Over-represented GO biological process terms in 415 significantly down-regulated genes in ADSCs from diseased sides

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| GO:ID | GO term | Term P value | Term P value corrected with Bonferroni step down | Group P value | Group P value corrected with Bonferroni step down | GO groups | % Associated genes | Nr. genes | Associated genes found |
| GO:0019722 | Calcium-mediated signaling | 0.000014 | 0.00067 | 0.0000028 | 0.0000057 | Group 0 | 7.738095284 | 13 | *CD4, CMKLR1, CXCL8, CXCR4, IGF1, JPH1, KDR, MCTP1, PLCG2, PLEK, SYK, TREM2, TRPM2* |
| GO:0050848 | Regulation of calcium-mediated signaling | 0.00085 | 0.013 | 0.0000028 | 0.0000057 | Group 0 | 8.433734894 | 7 | *CD4, CMKLR1, IGF1, JPH1, PLEK, SYK, TREM2* |
| GO:0002576 | Platelet degranulation | 0.001 | 0.014 | 0.0000028 | 0.0000057 | Group 0 | 6.521739006 | 9 | *F13A1, FCER1G, IGF1, IL6, PCDH7, PF4, PLEK, SRGN, SYK* |
| GO:0003170 | Heart valve development | 0.000074 | 0.0026 | 0.000032 | 0.000032 | Group 1 | 15.38461494 | 6 | *BMP2, GJA5, HEYL, PITX2, SOX9, TBX5* |
| GO:0010717 | Regulation of epithelial to mesenchymal transition | 0.01 | 0.01 | 0.000032 | 0.000032 | Group 1 | 6.944444656 | 5 | *ALX1, BMP2, EPHA3, LDLRAD4, TBX5* |
| GO:0001837 | Epithelial to mesenchymal transition | 0.0015 | 0.017 | 0.000032 | 0.000032 | Group 1 | 6.779661179 | 8 | *ALX1, BMP2, EPHA3, HEYL, IL6, LDLRAD4, SOX9, TBX5* |
| GO:0060393 | Regulation of pathway-restricted SMAD protein phosphorylation | 0.0061 | 0.024 | 0.000032 | 0.000032 | Group 1 | 7.936507702 | 5 | *BMP2, GDF6, INHBA, LDLRAD4, PMEPA1* |
| GO:0042119 | Neutrophil activation | 7E–14 | 7.4E–12 | 1.2E–14 | 3.7E–14 | Group 2 | 7.393715382 | 40 | *ACPP, ALOX5, BIN2, C3AR1, C5AR1, CD14, CD300A, CD53, CR1, CXCL8, CYBB, F2RL1, FCER1G, FCGR2A, FGR, FPR1, FUCA1, HK3, HSPA6, ITGAM, LAIR1, LILRA6, LYZ, MMP12, MMP8, NCKAP1L, NFAM1, OLFM4, OLR1, PTAFR, PTPN6, PTPRC, RNASE1, S100A9, SLC11A1, SYK, TMC6, TRPM2, TYROBP, VAMP8* |
| GO:0043299 | Leukocyte degranulation | 1.9E–13 | 2E–11 | 1.2E–14 | 3.7E–14 | Group 2 | 7.008546829 | 41 | *ACPP, ALOX5, BIN2, C3AR1, C5AR1, CD14, CD300A, CD53, CD84, CR1, CYBB, F2RL1, FCER1G, FCGR2A, FGR, FPR1, FUCA1, HCK, HK3, HSPA6, ITGAM, LAIR1, LILRA6, LYZ, MMP12, MMP8, NCKAP1L, NFAM1, OLFM4, OLR1, PTAFR, PTPN6, PTPRC, RNASE1, S100A9, SLC11A1, SYK, TMC6, TRPM2, TYROBP, VAMP8* |
| GO:0045055 | Regulated exocytosis | 4.1E–14 | 4.4E–12 | 1.2E–14 | 3.7E–14 | Group 2 | 6.195786953 | 50 | *ACPP, ALOX5, BIN2, C3AR1, C5AR1, CADPS, CD14, CD300A, CD53, CD84, CR1, CYBB, F13A1, F2RL1, FCER1G, FCGR2A, FGR, FPR1, FUCA1, HCK, HK3, HSPA6, IGF1, IL6, ITGAM, LAIR1, LILRA6, LYZ, MMP12, MMP8, NCKAP1L, NFAM1, OLFM4, OLR1, PCDH7, PF4, PLEK, PTAFR, PTPN6, PTPRC, RNASE1, S100A9, SLC11A1, SRGN, SYK, TMC6, TMEM27, TRPM2, TYROBP, VAMP8* |
| GO:0043312 | Neutrophil degranulation | 1.1E–12 | 1.1E–10 | 1.2E–14 | 3.7E–14 | Group 2 | 7.089552402 | 38 | *ACPP, ALOX5, BIN2, C3AR1, C5AR1, CD14, CD300A, CD53, CR1, CYBB, FCER1G, FCGR2A, FGR, FPR1, FUCA1, HK3, HSPA6, ITGAM, LAIR1, LILRA6, LYZ, MMP12, MMP8, NCKAP1L, NFAM1, OLFM4, OLR1, PTAFR, PTPN6, PTPRC, RNASE1, S100A9, SLC11A1, SYK, TMC6, TRPM2, TYROBP, VAMP8* |
| GO:0002757 | Immune response-activating signal transduction | 6.4E–15 | 7.2E–13 | 5.4E–17 | 2.1E–16 | Group 3 | 7.120253086 | 45 | *C3AR1, C5AR1, CARD11, CD14, CD180, CD209, CD28, CD300A, CD4, CD86, CLEC7A, CR1, F2RL1, FCER1G, FCGR1A, FCGR2A, FCGR3A, FGR, FPR1, FPR3, HAVCR2, HCK, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, ITGAM, LBP, LCP2, MARCO, NCKAP1L, NFAM1, PIK3AP1, PLCG2, PLPP4, PTPN22, PTPN6, PTPRC, RNASE1, S100A9, SYK, TLR8, TNFRSF21* |
| GO:0031294 | Lymphocyte costimulation | 2.1E–09 | 0.00000018 | 5.4E–17 | 2.1E–16 | Group 3 | 14.73684216 | 14 | *CARD11, CD28, CD4, CD86, EFNB2, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, ICOSLG, IL6, PTPN6, RNASE1* |
| GO:0045089 | Positive regulation of innate immune response | 0.00000036 | 0.000027 | 5.4E–17 | 2.1E–16 | Group 3 | 6.489675522 | 22 | *CARD11, CD14, CD180, CD1D, CD209, CD300A, CD86, CLEC7A, F2RL1, FCER1G, HAVCR2, HCK, ITGAM, LBP, MARCO, MMP12, PIK3AP1, PLCG2, PTPN22, S100A9, SYK, TLR8* |
| GO:0051251 | Positive regulation of lymphocyte activation | 2.2E–12 | 2.2E–10 | 5.4E–17 | 2.1E–16 | Group 3 | 8.645533562 | 30 | *AIF1, CARD11, CCL2, CD1D, CD28, CD4, CD74, CD86, EFNB2, GPAM, GPR183, HAVCR2, HLA-DMB, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, ICOSLG, IGF1, IL6, INPP5D, NCKAP1L, PTPN22, PTPN6, PTPRC, RNASE1, S100A9, SASH3, SYK* |
| GO:1903039 | Positive regulation of leukocyte cell-cell adhesion | 7.5E–15 | 8.3E–13 | 5.4E–17 | 2.1E–16 | Group 3 | 11.66666698 | 28 | *AIF1, CARD11, CCL2, CD1D, CD28, CD4, CD74, CD86, EFNB2, GPAM, HAVCR2, HLA-DMB, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, ICOSLG, IGF1, IL6, NCKAP1L, PTAFR, PTPN22, PTPN6, PTPRC, RNASE1, SASH3, SYK* |
| GO:0002429 | Immune response-activating cell surface receptor signaling pathway | 2.2E–11 | 0.000000002 | 5.4E–17 | 2.1E–16 | Group 3 | 7.053941727 | 34 | *C3AR1, C5AR1, CARD11, CD209, CD28, CD300A, CD4, CLEC7A, CR1, FCER1G, FCGR1A, FCGR2A, FCGR3A, FGR, FPR1, FPR3, HCK, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, LCP2, NCKAP1L, NFAM1, PLCG2, PLPP4, PTPN22, PTPN6, PTPRC, RNASE1, SYK, TNFRSF21* |
| GO:0050670 | Regulation of lymphocyte proliferation | 2.9E–15 | 3.2E–13 | 5.4E–17 | 2.1E–16 | Group 3 | 12.67605591 | 27 | *AIF1, CARD11, CD1D, CD209, CD28, CD300A, CD4, CD74, CD86, GPAM, GPR183, HAVCR2, HLA-DMB, HLA-DRB1, ICOSLG, IGF1, IL6, INPP5D, NCKAP1L, PTPN22, PTPN6, PTPRC, S100A9, SASH3, SYK, TNFRSF21, VSIG4* |
| GO:0050863 | Regulation of T cell activation | 1.6E–14 | 1.8E–12 | 5.4E–17 | 2.1E–16 | Group 3 | 9.696969986 | 32 | *AIF1, CARD11, CCL2, CD1D, CD209, CD28, CD300A, CD4, CD74, CD86, CYP26B1, EFNB2, GPAM, HAVCR2, HLA-DMB, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, ICOSLG, IGF1, IL6, NCKAP1L, PTPN22, PTPN6, PTPRC, RNASE1, SASH3, SYK, TNFRSF21, VSIG4* |
| GO:0002758 | Innate immune response-activating signal transduction | 0.00000043 | 0.000031 | 5.4E–17 | 2.1E–16 | Group 3 | 6.944444656 | 20 | *CARD11, CD14, CD180, CD209, CD300A, CD86, CLEC7A, F2RL1, FCER1G, HAVCR2, HCK, ITGAM, LBP, MARCO, PIK3AP1, PLCG2, PTPN22, S100A9, SYK, TLR8* |
| GO:0030098 | Lymphocyte differentiation | 0.00000019 | 0.000015 | 5.4E–17 | 2.1E–16 | Group 3 | 6.727828979 | 22 | *CARD11, CD1D, CD28, CD4, CD74, CD86, CYP26B1, FCER1G, GPR183, IL6, INHBA, INPP5D, MERTK, NCKAP1L, NFAM1, PLCG2, PTPN22, PTPN6, PTPRC, SASH3, SPI1, SYK* |
| GO:0002431 | Fc receptor mediated stimulatory signaling pathway | 0.00028 | 0.0073 | 5.4E–17 | 2.1E–16 | Group 3 | 6.586826324 | 11 | *FCER1G, FCGR1A, FCGR2A, FCGR3A, FGR, HCK, NCKAP1L, PLCG2, PLPP4, RNASE1, SYK* |
| GO:0038094 | Fc-gamma receptor signaling pathway | 0.00025 | 0.0073 | 5.4E–17 | 2.1E–16 | Group 3 | 6.666666508 | 11 | *FCER1G, FCGR1A, FCGR2A, FCGR3A, FGR, HCK, NCKAP1L, PLCG2, PLPP4, RNASE1, SYK* |
| GO:0050851 | Antigen receptor-mediated signaling pathway | 0.0000019 | 0.00011 | 5.4E–17 | 2.1E–16 | Group 3 | 6.574394226 | 19 | *CARD11, CD28, CD300A, CD4, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, LCP2, NCKAP1L, NFAM1, PLCG2, PTPN22, PTPN6, PTPRC, SYK, TNFRSF21* |
| GO:0002221 | Pattern recognition receptor signaling pathway | 0.0000062 | 0.00032 | 5.4E–17 | 2.1E–16 | Group 3 | 7.821228981 | 14 | *CD14, CD180, CD300A, CD86, CLEC7A, F2RL1, HAVCR2, ITGAM, LBP, MARCO, PIK3AP1, PTPN22, S100A9, TLR8* |
| GO:0050852 | T cell receptor signaling pathway | 0.00000057 | 0.000039 | 5.4E–17 | 2.1E–16 | Group 3 | 8.333333015 | 16 | *CARD11, CD28, CD300A, CD4, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, LCP2, PLCG2, PTPN22, PTPN6, PTPRC, TNFRSF21* |
| GO:0050853 | B cell receptor signaling pathway | 0.00073 | 0.012 | 5.4E–17 | 2.1E–16 | Group 3 | 7.619047642 | 8 | *CD300A, NCKAP1L, NFAM1, PLCG2, PTPN22, PTPN6, PTPRC, SYK* |
| GO:0002224 | Toll-like receptor signaling pathway | 0.0000078 | 0.00039 | 5.4E–17 | 2.1E–16 | Group 3 | 8.888889313 | 12 | *CD14, CD180, CD300A, CD86, F2RL1, HAVCR2, ITGAM, LBP, PIK3AP1, PTPN22, S100A9, TLR8* |
| GO:0002685 | Regulation of leukocyte migration | 1.2E–14 | 1.3E–12 | 5.9E–22 | 4.1E–21 | Group 4 | 13.95348835 | 24 | *AIF1, BDKRB1, C3AR1, C5AR1, CCL2, CD300A, CD74, CMKLR1, CXCL5, CXCL6, CXCL8, ENC1, F2RL1, IL33, IL6, ITGA2, LBP, NCKAP1L, PF4, PLA2G7, PLVAP, PTAFR, PTPN22, RNASE1* |
| GO:0030595 | Leukocyte chemotaxis | 2.9E–19 | 3.4E–17 | 5.9E–22 | 4.1E–21 | Group 4 | 14.69194317 | 31 | *AIF1, C3AR1, C5AR1, CCL13, CCL18, CCL2, CCL22, CCL26, CCL8, CD74, CMKLR1, CXCL5, CXCL6, CXCL8, CXCR4, EDNRB, F2RL1, FCER1G, GPR183, IL6, LBP, NCKAP1L, PCDHA6, PF4, PLA2G7, RNASE1, S100A9, SCG2, SYK, TREM1, TRPM2* |
| GO:0071674 | Mononuclear cell migration | 0.000000038 | 0.0000031 | 5.9E–22 | 4.1E–21 | Group 4 | 14.45783138 | 12 | *AIF1, C3AR1, C5AR1, CCL13, CCL18, CCL2, CCL22, CCL26, CCL8, CMKLR1, IL6, PLA2G7* |
| GO:0072676 | Lymphocyte migration | 0.00016 | 0.0049 | 5.9E–22 | 4.1E–21 | Group 4 | 9.523809433 | 8 | *AIF1, CCL13, CCL18, CCL2, CCL22, CCL26, CCL8, GPR183* |
| GO:0097529 | Myeloid leukocyte migration | 1E–16 | 1.2E–14 | 5.9E–22 | 4.1E–21 | Group 4 | 14.43850231 | 27 | *AIF1, C3AR1, C5AR1, CCL13, CCL18, CCL2, CCL22, CCL26, CCL8, CD300A, CD74, CMKLR1, CXCL5, CXCL6, CXCL8, EDNRB, FCER1G, IL6, LBP, NCKAP1L, PF4, PLA2G7, RNASE1, S100A9, SCG2, SYK, TREM1* |
| GO:0002687 | Positive regulation of leukocyte migration | 6.5E–14 | 7E–12 | 5.9E–22 | 4.1E–21 | Group 4 | 16.66666603 | 20 | *AIF1, BDKRB1, C3AR1, C5AR1, CCL2, CD74, CMKLR1, CXCL5, CXCL6, CXCL8, F2RL1, IL6, ITGA2, LBP, NCKAP1L, PF4, PLA2G7, PLVAP, PTAFR, RNASE1* |
| GO:0030335 | Positive regulation of cell migration | 0.000000002 | 0.00000017 | 5.9E–22 | 4.1E–21 | Group 4 | 6.744185925 | 29 | *AIF1, ANGPT1, BDKRB1, BMP2, C3AR1, C5AR1, CCL2, CCL26, CD74, CMKLR1, CXCL5, CXCL6, CXCL8, F2RL1, FGR, IGF1, IL6, ITGA2, KDR, LBP, MCAM, NCKAP1L, PF4, PLA2G7, PLVAP, PTAFR, PTPRC, RNASE1, SOX9* |
| GO:0071675 | Regulation of mononuclear cell migration | 0.00014 | 0.0047 | 5.9E–22 | 4.1E–21 | Group 4 | 13.63636398 | 6 | *AIF1, C3AR1, C5AR1, CCL2, CMKLR1, PLA2G7* |
| GO:0002548 | Monocyte chemotaxis | 0.0000025 | 0.00015 | 5.9E–22 | 4.1E–21 | Group 4 | 14.0625 | 9 | *AIF1, CCL13, CCL18, CCL2, CCL22, CCL26, CCL8, IL6, PLA2G7* |
| GO:0097530 | Granulocyte migration | 2.9E–16 | 3.4E–14 | 5.9E–22 | 4.1E–21 | Group 4 | 17.42424202 | 23 | *C3AR1, C5AR1, CCL13, CCL18, CCL2, CCL22, CCL26, CCL8, CD300A, CD74, CMKLR1, CXCL5, CXCL6, CXCL8, FCER1G, LBP, NCKAP1L, PF4, RNASE1, S100A9, SCG2, SYK, TREM1* |
| GO:0002690 | Positive regulation of leukocyte chemotaxis | 9.4E–12 | 8.9E–10 | 5.9E–22 | 4.1E–21 | Group 4 | 17.58241844 | 16 | *AIF1, C3AR1, C5AR1, CCL2, CD74, CMKLR1, CXCL5, CXCL6, CXCL8, F2RL1, IL6, LBP, NCKAP1L, PF4, PLA2G7, RNASE1* |
| GO:0048246 | Macrophage chemotaxis | 0.00032 | 0.0077 | 5.9E–22 | 4.1E–21 | Group 4 | 15.15151501 | 5 | *C3AR1, C5AR1, CCL2, CMKLR1, EDNRB* |
| GO:0002430 | Complement receptor mediated signaling pathway | 0.0000014 | 0.000093 | 5.9E–22 | 4.1E–21 | Group 4 | 41.66666794 | 5 | *C3AR1, C5AR1, CR1, FPR1, FPR3* |
| GO:0070371 | ERK1 and ERK2 cascade | 2.3E–13 | 2.4E–11 | 5.9E–22 | 4.1E–21 | Group 4 | 9.797297478 | 29 | *ANGPT1, BMP2, C5AR1, CCL13, CCL18, CCL2, CCL22, CCL26, CCL8, CD4, CD74, F2RL1, GPR183, HAVCR2, HLA-DRB1, HTR2A, IGF1, IL6, KDR, LIF, P2RY1, PTPN22, PTPN6, PTPRR, ROS1, S100A9, SOX9, SYK, TREM2* |
| GO:0030593 | Neutrophil chemotaxis | 7.2E–16 | 8.2E–14 | 5.9E–22 | 4.1E–21 | Group 4 | 20.83333397 | 20 | *C3AR1, C5AR1, CCL13, CCL18, CCL2, CCL22, CCL26, CCL8, CD74, CXCL5, CXCL6, CXCL8, FCER1G, LBP, NCKAP1L, PF4, RNASE1, S100A9, SYK, TREM1* |
| GO:0071622 | Regulation of granulocyte chemotaxis | 1.7E–10 | 0.000000015 | 5.9E–22 | 4.1E–21 | Group 4 | 22.64151001 | 12 | *C3AR1, C5AR1, CCL2, CD74, CMKLR1, CXCL5, CXCL6, CXCL8, LBP, NCKAP1L, PF4, RNASE1* |
| GO:0070372 | Regulation of ERK1 and ERK2 cascade | 1.4E–12 | 1.3E–10 | 5.9E–22 | 4.1E–21 | Group 4 | 9.854014397 | 27 | *ANGPT1, BMP2, C5AR1, CCL13, CCL18, CCL2, CCL22, CCL26, CCL8, CD4, CD74, F2RL1, GPR183, HAVCR2, HLA-DRB1, HTR2A, IL6, KDR, LIF, P2RY1, PTPN22, PTPN6, PTPRR, ROS1, S100A9, SYK, TREM2* |
| GO:0090023 | Positive regulation of neutrophil chemotaxis | 8.7E–11 | 7.9E–09 | 5.9E–22 | 4.1E–21 | Group 4 | 33.33333206 | 10 | *C3AR1, C5AR1, CD74, CXCL5, CXCL6, CXCL8, LBP, NCKAP1L, PF4, RNASE1* |
| GO:0070374 | Positive regulation of ERK1 and ERK2 cascade | 2E–11 | 1.9E–09 | 5.9E–22 | 4.1E–21 | Group 4 | 11 | 22 | *ANGPT1, BMP2, C5AR1, CCL13, CCL18, CCL2, CCL22, CCL26, CCL8, CD4, CD74, F2RL1, GPR183, HAVCR2, HLA-DRB1, HTR2A, IL6, KDR, P2RY1, PTPN22, S100A9, TREM2* |
| GO:0051250 | Negative regulation of lymphocyte activation | 0.0000045 | 0.00024 | 1.6E–21 | 9.7E–21 | Group 5 | 9.375 | 12 | *CD300A, CD74, HAVCR2, HLA-DRB1, INHBA, INPP5D, MERTK, PTPN22, PTPN6, SAMSN1, TNFRSF21, VSIG4* |
| GO:0002429 | Immune response-activating cell surface receptor signaling pathway | 2.2E–11 | 0.000000002 | 1.6E–21 | 9.7E–21 | Group 5 | 7.053941727 | 34 | *C3AR1, C5AR1, CARD11, CD209, CD28, CD300A, CD4, CLEC7A, CR1, FCER1G, FCGR1A, FCGR2A, FCGR3A, FGR, FPR1, FPR3, HCK, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, LCP2, NCKAP1L, NFAM1, PLCG2, PLPP4, PTPN22, PTPN6, PTPRC, RNASE1, SYK, TNFRSF21* |
| GO:0042098 | T cell proliferation | 8E–14 | 8.4E–12 | 1.6E–21 | 9.7E–21 | Group 5 | 12.8342247 | 24 | *AIF1, CARD11, CD1D, CD209, CD28, CD4, CD86, DOCK8, GPAM, HAVCR2, HLA-DMB, HLA-DRB1, ICOSLG, IGF1, IL6, NCKAP1L, PTPN22, PTPN6, PTPRC, SASH3, SLC11A1, SYK, TNFRSF21, VSIG4* |
| GO:0042100 | B cell proliferation | 0.0000011 | 0.000076 | 1.6E–21 | 9.7E–21 | Group 5 | 11.82795715 | 11 | *CARD11, CD180, CD300A, CD74, GPR183, INPP5D, NCKAP1L, PTPRC, S100A9, SASH3, TNFRSF21* |
| GO:0046631 | Alpha-beta T cell activation | 0.00038 | 0.0085 | 1.6E–21 | 9.7E–21 | Group 5 | 7.5 | 9 | *CD28, CD300A, CD86, GPR183, IL6, NCKAP1L, PTPN22, SASH3, SYK* |
| GO:0050670 | Regulation of lymphocyte proliferation | 2.9E–15 | 3.2E–13 | 1.6E–21 | 9.7E–21 | Group 5 | 12.67605591 | 27 | *AIF1, CARD11, CD1D, CD209, CD28, CD300A, CD4, CD74, CD86, GPAM, GPR183, HAVCR2, HLA-DMB, HLA-DRB1, ICOSLG, IGF1, IL6, INPP5D, NCKAP1L, PTPN22, PTPN6, PTPRC, S100A9, SASH3, SYK, TNFRSF21, VSIG4* |
| GO:0050863 | Regulation of T cell activation | 1.6E–14 | 1.8E–12 | 1.6E–21 | 9.7E–21 | Group 5 | 9.696969986 | 32 | *AIF1, CARD11, CCL2, CD1D, CD209, CD28, CD300A, CD4, CD74, CD86, CYP26B1, EFNB2, GPAM, HAVCR2, HLA-DMB, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, ICOSLG, IGF1, IL6, NCKAP1L, PTPN22, PTPN6, PTPRC, RNASE1, SASH3, SYK, TNFRSF21, VSIG4* |
| GO:0050864 | Regulation of B cell activation | 0.000000016 | 0.0000013 | 1.6E–21 | 9.7E–21 | Group 5 | 10.05917168 | 17 | *CARD11, CD28, CD300A, CD74, GPR183, IL6, INHBA, INPP5D, NCKAP1L, NFAM1, PTPN6, PTPRC, S100A9, SAMSN1, SASH3, SYK, TNFRSF21* |
| GO:1903038 | Negative regulation of leukocyte cell-cell adhesion | 0.000097 | 0.0034 | 1.6E–21 | 9.7E–21 | Group 5 | 9 | 9 | *CD300A, CD74, ENC1, HAVCR2, HLA-DRB1, PTPN22, PTPN6, TNFRSF21, VSIG4* |
| GO:0050672 | Negative regulation of lymphocyte proliferation | 0.00027 | 0.0077 | 1.6E–21 | 9.7E–21 | Group 5 | 10.14492798 | 7 | *CD300A, HAVCR2, HLA-DRB1, INPP5D, PTPN6, TNFRSF21, VSIG4* |
| GO:0050869 | Negative regulation of B cell activation | 0.00027 | 0.0075 | 1.6E–21 | 9.7E–21 | Group 5 | 15.625 | 5 | *CD300A, INHBA, INPP5D, SAMSN1, TNFRSF21* |
| GO:0030098 | Lymphocyte differentiation | 0.00000019 | 0.000015 | 1.6E–21 | 9.7E–21 | Group 5 | 6.727828979 | 22 | *CARD11, CD1D, CD28, CD4, CD74, CD86, CYP26B1, FCER1G, GPR183, IL6, INHBA, INPP5D, MERTK, NCKAP1L, NFAM1, PLCG2, PTPN22, PTPN6, PTPRC, SASH3, SPI1, SYK* |
| GO:0042129 | Regulation of T cell proliferation | 2.4E–13 | 2.5E–11 | 1.6E–21 | 9.7E–21 | Group 5 | 13.66459656 | 22 | *AIF1, CARD11, CD1D, CD209, CD28, CD4, CD86, GPAM, HAVCR2, HLA-DMB, HLA-DRB1, ICOSLG, IGF1, IL6, NCKAP1L, PTPN22, PTPN6, PTPRC, SASH3, SYK, TNFRSF21, VSIG4* |
| GO:0045639 | Positive regulation of myeloid cell differentiation | 0.0000045 | 0.00024 | 1.6E–21 | 9.7E–21 | Group 5 | 11.49425316 | 10 | *CA2, CD4, CD74, HLA-DRB1, HOXA5, INHBA, INPP5D, LIF, NCKAP1L, PF4* |
| GO:0050851 | Antigen receptor-mediated signaling pathway | 0.0000019 | 0.00011 | 1.6E–21 | 9.7E–21 | Group 5 | 6.574394226 | 19 | *CARD11, CD28, CD300A, CD4, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, LCP2, NCKAP1L, NFAM1, PLCG2, PTPN22, PTPN6, PTPRC, SYK, TNFRSF21* |
| GO:0050854 | Regulation of antigen receptor-mediated signaling pathway | 0.0022 | 0.02 | 1.6E–21 | 9.7E–21 | Group 5 | 10 | 5 | *CD300A, NFAM1, PTPN22, PTPN6, PTPRC* |
| GO:1902106 | Negative regulation of leukocyte differentiation | 0.0057 | 0.028 | 1.6E–21 | 9.7E–21 | Group 5 | 6.818181992 | 6 | *C1QC, CD74, INHBA, INPP5D, LILRA6, TMEM176B* |
| GO:0042130 | Negative regulation of T cell proliferation | 0.0031 | 0.018 | 1.6E–21 | 9.7E–21 | Group 5 | 9.259259224 | 5 | *HAVCR2, HLA-DRB1, PTPN6, TNFRSF21, VSIG4* |
| GO:0045619 | Regulation of lymphocyte differentiation | 0.0000032 | 0.00018 | 1.6E–21 | 9.7E–21 | Group 5 | 8.904109955 | 13 | *CARD11, CD28, CD74, CD86, CYP26B1, IL6, INHBA, INPP5D, NCKAP1L, NFAM1, PTPN6, SASH3, SYK* |
| GO:0030183 | B cell differentiation | 0.00036 | 0.0084 | 1.6E–21 | 9.7E–21 | Group 5 | 7.563024998 | 9 | *CARD11, GPR183, INHBA, INPP5D, NCKAP1L, NFAM1, PLCG2, PTPN6, SYK* |
| GO:0030217 | T cell differentiation | 0.000018 | 0.00083 | 1.6E–21 | 9.7E–21 | Group 5 | 6.696428776 | 15 | *CARD11, CD1D, CD28, CD4, CD74, CD86, CYP26B1, FCER1G, GPR183, IL6, NCKAP1L, PTPN22, PTPRC, SASH3, SYK* |
| GO:0034121 | Regulation of toll-like receptor signaling pathway | 0.0031 | 0.018 | 1.6E–21 | 9.7E–21 | Group 5 | 9.259259224 | 5 | *CD14, CD300A, F2RL1, LBP, PTPN22* |
| GO:0050852 | T cell receptor signaling pathway | 0.00000057 | 0.000039 | 1.6E–21 | 9.7E–21 | Group 5 | 8.333333015 | 16 | *CARD11, CD28, CD300A, CD4, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, LCP2, PLCG2, PTPN22, PTPN6, PTPRC, TNFRSF21* |
| GO:0050853 | B cell receptor signaling pathway | 0.00073 | 0.012 | 1.6E–21 | 9.7E–21 | Group 5 | 7.619047642 | 8 | *CD300A, NCKAP1L, NFAM1, PLCG2, PTPN22, PTPN6, PTPRC, SYK* |
| GO:0045577 | Regulation of B cell differentiation | 0.00000024 | 0.000018 | 1.6E–21 | 9.7E–21 | Group 5 | 28 | 7 | *CARD11, INHBA, INPP5D, NCKAP1L, NFAM1, PTPN6, SYK* |
| GO:0051209 | Release of sequestered calcium ion into cytosol | 0.0011 | 0.014 | 1.6E–21 | 9.7E–21 | Group 5 | 7.079646111 | 8 | *BDKRB1, HTR2A, JPH1, PLCG2, PTPN6, PTPRC, SNCA, TRPM2* |
| GO:0002757 | Immune response-activating signal transduction | 6.4E–15 | 7.2E–13 | 2.4E–21 | 1.2E–20 | Group 6 | 7.120253086 | 45 | *C3AR1, C5AR1, CARD11, CD14, CD180, CD209, CD28, CD300A, CD4, CD86, CLEC7A, CR1, F2RL1, FCER1G, FCGR1A, FCGR2A, FCGR3A, FGR, FPR1, FPR3, HAVCR2, HCK, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, ITGAM, LBP, LCP2, MARCO, NCKAP1L, NFAM1, PIK3AP1, PLCG2, PLPP4, PTPN22, PTPN6, PTPRC, RNASE1, S100A9, SYK, TLR8, TNFRSF21* |
| GO:0045807 | Positive regulation of endocytosis | 0.0000032 | 0.00018 | 2.4E–21 | 1.2E–20 | Group 6 | 9.677419662 | 12 | *ANGPT1, CCL2, CD14, F2RL1, FCER1G, ITGA2, MERTK, NCKAP1L, PLCG2, SLC11A1, SNCA, SYK* |
| GO:0051047 | Positive regulation of secretion | 0.00000043 | 0.000031 | 2.4E–21 | 1.2E–20 | Group 6 | 6.015037537 | 24 | *C1QTNF3, CD14, EDNRB, F2RL1, FCER1G, FGR, HAVCR2, HLA-DRB1, IGF1, IL33, IL6, INHBA, MMP12, P2RY1, PTAFR, PTPN22, S100A9, SNCA, SPP1, SYK, TLR8, TMEM27, TRPM2, VAMP8* |
| GO:0051048 | Negative regulation of secretion | 0.00000054 | 0.000037 | 2.4E–21 | 1.2E–20 | Group 6 | 7.9069767 | 17 | *ANGPT1, C1QTNF3, CD300A, CD74, CD84, F2RL1, IL33, IL6, INHBA, LIF, P2RY1, PTPN22, SNCA, SRGN, TLR8, TNFRSF21, VAMP8* |
| GO:0032496 | Response to lipopolysaccharide | 2.9E–13 | 2.9E–11 | 2.4E–21 | 1.2E–20 | Group 6 | 9.037900925 | 31 | *BDKRB1, C5AR1, CCL2, CD14, CD180, CD86, CSF2RB, CXCL5, CXCL6, CXCL8, EDNRB, HAVCR2, HCK, IL10RA, IL6, IRF8, LBP, LY86, MRC1, PCDHA6, PF4, PLCG2, PTAFR, PTPN22, S100A9, SLC11A1, SNCA, TNFRSF10C, TNFRSF10D, TNFRSF21, TREM2* |
| GO:0071219 | Cellular response to molecule of bacterial origin | 0.000000041 | 0.0000033 | 2.4E–21 | 1.2E–20 | Group 6 | 9.444444656 | 17 | *CCL2, CD14, CD180, CD86, CXCL8, EDNRB, HAVCR2, HCK, IL6, IRF8, LBP, LY86, MRC1, PTAFR, PTPN22, S100A9, TREM2* |
| GO:0033003 | Regulation of mast cell activation | 0.000009 | 0.00044 | 2.4E–21 | 1.2E–20 | Group 6 | 17.07317162 | 7 | *CD300A, CD84, FCER1G, FGR, PCDHA6, SYK, VAMP8* |
| GO:0045089 | Positive regulation of innate immune response | 0.00000036 | 0.000027 | 2.4E–21 | 1.2E–20 | Group 6 | 6.489675522 | 22 | *CARD11, CD14, CD180, CD1D, CD209, CD300A, CD86, CLEC7A, F2RL1, FCER1G, HAVCR2, HCK, ITGAM, LBP, MARCO, MMP12, PIK3AP1, PLCG2, PTPN22, S100A9, SYK, TLR8* |
| GO:0002429 | Immune response-activating cell surface receptor signaling pathway | 2.2E–11 | 0.000000002 | 2.4E–21 | 1.2E–20 | Group 6 | 7.053941727 | 34 | *C3AR1, C5AR1, CARD11, CD209, CD28, CD300A, CD4, CLEC7A, CR1, FCER1G, FCGR1A, FCGR2A, FCGR3A, FGR, FPR1, FPR3, HCK, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, LCP2, NCKAP1L, NFAM1, PLCG2, PLPP4, PTPN22, PTPN6, PTPRC, RNASE1, SYK, TNFRSF21* |
| GO:0050764 | Regulation of phagocytosis | 0.000000068 | 0.0000055 | 2.4E–21 | 1.2E–20 | Group 6 | 15.49295807 | 11 | *CCL2, CD300A, F2RL1, FCER1G, FGR, HCK, ITGA2, MERTK, NCKAP1L, SLC11A1, SYK* |
| GO:0050766 | Positive regulation of phagocytosis | 0.00003 | 0.0012 | 2.4E–21 | 1.2E–20 | Group 6 | 14.28571415 | 7 | *CCL2, F2RL1, FCER1G, ITGA2, MERTK, NCKAP1L, SLC11A1* |
| GO:0031663 | Lipopolysaccharide-mediated signaling pathway | 0.0000012 | 0.000081 | 2.4E–21 | 1.2E–20 | Group 6 | 15.25423717 | 9 | *CCL2, CD14, CD180, HCK, LBP, LY86, PTAFR, PTPN22, S100A9* |
| GO:0002758 | Innate immune response-activating signal transduction | 0.00000043 | 0.000031 | 2.4E–21 | 1.2E–20 | Group 6 | 6.944444656 | 20 | *CARD11, CD14, CD180, CD209, CD300A, CD86, CLEC7A, F2RL1, FCER1G, HAVCR2, HCK, ITGAM, LBP, MARCO, PIK3AP1, PLCG2, PTPN22, S100A9, SYK, TLR8* |
| GO:0002792 | Negative regulation of peptide secretion | 0.000072 | 0.0026 | 2.4E–21 | 1.2E–20 | Group 6 | 8.40336132 | 10 | *ANGPT1, C1QTNF3, CD74, F2RL1, IL33, IL6, PTPN22, SRGN, TLR8, TNFRSF21* |
| GO:0050663 | Cytokine secretion | 6.6E–10 | 0.000000057 | 2.4E–21 | 1.2E–20 | Group 6 | 10.20408154 | 20 | *ANGPT1, C1QTNF3, CARD11, CD14, F2RL1, FGR, GPAM, HAVCR2, HLA-DRB1, IL33, IL6, LCP2, MMP12, PTPN22, S100A9, SRGN, SYK, TLR8, TNFRSF21, TREM1* |
| GO:0002431 | Fc receptor mediated stimulatory signaling pathway | 0.00028 | 0.0073 | 2.4E–21 | 1.2E–20 | Group 6 | 6.586826324 | 11 | *FCER1G, FCGR1A, FCGR2A, FCGR3A, FGR, HCK, NCKAP1L, PLCG2, PLPP4, RNASE1, SYK* |
| GO:0038094 | Fc-gamma receptor signaling pathway | 0.00025 | 0.0073 | 2.4E–21 | 1.2E–20 | Group 6 | 6.666666508 | 11 | *FCER1G, FCGR1A, FCGR2A, FCGR3A, FGR, HCK, NCKAP1L, PLCG2, PLPP4, RNASE1, SYK* |
| GO:0050707 | Regulation of cytokine secretion | 0.000000014 | 0.0000012 | 2.4E–21 | 1.2E–20 | Group 6 | 10.11904716 | 17 | *ANGPT1, C1QTNF3, CD14, F2RL1, FGR, GPAM, HAVCR2, HLA-DRB1, IL33, IL6, MMP12, PTPN22, S100A9, SRGN, SYK, TLR8, TNFRSF21* |
| GO:0050714 | Positive regulation of protein secretion | 0.000012 | 0.00058 | 2.4E–21 | 1.2E–20 | Group 6 | 6.58436203 | 16 | *C1QTNF3, CD14, F2RL1, FGR, HAVCR2, HLA-DRB1, IGF1, IL33, IL6, MMP12, PTPN22, S100A9, SYK, TLR8, TMEM27, TRPM2* |
| GO:0050854 | Regulation of antigen receptor-mediated signaling pathway | 0.0022 | 0.02 | 2.4E–21 | 1.2E–20 | Group 6 | 10 | 5 | *CD300A, NFAM1, PTPN22, PTPN6, PTPRC* |
| GO:1903305 | Regulation of regulated secretory pathway | 0.0003 | 0.0075 | 2.4E–21 | 1.2E–20 | Group 6 | 7.758620739 | 9 | *CD300A, CD84, F2RL1, FCER1G, FGR, PTAFR, SYK, TMEM27, VAMP8* |
| GO:0002221 | Pattern recognition receptor signaling pathway | 0.0000062 | 0.00032 | 2.4E–21 | 1.2E–20 | Group 6 | 7.821228981 | 14 | *CD14, CD180, CD300A, CD86, CLEC7A, F2RL1, HAVCR2, ITGAM, LBP, MARCO, PIK3AP1, PTPN22, S100A9, TLR8* |
| GO:0050715 | Positive regulation of cytokine secretion | 0.0000071 | 0.00037 | 2.4E–21 | 1.2E–20 | Group 6 | 9.821428299 | 11 | *C1QTNF3, CD14, F2RL1, FGR, HAVCR2, IL33, MMP12, PTPN22, S100A9, SYK, TLR8* |
| GO:1903307 | Positive regulation of regulated secretory pathway | 0.000019 | 0.00085 | 2.4E–21 | 1.2E–20 | Group 6 | 15.21739101 | 7 | *F2RL1, FCER1G, FGR, PTAFR, SYK, TMEM27, VAMP8* |
| GO:0034121 | Regulation of toll-like receptor signaling pathway | 0.0031 | 0.018 | 2.4E–21 | 1.2E–20 | Group 6 | 9.259259224 | 5 | *CD14, CD300A, F2RL1, LBP, PTPN22* |
| GO:0043304 | Regulation of mast cell degranulation | 0.000012 | 0.00057 | 2.4E–21 | 1.2E–20 | Group 6 | 20.6896553 | 6 | *CD300A, CD84, FCER1G, FGR, SYK, VAMP8* |
| GO:0002224 | Toll-like receptor signaling pathway | 0.0000078 | 0.00039 | 2.4E–21 | 1.2E–20 | Group 6 | 8.888889313 | 12 | *CD14, CD180, CD300A, CD86, F2RL1, HAVCR2, ITGAM, LBP, PIK3AP1, PTPN22, S100A9, TLR8* |
| GO:0034142 | Toll-like receptor 4 signaling pathway | 0.000032 | 0.0012 | 2.4E–21 | 1.2E–20 | Group 6 | 17.64705849 | 6 | *CD14, F2RL1, ITGAM, LBP, PIK3AP1, PTPN22* |
| GO:0002757 | Immune response-activating signal transduction | 6.4E–15 | 7.2E–13 | 2.7E–24 | 2.1E–23 | Group 7 | 7.120253086 | 45 | *C3AR1, C5AR1, CARD11, CD14, CD180, CD209, CD28, CD300A, CD4, CD86, CLEC7A, CR1, F2RL1, FCER1G, FCGR1A, FCGR2A, FCGR3A, FGR, FPR1, FPR3, HAVCR2, HCK, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, ITGAM, LBP, LCP2, MARCO, NCKAP1L, NFAM1, PIK3AP1, PLCG2, PLPP4, PTPN22, PTPN6, PTPRC, RNASE1, S100A9, SYK, TLR8, TNFRSF21* |
| GO:0031294 | Lymphocyte costimulation | 2.1E–09 | 0.00000018 | 2.7E–24 | 2.1E–23 | Group 7 | 14.73684216 | 14 | *CARD11, CD28, CD4, CD86, EFNB2, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, ICOSLG, IL6, PTPN6, RNASE1* |
| GO:0042035 | Regulation of cytokine biosynthetic process | 0.000000087 | 0.0000069 | 2.7E–24 | 2.1E–23 | Group 7 | 12.14953232 | 13 | *CARD11, CD28, CD4, CD86, CYBB, IL6, INHBA, INPP5D, LBP, PTAFR, RNF128, SYK, TLR8* |
| GO:0051250 | Negative regulation of lymphocyte activation | 0.0000045 | 0.00024 | 2.7E–24 | 2.1E–23 | Group 7 | 9.375 | 12 | *CD300A, CD74, HAVCR2, HLA-DRB1, INHBA, INPP5D, MERTK, PTPN22, PTPN6, SAMSN1, TNFRSF21, VSIG4* |
| GO:0051251 | Positive regulation of lymphocyte activation | 2.2E–12 | 2.2E–10 | 2.7E–24 | 2.1E–23 | Group 7 | 8.645533562 | 30 | *AIF1, CARD11, CCL2, CD1D, CD28, CD4, CD74, CD86, EFNB2, GPAM, GPR183, HAVCR2, HLA-DMB, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, ICOSLG, IGF1, IL6, INPP5D, NCKAP1L, PTPN22, PTPN6, PTPRC, RNASE1, S100A9, SASH3, SYK* |
| GO:1903039 | Positive regulation of leukocyte cell-cell adhesion | 7.5E–15 | 8.3E–13 | 2.7E–24 | 2.1E–23 | Group 7 | 11.66666698 | 28 | *AIF1, CARD11, CCL2, CD1D, CD28, CD4, CD74, CD86, EFNB2, GPAM, HAVCR2, HLA-DMB, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, ICOSLG, IGF1, IL6, NCKAP1L, PTAFR, PTPN22, PTPN6, PTPRC, RNASE1, SASH3, SYK* |
| GO:1903706 | Regulation of hemopoiesis | 6.1E–10 | 0.000000054 | 2.7E–24 | 2.1E–23 | Group 7 | 7.831325531 | 26 | *C1QC, CA2, CARD11, CD28, CD4, CD74, CD86, CYP26B1, HLA-DRB1, HOXA5, HOXB8, IL6, INHBA, INPP5D, LIF, LILRA6, NCKAP1L, NFAM1, PF4, PTPN6, RBP1, SASH3, SPI1, SYK, TMEM176B, TYROBP* |
| GO:0002429 | Immune response-activating cell surface receptor signaling pathway | 2.2E–11 | 0.000000002 | 2.7E–24 | 2.1E–23 | Group 7 | 7.053941727 | 34 | *C3AR1, C5AR1, CARD11, CD209, CD28, CD300A, CD4, CLEC7A, CR1, FCER1G, FCGR1A, FCGR2A, FCGR3A, FGR, FPR1, FPR3, HCK, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, LCP2, NCKAP1L, NFAM1, PLCG2, PLPP4, PTPN22, PTPN6, PTPRC, RNASE1, SYK, TNFRSF21* |
| GO:0042098 | T cell proliferation | 8E–14 | 8.4E–12 | 2.7E–24 | 2.1E–23 | Group 7 | 12.8342247 | 24 | *AIF1, CARD11, CD1D, CD209, CD28, CD4, CD86, DOCK8, GPAM, HAVCR2, HLA-DMB, HLA-DRB1, ICOSLG, IGF1, IL6, NCKAP1L, PTPN22, PTPN6, PTPRC, SASH3, SLC11A1, SYK, TNFRSF21, VSIG4* |
| GO:0042100 | B cell proliferation | 0.0000011 | 0.000076 | 2.7E–24 | 2.1E–23 | Group 7 | 11.82795715 | 11 | *CARD11, CD180, CD300A, CD74, GPR183, INPP5D, NCKAP1L, PTPRC, S100A9, SASH3, TNFRSF21* |
| GO:0042108 | Positive regulation of cytokine biosynthetic process | 0.0000037 | 0.0002 | 2.7E–24 | 2.1E–23 | Group 7 | 13.43283558 | 9 | *CARD11, CD28, CD4, CD86, CYBB, LBP, PTAFR, SYK, TLR8* |
| GO:0046631 | Alpha-beta T cell activation | 0.00038 | 0.0085 | 2.7E–24 | 2.1E–23 | Group 7 | 7.5 | 9 | *CD28, CD300A, CD86, GPR183, IL6, NCKAP1L, PTPN22, SASH3, SYK* |
| GO:0050670 | Regulation of lymphocyte proliferation | 2.9E–15 | 3.2E–13 | 2.7E–24 | 2.1E–23 | Group 7 | 12.67605591 | 27 | *AIF1, CARD11, CD1D, CD209, CD28, CD300A, CD4, CD74, CD86, GPAM, GPR183, HAVCR2, HLA-DMB, HLA-DRB1, ICOSLG, IGF1, IL6, INPP5D, NCKAP1L, PTPN22, PTPN6, PTPRC, S100A9, SASH3, SYK, TNFRSF21, VSIG4* |
| GO:0050863 | Regulation of T cell activation | 1.6E–14 | 1.8E–12 | 2.7E–24 | 2.1E–23 | Group 7 | 9.696969986 | 32 | *AIF1, CARD11, CCL2, CD1D, CD209, CD28, CD300A, CD4, CD74, CD86, CYP26B1, EFNB2, GPAM, HAVCR2, HLA-DMB, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, ICOSLG, IGF1, IL6, NCKAP1L, PTPN22, PTPN6, PTPRC, RNASE1, SASH3, SYK, TNFRSF21, VSIG4* |
| GO:0050864 | Regulation of B cell activation | 0.000000016 | 0.0000013 | 2.7E–24 | 2.1E–23 | Group 7 | 10.05917168 | 17 | *CARD11, CD28, CD300A, CD74, GPR183, IL6, INHBA, INPP5D, NCKAP1L, NFAM1, PTPN6, PTPRC, S100A9, SAMSN1, SASH3, SYK, TNFRSF21* |
| GO:1903038 | Negative regulation of leukocyte cell-cell adhesion | 0.000097 | 0.0034 | 2.7E–24 | 2.1E–23 | Group 7 | 9 | 9 | *CD300A, CD74, ENC1, HAVCR2, HLA-DRB1, PTPN22, PTPN6, TNFRSF21, VSIG4* |
| GO:1903707 | Negative regulation of hemopoiesis | 0.00055 | 0.011 | 2.7E–24 | 2.1E–23 | Group 7 | 7.142857075 | 9 | *C1QC, CD74, HOXA5, HOXB8, INHBA, INPP5D, LILRA6, PF4, TMEM176B* |
| GO:1903708 | Positive regulation of hemopoiesis | 0.0000033 | 0.00019 | 2.7E–24 | 2.1E–23 | Group 7 | 8.235294342 | 14 | *CA2, CD4, CD74, CD86, HLA-DRB1, HOXA5, IL6, INHBA, INPP5D, LIF, NCKAP1L, PF4, SASH3, SYK* |
| GO:0002521 | Leukocyte differentiation | 4.3E–11 | 3.9E–09 | 2.7E–24 | 2.1E–23 | Group 7 | 6.882591248 | 34 | *C1QC, CA2, CARD11, CD1D, CD28, CD4, CD74, CD86, CYP26B1, F2RL1, FCER1G, GPR183, HLA-DRB1, IL6, INHBA, INPP5D, LIF, LILRA6, MERTK, NCKAP1L, NFAM1, PF4, PLCG2, PTPN22, PTPN6, PTPRC, RBP1, SASH3, SPI1, SYK, TMEM176B, TREM2, TRPM2, TYROBP* |
| GO:0030099 | Myeloid cell differentiation | 0.00000013 | 0.00001 | 2.7E–24 | 2.1E–23 | Group 7 | 6.628242016 | 23 | *C1QC, CA2, CD4, CD74, CD86, CDKN2B, F2RL1, GPR183, HLA-DRB1, HOXA5, HOXB7, HOXB8, INHBA, INPP5D, IRF8, LIF, LILRA6, NCKAP1L, PF4, PTPN6, RBP1, SPI1, TYROBP* |
| GO:0045637 | Regulation of myeloid cell differentiation | 0.00000043 | 0.000031 | 2.7E–24 | 2.1E–23 | Group 7 | 8.510638237 | 16 | *C1QC, CA2, CD4, CD74, HLA-DRB1, HOXA5, HOXB8, INHBA, INPP5D, LIF, LILRA6, NCKAP1L, PF4, RBP1, SPI1, TYROBP* |
| GO:0045646 | Regulation of erythrocyte differentiation | 0.0011 | 0.014 | 2.7E–24 | 2.1E–23 | Group 7 | 11.6279068 | 5 | *HOXA5, INHBA, INPP5D, NCKAP1L, SPI1* |
| GO:0050671 | Positive regulation of lymphocyte proliferation | 1.5E–12 | 1.4E–10 | 2.7E–24 | 2.1E–23 | Group 7 | 14.18439674 | 20 | *AIF1, CARD11, CD1D, CD28, CD4, CD74, CD86, GPAM, GPR183, HAVCR2, HLA-DMB, ICOSLG, IGF1, IL6, NCKAP1L, PTPN22, PTPRC, S100A9, SASH3, SYK* |
| GO:0050672 | Negative regulation of lymphocyte proliferation | 0.00027 | 0.0077 | 2.7E–24 | 2.1E–23 | Group 7 | 10.14492798 | 7 | *CD300A, HAVCR2, HLA-DRB1, INPP5D, PTPN6, TNFRSF21, VSIG4* |
| GO:0050869 | Negative regulation of B cell activation | 0.00027 | 0.0075 | 2.7E–24 | 2.1E–23 | Group 7 | 15.625 | 5 | *CD300A, INHBA, INPP5D, SAMSN1, TNFRSF21* |
| GO:0050871 | Positive regulation of B cell activation | 0.000029 | 0.0012 | 2.7E–24 | 2.1E–23 | Group 7 | 8.461538315 | 11 | *CARD11, CD28, CD74, GPR183, IL6, INPP5D, NCKAP1L, PTPRC, S100A9, SASH3, SYK* |
| GO:1902105 | Regulation of leukocyte differentiation | 3.4E–10 | 0.00000003 | 2.7E–24 | 2.1E–23 | Group 7 | 9.090909004 | 23 | *C1QC, CA2, CARD11, CD28, CD4, CD74, CD86, CYP26B1, HLA-DRB1, IL6, INHBA, INPP5D, LIF, LILRA6, NCKAP1L, NFAM1, PF4, PTPN6, RBP1, SASH3, SYK, TMEM176B, TYROBP* |
| GO:0030098 | Lymphocyte differentiation | 0.00000019 | 0.000015 | 2.7E–24 | 2.1E–23 | Group 7 | 6.727828979 | 22 | *CARD11, CD1D, CD28, CD4, CD74, CD86, CYP26B1, FCER1G, GPR183, IL6, INHBA, INPP5D, MERTK, NCKAP1L, NFAM1, PLCG2, PTPN22, PTPN6, PTPRC, SASH3, SPI1, SYK* |
| GO:0042129 | Regulation of T cell proliferation | 2.4E–13 | 2.5E–11 | 2.7E–24 | 2.1E–23 | Group 7 | 13.66459656 | 22 | *AIF1, CARD11, CD1D, CD209, CD28, CD4, CD86, GPAM, HAVCR2, HLA-DMB, HLA-DRB1, ICOSLG, IGF1, IL6, NCKAP1L, PTPN22, PTPN6, PTPRC, SASH3, SYK, TNFRSF21, VSIG4* |
| GO:0045638 | Negative regulation of myeloid cell differentiation | 0.00068 | 0.013 | 2.7E–24 | 2.1E–23 | Group 7 | 8.75 | 7 | *C1QC, HOXA5, HOXB8, INHBA, INPP5D, LILRA6, PF4* |
| GO:0045639 | Positive regulation of myeloid cell differentiation | 0.0000045 | 0.00024 | 2.7E–24 | 2.1E–23 | Group 7 | 11.49425316 | 10 | *CA2, CD4, CD74, HLA-DRB1, HOXA5, INHBA, INPP5D, LIF, NCKAP1L, PF4* |
| GO:0050851 | Antigen receptor-mediated signaling pathway | 0.0000019 | 0.00011 | 2.7E–24 | 2.1E–23 | Group 7 | 6.574394226 | 19 | *CARD11, CD28, CD300A, CD4, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, LCP2, NCKAP1L, NFAM1, PLCG2, PTPN22, PTPN6, PTPRC, SYK, TNFRSF21* |
| GO:0050854 | Regulation of antigen receptor-mediated signaling pathway | 0.0022 | 0.02 | 2.7E–24 | 2.1E–23 | Group 7 | 10 | 5 | *CD300A, NFAM1, PTPN22, PTPN6, PTPRC* |
| GO:1902106 | Negative regulation of leukocyte differentiation | 0.0057 | 0.028 | 2.7E–24 | 2.1E–23 | Group 7 | 6.818181992 | 6 | *C1QC, CD74, INHBA, INPP5D, LILRA6, TMEM176B* |
| GO:1902107 | Leukocyte chemotaxis | 0.0000084 | 0.00042 | 2.7E–24 | 2.1E–23 | Group 7 | 8.823529243 | 12 | *CA2, CD4, CD74, CD86, HLA-DRB1, IL6, INPP5D, LIF, NCKAP1L, PF4, SASH3, SYK* |
| GO:0002573 | Myeloid leukocyte differentiation | 0.0000012 | 0.00008 | 2.7E–24 | 2.1E–23 | Group 7 | 7.881773472 | 16 | *C1QC, CA2, CD4, CD74, CD86, F2RL1, GPR183, HLA-DRB1, INHBA, INPP5D, LIF, LILRA6, PF4, RBP1, SPI1, TYROBP* |
| GO:0002761 | Regulation of myeloid leukocyte differentiation | 0.000002 | 0.00012 | 2.7E–24 | 2.1E–23 | Group 7 | 10.08403397 | 12 | *C1QC, CA2, CD4, CD74, HLA-DRB1, INHBA, INPP5D, LIF, LILRA6, PF4, RBP1, TYROBP* |
| GO:0030890 | Positive regulation of B cell proliferation | 0.00001 | 0.00051 | 2.7E–24 | 2.1E–23 | Group 7 | 16.66666603 | 7 | *CARD11, CD74, GPR183, NCKAP1L, PTPRC, S100A9, SASH3* |
| GO:0042102 | Positive regulation of T cell proliferation | 7.1E–12 | 6.8E–10 | 2.7E–24 | 2.1E–23 | Group 7 | 16.34615326 | 17 | *AIF1, CARD11, CD1D, CD28, CD4, CD86, GPAM, HAVCR2, HLA-DMB, ICOSLG, IGF1, IL6, NCKAP1L, PTPN22, PTPRC, SASH3, SYK* |
| GO:0042130 | Negative regulation of T cell proliferation | 0.0031 | 0.018 | 2.7E–24 | 2.1E–23 | Group 7 | 9.259259224 | 5 | *HAVCR2, HLA-DRB1, PTPN6, TNFRSF21, VSIG4* |
| GO:0045619 | Regulation of lymphocyte differentiation | 0.0000032 | 0.00018 | 2.7E–24 | 2.1E–23 | Group 7 | 8.904109955 | 13 | *CARD11, CD28, CD74, CD86, CYP26B1, IL6, INHBA, INPP5D, NCKAP1L, NFAM1, PTPN6, SASH3, SYK* |
| GO:0045058 | T cell selection | 0.000026 | 0.0011 | 2.7E–24 | 2.1E–23 | Group 7 | 14.58333302 | 7 | *CARD11, CD1D, CD28, CD4, CD74, IL6, SYK* |
| GO:0030183 | B cell differentiation | 0.00036 | 0.0084 | 2.7E–24 | 2.1E–23 | Group 7 | 7.563024998 | 9 | *CARD11, GPR183, INHBA, INPP5D, NCKAP1L, NFAM1, PLCG2, PTPN6, SYK* |
| GO:0030217 | T cell differentiation | 0.000018 | 0.00083 | 2.7E–24 | 2.1E–23 | Group 7 | 6.696428776 | 15 | *CARD11, CD1D, CD28, CD4, CD74, CD86, CYP26B1, FCER1G, GPR183, IL6, NCKAP1L, PTPN22, PTPRC, SASH3, SYK* |
| GO:0002763 | Positive regulation of myeloid leukocyte differentiation | 0.00046 | 0.0097 | 2.7E–24 | 2.1E–23 | Group 7 | 11.11111069 | 6 | *CA2, CD4, CD74, HLA-DRB1, LIF, PF4* |
| GO:0045621 | Positive regulation of lymphocyte differentiation | 0.00092 | 0.013 | 2.7E–24 | 2.1E–23 | Group 7 | 8.333333015 | 7 | *CD74, CD86, IL6, INPP5D, NCKAP1L, SASH3, SYK* |
| GO:0050852 | T cell receptor signaling pathway | 0.00000057 | 0.000039 | 2.7E–24 | 2.1E–23 | Group 7 | 8.333333015 | 16 | *CARD11, CD28, CD300A, CD4, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, INPP5D, LCP2, PLCG2, PTPN22, PTPN6, PTPRC, TNFRSF21* |
| GO:0050853 | B cell receptor signaling pathway | 0.00073 | 0.012 | 2.7E–24 | 2.1E–23 | Group 7 | 7.619047642 | 8 | *CD300A, NCKAP1L, NFAM1, PLCG2, PTPN22, PTPN6, PTPRC, SYK* |
| GO:0030225 | Macrophage differentiation | 0.00071 | 0.012 | 2.7E–24 | 2.1E–23 | Group 7 | 12.82051277 | 5 | *C1QC, INHBA, LIF, PF4, SPI1* |
| GO:0045577 | Regulation of B cell differentiation | 0.00000024 | 0.000018 | 2.7E–24 | 2.1E–23 | Group 7 | 28 | 7 | *CARD11, INHBA, INPP5D, NCKAP1L, NFAM1, PTPN6, SYK* |
| GO:0045580 | Regulation of T cell differentiation | 0.00036 | 0.0084 | 2.7E–24 | 2.1E–23 | Group 7 | 7.563024998 | 9 | *CARD11, CD28, CD74, CD86, CYP26B1, IL6, NCKAP1L, SASH3, SYK* |
| GO:0046632 | Alpha-beta T cell differentiation | 0.0067 | 0.02 | 2.7E–24 | 2.1E–23 | Group 7 | 6.593406677 | 6 | *CD86, GPR183, IL6, NCKAP1L, SASH3, SYK* |
| GO:0035065 | Regulation of histone acetylation | 0.0026 | 0.018 | 2.7E–24 | 2.1E–23 | Group 7 | 9.615385056 | 5 | *LIF, MYOCD, NAP1L2, SNCA, SPI1* |
| GO:0014066 | Regulation of phosphatidylinositol 3-kinase signaling | 0.00014 | 0.0048 | NA | NA | None | 7.096774101 | 11 | *ANGPT1, CD28, CD86, F2RL1, FGR, IGF1, IL6, KDR, PIK3AP1, PTPN6, SOX9* |
| GO:0030260 | Entry into host cell | 0.00000022 | 0.000017 | NA | NA | None | 10.29411793 | 14 | *CD209, CD4, CD74, CD86, CR1, CXCL8, CXCR4, EFNB2, HLA-DRB1, HTR2A, ITGA2, MRC1, NECTIN4, VAMP8* |
| GO:0045844 | Positive regulation of striated muscle tissue development | 0.0079 | 0.015 | NA | NA | None | 7.462686539 | 5 | *CYP26B1, EFNB2, IGF1, MYOCD, TBX5* |
| GO:0048015 | Phosphatidylinositol-mediated signaling | 0.000072 | 0.0027 | NA | NA | None | 6.278027058 | 14 | *ANGPT1, CD28, CD86, F2RL1, FGR, HTR2A, IGF1, IL6, KDR, PIK3AP1, PIK3R5, PTAFR, PTPN6, SOX9* |
| GO:0048704 | Embryonic skeletal system morphogenesis | 0.0000014 | 0.00009 | NA | NA | None | 11.57894707 | 11 | *ALX1, HOXA2, HOXA3, HOXA5, HOXA6, HOXB5, HOXB6, HOXB7, HOXB8, MDFI, SATB2* |
| GO:0048705 | Skeletal system morphogenesis | 0.00000065 | 0.000044 | NA | NA | None | 7.798165321 | 17 | *ALX1, COL10A1, CYP26B1, FBN2, HOXA2, HOXA3, HOXA5, HOXA6, HOXB5, HOXB6, HOXB7, HOXB8, MDFI, RARB, SATB2, SOX9, STC1* |
| GO:0051153 | Regulation of striated muscle cell differentiation | 0.0025 | 0.02 | NA | NA | None | 7 | 7 | *BMP2, CCL8, CD53, CYP26B1, EFNB2, IGF1, MYOCD* |
| GO:0097028 | Dendritic cell differentiation | 0.00013 | 0.0044 | NA | NA | None | 13.95348835 | 6 | *CD86, F2RL1, SPI1, TMEM176B, TREM2, TRPM2* |
| GO:1903725 | Regulation of phospholipid metabolic process | 0.0019 | 0.019 | NA | NA | None | 8.450704575 | 6 | *ADGRF5, APOC2, FGR, HTR2A, PIK3R5, RNASE1* |
| GO:2000107 | Negative regulation of leukocyte apoptotic process | 0.00024 | 0.0072 | NA | NA | None | 12.5 | 6 | *CD74, DOCK8, FCER1G, GPAM, MERTK, S100A9* |

GO:ID: gene ontology term ID (biological process); GO term: name of gene ontology term; term P value: P value of enrichment test of the term; term corrected-P value: corrected P value of enrichment test of the term; group P value: P value of the group; group corrected P value: corrected P value of the group; GO groups: group ID of the term. “none” denotes unclustered terms; % associated genes: the percentage of genes in the gene list found to be associated with the term compared to all genes associated with the term; Nr. genes: the number of genes in the gene list found to be associated with the term; associated genes found: genes in the gene list found to be associated with the term. GO, gene ontology.