**Table S1：Signaling pathway enrichment analysis of differentially expressed genes**

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| --- | --- | --- | --- | --- |
| Description | GeneRatio | FDR | geneID | size |
| Glycerolipid metabolism | 6/83 | 5.53E-03 | PNPLA3/MOGAT1/CEL/PLPP4/GPAT3/LPL | 6 |
| Citrate cycle (TCA cycle) | 4/83 | 1.82E-02 | PCK2/DLST/ACO1/PC | 4 |
| Retinol metabolism | 5/83 | 3.13E-02 | ADH1C/DHRS4/RDH12/CYP3A7/CYP3A7-CYP3A51P | 5 |
| Chemical carcinogenesis | 5/83 | 3.27E-02 | ADH1C/GSTM3/CYP3A7/CYP3A7-CYP3A51P/GSTA3 | 5 |
| Peroxisome | 5/83 | 3.27E-02 | DHRS4/HAO2/ACOX2/PIPOX/DAO | 5 |
| Histidine metabolism | 3/83 | 3.27E-02 | FTCD/ASPA/AOC1 | 3 |
| Renin-angiotensin system | 3/83 | 3.27E-02 | KLK1/REN/AGTR1 | 3 |
| Arginine and proline metabolism | 4/83 | 3.27E-02 | SAT2/AGMAT/DAO/AOC1 | 4 |
| Steroid hormone biosynthesis | 4/83 | 5.68E-02 | CYP17A1/HSD11B2/CYP3A7/CYP3A7-CYP3A51P | 4 |
| Pentose and glucuronate interconversions | 3/83 | 7.74E-02 | DCXR/DHDH/SORD | 3 |
| Pyruvate metabolism | 3/83 | 9.14E-02 | PCK2/LDHD/PC | 3 |
| Metabolism of xenobiotics by cytochrome P450 | 4/83 | 9.14E-02 | ADH1C/GSTM3/DHDH/GSTA3 | 4 |
| PPAR signaling pathway | 4/83 | 9.14E-02 | PCK2/HMGCS2/ACOX2/LPL | 4 |
| Complement and coagulation cascades | 4/83 | 1.25E-01 | KLKB1/KNG1/SERPINA5/PLG | 4 |
| Glutathione metabolism | 3/83 | 2.03E-01 | GGT6/GSTM3/GSTA3 | 3 |
| Proximal tubule bicarbonate reclamation | 2/83 | 2.13E-01 | PCK2/SLC25A10 | 2 |
| Parathyroid hormone synthesis, secretion and action | 4/83 | 2.13E-01 | GATA3/SOST/SLC34A1/PTH1R | 4 |
| Vitamin digestion and absorption | 2/83 | 2.13E-01 | CUBN/SLC23A1 | 2 |
| Carbon metabolism | 4/83 | 2.52E-01 | DLST/HAO2/ACO1/PC | 4 |
| Glycolysis / Gluconeogenesis | 3/83 | 2.52E-01 | ADH1C/GALM/PCK2 | 3 |
| Glyoxylate and dicarboxylate metabolism | 2/83 | 2.65E-01 | HAO2/ACO1 | 2 |
| Drug metabolism - cytochrome P450 | 3/83 | 2.65E-01 | ADH1C/GSTM3/GSTA3 | 3 |
| Fructose and mannose metabolism | 2/83 | 3.01E-01 | KHK/SORD | 2 |
| Aldosterone-regulated sodium reabsorption | 2/83 | 3.54E-01 | SCNN1B/HSD11B2 | 2 |
| Glycine, serine and threonine metabolism | 2/83 | 3.80E-01 | PIPOX/DAO | 2 |
| Fat digestion and absorption | 2/83 | 3.80E-01 | CEL/MTTP | 2 |
| Regulation of actin cytoskeleton | 5/83 | 3.80E-01 | CYFIP2/EGF/KNG1/CXCL12/FGF9 | 5 |
| Tryptophan metabolism | 2/83 | 3.80E-01 | DLST/AOC1 | 2 |
| Glycerophospholipid metabolism | 3/83 | 4.25E-01 | PLPP4/GPAT3/ETNPPL | 3 |
| Staphylococcus aureus infection | 16/105 | 1.22E-11 | CFI/CFB/ICAM1/FCGR3B/FCGR3A/C2/KRT18/HLA-DRA/C1S/C1QB/FPR3/ITGB2/HLA-DQA1/FCGR2B/C3/C1QC | 16 |
| Complement and coagulation cascades | 13/105 | 4.95E-09 | CFI/CFB/SERPINA1/C2/CD46/F13A1/C1S/TFPI/VSIG4/C1QB/ITGB2/C3/C1QC | 13 |
| Tuberculosis | 14/105 | 4.81E-06 | FCGR3B/FCGR3A/HLA-DRA/LBP/CD14/IL10RA/STAT1/ITGB2/HLA-DQA1/CORO1A/FCGR2B/FCER1G/CTSS/C3 | 14 |
| Pertussis | 9/105 | 2.57E-05 | FOS/C2/C1S/CD14/LY96/C1QB/ITGB2/C3/C1QC | 9 |
| Mineral absorption | 8/105 | 2.75E-05 | MT1HL1/MT2A/MT1F/MT1H/MT1E/MT1X/MT1M/SLC34A2 | 8 |
| Malaria | 7/105 | 1.06E-04 | MET/ICAM1/SELE/CCL2/ITGB2/VCAM1/HBB | 7 |
| Leishmaniasis | 8/105 | 1.76E-04 | FOS/FCGR3B/FCGR3A/HLA-DRA/STAT1/ITGB2/HLA-DQA1/C3 | 8 |
| Rheumatoid arthritis | 8/105 | 5.71E-04 | FOS/ICAM1/HLA-DRA/CCL2/TNFSF13B/ITGB2/CCL20/HLA-DQA1 | 8 |
| Phagosome | 10/105 | 5.71E-04 | FCGR3B/FCGR3A/HLA-DRA/CD14/ITGB2/HLA-DQA1/CORO1A/FCGR2B/CTSS/C3 | 10 |
| AGE-RAGE signaling pathway in diabetic complications | 8/105 | 8.48E-04 | ICAM1/EGR1/COL4A1/COL4A2/SELE/CCL2/STAT1/VCAM1 | 8 |
| Systemic lupus erythematosus | 9/105 | 9.62E-04 | FCGR3B/FCGR3A/C2/HLA-DRA/C1S/C1QB/HLA-DQA1/C3/C1QC | 9 |
| TNF signaling pathway | 8/105 | 1.56E-03 | FOS/ICAM1/LIF/FAS/SELE/CCL2/CCL20/VCAM1 | 8 |
| African trypanosomiasis | 5/105 | 1.56E-03 | ICAM1/FAS/SELE/VCAM1/HBB | 5 |
| Cell adhesion molecules (CAMs) | 9/105 | 1.64E-03 | ICAM1/HLA-DRA/CLDN1/SELE/PTPRC/ITGB2/HLA-DQA1/VCAM1/VCAN | 9 |
| IL-17 signaling pathway | 7/105 | 2.70E-03 | FOS/S100A9/S100A8/HSP90B1/LCN2/CCL2/CCL20 | 7 |
| Fc gamma R-mediated phagocytosis | 6/105 | 1.54E-02 | FCGR3B/FCGR3A/ARPC1B/HCK/PTPRC/FCGR2B | 6 |
| Natural killer cell mediated cytotoxicity | 7/105 | 1.75E-02 | ICAM1/FCGR3B/FCGR3A/FAS/TYROBP/ITGB2/FCER1G | 7 |
| NF-kappa B signaling pathway | 6/105 | 2.09E-02 | ICAM1/LBP/CD14/LY96/TNFSF13B/VCAM1 | 6 |
| Chagas disease (American trypanosomiasis) | 6/105 | 2.09E-02 | FOS/FAS/C1QB/CCL2/C3/C1QC | 6 |
| Toll-like receptor signaling pathway | 6/105 | 2.19E-02 | FOS/SPP1/LBP/CD14/LY96/STAT1 | 6 |
| Toxoplasmosis | 6/105 | 3.02E-02 | HSPA6/HLA-DRA/LY96/IL10RA/STAT1/HLA-DQA1 | 6 |
| Legionellosis | 4/105 | 5.28E-02 | HSPA6/CD14/ITGB2/C3 | 4 |
| Osteoclast differentiation | 6/105 | 5.28E-02 | FOS/FCGR3B/FCGR3A/STAT1/TYROBP/FCGR2B | 6 |
| Asthma | 3/105 | 5.62E-02 | HLA-DRA/HLA-DQA1/FCER1G | 3 |
| Viral myocarditis | 4/105 | 5.62E-02 | ICAM1/HLA-DRA/ITGB2/HLA-DQA1 | 4 |
| Human T-cell leukemia virus 1 infection | 8/105 | 5.62E-02 | FOS/CDC20/ICAM1/EGR1/HLA-DRA/MMP7/ITGB2/HLA-DQA1 | 8 |
| Measles | 6/105 | 6.41E-02 | FOS/HSPA6/CD46/FAS/STAT1/FCGR2B | 6 |
| Fluid shear stress and atherosclerosis | 6/105 | 6.41E-02 | FOS/ICAM1/HSP90B1/SELE/CCL2/VCAM1 | 6 |
| Prion diseases | 3/105 | 6.74E-02 | EGR1/C1QB/C1QC | 3 |
| Kaposi sarcoma-associated herpesvirus infection | 7/105 | 6.75E-02 | FOS/ICAM1/FAS/HCK/STAT1/HIF1A/C3 | 7 |
| Nicotinate and nicotinamide metabolism | 3/105 | 7.35E-02 | NNMT/AOX1/NAMPT | 3 |
| Th17 cell differentiation | 5/105 | 7.43E-02 | FOS/HLA-DRA/STAT1/HLA-DQA1/HIF1A | 5 |
| Allograft rejection | 3/105 | 7.43E-02 | HLA-DRA/FAS/HLA-DQA1 | 3 |
| p53 signaling pathway | 4/105 | 7.80E-02 | SFN/CDK1/RRM2/FAS | 4 |
| Cytokine-cytokine receptor interaction | 9/105 | 7.80E-02 | OSMR/TNFRSF12A/LIF/FAS/IL32/IL10RA/CCL2/TNFSF13B/CCL20 | 9 |
| Leukocyte transendothelial migration | 5/105 | 8.03E-02 | EZR/ICAM1/CLDN1/ITGB2/VCAM1 | 5 |
| Graft-versus-host disease | 3/105 | 8.14E-02 | HLA-DRA/FAS/HLA-DQA1 | 3 |
| Type I diabetes mellitus | 3/105 | 9.00E-02 | HLA-DRA/FAS/HLA-DQA1 | 3 |
| Antigen processing and presentation | 4/105 | 9.00E-02 | HSPA6/HLA-DRA/HLA-DQA1/CTSS | 4 |
| Influenza A | 6/105 | 1.11E-01 | ICAM1/HLA-DRA/FAS/CCL2/STAT1/HLA-DQA1 | 6 |
| Intestinal immune network for IgA production | 3/105 | 1.18E-01 | HLA-DRA/TNFSF13B/HLA-DQA1 | 3 |
| ECM-receptor interaction | 4/105 | 1.24E-01 | ITGB6/SPP1/COL4A1/COL4A2 | 4 |
| Autoimmune thyroid disease | 3/105 | 1.36E-01 | HLA-DRA/FAS/HLA-DQA1 | 3 |
| Th1 and Th2 cell differentiation | 4/105 | 1.36E-01 | FOS/HLA-DRA/STAT1/HLA-DQA1 | 4 |
| Amoebiasis | 4/105 | 1.84E-01 | COL4A1/COL4A2/CD14/ITGB2 | 4 |
| Focal adhesion | 6/105 | 1.86E-01 | MET/ITGB6/SPP1/COL4A1/COL4A2/PPP1CB | 6 |
| Pathogenic Escherichia coli infection | 6/105 | 1.93E-01 | EZR/FOS/CLDN1/FAS/ARPC1B/HCK | 6 |
| Parathyroid hormone synthesis, secretion and action | 4/105 | 1.93E-01 | FOS/EGR1/CYP24A1/SLC34A2 | 4 |
| Proteoglycans in cancer | 6/105 | 1.93E-01 | EZR/MET/IQGAP1/FAS/PPP1CB/HIF1A | 6 |
| Inflammatory bowel disease (IBD) | 3/105 | 1.97E-01 | HLA-DRA/STAT1/HLA-DQA1 | 3 |
| Regulation of actin cytoskeleton | 6/105 | 2.12E-01 | EZR/ITGB6/IQGAP1/ARPC1B/ITGB2/PPP1CB | 6 |
| JAK-STAT signaling pathway | 5/105 | 2.12E-01 | OSMR/LIF/IL10RA/STAT1/AOX1 | 5 |
| Salmonella infection | 6/105 | 2.12E-01 | FOS/HSP90B1/ARPC1B/CD14/LY96/PTPRC | 6 |
| Mucin type O-glycan biosynthesis | 2/105 | 2.12E-01 | GCNT3/GALNT7 | 2 |
| Protein processing in endoplasmic reticulum | 5/105 | 2.24E-01 | HSPA6/SEC23A/TRAM1/HSP90B1/LMAN1 | 5 |
| Estrogen signaling pathway | 4/105 | 3.54E-01 | FOS/HSPA6/KRT18/HSP90B1 | 4 |
| PD-L1 expression and PD-1 checkpoint pathway in cancer | 3/105 | 3.61E-01 | FOS/STAT1/HIF1A | 3 |
| Epstein-Barr virus infection | 5/105 | 3.95E-01 | ICAM1/HLA-DRA/FAS/STAT1/HLA-DQA1 | 5 |
| Sphingolipid metabolism | 2/105 | 3.95E-01 | SGPP1/UGCG | 2 |
| Protein digestion and absorption | 3/105 | 3.96E-01 | COL7A1/COL4A1/COL4A2 | 3 |
| Choline metabolism in cancer | 3/105 | 4.16E-01 | FOS/SLC44A4/HIF1A | 3 |
| Hematopoietic cell lineage | 3/105 | 4.19E-01 | HLA-DRA/CD14/HLA-DQA1 | 3 |
| Viral protein interaction with cytokine and cytokine receptor | 3/105 | 4.21E-01 | IL10RA/CCL2/CCL20 | 3 |