

Figure S1. The correlation of SBDGs in rosacea.

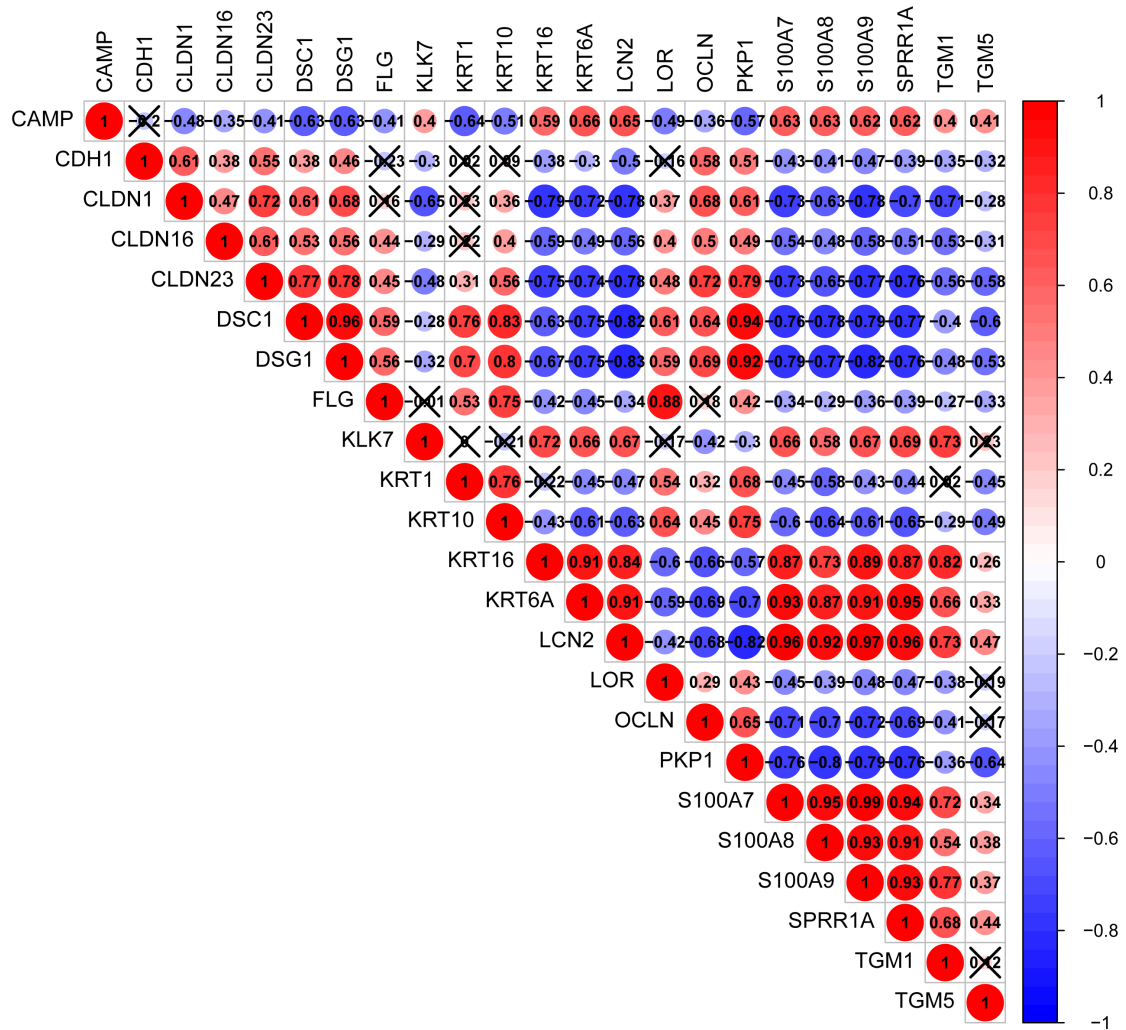


Figure S2. The immune cells in different subtypes of rosacea.

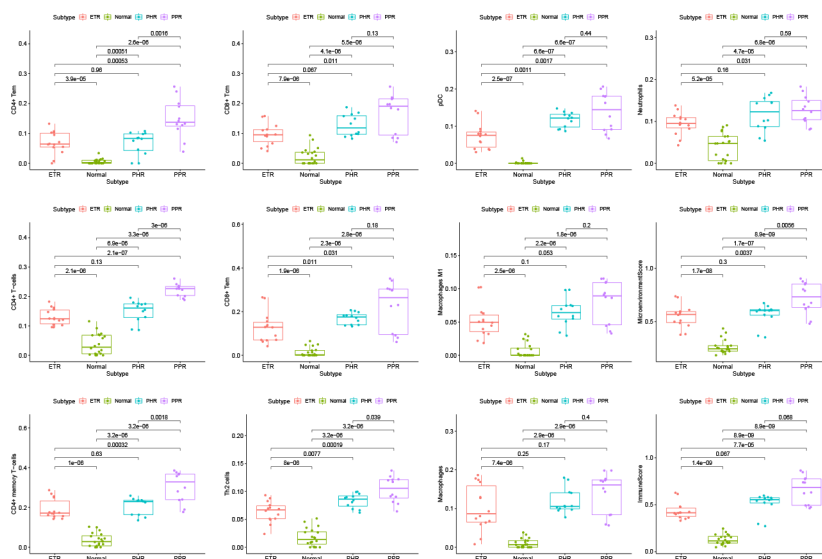


Figure S3. The 3 hub genes expression in rosacea was verified in Shih's study and epidermal transcriptome data.

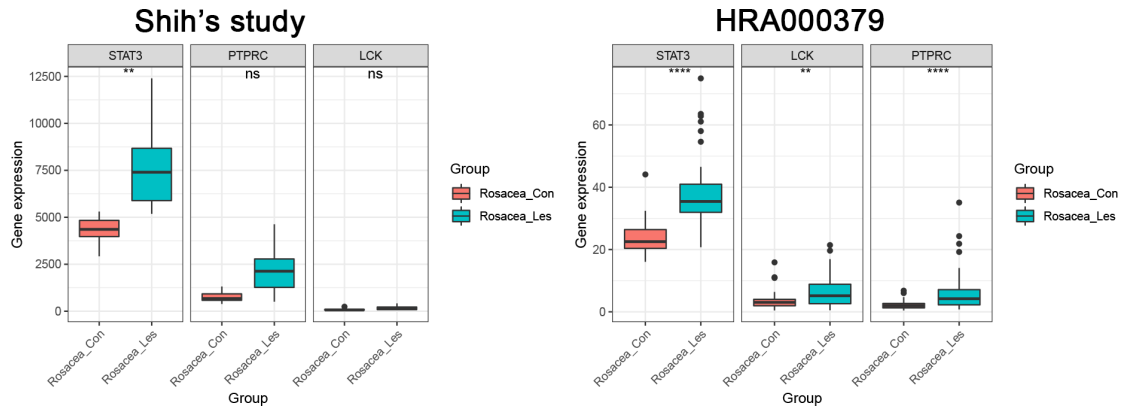


Figure S4. The expression and enrichment of STAT3-related genes in lightgreen. A, The expression of STAT3-related genes in rosacea and normal tissues. B, The expression of genes in 3 SBDs clusters. C, The heatmap of STAT3-related genes in 3 SBDs clusters. The enrichment of STAT3-related genes.

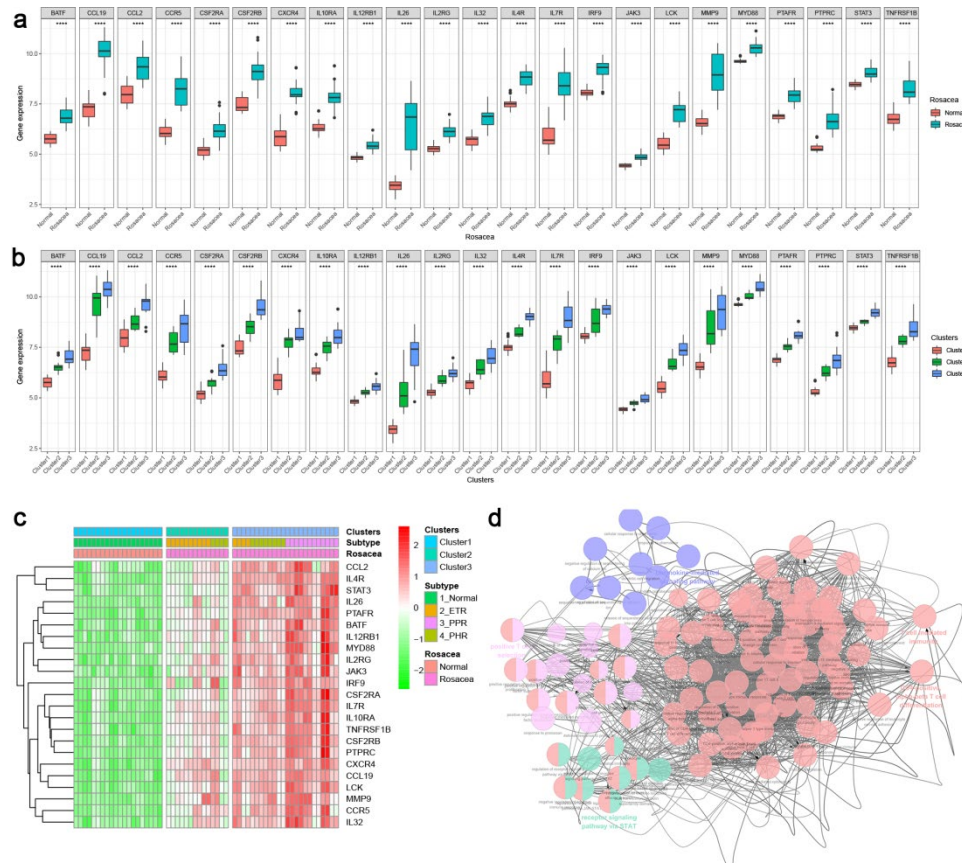


Figure S5. The KEGG analysis of genes from 3 subnetworks.

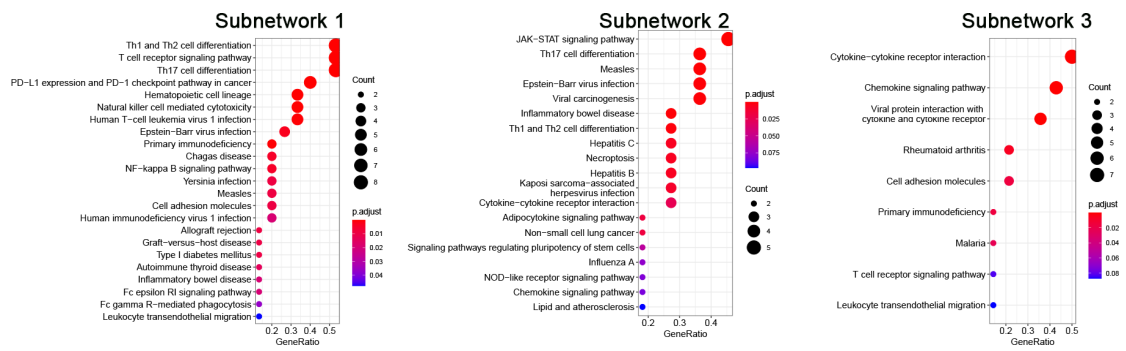


Figure S6. The correlation of SBDGs and rosacea related genes.

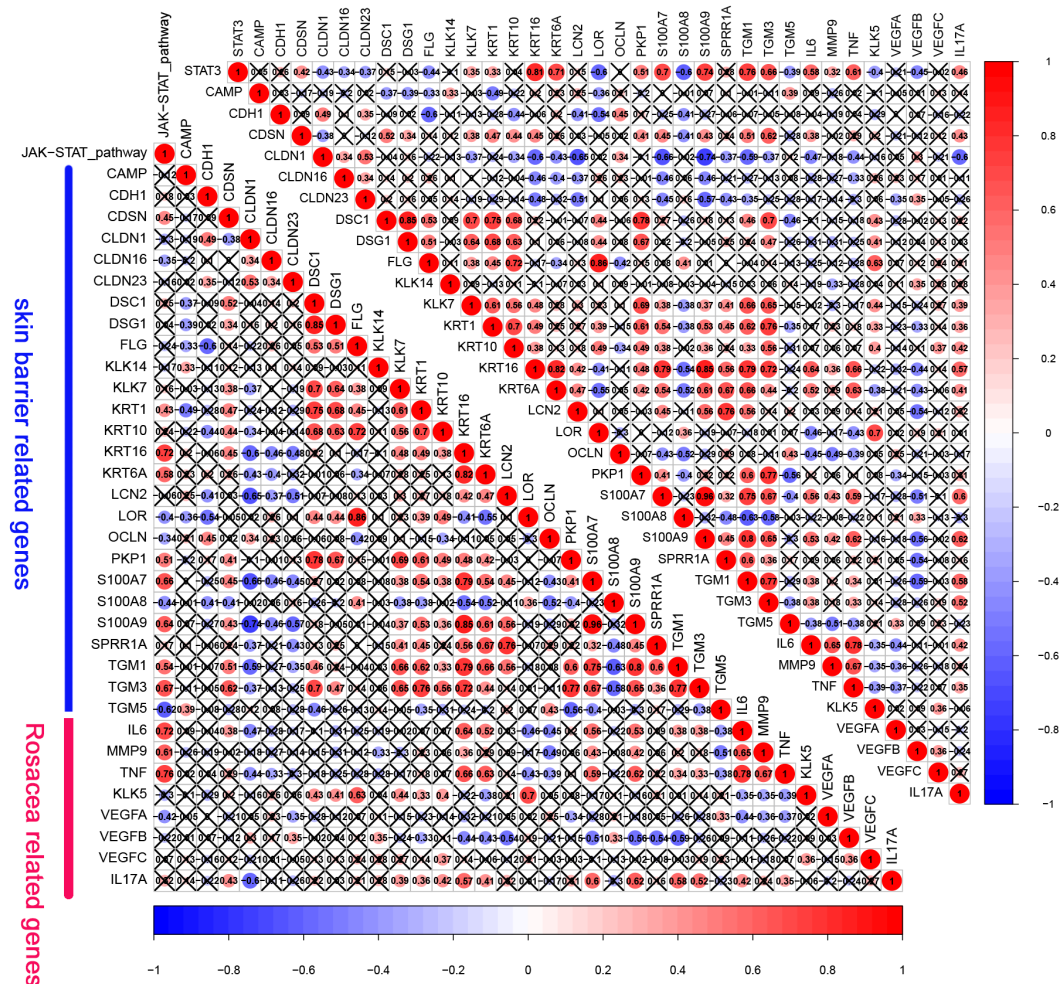
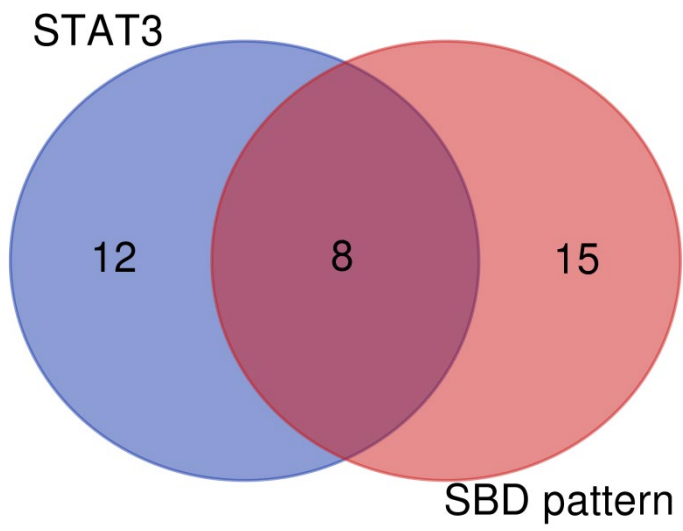


Figure S7. The ven of predicted drugs using STAT3-related genes and SBD pattern-related genes.















MF	GO:0079492 oligosaccharide binding	3/412	15/18352	0.004181	0.036105	0.029471	SELE/SELL/SELP	3
MF	GO:0015026 coreceptor activity	5/412	48/18352	0.004312	0.03687	0.029945	CXCR6/Y95TGA/CCR5/CD86	5
MF	GO:0043177 organic acid binding	12/412	224/18352	0.00485	0.04278	0.032877	SUGAP/ABPS/TCD3/CHAMP/SELE/GLUL/SELP/ALOX5AP/ST8SI44/VCA/PCN1/SGLT10	12
MF	GO:0005126 tumor necrosis factor receptor binding	4/412	31/18352	0.0048763	0.04278	0.032877	TNFR/TFN3/CD275/TNFRSF10B	4
MF	GO:0018783 transferase activity, transferring pentosyl groups	5/412	50/18352	0.005145	0.041895	0.034197	PNP/TFM/NAIMP/APP1/PABP9	5
MF	GO:0004601 peroxidase activity	5/412	52/18352	0.0060863	0.04865	0.039678	P/CEU/CPK2/PKCN/ALDOXAP/PTGS2	5





BP	GO:0007584 response to nutrient	8/207	171/18866	0.000613	0.016037	0.014352	PKLR/AACS/PPARG/BCKDHB/HLCS/GNPAT/ACSL1/LEP	8
BP	GO:0006084 acetyl-CoA metabolic process	4/207	39/18866	0.000776	0.019742	0.017668	MPC2/ACSS2/PMVK/MVD	4
BP	GO:0019433 triglyceride catabolic process	4/207	39/18866	0.000776	0.019742	0.017668	PNPLA4/LIPH/PNPLA3/ABHD5	4
BP	GO:0030730 sequestering of triglyceride	3/207	17/18866	0.000790	0.019742	0.017668	PPARG/FITM2/ABHD5	3
BP	GO:0046459 short-chain fatty acid metabolic process	3/207	17/18866	0.000790	0.019742	0.017668	PHYH/ACSS2/CRAT	3
BP	GO:0055089 fatty acid homeostasis	3/207	17/18866	0.000790	0.019742	0.017668	APOE/GPAM/DGAT2	3
BP	GO:0055090 acylglycerol homeostasis	4/207	39/18866	0.000857	0.021028	0.018818	APOE/NR1H3/FITM2/DGAT2	4
BP	GO:0070328 triglyceride homeostasis	4/207	39/18866	0.000857	0.021028	0.018818	APOE/NR1H3/FITM2/DGAT2	4
BP	GO:0035338 long-chain fatty-acyl-CoA biosynthetic process	3/207	19/18866	0.001108	0.026940	0.024109	ACSBG1/ACSL1/ELOVL3	3
BP	GO:0010878 cholesterol storage	3/207	20/18866	0.001293	0.030981	0.027725	NR1H3/PPARG/SOAT1	3
BP	GO:0044272 sulfur compound biosynthetic process	8/207	192/18866	0.001297	0.030981	0.027725	GSTM3/MPC2/SCD/ACSS2/ACSBG1/OGN/ACSL1/ELOVL3	8
BP	GO:0046503 glycerolipid catabolic process	5/207	74/18866	0.001321	0.031287	0.027999	PNPLA4/LIPH/GDP1/PNPLA3/ABHD5	5
BP	GO:0006089 lipid transport	12/207	393/18866	0.001385	0.032506	0.029093	SLC27A6/SLC25A17/APOE/ABC1/3/NR1H3/RBP4/PPARG/AQP9/THRS/ACSL1/LEP/SOAT1	12
BP	GO:0015909 long-chain fatty acid transport	5/207	75/18866	0.001403	0.032860	0.029227	SLC27A6/APOE/PPARG/THRS/ACSL1	5
BP	GO:1901616 organic hydroxy compound catabolic process	5/207	76/18866	0.001489	0.033959	0.03039	CYP4F3/CYP27A1/GKS/APOE/CYP39A1	5
BP	GO:0043651 linoleic acid metabolic process	3/207	21/18866	0.001497	0.033959	0.03039	ACSL1/ELOVL3/FA2D2	3
BP	GO:2000738 positive regulation of stem cell differentiation	3/207	21/18866	0.001497	0.033959	0.03039	GATA6/FOXCL/RBM24	3
BP	GO:0016101 diterpenoid metabolic process	6/207	114/18866	0.001620	0.036311	0.032495	PNPLA4/APOE/PCER/RBP4/DGAT2/SRD5A1	6
BP	GO:0062012 regulation of small molecule metabolic process	13/207	456/18866	0.001634	0.036311	0.032495	RORC/APOE/NR1H3/GPAM/SCD/FDPS/DHCR7/PPARG/PMVK/INSIG1/MVD/DGAT2/LEP	13
BP	GO:0009150 purine ribonucleotide metabolic process	12/207	401/18866	0.001640	0.036311	0.032495	PKLR/MPC2/GPAM/SCD/ACSS2/PMVK/ACSBG1/ENO3/ACSL1/ELOVL3/MVD/DGAT2	12
BP	GO:0009083 branched-chain amino acid catabolic process	3/207	22/18866	0.001719	0.037746	0.03378	PPM1K/BCKDHB/HIBCH	3
BP	GO:0046942 carboxylic acid transport	11/207	350/18866	0.001736	0.037819	0.033844	SLC27A6/SLC1A6/SLC25A17/APOE/MPC2/SLC25A18/PPARG/AQP9/THRS/ACSL1/LEP	11
BP	GO:0015849 organic acid transport	11/207	353/18866	0.001856	0.039949	0.035751	SLC27A6/SLC1A6/SLC25A17/APOE/MPC2/SLC25A18/PPARG/AQP9/THRS/ACSL1/LEP	11
BP	GO:0046401 neutral lipid catabolic process	4/207	48/18866	0.001878	0.039949	0.035751	PNPLA4/LIPH/PNPLA3/ABHD5	4
BP	GO:0046454 acylglycerol catabolic process	4/207	48/18866	0.001878	0.039949	0.035751	PNPLA4/LIPH/PNPLA3/ABHD5	4
BP	GO:0034284 response to monosaccharide	8/207	207/18866	0.002083	0.043971	0.03935	CTS/PKLR/MPC2/GPAM/AACS/CPB2/ACV1/CLP	8
BP	GO:0090208 positive regulation of triglyceride metabolic process	3/207	24/18866	0.002223	0.046226	0.041369	NR1H3/ABHD5/DGAT2	3
BP	GO:0009259 ribonucleotide metabolic process	12/207	416/18866	0.002224	0.046226	0.041369	PKLR/MPC2/GPAM/SCD/ACSS2/PMVK/ACSBG1/ENO3/ACSL1/ELOVL3/MVD/DGAT2	12
CC	GO:0005777 peroxisome	12/215	137/19559	3.81E-08	4.80E-06	4.50E-06	PHYH/ISOC1/SLC25A17/HACL1/PEX11A/HAO2/PCER/PXMP2/PMVK/CRAT/GNPAT/ACSL1	12
CC	GO:0042579 microbody	12/215	137/19559	3.81E-08	4.80E-06	4.50E-06	PHYH/ISOC1/SLC25A17/HACL1/PEX11A/HAO2/PCER/PXMP2/PMVK/CRAT/GNPAT/ACSL1	12
CC	GO:0005778 peroxisomal membrane	6/215	60/19559	5.02E-05	0.003164	0.00296	SLC25A17/PEX11A/PCER/PXMP2/GNPAT/ACSL1	6
CC	GO:0031903 microbody membrane	6/215	60/19559	5.02E-05	0.003164	0.00296	SLC25A17/PEX11A/PCER/PXMP2/GNPAT/ACSL1	6
CC	GO:0005782 peroxisomal matrix	5/215	52/19559	0.000262	0.010986	0.010279	PHYH/HACL1/HAO2/CRAT/GNPAT	5
CC	GO:0031907 microbody lumen	5/215	52/19559	0.000262	0.010986	0.010279	PHYH/HACL1/HAO2/CRAT/GNPAT	5
CC	GO:0005811 lipid droplet	6/215	93/19559	0.000566	0.020386	0.019075	PNPLA4/PLIN4/PLIN1/PNPLA3/ABHD5/DGAT2	6
MF	GO:0003374 O-acyltransferase activity	11/205	50/18352	6.59E-12	2.96E-09	2.50E-09	AGPAT1/GPAM/AGPAT3/PNPLA3/MOGAT2/CRAT/ABHD5/GNPAT/DGAT2/AWAT1/SOAT1	11
MF	GO:0016411 acylglycerol O-acyltransferase activity	6/205	23/18352	1.58E-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 acid-thiol ligase activity	6/205	36/18352	8.57E-07	7.74E-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	0.000488	0.000426	PCER/DHCR7/DHCR24/SRD5A1/MECR	5
MF	GO:0003841 L-acylglycerol-3-phosphate O-acyltransferase activity	4/205	15/18352	1.87E-05	0.000904	0.000789	AGPAT1/AGPAT3/PNPLA3/ABHD5	4
MF	GO:0042171 lysophosphatidic acid acyltransferase activity	4/205	17/18352	3.21E-05	0.001393	0.001217	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	0.001888	0.001623	PCER/DHCR7/DHCR24/CRAT/SRD5A1/MECR	6
MF	GO:0071617 lysophospholipid acyltransferase activity	4/205	19/18352	5.14E-05	0.001888	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	8.80E-05	0.002930	0.002565	PHYH/CYP4F3/CYP27A1/SCD/CYP39A1/NLRRP11/HEATR4/MSMO1/FA2D2	9
MF	GO:0005496 steroid binding	7/205	106/18352	0.000188	0.005815	0.006077	PGRMC2/NR3C2/RORC/NR1H3/PGRMC1/INSIG1/SOAT1	7
MF	GO:0004467 long-chain fatty acid-CoA ligase activity	3/205	13/18352	0.000362	0.010485	0.009138	SLC27A6/ACSBG1/ACSL1	3
MF	GO:0016874 ligase activity	8/205	165/18352	0.000543	0.014734	0.012865	SLC27A6/ACSS3/TLL7/AACS/ACSS2/HLCS/ACSBG1/ACSL1	8
MF	GO:0020037 heme binding	7/205	138/18352	0.000924	0.022874	0.019973	PGRMC2/CYP4F3/CYP27A1/CYB5A/FA2H/CYP39A1/PGRMC1	7
MF	GO:0004497 monoxygenase activity	6/205	101/18352	0.000949	0.022874	0.019973	CYP4F3/CYP27A1/CYP39A1/NLRRP11/HEATR4/MSMO1	6
MF	GO:0032218 amide binding	12/205	381/18352	0.001236	0.028233	0.024652	GHR/CRYAB/CTS/APOE/GSTM3/PGRMC1/DHCR24/PPARG/HLCS/PNPLA3/SRD5A1/SOAT1	12
MF	GO:0046906 tetrapyrrole binding	7/205	148/18352	0.001389	0.030134	0.026312	PGRMC2/CYP4F3/CYP27A1/CYB5A/FA2H/CYP39A1/PGRMC1	7
MF	GO:0005506 iron ion binding	7/205	151/18352	0.001559	0.032211	0.028125	PHYH/CYP4F3/CYP27A1/SCD/FA2H/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:0004879 nuclear receptor activity	4/205	52/18352	0.002692	0.048086	0.04251	NR3C2/RORC/NR1H3/PPARG	4
MF	GO:0098531 ligand-activated transcription factor activity	4/205	52/18352	0.002692	0.048086	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	geneID	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	Count
GO:0042110	cell activation	45/29
GO:0017159	leukocyte cell-cell adhesion	34/208
GO:0050865	regulation of T cell activation	33/218
GO:0053212	T cell chemotaxis	30/208
GO:0022405	positive regulation of cell-cell adhesion	27/208
GO:1903039	positive regulation of leukocyte cell-cell adhesion	25/208
GO:0002699	positive regulation of leukocyte activation	23/208
GO:0014711	regulation of cell-cell adhesion	31/208
GO:0050870	positive regulation of T cell activation	30/208
GO:0050887	positive regulation of cell activation	30/208
GO:1903031	regulation of cell-cell adhesion	27/208
GO:0030088	lymphocyte differentiation	28/208
GO:0050852	T cell receptor signaling pathway	22/208
GO:0050851	antigen receptor-mediated signaling pathway	22/208
GO:0015231	positive regulation of lymphocyte activation	27/208
GO:0045785	positive regulation of cell adhesion	28/208
GO:0002429	immune response-activating cell surface receptor signaling pathway	29/208
GO:0002753	immune response-activating cell surface receptor signaling pathway	29/208
GO:0007187	leukocyte apoptotic process	25/208
GO:0046561	lymphocyte proliferation	15/208
GO:0046631	alpha-beta T cell lymphocyte	16/208
GO:0029284	mononuclear cell proliferation	18/208
GO:0050670	regulation of lymphocyte proliferation	21/208
GO:0070661	cell proliferation	21/208
GO:0022944	regulation of mononuclear cell proliferation	18/208
GO:0042098	T cell proliferation	17/208
GO:0016017	defense response to virus	19/208
GO:0002010	negative regulation of leukocyte apoptotic process	10/208
GO:0046632	alpha-beta T cell differentiation	13/208
GO:0001819	positive regulation of cytokine production	24/208
GO:0002109	positive regulation of leukocyte apoptotic process	12/208
GO:0070662	positive regulation of leukocyte proliferation	15/208
GO:0009619	response to virus	21/208
GO:0042123	regulation of T cell proliferation	15/208
GO:0035711	positive, alpha-beta T cell activation	12/208
GO:0001895	cell killing	15/208
GO:0034341	regulation of interferon-gamma	16/208
GO:0043637	CD4-positive, alpha-beta T cell differentiation	11/208
GO:0046633	positive regulation of alpha-beta T cell activation	11/208
GO:0045058	T cell selection	9/208
GO:0050671	positive regulation of lymphocyte proliferation	13/208
GO:1902105	regulation of leukocyte differentiation	13/208
GO:0022945	positive regulation of mononuclear cell proliferation	13/208
GO:0043368	positive T cell selection	13/208
GO:1903708	positive regulation of hemopoiesis	8/208
GO:0006909	phagocytosis	14/208
GO:0002868	negative regulation of immune system process	15/208
GO:0046634	regulation of alpha-beta T cell activation	11/208
GO:0006325	cell chemotaxis	11/208
GO:0045580	regulation of T cell differentiation	13/208
GO:0070665	positive regulation of leukocyte proliferation	13/208
GO:0002691	regulation of immune effector process	22/208
GO:0045619	regulation of lymphocyte differentiation	14/208
GO:0042102	positive regulation of T cell proliferation	11/208
GO:1902107	positive regulation of leukocyte differentiation	13/208
GO:0002683	regulation of response to biotic stimulus	14/208
GO:0001909	leukocyte mediated cytotoxicity	11/208
GO:1903708	regulation of hemopoiesis	22/208
GO:0045680	positive regulation of T cell differentiation	10/208
GO:0002703	regulation of leukocyte mediated immunity	14/208
GO:200051	positive regulation of CD4-positive, alpha-beta T cell activation	7/208
GO:1909808	response to chemokine	10/208
GO:1909869	cellular response to chemokine	10/208
GO:0071346	cellular response to interferon-gamma	13/208
GO:0002449	leukocyte mediated immunity	11/208
GO:0041133	cell activation	17/208
GO:0057717	negative regulation of immune response	12/208
GO:0045621	positive regulation of lymphocyte differentiation	11/208
GO:0002723	positive regulation of interferon-gamma-1 production	8/208
GO:0030592	leukocyte chemotaxis	10/208
GO:0002286	T cell activation involved in immune response	10/208
GO:0022080	regulation of tumor necrosis factor production	10/208
GO:0029899	regulation of B cell proliferation	8/208
GO:0032652	regulation of interferon-gamma-1 production	10/208
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	8/208
GO:1903535	positive regulation of superfamily cytokine production	10/208
GO:0046637	regulation of alpha-beta T cell differentiation	8/208
GO:0070098	chemokine-mediated signaling pathway	8/208
GO:0002609	interferon-gamma production	10/208
GO:0022640	tumor necrosis factor production	8/208
GO:0002228	natural killer cell mediated immunity	8/208
GO:0036336	dendritic cell migration	10/208
GO:0072076	lymphocyte migration	10/208
GO:0051897	positive regulation of protein kinase B signaling	12/208
GO:0006333	interferon-gamma-mediated signaling pathway	8/208
GO:0046635	positive regulation of alpha-beta T cell differentiation	8/208
GO:0043371	positive regulation of CD4-positive, alpha-beta T cell differentiation	8/208
GO:0031341	regulation of cell killing	7/208
GO:0071708	tumor necrosis factor superfamily cytokine production	10/208
GO:0020585	regulation of antigen receptor-mediated signaling pathway	8/208
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	7/208
GO:0002612	interleukin-1 production	7/208
GO:1990299	neutrophil migration	10/208
GO:0048871	chemotaxis of number of cells	14/208
GO:0006037	type I interferon signaling pathway	9/208
GO:0071357	cellular response to type I interferon	9/208
GO:0002283	lymphocyte cell-cell adhesion involved in immune response	12/208
GO:0032651	regulation of interleukin-1 beta production	9/208
GO:0042100	cell proliferation	9/208
GO:0019026	viral life cycle	16/208
GO:0070227	lymphocyte apoptotic process	8/208
GO:0030439	myeloid cell differentiation	18/208
GO:0003494	response to type I interferon	9/208
GO:0045080	regulation of immune response	15/208
GO:0032713	positive regulation of interleukin-1 beta production	17/208
GO:0043312	neutrophil degranulation	19/208
GO:0032622	interleukin-2 production	9/208
GO:0032620	neutrophil chemotaxis	9/208
GO:0002283	neutrophil activation involved in immune response	19/208
GO:0002649	regulation of interferon-gamma production	9/208
GO:0002650	regulation of interferon-gamma-1 production	7/208
GO:0050853	B cell receptor signaling pathway	10/208
GO:0031295	T cell costimulation	7/208
GO:0032611	interleukin-1 beta production	7/208
GO:0032610	interleukin-12 production	7/208
GO:0007204	positive regulation of cytosolic calcium ion concentration	15/208
GO:0031294	lymphocyte costimulation	7/208
GO:0002460	immune response-based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	15/208
GO:0032653	regulation of interleukin-10 production	7/208
GO:0042093	T-helper cell differentiation	7/208
GO:0002265	natural killer cell mediated cytotoxicity	7/208
GO:0002486	response to lipopolysaccharide	15/208
GO:0001776	leukocyte homeostasis	15/208
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response	7/208
GO:0002407	dendritic cell chemotaxis	5/208
GO:0002287	alpha-beta T cell activation involved in immune response	7/208
GO:0002293	alpha-beta T cell differentiation involved in immune response	7/208
GO:0032613	interleukin-10 production	7/208
GO:0031340	positive regulation of defense response	7/208
GO:0002695	negative regulation of leukocyte activation	11/208
GO:0097530	granulocyte migration	11/208
GO:0002723	positive regulation of interferon-gamma production	7/208









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

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa04060	Cytokine-cytokine receptor interaction	24/129	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	24
hsa04659	Th17 cell differentiation	13/129	108/8091	1.33E-08	1.33E-06	9.60E-07	IL2RG/HLA-DRA/HLA-DMA/IL12RB1/JAK3/CD247/LAT/PRKQ/STAT3/CD3D/LCK/CD3G/IL4R	13
hsa04658	Th1 and Th2 cell differentiation	12/129	92/8091	1.98E-08	1.33E-06	9.60E-07	IL2RG/HLA-DRA/HLA-DMA/IL12RB1/JAK3/CD247/LAT/PRKQ/CD3D/LCK/CD3G/IL4R	12
hsa04062	Chemokine signaling pathway	16/129	192/8091	5.50E-08	2.76E-06	2.00E-06	PIK3CD/CX3CR1/CCL18/AVAV1/CCL2/CXCL16/CXCL13/CCR5/JAK3/CCR7/ITK/CXCR6/STAT3/CXCR4/CCL19/RAC2	16
hsa04660	T cell receptor signaling pathway	12/129	104/8091	8.03E-08	3.22E-06	2.32E-06	PIK3CD/CTLA4/AVAV1/COS/ITK/CD247/LAT/PRKQ/PTPRC/CD3D/LCK/CD3G	12
hsa05340	Primary immunodeficiency	8/129	38/8091	1.10E-07	3.22E-06	2.32E-06	CITTA/COS/IL2RG/JAK3/PTPRC/CD3D/IL7R/LCK	8
hsa05169	Epstein-Barr virus infection	16/129	202/8091	1.12E-07	3.22E-06	2.32E-06	IFNAR2/PIK3CD/IRF9/HLA-DRA/HLA-DMA/JAK3/BCL2L11/E2F3/MYD88/TRAFF3/CD247/ITGAL/IRF7/STAT3/CD3D/CD3G	16
hsa04650	Natural killer cell mediated cytotoxicity	13/129	131/8091	1.38E-07	3.47E-06	2.51E-06	IFNAR2/PIK3CD/SH2D1A/MICB/HCST/VAV1/CD247/CD48/ITGAL/LAT/GZMB/LCK/RAC2	13
hsa04061	Viral protein interaction with cytokine and cytokine receptor	11/129	100/8091	4.69E-07	1.05E-05	7.57E-06	CX3CR1/CCL18/CCL2/IL2RG/CXCL13/CCR5/CCR7/TNFRSF1B/IL10RA/CXCR4/CCL19	11
hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	10/129	89/8091	1.31E-06	2.63E-05	1.90E-05	PIK3CD/MYD88/CD247/BATF/LAT/PRKQ/STAT3/CD3D/LCK/CD3G	10
hsa04630	JAK-STAT signaling pathway	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	13
hsa05162	Measles	12/129	139/8091	1.93E-06	3.23E-05	2.34E-05	IFNAR2/PIK3CD/IRF9/IL2RG/JAK3/MYD88/TRAFF3/IRF7/SLAMF1/STAT3/CD3D/CD3G	12
hsa04621	NOD-like receptor signaling pathway	13/129	184/8091	6.70E-06	0.000104	7.49E-05	IFNAR2/CARD6/IRF9/CCL2/IFI16/GSDMD/BIRC3/MYD88/TRAFF3/IRF7/AIM2/NAMPT/CYBA	13
hsa04640	Hematopoietic cell lineage	9/129	99/8091	2.60E-05	0.000373	0.00027	CSF2RA/CD5/HLA-DRA/HLA-DMA/CD3D/CD2/IL7R/CD3G/IL4R	9
hsa04670	Leukocyte transendothelial migration	9/129	114/8091	7.96E-05	0.001066	0.00077	PIK3CD/AVAV1/MMP9/RHOH/ITK/ITGAL/CXCR4/RAC2/CYBA	9
hsa04064	NF-kappa B signaling pathway	8/129	104/8091	0.00024	0.003016	0.00218	BIRC3/MYD88/TRAFF3/LAT/PRKQ/CCL19/LCK/LTB	8
hsa04210	Apoptosis	9/129	136/8091	0.000306	0.003619	0.002615	CTSF/PIK3CD/CTSL/PARP4/BIRC3/BCL2L11/GZMB/CSF2RB/CTSC	9
hsa05145	Toxoplasmosis	8/129	112/8091	0.000399	0.004266	0.003083	CITTA/BIRC3/HLA-DRA/HLA-DMA/CCR5/MYD88/IL10RA/STAT3	8
hsa05164	Influenza A	10/129	172/8091	0.000403	0.004266	0.003083	IFNAR2/CITTA/PIK3CD/IRF9/CCL2/HLA-DRA/HLA-DMA/MYD88/TRAFF3/IRF7	10
hsa05321	Inflammatory bowel disease	6/129	65/8091	0.000559	0.00562	0.004061	IL2RG/HLA-DRA/HLA-DMA/IL12RB1/STAT3/IL4R	6
hsa04514	Cell adhesion molecules	9/129	149/8091	0.000599	0.005736	0.004145	CTLA4/ICOS/SELL/HLA-DRA/HLA-DMA/ITGAL/PTPRC/SELPLG/CD2	9
hsa05323	Rheumatoid arthritis	7/129	93/8091	0.000676	0.006176	0.004463	CTLA4/CTSL/CCL2/HLA-DRA/HLA-DMA/ITGAL/LTB	7
hsa05135	Yersinia infection	8/129	137/8091	0.001504	0.013141	0.009497	PIK3CD/AVAV1/CCL2/MYD88/LAT/ARPC1B/LCK/RAC2	8
hsa05170	Human immunodeficiency virus 1 infection	10/129	184/8091	0.002009	0.016327	0.0118	PIK3CD/APOBEC3G/CCR5/MYD88/CD247/TNFRSF1B/CXCR4/CD3D/CD3G/RAC2	10
hsa05132	Salmonella infection	11/129	249/8091	0.002031	0.016327	0.0118	ARHGEF26/DYNLRB2/TUBB6/PIK3CD/NCKAP1L/RHOH/GSDMD/BIRC3/MYD88/PTPRC/ARPC1B	11
hsa00760	Nicotine and nicotinamide metabolism	4/129	35/8091	0.002202	0.017025	0.012304	NMNAT3/NAMPT/NT5C2/PPN	4
hsa05166	Human T-cell leukemia virus 1 infection	10/129	219/8091	0.002549	0.018976	0.013714	PIK3CD/IL2RG/HLA-DRA/HLA-DMA/JAK3/E2F3/ITGAL/CD3D/LCK/CD3G	10
hsa05167	Kaposi sarcoma-associated herpesvirus infection	9/129	194/8091	0.003748	0.026908	0.019446	IFNAR2/PIK3CD/MICB/IRF9/CCR5/E2F3/TRAFF3/IRF7/STAT3	9
hsa05150	Staphylococcus aureus infection	6/129	96/8091	0.004203	0.027974	0.020217	HLA-DRA/HLA-DMA/ITGAL/SELPLG/CFB/PTAFR	6
hsa05161	Hepatitis B	8/129	162/8091	0.004267	0.027974	0.020217	PIK3CD/MMP9/JAK3/E2F3/MYD88/TRAFF3/IRF7/STAT3	8
hsa04666	Fc gamma R-mediated phagocytosis	6/129	97/8091	0.004423	0.027974	0.020217	PIK3CD/AVAV1/LAT/PTPRC/ARPC1B/RAC2	6
hsa04664	Fc epsilon RI signaling pathway	5/129	68/8091	0.004454	0.027974	0.020217	PIK3CD/AVAV1/LAT/ALOX5AP/RAC2	5
hsa04920	Adipocytokine signaling pathway	5/129	69/8091	0.004741	0.028879	0.020871	PRKAB2/IRS2/TNFRSF1B/PRKQ/STAT3	5
hsa05142	Chagas disease	6/129	102/8091	0.005651	0.03341	0.024146	PIK3CD/CCL2/MYD88/CD247/CD3D/CD3G	6
hsa05418	Fluid shear stress and atherosclerosis	7/129	139/8091	0.006666	0.038281	0.027666	GSTO2/PIK3CD/MMP9/CTSL/CCL2/RAC2/CYBA	7
hsa05417	Lipid and atherosclerosis	9/129	215/8091	0.007286	0.040683	0.029401	PIK3CD/AVAV1/MMP9/CCL2/MYD88/TRAFF3/IRF7/STAT3/CYBA	9
hsa04672	Intestinal immune network for IgA production	4/129	49/8091	0.007509	0.040792	0.029481	ICOS/HLA-DRA/HLA-DMA/CXCR4	4
hsa04668	TNF signaling pathway	6/129	112/8091	0.008831	0.046709	0.033757	PIK3CD/MMP9/CCL2/BIRC3/TRAFF3/TNFRSF1B	6
hsa05320	Autoimmune thyroid disease	4/129	53/8091	0.009885	0.050944	0.036817	CTLA4/HLA-DRA/HLA-DMA/GZMB	4
hsa04145	Phagosome	7/129	152/8091	0.010665	0.05318	0.038434	TUBB6/CTSL/HLA-DRA/HLA-DMA/CORO1A/CLEC7A/CYBA	7
hsa04613	Neutrophil extracellular trap formation	8/129	190/8091	0.010848	0.05318	0.038434	HDAC11/PIK3CD/GSDMD/ITGAL/SELPLG/RAC2/CLEC7A/CYBA	8
hsa05160	Hepatitis C	7/129	157/8091	0.012592	0.060261	0.043551	IFNAR2/PIK3CD/IRF9/E2F3/TRAFF3/IRF7/STAT3	7
hsa05416	Viral myocarditis	4/129	60/8091	0.015119	0.070674	0.051077	HLA-DRA/HLA-DMA/ITGAL/RAC2	4
hsa05203	Viral carcinogenesis	8/129	204/8091	0.016109	0.073589	0.053183	HDAC11/PIK3CD/IRF9/CCR5/JAK3/TRAFF3/IRF7/STAT3	8
hsa04068	FoxO signaling pathway	6/129	131/8091	0.01809	0.080803	0.058396	PRKAB2/IRS2/PIK3CD/BCL2L11/STAT3/IL7R	6
hsa05330	Allograft rejection	3/129	38/8091	0.02255	0.097247	0.070281	HLA-DRA/HLA-DMA/GZMB	3
hsa04810	Regulation of actin cytoskeleton	8/129	218/8091	0.023015	0.098425	0.071132	PIK3CD/NCKAP1L/AVAV1/FGD3/ITGAL/CXCR4/ARPC1B/RAC2	8

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