Five hundred and forty-four down-regulated gene sets in ADSCs from diseased sides compared to normal sides revealed by gene set enrichment analysis

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| Group | ID | Description | Set size | Enrichment score | NES | P value | P.adjust | leading\_edge | core\_enrichment |
| G1 | GO:0001568 | Blood vessel development | 475 | –0.439121524 | –1.749978145 | 0.001218027 | 0.023352669 | tags =29%, list =10%, signal =27% | *EGFL7/CHRNA7/ATP7A/RSPO3/SMO/GPI/MMP19/EPHB2/PROX1/ARHGAP22/TGFB1/ZMIZ1/LEP/ITGB1/ZFPM2/LTBP1/C19orf10/HIF1A/ROBO1/PDGFRA/FLT1/PLCG1/PTPRB/FN1/PDGFA/EPAS1/TSPAN12/MYH10/HIPK2/ITGA5/TGFBR2/COL15A1/VASH2/PTN/GPR56/EGLN1/RAMP1/HEY1/SERPINE1/RORA/PDGFB/PTK7/VEGFA/HSPB1/NKX3-1/COL4A2/GATA6/CALCRL/PAX6/B4GALT1/COL3A1/FAP/PTGS2/F3/ITGB3/MFGE8/GPC3/NOTCH3/RUNX1/COL4A1/CTGF/SOX4/ANGPTL4/HAND2/EPGN/SFRP1/TBX3/ITGB2/VAV3/EPHA2/FGF2/ANTXR1/HPGD/PCSK5/FOXO1/MDM2/XDH/PDE3B/ADAM8/PRICKLE1/FZD8/IL18/ACTA2/LOXL2/SPARC/HOXA7/BAI1/MEIS1/SAT1/CDH2/HMOX1/MYLK/WNT11/RGCC/EYA1/CHD7/LYL1/EDNRA/STRA6/IL1B/NRP2/ANGPT4/WNT5A/SRPX2/NRCAM/HAS2/APOE/HOXB3/SULF1/ANGPT1/TIE1/NDNF/EFNB2/MYOCD/CCL2/PRKCB/C5AR1/IL1A/ENPEP/SERPINB7/IL6/SYK/C3AR1/STAB1/CYBB/SPI1/TBX5/PF4/KDR/MCAM/FOXS1/HOXA3/HOXA5/SCG2/IL8/PITX2* |
| G1 | GO:0001525 | Angiogenesis | 337 | –0.438480521 | –1.710347527 | 0.00128041 | 0.023352669 | tags =27%, list =13%, signal =24% | *HIF1A/ROBO1/PDGFRA/FLT1/PLCG1/PTPRB/FN1/PDGFA/EPAS1/TSPAN12/HIPK2/ITGA5/TGFBR2/COL15A1/VASH2/PTN/GPR56/EGLN1/RAMP1/HEY1/SERPINE1/RORA/VEGFA/HSPB1/COL4A2/GATA6/CALCRL/B4GALT1/FAP/PTGS2/F3/ITGB3/MFGE8/NOTCH3/RUNX1/COL4A1/CTGF/ANGPTL4/HAND2/EPGN/SFRP1/ITGB2/VAV3/EPHA2/FGF2/PDE3B/ADAM8/FZD8/IL18/LOXL2/SPARC/HOXA7/BAI1/MEIS1/SAT1/HMOX1/RGCC/EDNRA/IL1B/NRP2/ANGPT4/WNT5A/SRPX2/NRCAM/HOXB3/SULF1/ANGPT1/TIE1/NDNF/EFNB2/CCL2/PRKCB/C5AR1/IL1A/ENPEP/IL6/SYK/C3AR1/STAB1/CYBB/SPI1/PF4/KDR/MCAM/HOXA3/HOXA5/SCG2/IL8/PITX2* |
| G1 | GO:0001523 | Retinoid metabolic process | 53 | –0.5986337 | –1.858153374 | 0.001550388 | 0.023352669 | tags =40%, list =12%, signal =35% | *AKR1C1/GPC4/ALDH1A3/SDC1/GPC2/RDH10/ADH4/CRABP2/GPC3/RBP4/DGAT2/DHRS9/DHRS3/STRA6/LPL/APOE/CYP26B1/AKR1B10/RBP1/APOC2* |
| G1 | GO:0001774 | Microglial cell activation | 11 | –0.849570257 | –1.872748635 | 0.001805054 | 0.024097005 | tags =64%, list =7%, signal =59% | *CLU/TLR8/TLR7/AIF1/IL33/SNCA* |
| G1 | GO:0001501 | Skeletal system development | 392 | –0.390023533 | –1.536059072 | 0.0025 | 0.030326036 | tags =27%, list =15%, signal =24% | *SERPINH1/SPNS2/IMPAD1/LEPRE1/HOXC5/TGFB1/HYAL2/LEP/MAPK3/JAG2/INHA/PTGER4/HIF1A/GSC/CSRNP1/PDGFRA/TIMP1/HOXD3/FAM101B/WNT5B/HOXC6/SERP1/HHIP/TGFBR2/RP11-834C11.14/ATP6AP1/GLI2/HOXD1/ACVR2A/HOXC9/EN1/GDF11/PAPSS2/COL5A2/COL11A2/RDH10/HOXB2/COL27A1/COL3A1/COL11A1/HSD17B1/HOXA9/RUNX1/CTGF/SOX4/HAND2/SFRP1/TBX3/HAPLN1/EPHA2/FGF2/RBP4/PCSK5/SCIN/VCAN/ADAMTS12/MMP9/SNAI1/LOXL2/SPARC/HOXA7/ZFPM1/MEIS1/HOXB4/MMP16/WNT11/EYA1/CHD7/DHRS3/MSX2/SIGLEC15/HOXC8/MGP/WNT5A/HAS2/TGFB3/MDFI/HOXB3/SULF1/CYP26B1/PTPN6/GDF6/ACP5/RUNX3/HOXB5/FBN2/PTPRC/EXTL1/SOX9/RARB/CMKLR1/SATB2/STC1/HOXB7/HOXB6/COL10A1/IGF1/TYROBP/ALX1/HOXA6/HOXA3/BMP2/HOXA2/HOXA5/PITX2/HOXB8* |
| G1 | GO:0001667 | Ameboidal-type cell migration | 265 | –0.393348844 | –1.50647722 | 0.002642008 | 0.030326036 | tags =17%, list =10%, signal =16% | *TNS1/FERMT1/PTP4A3/PDGFB/VEGFA/HSPB1/ARSB/ARHGDIB/RET/FAP/PTGS2/ITGB3/GDNF/DPP4/HAND2/ITGB2/EPHA2/FGF2/MMP9/HBEGF/PRR5L/LOXL2/SPARC/WNT11/RGCC/NRP2/ANGPT4/WNT5A/SRPX2/HAS2/PTPRR/APOE/ANGPT1/EFNB2/ITGA2/SOX9/STC1/SEMA6B/KDR/EDNRB/ALX1/HAS1/SCG2/PITX2* |
| G1 | GO:0001706 | Endoderm formation | 44 | –0.574258305 | –1.697851654 | 0.004823151 | 0.038245256 | tags =36%, list =12%, signal =32% | *ITGA5/ITGB5/DUSP6/COL5A2/COL4A2/GATA6/MMP15/COL11A1/DUSP4/ITGB2/MMP9/VTN/COL7A1/MMP8/INHBA* |
| G1 | GO:0001754 | Eye photoreceptor cell differentiation | 25 | –0.641185693 | –1.712517558 | 0.004942339 | 0.038529311 | tags =40%, list =17%, signal =33% | *PDE6C/GNAT2/SOX8/PTN/VEGFA/PAX6/MYO7A/SDK2/SOX9* |
| G1 | GO:0001704 | Formation of primary germ layer | 93 | –0.446824546 | –1.504339985 | 0.006125574 | 0.04452057 | tags =27%, list =12%, signal =24% | *ITGA5/ITGB5/DUSP6/COL5A2/COL4A2/GATA6/MMP15/COL11A1/ITGB3/DUSP4/ITGB2/EPHA2/MMP9/SNAI1/FZD7/WNT11/EYA1/VTN/COL7A1/WNT5A/ITGA2/EYA2/MMP8/INHBA* |
| G10 | GO:0002694 | Regulation of leukocyte activation | 315 | –0.552834451 | –2.145727548 | 0.001282051 | 0.023352669 | tags =25%, list =6%, signal =24% | *RASGRP1/MILR1/RORA/BTK/MICA/TNFSF4/STXBP2/DPP4/UNC13D/SFRP1/VAV3/LAT/PRKCZ/ADAM8/CORO1A/CDKN1A/IL18/CD83/MNDA/HMOX1/LST1/CAMK4/HLA-DPA1/IL1B/LYN/CD300A/WNT5A/IL36B/TBC1D10C/INPP5D/CYP26B1/PAG1/F2RL1/IL1RL1/PTPN6/HAVCR2/VAMP8/EFNB2/NCKAP1L/CD1D/CCL2/FGR/PTPN22/TNFRSF21/PTPRC/LBP/CD86/CD4/GPAM/SASH3/NFAM1/SAMSN1/MERTK/IL6/CD28/SYK/AIF1/PTAFR/CD84/GPR183/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/CD209/INHBA/FCER1G/IGF1/VSIG4/GPR116/HLA-DQB1/HLA-DRB1/HLA-DRB5/IL33/CD74/SNCA/HLA-DRA* |
| G10 | GO:0002521 | Leukocyte differentiation | 333 | –0.503394723 | –1.962393867 | 0.00128866 | 0.023352669 | tags =29%, list =14%, signal =25% | *TUSC2/CEBPB/LEP/JAG2/ITGB1/LGALS9/INHA/PTGER4/FSTL3/HLA-DOA/IL11/TNFRSF11A/TNFSF9/SATB1/SPN/IL15/TFRC/BATF2/TLR4/TGFBR2/PREX1/CCR1/ATP6AP1/GLI2/IL2RA/DOCK2/CSF1R/RASGRP1/RORA/VEGFA/IFNE/BTK/SH3PXD2A/TSPAN2/TNFSF4/ITM2A/GPC3/RUNX1/SOX4/SFRP1/EPHA2/RSAD2/DCSTAMP/PRKCZ/MMP9/ADAM8/FZD8/FZD7/IL18/CD83/HOXA7/ZFPM1/TNFSF8/TPD52/CAMK4/CHD7/LYL1/SIGLEC15/TMEM176A/LILRB4/LYN/BLNK/IL36B/LILRA6/PLCG2/CA2/INPP5D/CYP26B1/TMEM176B/F2RL1/PTPN6/NCKAP1L/CD1D/PTPN22/PTPRC/TREM2/CD86/CD4/SASH3/NFAM1/MERTK/IL6/CD28/SYK/GPR183/CARD11/SPI1/INHBA/FCER1G/PF4/LIF/TYROBP/CD74/C1QC* |
| G10 | GO:0002683 | Negative regulation of immune system process | 274 | –0.515703775 | –1.983206414 | 0.001295337 | 0.023352669 | tags =18%, list =4%, signal =17% | *A2M/HOXA7/ZFPM1/MEIS1/MNDA/HMOX1/LST1/CR1/PADI2/TMEM176A/LILRB4/LYN/CD300A/LILRA6/TGFB3/TBC1D10C/INPP5D/ANGPT1/PAG1/TMEM176B/F2RL1/IL1RL1/PTPN6/HAVCR2/CCL2/PTPN22/TNFRSF21/PTPRC/PIK3AP1/CD86/GPAM/SOX9/SAMSN1/MERTK/CD14/CD84/HIST1H4H/INHBA/FCER1G/PF4/VSIG4/GPR116/IL33/CD74/HOXA5/C1QC/HOXB8* |
| G10 | GO:0002697 | Regulation of immune effector process | 229 | –0.490428426 | –1.86488756 | 0.001321004 | 0.023352669 | tags =24%, list =9%, signal =22% | *DOCK2/RAC2/RASGRP1/BTK/CADM1/SPON2/CFH/MICA/TNFSF4/STXBP2/UNC13D/RBP4/RSAD2/PRKCZ/IL18/DUSP10/A2M/WAS/C7/CFI/HMOX1/AC005013.1/CR1/VTN/IL1B/LYN/CD300A/WNT5A/TGFB3/ANGPT1/F2RL1/PTPN6/HAVCR2/VAMP8/CCL2/FGR/PTPRC/LBP/CD86/CD4/C5AR1/SASH3/IL6/CD28/SYK/PTAFR/C3AR1/CD84/HCK/HLA-DMB/FCER1G/IL33/CD74* |
| G10 | GO:0002696 | Positive regulation of leukocyte activation | 206 | –0.572871337 | –2.158999482 | 0.001349528 | 0.023352669 | tags =23%, list =6%, signal =22% | *VAV3/PRKCZ/ADAM8/CORO1A/CDKN1A/IL18/CD83/HLA-DPA1/IL1B/LYN/WNT5A/IL36B/INPP5D/F2RL1/IL1RL1/PTPN6/HAVCR2/VAMP8/EFNB2/NCKAP1L/CD1D/CCL2/FGR/PTPRC/LBP/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/PTAFR/GPR183/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/FCER1G/IGF1/HLA-DQB1/HLA-DRB1/HLA-DRB5/IL33/CD74/HLA-DRA* |
| G10 | GO:0002573 | Myeloid leukocyte differentiation | 144 | –0.519874436 | –1.87150618 | 0.00141844 | 0.023352669 | tags =27%, list =14%, signal =23% | *CEBPB/INHA/FSTL3/TNFRSF11A/TFRC/BATF2/TLR4/TGFBR2/CCR1/ATP6AP1/CSF1R/VEGFA/SH3PXD2A/TSPAN2/GPC3/RUNX1/SFRP1/EPHA2/DCSTAMP/MMP9/HOXA7/ZFPM1/CAMK4/SIGLEC15/LILRB4/LYN/LILRA6/CA2/INPP5D/F2RL1/CD86/GPR183/SPI1/INHBA/PF4/LIF/TYROBP/C1QC* |
| G10 | GO:0002685 | Regulation of leukocyte migration | 108 | –0.630352201 | –2.172668194 | 0.001470588 | 0.023352669 | tags =37%, list =10%, signal =33% | *CXCL2/GCSAM/RAC2/GCSAML/SERPINE1/VEGFA/PLCB1/CXCL14/ADAM8/HOXA7/HMOX1/PADI2/LYN/CD300A/WNT5A/F2RL1/BDKRB1/NCKAP1L/CCL2/ITGA2/LBP/C5AR1/IL1A/IL6/AIF1/PTAFR/CCL8/CMKLR1/C3AR1/CXCL1/PF4/CXCL6/CXCL3/PLA2G7/IL33/CD74/PLVAP/CXCL5/IL8* |
| G10 | GO:0002699 | Positive regulation of immune effector process | 108 | –0.588534167 | –2.02853177 | 0.001470588 | 0.023352669 | tags =31%, list =9%, signal =28% | *RASGRP1/BTK/CADM1/SPON2/TNFSF4/STXBP2/UNC13D/RBP4/RSAD2/PRKCZ/IL18/HMOX1/IL1B/LYN/CD300A/WNT5A/F2RL1/VAMP8/CCL2/FGR/LBP/CD86/SASH3/IL6/CD28/SYK/PTAFR/CD84/HLA-DMB/FCER1G/IL33/CD74* |
| G10 | GO:0002703 | Regulation of leukocyte mediated immunity | 107 | –0.511482634 | –1.76015583 | 0.001477105 | 0.023352669 | tags =36%, list =15%, signal =30% | *ARRB2/TGFB1/LEP/BST2/LGALS9/SPN/TFRC/TLR4/RAC2/RASGRP1/BTK/CADM1/MICA/TNFSF4/STXBP2/UNC13D/RSAD2/PRKCZ/WAS/HMOX1/CR1/IL1B/LYN/CD300A/F2RL1/PTPN6/HAVCR2/VAMP8/FGR/PTPRC/SASH3/IL6/CD28/SYK/PTAFR/CD84/FCER1G* |
| G10 | GO:0002576 | Platelet degranulation | 79 | –0.518289394 | –1.716234007 | 0.001531394 | 0.023352669 | tags =43%, list =19%, signal =35% | *ACTN1/TGFB2/THBS1/STXBP1/GAS6/CYB5R1/TGFB1/TF/TIMP1/FN1/PDGFA/FAM3C/ALDOA/SERPINE1/PDGFB/VEGFA/VWF/P2RX1/ITGB3/A2M/SPARC/CLU/ISLR/LYN/TGFB3/SRGN/F13A1/PLEK/SYK/PCDH7/FCER1G/PF4/IGF1* |
| G10 | GO:0002695 | Negative regulation of leukocyte activation | 96 | –0.572778531 | –1.933525927 | 0.001533742 | 0.023352669 | tags =33%, list =16%, signal =28% | *PELI1/JAK3/TGFB1/CEBPB/LGALS9/INHA/SPN/IL2RA/MILR1/MICA/TNFSF4/SFRP1/MNDA/HMOX1/LST1/LYN/CD300A/TBC1D10C/INPP5D/PAG1/PTPN6/HAVCR2/PTPN22/TNFRSF21/SAMSN1/MERTK/CD84/INHBA/VSIG4/GPR116/CD74* |
| G10 | GO:0002526 | Acute inflammatory response | 80 | –0.53742531 | –1.773601 | 0.001540832 | 0.023352669 | tags =28%, list =8%, signal =25% | *CFH/B4GALT1/TNFSF4/PTGS2/F3/ADAM8/PTGER3/A2M/C7/CFI/CR1/VTN/IL1B/LBP/C5AR1/IL1A/IL6/C3AR1/FCER1G/EDNRB/CD163* |
| G10 | GO:0002698 | Negative regulation of immune effector process | 70 | –0.530222137 | –1.711949734 | 0.001545595 | 0.023352669 | tags =30%, list =15%, signal =26% | *ARRB2/TGFB1/BST2/LGALS9/SPN/IL2RA/MICA/TNFSF4/DUSP10/A2M/HMOX1/CR1/CD300A/TGFB3/ANGPT1/PTPN6/HAVCR2/PTPRC/CD84/IL33* |
| G10 | GO:0002700 | Regulation of production of molecular mediator of immune response | 69 | –0.573963127 | –1.845588738 | 0.001545595 | 0.023352669 | tags =35%, list =8%, signal =32% | *JAK3/TGFB1/BST2/TFRC/TLR4/BTK/SPON2/TNFSF4/RBP4/RSAD2/PRKCZ/HMOX1/AC005013.1/WNT5A/TGFB3/ANGPT1/F2RL1/SASH3/IL6/CD28/FCER1G/IL33/CD74* |
| G10 | GO:0002688 | Regulation of leukocyte chemotaxis | 66 | –0.650394917 | –2.07021373 | 0.001550388 | 0.023352669 | tags =30%, list =3%, signal =29% | *LYN/WNT5A/F2RL1/NCKAP1L/CCL2/LBP/C5AR1/IL6/AIF1/CMKLR1/C3AR1/CXCL1/PF4/CXCL6/CXCL3/PLA2G7/CD74/CXCL5/IL8* |
| G10 | GO:0002690 | Positive regulation of leukocyte chemotaxis | 54 | –0.717688565 | –2.227355932 | 0.001550388 | 0.023352669 | tags =33%, list =3%, signal =33% | *F2RL1/NCKAP1L/CCL2/LBP/C5AR1/IL6/AIF1/CMKLR1/C3AR1/CXCL1/PF4/CXCL6/CXCL3/PLA2G7/CD74/CXCL5/IL8* |
| G10 | GO:0002687 | Positive regulation of leukocyte migration | 75 | –0.70588195 | –2.306019132 | 0.0015625 | 0.023352669 | tags =41%, list =3%, signal =40% | *CXCL2/RAC2/SERPINE1/VEGFA/CXCL14/ADAM8/WNT5A/F2RL1/BDKRB1/NCKAP1L/CCL2/ITGA2/LBP/C5AR1/IL1A/IL6/AIF1/PTAFR/CCL8/CMKLR1/C3AR1/CXCL1/PF4/CXCL6/CXCL3/PLA2G7/CD74/PLVAP/CXCL5/IL8* |
| G10 | GO:0002705 | Positive regulation of leukocyte mediated immunity | 60 | –0.528169537 | –1.65693843 | 0.001574803 | 0.023352669 | tags =27%, list =9%, signal =24% | *BTK/CADM1/TNFSF4/RSAD2/PRKCZ/IL1B/F2RL1/VAMP8/FGR/SASH3/IL6/CD28/SYK/PTAFR/FCER1G* |
| G10 | GO:0002718 | Regulation of cytokine production involved in immune response | 41 | –0.647389123 | –1.905598493 | 0.001612903 | 0.023352669 | tags =49%, list =15%, signal =41% | *JAK3/TGFB1/BST2/TLR4/BTK/SPON2/TNFSF4/RSAD2/PRKCZ/HMOX1/AC005013.1/WNT5A/TGFB3/ANGPT1/F2RL1/SASH3/IL6/FCER1G/CD74* |
| G10 | GO:0002673 | Regulation of acute inflammatory response | 46 | –0.576219184 | –1.726398904 | 0.003205128 | 0.030486975 | tags =35%, list =8%, signal =32% | *CFH/PTGS2/ADAM8/PTGER3/A2M/C7/CFI/CR1/VTN/IL1B/C5AR1/IL6/C3AR1/FCER1G/EDNRB* |
| G10 | GO:0002702 | Positive regulation of production of molecular mediator of immune response | 45 | –0.593601411 | –1.768537365 | 0.003220612 | 0.030486975 | tags =33%, list =8%, signal =31% | *TLR4/SPON2/TNFSF4/RBP4/RSAD2/PRKCZ/WNT5A/F2RL1/SASH3/IL6/CD28/FCER1G/IL33/CD74* |
| G10 | GO:0002720 | Positive regulation of cytokine production involved in immune response | 25 | –0.650613922 | –1.737699043 | 0.003294893 | 0.03079065 | tags =44%, list =8%, signal =41% | *SPON2/TNFSF4/RSAD2/PRKCZ/WNT5A/F2RL1/SASH3/IL6/FCER1G/CD74* |
| G10 | GO:0002532 | Production of molecular mediator involved in inflammatory response | 31 | –0.635342105 | –1.76718343 | 0.003322259 | 0.03079065 | tags =45%, list =14%, signal =39% | *C5orf30/TLR4/IL1R2/SERPINE1/P2RX1/BTK/DUSP10/LYN/VAMP8/LBP/SYK/ALOX5/FCER1G* |
| G10 | GO:0002548 | Monocyte chemotaxis | 27 | –0.638108424 | –1.722849992 | 0.003338898 | 0.030830257 | tags =52%, list =13%, signal =45% | *TNFRSF11A/CCR1/SERPINE1/PDGFB/LYN/CCL26/CCL22/CCL2/IL6/AIF1/CCL8/CCL13/PLA2G7* |
| G10 | GO:0002701 | Negative regulation of production of molecular mediator of immune response | 18 | –0.690730541 | –1.726441518 | 0.005181347 | 0.039554788 | tags =44%, list =15%, signal =38% | *JAK3/TGFB1/BST2/HMOX1/TGFB3/ANGPT1/IL33* |
| G100 | GO:1903037 | Regulation of leukocyte cell-cell adhesion | 216 | –0.532032113 | –2.008860132 | 0.001347709 | 0.023352669 | tags =21%, list =6%, signal =20% | *LAT/PRKCZ/ADAM8/CORO1A/IL18/CD83/CAMK4/HLA-DPA1/IL1B/LYN/CD300A/IL36B/HAS2/CYP26B1/PAG1/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/PTAFR/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/CD209/IGF1/VSIG4/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G100 | GO:1901342 | Regulation of vasculature development | 181 | –0.466997556 | –1.721709124 | 0.001396648 | 0.023352669 | tags =29%, list =10%, signal =27% | *HIF1A/FLT1/PLCG1/TSPAN12/HIPK2/ITGA5/TGFBR2/VASH2/PTN/EGLN1/HEY1/SERPINE1/PDGFB/VEGFA/HSPB1/COL4A2/GATA6/PTGS2/F3/RUNX1/ANGPTL4/SFRP1/ITGB2/EPHA2/FGF2/XDH/PDE3B/SPARC/BAI1/HMOX1/RGCC/IL1B/ANGPT4/WNT5A/SRPX2/SULF1/TIE1/EFNB2/MYOCD/CCL2/PRKCB/C5AR1/IL1A/SERPINB7/IL6/C3AR1/STAB1/CYBB/PF4/KDR/HOXA5/IL8* |
| G100 | GO:1902105 | Regulation of leukocyte differentiation | 179 | –0.513384518 | –1.888984956 | 0.00140056 | 0.023352669 | tags =30%, list =15%, signal =26% | *JAK3/TGFB1/CEBPB/LGALS9/INHA/FSTL3/HLA-DOA/TNFSF9/IL15/TLR4/TGFBR2/CCR1/ATP6AP1/GLI2/IL2RA/RASGRP1/BTK/TNFSF4/RUNX1/SFRP1/DCSTAMP/PRKCZ/ADAM8/IL18/CD83/HOXA7/ZFPM1/CAMK4/SIGLEC15/TMEM176A/LILRB4/LYN/IL36B/LILRA6/CA2/INPP5D/CYP26B1/TMEM176B/PTPN6/NCKAP1L/CD86/SASH3/NFAM1/IL6/CD28/SYK/CARD11/INHBA/PF4/LIF/TYROBP/CD74/C1QC* |
| G100 | GO:1903039 | Positive regulation of leukocyte cell-cell adhesion | 150 | –0.597849524 | –2.145869956 | 0.001436782 | 0.023352669 | tags =31%, list =6%, signal =30% | *SPN/IL15/TFRC/TGFBR2/HLA-DPB1/GLI2/IL2RA/RASGRP1/TNFSF4/DPP4/PRKCZ/ADAM8/CORO1A/IL18/CD83/HLA-DPA1/IL1B/LYN/IL36B/HAS2/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/PTAFR/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/IGF1/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G100 | GO:1903169 | Regulation of calcium ion transmembrane transport | 85 | –0.510624359 | –1.698593401 | 0.001517451 | 0.023352669 | tags =29%, list =17%, signal =25% | *CAPN3/HTT/C19orf26/TGFB1/DMD/STIM2/ADRA2A/PLCG1/EHD3/OPRL1/DRD4/F2RL3/ATP1B1/CORO1A/CHD7/JPH2/LYN/TSPAN13/PLCG2/PTPN6/BDKRB1/PLN/JPH1/SNCA* |
| G100 | GO:1902656 | Calcium ion import into cytosol | 77 | –0.529888525 | –1.745406546 | 0.00154321 | 0.023352669 | tags =21%, list =6%, signal =20% | *FGF2/CORO1A/CHD7/JPH2/LYN/PLCG2/CCR5/PTPN6/BDKRB1/PTPRC/PLN/JPH1/HTR2A/TRPM2/SNCA* |
| G100 | GO:1903305 | Regulation of regulated secretory pathway | 77 | –0.537174403 | –1.769405592 | 0.00154321 | 0.023352669 | tags =35%, list =17%, signal =29% | *CDK5/C19orf26/SYT15/CACNA1A/LGALS9/ADRA2A/RIMS3/RAC2/NLGN1/SYTL1/STXBP2/UNC13D/SYTL3/SYN1/RIMS1/HMOX1/TMEM27/LYN/CD300A/F2RL1/VAMP8/FGR/SYK/PTAFR/CD84/FCER1G* |
| G100 | GO:1902106 | Negative regulation of leukocyte differentiation | 58 | –0.596975752 | –1.865781233 | 0.001574803 | 0.023352669 | tags =22%, list =7%, signal =21% | *SFRP1/HOXA7/ZFPM1/TMEM176A/LILRB4/LYN/LILRA6/INPP5D/TMEM176B/INHBA/CD74/C1QC* |
| G100 | GO:1900543 | Negative regulation of purine nucleotide metabolic process | 34 | –0.639234843 | –1.835786642 | 0.001623377 | 0.023352669 | tags =38%, list =14%, signal =33% | *ADRA2A/DDIT4/OPRL1/EGLN1/C12orf5/APLP1/DRD4/PID1/FBP1/EDNRA/EDNRB/SNCA* |
| G100 | GO:1902622 | Regulation of neutrophil migration | 25 | –0.775379249 | –2.07092983 | 0.001647446 | 0.023352669 | tags =48%, list =5%, signal =46% | *RAC2/ADAM8/NCKAP1L/LBP/C5AR1/IL1A/C3AR1/CXCL1/CXCL3/CD74/IL8* |
| G100 | GO:1902624 | Positive regulation of neutrophil migration | 21 | –0.795047807 | –2.056604138 | 0.001686341 | 0.023352669 | tags =57%, list =5%, signal =55% | *RAC2/ADAM8/NCKAP1L/LBP/C5AR1/IL1A/C3AR1/CXCL1/CXCL3/CD74/IL8* |
| G100 | GO:1903034 | Regulation of response to wounding | 107 | –0.498035084 | –1.713879023 | 0.00295421 | 0.030486975 | tags =34%, list =13%, signal =30% | *CASK/ADRA2A/PRKG1/PTPRF/SCARF1/GJD4/GP1BA/PDGFA/KANK1/TLR4/TGFBR2/SERPINE1/PDGFB/WFDC1/ENPP4/PLAUR/FAM46A/PLAT/FAP/F3/SERPINE2/FGF2/PLAU/HBEGF/MYLK/VTN/LYN/APOE/F2RL1/PLEK/SYK/SERPINB2/FCER1G/S100A9/SPP1* |
| G100 | GO:1902107 | Positive regulation of leukocyte differentiation | 102 | –0.487586967 | –1.656687729 | 0.002994012 | 0.030486975 | tags =26%, list =12%, signal =23% | *IL15/TGFBR2/CCR1/ATP6AP1/GLI2/IL2RA/RASGRP1/BTK/TNFSF4/RUNX1/DCSTAMP/PRKCZ/ADAM8/IL18/CD83/IL36B/CA2/INPP5D/NCKAP1L/CD86/SASH3/IL6/SYK/PF4/LIF/CD74* |
| G100 | GO:1901343 | Negative regulation of vasculature development | 57 | –0.531455304 | –1.66128691 | 0.003115265 | 0.030486975 | tags =30%, list =9%, signal =27% | *SERPINE1/PDGFB/COL4A2/EPHA2/XDH/PDE3B/SPARC/BAI1/RGCC/ANGPT4/SULF1/TIE1/CCL2/STAB1/PF4/HOXA5* |
| G100 | GO:1903036 | Positive regulation of response to wounding | 39 | –0.582300135 | –1.700449529 | 0.004846527 | 0.038245256 | tags =33%, list =12%, signal =29% | *SCARF1/KANK1/TLR4/TGFBR2/SERPINE1/ENPP4/F3/HBEGF/MYLK/VTN/PLEK/S100A9* |
| G100 | GO:1903307 | Positive regulation of regulated secretory pathway | 32 | –0.597145559 | –1.674144546 | 0.006578947 | 0.046053749 | tags =28%, list =8%, signal =26% | *UNC13D/TMEM27/F2RL1/VAMP8/FGR/SYK/PTAFR/FCER1G* |
| G101 | GO:1903530 | Regulation of secretion by cell | 409 | –0.437820938 | –1.729784588 | 0.001240695 | 0.023352669 | tags =29%, list =17%, signal =25% | *ATP13A2/C2CD2L/STXBP1/GAS6/CDK5/STXBP6/NR1D1/CHRNA7/MIF/SSC5D/IL1RAP/C19orf26/LEPRE1/TGFB1/SYT15/NSF/CACNA1A/HYAL2/LEP/TLR6/LGALS9/INHA/PTGER4/HIF1A/PARK2/SLC25A4/CD38/TNFRSF9/IRS2/IL11/ADRA2A/FN1/ITPR2/IRS1/ITPR1/SERP1/ARNTL/TLR4/UCN/RHBDF2/ATP6AP1/RIMS3/IL36RN/IL1R2/SYBU/NCS1/SDC1/RAC2/CSF1R/RASGRP1/RAB11FIP1/SIRT4/NLGN1/NKX3-1/SYTL1/CADM1/TNFSF4/TLR2/STXBP2/SMPD3/GDNF/UCP2/DRD4/SOX4/UNC13D/SFRP1/CAMK2A/SYTL3/RBP4/RSAD2/TLR1/PRKCZ/SYN1/P2RY1/ADAM8/RIMS1/TLR8/ADCY5/HMOX1/GPR27/RGCC/CHD7/IL1B/TMEM27/LYN/CD300A/RPH3AL/WNT5A/SLC2A1/TGFB3/LPL/KCNS3/ANGPT1/F2RL1/IL1RL1/C1QTNF3/HAVCR2/VAMP8/FGR/PTPN22/TNFRSF21/SRGN/IL1A/GPAM/IL6/SYK/CD14/PTAFR/CD84/HTR2A/INHBA/FCER1G/LIF/IGF1/TRPM2/IL33/SNCA* |
| G101 | GO:1903706 | Regulation of hemopoiesis | 241 | –0.491048269 | –1.867855313 | 0.001335113 | 0.023352669 | tags =26%, list =14%, signal =23% | *CEBPB/LEP/LGALS9/INHA/HIF1A/FSTL3/HLA-DOA/TNFSF9/IL15/TLR4/TGFBR2/CCR1/ATP6AP1/GLI2/IL2RA/ACVR2A/MEIS2/RASGRP1/BTK/TNFSF4/HOXA9/RUNX1/SFRP1/DCSTAMP/SCIN/PRKCZ/ADAM8/IL18/CD83/HOXA7/ZFPM1/MEIS1/CAMK4/SIGLEC15/TMEM176A/LILRB4/LYN/IL36B/LILRA6/CA2/INPP5D/CYP26B1/TMEM176B/PTPN6/NCKAP1L/CD86/SASH3/NFAM1/IL6/CD28/SYK/HIST1H4H/CARD11/SPI1/INHBA/PF4/LIF/TYROBP/CD74/HOXA5/C1QC/HOXB8* |
| G101 | GO:1903532 | Positive regulation of secretion by cell | 224 | –0.440359019 | –1.665277932 | 0.00135318 | 0.023352669 | tags =24%, list =14%, signal =21% | *HYAL2/LEP/LGALS9/INHA/PTGER4/HIF1A/CD38/IRS2/SERP1/UCN/ATP6AP1/NCS1/SDC1/CSF1R/RASGRP1/NLGN1/NKX3-1/CADM1/TNFSF4/SMPD3/GDNF/SOX4/UNC13D/RBP4/PRKCZ/P2RY1/ADAM8/GPR27/RGCC/IL1B/TMEM27/RPH3AL/WNT5A/TGFB3/LPL/F2RL1/IL1RL1/C1QTNF3/HAVCR2/VAMP8/FGR/PTPN22/IL1A/IL6/SYK/CD14/PTAFR/INHBA/FCER1G/IGF1/TRPM2/IL33/SNCA* |
| G101 | GO:1903708 | Positive regulation of hemopoiesis | 128 | –0.468089596 | –1.655362714 | 0.001428571 | 0.023352669 | tags =27%, list =14%, signal =24% | *LEP/LGALS9/HIF1A/TNFSF9/IL15/TGFBR2/CCR1/ATP6AP1/GLI2/IL2RA/ACVR2A/RASGRP1/BTK/TNFSF4/RUNX1/DCSTAMP/SCIN/PRKCZ/ADAM8/IL18/CD83/IL36B/CA2/INPP5D/NCKAP1L/CD86/SASH3/IL6/SYK/INHBA/PF4/LIF/CD74/HOXA5* |
| G101 | GO:1903531 | Negative regulation of secretion by cell | 115 | –0.535800009 | –1.855121864 | 0.001451379 | 0.023352669 | tags =37%, list =16%, signal =31% | *STXBP6/SSC5D/C19orf26/LEP/LGALS9/INHA/PTGER4/PARK2/TNFRSF9/IL11/ADRA2A/FN1/IRS1/UCN/RHBDF2/IL36RN/IL1R2/RAB11FIP1/SIRT4/TNFSF4/UCP2/DRD4/SFRP1/RSAD2/P2RY1/HMOX1/RGCC/IL1B/CD300A/ANGPT1/F2RL1/C1QTNF3/VAMP8/PTPN22/TNFRSF21/SRGN/IL6/CD84/INHBA/LIF/IL33/SNCA* |
| G101 | GO:1903707 | Negative regulation of hemopoiesis | 91 | –0.597925863 | –2.012741582 | 0.00152207 | 0.023352669 | tags =21%, list =7%, signal =20% | *HOXA9/SFRP1/HOXA7/ZFPM1/MEIS1/TMEM176A/LILRB4/LYN/LILRA6/INPP5D/TMEM176B/HIST1H4H/INHBA/PF4/CD74/HOXA5/C1QC/HOXB8* |
| G101 | GO:1903555 | Regulation of tumor necrosis factor superfamily cytokine production | 83 | –0.555461838 | –1.841715441 | 0.001533742 | 0.023352669 | tags =30%, list =9%, signal =28% | *LEP/LGALS9/SPN/TLR4/RASGRP1/HSPB1/SPON2/TLR2/TLR1/ADAM8/CLU/ANGPT1/HAVCR2/ACP5/CCL2/PTPN22/LBP/CD86/SASH3/CD14/PTAFR/CYBB/FCER1G/PF4* |
| G101 | GO:1903557 | Positive regulation of tumor necrosis factor superfamily cytokine production | 50 | –0.669877771 | –2.040479109 | 0.001572327 | 0.023352669 | tags =42%, list =14%, signal =36% | *LGALS9/SPN/TLR4/RASGRP1/HSPB1/SPON2/TLR2/TLR1/ADAM8/CLU/HAVCR2/CCL2/LBP/CD86/SASH3/CD14/PTAFR/CYBB/FCER1G/PF4* |
| G101 | GO:1904035 | Regulation of epithelial cell apoptotic process | 48 | –0.5628341 | –1.693519991 | 0.003169572 | 0.030486975 | tags =21%, list =9%, signal =19% | *ANGPTL4/HMOX1/RGCC/SFRP4/ANGPT1/NDNF/IL6/KDR/SCG2* |
| G101 | GO:1904018 | Positive regulation of vasculature development | 111 | –0.469888506 | –1.62198152 | 0.004379562 | 0.037118229 | tags =31%, list =13%, signal =27% | *HIF1A/FLT1/PLCG1/HIPK2/ITGA5/TGFBR2/VASH2/SERPINE1/PDGFB/VEGFA/HSPB1/GATA6/PTGS2/F3/RUNX1/ANGPTL4/ITGB2/FGF2/HMOX1/IL1B/ANGPT4/WNT5A/SRPX2/EFNB2/MYOCD/PRKCB/C5AR1/IL1A/SERPINB7/C3AR1/CYBB/KDR/IL8* |
| G102 | GO:1904036 | Negative regulation of epithelial cell apoptotic process | 24 | –0.708336449 | –1.875572189 | 0.001655629 | 0.023352669 | tags =29%, list =9%, signal =27% | *ANGPTL4/HMOX1/ANGPT1/NDNF/KDR/SCG2* |
| G103 | GO:2000147 | Positive regulation of cell motility | 328 | –0.498206518 | –1.937834589 | 0.00128866 | 0.023352669 | tags =27%, list =13%, signal =24% | *MYADM/PDGFRA/FLT1/IRS2/ADRA2A/PLCG1/NOX4/FN1/PDGFA/SEMA6D/WNT5B/ITGA5/TGFBR2/CCR1/CXCL2/FAM83H/RAC2/CSF1R/SERPINE1/KIAA1598/PDGFB/VEGFA/HSPB1/PTP4A1/FAM115C/CXCL14/RET/PTGS2/F3/ITGB3/LRRC15/ATP8A1/FGF2/PLAU/MDM2/MMP9/SNAI1/HBEGF/ADAM8/CORO1A/SPARC/P2RY6/SPOCK2/MYLK/WNT11/VTN/NRP2/LYN/ANGPT4/CXCL16/WNT5A/SRPX2/HAS2/CCL26/ANGPT1/F2RL1/BDKRB1/NCKAP1L/CCL2/FGR/PTPRC/ITGA2/LBP/C5AR1/IL1A/SOX9/IL6/AIF1/PTAFR/CCL8/CMKLR1/C3AR1/CXCL1/SEMA6B/PF4/IGF1/KDR/CXCL6/MCAM/CXCL3/PLA2G7/CD74/BMP2/PLVAP/CXCL5/IL8* |
| G103 | GO:2000181 | Negative regulation of blood vessel morphogenesis | 55 | –0.525285964 | –1.636503331 | 0.001547988 | 0.023352669 | tags =29%, list =9%, signal =26% | *SERPINE1/COL4A2/EPHA2/XDH/PDE3B/SPARC/BAI1/RGCC/ANGPT4/SULF1/TIE1/CCL2/STAB1/PF4/HOXA5* |
| G103 | GO:1990266 | Neutrophil migration | 51 | –0.771229982 | –2.355743217 | 0.001574803 | 0.023352669 | tags =53%, list =11%, signal =47% | *PREX1/CXCL2/RAC2/ITGA1/ITGB2/VAV3/ADAM8/IL1B/CCL26/CCL22/NCKAP1L/CCL2/TREM1/LBP/C5AR1/IL1A/SYK/CCL8/C3AR1/CXCL1/FCER1G/S100A9/CXCL3/CCL13/CD74/IL8* |
| G103 | GO:1905207 | Regulation of cardiocyte differentiation | 26 | –0.653957593 | –1.757242452 | 0.001655629 | 0.023352669 | tags =27%, list =8%, signal =25% | *PRICKLE1/EFNB2/MYOCD/TBX5/IGF1/BMP2* |
| G103 | GO:2000725 | Regulation of cardiac muscle cell differentiation | 21 | –0.66299523 | –1.715014772 | 0.001686341 | 0.023352669 | tags =24%, list =2%, signal =23% | *EFNB2/MYOCD/IGF1/BMP2* |
| G103 | GO:2000516 | Positive regulation of CD4-positive, alpha-beta T cell activation | 20 | –0.741541285 | –1.906326919 | 0.001694915 | 0.023352669 | tags =40%, list =7%, signal =37% | *PRKCZ/IL18/CD83/NCKAP1L/CD86/SASH3/IL6* |
| G103 | GO:2000352 | Negative regulation of endothelial cell apoptotic process | 18 | –0.732862795 | –1.83174868 | 0.001727116 | 0.023440094 | tags =33%, list =9%, signal =30% | *ANGPTL4/ANGPT1/NDNF/KDR/SCG2* |
| G103 | GO:2000351 | Regulation of endothelial cell apoptotic process | 28 | –0.631344069 | –1.720607333 | 0.003344482 | 0.030830257 | tags =43%, list =9%, signal =39% | *MAPK7/THBS1/GAS6/COL18A1/SERPINE1/ANGPTL4/RGCC/ANGPT1/NDNF/KDR/SCG2* |
| G103 | GO:2001239 | Regulation of extrinsic apoptotic signaling pathway in absence of ligand | 39 | –0.559846159 | –1.634878785 | 0.006462036 | 0.045366307 | tags =23%, list =7%, signal =21% | *GDNF/IFI6/EYA1/IL1B/IL1A/EYA2/INHBA/PF4* |
| G103 | GO:2000021 | Regulation of ion homeostasis | 132 | –0.429259537 | –1.519955937 | 0.00723589 | 0.049451646 | tags =17%, list =6%, signal =16% | *IFI6/FGF2/CORO1A/MLLT11/CHD7/JPH2/LYN/PLCG2/CA2/CCR5/SLC30A3/PTPN6/BDKRB1/PTPRC/CD4/PLN/JPH1/HTR2A/KDR/EDNRB/SNCA* |
| G103 | GO:1905153 | Regulation of membrane invagination | 10 | –0.798434599 | –1.721786112 | 0.007366483 | 0.049685189 | tags =40%, list =3%, signal =39% | *F2RL1/NCKAP1L/ITGA2* |
| G103 | GO:2001028 | Positive regulation of endothelial cell chemotaxis | 10 | –0.798507549 | –1.721943426 | 0.007366483 | 0.049685189 | tags =40%, list =8%, signal =37% | *HSPB1/FGF2/KDR* |
| G11 | GO:0002764 | Immune response-regulating signaling pathway | 379 | –0.529374138 | –2.084125568 | 0.00125 | 0.023352669 | tags =16%, list =6%, signal =16% | *VAV3/LAT/RSAD2/TLR1/LGMN/CTSS/LIMK1/ADAM8/WAS/MNDA/TLR8/TLR7/AC005013.1/CR1/HLA-DPA1/LYN/CD300A/SKAP2/CYFIP2/PLCG2/INPP5D/MARCO/PAG1/F2RL1/PTPN6/HAVCR2/NCKAP1L/FGR/CLEC7A/PTPN22/TNFRSF21/PTPRC/PIK3AP1/PPAPDC1A/PRKCB/LBP/CD86/CD4/C5AR1/NFAM1/CD180/LCP2/CD28/SYK/CD14/ITGAM/C3AR1/CARD11/HLA-DQA1/HCK/CD209/FCGR1A/FCER1G/FPR1/HLA-DQB1/FPR3/HLA-DRB1/FCGR2A/HLA-DRB5/FCGR3A/HLA-DRA* |
| G11 | GO:0002757 | Immune response-activating signal transduction | 355 | –0.550818137 | –2.152396805 | 0.001272265 | 0.023352669 | tags =17%, list =6%, signal =17% | *VAV3/LAT/RSAD2/TLR1/LGMN/CTSS/LIMK1/ADAM8/WAS/MNDA/TLR8/TLR7/AC005013.1/CR1/HLA-DPA1/LYN/CD300A/SKAP2/CYFIP2/PLCG2/INPP5D/MARCO/PAG1/F2RL1/PTPN6/HAVCR2/NCKAP1L/FGR/CLEC7A/PTPN22/TNFRSF21/PTPRC/PIK3AP1/PPAPDC1A/PRKCB/LBP/CD86/CD4/C5AR1/NFAM1/CD180/LCP2/CD28/SYK/CD14/ITGAM/C3AR1/CARD11/HLA-DQA1/HCK/CD209/FCGR1A/FCER1G/FPR1/HLA-DQB1/FPR3/HLA-DRB1/FCGR2A/HLA-DRB5/FCGR3A/HLA-DRA* |
| G11 | GO:0002768 | Immune response-regulating cell surface receptor signaling pathway | 272 | –0.543728168 | –2.090003036 | 0.001298701 | 0.023352669 | tags =16%, list =6%, signal =15% | *LAT/LIMK1/WAS/MNDA/CR1/HLA-DPA1/LYN/CD300A/CYFIP2/PLCG2/INPP5D/PAG1/PTPN6/NCKAP1L/FGR/CLEC7A/PTPN22/TNFRSF21/PTPRC/PPAPDC1A/PRKCB/CD4/C5AR1/NFAM1/LCP2/CD28/SYK/C3AR1/CARD11/HLA-DQA1/HCK/CD209/FCGR1A/FCER1G/FPR1/HLA-DQB1/FPR3/HLA-DRB1/FCGR2A/HLA-DRB5/FCGR3A/HLA-DRA* |
| G11 | GO:0002758 | Innate immune response-activating signal transduction | 206 | –0.454600387 | –1.713267773 | 0.001349528 | 0.023352669 | tags =13%, list =6%, signal =12% | *RSAD2/TLR1/LGMN/CTSS/ADAM8/TLR8/TLR7/AC005013.1/LYN/PLCG2/MARCO/F2RL1/HAVCR2/CLEC7A/PTPN22/PIK3AP1/LBP/CD86/CD180/SYK/CD14/ITGAM/CARD11/HCK/CD209/FCER1G* |
| G11 | GO:0002761 | Regulation of myeloid leukocyte differentiation | 84 | –0.56235424 | –1.86852613 | 0.00152207 | 0.023352669 | tags =29%, list =6%, signal =27% | *CEBPB/INHA/FSTL3/TLR4/CCR1/ATP6AP1/RUNX1/SFRP1/DCSTAMP/HOXA7/ZFPM1/CAMK4/SIGLEC15/LILRB4/LYN/LILRA6/CA2/INPP5D/INHBA/PF4/LIF/TYROBP/C1QC* |
| G11 | GO:0003231 | Cardiac ventricle development | 84 | –0.478124906 | –1.588658564 | 0.00152207 | 0.023352669 | tags =31%, list =15%, signal =27% | *TGFB1/ZFPM2/LTBP1/HIF1A/TPM1/PPP1R13L/TGFBR2/SALL4/EGLN1/HEY1/PTK7/COL11A1/SOX4/HAND2/TBX3/MDM2/ZFPM1/WNT11/CHD7/STRA6/WNT5A/HEYL/MYOCD/TBX5/PITX2* |
| G11 | GO:0003279 | Cardiac septum development | 82 | –0.503772257 | –1.673573206 | 0.001531394 | 0.023352669 | tags =45%, list =21%, signal =36% | *PLXND1/LUZP1/TBX2/TAB1/TGFB2/NDST1/HEG1/LMO4/TRIP11/NOTCH2/SMO/PROX1/ZFPM2/LTBP1/MYH10/TGFBR2/SALL4/EGLN1/HEY1/PTK7/GATA6/SOX4/TBX3/PCSK5/MDM2/ZFPM1/WNT11/CHD7/DHRS3/MSX2/STRA6/WNT5A/HEYL/RARB/TBX5/PITX2* |
| G11 | GO:0003281 | Ventricular septum development | 55 | –0.513148863 | –1.598690775 | 0.001547988 | 0.023352669 | tags =40%, list =19%, signal =33% | *HEG1/LMO4/TRIP11/PROX1/ZFPM2/LTBP1/TGFBR2/SALL4/EGLN1/HEY1/PTK7/SOX4/TBX3/MDM2/ZFPM1/WNT11/STRA6/WNT5A/HEYL/TBX5/PITX2* |
| G11 | GO:0002762 | Negative regulation of myeloid leukocyte differentiation | 36 | –0.631366947 | –1.845574 | 0.001569859 | 0.023352669 | tags =33%, list =6%, signal =31% | *FSTL3/TLR4/SFRP1/HOXA7/ZFPM1/LILRB4/LYN/LILRA6/INPP5D/INHBA/C1QC* |
| G11 | GO:0003170 | Heart valve development | 33 | –0.608543383 | –1.725974807 | 0.001633987 | 0.023352669 | tags =33%, list =6%, signal =31% | *HEY1/SOX4/MDM2/ZFPM1/STRA6/HEYL/SOX9/TBX5/BMP2/PITX2* |
| G11 | GO:0002886 | Regulation of myeloid leukocyte mediated immunity | 31 | –0.684580231 | –1.90413768 | 0.00166113 | 0.023352669 | tags =45%, list =9%, signal =41% | *BTK/STXBP2/UNC13D/HMOX1/LYN/CD300A/F2RL1/VAMP8/FGR/SYK/PTAFR/CD84/FCER1G* |
| G11 | GO:0003171 | Atrioventricular valve development | 20 | –0.716679916 | –1.842414231 | 0.001694915 | 0.023352669 | tags =45%, list =11%, signal =40% | *HEY1/SOX4/MDM2/ZFPM1/HEYL/TBX5/BMP2/PITX2* |
| G11 | GO:0002828 | Regulation of type 2 immune response | 18 | –0.769127741 | –1.92239084 | 0.001727116 | 0.023440094 | tags =44%, list =7%, signal =41% | *RSAD2/PRKCZ/IL18/CD86/IL6/IL33/CD74* |
| G11 | GO:0002830 | Positive regulation of type 2 immune response | 10 | –0.907528488 | –1.957041879 | 0.001841621 | 0.024395555 | tags =80%, list =7%, signal =74% | *RSAD2/PRKCZ/IL18/CD86/IL6/IL33/CD74* |
| G11 | GO:0002822 | Regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 82 | –0.462938744 | –1.537920891 | 0.003062787 | 0.030486975 | tags =22%, list =8%, signal =20% | *TNFSF4/RSAD2/PRKCZ/WAS/CR1/IL1B/IL1RL1/PTPN6/HAVCR2/PTPRC/CD4/SASH3/SLC11A1/IL6/CD28/FCER1G/IL33* |
| G11 | GO:0002790 | Peptide secretion | 157 | –0.416928317 | –1.508011185 | 0.004243281 | 0.036564598 | tags =24%, list =14%, signal =20% | *LEP/HIF1A/PARK2/SLC25A4/CD38/IRS2/ADRA2A/ITPR2/IRS1/ITPR1/SERP1/ARNTL/UCN/SYBU/SIRT4/EXOC3L1/SMPD3/UCP2/SOX4/SFRP1/RBP4/ABCA1/ADCY5/PTPRN/GPR27/CHD7/IL1B/TMEM27/VGF/SLC2A1/KCNS3/IL1RN/IL6/TRPM2/S100A9/CD74* |
| G11 | GO:0002819 | Regulation of adaptive immune response | 92 | –0.47710307 | –1.608034397 | 0.004552352 | 0.037949001 | tags =23%, list =8%, signal =21% | *TNFSF4/RSAD2/PRKCZ/DUSP10/WAS/CR1/IL1B/CD48/IL1RL1/PTPN6/HAVCR2/PTPRC/CD4/SASH3/SLC11A1/SAMSN1/IL6/CD28/FCER1G/IL33* |
| G11 | GO:0002820 | Negative regulation of adaptive immune response | 22 | –0.678039517 | –1.779133402 | 0.005 | 0.038706237 | tags =36%, list =7%, signal =34% | *CR1/IL1RL1/PTPN6/HAVCR2/PTPRC/SAMSN1/IL33* |
| G11 | GO:0003205 | Cardiac chamber development | 116 | –0.449947955 | –1.558619902 | 0.005797101 | 0.042797226 | tags =34%, list =18%, signal =28% | *HEG1/LMO4/TRIP11/NOTCH2/SMO/PROX1/TGFB1/ZFPM2/LTBP1/HIF1A/TPM1/PPP1R13L/MYH10/TGFBR2/SALL4/EGLN1/HEY1/PTK7/GATA6/COL11A1/SOX4/HAND2/TBX3/RBP4/PCSK5/MDM2/ZFPM1/WNT11/CHD7/DHRS3/MSX2/STRA6/WNT5A/HEYL/MYOCD/RARB/TBX5/PITX2* |
| G11 | GO:0003179 | Heart valve morphogenesis | 29 | –0.609064781 | –1.670283197 | 0.006745363 | 0.046531263 | tags =48%, list =19%, signal =39% | *OLFM1/NOTCH2/TGFB1/TGFBR2/HEY1/SOX4/MDM2/ZFPM1/STRA6/HEYL/SOX9/TBX5/BMP2* |
| G11 | GO:0002823 | Negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 20 | –0.65546351 | –1.685041358 | 0.006779661 | 0.046705339 | tags =45%, list =7%, signal =42% | *SPN/TNFSF4/CR1/IL1RL1/PTPN6/HAVCR2/PTPRC/IL33* |
| G11 | GO:0002888 | Positive regulation of myeloid leukocyte mediated immunity | 15 | –0.72357149 | –1.711361593 | 0.007067138 | 0.048362498 | tags =47%, list =2%, signal =46% | *F2RL1/VAMP8/FGR/SYK/PTAFR/FCER1G* |
| G12 | GO:0005975 | Carbohydrate metabolic process | 446 | –0.357322003 | –1.417082889 | 0.004926108 | 0.038460964 | tags =23%, list =16%, signal =20% | *PGAM1/GYG2/HYAL3/B3GAT3/GPI/GBA/KIAA1161/ALDH1B1/PHKA1/GPD1L/GNMT/IMPAD1/AKR1B1/PPP1R3B/TGFB1/CHST2/CACNA1A/PGM1/HYAL2/LEP/ME1/GLA/TPI1/TREH/HIF1A/PARK2/SLC2A8/ATF3/MLEC/IRS2/NPY1R/ST3GAL1/GLB1L3/SORBS1/IRS1/ENO3/DDIT4/PGM2L1/SERP1/HHIP/GM2A/MANBA/MPI/A4GNT/MTMR7/ENO2/OVGP1/GAPDH/IPPK/ALDOC/GNPTAB/GLB1L2/ALDOA/LDHA/SYNJ1/C12orf5/PKM/PDK1/RORA/PGK1/MLXIP/NPL/PDGFB/SIK1/KL/CHST1/B4GALT1/ST3GAL6/MGAM/FABP5/GCNT3/LCTL/RBP4/PDK4/GYS1/CHST7/FOXO1/PFKFB4/P2RY1/PDK3/FBP1/DGAT2/B4GALNT1/ST8SIA4/ST6GAL1/HAS3/HAS2/SLC2A1/PPP1R3C/C1QTNF3/HK3/MGAT4A/FUCA1/PLEK/IL6/PTAFR/HTR2A/IGF1/SDS/SNCA/HAS1* |
| G13 | GO:0006006 | Glucose metabolic process | 163 | –0.452228095 | –1.646913928 | 0.001396648 | 0.023352669 | tags =26%, list =16%, signal =22% | *NR1D1/PGAM1/GPI/GNMT/PPP1R3B/CACNA1A/PGM1/LEP/TPI1/PARK2/ATF3/IRS2/NPY1R/SORBS1/IRS1/ENO3/PGM2L1/SERP1/ENO2/GAPDH/ALDOC/ALDOA/C12orf5/PKM/PDK1/RORA/PGK1/SIK1/FABP5/RBP4/PDK4/FOXO1/PFKFB4/PDK3/FBP1/DGAT2/C1QTNF3/HK3/IL6/IGF1/SDS* |
| G13 | GO:0006094 | Gluconeogenesis | 63 | –0.55992311 | –1.775345765 | 0.001547988 | 0.023352669 | tags =37%, list =16%, signal =31% | *NR1D1/PGAM1/GPI/GNMT/PGM1/LEP/TPI1/ATF3/ENO3/ENO2/GAPDH/ALDOC/ALDOA/PGK1/SIK1/RBP4/FOXO1/FBP1/DGAT2/C1QTNF3/IL6/SDS* |
| G13 | GO:0006007 | Glucose catabolic process | 23 | –0.700000335 | –1.851061418 | 0.001636661 | 0.023352669 | tags =83%, list =25%, signal =62% | *PFKM/HK2/PFKFB2/PFKFB3/PFKL/PGAM1/GPI/TPI1/ENO3/ENO2/GAPDH/ALDOC/ALDOA/C12orf5/PKM/PGK1/PFKFB4/HK3* |
| G13 | GO:0006109 | Regulation of carbohydrate metabolic process | 117 | –0.481287033 | –1.669458579 | 0.002902758 | 0.030486975 | tags =28%, list =16%, signal =24% | *NR1D1/PGAM1/GNMT/PPP1R3B/TGFB1/LEP/HIF1A/PARK2/IRS2/SORBS1/IRS1/DDIT4/C12orf5/PDK1/RORA/MLXIP/PDGFB/SIK1/PDK4/FOXO1/P2RY1/PDK3/FBP1/DGAT2/HAS2/C1QTNF3/PLEK/IL6/PTAFR/HTR2A/IGF1/SNCA* |
| G13 | GO:0006024 | Glycosaminoglycan biosynthetic process | 96 | –0.454701928 | –1.534935265 | 0.006134969 | 0.044526052 | tags =41%, list =18%, signal =33% | *GPC6/SLC35D1/B3GNT2/GALNT5/AGRN/B4GALT7/NDST1/HSPG2/HS3ST3B1/B3GAT3/TGFB1/CHST2/ST3GAL1/CHPF2/DSE/GPC4/SDC1/B4GALT6/PDGFB/GPC2/CHPF/CHST1/B4GALT1/ST3GAL6/CHSY3/GPC3/HS3ST3A1/B3GNT7/CHST7/VCAN/HS3ST1/IL1B/HAS3/HAS2/ANGPT1/EXTL1/HS3ST2/HAS1* |
| G14 | GO:0006720 | Isoprenoid metabolic process | 85 | –0.516666046 | –1.71869109 | 0.001517451 | 0.023352669 | tags =27%, list =12%, signal =24% | *AKR1C1/GPC4/ALDH1A3/SDC1/STAR/GPC2/RDH10/ADH4/CRABP2/GPC3/CYP2E1/RBP4/DGAT2/DHRS9/DHRS3/STRA6/LPL/APOE/CYP26B1/AKR1B10/RBP1/APOC2* |
| G14 | GO:0006721 | Terpenoid metabolic process | 66 | –0.571592956 | –1.819386275 | 0.001550388 | 0.023352669 | tags =35%, list =12%, signal =31% | *AKR1C1/GPC4/ALDH1A3/SDC1/STAR/GPC2/RDH10/ADH4/CRABP2/GPC3/CYP2E1/RBP4/DGAT2/DHRS9/DHRS3/STRA6/LPL/APOE/CYP26B1/AKR1B10/RBP1/APOC2* |
| G14 | GO:0006734 | NADH metabolic process | 28 | –0.656271336 | –1.788541826 | 0.001672241 | 0.023352669 | tags =71%, list =25%, signal =54% | *PFKM/HK2/PFKFB2/PFKFB3/PFKL/PGAM1/GPI/GPD1L/TPI1/ENO3/ENO2/GAPDH/ALDOC/ALDOA/C12orf5/PKM/PGK1/PFKFB4/HK3* |
| G14 | GO:0006735 | NADH regeneration | 20 | –0.726883421 | –1.868645024 | 0.001694915 | 0.023352669 | tags =90%, list =25%, signal =68% | *PFKM/HK2/PFKFB2/PFKFB3/PFKL/PGAM1/GPI/TPI1/ENO3/ENO2/GAPDH/ALDOC/ALDOA/PKM/PGK1/PFKFB4/HK3* |
| G15 | GO:0006873 | Cellular ion homeostasis | 388 | –0.417705899 | –1.648606293 | 0.001234568 | 0.023352669 | tags =27%, list =17%, signal =23% | *FTL/ATP13A2/ATP6V1F/MYO5A/ATP6V1G1/CAPN3/SLC9A4/BCAP31/HTT/CHRNA7/ATP7A/ATP6V1G2/ATP6V0E1/ATP6V1A/SLC46A1/ATP6V0A1/TGFB1/CACNA1A/SLC22A17/GNAT2/ATP13A3/ATP6V1E1/PTGER4/TF/HIF1A/DMD/ABCG2/STIM2/CD38/PDGFRA/PLCG1/TTPA/ITPR2/TRPC4/CD52/SLC4A3/LETM2/TFRC/ITPR1/SLC11A2/OPRL1/CCR1/SLC26A1/ATP6V0C/SLC30A10/EGLN1/FTH1/ATP2B1/MT2A/SLC4A11/DRD4/F2RL3/SLC9A7/ATP1B1/FGF2/KCNMA1/P2RY1/PTGER3/CORO1A/CDH23/SLC24A3/ATP2A3/CHRNA9/ADCY5/HMOX1/CHD7/SLC4A4/EDNRA/GNA15/ATP6V0D2/JPH2/LYN/PLCG2/CA2/APOE/CCR5/F2RL1/SLC30A3/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/C5AR1/SLC11A1/PTGDR/GRIK2/PLN/JPH1/CCL8/C3AR1/STC1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/S100A9/EDNRB/FPR3/CCL13/SNCA/CALB2* |
| G15 | GO:0006875 | Cellular metal ion homeostasis | 317 | –0.446761937 | –1.732503415 | 0.00129199 | 0.023352669 | tags =25%, list =15%, signal =22% | *TGFB1/CACNA1A/SLC22A17/GNAT2/ATP13A3/PTGER4/TF/HIF1A/DMD/ABCG2/STIM2/CD38/PDGFRA/PLCG1/ITPR2/TRPC4/CD52/LETM2/TFRC/ITPR1/SLC11A2/OPRL1/CCR1/SLC30A10/EGLN1/FTH1/ATP2B1/MT2A/DRD4/F2RL3/ATP1B1/FGF2/KCNMA1/P2RY1/PTGER3/CORO1A/CDH23/SLC24A3/ATP2A3/CHRNA9/ADCY5/HMOX1/CHD7/EDNRA/GNA15/JPH2/LYN/PLCG2/APOE/CCR5/F2RL1/SLC30A3/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/C5AR1/SLC11A1/PTGDR/GRIK2/PLN/JPH1/CCL8/C3AR1/STC1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/S100A9/EDNRB/FPR3/CCL13/SNCA/CALB2* |
| G15 | GO:0006887 | Exocytosis | 300 | –0.449972341 | –1.737248157 | 0.001293661 | 0.023352669 | tags =31%, list =19%, signal =26% | *ACTN1/TGFB2/THBS1/SCRN1/PI4K2A/RSG1/ATP13A2/STXBP1/MYO5A/GAS6/CDK5/STXBP6/STEAP2/CYB5R1/C19orf26/TGFB1/SYT15/NSF/CACNA1A/SCAMP1/DNAJC5/LGALS9/TF/ADRA2A/TIMP1/FN1/PDGFA/MYH10/FAM3C/VMP1/CCR1/ATP6AP1/RIMS3/SLC17A9/ALDOA/SYNJ1/NCS1/LIN7A/SDC1/RAC2/ABCA12/RASGRP1/RAB11FIP1/SERPINE1/MILR1/NLGN1/LAT2/PDGFB/VEGFA/SYTL1/VWF/P2RX1/BTK/ARHGAP44/EXOC3L1/STXBP2/SMPD3/ITGB3/UNC13D/SYTL3/LAT/SCIN/SYN1/CORO1A/A2M/SPARC/CLU/ISLR/RIMS1/HMOX1/TMEM27/LYN/CD300A/RPH3AL/TGFB3/F2RL1/VAMP8/FGR/SRGN/F13A1/PLEK/SYK/PTAFR/CCL8/CD84/HCK/PCDH7/CADPS/FCER1G/PF4/IGF1/SNCA* |
| G15 | GO:0006874 | Cellular calcium ion homeostasis | 242 | –0.481873573 | –1.832746422 | 0.001340483 | 0.023352669 | tags =19%, list =6%, signal =18% | *F2RL3/ATP1B1/FGF2/P2RY1/PTGER3/CORO1A/CDH23/SLC24A3/ATP2A3/CHRNA9/ADCY5/CHD7/EDNRA/GNA15/JPH2/LYN/PLCG2/APOE/CCR5/F2RL1/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/C5AR1/PTGDR/GRIK2/PLN/JPH1/CCL8/C3AR1/STC1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/EDNRB/FPR3/CCL13/SNCA/CALB2* |
| G15 | GO:0006816 | Calcium ion transport | 245 | –0.439120177 | –1.670309571 | 0.001344086 | 0.023352669 | tags =29%, list =16%, signal =25% | *CAPN3/CDK5/HOMER1/HTT/CHRNA7/CATSPER2/C19orf26/ARRB2/TGFB1/CACNA1A/DMD/STIM2/CASK/ADRA2A/CYP27B1/PLCG1/ITPR2/EHD3/TRPC4/TRPV2/ITPR1/OPRL1/UCN/CCR1/TRPV3/NCS1/DENND5B/RAMP1/ATP2B1/PDGFB/P2RX1/CALCRL/PTGS2/CACNA1H/DRD4/F2RL3/MCOLN2/CTGF/ATP1B1/CAMK2A/FGF2/EPPIN/PKD1L1/CORO1A/CDH23/SLC24A3/MCOLN3/ATP2A3/CHRNA9/MYLK/CHD7/JPH2/LYN/TSPAN13/PLCG2/CCR5/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/PLN/JPH1/CCL8/CD84/STC1/HTR2A/TRPM2/SNCA* |
| G16 | GO:0006897 | Endocytosis | 485 | –0.421288554 | –1.681748745 | 0.001207729 | 0.023352669 | tags =15%, list =8%, signal =14% | *CALCRL/APLP1/ADRBK2/SYP/MFGE8/GPC3/STON1/TINAGL1/DNM3/UNC13D/ITGB2/VAV3/CD93/APOC1/LIMK1/CORO1A/LRP1B/APOBR/LOXL2/SPARC/MYO7A/WAS/ABCA1/IGJ/CFI/VTN/SFRP4/IL1B/LYN/CD300A/CXCL16/WNT5A/CYFIP2/PLCG2/DNER/IRF8/APOE/ARC/MARCO/ANGPT1/BIN2/F2RL1/OLR1/MSR1/NCKAP1L/CCL2/FGR/CLEC7A/TREM2/ITGA2/PPAPDC1A/LBP/APOC2/SLC11A1/MERTK/SYK/AIF1/CD14/CD163L1/SIGLEC1/STAB1/HCK/CD209/FCGR1A/TGM2/FCER1G/FCGR2A/FOLR2/FCGR3A/SNCA/CD163/IL8* |
| G16 | GO:0006935 | Chemotaxis | 376 | –0.492970991 | –1.939321111 | 0.001248439 | 0.023352669 | tags =22%, list =9%, signal =20% | *CSF1R/SERPINE1/DRAXIN/PDGFB/VEGFA/HSPB1/PLAUR/EGR2/SPON2/CXCL14/ITGA1/PAX6/F3/ITGB3/KIF26B/PLXNB3/ITGB2/VAV3/EPHA2/FGF2/PLAU/ETV1/HBEGF/FLRT3/ADAM8/CORO1A/EFNA3/SPTBN2/PADI2/IL1B/NRP2/LYN/CXCL16/WNT5A/DPYSL4/NRCAM/CCL26/CCR5/ANGPT1/BIN2/CCL22/F2RL1/EFNB2/NCKAP1L/CCL2/KIF5A/TREM1/ITGA2/LBP/C5AR1/IL6/SYK/GAP43/AIF1/PTAFR/CCL8/CMKLR1/C3AR1/GPR183/ROBO2/CXCR4/CXCL1/SEMA6B/FCER1G/PF4/UNC5C/FPR1/KDR/S100A9/EDNRB/FPR3/KAL1/CXCL6/CXCL3/CCL13/PLA2G7/CD74/HOXA2/SCG2/CXCL5/IL8* |
| G16 | GO:0006898 | Receptor-mediated endocytosis | 201 | –0.427865755 | –1.6072687 | 0.001364256 | 0.023352669 | tags =19%, list =9%, signal =17% | *SYNJ1/RAMP1/SERPINE1/NLGN1/VEGFA/CALCRL/ADRBK2/TINAGL1/DNM3/ITGB2/APOC1/LRP1B/APOBR/LOXL2/SPARC/IGJ/CFI/VTN/SFRP4/CXCL16/PLCG2/APOE/MARCO/ANGPT1/OLR1/MSR1/APOC2/SYK/CD14/CD163L1/STAB1/FCGR1A/FCER1G/FOLR2/SNCA/CD163/IL8* |
| G16 | GO:0006909 | Phagocytosis | 176 | –0.538489275 | –1.978317691 | 0.001383126 | 0.023352669 | tags =22%, list =7%, signal =20% | *UNC13D/ITGB2/VAV3/CD93/LIMK1/CORO1A/MYO7A/WAS/ABCA1/IL1B/LYN/CD300A/CYFIP2/PLCG2/IRF8/MARCO/BIN2/F2RL1/NCKAP1L/CCL2/FGR/CLEC7A/TREM2/ITGA2/PPAPDC1A/LBP/SLC11A1/MERTK/SYK/AIF1/CD14/HCK/FCGR1A/TGM2/FCER1G/FCGR2A/FCGR3A* |
| G16 | GO:0006911 | Phagocytosis, engulfment | 26 | –0.80141746 | –2.153480282 | 0.001655629 | 0.023352669 | tags =42%, list =7%, signal =40% | *ABCA1/CD300A/BIN2/F2RL1/NCKAP1L/TREM2/ITGA2/AIF1/FCGR1A/FCER1G* |
| G17 | GO:0006954 | Inflammatory response | 450 | –0.512030447 | –2.032161036 | 0.001233046 | 0.023352669 | tags =26%, list =9%, signal =24% | *CSF1R/TNFRSF10A/RASGRP1/SERPINE1/RORA/TPST1/P2RX1/WFDC1/BTK/NFKBIZ/CFH/CALCRL/TSPAN2/CHST1/B4GALT1/THEMIS2/TNFSF4/TLR2/PTGS2/F3/GGT1/UNC13D/ITGB2/EPHA2/LAT/TLR1/PRKCZ/ADAMTS12/ADAM8/PTGER3/IL18/DUSP10/A2M/C7/F11R/CFI/TLR8/TLR7/HMOX1/AC005013.1/CR1/CAMK4/VTN/IL1B/LYN/WNT5A/BLNK/IL36B/LPL/APOE/CCL26/CCR5/CYP26B1/CCL22/F2RL1/IL1RL1/SCUBE1/OLR1/C1QTNF3/HAVCR2/VAMP8/BDKRB1/ACP5/FABP4/CCL2/CLEC7A/LYZ/TNFRSF21/TNFRSF10D/ITGA2/PIK3AP1/TNFRSF10C/LBP/C5AR1/IL1A/SCN9A/NFAM1/SLC11A1/AOC3/PTGDR/CD180/IL6/CD28/SYK/AIF1/CD14/PTAFR/CCL8/C3AR1/SIGLEC1/STAB1/HCK/CYBB/ALOX5/CXCR4/CXCL1/TGM2/FCER1G/PF4/LY86/FPR1/S100A9/EDNRB/FPR3/CXCL6/FOLR2/CXCL3/CCL13/PLA2G7/IL33/BMP2/SPP1/CD163/SCG2/CXCL5/IL8* |
| G17 | GO:0007156 | Homophilic cell adhesion via plasma membrane adhesion molecules | 110 | –0.630702173 | –2.180364618 | 0.001455604 | 0.023352669 | tags =45%, list =13%, signal =39% | *PCDHGB1/PCDHB15/CELSR3/FAT3/PCDHGA4/PCDHGC5/PCDHA7/CLSTN2/PCDHB14/PCDH1/PCDHGA3/CADM1/PCDHGA2/RET/PCDHB6/PCDHB4/PLXNB3/PCDHB7/CELSR1/PCDHB5/PCDHB8/PCDHB2/CDH23/DSC2/PCDHA12/CDH2/PCDHB10/DSG2/ESAM/PCDHA13/PCDHB9/PCDHB3/SDK2/PCDHB12/PVRL4/CDH6/PCDHA3/PCDHA6/CADM3/PCDHA11/PCDHA10/CD84/ROBO2/PCDH10/PCDH7/PCDH9/CDH10/AMIGO2* |
| G17 | GO:0006959 | Humoral immune response | 89 | –0.613883162 | –2.060517703 | 0.001515152 | 0.023352669 | tags =39%, list =8%, signal =36% | *SPON2/CFH/HIST1H2BJ/CFHR1/A2M/CD83/C7/CLU/HIST1H2BK/IGJ/HIST1H2BC/CFI/HIST2H2BE/CR1/RGCC/VTN/ST6GAL1/BLNK/PTPN6/CCL2/TREM1/TNFRSF21/TREM2/C5AR1/IL6/CD28/C3AR1/GPR183/C1QA/VSIG4/LY86/HLA-DQB1/C1QB/C1QC* |
| G17 | GO:0006939 | Smooth muscle contraction | 66 | –0.528789249 | –1.683141636 | 0.001550388 | 0.023352669 | tags =27%, list =8%, signal =25% | *CALCRL/PTGS2/GDNF/KCNMA1/MYH11/PTGER3/ACTA2/RGS2/MYLK/CNN1/EDNRA/SULF1/MYOCD/ITGA2/PTAFR/HTR2A/EDNRB* |
| G17 | GO:0006956 | Complement activation | 39 | –0.586961639 | –1.714062188 | 0.004846527 | 0.038245256 | tags =38%, list =5%, signal =36% | *CFHR1/A2M/C7/CLU/CFI/CR1/RGCC/VTN/C5AR1/C3AR1/C1QA/VSIG4/C1QB/C1QC* |
| G18 | GO:0007159 | Leukocyte cell-cell adhesion | 334 | –0.490021215 | –1.907294923 | 0.001298701 | 0.023352669 | tags =25%, list =6%, signal =23% | *SATB1/SPN/IL15/TFRC/ITGA5/KIF13B/TGFBR2/HLA-DPB1/PREX1/GLI2/IL2RA/DOCK2/RAC2/RASGRP1/RORA/IFNE/MICA/TNFSF4/DPP4/SOX4/ITGB2/LAT/RSAD2/PRKCZ/ADAM8/FZD8/CORO1A/FZD7/IL18/CD83/WAS/LCP1/ZFPM1/TNFSF8/CAMK4/CHD7/HLA-DPA1/IL1B/LYN/CD300A/IL36B/HAS2/CYP26B1/PAG1/F2RL1/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/DOCK8/CLEC7A/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/SLC11A1/IL6/CD28/SYK/AIF1/PTAFR/GPR183/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/CD209/FCER1G/IGF1/VSIG4/S100A9/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G18 | GO:0007157 | Heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules | 30 | –0.607838189 | –1.678134526 | 0.006722689 | 0.04643702 | tags =33%, list =11%, signal =30% | *TENM4/NLGN1/AMIGO3/CADM1/CDH2/PVRL4/CADM3/CD209/AMIGO2* |
| G19 | GO:0007186 | G-protein coupled receptor signaling pathway | 421 | –0.459636636 | –1.82241452 | 0.001230012 | 0.023352669 | tags =22%, list =11%, signal =20% | *OPRL1/UCN/P2RY8/PREX1/CCR1/CXCL2/GPR146/GNRHR2/RAPGEFL1/GPR56/RAC2/LPAR6/RAMP1/GNB3/PLCB1/GPR65/CALCRL/APLP1/F2RL2/SYP/DRD4/F2RL3/GPR156/OR2W3/PPAP2A/CELSR1/SFRP1/CAMK2A/GPR113/HPGD/GPR63/P2RY1/HOMER2/FZD8/ADCY8/PTGER3/FZD7/PREX2/ABCA1/GNG2/BAI1/P2RY6/GPR160/RGS2/ADCY5/GPR27/EDNRA/GNA15/S1PR5/SFRP4/UCN2/RPH3AL/RGS4/GABRA5/CA2/APOE/CCL26/CCR5/CCL22/F2RL1/PTPN6/BDKRB1/SUCNR1/CCL2/OR7A5/PIK3R5/C5AR1/PTGDR/PLN/PLEK/GAP43/PTAFR/CCL8/CMKLR1/C3AR1/GPR183/GPR34/HTR2A/CXCR4/CXCL1/TGM2/ACPP/PF4/GPR116/FPR1/EDNRB/FPR3/CXCL6/CXCL3/CCL13/SNCA/CXCL5/IL8* |
| G2 | GO:0001816 | Cytokine production | 464 | –0.442702467 | –1.763205865 | 0.001222494 | 0.023352669 | tags =27%, list =15%, signal =24% | *MIF/SSC5D/POLR3G/GBA/IL1RAP/HERC5/TRIB2/JAK3/POLR3A/ARRB2/TGFB1/TUSC2/HYAL2/CEBPB/LEP/BST2/TLR6/POLR2K/C5orf30/LGALS9/INHA/PTGER4/HIF1A/MAPK13/TNFRSF9/ADRA2A/FN1/SPN/IL15/TLR4/UCN/HLA-DPB1/NLRC4/IL36RN/GPR56/IL1R2/CSF1R/RASGRP1/SERPINE1/RORA/DENND1B/HSPB1/PLCB1/BTK/CADM1/GATA6/SPON2/TNFSF4/TLR2/PTGS2/RUNX1/EPHA2/RSAD2/PCSK5/TLR1/PRKCZ/ADAM8/IL18/CD83/IGF2BP3/ABCA1/ZFPM1/IGF2BP1/CLU/F11R/TLR8/TLR7/HMOX1/AC005013.1/WNT11/RGCC/HLA-DPA1/IL1B/LYN/WNT5A/IL36B/PLCG2/TGFB3/LPL/IRF8/INPP5D/SULF1/ANGPT1/F2RL1/IL1RL1/C1QTNF3/HAVCR2/ACP5/NCKAP1L/FABP4/CCL2/FGR/PTPN22/TREM1/TNFRSF21/RNF128/SRGN/LBP/CD86/CD4/C5AR1/IL1A/GPAM/SASH3/NFAM1/SLC11A1/SERPINB7/LCP2/IL6/CD28/SYK/CD14/PTAFR/CMKLR1/C3AR1/CD84/CARD11/CYBB/INHBA/FCER1G/PF4/VSIG4/S100A9/IL33/CD74* |
| G20 | GO:0007204 | Positive regulation of cytosolic calcium ion concentration | 162 | –0.495268688 | –1.803433232 | 0.001390821 | 0.023352669 | tags =20%, list =6%, signal =19% | *FGF2/P2RY1/PTGER3/CORO1A/CHRNA9/ADCY5/CHD7/EDNRA/GNA15/JPH2/LYN/PLCG2/CCR5/F2RL1/PTPN6/BDKRB1/PTPRC/CD4/C5AR1/PTGDR/PLN/JPH1/C3AR1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/EDNRB/FPR3/SNCA* |
| G20 | GO:0007200 | Phospholipase C-activating G-protein coupled receptor signaling pathway | 46 | –0.577030045 | –1.72882831 | 0.003205128 | 0.030486975 | tags =28%, list =6%, signal =27% | *P2RY1/PTGER3/P2RY6/GPR27/GNA15/C5AR1/C3AR1/HTR2A/TGM2/FPR1/EDNRB/FPR3* |
| G21 | GO:0007229 | Integrin-mediated signaling pathway | 74 | –0.558021246 | –1.819842059 | 0.00155521 | 0.023352669 | tags =28%, list =12%, signal =25% | *ITGA9/ITGA5/ITGB5/NEDD9/ITGA1/COL3A1/ITGB3/CTGF/ITGB2/VAV3/LAT/ITGAX/FGR/ITGA2/PLEK/SYK/ITGAM/HCK/FCER1G/TYROBP* |
| G22 | GO:0007271 | Synaptic transmission, cholinergic | 14 | –0.732960901 | –1.711816891 | 0.005217391 | 0.039712286 | tags =57%, list =17%, signal =47% | *CHRNA7/LAMA2/CACNA1A/CHRNE/LYPD1/CHRNA9/APOE* |
| G23 | GO:0007599 | Hemostasis | 249 | –0.45290039 | –1.730088715 | 0.001321004 | 0.023352669 | tags =27%, list =14%, signal =24% | *BLOC1S3/ZFPM2/CSRP1/PDGFRA/ADRA2A/PRKG1/ITPR2/EHD3/GP1BA/PDGFA/DGKG/ITPR1/TLR4/RAC2/P2RX6/PAPSS2/SERPINE1/PDGFB/HSPB1/VWF/P2RX1/ENPP4/PLAUR/GATA6/FAM46A/F2RL2/COL3A1/PLAT/FAP/F3/ITGB3/F2RL3/SERPINE2/VAV3/LAT/PLAU/P2RY1/PROCR/A2M/WAS/GNG2/ZFPM1/VTN/GNA15/LYN/PLCG2/APOE/F2RL1/SCUBE1/PTPN6/DOCK8/PIK3R5/ITGA2/HIST2H3C/HIST2H3A/PRKCB/F13A1/LCP2/PLEK/MERTK/IL6/SYK/SERPINB2/TFPI2/FCER1G/PF4/S100A9* |
| G23 | GO:0007596 | Blood coagulation | 245 | –0.458872036 | –1.745440985 | 0.001344086 | 0.023352669 | tags =28%, list =14%, signal =24% | *BLOC1S3/ZFPM2/CSRP1/PDGFRA/ADRA2A/PRKG1/ITPR2/EHD3/GP1BA/PDGFA/DGKG/ITPR1/TLR4/RAC2/P2RX6/PAPSS2/SERPINE1/PDGFB/HSPB1/VWF/P2RX1/ENPP4/PLAUR/GATA6/FAM46A/F2RL2/COL3A1/PLAT/FAP/F3/ITGB3/F2RL3/SERPINE2/VAV3/LAT/PLAU/P2RY1/PROCR/A2M/WAS/GNG2/ZFPM1/VTN/GNA15/LYN/PLCG2/APOE/F2RL1/SCUBE1/PTPN6/DOCK8/PIK3R5/ITGA2/HIST2H3C/HIST2H3A/PRKCB/F13A1/LCP2/PLEK/MERTK/IL6/SYK/SERPINB2/TFPI2/FCER1G/PF4/S100A9* |
| G23 | GO:0007416 | Synapse assembly | 96 | –0.495757958 | –1.673527924 | 0.003067485 | 0.030486975 | tags =29%, list =10%, signal =26% | *NRXN2/PCDHB14/SYNDIG1/NLGN1/AMIGO3/PCDHB6/PCDHB4/DNM3/PCDHB5/PCDHB2/FLRT3/BAI1/SPTBN2/CDH2/PCDHB10/SPOCK2/LRRN1/SLITRK4/PCDHB9/PCDHB3/WNT5A/SDK2/SRPX2/NRCAM/DNER/ROBO2/AMIGO2* |
| G23 | GO:0007566 | Embryo implantation | 39 | –0.575935644 | –1.681863763 | 0.004846527 | 0.038245256 | tags =33%, list =12%, signal =29% | *TGFBR2/VMP1/IGFBP7/DDR1/ARHGDIB/PTGS2/PCSK5/MMP9/IL1B/STC1/LIF/SPP1* |
| G23 | GO:0007565 | Female pregnancy | 131 | –0.43371669 | –1.537327129 | 0.005747126 | 0.042611428 | tags =26%, list =15%, signal =22% | *AKR1B1/TGFB1/LEP/LGALS9/CD38/CYP27B1/TIMP1/AR/UCN/TGFBR2/VMP1/OVGP1/IGFBP7/DDR1/ARHGDIB/PTGS2/UCP2/PAPPA/HPGD/PCSK5/CTSV/MMP9/FOSB/DSG2/IL1B/TGFB3/HAVCR2/MMP7/CCL2/ITGA2/STC1/LIF/SPP1* |
| G23 | GO:0007584 | Response to nutrient | 126 | –0.448881463 | –1.574851794 | 0.005780347 | 0.042734759 | tags =22%, list =12%, signal =20% | *TTPA/IL15/TGFBR2/LDHA/PTN/ATP2B1/STAR/ARSB/TNC/PTGS2/CCND1/SFRP1/MDM2/SPARC/ABCA1/HMOX1/LIPG/CCL2/ITGA2/CD4/BCHE/CDKN2B/CYBB/STC1/FOLR2/SPP1/PITX2* |
| G24 | GO:0009306 | Protein secretion | 332 | –0.432764663 | –1.686489412 | 0.00128866 | 0.023352669 | tags =26%, list =15%, signal =22% | *LEPRE1/TGFB1/CACNA1A/HYAL2/LEP/TLR6/LGALS9/PTGER4/HIF1A/PARK2/SLC25A4/CD38/TNFRSF9/IRS2/ADRA2A/FN1/ITPR2/IRS1/ITPR1/SERP1/ARNTL/TLR4/NLRC4/RHBDF2/GNPTAB/IL36RN/IL1R2/SYBU/CSF1R/RASGRP1/RAB11FIP1/SIRT4/CADM1/TNFSF4/TLR2/LTBP2/UCP2/DRD4/SOX4/SFRP1/RBP4/RSAD2/PCSK5/TLR1/PRKCZ/ADAM8/ABCA1/TLR8/ADCY5/PTPRN/GPR27/RGCC/IL1B/TMEM27/LYN/RPH3AL/VGF/WNT5A/SLC2A1/TGFB3/LPL/KCNS3/ANGPT1/F2RL1/IL1RL1/C1QTNF3/HAVCR2/FGR/PTPN22/TREM1/TNFRSF21/SRGN/IL1A/GPAM/IL1RN/LCP2/PLEK/IL6/SYK/CD14/IGF1/TRPM2/IL33/SCG2* |
| G24 | GO:0008037 | Cell recognition | 79 | –0.486785068 | –1.611912377 | 0.001531394 | 0.023352669 | tags =25%, list =11%, signal =23% | *CELSR3/OVGP1/DOCK2/CADM1/CATSPERG/B4GALT1/MFGE8/VCAN/NRCAM/PVRL4/HAVCR2/DOCK8/CLEC7A/CADM3/OPCML/EPHA3/GAP43/ROBO2/CD209* |
| G25 | GO:0009611 | Response to wounding | 452 | –0.419988758 | –1.66619471 | 0.001233046 | 0.023352669 | tags =27%, list =14%, signal =24% | *TGFB1/NINJ2/MAPK3/BLOC1S3/ZFPM2/CSRP1/HIF1A/CHL1/PDGFRA/CASK/ADRA2A/PRKG1/PTPRF/TIMP1/SCARF1/GJD4/TPM1/DCBLD2/FN1/ITPR2/EHD3/GP1BA/PDGFA/ENO3/MYH10/DGKG/WNT5B/ITGA9/ITPR1/KANK1/ITGA5/TLR4/TGFBR2/CCR1/SLC1A3/ID3/DDR1/SDC1/NINJ1/RAC2/P2RX6/PAPSS2/SERPINE1/PDGFB/PTK7/HSPB1/VWF/P2RX1/WFDC1/ENPP4/PLAUR/NREP/GATA6/PAX6/FAM46A/F2RL2/B4GALT1/COL3A1/TNC/PLAT/FAP/F3/ITGB3/FABP5/F2RL3/SERPINE2/CTGF/CELSR1/VAV3/FGF2/LAT/PLAU/ABHD2/HBEGF/P2RY1/FLRT3/FZD7/PROCR/A2M/SPARC/WAS/GNG2/ZFPM1/HMOX1/MYLK/VTN/GNA15/MSX2/LYN/WNT5A/PLCG2/DYSF/TGFB3/APOE/NDNF/F2RL1/SCUBE1/PTPN6/CCL2/DOCK8/PIK3R5/ITGA2/HIST2H3C/HIST2H3A/PRKCB/F13A1/IL1A/SLC11A1/LCP2/PLEK/MERTK/IL6/SYK/GAP43/AIF1/SERPINB2/TFPI2/FCER1G/PF4/IGF1/S100A9/MCAM/SPP1* |
| G25 | GO:0009617 | Response to bacterium | 319 | –0.503190254 | –1.951909882 | 0.00128866 | 0.023352669 | tags =22%, list =9%, signal =21% | *CMPK2/SERPINE1/STAR/IFNE/SPON2/MICA/TNFSF4/TLR2/PTGS2/EPHA2/EPPIN/HIST1H2BJ/TLR1/MPO/IL18/DUSP10/SPARC/ABCA1/HIST1H2BK/IGJ/HIST1H2BC/HIST2H2BE/TNFSF8/IL1B/LYN/CXCL16/VGF/WNT5A/PLCG2/IRF8/CCR5/F2RL1/HAVCR2/BDKRB1/ACP5/CD1D/CCL2/FGR/PTPN22/LYZ/TREM1/TNFRSF21/CSF2RB/TNFRSF10D/TREM2/TNFRSF10C/LBP/CD86/CD4/C5AR1/SLC11A1/CD180/IL6/SYK/CD14/PTAFR/STAB1/HCK/CXCL1/IL10RA/FCER1G/PF4/LY86/S100A9/EDNRB/CXCL6/CXCL3/SNCA/CXCL5/IL8* |
| G25 | GO:0009914 | Hormone transport | 191 | –0.446496607 | –1.656318897 | 0.001392758 | 0.023352669 | tags =26%, list =14%, signal =22% | *LEP/INHA/HIF1A/PARK2/SLC25A4/CD38/IRS2/IL11/ADRA2A/ITPR2/IRS1/ITPR1/SERP1/ARNTL/UCN/SLC16A2/SYBU/RAB11FIP1/SIRT4/NKX3-1/SLC16A10/BTK/EXOC3L1/SMPD3/UCP2/SOX4/SFRP1/TBX3/RBP4/P2RY1/ADCY5/PTPRN/GPR27/CHD7/IL1B/TMEM27/LYN/VGF/SLC2A1/KCNS3/C1QTNF3/VAMP8/IL1RN/IL6/HTR2A/INHBA/LIF/TRPM2* |
| G25 | GO:0010310 | Regulation of hydrogen peroxide metabolic process | 10 | –0.826951551 | –1.78328156 | 0.007366483 | 0.049685189 | tags =30%, list =9%, signal =27% | *SNCA/MMP3* |
| G26 | GO:0010324 | Membrane invagination | 42 | –0.62618967 | –1.849924124 | 0.001618123 | 0.023352669 | tags =26%, list =7%, signal =25% | *ABCA1/CD300A/BIN2/F2RL1/NCKAP1L/TREM2/ITGA2/AIF1/FCGR1A/FCER1G* |
| G27 | GO:0010543 | Regulation of platelet activation | 21 | –0.705639414 | –1.82532538 | 0.001686341 | 0.023352669 | tags =52%, list =13%, signal =46% | *PRKG1/PDGFA/TLR4/PDGFB/SERPINE2/LYN/APOE/PLEK/SYK/FCER1G* |
| G27 | GO:0010517 | Regulation of phospholipase activity | 44 | –0.540662284 | –1.598521685 | 0.006430868 | 0.045354927 | tags =32%, list =13%, signal =28% | *FLT1/PLCB2/PLA2G5/FGF2/PRKCZ/RGS2/EDNRA/GNA15/APOC2/C5AR1/PTAFR/HTR2A/SNCA* |
| G28 | GO:0010712 | Regulation of collagen metabolic process | 28 | –0.659356843 | –1.796950783 | 0.001672241 | 0.023352669 | tags =39%, list =14%, signal =34% | *ITGB1/UCN/FAP/CTGF/RGCC/TGFB3/CCL2/ITGA2/SERPINB7/IL6* |
| G28 | GO:0010675 | Regulation of cellular carbohydrate metabolic process | 98 | –0.482707781 | –1.637151396 | 0.003021148 | 0.030486975 | tags =28%, list =16%, signal =23% | *NR1D1/PGAM1/GNMT/PPP1R3B/LEP/PARK2/IRS2/SORBS1/IRS1/DDIT4/C12orf5/PDK1/RORA/SIK1/PDK4/FOXO1/P2RY1/PDK3/FBP1/DGAT2/C1QTNF3/PLEK/IL6/PTAFR/IGF1/SNCA* |
| G28 | GO:0010634 | Positive regulation of epithelial cell migration | 91 | –0.468165122 | –1.575940207 | 0.00456621 | 0.037949001 | tags =34%, list =21%, signal =27% | *FGF7/GLIPR2/JUN/TGFB2/THBS1/ZNF580/BCAR1/PROX1/TGFB1/HIF1A/PLCG1/TGFBR2/PDGFB/VEGFA/HSPB1/PTGS2/ITGB3/FGF2/MMP9/HBEGF/SPARC/NRP2/ANGPT4/WNT5A/SRPX2/HAS2/ANGPT1/ITGA2/SOX9/KDR* |
| G28 | GO:0010714 | Positive regulation of collagen metabolic process | 17 | –0.706071964 | –1.723022092 | 0.005272408 | 0.039836829 | tags =47%, list =14%, signal =40% | *UCN/CTGF/RGCC/TGFB3/CCL2/ITGA2/SERPINB7* |
| G29 | GO:0010817 | Regulation of hormone levels | 289 | –0.435544503 | –1.679712889 | 0.001297017 | 0.023352669 | tags =26%, list =15%, signal =23% | *DKK3/FDXR/CACNA1A/LEP/INHA/HIF1A/PARK2/SLC25A4/AKR1C2/CD38/IRS2/IL11/ADRA2A/ALDH8A1/TG/ITPR2/IRS1/AKR1C1/ITPR1/SULT1B1/SERP1/ARNTL/UCN/SOX8/SLC16A2/ALDH1A3/SYBU/RAB11FIP1/SIRT4/STAR/CTSZ/HSD17B14/NKX3-1/SLC16A10/BTK/RDH10/ADH4/EXOC3L1/SMPD3/CRABP2/HSD17B1/CACNA1H/UCP2/SOX4/SFRP1/TBX3/RBP4/PCSK5/DDO/P2RY1/DGAT2/DHRS9/ADCY5/PTPRN/GPR27/CHD7/DHRS3/IL1B/TMEM27/LYN/VGF/SLC2A1/KCNS3/CYP26B1/C1QTNF3/VAMP8/RBP1/ENPEP/IL1RN/IL6/HTR2A/INHBA/LIF/TRPM2/BMP2* |
| G3 | GO:0001817 | Regulation of cytokine production | 423 | –0.45154761 | –1.790656474 | 0.001230012 | 0.023352669 | tags =28%, list =15%, signal =24% | *MIF/SSC5D/POLR3G/GBA/IL1RAP/HERC5/TRIB2/JAK3/POLR3A/ARRB2/TGFB1/TUSC2/HYAL2/CEBPB/LEP/BST2/TLR6/POLR2K/C5orf30/LGALS9/INHA/PTGER4/HIF1A/MAPK13/TNFRSF9/ADRA2A/FN1/SPN/IL15/TLR4/UCN/HLA-DPB1/IL36RN/IL1R2/CSF1R/RASGRP1/SERPINE1/RORA/HSPB1/PLCB1/BTK/CADM1/GATA6/SPON2/TNFSF4/TLR2/PTGS2/RUNX1/EPHA2/RSAD2/TLR1/PRKCZ/ADAM8/IL18/CD83/IGF2BP3/ZFPM1/IGF2BP1/CLU/F11R/TLR8/TLR7/HMOX1/AC005013.1/WNT11/RGCC/HLA-DPA1/IL1B/LYN/WNT5A/IL36B/PLCG2/TGFB3/LPL/IRF8/INPP5D/SULF1/ANGPT1/F2RL1/IL1RL1/C1QTNF3/HAVCR2/ACP5/NCKAP1L/CCL2/FGR/PTPN22/TNFRSF21/RNF128/SRGN/LBP/CD86/CD4/C5AR1/IL1A/GPAM/SASH3/NFAM1/SLC11A1/SERPINB7/IL6/CD28/SYK/CD14/PTAFR/CMKLR1/C3AR1/CD84/CARD11/CYBB/INHBA/FCER1G/PF4/VSIG4/IL33/CD74* |
| G3 | GO:0001819 | Positive regulation of cytokine production | 283 | –0.470442412 | –1.813438675 | 0.001293661 | 0.023352669 | tags =29%, list =9%, signal =26% | *IL1RAP/POLR3A/TGFB1/TUSC2/HYAL2/CEBPB/LEP/TLR6/POLR2K/LGALS9/PTGER4/HIF1A/MAPK13/ADRA2A/SPN/IL15/TLR4/UCN/HLA-DPB1/CSF1R/RASGRP1/SERPINE1/RORA/HSPB1/PLCB1/CADM1/SPON2/TNFSF4/TLR2/PTGS2/RUNX1/RSAD2/TLR1/PRKCZ/ADAM8/IL18/CD83/ZFPM1/CLU/TLR8/TLR7/HMOX1/WNT11/RGCC/HLA-DPA1/IL1B/WNT5A/IL36B/PLCG2/LPL/IRF8/SULF1/F2RL1/IL1RL1/C1QTNF3/HAVCR2/CCL2/FGR/PTPN22/LBP/CD86/CD4/C5AR1/IL1A/SASH3/NFAM1/SLC11A1/SERPINB7/IL6/CD28/SYK/CD14/PTAFR/C3AR1/CARD11/CYBB/FCER1G/PF4/IL33/CD74* |
| G3 | GO:0001818 | Negative regulation of cytokine production | 162 | –0.497212337 | –1.810510685 | 0.001390821 | 0.023352669 | tags =31%, list =15%, signal =27% | *GAS6/CHRNA7/SSC5D/GBA/HERC5/TRIB2/JAK3/ARRB2/TGFB1/TUSC2/BST2/C5orf30/LGALS9/INHA/PTGER4/TNFRSF9/FN1/TLR4/IL36RN/IL1R2/BTK/GATA6/TNFSF4/EPHA2/CD83/ZFPM1/HMOX1/WNT11/RGCC/TGFB3/INPP5D/ANGPT1/F2RL1/IL1RL1/C1QTNF3/HAVCR2/ACP5/NCKAP1L/PTPN22/TNFRSF21/RNF128/SRGN/LBP/SLC11A1/IL6/CMKLR1/CD84/INHBA/VSIG4/IL33* |
| G30 | GO:0010942 | Positive regulation of cell death | 500 | –0.329980311 | –1.320229841 | 0.005980861 | 0.043777526 | tags =20%, list =17%, signal =17% | *APBB2/NACC2/MAP2K6/CHEK2/CDK5/SORT1/BCAP31/FAS/OBSCN/COL18A1/TRIM35/MAGED1/CDKN2A/TGFB1/HYAL2/LEP/ITGB1/LGALS9/NET1/ZMAT3/PARK2/ROBO1/SFN/ATF3/CSRNP3/IFI27/TNFRSF10B/NOX4/DDIT4/ZNF622/ACER2/NLRC4/ID3/SQSTM1/LDHA/DUSP6/PTN/ALDH1A3/C12orf5/TNFRSF10A/FAM162A/GADD45A/CTD-2207O23.3/NKX3-1/SIK1/P2RX1/ITM2C/PLAUR/ITGA1/RET/B4GALT1/FAP/PTGS2/SKIL/F3/PPP1R13B/UCP2/CTGF/SOX4/SFRP1/CAMK2A/VAV3/KCNMA1/SCIN/FOXO1/XDH/MMP9/ADAM8/KALRN/CDKN1A/TPD52L1/CLU/BNIP3/MNDA/RASGRF2/PIDD/HMOX1/WNT11/MLLT11/RGCC/MSX2/SFRP4/LYN/WNT5A/GADD45G/TGFB3/INPP5D/GRIK2/RARB/IL6/FGD2/TGM2/BCL2A1/INHBA/TRPM2/UNC5C/S100A9/SNCA/BMP2/MMP3/HOXA5* |
| G31 | GO:0014068 | Positive regulation of phosphatidylinositol 3-kinase signaling | 53 | –0.520809074 | –1.616586466 | 0.003100775 | 0.030486975 | tags =34%, list =14%, signal =29% | *C19orf10/PDGFRA/FLT1/PDGFA/PDGFB/NKX3-1/PRR5L/IL18/ANGPT1/F2RL1/PTPN6/FGR/PIK3AP1/SOX9/CD28/IGF1/KDR* |
| G32 | GO:0014074 | Response to purine-containing compound | 103 | –0.470492013 | –1.604363336 | 0.002985075 | 0.030486975 | tags =23%, list =12%, signal =21% | *ITPR2/HCN2/AP000322.53/LDHA/SDC1/P2RX6/STAR/P2RX1/PLA2G5/KCNE1/PTGS2/SPARC/FOSB/PTPRN/IL1B/VGF/SELL/AQP9/CCL2/IL6/PTAFR/STC1/TRPM2* |
| G32 | GO:0014909 | Smooth muscle cell migration | 54 | –0.526710192 | –1.634652033 | 0.003100775 | 0.030486975 | tags =33%, list =12%, signal =29% | *NOX4/PDGFA/SEMA6D/DDR1/SERPINE1/PDGFB/PLAT/ITGB3/PLAU/MDM2/NDRG4/P2RY6/VTN/HAS2/ITGA2/AIF1/IGF1* |
| G32 | GO:0014910 | Regulation of smooth muscle cell migration | 47 | –0.547802783 | –1.644235803 | 0.004769475 | 0.038245256 | tags =32%, list =12%, signal =28% | *NOX4/PDGFA/SEMA6D/SERPINE1/PDGFB/PLAU/MDM2/NDRG4/P2RY6/VTN/HAS2/ITGA2/AIF1/IGF1* |
| G32 | GO:0014911 | Positive regulation of smooth muscle cell migration | 26 | –0.630658507 | –1.694635727 | 0.006622517 | 0.046053749 | tags =38%, list =12%, signal =34% | *SEMA6D/PDGFB/MDM2/P2RY6/VTN/HAS2/ITGA2/AIF1/IGF1* |
| G33 | GO:0015833 | Peptide transport | 170 | –0.420007506 | –1.538774411 | 0.001386963 | 0.023352669 | tags =24%, list =14%, signal =21% | *LEP/HIF1A/PARK2/SLC25A4/CD38/IRS2/ADRA2A/ITPR2/IRS1/ITPR1/SERP1/ARNTL/UCN/SLC15A3/SYBU/SIRT4/DISP1/EXOC3L1/SMPD3/UCP2/SOX4/SFRP1/RBP4/ABCA1/ADCY5/PTPRN/GPR27/CHD7/IL1B/TMEM27/VGF/SLC2A1/CA2/KCNS3/IL1RN/IL6/CD209/TRPM2/S100A9/CD74* |
| G33 | GO:0015844 | Monoamine transport | 37 | –0.622793601 | –1.824481646 | 0.001597444 | 0.023352669 | tags =30%, list =8%, signal =27% | *SLC29A4/GDNF/DRD4/P2RY1/SYK/HTR2A/CADPS/FCER1G/SNCA/SLC22A3* |
| G34 | GO:0019221 | Cytokine-mediated signaling pathway | 402 | –0.420048629 | –1.65649024 | 0.001248439 | 0.023352669 | tags =18%, list =11%, signal =17% | *LRRC19/RNF31/CCR1/CXCL2/IL2RA/IL36RN/LRRC66/IL1R2/CSF1R/TNFRSF10A/CDIP1/PDGFB/IFNE/MT2A/PLCB1/TNFSF4/F3/LRRC15/IFI6/CAMK2A/RSAD2/KRT18/PODNL1/FLRT3/IL18/PTPRN/PADI2/CNTFR/HLA-DPA1/IL1B/WNT5A/IL36B/IRF8/CCL26/CCR5/ANGPT1/CCL22/F2RL1/IL1RL1/PTPN6/CCL2/TNFRSF21/CSF2RB/PTPRC/TNFRSF10D/TREM2/TNFRSF10C/IL1A/IL1RN/IL6/SYK/PTAFR/CCL8/CMKLR1/HLA-DQA1/HCK/FCGR1A/CXCR4/CXCL1/IL10RA/PF4/HLA-DQB1/HLA-DRB1/CXCL6/CXCL3/CCL13/HLA-DRB5/CD74/HLA-DRA/PLVAP/CXCL5/IL8* |
| G34 | GO:0016051 | Carbohydrate biosynthetic process | 153 | –0.482999306 | –1.747237284 | 0.001416431 | 0.023352669 | tags =29%, list =16%, signal =24% | *NR1D1/PGAM1/GYG2/GPI/GNMT/IMPAD1/AKR1B1/PPP1R3B/TGFB1/PGM1/LEP/TPI1/ATF3/IRS2/SORBS1/IRS1/ENO3/ENO2/GAPDH/ALDOC/ALDOA/PGK1/PDGFB/SIK1/B4GALT1/RBP4/GYS1/FOXO1/P2RY1/FBP1/DGAT2/HAS3/HAS2/SLC2A1/PPP1R3C/C1QTNF3/PLEK/IL6/PTAFR/IGF1/SDS/SNCA/HAS1* |
| G34 | GO:0015850 | Organic hydroxy compound transport | 115 | –0.508472604 | –1.760505093 | 0.001451379 | 0.023352669 | tags =21%, list =9%, signal =19% | *STAR/P2RX1/GDNF/DRD4/RBP4/APOC1/P2RY1/ABCA1/CLU/ABCB4/APOE/LIPG/CES1/AQP9/MSR1/APOC2/SYK/HTR2A/CADPS/FCER1G/SLCO2B1/SNCA/SLC22A3* |
| G34 | GO:0019319 | Hexose biosynthetic process | 66 | –0.562569042 | –1.790663063 | 0.001550388 | 0.023352669 | tags =36%, list =16%, signal =31% | *NR1D1/PGAM1/GPI/GNMT/AKR1B1/PGM1/LEP/TPI1/ATF3/ENO3/ENO2/GAPDH/ALDOC/ALDOA/PGK1/SIK1/RBP4/FOXO1/FBP1/DGAT2/C1QTNF3/IL6/SDS* |
| G34 | GO:0019724 | B cell mediated immunity | 74 | –0.519170481 | –1.693140332 | 0.00155521 | 0.023352669 | tags =23%, list =8%, signal =21% | *TNFSF4/GCNT3/C7/CLU/CFI/TLR8/CR1/INPP5D/PTPN6/CD28/C1QA/FCER1G/HLA-DQB1/CD74/C1QB/C1QC* |
| G34 | GO:0016064 | Immunoglobulin mediated immune response | 73 | –0.524197104 | –1.699626357 | 0.001564945 | 0.023352669 | tags =23%, list =8%, signal =22% | *TNFSF4/GCNT3/C7/CLU/CFI/TLR8/CR1/INPP5D/PTPN6/CD28/C1QA/FCER1G/HLA-DQB1/CD74/C1QB/C1QC* |
| G34 | GO:0016101 | Diterpenoid metabolic process | 59 | –0.58101735 | –1.824797014 | 0.001567398 | 0.023352669 | tags =37%, list =12%, signal =33% | *AKR1C1/GPC4/ALDH1A3/SDC1/STAR/GPC2/RDH10/ADH4/CRABP2/GPC3/RBP4/DGAT2/DHRS9/DHRS3/STRA6/LPL/APOE/CYP26B1/AKR1B10/RBP1/APOC2* |
| G34 | GO:0016339 | Calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules | 24 | –0.660300611 | –1.748380255 | 0.001655629 | 0.023352669 | tags =46%, list =9%, signal =42% | *NLGN1/PCDHB6/PCDHB4/PCDHB5/PCDHB2/CDH23/CDH2/PCDHB10/PCDHB9/PCDHB3* |
| G34 | GO:0017157 | Regulation of exocytosis | 116 | –0.477453166 | –1.653897965 | 0.002898551 | 0.030486975 | tags =30%, list =17%, signal =25% | *STXBP1/CDK5/STXBP6/C19orf26/SYT15/NSF/CACNA1A/LGALS9/ADRA2A/ATP6AP1/RIMS3/NCS1/SDC1/RAC2/NLGN1/SYTL1/STXBP2/SMPD3/UNC13D/SYTL3/SYN1/RIMS1/HMOX1/TMEM27/LYN/CD300A/F2RL1/VAMP8/FGR/SYK/PTAFR/CD84/FCER1G/SNCA* |
| G34 | GO:0019722 | Calcium-mediated signaling | 103 | –0.499958677 | –1.704843757 | 0.002985075 | 0.030486975 | tags =20%, list =6%, signal =19% | *LAT2/BTK/ATP1B1/LAT/HOMER2/JPH2/PLCG2/CCR5/TREM2/CD4/MCTP1/PLN/PLEK/JPH1/SYK/CMKLR1/CXCR4/IGF1/KDR/IL8* |
| G34 | GO:0019674 | NAD metabolic process | 43 | –0.5581678 | –1.649847029 | 0.006451613 | 0.045354927 | tags =58%, list =25%, signal =44% | *PFKP/PNP/PFKM/HK2/PFKFB2/PFKFB3/PFKL/PGAM1/GPI/GPD1L/NADSYN1/TPI1/ENO3/ENO2/GAPDH/ALDOC/ALDOA/LDHA/C12orf5/PKM/PGK1/QPRT/PFKFB4/HK3* |
| G35 | GO:0019882 | Antigen processing and presentation | 191 | –0.427412865 | –1.585526056 | 0.001392758 | 0.023352669 | tags =13%, list =5%, signal =13% | *CTSV/CTSS/WAS/SPTBN2/HLA-DMA/HLA-DPA1/ABCB4/CD1D/KIF5A/TREM2/NCF4/NCF2/SLC11A1/HLA-DQA1/HLA-DMB/CYBB/CD209/FCGR1A/FCER1G/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G35 | GO:0019884 | Antigen processing and presentation of exogenous antigen | 146 | –0.458925212 | –1.652679618 | 0.00141844 | 0.023352669 | tags =15%, list =6%, signal =14% | *LGMN/CTSV/CTSS/SPTBN2/HLA-DMA/HLA-DPA1/ABCB4/CD1D/KIF5A/NCF4/NCF2/HLA-DQA1/HLA-DMB/CYBB/FCGR1A/FCER1G/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G35 | GO:0019886 | Antigen processing and presentation of exogenous peptide antigen via MHC class II | 81 | –0.469751384 | –1.551321704 | 0.00462963 | 0.037949001 | tags =20%, list =6%, signal =19% | *LGMN/CTSV/CTSS/SPTBN2/HLA-DMA/HLA-DPA1/KIF5A/HLA-DQA1/HLA-DMB/FCER1G/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G36 | GO:0030003 | Cellular cation homeostasis | 381 | –0.422415565 | –1.66188756 | 0.001251564 | 0.023352669 | tags =28%, list =17%, signal =23% | *FTL/ATP13A2/ATP6V1F/MYO5A/ATP6V1G1/CAPN3/SLC9A4/BCAP31/HTT/CHRNA7/ATP7A/ATP6V1G2/ATP6V0E1/ATP6V1A/SLC46A1/ATP6V0A1/TGFB1/CACNA1A/SLC22A17/GNAT2/ATP13A3/ATP6V1E1/PTGER4/TF/HIF1A/DMD/ABCG2/STIM2/CD38/PDGFRA/PLCG1/TTPA/ITPR2/TRPC4/CD52/SLC4A3/LETM2/TFRC/ITPR1/SLC11A2/OPRL1/CCR1/SLC26A1/ATP6V0C/SLC30A10/EGLN1/FTH1/ATP2B1/MT2A/SLC4A11/DRD4/F2RL3/SLC9A7/ATP1B1/FGF2/KCNMA1/P2RY1/PTGER3/CORO1A/CDH23/SLC24A3/ATP2A3/CHRNA9/ADCY5/HMOX1/CHD7/SLC4A4/EDNRA/GNA15/ATP6V0D2/JPH2/LYN/PLCG2/CA2/APOE/CCR5/F2RL1/SLC30A3/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/C5AR1/SLC11A1/PTGDR/GRIK2/PLN/JPH1/CCL8/C3AR1/STC1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/S100A9/EDNRB/FPR3/CCL13/SNCA/CALB2* |
| G36 | GO:0023061 | Signal release | 275 | –0.419545236 | –1.612847072 | 0.00130039 | 0.023352669 | tags =24%, list =14%, signal =21% | *CACNA1A/LEP/DNAJC5/INHA/HIF1A/PARK2/SLC25A4/CD38/SYN3/CASK/IRS2/IL11/ADRA2A/ITPR2/IRS1/ITPR1/SERP1/ARNTL/UCN/NRXN2/RIMS3/SYNJ1/SYBU/LIN7A/RAB11FIP1/SIRT4/NLGN1/NKX3-1/SYTL1/BTK/PPFIA3/EXOC3L1/SMPD3/UCP2/SOX4/SFRP1/TBX3/CAMK2A/SYTL3/RBP4/PPFIA4/SYN1/P2RY1/RIMS1/ADCY5/PTPRN/GPR27/CHD7/IL1B/TMEM27/LYN/VGF/SLC2A1/KCNS3/C1QTNF3/VAMP8/IL1RN/IL6/HTR2A/CADPS/INHBA/LIF/TRPM2/SNCA* |
| G36 | GO:0022407 | Regulation of cell-cell adhesion | 263 | –0.492040455 | –1.884206496 | 0.001317523 | 0.023352669 | tags =20%, list =6%, signal =19% | *KIF26B/SERPINE2/DPP4/LAT/PRKCZ/ADAM8/CORO1A/IL18/CD83/SPINT2/CAMK4/RGCC/HLA-DPA1/IL1B/LYN/CD300A/WNT5A/IL36B/HAS2/CYP26B1/PAG1/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/IL1RN/IL6/CD28/SYK/AIF1/PTAFR/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/CD209/IGF1/VSIG4/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G36 | GO:0030099 | Myeloid cell differentiation | 261 | –0.462933912 | –1.769313385 | 0.00132626 | 0.023352669 | tags =22%, list =14%, signal =19% | *CEBPB/LEP/INHA/HIF1A/FSTL3/IL11/TNFRSF11A/EPAS1/HIPK2/TFRC/BATF2/TLR4/SLC11A2/TGFBR2/CCR1/ATP6AP1/ACVR2A/MEIS2/CSF1R/VEGFA/SH3PXD2A/TSPAN2/GPC3/HOXA9/RUNX1/SFRP1/EPHA2/DCSTAMP/SCIN/MMP9/HOXA7/ZFPM1/MEIS1/CAMK4/SIGLEC15/LILRB4/LYN/LILRA6/IRF8/CA2/INPP5D/F2RL1/PTPN6/NCKAP1L/CD86/CDKN2B/GPR183/HIST1H4H/SPI1/INHBA/HOXB7/PF4/LIF/TYROBP/HOXA5/C1QC/HOXB8* |
| G36 | GO:0030098 | Lymphocyte differentiation | 217 | –0.485045836 | –1.831155209 | 0.001349528 | 0.023352669 | tags =31%, list =15%, signal =26% | *NOTCH2/JAK3/TGFB1/TUSC2/LEP/JAG2/ITGB1/LGALS9/INHA/PTGER4/HLA-DOA/IL11/TNFSF9/SATB1/SPN/IL15/TGFBR2/PREX1/GLI2/IL2RA/DOCK2/RASGRP1/RORA/IFNE/BTK/TNFSF4/ITM2A/SOX4/SFRP1/RSAD2/PRKCZ/ADAM8/FZD8/FZD7/IL18/CD83/ZFPM1/TNFSF8/TPD52/CAMK4/CHD7/LYL1/BLNK/IL36B/PLCG2/INPP5D/CYP26B1/PTPN6/NCKAP1L/CD1D/PTPN22/PTPRC/CD86/CD4/SASH3/NFAM1/MERTK/IL6/CD28/SYK/GPR183/CARD11/SPI1/INHBA/FCER1G/CD74* |
| G36 | GO:0019932 | Second-messenger-mediated signaling | 164 | –0.479744406 | –1.748579516 | 0.001390821 | 0.023352669 | tags =20%, list =8%, signal =18% | *BTK/PDE10A/RASD2/ATP1B1/LAT/PDE3B/HOMER2/ADCY8/RGS2/ADCY5/JPH2/PLCG2/APOE/CCR5/NDNF/TREM2/CD4/SOX9/MCTP1/PLN/PLEK/JPH1/SYK/CMKLR1/CXCR4/PF4/IGF1/FPR1/KDR/EDNRB/IL8* |
| G36 | GO:0022409 | Positive regulation of cell-cell adhesion | 164 | –0.578010093 | –2.106739748 | 0.001390821 | 0.023352669 | tags =24%, list =7%, signal =23% | *KIF26B/DPP4/PRKCZ/ADAM8/CORO1A/IL18/CD83/HLA-DPA1/IL1B/LYN/WNT5A/IL36B/HAS2/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/PTAFR/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/IGF1/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G36 | GO:0030100 | Regulation of endocytosis | 159 | –0.439311728 | –1.59319273 | 0.001408451 | 0.023352669 | tags =17%, list =9%, signal =16% | *NLGN1/VEGFA/MFGE8/GPC3/STON1/APOC1/VTN/SFRP4/IL1B/CD300A/WNT5A/PLCG2/ANGPT1/F2RL1/NCKAP1L/CCL2/FGR/ITGA2/APOC2/SLC11A1/MERTK/SYK/CD14/HCK/FCER1G/SNCA* |
| G36 | GO:0022617 | Extracellular matrix disassembly | 67 | –0.550049009 | –1.757839363 | 0.001560062 | 0.023352669 | tags =28%, list =9%, signal =26% | *MMP11/MMP15/FAP/DPP4/CTSV/MMP9/CTSS/ADAM8/A2M/LCP1/MMP16/MMP10/MMP7/FBN2/MMP8/MMP1/SPP1/MMP3* |
| G37 | GO:0030155 | Regulation of cell adhesion | 483 | –0.441816931 | –1.763466096 | 0.001207729 | 0.023352669 | tags =23%, list =13%, signal =21% | *HLA-DOA/CASK/PRKG1/TNFSF9/TPM1/FN1/SPN/LPXN/CYTH1/IL15/TFRC/KANK1/ITGA5/TGFBR2/HLA-DPB1/PREX1/ACER2/GLI2/IL2RA/NUAK1/PTN/DDR1/GPR56/NINJ1/RAC2/RASGRP1/SERPINE1/VEGFA/RAC3/SERPINI1/ARHGDIB/ADAM22/RET/TNC/TNFSF4/KIF26B/PLXNB3/SERPINE2/DPP4/UNC13D/SFRP1/VAV3/EPHA2/LAT/PLAU/OLFM4/PRKCZ/RND1/PDE3B/ADAM8/CORO1A/FZD7/IL18/CD83/HOXA7/SPINT2/SPOCK2/PLEKHA2/CAMK4/RGCC/VTN/HLA-DPA1/IL1B/LYN/CD300A/WNT5A/IL36B/HAS2/ANGPT1/CYP26B1/PAG1/NDNF/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/PTPN22/TNFRSF21/PTPRC/ITGA2/ADAMDEC1/CD86/CD4/EPHA3/GPAM/SASH3/SOX9/IL1RN/EDIL3/IL6/CD28/SYK/AIF1/PTAFR/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/CD209/TGM2/IGF1/VSIG4/KDR/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA/BMP2/IL8* |
| G37 | GO:0030168 | Platelet activation | 122 | –0.55780098 | –1.947139436 | 0.001445087 | 0.023352669 | tags =34%, list =14%, signal =30% | *ARRB2/MAPK3/BLOC1S3/CSRP1/PDGFRA/ADRA2A/PRKG1/ITPR2/GP1BA/PDGFA/DGKG/ITPR1/TLR4/RAC2/PDGFB/HSPB1/VWF/P2RX1/F2RL2/COL3A1/ITGB3/F2RL3/SERPINE2/VAV3/LAT/P2RY1/GNG2/GNA15/LYN/PLCG2/APOE/PTPN6/PIK3R5/PRKCB/LCP2/PLEK/MERTK/IL6/SYK/FCER1G/PF4* |
| G37 | GO:0030183 | B cell differentiation | 79 | –0.495507837 | –1.640796455 | 0.001531394 | 0.023352669 | tags =20%, list =8%, signal =19% | *BTK/ITM2A/SFRP1/TPD52/LYL1/BLNK/PLCG2/INPP5D/PTPN6/NCKAP1L/NFAM1/SYK/GPR183/CARD11/INHBA* |
| G37 | GO:0030193 | Regulation of blood coagulation | 56 | –0.544751717 | –1.700063657 | 0.00155521 | 0.023352669 | tags =43%, list =13%, signal =38% | *PRKG1/GP1BA/PDGFA/TLR4/SERPINE1/PDGFB/ENPP4/PLAUR/FAM46A/PLAT/FAP/F3/SERPINE2/PLAU/VTN/LYN/APOE/F2RL1/PLEK/SYK/SERPINB2/FCER1G/S100A9* |
| G38 | GO:0030198 | Extracellular matrix organization | 264 | –0.446818696 | –1.711915142 | 0.001315789 | 0.023352669 | tags =25%, list =9%, signal =23% | *SERPINE1/COL5A2/COL11A2/PDGFB/MMP11/CRISPLD2/VWF/COL4A2/COL27A1/THSD4/ITGA1/MMP15/B4GALT1/COL3A1/TNC/COL11A1/FAP/ITGB3/LTBP2/COL4A1/DPP4/CTGF/DPT/ITGB2/HAPLN1/FGF2/ANTXR1/VCAN/MYH11/CTSV/MMP9/CTSS/ADAM8/A2M/LOXL2/SPARC/LCP1/P4HA1/F11R/SPINT2/SPOCK2/MPZL3/MMP16/ITGAX/RGCC/VTN/MMP10/COL7A1/HAS3/HAS2/SULF1/NDNF/MMP7/FBN2/ITGA2/SOX9/ITGAM/MMP8/COL10A1/KDR/MMP1/SNCA/SPP1/MMP3/HAS1* |
| G39 | GO:0030217 | T cell differentiation | 152 | –0.477403293 | –1.7218418 | 0.001422475 | 0.023352669 | tags =30%, list =14%, signal =26% | *LEP/JAG2/LGALS9/PTGER4/HLA-DOA/TNFSF9/SATB1/SPN/IL15/TGFBR2/PREX1/GLI2/IL2RA/DOCK2/RASGRP1/RORA/TNFSF4/SOX4/RSAD2/PRKCZ/ADAM8/FZD8/FZD7/IL18/CD83/ZFPM1/TNFSF8/CAMK4/CHD7/IL36B/CYP26B1/NCKAP1L/CD1D/PTPN22/PTPRC/CD86/CD4/SASH3/IL6/CD28/SYK/GPR183/CARD11/FCER1G/CD74* |
| G39 | GO:0030203 | Glycosaminoglycan metabolic process | 130 | –0.422660345 | –1.497957562 | 0.005714286 | 0.042490208 | tags =33%, list =16%, signal =28% | *B4GALT7/NDST1/HSPG2/HS3ST3B1/HYAL3/B3GAT3/IMPAD1/TGFB1/CHST2/HYAL2/ST3GAL1/IL15/CHPF2/DSE/GPC4/SDC1/B4GALT6/PDGFB/GPC2/ARSB/CHPF/CHST1/B4GALT1/ST3GAL6/CHSY3/GPC3/HS3ST3A1/B3GNT7/FGF2/CHST7/VCAN/SPOCK2/HS3ST1/IL1B/HAS3/HAS2/ANGPT1/NDNF/EXTL1/FUCA1/HS3ST2/HAS1* |
| G4 | GO:0001935 | Endothelial cell proliferation | 95 | –0.482191527 | –1.63001238 | 0.00304878 | 0.030486975 | tags =34%, list =8%, signal =31% | *GJA1/ZNF580/ERN1/EGFL7/PROX1/LEP/C19orf10/HIF1A/RPTOR/VASH2/PDGFB/VEGFA/F3/ITGB3/PLXNB3/EPHA2/FGF2/XDH/LOXL2/SPARC/HMOX1/RGCC/NRP2/WNT5A/APOE/CCL26/SULF1/CCL2/KDR/BMP2/SCG2* |
| G4 | GO:0001837 | Epithelial to mesenchymal transition | 93 | –0.456613459 | –1.537296665 | 0.006125574 | 0.04452057 | tags =27%, list =14%, signal =23% | *SDHAF2/HIF1A/GSC/FAM101B/TGFBR2/BCL9L/LOXL3/HEY1/SFRP1/SNAI1/LOXL2/WNT11/RGCC/MSX2/WNT5A/HAS2/TGFB3/HEYL/LDLRAD4/EPHA3/SOX9/TBX5/ALX1/BMP2* |
| G40 | GO:0030335 | Positive regulation of cell migration | 321 | –0.505151723 | –1.96094512 | 0.001293661 | 0.023352669 | tags =27%, list =13%, signal =24% | *MYADM/PDGFRA/FLT1/IRS2/ADRA2A/PLCG1/NOX4/FN1/PDGFA/SEMA6D/WNT5B/ITGA5/TGFBR2/CCR1/CXCL2/FAM83H/RAC2/CSF1R/SERPINE1/KIAA1598/PDGFB/VEGFA/HSPB1/PTP4A1/FAM115C/CXCL14/RET/PTGS2/F3/ITGB3/LRRC15/ATP8A1/FGF2/PLAU/MDM2/MMP9/SNAI1/HBEGF/ADAM8/CORO1A/SPARC/P2RY6/MYLK/WNT11/VTN/NRP2/LYN/ANGPT4/CXCL16/WNT5A/SRPX2/HAS2/CCL26/ANGPT1/F2RL1/BDKRB1/NCKAP1L/CCL2/FGR/PTPRC/ITGA2/LBP/C5AR1/IL1A/SOX9/IL6/AIF1/PTAFR/CCL8/CMKLR1/C3AR1/CXCL1/SEMA6B/PF4/IGF1/KDR/CXCL6/MCAM/CXCL3/PLA2G7/CD74/BMP2/PLVAP/CXCL5/IL8* |
| G40 | GO:0030595 | Leukocyte chemotaxis | 119 | –0.648112618 | –2.254644133 | 0.001445087 | 0.023352669 | tags =39%, list =6%, signal =37% | *CCR1/CXCL2/RAC2/SERPINE1/PDGFB/CXCL14/ITGA1/ITGB2/VAV3/ADAM8/CORO1A/PADI2/IL1B/LYN/CXCL16/WNT5A/CCL26/CCR5/CCL22/F2RL1/NCKAP1L/CCL2/TREM1/LBP/C5AR1/IL6/SYK/AIF1/CCL8/CMKLR1/C3AR1/GPR183/CXCR4/CXCL1/FCER1G/PF4/S100A9/EDNRB/CXCL6/CXCL3/CCL13/PLA2G7/CD74/SCG2/CXCL5/IL8* |
| G40 | GO:0030260 | Entry into host cell | 93 | –0.49965221 | –1.682196746 | 0.001531394 | 0.023352669 | tags =28%, list =7%, signal =26% | *GAS6/P4HB/CXADR/HYAL2/ITGB1/LGALS9/TFRC/ITGA5/ITGB5/ITGB3/DPP4/F11R/SLC52A1/CR1/PVRL4/CCR5/VAMP8/EFNB2/ITGA2/CD86/CD4/CD209/HTR2A/CXCR4/IL8* |
| G40 | GO:0030574 | Collagen catabolic process | 56 | –0.55430266 | –1.729870285 | 0.00155521 | 0.023352669 | tags =46%, list =11%, signal =41% | *CTSD/MMP19/ITGB1/COL25A1/COL15A1/COL4A5/COL5A2/COL11A2/MMP11/COL4A2/MMP15/COL3A1/COL11A1/FAP/COL4A1/MMP9/CTSS/MMP16/MMP10/COL7A1/MMP7/MMP8/COL10A1/MMP1/MMP3* |
| G40 | GO:0030316 | Osteoclast differentiation | 67 | –0.581976237 | –1.859871977 | 0.001560062 | 0.023352669 | tags =33%, list =15%, signal =28% | *CEBPB/FSTL3/TNFRSF11A/TFRC/TLR4/CCR1/ATP6AP1/CSF1R/SH3PXD2A/GPC3/SFRP1/EPHA2/DCSTAMP/CAMK4/SIGLEC15/LILRB4/LILRA6/CA2/INPP5D/GPR183/TYROBP* |
| G40 | GO:0031294 | Lymphocyte costimulation | 51 | –0.691383909 | –2.111851188 | 0.001574803 | 0.023352669 | tags =31%, list =7%, signal =29% | *DPP4/HLA-DPA1/LYN/PTPN6/EFNB2/CD86/CD4/CD28/CARD11/HLA-DQA1/ICOSLG/HLA-DQB1/HLA-DRB1/HLA-DRB5/HLA-DRA* |
| G40 | GO:0031295 | T cell costimulation | 51 | –0.691383909 | –2.111851188 | 0.001574803 | 0.023352669 | tags =31%, list =7%, signal =29% | *DPP4/HLA-DPA1/LYN/PTPN6/EFNB2/CD86/CD4/CD28/CARD11/HLA-DQA1/ICOSLG/HLA-DQB1/HLA-DRB1/HLA-DRB5/HLA-DRA* |
| G40 | GO:0030593 | Neutrophil chemotaxis | 46 | –0.777101861 | –2.328259524 | 0.001602564 | 0.023352669 | tags =54%, list =11%, signal =48% | *PREX1/CXCL2/RAC2/ITGA1/ITGB2/VAV3/IL1B/CCL26/CCL22/NCKAP1L/CCL2/TREM1/LBP/C5AR1/SYK/CCL8/C3AR1/CXCL1/FCER1G/S100A9/CXCL3/CCL13/CD74/IL8* |
| G40 | GO:0030888 | Regulation of B cell proliferation | 40 | –0.66829713 | –1.954837914 | 0.001620746 | 0.023352669 | tags =42%, list =13%, signal =37% | *IRS2/TFRC/TLR4/VAV3/CDKN1A/MNDA/LYN/CD300A/INPP5D/NCKAP1L/TNFRSF21/PTPRC/SASH3/GPR183/CARD11/CD74* |
| G40 | GO:0030890 | Positive regulation of B cell proliferation | 28 | –0.65563721 | –1.786813636 | 0.001672241 | 0.023352669 | tags =50%, list =16%, signal =42% | *MIF/CD38/IRS2/TFRC/TLR4/VAV3/CDKN1A/NCKAP1L/PTPRC/SASH3/GPR183/CARD11/CD74* |
| G40 | GO:0030851 | Granulocyte differentiation | 20 | –0.703381055 | –1.808226011 | 0.001694915 | 0.023352669 | tags =25%, list =6%, signal =23% | *ZFPM1/INPP5D/SPI1/C1QC* |
| G40 | GO:0030323 | Respiratory tube development | 140 | –0.449629788 | –1.608718835 | 0.002890173 | 0.030486975 | tags =29%, list =14%, signal =25% | *MAPK3/CCDC40/TRAF4/ZFPM2/FSTL3/PDGFA/EPAS1/HHIP/TGFBR2/GLI2/PTN/ABCA12/CTSZ/PTK7/VEGFA/CRISPLD2/RDH10/GATA6/TNC/HSD11B1/TNS3/GPC3/CTGF/CELSR1/RBP4/PCSK5/SPARC/WNT11/EYA1/STRA6/WNT5A/TGFB3/MYOCD/SOX9/TBX5/LIF/SIM2/HOXA5/PITX2* |
| G40 | GO:0030324 | Lung development | 136 | –0.445620638 | –1.587078188 | 0.004360465 | 0.03701726 | tags =28%, list =14%, signal =24% | *MAPK3/CCDC40/ZFPM2/FSTL3/PDGFA/EPAS1/HHIP/TGFBR2/GLI2/PTN/ABCA12/CTSZ/PTK7/VEGFA/CRISPLD2/RDH10/GATA6/TNC/HSD11B1/TNS3/GPC3/CTGF/CELSR1/RBP4/SPARC/WNT11/EYA1/STRA6/WNT5A/TGFB3/MYOCD/SOX9/TBX5/LIF/SIM2/HOXA5/PITX2* |
| G40 | GO:0031076 | Embryonic camera-type eye development | 27 | –0.628718792 | –1.697498615 | 0.005008347 | 0.038706237 | tags =37%, list =15%, signal =32% | *NES/PPP1R13L/HIPK2/ALDH1A3/RDH10/PAX6/STRA6/WNT5A/PITX2* |
| G40 | GO:0030809 | Negative regulation of nucleotide biosynthetic process | 20 | –0.657442394 | –1.690128601 | 0.005084746 | 0.038932682 | tags =40%, list =14%, signal =34% | *ADRA2A/OPRL1/APLP1/DRD4/PID1/EDNRA/EDNRB* |
| G40 | GO:0030540 | Female genitalia development | 12 | –0.7988699 | –1.805514045 | 0.006993007 | 0.047918836 | tags =50%, list =6%, signal =47% | *RBP4/CHD7/STRA6/WNT5A/MERTK* |
| G41 | GO:0031347 | Regulation of defense response | 483 | –0.409487134 | –1.634425093 | 0.001207729 | 0.023352669 | tags =16%, list =9%, signal =15% | *SERPINE1/RORA/WFDC1/BTK/CADM1/CFH/MICA/CALCRL/TNFSF4/TLR2/PTGS2/GGT1/ITGB2/RSAD2/TLR1/LGMN/ADAMTS12/CTSS/ADAM8/PTGER3/IL18/DUSP10/A2M/C7/CFI/TLR8/TLR7/AC005013.1/CR1/VTN/IL1B/LYN/WNT5A/PLCG2/LPL/APOE/MARCO/CCL26/F2RL1/IL1RL1/PTPN6/C1QTNF3/HAVCR2/VAMP8/ACP5/FABP4/CD1D/CCL2/FGR/CLEC7A/PTPN22/ITGA2/PIK3AP1/LBP/CD86/CD4/C5AR1/CD180/IL6/CD28/SYK/CD14/CCL8/ITGAM/C3AR1/CARD11/HCK/CD209/TGM2/FCER1G/S100A9/EDNRB/CCL13/PLA2G7/IL33* |
| G41 | GO:0031349 | Positive regulation of defense response | 300 | –0.479899399 | –1.852790203 | 0.001293661 | 0.023352669 | tags =18%, list =7%, signal =17% | *SERPINE1/BTK/CADM1/TNFSF4/TLR2/PTGS2/ITGB2/RSAD2/TLR1/LGMN/CTSS/ADAM8/PTGER3/IL18/TLR8/TLR7/AC005013.1/IL1B/LYN/WNT5A/PLCG2/LPL/MARCO/CCL26/F2RL1/IL1RL1/HAVCR2/VAMP8/FABP4/CD1D/CCL2/CLEC7A/PTPN22/ITGA2/PIK3AP1/LBP/CD86/CD180/IL6/CD28/SYK/CD14/CCL8/ITGAM/CARD11/HCK/CD209/TGM2/FCER1G/S100A9/CCL13/PLA2G7/IL33* |
| G42 | GO:0031663 | Lipopolysaccharide-mediated signaling pathway | 42 | –0.711402117 | –2.101663444 | 0.001618123 | 0.023352669 | tags =38%, list =7%, signal =36% | *TGFB1/MAPK3/TLR4/TLR2/IL18/IL1B/LYN/CCL2/PTPN22/LBP/CD180/CD14/PTAFR/HCK/LY86* |
| G42 | GO:0031623 | Receptor internalization | 62 | –0.503253752 | –1.593663732 | 0.00466563 | 0.037949001 | tags =21%, list =9%, signal =19% | *VEGFA/CALCRL/ADRBK2/DNM3/ITGB2/SFRP4/PLCG2/ANGPT1/SYK/FCER1G/SNCA/IL8* |
| G43 | GO:0032101 | Regulation of response to external stimulus | 491 | –0.441169992 | –1.763225886 | 0.001201923 | 0.023352669 | tags =23%, list =13%, signal =21% | *MAPK13/PDGFRA/CASK/TNFRSF11A/PRKG1/CYP27B1/PTPRF/SCARF1/GJD4/SPN/GP1BA/PDGFA/IL15/SEMA6D/TLR4/UCN/TGFBR2/CCR1/CXCL2/IL2RA/DOCK2/IL1R2/RAC2/SERPINE1/RORA/PDGFB/VEGFA/HSPB1/WFDC1/BTK/ENPP4/PLAUR/CXCL14/CFH/CALCRL/FAM46A/PLAT/TNFSF4/FAP/TLR2/PTGS2/F3/SERPINE2/GGT1/FGF2/PLAU/ADAMTS12/ADAM8/PTGER3/IL18/DUSP10/A2M/C7/CFI/TLR7/CR1/PADI2/VTN/IL1B/LYN/WNT5A/LPL/APOE/CCL26/F2RL1/IL1RL1/C1QTNF3/HAVCR2/VAMP8/EFNB2/ACP5/NCKAP1L/FABP4/CCL2/ITGA2/PIK3AP1/LBP/CD4/C5AR1/CD180/PLEK/IL6/CD28/SYK/AIF1/SERPINB2/CCL8/CMKLR1/C3AR1/GPR183/HCK/ROBO2/CXCR4/CXCL1/TGM2/SEMA6B/FCER1G/PF4/LY86/KDR/S100A9/EDNRB/CXCL6/CXCL3/CCL13/PLA2G7/IL33/CD74/SPP1/SCG2/CXCL5/IL8* |
| G43 | GO:0032103 | Positive regulation of response to external stimulus | 174 | –0.614269004 | –2.249412327 | 0.001390821 | 0.023352669 | tags =30%, list =9%, signal =28% | *SERPINE1/PDGFB/VEGFA/HSPB1/BTK/CXCL14/TNFSF4/TLR2/PTGS2/F3/FGF2/ADAM8/PTGER3/IL18/TLR7/IL1B/WNT5A/LPL/CCL26/F2RL1/IL1RL1/HAVCR2/VAMP8/NCKAP1L/FABP4/CCL2/ITGA2/LBP/C5AR1/CD180/IL6/CD28/AIF1/CCL8/CMKLR1/C3AR1/CXCL1/TGM2/FCER1G/PF4/LY86/KDR/S100A9/CXCL6/CXCL3/CCL13/PLA2G7/IL33/CD74/SCG2/CXCL5/IL8* |
| G44 | GO:0032496 | Response to lipopolysaccharide | 228 | –0.520461511 | –1.979340229 | 0.001328021 | 0.023352669 | tags =21%, list =5%, signal =21% | *CMPK2/SERPINE1/STAR/SPON2/TNFSF4/TLR2/PTGS2/MPO/IL18/DUSP10/SPARC/ABCA1/IL1B/LYN/CXCL16/WNT5A/PLCG2/IRF8/CCR5/HAVCR2/BDKRB1/ACP5/CCL2/PTPN22/TNFRSF21/CSF2RB/TNFRSF10D/TREM2/TNFRSF10C/LBP/CD86/C5AR1/SLC11A1/CD180/IL6/CD14/PTAFR/HCK/CXCL1/IL10RA/PF4/LY86/EDNRB/CXCL6/CXCL3/SNCA/CXCL5/IL8* |
| G44 | GO:0032943 | Mononuclear cell proliferation | 166 | –0.546187742 | –1.994321955 | 0.001386963 | 0.023352669 | tags =33%, list =14%, signal =29% | *CEBPB/LEP/LGALS9/CD38/IRS2/TNFSF9/SATB1/SPN/IL15/TFRC/TLR4/HLA-DPB1/IL2RA/DOCK2/RAC2/IFNE/TNFSF4/VAV3/CORO1A/CDKN1A/IL18/MNDA/LST1/HLA-DPA1/IL1B/LYN/CD300A/INPP5D/PTPN6/HAVCR2/NCKAP1L/CD1D/DOCK8/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/SLC11A1/CD180/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DMB/ICOSLG/CD209/IGF1/VSIG4/CD74* |
| G44 | GO:0032944 | Regulation of mononuclear cell proliferation | 130 | –0.615009662 | –2.179665979 | 0.001428571 | 0.023352669 | tags =38%, list =14%, signal =33% | *CEBPB/LEP/LGALS9/CD38/IRS2/TNFSF9/SPN/IL15/TFRC/TLR4/HLA-DPB1/IL2RA/RAC2/TNFSF4/VAV3/CORO1A/CDKN1A/IL18/MNDA/LST1/HLA-DPA1/IL1B/LYN/CD300A/INPP5D/PTPN6/HAVCR2/NCKAP1L/CD1D/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DMB/ICOSLG/CD209/IGF1/VSIG4/CD74* |
| G44 | GO:0032845 | Negative regulation of homeostatic process | 136 | –0.465758693 | –1.658799883 | 0.001453488 | 0.023352669 | tags =16%, list =6%, signal =15% | *F2RL3/FGF2/CORO1A/CHD7/JPH2/LYN/PLCG2/INPP5D/CCR5/PTPN6/BDKRB1/PTPRC/GPAM/PLN/JPH1/IL6/HTR2A/FCER1G/CD74/SNCA/HOXA5* |
| G44 | GO:0032946 | Positive regulation of mononuclear cell proliferation | 88 | –0.648421211 | –2.174835085 | 0.00149925 | 0.023352669 | tags =44%, list =16%, signal =37% | *MIF/JAK3/LEP/LGALS9/CD38/IRS2/TNFSF9/SPN/IL15/TFRC/TLR4/HLA-DPB1/IL2RA/TNFSF4/VAV3/CORO1A/CDKN1A/IL18/HLA-DPA1/IL1B/HAVCR2/NCKAP1L/CD1D/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DMB/ICOSLG/IGF1/CD74* |
| G44 | GO:0032635 | Interleukin-6 production | 85 | –0.540724804 | –1.798722618 | 0.001517451 | 0.023352669 | tags =39%, list =15%, signal =33% | *GBA/IL1RAP/ARRB2/HYAL2/CEBPB/LEP/TLR6/LGALS9/MAPK13/TLR4/UCN/IL36RN/SPON2/TNFSF4/TLR2/TLR1/TLR7/IL1B/WNT5A/IL36B/INPP5D/F2RL1/C1QTNF3/HAVCR2/NCKAP1L/PTPN22/LBP/IL1A/IL6/PTAFR/FCER1G/IL33* |
| G44 | GO:0032640 | Tumor necrosis factor production | 82 | –0.529760361 | –1.759907843 | 0.001531394 | 0.023352669 | tags =30%, list =9%, signal =28% | *CHRNA7/ARRB2/LEP/LGALS9/SPN/TLR4/RASGRP1/HSPB1/SPON2/TLR2/TLR1/CLU/ANGPT1/HAVCR2/ACP5/CCL2/PTPN22/LBP/SASH3/CD14/PTAFR/CYBB/FCER1G/PF4* |
| G44 | GO:0032680 | Regulation of tumor necrosis factor production | 80 | –0.536447958 | –1.770375561 | 0.001540832 | 0.023352669 | tags =31%, list =14%, signal =27% | *CHRNA7/ARRB2/LEP/LGALS9/SPN/TLR4/RASGRP1/HSPB1/SPON2/TLR2/TLR1/CLU/ANGPT1/HAVCR2/ACP5/CCL2/PTPN22/LBP/SASH3/CD14/PTAFR/CYBB/FCER1G/PF4* |
| G44 | GO:0032675 | Regulation of interleukin-6 production | 81 | –0.540871052 | –1.786189528 | 0.00154321 | 0.023352669 | tags =40%, list =15%, signal =34% | *GBA/IL1RAP/ARRB2/HYAL2/CEBPB/TLR6/LGALS9/MAPK13/TLR4/UCN/IL36RN/SPON2/TNFSF4/TLR2/TLR1/TLR7/IL1B/WNT5A/IL36B/INPP5D/F2RL1/C1QTNF3/HAVCR2/NCKAP1L/PTPN22/LBP/IL1A/IL6/PTAFR/FCER1G/IL33* |
| G44 | GO:0032642 | Regulation of chemokine production | 54 | –0.666648666 | –2.068952934 | 0.001550388 | 0.023352669 | tags =39%, list =7%, signal =36% | *HIF1A/TLR4/CSF1R/TLR2/EPHA2/ZFPM1/TLR7/HMOX1/IL1B/WNT5A/LPL/F2RL1/IL1RL1/C1QTNF3/HAVCR2/LBP/IL1A/IL6/IL33/CD74* |
| G44 | GO:0032609 | Interferon-gamma production | 67 | –0.588546501 | –1.880869139 | 0.001560062 | 0.023352669 | tags =33%, list =11%, signal =29% | *HLA-DPB1/IL36RN/RASGRP1/TNFSF4/IL18/ZFPM1/TLR8/TLR7/HLA-DPA1/IL1B/WNT5A/IRF8/F2RL1/IL1RL1/HAVCR2/PTPN22/SASH3/SLC11A1/CD14/INHBA/IL33* |
| G44 | GO:0032602 | Chemokine production | 59 | –0.683693822 | –2.147272271 | 0.001567398 | 0.023352669 | tags =42%, list =7%, signal =40% | *LGALS9/HIF1A/TLR4/CSF1R/TNFSF4/TLR2/EPHA2/IL18/ZFPM1/TLR7/HMOX1/IL1B/WNT5A/LPL/F2RL1/IL1RL1/C1QTNF3/HAVCR2/LBP/IL1A/IL6/S100A9/IL33/CD74* |
| G44 | GO:0032649 | Regulation of interferon-gamma production | 61 | –0.599132619 | –1.887028575 | 0.001567398 | 0.023352669 | tags =38%, list =11%, signal =34% | *INHA/TLR4/HLA-DPB1/IL36RN/RASGRP1/TNFSF4/IL18/ZFPM1/TLR8/TLR7/HLA-DPA1/IL1B/WNT5A/IRF8/IL1RL1/HAVCR2/PTPN22/SASH3/SLC11A1/CD14/INHBA/IL33* |
| G44 | GO:0032418 | Lysosome localization | 49 | –0.610491412 | –1.851031453 | 0.001577287 | 0.023352669 | tags =33%, list =9%, signal =30% | *RASGRP1/MILR1/LAT2/BTK/STXBP2/UNC13D/LAT/HMOX1/LYN/CD300A/VAMP8/FGR/SYK/CD84/FCER1G* |
| G44 | GO:0032760 | Positive regulation of tumor necrosis factor production | 48 | –0.652543204 | –1.963447063 | 0.001584786 | 0.023352669 | tags =40%, list =14%, signal =34% | *LGALS9/SPN/TLR4/RASGRP1/HSPB1/SPON2/TLR2/TLR1/CLU/HAVCR2/CCL2/LBP/SASH3/CD14/PTAFR/CYBB/FCER1G/PF4* |
| G44 | GO:0032729 | Positive regulation of interferon-gamma production | 42 | –0.655631568 | –1.936903007 | 0.001618123 | 0.023352669 | tags =40%, list =11%, signal =36% | *HLA-DPB1/RASGRP1/TNFSF4/IL18/ZFPM1/TLR8/TLR7/HLA-DPA1/IL1B/WNT5A/IRF8/HAVCR2/PTPN22/SASH3/SLC11A1/CD14* |
| G44 | GO:0032722 | Positive regulation of chemokine production | 40 | –0.725065686 | –2.120891786 | 0.001620746 | 0.023352669 | tags =42%, list =14%, signal =37% | *HIF1A/TLR4/CSF1R/TLR2/TLR7/HMOX1/IL1B/WNT5A/LPL/IL1RL1/HAVCR2/LBP/IL1A/IL6/IL33/CD74* |
| G44 | GO:0032743 | Positive regulation of interleukin-2 production | 25 | –0.681584583 | –1.820417358 | 0.001647446 | 0.023352669 | tags =40%, list =7%, signal =37% | *RUNX1/CD83/IL1B/CD86/CD4/IL1A/SASH3/CD28/CARD11* |
| G44 | GO:0032633 | Interleukin-4 production | 21 | –0.667616019 | –1.726967681 | 0.001686341 | 0.023352669 | tags =57%, list =7%, signal =53% | *CEBPB/LGALS9/TNFSF4/PRKCZ/CD83/ZFPM1/HAVCR2/CD86/SASH3/CD28/IL33* |
| G44 | GO:0032755 | Positive regulation of interleukin-6 production | 53 | –0.526921904 | –1.635560635 | 0.003100775 | 0.030486975 | tags =42%, list =15%, signal =35% | *HYAL2/TLR6/LGALS9/MAPK13/TLR4/UCN/SPON2/TNFSF4/TLR2/TLR1/TLR7/IL1B/WNT5A/IL36B/F2RL1/LBP/IL1A/IL6/PTAFR/FCER1G/IL33* |
| G44 | GO:0032623 | Interleukin-2 production | 45 | –0.615965989 | –1.835168931 | 0.003220612 | 0.030486975 | tags =33%, list =7%, signal =31% | *RUNX1/IL18/CD83/IL1B/HAVCR2/CD86/CD4/IL1A/GPAM/SASH3/SLC11A1/CD28/CARD11/VSIG4* |
| G44 | GO:0032945 | Negative regulation of mononuclear cell proliferation | 42 | –0.577036283 | –1.704712472 | 0.003236246 | 0.030486975 | tags =36%, list =16%, signal =30% | *TGFB1/CEBPB/LGALS9/SPN/IL2RA/MNDA/LST1/LYN/CD300A/INPP5D/PTPN6/HAVCR2/TNFRSF21/VSIG4* |
| G44 | GO:0032673 | Regulation of interleukin-4 production | 17 | –0.71216391 | –1.737888222 | 0.003514938 | 0.031944406 | tags =65%, list =7%, signal =60% | *LGALS9/TNFSF4/PRKCZ/CD83/ZFPM1/HAVCR2/CD86/SASH3/CD28/IL33* |
| G44 | GO:0032844 | Regulation of homeostatic process | 339 | –0.378285468 | –1.476473045 | 0.003826531 | 0.033706175 | tags =19%, list =13%, signal =17% | *PARK2/DMD/CD38/ADRA2A/TNFRSF11A/PLCG1/ITPR2/SLX1A/TFRC/ITPR1/ATP6AP1/IL2RA/ACVR2A/SLC30A10/SYBU/CSF1R/RORA/NEK7/PTGS2/ITGB3/UCP2/F2RL3/IFI6/FGF2/PDK4/DCSTAMP/FOXO1/ADAM8/PTGER3/CORO1A/ZFPM1/ADCY5/GPR27/MLLT11/CHD7/SIGLEC15/IL1B/TMEM27/JPH2/LYN/PLCG2/CA2/INPP5D/CCR5/SLC30A3/PTPN6/BDKRB1/NCKAP1L/PTPRC/CD4/GPAM/PLN/JPH1/IL6/SYK/SPI1/HTR2A/INHBA/FCER1G/KDR/EDNRB/CD74/SNCA/SPP1/HOXA5* |
| G44 | GO:0032663 | Regulation of interleukin-2 production | 38 | –0.588886133 | –1.728276118 | 0.004807692 | 0.038245256 | tags =32%, list =7%, signal =29% | *RUNX1/CD83/IL1B/HAVCR2/CD86/CD4/IL1A/SASH3/CD28/CARD11/VSIG4* |
| G44 | GO:0032715 | Negative regulation of interleukin-6 production | 28 | –0.613760214 | –1.672685906 | 0.006688963 | 0.046379968 | tags =39%, list =16%, signal =33% | *CHRNA7/GBA/ARRB2/TLR4/IL36RN/INPP5D/C1QTNF3/HAVCR2/NCKAP1L/PTPN22* |
| G45 | GO:0032963 | Collagen metabolic process | 91 | –0.534486038 | –1.799190069 | 0.00152207 | 0.023352669 | tags =43%, list =16%, signal =36% | *CTSD/MMP19/SERPINH1/LEPRE1/TGFB1/ITGB1/HIF1A/COL25A1/UCN/COL15A1/COL4A5/COL5A2/COL11A2/MMP11/COL4A2/MMP15/COL3A1/COL11A1/FAP/COL4A1/CTGF/LEPREL1/MMP9/CTSS/MMP16/RGCC/MMP10/COL7A1/TGFB3/MMP7/CCL2/ITGA2/SERPINB7/IL6/MMP8/COL10A1/MMP1/MMP3* |
| G45 | GO:0032965 | Regulation of collagen biosynthetic process | 24 | –0.66953791 | –1.772839285 | 0.001655629 | 0.023352669 | tags =38%, list =6%, signal =35% | *UCN/CTGF/RGCC/TGFB3/CCL2/ITGA2/SERPINB7/IL6* |
| G45 | GO:0033006 | Regulation of mast cell activation involved in immune response | 24 | –0.711519965 | –1.884001678 | 0.001655629 | 0.023352669 | tags =46%, list =9%, signal =42% | *STXBP2/UNC13D/HMOX1/LYN/CD300A/VAMP8/FGR/SYK/CD84/FCER1G* |
| G45 | GO:0033003 | Regulation of mast cell activation | 28 | –0.696987348 | –1.899505518 | 0.001672241 | 0.023352669 | tags =43%, list =9%, signal =39% | *MILR1/STXBP2/UNC13D/HMOX1/LYN/CD300A/VAMP8/FGR/SYK/CD84/FCER1G* |
| G45 | GO:0032967 | Positive regulation of collagen biosynthetic process | 17 | –0.706071964 | –1.723022092 | 0.005272408 | 0.039836829 | tags =47%, list =14%, signal =40% | *UCN/CTGF/RGCC/TGFB3/CCL2/ITGA2/SERPINB7* |
| G45 | GO:0033008 | Positive regulation of mast cell activation involved in immune response | 10 | –0.792924841 | –1.709904583 | 0.007366483 | 0.049685189 | tags =40%, list =2%, signal =39% | *FGR/SYK/FCER1G* |
| G46 | GO:0033273 | Response to vitamin | 65 | –0.53277853 | –1.695284187 | 0.00154321 | 0.023352669 | tags =31%, list =9%, signal =28% | *LEP/CYP27B1/IL15/PTN/ATP2B1/TNC/PTGS2/CCND1/SFRP1/MDM2/SPARC/CCL2/ITGA2/CD4/BCHE/STC1/FOLR2/SPP1/PITX2* |
| G47 | GO:0033628 | Regulation of cell adhesion mediated by integrin | 30 | –0.596483583 | –1.646786452 | 0.006722689 | 0.04643702 | tags =43%, list =12%, signal =38% | *ACER2/SERPINE1/RAC3/RET/DPP4/EPHA2/PLAU/PDE3B/LYN/PTPN6/NCKAP1L/SYK* |
| G48 | GO:0034341 | Response to interferon-gamma | 109 | –0.552118993 | –1.906400119 | 0.001457726 | 0.023352669 | tags =19%, list =3%, signal =19% | *CXCL16/WNT5A/IRF8/CCL26/CCL22/CCL2/CD86/SLC11A1/AIF1/PTAFR/CCL8/HLA-DQA1/HCK/FCGR1A/HLA-DQB1/HLA-DRB1/CCL13/HLA-DRB5/SNCA/HLA-DRA* |
| G48 | GO:0034142 | Toll-like receptor 4 signaling pathway | 24 | –0.750142567 | –1.986268725 | 0.001655629 | 0.023352669 | tags =54%, list =6%, signal =51% | *PELI1/NR1D1/TLR4/ITGB2/AC005013.1/LYN/F2RL1/PTPN22/PIK3AP1/LBP/CD14/ITGAM* |
| G48 | GO:0034105 | Positive regulation of tissue remodeling | 19 | –0.752544804 | –1.908058925 | 0.001733102 | 0.023440094 | tags =53%, list =11%, signal =47% | *TFRC/ATP6AP1/B4GALT1/DCSTAMP/ADAM8/IL18/CA2/SYK/SPP1* |
| G48 | GO:0034162 | Toll-like receptor 9 signaling pathway | 16 | –0.779877414 | –1.872757509 | 0.001751313 | 0.02350135 | tags =31%, list =5%, signal =30% | *TLR8/TLR7/HAVCR2/PIK3AP1* |
| G48 | GO:0034764 | Positive regulation of transmembrane transport | 84 | –0.476487033 | –1.583216427 | 0.00304414 | 0.030486975 | tags =32%, list =17%, signal =27% | *FAM115A/CAPN3/HTT/STK39/AKAP9/RNF207/DMD/STIM2/PLCG1/EHD3/SHANK3/AP000322.53/KCNMB1/KCNE1/PDZK1/DRD4/F2RL3/ATP1B1/CTSS/JPH2/PLCG2/CA2/ARC/BDKRB1/PTAFR/SNCA* |
| G48 | GO:0034123 | Positive regulation of toll-like receptor signaling pathway | 17 | –0.707608631 | –1.72677201 | 0.005272408 | 0.039836829 | tags =35%, list =7%, signal =33% | *RSAD2/F2RL1/PTPN22/PIK3AP1/LBP* |
| G48 | GO:0034765 | Regulation of ion transmembrane transport | 249 | –0.380384878 | –1.453077982 | 0.005284016 | 0.039860454 | tags =26%, list =17%, signal =22% | *FAM115A/CAPN3/SCN3B/HOMER1/HTT/STK39/CATSPER2/C19orf26/GPD1L/TGFB1/CACNA1A/AKAP9/RNF207/DMD/STIM2/IRS2/ADRA2A/PLCG1/EHD3/SHANK3/KCND2/KCNQ5/HCN2/AP000322.53/OPRL1/KCNMB1/KCNAB2/NLGN1/FAM115C/KCNE1/PDZK1/CACNA1H/DRD4/F2RL3/KCNRG/ATP1B1/KCNH1/KCNMA1/SHANK1/MMP9/CTSS/KCNE4/CORO1A/CHD7/JPH2/LYN/TSPAN13/PLCG2/ARC/KCNS3/KCNQ3/PTPN6/NETO2/BDKRB1/SCN9A/SCN2A/PLN/JPH1/KCNJ5/PTAFR/CYBB/KCNC3/SNCA* |
| G48 | GO:0034762 | Regulation of transmembrane transport | 262 | –0.376803919 | –1.442199949 | 0.00660502 | 0.046053749 | tags =25%, list =17%, signal =21% | *FAM115A/CAPN3/SCN3B/HOMER1/HTT/STK39/CATSPER2/C19orf26/OAZ3/GPD1L/TGFB1/CACNA1A/AKAP9/RNF207/DMD/STIM2/IRS2/ADRA2A/PLCG1/EHD3/SHANK3/KCND2/KCNQ5/HCN2/AP000322.53/OPRL1/KCNMB1/KCNAB2/NLGN1/FAM115C/KCNE1/PDZK1/CACNA1H/DRD4/F2RL3/KCNRG/ATP1B1/KCNH1/KCNMA1/SHANK1/MMP9/CTSS/KCNE4/CORO1A/CHD7/JPH2/LYN/TSPAN13/PLCG2/CA2/ARC/KCNS3/KCNQ3/PTPN6/NETO2/BDKRB1/SCN9A/SCN2A/PLN/JPH1/KCNJ5/PTAFR/CYBB/KCNC3/SNCA* |
| G49 | GO:0034767 | Positive regulation of ion transmembrane transport | 78 | –0.471068902 | –1.557042088 | 0.001545595 | 0.023352669 | tags =33%, list =17%, signal =28% | *FAM115A/CAPN3/HTT/STK39/AKAP9/RNF207/DMD/STIM2/PLCG1/EHD3/SHANK3/AP000322.53/KCNMB1/KCNE1/PDZK1/DRD4/F2RL3/ATP1B1/CTSS/JPH2/PLCG2/ARC/BDKRB1/PTAFR/SNCA* |
| G49 | GO:0035051 | Cardiocyte differentiation | 90 | –0.452099964 | –1.518371281 | 0.00610687 | 0.044510187 | tags =31%, list =17%, signal =26% | *ECE2/CXADR/PROX1/TGFB1/MAPK3/ITGB1/PDGFRA/NOX4/MYH10/TENM4/NEBL/VEGFA/SIK1/GATA6/NEXN/HAND2/TBX3/MYH11/PRICKLE1/FHOD3/EFNB2/MYOCD/RARB/TBX5/IGF1/BMP2/PITX2* |
| G5 | GO:0001944 | Vasculature development | 494 | –0.430469287 | –1.720508034 | 0.001201923 | 0.023352669 | tags =21%, list =10%, signal =20% | *PTN/GPR56/EGLN1/RAMP1/HEY1/SERPINE1/RORA/PDGFB/PTK7/VEGFA/HSPB1/NKX3-1/COL4A2/GATA6/CALCRL/PAX6/B4GALT1/COL3A1/FAP/PTGS2/F3/ITGB3/MFGE8/GPC3/NOTCH3/RUNX1/COL4A1/CTGF/SOX4/ANGPTL4/HAND2/EPGN/SFRP1/TBX3/ITGB2/VAV3/EPHA2/FGF2/ANTXR1/HPGD/PCSK5/FOXO1/MDM2/XDH/PDE3B/ADAM8/PRICKLE1/FZD8/IL18/ACTA2/LOXL2/SPARC/HOXA7/BAI1/MEIS1/SAT1/CDH2/HMOX1/MYLK/WNT11/RGCC/EYA1/CHD7/LYL1/EDNRA/STRA6/IL1B/NRP2/ANGPT4/WNT5A/SRPX2/NRCAM/HAS2/APOE/HOXB3/SULF1/ANGPT1/TIE1/NDNF/EFNB2/MYOCD/CCL2/PRKCB/C5AR1/IL1A/ENPEP/SERPINB7/IL6/SYK/C3AR1/STAB1/CYBB/SPI1/TBX5/PF4/LIF/KDR/MCAM/FOXS1/HOXA3/HOXA5/SCG2/IL8/PITX2* |
| G5 | GO:0002218 | Activation of innate immune response | 212 | –0.440386089 | –1.662532423 | 0.001340483 | 0.023352669 | tags =13%, list =6%, signal =12% | *RSAD2/TLR1/LGMN/CTSS/ADAM8/TLR8/TLR7/AC005013.1/LYN/PLCG2/MARCO/F2RL1/HAVCR2/CLEC7A/PTPN22/PIK3AP1/LBP/CD86/CD180/SYK/CD14/ITGAM/CARD11/HCK/CD209/FCER1G* |
| G5 | GO:0002221 | Pattern recognition receptor signaling pathway | 130 | –0.472034555 | –1.672945524 | 0.001428571 | 0.023352669 | tags =17%, list =8%, signal =16% | *TLR2/ITGB2/RSAD2/TLR1/LGMN/CTSS/TLR8/TLR7/AC005013.1/LYN/MARCO/F2RL1/HAVCR2/CLEC7A/PTPN22/PIK3AP1/LBP/CD86/CD180/CD14/ITGAM* |
| G5 | GO:0002224 | Toll-like receptor signaling pathway | 101 | –0.515731512 | –1.750323163 | 0.001503759 | 0.023352669 | tags =20%, list =8%, signal =18% | *TLR2/ITGB2/RSAD2/TLR1/LGMN/CTSS/TLR8/TLR7/AC005013.1/LYN/F2RL1/HAVCR2/PTPN22/PIK3AP1/LBP/CD86/CD180/CD14/ITGAM* |
| G5 | GO:0001936 | Regulation of endothelial cell proliferation | 80 | –0.501104393 | –1.653735383 | 0.001540832 | 0.023352669 | tags =31%, list =15%, signal =27% | *PROX1/LEP/C19orf10/HIF1A/RPTOR/VASH2/PDGFB/VEGFA/F3/ITGB3/PLXNB3/FGF2/XDH/SPARC/RGCC/NRP2/WNT5A/APOE/CCL26/SULF1/CCL2/KDR/BMP2/SCG2* |
| G5 | GO:0001937 | Negative regulation of endothelial cell proliferation | 25 | –0.685983979 | –1.832167533 | 0.001647446 | 0.023352669 | tags =24%, list =5%, signal =23% | *SPARC/RGCC/APOE/SULF1/SCG2* |
| G50 | GO:0035065 | Regulation of histone acetylation | 43 | –0.55619755 | –1.644023311 | 0.006451613 | 0.045354927 | tags =14%, list =3%, signal =14% | *MYOCD/SPI1/LIF/SNCA/NAP1L2* |
| G51 | GO:0035270 | Endocrine system development | 83 | –0.477723896 | –1.583963857 | 0.003067485 | 0.030486975 | tags =28%, list =15%, signal =24% | *DKK3/MAPK3/FSTL3/TG/HOXD3/ARNTL/GLI2/POU3F2/GATA6/PAX6/SOX4/FOXO1/WNT11/STRA6/WNT5A/HOXB3/SOX9/IL6/HOXA3/BMP2/HOXA5/PITX2* |
| G52 | GO:0035987 | Endodermal cell differentiation | 37 | –0.623633349 | –1.826941696 | 0.001597444 | 0.023352669 | tags =41%, list =12%, signal =36% | *ITGA5/ITGB5/DUSP6/COL5A2/COL4A2/GATA6/MMP15/COL11A1/ITGB2/MMP9/VTN/COL7A1/MMP8/INHBA* |
| G52 | GO:0036230 | Granulocyte activation | 20 | –0.778580035 | –2.001544769 | 0.001694915 | 0.023352669 | tags =45%, list =3%, signal =44% | *STXBP2/CD300A/F2RL1/SYK/PTAFR/FCER1G/TYROBP/IL8* |
| G52 | GO:0035295 | Tube development | 450 | –0.340715652 | –1.352241994 | 0.006165228 | 0.044612401 | tags =19%, list =12%, signal =17% | *EPAS1/C2CD3/AR/HHIP/TGFBR2/SALL4/SOX8/GLI2/PTN/DDR1/GPR56/C12orf5/EN1/SDC1/CSF1R/ABCA12/GDF11/CTSZ/PTK7/VEGFA/CRISPLD2/NKX3-1/RDH10/MICAL2/GATA6/IRX2/RET/PAX6/B4GALT1/COL3A1/TNC/CTHRC1/ITGB3/HSD11B1/TNS3/GDNF/GPC3/KIF26B/COL4A1/SERPINE2/CTGF/SOX4/CELSR1/HAND2/SFRP1/TBX3/EPHA2/FGF2/RBP4/PCSK5/ADAMTS12/PRICKLE1/CDKN1A/NDRG4/SPARC/SPINT2/WNT11/EYA1/CHD7/EDNRA/MSX2/STRA6/WNT5A/TGFB3/HEYL/EFNB2/MYOCD/ST14/DACT1/SOX9/RARB/ROBO2/SPI1/TBX5/TGM2/HOXB7/LIF/EDNRB/ALX1/SIM2/BMP2/HOXA5/IL8/PITX2* |
| G52 | GO:0035710 | CD4-positive, alpha-beta T cell activation | 45 | –0.54167001 | –1.613816333 | 0.006441224 | 0.045354927 | tags =40%, list =15%, signal =34% | *JAK3/CEBPB/LGALS9/PTGER4/SATB1/RORA/TNFSF4/RSAD2/PRKCZ/IL18/CD83/ZFPM1/NCKAP1L/CD86/SASH3/IL6/GPR183* |
| G53 | GO:0040017 | Positive regulation of locomotion | 335 | –0.500259867 | –1.947943119 | 0.001293661 | 0.023352669 | tags =26%, list =13%, signal =23% | *PDGFRA/FLT1/IRS2/ADRA2A/PLCG1/NOX4/FN1/PDGFA/SEMA6D/WNT5B/ITGA5/TGFBR2/CCR1/CXCL2/FAM83H/RAC2/CSF1R/SERPINE1/KIAA1598/PDGFB/VEGFA/HSPB1/PTP4A1/FAM115C/CXCL14/RET/PTGS2/F3/ITGB3/LRRC15/ATP8A1/FGF2/PLAU/MDM2/MMP9/SNAI1/HBEGF/ADAM8/CORO1A/SPARC/P2RY6/SPOCK2/MYLK/WNT11/VTN/NRP2/LYN/ANGPT4/CXCL16/WNT5A/SRPX2/HAS2/CCL26/ANGPT1/F2RL1/BDKRB1/NCKAP1L/CCL2/FGR/PTPRC/ITGA2/LBP/C5AR1/IL1A/SOX9/IL6/AIF1/PTAFR/CCL8/CMKLR1/C3AR1/CXCL1/SEMA6B/PF4/IGF1/KDR/CXCL6/MCAM/CXCL3/PLA2G7/CD74/BMP2/PLVAP/SCG2/CXCL5/IL8* |
| G53 | GO:0038093 | Fc receptor signaling pathway | 168 | –0.451362207 | –1.652193115 | 0.001392758 | 0.023352669 | tags =11%, list =6%, signal =10% | *LAT/LIMK1/WAS/LYN/CYFIP2/PLCG2/NCKAP1L/FGR/PPAPDC1A/LCP2/SYK/CARD11/HCK/FCGR1A/FCER1G/FCGR2A/FCGR3A* |
| G53 | GO:0038094 | Fc-gamma receptor signaling pathway | 69 | –0.654288922 | –2.103877775 | 0.001545595 | 0.023352669 | tags =22%, list =6%, signal =21% | *LIMK1/WAS/LYN/CYFIP2/PLCG2/NCKAP1L/FGR/PPAPDC1A/SYK/HCK/FCGR1A/FCER1G/FCGR2A/FCGR3A* |
| G53 | GO:0042035 | Regulation of cytokine biosynthetic process | 63 | –0.653356357 | –2.071594151 | 0.001547988 | 0.023352669 | tags =35%, list =5%, signal =33% | *IGF2BP3/ZFPM1/IGF2BP1/TLR8/TLR7/HMOX1/IL1B/WNT5A/INPP5D/RNF128/LBP/CD86/CD4/IL1A/IL6/CD28/SYK/PTAFR/CARD11/CYBB/INHBA* |
| G53 | GO:0038096 | Fc-gamma receptor signaling pathway involved in phagocytosis | 67 | –0.64325226 | –2.055697081 | 0.001560062 | 0.023352669 | tags =21%, list =6%, signal =20% | *LIMK1/WAS/LYN/CYFIP2/PLCG2/NCKAP1L/FGR/PPAPDC1A/SYK/HCK/FCGR1A/FCGR2A/FCGR3A* |
| G53 | GO:0038034 | Signal transduction in absence of ligand | 60 | –0.505123196 | –1.584638978 | 0.006299213 | 0.045145817 | tags =17%, list =7%, signal =16% | *GDNF/IFI6/EYA1/IL1B/IL1A/EYA2/BCL2A1/INHBA/PF4* |
| G54 | GO:0042060 | Wound healing | 375 | –0.457294363 | –1.800106762 | 0.00124533 | 0.023352669 | tags =29%, list =14%, signal =25% | *TGFB1/NINJ2/MAPK3/BLOC1S3/ZFPM2/CSRP1/HIF1A/PDGFRA/CASK/ADRA2A/PRKG1/TIMP1/GJD4/TPM1/DCBLD2/FN1/ITPR2/EHD3/GP1BA/PDGFA/ENO3/MYH10/DGKG/WNT5B/ITGA9/ITPR1/KANK1/ITGA5/TLR4/TGFBR2/DDR1/SDC1/NINJ1/RAC2/P2RX6/PAPSS2/SERPINE1/PDGFB/PTK7/HSPB1/VWF/P2RX1/WFDC1/ENPP4/PLAUR/GATA6/FAM46A/F2RL2/B4GALT1/COL3A1/TNC/PLAT/FAP/F3/ITGB3/F2RL3/SERPINE2/CELSR1/VAV3/FGF2/LAT/PLAU/HBEGF/P2RY1/FZD7/PROCR/A2M/SPARC/WAS/GNG2/ZFPM1/HMOX1/MYLK/VTN/GNA15/MSX2/LYN/WNT5A/PLCG2/DYSF/TGFB3/APOE/NDNF/F2RL1/SCUBE1/PTPN6/DOCK8/PIK3R5/ITGA2/HIST2H3C/HIST2H3A/PRKCB/F13A1/IL1A/SLC11A1/LCP2/PLEK/MERTK/IL6/SYK/GAP43/SERPINB2/TFPI2/FCER1G/PF4/IGF1/S100A9/MCAM* |
| G54 | GO:0042089 | Cytokine biosynthetic process | 71 | –0.638561624 | –2.066193968 | 0.001550388 | 0.023352669 | tags =34%, list =5%, signal =32% | *TLR1/IL18/IGF2BP3/ZFPM1/IGF2BP1/TLR8/TLR7/HMOX1/IL1B/WNT5A/INPP5D/RNF128/LBP/CD86/CD4/IL1A/IL6/CD28/SYK/PTAFR/CARD11/CYBB/INHBA* |
| G55 | GO:0042098 | T cell proliferation | 117 | –0.572888714 | –1.987200802 | 0.001451379 | 0.023352669 | tags =35%, list =15%, signal =30% | *TGFB1/CEBPB/LEP/LGALS9/TNFSF9/SATB1/SPN/IL15/TFRC/HLA-DPB1/IL2RA/DOCK2/RAC2/TNFSF4/CORO1A/IL18/HLA-DPA1/IL1B/PTPN6/HAVCR2/NCKAP1L/CD1D/DOCK8/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/SLC11A1/IL6/CD28/SYK/AIF1/CARD11/HLA-DMB/ICOSLG/CD209/IGF1/VSIG4* |
| G55 | GO:0042102 | Positive regulation of T cell proliferation | 64 | –0.688814328 | –2.186563171 | 0.001545595 | 0.023352669 | tags =45%, list =14%, signal =39% | *LGALS9/TNFSF9/SPN/IL15/TFRC/HLA-DPB1/IL2RA/TNFSF4/CORO1A/IL18/HLA-DPA1/IL1B/HAVCR2/NCKAP1L/CD1D/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/CARD11/HLA-DMB/ICOSLG/IGF1* |
| G55 | GO:0042100 | B cell proliferation | 51 | –0.611231447 | –1.867023287 | 0.001574803 | 0.023352669 | tags =37%, list =13%, signal =33% | *IRS2/TFRC/TLR4/IFNE/VAV3/CDKN1A/MNDA/LYN/CD300A/INPP5D/NCKAP1L/TNFRSF21/PTPRC/SASH3/CD180/GPR183/CARD11/CD74* |
| G55 | GO:0042092 | Type 2 immune response | 21 | –0.755295419 | –1.953773937 | 0.001686341 | 0.023352669 | tags =43%, list =8%, signal =39% | *TNFSF4/RSAD2/PRKCZ/IL18/CD86/IL6/IL33/CD74* |
| G56 | GO:0042330 | Taxis | 377 | –0.492215082 | –1.936542543 | 0.001248439 | 0.023352669 | tags =22%, list =9%, signal =20% | *CSF1R/SERPINE1/DRAXIN/PDGFB/VEGFA/HSPB1/PLAUR/EGR2/SPON2/CXCL14/ITGA1/PAX6/F3/ITGB3/KIF26B/PLXNB3/ITGB2/VAV3/EPHA2/FGF2/PLAU/ETV1/HBEGF/FLRT3/ADAM8/CORO1A/EFNA3/SPTBN2/PADI2/IL1B/NRP2/LYN/CXCL16/WNT5A/DPYSL4/NRCAM/CCL26/CCR5/ANGPT1/BIN2/CCL22/F2RL1/EFNB2/NCKAP1L/CCL2/KIF5A/TREM1/ITGA2/LBP/C5AR1/IL6/SYK/GAP43/AIF1/PTAFR/CCL8/CMKLR1/C3AR1/GPR183/ROBO2/CXCR4/CXCL1/SEMA6B/FCER1G/PF4/UNC5C/FPR1/KDR/S100A9/EDNRB/FPR3/KAL1/CXCL6/CXCL3/CCL13/PLA2G7/CD74/HOXA2/SCG2/CXCL5/IL8* |
| G56 | GO:0042110 | T cell activation | 304 | –0.502584073 | –1.941159591 | 0.001302083 | 0.023352669 | tags =25%, list =12%, signal =23% | *SATB1/SPN/IL15/TFRC/KIF13B/TGFBR2/HLA-DPB1/PREX1/GLI2/IL2RA/DOCK2/RAC2/RASGRP1/RORA/IFNE/MICA/TNFSF4/DPP4/SOX4/LAT/RSAD2/PRKCZ/ADAM8/FZD8/CORO1A/FZD7/IL18/CD83/WAS/LCP1/ZFPM1/TNFSF8/CAMK4/CHD7/HLA-DPA1/IL1B/LYN/CD300A/IL36B/CYP26B1/PAG1/F2RL1/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/DOCK8/CLEC7A/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/SLC11A1/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/CD209/FCER1G/IGF1/VSIG4/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G56 | GO:0042113 | B cell activation | 159 | –0.525350529 | –1.905218075 | 0.001408451 | 0.023352669 | tags =32%, list =16%, signal =27% | *PELI1/CHRNA7/MIF/NOTCH2/JAK3/TGFB1/BST2/ITGB1/INHA/CD38/IRS2/IL11/TFRC/TLR4/LAT2/IFNE/BTK/TNFSF4/ITM2A/SFRP1/VAV3/CDKN1A/MNDA/TPD52/LYL1/LYN/CD300A/SKAP2/BLNK/PLCG2/TBC1D10C/INPP5D/PTPN6/NCKAP1L/TNFRSF21/PTPRC/PRKCB/CD86/SASH3/NFAM1/CD180/SAMSN1/IL6/CD28/SYK/GPR183/CARD11/ICOSLG/INHBA/CD74* |
| G56 | GO:0042742 | Defense response to bacterium | 102 | –0.531239659 | –1.805007685 | 0.001497006 | 0.023352669 | tags =32%, list =9%, signal =30% | *IFNE/SPON2/MICA/TLR2/EPHA2/EPPIN/HIST1H2BJ/TLR1/MPO/HIST1H2BK/IGJ/HIST1H2BC/HIST2H2BE/TNFSF8/VGF/IRF8/F2RL1/HAVCR2/ACP5/FGR/LYZ/TREM1/LBP/CD4/C5AR1/SLC11A1/IL6/SYK/STAB1/FCER1G/S100A9/CXCL6* |
| G56 | GO:0042129 | Regulation of T cell proliferation | 96 | –0.616604842 | –2.08147021 | 0.001533742 | 0.023352669 | tags =39%, list =15%, signal =33% | *TGFB1/CEBPB/LEP/LGALS9/TNFSF9/SPN/IL15/TFRC/HLA-DPB1/IL2RA/RAC2/TNFSF4/CORO1A/IL18/HLA-DPA1/IL1B/PTPN6/HAVCR2/NCKAP1L/CD1D/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/CARD11/HLA-DMB/ICOSLG/CD209/IGF1/VSIG4* |
| G56 | GO:0042107 | Cytokine metabolic process | 73 | –0.64670833 | –2.096849668 | 0.001564945 | 0.023352669 | tags =34%, list =5%, signal =33% | *TLR1/IL18/IGF2BP3/ZFPM1/IGF2BP1/TLR8/TLR7/HMOX1/IL1B/WNT5A/INPP5D/TREM1/RNF128/LBP/CD86/CD4/IL1A/IL6/CD28/SYK/PTAFR/CARD11/CYBB/INHBA* |
| G56 | GO:0042116 | Macrophage activation | 41 | –0.777010245 | –2.287139988 | 0.001612903 | 0.023352669 | tags =46%, list =8%, signal =43% | *TLR2/TLR1/CD93/CLU/TLR8/TLR7/WNT5A/IL1RL1/HAVCR2/LBP/SLC11A1/SYK/AIF1/TYROBP/GPR116/IL33/CD74/SNCA* |
| G56 | GO:0042108 | Positive regulation of cytokine biosynthetic process | 39 | –0.716671198 | –2.092843756 | 0.001615509 | 0.023352669 | tags =49%, list =5%, signal =46% | *TLR4/HSPB1/TLR1/ZFPM1/TLR8/TLR7/HMOX1/IL1B/WNT5A/LBP/CD86/CD4/IL1A/CD28/SYK/PTAFR/CARD11/CYBB* |
| G56 | GO:0042119 | Neutrophil activation | 16 | –0.83821684 | –2.012850805 | 0.001751313 | 0.02350135 | tags =56%, list =7%, signal =52% | *STXBP2/CD300A/F2RL1/SYK/PTAFR/FCER1G/TYROBP/IL8* |
| G56 | GO:0042698 | Ovulation cycle | 81 | –0.462917208 | –1.528752307 | 0.00617284 | 0.044612401 | tags =28%, list =17%, signal =24% | *NRIP1/CHRNA7/MMP19/ARRB2/CEBPB/LEP/INHA/TIMP4/PDGFRA/OPRL1/PTN/VEGFA/MSH4/PTPRN/VGF/HAS2/TGFB3/MMP7/ROBO2/INHBA/TRPM2/HAS1* |
| G57 | GO:0042886 | Amide transport | 184 | –0.447629653 | –1.655094299 | 0.001375516 | 0.023352669 | tags =26%, list =15%, signal =22% | *CACNA1A/LEP/HIF1A/PARK2/SLC25A4/CD38/IRS2/ADRA2A/ITPR2/IRS1/ITPR1/SERP1/ARNTL/UCN/SLC15A3/SYBU/ABCA12/SIRT4/DISP1/EXOC3L1/SMPD3/UCP2/SOX4/SFRP1/RBP4/SLC19A2/ABCA1/ADCY5/PTPRN/GPR27/CHD7/IL1B/TMEM27/VGF/SLC2A1/CA2/KCNS3/AQP9/SLC14A1/IL1RN/IL6/CD209/TRPM2/S100A9/FOLR2/CD74* |
| G57 | GO:0042743 | Hydrogen peroxide metabolic process | 28 | –0.685494165 | –1.868183049 | 0.001672241 | 0.023352669 | tags =21%, list =9%, signal =20% | *RAC2/MPO/CYBB/SNCA/MMP3* |
| G57 | GO:0043030 | Regulation of macrophage activation | 20 | –0.797687097 | –2.050664497 | 0.001694915 | 0.023352669 | tags =45%, list =3%, signal =44% | *WNT5A/IL1RL1/HAVCR2/LBP/GPR116/IL33/CD74/SNCA* |
| G57 | GO:0043032 | Positive regulation of macrophage activation | 10 | –0.886605682 | –1.911922846 | 0.001841621 | 0.024395555 | tags =50%, list =3%, signal =49% | *IL1RL1/HAVCR2/LBP/IL33* |
| G58 | GO:0043062 | Extracellular structure organization | 264 | –0.446818696 | –1.711915142 | 0.001315789 | 0.023352669 | tags =25%, list =9%, signal =23% | *SERPINE1/COL5A2/COL11A2/PDGFB/MMP11/CRISPLD2/VWF/COL4A2/COL27A1/THSD4/ITGA1/MMP15/B4GALT1/COL3A1/TNC/COL11A1/FAP/ITGB3/LTBP2/COL4A1/DPP4/CTGF/DPT/ITGB2/HAPLN1/FGF2/ANTXR1/VCAN/MYH11/CTSV/MMP9/CTSS/ADAM8/A2M/LOXL2/SPARC/LCP1/P4HA1/F11R/SPINT2/SPOCK2/MPZL3/MMP16/ITGAX/RGCC/VTN/MMP10/COL7A1/HAS3/HAS2/SULF1/NDNF/MMP7/FBN2/ITGA2/SOX9/ITGAM/MMP8/COL10A1/KDR/MMP1/SNCA/SPP1/MMP3/HAS1* |
| G58 | GO:0043255 | Regulation of carbohydrate biosynthetic process | 68 | –0.528760767 | –1.696720027 | 0.001538462 | 0.023352669 | tags =32%, list =16%, signal =27% | *NR1D1/GNMT/PPP1R3B/TGFB1/LEP/IRS2/SORBS1/IRS1/PDGFB/SIK1/FOXO1/P2RY1/FBP1/DGAT2/HAS2/C1QTNF3/PLEK/IL6/PTAFR/IGF1/SNCA* |
| G58 | GO:0043407 | Negative regulation of MAP kinase activity | 62 | –0.53451507 | –1.692659576 | 0.00155521 | 0.023352669 | tags =44%, list =21%, signal =35% | *PAQR3/SPRY1/MAPK7/PTPN1/GSTP1/DUSP19/DUSP3/DAB2IP/GBA/SPRED2/DUSP16/HYAL2/DUSP6/DUSP8/DUSP4/SFRP1/UCHL1/DUSP10/RGS2/IL1B/LYN/CD300A/RGS4/APOE/PTPN6/PTPN22* |
| G58 | GO:0043299 | Leukocyte degranulation | 49 | –0.679040628 | –2.05887509 | 0.001577287 | 0.023352669 | tags =41%, list =9%, signal =37% | *RASGRP1/MILR1/LAT2/BTK/STXBP2/UNC13D/LAT/CORO1A/HMOX1/LYN/CD300A/F2RL1/VAMP8/FGR/SYK/PTAFR/CD84/HCK/FCER1G* |
| G58 | GO:0043303 | Mast cell degranulation | 34 | –0.685369688 | –1.968279002 | 0.001623377 | 0.023352669 | tags =47%, list =9%, signal =43% | *RASGRP1/MILR1/LAT2/BTK/STXBP2/UNC13D/LAT/HMOX1/LYN/CD300A/VAMP8/FGR/SYK/CD84/FCER1G* |
| G58 | GO:0043536 | Positive regulation of blood vessel endothelial cell migration | 23 | –0.688617946 | –1.820962145 | 0.001636661 | 0.023352669 | tags =48%, list =14%, signal =41% | *TGFB1/PLCG1/PDGFB/VEGFA/HSPB1/PTGS2/FGF2/ANGPT4/SRPX2/ANGPT1* |
| G58 | GO:0043304 | Regulation of mast cell degranulation | 24 | –0.711519965 | –1.884001678 | 0.001655629 | 0.023352669 | tags =46%, list =9%, signal =42% | *STXBP2/UNC13D/HMOX1/LYN/CD300A/VAMP8/FGR/SYK/CD84/FCER1G* |
| G58 | GO:0043300 | Regulation of leukocyte degranulation | 31 | –0.714984825 | –1.98870707 | 0.00166113 | 0.023352669 | tags =42%, list =9%, signal =38% | *STXBP2/UNC13D/HMOX1/LYN/CD300A/F2RL1/VAMP8/FGR/SYK/PTAFR/CD84/FCER1G* |
| G58 | GO:0043372 | Positive regulation of CD4-positive, alpha-beta T cell differentiation | 19 | –0.74915676 | –1.899468624 | 0.001733102 | 0.023440094 | tags =42%, list =7%, signal =39% | *PRKCZ/IL18/CD83/NCKAP1L/CD86/SASH3/IL6* |
| G58 | GO:0043302 | Positive regulation of leukocyte degranulation | 15 | –0.83163553 | –1.966950225 | 0.001766784 | 0.023647377 | tags =40%, list =2%, signal =39% | *VAMP8/FGR/SYK/PTAFR/FCER1G* |
| G58 | GO:0043269 | Regulation of ion transport | 348 | –0.383117346 | –1.496346391 | 0.00255102 | 0.030326036 | tags =27%, list =17%, signal =23% | *FAM115A/MAP2K6/CAPN3/SCN3B/HOMER1/HTT/STK39/MIF/CATSPER2/C19orf26/GPD1L/ARRB2/TGFB1/CACNA1A/AKAP9/LEP/RNF207/DMD/STIM2/CASK/IRS2/ADRA2A/TNFRSF11A/PLCG1/EHD3/TRPV2/SHANK3/KCND2/KCNQ5/HCN2/AP000322.53/OPRL1/UCN/KCNMB1/KCNAB2/CCR1/TRPV3/NLGN1/PDGFB/SIK1/P2RX1/FAM115C/KCNE1/PTGS2/PDZK1/CACNA1H/DRD4/F2RL3/KCNRG/SERPINE2/ATP1B1/CAMK2A/KCNH1/EPPIN/KCNMA1/SHANK1/MMP9/P2RY1/CTSS/KCNE4/CORO1A/MYLK/CHD7/SFRP4/IL1B/JPH2/LYN/TSPAN13/PLCG2/CA2/ARC/KCNS3/KCNQ3/ROS1/PTPN6/NETO2/BDKRB1/CCL2/CD4/SCN9A/SCN2A/PLN/JPH1/SYK/KCNJ5/PTAFR/CD84/CYBB/STC1/HTR2A/KCNC3/SNCA* |
| G58 | GO:0043367 | CD4-positive, alpha-beta T cell differentiation | 41 | –0.550306922 | –1.619835742 | 0.00483871 | 0.038245256 | tags =41%, list =15%, signal =35% | *JAK3/LGALS9/PTGER4/SATB1/RORA/TNFSF4/RSAD2/PRKCZ/IL18/CD83/ZFPM1/NCKAP1L/CD86/SASH3/IL6/GPR183* |
| G58 | GO:0043410 | Positive regulation of MAPK cascade | 354 | –0.364470711 | –1.425383587 | 0.00635324 | 0.045290946 | tags =23%, list =14%, signal =21% | *MAPK3/TLR6/ANKRD6/TRAF4/LGALS9/C19orf10/PDGFRA/FLT1/RELT/IL11/ADRA2A/TNFRSF11A/PLCG1/NOX4/PDGFA/HIPK2/AR/TLR4/ZNF622/CCR1/ATP6AP1/GAREM/DUSP6/CSF1R/RASGRP1/GADD45A/PDGFB/VEGFA/PLCB1/MUC20/PLA2G5/KL/ITGA1/DRD4/TNIK/CTGF/HAND2/TGFA/EPGN/FGF2/PRKCZ/XDH/SCIMP/P2RY1/ADAM8/FZD8/FZD7/NDRG4/NRK/TPD52L1/CDH2/IL1B/WNT5A/GADD45G/TGFB3/MDFI/CCL26/ANGPT1/CCL22/F2RL1/HAVCR2/GDF6/CCL2/PTPN22/PIK3R5/TREM2/C5AR1/IL1A/IL6/SYK/CCL8/FGD2/GPR183/HTR2A/CXCR4/LIF/IGF1/FPR1/KDR/CCL13/CD74/BMP2* |
| G58 | GO:0043306 | Positive regulation of mast cell degranulation | 10 | –0.792924841 | –1.709904583 | 0.007366483 | 0.049685189 | tags =40%, list =2%, signal =39% | *FGR/SYK/FCER1G* |
| G59 | GO:0044259 | Multicellular organismal macromolecule metabolic process | 94 | –0.525917935 | –1.773804344 | 0.001536098 | 0.023352669 | tags =43%, list =16%, signal =36% | *CTSD/MMP19/SERPINH1/LEPRE1/TGFB1/ITGB1/HIF1A/COL25A1/UCN/COL15A1/COL4A5/COL5A2/COL11A2/MMP11/COL4A2/MMP15/COL3A1/COL11A1/FAP/COL4A1/CTGF/LEPREL1/MMP9/CTSS/MMP16/RGCC/MMP10/COL7A1/TGFB3/MMP7/CCL2/ITGA2/ENPEP/SERPINB7/IL6/MMP8/COL10A1/MMP1/MMP3* |
| G59 | GO:0044236 | Multicellular organism metabolic process | 104 | –0.492194195 | –1.686216017 | 0.002962963 | 0.030486975 | tags =38%, list =16%, signal =33% | *CTSD/MMP19/SERPINH1/LEPRE1/TGFB1/ITGB1/HIF1A/COL25A1/UCN/COL15A1/COL4A5/COL5A2/COL11A2/MMP11/COL4A2/MMP15/COL3A1/COL11A1/FAP/COL4A1/CTGF/LEPREL1/MMP9/CTSS/MMP16/RGCC/MMP10/COL7A1/TGFB3/MMP7/CCL2/ITGA2/ENPEP/SERPINB7/IL6/MMP8/COL10A1/MMP1/MMP3* |
| G59 | GO:0044246 | Regulation of multicellular organismal metabolic process | 29 | –0.644603165 | –1.767742723 | 0.003372681 | 0.03103469 | tags =38%, list =14%, signal =33% | *ITGB1/UCN/FAP/CTGF/RGCC/TGFB3/CCL2/ITGA2/SERPINB7/IL6* |
| G59 | GO:0044262 | Cellular carbohydrate metabolic process | 204 | –0.407016608 | –1.530221023 | 0.004092769 | 0.035385975 | tags =24%, list =16%, signal =20% | *NR1D1/PGAM1/GYG2/PHKA1/GNMT/IMPAD1/AKR1B1/PPP1R3B/PGM1/LEP/TPI1/TREH/PARK2/IRS2/SORBS1/IRS1/DDIT4/MTMR7/IPPK/GNPTAB/SYNJ1/C12orf5/PDK1/RORA/SIK1/B4GALT1/MGAM/PDK4/GYS1/FOXO1/PFKFB4/P2RY1/PDK3/FBP1/DGAT2/HAS3/HAS2/SLC2A1/PPP1R3C/C1QTNF3/HK3/PLEK/IL6/PTAFR/IGF1/SNCA/HAS1* |
| G59 | GO:0044253 | Positive regulation of multicellular organismal metabolic process | 17 | –0.706071964 | –1.723022092 | 0.005272408 | 0.039836829 | tags =47%, list =14%, signal =40% | *UCN/CTGF/RGCC/TGFB3/CCL2/ITGA2/SERPINB7* |
| G59 | GO:0044243 | Multicellular organism catabolic process | 60 | –0.514797378 | –1.614988178 | 0.006299213 | 0.045145817 | tags =38%, list =11%, signal =34% | *COL15A1/COL4A5/COL5A2/COL11A2/MMP11/COL4A2/MMP15/COL3A1/COL11A1/FAP/COL4A1/MMP9/CTSS/MMP16/MMP10/COL7A1/MMP7/ENPEP/MMP8/COL10A1/MMP1/MMP3* |
| G6 | GO:0002252 | Immune effector process | 491 | –0.46528781 | –1.859617666 | 0.001201923 | 0.023352669 | tags =20%, list =9%, signal =19% | *RASGRP1/IFI44L/MILR1/RORA/RAET1E/LAT2/DENND1B/IFNE/BTK/CADM1/SPON2/CFH/MICA/TNFSF4/STXBP2/ITM2A/GCNT3/UNC13D/VAV3/LAT/RBP4/RSAD2/CFHR1/PRKCZ/LIMK1/MPO/CORO1A/IL18/DUSP10/A2M/WAS/LCP1/C7/ZFPM1/CLU/BNIP3/CFI/TLR8/SLAMF7/TLR7/HMOX1/AC005013.1/CR1/RGCC/VTN/IL1B/LYN/CD300A/WNT5A/CYFIP2/PLCG2/TGFB3/INPP5D/ANGPT1/F2RL1/PTPN6/KLRD1/HAVCR2/VAMP8/NCKAP1L/CCL2/FGR/CLEC7A/TREM1/PTPRC/PPAPDC1A/LBP/CD86/CD4/C5AR1/GPAM/SASH3/SLC11A1/CD180/IL6/CD28/SYK/PTAFR/C3AR1/CD84/GPR183/HCK/HLA-DMB/FCGR1A/C1QA/FCER1G/VSIG4/TYROBP/HLA-DQB1/FCGR2A/CXCL6/IL33/CD74/FCGR3A/C1QB/C1QC/CXCL5* |
| G6 | GO:0002253 | Activation of immune response | 394 | –0.543242257 | –2.140418734 | 0.001248439 | 0.023352669 | tags =19%, list =6%, signal =18% | *VAV3/LAT/RSAD2/TLR1/CFHR1/LGMN/CTSS/LIMK1/ADAM8/A2M/WAS/C7/CLU/MNDA/CFI/TLR8/TLR7/AC005013.1/CR1/RGCC/VTN/HLA-DPA1/LYN/CD300A/SKAP2/CYFIP2/PLCG2/INPP5D/MARCO/PAG1/F2RL1/PTPN6/HAVCR2/NCKAP1L/FGR/CLEC7A/PTPN22/TNFRSF21/PTPRC/PIK3AP1/PPAPDC1A/PRKCB/LBP/CD86/CD4/C5AR1/NFAM1/CD180/LCP2/CD28/SYK/CD14/ITGAM/C3AR1/CARD11/HLA-DQA1/HCK/CD209/FCGR1A/C1QA/FCER1G/VSIG4/FPR1/HLA-DQB1/FPR3/HLA-DRB1/FCGR2A/HLA-DRB5/FCGR3A/HLA-DRA/C1QB/C1QC* |
| G6 | GO:0002429 | Immune response-activating cell surface receptor signaling pathway | 249 | –0.571871038 | –2.184559012 | 0.001321004 | 0.023352669 | tags =17%, list =6%, signal =17% | *LAT/LIMK1/WAS/MNDA/CR1/HLA-DPA1/LYN/CD300A/CYFIP2/PLCG2/INPP5D/PAG1/PTPN6/NCKAP1L/FGR/CLEC7A/PTPN22/TNFRSF21/PTPRC/PPAPDC1A/PRKCB/CD4/C5AR1/NFAM1/LCP2/CD28/SYK/C3AR1/CARD11/HLA-DQA1/HCK/CD209/FCGR1A/FCER1G/FPR1/HLA-DQB1/FPR3/HLA-DRB1/FCGR2A/HLA-DRB5/FCGR3A/HLA-DRA* |
| G6 | GO:0002237 | Response to molecule of bacterial origin | 238 | –0.509675477 | –1.939178814 | 0.001335113 | 0.023352669 | tags =21%, list =9%, signal =19% | *CMPK2/SERPINE1/STAR/SPON2/TNFSF4/TLR2/PTGS2/TLR1/MPO/IL18/DUSP10/SPARC/ABCA1/IL1B/LYN/CXCL16/WNT5A/PLCG2/IRF8/CCR5/HAVCR2/BDKRB1/ACP5/CCL2/PTPN22/TNFRSF21/CSF2RB/TNFRSF10D/TREM2/TNFRSF10C/LBP/CD86/C5AR1/SLC11A1/CD180/IL6/CD14/PTAFR/HCK/CXCL1/IL10RA/PF4/LY86/EDNRB/CXCL6/CXCL3/SNCA/CXCL5/IL8* |
| G6 | GO:0002250 | Adaptive immune response | 223 | –0.527594334 | –1.996661534 | 0.001349528 | 0.023352669 | tags =27%, list =8%, signal =25% | *RAET1E/LAT2/DENND1B/IFNE/BTK/MICA/TNFSF4/GCNT3/RNF125/UNC13D/LAT/RSAD2/PRKCZ/CTSS/IL18/DUSP10/WAS/C7/CLU/IGJ/CFI/TLR8/SLAMF7/CR1/CAMK4/LILRB4/IL1B/LYN/LILRA6/INPP5D/CD48/PAG1/IL1RL1/PTPN6/HAVCR2/TNFRSF21/PTPRC/PRKCB/CD86/CD4/SASH3/SLC11A1/LAIR1/SAMSN1/IL6/CD28/SYK/CD84/GPR183/ICOSLG/CD209/C1QA/FCER1G/LILRB5/HLA-DQB1/IL33/CD74/C1QB/C1QC* |
| G6 | GO:0002263 | Cell activation involved in immune response | 147 | –0.552715793 | –1.991790546 | 0.00141844 | 0.023352669 | tags =28%, list =10%, signal =25% | *RAC2/RASGRP1/MILR1/RORA/LAT2/IFNE/BTK/TNFSF4/STXBP2/ITM2A/UNC13D/LAT/PRKCZ/CORO1A/IL18/LCP1/ZFPM1/HMOX1/LYN/CD300A/PLCG2/F2RL1/HAVCR2/VAMP8/FGR/CLEC7A/LBP/CD86/SLC11A1/CD180/IL6/CD28/SYK/PTAFR/CD84/GPR183/HLA-DMB/FCER1G/TYROBP/IL33* |
| G6 | GO:0002366 | Leukocyte activation involved in immune response | 146 | –0.553620679 | –1.99369655 | 0.00141844 | 0.023352669 | tags =28%, list =10%, signal =26% | *RAC2/RASGRP1/MILR1/RORA/LAT2/IFNE/BTK/TNFSF4/STXBP2/ITM2A/UNC13D/LAT/PRKCZ/CORO1A/IL18/LCP1/ZFPM1/HMOX1/LYN/CD300A/PLCG2/F2RL1/HAVCR2/VAMP8/FGR/CLEC7A/LBP/CD86/SLC11A1/CD180/IL6/CD28/SYK/PTAFR/CD84/GPR183/HLA-DMB/FCER1G/TYROBP/IL33* |
| G6 | GO:0002274 | Myeloid leukocyte activation | 114 | –0.671852409 | –2.325838632 | 0.001459854 | 0.023352669 | tags =41%, list =11%, signal =37% | *TLR4/TGFBR2/PREX1/DOCK2/RAC2/RASGRP1/MILR1/RORA/LAT2/BTK/TLR2/STXBP2/UNC13D/LAT/DCSTAMP/TLR1/CD93/CLU/TLR8/TLR7/HMOX1/CAMK4/LYN/CD300A/WNT5A/F2RL1/IL1RL1/HAVCR2/VAMP8/FGR/LBP/CD86/SLC11A1/LCP2/SYK/AIF1/PTAFR/CD84/SPI1/FCER1G/TYROBP/GPR116/IL33/CD74/SNCA/IL8* |
| G6 | GO:0002431 | Fc receptor mediated stimulatory signaling pathway | 72 | –0.646121401 | –2.097832824 | 0.001545595 | 0.023352669 | tags =21%, list =6%, signal =20% | *LIMK1/WAS/LYN/CYFIP2/PLCG2/NCKAP1L/FGR/PPAPDC1A/SYK/HCK/FCGR1A/FCER1G/FCGR2A/FCGR3A* |
| G6 | GO:0002275 | Myeloid cell activation involved in immune response | 54 | –0.698701548 | –2.168429474 | 0.001550388 | 0.023352669 | tags =43%, list =10%, signal =39% | *RAC2/RASGRP1/MILR1/LAT2/BTK/STXBP2/UNC13D/LAT/HMOX1/LYN/CD300A/F2RL1/HAVCR2/VAMP8/FGR/LBP/SYK/PTAFR/CD84/FCER1G/TYROBP/IL33* |
| G6 | GO:0002433 | Immune response-regulating cell surface receptor signaling pathway involved in phagocytosis | 67 | –0.64325226 | –2.055697081 | 0.001560062 | 0.023352669 | tags =21%, list =6%, signal =20% | *LIMK1/WAS/LYN/CYFIP2/PLCG2/NCKAP1L/FGR/PPAPDC1A/SYK/HCK/FCGR1A/FCGR2A/FCGR3A* |
| G6 | GO:0002367 | Cytokine production involved in immune response | 52 | –0.622146238 | –1.917200489 | 0.001567398 | 0.023352669 | tags =48%, list =8%, signal =44% | *MIF/JAK3/TGFB1/BST2/TLR4/DENND1B/BTK/SPON2/TNFSF4/TLR2/RSAD2/PRKCZ/HMOX1/AC005013.1/WNT5A/TGFB3/ANGPT1/F2RL1/TREM1/SASH3/SLC11A1/IL6/FCER1G/CD74* |
| G6 | GO:0002286 | T cell activation involved in immune response | 51 | –0.569683255 | –1.74011319 | 0.001574803 | 0.023352669 | tags =29%, list =8%, signal =27% | *IFNE/TNFSF4/PRKCZ/IL18/LCP1/ZFPM1/F2RL1/HAVCR2/CD86/SLC11A1/IL6/GPR183/HLA-DMB/FCER1G* |
| G6 | GO:0002279 | Mast cell activation involved in immune response | 34 | –0.685369688 | –1.968279002 | 0.001623377 | 0.023352669 | tags =47%, list =9%, signal =43% | *RASGRP1/MILR1/LAT2/BTK/STXBP2/UNC13D/LAT/HMOX1/LYN/CD300A/VAMP8/FGR/SYK/CD84/FCER1G* |
| G6 | GO:0002285 | Lymphocyte activation involved in immune response | 98 | –0.476537377 | –1.616223858 | 0.003021148 | 0.030486975 | tags =30%, list =15%, signal =25% | *NOTCH2/JAK3/TGFB1/LGALS9/PTGER4/TFRC/TLR4/RORA/IFNE/TNFSF4/ITM2A/UNC13D/PRKCZ/CORO1A/IL18/LCP1/ZFPM1/PLCG2/F2RL1/HAVCR2/CD86/SLC11A1/CD180/IL6/CD28/GPR183/HLA-DMB/FCER1G* |
| G6 | GO:0002369 | T cell cytokine production | 17 | –0.713814355 | –1.741915791 | 0.003514938 | 0.031944406 | tags =41%, list =8%, signal =38% | *TNFSF4/RSAD2/PRKCZ/SASH3/SLC11A1/IL6* |
| G6 | GO:0002283 | Neutrophil activation involved in immune response | 10 | –0.849133605 | –1.831116101 | 0.003683241 | 0.033008247 | tags =50%, list =7%, signal =47% | *SYK/PTAFR/FCER1G/TYROBP* |
| G6 | GO:0002228 | Natural killer cell mediated immunity | 35 | –0.594281193 | –1.727231497 | 0.006389776 | 0.045290946 | tags =40%, list =14%, signal =34% | *LEP/LGALS9/ULBP2/RASGRP1/RAET1E/CADM1/MICA/UNC13D/CORO1A/SLAMF7/PTPN6/KLRD1/HAVCR2* |
| G60 | GO:0044409 | Entry into host | 93 | –0.49965221 | –1.682196746 | 0.001531394 | 0.023352669 | tags =28%, list =7%, signal =26% | *GAS6/P4HB/CXADR/HYAL2/ITGB1/LGALS9/TFRC/ITGA5/ITGB5/ITGB3/DPP4/F11R/SLC52A1/CR1/PVRL4/CCR5/VAMP8/EFNB2/ITGA2/CD86/CD4/CD209/HTR2A/CXCR4/IL8* |
| G60 | GO:0044283 | Small molecule biosynthetic process | 369 | –0.372250732 | –1.461158107 | 0.003773585 | 0.033468645 | tags =22%, list =17%, signal =18% | *PTGES/RFK/ACN9/MTHFD2L/GGT7/NR1D1/PGAM1/PLOD1/MIF/GPI/GBA/PNPO/PROX1/FADS1/GNMT/IMPAD1/AKR1B1/DKK3/PGM1/LEP/TPI1/ATF3/CYP27B1/ALDH8A1/ENO3/GLS/SLC1A3/ACER2/ENO2/NOXRED1/GAPDH/IPPK/ALDOC/ALDOA/ALDH1A3/PGK1/STAR/SCD/SIK1/RDH10/PLA2G5/ACLY/PTGS2/HSD17B1/CACNA1H/GGT1/FGF2/RBP4/PDK4/ASPA/FOXO1/SNAI1/APOC1/P2RY1/FBP1/MPO/DGAT2/DHRS9/PADI2/IL1B/PLCG2/HPGDS/LPL/APOE/CES1/C1QTNF3/ACADL/RBP1/ALOX5AP/APOC2/PLEK/IL6/SYK/PTAFR/ALOX5/SDS/CD74/SNCA/BMP2* |
| G61 | GO:0045088 | Regulation of innate immune response | 280 | –0.409988321 | –1.577541132 | 0.001305483 | 0.023352669 | tags =14%, list =8%, signal =13% | *CADM1/MICA/TLR2/ITGB2/RSAD2/TLR1/LGMN/CTSS/ADAM8/DUSP10/A2M/TLR8/TLR7/AC005013.1/CR1/LYN/WNT5A/PLCG2/MARCO/F2RL1/PTPN6/HAVCR2/CD1D/FGR/CLEC7A/PTPN22/PIK3AP1/LBP/CD86/CD180/SYK/CD14/ITGAM/CARD11/HCK/CD209/FCER1G* |
| G61 | GO:0045089 | Positive regulation of innate immune response | 240 | –0.411136555 | –1.566111313 | 0.001328021 | 0.023352669 | tags =13%, list =8%, signal =12% | *CADM1/TLR2/ITGB2/RSAD2/TLR1/LGMN/CTSS/ADAM8/TLR8/TLR7/AC005013.1/LYN/WNT5A/PLCG2/MARCO/F2RL1/HAVCR2/CD1D/CLEC7A/PTPN22/PIK3AP1/LBP/CD86/CD180/SYK/CD14/ITGAM/CARD11/HCK/CD209/FCER1G* |
| G61 | GO:0045055 | Regulated exocytosis | 204 | –0.479119607 | –1.801299706 | 0.001364256 | 0.023352669 | tags =31%, list =15%, signal =27% | *C19orf26/TGFB1/SYT15/CACNA1A/DNAJC5/LGALS9/TF/ADRA2A/TIMP1/FN1/PDGFA/FAM3C/RIMS3/ALDOA/SYNJ1/RAC2/ABCA12/RASGRP1/RAB11FIP1/SERPINE1/MILR1/NLGN1/LAT2/PDGFB/VEGFA/SYTL1/VWF/P2RX1/BTK/STXBP2/ITGB3/UNC13D/SYTL3/LAT/SCIN/SYN1/CORO1A/A2M/SPARC/CLU/ISLR/RIMS1/HMOX1/TMEM27/LYN/CD300A/TGFB3/F2RL1/VAMP8/FGR/SRGN/F13A1/PLEK/SYK/PTAFR/CD84/HCK/PCDH7/CADPS/FCER1G/PF4/IGF1* |
| G61 | GO:0045580 | Regulation of T cell differentiation | 83 | –0.484308646 | –1.605796565 | 0.001533742 | 0.023352669 | tags =31%, list =15%, signal =27% | *TGFB1/LGALS9/HLA-DOA/TNFSF9/IL15/TGFBR2/GLI2/IL2RA/RASGRP1/TNFSF4/PRKCZ/ADAM8/IL18/CD83/CAMK4/IL36B/CYP26B1/NCKAP1L/CD86/SASH3/IL6/CD28/SYK/CARD11/CD74* |
| G61 | GO:0045582 | Positive regulation of T cell differentiation | 52 | –0.559971293 | –1.725602714 | 0.001567398 | 0.023352669 | tags =37%, list =14%, signal =31% | *LGALS9/TNFSF9/TGFBR2/GLI2/IL2RA/RASGRP1/TNFSF4/PRKCZ/ADAM8/IL18/CD83/IL36B/NCKAP1L/CD86/SASH3/IL6/SYK/CD74* |
| G61 | GO:0045576 | Mast cell activation | 38 | –0.684971168 | –2.010268618 | 0.001602564 | 0.023352669 | tags =45%, list =9%, signal =41% | *RASGRP1/MILR1/LAT2/BTK/STXBP2/UNC13D/LAT/HMOX1/LYN/CD300A/VAMP8/FGR/LCP2/SYK/CD84/FCER1G* |
| G61 | GO:0045577 | Regulation of B cell differentiation | 22 | –0.717918956 | –1.883774562 | 0.001666667 | 0.023352669 | tags =41%, list =8%, signal =38% | *SFRP1/INPP5D/PTPN6/NCKAP1L/NFAM1/SYK/CARD11/INHBA* |
| G61 | GO:0044706 | Multi-multicellular organism process | 144 | –0.447871245 | –1.61230048 | 0.002836879 | 0.030380747 | tags =28%, list =15%, signal =24% | *AKR1B1/TGFB1/LEP/LGALS9/CD38/CYP27B1/TIMP1/AR/UCN/TGFBR2/VMP1/OVGP1/IGFBP7/ACVR2A/DDR1/P2RX1/ARHGDIB/B4GALT1/PTGS2/UCP2/SERPINE2/PAPPA/HPGD/PCSK5/DDO/CTSV/MMP9/NRK/FOSB/DSG2/IL1B/TGFB3/HAVCR2/MMP7/CCL2/ITGA2/PTAFR/STC1/LIF/SPP1* |
| G61 | GO:0044723 | Single-organism carbohydrate metabolic process | 358 | –0.368452873 | –1.441179174 | 0.005063291 | 0.038932682 | tags =22%, list =16%, signal =19% | *NR1D1/PGAM1/GYG2/GPI/PHKA1/GNMT/IMPAD1/AKR1B1/PPP1R3B/TGFB1/CACNA1A/PGM1/LEP/GLA/TPI1/TREH/HIF1A/PARK2/ATF3/IRS2/NPY1R/ST3GAL1/SORBS1/IRS1/ENO3/DDIT4/PGM2L1/SERP1/GM2A/MANBA/MPI/MTMR7/ENO2/GAPDH/IPPK/ALDOC/GNPTAB/ALDOA/LDHA/SYNJ1/C12orf5/PKM/PDK1/RORA/PGK1/PDGFB/SIK1/CHST1/B4GALT1/ST3GAL6/MGAM/FABP5/RBP4/PDK4/GYS1/FOXO1/PFKFB4/P2RY1/PDK3/FBP1/DGAT2/ST8SIA4/ST6GAL1/HAS3/HAS2/SLC2A1/PPP1R3C/C1QTNF3/HK3/MGAT4A/FUCA1/PLEK/IL6/PTAFR/HTR2A/IGF1/SDS/SNCA/HAS1* |
| G61 | GO:0044849 | Estrous cycle | 15 | –0.746814731 | –1.766335553 | 0.005300353 | 0.039872585 | tags =40%, list =11%, signal =36% | *PTN/HAS2/MMP7/TRPM2/HAS1* |
| G62 | GO:0045596 | Negative regulation of cell differentiation | 430 | –0.392927049 | –1.55860365 | 0.001228501 | 0.023352669 | tags =18%, list =12%, signal =16% | *LINGO1/SEMA6D/KANK1/ARNTL/TLR4/ID3/SOX8/GLI2/PTN/GPR56/MEIS2/GDF11/DRAXIN/COL5A2/RORA/NLGN1/PDGFB/MMP11/ITM2C/PPAPDC3/CXCL14/PAX6/COL3A1/TNFSF4/SKIL/ITGB3/NOTCH3/HOXA9/BHLHE41/CCND1/RAP1GAP2/DNM3/HAND2/SFRP1/TBX3/FOXO1/MDM2/XDH/ADAMTS12/SNAI1/PLK2/PRICKLE1/FZD7/IL18/DUSP10/HOXA7/ABCA1/ZFPM1/MEIS1/MSX2/TMEM176A/LILRB4/LYN/WNT5A/LILRA6/INPP5D/TMEM176B/LDLRAD4/MYOCD/SOX9/NR2F1/RARB/IL6/HIST1H4H/TBX5/SEMA6B/INHBA/PF4/IGF1/EDNRB/CD74/BMP2/SPP1/HOXA2/HOXA5/C1QC/HOXB8* |
| G62 | GO:0045637 | Regulation of myeloid cell differentiation | 141 | –0.524549428 | –1.880610186 | 0.001436782 | 0.023352669 | tags =25%, list =6%, signal =23% | *LEP/INHA/HIF1A/FSTL3/TLR4/CCR1/ATP6AP1/ACVR2A/MEIS2/HOXA9/RUNX1/SFRP1/DCSTAMP/SCIN/HOXA7/ZFPM1/MEIS1/CAMK4/SIGLEC15/LILRB4/LYN/LILRA6/CA2/INPP5D/NCKAP1L/HIST1H4H/SPI1/INHBA/PF4/LIF/TYROBP/HOXA5/C1QC/HOXB8* |
| G62 | GO:0045638 | Negative regulation of myeloid cell differentiation | 65 | –0.627420178 | –1.996430875 | 0.00154321 | 0.023352669 | tags =23%, list =6%, signal =22% | *SFRP1/HOXA7/ZFPM1/MEIS1/LILRB4/LYN/LILRA6/INPP5D/HIST1H4H/INHBA/PF4/HOXA5/C1QC/HOXB8* |
| G62 | GO:0045621 | Positive regulation of lymphocyte differentiation | 64 | –0.507878969 | –1.612204342 | 0.001545595 | 0.023352669 | tags =34%, list =14%, signal =30% | *LGALS9/TNFSF9/IL15/TGFBR2/GLI2/IL2RA/RASGRP1/BTK/TNFSF4/PRKCZ/ADAM8/IL18/CD83/IL36B/INPP5D/NCKAP1L/CD86/SASH3/IL6/SYK/CD74* |
| G62 | GO:0045619 | Regulation of lymphocyte differentiation | 105 | –0.484806013 | –1.663691317 | 0.002967359 | 0.030486975 | tags =31%, list =15%, signal =27% | *TGFB1/LGALS9/INHA/HLA-DOA/TNFSF9/IL15/TGFBR2/GLI2/IL2RA/RASGRP1/BTK/TNFSF4/SFRP1/PRKCZ/ADAM8/IL18/CD83/CAMK4/IL36B/INPP5D/CYP26B1/PTPN6/NCKAP1L/CD86/SASH3/NFAM1/IL6/CD28/SYK/CARD11/INHBA/CD74* |
| G62 | GO:0045639 | Positive regulation of myeloid cell differentiation | 62 | –0.49323052 | –1.561922965 | 0.00466563 | 0.037949001 | tags =21%, list =10%, signal =19% | *ATP6AP1/ACVR2A/RUNX1/DCSTAMP/SCIN/CA2/INPP5D/NCKAP1L/INHBA/PF4/LIF/HOXA5* |
| G62 | GO:0045646 | Regulation of erythrocyte differentiation | 35 | –0.574436291 | –1.66955385 | 0.006389776 | 0.045290946 | tags =20%, list =4%, signal =19% | *LYN/INPP5D/NCKAP1L/SPI1/INHBA/HOXA5* |
| G62 | GO:0045670 | Regulation of osteoclast differentiation | 44 | –0.560382241 | –1.656825693 | 0.006430868 | 0.045354927 | tags =32%, list =15%, signal =27% | *CEBPB/FSTL3/TLR4/CCR1/ATP6AP1/SFRP1/CAMK4/SIGLEC15/LILRB4/LILRA6/CA2/INPP5D/TYROBP* |
| G63 | GO:0045785 | Positive regulation of cell adhesion | 279 | –0.498011742 | –1.916332955 | 0.00130719 | 0.023352669 | tags =26%, list =12%, signal =23% | *TPM1/FN1/SPN/IL15/TFRC/ITGA5/TGFBR2/HLA-DPB1/PREX1/GLI2/IL2RA/PTN/GPR56/NINJ1/RASGRP1/VEGFA/RAC3/RET/TNFSF4/KIF26B/DPP4/UNC13D/SFRP1/VAV3/OLFM4/PRKCZ/ADAM8/CORO1A/IL18/CD83/SPOCK2/PLEKHA2/VTN/HLA-DPA1/IL1B/LYN/WNT5A/IL36B/HAS2/ANGPT1/NDNF/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/PTPRC/ITGA2/CD86/CD4/GPAM/SASH3/EDIL3/IL6/CD28/SYK/AIF1/PTAFR/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/TGM2/IGF1/KDR/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G63 | GO:0045765 | Regulation of angiogenesis | 163 | –0.459136178 | –1.672071629 | 0.001396648 | 0.023352669 | tags =29%, list =13%, signal =25% | *HIF1A/FLT1/PLCG1/TSPAN12/HIPK2/ITGA5/TGFBR2/VASH2/PTN/EGLN1/SERPINE1/VEGFA/HSPB1/COL4A2/GATA6/PTGS2/F3/RUNX1/ANGPTL4/SFRP1/ITGB2/EPHA2/FGF2/PDE3B/SPARC/BAI1/HMOX1/RGCC/IL1B/ANGPT4/WNT5A/SRPX2/SULF1/TIE1/CCL2/PRKCB/C5AR1/IL1A/IL6/C3AR1/STAB1/CYBB/PF4/KDR/HOXA5/IL8* |
| G63 | GO:0045807 | Positive regulation of endocytosis | 87 | –0.518658433 | –1.739569712 | 0.001490313 | 0.023352669 | tags =25%, list =10%, signal =23% | *SERPINE1/NLGN1/VEGFA/MFGE8/GPC3/VTN/SFRP4/IL1B/WNT5A/PLCG2/ANGPT1/F2RL1/NCKAP1L/CCL2/ITGA2/SLC11A1/MERTK/SYK/CD14/FCER1G/SNCA* |
| G63 | GO:0045730 | Respiratory burst | 20 | –0.737011048 | –1.894680754 | 0.001694915 | 0.023352669 | tags =50%, list =12%, signal =44% | *RAC2/MPO/DUSP10/IGJ/LBP/NCF2/SLC11A1/HCK/CYBB* |
| G63 | GO:0045766 | Positive regulation of angiogenesis | 96 | –0.470165909 | –1.587136958 | 0.003067485 | 0.030486975 | tags =31%, list =13%, signal =27% | *HIF1A/FLT1/PLCG1/HIPK2/ITGA5/TGFBR2/VASH2/SERPINE1/VEGFA/HSPB1/GATA6/PTGS2/F3/RUNX1/ANGPTL4/ITGB2/FGF2/HMOX1/IL1B/ANGPT4/WNT5A/SRPX2/PRKCB/C5AR1/IL1A/C3AR1/CYBB/KDR/IL8* |
| G63 | GO:0045780 | Positive regulation of bone resorption | 10 | –0.803986499 | –1.73375852 | 0.007366483 | 0.049685189 | tags =70%, list =11%, signal =62% | *ATP6AP1/DCSTAMP/ADAM8/CA2/SYK/SPP1* |
| G64 | GO:0046364 | Monosaccharide biosynthetic process | 70 | –0.545652967 | –1.761771881 | 0.001545595 | 0.023352669 | tags =34%, list =16%, signal =29% | *NR1D1/PGAM1/GPI/GNMT/AKR1B1/PGM1/LEP/TPI1/ATF3/ENO3/ENO2/GAPDH/ALDOC/ALDOA/PGK1/SIK1/RBP4/FOXO1/FBP1/DGAT2/C1QTNF3/IL6/SDS* |
| G64 | GO:0046631 | Alpha-beta T cell activation | 74 | –0.493993737 | –1.611032889 | 0.00155521 | 0.023352669 | tags =34%, list =15%, signal =29% | *JAK3/CEBPB/LGALS9/PTGER4/SATB1/IL15/TGFBR2/DOCK2/RORA/TNFSF4/RSAD2/PRKCZ/IL18/CD83/ZFPM1/TNFSF8/CD300A/NCKAP1L/CD86/SASH3/IL6/CD28/SYK/GPR183* |
| G64 | GO:0045833 | Negative regulation of lipid metabolic process | 59 | –0.528638561 | –1.660291328 | 0.001567398 | 0.023352669 | tags =32%, list =15%, signal =28% | *ORMDL3/DKK3/ADRA2A/CYP27B1/METTL20/PDGFA/SIRT4/PDGFB/SIK1/PDE3B/SNAI1/APOC1/DGAT2/IL1B/APOE/ACADL/APOC2/BMP2* |
| G64 | GO:0045980 | Negative regulation of nucleotide metabolic process | 35 | –0.625586109 | –1.818216769 | 0.001597444 | 0.023352669 | tags =37%, list =14%, signal =32% | *ADRA2A/DDIT4/OPRL1/EGLN1/C12orf5/APLP1/DRD4/PID1/FBP1/EDNRA/EDNRB/SNCA* |
| G64 | GO:0046635 | Positive regulation of alpha-beta T cell activation | 34 | –0.659895224 | –1.895120161 | 0.001623377 | 0.023352669 | tags =35%, list =7%, signal =33% | *TGFBR2/TNFSF4/PRKCZ/IL18/CD83/NCKAP1L/CD86/SASH3/IL6/CD28/SYK* |
| G64 | GO:0046638 | Positive regulation of alpha-beta T cell differentiation | 29 | –0.660151488 | –1.810382035 | 0.001686341 | 0.023352669 | tags =38%, list =7%, signal =35% | *TGFBR2/TNFSF4/PRKCZ/IL18/CD83/NCKAP1L/CD86/SASH3/IL6/SYK* |
| G64 | GO:0045921 | Positive regulation of exocytosis | 59 | –0.499814105 | –1.569762566 | 0.004702194 | 0.037949001 | tags =22%, list =10%, signal =20% | *NCS1/SDC1/NLGN1/SMPD3/UNC13D/TMEM27/F2RL1/VAMP8/FGR/SYK/PTAFR/FCER1G* |
| G64 | GO:0046634 | Regulation of alpha-beta T cell activation | 46 | –0.54755743 | –1.640525991 | 0.004807692 | 0.038245256 | tags =24%, list =7%, signal =22% | *PRKCZ/IL18/CD83/CD300A/NCKAP1L/CD86/SASH3/IL6/CD28/SYK* |
| G65 | GO:0046649 | Lymphocyte activation | 434 | –0.491740954 | –1.947738255 | 0.001234568 | 0.023352669 | tags =27%, list =14%, signal =24% | *CEBPB/LEP/BST2/JAG2/ITGB1/LGALS9/INHA/ULBP2/PTGER4/CD38/HLA-DOA/IRS2/IL11/TNFSF9/SATB1/SPN/IL15/TFRC/TLR4/KIF13B/TGFBR2/HLA-DPB1/PREX1/GLI2/IL2RA/DOCK2/RAC2/RASGRP1/RORA/LAT2/IFNE/BTK/MICA/TNFSF4/ITM2A/DPP4/SOX4/UNC13D/SFRP1/ITGB2/VAV3/LAT/RSAD2/PRKCZ/ADAM8/FZD8/CORO1A/FZD7/CDKN1A/IL18/CD83/WAS/LCP1/ZFPM1/MNDA/SLAMF7/TNFSF8/TPD52/LST1/CAMK4/CHD7/LYL1/HLA-DPA1/IL1B/LYN/CD300A/SKAP2/BLNK/IL36B/PLCG2/TBC1D10C/INPP5D/CYP26B1/PAG1/F2RL1/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/DOCK8/CLEC7A/PTPN22/TNFRSF21/PTPRC/PRKCB/CD86/CD4/GPAM/SASH3/NFAM1/SLC11A1/CD180/SAMSN1/MERTK/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/SPI1/CD209/INHBA/FCER1G/IGF1/VSIG4/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G65 | GO:0046651 | Lymphocyte proliferation | 164 | –0.554494996 | –2.021031572 | 0.001390821 | 0.023352669 | tags =34%, list =14%, signal =29% | *CEBPB/LEP/LGALS9/CD38/IRS2/TNFSF9/SATB1/SPN/IL15/TFRC/TLR4/HLA-DPB1/IL2RA/DOCK2/RAC2/IFNE/TNFSF4/VAV3/CORO1A/CDKN1A/IL18/MNDA/LST1/HLA-DPA1/IL1B/LYN/CD300A/INPP5D/PTPN6/HAVCR2/NCKAP1L/CD1D/DOCK8/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/SLC11A1/CD180/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DMB/ICOSLG/CD209/IGF1/VSIG4/CD74* |
| G66 | GO:0046879 | Hormone secretion | 187 | –0.44201444 | –1.632690003 | 0.001408451 | 0.023352669 | tags =25%, list =14%, signal =22% | *LEP/INHA/HIF1A/PARK2/SLC25A4/CD38/IRS2/IL11/ADRA2A/ITPR2/IRS1/ITPR1/SERP1/ARNTL/UCN/SYBU/RAB11FIP1/SIRT4/NKX3-1/BTK/EXOC3L1/SMPD3/UCP2/SOX4/SFRP1/TBX3/RBP4/P2RY1/ADCY5/PTPRN/GPR27/CHD7/IL1B/TMEM27/LYN/VGF/SLC2A1/KCNS3/C1QTNF3/VAMP8/IL1RN/IL6/HTR2A/INHBA/LIF/TRPM2* |
| G66 | GO:0048002 | Antigen processing and presentation of peptide antigen | 159 | –0.460343316 | –1.669465161 | 0.001408451 | 0.023352669 | tags =15%, list =5%, signal =14% | *LGMN/CTSV/CTSS/SPTBN2/HLA-DMA/HLA-DPA1/ABCB4/KIF5A/TREM2/NCF4/NCF2/SLC11A1/HLA-DQA1/HLA-DMB/CYBB/CD209/FCGR1A/FCER1G/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G66 | GO:0046883 | Regulation of hormone secretion | 155 | –0.428051411 | –1.548211898 | 0.001420455 | 0.023352669 | tags =25%, list =14%, signal =22% | *LEP/INHA/HIF1A/PARK2/SLC25A4/CD38/IRS2/IL11/ADRA2A/ITPR2/IRS1/ITPR1/SERP1/ARNTL/UCN/SYBU/RAB11FIP1/SIRT4/NKX3-1/UCP2/SOX4/SFRP1/RBP4/P2RY1/ADCY5/GPR27/CHD7/IL1B/TMEM27/SLC2A1/KCNS3/C1QTNF3/VAMP8/IL6/HTR2A/INHBA/LIF/TRPM2* |
| G66 | GO:0046718 | Viral entry into host cell | 89 | –0.464296894 | –1.558426797 | 0.006060606 | 0.044298302 | tags =28%, list =17%, signal =24% | *GAS6/P4HB/CXADR/HYAL2/ITGB1/LGALS9/TFRC/ITGA5/ITGB5/ITGB3/DPP4/F11R/SLC52A1/CR1/PVRL4/CCR5/VAMP8/EFNB2/ITGA2/CD86/CD4/CD209/HTR2A/CXCR4* |
| G66 | GO:0046660 | Female sex differentiation | 81 | –0.455537385 | –1.504380948 | 0.00617284 | 0.044612401 | tags =27%, list =16%, signal =23% | *MMP19/ARRB2/CEBPB/LEP/ZFPM2/INHA/PDGFRA/VEGFA/SFRP1/TBX3/RBP4/MSH4/PTPRN/CHD7/STRA6/VGF/WNT5A/MERTK/ROBO2/INHBA/PITX2* |
| G66 | GO:0046852 | Positive regulation of bone remodeling | 10 | –0.803986499 | –1.73375852 | 0.007366483 | 0.049685189 | tags =70%, list =11%, signal =62% | *ATP6AP1/DCSTAMP/ADAM8/CA2/SYK/SPP1* |
| G67 | GO:0048598 | Embryonic morphogenesis | 447 | –0.394284692 | –1.564317636 | 0.001230012 | 0.023352669 | tags =25%, list =15%, signal =22% | *RSPO3/SMO/GPI/NKX3-2/EPHB2/PROX1/IMPAD1/TGFB1/MAPK3/CCDC40/JAG2/ITGB1/HIF1A/RNF207/GSC/MYADM/PDGFRA/FLT1/HOXD3/FN1/HIPK2/C2CD3/AR/ITGA5/TENM4/TGFBR2/SALL4/ITGB5/SOX8/GLI2/DUSP6/ACVR2A/ALDH1A3/HOXC9/EN1/COL5A2/PTK7/COL4A2/RDH10/HOXB2/MICAL2/GATA6/IRX2/MMP15/RET/PAX6/COL11A1/CTHRC1/ITGB3/GDNF/CRABP2/GPC3/HOXA9/DUSP4/SOX4/CELSR1/HAND2/SFRP1/TBX3/ITGB2/EPHA2/FGF2/RBP4/GJB5/AFF3/MMP9/SNAI1/FLRT3/PRICKLE1/FZD7/NDRG4/MYO7A/HOXA7/SPINT2/HOXB4/CHRNA9/MMP16/WNT11/EYA1/CHD7/VTN/MSX2/STRA6/COL7A1/WNT5A/TGFB3/MDFI/HOXB3/SULF1/CYP26B1/HOXB5/FBN2/ITGA2/ST14/DACT1/SOX9/IL1RN/RARB/EYA2/SATB2/TBX5/MMP8/INHBA/HOXB7/HOXB6/ALX1/HOXA6/HOXA3/HOXA2/HOXA5/PITX2/HOXB8* |
| G67 | GO:0048514 | Blood vessel morphogenesis | 400 | –0.446443829 | –1.760722842 | 0.001248439 | 0.023352669 | tags =29%, list =15%, signal =25% | *SMO/GPI/MMP19/EPHB2/PROX1/ARHGAP22/TGFB1/ZMIZ1/LEP/ITGB1/ZFPM2/C19orf10/HIF1A/ROBO1/PDGFRA/FLT1/PLCG1/PTPRB/FN1/PDGFA/EPAS1/TSPAN12/HIPK2/ITGA5/TGFBR2/COL15A1/VASH2/PTN/GPR56/EGLN1/RAMP1/HEY1/SERPINE1/RORA/VEGFA/HSPB1/COL4A2/GATA6/CALCRL/B4GALT1/COL3A1/FAP/PTGS2/F3/ITGB3/MFGE8/NOTCH3/RUNX1/COL4A1/CTGF/SOX4/ANGPTL4/HAND2/EPGN/SFRP1/ITGB2/VAV3/EPHA2/FGF2/HPGD/XDH/PDE3B/ADAM8/FZD8/IL18/LOXL2/SPARC/HOXA7/BAI1/MEIS1/SAT1/CDH2/HMOX1/MYLK/WNT11/RGCC/EYA1/CHD7/EDNRA/STRA6/IL1B/NRP2/ANGPT4/WNT5A/SRPX2/NRCAM/HAS2/APOE/HOXB3/SULF1/ANGPT1/TIE1/NDNF/EFNB2/MYOCD/CCL2/PRKCB/C5AR1/IL1A/ENPEP/IL6/SYK/C3AR1/STAB1/CYBB/SPI1/TBX5/PF4/KDR/MCAM/HOXA3/HOXA5/SCG2/IL8/PITX2* |
| G67 | GO:0048010 | Vascular endothelial growth factor receptor signaling pathway | 83 | –0.492178641 | –1.631890692 | 0.001533742 | 0.023352669 | tags =24%, list =13%, signal =21% | *MAPK13/FLT1/ITGA5/VEGFA/HSPB1/ITGB3/VAV3/VTN/IL1B/NRP2/CYFIP2/SULF1/NCKAP1L/CCL2/PRKCB/NCF4/NCF2/CYBB/KDR* |
| G67 | GO:0048247 | Lymphocyte chemotaxis | 22 | –0.748293079 | –1.963474368 | 0.001666667 | 0.023352669 | tags =50%, list =7%, signal =46% | *ADAM8/PADI2/CXCL16/WNT5A/CCL26/CCL22/CCL2/CCL8/GPR183/CCL13* |
| G67 | GO:0048568 | Embryonic organ development | 317 | –0.399628245 | –1.549723114 | 0.002583979 | 0.030326036 | tags =26%, list =15%, signal =22% | *SMO/NKX3-2/EPHB2/PROX1/TGFB1/CEBPB/MAPK3/CCDC40/ZFPM2/HIF1A/RNF207/GSC/PDGFRA/TTPA/NES/HOXD3/PPP1R13L/PDGFA/EPAS1/HIPK2/C2CD3/TGFBR2/ID3/GLI2/ALDH1A3/HOXC9/EGLN1/EN1/HEY1/PDGFB/PTK7/VEGFA/RDH10/HOXB2/MICAL2/PAX6/COL11A1/CTHRC1/CELSR1/HAND2/TBX3/EPHA2/RBP4/GJB5/PCSK5/SNAI1/NDRG4/NRK/MYO7A/HOXA7/ZFPM1/SPINT2/HOXB4/CHRNA9/MMP16/WNT11/EYA1/CHD7/STRA6/WNT5A/TGFB3/MDFI/HOXB3/HOXB5/FBN2/ST14/SOX9/RARB/SATB2/HOXB7/HOXB6/LIF/KDR/ALX1/HOXA6/HOXA3/HOXA2/HOXA5/IL8/PITX2/HOXB8* |
| G67 | GO:0048593 | Camera-type eye morphogenesis | 76 | –0.465606788 | –1.52681817 | 0.003100775 | 0.030486975 | tags =28%, list =15%, signal =24% | *PROX1/GNAT2/HIF1A/TSPAN12/HIPK2/TSKU/SOX8/PTN/ALDH1A3/GDF11/VEGFA/PAX6/EPHA2/RBP4/MEIS1/STRA6/WNT5A/SDK2/SOX9/PITX2* |
| G67 | GO:0048562 | Embryonic organ morphogenesis | 214 | –0.406856532 | –1.534922142 | 0.004043127 | 0.035074464 | tags =19%, list =8%, signal =17% | *RDH10/HOXB2/MICAL2/PAX6/COL11A1/CTHRC1/CELSR1/HAND2/TBX3/EPHA2/RBP4/NDRG4/MYO7A/HOXA7/HOXB4/CHRNA9/MMP16/WNT11/EYA1/CHD7/STRA6/WNT5A/TGFB3/MDFI/HOXB3/HOXB5/FBN2/SOX9/RARB/SATB2/HOXB7/HOXB6/ALX1/HOXA6/HOXA3/HOXA2/HOXA5/PITX2/HOXB8* |
| G67 | GO:0048660 | Regulation of smooth muscle cell proliferation | 95 | –0.446180283 | –1.508279065 | 0.006097561 | 0.044505286 | tags =22%, list =8%, signal =20% | *IL15/TGFBR2/PDGFB/CALCRL/PTGS2/NOTCH3/MDM2/MMP9/HBEGF/NDRG4/IL18/HMOX1/CNN1/TGFB3/ITGA2/IL6/AIF1/PTAFR/TGM2/IGF1* |
| G68 | GO:0048704 | Embryonic skeletal system morphogenesis | 78 | –0.503918222 | –1.665620203 | 0.001545595 | 0.023352669 | tags =26%, list =4%, signal =25% | *HOXB2/COL11A1/HOXA7/HOXB4/MMP16/EYA1/TGFB3/MDFI/HOXB3/HOXB5/SATB2/HOXB7/HOXB6/ALX1/HOXA6/HOXA3/HOXA2/HOXA5/HOXB8* |
| G68 | GO:0048661 | Positive regulation of smooth muscle cell proliferation | 60 | –0.554858662 | –1.740665781 | 0.001574803 | 0.023352669 | tags =25%, list =8%, signal =23% | *CALCRL/PTGS2/NOTCH3/MDM2/MMP9/HBEGF/IL18/HMOX1/ITGA2/IL6/AIF1/PTAFR/TGM2/IGF1* |
| G69 | GO:0048705 | Skeletal system morphogenesis | 167 | –0.443147661 | –1.622962549 | 0.001383126 | 0.023352669 | tags =21%, list =8%, signal =19% | *HOXB2/COL27A1/COL11A1/CTGF/SFRP1/HOXA7/HOXB4/MMP16/EYA1/DHRS3/MSX2/HOXC8/MGP/HAS2/TGFB3/MDFI/HOXB3/CYP26B1/ACP5/HOXB5/FBN2/SOX9/RARB/SATB2/STC1/HOXB7/HOXB6/COL10A1/ALX1/HOXA6/HOXA3/HOXA2/HOXA5/HOXB8* |
| G69 | GO:0048706 | Embryonic skeletal system development | 102 | –0.489580018 | –1.66345957 | 0.002994012 | 0.030486975 | tags =34%, list =11%, signal =31% | *PDGFRA/HOXD3/HOXC6/TGFBR2/RP11-834C11.14/HOXD1/ACVR2A/HOXC9/RDH10/HOXB2/COL11A1/HOXA9/RBP4/PCSK5/HOXA7/HOXB4/MMP16/WNT11/EYA1/WNT5A/TGFB3/MDFI/HOXB3/SULF1/HOXB5/SATB2/HOXB7/HOXB6/ALX1/HOXA6/HOXA3/HOXA2/HOXA5/HOXB8* |
| G7 | GO:0002443 | Leukocyte mediated immunity | 200 | –0.51706592 | –1.939904903 | 0.001362398 | 0.023352669 | tags =26%, list =9%, signal =24% | *RASGRP1/MILR1/RAET1E/LAT2/DENND1B/BTK/CADM1/SPON2/MICA/TNFSF4/STXBP2/GCNT3/UNC13D/LAT/RSAD2/PRKCZ/CORO1A/WAS/C7/CLU/CFI/TLR8/SLAMF7/HMOX1/CR1/IL1B/LYN/CD300A/INPP5D/F2RL1/PTPN6/KLRD1/HAVCR2/VAMP8/FGR/TREM1/PTPRC/SASH3/SLC11A1/IL6/CD28/SYK/PTAFR/CD84/C1QA/FCER1G/HLA-DQB1/CXCL6/CD74/C1QB/C1QC/CXCL5* |
| G7 | GO:0002440 | Production of molecular mediator of immune response | 108 | –0.516459567 | –1.780108442 | 0.001470588 | 0.023352669 | tags =24%, list =8%, signal =22% | *BTK/SPON2/TNFSF4/TLR2/ITM2A/GCNT3/RBP4/RSAD2/PRKCZ/HMOX1/AC005013.1/WNT5A/TGFB3/ANGPT1/F2RL1/TREM1/PTPRC/SASH3/SLC11A1/IL6/CD28/FCER1G/HLA-DQB1/IL33/CD74* |
| G7 | GO:0002444 | Myeloid leukocyte mediated immunity | 57 | –0.660773714 | –2.065525949 | 0.001557632 | 0.023352669 | tags =40%, list =9%, signal =37% | *RASGRP1/MILR1/LAT2/BTK/SPON2/STXBP2/UNC13D/LAT/HMOX1/LYN/CD300A/F2RL1/VAMP8/FGR/TREM1/IL6/SYK/PTAFR/CD84/FCER1G/CXCL6/CXCL5* |
| G7 | GO:0002446 | Neutrophil mediated immunity | 19 | –0.784700251 | –1.989588275 | 0.001733102 | 0.023440094 | tags =42%, list =2%, signal =41% | *F2RL1/TREM1/IL6/SYK/PTAFR/CXCL6/CXCL5* |
| G70 | GO:0048729 | Tissue morphogenesis | 481 | –0.363052861 | –1.449277656 | 0.001207729 | 0.023352669 | tags =17%, list =11%, signal =16% | *CELSR3/AR/ITGA5/HHIP/TGFBR2/SALL4/SOX8/GLI2/GPC4/DDR1/ALDH1A3/EGLN1/CSF1R/HEY1/CTSZ/PTK7/VEGFA/NKX3-1/RDH10/HOXB2/MICAL2/IRX2/RET/B4GALT1/COL3A1/TNC/COL11A1/CTHRC1/ITGB3/GDNF/GPC3/GCNT3/KIF26B/COL4A1/SOX4/CELSR1/HAND2/SFRP1/TBX3/EPHA2/FGF2/MDM2/CTSV/ADAMTS12/SNAI1/HBEGF/FLRT3/PRICKLE1/FZD7/NDRG4/ACTA2/ZFPM1/SPINT2/HOXB4/MYLK/WNT11/EYA1/CHD7/EDNRA/MSX2/WNT5A/HEYL/CA2/SULF1/EFNB2/ITGA2/ST14/DACT1/SOX9/IL6/ACTG2/EYA2/STC1/SPI1/TBX5/TGM2/INHBA/HOXB7/LIF/ALX1/BMP2/HOXA5/PITX2* |
| G70 | GO:0048738 | Cardiac muscle tissue development | 135 | –0.448392019 | –1.59587998 | 0.004341534 | 0.03701726 | tags =27%, list =15%, signal =24% | *TGFB1/ITGB1/ZFPM2/PDGFRA/TPM1/PPP1R13L/NOX4/MYH10/TENM4/TGFBR2/EGLN1/NEBL/VEGFA/SIK1/GATA6/NEXN/COL11A1/TBX3/FGF2/RBP4/MYH11/NDRG4/ZFPM1/DSG2/CHD7/FHOD3/JPH2/WNT5A/EFNB2/MYOCD/RARB/PLN/TBX5/IGF1/BMP2/PITX2* |
| G71 | GO:0050670 | Regulation of lymphocyte proliferation | 129 | –0.616066908 | –2.18096517 | 0.001424501 | 0.023352669 | tags =38%, list =14%, signal =33% | *CEBPB/LEP/LGALS9/CD38/IRS2/TNFSF9/SPN/IL15/TFRC/TLR4/HLA-DPB1/IL2RA/RAC2/TNFSF4/VAV3/CORO1A/CDKN1A/IL18/MNDA/LST1/HLA-DPA1/IL1B/LYN/CD300A/INPP5D/PTPN6/HAVCR2/NCKAP1L/CD1D/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DMB/ICOSLG/CD209/IGF1/VSIG4/CD74* |
| G71 | GO:0050663 | Cytokine secretion | 116 | –0.49901506 | –1.728588372 | 0.001449275 | 0.023352669 | tags =39%, list =15%, signal =33% | *SSC5D/IL1RAP/HYAL2/LEP/TLR6/LGALS9/PTGER4/TNFRSF9/FN1/TLR4/NLRC4/IL36RN/IL1R2/CSF1R/RASGRP1/CADM1/TNFSF4/TLR2/TLR1/PRKCZ/ABCA1/TLR8/RGCC/IL1B/LYN/WNT5A/LPL/ANGPT1/F2RL1/IL1RL1/C1QTNF3/HAVCR2/FGR/PTPN22/TREM1/TNFRSF21/SRGN/IL1A/GPAM/LCP2/IL6/SYK/CD14/IL33* |
| G71 | GO:0050671 | Positive regulation of lymphocyte proliferation | 87 | –0.650011304 | –2.180124538 | 0.001490313 | 0.023352669 | tags =45%, list =16%, signal =38% | *MIF/JAK3/LEP/LGALS9/CD38/IRS2/TNFSF9/SPN/IL15/TFRC/TLR4/HLA-DPB1/IL2RA/TNFSF4/VAV3/CORO1A/CDKN1A/IL18/HLA-DPA1/IL1B/HAVCR2/NCKAP1L/CD1D/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DMB/ICOSLG/IGF1/CD74* |
| G71 | GO:0050672 | Negative regulation of lymphocyte proliferation | 42 | –0.577036283 | –1.704712472 | 0.003236246 | 0.030486975 | tags =36%, list =16%, signal =30% | *TGFB1/CEBPB/LGALS9/SPN/IL2RA/MNDA/LST1/LYN/CD300A/INPP5D/PTPN6/HAVCR2/TNFRSF21/VSIG4* |
| G71 | GO:0048871 | Multicellular organismal homeostasis | 227 | –0.397716465 | –1.51148645 | 0.00397878 | 0.034809257 | tags =28%, list =16%, signal =24% | *HOMER1/LCN1/CXADR/NR1D1/STK39/SMO/GBA/AKR1B1/HYAL2/MYO5B/TF/SFN/CD38/TNFRSF11A/PPP1R13L/NOX4/EPAS1/TFRC/TLR4/SLC11A2/ATP6AP1/RAC2/CSF1R/ABCA12/FLG/VEGFA/HSPB1/RAC3/PTGS2/ITGB3/CTGF/RBP4/PDK4/DCSTAMP/FOXO1/ADAM8/HOMER2/ADCY8/PTGER3/CORO1A/CDH23/IGJ/ADCY5/SIGLEC15/IL1B/HAS2/CA2/INPP5D/CYP26B1/ACADL/ACP5/LYZ/IL1A/SASH3/SOX9/SLC11A1/IL6/SYK/HTR2A/GPR116/EDNRB/SPP1* |
| G71 | GO:0048863 | Stem cell differentiation | 121 | –0.445272178 | –1.55354708 | 0.005755396 | 0.042611428 | tags =19%, list =8%, signal =18% | *SHC4/GATA6/RET/GDNF/HAND2/SFRP1/PRICKLE1/A2M/HOXA7/HOXB4/EDNRA/MSX2/MYOCD/PTPRC/SOX9/BCHE/TBX5/SEMA6B/LIF/EDNRB/ALX1/PITX2* |
| G72 | GO:0050708 | Regulation of protein secretion | 265 | –0.438657064 | –1.680002074 | 0.001321004 | 0.023352669 | tags =28%, list =15%, signal =24% | *SSC5D/IL1RAP/LEPRE1/TGFB1/CACNA1A/HYAL2/LEP/TLR6/LGALS9/PTGER4/HIF1A/PARK2/SLC25A4/CD38/TNFRSF9/IRS2/ADRA2A/FN1/ITPR2/IRS1/ITPR1/SERP1/ARNTL/TLR4/RHBDF2/IL36RN/IL1R2/SYBU/CSF1R/RASGRP1/RAB11FIP1/SIRT4/CADM1/TNFSF4/TLR2/UCP2/DRD4/SOX4/SFRP1/RBP4/RSAD2/TLR1/PRKCZ/ADAM8/TLR8/ADCY5/GPR27/RGCC/IL1B/TMEM27/LYN/RPH3AL/WNT5A/SLC2A1/TGFB3/LPL/KCNS3/ANGPT1/F2RL1/IL1RL1/C1QTNF3/HAVCR2/FGR/PTPN22/TNFRSF21/SRGN/IL1A/GPAM/IL6/SYK/CD14/IGF1/TRPM2/IL33* |
| G72 | GO:0050727 | Regulation of inflammatory response | 203 | –0.475394241 | –1.787866495 | 0.001358696 | 0.023352669 | tags =24%, list =9%, signal =22% | *RORA/WFDC1/BTK/CFH/CALCRL/TNFSF4/TLR2/PTGS2/GGT1/ADAMTS12/ADAM8/PTGER3/IL18/DUSP10/A2M/C7/CFI/TLR7/CR1/VTN/IL1B/LYN/WNT5A/LPL/APOE/CCL26/IL1RL1/C1QTNF3/VAMP8/ACP5/FABP4/CCL2/ITGA2/PIK3AP1/LBP/C5AR1/IL6/CD28/CCL8/C3AR1/HCK/TGM2/FCER1G/S100A9/EDNRB/CCL13/PLA2G7/IL33* |
| G72 | GO:0050714 | Positive regulation of protein secretion | 144 | –0.45968478 | –1.654828255 | 0.00141844 | 0.023352669 | tags =20%, list =9%, signal =18% | *RASGRP1/CADM1/TNFSF4/SOX4/RBP4/PRKCZ/ADAM8/GPR27/RGCC/IL1B/TMEM27/RPH3AL/WNT5A/TGFB3/LPL/F2RL1/IL1RL1/C1QTNF3/HAVCR2/FGR/PTPN22/IL1A/IL6/SYK/CD14/IGF1/TRPM2/IL33* |
| G72 | GO:0050707 | Regulation of cytokine secretion | 99 | –0.523948283 | –1.781295182 | 0.001494768 | 0.023352669 | tags =40%, list =15%, signal =34% | *SSC5D/IL1RAP/HYAL2/TLR6/LGALS9/PTGER4/TNFRSF9/FN1/TLR4/IL36RN/IL1R2/CSF1R/RASGRP1/CADM1/TNFSF4/TLR2/TLR1/PRKCZ/TLR8/RGCC/IL1B/LYN/WNT5A/LPL/ANGPT1/F2RL1/IL1RL1/C1QTNF3/HAVCR2/FGR/PTPN22/TNFRSF21/SRGN/IL1A/GPAM/IL6/SYK/CD14/IL33* |
| G72 | GO:0050729 | Positive regulation of inflammatory response | 68 | –0.650432874 | –2.087148958 | 0.001538462 | 0.023352669 | tags =41%, list =9%, signal =38% | *BTK/TNFSF4/TLR2/PTGS2/ADAM8/PTGER3/IL18/TLR7/IL1B/WNT5A/LPL/CCL26/IL1RL1/VAMP8/FABP4/CCL2/ITGA2/LBP/IL6/CD28/CCL8/TGM2/FCER1G/S100A9/CCL13/PLA2G7/IL33* |
| G72 | GO:0050709 | Negative regulation of protein secretion | 74 | –0.530307999 | –1.729462468 | 0.00155521 | 0.023352669 | tags =35%, list =13%, signal =31% | *PARK2/TNFRSF9/ADRA2A/FN1/IRS1/RHBDF2/IL36RN/IL1R2/RAB11FIP1/SIRT4/TNFSF4/UCP2/DRD4/SFRP1/RSAD2/RGCC/IL1B/ANGPT1/F2RL1/C1QTNF3/PTPN22/TNFRSF21/SRGN/IL6/IL33* |
| G72 | GO:0050710 | Negative regulation of cytokine secretion | 33 | –0.598068668 | –1.696266007 | 0.001633987 | 0.023352669 | tags =48%, list =16%, signal =41% | *SSC5D/PTGER4/TNFRSF9/FN1/IL36RN/IL1R2/TNFSF4/RGCC/ANGPT1/F2RL1/C1QTNF3/PTPN22/TNFRSF21/SRGN/IL6* |
| G72 | GO:0050678 | Regulation of epithelial cell proliferation | 226 | –0.40131386 | –1.520481915 | 0.004016064 | 0.034898447 | tags =27%, list =8%, signal =25% | *INTU/KDM5B/EAF2/NR1D1/EGFL7/MAGED1/SMO/PROX1/TGFB1/LEP/C19orf10/HIF1A/ROBO1/RPTOR/SFN/CASK/AR/A4GNT/VASH2/PTN/PDGFB/VEGFA/NKX3-1/WFDC1/PAX6/B4GALT1/F3/ITGB3/GPC3/PLXNB3/CCND1/TGFA/EPGN/SFRP1/FGF2/XDH/CTSV/FZD7/SPARC/PTPRN/RGCC/EYA1/NRP2/WNT5A/HAS2/APOE/CCL26/SULF1/EFNB2/RUNX3/CCL2/C5AR1/SOX9/IL6/CDKN2B/IGF1/KDR/EDNRB/BMP2/HOXA5/SCG2* |
| G72 | GO:0050679 | Positive regulation of epithelial cell proliferation | 117 | –0.449124999 | –1.557896909 | 0.004354136 | 0.03701726 | tags =24%, list =10%, signal =22% | *PTN/PDGFB/VEGFA/B4GALT1/F3/ITGB3/PLXNB3/CCND1/TGFA/EPGN/SFRP1/FGF2/FZD7/PTPRN/EYA1/NRP2/WNT5A/HAS2/CCL26/CCL2/C5AR1/SOX9/IL6/IGF1/KDR/BMP2/SCG2* |
| G72 | GO:0050680 | Negative regulation of epithelial cell proliferation | 98 | –0.45419877 | –1.540460255 | 0.004531722 | 0.037949001 | tags =33%, list =19%, signal =27% | *THBS1/GJA1/PTPRK/DAB2IP/INTU/EAF2/MAGED1/TGFB1/ROBO1/SFN/CASK/AR/A4GNT/PTN/NKX3-1/WFDC1/PAX6/GPC3/SFRP1/XDH/CTSV/SPARC/RGCC/WNT5A/APOE/SULF1/EFNB2/RUNX3/SOX9/CDKN2B/SCG2* |
| G72 | GO:0050715 | Positive regulation of cytokine secretion | 62 | –0.493370808 | –1.562367216 | 0.00466563 | 0.037949001 | tags =29%, list =9%, signal =27% | *RASGRP1/CADM1/PRKCZ/RGCC/IL1B/WNT5A/LPL/F2RL1/IL1RL1/C1QTNF3/HAVCR2/FGR/PTPN22/IL1A/SYK/CD14/IL33* |
| G72 | GO:0050673 | Epithelial cell proliferation | 265 | –0.372240614 | –1.425635319 | 0.00660502 | 0.046053749 | tags =30%, list =19%, signal =25% | *THBS1/GJA1/ZNF580/PTPRK/NCSTN/BCL2L2/ERN1/DAB2IP/MAP2K1/INTU/KDM5B/BTRC/EAF2/NR1D1/EGFL7/MAGED1/SMO/PROX1/TGFB1/CEBPB/LEP/BTBD10/C19orf10/HIF1A/ROBO1/RPTOR/SFN/CASK/AR/A4GNT/FERMT1/VASH2/ACVR2A/PTN/PDGFB/VEGFA/NKX3-1/WFDC1/PAX6/B4GALT1/FAP/F3/ITGB3/GPC3/PLXNB3/CCND1/TGFA/EPGN/SFRP1/EPHA2/FGF2/XDH/CTSV/FZD7/LOXL2/SPARC/HMOX1/PTPRN/RGCC/EYA1/NRP2/WNT5A/HAS2/APOE/CCL26/SULF1/EFNB2/RUNX3/CCL2/C5AR1/SOX9/IL6/CDKN2B/IGF1/KDR/EDNRB/BMP2/HOXA5/SCG2* |
| G73 | GO:0050778 | Positive regulation of immune response | 480 | –0.512999617 | –2.04741298 | 0.00120919 | 0.023352669 | tags =18%, list =6%, signal =17% | *VAV3/LAT/RSAD2/TLR1/CFHR1/PRKCZ/LGMN/CTSS/LIMK1/ADAM8/IL18/A2M/WAS/C7/CLU/MNDA/CFI/TLR8/TLR7/AC005013.1/CR1/RGCC/VTN/HLA-DPA1/IL1B/LYN/CD300A/SKAP2/WNT5A/CYFIP2/PLCG2/INPP5D/MARCO/PAG1/F2RL1/PTPN6/HAVCR2/VAMP8/NCKAP1L/CD1D/FGR/CLEC7A/PTPN22/TNFRSF21/PTPRC/PIK3AP1/PPAPDC1A/PRKCB/LBP/CD86/CD4/C5AR1/SASH3/NFAM1/SLC11A1/CD180/LCP2/IL6/CD28/SYK/CD14/PTAFR/ITGAM/C3AR1/CARD11/HLA-DQA1/HCK/HLA-DMB/CD209/FCGR1A/C1QA/FCER1G/VSIG4/FPR1/HLA-DQB1/FPR3/HLA-DRB1/FCGR2A/HLA-DRB5/IL33/CD74/FCGR3A/HLA-DRA/C1QB/C1QC* |
| G73 | GO:0050801 | Ion homeostasis | 464 | –0.387465469 | –1.543206643 | 0.001222494 | 0.023352669 | tags =26%, list =17%, signal =22% | *WNK4/FTL/ATP13A2/ATP6V1F/MYO5A/ATP6V1G1/CAPN3/SCN3B/SLC9A4/BCAP31/HTT/STEAP2/STK39/CHRNA7/ATP7A/ATP6V1G2/ATP6V0E1/ATP6V1A/GPD1L/SLC46A1/ATP6V0A1/TGFB1/CACNA1A/SLC22A17/HYAL2/GNAT2/ATP13A3/ATP6V1E1/PTGER4/TF/HIF1A/PARK2/DMD/ABCG2/STIM2/CD38/PDGFRA/CYP27B1/PLCG1/TTPA/ITPR2/TRPC4/EPAS1/CD52/SLC4A3/LETM2/TFRC/ITPR1/SLC11A2/OPRL1/CCR1/SLC26A1/ATP6AP1/ATP6V0C/SLC30A10/EGLN1/FTH1/ATP2B1/MT2A/KL/SLC4A11/DRD4/F2RL3/SLC9A7/ATP1B1/IFI6/FGF2/PDK4/KCNMA1/P2RY1/PTGER3/CORO1A/CDH23/SLC24A3/ATP2A3/CHRNA9/ADCY5/HMOX1/MLLT11/CHD7/SLC4A4/EDNRA/GNA15/ATP6V0D2/SFRP4/JPH2/LYN/PLCG2/CA2/APOE/CCR5/F2RL1/SLC30A3/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/C5AR1/SLC11A1/PTGDR/GRIK2/PLN/JPH1/CCL8/C3AR1/STC1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/KDR/S100A9/EDNRB/FPR3/CCL13/SNCA/CALB2* |
| G73 | GO:0050777 | Negative regulation of immune response | 81 | –0.530197678 | –1.750941442 | 0.00154321 | 0.023352669 | tags =32%, list =7%, signal =30% | *ARRB2/TGFB1/BST2/LGALS9/SPN/IL2RA/MICA/COL3A1/TNFSF4/DUSP10/A2M/HMOX1/CR1/LYN/CD300A/TGFB3/INPP5D/ANGPT1/IL1RL1/PTPN6/HAVCR2/PTPRC/SAMSN1/CD84/IL33* |
| G73 | GO:0050755 | Chemokine metabolic process | 10 | –0.903396019 | –1.948130407 | 0.001841621 | 0.024395555 | tags =60%, list =4%, signal =57% | *HMOX1/IL1B/WNT5A/TREM1/IL6* |
| G73 | GO:0050764 | Regulation of phagocytosis | 49 | –0.556423898 | –1.687096846 | 0.004731861 | 0.038098876 | tags =27%, list =3%, signal =26% | *IL1B/CD300A/F2RL1/NCKAP1L/CCL2/FGR/ITGA2/SLC11A1/MERTK/SYK/HCK/FCER1G* |
| G74 | GO:0050808 | Synapse organization | 170 | –0.438336841 | –1.605927287 | 0.001386963 | 0.023352669 | tags =23%, list =11%, signal =21% | *CLSTN2/NRXN2/PTN/PCDHB14/SYNDIG1/COL4A5/NLGN1/ZC4H2/AMIGO3/PCDHB6/PCDHB4/TNC/GDNF/COL4A1/DNM3/PCDHB5/PCDHB2/SHANK1/FLRT3/BAI1/SPTBN2/CDH2/PCDHB10/SPOCK2/LRRN1/SLITRK4/PCDHB9/PCDHB3/WNT5A/SDK2/SRPX2/NRCAM/DNER/APOE/ROBO2/IL10RA/AMIGO2/SNCA* |
| G75 | GO:0050817 | Coagulation | 246 | –0.458437725 | –1.742681097 | 0.001347709 | 0.023352669 | tags =28%, list =14%, signal =24% | *BLOC1S3/ZFPM2/CSRP1/PDGFRA/ADRA2A/PRKG1/ITPR2/EHD3/GP1BA/PDGFA/DGKG/ITPR1/TLR4/RAC2/P2RX6/PAPSS2/SERPINE1/PDGFB/HSPB1/VWF/P2RX1/ENPP4/PLAUR/GATA6/FAM46A/F2RL2/COL3A1/PLAT/FAP/F3/ITGB3/F2RL3/SERPINE2/VAV3/LAT/PLAU/P2RY1/PROCR/A2M/WAS/GNG2/ZFPM1/VTN/GNA15/LYN/PLCG2/APOE/F2RL1/SCUBE1/PTPN6/DOCK8/PIK3R5/ITGA2/HIST2H3C/HIST2H3A/PRKCB/F13A1/LCP2/PLEK/MERTK/IL6/SYK/SERPINB2/TFPI2/FCER1G/PF4/S100A9* |
| G76 | GO:0050818 | Regulation of coagulation | 59 | –0.547979933 | –1.721036637 | 0.001567398 | 0.023352669 | tags =42%, list =13%, signal =37% | *PRKG1/GP1BA/PDGFA/TLR4/SERPINE1/PDGFB/ENPP4/PLAUR/FAM46A/PLAT/FAP/F3/SERPINE2/PLAU/PROCR/VTN/LYN/APOE/F2RL1/PLEK/SYK/SERPINB2/FCER1G/S100A9* |
| G77 | GO:0050865 | Regulation of cell activation | 342 | –0.544739001 | –2.127911104 | 0.001273885 | 0.023352669 | tags =29%, list =13%, signal =26% | *PDGFRA/HLA-DOA/IRS2/PRKG1/TNFSF9/GJD4/SPN/PDGFA/IL15/TFRC/TLR4/TGFBR2/HLA-DPB1/GLI2/IL2RA/RAC2/RASGRP1/MILR1/RORA/PDGFB/BTK/MICA/TNFSF4/STXBP2/SERPINE2/DPP4/CTGF/UNC13D/SFRP1/VAV3/LAT/PRKCZ/ADAM8/CORO1A/CDKN1A/IL18/CD83/MNDA/HMOX1/LST1/CAMK4/HLA-DPA1/IL1B/LYN/CD300A/WNT5A/IL36B/TBC1D10C/INPP5D/APOE/CYP26B1/PAG1/F2RL1/IL1RL1/PTPN6/HAVCR2/VAMP8/EFNB2/NCKAP1L/CD1D/CCL2/FGR/PTPN22/TNFRSF21/PTPRC/LBP/CD86/CD4/GPAM/SASH3/NFAM1/SAMSN1/PLEK/MERTK/IL6/CD28/SYK/AIF1/PTAFR/CD84/GPR183/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/CD209/INHBA/FCER1G/IGF1/VSIG4/GPR116/HLA-DQB1/HLA-DRB1/HLA-DRB5/IL33/CD74/SNCA/HLA-DRA* |
| G77 | GO:0050867 | Positive regulation of cell activation | 213 | –0.572388454 | –2.159733516 | 0.001345895 | 0.023352669 | tags =23%, list =6%, signal =22% | *CTGF/VAV3/PRKCZ/ADAM8/CORO1A/CDKN1A/IL18/CD83/HLA-DPA1/IL1B/LYN/WNT5A/IL36B/INPP5D/F2RL1/IL1RL1/PTPN6/HAVCR2/VAMP8/EFNB2/NCKAP1L/CD1D/CCL2/FGR/PTPRC/LBP/CD86/CD4/GPAM/SASH3/PLEK/IL6/CD28/SYK/AIF1/PTAFR/GPR183/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/FCER1G/IGF1/HLA-DQB1/HLA-DRB1/HLA-DRB5/IL33/CD74/HLA-DRA* |
| G77 | GO:0050863 | Regulation of T cell activation | 205 | –0.543458029 | –2.04260729 | 0.001364256 | 0.023352669 | tags =21%, list =6%, signal =20% | *LAT/PRKCZ/ADAM8/CORO1A/IL18/CD83/CAMK4/HLA-DPA1/IL1B/LYN/CD300A/IL36B/CYP26B1/PAG1/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/CD209/IGF1/VSIG4/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G77 | GO:0050851 | Antigen receptor-mediated signaling pathway | 168 | –0.547375132 | –2.003644547 | 0.001392758 | 0.023352669 | tags =23%, list =11%, signal =21% | *PLCG1/LPXN/HLA-DPB1/RNF31/GCSAM/KLHL6/GCSAML/LAT2/DENND1B/BTK/THEMIS2/VAV3/LAT/WAS/MNDA/HLA-DPA1/LYN/CD300A/PLCG2/INPP5D/PAG1/PTPN6/NCKAP1L/PTPN22/TNFRSF21/PTPRC/PRKCB/CD4/NFAM1/LCP2/CD28/SYK/CARD11/HLA-DQA1/HLA-DQB1/HLA-DRB1/HLA-DRB5/HLA-DRA* |
| G77 | GO:0050870 | Positive regulation of T cell activation | 144 | –0.590447648 | –2.125564067 | 0.00141844 | 0.023352669 | tags =31%, list =12%, signal =28% | *SPN/IL15/TFRC/TGFBR2/HLA-DPB1/GLI2/IL2RA/RASGRP1/TNFSF4/DPP4/PRKCZ/ADAM8/CORO1A/IL18/CD83/HLA-DPA1/IL1B/LYN/IL36B/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/IGF1/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G77 | GO:0050852 | T cell receptor signaling pathway | 140 | –0.531891959 | –1.903042539 | 0.001445087 | 0.023352669 | tags =15%, list =4%, signal =14% | *LAT/WAS/HLA-DPA1/CD300A/PLCG2/INPP5D/PAG1/PTPN6/PTPN22/TNFRSF21/PTPRC/CD4/LCP2/CD28/CARD11/HLA-DQA1/HLA-DQB1/HLA-DRB1/HLA-DRB5/HLA-DRA* |
| G77 | GO:0050866 | Negative regulation of cell activation | 111 | –0.566778826 | –1.95643173 | 0.001459854 | 0.023352669 | tags =34%, list =16%, signal =29% | *PELI1/JAK3/TGFB1/CEBPB/LGALS9/INHA/PDGFRA/PRKG1/SPN/PDGFA/IL2RA/MILR1/PDGFB/MICA/TNFSF4/SERPINE2/SFRP1/MNDA/HMOX1/LST1/LYN/CD300A/TBC1D10C/INPP5D/APOE/PAG1/PTPN6/HAVCR2/PTPN22/TNFRSF21/SAMSN1/MERTK/CD84/INHBA/VSIG4/GPR116/CD74* |
| G77 | GO:0050864 | Regulation of B cell activation | 81 | –0.619401279 | –2.045530213 | 0.00154321 | 0.023352669 | tags =41%, list =8%, signal =38% | *PELI1/MIF/TGFB1/INHA/CD38/IRS2/TFRC/TLR4/BTK/TNFSF4/SFRP1/VAV3/CDKN1A/MNDA/LYN/CD300A/TBC1D10C/INPP5D/PTPN6/NCKAP1L/TNFRSF21/PTPRC/SASH3/NFAM1/SAMSN1/IL6/CD28/SYK/GPR183/CARD11/INHBA/CD74* |
| G77 | GO:0050848 | Regulation of calcium-mediated signaling | 55 | –0.541556491 | –1.687193381 | 0.001547988 | 0.023352669 | tags =16%, list =3%, signal =16% | *TREM2/CD4/PLN/PLEK/JPH1/SYK/CMKLR1/IGF1* |
| G77 | GO:0050871 | Positive regulation of B cell activation | 53 | –0.591280063 | –1.835327755 | 0.001550388 | 0.023352669 | tags =40%, list =16%, signal =33% | *MIF/TGFB1/CD38/IRS2/TFRC/TLR4/BTK/TNFSF4/VAV3/CDKN1A/INPP5D/NCKAP1L/PTPRC/SASH3/IL6/CD28/SYK/GPR183/CARD11/CD74* |
| G77 | GO:0050853 | B cell receptor signaling pathway | 35 | –0.712503676 | –2.070835835 | 0.001597444 | 0.023352669 | tags =54%, list =13%, signal =47% | *LPXN/GCSAM/KLHL6/GCSAML/LAT2/BTK/VAV3/MNDA/LYN/CD300A/PLCG2/PTPN6/NCKAP1L/PTPN22/PTPRC/PRKCB/NFAM1/SYK* |
| G77 | GO:0050869 | Negative regulation of B cell activation | 23 | –0.743588727 | –1.96632535 | 0.001636661 | 0.023352669 | tags =39%, list =6%, signal =37% | *MNDA/LYN/CD300A/TBC1D10C/INPP5D/TNFRSF21/SAMSN1/INHBA* |
| G77 | GO:0050850 | Positive regulation of calcium-mediated signaling | 25 | –0.662494047 | –1.7694292 | 0.001647446 | 0.023352669 | tags =20%, list =3%, signal =19% | *TREM2/CD4/SYK/IGF1* |
| G77 | GO:0050868 | Negative regulation of T cell activation | 58 | –0.508740825 | –1.590012796 | 0.003149606 | 0.030486975 | tags =29%, list =17%, signal =24% | *PELI1/JAK3/TGFB1/CEBPB/LGALS9/SPN/IL2RA/TNFSF4/CD300A/PAG1/PTPN6/HAVCR2/PTPN22/TNFRSF21/VSIG4/CD74* |
| G77 | GO:0050855 | Regulation of B cell receptor signaling pathway | 13 | –0.811592807 | –1.87066717 | 0.003502627 | 0.031944406 | tags =69%, list =12%, signal =61% | *GCSAM/GCSAML/LYN/CD300A/PTPN6/PTPN22/PRKCB/NFAM1* |
| G77 | GO:0050857 | Positive regulation of antigen receptor-mediated signaling pathway | 13 | –0.799922525 | –1.843767951 | 0.003502627 | 0.031944406 | tags =31%, list =3%, signal =30% | *PTPRC/PRKCB/NFAM1* |
| G77 | GO:0050854 | Regulation of antigen receptor-mediated signaling pathway | 35 | –0.571603735 | –1.661321248 | 0.006389776 | 0.045290946 | tags =29%, list =12%, signal =25% | *GCSAM/GCSAML/LYN/CD300A/PTPN6/PTPN22/PTPRC/PRKCB/NFAM1* |
| G78 | GO:0051046 | Regulation of secretion | 442 | –0.449895659 | –1.785173279 | 0.001234568 | 0.023352669 | tags =29%, list =17%, signal =25% | *PFKL/ATP13A2/C2CD2L/STXBP1/MAP2K6/GAS6/KDM5B/CDK5/STXBP6/NR1D1/STK39/CHRNA7/MIF/SSC5D/IL1RAP/C19orf26/LEPRE1/TGFB1/SYT15/NSF/CACNA1A/HYAL2/LEP/TLR6/LGALS9/INHA/PTGER4/HIF1A/PARK2/SLC25A4/CD38/TNFRSF9/IRS2/IL11/ADRA2A/TNFRSF11A/FN1/ITPR2/IRS1/ITPR1/SERP1/ARNTL/TLR4/OPRL1/UCN/RHBDF2/ATP6AP1/RIMS3/IL36RN/IL1R2/SYBU/NCS1/SDC1/RAC2/CSF1R/RASGRP1/RAB11FIP1/SIRT4/NLGN1/NKX3-1/SYTL1/CADM1/TNFSF4/TLR2/STXBP2/SMPD3/GDNF/UCP2/DRD4/SOX4/UNC13D/SFRP1/CAMK2A/SYTL3/RBP4/RSAD2/TLR1/SCIN/PRKCZ/SYN1/P2RY1/ADAM8/PTGER3/RIMS1/TLR8/ADCY5/HMOX1/GPR27/RGCC/CHD7/IL1B/TMEM27/LYN/CD300A/RPH3AL/WNT5A/SLC2A1/TGFB3/LPL/KCNS3/ANGPT1/F2RL1/IL1RL1/C1QTNF3/HAVCR2/VAMP8/FGR/PTPN22/TNFRSF21/SRGN/IL1A/GPAM/IL6/SYK/CD14/PTAFR/CD84/STC1/HTR2A/INHBA/FCER1G/LIF/IGF1/TRPM2/S100A9/EDNRB/IL33/CD74/SNCA* |
| G78 | GO:0050878 | Regulation of body fluid levels | 340 | –0.424125537 | –1.654663142 | 0.001278772 | 0.023352669 | tags =28%, list =16%, signal =24% | *STK39/ATP7A/GNAQ/GPI/GBA/PTPRO/EPHB2/ARRB2/HYAL2/MYO5B/MAPK3/BLOC1S3/ZFPM2/CSRP1/HIF1A/SFN/PDGFRA/ADRA2A/PRKG1/ITPR2/EHD3/GP1BA/PDGFA/DGKG/ITPR1/TLR4/OPRL1/UCN/DDR1/RAC2/ABCA12/P2RX6/PAPSS2/SERPINE1/FLG/PDGFB/VEGFA/HSPB1/VWF/P2RX1/ENPP4/PLAUR/GATA6/FAM46A/F2RL2/COL3A1/PLAT/FAP/F3/ITGB3/F2RL3/CCND1/SERPINE2/VAV3/LAT/PLAU/XDH/P2RY1/ADCY8/PROCR/A2M/WAS/GNG2/ZFPM1/ADCY5/VTN/GNA15/LYN/HAS2/PLCG2/APOE/CYP26B1/F2RL1/SCUBE1/PTPN6/VAMP8/DOCK8/PIK3R5/ITGA2/HIST2H3C/HIST2H3A/PRKCB/F13A1/LCP2/PLEK/MERTK/IL6/SYK/SERPINB2/TFPI2/FCER1G/PF4/S100A9/EDNRB* |
| G78 | GO:0051051 | Negative regulation of transport | 324 | –0.415428263 | –1.614607075 | 0.00129199 | 0.023352669 | tags =24%, list =17%, signal =20% | *PFKL/DAB2IP/GAS6/CDK5/STXBP6/STK39/SSC5D/C19orf26/OAZ3/TGFB1/LEP/BST2/LGALS9/INHA/PTGER4/PARK2/TNFRSF9/IRS2/IL11/ADRA2A/FN1/IRS1/AP000322.53/OPRL1/UCN/RHBDF2/IL36RN/IL1R2/RAB11FIP1/SIRT4/GOPC/FAM115C/KCNE1/TNFSF4/PTGS2/ITGB3/UCP2/DRD4/KCNRG/SERPINE2/SOX4/PKIA/SFRP1/EPPIN/PID1/RSAD2/MMP9/APOC1/P2RY1/PTGER3/CORO1A/HMOX1/RGCC/SFRP4/IL1B/CD300A/MDFI/TBC1D10C/ANGPT1/F2RL1/C1QTNF3/VAMP8/PTPN22/TNFRSF21/SRGN/PRKCB/APOC2/PLN/IL6/CD84/STC1/HTR2A/INHBA/LIF/IL33/CD74/SNCA* |
| G78 | GO:0050900 | Leukocyte migration | 255 | –0.603273703 | –2.304790941 | 0.001331558 | 0.023352669 | tags =32%, list =9%, signal =29% | *GCSAML/SERPINE1/PDGFB/VEGFA/PLCB1/CXCL14/ITGA1/RET/B4GALT1/ITGB3/ATP1B1/ITGB2/VAV3/SLC16A3/MMP9/ADAM8/CORO1A/PROCR/HOXA7/F11R/HMOX1/PADI2/ITGAX/ESAM/IL1B/LYN/CD300A/ANGPT4/CXCL16/WNT5A/SELL/INPP5D/CD48/CCL26/CCR5/ANGPT1/CCL22/F2RL1/PTPN6/OLR1/BDKRB1/NCKAP1L/CCL2/DOCK8/TREM1/ITGA2/LBP/C5AR1/IL1A/MERTK/IL6/SYK/AIF1/PTAFR/CCL8/ITGAM/CMKLR1/C3AR1/CD84/GPR183/HCK/CXCR4/CXCL1/FCER1G/PF4/FPR1/MMP1/S100A9/EDNRB/FPR3/CXCL6/CXCL3/CCL13/PLA2G7/IL33/CD74/PLVAP/SCG2/CXCL5/IL8* |
| G78 | GO:0051047 | Positive regulation of secretion | 241 | –0.444892285 | –1.692286626 | 0.001335113 | 0.023352669 | tags =24%, list =14%, signal =21% | *HYAL2/LEP/LGALS9/INHA/PTGER4/HIF1A/CD38/IRS2/TNFRSF11A/SERP1/OPRL1/UCN/ATP6AP1/NCS1/SDC1/CSF1R/RASGRP1/NLGN1/NKX3-1/CADM1/TNFSF4/SMPD3/GDNF/SOX4/UNC13D/RBP4/SCIN/PRKCZ/P2RY1/ADAM8/GPR27/RGCC/IL1B/TMEM27/RPH3AL/WNT5A/TGFB3/LPL/F2RL1/IL1RL1/C1QTNF3/HAVCR2/VAMP8/FGR/PTPN22/IL1A/IL6/SYK/CD14/PTAFR/INHBA/FCER1G/IGF1/TRPM2/S100A9/EDNRB/IL33/SNCA* |
| G78 | GO:0051048 | Negative regulation of secretion | 127 | –0.534083445 | –1.880138522 | 0.001445087 | 0.023352669 | tags =38%, list =17%, signal =32% | *PFKL/GAS6/STXBP6/STK39/SSC5D/C19orf26/LEP/LGALS9/INHA/PTGER4/PARK2/TNFRSF9/IL11/ADRA2A/FN1/IRS1/UCN/RHBDF2/IL36RN/IL1R2/RAB11FIP1/SIRT4/TNFSF4/UCP2/DRD4/SFRP1/RSAD2/P2RY1/PTGER3/HMOX1/RGCC/IL1B/CD300A/ANGPT1/F2RL1/C1QTNF3/VAMP8/PTPN22/TNFRSF21/SRGN/IL6/CD84/INHBA/LIF/IL33/CD74/SNCA* |
| G78 | GO:0050920 | Regulation of chemotaxis | 135 | –0.567250202 | –2.018910244 | 0.001447178 | 0.023352669 | tags =27%, list =9%, signal =24% | *SERPINE1/PDGFB/VEGFA/HSPB1/CXCL14/F3/FGF2/PADI2/LYN/WNT5A/F2RL1/EFNB2/NCKAP1L/CCL2/ITGA2/LBP/C5AR1/IL6/AIF1/CMKLR1/C3AR1/GPR183/ROBO2/CXCR4/CXCL1/SEMA6B/PF4/KDR/CXCL6/CXCL3/PLA2G7/CD74/SCG2/CXCL5/IL8* |
| G78 | GO:0050921 | Positive regulation of chemotaxis | 86 | –0.670458708 | –2.23743729 | 0.00149925 | 0.023352669 | tags =36%, list =10%, signal =32% | *CXCL2/RAC2/SERPINE1/PDGFB/VEGFA/HSPB1/CXCL14/F3/FGF2/WNT5A/F2RL1/NCKAP1L/CCL2/ITGA2/LBP/C5AR1/IL6/AIF1/CMKLR1/C3AR1/CXCL1/PF4/KDR/CXCL6/CXCL3/PLA2G7/CD74/SCG2/CXCL5/IL8* |
| G78 | GO:0050918 | Positive chemotaxis | 38 | –0.62570897 | –1.8363446 | 0.001602564 | 0.023352669 | tags =34%, list =8%, signal =31% | *VEGFA/F3/PLXNB3/FGF2/CORO1A/WNT5A/ANGPT1/F2RL1/ITGA2/KDR/SCG2/IL8* |
| G79 | GO:0051208 | Sequestering of calcium ion | 79 | –0.50126899 | –1.65987361 | 0.001531394 | 0.023352669 | tags =19%, list =6%, signal =18% | *FGF2/CORO1A/CHD7/JPH2/LYN/PLCG2/CCR5/PTPN6/BDKRB1/PTPRC/PLN/JPH1/HTR2A/SNCA* |
| G79 | GO:0051209 | Release of sequestered calcium ion into cytosol | 75 | –0.508025149 | –1.659648205 | 0.0015625 | 0.023352669 | tags =20%, list =6%, signal =19% | *FGF2/CORO1A/CHD7/JPH2/LYN/PLCG2/CCR5/PTPN6/BDKRB1/PTPRC/PLN/JPH1/HTR2A/SNCA* |
| G79 | GO:0051180 | Vitamin transport | 22 | –0.726479767 | –1.906237596 | 0.001666667 | 0.023352669 | tags =50%, list =17%, signal =42% | *SLC23A2/SLC46A1/SLC23A1/TTPA/SLC19A2/SLC52A1/SLC19A3/STRA6/SLC2A1/FOLR2* |
| G8 | GO:0002460 | Adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 155 | –0.447065898 | –1.616985073 | 0.001420455 | 0.023352669 | tags =23%, list =8%, signal =21% | *RAET1E/DENND1B/BTK/MICA/TNFSF4/GCNT3/UNC13D/RSAD2/PRKCZ/IL18/WAS/C7/CLU/CFI/TLR8/CR1/IL1B/INPP5D/IL1RL1/PTPN6/HAVCR2/PTPRC/CD4/SASH3/SLC11A1/IL6/CD28/C1QA/FCER1G/HLA-DQB1/IL33/CD74/C1QB/C1QC* |
| G8 | GO:0002449 | Lymphocyte mediated immunity | 149 | –0.468679229 | –1.685365572 | 0.001430615 | 0.023352669 | tags =23%, list =9%, signal =22% | *RAET1E/DENND1B/BTK/CADM1/MICA/TNFSF4/GCNT3/UNC13D/RSAD2/PRKCZ/CORO1A/WAS/C7/CLU/CFI/TLR8/SLAMF7/CR1/IL1B/INPP5D/PTPN6/KLRD1/HAVCR2/PTPRC/SASH3/SLC11A1/IL6/CD28/C1QA/FCER1G/HLA-DQB1/CD74/C1QB/C1QC* |
| G8 | GO:0002448 | Mast cell mediated immunity | 36 | –0.683689075 | –1.998518906 | 0.001569859 | 0.023352669 | tags =47%, list =9%, signal =43% | *RASGRP1/MILR1/LAT2/BTK/SPON2/STXBP2/UNC13D/LAT/HMOX1/LYN/CD300A/VAMP8/FGR/SYK/CD84/FCER1G* |
| G80 | GO:0051235 | Maintenance of location | 236 | –0.415074351 | –1.580876024 | 0.001324503 | 0.023352669 | tags =15%, list =9%, signal =14% | *FTH1/PLIN2/GOPC/ITGB3/F2RL3/FGF2/SCIN/SHANK1/CORO1A/DGAT2/ABCA1/B4GALNT1/CHD7/IL1B/JPH2/LYN/PLCG2/MDFI/LPL/APOE/CCR5/SLC30A3/PTPN6/MSR1/BDKRB1/FBN2/PTPRC/SRGN/CD4/PLN/JPH1/IL6/HTR2A/S100A9/SNCA* |
| G81 | GO:0055080 | Cation homeostasis | 428 | –0.398443793 | –1.580934108 | 0.001231527 | 0.023352669 | tags =26%, list =17%, signal =22% | *ATP13A2/ATP6V1F/MYO5A/ATP6V1G1/CAPN3/SLC9A4/BCAP31/HTT/STEAP2/CHRNA7/ATP7A/ATP6V1G2/ATP6V0E1/ATP6V1A/SLC46A1/ATP6V0A1/TGFB1/CACNA1A/SLC22A17/HYAL2/GNAT2/ATP13A3/ATP6V1E1/PTGER4/TF/HIF1A/PARK2/DMD/ABCG2/STIM2/CD38/PDGFRA/CYP27B1/PLCG1/TTPA/ITPR2/TRPC4/EPAS1/CD52/SLC4A3/LETM2/TFRC/ITPR1/SLC11A2/OPRL1/CCR1/SLC26A1/ATP6AP1/ATP6V0C/SLC30A10/EGLN1/FTH1/ATP2B1/MT2A/KL/SLC4A11/DRD4/F2RL3/SLC9A7/ATP1B1/FGF2/PDK4/KCNMA1/P2RY1/PTGER3/CORO1A/CDH23/SLC24A3/ATP2A3/CHRNA9/ADCY5/HMOX1/CHD7/SLC4A4/EDNRA/GNA15/ATP6V0D2/JPH2/LYN/PLCG2/CA2/APOE/CCR5/F2RL1/SLC30A3/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/C5AR1/SLC11A1/PTGDR/GRIK2/PLN/JPH1/CCL8/C3AR1/STC1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/S100A9/EDNRB/FPR3/CCL13/SNCA/CALB2* |
| G81 | GO:0055065 | Metal ion homeostasis | 362 | –0.411064118 | –1.608340613 | 0.001269036 | 0.023352669 | tags =23%, list =15%, signal =20% | *TGFB1/CACNA1A/SLC22A17/HYAL2/GNAT2/ATP13A3/PTGER4/TF/HIF1A/PARK2/DMD/ABCG2/STIM2/CD38/PDGFRA/CYP27B1/PLCG1/ITPR2/TRPC4/EPAS1/CD52/LETM2/TFRC/ITPR1/SLC11A2/OPRL1/CCR1/SLC30A10/EGLN1/FTH1/ATP2B1/MT2A/KL/DRD4/F2RL3/ATP1B1/FGF2/KCNMA1/P2RY1/PTGER3/CORO1A/CDH23/SLC24A3/ATP2A3/CHRNA9/ADCY5/HMOX1/CHD7/EDNRA/GNA15/JPH2/LYN/PLCG2/APOE/CCR5/F2RL1/SLC30A3/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/C5AR1/SLC11A1/PTGDR/GRIK2/PLN/JPH1/CCL8/C3AR1/STC1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/S100A9/EDNRB/FPR3/CCL13/SNCA/CALB2* |
| G81 | GO:0051272 | Positive regulation of cellular component movement | 335 | –0.490447403 | –1.909734732 | 0.001293661 | 0.023352669 | tags =26%, list =13%, signal =23% | *RNF207/MYADM/PDGFRA/FLT1/IRS2/ADRA2A/PLCG1/NOX4/FN1/PDGFA/SEMA6D/WNT5B/ITGA5/TGFBR2/CCR1/CXCL2/FAM83H/RAC2/CSF1R/SERPINE1/KIAA1598/PDGFB/VEGFA/HSPB1/PTP4A1/FAM115C/CXCL14/RET/PTGS2/F3/ITGB3/LRRC15/ATP8A1/FGF2/PLAU/MDM2/MMP9/SNAI1/HBEGF/ADAM8/CORO1A/SPARC/P2RY6/SPOCK2/MYLK/WNT11/VTN/NRP2/LYN/ANGPT4/CXCL16/WNT5A/SRPX2/HAS2/CCL26/ANGPT1/F2RL1/BDKRB1/NCKAP1L/CCL2/FGR/PTPRC/ITGA2/LBP/C5AR1/IL1A/SOX9/IL6/AIF1/PTAFR/CCL8/CMKLR1/C3AR1/CXCL1/SEMA6B/PF4/IGF1/KDR/CXCL6/MCAM/CXCL3/PLA2G7/CD74/BMP2/PLVAP/CXCL5/IL8* |
| G81 | GO:0051249 | Regulation of lymphocyte activation | 274 | –0.523971874 | –2.01500247 | 0.001295337 | 0.023352669 | tags =20%, list =6%, signal =19% | *SFRP1/VAV3/LAT/PRKCZ/ADAM8/CORO1A/CDKN1A/IL18/CD83/MNDA/LST1/CAMK4/HLA-DPA1/IL1B/LYN/CD300A/IL36B/TBC1D10C/INPP5D/CYP26B1/PAG1/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/NFAM1/SAMSN1/MERTK/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/CD209/INHBA/IGF1/VSIG4/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G81 | GO:0055074 | Calcium ion homeostasis | 249 | –0.470583463 | –1.797638414 | 0.001321004 | 0.023352669 | tags =18%, list =6%, signal =17% | *F2RL3/ATP1B1/FGF2/P2RY1/PTGER3/CORO1A/CDH23/SLC24A3/ATP2A3/CHRNA9/ADCY5/CHD7/EDNRA/GNA15/JPH2/LYN/PLCG2/APOE/CCR5/F2RL1/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/C5AR1/PTGDR/GRIK2/PLN/JPH1/CCL8/C3AR1/STC1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/EDNRB/FPR3/CCL13/SNCA/CALB2* |
| G81 | GO:0051480 | Regulation of cytosolic calcium ion concentration | 173 | –0.48872301 | –1.788762917 | 0.001392758 | 0.023352669 | tags =20%, list =6%, signal =19% | *FGF2/P2RY1/PTGER3/CORO1A/CDH23/CHRNA9/ADCY5/CHD7/EDNRA/GNA15/JPH2/LYN/PLCG2/CCR5/F2RL1/PTPN6/BDKRB1/PTPRC/CD4/C5AR1/PTGDR/PLN/JPH1/C3AR1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/EDNRB/FPR3/SNCA/CALB2* |
| G81 | GO:0051251 | Positive regulation of lymphocyte activation | 187 | –0.537215025 | –1.984336983 | 0.001408451 | 0.023352669 | tags =28%, list =13%, signal =25% | *IRS2/TNFSF9/SPN/IL15/TFRC/TLR4/TGFBR2/HLA-DPB1/GLI2/IL2RA/RASGRP1/BTK/TNFSF4/DPP4/VAV3/PRKCZ/ADAM8/CORO1A/CDKN1A/IL18/CD83/HLA-DPA1/IL1B/LYN/IL36B/INPP5D/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/IGF1/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G81 | GO:0051924 | Regulation of calcium ion transport | 135 | –0.462073821 | –1.644575122 | 0.001447178 | 0.023352669 | tags =31%, list =17%, signal =26% | *CAPN3/HOMER1/HTT/C19orf26/ARRB2/TGFB1/DMD/STIM2/CASK/ADRA2A/PLCG1/EHD3/TRPV2/OPRL1/UCN/CCR1/TRPV3/PDGFB/P2RX1/PTGS2/DRD4/F2RL3/ATP1B1/CAMK2A/EPPIN/CORO1A/MYLK/CHD7/JPH2/LYN/TSPAN13/PLCG2/PTPN6/BDKRB1/CCL2/CD4/PLN/JPH1/CD84/STC1/SNCA* |
| G81 | GO:0051238 | Sequestering of metal ion | 91 | –0.511882085 | –1.723100507 | 0.00152207 | 0.023352669 | tags =32%, list =18%, signal =26% | *FTL/MYO5A/CAPN3/HTT/TGFB1/DMD/PLCG1/ITPR2/ITPR1/SLC30A10/FTH1/F2RL3/FGF2/CORO1A/CHD7/JPH2/LYN/PLCG2/CCR5/SLC30A3/PTPN6/BDKRB1/PTPRC/PLN/JPH1/HTR2A/S100A9/SNCA* |
| G81 | GO:0051806 | Entry into cell of other organism involved in symbiotic interaction | 93 | –0.49965221 | –1.682196746 | 0.001531394 | 0.023352669 | tags =28%, list =7%, signal =26% | *GAS6/P4HB/CXADR/HYAL2/ITGB1/LGALS9/TFRC/ITGA5/ITGB5/ITGB3/DPP4/F11R/SLC52A1/CR1/PVRL4/CCR5/VAMP8/EFNB2/ITGA2/CD86/CD4/CD209/HTR2A/CXCR4/IL8* |
| G81 | GO:0051828 | Entry into other organism involved in symbiotic interaction | 93 | –0.49965221 | –1.682196746 | 0.001531394 | 0.023352669 | tags =28%, list =7%, signal =26% | *GAS6/P4HB/CXADR/HYAL2/ITGB1/LGALS9/TFRC/ITGA5/ITGB5/ITGB3/DPP4/F11R/SLC52A1/CR1/PVRL4/CCR5/VAMP8/EFNB2/ITGA2/CD86/CD4/CD209/HTR2A/CXCR4/IL8* |
| G81 | GO:0051250 | Negative regulation of lymphocyte activation | 83 | –0.574909791 | –1.906197988 | 0.001533742 | 0.023352669 | tags =34%, list =16%, signal =28% | *PELI1/JAK3/TGFB1/CEBPB/LGALS9/INHA/SPN/IL2RA/MICA/TNFSF4/SFRP1/MNDA/LST1/LYN/CD300A/TBC1D10C/INPP5D/PAG1/PTPN6/HAVCR2/PTPN22/TNFRSF21/SAMSN1/MERTK/INHBA/VSIG4/CD74* |
| G81 | GO:0051282 | Regulation of sequestering of calcium ion | 76 | –0.507436439 | –1.663985996 | 0.001550388 | 0.023352669 | tags =20%, list =6%, signal =19% | *FGF2/CORO1A/CHD7/JPH2/LYN/PLCG2/CCR5/PTPN6/BDKRB1/PTPRC/PLN/JPH1/HTR2A/SNCA* |
| G81 | GO:0055007 | Cardiac muscle cell differentiation | 74 | –0.485439087 | –1.583134109 | 0.00155521 | 0.023352669 | tags =28%, list =15%, signal =24% | *TGFB1/ITGB1/PDGFRA/NOX4/MYH10/NEBL/VEGFA/SIK1/GATA6/NEXN/TBX3/MYH11/FHOD3/EFNB2/MYOCD/RARB/TBX5/IGF1/BMP2/PITX2* |
| G81 | GO:0051283 | Negative regulation of sequestering of calcium ion | 75 | –0.508025149 | –1.659648205 | 0.0015625 | 0.023352669 | tags =20%, list =6%, signal =19% | *FGF2/CORO1A/CHD7/JPH2/LYN/PLCG2/CCR5/PTPN6/BDKRB1/PTPRC/PLN/JPH1/HTR2A/SNCA* |
| G81 | GO:0051279 | Regulation of release of sequestered calcium ion into cytosol | 52 | –0.540219657 | –1.664736243 | 0.003134796 | 0.030486975 | tags =31%, list =6%, signal =29% | *CAPN3/HTT/TGFB1/DMD/PLCG1/F2RL3/CORO1A/CHD7/JPH2/LYN/PTPN6/BDKRB1/PLN/JPH1/SNCA* |
| G81 | GO:0051591 | Response to camp | 66 | –0.49937782 | –1.589524753 | 0.004651163 | 0.037949001 | tags =35%, list =20%, signal =28% | *NME1/JUN/COL1A1/PER1/MMP19/AKAP9/NOX4/ITPR2/HCN2/AP000322.53/LDHA/SDC1/STAR/PLA2G5/KCNE1/SPARC/FOSB/PTPRN/VGF/AQP9/PTAFR/STC1* |
| G82 | GO:0055082 | Cellular chemical homeostasis | 485 | –0.406655896 | –1.623336397 | 0.001207729 | 0.023352669 | tags =26%, list =17%, signal =22% | *ERN1/ATP13A2/ATP6V1F/C2CD2L/MYO5A/ATP6V1G1/GAS6/CAPN3/SLC9A4/BCAP31/HTT/NR1D1/CHRNA7/ATP7A/ATP6V1G2/ATP6V0E1/ATP6V1A/SLC46A1/ATP6V0A1/ORMDL3/TGFB1/CACNA1A/SLC22A17/GNAT2/ATP13A3/ATP6V1E1/PTGER4/TF/HIF1A/DMD/ABCG2/STIM2/CD38/PDGFRA/IRS2/ADRA2A/PLCG1/TTPA/NOX4/ITPR2/C10orf2/TRPC4/CD52/SLC4A3/LETM2/TFRC/ITPR1/SLC11A2/OPRL1/CCR1/SLC26A1/ATP6V0C/SLC30A10/EGLN1/SYBU/FTH1/ATP2B1/STAR/MT2A/SLC4A11/UCP2/DRD4/F2RL3/SLC9A7/SOX4/ATP1B1/FGF2/KCNMA1/FOXO1/P2RY1/PDK3/PTGER3/CORO1A/CDH23/SLC24A3/ATP2A3/DGAT2/CHRNA9/ADCY5/HMOX1/PTPRN/GPR27/CHD7/SLC4A4/EDNRA/GNA15/ATP6V0D2/TMEM27/JPH2/LYN/PLCG2/CA2/APOE/CCR5/F2RL1/SLC30A3/PTPN6/AQP9/C1QTNF3/HK3/BDKRB1/CCL2/PTPRC/PRKCB/CD4/C5AR1/SLC11A1/PTGDR/GRIK2/PLN/JPH1/CCL8/C3AR1/STC1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/S100A9/EDNRB/FPR3/CCL13/SNCA/CALB2* |
| G82 | GO:0055090 | Acylglycerol homeostasis | 19 | –0.668530855 | –1.695043616 | 0.006932409 | 0.047630272 | tags =42%, list =8%, signal =39% | *ANGPTL4/IL18/DGAT2/LPL/APOE/C1QTNF3/APOC2* |
| G83 | GO:0055094 | Response to lipoprotein particle | 16 | –0.781924354 | –1.877672925 | 0.001751313 | 0.02350135 | tags =44%, list =6%, signal =41% | *ITGB2/ABCA1/SIGLEC15/CCL2/SYK/FCER1G* |
| G83 | GO:0060039 | Pericardium development | 14 | –0.745078413 | –1.740117121 | 0.003478261 | 0.031944406 | tags =36%, list =6%, signal =34% | *FLRT3/WNT5A/TBX5/BMP2* |
| G84 | GO:0060135 | Maternal process involved in female pregnancy | 45 | –0.59939089 | –1.785786159 | 0.003220612 | 0.030486975 | tags =29%, list =15%, signal =25% | *LGALS9/CYP27B1/AR/PTGS2/CTSV/DSG2/HAVCR2/MMP7/CCL2/STC1/LIF/SPP1* |
| G85 | GO:0060326 | Cell chemotaxis | 163 | –0.618133135 | –2.251103108 | 0.001396648 | 0.023352669 | tags =33%, list =9%, signal =30% | *SERPINE1/PDGFB/VEGFA/HSPB1/CXCL14/ITGA1/PLXNB3/ITGB2/VAV3/EPHA2/FGF2/HBEGF/ADAM8/CORO1A/PADI2/IL1B/LYN/CXCL16/WNT5A/CCL26/CCR5/BIN2/CCL22/F2RL1/NCKAP1L/CCL2/TREM1/LBP/C5AR1/IL6/SYK/AIF1/CCL8/CMKLR1/C3AR1/GPR183/CXCR4/CXCL1/FCER1G/PF4/FPR1/KDR/S100A9/EDNRB/FPR3/CXCL6/CXCL3/CCL13/PLA2G7/CD74/SCG2/CXCL5/IL8* |
| G85 | GO:0060348 | Bone development | 146 | –0.459721276 | –1.6555464 | 0.00141844 | 0.023352669 | tags =16%, list =4%, signal =15% | *ZFPM1/MEIS1/HOXB4/MMP16/DHRS3/MSX2/SIGLEC15/HAS2/TGFB3/SULF1/CYP26B1/PTPN6/ACP5/PTPRC/SOX9/RARB/STC1/COL10A1/IGF1/TYROBP/BMP2/PITX2* |
| G85 | GO:0060191 | Regulation of lipase activity | 55 | –0.508720609 | –1.58489476 | 0.001547988 | 0.023352669 | tags =29%, list =8%, signal =27% | *FLT1/PLCB2/PLA2G5/ANGPTL4/FGF2/PRKCZ/APOC1/RGS2/EDNRA/GNA15/APOC2/C5AR1/PTAFR/HTR2A/SNCA* |
| G85 | GO:0060333 | Interferon-gamma-mediated signaling pathway | 70 | –0.508358306 | –1.641357095 | 0.00309119 | 0.030486975 | tags =16%, list =3%, signal =15% | *HLA-DPA1/IRF8/PTAFR/HLA-DQA1/HCK/FCGR1A/HLA-DQB1/HLA-DRB1/HLA-DRB5/HLA-DRA* |
| G86 | GO:0060401 | Cytosolic calcium ion transport | 88 | –0.507811796 | –1.703224527 | 0.00149925 | 0.023352669 | tags =20%, list =6%, signal =19% | *CTGF/FGF2/CORO1A/CHD7/JPH2/LYN/PLCG2/CCR5/PTPN6/BDKRB1/PTPRC/CD4/PLN/JPH1/HTR2A/TRPM2/SNCA* |
| G86 | GO:0060402 | Calcium ion transport into cytosol | 86 | –0.500718059 | –1.670983231 | 0.00149925 | 0.023352669 | tags =20%, list =6%, signal =19% | *FGF2/CORO1A/CHD7/JPH2/LYN/PLCG2/CCR5/PTPN6/BDKRB1/PTPRC/CD4/PLN/JPH1/HTR2A/TRPM2/SNCA* |
| G86 | GO:0060444 | Branching involved in mammary gland duct morphogenesis | 20 | –0.687423858 | –1.767203839 | 0.001694915 | 0.023352669 | tags =50%, list =17%, signal =42% | *KDM5B/BTRC/TGFB1/AR/DDR1/TBX3/EPHA2/MSX2/WNT5A* |
| G86 | GO:0060395 | SMAD protein signal transduction | 37 | –0.599042089 | –1.754901294 | 0.004792332 | 0.038245256 | tags =38%, list =21%, signal =30% | *JUN/TGFB2/CERS1/TGFB1/INHA/HIPK2/GDF11/GDF15/BTBD11/TGFB3/GDF6/INHBA/BMP2* |
| G86 | GO:0060425 | Lung morphogenesis | 39 | –0.563650636 | –1.645988729 | 0.004846527 | 0.038245256 | tags =26%, list =11%, signal =23% | *TGFBR2/CTSZ/RDH10/TNC/CELSR1/SOX9/LIF/HOXA5/PITX2* |
| G86 | GO:0060443 | Mammary gland morphogenesis | 36 | –0.568862281 | –1.662864107 | 0.006279435 | 0.045145817 | tags =39%, list =17%, signal =33% | *KDM5B/BTRC/TGFB1/AR/TGFBR2/GLI2/DDR1/CSF1R/B4GALT1/TBX3/EPHA2/MSX2/WNT5A* |
| G87 | GO:0060541 | Respiratory system development | 159 | –0.426447964 | –1.546541449 | 0.002816901 | 0.030326036 | tags =27%, list =14%, signal =23% | *MAPK3/CCDC40/ZFPM2/FSTL3/PDGFA/EPAS1/HHIP/TGFBR2/GLI2/PTN/ALDH1A3/ABCA12/HYDIN/CTSZ/PTK7/VEGFA/CRISPLD2/RDH10/DISP1/GATA6/TNC/HSD11B1/TNS3/GPC3/CTGF/CELSR1/RBP4/SPARC/MSC/WNT11/EYA1/CHD7/STRA6/WNT5A/TGFB3/MYOCD/SOX9/TBX5/LIF/SIM2/HOXA5/PITX2* |
| G88 | GO:0070371 | ERK1 and ERK2 cascade | 176 | –0.485630079 | –1.784122027 | 0.001383126 | 0.023352669 | tags =30%, list =14%, signal =26% | *LGALS9/PTGER4/ATF3/PDGFRA/TNFRSF11A/NOX4/FN1/PDGFA/TLR4/CCR1/ATP6AP1/GAREM/DUSP6/CSF1R/RASGRP1/PDGFB/PLA2G5/DUSP4/CTGF/HAND2/EPHA2/FGF2/PRKCZ/SCIMP/P2RY1/NDRG4/LYN/PTPRR/TBC1D10C/CCL26/ANGPT1/ROS1/CCL22/F2RL1/PTPN6/HAVCR2/CCL2/PTPN22/TREM2/C5AR1/SOX9/IL6/SYK/CCL8/GPR183/HTR2A/LIF/IGF1/KDR/CCL13/CD74/BMP2* |
| G88 | GO:0061041 | Regulation of wound healing | 89 | –0.529542294 | –1.777424986 | 0.001515152 | 0.023352669 | tags =37%, list =13%, signal =33% | *CASK/ADRA2A/PRKG1/GJD4/GP1BA/PDGFA/KANK1/TLR4/TGFBR2/SERPINE1/PDGFB/WFDC1/ENPP4/PLAUR/FAM46A/PLAT/FAP/F3/SERPINE2/FGF2/PLAU/HBEGF/MYLK/VTN/LYN/APOE/F2RL1/PLEK/SYK/SERPINB2/FCER1G/S100A9* |
| G88 | GO:0070098 | Chemokine-mediated signaling pathway | 35 | –0.729151685 | –2.119221962 | 0.001597444 | 0.023352669 | tags =46%, list =3%, signal =44% | *CCL26/CCR5/CCL22/CCL2/TREM2/CCL8/CMKLR1/CXCR4/CXCL1/PF4/CXCL6/CXCL3/CCL13/CXCL5/IL8* |
| G88 | GO:0061615 | Glycolytic process through fructose-6-phosphate | 21 | –0.677052833 | –1.751378529 | 0.001686341 | 0.023352669 | tags =86%, list =25%, signal =64% | *PFKM/HK2/PFKFB2/PFKFB3/PFKL/PGAM1/GPI/TPI1/ENO3/ENO2/GAPDH/ALDOC/ALDOA/PKM/PGK1/PFKFB4/HK3* |
| G88 | GO:0061620 | Glycolytic process through glucose-6-phosphate | 21 | –0.677052833 | –1.751378529 | 0.001686341 | 0.023352669 | tags =86%, list =25%, signal =64% | *PFKM/HK2/PFKFB2/PFKFB3/PFKL/PGAM1/GPI/TPI1/ENO3/ENO2/GAPDH/ALDOC/ALDOA/PKM/PGK1/PFKFB4/HK3* |
| G88 | GO:0061621 | Canonical glycolysis | 20 | –0.726883421 | –1.868645024 | 0.001694915 | 0.023352669 | tags =90%, list =25%, signal =68% | *PFKM/HK2/PFKFB2/PFKFB3/PFKL/PGAM1/GPI/TPI1/ENO3/ENO2/GAPDH/ALDOC/ALDOA/PKM/PGK1/PFKFB4/HK3* |
| G88 | GO:0061718 | Glucose catabolic process to pyruvate | 20 | –0.726883421 | –1.868645024 | 0.001694915 | 0.023352669 | tags =90%, list =25%, signal =68% | *PFKM/HK2/PFKFB2/PFKFB3/PFKL/PGAM1/GPI/TPI1/ENO3/ENO2/GAPDH/ALDOC/ALDOA/PKM/PGK1/PFKFB4/HK3* |
| G88 | GO:0060627 | Regulation of vesicle-mediated transport | 332 | –0.371940207 | –1.449455733 | 0.005154639 | 0.039409281 | tags =15%, list =10%, signal =14% | *RIMS3/DOCK2/NCS1/SDC1/RAC2/SERPINE1/NLGN1/VEGFA/SYTL1/STXBP2/SMPD3/MFGE8/GPC3/STON1/UNC13D/SYTL3/SYN1/APOC1/CORO1A/NDRG4/RIMS1/HMOX1/VTN/SFRP4/IL1B/TMEM27/LYN/CD300A/WNT5A/PLCG2/TBC1D10C/ANGPT1/F2RL1/VAMP8/NCKAP1L/CCL2/FGR/ITGA2/APOC2/SLC11A1/MERTK/SYK/CD14/PTAFR/CD84/HCK/FCER1G/SNCA* |
| G88 | GO:0060562 | Epithelial tube morphogenesis | 242 | –0.383041987 | –1.456852732 | 0.00536193 | 0.040277007 | tags =20%, list =11%, signal =18% | *AR/HHIP/TGFBR2/SALL4/SOX8/GLI2/DDR1/CSF1R/CTSZ/PTK7/VEGFA/NKX3-1/RDH10/MICAL2/IRX2/RET/B4GALT1/TNC/CTHRC1/GDNF/GPC3/KIF26B/COL4A1/SOX4/CELSR1/HAND2/SFRP1/TBX3/EPHA2/FGF2/ADAMTS12/PRICKLE1/NDRG4/SPINT2/WNT11/EYA1/EDNRA/MSX2/WNT5A/EFNB2/ST14/SOX9/SPI1/HOXB7/ALX1/BMP2/HOXA5/PITX2* |
| G88 | GO:0070302 | Regulation of stress-activated protein kinase signaling cascade | 170 | –0.407744256 | –1.493845748 | 0.00554785 | 0.04142949 | tags =23%, list =14%, signal =20% | *MAPK3/TLR6/ANKRD6/TRAF4/PARK2/TNFRSF11A/HIPK2/TLR4/ZNF622/RASGRP1/GADD45A/VEGFA/PLCB1/TNIK/CTGF/HAND2/SFRP1/FOXO1/XDH/FZD8/FZD7/DUSP10/NRK/TPD52L1/IL1B/LYN/WNT5A/GADD45G/MDFI/F2RL1/GDF6/PTPN22/IL1A/DACT1/GRIK2/SYK/FGD2/BMP2* |
| G88 | GO:0061045 | Negative regulation of wound healing | 42 | –0.544470741 | –1.608505549 | 0.006472492 | 0.045377892 | tags =40%, list =13%, signal =35% | *CASK/PRKG1/GP1BA/PDGFA/SERPINE1/PDGFB/WFDC1/PLAUR/PLAT/FAP/SERPINE2/FGF2/PLAU/VTN/APOE/SERPINB2* |
| G88 | GO:0070328 | Triglyceride homeostasis | 19 | –0.668530855 | –1.695043616 | 0.006932409 | 0.047630272 | tags =42%, list =8%, signal =39% | *ANGPTL4/IL18/DGAT2/LPL/APOE/C1QTNF3/APOC2* |
| G89 | GO:0070486 | Leukocyte aggregation | 310 | –0.509163937 | –1.971787242 | 0.00128866 | 0.023352669 | tags =25%, list =6%, signal =24% | *SATB1/SPN/IL15/TFRC/KIF13B/TGFBR2/HLA-DPB1/PREX1/GLI2/IL2RA/DOCK2/RAC2/RASGRP1/RORA/IFNE/MICA/TNFSF4/DPP4/SOX4/LAT/RSAD2/PRKCZ/ADAM8/FZD8/CORO1A/FZD7/IL18/CD83/WAS/LCP1/ZFPM1/TNFSF8/CAMK4/CHD7/HLA-DPA1/IL1B/LYN/CD300A/IL36B/HAS2/CYP26B1/PAG1/F2RL1/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/DOCK8/CLEC7A/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/SLC11A1/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/CD209/FCER1G/IGF1/VSIG4/S100A9/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G89 | GO:0070489 | T cell aggregation | 304 | –0.502584073 | –1.941159591 | 0.001302083 | 0.023352669 | tags =25%, list =12%, signal =23% | *SATB1/SPN/IL15/TFRC/KIF13B/TGFBR2/HLA-DPB1/PREX1/GLI2/IL2RA/DOCK2/RAC2/RASGRP1/RORA/IFNE/MICA/TNFSF4/DPP4/SOX4/LAT/RSAD2/PRKCZ/ADAM8/FZD8/CORO1A/FZD7/IL18/CD83/WAS/LCP1/ZFPM1/TNFSF8/CAMK4/CHD7/HLA-DPA1/IL1B/LYN/CD300A/IL36B/CYP26B1/PAG1/F2RL1/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/DOCK8/CLEC7A/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/SLC11A1/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/CD209/FCER1G/IGF1/VSIG4/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G89 | GO:0070372 | Regulation of ERK1 and ERK2 cascade | 164 | –0.495934041 | –1.80758774 | 0.001390821 | 0.023352669 | tags =35%, list =13%, signal =31% | *DAB2IP/MAP2K1/C3orf33/GAS6/ACKR3/MIF/ARRB2/MAPK3/LGALS9/ATF3/PDGFRA/TNFRSF11A/NOX4/FN1/PDGFA/TLR4/CCR1/ATP6AP1/GAREM/DUSP6/CSF1R/RASGRP1/PDGFB/PLA2G5/DUSP4/CTGF/HAND2/EPHA2/FGF2/PRKCZ/SCIMP/P2RY1/NDRG4/LYN/PTPRR/TBC1D10C/CCL26/ANGPT1/ROS1/CCL22/F2RL1/PTPN6/HAVCR2/CCL2/PTPN22/TREM2/C5AR1/IL6/SYK/CCL8/GPR183/HTR2A/LIF/KDR/CCL13/CD74/BMP2* |
| G89 | GO:0070374 | Positive regulation of ERK1 and ERK2 cascade | 107 | –0.538476963 | –1.853050921 | 0.001477105 | 0.023352669 | tags =36%, list =14%, signal =31% | *MAPK3/LGALS9/PDGFRA/TNFRSF11A/NOX4/PDGFA/TLR4/CCR1/ATP6AP1/GAREM/CSF1R/RASGRP1/PDGFB/PLA2G5/CTGF/HAND2/FGF2/PRKCZ/SCIMP/P2RY1/NDRG4/CCL26/ANGPT1/CCL22/F2RL1/HAVCR2/CCL2/PTPN22/TREM2/C5AR1/IL6/CCL8/GPR183/HTR2A/KDR/CCL13/CD74/BMP2* |
| G9 | GO:0002478 | Antigen processing and presentation of exogenous peptide antigen | 143 | –0.450843263 | –1.620050654 | 0.001426534 | 0.023352669 | tags =15%, list =6%, signal =14% | *LGMN/CTSV/CTSS/SPTBN2/HLA-DMA/HLA-DPA1/ABCB4/KIF5A/NCF4/NCF2/HLA-DQA1/HLA-DMB/CYBB/FCGR1A/FCER1G/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G9 | GO:0002504 | Antigen processing and presentation of peptide or polysaccharide antigen via MHC class II | 86 | –0.470246001 | –1.569292673 | 0.00149925 | 0.023352669 | tags =20%, list =6%, signal =19% | *LGMN/CTSV/CTSS/SPTBN2/HLA-DMA/HLA-DPA1/KIF5A/TREM2/HLA-DQA1/HLA-DMB/FCER1G/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G9 | GO:0002495 | Antigen processing and presentation of peptide antigen via MHC class II | 85 | –0.473512727 | –1.575141452 | 0.001517451 | 0.023352669 | tags =20%, list =6%, signal =19% | *LGMN/CTSV/CTSS/SPTBN2/HLA-DMA/HLA-DPA1/KIF5A/TREM2/HLA-DQA1/HLA-DMB/FCER1G/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G90 | GO:0070588 | Calcium ion transmembrane transport | 175 | –0.41233167 | –1.513552575 | 0.001383126 | 0.023352669 | tags =27%, list =17%, signal =23% | *GAS6/CAPN3/HTT/CATSPER2/C19orf26/TGFB1/CACNA1A/DMD/STIM2/ADRA2A/PLCG1/ITPR2/EHD3/TRPC4/TRPV2/ITPR1/OPRL1/TRPV3/NCS1/DENND5B/ATP2B1/CACNA1H/DRD4/F2RL3/MCOLN2/ATP1B1/FGF2/PKD1L1/CORO1A/SLC24A3/MCOLN3/ATP2A3/CHRNA9/CHD7/JPH2/LYN/TSPAN13/PLCG2/CCR5/PTPN6/BDKRB1/PTPRC/PLN/JPH1/HTR2A/TRPM2/SNCA* |
| G90 | GO:0070555 | Response to interleukin-1 | 77 | –0.576814377 | –1.899976208 | 0.00154321 | 0.023352669 | tags =32%, list =14%, signal =28% | *CEBPB/MAPK3/LGALS9/HIF1A/CD38/TNFRSF11A/IL1R2/RORA/NKX3-1/PLCB1/SFRP1/ADAMTS12/HAS2/CCL26/CCL22/CCL2/IL1A/SOX9/IL1RN/IL6/CCL8/CCL13/SNCA/IL8* |
| G90 | GO:0070509 | Calcium ion import | 110 | –0.489284275 | –1.691476845 | 0.002911208 | 0.030486975 | tags =33%, list =17%, signal =27% | *CAPN3/CDK5/HOMER1/HTT/TGFB1/DMD/CASK/PLCG1/ITPR2/TRPC4/TRPV2/ITPR1/UCN/TRPV3/PDGFB/CACNA1H/F2RL3/FGF2/EPPIN/CORO1A/CHD7/JPH2/LYN/PLCG2/CCR5/PTPN6/BDKRB1/CCL2/PTPRC/PLN/JPH1/STC1/HTR2A/TRPM2/SNCA* |
| G90 | GO:0070527 | Platelet aggregation | 41 | –0.562277428 | –1.655071087 | 0.00483871 | 0.038245256 | tags =46%, list =26%, signal =35% | *ABAT/RAP2B/TLN1/PRKCD/MYL9/STXBP1/GAS6/CSRP1/PDGFRA/PRKG1/GP1BA/HSPB1/ITGB3/SERPINE2/LYN/PTPN6/PLEK/SYK* |
| G90 | GO:0070493 | Thrombin receptor signaling pathway | 10 | –0.800935065 | –1.727178248 | 0.007366483 | 0.049685189 | tags =70%, list =12%, signal =62% | *F2RL2/F2RL3/HPGD/F2RL1/PLEK/SNCA* |
| G91 | GO:0070838 | Divalent metal ion transport | 288 | –0.416131864 | –1.60438486 | 0.001297017 | 0.023352669 | tags =27%, list =16%, signal =23% | *CAPN3/CDK5/HOMER1/HTT/CHRNA7/CATSPER2/C19orf26/ARRB2/TGFB1/CACNA1A/TF/DMD/STIM2/CASK/ADRA2A/CYP27B1/PLCG1/SLC41A2/ITPR2/EHD3/TRPC4/TRPV2/ITPR1/SLC11A2/OPRL1/UCN/CCR1/SLC30A10/TRPV3/NCS1/DENND5B/RAMP1/ATP2B1/PDGFB/P2RX1/CALCRL/PTGS2/CACNA1H/DRD4/F2RL3/MCOLN2/CTGF/ATP1B1/CAMK2A/FGF2/EPPIN/PKD1L1/CORO1A/CDH23/SLC24A3/MCOLN3/ATP2A3/CHRNA9/MYLK/CHD7/JPH2/LYN/TSPAN13/PLCG2/CCR5/SLC30A3/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/SLC11A1/PLN/JPH1/CCL8/CD84/STC1/HTR2A/TRPM2/SNCA* |
| G91 | GO:0070661 | Leukocyte proliferation | 177 | –0.54559394 | –2.008813875 | 0.001381215 | 0.023352669 | tags =23%, list =4%, signal =22% | *CDKN1A/IL18/CLU/MNDA/LST1/HLA-DPA1/IL1B/LYN/CD300A/INPP5D/F2RL1/PTPN6/HAVCR2/NCKAP1L/CD1D/DOCK8/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/SLC11A1/CD180/IL6/CD28/SYK/AIF1/CCL8/GPR183/CARD11/HLA-DMB/ICOSLG/CD209/IGF1/VSIG4/IL33/CD74* |
| G91 | GO:0071216 | Cellular response to biotic stimulus | 142 | –0.574533223 | –2.061765726 | 0.00143472 | 0.023352669 | tags =23%, list =9%, signal =21% | *CMPK2/SERPINE1/STAR/BTK/SPON2/TNFSF4/TLR2/TLR1/IL18/ABCA1/IL1B/LYN/CXCL16/WNT5A/IRF8/CCR5/HAVCR2/CCL2/CLEC7A/PTPN22/TREM2/LBP/CD86/CD180/IL6/SYK/CD14/PTAFR/HCK/LY86/EDNRB/IL8* |
| G91 | GO:0071222 | Cellular response to lipopolysaccharide | 117 | –0.582149984 | –2.019325719 | 0.001451379 | 0.023352669 | tags =23%, list =9%, signal =21% | *SERPINE1/STAR/SPON2/TNFSF4/TLR2/IL18/ABCA1/IL1B/LYN/CXCL16/WNT5A/IRF8/CCR5/HAVCR2/CCL2/PTPN22/LBP/CD86/CD180/IL6/CD14/PTAFR/HCK/LY86/EDNRB/IL8* |
| G91 | GO:0070663 | Regulation of leukocyte proliferation | 136 | –0.600064206 | –2.137129056 | 0.001453488 | 0.023352669 | tags =37%, list =4%, signal =35% | *CEBPB/LEP/LGALS9/CD38/IRS2/TNFSF9/SPN/IL15/TFRC/TLR4/HLA-DPB1/IL2RA/RAC2/TNFSF4/VAV3/CORO1A/CDKN1A/IL18/MNDA/LST1/HLA-DPA1/IL1B/LYN/CD300A/INPP5D/PTPN6/HAVCR2/NCKAP1L/CD1D/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/CCL8/GPR183/CARD11/HLA-DMB/ICOSLG/CD209/IGF1/VSIG4/CD74* |
| G91 | GO:0071219 | Cellular response to molecule of bacterial origin | 123 | –0.584875716 | –2.042042537 | 0.001453488 | 0.023352669 | tags =24%, list =9%, signal =22% | *SERPINE1/STAR/SPON2/TNFSF4/TLR2/TLR1/IL18/ABCA1/IL1B/LYN/CXCL16/WNT5A/IRF8/CCR5/HAVCR2/CCL2/PTPN22/TREM2/LBP/CD86/CD180/IL6/CD14/PTAFR/HCK/LY86/EDNRB/IL8* |
| G91 | GO:0070665 | Positive regulation of leukocyte proliferation | 91 | –0.637945392 | –2.147455559 | 0.00152207 | 0.023352669 | tags =44%, list =14%, signal =38% | *MIF/JAK3/LEP/LGALS9/CD38/IRS2/TNFSF9/SPN/IL15/TFRC/TLR4/HLA-DPB1/IL2RA/TNFSF4/VAV3/CORO1A/CDKN1A/IL18/HLA-DPA1/IL1B/LYN/HAVCR2/NCKAP1L/CD1D/PTPRC/CD86/CD4/GPAM/SASH3/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DMB/ICOSLG/IGF1/CD74* |
| G91 | GO:0070664 | Negative regulation of leukocyte proliferation | 46 | –0.568391262 | –1.702945823 | 0.003205128 | 0.030486975 | tags =41%, list =4%, signal =40% | *CD276/KIAA0922/PELI1/TGFB1/CEBPB/LGALS9/SPN/IL2RA/MNDA/LST1/LYN/CD300A/INPP5D/PTPN6/HAVCR2/TNFRSF21/CCL8/VSIG4* |
| G92 | GO:0071229 | Cellular response to acid chemical | 129 | –0.428834591 | –1.518135927 | 0.005698006 | 0.042430381 | tags =26%, list =14%, signal =22% | *LEP/AKR1C2/RPTOR/SESN3/AKR1C1/WNT5B/KCNMB1/ID3/COL5A2/PTK7/RRAGD/RET/COL3A1/TNC/COL4A1/PDK4/PID1/PDK3/FZD7/ABCA1/WNT11/ABCB4/LYN/WNT5A/CYP26B1/CCL2/EPHA3/SOX9/PTAFR/CYBB/FOLR2/HOXA2* |
| G93 | GO:0071346 | Cellular response to interferon-gamma | 94 | –0.540670038 | –1.82355991 | 0.001536098 | 0.023352669 | tags =18%, list =3%, signal =18% | *WNT5A/IRF8/CCL26/CCL22/CCL2/AIF1/PTAFR/CCL8/HLA-DQA1/HCK/FCGR1A/HLA-DQB1/HLA-DRB1/CCL13/HLA-DRB5/HLA-DRA* |
| G93 | GO:0071347 | Cellular response to interleukin-1 | 58 | –0.589324523 | –1.84186817 | 0.001574803 | 0.023352669 | tags =36%, list =9%, signal =33% | *CEBPB/MAPK3/HIF1A/IL1R2/RORA/NKX3-1/PLCB1/SFRP1/ADAMTS12/HAS2/CCL26/CCL22/CCL2/IL1A/SOX9/IL1RN/IL6/CCL8/CCL13/IL8* |
| G93 | GO:0071260 | Cellular response to mechanical stimulus | 59 | –0.496229442 | –1.558504241 | 0.004702194 | 0.037949001 | tags =29%, list =16%, signal =24% | *BAG3/TGFB1/MAPK3/PTGER4/TNFRSF10B/TLR4/TNFRSF10A/GADD45A/PTGS2/BNIP3/TLR8/TLR7/IL1B/MMP7/ITGA2/SOX9* |
| G94 | GO:0071396 | Cellular response to lipid | 389 | –0.418339149 | –1.648005794 | 0.001246883 | 0.023352669 | tags =15%, list =9%, signal =14% | *ATP2B1/CMPK2/SERPINE1/RORA/STAR/PTK7/NKX3-1/SPON2/RET/TNC/TNFSF4/TLR2/PPAP2A/SFRP1/PDK4/PID1/ABHD2/FOXO1/PDK3/FZD7/FBXO32/IL18/DGAT2/ABCA1/ADCY5/WNT11/PADI2/MSX2/IL1B/ABCB4/LYN/CXCL16/WNT5A/IRF8/HEYL/CCR5/CYP26B1/HAVCR2/CCL2/PTPN22/ITGA2/LBP/CD86/EPHA3/SOX9/NR2F1/RARB/CD180/IL6/CD14/PTAFR/HCK/STC1/PMEPA1/INHBA/LY86/EDNRB/HOXA2/IL8* |
| G94 | GO:0071593 | Lymphocyte aggregation | 305 | –0.502319292 | –1.941929704 | 0.001295337 | 0.023352669 | tags =25%, list =12%, signal =23% | *SATB1/SPN/IL15/TFRC/KIF13B/TGFBR2/HLA-DPB1/PREX1/GLI2/IL2RA/DOCK2/RAC2/RASGRP1/RORA/IFNE/MICA/TNFSF4/DPP4/SOX4/LAT/RSAD2/PRKCZ/ADAM8/FZD8/CORO1A/FZD7/IL18/CD83/WAS/LCP1/ZFPM1/TNFSF8/CAMK4/CHD7/HLA-DPA1/IL1B/LYN/CD300A/IL36B/CYP26B1/PAG1/F2RL1/PTPN6/HAVCR2/EFNB2/NCKAP1L/CD1D/CCL2/DOCK8/CLEC7A/PTPN22/TNFRSF21/PTPRC/CD86/CD4/GPAM/SASH3/SLC11A1/IL6/CD28/SYK/AIF1/GPR183/CARD11/HLA-DQA1/HLA-DMB/ICOSLG/CD209/FCER1G/IGF1/VSIG4/HLA-DQB1/HLA-DRB1/HLA-DRB5/CD74/HLA-DRA* |
| G94 | GO:0071706 | Tumor necrosis factor superfamily cytokine production | 86 | –0.548786056 | –1.831394495 | 0.00149925 | 0.023352669 | tags =29%, list =9%, signal =27% | *LEP/LGALS9/SPN/TLR4/RASGRP1/HSPB1/SPON2/TLR2/TLR1/ADAM8/CLU/ANGPT1/HAVCR2/ACP5/CCL2/PTPN22/LBP/CD86/SASH3/CD14/PTAFR/CYBB/FCER1G/PF4* |
| G94 | GO:0071621 | Granulocyte chemotaxis | 56 | –0.746519315 | –2.329740906 | 0.00155521 | 0.023352669 | tags =48%, list =6%, signal =46% | *PREX1/CXCL2/RAC2/ITGA1/ITGB2/VAV3/IL1B/CCL26/CCL22/NCKAP1L/CCL2/TREM1/LBP/C5AR1/SYK/CCL8/CMKLR1/C3AR1/CXCL1/FCER1G/S100A9/CXCL3/CCL13/CD74/SCG2/IL8* |
| G94 | GO:0071674 | Mononuclear cell migration | 37 | –0.641352056 | –1.878848872 | 0.001597444 | 0.023352669 | tags =54%, list =15%, signal =46% | *TGFB1/FLT1/TNFRSF11A/CCR1/SERPINE1/PDGFB/PLCB1/LYN/CCL26/CCL22/CCL2/C5AR1/IL6/AIF1/CCL8/CMKLR1/C3AR1/CCL13/PLA2G7* |
| G94 | GO:0071622 | Regulation of granulocyte chemotaxis | 28 | –0.800395406 | –2.181324374 | 0.001672241 | 0.023352669 | tags =36%, list =2%, signal =35% | *CCL2/LBP/C5AR1/CMKLR1/C3AR1/CXCL1/CXCL3/CD74/IL8* |
| G94 | GO:0071624 | Positive regulation of granulocyte chemotaxis | 18 | –0.817225895 | –2.042609428 | 0.001727116 | 0.023440094 | tags =56%, list =2%, signal =55% | *RAC2/NCKAP1L/LBP/C5AR1/C3AR1/CXCL1/CXCL3/CD74/IL8* |
| G94 | GO:0072132 | Mesenchyme morphogenesis | 37 | –0.564293323 | –1.653104348 | 0.006389776 | 0.045290946 | tags =32%, list =5%, signal =31% | *HEY1/MDM2/SNAI1/ACTA2/WNT11/MSX2/WNT5A/HEYL/SOX9/ACTG2/BMP2* |
| G95 | GO:0072358 | Cardiovascular system development | 498 | –0.429555341 | –1.718331568 | 0.001193317 | 0.023352669 | tags =21%, list =10%, signal =20% | *PTN/GPR56/EGLN1/RAMP1/HEY1/SERPINE1/RORA/PDGFB/PTK7/VEGFA/HSPB1/NKX3-1/COL4A2/GATA6/CALCRL/PAX6/B4GALT1/COL3A1/FAP/PTGS2/F3/ITGB3/MFGE8/GPC3/NOTCH3/RUNX1/COL4A1/CTGF/SOX4/ANGPTL4/HAND2/EPGN/SFRP1/TBX3/ITGB2/VAV3/EPHA2/FGF2/ANTXR1/HPGD/PCSK5/FOXO1/MDM2/XDH/PDE3B/ADAM8/PRICKLE1/FZD8/IL18/ACTA2/LOXL2/SPARC/HOXA7/BAI1/MEIS1/SAT1/CDH2/HMOX1/MYLK/WNT11/RGCC/EYA1/CHD7/LYL1/EDNRA/STRA6/IL1B/NRP2/ANGPT4/WNT5A/SRPX2/NRCAM/HAS2/APOE/HOXB3/SULF1/ANGPT1/TIE1/NDNF/EFNB2/MYOCD/CCL2/PRKCB/C5AR1/IL1A/ENPEP/SERPINB7/IL6/SYK/C3AR1/STAB1/CYBB/SPI1/TBX5/PF4/LIF/KDR/MCAM/FOXS1/HOXA3/HOXA5/SCG2/IL8/PITX2* |
| G96 | GO:0072511 | Divalent inorganic cation transport | 289 | –0.414711667 | –1.599369356 | 0.001297017 | 0.023352669 | tags =27%, list =16%, signal =23% | *CAPN3/CDK5/HOMER1/HTT/CHRNA7/CATSPER2/C19orf26/ARRB2/TGFB1/CACNA1A/TF/DMD/STIM2/CASK/ADRA2A/CYP27B1/PLCG1/SLC41A2/ITPR2/EHD3/TRPC4/TRPV2/ITPR1/SLC11A2/OPRL1/UCN/CCR1/SLC30A10/TRPV3/NCS1/DENND5B/RAMP1/ATP2B1/PDGFB/P2RX1/CALCRL/PTGS2/CACNA1H/DRD4/F2RL3/MCOLN2/CTGF/ATP1B1/CAMK2A/FGF2/EPPIN/PKD1L1/CORO1A/CDH23/SLC24A3/MCOLN3/ATP2A3/CHRNA9/MYLK/CHD7/JPH2/LYN/TSPAN13/PLCG2/CCR5/SLC30A3/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/SLC11A1/PLN/JPH1/CCL8/CD84/STC1/HTR2A/TRPM2/SNCA* |
| G96 | GO:0072507 | Divalent inorganic cation homeostasis | 275 | –0.466845592 | –1.794682627 | 0.00130039 | 0.023352669 | tags =17%, list =6%, signal =17% | *F2RL3/ATP1B1/FGF2/P2RY1/PTGER3/CORO1A/CDH23/SLC24A3/ATP2A3/CHRNA9/ADCY5/CHD7/EDNRA/GNA15/JPH2/LYN/PLCG2/APOE/CCR5/F2RL1/SLC30A3/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/C5AR1/SLC11A1/PTGDR/GRIK2/PLN/JPH1/CCL8/C3AR1/STC1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/S100A9/EDNRB/FPR3/CCL13/SNCA/CALB2* |
| G96 | GO:0072503 | Cellular divalent inorganic cation homeostasis | 262 | –0.484736554 | –1.855307225 | 0.001321004 | 0.023352669 | tags =18%, list =6%, signal =17% | *F2RL3/ATP1B1/FGF2/P2RY1/PTGER3/CORO1A/CDH23/SLC24A3/ATP2A3/CHRNA9/ADCY5/CHD7/EDNRA/GNA15/JPH2/LYN/PLCG2/APOE/CCR5/F2RL1/SLC30A3/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/C5AR1/SLC11A1/PTGDR/GRIK2/PLN/JPH1/CCL8/C3AR1/STC1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/S100A9/EDNRB/FPR3/CCL13/SNCA/CALB2* |
| G96 | GO:0090279 | Regulation of calcium ion import | 70 | –0.53078237 | –1.71375858 | 0.001545595 | 0.023352669 | tags =36%, list =17%, signal =30% | *CAPN3/HOMER1/HTT/TGFB1/DMD/CASK/PLCG1/TRPV2/UCN/TRPV3/PDGFB/F2RL3/EPPIN/CORO1A/CHD7/JPH2/LYN/PTPN6/BDKRB1/CCL2/PLN/JPH1/STC1/SNCA* |
| G96 | GO:0090303 | Positive regulation of wound healing | 33 | –0.599838753 | –1.70128639 | 0.001633987 | 0.023352669 | tags =36%, list =12%, signal =32% | *KANK1/TLR4/TGFBR2/SERPINE1/ENPP4/F3/HBEGF/MYLK/VTN/PLEK/S100A9* |
| G96 | GO:0090022 | Regulation of neutrophil chemotaxis | 22 | –0.795126704 | –2.086362877 | 0.001666667 | 0.023352669 | tags =45%, list =2%, signal =45% | *RAC2/NCKAP1L/LBP/C5AR1/C3AR1/CXCL1/CXCL3/CD74/IL8* |
| G96 | GO:0090023 | Positive regulation of neutrophil chemotaxis | 18 | –0.817225895 | –2.042609428 | 0.001727116 | 0.023440094 | tags =56%, list =2%, signal =55% | *RAC2/NCKAP1L/LBP/C5AR1/C3AR1/CXCL1/CXCL3/CD74/IL8* |
| G96 | GO:0072376 | Protein activation cascade | 48 | –0.542583467 | –1.632587556 | 0.004754358 | 0.038220293 | tags =35%, list =8%, signal =33% | *CFH/F3/CFHR1/A2M/C7/CLU/CFI/CR1/RGCC/VTN/C5AR1/C3AR1/C1QA/VSIG4/C1QB/C1QC* |
| G96 | GO:0072676 | Lymphocyte migration | 41 | –0.58800424 | –1.730798299 | 0.00483871 | 0.038245256 | tags =37%, list =10%, signal =33% | *GCSAML/CXCL14/RET/ADAM8/PADI2/CXCL16/WNT5A/CCL26/CCL22/CCL2/AIF1/CCL8/GPR183/CCL13* |
| G96 | GO:0072577 | Endothelial cell apoptotic process | 34 | –0.585027665 | –1.680111753 | 0.00487013 | 0.038314167 | tags =38%, list =21%, signal =30% | *MAPK7/THBS1/DAB2IP/GAS6/COL18A1/SERPINE1/ANGPTL4/RGCC/ANGPT1/NDNF/KDR/SCG2* |
| G96 | GO:0090195 | Chemokine secretion | 10 | –0.806104152 | –1.738325139 | 0.007366483 | 0.049685189 | tags =50%, list =9%, signal =46% | *LPL/F2RL1/IL1RL1/IL33* |
| G97 | GO:0097529 | Myeloid leukocyte migration | 97 | –0.620223933 | –2.094702158 | 0.001526718 | 0.023352669 | tags =40%, list =11%, signal =36% | *PREX1/CCR1/CXCL2/RAC2/SERPINE1/PDGFB/PLCB1/ITGA1/ITGB2/VAV3/ADAM8/IL1B/LYN/CD300A/CCL26/CCL22/NCKAP1L/CCL2/TREM1/LBP/C5AR1/IL1A/IL6/SYK/AIF1/CCL8/CMKLR1/C3AR1/CXCL1/FCER1G/S100A9/EDNRB/CXCL3/CCL13/PLA2G7/CD74/SCG2/IL8* |
| G97 | GO:0097192 | Extrinsic apoptotic signaling pathway in absence of ligand | 60 | –0.505123196 | –1.584638978 | 0.006299213 | 0.045145817 | tags =17%, list =7%, signal =16% | *GDNF/IFI6/EYA1/IL1B/IL1A/EYA2/BCL2A1/INHBA/PF4* |
| G98 | GO:0098771 | Inorganic ion homeostasis | 437 | –0.395935306 | –1.56985802 | 0.001230012 | 0.023352669 | tags =26%, list =17%, signal =22% | *ATP13A2/ATP6V1F/MYO5A/ATP6V1G1/CAPN3/SLC9A4/BCAP31/HTT/STEAP2/CHRNA7/ATP7A/ATP6V1G2/ATP6V0E1/ATP6V1A/SLC46A1/ATP6V0A1/TGFB1/CACNA1A/SLC22A17/HYAL2/GNAT2/ATP13A3/ATP6V1E1/PTGER4/TF/HIF1A/PARK2/DMD/ABCG2/STIM2/CD38/PDGFRA/CYP27B1/PLCG1/TTPA/ITPR2/TRPC4/EPAS1/CD52/SLC4A3/LETM2/TFRC/ITPR1/SLC11A2/OPRL1/CCR1/SLC26A1/ATP6AP1/ATP6V0C/SLC30A10/EGLN1/FTH1/ATP2B1/MT2A/KL/SLC4A11/DRD4/F2RL3/SLC9A7/ATP1B1/FGF2/PDK4/KCNMA1/P2RY1/PTGER3/CORO1A/CDH23/SLC24A3/ATP2A3/CHRNA9/ADCY5/HMOX1/CHD7/SLC4A4/EDNRA/GNA15/ATP6V0D2/SFRP4/JPH2/LYN/PLCG2/CA2/APOE/CCR5/F2RL1/SLC30A3/PTPN6/BDKRB1/CCL2/PTPRC/PRKCB/CD4/C5AR1/SLC11A1/PTGDR/GRIK2/PLN/JPH1/CCL8/C3AR1/STC1/HTR2A/CXCR4/TGM2/TRPM2/FPR1/S100A9/EDNRB/FPR3/CCL13/SNCA/CALB2* |
| G98 | GO:0098542 | Defense response to other organism | 275 | –0.416805817 | –1.602315996 | 0.00130039 | 0.023352669 | tags =26%, list =15%, signal =22% | *POLR3G/HERC5/APOBEC3C/POLR3A/ZNF175/TGFB1/TUSC2/HYAL2/CEBPB/BST2/MAPK3/AP1S3/TLR6/SPN/DDIT4/IL15/BATF2/TLR4/NLRC4/IL2RA/DOCK2/IL36RN/SERINC5/IFI44L/SERPINE1/IFNE/SPON2/MICA/TNFSF4/TLR2/UNC13D/EPHA2/EPPIN/HIST1H2BJ/RSAD2/TLR1/MPO/HIST1H2BK/IGJ/HIST1H2BC/BNIP3/TLR8/HIST2H2BE/TLR7/TNFSF8/VGF/IRF8/F2RL1/HAVCR2/ACP5/FGR/CLEC7A/LYZ/TREM1/PTPRC/LBP/CD86/CD4/C5AR1/GPAM/SLC11A1/IL6/CD28/SYK/STAB1/HCK/FCER1G/S100A9/CXCL6/IL33* |
| G98 | GO:0098742 | Cell-cell adhesion via plasma-membrane adhesion molecules | 152 | –0.574720009 | –2.072832235 | 0.001422475 | 0.023352669 | tags =39%, list =13%, signal =34% | *ROBO1/PCDHGB1/PCDHB15/CELSR3/FAT3/PCDHGA4/ITGA5/TENM4/TGFBR2/PCDHGC5/PCDHA7/CLSTN2/PCDHB14/PCDH1/PCDHGA3/NLGN1/AMIGO3/CADM1/PCDHGA2/RET/PCDHB6/PCDHB4/PLXNB3/PCDHB7/CELSR1/PCDHB5/PCDHB8/PCDHB2/CDH23/DSC2/PCDHA12/CDH2/PCDHB10/DSG2/ESAM/PCDHA13/PCDHB9/PCDHB3/SDK2/PCDHB12/PVRL4/CLDN14/CDH6/PCDHA3/PCDHA6/CADM3/PCDHA11/IL1RN/PCDHA10/CD84/ROBO2/PCDH10/CD209/PCDH7/PCDH9/CDH10/AMIGO2/BMP2* |
| G98 | GO:0097553 | Calcium ion transmembrane import into cytosol | 77 | –0.529888525 | –1.745406546 | 0.00154321 | 0.023352669 | tags =21%, list =6%, signal =20% | *FGF2/CORO1A/CHD7/JPH2/LYN/PLCG2/CCR5/PTPN6/BDKRB1/PTPRC/PLN/JPH1/HTR2A/TRPM2/SNCA* |
| G98 | GO:0097530 | Granulocyte migration | 63 | –0.744500813 | –2.36058548 | 0.001547988 | 0.023352669 | tags =48%, list =6%, signal =45% | *PREX1/CXCL2/RAC2/ITGA1/ITGB2/VAV3/ADAM8/IL1B/CD300A/CCL26/CCL22/NCKAP1L/CCL2/TREM1/LBP/C5AR1/IL1A/SYK/CCL8/CMKLR1/C3AR1/CXCL1/FCER1G/S100A9/CXCL3/CCL13/CD74/SCG2/IL8* |
| G98 | GO:0099024 | Plasma membrane invagination | 34 | –0.660524291 | –1.896926747 | 0.001623377 | 0.023352669 | tags =32%, list =7%, signal =30% | *ABCA1/CD300A/BIN2/F2RL1/NCKAP1L/TREM2/ITGA2/AIF1/FCGR1A/FCER1G* |
| G98 | GO:0098660 | Inorganic ion transmembrane transport | 469 | –0.352365709 | –1.402679237 | 0.004901961 | 0.03838876 | tags =25%, list =17%, signal =21% | *TMEM38B/MYO5A/ATP6V1G1/SLC23A2/TMEM38A/GAS6/CAPN3/SCN3B/SLC9A4/HTT/STK39/ATP7A/SLC36A1/CATSPER2/ATP6V1G2/SCNN1D/C19orf26/ATP6V0E1/ATP6V1A/SLC12A7/GPD1L/SLC46A1/ATP6V0A1/TGFB1/CACNA1A/AKAP9/SLC23A1/TTYH3/SLC12A4/ATP6V1E1/RNF207/DMD/KCNMB3/STIM2/ADRA2A/PLCG1/SLC6A8/ITPR2/EHD3/TRPC4/TRPV2/SLC4A3/KCND2/KCNQ5/HCN2/ITPR1/SLC11A2/AP000322.53/OPRL1/KCNMB1/ANO7/KCNAB2/ANO4/SLC26A1/ATP6AP1/ATP6V0C/SLC30A10/TRPV3/NCS1/DENND5B/ATP2B1/NDUFA4L2/KCNE1/SLC4A11/TTYH2/CACNA1H/DRD4/F2RL3/KCNRG/MCOLN2/SLC9A7/ATP1B1/FGF2/KCNH1/PKD1L1/KCNMA1/SLC37A2/KCNE4/CORO1A/SLC24A3/MCOLN3/ATP2A3/SLC9B1/ANO3/CHRNA9/CHD7/SLC4A4/ATP6V0D2/JPH2/LYN/TSPAN13/ATP5L2/C15orf48/PLCG2/GABRA5/CLCA2/KCNS3/CCR5/KCNQ3/SLC30A3/PTPN6/BDKRB1/PTPRC/SCN9A/SCN2A/SLC11A1/PLN/JPH1/KCNJ5/PTAFR/HTR2A/KCNC3/TRPM2/SNCA* |
| G98 | GO:0098655 | Cation transmembrane transport | 447 | –0.356570028 | –1.414685363 | 0.004920049 | 0.038460964 | tags =26%, list =17%, signal =22% | *ATP13A2/ATP6V1F/TMEM38B/MYO5A/ATP6V1G1/SLC23A2/TMEM38A/GAS6/CAPN3/SCN3B/SLC9A4/HOMER1/HTT/STK39/CHRNA7/ATP7A/SLC36A1/CATSPER2/ATP6V1G2/SCNN1D/C19orf26/ATP6V0E1/ATP6V1A/SLC12A7/GPD1L/SLC46A1/ATP6V0A1/TGFB1/CACNA1A/AKAP9/SLC23A1/SLC12A4/ATP13A3/ATP6V1E1/RNF207/DMD/KCNMB3/STIM2/ADRA2A/PLCG1/SLC41A2/SLC6A8/ITPR2/EHD3/TRPC4/TRPV2/KCND2/KCNQ5/HCN2/ITPR1/SLC11A2/AP000322.53/OPRL1/KCNMB1/KCNAB2/CHRNE/ATP6AP1/ATP6V0C/SLC30A10/TRPV3/NCS1/DENND5B/P2RX6/ATP2B1/P2RX1/NDUFA4L2/KCNE1/SLC4A11/CACNA1H/DRD4/F2RL3/KCNRG/MCOLN2/SLC9A7/ATP1B1/ATP8A1/FGF2/KCNH1/PKD1L1/KCNMA1/MMP9/CTSS/KCNE4/CORO1A/SLC24A3/MCOLN3/ATP2A3/SLC9B1/CHRNA9/CHD7/SLC4A4/ATP6V0D2/JPH2/LYN/TSPAN13/ATP5L2/C15orf48/PLCG2/KCNS3/CCR5/KCNQ3/SLC30A3/PTPN6/BDKRB1/PTPRC/SCN9A/SCN2A/SLC11A1/PLN/JPH1/KCNJ5/HTR2A/KCNC3/TRPM2/SNCA* |
| G98 | GO:0098662 | Inorganic cation transmembrane transport | 416 | –0.350546522 | –1.386849187 | 0.006203474 | 0.04477101 | tags =25%, list =17%, signal =21% | *TMEM38B/MYO5A/ATP6V1G1/SLC23A2/TMEM38A/GAS6/CAPN3/SCN3B/SLC9A4/HTT/STK39/ATP7A/SLC36A1/CATSPER2/ATP6V1G2/SCNN1D/C19orf26/ATP6V0E1/ATP6V1A/SLC12A7/GPD1L/SLC46A1/ATP6V0A1/TGFB1/CACNA1A/AKAP9/SLC23A1/SLC12A4/ATP6V1E1/RNF207/DMD/KCNMB3/STIM2/ADRA2A/PLCG1/SLC6A8/ITPR2/EHD3/TRPC4/TRPV2/KCND2/KCNQ5/HCN2/ITPR1/SLC11A2/AP000322.53/OPRL1/KCNMB1/KCNAB2/ATP6AP1/ATP6V0C/SLC30A10/TRPV3/NCS1/DENND5B/ATP2B1/NDUFA4L2/KCNE1/SLC4A11/CACNA1H/DRD4/F2RL3/KCNRG/MCOLN2/SLC9A7/ATP1B1/FGF2/KCNH1/PKD1L1/KCNMA1/KCNE4/CORO1A/SLC24A3/MCOLN3/ATP2A3/SLC9B1/CHRNA9/CHD7/SLC4A4/ATP6V0D2/JPH2/LYN/TSPAN13/ATP5L2/C15orf48/PLCG2/KCNS3/CCR5/KCNQ3/SLC30A3/PTPN6/BDKRB1/PTPRC/SCN9A/SCN2A/SLC11A1/PLN/JPH1/KCNJ5/HTR2A/KCNC3/TRPM2/SNCA* |
| G99 | GO:1900046 | Regulation of hemostasis | 56 | –0.544751717 | –1.700063657 | 0.00155521 | 0.023352669 | tags =43%, list =13%, signal =38% | *PRKG1/GP1BA/PDGFA/TLR4/SERPINE1/PDGFB/ENPP4/PLAUR/FAM46A/PLAT/FAP/F3/SERPINE2/PLAU/VTN/LYN/APOE/F2RL1/PLEK/SYK/SERPINB2/FCER1G/S100A9* |
| G99 | GO:1900372 | Negative regulation of purine nucleotide biosynthetic process | 20 | –0.657442394 | –1.690128601 | 0.005084746 | 0.038932682 | tags =40%, list =14%, signal =34% | *ADRA2A/OPRL1/APLP1/DRD4/PID1/EDNRA/EDNRB* |

Group: group ID; terms with the same group ID indicate high semantical similarities among them; ID: gene set id; description: description of the gene set; set size: the number of genes in the gene set; enrichment score: the degree to which a gene set is over-represented at the top (up-regulated) or bottom (down-regulated) of the list of genes ranked by expression fold change; NES: normalized enrichment score; P value: the P value of the enrichment score calculated using permutation test; P.adjust: adjusted P value for multiple hypothesis testing; leading\_edge: “tags” indicates the percentage of genes contributing to the enrichment score; “list” indicates where in the list the enrichment score is attained; “Signal” indicates enrichment signal strength; core\_enrichment: the core enriched genes that contribute to the enrichment. GO, gene ontology.