative regulation of IL-15	3
GO:051208-sequestration of calcium ion	7
GO:003328-myeloid cell apoptotic process	4
GO:0090222-regulation of neutrophil chemotaxis	6
GO:0032479-regulation of type I interferon production	7
GO:0000251-negative regulation of tumor necrosis factor	11
GO:0403020-regulation of macrophage activation	5
GO:0002756-MyD88-independent type-I-like receptor signaling pathway	4
GO:0070232-regulation of T cell apoptosis process	4
GO:0032695-type I interferon production	7
GO:0000205-negative regulation of interleukin-10 signaling pathway	3
GO:0000232-production of molecular mediator involved in inflammatory response	6
GO:003577-regulation of interleukin-8 production	6
GO:1904894-positive regulation of receptor signaling pathway via STAT	6
GO:0045622-regulation of T helper cell differentiation	4
GO:0002951-T helper cell lineage commitment	3
GO:0000209-regulation of viral life cycle	9
GO:0047189-viral entry into host cell	7
GO:0032733-positive regulation of interleukin-10 production	4
GO:000216-negative regulation of natural killer cell mediated immunity	3
GO:0029595-negative regulation of interleukin-12 production	3
GO:0000205-negative regulation of interleukin-12 production by integrin	3
GO:0044764-multi-organism cellular process	3
GO:0032175-negative regulation of interleukin-6 production	5
GO:1903038-negative regulation of leukocyte-cell adhesion	7
GO:000348-negative regulation of defense response	10
GO:0000205-negative regulation of autocrine mediated immunity	7
GO:004862-positive regulation of proteolysis	12
GO:0032537-interleukin-8 production	6
GO:0042116-macrophage activation	6
GO:0045639-positive regulation of myeloid cell differentiation	9
GO:0000205-cell recognition	9
GO:0091553-positive regulation of membrane import into cytosol	7
GO:0049425-regulation of receptor signaling pathway via JAK-STAT	7
GO:0002456-T cell mediated immunity	6
GO:048525-negative regulation of viral process	6
GO:0002534-cytokine production involved in inflammatory response	5
GO:0000205-negative regulation of leukocyte mediated cytotoxicity	9
GO:0027009-regulation of production of molecular mediator of immune response	7
GO:003527-cell adhesion mediated by integrin	5
GO:046579-positive regulation of Ras protein signal transduction	5
GO:0045631-T helper 1 cell differentiation	3
GO:003577-positive regulation of neuroinflammatory response	3
GO:0434232-positive regulation of λ -kappaB kinase/NF- κ B signaling	8
GO:0044699-entry into host	7
GO:0002709-regulation of T cell mediated immunity	5
GO:0022408-negative regulation of cell-cell adhesion	8
GO:0000205-negative regulation of GTPase activity	9
GO:0001616-positive regulation of type I endopeptidase activity	4
GO:0001913-T cell mediated cytotoxicity	5
GO:0003821-positive regulation of adaptive immune response	6
GO:0032418-lysosome localization	3
GO:003323-positive regulation of cell adhesion mediated by integrin	3
GO:0045639-positive regulation of interferon-alpha	3
GO:1903078-regulation of microbial cell activation	3
GO:033777-T cell differentiation in thymus	5
GO:0002626-myeloid cell homeostasis	7
GO:0051057-positive regulation of type I GTPase mediated signal transduction	5
GO:0000205-negative regulation of T cell receptor signaling pathway	3
GO:005729-positive regulation of inflammatory response	7
GO:0094024-leukocyte transport, cytosol	7
GO:0002833-positive regulation of response to biotic stimulus	9
GO:0032693-negative regulation of interleukin-10 production	3
GO:0035456-cellular response to interferon-beta	3
GO:003577-positive regulation of T cell receptor signaling pathway	3
GO:1900717-positive regulation of cytokine production involved in inflammatory response	3
GO:0031589-cell-substrate adhesion	11
GO:0001774-microglial cell activation	4
GO:0002695-cytokine secretion involved in inflammatory response	4
GO:0032694-positive regulation of interleukin-4 production	3
GO:0332622-inegrin activation	3
GO:0002688-regulation of leukocyte chemotaxis	6
GO:0032457-regulation of interferon-alpha production	3
GO:034162-toll-like receptor 9 signaling pathway	3
GO:0001821-positive regulation of type I receptor signaling pathway	8
GO:0001812-positive regulation of leukocyte mediated response	4
GO:0071522-regulation of granulocyte chemotaxis	4
GO:0052126-movement in host environment	7
GO:000911-phagocytosis, engulfment	6
GO:0007759-leukocyte adhesion; vascular endothelial cell	6
GO:0001616-positive regulation of location in cell	8
GO:0032874-positive regulation of stress-activated MAPK cascade	7
GO:0001783-B cell apoptotic process	3
GO:0044668-modulation by symbol of host cellular process	3
GO:0041249-positive regulation of phosphoinositide 3-kinase signaling	6
GO:0070304-positive regulation of interleukin-3 production	4
GO:0001763-establishment or maintenance of cell polarity	8
GO:0032720-negative regulation of tumor necrosis factor production	4
GO:0032597-interferon-alpha production	3
GO:0000205-negative regulation of T cell receptor signaling	3
GO:0046427-positive regulation of receptor signaling pathway via JAK-STAT	5
GO:032102-negative regulation of response to external stimulus	12
GO:000015-acfil filament organization	12
GO:005248-regulation of endopeptidase activity	12
GO:1903595-negative regulation of tumor necrosis factor superfamily cytokine production	4
GO:0000205-negative regulation of type I endopeptidase activity	7
GO:0320898-negative regulation of NF- κ B transcription factor activity	5
GO:2000117-negative regulation of cysteine-type endopeptidase activity	5
GO:009924-plasma membrane invagination	5
GO:0040323-positive regulation of myeloid cell apoptotic process	3
GO:0059209-regulation of macrophage activation	3
GO:0059209-regulation of chemotaxis	8
GO:0010950-positive regulation of endopeptidase activity	7
GO:0051495-positive regulation of cytoskeleton organization	8
GO:003273-positive regulation of protein polymerization	6
GO:0000205-negative regulation of protein polymerization	5
GO:0032717-regulation of protein polymerization	8
GO:0002690-positive regulation of leukocyte chemotaxis	8
GO:0018822-antigen processing and presentation	5
GO:0046330-positive regulation of JNK cascade	6
GO:0043289-positive regulation of glial cell differentiation	4
GO:0059209-regulation of chemotaxis	7
GO:002433-immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	6
GO:000272-endosome of neurons	6
GO:0008365-enzyme heparan sulfate	6
GO:0032457-regulation of receptor signaling pathway involved in phagocytosis	6
GO:0051099-positive regulation of DNA-binding transcription factor activity	12
GO:0050303-defense response to Gram-positive bacteria	5
GO:034113-heterotypic cell-cell adhesion	5
GO:003272-regulation of stress-activated MAPK cascade	8
GO:038994Fc-gamma receptor signaling pathway	8
GO:00100342-membrane invagination	6

BP	GO:001454 extracellular receptor activity	2/28
BP	GO:007024 regulation of nucleotide-binding oligomerization domain containing signaling pathway	2/28
BP	GO:190426 positive regulation of defense response to bacterium	2/28
BP	GO:200019 regulation of macrophage apoptotic process	2/28
BP	GO:009164 arachidonic acid metabolic process	3/208
BP	GO:000265 Ras protein signal transduction	10/208
BP	GO:000266 Ras protein-mediated protein kinase signaling cascade	3/208
BP	GO:095921 positive regulation of chemotaxis	6/208
BP	GO:0002431 Fc receptor mediated stimulatory signaling pathway	6/208
BP	GO:004815 phosphatidylinositol-mediated signaling	6/208
BP	GO:0002025 positive regulation of Ras protein signal transduction	7/208
BP	GO:0002430 Fc receptor-mediated signaling pathway	3/208
BP	GO:000830 intracellular signaling pathway in response to DNA damage	3/208
BP	GO:002547 regulation of peptidephage activity	5/208
BP	GO:001540 killing of cells of other organism	12/208
BP	GO:004578 regulation of Ras protein signal transduction	4/208
BP	GO:0002432 positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-coupled signaling pathway	6/208
BP	GO:0002842 positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	5/208
BP	GO:0002604 regulation of lymphocytic cell antigen processing and presentation	2/208
BP	GO:0002605 positive regulation of antigen presentation	2/208
BP	GO:004560 negative thymic T cell selection	2/208
BP	GO:004643 regulation of gamma-delta T cell activation	2/208
BP	GO:0051712 positive regulation of killing of cells of other organism	2/208
BP	GO:009748 dendrite cell apoptosis process	2/208
BP	GO:200019 positive regulation of T helper 1 type immune response	2/208
BP	GO:0006698 positive regulation of dendrite cell apoptosis process	2/208
BP	GO:190015 regulation of cytokine production involved in inflammatory response	4/208
BP	GO:0002708 positive regulation of lymphocyte mediated immunity	5/208
BP	GO:0050711 positive regulation of B cell activation	6/208
BP	GO:0002914 regulation of T cell mediated immunity	3/208
BP	GO:0002401 positive regulation of cell cycle progression	10/208
BP	GO:0010952 positive regulation of peptidephage activity	2/208
BP	GO:0002440 production of molecular mediator of immune response	7/208
BP	GO:0002755 MyD88-dependent toll-like receptor signaling pathway	3/208
BP	GO:0014055 phosphatidylinositol-3-kinase signaling	6/208
BP	GO:0002551 mast cell chemotaxis	2/208
BP	GO:0038110 interleukin-2-mediated signaling pathway	2/208
BP	GO:0042492 gamma-delta T cell differentiation	2/208
BP	GO:0070269 pyroptosis	2/208
BP	GO:0002401 positive regulation of cysteine-type endopeptidase activity	2/208
BP	GO:0039179 zymogen inhibition	2/208
BP	GO:009322 regulation of superoxide metabolic process	3/208
CC	GO:000172 immunological synapse	10/12
CC	GO:0009897 external side of plasma membrane	21/12
CC	GO:0042529 mast cell granule	4/12
CC	GO:0002604 membrane signaling receptor complex	12/12
CC	GO:0001891 phagosome cup	4/12
CC	GO:002102 podosome	4/12
CC	GO:0070820 tertiary granule	8/12
CC	GO:0034774 secondary granule lumen	11/12
CC	GO:0002551 T cell granule complex	7/12
CC	GO:0002025 exoplasmic vesicle lumen	11/12
CC	GO:03193 vesicle lumen	11/12
CC	GO:045121 membrane raft	11/12
CC	GO:008857 membrane microdomain	11/12
CC	GO:0002657 membrane region	11/12
CC	GO:0002657 exoplasmic membrane	11/12
MF	GO:0004996 cytokine receptor activity	14/209
MF	GO:0140373 immune receptor activity	15/209
MF	GO:0019955 cytokine binding	12/209
MF	GO:0014933 C-chemokine receptor activity	5/209
MF	GO:0002657 chemokine binding	5/209
MF	GO:0424934 domain binding	6/209
MF	GO:0001537 G protein-coupled chemoattractant receptor activity	5/209
MF	GO:0004950 chemokine receptor activity	5/209
MF	GO:004548 phosphatidylinositol-3-kinase binding	5/209
MF	GO:0002657 membrane receptor activity	5/209
MF	GO:0424379 chemokine receptor binding	6/209
MF	GO:0049201 CCR chemokine receptor binding	7/209
MF	GO:0008009 chemokine activity	5/209
MF	GO:0016763 transferase activity, transferring pentosyl groups	5/209
MF	GO:000126 cytokine receptor binding	11/209
MF	GO:0002657 G protein-coupled purinic nucleotide receptor activity	3/209
MF	GO:0017124 SH3 domain binding	7/209
MF	GO:000125 cytokine activity	7/209
MF	GO:0019903 protein phosphatase binding	9/209
MF	GO:0001641 arachidonic nucleotide receptor activity	7/209
MF	GO:0002657 nucleotide receptor activity	3/209
MF	GO:0019902 phosphatase binding	8/209
MF	GO:0017048 Rho GTPase binding	7/209
MF	GO:0004364 glutathione transferase activity	3/209
CC	GO:0009897 external side of plasma membrane	21/12
CC	GO:0042529 mast cell granule	4/12
CC	GO:0002604 membrane signaling receptor complex	12/12
CC	GO:0001891 phagosome cup	4/12
CC	GO:002102 podosome	4/12
CC	GO:0070820 tertiary granule	8/12
CC	GO:0034774 secondary granule lumen	11/12
CC	GO:0002551 T cell granule complex	7/12
CC	GO:0002025 exoplasmic vesicle lumen	11/12
CC	GO:03193 vesicle lumen	11/12
CC	GO:045121 membrane raft	11/12
CC	GO:008857 membrane microdomain	11/12
CC	GO:0002657 membrane region	11/12
CC	GO:0002657 exoplasmic membrane	11/12
MF	GO:0004996 cytokine receptor activity	10/209
MF	GO:0140373 immune receptor activity	14/209
MF	GO:0019955 cytokine binding	15/209
MF	GO:0014933 C-chemokine receptor activity	12/209
MF	GO:0002657 chemokine binding	5/209
MF	GO:0424934 domain binding	6/209
MF	GO:0001537 G protein-coupled chemoattractant receptor activity	6/209
MF	GO:0004950 chemokine receptor activity	6/209
MF	GO:004548 phosphatidylinositol-3-kinase binding	6/209
MF	GO:0002657 membrane receptor activity	6/209
MF	GO:0424379 chemokine receptor binding	7/209
MF	GO:0049201 CCR chemokine receptor binding	7/209
MF	GO:0008009 chemokine activity	5/209
MF	GO:0016763 transferase activity, transferring pentosyl groups	5/209
MF	GO:000126 cytokine receptor binding	11/209
MF	GO:0002657 G protein-coupled purinic nucleotide receptor activity	3/209
MF	GO:0017124 SH3 domain binding	7/209
MF	GO:000125 cytokine activity	7/209
MF	GO:0019903 protein phosphatase binding	9/209
MF	GO:0001641 arachidonic nucleotide receptor activity	7/209
MF	GO:0002657 nucleotide receptor activity	3/209
MF	GO:0019902 phosphatase binding	8/209
MF	GO:0017048 Rho GTPase binding	7/209
MF	GO:0004364 glutathione transferase activity	3/209
BP	GO:000294 T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell	2/28
BP	GO:001454 extracellular receptor activity	2/28
BP	GO:007024 regulation of nucleotide-binding oligomerization domain containing signaling pathway	2/28
BP	GO:190426 positive regulation of defense response to bacterium	2/28
BP	GO:200019 regulation of macrophage apoptotic process	2/28
BP	GO:009164 arachidonic acid metabolic process	3/208
BP	GO:000265 Ras protein signal transduction	10/208
BP	GO:000266 Ras protein-mediated protein kinase signaling cascade	3/208
BP	GO:095921 positive regulation of chemotaxis	6/208
BP	GO:0002431 Fc receptor mediated stimulatory signaling pathway	6/208
BP	GO:004815 phosphatidylinositol-mediated signaling	6/208
BP	GO:0002025 positive regulation of Ras protein signal transduction	7/208
BP	GO:0002430 Fc receptor-mediated signaling pathway	3/208
BP	GO:000830 intracellular signaling pathway in response to DNA damage	3/208
BP	GO:002547 regulation of peptidephage activity	5/208
BP	GO:001540 killing of cells of other organism	12/208
BP	GO:004578 regulation of Ras protein signal transduction	4/208
BP	GO:0002432 positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-coupled signaling pathway	6/208
BP	GO:0002842 positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	5/208
BP	GO:0002604 regulation of lymphocytic cell antigen processing and presentation	2/208
BP	GO:0002605 positive regulation of antigen presentation	2/208
BP	GO:004560 negative thymic T cell selection	2/208
BP	GO:004643 regulation of gamma-delta T cell activation	2/208
BP	GO:0051712 positive regulation of killing of cells of other organism	2/208
BP	GO:009748 dendrite cell apoptosis process	2/208
BP	GO:200019 positive regulation of T helper 1 type immune response	2/208
BP	GO:0006698 positive regulation of dendrite cell apoptosis process	2/208
BP	GO:190015 regulation of cytokine production involved in inflammatory response	4/208
BP	GO:0002708 positive regulation of lymphocyte mediated immunity	5/208
BP	GO:0050711 positive regulation of B cell activation	6/208
BP	GO:0002914 regulation of T cell mediated immunity	3/208
BP	GO:0002401 positive regulation of cell cycle progression	10/208
BP	GO:0010952 positive regulation of peptidephage activity	2/208
BP	GO:0002440 production of molecular mediator of immune response	7/208
BP	GO:0002755 MyD88-dependent toll-like receptor signaling pathway	3/208
BP	GO:0014055 phosphatidylinositol-3-kinase signaling	6/208
BP	GO:0002551 mast cell chemotaxis	2/208
BP	GO:0038110 interleukin-2-mediated signaling pathway	2/208
BP	GO:0042492 gamma-delta T cell differentiation	2/208
BP	GO:0070269 pyroptosis	2/208
BP	GO:0002401 positive regulation of cysteine-type endopeptidase activity	2/208
BP	GO:0039179 zymogen inhibition	2/208
BP	GO:009322 regulation of superoxide metabolic process	3/208
CC	GO:000172 immunological synapse	10/12
CC	GO:0009897 external side of plasma membrane	21/12
CC	GO:0042529 mast cell granule	4/12
CC	GO:0002604 membrane signaling receptor complex	12/12
CC	GO:0001891 phagosome cup	4/12
CC	GO:002102 podosome	4/12
CC	GO:0070820 tertiary granule	8/12
CC	GO:0034774 secondary granule lumen	11/12
CC	GO:0002551 T cell granule complex	7/12
CC	GO:0002025 exoplasmic vesicle lumen	11/12
CC	GO:03193 vesicle lumen	11/12
CC	GO:045121 membrane raft	11/12
CC	GO:008857 membrane microdomain	11/12
CC	GO:0002657 membrane region	11/12
CC	GO:0002657 exoplasmic membrane	11/12
MF	GO:0004996 cytokine receptor activity	12/12
MF	GO:0140373 immune receptor activity	16/12
MF	GO:0019955 cytokine binding	11/12
MF	GO:0014933 C-chemokine receptor activity	5/12
MF	GO:0002657 chemokine binding	5/12
MF	GO:0424934 domain binding	6/12
MF	GO:0001537 G protein-coupled chemoattractant receptor activity	5/12
MF	GO:0004950 chemokine receptor activity	5/12
MF	GO:004548 phosphatidylinositol-3-kinase binding	5/12
MF	GO:0002657 membrane receptor activity	5/12
MF	GO:0424379 chemokine receptor binding	7/12
MF	GO:0049201 CCR chemokine receptor binding	7/12
MF	GO:0008009 chemokine activity	5/12
MF	GO:0016763 transferase activity, transferring pentosyl groups	5/12
MF	GO:000126 cytokine receptor binding	11/12
MF	GO:0002657 G protein-coupled purinic nucleotide receptor activity	3/12
MF	GO:0017124 SH3 domain binding	7/12
MF	GO:000125 cytokine activity	7/12
MF	GO:0019903 protein phosphatase binding	9/12
MF	GO:0001641 arachidonic nucleotide receptor activity	7/12
MF	GO:0002657 nucleotide receptor activity	3/12
MF	GO:0019902 phosphatase binding	8/12
MF	GO:0017048 Rho GTPase binding	7/12
MF	GO:0004364 glutathione transferase activity	3/12
CC	GO:0009897 external side of plasma membrane	21/12
CC	GO:0042529 mast cell granule	4/12
CC	GO:0002604 membrane signaling receptor complex	12/12
CC	GO:0001891 phagosome cup	4/12
CC	GO:002102 podosome	4/12
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CC	GO:0002025 exoplasmic vesicle lumen	11/12
CC	GO:03193 vesicle lumen	11/12
CC	GO:045121 membrane raft	11/12
CC	GO:008857 membrane microdomain	11/12
CC	GO:0002657 membrane region	11/12
CC	GO:0002657 exoplasmic membrane	11/12
MF	GO:0004996 cytokine receptor activity	14/12
MF	GO:0140373 immune receptor activity	18/12
MF	GO:0019955 cytokine binding	13/12
MF	GO:0014933 C-chemokine receptor activity	5/12
MF	GO:0002657 chemokine binding	5/12
MF	GO:0424934 domain binding	6/12
MF	GO:0001537 G protein-coupled chemoattractant receptor activity	5/12
MF	GO:0004950 chemokine receptor activity	5/12
MF	GO:004548 phosphatidylinositol-3-kinase binding	5/12
MF	GO:0002657 membrane receptor activity	5/12
MF	GO:0424379 chemokine receptor binding	7/12
MF	GO:0049201 CCR chemokine receptor binding	7/12
MF	GO:0008009 chemokine activity	5/12
MF	GO:0016763 transferase activity, transferring pentosyl groups	5/12
MF	GO:000126 cytokine receptor binding	11/12
MF	GO:0002657 G protein-coupled purinic nucleotide receptor activity	3/12
MF	GO:0017124 SH3 domain binding	7/12
MF	GO:000125 cytokine activity	7/12
MF	GO:0019903 protein phosphatase binding	9/12
MF	GO:0001641 arachidonic nucleotide receptor activity	7/12
MF	GO:0002657 nucleotide receptor activity	3/12
MF	GO:0019902 phosphatase binding	8/12
MF	GO:0017048 Rho GTPase binding	7/12
MF	GO:0004364 glutathione transferase activity	3/12
BP	GO:000294 T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell	2/28
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BP	GO:007024 regulation of nucleotide-binding oligomerization domain containing signaling pathway	2/28
BP	GO:190426 positive regulation of defense response to bacterium	2/28
BP	GO:200019 regulation of macrophage apoptotic process	2/28
BP	GO:009164 arachidonic acid metabolic process	3/208
BP	GO:000265 Ras protein signal transduction	10/208
BP	GO:000266 Ras protein-mediated protein kinase signaling cascade	3/208
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BP	GO:002547 regulation of peptidephage activity	5/208
BP	GO:001540 killing of cells of other organism	12/208
BP	GO:004578 regulation of Ras protein signal transduction	4/208
BP	GO:0002432 positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-coupled signaling pathway	6/208
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BP	GO:004560 negative thymic T cell selection	2/208
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BP	GO:009748 dendrite cell apoptosis process	2/208
BP	GO:200019 positive regulation of T helper 1 type immune response	2/208
BP	GO:0006698 positive regulation of dendrite cell apoptosis process	2/208
BP	GO:190015 regulation of cytokine production involved in inflammatory response	4/208
BP	GO:0002708 positive regulation of lymphocyte mediated immunity	5/208
BP	GO:0050711 positive regulation of B cell activation	6/208
BP	GO:0002914 regulation of T cell mediated immunity	3/208
BP	GO:0002401 positive regulation of cell cycle progression	10/208
BP	GO:0010952 positive regulation of peptidephage activity	2/208
BP	GO:0002440 production of molecular mediator of immune response	7/208
BP	GO:00027	

Table S6. The KEGG enrichment analysis of key genes in lightgreen

ID	Description	GeneRatio	BgRatio	pvalue	p-adjust	qvalue	genelD	Count	
hsa04060	Cytokine-cytokine receptor interaction	24	295/8091	2.83E-11	5.68E-09	4.11E-09	IFNAR2/ CX3CR1/ CCL18/ TNFRSF21/ CSF2RA/ CCL2/ CXCL16/ OSMR/ IL2RG/ CXCL13/ IL32/ CCR5/ IL12RB1/ CCR7/ TNFRSF1B/ IL10RA/ CXCR6/ CXCR4/ CCL19/ IL26/ CSF2RB/ IL7R/ LTB/ IL4R		
hsa04659	Th17 cell differentiation	13	108/8091	1.33E-08	1.33E-06	9.60E-07	IL2RG/ HLA-DRA/ HLA-DMA/ IL12RB1/ JAK3/ CD247/ LAT/ PRKCQ/ STAT3/ CD3D/ LCK/ CD3G/ IL4R		
hsa04658	Th1 and Th2 cell differentiation	12	92/8091	1.98E-08	1.33E-06	9.60E-07	IL2RG/ HLA-DRA/ HLA-DMA/ IL12RB1/ JAK3/ CD247/ LAT/ PRKCQ/ CD3D/ LCK/ CD3G/ IL4R		
hsa04652	Chemokine signaling pathway	16	192/8091	5.50E-08	2.76E-06	2.00E-06	PIK3CD/ CX3CR1/ CCL18/ VAV1/ CCL2/ CXCL16/ CXCL13/ CCR5/ JAK3/ CCR7/ ITK/ CXCR6/ STAT3/ CXCR4/ CCL19/ RAC2		
hsa04660	T cell receptor signaling pathway	12	129/8091	10.4E-08	3.22E-06	2.32E-06	PIK3CD/ CTLA4/ VAV1/ ICOS/ ITK/ CD247/ LAT/ PRKCQ/ PTPRC/ CD3D/ LCK/ CD3G		
hsa05340	Primary immunodeficiency	8	38/8091	1.01E-07	3.22E-06	2.32E-06	CIITA/ ICOS/ IL2RG/ JAK3/ PTPRC/ CD3D/ IL7R/ LCK		
hsa05169	Epstein-Barr virus infection	16	16/129	202/8091	1.12E-07	3.22E-06	2.32E-06	IFNAR2/ PIK3CD/ IRF9/ HLA-DRA/ HLA-DMA/ JAK3/ BCL2L11/ E2F3/ MYD88/ TRAF3/ CD247/ ITGAL/ IRF7/ STAT3/ CD3D/ CD3G	
hsa04650	Natural killer cell mediated cytotoxicity	13	13/129	131/8091	1.38E-07	3.47E-06	2.51E-06	IFNAR2/ PIK3CD/ SH2D1A/ MIBC/ HCST/ VAV1/ CD247/ CD48/ ITGAL/ LAT/ GZMB/ LCK/ RAC2	
hsa04061	Viral protein interaction with cytokine and cytokine receptor	11	109/8091	4.69E-07	1.05E-06	9.75E-06	CX3CR1/ CCL18/ IL2RG/ CXCL13/ CCR5/ ICOS/ ITK/ CD247/ LAT/ PRKCQ/ PTPRC/ CD3D/ LCK/ CD3G		
hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	10	10/129	89/8091	1.31E-06	2.63E-05	1.90E-05	PIK3CD/ MYD88/ CD247/ BATF/ LAT/ PRKCQ/ STAT3/ CD3D/ LCK/ CD3G	
hsa04630	JAK-STAT signaling pathway	13	13/129	162/8091	1.62E-06	2.96E-05	2.14E-05	IFNAR2/ PIK3CD/ IRF9/ CSF2RA/ OSMR/ IL2RG/ IL12RB1/ JAK3/ IL10RA/ STAT3/ CSF2RB/ IL7R/ IL4R	
hsa05162	Measles	12	12/129	139/8091	1.93E-06	3.23E-05	2.34E-05	IFNAR2/ PIK3CD/ IRF9/ IL2RG/ JAK3/ MYD88/ TRAF3/ IRF7/ SLAMF1/ STAT3/ CD3D/ CD3G	
hsa04621	NOD-like receptor signaling pathway	13	13/129	184/8091	6.70E-06	0.000104	7.49E-06	IFNAR2/ CARD6/ IRF9/ CCL2/ IFI16/ GSDMD/ BIRC3/ MYD88/ TRAF3/ IRF7/ AIM2/ NAMPT/ CYBA	
hsa04640	Hematopoietic cell lineage	9	9/129	99/8091	2.60E-05	0.000373	0.00027	CSF2RA/ CD5/ HLA-DRA/ HLA-DMA/ CD3D/ CD22/ ILTR/ CD3G/ IL4R	
hsa04670	Leukocyte transendothelial migration	9	9/129	114/8091	7.96E-05	0.001066	0.00077	PIK3CD/ VAV1/ MMP9/ RH0H/ ITK/ ITGAL/ CXCR4/ RAC2/ CYBA	
hsa04664	NF-kappa B signaling pathway	8	8/129	104/8091	0.00024	0.003016	0.00218	BIRC3/ MYD88/ TRAF3/ LAT/ PRKCQ/ CCL19/ LCK/ LTB	
hsa04210	Apoptosis	9	9/129	136/8091	0.000306	0.003619	0.002615	CTSF/ PIK3CD/ CTSL/ PARP4/ BIRC3/ BCL2L11/ GZMB/ CSF2RB/ CTSC	
hsa05145	Toxoplasmosis	8	8/129	112/8091	0.000399	0.004266	0.003083	CIITA/ BIRC3/ HLA-DRA/ HLA-DMA/ CCR5/ MYD88/ IL10RA/ STAT3	
hsa05164	Influenza A	10	10/129	172/8091	0.000403	0.004266	0.003083	IFNAR2/ CIITA/ PIK3CD/ IRF9/ CCL2/ HLA-DRA/ HLA-DMA/ MYD88/ TRAF3/ IRF7	
hsa05321	Inflammatory bowel disease	6	6/129	65/8091	0.000559	0.00562	0.004061	IL2RG/ HLA-DRA/ HLA-DMA/ IL12RB1/ STAT3/ IL4R	
hsa04514	Cell adhesion molecules	9	9/129	149/8091	0.000599	0.005736	0.004145	CTLA4/ ICOS/ SELL/ HLA-DRA/ HLA-DMA/ ITGAL/ PTPRC/ SELPLG/ CD2	
hsa05323	Rheumatoid arthritis	7	7/129	93/8091	0.000676	0.006176	0.004463	CTLA4/ CTSL/ CCL2/ HLA-DRA/ HLA-DMA/ ITGAL/ LTB	
hsa05135	Yersinia infection	8	8/129	137/8091	0.001504	0.013141	0.009497	PIK3CD/ VAV1/ CCL2/ MYD88/ LAT/ ARPC1B/ LCK/ RAC2	
hsa05170	Human immunodeficiency virus 1 infection	10	10/129	212/8091	0.002009	0.016327	0.0118	PIK3CD/ APOBEC3G/ CCR5/ MYD88/ CD247/ TNFRSF1B/ CXCR4/ CD3D/ CD3G/ RAC2	
hsa05132	Salmonella infection	11	11/129	249/8091	0.002031	0.016327	0.0118	ARHGEF26/ DYNLRB2/ TUBB6/ PIK3CD/ NCKAP1L/ RH0H/ GSDMD/ BIRC3/ MYD88/ PTPRC/ ARPC1B	
hsa00760	Nicotinate and nicotinamide metabolism	4	4/129	35/8091	0.002202	0.017025	0.012304	MNMAT3/ NAMPT/ NT5C2/ PNP	
hsa05166	Human T-cell leukemia virus 1 infection	10	10/129	219/8091	0.002549	0.018976	0.013714	PIK3CD/ IL2RG/ HLA-DRA/ HLA-DMA/ JAK3/ E2F3/ ITGAL/ CD3D/ LCK/ CD3G	
hsa05167	Kaposi's sarcoma-associated herpesvirus infection	9	9/129	194/8091	0.003748	0.026908	0.019446	IFNAR2/ PIK3CD/ MIBC/ IRF9/ CCR5/ E2F3/ TRAF3/ IRF7/ STAT3	
hsa05150	Staphylococcus aureus infection	6	6/129	96/8091	0.004203	0.027974	0.020217	HLA-DRA/ HLA-DMA/ ITGAL/ SELPLG/ CFB/ PTAFR	
hsa05161	Hepatitis B	8	8/129	162/8091	0.004267	0.027974	0.020217	PIK3CD/ MMP9/ JAK3/ E2F3/ MYD88/ TRAF3/ IRF7/ STAT3	
hsa04666	Fc gamma R-mediated phagocytosis	6	6/129	97/8091	0.004423	0.027974	0.020217	PIK3CD/ VAV1/ LAT/ PTPRC/ ARPC1B/ RAC2	
hsa04664	Fc epsilon RI signaling pathway	5	5/129	68/8091	0.004454	0.027974	0.020217	PIK3CD/ VAV1/ LAT/ ALOX5AP/ RAC2	
hsa04920	Adipocytokine signaling pathway	5	5/129	69/8091	0.004741	0.028879	0.020871	PRKAB2/ IRS2/ TNFRSF1B/ PRKCQ/ STAT3	
hsa05142	Chagas disease	6	6/129	102/8091	0.005651	0.03341	0.024146	PIK3CD/ CCL2/ MYD88/ CD247/ CD3D/ CD3G	
hsa05418	Fluid shear stress and atherosclerosis	7	7/129	139/8091	0.006666	0.038281	0.027666	GSTO2/ PIK3CD/ MMP9/ CTSL/ CCL2/ RAC2/ CYBA	
hsa05417	Lipid and atherosclerosis	9	9/129	215/8091	0.007286	0.040683	0.029401	PIK3CD/ VAV1/ MMP9/ CCL2/ MYD88/ TRAF3/ IRF7/ STAT3/ CYBA	
hsa04672	Intestinal immune network for IgA production	4	4/129	49/8091	0.007509	0.040792	0.029481	ICOS/ HLA-DRA/ HLA-DMA/ CXCR4	
hsa04668	TNF signaling pathway	6	6/129	112/8091	0.008831	0.046709	0.033757	PIK3CD/ MMP9/ CCL2/ BIRC3/ TRAF3/ TNFRSF1B	
hsa05320	Autoimmune thyroid disease	4	4/129	53/8091	0.009885	0.050944	0.036817	CTLA4/ HLA-DRA/ HLA-DMA/ GZMB	
hsa04145	Phagosome	7	7/129	152/8091	0.010665	0.053180	0.038434	TUBB6/ CTSL/ HLA-DRA/ HLA-DMA/ CORO1A/ CLEC7A/ CYBA	
hsa04613	Neutrophil extracellular trap formation	8	8/129	190/8091	0.010848	0.053180	0.038434	HDAC11/ PIK3CD/ GSDMD/ ITGAL/ SELPLG/ RAC2/ CLEC7A/ CYBA	
hsa05160	Hepatitis C	7	7/129	157/8091	0.012592	0.062061	0.043551	IFNAR2/ PIK3CD/ IRF9/ E2F3/ TRAF3/ IRF7/ STAT3	
hsa05416	Viral myocarditis	4	4/129	60/8091	0.015119	0.070674	0.051077	HLA-DRA/ HLA-DMA/ ITGAL/ RAC2	
hsa05203	Viral carcinogenesis	8	8/129	204/8091	0.016109	0.073589	0.053183	HDAC11/ PIK3CD/ IRF9/ CCR5/ JAK3/ TRAF3/ IRF7/ STAT3	
hsa04068	FoxO signaling pathway	6	6/129	131/8091	0.01809	0.080803	0.058396	PRKAB2/ IRS2/ PIK3CD/ BCL2L11/ STAT3/ IL7R	
hsa05330	Allograft rejection	3	3/129	38/8091	0.022255	0.097247	0.070281	HLA-DRA/ HLA-DMA/ GZMB	
hsa04810	Regulation of actin cytoskeleton	8	8/129	218/8091	0.023015	0.098425	0.071132	PIK3CD/ NCKAP1L/ VAV1/ FGD3/ ITGAL/ CXCR4/ ARPC1B/ RAC2	

Table S7.Potential targeted therapeutic drugs for STAT3 in rosacea

cmap name	mean	n	enrichment p	specificity	percent non-null
naringenin	-0.286	4	-0.873 0.00056	0	50
ikarugamycin	-0.507	3	-0.871 0.00423	0.0152	66
levobunolol	-0.295	4	-0.844 0.00105	0.0064	50
azapropazone	-0.448	3	-0.837 0.00863	0	66
diphenhydramine	-0.401	5	-0.818 0.00048	0	60
rifampicin	-0.264	4	-0.752 0.00764	0.0357	50
Prestwick-1103	-0.366	4	-0.75 0.00784	0.0464	50
demecarium bromide	-0.595	4	-0.724 0.0118	0.0116	75
semustine	0.554	4	0.703 0.01611	0.1412	75
terbutaline	0.226	4	0.705 0.01574	0.0122	50
etamsylate	0.539	4	0.71 0.01456	0.0273	75
methacholine chloride	0.417	3	0.804 0.01508	0.0165	66
ivermectin	0.638	5	0.81 0.0006	0.0269	80
pyridoxine	0.329	4	0.829 0.00127	0	50
clofibrate	0.523	2	0.851 0.04455	0.0364	100
arachidonic acid	0.511	3	0.855 0.00585	0	100
puromycin	0.704	4	0.873 0.00036	0.0955	100
5230742	0.696	2	0.945 0.00567	0.0078	100
benfluorex	0.767	4	0.951 0	0	100
rottlerin	0.813	3	0.98 0.00004	0.0052	100

Table S8.Potential targeted therapeutic drugs for SBD pattern in rosacea

cmap name	mean	n	enrichment p	specificity	percent non-null
ikarugamycin	-0.484	3	-0.865 0.00497	0.0152	66
yohimbic acid	-0.341	3	-0.863 0.00529	0.0059	66
chenodeoxycholic acid	-0.335	4	-0.796 0.00342	0.0461	50
timolol	-0.311	4	-0.785 0.00434	0.0224	50
ribavirin	-0.246	4	-0.76 0.00684	0.0461	50
Prestwick-1103	-0.313	4	-0.746 0.00828	0.0464	50
indoprofen	-0.416	4	-0.744 0.00849	0.04	75
heptaminol	-0.435	5	-0.731 0.00284	0.0274	60
clorsulon	-0.517	4	-0.717 0.01293	0.0426	75
iopromide	-0.369	4	-0.71 0.01466	0.0515	75
furazolidone	-0.316	4	-0.709 0.01484	0.0255	50
cicloheximide	0.572	4	0.704 0.01597	0.1695	75
benfluorex	0.536	4	0.712 0.01396	0.0349	75
glycocholic acid	0.441	4	0.738 0.00917	0	75
albendazole	0.41	3	0.743 0.03315	0.0523	66
ivermectin	0.626	5	0.769 0.0014	0.0376	80
rottlerin	0.51	3	0.79 0.01857	0.1606	66
puromycin	0.703	4	0.871 0.00038	0.0955	100
clofibrate	0.551	2	0.875 0.03131	0.0303	100
5230742	0.656	2	0.924 0.01125	0.0078	100
5182598	0.727	2	0.959 0.003	0.0392	100
5224221	0.79	2	0.976 0.00093	0.1006	100
5255229	0.861	2	0.995 0.00002	0	100