Supplementary Table.5 GO and KEGG functional analysis of CCL22 correlated genes

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Description | pvalue | p.adju | qvalue | geneID | Count |
| BP | T cell activation | 2.47036E-13 | 2.6754E-10 | 1.58623E-10 | CD1C/CD5/CD28/CCR6/CCR7/FUT7/NCKAP1L/IRF4/SPN/TESPA1/FOXP3/SASH3/JAML/BTLA/CCR2 | 15 |
| BP | lymphocyte differentiation | 2.49618E-12 | 1.35168E-09 | 8.01406E-10 | CD28/CCR6/CCR7/FLT3/FUT7/NCKAP1L/IRF4/SPN/TESPA1/IKZF1/FOXP3/SASH3/CCR2 | 13 |
| BP | T cell differentiation | 1.45946E-11 | 5.26866E-09 | 3.12376E-09 | CD28/CCR6/CCR7/FUT7/NCKAP1L/IRF4/SPN/TESPA1/FOXP3/SASH3/CCR2 | 11 |
| BP | regulation of T cell activation | 2.59852E-10 | 7.03549E-08 | 4.17131E-08 | CD5/CD28/CCR7/NCKAP1L/IRF4/SPN/TESPA1/FOXP3/SASH3/BTLA/CCR2 | 11 |
| BP | leukocyte cell-cell adhesion | 5.4935E-10 | 1.18989E-07 | 7.05481E-08 | CD5/CD28/CCR7/NCKAP1L/SELPLG/SPN/TESPA1/FOXP3/SASH3/BTLA/CCR2 | 11 |
| BP | positive regulation of T cell activation | 1.62323E-09 | 2.77154E-07 | 1.64323E-07 | CD5/CD28/CCR7/NCKAP1L/TESPA1/FOXP3/SASH3/BTLA/CCR2 | 9 |
| BP | alpha-beta T cell activation | 1.79139E-09 | 2.77154E-07 | 1.64323E-07 | CD28/FUT7/NCKAP1L/IRF4/SPN/FOXP3/SASH3/CCR2 | 8 |
| BP | chemokine-mediated signaling pathway | 2.18817E-09 | 2.96224E-07 | 1.7563E-07 | CXCR5/CCR4/CCR6/CCR7/CCR8/CCL17/CCR2 | 7 |
| BP | positive regulation of leukocyte cell-cell adhesion | 3.17208E-09 | 3.72101E-07 | 2.20617E-07 | CD5/CD28/CCR7/NCKAP1L/TESPA1/FOXP3/SASH3/BTLA/CCR2 | 9 |
| BP | regulation of leukocyte cell-cell adhesion | 3.43584E-09 | 3.72101E-07 | 2.20617E-07 | CD5/CD28/CCR7/NCKAP1L/SPN/TESPA1/FOXP3/SASH3/BTLA/CCR2 | 10 |
| BP | response to chemokine | 4.35361E-09 | 3.92913E-07 | 2.32956E-07 | CXCR5/CCR4/CCR6/CCR7/CCR8/CCL17/CCR2 | 7 |
| BP | cellular response to chemokine | 4.35361E-09 | 3.92913E-07 | 2.32956E-07 | CXCR5/CCR4/CCR6/CCR7/CCR8/CCL17/CCR2 | 7 |
| BP | positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 5.39447E-09 | 4.49401E-07 | 2.66448E-07 | CD1B/CD1C/CD1E/CD28/FOXP3/SASH3/CCR2 | 7 |
| BP | positive regulation of adaptive immune response | 7.59849E-09 | 5.87797E-07 | 3.48502E-07 | CD1B/CD1C/CD1E/CD28/FOXP3/SASH3/CCR2 | 7 |
| BP | homeostasis of number of cells | 9.11102E-09 | 6.57815E-07 | 3.90015E-07 | CCR4/CCR7/FLT3/NCKAP1L/RASSF2/IKZF1/FOXP3/SASH3/CCR2 | 9 |
| BP | positive regulation of cell-cell adhesion | 1.24476E-08 | 8.42549E-07 | 4.99543E-07 | CD5/CD28/CCR7/NCKAP1L/TESPA1/FOXP3/SASH3/BTLA/CCR2 | 9 |
| BP | adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 1.76837E-08 | 1.12655E-06 | 6.67929E-07 | CD1B/CD1C/CD1E/CD28/CCR6/IRF4/SPN/FOXP3/SASH3/CCR2 | 10 |
| BP | regulation of T cell mediated immunity | 2.12315E-08 | 1.27743E-06 | 7.57381E-07 | CD1B/CD1C/CD1E/FOXP3/SASH3/CCR2 | 6 |
| BP | regulation of lymphocyte activation | 2.43023E-08 | 1.38523E-06 | 8.21298E-07 | CD5/CD28/CCR7/NCKAP1L/IRF4/SPN/TESPA1/FOXP3/SASH3/BTLA/CCR2 | 11 |
| BP | CD4-positive, alpha-beta T cell differentiation | 2.97721E-08 | 1.61216E-06 | 9.55841E-07 | FUT7/NCKAP1L/IRF4/SPN/FOXP3/SASH3 | 6 |
| BP | regulation of cell-cell adhesion | 4.9885E-08 | 2.4557E-06 | 1.45597E-06 | CD5/CD28/CCR7/NCKAP1L/SPN/TESPA1/FOXP3/SASH3/BTLA/CCR2 | 10 |
| BP | positive regulation of cell adhesion | 4.9885E-08 | 2.4557E-06 | 1.45597E-06 | CD5/CD28/CCR7/NCKAP1L/SPOCK2/TESPA1/FOXP3/SASH3/BTLA/CCR2 | 10 |
| BP | regulation of T cell differentiation | 5.34297E-08 | 2.51584E-06 | 1.49163E-06 | CD28/NCKAP1L/IRF4/TESPA1/FOXP3/SASH3/CCR2 | 7 |
| BP | cell chemotaxis | 5.66018E-08 | 2.55415E-06 | 1.51435E-06 | CXCR5/CCR4/CCR6/CCR7/CCR8/NCKAP1L/CCL17/JAML/CCR2 | 9 |
| BP | regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 7.14748E-08 | 3.09629E-06 | 1.83577E-06 | CD1B/CD1C/CD1E/CD28/FOXP3/SASH3/CCR2 | 7 |
| BP | regulation of lymphocyte mediated immunity | 8.61693E-08 | 3.58928E-06 | 2.12807E-06 | CD1B/CD1C/CD1E/CD28/FOXP3/SASH3/CCR2 | 7 |
| BP | CD4-positive, alpha-beta T cell activation | 1.10774E-07 | 4.41382E-06 | 2.61693E-06 | FUT7/NCKAP1L/IRF4/SPN/FOXP3/SASH3 | 6 |
| BP | T cell selection | 1.15101E-07 | 4.41382E-06 | 2.61693E-06 | CD28/CCR7/IRF4/SPN/FOXP3 | 5 |
| BP | regulation of alpha-beta T cell activation | 1.18191E-07 | 4.41382E-06 | 2.61693E-06 | CD28/NCKAP1L/IRF4/FOXP3/SASH3/CCR2 | 6 |
| BP | positive regulation of lymphocyte activation | 1.26262E-07 | 4.48026E-06 | 2.65632E-06 | CD5/CD28/CCR7/NCKAP1L/TESPA1/FOXP3/SASH3/BTLA/CCR2 | 9 |
| BP | positive regulation of T cell mediated immunity | 1.28244E-07 | 4.48026E-06 | 2.65632E-06 | CD1B/CD1C/CD1E/FOXP3/SASH3 | 5 |
| BP | regulation of adaptive immune response | 1.40355E-07 | 4.75015E-06 | 2.81634E-06 | CD1B/CD1C/CD1E/CD28/FOXP3/SASH3/CCR2 | 7 |
| BP | alpha-beta T cell differentiation | 1.93567E-07 | 6.35251E-06 | 3.76637E-06 | FUT7/NCKAP1L/IRF4/SPN/FOXP3/SASH3 | 6 |
| BP | regulation of lymphocyte differentiation | 2.03872E-07 | 6.49392E-06 | 3.85021E-06 | CD28/NCKAP1L/IRF4/TESPA1/FOXP3/SASH3/CCR2 | 7 |
| BP | regulation of interleukin-2 production | 2.34206E-07 | 7.24701E-06 | 4.29671E-06 | CD28/IRF4/FOXP3/SASH3/CCR2 | 5 |
| BP | positive regulation of lymphocyte mediated immunity | 2.43955E-07 | 7.33899E-06 | 4.35125E-06 | CD1B/CD1C/CD1E/CD28/FOXP3/SASH3 | 6 |
| BP | T cell mediated immunity | 2.58105E-07 | 7.55481E-06 | 4.47921E-06 | CD1B/CD1C/CD1E/FOXP3/SASH3/CCR2 | 6 |
| BP | positive regulation of interleukin-4 production | 3.01339E-07 | 8.58816E-06 | 5.09188E-06 | CD28/IRF4/FOXP3/SASH3 | 4 |
| BP | regulation of leukocyte differentiation | 3.52069E-07 | 9.77669E-06 | 5.79655E-06 | CD28/NCKAP1L/IRF4/RASSF2/TESPA1/FOXP3/SASH3/CCR2 | 8 |
| BP | leukocyte migration | 3.62296E-07 | 9.80916E-06 | 5.8158E-06 | CXCR5/CCR6/CCR7/FUT7/NCKAP1L/CCL17/SELPLG/SPN/JAML/CCR2 | 10 |
| BP | positive regulation of leukocyte activation | 3.75273E-07 | 9.9127E-06 | 5.87719E-06 | CD5/CD28/CCR7/NCKAP1L/TESPA1/FOXP3/SASH3/BTLA/CCR2 | 9 |
| BP | regulation of cytokine biosynthetic process | 3.97467E-07 | 1.0249E-05 | 6.07656E-06 | CD28/IRF4/LTB/SPN/FOXP3/CCR2 | 6 |
| BP | interleukin-2 production | 4.72085E-07 | 1.16197E-05 | 6.88927E-06 | CD28/IRF4/FOXP3/SASH3/CCR2 | 5 |
| BP | positive regulation of alpha-beta T cell activation | 4.72085E-07 | 1.16197E-05 | 6.88927E-06 | CD28/NCKAP1L/FOXP3/SASH3/CCR2 | 5 |
| BP | positive regulation of cell activation | 5.08123E-07 | 1.22288E-05 | 7.25041E-06 | CD5/CD28/CCR7/NCKAP1L/TESPA1/FOXP3/SASH3/BTLA/CCR2 | 9 |
| BP | regulation of interleukin-4 production | 5.92845E-07 | 1.39576E-05 | 8.27542E-06 | CD28/IRF4/FOXP3/SASH3 | 4 |
| BP | cytokine biosynthetic process | 6.22652E-07 | 1.43475E-05 | 8.50656E-06 | CD28/IRF4/LTB/SPN/FOXP3/CCR2 | 6 |
| BP | cytokine metabolic process | 6.5308E-07 | 1.45744E-05 | 8.64109E-06 | CD28/IRF4/LTB/SPN/FOXP3/CCR2 | 6 |
| BP | regulation of leukocyte mediated immunity | 6.59415E-07 | 1.45744E-05 | 8.64109E-06 | CD1B/CD1C/CD1E/CD28/FOXP3/SASH3/CCR2 | 7 |
| BP | positive regulation of cytokine biosynthetic process | 6.97985E-07 | 1.51184E-05 | 8.96359E-06 | CD28/IRF4/LTB/SPN/CCR2 | 5 |
| BP | T cell differentiation in thymus | 8.69809E-07 | 1.84707E-05 | 1.09512E-05 | CD28/CCR6/CCR7/TESPA1/FOXP3 | 5 |
| BP | positive regulation of interleukin-2 production | 9.20646E-07 | 1.91742E-05 | 1.13683E-05 | CD28/IRF4/SASH3/CCR2 | 4 |
| BP | B cell activation | 9.45489E-07 | 1.93201E-05 | 1.14548E-05 | CXCR5/CD28/CCR6/FLT3/NCKAP1L/PRKCB/FOXP3/SASH3 | 8 |
| BP | positive regulation of leukocyte mediated immunity | 9.85902E-07 | 1.97728E-05 | 1.17232E-05 | CD1B/CD1C/CD1E/CD28/FOXP3/SASH3 | 6 |
| BP | positive regulation of immune effector process | 1.06884E-06 | 2.10464E-05 | 1.24783E-05 | CD1B/CD1C/CD1E/CD28/FOXP3/SASH3/CCR2 | 7 |
| BP | leukocyte chemotaxis | 1.3629E-06 | 2.59747E-05 | 1.54003E-05 | CXCR5/CCR6/CCR7/NCKAP1L/CCL17/JAML/CCR2 | 7 |
| BP | interleukin-4 production | 1.36709E-06 | 2.59747E-05 | 1.54003E-05 | CD28/IRF4/FOXP3/SASH3 | 4 |
| BP | regulation of immune effector process | 1.77138E-06 | 3.30759E-05 | 1.96105E-05 | CD1B/CD1C/CD1E/CD28/IRF4/CFP/FOXP3/SASH3/CCR2 | 9 |
| BP | regulation of hemopoiesis | 2.38935E-06 | 4.38587E-05 | 2.60036E-05 | CD28/NCKAP1L/IRF4/PRKCB/RASSF2/TESPA1/FOXP3/SASH3/CCR2 | 9 |
| BP | lymphocyte mediated immunity | 2.44166E-06 | 4.40719E-05 | 2.613E-05 | CD1B/CD1C/CD1E/CD28/CCR6/FOXP3/SASH3/CCR2 | 8 |
| BP | regulation of T cell proliferation | 2.50058E-06 | 4.43955E-05 | 2.63219E-05 | CD28/NCKAP1L/SPN/FOXP3/SASH3/CCR2 | 6 |
| BP | regulation of tumor necrosis factor production | 2.89604E-06 | 5.05873E-05 | 2.9993E-05 | SLAMF1/SPN/LILRA4/FOXP3/SASH3/CCR2 | 6 |
| BP | tumor necrosis factor production | 3.22492E-06 | 5.45718E-05 | 3.23553E-05 | SLAMF1/SPN/LILRA4/FOXP3/SASH3/CCR2 | 6 |
| BP | regulation of tumor necrosis factor superfamily cytokine production | 3.22492E-06 | 5.45718E-05 | 3.23553E-05 | SLAMF1/SPN/LILRA4/FOXP3/SASH3/CCR2 | 6 |
| BP | tumor necrosis factor superfamily cytokine production | 3.84034E-06 | 6.3986E-05 | 3.7937E-05 | SLAMF1/SPN/LILRA4/FOXP3/SASH3/CCR2 | 6 |
| BP | positive regulation of T cell proliferation | 3.97327E-06 | 6.51978E-05 | 3.86554E-05 | CD28/NCKAP1L/FOXP3/SASH3/CCR2 | 5 |
| BP | G protein-coupled purinergic nucleotide receptor signaling pathway | 4.20135E-06 | 6.79114E-05 | 4.02644E-05 | P2RY14/P2RY10/P2RY13 | 3 |
| BP | lymphocyte proliferation | 4.92881E-06 | 7.84986E-05 | 4.65414E-05 | CD28/FLT3/NCKAP1L/SPN/FOXP3/SASH3/CCR2 | 7 |
| BP | mononuclear cell proliferation | 5.17161E-06 | 8.11717E-05 | 4.81263E-05 | CD28/FLT3/NCKAP1L/SPN/FOXP3/SASH3/CCR2 | 7 |
| BP | regulation of CD4-positive, alpha-beta T cell differentiation | 5.80723E-06 | 8.98461E-05 | 5.32693E-05 | NCKAP1L/IRF4/FOXP3/SASH3 | 4 |
| BP | lymphocyte activation involved in immune response | 5.89901E-06 | 8.99807E-05 | 5.33491E-05 | CD1C/CD28/CCR6/IRF4/SPN/FOXP3 | 6 |
| BP | T cell proliferation | 6.48269E-06 | 9.75105E-05 | 5.78135E-05 | CD28/NCKAP1L/SPN/FOXP3/SASH3/CCR2 | 6 |
| BP | antigen processing and presentation via MHC class Ib | 8.18291E-06 | 0.000121399 | 7.19766E-05 | CD1B/CD1C/CD1E | 3 |
| BP | lymphocyte migration | 8.52911E-06 | 0.000124825 | 7.4008E-05 | CCR6/CCR7/CCL17/SPN/CCR2 | 5 |
| BP | regulation of interleukin-10 production | 8.7335E-06 | 0.000126112 | 7.4771E-05 | CD28/IRF4/FOXP3/SASH3 | 4 |
| BP | leukocyte proliferation | 8.95272E-06 | 0.000127576 | 7.56394E-05 | CD28/FLT3/NCKAP1L/SPN/FOXP3/SASH3/CCR2 | 7 |
| BP | interferon-gamma production | 9.30602E-06 | 0.000130889 | 7.76032E-05 | CCR7/SPN/FOXP3/SASH3/CCR2 | 5 |
| BP | CD4-positive, alpha-beta T cell lineage commitment | 9.91885E-06 | 0.000137719 | 8.16531E-05 | IRF4/SPN/FOXP3 | 3 |
| BP | interleukin-10 production | 1.09417E-05 | 0.000149998 | 8.89332E-05 | CD28/IRF4/FOXP3/SASH3 | 4 |
| BP | T cell costimulation | 1.17617E-05 | 0.000159224 | 9.4403E-05 | CD5/CD28/CCR7/BTLA | 4 |
| BP | lymphocyte costimulation | 1.26261E-05 | 0.000168816 | 0.00010009 | CD5/CD28/CCR7/BTLA | 4 |
| BP | regulation of lymphocyte proliferation | 1.30535E-05 | 0.000172402 | 0.000102216 | CD28/NCKAP1L/SPN/FOXP3/SASH3/CCR2 | 6 |
| BP | regulation of mononuclear cell proliferation | 1.3414E-05 | 0.000175028 | 0.000103773 | CD28/NCKAP1L/SPN/FOXP3/SASH3/CCR2 | 6 |
| BP | positive regulation of cytosolic calcium ion concentration | 1.39258E-05 | 0.000177366 | 0.00010516 | CXCR5/CCR4/CCR6/CCR7/CCR8/P2RY10/CCR2 | 7 |
| BP | alpha-beta T cell lineage commitment | 1.40845E-05 | 0.000177366 | 0.00010516 | IRF4/SPN/FOXP3 | 3 |
| BP | regulation of interleukin-2 biosynthetic process | 1.40845E-05 | 0.000177366 | 0.00010516 | CD28/IRF4/FOXP3 | 3 |
| BP | CD4-positive or CD8-positive, alpha-beta T cell lineage commitment | 1.65407E-05 | 0.000200756 | 0.000119027 | IRF4/SPN/FOXP3 | 3 |
| BP | cellular extravasation | 1.65582E-05 | 0.000200756 | 0.000119027 | SELPLG/SPN/JAML/CCR2 | 4 |
| BP | regulation of CD4-positive, alpha-beta T cell activation | 1.65582E-05 | 0.000200756 | 0.000119027 | NCKAP1L/IRF4/FOXP3/SASH3 | 4 |
| BP | cellular calcium ion homeostasis | 1.67488E-05 | 0.000200756 | 0.000119027 | CXCR5/CCR4/CCR6/CCR7/CCR8/PRKCB/P2RY10/CCR2 | 8 |
| BP | calcium-mediated signaling | 1.70354E-05 | 0.000200756 | 0.000119027 | CXCR5/CCR4/CCR6/CCR7/CCR8/CCR2 | 6 |
| BP | positive regulation of leukocyte migration | 1.70541E-05 | 0.000200756 | 0.000119027 | CCR6/CCR7/NCKAP1L/SPN/CCR2 | 5 |
| BP | positive regulation of lymphocyte proliferation | 1.83823E-05 | 0.000211913 | 0.000125642 | CD28/NCKAP1L/FOXP3/SASH3/CCR2 | 5 |
| BP | positive regulation of cytokine production | 1.83932E-05 | 0.000211913 | 0.000125642 | CD28/CCR7/IRF4/LTB/SPN/FOXP3/SASH3/CCR2 | 8 |
| BP | regulation of alpha-beta T cell differentiation | 1.88306E-05 | 0.000212881 | 0.000126216 | NCKAP1L/IRF4/FOXP3/SASH3 | 4 |
| BP | regulation of leukocyte proliferation | 1.888E-05 | 0.000212881 | 0.000126216 | CD28/NCKAP1L/SPN/FOXP3/SASH3/CCR2 | 6 |
| BP | positive regulation of mononuclear cell proliferation | 1.9076E-05 | 0.000212881 | 0.000126216 | CD28/NCKAP1L/FOXP3/SASH3/CCR2 | 5 |
| BP | purinergic nucleotide receptor signaling pathway | 1.92634E-05 | 0.000212881 | 0.000126216 | P2RY14/P2RY10/P2RY13 | 3 |
| BP | calcium ion homeostasis | 2.04815E-05 | 0.000224055 | 0.000132841 | CXCR5/CCR4/CCR6/CCR7/CCR8/PRKCB/P2RY10/CCR2 | 8 |
| BP | positive regulation of chemotaxis | 2.20571E-05 | 0.000236409 | 0.000140166 | CCR4/CCR6/CCR7/NCKAP1L/CCR2 | 5 |
| BP | antigen processing and presentation of endogenous antigen | 2.22657E-05 | 0.000236409 | 0.000140166 | CD1B/CD1C/CD1E | 3 |
| BP | interleukin-2 biosynthetic process | 2.22657E-05 | 0.000236409 | 0.000140166 | CD28/IRF4/FOXP3 | 3 |
| BP | positive regulation of leukocyte proliferation | 2.53889E-05 | 0.000266953 | 0.000158275 | CD28/NCKAP1L/FOXP3/SASH3/CCR2 | 5 |
| BP | cellular divalent inorganic cation homeostasis | 2.83908E-05 | 0.000292412 | 0.00017337 | CXCR5/CCR4/CCR6/CCR7/CCR8/PRKCB/P2RY10/CCR2 | 8 |
| BP | regulation of cytosolic calcium ion concentration | 2.87016E-05 | 0.000292412 | 0.00017337 | CXCR5/CCR4/CCR6/CCR7/CCR8/P2RY10/CCR2 | 7 |
| BP | dendritic cell chemotaxis | 2.91602E-05 | 0.000292412 | 0.00017337 | CCR6/CCR7/CCR2 | 3 |
| BP | G protein-coupled purinergic receptor signaling pathway | 2.91602E-05 | 0.000292412 | 0.00017337 | P2RY14/P2RY10/P2RY13 | 3 |
| BP | positive regulation of antigen receptor-mediated signaling pathway | 2.91602E-05 | 0.000292412 | 0.00017337 | CCR7/PRKCB/TESPA1 | 3 |
| BP | leukocyte tethering or rolling | 3.30781E-05 | 0.000328657 | 0.000194859 | SELPLG/SPN/CCR2 | 3 |
| BP | positive regulation of T cell mediated cytotoxicity | 3.73267E-05 | 0.000364187 | 0.000215925 | CD1B/CD1C/CD1E | 3 |
| BP | T cell lineage commitment | 3.73267E-05 | 0.000364187 | 0.000215925 | IRF4/SPN/FOXP3 | 3 |
| BP | dendritic cell migration | 4.19184E-05 | 0.000405336 | 0.000240322 | CCR6/CCR7/CCR2 | 3 |
| BP | positive regulation of T cell differentiation | 5.5993E-05 | 0.000536641 | 0.000318172 | NCKAP1L/TESPA1/FOXP3/SASH3 | 4 |
| BP | positive regulation of CD4-positive, alpha-beta T cell differentiation | 5.78767E-05 | 0.000549829 | 0.000325991 | NCKAP1L/FOXP3/SASH3 | 3 |
| BP | regulation of T cell cytokine production | 6.39647E-05 | 0.00060078 | 0.000356199 | FOXP3/SASH3/CCR2 | 3 |
| BP | leukocyte homeostasis | 6.43495E-05 | 0.00060078 | 0.000356199 | FLT3/NCKAP1L/FOXP3/CCR2 | 4 |
| BP | positive regulation of leukocyte chemotaxis | 6.73267E-05 | 0.000623203 | 0.000369494 | CCR6/CCR7/NCKAP1L/CCR2 | 4 |
| BP | purinergic receptor signaling pathway | 7.04573E-05 | 0.000646654 | 0.000383398 | P2RY14/P2RY10/P2RY13 | 3 |
| BP | regulation of T cell mediated cytotoxicity | 7.73663E-05 | 0.000704098 | 0.000417456 | CD1B/CD1C/CD1E | 3 |
| BP | positive T cell selection | 8.47037E-05 | 0.000758133 | 0.000449493 | IRF4/SPN/FOXP3 | 3 |
| BP | regulatory T cell differentiation | 8.47037E-05 | 0.000758133 | 0.000449493 | CD28/FUT7/FOXP3 | 3 |
| BP | positive regulation of lymphocyte differentiation | 9.10584E-05 | 0.00080833 | 0.000479255 | NCKAP1L/TESPA1/FOXP3/SASH3 | 4 |
| BP | positive regulation of interleukin-10 production | 0.000100711 | 0.000879594 | 0.000521507 | CD28/IRF4/SASH3 | 3 |
| BP | positive regulation of CD4-positive, alpha-beta T cell activation | 0.000100711 | 0.000879594 | 0.000521507 | NCKAP1L/FOXP3/SASH3 | 3 |
| BP | regulation of interferon-gamma production | 0.000120357 | 0.001042777 | 0.000618257 | CCR7/FOXP3/SASH3/CCR2 | 4 |
| BP | regulation of leukocyte migration | 0.000129933 | 0.001116809 | 0.000662151 | CCR6/CCR7/NCKAP1L/SPN/CCR2 | 5 |
| BP | antigen receptor-mediated signaling pathway | 0.000134221 | 0.001140527 | 0.000676213 | CD28/CCR7/NCKAP1L/PRKCB/TESPA1/FOXP3 | 6 |
| BP | neutrophil chemotaxis | 0.000134799 | 0.001140527 | 0.000676213 | CCR7/NCKAP1L/CCL17/JAML | 4 |
| BP | T cell cytokine production | 0.000138379 | 0.001161736 | 0.000688788 | FOXP3/SASH3/CCR2 | 3 |
| BP | T cell activation involved in immune response | 0.000145099 | 0.001208785 | 0.000716683 | CD1C/IRF4/SPN/FOXP3 | 4 |
| BP | positive regulation of response to external stimulus | 0.000151226 | 0.001250216 | 0.000741247 | CD28/CCR4/CCR6/CCR7/NCKAP1L/CCR2 | 6 |
| BP | dendritic cell differentiation | 0.000160222 | 0.001314546 | 0.000779388 | CCR7/FLT3/IRF4 | 3 |
| BP | immune response-activating cell surface receptor signaling pathway | 0.000167667 | 0.001365288 | 0.000809472 | CD28/CCR7/NCKAP1L/PRKCB/TESPA1/CLEC10A/FOXP3 | 7 |
| BP | myeloid leukocyte migration | 0.000179328 | 0.001449348 | 0.000859311 | CCR7/NCKAP1L/CCL17/JAML/CCR2 | 5 |
| BP | leukocyte adhesion to vascular endothelial cell | 0.00018419 | 0.001466749 | 0.000869628 | SELPLG/SPN/CCR2 | 3 |
| BP | regulation of T cell migration | 0.00018419 | 0.001466749 | 0.000869628 | CCR6/SPN/CCR2 | 3 |
| BP | regulation of leukocyte chemotaxis | 0.00019206 | 0.001518256 | 0.000900166 | CCR6/CCR7/NCKAP1L/CCR2 | 4 |
| BP | regulation of chemotaxis | 0.00020885 | 0.001639019 | 0.000971766 | CCR4/CCR6/CCR7/NCKAP1L/CCR2 | 5 |
| BP | neutrophil migration | 0.000219253 | 0.001698864 | 0.001007248 | CCR7/NCKAP1L/CCL17/JAML | 4 |
| BP | somatic recombination of immunoglobulin genes involved in immune response | 0.000224319 | 0.001698864 | 0.001007248 | CD28/CCR6/FOXP3 | 3 |
| BP | somatic diversification of immunoglobulins involved in immune response | 0.000224319 | 0.001698864 | 0.001007248 | CD28/CCR6/FOXP3 | 3 |
| BP | isotype switching | 0.000224319 | 0.001698864 | 0.001007248 | CD28/CCR6/FOXP3 | 3 |
| BP | positive regulation of alpha-beta T cell differentiation | 0.000224319 | 0.001698864 | 0.001007248 | NCKAP1L/FOXP3/SASH3 | 3 |
| BP | T cell mediated cytotoxicity | 0.000253981 | 0.00191015 | 0.001132519 | CD1B/CD1C/CD1E | 3 |
| BP | granulocyte chemotaxis | 0.000257018 | 0.001919657 | 0.001138155 | CCR7/NCKAP1L/CCL17/JAML | 4 |
| BP | regulation of phosphatidylinositol 3-kinase signaling | 0.000265098 | 0.001966443 | 0.001165894 | CD28/FLT3/PIK3R5/PPP1R16B | 4 |
| BP | vestibulocochlear nerve development | 0.000275561 | 0.002002905 | 0.001187512 | DCANP1/TIFAB | 2 |
| BP | peristalsis | 0.000275561 | 0.002002905 | 0.001187512 | DCANP1/TIFAB | 2 |
| BP | learned vocalization behavior or vocal learning | 0.000275561 | 0.002002905 | 0.001187512 | DCANP1/TIFAB | 2 |
| BP | somatic recombination of immunoglobulin gene segments | 0.000303049 | 0.002188014 | 0.001297263 | CD28/CCR6/FOXP3 | 3 |
| BP | cellular defense response | 0.000320666 | 0.002284747 | 0.001354615 | CCR6/SPN/CCR2 | 3 |
| BP | negative regulation of interleukin-6 production | 0.000320666 | 0.002284747 | 0.001354615 | NCKAP1L/SLAMF1/FOXP3 | 3 |
| BP | positive regulation of T cell differentiation in thymus | 0.000336257 | 0.002349457 | 0.001392981 | TESPA1/FOXP3 | 2 |
| BP | negative thymic T cell selection | 0.000336257 | 0.002349457 | 0.001392981 | CD28/CCR7 | 2 |
| BP | regulation of relaxation of muscle | 0.000336257 | 0.002349457 | 0.001392981 | DCANP1/TIFAB | 2 |
| BP | regulation of interleukin-12 production | 0.000338931 | 0.002352964 | 0.00139506 | CCR7/LTB/SLAMF1 | 3 |
| BP | regulation of phosphatidylinositol 3-kinase activity | 0.000357854 | 0.002468506 | 0.001463565 | CCR7/FLT3/PIK3R5 | 3 |
| BP | positive regulation of leukocyte mediated cytotoxicity | 0.000377444 | 0.002554822 | 0.001514741 | CD1B/CD1C/CD1E | 3 |
| BP | immunoglobulin production involved in immunoglobulin mediated immune response | 0.000377444 | 0.002554822 | 0.001514741 | CD28/CCR6/FOXP3 | 3 |
| BP | interleukin-12 production | 0.000377444 | 0.002554822 | 0.001514741 | CCR7/LTB/SLAMF1 | 3 |
| BP | positive regulation of inflammatory response to antigenic stimulus | 0.00040286 | 0.002644229 | 0.00156775 | CD28/CCR7 | 2 |
| BP | trigeminal nerve development | 0.00040286 | 0.002644229 | 0.00156775 | DCANP1/TIFAB | 2 |
| BP | negative T cell selection | 0.00040286 | 0.002644229 | 0.00156775 | CD28/CCR7 | 2 |
| BP | saliva secretion | 0.00040286 | 0.002644229 | 0.00156775 | DCANP1/TIFAB | 2 |
| BP | regulation of isotype switching to IgG isotypes | 0.00040286 | 0.002644229 | 0.00156775 | CD28/FOXP3 | 2 |
| BP | regulation of production of molecular mediator of immune response | 0.000409378 | 0.00267082 | 0.001583516 | CD28/FOXP3/SASH3/CCR2 | 4 |
| BP | T-helper cell differentiation | 0.000418666 | 0.002715063 | 0.001609747 | IRF4/SPN/FOXP3 | 3 |
| BP | granulocyte migration | 0.000432133 | 0.002785714 | 0.001651636 | CCR7/NCKAP1L/CCL17/JAML | 4 |
| BP | CD4-positive, alpha-beta T cell differentiation involved in immune response | 0.000462677 | 0.002964967 | 0.001757914 | IRF4/SPN/FOXP3 | 3 |
| BP | positive regulation of leukocyte differentiation | 0.000467941 | 0.002975707 | 0.001764282 | NCKAP1L/TESPA1/FOXP3/SASH3 | 4 |
| BP | auditory behavior | 0.000475344 | 0.002975707 | 0.001764282 | DCANP1/TIFAB | 2 |
| BP | positive regulation of interleukin-2 biosynthetic process | 0.000475344 | 0.002975707 | 0.001764282 | CD28/IRF4 | 2 |
| BP | isotype switching to IgG isotypes | 0.000475344 | 0.002975707 | 0.001764282 | CD28/FOXP3 | 2 |
| BP | alpha-beta T cell activation involved in immune response | 0.000485752 | 0.003006113 | 0.001782309 | IRF4/SPN/FOXP3 | 3 |
| BP | alpha-beta T cell differentiation involved in immune response | 0.000485752 | 0.003006113 | 0.001782309 | IRF4/SPN/FOXP3 | 3 |
| BP | myeloid cell homeostasis | 0.000505818 | 0.003100259 | 0.001838128 | NCKAP1L/IKZF1/FOXP3/CCR2 | 4 |
| BP | somatic diversification of immune receptors via germline recombination within a single locus | 0.000509553 | 0.003100259 | 0.001838128 | CD28/CCR6/FOXP3 | 3 |
| BP | somatic cell DNA recombination | 0.000509553 | 0.003100259 | 0.001838128 | CD28/CCR6/FOXP3 | 3 |
| BP | phosphatidylinositol 3-kinase signaling | 0.000518915 | 0.003139581 | 0.001861442 | CD28/FLT3/PIK3R5/PPP1R16B | 4 |
| BP | regulation of immunoglobulin production | 0.000534089 | 0.003195684 | 0.001894705 | CD28/FOXP3/SASH3 | 3 |
| BP | regulation of lymphocyte migration | 0.000534089 | 0.003195684 | 0.001894705 | CCR6/SPN/CCR2 | 3 |
| BP | genitalia morphogenesis | 0.000553678 | 0.003256977 | 0.001931045 | DCANP1/TIFAB | 2 |
| BP | gamma-delta T cell activation | 0.000553678 | 0.003256977 | 0.001931045 | NCKAP1L/JAML | 2 |
| BP | positive regulation of T cell receptor signaling pathway | 0.000553678 | 0.003256977 | 0.001931045 | CCR7/TESPA1 | 2 |
| BP | somatic diversification of immunoglobulins | 0.00055937 | 0.003256977 | 0.001931045 | CD28/CCR6/FOXP3 | 3 |
| BP | regulation of lipid kinase activity | 0.00055937 | 0.003256977 | 0.001931045 | CCR7/FLT3/PIK3R5 | 3 |
| BP | myeloid cell differentiation | 0.000585195 | 0.00335446 | 0.001988843 | CCR7/NCKAP1L/IRF4/PRKCB/RASSF2/IKZF1 | 6 |
| BP | regulation of antigen receptor-mediated signaling pathway | 0.000585404 | 0.00335446 | 0.001988843 | CCR7/PRKCB/TESPA1 | 3 |
| BP | T cell migration | 0.000585404 | 0.00335446 | 0.001988843 | CCR6/SPN/CCR2 | 3 |
| BP | tripartite regional subdivision | 0.000637835 | 0.003597786 | 0.002133109 | DCANP1/TIFAB | 2 |
| BP | mechanosensory behavior | 0.000637835 | 0.003597786 | 0.002133109 | DCANP1/TIFAB | 2 |
| BP | anterior/posterior axis specification, embryo | 0.000637835 | 0.003597786 | 0.002133109 | DCANP1/TIFAB | 2 |
| BP | T cell differentiation involved in immune response | 0.000668122 | 0.003729773 | 0.002211364 | IRF4/SPN/FOXP3 | 3 |
| BP | positive regulation of cell killing | 0.000668122 | 0.003729773 | 0.002211364 | CD1B/CD1C/CD1E | 3 |
| BP | negative regulation of tumor necrosis factor production | 0.000727202 | 0.004021383 | 0.002384258 | SLAMF1/LILRA4/FOXP3 | 3 |
| BP | T-helper cell lineage commitment | 0.000727785 | 0.004021383 | 0.002384258 | IRF4/SPN | 2 |
| BP | production of molecular mediator of immune response | 0.000738191 | 0.004058177 | 0.002406073 | CD28/CCR6/FOXP3/SASH3/CCR2 | 5 |
| BP | second-messenger-mediated signaling | 0.000775362 | 0.004240993 | 0.002514463 | CXCR5/CCR4/CCR6/CCR7/CCR8/CCR2 | 6 |
| BP | negative regulation of tumor necrosis factor superfamily cytokine production | 0.000789513 | 0.004296694 | 0.002547488 | SLAMF1/LILRA4/FOXP3 | 3 |
| BP | B cell activation involved in immune response | 0.000821901 | 0.004437069 | 0.002630716 | CD28/CCR6/FOXP3 | 3 |
| BP | lymph node development | 0.0008235 | 0.004437069 | 0.002630716 | CXCR5/LTB | 2 |
| BP | somatic diversification of immune receptors | 0.000889187 | 0.004767276 | 0.002826494 | CD28/CCR6/FOXP3 | 3 |
| BP | negative regulation of adenylate cyclase activity | 0.000924953 | 0.004886458 | 0.002897156 | P2RY13/CCR2 | 2 |
| BP | vocalization behavior | 0.000924953 | 0.004886458 | 0.002897156 | DCANP1/TIFAB | 2 |
| BP | craniofacial suture morphogenesis | 0.000924953 | 0.004886458 | 0.002897156 | DCANP1/TIFAB | 2 |
| BP | regulation of leukocyte mediated cytotoxicity | 0.000996516 | 0.005238963 | 0.003106155 | CD1B/CD1C/CD1E | 3 |
| BP | blastoderm segmentation | 0.001032114 | 0.005322758 | 0.003155836 | DCANP1/TIFAB | 2 |
| BP | negative regulation of interleukin-17 production | 0.001032114 | 0.005322758 | 0.003155836 | NCKAP1L/FOXP3 | 2 |
| BP | positive regulation of alpha-beta T cell proliferation | 0.001032114 | 0.005322758 | 0.003155836 | CD28/CCR2 | 2 |
| BP | negative regulation of digestive system process | 0.001032114 | 0.005322758 | 0.003155836 | DCANP1/TIFAB | 2 |
| BP | phosphatidylinositol-mediated signaling | 0.00110087 | 0.005650435 | 0.003350115 | CD28/FLT3/PIK3R5/PPP1R16B | 4 |
| BP | negative regulation of cyclase activity | 0.001144955 | 0.005821532 | 0.003451557 | P2RY13/CCR2 | 2 |
| BP | positive regulation of tumor necrosis factor biosynthetic process | 0.001144955 | 0.005821532 | 0.003451557 | SPN/CCR2 | 2 |
| BP | inositol lipid-mediated signaling | 0.001169884 | 0.005892951 | 0.003493901 | CD28/FLT3/PIK3R5/PPP1R16B | 4 |
| BP | regulation of B cell activation | 0.001169884 | 0.005892951 | 0.003493901 | CD28/NCKAP1L/FOXP3/SASH3 | 4 |
| BP | positive regulation of hemopoiesis | 0.001193549 | 0.005984321 | 0.003548074 | NCKAP1L/TESPA1/FOXP3/SASH3 | 4 |
| BP | regulation of cytokine production involved in immune response | 0.001235019 | 0.006163712 | 0.003654434 | FOXP3/SASH3/CCR2 | 3 |
| BP | phasic smooth muscle contraction | 0.001263449 | 0.006248015 | 0.003704417 | DCANP1/TIFAB | 2 |
| BP | thymic T cell selection | 0.001263449 | 0.006248015 | 0.003704417 | CD28/CCR7 | 2 |
| BP | positive regulation of tumor necrosis factor production | 0.001321819 | 0.006506954 | 0.00385794 | SPN/SASH3/CCR2 | 3 |
| BP | positive regulation of phosphatidylinositol 3-kinase signaling | 0.001366622 | 0.006697067 | 0.003970658 | CD28/FLT3/PIK3R5 | 3 |
| BP | immunoglobulin production | 0.001395108 | 0.006805866 | 0.004035164 | CD28/CCR6/FOXP3/SASH3 | 4 |
| BP | positive regulation of tumor necrosis factor superfamily cytokine production | 0.001412371 | 0.006828562 | 0.00404862 | SPN/SASH3/CCR2 | 3 |
| BP | regulation of phospholipid metabolic process | 0.001412371 | 0.006828562 | 0.00404862 | CCR7/FLT3/PIK3R5 | 3 |
| BP | mononuclear cell migration | 0.001506736 | 0.007252421 | 0.004299924 | CCL17/JAML/CCR2 | 3 |
| BP | negative regulation of lyase activity | 0.001517282 | 0.00727087 | 0.004310863 | P2RY13/CCR2 | 2 |
| BP | T cell receptor signaling pathway | 0.001649051 | 0.007747745 | 0.004593599 | CD28/CCR7/TESPA1/FOXP3 | 4 |
| BP | regulation of inflammatory response to antigenic stimulus | 0.001652566 | 0.007747745 | 0.004593599 | CD28/CCR7 | 2 |
| BP | regulation of T cell differentiation in thymus | 0.001652566 | 0.007747745 | 0.004593599 | TESPA1/FOXP3 | 2 |
| BP | positive regulation of neutrophil chemotaxis | 0.001652566 | 0.007747745 | 0.004593599 | CCR7/NCKAP1L | 2 |
| BP | cochlea morphogenesis | 0.001652566 | 0.007747745 | 0.004593599 | DCANP1/TIFAB | 2 |
| BP | tolerance induction | 0.001793391 | 0.008371736 | 0.00496356 | CCR4/FOXP3 | 2 |
| BP | regulation of cell killing | 0.001923477 | 0.008901388 | 0.005277588 | CD1B/CD1C/CD1E | 3 |
| BP | response to auditory stimulus | 0.00193973 | 0.008901388 | 0.005277588 | DCANP1/TIFAB | 2 |
| BP | positive regulation of granulocyte chemotaxis | 0.00193973 | 0.008901388 | 0.005277588 | CCR7/NCKAP1L | 2 |
| BP | T-helper 17 cell differentiation | 0.00193973 | 0.008901388 | 0.005277588 | IRF4/FOXP3 | 2 |
| BP | humoral immune response | 0.001948815 | 0.008905344 | 0.005279934 | CD28/CCR6/CCR7/CFP/CCR2 | 5 |
| BP | positive regulation of ERK1 and ERK2 cascade | 0.00207031 | 0.009420779 | 0.005585532 | CCR7/FLT3/CCL17/SLAMF1 | 4 |
| BP | cytokine production involved in immune response | 0.0021562 | 0.009770564 | 0.005792918 | FOXP3/SASH3/CCR2 | 3 |
| BP | myeloid dendritic cell activation | 0.002248839 | 0.010105777 | 0.005991664 | IRF4/SLAMF1 | 2 |
| BP | regulation of adenylate cyclase activity | 0.002248839 | 0.010105777 | 0.005991664 | P2RY13/CCR2 | 2 |
| BP | cranial nerve morphogenesis | 0.002411554 | 0.010703741 | 0.006346195 | DCANP1/TIFAB | 2 |
| BP | T-helper 17 type immune response | 0.002411554 | 0.010703741 | 0.006346195 | IRF4/FOXP3 | 2 |
| BP | positive regulation of neutrophil migration | 0.002411554 | 0.010703741 | 0.006346195 | CCR7/NCKAP1L | 2 |
| BP | leukocyte mediated cytotoxicity | 0.002470784 | 0.010921027 | 0.006475022 | CD1B/CD1C/CD1E | 3 |
| BP | antigen processing and presentation | 0.002480676 | 0.010921027 | 0.006475022 | CD1B/CD1C/CD1E/CCR7 | 4 |
| BP | B cell homeostasis | 0.002579674 | 0.011175147 | 0.006625688 | NCKAP1L/FOXP3 | 2 |
| BP | regulation of alpha-beta T cell proliferation | 0.002579674 | 0.011175147 | 0.006625688 | CD28/CCR2 | 2 |
| BP | homeostasis of number of cells within a tissue | 0.002579674 | 0.011175147 | 0.006625688 | SASH3/CCR2 | 2 |
| BP | regulation of neutrophil chemotaxis | 0.002579674 | 0.011175147 | 0.006625688 | CCR7/NCKAP1L | 2 |
| BP | relaxation of muscle | 0.002753171 | 0.01183208 | 0.007015181 | DCANP1/TIFAB | 2 |
| BP | positive regulation of T cell migration | 0.002753171 | 0.01183208 | 0.007015181 | SPN/CCR2 | 2 |
| BP | positive regulation of phosphatidylinositol 3-kinase activity | 0.002932019 | 0.01250148 | 0.007412065 | CCR7/FLT3 | 2 |
| BP | regulation of regulatory T cell differentiation | 0.002932019 | 0.01250148 | 0.007412065 | CD28/FOXP3 | 2 |
| BP | negative regulation of secretion | 0.002988823 | 0.012693707 | 0.007526035 | FOXP3/DCANP1/TIFAB/CCR2 | 4 |
| BP | regulation of isotype switching | 0.00311619 | 0.013131647 | 0.007785688 | CD28/FOXP3 | 2 |
| BP | alpha-beta T cell proliferation | 0.00311619 | 0.013131647 | 0.007785688 | CD28/CCR2 | 2 |
| BP | regulation of interleukin-17 production | 0.003305657 | 0.013769335 | 0.008163769 | NCKAP1L/FOXP3 | 2 |
| BP | tumor necrosis factor biosynthetic process | 0.003305657 | 0.013769335 | 0.008163769 | SPN/CCR2 | 2 |
| BP | regulation of tumor necrosis factor biosynthetic process | 0.003305657 | 0.013769335 | 0.008163769 | SPN/CCR2 | 2 |
| BP | positive regulation of interleukin-12 production | 0.003500395 | 0.014469192 | 0.008578711 | CCR7/LTB | 2 |
| BP | regulation of T-helper cell differentiation | 0.003500395 | 0.014469192 | 0.008578711 | IRF4/FOXP3 | 2 |
| BP | embryonic axis specification | 0.003700377 | 0.015122672 | 0.008966157 | DCANP1/TIFAB | 2 |
| BP | positive regulation of lipid kinase activity | 0.003700377 | 0.015122672 | 0.008966157 | CCR7/FLT3 | 2 |
| BP | regulation of neutrophil migration | 0.003700377 | 0.015122672 | 0.008966157 | CCR7/NCKAP1L | 2 |
| BP | secretion by tissue | 0.003905575 | 0.015782605 | 0.009357427 | DCANP1/TIFAB | 2 |
| BP | T cell homeostasis | 0.003905575 | 0.015782605 | 0.009357427 | NCKAP1L/FOXP3 | 2 |
| BP | positive regulation of lymphocyte migration | 0.003905575 | 0.015782605 | 0.009357427 | SPN/CCR2 | 2 |
| BP | interleukin-17 production | 0.004115964 | 0.016570965 | 0.009824842 | NCKAP1L/FOXP3 | 2 |
| BP | regulation of T cell receptor signaling pathway | 0.004331518 | 0.017374199 | 0.010301076 | CCR7/TESPA1 | 2 |
| BP | regulation of digestive system process | 0.004552209 | 0.01819204 | 0.010785969 | DCANP1/TIFAB | 2 |
| BP | positive regulation of B cell proliferation | 0.004778013 | 0.018954535 | 0.011238049 | NCKAP1L/SASH3 | 2 |
| BP | negative regulation of toll-like receptor signaling pathway | 0.004778013 | 0.018954535 | 0.011238049 | IRF4/LILRA4 | 2 |
| BP | positive regulation of immunoglobulin production | 0.005008903 | 0.019797961 | 0.011738112 | CD28/SASH3 | 2 |
| BP | regulation of cyclase activity | 0.005244852 | 0.020559369 | 0.012189547 | P2RY13/CCR2 | 2 |
| BP | T-helper 1 type immune response | 0.005244852 | 0.020559369 | 0.012189547 | SPN/CCR2 | 2 |
| BP | positive regulation of JNK cascade | 0.005258491 | 0.020559369 | 0.012189547 | CCR7/SLAMF1/RASSF2 | 3 |
| BP | positive regulation of B cell activation | 0.005469589 | 0.02121843 | 0.012580301 | CD28/NCKAP1L/SASH3 | 3 |
| BP | regulation of filopodium assembly | 0.005485836 | 0.02121843 | 0.012580301 | CCR7/PPP1R16B | 2 |
| BP | regulation of granulocyte chemotaxis | 0.005485836 | 0.02121843 | 0.012580301 | CCR7/NCKAP1L | 2 |
| BP | negative regulation of immune system process | 0.005977829 | 0.022895324 | 0.013574522 | IRF4/SPN/LILRA4/FOXP3/CCR2 | 5 |
| BP | inflammatory response to antigenic stimulus | 0.005982804 | 0.022895324 | 0.013574522 | CD28/CCR7 | 2 |
| BP | regulation of lyase activity | 0.005982804 | 0.022895324 | 0.013574522 | P2RY13/CCR2 | 2 |
| BP | genitalia development | 0.006238737 | 0.023790675 | 0.014105372 | DCANP1/TIFAB | 2 |
| BP | negative regulation of cytokine production | 0.006464388 | 0.024564674 | 0.014564272 | NCKAP1L/SLAMF1/LILRA4/FOXP3 | 4 |
| BP | positive regulation of phospholipid metabolic process | 0.006499601 | 0.024612126 | 0.014592406 | CCR7/FLT3 | 2 |
| BP | regulation of interleukin-6 production | 0.006601385 | 0.024910455 | 0.014769283 | NCKAP1L/SLAMF1/FOXP3 | 3 |
| BP | positive regulation of inflammatory response | 0.006721652 | 0.025276213 | 0.01498614 | CD28/CCR7/CCR2 | 3 |
| BP | negative regulation of leukocyte mediated immunity | 0.006765372 | 0.025294533 | 0.014997002 | FOXP3/CCR2 | 2 |
| BP | regulation of ERK1 and ERK2 cascade | 0.006773236 | 0.025294533 | 0.014997002 | CCR7/FLT3/CCL17/SLAMF1 | 4 |
| BP | anterior/posterior axis specification | 0.007036024 | 0.026185617 | 0.015525321 | DCANP1/TIFAB | 2 |
| BP | JAK-STAT cascade | 0.007090287 | 0.026297193 | 0.015591474 | FLT3/IL10RA/CCR2 | 3 |
| BP | regulation of inflammatory response | 0.007243856 | 0.026661246 | 0.015807319 | CD28/CCR7/CFP/FOXP3/CCR2 | 5 |
| BP | regulation of B cell mediated immunity | 0.007311533 | 0.026661246 | 0.015807319 | CD28/FOXP3 | 2 |
| BP | regulation of immunoglobulin mediated immune response | 0.007311533 | 0.026661246 | 0.015807319 | CD28/FOXP3 | 2 |
| BP | cranial nerve development | 0.007311533 | 0.026661246 | 0.015807319 | DCANP1/TIFAB | 2 |
| BP | cochlea development | 0.007311533 | 0.026661246 | 0.015807319 | DCANP1/TIFAB | 2 |
| BP | neuromuscular process controlling balance | 0.007591872 | 0.027590596 | 0.016358326 | DCANP1/TIFAB | 2 |
| BP | interleukin-6 production | 0.007730998 | 0.028002245 | 0.016602391 | NCKAP1L/SLAMF1/FOXP3 | 3 |
| BP | ERK1 and ERK2 cascade | 0.00819524 | 0.029584816 | 0.017540689 | CCR7/FLT3/CCL17/SLAMF1 | 4 |
| BP | STAT cascade | 0.008404966 | 0.030241124 | 0.017929811 | FLT3/IL10RA/CCR2 | 3 |
| BP | cell killing | 0.008683951 | 0.031141455 | 0.018463612 | CD1B/CD1C/CD1E | 3 |
| BP | positive regulation of stress-activated MAPK cascade | 0.009258161 | 0.033091052 | 0.019619519 | CCR7/SLAMF1/RASSF2 | 3 |
| BP | positive regulation of stress-activated protein kinase signaling cascade | 0.009405113 | 0.033505715 | 0.01986537 | CCR7/SLAMF1/RASSF2 | 3 |
| BP | negative regulation of T cell proliferation | 0.009687426 | 0.034229554 | 0.020294531 | SPN/FOXP3 | 2 |
| BP | filopodium assembly | 0.009687426 | 0.034229554 | 0.020294531 | CCR7/PPP1R16B | 2 |
| BP | negative regulation of leukocyte activation | 0.009703114 | 0.034229554 | 0.020294531 | SPN/FOXP3/CCR2 | 3 |
| BP | positive regulation of protein kinase B signaling | 0.009854169 | 0.034649563 | 0.020543552 | CD28/CCR7/PIK3R5 | 3 |
| BP | regulation of B cell proliferation | 0.010328225 | 0.036198926 | 0.021462161 | NCKAP1L/SASH3 | 2 |
| BP | lymphocyte homeostasis | 0.010655514 | 0.037105859 | 0.021999877 | NCKAP1L/FOXP3 | 2 |
| BP | embryonic pattern specification | 0.010655514 | 0.037105859 | 0.021999877 | DCANP1/TIFAB | 2 |
| BP | antigen processing and presentation of exogenous antigen | 0.010789411 | 0.037451704 | 0.022204927 | CD1B/CD1C/CD1E | 3 |
| BP | regulation of JNK cascade | 0.011275723 | 0.039014722 | 0.023131633 | CCR7/SLAMF1/RASSF2 | 3 |
| BP | lymphocyte chemotaxis | 0.011323751 | 0.039056123 | 0.023156179 | CCL17/CCR2 | 2 |
| BP | monocyte chemotaxis | 0.011664651 | 0.039851158 | 0.023627552 | CCL17/CCR2 | 2 |
| BP | positive regulation of interferon-gamma production | 0.011664651 | 0.039851158 | 0.023627552 | SASH3/CCR2 | 2 |
| BP | negative regulation of protein dephosphorylation | 0.011664651 | 0.039851158 | 0.023627552 | NCKAP1L/PPP1R16B | 2 |
| BP | cranial skeletal system development | 0.01201004 | 0.040902118 | 0.02425066 | DCANP1/TIFAB | 2 |
| BP | regulation of toll-like receptor signaling pathway | 0.013436014 | 0.045615057 | 0.027044938 | IRF4/LILRA4 | 2 |
| BP | negative regulation of cell activation | 0.013711849 | 0.046406038 | 0.027513907 | SPN/FOXP3/CCR2 | 3 |
| BP | negative regulation of mononuclear cell proliferation | 0.014551475 | 0.048941762 | 0.029017325 | SPN/FOXP3 | 2 |
| BP | negative regulation of lymphocyte proliferation | 0.014551475 | 0.048941762 | 0.029017325 | SPN/FOXP3 | 2 |
| BP | myeloid leukocyte differentiation | 0.014649048 | 0.049117396 | 0.029121457 | CCR7/IRF4/RASSF2 | 3 |
| BP | establishment or maintenance of cell polarity | 0.015820761 | 0.052882358 | 0.031353684 | CCR7/NCKAP1L/SPN | 3 |
| BP | negative regulation of leukocyte proliferation | 0.016496301 | 0.05497075 | 0.032591882 | SPN/FOXP3 | 2 |
| BP | JNK cascade | 0.016630558 | 0.055248141 | 0.032756345 | CCR7/SLAMF1/RASSF2 | 3 |
| BP | nerve development | 0.016897918 | 0.055964665 | 0.033181169 | DCANP1/TIFAB | 2 |
| BP | immunoglobulin mediated immune response | 0.017463359 | 0.05766103 | 0.034186935 | CD28/CCR6/FOXP3 | 3 |
| BP | B cell mediated immunity | 0.018103093 | 0.05959164 | 0.035331584 | CD28/CCR6/FOXP3 | 3 |
| BP | positive regulation of GTPase activity | 0.018683896 | 0.061317149 | 0.03635463 | CCR7/NCKAP1L/CCL17/ARHGAP30 | 4 |
| BP | axis specification | 0.019394287 | 0.063456233 | 0.037622882 | DCANP1/TIFAB | 2 |
| BP | positive regulation of JAK-STAT cascade | 0.021139435 | 0.068957857 | 0.040884767 | FLT3/IL10RA | 2 |
| BP | regulation of stress-activated MAPK cascade | 0.021734885 | 0.07068733 | 0.041910163 | CCR7/SLAMF1/RASSF2 | 3 |
| BP | regulation of stress-activated protein kinase signaling cascade | 0.02221496 | 0.072032341 | 0.042707613 | CCR7/SLAMF1/RASSF2 | 3 |
| BP | positive regulation of STAT cascade | 0.022489769 | 0.07270573 | 0.043106863 | FLT3/IL10RA | 2 |
| BP | body fluid secretion | 0.022947664 | 0.073965237 | 0.043853618 | DCANP1/TIFAB | 2 |
| BP | regulation of protein kinase B signaling | 0.023440562 | 0.075329758 | 0.044662636 | CD28/CCR7/PIK3R5 | 3 |
| BP | positive regulation of production of molecular mediator of immune response | 0.023874999 | 0.076273228 | 0.045222014 | CD28/SASH3 | 2 |
| BP | B cell proliferation | 0.023874999 | 0.076273228 | 0.045222014 | NCKAP1L/SASH3 | 2 |
| BP | vascular endothelial growth factor receptor signaling pathway | 0.024344397 | 0.077037612 | 0.045675214 | NCKAP1L/PRKCB | 2 |
| BP | positive regulation of cold-induced thermogenesis | 0.024817587 | 0.077037612 | 0.045675214 | IRF4/CCR2 | 2 |
| BP | establishment of T cell polarity | 0.024896735 | 0.077037612 | 0.045675214 | CCR7 | 1 |
| BP | negative regulation of B cell mediated immunity | 0.024896735 | 0.077037612 | 0.045675214 | FOXP3 | 1 |
| BP | negative regulation of immunoglobulin mediated immune response | 0.024896735 | 0.077037612 | 0.045675214 | FOXP3 | 1 |
| BP | positive regulation of isotype switching to IgG isotypes | 0.024896735 | 0.077037612 | 0.045675214 | CD28 | 1 |
| BP | positive regulation of B cell receptor signaling pathway | 0.024896735 | 0.077037612 | 0.045675214 | PRKCB | 1 |
| BP | interleukin-12 secretion | 0.024896735 | 0.077037612 | 0.045675214 | CCR7 | 1 |
| BP | dendritic cell apoptotic process | 0.024896735 | 0.077037612 | 0.045675214 | CCR7 | 1 |
| BP | negative regulation of T-helper 17 type immune response | 0.024896735 | 0.077037612 | 0.045675214 | FOXP3 | 1 |
| BP | regulation of dendritic cell apoptotic process | 0.024896735 | 0.077037612 | 0.045675214 | CCR7 | 1 |
| BP | regulation of myeloid cell differentiation | 0.025217412 | 0.07780757 | 0.046131718 | NCKAP1L/PRKCB/RASSF2 | 3 |
| BP | inner ear morphogenesis | 0.025294548 | 0.077823851 | 0.04614137 | DCANP1/TIFAB | 2 |
| BP | positive regulation of actin filament polymerization | 0.025775258 | 0.0790782 | 0.046885068 | CCR7/NCKAP1L | 2 |
| BP | digestive system process | 0.026259697 | 0.080110568 | 0.047497154 | DCANP1/TIFAB | 2 |
| BP | segmentation | 0.026259697 | 0.080110568 | 0.047497154 | DCANP1/TIFAB | 2 |
| BP | regulation of DNA recombination | 0.026747843 | 0.080497457 | 0.047726538 | CD28/FOXP3 | 2 |
| BP | establishment of lymphocyte polarity | 0.027352783 | 0.080497457 | 0.047726538 | CCR7 | 1 |
| BP | pro-B cell differentiation | 0.027352783 | 0.080497457 | 0.047726538 | FLT3 | 1 |
| BP | T cell tolerance induction | 0.027352783 | 0.080497457 | 0.047726538 | FOXP3 | 1 |
| BP | regulation of dendritic cell antigen processing and presentation | 0.027352783 | 0.080497457 | 0.047726538 | CCR7 | 1 |
| BP | negative regulation of immunoglobulin production | 0.027352783 | 0.080497457 | 0.047726538 | FOXP3 | 1 |
| BP | negative regulation of myeloid leukocyte mediated immunity | 0.027352783 | 0.080497457 | 0.047726538 | CCR2 | 1 |
| BP | regulation of transforming growth factor beta1 production | 0.027352783 | 0.080497457 | 0.047726538 | FOXP3 | 1 |
| BP | negative regulation of activated T cell proliferation | 0.027352783 | 0.080497457 | 0.047726538 | FOXP3 | 1 |
| BP | response to interleukin-18 | 0.027352783 | 0.080497457 | 0.047726538 | ALOX5 | 1 |
| BP | T cell extravasation | 0.027352783 | 0.080497457 | 0.047726538 | CCR2 | 1 |
| BP | positive regulation of flagellated sperm motility | 0.027352783 | 0.080497457 | 0.047726538 | CCR6 | 1 |
| BP | positive regulation of glial cell migration | 0.027352783 | 0.080497457 | 0.047726538 | CCR2 | 1 |
| BP | neuromuscular process | 0.029753415 | 0.086300552 | 0.051167164 | DCANP1/TIFAB | 2 |
| BP | dendritic cell antigen processing and presentation | 0.029802776 | 0.086300552 | 0.051167164 | CCR7 | 1 |