

Table S1 Lists for KEGG enrichment results of 971 DEGs

Category	Subcategory	ID	Description	Gene ratio	Bg ratio	P value	P.adjust	Q value	Gene ID	Count
Organismal systems	Immune system	hsa04610	Complement and coagulation cascades	21/433	86/8673	8.08E-10	2.38E-07	2.26E-07	C6/SERPINE1/VTN/F3/C4BPB/F13A1/C3/VSIG4/C1QC/C1R/BDKRB2/F2/C1S/SERPINA5/SERPINA1/CFD/F5/CR1/CFB/C2/CFI	21
Environmental information processing	Signaling molecules and interaction	hsa04080	Neuroactive ligand-receptor interaction	43/433	367/8673	1.20E-07	1.77E-05	1.68E-05	TAC1/UTS2/PTGER3/GAL/SCT/P2RX5/P2RX6/CTSG/HTR2A/GRIK5/GLP1R/CNR1/PTGFR/GPR83/PTGER2/C3/EDN2/SPX/CGA/HTR2B/GABBR2/CHRNA1/ADCYAP1/ADRA2A/EDNRA/GRM1/GRIA1/PAQR6/SSTR5/GRIK2/GABBR3/GALR1/BDKRB2/FPR2/FPR1/NMUR1/CALCB/F2/AGTR2/UTS2R/GRID1/GRIN2A/ADRA2C	43
Human diseases	Infectious disease: bacterial	hsa05150	Staphylococcus aureus infection	16/433	96/8673	1.87E-05	0.001832	0.001745	C3/DSG1/IL10/FCGR2A/C1QC/C1R/CAMP/FPR2/FPR1/C1S/FCAR/CFD/FCGR3A/CFB/C2/CFI	16
Environmental information processing	Signaling molecules and interaction	hsa04061	Viral protein interaction with cytokine and cytokine receptor	16/433	100/8673	3.16E-05	0.002323	0.002212	CCL26/IL20RA/CCL17/CCL2/CXCL6/TNFSF14/CCR7/IL10/CCL21/CXCL14/CXCL5/CCR1/CX3CR1/CCL11/CCL19/CCL13	16
Environmental information processing	Signaling molecules and interaction	hsa04060	Cytokine-cytokine receptor interaction	30/433	297/8673	0.000174	0.010202	0.009716	TNFRSF12A/CCL26/IL20RA/RELT/NGFR/CCL17/AMH/CCL2/BMP5/CSF3R/CXCL6/TNFSF14/CCR7/LIF/IL15RA/AMHR2/IL10/IL1RN/CCL21/OSMR/CXCL14/GDF6/CXCL5/CCR1/TNFRSF11B/CX3CR1/CCL11/CCL19/CLCF1/CCL13	30
Organismal systems	Immune system	hsa04062	Chemokine signaling pathway	21/433	192/8673	0.000576	0.025902	0.024669	FGR/CCL26/WAS/PLCB4/HCK/CCL17/JAK3/CCL2/CXCL6/CCR7/CCL21/CXCL14/SHC3/CXCL5/CCR1/PRKCD/CX3CR1/STAT3/CCL11/CCL19/CCL13	21
Cellular processes	Cell motility	hsa04814	Motor proteins	21/433	193/8673	0.000617	0.025902	0.024669	TUBA3D/MYL12A/TUBB4A/DNAH11/MYL7/KIF25/TUBA4A/KIF1A/TNNT3/MYO1G/TUBA3E/KIF5A/DYNC111/TNNI1/DNAI3/KIF26B/ACTG2/TUBA1C/KIF19/MYL4/KIFC1	21
Organismal systems	Endocrine system	hsa03320	PPAR signaling pathway	11/433	75/8673	0.001148	0.039527	0.037645	SCD/PCK2/PLTP/SLC27A6/APOA1/HMGCS2/PLIN1/PLIN4/ANGPTL4/ADIPOQ/MMP1	11
Human diseases	Infectious disease: bacterial	hsa05133	Pertussis	11/433	76/8673	0.001283	0.039527	0.037645	C4BPB/CXCL6/C3/IL10/LY96/C1QC/C1R/CXCL5/CD14/C1S/C2	11
Cellular processes	Transport and catabolism	hsa04145	Phagosome	17/433	152/8673	0.001473	0.039527	0.037645	MPO/MARCO/TUBA3D/CD209/TUBB4A/C3/TUBA4A/SFTPD/FCGR2A/TUBA3E/DYNC111/C1R/TUBA1C/CD14/FCAR/FCGR3A/ATP6V1G2	17
Environmental information processing	Signaling molecules and interaction	hsa04512	ECM-receptor interaction	12/433	89/8673	0.001479	0.039527	0.037645	ITGA3/TNC/COL9A2/COL1A1/VTN/COL9A1/SPP1/SV2C/FRAS1/COL2A1/FREM2/NPNT	12

KEGG, Kyoto Encyclopedia of Genes and Genomes; DEGs, differential expressed genes.

Table S2 Lists for the signaling pathways related to inflammatory

Enrich	Pathway
KEGG	Complement and coagulation cascades
KEGG	Neuroactive ligand-receptor interaction
KEGG	Staphylococcus aureus infection
KEGG	Viral protein interaction with cytokine and cytokine receptor
KEGG	Cytokine-cytokine receptor interaction
KEGG	Chemokine signaling pathway
KEGG	Motor proteins
KEGG	PPAR signaling pathway
KEGG	Pertussis
KEGG	Phagosome
GO-BP	Chemotaxis
GO-BP	Humoral immune response
GO-BP	Complement activation classical pathway
GO-BP	Leukocyte chemotaxis
GO-BP	Leukocyte migration
GO-BP	Leukocyte-mediated immunity
GO-BP	Acute inflammatory response
GO-BP	Immune response-regulating cell surface receptor signaling pathway
GO-BP	Cell chemotaxis
GO-BP	Immunoglobulin-mediated immune response
GO-BP	Leukocyte migration involved in inflammatory response
GO-BP	Neutrophil chemotaxis
GO-BP	B cell-mediated immunity
GO-BP	Granulocyte chemotaxis
GO-BP	Regulation of inflammatory response
GO-BP	Immune response-activating cell surface receptor signaling pathway
GO-BP	Antimicrobial humoral response
GO-BP	Response to lipopolysaccharide
GO-BP	Myeloid leukocyte migration
GO-BP	Defense response to bacterium

Table S2 (*continued*)**Table S2** (*continued*)

Enrich	Pathway
GO-BP	Regulation of immune effector process
GO-BP	Monocyte chemotaxis
GO-BP	Negative regulation of heterotypic cell-cell adhesion
GO-BP	Regulation of cell-cell adhesion involved in gastrulation
GO-BP	Neutrophil-mediated killing of bacterium
GO-BP	Lymphocyte-mediated immunity
GO-BP	Myeloid leukocyte activation
GO-BP	Negative regulation of cell adhesion
GO-BP	Positive regulation of ERK1 and ERK2 cascade
GO-BP	Granulocyte migration
GO-BP	Regulation of immune effector process
GO-BP	Monocyte chemotaxis
GO-BP	Negative regulation of heterotypic cell-cell adhesion
GO-BP	Regulation of cell-cell adhesion involved in gastrulation
GO-BP	Neutrophil-mediated killing of symbiont cell
GO-MF	Chemokine activity
GO-MF	Cytokine activity
GO-MF	Cytokine receptor binding
GO-MF	Immune receptor activity
GO-MF	Carbohydrate binding
GO-MF	Glycosaminoglycan binding
GO-MF	Lipopolysaccharide binding
GO-MF	Antigen binding
GO-MF	RAGE receptor binding
GO-MF	Serine-type endopeptidase activity
GO-MF	Protease binding
GO-MF	Prostaglandin receptor activity
GO-MF	Oxygen binding
GO-MF	Phospholipase activity
GO-MF	lipase activity

KEGG, Kyoto Encyclopedia of Genes and Genomes; GO, Gene Ontology; BP, biological process; MF, molecular function.

Table S3 Lists for KEGG enrichment pathways of 29 DE-IRGs

Category	Subcategory	ID	Description	Gene ratio	Bg ratio	P value	Padjust	qvalue	Gene ID	Count
Environmental information processing	Signaling molecules and interaction	hsa04060	Cytokine-cytokine receptor interaction	9/23	297/8673	3.07E-08	2.00E-06	1.42E-06	CCL17/CCL2/CCR7/CSF3R/CXCL6/IL10/IL15RA/LIF/OSMR	9
Environmental information processing	Signaling molecules and interaction	hsa04061	Viral protein interaction with cytokine and cytokine receptor	5/23	100/8673	5.26E-06	0.000171	0.000122	CCL17/CCL2/CCR7/CXCL6/IL10	5
Environmental information processing	Signal transduction	hsa04630	JAK-STAT signaling pathway	5/23	166/8673	6.15E-05	0.001333	0.00095	CSF3R/IL10/IL15RA/LIF/OSMR	5
Human diseases	Endocrine and metabolic disease	hsa04933	AGE-RAGE signaling pathway in diabetic complications	4/23	100/8673	0.000125	0.002023	0.001442	CCL2/F3/SELE/SERPINE1	4
Environmental information processing	Signal transduction	hsa04668	TNF signaling pathway	4/23	114/8673	0.000207	0.002687	0.001915	CCL2/CXCL6/LIF/SELE	4
Human diseases	Infectious disease: parasitic	hsa05144	Malaria	3/23	50/8673	0.000294	0.003189	0.002273	CCL2/IL10/SELE	3
Human diseases	Infectious disease: bacterial	hsa05133	Pertussis	3/23	76/8673	0.00101	0.009374	0.00668	CD14/CXCL6/IL10	3
Organismal systems	Immune system	hsa04062	Chemokine signaling pathway	4/23	192/8673	0.001482	0.01204	0.008579	CCL17/CCL2/CCR7/CXCL6	4
Organismal systems	Immune system	hsa04657	IL-17 signaling pathway	3/23	94/8673	0.001866	0.013476	0.009603	CCL17/CCL2/CXCL6	3
Human diseases	Infectious disease: parasitic	hsa05142	Chagas disease	3/23	102/8673	0.002357	0.015323	0.010918	CCL2/IL10/SERPINE1	3
Human diseases	Infectious disease: parasitic	hsa05143	African trypanosomiasis	2/23	37/8673	0.004235	0.025023	0.01783	IL10/SELE	2
Human diseases	Infectious disease: bacterial	hsa05135	Yersinia infection	3/23	137/8673	0.005418	0.029349	0.020913	CCL2/IL10/MEFV	3
Organismal systems	Immune system	hsa04672	Intestinal immune network for IgA production	2/23	49/8673	0.007335	0.036673	0.026131	IL10/IL15RA	2

KEGG, Kyoto Encyclopedia of Genes and Genomes; DE-IRGs, differential expressed inflammation related genes.