**Table S3**: The functional analyses of up-regulated genes to identify the top 10 GO terms.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Category** | **Term** | **Gene Count** | **Overlapped Gene** | **P Value** |
| GO\_BP | Immune response | 23 | CIITA, GPR183, CRIP1, CCL3, HLA-DRB1, CMKLR1, CCR1, HLA-DRB3, IL19, IL32, HLA-DQA2, C1QC, IL10, CCL18, SLC11A1, LILRB2, CCL23, RGS1, CCR5, FCGR1B, FCGR3A, HLA-DRA, LCP2 | 3.17E-11 |
| GO\_BP | Inflammatory response | 20 | HAVCR2, CIITA, CCL3, CCR1, IL19, LYZ, ITGB2, FPR3, IL10, CCL18, SLC11A1, CYBB, NLRC4, CCL23, CCR5, CXCR4, STAB1, CCL3L3, PLA2G4C, CSF1R | 1.56E-09 |
| GO\_CC | Plasma membrane | 69 | KCNH1, MSR1, PLXNA4, CD53, DYSF, SLC1A3, CXCR4, FCGR3A, ANGPT2, PARVG, LAIR1, FMNL3, TMEM204, CMKLR1, PTPRRC, HLA-DQA2, CD163, CD84, LILRB2, CRHR2, CD163L1, CCR5, ARRB1, CD33, TREM2, SH3GL2, LCP1, GAP43, HLA-DRA, GPR183, HLA-DRB1, FGR, HLA-DRB3, CCR1, CYTH4, ITGA11, IFI30, OXTR, PCDHB14, ITGB2, FPR3, CDH4, EPHB1, KCNMB1, KCNMB2, SLC11A1, SORBS1, FAT3, TEK, FCGR1B, FCER1G, APBA2, SUCNR1, SELPLG, TYROBP, CSF1R, CARD9, GNAO1, CPPED1, PODXL, LSP1, CYBB, RGS1, STAB1, CD300A, RGS5, PECAM1, ECSCR, GFRA1 | 6.52E-08 |
| GO\_CC | Integral component of plasma membrane | 34 | KCNH1, GPR183, MSR1, PLXNA4, HLA-DRB1, HLA-DRB3, CCR1, OXTR, FPR3, CD53, CDH4, EPHB1, KCNMB2, SLC11A1, TEK, FCER1G, PCDHA11, SELPLG, TYROBP, CSF1R, PTPRB, CMKLR1, PODXL, HLA-DQA2, DCSTAMP, CD163, CD84, CRHR2, LILRB2, CYBB, CCR5, STAB1, CD33, HLA-DRA | 3.88E-07 |
| GO\_BP | Positive regulation of ERK1 and ERK2 cascade | 12 | HAVCR2, GPR183, CCL3, CCL23, ARRB1, CCR1, CCL3L3, TEK, FGF1, TREM2, CCL18, CSF1R | 5.58E-07 |
| GO\_BP | Leukocyte migration | 10 | CD84, PODXL, PECAM1, TEK, FCER1G, FPR3, ITGB2, ANGPT2, SELPLG, MMP1 | 1.64E-06 |
| GO\_BP | Chemokine-mediated signaling pathway | 8 | CCL3, CCL23, CCR5, CMKLR1, CXCR4, CCR1, CCL3L3, CCL18 | 3.55E-06 |
| GO\_BP | Cell adhesion | 17 | PARVG, CCR1, PODXL, ITGA11, IL32, ITGB2, AJAP1, CDH4, SORBS1, SORBS2, STAB1, CD300A, CD33, PECAM1, PCDHA11, LOXL2, SELPLG | 4.24E-06 |
| GO\_MF | Actin binding | 13 | PARVG, FMNL3, NCALD, DAAM2, TPM1, LSP1, SORBS1, TAGLN, CCR5, GMFG, CXCR4, CNN1, LCP1 | 7.71E-06 |
| GO\_BP | Chemotaxis | 9 | LSP1, CCL3, CCL23, CCR5, CMKLR1, CXCR4, CCR1, ECSCR, CCL18 | 1.51E-05 |

**Table S4**: The functional analyses of down-regulated genes to identify the top 10 GO terms.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Category** | **Term** | **Gene Count** | **Overlapped Gene** | **P Value** |
| GO\_CC | Basolateral plasma membrane | 14 | PALM, SLC8A2, SLC7A8, CFTR, ATP12A, CXADR, AQP3, CD1D, CA9, NDRG4, P2RY1, MAP7, SLC40A1, PIANP | 9.60E-06 |
| GO\_CC | Extracellular region | 50 | NRTN, GDF7, EFNA1, NPNT, IL18, FST, BTC, IGFBP6, SNCA, FGF10, CXADR, SERPINA3, CNTNAP3, PRSS37, KLK13, HHIPL2, COLEC10, DLL1, WFDC12, MELTF, CNTN4, WFDC2, CCK, CRHR1-IT1, C6, CLU, KITLG, FAM132A, CXCL6, MDK, EPHB2, LIF, PRRG4, PRSS2, PRSS3, PTH, TNFRSF18, DEFB1, ANGPTL4, KLK6, DEFB103B, MUC20, HGF, COL4A6, B3GAT1, LAMA3, PRSS27, WIF1, IGFBP2, NXPE1 | 2.09E-05 |
| GO\_CC | Extracellular space | 44 | SPINK13, CCK, LYPD3, SPOCK3, MSMB, GDF7, IL18, SNCA, CLU, IGFBP6, BTC, SORL1, FAM20C, KITLG, FGF10, FAM132A, CXCL6, GPRC5B, CXADR, CPZ, ALDH3A1, LIF, PRSS2, PTH, PRSS3, SERPINA3, SEMA3B, DEFB1, KLK13, ANGPTL4, FLRT3, KLK6, CPA6, LGALS4, DEFB103B, KLK5, PIGR, HGF, TNFSF9, MUC4, MELTF, CMTM8, IGFBP2, WFDC2 | 2.32E-05 |
| GO\_BP | Retinal metabolic process | 5 | AKR1C3, RDH10, ALDH1A3, AKR1C1, BCO2 | 3.47E-05 |
| GO\_MF | Receptor binding | 17 | FRK, NRTN, EFNA1, IGFBP6, LRRC4B, CXADR, TNFSF9, EPHB2, LIF, RND1, LAMA3, ITGB8, PTK6, C1QL1, MAP7, IGFBP2, SLC27A2 | 2.94E-04 |
| GO\_MF | Gamma-glutamyltransferase activity | 4 | GGT5, GGT3P, GGTLC2, GGTLC1 | 5.02E-04 |
| GO\_MF | Indanol dehydrogenase activity | 3 | AKR1C3, AKR1B10, AKR1C1 | 8.19E-04 |
| **Category** | **Term** | **Gene Count** | **Overlapped Gene** | **P Value** |
| GO\_BP | Activation of MAPK activity | 8 | DUSP5, ADORA2B, EFNA1, MUC20, LPAR3, FGF10, MAPK10, HGF | 0.002184644 |
| GO\_MF | Retinol dehydrogenase activity | 4 | AKR1C3, RDH10, DHRS3, ADH1A | 0.003093998 |
| GO\_BP | Leukotriene biosynthetic process | 4 | GGT5, GGT3P, GGTLC2, GGTLC1 | 0.004323082 |

**Table S5**: The gene lists of the significantly enriched KEGG pathways

|  |  |  |  |
| --- | --- | --- | --- |
| **Term** | **Gene Count** | **Overlapped Gene** | **P Value** |
| Rheumatoid arthritis | 10 | CCL3, HLA-DRB1, HLA-DRB3, CCL3L3, TEK, ITGB2, ATP6V0D2, HLA-DQA2, MMP1, HLA-DRA | 7.45E-07 |
| Asthma | 6 | HLA-DRB1, HLA-DRB3, FCER1G, HLA-DQA2, IL10, HLA-DRA | 2.26E-05 |
| Chemokine signaling pathway | 11 | CCL3, CCL23, PLCB4, CCR5, FGR, CXCR4, NCF1, ARRB1, CCR1, CCL3L3, CCL18 | 5.82E-05 |
| Osteoclast differentiation | 9 | LILRB2, CYBB, LILRB5, NCF1, FCGR3A, TREM2, CSF1R, TYROBP, LCP2 | 1.40E-04 |
| Intestinal immune network for IgA production | 6 | HLA-DRB1, CXCR4, HLA-DRB3, HLA-DQA2, IL10, HLA-DRA | 2.08E-04 |
| Phagosome | 9 | MSR1, HLA-DRB1, NCF1, HLA-DRB3, ITGB2, FCGR3A, ATP6V0D2, HLA-DQA2, HLA-DRA | 3.55E-04 |
| Pathways in cancer | 15 | PTGER3, PTGS2, PPARG, SMAD3, KITLG, FGF10, LPAR3, LPAR2, HGF, MAPK10, MECOM, STAT3, COL4A6, LAMA3, LPAR5 | 0.003773286 |
| Rap1 signaling pathway | 10 | ADORA2B, LPAR5, EFNA1, P2RY1, SIPA1L2, KITLG, LPAR3, FGF10, LPAR2, HGF | 0.006259875 |
| Metabolism of xenobiotics by cytochrome P450 | 6 | UGT1A6, ALDH1A3, ADH1A, AKR1C1, DHDH, ALDH3A1 | 0.006407175 |
| Chemical carcinogenesis | 6 | UGT1A6, CYP3A7, PTGS2, ALDH1A3, ADH1A, ALDH3A1 | 0.008868448 |
| **Term** | **Gene Count** | **Overlapped Gene** | **P Value** |
| Retinol metabolism | 5 | UGT1A6, RDH10, DHRS3, CYP3A7, ADH1A | 0.018866178 |
| Drug metabolism - cytochrome P450 | 5 | UGT1A6, ALDH1A3, FMO3, ADH1A, ALDH3A1 | 0.023042317 |
| Cell adhesion molecules (CAMs) | 7 | LRRC4, F11R, OCLN, ITGB8, LRRC4B, CNTNAP2, CLDN23 | 0.0258561 |
| Neuroactive ligand-receptor interaction | 10 | MCHR1, GABRE, PTGER3, RXFP1, ADORA2B, PRSS2, P2RY1, PRSS3, LPAR3, LPAR2 | 0.03270952 |
| PI3K-Akt signaling pathway | 11 | LAMA3, LPAR5, ITGB8, EFNA1, KITLG, LPAR3, FGF10, LPAR2, HGF, BCL2L11, COL4A6 | 0.0485844 |
| PPAR signaling pathway | 4 | PPARG, SLC27A6, SLC27A2, ANGPTL4 | 0.09149798 |