

Pathway enrichment GO LD vs DD

| ID         | Description                                                     | GeneRatio | BgRatio | pvalue      | p.adjust    | qvalue      | geneID                                                                                                   | Count |
|------------|-----------------------------------------------------------------|-----------|---------|-------------|-------------|-------------|----------------------------------------------------------------------------------------------------------|-------|
| GO:0043687 | post-translational protein modification                         | 15/182    | 21/749  | 4,97E-06    | 0,010963518 | 0,010963518 | HIF1A/TIMP1/C3/PSMB8/SOCS3/ASB15/PSME2/PSMB10/APOL1/TNC/VCAN/APOE/PSME1/FN1/KLHL13                       | 15    |
| GO:0002283 | neutrophil activation involved in immune response               | 30/182    | 69/749  | 0,000183439 | 0,134766565 | 0,134766565 | SERPINA3/S100A9/LTF/FPR1/S100A8/C3/SLPI/FCER1G/FCGR3B/MME/LCN2/IMPDH1/ALOX5/FCGR2A/CD59/CTSS/CXCL1       | 30    |
| GO:0043312 | neutrophil degranulation                                        | 30/182    | 69/749  | 0,000183439 | 0,134766565 | 0,134766565 | SERPINA3/S100A9/LTF/FPR1/S100A8/C3/SLPI/FCER1G/FCGR3B/MME/LCN2/IMPDH1/ALOX5/FCGR2A/CD59/CTSS/CXCL1       | 30    |
| GO:0002446 | neutrophil mediated immunity                                    | 30/182    | 70/749  | 0,000252884 | 0,139339102 | 0,139339102 | SERPINA3/S100A9/LTF/FPR1/S100A8/C3/SLPI/FCER1G/FCGR3B/MME/LCN2/IMPDH1/ALOX5/FCGR2A/CD59/CTSS/CXCL1       | 30    |
| GO:0045055 | regulated exocytosis                                            | 37/182    | 99/749  | 0,001252391 | 0,460044793 | 0,460044793 | SERPINA3/S100A9/LTF/FPR1/TIMP1/S100A8/C3/SLPI/SERPING1/FCER1G/FCGR3B/MME/LCN2/IMPDH1/IL4R/TGFB1/ALC      | 37    |
| GO:0042119 | neutrophil activation                                           | 30/182    | 75/749  | 0,001080622 | 0,460044793 | 0,460044793 | SERPINA3/S100A9/LTF/FPR1/S100A8/C3/SLPI/FCER1G/FCGR3B/MME/LCN2/IMPDH1/ALOX5/FCGR2A/CD59/CTSS/CXCL1       | 30    |
| GO:0002275 | myeloid cell activation involved in immune response             | 31/182    | 81/749  | 0,002131119 | 0,521887302 | 0,521887302 | SERPINA3/S100A9/LTF/FPR1/S100A8/C3/SLPI/FCER1G/FCGR3B/MME/LCN2/IMPDH1/IL4R/ALOX5/FCGR2A/CD59/CTSS/C      | 31    |
| GO:0043299 | leukocyte degranulation                                         | 31/182    | 81/749  | 0,002131119 | 0,521887302 | 0,521887302 | SERPINA3/S100A9/LTF/FPR1/S100A8/C3/SLPI/FCER1G/FCGR3B/MME/LCN2/IMPDH1/IL4R/ALOX5/FCGR2A/CD59/CTSS/C      | 31    |
| GO:0036230 | granulocyte activation                                          | 30/182    | 77/749  | 0,001810774 | 0,521887302 | 0,521887302 | SERPINA3/S100A9/LTF/FPR1/S100A8/C3/SLPI/FCER1G/FCGR3B/MME/LCN2/IMPDH1/ALOX5/FCGR2A/CD59/CTSS/CXCL1       | 30    |
| GO:0002444 | myeloid leukocyte mediated immunity                             | 31/182    | 82/749  | 0,002695502 | 0,568502765 | 0,568502765 | SERPINA3/S100A9/LTF/FPR1/S100A8/C3/SLPI/FCER1G/FCGR3B/MME/LCN2/IMPDH1/IL4R/ALOX5/FCGR2A/CD59/CTSS/C      | 31    |
| GO:0070741 | response to interleukin-6                                       | 9/182     | 15/749  | 0,003095296 | 0,568502765 | 0,568502765 | JAK1/STAT3/SOCS3/ICAM1/STAT1/IL6R/ABCC2/NFKB1/IL6ST                                                      | 9     |
| GO:0071354 | cellular response to interleukin-6                              | 9/182     | 15/749  | 0,003095296 | 0,568502765 | 0,568502765 | JAK1/STAT3/SOCS3/ICAM1/STAT1/IL6R/ABCC2/NFKB1/IL6ST                                                      | 9     |
| GO:0051248 | negative regulation of protein metabolic process                | 41/182    | 118/749 | 0,003546836 | 0,569294933 | 0,569294933 | SERPINA3/LTF/BCL3/RARRES1/TIMP1/STAT3/C3/SLPI/SERPING1/SOCS3/HDAC6/JAK3/TGFB1/SOCS1/DNMT1/BAX/CDKN       | 41    |
| GO:0006887 | exocytosis                                                      | 37/182    | 104/749 | 0,003616211 | 0,569294933 | 0,569294933 | SERPINA3/S100A9/LTF/FPR1/TIMP1/S100A8/C3/SLPI/SERPING1/FCER1G/FCGR3B/MME/LCN2/IMPDH1/IL4R/TGFB1/ALC      | 37    |
| GO:0002526 | acute inflammatory response                                     | 16/182    | 36/749  | 0,005294568 | 0,77794851  | 0,77794851  | SERPINA3/OSMR/CD163/STAT3/S100A8/C3/FCER1G/ICAM1/VCAM1/SIGIRR/IL6R/APOL2/FN1/EPO/GATA3/IL6ST             | 16    |
| GO:0002263 | cell activation involved in immune response                     | 45/182    | 143/749 | 0,018756774 | 0,961873513 | 0,961873513 | SERPINA3/S100A9/LTF/BCL3/FPR1/BCL6/STAT3/S100A8/C3/SLPI/FCER1G/FCGR3B/MME/LCN2/ICAM1/IMPDH1/RELB/JA      | 45    |
| GO:0002366 | leukocyte activation involved in immune response                | 45/182    | 143/749 | 0,018756774 | 0,961873513 | 0,961873513 | SERPINA3/S100A9/LTF/BCL3/FPR1/BCL6/STAT3/S100A8/C3/SLPI/FCER1G/FCGR3B/MME/LCN2/ICAM1/IMPDH1/RELB/JA      | 45    |
| GO:0006508 | proteolysis                                                     | 44/182    | 136/749 | 0,011713066 | 0,961873513 | 0,961873513 | SERPINA3/S100A9/HIF1A/LTF/RARRES1/C15/TIMP1/STAT3/S100A8/C3/SLPI/ADAMTS1/SERPING1/CFB/PSMB8/MME/HC       | 44    |
| GO:0010243 | response to organonitrogen compound                             | 39/182    | 119/749 | 0,01432309  | 0,961873513 | 0,961873513 | TIMP1/STAT3/COL4A1/NNMT/FCER1G/SOCS3/MAPK13/COL1A1/NR4A1/COL3A1/ICAM1/JAK3/STAT1/TGFB1/SOCS1/XBI         | 39    |
| GO:0032269 | negative regulation of cellular protein metabolic process       | 35/182    | 102/749 | 0,009324985 | 0,961873513 | 0,961873513 | SERPINA3/LTF/RARRES1/TIMP1/STAT3/C3/SLPI/SERPING1/SOCS3/HDAC6/TGFB1/SOCS1/DNMT1/BAX/CDKN1A/AGT/FKI       | 35    |
| GO:0009636 | response to toxic substance                                     | 27/182    | 76/749  | 0,013801829 | 0,961873513 | 0,961873513 | S100A9/SOD2/STAT3/S100A8/MAPK13/LCN2/HDAC6/COL1A1/ICAM1/STAT1/BAX/AHR/CDKN1A/VCAM1/STAT6/TNC/EC          | 27    |
| GO:1901699 | cellular response to nitrogen compound                          | 26/182    | 74/749  | 0,018314714 | 0,961873513 | 0,961873513 | STAT3/COL4A1/SOCS3/MAPK13/COL1A1/NR4A1/COL3A1/ICAM1/JAK3/STAT1/TGFB1/SOCS1/XBP1/DNMT1/AHR/VCAM:          | 26    |
| GO:0071417 | cellular response to organonitrogen compound                    | 25/182    | 71/749  | 0,0200754   | 0,961873513 | 0,961873513 | STAT3/COL4A1/SOCS3/MAPK13/COL1A1/NR4A1/COL3A1/ICAM1/JAK3/STAT1/TGFB1/SOCS1/XBP1/DNMT1/AHR/VCAM:          | 25    |
| GO:0043434 | response to peptide hormone                                     | 20/182    | 50/749  | 0,007992089 | 0,961873513 | 0,961873513 | TIMP1/STAT3/SOCS3/COL1A1/NR4A1/ICAM1/JAK3/STAT1/TGFB1/SOCS1/XBP1/STAT6/AGT/EGR1/TLR2/ABCC2/TNFSF10       | 20    |
| GO:0060759 | regulation of response to cytokine stimulus                     | 20/182    | 51/749  | 0,010337067 | 0,961873513 | 0,961873513 | HIF1A/JAK1/CD24/IFNGR2/IL1R1/SOCS3/TNFRSF1A/IFNAR2/STAT1/SOCS1/SIGIRR/TLR4/TLR2/IRF7/IL1R2/TBK1/BIRC3/C. | 20    |
| GO:0030198 | extracellular matrix organization                               | 20/182    | 53/749  | 0,016678171 | 0,961873513 | 0,961873513 | BCL3/TIMP1/COL4A1/ITGB6/TNFRSF1A/COL1A1/COL3A1/ICAM1/TGFB1/VCAM1/AGT/TNC/NFKB2/CTSS/VCAN/TNFRSF1         | 20    |
| GO:0043062 | extracellular structure organization                            | 20/182    | 53/749  | 0,016678171 | 0,961873513 | 0,961873513 | BCL3/TIMP1/COL4A1/ITGB6/TNFRSF1A/COL1A1/COL3A1/ICAM1/TGFB1/VCAM1/AGT/TNC/NFKB2/CTSS/VCAN/TNFRSF1         | 20    |
| GO:0071214 | cellular response to abiotic stimulus                           | 20/182    | 53/749  | 0,016678171 | 0,961873513 | 0,961873513 | MAPK13/TNFRSF1A/MME/LTBR/COL1A1/RELB/TGFB1/BAX/CDKN1A/AGT/EGR1/TLR4/MYD88/MYC/ERRFI1/NOX4/EPO/IF         | 20    |
| GO:0104004 | cellular response to environmental stimulus                     | 20/182    | 53/749  | 0,016678171 | 0,961873513 | 0,961873513 | MAPK13/TNFRSF1A/MME/LTBR/COL1A1/RELB/TGFB1/BAX/CDKN1A/AGT/EGR1/TLR4/MYD88/MYC/ERRFI1/NOX4/EPO/IF         | 20    |
| GO:0032446 | protein modification by small protein conjugation               | 16/182    | 40/749  | 0,017489693 | 0,961873513 | 0,961873513 | HIF1A/PSMB8/SOCS3/ASB15/HDAC6/PSME2/PSMB10/SOCS1/EGR1/FKBP1A/BIRC3/PSME1/DCAF12/KLHL13/ISG15/RNF:        | 16    |
| GO:0097193 | intrinsic apoptotic signaling pathway                           | 15/182    | 37/749  | 0,018599307 | 0,961873513 | 0,961873513 | S100A9/HIF1A/BCL3/SOD2/S100A8/CD24/MUC1/TNFRSF1A/XBP1/BAX/CDKN1A/TNFRSF1B/EPO/CASP4/PLAUR                | 15    |
| GO:0071375 | cellular response to peptide hormone stimulus                   | 13/182    | 30/749  | 0,0152262   | 0,961873513 | 0,961873513 | STAT3/SOCS3/NR4A1/JAK3/STAT1/TGFB1/SOCS1/XBP1/STAT6/AGT/ERRFI1/GDF15/NFKB1                               | 13    |
| GO:0010212 | response to ionizing radiation                                  | 10/182    | 21/749  | 0,015599381 | 0,961873513 | 0,961873513 | ICAM1/TGFB1/BAX/CDKN1A/VCAM1/EGR1/MYC/NOX4/GATA3/THBD                                                    | 10    |
| GO:0021782 | glial cell development                                          | 9/182     | 17/749  | 0,009433689 | 0,961873513 | 0,961873513 | S100A8/C1QA/TGFB1/LDLR/TLR4/TLR2/C5AR1/IFNGR1/ADORA2A                                                    | 9     |
| GO:0043618 | regulation of transcription from RNA polymerase II promoter in  | 9/182     | 17/749  | 0,009433689 | 0,961873513 | 0,961873513 | HIF1A/PSMB8/MUC1/PSME2/PSMB10/EGR1/PSME1/EPO/ATF3                                                        | 9     |
| GO:0043620 | regulation of DNA-templated transcription in response to stress | 9/182     | 18/749  | 0,014959918 | 0,961873513 | 0,961873513 | HIF1A/PSMB8/MUC1/PSME2/PSMB10/EGR1/PSME1/EPO/ATF3                                                        | 9     |
| GO:0045071 | negative regulation of viral genome replication                 | 8/182     | 15/749  | 0,013672102 | 0,961873513 | 0,961873513 | LTF/IFITM3/SLPI/IFITM2/IFITM1/ISG20/IFIT1/ISG15                                                          | 8     |
| GO:0046916 | cellular transition metal ion homeostasis                       | 8/182     | 15/749  | 0,013672102 | 0,961873513 | 0,961873513 | S100A9/HIF1A/LTF/S100A8/LCN2/MT1A/SLC11A1/MYC                                                            | 8     |
| GO:0043487 | regulation of RNA stability                                     | 7/182     | 12/749  | 0,011508766 | 0,961873513 | 0,961873513 | PSMB8/PSME2/PSMB10/MYD88/SLC11A1/TNFRSF1B/PSME1                                                          | 7     |
| GO:0097242 | amyloid-beta clearance                                          | 7/182     | 12/749  | 0,011508766 | 0,961873513 | 0,961873513 | C3/MME/LDLR/APOE/ITGB2/C5AR1/IFNGR1                                                                      | 7     |
| GO:0009308 | amine metabolic process                                         | 7/182     | 13/749  | 0,019877161 | 0,961873513 | 0,961873513 | PSMB8/PSME2/PSMB10/VCAM1/ABCC2/ITGB2/PSME1                                                               | 7     |
| GO:0061418 | regulation of transcription from RNA polymerase II promoter in  | 7/182     | 13/749  | 0,019877161 | 0,961873513 | 0,961873513 | HIF1A/PSMB8/PSME2/PSMB10/EGR1/PSME1/EPO                                                                  | 7     |
| GO:0097327 | response to antineoplastic agent                                | 7/182     | 13/749  | 0,019877161 | 0,961873513 | 0,961873513 | MAPK13/ICAM1/TGFB1/EGR1/ABCC2/ERRFI1/EPO                                                                 | 7     |
| GO:0044839 | cell cycle G2/M phase transition                                | 6/182     | 10/749  | 0,016480038 | 0,961873513 | 0,961873513 | PSMB8/ABCB1/PSME2/PSMB10/CDKN1A/PSME1                                                                    | 6     |
| GO:0070102 | interleukin-6-mediated signaling pathway                        | 6/182     | 10/749  | 0,016480038 | 0,961873513 | 0,961873513 | JAK1/STAT3/SOCS3/STAT1/IL6R/IL6ST                                                                        | 6     |
| GO:1901532 | regulation of hematopoietic progenitor cell differentiation     | 6/182     | 10/749  | 0,016480038 | 0,961873513 | 0,961873513 | PSMB8/PSME2/PSMB10/KITLG/PSME1/GATA3                                                                     | 6     |
| GO:0051649 | establishment of localization in cell                           | 52/182    | 174/749 | 0,032873609 | 0,96315198  | 0,96315198  | SERPINA3/S100A9/HIF1A/LTF/FPR1/TIMP1/STAT3/S100A8/C3/CD24/SLPI/SERPING1/FCER1G/FCGR3B/EHD3/MME/LCN2      | 52    |
| GO:1901698 | response to nitrogen compound                                   | 40/182    | 126/749 | 0,023337636 | 0,96315198  | 0,96315198  | TIMP1/STAT3/COL4A1/NNMT/FCER1G/SOCS3/MAPK13/COL1A1/NR4A1/COL3A1/ICAM1/JAK3/STAT1/TGFB1/SOCS1/XBI         | 40    |
| GO:0002274 | myeloid leukocyte activation                                    | 38/182    | 121/749 | 0,032458947 | 0,96315198  | 0,96315198  | SERPINA3/S100A9/LTF/FPR1/S100A8/C3/SLPI/FCER1G/FCGR3B/MME/LCN2/LTBR/IMPDH1/C1QA/RELB/IL4R/TGFB1/ALC      | 38    |
| GO:0001959 | regulation of cytokine-mediated signaling pathway               | 18/182    | 48/749  | 0,024545715 | 0,96315198  | 0,96315198  | HIF1A/JAK1/CD24/IFNGR2/IL1R1/SOCS3/TNFRSF1A/IFNAR2/STAT1/SOCS1/SIGIRR/IRF7/IL1R2/TBK1/BIRC3/CASP4/IFNGF  | 18    |
| GO:1901653 | cellular response to peptide                                    | 17/182    | 46/749  | 0,033212137 | 0,96315198  | 0,96315198  | STAT3/SOCS3/NR4A1/ICAM1/JAK3/STAT1/TGFB1/SOCS1/XBP1/VCAM1/STAT6/AGT/TLR4/ERRFI1/GDF15/CASP4/NFKB1        | 17    |
| GO:0016567 | protein ubiquitination                                          | 15/182    | 38/749  | 0,024219084 | 0,96315198  | 0,96315198  | HIF1A/PSMB8/SOCS3/ASB15/HDAC6/PSME2/PSMB10/SOCS1/FKBP1A/BIRC3/PSME1/DCAF12/KLHL13/ISG15/RNF149           | 15    |
| GO:0032479 | regulation of type I interferon production                      | 13/182    | 32/749  | 0,027517007 | 0,96315198  | 0,96315198  | RELB/STAT1/STAT6/NFKB2/TLR4/MYD88/TLR2/IRF7/TBK1/LILRB1/CD14/NFKB1/ISG15                                 | 13    |
| GO:0032606 | type I interferon production                                    | 13/182    | 32/749  | 0,027517007 | 0,96315198  | 0,96315198  | RELB/STAT1/STAT6/NFKB2/TLR4/MYD88/TLR2/IRF7/TBK1/LILRB1/CD14/NFKB1/ISG15                                 | 13    |
| GO:0008202 | steroid metabolic process                                       | 11/182    | 26/749  | 0,030556761 | 0,96315198  | 0,96315198  | HSD11B1/AGT/APOL1/LDLR/EGR1/APOE/RORC/APOL2/TIPARP/G6PD/NFKB1                                            | 11    |
| GO:0032481 | positive regulation of type I interferon production             | 10/182    | 23/749  | 0,031765275 | 0,96315198  | 0,96315198  | STAT1/STAT6/NFKB2/TLR4/MYD88/TLR2/IRF7/TBK1/CD14/NFKB1                                                   | 10    |
| GO:0032868 | response to insulin                                             | 10/182    | 23/749  | 0,031765275 | 0,96315198  | 0,96315198  | SOCS3/ICAM1/STAT1/SOCS1/XBP1/AGT/EGR1/TLR2/TNFSF10/ERRFI1                                                | 10    |

|            |                                                            |         |         |             |             |             |                                                                                                         |     |
|------------|------------------------------------------------------------|---------|---------|-------------|-------------|-------------|---------------------------------------------------------------------------------------------------------|-----|
| GO:1901987 | regulation of cell cycle phase transition                  | 10/182  | 23/749  | 0,031765275 | 0,96315198  | 0,96315198  | ADAMTS1/PSMB8/MUC1/PSME2/PSMB10/TGFB1/BAX/CDKN1A/PSME1/PTPN6                                            | 10  |
| GO:1901990 | regulation of mitotic cell cycle phase transition          | 10/182  | 23/749  | 0,031765275 | 0,96315198  | 0,96315198  | ADAMTS1/PSMB8/MUC1/PSME2/PSMB10/TGFB1/BAX/CDKN1A/PSME1/PTPN6                                            | 10  |
| GO:0045444 | fat cell differentiation                                   | 9/182   | 19/749  | 0,022553002 | 0,96315198  | 0,96315198  | PSMB8/HDAC6/NR4A1/TGFB1/SOCS1/XBP1/RORC/CMKLR1/GATA3                                                    | 9   |
| GO:0071478 | cellular response to radiation                             | 9/182   | 19/749  | 0,022553002 | 0,96315198  | 0,96315198  | MAPK13/MME/TGFB1/BAX/CDKN1A/EGR1/MYC/NOX4/GATA3                                                         | 9   |
| GO:0048525 | negative regulation of viral process                       | 9/182   | 20/749  | 0,032560176 | 0,96315198  | 0,96315198  | LTF/IFITM3/SLPI/IFITM2/IFITM1/STAT1/ISG20/IFIT1/ISG15                                                   | 9   |
| GO:0006953 | acute-phase response                                       | 8/182   | 16/749  | 0,021741599 | 0,96315198  | 0,96315198  | SERPINA3/CD163/STAT3/SIGIRR/IL6R/APOL2/FN1/EPO                                                          | 8   |
| GO:0045471 | response to ethanol                                        | 8/182   | 16/749  | 0,021741599 | 0,96315198  | 0,96315198  | STAT3/S100A8/ICAM1/VCAM1/TNC/G6PD/CD14/GATA3                                                            | 8   |
| GO:1903901 | negative regulation of viral life cycle                    | 8/182   | 16/749  | 0,021741599 | 0,96315198  | 0,96315198  | LTF/IFITM3/SLPI/IFITM2/IFITM1/ISG20/IFIT1/ISG15                                                         | 8   |
| GO:0006401 | RNA catabolic process                                      | 8/182   | 17/749  | 0,032681963 | 0,96315198  | 0,96315198  | PSMB8/PSME2/PSMB10/MYD88/SLC11A1/TNFRSF1B/ISG20/PSME1                                                   | 8   |
| GO:0071466 | cellular response to xenobiotic stimulus                   | 8/182   | 17/749  | 0,032681963 | 0,96315198  | 0,96315198  | ICAM1/TGFB1/AHR/EGR1/RORC/S100A12/ABCC2/ERRFI1                                                          | 8   |
| GO:0014002 | astrocyte development                                      | 7/182   | 14/749  | 0,031723183 | 0,96315198  | 0,96315198  | S100A8/C1QA/LDLR/TLR4/C5AR1/IFNGR1/ADORA2A                                                              | 7   |
| GO:0061515 | myeloid cell development                                   | 7/182   | 14/749  | 0,031723183 | 0,96315198  | 0,96315198  | LTF/BCL6/TLR2/G6PD/LILRB1/EPO/PTPN6                                                                     | 7   |
| GO:0090184 | positive regulation of kidney development                  | 7/182   | 14/749  | 0,031723183 | 0,96315198  | 0,96315198  | CD24/TGFB1/AGT/EGR1/IL6R/MYC/GATA3                                                                      | 7   |
| GO:0043488 | regulation of mRNA stability                               | 6/182   | 11/749  | 0,029030093 | 0,96315198  | 0,96315198  | PSMB8/PSME2/PSMB10/MYD88/SLC11A1/PSME1                                                                  | 6   |
| GO:0050832 | defense response to fungus                                 | 6/182   | 11/749  | 0,029030093 | 0,96315198  | 0,96315198  | S100A9/LTF/S100A8/TGFB1/IL17RA/S100A12                                                                  | 6   |
| GO:0055094 | response to lipoprotein particle                           | 6/182   | 11/749  | 0,029030093 | 0,96315198  | 0,96315198  | FCER1G/LDLR/TLR4/MYD88/APOE/ITGB2                                                                       | 6   |
| GO:0060330 | regulation of response to interferon-gamma                 | 6/182   | 11/749  | 0,029030093 | 0,96315198  | 0,96315198  | JAK1/IFNGR2/SOCS3/STAT1/SOCS1/IFNGR1                                                                    | 6   |
| GO:0060334 | regulation of interferon-gamma-mediated signaling pathway  | 6/182   | 11/749  | 0,029030093 | 0,96315198  | 0,96315198  | JAK1/IFNGR2/SOCS3/STAT1/SOCS1/IFNGR1                                                                    | 6   |
| GO:0071402 | cellular response to lipoprotein particle stimulus         | 6/182   | 11/749  | 0,029030093 | 0,96315198  | 0,96315198  | FCER1G/LDLR/TLR4/MYD88/APOE/ITGB2                                                                       | 6   |
| GO:0051172 | negative regulation of nitrogen compound metabolic process | 56/182  | 190/749 | 0,035126238 | 0,981771842 | 0,981771842 | SERPINA3/LTF/BCL3/RARRES1/BCL6/TIMP1/STAT3/C3/SLPI/SERPING1/SOCS3/MUC1/HDAC6/MAF/RELB/JAK3/STAT1/TG     | 56  |
| GO:0007568 | aging                                                      | 19/182  | 53/749  | 0,034404931 | 0,981771842 | 0,981771842 | SOD2/BCL6/TIMP1/STAT3/SERPING1/MME/ICAM1/C1QA/TGFB1/CDKN1A/VCAM1/AGT/NFKB2/TNFRSF1B/ITGB2/NOX4,         | 19  |
| GO:0034340 | response to type I interferon                              | 16/182  | 43/749  | 0,036081452 | 0,981771842 | 0,981771842 | JAK1/IFITM3/IFITM2/IFITM1/PSMB8/GBP2/IFNAR2/STAT1/EGR1/MYD88/IRF7/TBK1/ISG20/IFIT1/ISG15/PTPN6          | 16  |
| GO:0060337 | type I interferon signaling pathway                        | 16/182  | 43/749  | 0,036081452 | 0,981771842 | 0,981771842 | JAK1/IFITM3/IFITM2/IFITM1/PSMB8/GBP2/IFNAR2/STAT1/EGR1/MYD88/IRF7/TBK1/ISG20/IFIT1/ISG15/PTPN6          | 16  |
| GO:0071357 | cellular response to type I interferon                     | 16/182  | 43/749  | 0,036081452 | 0,981771842 | 0,981771842 | JAK1/IFITM3/IFITM2/IFITM1/PSMB8/GBP2/IFNAR2/STAT1/EGR1/MYD88/IRF7/TBK1/ISG20/IFIT1/ISG15/PTPN6          | 16  |
| GO:0006950 | response to stress                                         | 130/182 | 495/749 | 0,047547896 | 0,999954951 | 0,999954951 | SERPINA3/OSMR/S100A9/HIF1A/LTF/BCL3/C1QB/JAK1/CD163/IFITM3/C1S/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/    | 130 |
| GO:0042221 | response to chemical                                       | 127/182 | 493/749 | 0,113736612 | 0,999954951 | 0,999954951 | OSMR/S100A9/HIF1A/LTF/JAK1/IFITM3/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/CD24/COL4A1/SLPI/IFITM2/NNMT/IFI    | 127 |
| GO:0044238 | primary metabolic process                                  | 121/182 | 500/749 | 0,573378179 | 0,999954951 | 0,999954951 | SERPINA3/ALDH3A2/S100A9/HIF1A/LTF/BCL3/PLAAT4/RARRES1/JAK1/C1S/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/    | 121 |
| GO:0048583 | regulation of response to stimulus                         | 119/182 | 490/749 | 0,542186879 | 0,999954951 | 0,999954951 | OSMR/S100A9/HIF1A/LTF/BCL3/C1QB/JAK1/C1S/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/IFITM1/SERPING1/C    | 119 |
| GO:0010033 | response to organic substance                              | 117/182 | 453/749 | 0,131237423 | 0,999954951 | 0,999954951 | OSMR/HIF1A/LTF/JAK1/IFITM3/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/CD24/COL4A1/SLPI/IFITM2/NNMT/IFITM1/FCE    | 117 |
| GO:0070887 | cellular response to chemical stimulus                     | 116/182 | 448/749 | 0,124054102 | 0,999954951 | 0,999954951 | OSMR/S100A9/HIF1A/LTF/JAK1/IFITM3/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/CD24/COL4A1/IFITM2/IFITM1/FCER1G    | 116 |
| GO:0019222 | regulation of metabolic process                            | 111/182 | 468/749 | 0,715315845 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/BCL3/RARRES1/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/ITGB6/SLPI/SERPING1/   | 111 |
| GO:0009605 | response to external stimulus                              | 110/182 | 441/749 | 0,343461212 | 0,999954951 | 0,999954951 | OSMR/S100A9/LTF/BCL3/C1QB/JAK1/IFITM3/C1S/FPR1/BCL6/S100A8/C3/CD24/SLPI/IFITM2/IFITM1/SERPING1/C9/CFB/  | 110 |
| GO:0006955 | immune response                                            | 110/182 | 460/749 | 0,655813225 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/LTF/BCL3/C1QB/JAK1/IFITM3/C1S/FPR1/BCL6/STAT3/S100A8/C3/CD24/SLPI/IFITM2/IFITM1/SERPINC | 110 |
| GO:0032502 | developmental process                                      | 110/182 | 462/749 | 0,686708396 | 0,999954951 | 0,999954951 | ALDH3A2/S100A9/HIF1A/LTF/BCL3/PLAAT4/C1QB/JAK1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/COL4A1/ADAMTS1      | 110 |
| GO:0060255 | regulation of macromolecule metabolic process              | 109/182 | 456/749 | 0,657191069 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/BCL3/RARRES1/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/ITGB6/SLPI/SERPING1/   | 109 |
| GO:0007166 | cell surface receptor signaling pathway                    | 109/182 | 465/749 | 0,785187296 | 0,999954951 | 0,999954951 | OSMR/HIF1A/LTF/BCL3/JAK1/IFITM3/FPR1/SOD2/BCL6/TIMP1/STAT3/C3/CD24/COL4A1/ITGB6/ADAMTS1/IFITM2/IFITV    | 109 |
| GO:1901564 | organonitrogen compound metabolic process                  | 107/182 | 418/749 | 0,199007491 | 0,999954951 | 0,999954951 | SERPINA3/ALDH3A2/S100A9/HIF1A/LTF/BCL3/PLAAT4/RARRES1/JAK1/C1S/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/CD24/    | 107 |
| GO:0044260 | cellular macromolecule metabolic process                   | 107/182 | 446/749 | 0,628440726 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/BCL3/RARRES1/JAK1/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/SLPI/SERPING1/F   | 107 |
| GO:0048856 | anatomical structure development                           | 106/182 | 444/749 | 0,661386407 | 0,999954951 | 0,999954951 | ALDH3A2/S100A9/HIF1A/LTF/BCL3/PLAAT4/C1QB/JAK1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/COL4A1/ADAMTS1      | 106 |
| GO:0048519 | negative regulation of biological process                  | 105/182 | 423/749 | 0,384811379 | 0,999954951 | 0,999954951 | SERPINA3/HIF1A/LTF/BCL3/PLAAT4/RARRES1/IFITM3/SOD2/BCL6/TIMP1/STAT3/C3/CD24/SLPI/ADAMTS1/IFITM2/IFITM   | 105 |
| GO:0051179 | localization                                               | 105/182 | 448/749 | 0,776002904 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/BCL3/CD163/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/ITGB6/SLPI/ADAMTS1/IFI   | 105 |
| GO:0071310 | cellular response to organic substance                     | 104/182 | 418/749 | 0,37090083  | 0,999954951 | 0,999954951 | OSMR/HIF1A/LTF/JAK1/IFITM3/FPR1/SOD2/BCL6/TIMP1/STAT3/CD24/COL4A1/IFITM2/IFITM1/FCER1G/IFNGR2/SOST/P    | 104 |
| GO:0006952 | defense response                                           | 103/182 | 386/749 | 0,068762447 | 0,999954951 | 0,999954951 | SERPINA3/OSMR/S100A9/HIF1A/LTF/BCL3/C1QB/JAK1/CD163/IFITM3/C1S/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/ITGB6,   | 103 |
| GO:0007275 | multicellular organism development                         | 102/182 | 425/749 | 0,620302878 | 0,999954951 | 0,999954951 | ALDH3A2/S100A9/HIF1A/LTF/BCL3/PLAAT4/C1QB/JAK1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/COL4A1/ADAMTS1      | 102 |
| GO:0048731 | system development                                         | 100/182 | 411/749 | 0,525758677 | 0,999954951 | 0,999954951 | ALDH3A2/S100A9/HIF1A/LTF/BCL3/PLAAT4/C1QB/JAK1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/COL4A1/ADAMTS1      | 100 |
| GO:0019538 | protein metabolic process                                  | 99/182  | 386/749 | 0,211298299 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/BCL3/RARRES1/JAK1/C1S/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/CD24/SLPI/ADAMTS1/SEF   | 99  |
| GO:0080090 | regulation of primary metabolic process                    | 97/182  | 404/749 | 0,612608747 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/BCL3/RARRES1/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/SLPI/SERPING1/SOST/F   | 97  |
| GO:0044419 | interspecies interaction between organisms                 | 96/182  | 383/749 | 0,339230369 | 0,999954951 | 0,999954951 | S100A9/LTF/BCL3/C1QB/JAK1/IFITM3/C1S/STAT3/S100A8/C3/CD24/ITGB6/SLPI/IFITM2/IFITM1/SERPING1/C9/HAVCR1/I | 96  |
| GO:0051171 | regulation of nitrogen compound metabolic process          | 96/182  | 400/749 | 0,614298524 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/BCL3/RARRES1/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/SLPI/SERPING1/SOST/F   | 96  |
| GO:0031323 | regulation of cellular metabolic process                   | 96/182  | 412/749 | 0,785325698 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/BCL3/RARRES1/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/SLPI/SERPING1/SOST/F   | 96  |
| GO:0051239 | regulation of multicellular organismal process             | 95/182  | 376/749 | 0,296630357 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/PLAAT4/JAK1/SOD2/BCL6/TIMP1/STAT3/C3/CD24/ITGB6/IFITM1/SERPING1/FCER1G/SOST/PSM   | 95  |
| GO:0048523 | negative regulation of cellular process                    | 94/182  | 386/749 | 0,520185877 | 0,999954951 | 0,999954951 | SERPINA3/HIF1A/LTF/BCL3/PLAAT4/RARRES1/SOD2/BCL6/TIMP1/STAT3/C3/SLPI/ADAMTS1/IFITM1/SERPING1/FCER1G/    | 94  |
| GO:0010467 | gene expression                                            | 93/182  | 393/749 | 0,695474483 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/C3/CD24/ITGB6/FCER1G/SOST/PSMB8/IL1R1/MUC1/MAPK13/TNF      | 93  |
| GO:0030154 | cell differentiation                                       | 89/182  | 355/749 | 0,351057487 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/PLAAT4/SOD2/BCL6/STAT3/S100A8/C3/CD24/COL4A1/IFITM1/FCER1G/PSMB8/SOCS3/TNFRSF     | 89  |
| GO:0048869 | cellular developmental process                             | 89/182  | 359/749 | 0,414306521 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/PLAAT4/SOD2/BCL6/STAT3/S100A8/C3/CD24/COL4A1/IFITM1/FCER1G/PSMB8/SOCS3/TNFRSF     | 89  |
| GO:0023051 | regulation of signaling                                    | 89/182  | 369/749 | 0,578485207 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/JAK1/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/IFNGR2/SOST/PSMB8/IL1R1/SOCS3/N    | 89  |
| GO:0009893 | positive regulation of metabolic process                   | 89/182  | 395/749 | 0,899087023 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/FPR1/BCL6/STAT3/S100A8/C3/CD24/FCER1G/SOST/IL1R1/SOCS3/MUC1/MAPK13/TNFRSF1A/L     | 89  |
| GO:0010646 | regulation of cell communication                           | 88/182  | 368/749 | 0,628160744 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/JAK1/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/IFNGR2/SOST/PSMB8/IL1R1/SOCS3/N    | 88  |
| GO:0044267 | cellular protein metabolic process                         | 87/182  | 347/749 | 0,354321879 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/BCL3/RARRES1/JAK1/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/CD24/SLPI/SERPING1/PSMB8/   | 87  |



|            |                                                            |        |         |             |             |             |                                                                                                         |    |
|------------|------------------------------------------------------------|--------|---------|-------------|-------------|-------------|---------------------------------------------------------------------------------------------------------|----|
| GO:0010468 | regulation of gene expression                              | 87/182 | 371/749 | 0,732924146 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/C3/CD24/ITGB6/FCER1G/SOST/PSMB8/IL1R1/MUC1/MAPK13/TNF      | 87 |
| GO:0010604 | positive regulation of macromolecule metabolic process     | 87/182 | 381/749 | 0,849905978 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/FPR1/BCL6/STAT3/S100A8/C3/CD24/FCER1G/SOST/IL1R1/SOCS3/MUC1/MAPK13/TNFRSF1A/L     | 87 |
| GO:0034097 | response to cytokine                                       | 86/182 | 328/749 | 0,159667169 | 0,999954951 | 0,999954951 | OSMR/HIF1A/JAK1/IFITM3/FPR1/SOD2/BCL6/TIMP1/STAT3/CD24/IFITM2/IFITM1/FCER1G/IFNGR2/PSMB8/IL1R1/SOCS3    | 86 |
| GO:0006810 | transport                                                  | 86/182 | 349/749 | 0,452295197 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/CD163/FPR1/TIMP1/STAT3/S100A8/C3/CD24/ITGB6/SLPI/SERPING1/FCER1G/PSMB8/TNF    | 86 |
| GO:0051234 | establishment of localization                              | 86/182 | 351/749 | 0,485318297 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/CD163/FPR1/TIMP1/STAT3/S100A8/C3/CD24/ITGB6/SLPI/SERPING1/FCER1G/PSMB8/TNF    | 86 |
| GO:0048584 | positive regulation of response to stimulus                | 86/182 | 387/749 | 0,927218995 | 0,999954951 | 0,999954951 | OSMR/S100A9/HIF1A/LTF/C1QB/C1S/FPR1/STAT3/S100A8/C3/CD24/SERPING1/C9/CFB/FCER1G/PSMB8/IL1R1/SOCS3/N     | 86 |
| GO:0043207 | response to external biotic stimulus                       | 84/182 | 337/749 | 0,3907474   | 0,999954951 | 0,999954951 | S100A9/LTF/BCL3/C1QB/JAK1/IFITM3/C1S/S100A8/C3/CD24/SLPI/IFITM2/IFITM1/SERPING1/C9/CFB/FCER1G/IFNGR2/P: | 84 |
| GO:0051707 | response to other organism                                 | 84/182 | 337/749 | 0,3907474   | 0,999954951 | 0,999954951 | S100A9/LTF/BCL3/C1QB/JAK1/IFITM3/C1S/S100A8/C3/CD24/SLPI/IFITM2/IFITM1/SERPING1/C9/CFB/FCER1G/IFNGR2/P: | 84 |
| GO:0009607 | response to biotic stimulus                                | 84/182 | 338/749 | 0,406832719 | 0,999954951 | 0,999954951 | S100A9/LTF/BCL3/C1QB/JAK1/IFITM3/C1S/S100A8/C3/CD24/SLPI/IFITM2/IFITM1/SERPING1/C9/CFB/FCER1G/IFNGR2/P: | 84 |
| GO:0002682 | regulation of immune system process                        | 83/182 | 362/749 | 0,824122632 | 0,999954951 | 0,999954951 | HIF1A/LTF/C1QB/JAK1/C1S/FPR1/BCL6/STAT3/C3/CD24/IFITM1/SERPING1/C9/CFB/FCER1G/IFNGR2/PSMB8/IL1R1/SOCS   | 83 |
| GO:0071840 | cellular component organization or biogenesis              | 81/182 | 331/749 | 0,494521364 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL3/C1QB/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/COL4A1/ITGB6/C9/FCER1G/SOST/MUC1/TNFRS      | 81 |
| GO:0071345 | cellular response to cytokine stimulus                     | 80/182 | 314/749 | 0,289713231 | 0,999954951 | 0,999954951 | OSMR/HIF1A/JAK1/IFITM3/FPR1/SOD2/BCL6/TIMP1/STAT3/CD24/IFITM2/IFITM1/FCER1G/IFNGR2/PSMB8/IL1R1/SOCS3    | 80 |
| GO:0016043 | cellular component organization                            | 80/182 | 329/749 | 0,529654509 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL3/C1QB/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/COL4A1/ITGB6/C9/FCER1G/SOST/MUC1/TNFRS      | 80 |
| GO:0009966 | regulation of signal transduction                          | 80/182 | 334/749 | 0,611329223 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/JAK1/FPR1/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/CD24/IFNGR2/SOST/PSMB8/IL1R1/SOCS3/N    | 80 |
| GO:0048513 | animal organ development                                   | 79/182 | 341/749 | 0,771918264 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/PLAAT4/C1QB/BCL6/TIMP1/STAT3/CD24/COL4A1/ADAMTS1/NNMT/FCER1G/PSMB8/SOCS3/TNFRSF1A        | 79 |
| GO:0065008 | regulation of biological quality                           | 78/182 | 304/749 | 0,263854654 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/BCL3/FPR1/SOD2/BCL6/STAT3/S100A8/C3/CD24/SERPING1/FCER1G/PSMB8/EHD3/ABC       | 78 |
| GO:0051246 | regulation of protein metabolic process                    | 77/182 | 293/749 | 0,177135497 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/LTF/BCL3/RARRES1/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/CD24/SLPI/SERPING1/PSMB8/SOCS3/MUC     | 77 |
| GO:0051173 | positive regulation of nitrogen compound metabolic process | 76/182 | 329/749 | 0,776972396 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/FPR1/BCL6/STAT3/S100A8/C3/CD24/SOST/SOCS3/MUC1/TNFRSF1A/LTBR/HDAC6/COL1A1/NR      | 76 |
| GO:0001775 | cell activation                                            | 76/182 | 333/749 | 0,823365352 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/LTF/BCL3/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/CD24/SLPI/FCER1G/FCGR3B/MME/LCN2/LTBR/COL1     | 76 |
| GO:0009058 | biosynthetic process                                       | 75/182 | 327/749 | 0,802636866 | 0,999954951 | 0,999954951 | ALDH3A2/S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/C3/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1        | 75 |
| GO:0031325 | positive regulation of cellular metabolic process          | 75/182 | 338/749 | 0,904514053 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/FPR1/BCL6/STAT3/S100A8/C3/CD24/SOST/SOCS3/MUC1/TNFRSF1A/LTBR/HDAC6/COL1A1/NR      | 75 |
| GO:1901576 | organic substance biosynthetic process                     | 74/182 | 319/749 | 0,755007542 | 0,999954951 | 0,999954951 | ALDH3A2/S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/C3/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1        | 74 |
| GO:0044249 | cellular biosynthetic process                              | 73/182 | 321/749 | 0,82808039  | 0,999954951 | 0,999954951 | ALDH3A2/S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/C3/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1        | 73 |
| GO:0006464 | cellular protein modification process                      | 72/182 | 292/749 | 0,460667862 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/JAK1/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/CD24/PSMB8/SOCS3/MUC1/MAPK13/TNFRSF1A/ASB15/      | 72 |
| GO:0036211 | protein modification process                               | 72/182 | 292/749 | 0,460667862 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/JAK1/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/CD24/PSMB8/SOCS3/MUC1/MAPK13/TNFRSF1A/ASB15/      | 72 |
| GO:0043412 | macromolecule modification                                 | 72/182 | 295/749 | 0,511403764 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/JAK1/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/CD24/PSMB8/SOCS3/MUC1/MAPK13/TNFRSF1A/ASB15/      | 72 |
| GO:0050793 | regulation of developmental process                        | 72/182 | 297/749 | 0,545098555 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/PLAAT4/JAK1/SOD2/BCL6/TIMP1/STAT3/C3/CD24/IFITM1/PSMB8/SOCS3/TNFRSF1A/MME/HDAC6/C      | 72 |
| GO:1901360 | organic cyclic compound metabolic process                  | 72/182 | 297/749 | 0,545098555 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/MME/HDAC6/COL1A1/NR4         | 72 |
| GO:0035556 | intracellular signal transduction                          | 72/182 | 307/749 | 0,703555228 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/JAK1/FPR1/SOD2/BCL6/S100A8/CD24/PSMB8/SOCS3/MUC1/MAPK13/TNFRSF1A/ASB15/LTBR,      | 72 |
| GO:0098542 | defense response to other organism                         | 71/182 | 268/749 | 0,169463214 | 0,999954951 | 0,999954951 | S100A9/LTF/BCL3/C1QB/JAK1/IFITM3/C1S/S100A8/C3/SLPI/IFITM2/IFITM1/SERPING1/C9/CFB/FCER1G/IFNGR2/PSMB8/  | 71 |
| GO:0019221 | cytokine-mediated signaling pathway                        | 71/182 | 275/749 | 0,257135263 | 0,999954951 | 0,999954951 | OSMR/HIF1A/JAK1/IFITM3/FPR1/SOD2/BCL6/TIMP1/STAT3/CD24/IFITM2/IFITM1/FCER1G/IFNGR2/PSMB8/IL1R1/SOCS3    | 71 |
| GO:0065009 | regulation of molecular function                           | 71/182 | 275/749 | 0,257135263 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/BCL3/PLAAT4/RARRES1/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/CD24/SLPI/SERPING1/PSMI   | 71 |
| GO:0002252 | immune effector process                                    | 69/182 | 261/749 | 0,181677001 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/LTF/BCL3/C1QB/IFITM3/C1S/FPR1/BCL6/STAT3/S100A8/C3/SLPI/IFITM2/IFITM1/SERPING1/C9/CFB/F | 69 |
| GO:0032268 | regulation of cellular protein metabolic process           | 69/182 | 268/749 | 0,273215707 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/LTF/BCL3/RARRES1/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/CD24/SLPI/SERPING1/SOCS3/MUC1/TNFRS    | 69 |
| GO:0034641 | cellular nitrogen compound metabolic process               | 69/182 | 305/749 | 0,83472259  | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/PLAAT4/SOD2/BCL6/STAT3/S100A8/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/MME/HDAC6/COL         | 69 |
| GO:0045321 | leukocyte activation                                       | 69/182 | 306/749 | 0,844915592 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/LTF/BCL3/FPR1/BCL6/STAT3/S100A8/C3/CD24/SLPI/FCER1G/FCGR3B/MME/LCN2/LTBR/ICAM1/IMPE     | 69 |
| GO:0009892 | negative regulation of metabolic process                   | 67/182 | 259/749 | 0,260650843 | 0,999954951 | 0,999954951 | SERPINA3/HIF1A/LTF/BCL3/RARRES1/BCL6/TIMP1/STAT3/C3/CD24/SLPI/SERPING1/PSMB8/SOCS3/MUC1/HDAC6/PSME      | 67 |
| GO:0051240 | positive regulation of multicellular organismal process    | 67/182 | 286/749 | 0,699356161 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/PLAAT4/JAK1/SOD2/BCL6/STAT3/C3/CD24/IFITM1/FCER1G/IL1R1/MAPK13/MME/LCN2/HDAC      | 67 |
| GO:0050776 | regulation of immune response                              | 66/182 | 269/749 | 0,488689741 | 0,999954951 | 0,999954951 | C1QB/JAK1/C1S/FPR1/BCL6/C3/CD24/IFITM1/SERPING1/C9/CFB/FCER1G/IFNGR2/PSMB8/IL1R1/SOCS3/MUC1/IFNAR2/I    | 66 |
| GO:0046483 | heterocycle metabolic process                              | 66/182 | 284/749 | 0,73033796  | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/MME/HDAC6/COL1A1/NR4         | 66 |
| GO:0010605 | negative regulation of macromolecule metabolic process     | 65/182 | 248/749 | 0,220846053 | 0,999954951 | 0,999954951 | SERPINA3/HIF1A/LTF/BCL3/RARRES1/BCL6/TIMP1/STAT3/C3/CD24/SLPI/SERPING1/PSMB8/SOCS3/MUC1/HDAC6/PSME      | 65 |
| GO:1901362 | organic cyclic compound biosynthetic process               | 65/182 | 262/749 | 0,438850418 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PS        | 65 |
| GO:0008219 | cell death                                                 | 65/182 | 266/749 | 0,507853042 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/TIMP1/STAT3/S100A8/CD24/FCER1G/SOCS3/MUC1/TNFRSF1A/LCN2/KRT8/LTBR/I     | 65 |
| GO:0009059 | macromolecule biosynthetic process                         | 65/182 | 288/749 | 0,831377591 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC       | 65 |
| GO:0006725 | cellular aromatic compound metabolic process               | 64/182 | 285/749 | 0,8436254   | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PS        | 64 |
| GO:0045087 | innate immune response                                     | 63/182 | 229/749 | 0,103062112 | 0,999954951 | 0,999954951 | S100A9/LTF/C1QB/JAK1/IFITM3/C1S/S100A8/C3/SLPI/IFITM2/IFITM1/SERPING1/C9/CFB/FCER1G/IFNGR2/PSMB8/SOCS   | 63 |
| GO:0080134 | regulation of response to stress                           | 63/182 | 231/749 | 0,120424069 | 0,999954951 | 0,999954951 | OSMR/S100A9/HIF1A/JAK1/SOD2/BCL6/S100A8/C3/SERPING1/FCER1G/IFNGR2/PSMB8/IL1R1/SOCS3/MUC1/MAPK13/T       | 63 |
| GO:0018130 | heterocycle biosynthetic process                           | 63/182 | 258/749 | 0,511786452 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PS        | 63 |
| GO:0019438 | aromatic compound biosynthetic process                     | 63/182 | 258/749 | 0,511786452 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PS        | 63 |
| GO:0044271 | cellular nitrogen compound biosynthetic process            | 63/182 | 278/749 | 0,813247415 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PS        | 63 |
| GO:0006139 | nucleobase-containing compound metabolic process           | 63/182 | 279/749 | 0,82444055  | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PS        | 63 |
| GO:0031326 | regulation of cellular biosynthetic process                | 63/182 | 281/749 | 0,845489543 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/C3/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME:       | 63 |
| GO:0009889 | regulation of biosynthetic process                         | 63/182 | 284/749 | 0,873739607 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/C3/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME:       | 63 |
| GO:0012501 | programmed cell death                                      | 62/182 | 251/749 | 0,461374697 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/TIMP1/STAT3/S100A8/CD24/FCER1G/SOCS3/MUC1/TNFRSF1A/LCN2/KRT8/LTBR/I     | 62 |
| GO:0034654 | nucleobase-containing compound biosynthetic process        | 62/182 | 256/749 | 0,548506669 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/NNMT/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PS        | 62 |
| GO:0010647 | positive regulation of cell communication                  | 62/182 | 278/749 | 0,857180471 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/STAT3/S100A8/C3/CD24/PSMB8/IL1R1/SOCS3/TNFRSF1A/MME/LTBR/HDAC6/COL1A1/COL3A:      | 62 |
| GO:0023056 | positive regulation of signaling                           | 62/182 | 278/749 | 0,857180471 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/STAT3/S100A8/C3/CD24/PSMB8/IL1R1/SOCS3/TNFRSF1A/MME/LTBR/HDAC6/COL1A1/COL3A:      | 62 |
| GO:0006954 | inflammatory response                                      | 61/182 | 217/749 | 0,073161474 | 0,999954951 | 0,999954951 | SERPINA3/OSMR/S100A9/HIF1A/CD163/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/ITGB6/FCER1G/IL1R1/SOCS3/MAPK13/TN     | 61 |
| GO:0090304 | nucleic acid metabolic process                             | 61/182 | 266/749 | 0,768550762 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC       | 61 |

|            |                                                              |        |         |             |             |             |                                                                                                       |    |
|------------|--------------------------------------------------------------|--------|---------|-------------|-------------|-------------|-------------------------------------------------------------------------------------------------------|----|
| GO:0010556 | regulation of macromolecule biosynthetic process             | 61/182 | 268/749 | 0,79385475  | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC     | 61 |
| GO:0034645 | cellular macromolecule biosynthetic process                  | 61/182 | 268/749 | 0,79385475  | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC     | 61 |
| GO:0050790 | regulation of catalytic activity                             | 60/182 | 221/749 | 0,139558814 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/PLAAT4/RARRES1/FPR1/BCL6/TIMP1/STAT3/S100A8/C3/CD24/SLPI/SERPING1/PSMB8/SO  | 60 |
| GO:0032101 | regulation of response to external stimulus                  | 60/182 | 226/749 | 0,196957968 | 0,999954951 | 0,999954951 | OSMR/S100A9/LTF/JAK1/BCL6/S100A8/C3/SERPING1/FCER1G/IFNGR2/PSMB8/IL1R1/SOCS3/MUC1/MAPK13/TNFRSF1A     | 60 |
| GO:0006915 | apoptotic process                                            | 60/182 | 247/749 | 0,535341402 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/TIMP1/STAT3/S100A8/CD24/FCER1G/SOCS3/MUC1/TNFRSF1A/LCN2/KRT8/LTBR/I   | 60 |
| GO:2000026 | regulation of multicellular organismal development           | 60/182 | 258/749 | 0,715269694 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/PLAAT4/JAK1/SOD2/BCL6/TIMP1/STAT3/C3/CD24/PSMB8/TNFRSF1A/MME/COL1A1/COL3A1/PSME2     | 60 |
| GO:0006796 | phosphate-containing compound metabolic process              | 60/182 | 272/749 | 0,878948422 | 0,999954951 | 0,999954951 | HIF1A/LTF/PLAAT4/JAK1/FPR1/STAT3/C3/CD24/NNMT/PSMB8/SOCS3/MAPK13/TNFRSF1A/LTBR/HDAC6/PSME2/ICAM1      | 60 |
| GO:0006793 | phosphorus metabolic process                                 | 60/182 | 273/749 | 0,887298814 | 0,999954951 | 0,999954951 | HIF1A/LTF/PLAAT4/JAK1/FPR1/STAT3/C3/CD24/NNMT/PSMB8/SOCS3/MAPK13/TNFRSF1A/LTBR/HDAC6/PSME2/ICAM1      | 60 |
| GO:0032879 | regulation of localization                                   | 60/182 | 301/749 | 0,991516148 | 0,999954951 | 0,999954951 | HIF1A/SOD2/BCL6/TIMP1/STAT3/S100A8/C3/ADAMTS1/IFITM1/FCER1G/IL1R1/TNFRSF1A/EHD3/ABCB1/HDAC6/COL1A1    | 60 |
| GO:1901700 | response to oxygen-containing compound                       | 59/182 | 225/749 | 0,23752965  | 0,999954951 | 0,999954951 | HIF1A/LTF/SOD2/TIMP1/STAT3/S100A8/COL4A1/SLPI/SOCS3/MAPK13/LCN2/KRT8/HDAC6/COL1A1/NR4A1/COL3A1/ICA    | 59 |
| GO:0001816 | cytokine production                                          | 59/182 | 229/749 | 0,297264634 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/BCL6/STAT3/S100A8/C3/CD24/ITGB6/FCER1G/IL1R1/MAPK13/MAF/RELB/JAK3/STAT1/IL4R/TG | 59 |
| GO:0016070 | RNA metabolic process                                        | 59/182 | 249/749 | 0,639790384 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC     | 59 |
| GO:0008283 | cell population proliferation                                | 59/182 | 282/749 | 0,961775555 | 0,999954951 | 0,999954951 | OSMR/HIF1A/LTF/PLAAT4/RARRES1/SOD2/BCL6/TIMP1/STAT3/CD24/ADAMTS1/IFITM1/ABCB1/NR4A1/IMPDH1/PSMB1      | 59 |
| GO:0045595 | regulation of cell differentiation                           | 58/182 | 226/749 | 0,314064166 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/PLAAT4/SOD2/BCL6/STAT3/CD24/IFITM1/PSMB8/SOCS3/TNFRSF1A/MME/HDAC6/COL1A1/COL3A1/     | 58 |
| GO:0032774 | RNA biosynthetic process                                     | 58/182 | 240/749 | 0,55714386  | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC     | 58 |
| GO:0019219 | regulation of nucleobase-containing compound metabolic proce | 58/182 | 251/749 | 0,734602744 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC     | 58 |
| GO:0002684 | positive regulation of immune system process                 | 58/182 | 273/749 | 0,941908344 | 0,999954951 | 0,999954951 | HIF1A/C1QB/C1S/FPR1/BCL6/STAT3/C3/CD24/SERPING1/C9/CFB/FCER1G/PSMB8/IL1R1/MUC1/PSME2/ICAM1/C1QA/PS    | 58 |
| GO:0010628 | positive regulation of gene expression                       | 58/182 | 288/749 | 0,986160785 | 0,999954951 | 0,999954951 | HIF1A/BCL3/STAT3/C3/FCER1G/SOST/IL1R1/MUC1/MAPK13/TNFRSF1A/LCN2/COL1A1/NR4A1/MAF/RELB/STAT1/IL4R/T    | 58 |
| GO:2000112 | regulation of cellular macromolecule biosynthetic process    | 57/182 | 250/749 | 0,777916461 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC     | 57 |
| GO:0051641 | cellular localization                                        | 56/182 | 203/749 | 0,118902945 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/BCL3/FPR1/TIMP1/STAT3/S100A8/C3/CD24/SLPI/SERPING1/FCER1G/TNFRSF1A/FCGR3B/I | 56 |
| GO:0046903 | secretion                                                    | 56/182 | 214/749 | 0,253393076 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/FPR1/TIMP1/S100A8/C3/ITGB6/SLPI/SERPING1/FCER1G/TNFRSF1A/FCGR3B/MME/LCN2/I  | 56 |
| GO:0051247 | positive regulation of protein metabolic process             | 56/182 | 236/749 | 0,630517902 | 0,999954951 | 0,999954951 | S100A9/LTF/BCL3/FPR1/BCL6/STAT3/S100A8/C3/CD24/SOCS3/MUC1/TNFRSF1A/LTBR/HDAC6/PSME2/ICAM1/FCGR1A/     | 56 |
| GO:2001141 | regulation of RNA biosynthetic process                       | 56/182 | 237/749 | 0,647124752 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC     | 56 |
| GO:0006351 | transcription, DNA-templated                                 | 56/182 | 238/749 | 0,663428279 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC     | 56 |
| GO:0009653 | anatomical structure morphogenesis                           | 56/182 | 238/749 | 0,663428279 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/JAK1/BCL6/STAT3/C3/COL4A1/ADAMTS1/PSMB8/LYVE1/SOCS3/TNFRSF1A/KRT8/HDAC6/COL1A1/NR4     | 56 |
| GO:0097659 | nucleic acid-templated transcription                         | 56/182 | 238/749 | 0,663428279 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC     | 56 |
| GO:0051252 | regulation of RNA metabolic process                          | 56/182 | 239/749 | 0,679403514 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC     | 56 |
| GO:0031324 | negative regulation of cellular metabolic process            | 55/182 | 196/749 | 0,092281125 | 0,999954951 | 0,999954951 | SERPINA3/HIF1A/LTF/BCL3/RARRES1/BCL6/TIMP1/STAT3/C3/SLPI/SERPING1/SOCS3/MUC1/HDAC6/MAF/RELB/JAK3/ST   | 55 |
| GO:0032940 | secretion by cell                                            | 55/182 | 204/749 | 0,172504363 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/FPR1/TIMP1/S100A8/C3/ITGB6/SLPI/SERPING1/FCER1G/TNFRSF1A/FCGR3B/MME/LCN2/I  | 55 |
| GO:0140352 | export from cell                                             | 55/182 | 204/749 | 0,172504363 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/FPR1/TIMP1/S100A8/C3/ITGB6/SLPI/SERPING1/FCER1G/TNFRSF1A/FCGR3B/MME/LCN2/I  | 55 |
| GO:0001817 | regulation of cytokine production                            | 55/182 | 211/749 | 0,268994344 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/BCL6/STAT3/C3/CD24/ITGB6/FCER1G/IL1R1/MAPK13/RELB/JAK3/STAT1/IL4R/TGFB1/SOCS1/XBP1/STA | 55 |
| GO:0009967 | positive regulation of signal transduction                   | 55/182 | 246/749 | 0,830607248 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/STAT3/S100A8/C3/CD24/PSMB8/IL1R1/SOCS3/TNFRSF1A/LTBR/HDAC6/COL1A1/COL3A1/PSM    | 55 |
| GO:0010941 | regulation of cell death                                     | 54/182 | 233/749 | 0,715469153 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/TIMP1/STAT3/S100A8/FCER1G/SOCS3/MUC1/TNFRSF1A/LTBR/HDAC6/ICAM1/C1C    | 54 |
| GO:0006355 | regulation of transcription, DNA-templated                   | 54/182 | 235/749 | 0,744743385 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC     | 54 |
| GO:1903506 | regulation of nucleic acid-templated transcription           | 54/182 | 235/749 | 0,744743385 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/STAT3/S100A8/SOST/PSMB8/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/PSME2/IC     | 54 |
| GO:0048585 | negative regulation of response to stimulus                  | 53/182 | 214/749 | 0,459718613 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/SOD2/BCL6/SERPING1/SOST/PSMB8/SOCS3/MUC1/TNFRSF1A/COL3A1/PSME2/ICAM1/PSMB10/JAK3/S     | 53 |
| GO:0016310 | phosphorylation                                              | 53/182 | 246/749 | 0,907289543 | 0,999954951 | 0,999954951 | HIF1A/LTF/JAK1/FPR1/STAT3/C3/CD24/PSMB8/SOCS3/MAPK13/TNFRSF1A/LTBR/HDAC6/PSME2/ICAM1/PSMB10/FCGR      | 53 |
| GO:0032270 | positive regulation of cellular protein metabolic process    | 52/182 | 217/749 | 0,588732421 | 0,999954951 | 0,999954951 | S100A9/LTF/BCL3/FPR1/BCL6/STAT3/S100A8/C3/CD24/SOCS3/MUC1/TNFRSF1A/LTBR/HDAC6/PSME2/ICAM1/FCGR1A/     | 52 |
| GO:0042127 | regulation of cell population proliferation                  | 52/182 | 254/749 | 0,968046152 | 0,999954951 | 0,999954951 | OSMR/HIF1A/LTF/PLAAT4/RARRES1/SOD2/BCL6/TIMP1/STAT3/CD24/ADAMTS1/IFITM1/NR4A1/JAK3/STAT1/IL4R/TGFB    | 52 |
| GO:0031399 | regulation of protein modification process                   | 51/182 | 211/749 | 0,555277054 | 0,999954951 | 0,999954951 | LTF/FPR1/BCL6/STAT3/C3/CD24/SOCS3/MUC1/TNFRSF1A/LTBR/HDAC6/ICAM1/FCGR1A/TGFB1/SOCS1/DNMT1/BAX/CD      | 51 |
| GO:0006468 | protein phosphorylation                                      | 51/182 | 235/749 | 0,887883812 | 0,999954951 | 0,999954951 | LTF/JAK1/FPR1/STAT3/C3/CD24/PSMB8/SOCS3/MAPK13/TNFRSF1A/LTBR/HDAC6/PSME2/ICAM1/PSMB10/FCGR1A/JAK      | 51 |
| GO:0016192 | vesicle-mediated transport                                   | 50/182 | 182/749 | 0,147479822 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/LTF/CD163/FPR1/TIMP1/S100A8/C3/SLPI/SERPING1/FCER1G/FCGR3B/EHD3/MME/LCN2/IMPDH1/FC    | 50 |
| GO:0043067 | regulation of programmed cell death                          | 50/182 | 215/749 | 0,695448145 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/TIMP1/STAT3/S100A8/FCER1G/SOCS3/MUC1/TNFRSF1A/LTBR/HDAC6/ICAM1/JAK    | 50 |
| GO:0002443 | leukocyte mediated immunity                                  | 49/182 | 182/749 | 0,197178568 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/LTF/BCL3/C1QB/C1S/FPR1/BCL6/S100A8/C3/SLPI/SERPING1/C9/FCER1G/IL1R1/FCGR3B/MME/LCN2/  | 49 |
| GO:0051241 | negative regulation of multicellular organismal process      | 49/182 | 186/749 | 0,255836409 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/BCL6/TIMP1/STAT3/CD24/SERPING1/SOST/TNFRSF1A/COL3A1/RELB/JAK3/STAT1/IL4R/TGFB1/SOCS1/L | 49 |
| GO:0044093 | positive regulation of molecular function                    | 49/182 | 197/749 | 0,44836764  | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/PLAAT4/FPR1/STAT3/S100A8/CD24/EHD3/ABCB1/PSME2/ICAM1/FCGR1A/TGFB1/SOCS1/BAX/CDKN     | 49 |
| GO:0042981 | regulation of apoptotic process                              | 49/182 | 211/749 | 0,698292343 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/SOD2/BCL6/TIMP1/STAT3/S100A8/FCER1G/SOCS3/MUC1/TNFRSF1A/LTBR/ICAM1/JAK3/STAT1   | 49 |
| GO:0033036 | macromolecule localization                                   | 49/182 | 212/749 | 0,713992564 | 0,999954951 | 0,999954951 | HIF1A/BCL3/BCL6/STAT3/C3/CD24/ITGB6/FCER1G/TNFRSF1A/EHD3/ABCB1/GBP2/HDAC6/COL1A1/IL4R/TGFB1/SOCS1/    | 49 |
| GO:1902531 | regulation of intracellular signal transduction              | 49/182 | 216/749 | 0,772315166 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL3/FPR1/SOD2/BCL6/S100A8/CD24/MUC1/TNFRSF1A/LTBR/COL3A1/ICAM1/STAT1/TGFB1/XBP1/I   | 49 |
| GO:0031347 | regulation of defense response                               | 48/182 | 169/749 | 0,095885043 | 0,999954951 | 0,999954951 | OSMR/S100A9/JAK1/BCL6/S100A8/C3/SERPING1/FCER1G/IFNGR2/PSMB8/IL1R1/SOCS3/MUC1/MAPK13/TNFRSF1A/IFN     | 48 |
| GO:0007267 | cell-cell signaling                                          | 48/182 | 210/749 | 0,746987795 | 0,999954951 | 0,999954951 | S100A9/HIF1A/STAT3/S100A8/C3/CD24/ITGB6/FCER1G/SOST/PSMB8/MME/COL1A1/PSME2/C1QA/PSMB10/IL4R/SOCS      | 48 |
| GO:0042592 | homeostatic process                                          | 47/182 | 197/749 | 0,601598616 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/HIF1A/LTF/FPR1/SOD2/BCL6/STAT3/S100A8/CD24/FCER1G/LCN2/ICAM1/JAK3/STAT1/IL4R/TGFB1/XI | 47 |
| GO:0071702 | organic substance transport                                  | 47/182 | 199/749 | 0,637166073 | 0,999954951 | 0,999954951 | HIF1A/STAT3/S100A8/C3/CD24/ITGB6/FCER1G/EHD3/ABCB1/HDAC6/COL1A1/IL4R/TGFB1/SOCS1/XBP1/BAX/CDKN1A/II   | 47 |
| GO:0019220 | regulation of phosphate metabolic process                    | 47/182 | 209/749 | 0,791426904 | 0,999954951 | 0,999954951 | HIF1A/LTF/FPR1/STAT3/C3/CD24/SOCS3/TNFRSF1A/LTBR/HDAC6/ICAM1/FCGR1A/TGFB1/SOCS1/BAX/CDKN1A/AGT/LDI    | 47 |
| GO:0051174 | regulation of phosphorus metabolic process                   | 47/182 | 209/749 | 0,791426904 | 0,999954951 | 0,999954951 | HIF1A/LTF/FPR1/STAT3/C3/CD24/SOCS3/TNFRSF1A/LTBR/HDAC6/ICAM1/FCGR1A/TGFB1/SOCS1/BAX/CDKN1A/AGT/LDI    | 47 |
| GO:0040011 | locomotion                                                   | 47/182 | 244/749 | 0,990704061 | 0,999954951 | 0,999954951 | S100A9/HIF1A/FPR1/SOD2/TIMP1/STAT3/S100A8/CD24/ITGB6/ADAMTS1/IFITM1/FCER1G/IL1R1/HDAC6/COL1A1/NR4A    | 47 |
| GO:0009888 | tissue development                                           | 46/182 | 179/749 | 0,341693139 | 0,999954951 | 0,999954951 | ALDH3A2/HIF1A/LTF/PLAAT4/TIMP1/CD24/COL4A1/PSMB8/SOCS3/TNFRSF1A/KRT8/COL1A1/COL3A1/PSME2/ICAM1/M      | 46 |
| GO:0010629 | negative regulation of gene expression                       | 46/182 | 195/749 | 0,640023004 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/BCL6/STAT3/CD24/PSMB8/MUC1/HDAC6/PSME2/MAF/PSMB10/RELB/JAK3/STAT1/TGFB1/DNMT1/AH       | 46 |
| GO:0051094 | positive regulation of developmental process                 | 46/182 | 202/749 | 0,752971372 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/PLAAT4/JAK1/SOD2/BCL6/STAT3/C3/CD24/IFITM1/SOCS3/TNFRSF1A/MME/COL1A1/STAT1/IL4R/NFI  | 46 |

|            |                                                              |        |         |             |             |             |                                                                                                       |    |
|------------|--------------------------------------------------------------|--------|---------|-------------|-------------|-------------|-------------------------------------------------------------------------------------------------------|----|
| GO:1901701 | cellular response to oxygen-containing compound              | 45/182 | 165/749 | 0,18203504  | 0,999954951 | 0,999954951 | HIF1A/LTF/SOD2/STAT3/COL4A1/SOCS3/MAPK13/LCN2/HDAC6/COL1A1/NR4A1/COL3A1/ICAM1/JAK3/STAT1/TGFB1/SC     | 45 |
| GO:0006928 | movement of cell or subcellular component                    | 45/182 | 241/749 | 0,995367795 | 0,999954951 | 0,999954951 | S100A9/HIF1A/SOD2/BCL6/TIMP1/STAT3/S100A8/CD24/ITGB6/ADAMTS1/IFITM1/FCER1G/IL1R1/HDAC6/COL1A1/NR4A    | 45 |
| GO:0042325 | regulation of phosphorylation                                | 44/182 | 200/749 | 0,836832357 | 0,999954951 | 0,999954951 | HIF1A/LTF/FPR1/STAT3/C3/CD24/SOCS3/TNFRSF1A/LTBR/HDAC6/ICAM1/FCGR1A/TGFB1/SOCS1/BAX/CDKN1A/AGT/EG     | 44 |
| GO:0048870 | cell motility                                                | 44/182 | 234/749 | 0,993642161 | 0,999954951 | 0,999954951 | S100A9/HIF1A/SOD2/TIMP1/STAT3/S100A8/CD24/ITGB6/ADAMTS1/IFITM1/FCER1G/IL1R1/HDAC6/COL1A1/NR4A1/COI    | 44 |
| GO:0051674 | localization of cell                                         | 44/182 | 234/749 | 0,993642161 | 0,999954951 | 0,999954951 | S100A9/HIF1A/SOD2/TIMP1/STAT3/S100A8/CD24/ITGB6/ADAMTS1/IFITM1/FCER1G/IL1R1/HDAC6/COL1A1/NR4A1/COI    | 44 |
| GO:0048468 | cell development                                             | 43/182 | 169/749 | 0,38168859  | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL6/STAT3/S100A8/C3/TNFRSF1A/MME/KRT8/HDAC6/COL3A1/ICAM1/C1QA/MAF/TGFB1/XBP1/B/     | 43 |
| GO:0048534 | hematopoietic or lymphoid organ development                  | 43/182 | 205/749 | 0,920034809 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/BCL6/STAT3/FCER1G/PSMB8/LTBR/PSME2/PSMB10/RELB/JAK3/STAT1/IL4R/NFKBIZ/TGFB1/SOCS1/XBP  | 43 |
| GO:0002520 | immune system development                                    | 43/182 | 217/749 | 0,973940825 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/BCL6/STAT3/FCER1G/PSMB8/LTBR/PSME2/PSMB10/RELB/JAK3/STAT1/IL4R/NFKBIZ/TGFB1/SOCS1/XBP  | 43 |
| GO:0016477 | cell migration                                               | 43/182 | 229/749 | 0,993188953 | 0,999954951 | 0,999954951 | S100A9/HIF1A/SOD2/TIMP1/STAT3/S100A8/CD24/ITGB6/ADAMTS1/IFITM1/FCER1G/IL1R1/HDAC6/COL1A1/NR4A1/COI    | 43 |
| GO:0009719 | response to endogenous stimulus                              | 42/182 | 177/749 | 0,615726476 | 0,999954951 | 0,999954951 | TIMP1/STAT3/COL4A1/FCER1G/SOST/SOCS3/MAPK13/HDAC6/COL1A1/NR4A1/COL3A1/ICAM1/JAK3/STAT1/TGFB1/SOC      | 42 |
| GO:0001932 | regulation of protein phosphorylation                        | 42/182 | 193/749 | 0,853679636 | 0,999954951 | 0,999954951 | LTF/FPR1/STAT3/C3/CD24/SOCS3/TNFRSF1A/LTBR/HDAC6/ICAM1/FCGR1A/TGFB1/SOCS1/BAX/CDKN1A/AGT/EGR1/TLR     | 42 |
| GO:0008104 | protein localization                                         | 42/182 | 195/749 | 0,873875398 | 0,999954951 | 0,999954951 | HIF1A/BCL3/BCL6/STAT3/CD24/ITGB6/FCER1G/TNFRSF1A/EHD3/GBP2/HDAC6/COL1A1/IL4R/TGFB1/SOCS1/XBP1/BAX/C   | 42 |
| GO:0046649 | lymphocyte activation                                        | 42/182 | 235/749 | 0,998234915 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/CD24/FCER1G/ICAM1/IMPDPH1/PSMB10/RELB/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/BAX/AHR/CDK   | 42 |
| GO:0010648 | negative regulation of cell communication                    | 41/182 | 169/749 | 0,542082055 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/SOD2/BCL6/SOST/PSMB8/SOCS3/MUC1/PSME2/ICAM1/PSMB10/STAT1/TGFB1/SOCS1/XBP1/BAX/AGT      | 41 |
| GO:0023057 | negative regulation of signaling                             | 41/182 | 170/749 | 0,561602666 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/SOD2/BCL6/SOST/PSMB8/SOCS3/MUC1/PSME2/ICAM1/PSMB10/STAT1/TGFB1/SOCS1/XBP1/BAX/AGT      | 41 |
| GO:0071705 | nitrogen compound transport                                  | 41/182 | 180/749 | 0,739013212 | 0,999954951 | 0,999954951 | HIF1A/STAT3/S100A8/CD24/ITGB6/FCER1G/EHD3/ABCB1/HDAC6/COL1A1/IL4R/TGFB1/SOCS1/XBP1/BAX/CDKN1A/IL17I   | 41 |
| GO:0050778 | positive regulation of immune response                       | 41/182 | 191/749 | 0,876669286 | 0,999954951 | 0,999954951 | C1QB/C1S/FPR1/C3/SERPING1/C9/CFB/FCER1G/PSMB8/IL1R1/MUC1/PSME2/C1QA/PSMB10/RELB/FCGR1A/IL4R/NFKBI     | 41 |
| GO:0030097 | hemopoiesis                                                  | 41/182 | 196/749 | 0,917624422 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/BCL6/STAT3/FCER1G/PSMB8/LTBR/PSME2/PSMB10/RELB/JAK3/STAT1/IL4R/NFKBIZ/TGFB1/SOCS1/XBP  | 41 |
| GO:0009891 | positive regulation of biosynthetic process                  | 41/182 | 208/749 | 0,973348927 | 0,999954951 | 0,999954951 | HIF1A/BCL3/STAT3/SOST/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/ICAM1/MAF/RELB/STAT1/TGFB1/XBP1/AHR/STAT6      | 41 |
| GO:0009628 | response to abiotic stimulus                                 | 40/182 | 141/749 | 0,127428679 | 0,999954951 | 0,999954951 | HIF1A/BCL3/CD24/SOST/PSMB8/MAPK13/TNFRSF1A/ABCB1/MME/KRT8/LTBR/COL1A1/COL3A1/PSME2/ICAM1/PSMB10       | 40 |
| GO:0051128 | regulation of cellular component organization                | 40/182 | 168/749 | 0,602942632 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/S100A8/C3/SOST/MUC1/TNFRSF1A/EHD3/LCN2/HDAC6/ICAM1/IL4R/TGFB1/DNMT1/BAX/CXCL16/     | 40 |
| GO:0006366 | transcription by RNA polymerase II                           | 40/182 | 182/749 | 0,825722563 | 0,999954951 | 0,999954951 | HIF1A/BCL3/SOD2/BCL6/STAT3/PSMB8/MUC1/TNFRSF1A/NR4A1/PSME2/MAF/PSMB10/RELB/STAT1/TGFB1/XBP1/DNM       | 40 |
| GO:0031328 | positive regulation of cellular biosynthetic process         | 40/182 | 205/749 | 0,977005522 | 0,999954951 | 0,999954951 | HIF1A/BCL3/STAT3/SOST/MUC1/TNFRSF1A/COL1A1/NR4A1/ICAM1/MAF/RELB/STAT1/TGFB1/XBP1/AHR/STAT6/AGT/LL     | 40 |
| GO:0051049 | regulation of transport                                      | 40/182 | 208/749 | 0,983393034 | 0,999954951 | 0,999954951 | HIF1A/S100A8/C3/FCER1G/TNFRSF1A/EHD3/ABCB1/ICAM1/IL4R/TGFB1/SOCS1/XBP1/BAX/IL17RA/AGT/FKBP1A/TLR4/C   | 40 |
| GO:0043085 | positive regulation of catalytic activity                    | 39/182 | 157/749 | 0,466640454 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/PLAAT4/FPR1/STAT3/S100A8/CD24/PSME2/ICAM1/FCGR1A/TGFB1/SOCS1/BAX/CDKN1A/AGT/EGR1     | 39 |
| GO:0001819 | positive regulation of cytokine production                   | 39/182 | 159/749 | 0,507142806 | 0,999954951 | 0,999954951 | HIF1A/BCL3/STAT3/C3/FCER1G/IL1R1/MAPK13/STAT1/IL4R/TGFB1/XBP1/STAT6/IL17RA/AGT/CD276/LY96/EGR1/NFKB2  | 39 |
| GO:0072359 | circulatory system development                               | 39/182 | 159/749 | 0,507142806 | 0,999954951 | 0,999954951 | HIF1A/JAK1/SOD2/STAT3/C3/COL4A1/ADAMTS1/SOCS3/TNFRSF1A/COL1A1/NR4A1/COL3A1/STAT1/TGFB1/XBP1/DNMT      | 39 |
| GO:0033554 | cellular response to stress                                  | 39/182 | 164/749 | 0,605984104 | 0,999954951 | 0,999954951 | HIF1A/BCL3/SOD2/BCL6/PSMB8/MUC1/MAPK13/TNFRSF1A/LCN2/LTBR/HDAC6/PSME2/ICAM1/PSMB10/RELB/XBP1/BA       | 39 |
| GO:0009617 | response to bacterium                                        | 39/182 | 170/749 | 0,713812222 | 0,999954951 | 0,999954951 | S100A9/LTF/BCL3/S100A8/C3/CD24/SLPI/FCER1G/TNFRSF1A/GBP2/LCN2/ICAM1/TGFB1/XBP1/VCAM1/SIGIRR/LY96/NFI  | 39 |
| GO:0022610 | biological adhesion                                          | 39/182 | 235/749 | 0,999764662 | 0,999954951 | 0,999954951 | S100A9/LTF/BCL6/S100A8/CD24/ITGB6/LYVE1/MUC1/COL1A1/COL3A1/MEGF11/ICAM1/JAK3/IL4R/NFKBIZ/TGFB1/SOC    | 39 |
| GO:0009968 | negative regulation of signal transduction                   | 38/182 | 153/749 | 0,468595999 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/SOD2/BCL6/SOST/PSMB8/SOCS3/MUC1/PSME2/ICAM1/PSMB10/STAT1/TGFB1/SOCS1/XBP1/BAX/AGT      | 38 |
| GO:0042886 | amide transport                                              | 38/182 | 166/749 | 0,717386457 | 0,999954951 | 0,999954951 | HIF1A/STAT3/S100A8/CD24/ITGB6/EHD3/ABCB1/HDAC6/COL1A1/IL4R/TGFB1/SOCS1/XBP1/BAX/CDKN1A/IL17RA/AGT/    | 38 |
| GO:0031401 | positive regulation of protein modification process          | 38/182 | 173/749 | 0,820089706 | 0,999954951 | 0,999954951 | LTF/FPR1/BCL6/STAT3/C3/CD24/SOCS3/MUC1/TNFRSF1A/LTBR/HDAC6/ICAM1/FCGR1A/TGFB1/SOCS1/DNMT1/CDKN1A/     | 38 |
| GO:0006357 | regulation of transcription by RNA polymerase II             | 38/182 | 176/749 | 0,855312338 | 0,999954951 | 0,999954951 | HIF1A/BCL3/SOD2/BCL6/STAT3/PSMB8/MUC1/TNFRSF1A/NR4A1/PSME2/MAF/PSMB10/RELB/STAT1/TGFB1/XBP1/DNM       | 38 |
| GO:0007155 | cell adhesion                                                | 38/182 | 234/749 | 0,99986858  | 0,999954951 | 0,999954951 | S100A9/BCL6/S100A8/CD24/ITGB6/LYVE1/MUC1/COL1A1/COL3A1/MEGF11/ICAM1/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/X    | 38 |
| GO:0045597 | positive regulation of cell differentiation                  | 37/182 | 154/749 | 0,572857965 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/PLAAT4/SOD2/BCL6/STAT3/CD24/IFITM1/SOCS3/MME/COL1A1/STAT1/IL4R/NFKBIZ/TGFB1/SOCS1/   | 37 |
| GO:0015833 | peptide transport                                            | 37/182 | 164/749 | 0,753275145 | 0,999954951 | 0,999954951 | HIF1A/STAT3/S100A8/CD24/ITGB6/EHD3/HDAC6/COL1A1/IL4R/TGFB1/SOCS1/XBP1/BAX/CDKN1A/IL17RA/AGT/TLR4/AF   | 37 |
| GO:0033993 | response to lipid                                            | 37/182 | 172/749 | 0,858597787 | 0,999954951 | 0,999954951 | LTF/STAT3/S100A8/SLPI/LCN2/HDAC6/COL1A1/NR4A1/ICAM1/TGFB1/XBP1/AHR/CDKN1A/VCAM1/AGT/SIGIRR/LDLR/TI    | 37 |
| GO:0002250 | adaptive immune response                                     | 37/182 | 185/749 | 0,954238944 | 0,999954951 | 0,999954951 | BCL3/C1QB/C1S/BCL6/STAT3/C3/SERPING1/C9/FCER1G/IL1R1/ICAM1/C1QA/RELB/JAK3/IL4R/NFKBIZ/TGFB1/STAT6/IL1 | 37 |
| GO:0010557 | positive regulation of macromolecule biosynthetic process    | 37/182 | 195/749 | 0,984039995 | 0,999954951 | 0,999954951 | HIF1A/BCL3/STAT3/SOST/MUC1/TNFRSF1A/HDAC6/COL1A1/NR4A1/MAF/RELB/STAT1/TGFB1/XBP1/AHR/STAT6/AGT/CI     | 37 |
| GO:0015031 | protein transport                                            | 36/182 | 160/749 | 0,757061896 | 0,999954951 | 0,999954951 | HIF1A/STAT3/CD24/ITGB6/EHD3/HDAC6/COL1A1/IL4R/TGFB1/SOCS1/XBP1/BAX/CDKN1A/IL17RA/AGT/TLR4/APOE/TLR    | 36 |
| GO:0045184 | establishment of protein localization                        | 36/182 | 164/749 | 0,814408844 | 0,999954951 | 0,999954951 | HIF1A/STAT3/CD24/ITGB6/EHD3/HDAC6/COL1A1/IL4R/TGFB1/SOCS1/XBP1/BAX/CDKN1A/IL17RA/AGT/TLR4/APOE/TLR    | 36 |
| GO:0045935 | positive regulation of nucleobase-containing compound metabo | 36/182 | 179/749 | 0,94662968  | 0,999954951 | 0,999954951 | HIF1A/BCL3/STAT3/SOST/MUC1/TNFRSF1A/COL1A1/NR4A1/MAF/RELB/STAT1/TGFB1/XBP1/BAX/AHR/STAT6/AGT/EGR      | 36 |
| GO:0032103 | positive regulation of response to external stimulus         | 35/182 | 149/749 | 0,638403891 | 0,999954951 | 0,999954951 | OSMR/S100A9/S100A8/C3/FCER1G/PSMB8/MUC1/MAPK13/TNFRSF1A/PSME2/PSMB10/RELB/NFKBIZ/TGFB1/IL17RA/A       | 35 |
| GO:0060548 | negative regulation of cell death                            | 35/182 | 152/749 | 0,694106099 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/SOD2/BCL6/TIMP1/STAT3/FCER1G/SOCS3/MUC1/ICAM1/JAK3/XBP1/DNMT1/BAX/CDKN1A/KITLG/MYI     | 35 |
| GO:0048878 | chemical homeostasis                                         | 34/182 | 125/749 | 0,235599199 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/SOD2/STAT3/S100A8/CD24/LCN2/ICAM1/STAT1/TGFB1/XBP1/BAX/AGT/LDLR/SLC12A3/FKBP1   | 34 |
| GO:0043066 | negative regulation of apoptotic process                     | 34/182 | 139/749 | 0,519361108 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/SOD2/BCL6/TIMP1/STAT3/FCER1G/SOCS3/MUC1/ICAM1/JAK3/XBP1/DNMT1/BAX/CDKN1A/KITLG/MYI     | 34 |
| GO:0043069 | negative regulation of programmed cell death                 | 34/182 | 141/749 | 0,56139455  | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL3/SOD2/BCL6/TIMP1/STAT3/FCER1G/SOCS3/MUC1/ICAM1/JAK3/XBP1/DNMT1/BAX/CDKN1A/KITLG/MYI     | 34 |
| GO:0007399 | nervous system development                                   | 34/182 | 151/749 | 0,749089508 | 0,999954951 | 0,999954951 | ALDH3A2/S100A9/HIF1A/BCL6/STAT3/S100A8/C3/COL4A1/MME/HDAC6/COL3A1/C1QA/TGFB1/XBP1/BAX/VCAM1/AGT       | 34 |
| GO:0051254 | positive regulation of RNA metabolic process                 | 34/182 | 168/749 | 0,934366835 | 0,999954951 | 0,999954951 | HIF1A/BCL3/STAT3/SOST/MUC1/TNFRSF1A/COL1A1/NR4A1/MAF/RELB/STAT1/TGFB1/XBP1/AHR/STAT6/AGT/EGR1/NF      | 34 |
| GO:0010562 | positive regulation of phosphorus metabolic process          | 34/182 | 173/749 | 0,959681182 | 0,999954951 | 0,999954951 | HIF1A/LTF/FPR1/STAT3/C3/CD24/SOCS3/TNFRSF1A/LTBR/HDAC6/ICAM1/FCGR1A/TGFB1/SOCS1/CDKN1A/AGT/EGR1/TI    | 34 |
| GO:0045937 | positive regulation of phosphate metabolic process           | 34/182 | 173/749 | 0,959681182 | 0,999954951 | 0,999954951 | HIF1A/LTF/FPR1/STAT3/C3/CD24/SOCS3/TNFRSF1A/LTBR/HDAC6/ICAM1/FCGR1A/TGFB1/SOCS1/CDKN1A/AGT/EGR1/TI    | 34 |
| GO:0051336 | regulation of hydrolase activity                             | 33/182 | 129/749 | 0,39276261  | 0,999954951 | 0,999954951 | SERPINA3/S100A9/LTF/RARRES1/BCL6/TIMP1/STAT3/S100A8/C3/SLPI/SERPING1/PSMB8/PSME2/ICAM1/BAX/AGT/FKBP   | 33 |
| GO:0045893 | positive regulation of transcription, DNA-templated          | 33/182 | 164/749 | 0,936855485 | 0,999954951 | 0,999954951 | HIF1A/BCL3/STAT3/SOST/MUC1/TNFRSF1A/COL1A1/NR4A1/MAF/RELB/STAT1/TGFB1/XBP1/AHR/STAT6/AGT/EGR1/NF      | 33 |
| GO:1902680 | positive regulation of RNA biosynthetic process              | 33/182 | 165/749 | 0,942613213 | 0,999954951 | 0,999954951 | HIF1A/BCL3/STAT3/SOST/MUC1/TNFRSF1A/COL1A1/NR4A1/MAF/RELB/STAT1/TGFB1/XBP1/AHR/STAT6/AGT/EGR1/NF      | 33 |
| GO:1903508 | positive regulation of nucleic acid-templated transcription  | 33/182 | 165/749 | 0,942613213 | 0,999954951 | 0,999954951 | HIF1A/BCL3/STAT3/SOST/MUC1/TNFRSF1A/COL1A1/NR4A1/MAF/RELB/STAT1/TGFB1/XBP1/AHR/STAT6/AGT/EGR1/NF      | 33 |
| GO:0042110 | T cell activation                                            | 33/182 | 179/749 | 0,987362996 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/CD24/FCER1G/ICAM1/PSMB10/RELB/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/BAX/VCAM1/STAT6/CD    | 33 |
| GO:0042493 | response to drug                                             | 32/182 | 119/749 | 0,270691855 | 0,999954951 | 0,999954951 | STAT3/S100A8/NNMT/MAPK13/ABCB1/LCN2/HDAC6/COL1A1/ICAM1/STAT1/TGFB1/AHR/CDKN1A/VCAM1/STAT6/AGT/        | 32 |
| GO:0044403 | symbiotic process                                            | 32/182 | 130/749 | 0,502916571 | 0,999954951 | 0,999954951 | LTF/IFITM3/STAT3/ITGB6/SLPI/IFITM2/IFITM1/HAVCR1/PSMB8/TNFRSF1A/KRT8/LTBR/ICAM1/C1QA/PSMB10/STAT1/TC  | 32 |

|            |                                                              |        |         |             |             |             |                                                                                                       |    |
|------------|--------------------------------------------------------------|--------|---------|-------------|-------------|-------------|-------------------------------------------------------------------------------------------------------|----|
| GO:0071495 | cellular response to endogenous stimulus                     | 32/182 | 138/749 | 0,668896973 | 0,999954951 | 0,999954951 | STAT3/COL4A1/SOST/SOCS3/MAPK13/HDAC6/COL1A1/NR4A1/COL3A1/ICAM1/JAK3/STAT1/TGFB1/SOCS1/XBP1/DNMT       | 32 |
| GO:0048646 | anatomical structure formation involved in morphogenesis     | 32/182 | 150/749 | 0,854267337 | 0,999954951 | 0,999954951 | HIF1A/BCL3/JAK1/BCL6/STAT3/C3/COL4A1/ADAMTS1/KRT8/COL1A1/NR4A1/MEGF11/STAT1/IL4R/TGFB1/XBP1/AGT/FK    | 32 |
| GO:0042327 | positive regulation of phosphorylation                       | 32/182 | 165/749 | 0,963328047 | 0,999954951 | 0,999954951 | HIF1A/LTF/FPR1/STAT3/C3/CD24/SOCS3/TNFRSF1A/LTBR/HDAC6/ICAM1/FCGR1A/TGFB1/SOCS1/CDKN1A/AGT/EGR1/TI    | 32 |
| GO:1902533 | positive regulation of intracellular signal transduction     | 32/182 | 169/749 | 0,976205457 | 0,999954951 | 0,999954951 | S100A9/LTF/FPR1/S100A8/CD24/TNFRSF1A/LTBR/COL3A1/ICAM1/TGFB1/BAX/AGT/FKBP1A/TLR4/KITLG/MYD88/APOE/    | 32 |
| GO:0009056 | catabolic process                                            | 31/182 | 123/749 | 0,43892246  | 0,999954951 | 0,999954951 | ALDH3A2/S100A9/HIF1A/PLAAT4/TIMP1/STAT3/S100A8/PSMB8/LYVE1/MME/HDAC6/PSME2/PSMB10/TGFB1/XBP1/BA       | 31 |
| GO:0016032 | viral process                                                | 31/182 | 123/749 | 0,43892246  | 0,999954951 | 0,999954951 | LTF/IFITM3/STAT3/ITGB6/SLPI/IFITM2/IFITM1/HAVCR1/PSMB8/TNFRSF1A/KRT8/LTBR/ICAM1/C1QA/PSMB10/STAT1/TG  | 31 |
| GO:0006996 | organelle organization                                       | 31/182 | 147/749 | 0,869260087 | 0,999954951 | 0,999954951 | S100A9/HIF1A/SOD2/BCL6/STAT3/S100A8/MUC1/EHD3/KRT8/HDAC6/ICAM1/TGFB1/DNMT1/BAX/CD59/SLAMF8/APOE       | 31 |
| GO:0000165 | MAPK cascade                                                 | 31/182 | 149/749 | 0,889467458 | 0,999954951 | 0,999954951 | JAK1/FPR1/CD24/PSMB8/MAPK13/LTBR/PSME2/ICAM1/PSMB10/JAK3/TGFB1/AGT/TLR4/KITLG/APOE/MAPK11/MYC/SI      | 31 |
| GO:0023014 | signal transduction by protein phosphorylation               | 31/182 | 149/749 | 0,889467458 | 0,999954951 | 0,999954951 | JAK1/FPR1/CD24/PSMB8/MAPK13/LTBR/PSME2/ICAM1/PSMB10/JAK3/TGFB1/AGT/TLR4/KITLG/APOE/MAPK11/MYC/SI      | 31 |
| GO:0002521 | leukocyte differentiation                                    | 31/182 | 160/749 | 0,961267531 | 0,999954951 | 0,999954951 | LTF/BCL3/BCL6/STAT3/FCER1G/LTBR/RELB/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/BAX/VCAM1/STAT6/EGR1/TLR4/KITL | 31 |
| GO:0001934 | positive regulation of protein phosphorylation               | 31/182 | 162/749 | 0,968698974 | 0,999954951 | 0,999954951 | LTF/FPR1/STAT3/C3/CD24/SOCS3/TNFRSF1A/LTBR/HDAC6/ICAM1/FCGR1A/TGFB1/SOCS1/CDKN1A/AGT/EGR1/TLR4/KIT    | 31 |
| GO:0008284 | positive regulation of cell population proliferation         | 31/182 | 173/749 | 0,991391714 | 0,999954951 | 0,999954951 | OSMR/HIF1A/LTF/BCL6/TIMP1/STAT3/CD24/ADAMTS1/NR4A1/JAK3/STAT1/TGFB1/XBP1/DNMT1/CDKN1A/VCAM1/AGT       | 31 |
| GO:0050865 | regulation of cell activation                                | 31/182 | 192/749 | 0,999413202 | 0,999954951 | 0,999954951 | BCL6/CD24/FCER1G/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/AHR/CDKN1A/VCAM1/STAT6/LDLR/CD276/TLR4/SLAMF8/A    | 31 |
| GO:0030162 | regulation of proteolysis                                    | 30/182 | 95/749  | 0,052729636 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/LTF/RARRES1/TIMP1/STAT3/S100A8/C3/SLPI/SERPING1/PSMB8/HDAC6/PSME2/BAX/AGT/APOE/TNF    | 30 |
| GO:0044281 | small molecule metabolic process                             | 30/182 | 97/749  | 0,068469899 | 0,999954951 | 0,999954951 | ALDH3A2/HIF1A/STAT3/C3/NNMT/PSMB8/LYVE1/TNFRSF1A/MME/PSME2/IMPDH1/PSMB10/TGFB1/XBP1/ALOX5/APOI        | 30 |
| GO:0097190 | apoptotic signaling pathway                                  | 30/182 | 107/749 | 0,195929669 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL3/SOD2/S100A8/CD24/MUC1/TNFRSF1A/LCN2/KRT8/LTBR/ICAM1/TGFB1/XBP1/BAX/CDKN1A/AGT/L     | 30 |
| GO:0051338 | regulation of transferase activity                           | 30/182 | 119/749 | 0,4405941   | 0,999954951 | 0,999954951 | LTF/PLAAT4/FPR1/CD24/SOCS3/FCGR1A/TGFB1/SOCS1/CDKN1A/AGT/EGR1/TLR4/KITLG/SLAMF8/APOE/MAPK11/IL6R/S    | 30 |
| GO:0044092 | negative regulation of molecular function                    | 30/182 | 120/749 | 0,463079257 | 0,999954951 | 0,999954951 | SERPINA3/LTF/RARRES1/TIMP1/C3/SLPI/SERPING1/SOCS3/HDAC6/SOCS1/BAX/CDKN1A/AGT/SIGIRR/IL18BP/FKBP1A/AF  | 30 |
| GO:0051093 | negative regulation of developmental process                 | 30/182 | 121/749 | 0,485564808 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL6/TIMP1/STAT3/COL3A1/JAK3/STAT1/IL4R/TGFB1/SOCS1/XBP1/DNMT1/CDKN1A/AGT/LDLR/TLR4/APOE/   | 30 |
| GO:0002460 | adaptive immune response based on somatic recombination of i | 30/182 | 124/749 | 0,552328567 | 0,999954951 | 0,999954951 | BCL3/C1QB/C1S/BCL6/STAT3/C3/SERPING1/C9/FCER1G/IL1R1/ICAM1/C1QA/RELB/JAK3/IL4R/NFKBIZ/TGFB1/STAT6/IL1 | 30 |
| GO:0018193 | peptidyl-amino acid modification                             | 30/182 | 133/749 | 0,732507571 | 0,999954951 | 0,999954951 | S100A9/JAK1/STAT3/S100A8/CD24/SOCS3/MUC1/MAPK13/TNFRSF1A/HDAC6/ICAM1/FCGR1A/JAK3/TGFB1/SOCS1/DN       | 30 |
| GO:0002697 | regulation of immune effector process                        | 30/182 | 141/749 | 0,850572767 | 0,999954951 | 0,999954951 | C1QB/C1S/BCL6/C3/SERPING1/C9/CFB/FCER1G/IL1R1/ICAM1/C1QA/JAK3/STAT1/IL4R/NFKBIZ/TGFB1/XBP1/STAT6/CD5  | 30 |
| GO:0051270 | regulation of cellular component movement                    | 30/182 | 156/749 | 0,963224699 | 0,999954951 | 0,999954951 | HIF1A/SOD2/BCL6/TIMP1/STAT3/ADAMTS1/IFITM1/IL1R1/HDAC6/COL1A1/COL3A1/ICAM1/TGFB1/XBP1/CXCL16/AGT/K    | 30 |
| GO:0040012 | regulation of locomotion                                     | 30/182 | 158/749 | 0,970387871 | 0,999954951 | 0,999954951 | HIF1A/SOD2/TIMP1/STAT3/ADAMTS1/IFITM1/IL1R1/HDAC6/COL1A1/COL3A1/ICAM1/TGFB1/XBP1/CXCL16/AGT/KITLG/    | 30 |
| GO:0050727 | regulation of inflammatory response                          | 29/182 | 99/749  | 0,132489465 | 0,999954951 | 0,999954951 | OSMR/S100A9/BCL6/S100A8/C3/FCER1G/IL1R1/SOCS3/MAPK13/TNFRSF1A/NFKBIZ/IL17RA/AGT/LDLR/TLR4/SLAMF8/M    | 29 |
| GO:0002831 | regulation of response to biotic stimulus                    | 29/182 | 101/749 | 0,161581282 | 0,999954951 | 0,999954951 | LTF/JAK1/SERPING1/FCER1G/IFNGR2/PSMB8/SOCS3/MUC1/IFNAR2/PSME2/PSMB10/RELB/STAT1/SOCS1/SIGIRR/LY96/    | 29 |
| GO:0044248 | cellular catabolic process                                   | 29/182 | 108/749 | 0,288588654 | 0,999954951 | 0,999954951 | ALDH3A2/S100A9/HIF1A/TIMP1/STAT3/S100A8/PSMB8/LYVE1/MME/HDAC6/PSME2/PSMB10/TGFB1/XBP1/BAX/LDLR/       | 29 |
| GO:0022008 | neurogenesis                                                 | 29/182 | 119/749 | 0,533180043 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/STAT3/S100A8/C3/MME/HDAC6/COL3A1/C1QA/TGFB1/XBP1/BAX/VCAM1/AGT/LDLR/TNC/TLR4/A      | 29 |
| GO:0003008 | system process                                               | 29/182 | 129/749 | 0,737073243 | 0,999954951 | 0,999954951 | SERPINA3/HIF1A/SOD2/SERPING1/TNFRSF1A/EHD3/MME/COL1A1/ICAM1/STAT1/TGFB1/AGT/LDLR/TLR4/APOE/TLR2/L     | 29 |
| GO:0022603 | regulation of anatomical structure morphogenesis             | 29/182 | 129/749 | 0,737073243 | 0,999954951 | 0,999954951 | HIF1A/JAK1/BCL6/STAT3/C3/PSMB8/TNFRSF1A/PSME2/ICAM1/PSMB10/STAT1/IL4R/TGFB1/XBP1/BAX/AGT/APOE/LST1    | 29 |
| GO:2000145 | regulation of cell motility                                  | 29/182 | 153/749 | 0,968786799 | 0,999954951 | 0,999954951 | HIF1A/SOD2/TIMP1/STAT3/ADAMTS1/IFITM1/IL1R1/HDAC6/COL1A1/COL3A1/ICAM1/TGFB1/XBP1/CXCL16/AGT/KITLG/    | 29 |
| GO:0044085 | cellular component biogenesis                                | 29/182 | 163/749 | 0,99047802  | 0,999954951 | 0,999954951 | SOD2/C9/FCER1G/SOST/TNFRSF1A/EHD3/LCN2/KRT8/HDAC6/COL1A1/ICAM1/TGFB1/DNMT1/BAX/AGT/CD59/FKBP1A/       | 29 |
| GO:0002694 | regulation of leukocyte activation                           | 29/182 | 184/749 | 0,999535937 | 0,999954951 | 0,999954951 | BCL6/CD24/FCER1G/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/AHR/CDKN1A/VCAM1/STAT6/LDLR/CD276/TLR4/SLAMF8/L    | 29 |
| GO:0031349 | positive regulation of defense response                      | 28/182 | 110/749 | 0,42091196  | 0,999954951 | 0,999954951 | OSMR/S100A9/S100A8/C3/FCER1G/PSMB8/MUC1/MAPK13/TNFRSF1A/PSME2/PSMB10/RELB/NFKBIZ/IL17RA/AGT/LDL       | 28 |
| GO:0043549 | regulation of kinase activity                                | 28/182 | 113/749 | 0,49029611  | 0,999954951 | 0,999954951 | LTF/FPR1/CD24/SOCS3/FCGR1A/TGFB1/SOCS1/CDKN1A/AGT/EGR1/TLR4/KITLG/SLAMF8/APOE/MAPK11/IL6R/SLC11A1/    | 28 |
| GO:0001944 | vasculature development                                      | 28/182 | 127/749 | 0,775536447 | 0,999954951 | 0,999954951 | HIF1A/JAK1/SOD2/STAT3/C3/COL4A1/SOCS3/COL1A1/NR4A1/COL3A1/STAT1/TGFB1/XBP1/DNMT1/BAX/AHR/AGT/LDL      | 28 |
| GO:0072358 | cardiovascular system development                            | 28/182 | 127/749 | 0,775536447 | 0,999954951 | 0,999954951 | HIF1A/JAK1/SOD2/STAT3/C3/COL4A1/SOCS3/COL1A1/NR4A1/COL3A1/STAT1/TGFB1/XBP1/DNMT1/BAX/AHR/AGT/LDL      | 28 |
| GO:0030334 | regulation of cell migration                                 | 28/182 | 149/749 | 0,970593592 | 0,999954951 | 0,999954951 | HIF1A/SOD2/TIMP1/STAT3/ADAMTS1/IFITM1/IL1R1/HDAC6/COL1A1/COL3A1/ICAM1/TGFB1/XBP1/CXCL16/AGT/KITLG/    | 28 |
| GO:0051050 | positive regulation of transport                             | 28/182 | 153/749 | 0,981487484 | 0,999954951 | 0,999954951 | HIF1A/S100A8/C3/FCER1G/EHD3/ABCB1/IL4R/TGFB1/XBP1/BAX/IL17RA/AGT/TLR4/CTSS/APOE/TLR2/MAPK11/SLC11A1   | 28 |
| GO:0035295 | tube development                                             | 28/182 | 154/749 | 0,983580587 | 0,999954951 | 0,999954951 | HIF1A/JAK1/STAT3/C3/CD24/COL4A1/MME/NR4A1/COL3A1/STAT1/TGFB1/XBP1/BAX/CDKN1A/HSD11B1/AGT/LDLR/TN      | 28 |
| GO:0022607 | cellular component assembly                                  | 28/182 | 160/749 | 0,992284935 | 0,999954951 | 0,999954951 | SOD2/C9/FCER1G/SOST/TNFRSF1A/EHD3/LCN2/KRT8/HDAC6/COL1A1/ICAM1/TGFB1/DNMT1/BAX/AGT/CD59/FKBP1A/       | 28 |
| GO:0030155 | regulation of cell adhesion                                  | 28/182 | 179/749 | 0,999519375 | 0,999954951 | 0,999954951 | BCL6/CD24/MUC1/COL1A1/ICAM1/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/VCAM1/TNC/CD276/LILRB2/IL6R/TGFB1/ARH   | 28 |
| GO:1901575 | organic substance catabolic process                          | 27/182 | 98/749  | 0,24596301  | 0,999954951 | 0,999954951 | ALDH3A2/HIF1A/PLAAT4/TIMP1/STAT3/PSMB8/LYVE1/HDAC6/PSME2/PSMB10/TGFB1/XBP1/BAX/LDLR/CTSS/VCAN/MY      | 27 |
| GO:0006811 | ion transport                                                | 27/182 | 100/749 | 0,28705723  | 0,999954951 | 0,999954951 | LTF/FCER1G/EHD3/ABCB1/LCN2/ICAM1/TGFB1/BAX/AGT/APOL1/LDLR/SLC12A3/FKBP1A/CTSS/APOE/LILRB2/SLC11A1/    | 27 |
| GO:0019725 | cellular homeostasis                                         | 27/182 | 101/749 | 0,30853291  | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/S100A8/CD24/LCN2/ICAM1/TGFB1/XBP1/BAX/AGT/SLC12A3/FKBP1A/SLAMF8/MT1A/APOE/SL    | 27 |
| GO:0045859 | regulation of protein kinase activity                        | 27/182 | 105/749 | 0,398948092 | 0,999954951 | 0,999954951 | LTF/FPR1/CD24/SOCS3/FCGR1A/TGFB1/SOCS1/CDKN1A/AGT/EGR1/TLR4/KITLG/APOE/MAPK11/IL6R/SLC11A1/S100A12    | 27 |
| GO:0000003 | reproduction                                                 | 27/182 | 106/749 | 0,422287085 | 0,999954951 | 0,999954951 | HIF1A/BCL6/TIMP1/STAT3/ADAMTS1/SOCS3/MME/KRT8/ICAM1/IL4R/TGFB1/BAX/AGT/TNC/EGR1/KITLG/APOL2/ARHGI     | 27 |
| GO:0022414 | reproductive process                                         | 27/182 | 106/749 | 0,422287085 | 0,999954951 | 0,999954951 | HIF1A/BCL6/TIMP1/STAT3/ADAMTS1/SOCS3/MME/KRT8/ICAM1/IL4R/TGFB1/BAX/AGT/TNC/EGR1/KITLG/APOL2/ARHGI     | 27 |
| GO:0009725 | response to hormone                                          | 27/182 | 107/749 | 0,445756748 | 0,999954951 | 0,999954951 | TIMP1/STAT3/SOST/SOCS3/HDAC6/COL1A1/NR4A1/ICAM1/JAK3/STAT1/TGFB1/SOCS1/XBP1/CDKN1A/STAT6/AGT/TNC/     | 27 |
| GO:0002253 | activation of immune response                                | 27/182 | 114/749 | 0,607002128 | 0,999954951 | 0,999954951 | C1QB/C1S/FPR1/C3/SERPING1/C9/CFB/FCER1G/PSMB8/MUC1/PSME2/C1QA/PSMB10/RELB/FCGR1A/NFKBIZ/BAX/FCGF      | 27 |
| GO:0002237 | response to molecule of bacterial origin                     | 27/182 | 115/749 | 0,628726653 | 0,999954951 | 0,999954951 | LTF/S100A8/CD24/SLPI/LCN2/ICAM1/TGFB1/XBP1/VCAM1/SIGIRR/LY96/NFKB2/TLR4/CXCL1/TLR2/LILRB2/SLC11A1/TNF | 27 |
| GO:1903706 | regulation of hemopoiesis                                    | 27/182 | 120/749 | 0,728684559 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL6/STAT3/PSMB8/PSME2/PSMB10/JAK3/STAT1/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/TLR4/KITLG/SLAMF8/LIL | 27 |
| GO:0045944 | positive regulation of transcription by RNA polymerase II    | 27/182 | 141/749 | 0,956991089 | 0,999954951 | 0,999954951 | HIF1A/BCL3/STAT3/MUC1/TNFRSF1A/NR4A1/MAF/RELB/STAT1/TGFB1/XBP1/AHR/STAT6/EGR1/NFKB2/TLR4/TLR2/IRF7    | 27 |
| GO:0055082 | cellular chemical homeostasis                                | 26/182 | 94/749  | 0,24434924  | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/S100A8/CD24/LCN2/ICAM1/TGFB1/XBP1/BAX/AGT/FKBP1A/SLAMF8/MT1A/APOE/SLC11A1/M     | 26 |
| GO:0009611 | response to wounding                                         | 26/182 | 97/749  | 0,307943502 | 0,999954951 | 0,999954951 | HIF1A/TIMP1/S100A8/SERPING1/FCER1G/LYVE1/EHD3/COL1A1/COL3A1/TGFB1/XBP1/BAX/CDKN1A/CD59/TNC/TLR4/AI    | 26 |
| GO:0050801 | ion homeostasis                                              | 26/182 | 97/749  | 0,307943502 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/S100A8/CD24/LCN2/TGFB1/XBP1/BAX/AGT/SLC12A3/FKBP1A/SLAMF8/MT1A/APOE/SLC11A1/    | 26 |
| GO:0009887 | animal organ morphogenesis                                   | 26/182 | 106/749 | 0,51902422  | 0,999954951 | 0,999954951 | HIF1A/LTF/STAT3/ADAMTS1/PSMB8/COL1A1/COL3A1/PSME2/MEGF11/PSMB10/STAT1/TGFB1/XBP1/BAX/STAT6/AGT/I      | 26 |
| GO:0032496 | response to lipopolysaccharide                               | 26/182 | 111/749 | 0,633044715 | 0,999954951 | 0,999954951 | LTF/S100A8/SLPI/LCN2/ICAM1/TGFB1/XBP1/VCAM1/SIGIRR/LY96/NFKB2/TLR4/CXCL1/TLR2/LILRB2/SLC11A1/TNFRSF1B | 26 |
| GO:0009890 | negative regulation of biosynthetic process                  | 26/182 | 113/749 | 0,675263848 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/MUC1/HDAC6/MAF/RELB/JAK3/STAT1/TGFB1/DNMT1/AHR/STAT6/SIGIRR/EGR1/APOE/IRF7/RORC/N     | 26 |



|            |                                                                 |        |         |             |             |             |                                                                                                        |    |
|------------|-----------------------------------------------------------------|--------|---------|-------------|-------------|-------------|--------------------------------------------------------------------------------------------------------|----|
| GO:0071396 | cellular response to lipid                                      | 26/182 | 116/749 | 0,733692273 | 0,999954951 | 0,999954951 | LTF/LCN2/HDAC6/COL1A1/NR4A1/ICAM1/TGFB1/XBP1/AHR/SIGIRR/LDLR/TNC/LY96/TLR4/CXCL1/TLR2/LILRB2/RORC/TN   | 26 |
| GO:0002790 | peptide secretion                                               | 26/182 | 117/749 | 0,751725347 | 0,999954951 | 0,999954951 | HIF1A/S100A8/ITGB6/IL4R/TGFB1/SOCS1/XBP1/IL17RA/AGT/TLR4/APOE/TLR2/MAPK11/TNFRSF1B/S100A12/IL1R2/HNF   | 26 |
| GO:0060429 | epithelium development                                          | 26/182 | 120/749 | 0,801209233 | 0,999954951 | 0,999954951 | HIF1A/PLAAT4/CD24/COL4A1/PSMB8/SOCS3/TNFRSF1A/KRT8/PSME2/ICAM1/MAF/PSMB10/STAT1/TGFB1/XBP1/BAX/C       | 26 |
| GO:0051249 | regulation of lymphocyte activation                             | 26/182 | 172/749 | 0,999689149 | 0,999954951 | 0,999954951 | BCL6/CD24/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/AHR/CDKN1A/VCAM1/STAT6/CD276/TLR4/SLAMF8/LILRB2/LST1/IL6   | 26 |
| GO:0098609 | cell-cell adhesion                                              | 26/182 | 176/749 | 0,999842649 | 0,999954951 | 0,999954951 | S100A9/BCL6/S100A8/CD24/MEGF11/ICAM1/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/VCAM1/CD276/LILRB2/IL6R/PVR/C   | 26 |
| GO:0043086 | negative regulation of catalytic activity                       | 25/182 | 85/749  | 0,150941964 | 0,999954951 | 0,999954951 | SERPINA3/LTF/RARRES1/TIMP1/C3/SLPI/SERPING1/SOCS3/HDAC6/SOCS1/CDKN1A/AGT/FKBP1A/APOE/TRIB1/ERRFI1/BI   | 25 |
| GO:0098771 | inorganic ion homeostasis                                       | 25/182 | 90/749  | 0,242556272 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/S100A8/CD24/LCN2/TGFB1/BAX/AGT/SLC12A3/FKBP1A/SLAMF8/MT1A/APOE/SLC11A1/MYC/I     | 25 |
| GO:0008285 | negative regulation of cell population proliferation            | 25/182 | 106/749 | 0,615342975 | 0,999954951 | 0,999954951 | PLAAT4/RARRES1/SOD2/BCL6/STAT3/ADAMTS1/IFITM1/STAT1/TGFB1/BAX/CDKN1A/APOE/CXCL1/TLR2/LILRB2/MAPK1      | 25 |
| GO:0010558 | negative regulation of macromolecule biosynthetic process       | 25/182 | 107/749 | 0,637538342 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/MUC1/HDAC6/MAF/RELB/JAK3/STAT1/TGFB1/DNMT1/AHR/STAT6/SIGIRR/EGR1/IRF7/RORC/MYC/ER      | 25 |
| GO:0023061 | signal release                                                  | 25/182 | 109/749 | 0,680139192 | 0,999954951 | 0,999954951 | HIF1A/ITGB6/FCER1G/IL4R/SOCS1/XBP1/IL17RA/AGT/TLR4/TLR2/MAPK11/TNFRSF1B/S100A12/IL1R2/HNF1A/CD58/FN1   | 25 |
| GO:0031327 | negative regulation of cellular biosynthetic process            | 25/182 | 110/749 | 0,70044785  | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/MUC1/HDAC6/MAF/RELB/JAK3/STAT1/TGFB1/DNMT1/AHR/STAT6/SIGIRR/EGR1/IRF7/RORC/MYC/ER      | 25 |
| GO:0051130 | positive regulation of cellular component organization          | 25/182 | 110/749 | 0,70044785  | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/C3/MUC1/LCN2/HDAC6/ICAM1/IL4R/TGFB1/DNMT1/BAX/AGT/TLR4/APOE/TNFSF10/NOX4/FN1/CI      | 25 |
| GO:0048699 | generation of neurons                                           | 25/182 | 111/749 | 0,720041785 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/STAT3/C3/MME/HDAC6/COL3A1/C1QA/TGFB1/XBP1/BAX/VCAM1/AGT/LDLR/TNC/APOE/TLR2/LST       | 25 |
| GO:0009306 | protein secretion                                               | 25/182 | 113/749 | 0,756964471 | 0,999954951 | 0,999954951 | HIF1A/ITGB6/IL4R/TGFB1/SOCS1/XBP1/IL17RA/AGT/TLR4/APOE/TLR2/MAPK11/TNFRSF1B/S100A12/IL1R2/HNF1A/CD58   | 25 |
| GO:0035592 | establishment of protein localization to extracellular region   | 25/182 | 113/749 | 0,756964471 | 0,999954951 | 0,999954951 | HIF1A/ITGB6/IL4R/TGFB1/SOCS1/XBP1/IL17RA/AGT/TLR4/APOE/TLR2/MAPK11/TNFRSF1B/S100A12/IL1R2/HNF1A/CD58   | 25 |
| GO:0071692 | protein localization to extracellular region                    | 25/182 | 113/749 | 0,756964471 | 0,999954951 | 0,999954951 | HIF1A/ITGB6/IL4R/TGFB1/SOCS1/XBP1/IL17RA/AGT/TLR4/APOE/TLR2/MAPK11/TNFRSF1B/S100A12/IL1R2/HNF1A/CD58   | 25 |
| GO:0010942 | positive regulation of cell death                               | 25/182 | 117/749 | 0,821255808 | 0,999954951 | 0,999954951 | S100A9/SOD2/BCL6/S100A8/TNFRSF1A/LTBR/HDAC6/C1QA/TGFB1/BAX/CDKN1A/AGT/EGR1/TLR4/TNFRSF1B/MYC/FGC       | 25 |
| GO:0001568 | blood vessel development                                        | 25/182 | 119/749 | 0,848550446 | 0,999954951 | 0,999954951 | HIF1A/JAK1/STAT3/C3/COL4A1/SOCS3/COL1A1/NR4A1/COL3A1/STAT1/TGFB1/XBP1/BAX/AHR/AGT/LDLR/EGR1/APOE/I     | 25 |
| GO:0051046 | regulation of secretion                                         | 25/182 | 126/749 | 0,920310847 | 0,999954951 | 0,999954951 | HIF1A/S100A8/FCER1G/TNFRSF1A/IL4R/TGFB1/SOCS1/XBP1/IL17RA/AGT/TLR4/APOE/TLR2/MAPK11/TNFRSF1B/IL1R2/C   | 25 |
| GO:0050900 | leukocyte migration                                             | 25/182 | 139/749 | 0,981096483 | 0,999954951 | 0,999954951 | S100A9/S100A8/FCER1G/IL1R1/COL1A1/ICAM1/TGFB1/CXCL16/VCAM1/IL17RA/KITLG/SLAMF8/CXCL1/IL6R/S100A12/CI   | 25 |
| GO:0052547 | regulation of peptidase activity                                | 24/182 | 75/749  | 0,069813347 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/LTF/RARRES1/TIMP1/STAT3/S100A8/C3/SLPI/SERPING1/PSMB8/PSME2/BAX/AGT/MYC/TNFSF10/BIR    | 24 |
| GO:0006629 | lipid metabolic process                                         | 24/182 | 76/749  | 0,080214955 | 0,999954951 | 0,999954951 | SERPINA3/ALDH3A2/PLAAT4/C3/SOCS3/TNFRSF1A/TGFB1/SOCS1/XBP1/BAX/ALOX5/HSD11B1/AGT/APOL1/LDLR/EGR1/      | 24 |
| GO:0045088 | regulation of innate immune response                            | 24/182 | 79/749  | 0,117574708 | 0,999954951 | 0,999954951 | JAK1/SERPING1/FCER1G/IFNGR2/PSMB8/SOCS3/MUC1/IFNAR2/PSME2/PSMB10/RELB/STAT1/SOCS1/SLAMF8/APOE/IRI      | 24 |
| GO:0055085 | transmembrane transport                                         | 24/182 | 80/749  | 0,13212535  | 0,999954951 | 0,999954951 | C3/PSMB8/EHD3/ABCB1/PSME2/PSMB10/TGFB1/BAX/AGT/APOL1/SLC12A3/FKBP1A/CTSS/SLC11A1/ABCC2/TAP2/HNF1       | 24 |
| GO:0034612 | response to tumor necrosis factor                               | 24/182 | 84/749  | 0,200608889 | 0,999954951 | 0,999954951 | PSMB8/TNFRSF1A/GBP2/LCN2/KRT8/LTBR/COL1A1/PSME2/ICAM1/PSMB10/STAT1/CXCL16/VCAM1/TNFRSF1B/ABCC2/I       | 24 |
| GO:0055080 | cation homeostasis                                              | 24/182 | 89/749  | 0,306394427 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/S100A8/CD24/LCN2/TGFB1/BAX/AGT/SLC12A3/FKBP1A/SLAMF8/MT1A/APOE/SLC11A1/MYC/I     | 24 |
| GO:0014070 | response to organic cyclic compound                             | 24/182 | 111/749 | 0,796146816 | 0,999954951 | 0,999954951 | STAT3/HDAC6/COL1A1/NR4A1/ICAM1/STAT1/TGFB1/AHR/CDKN1A/AGT/TNC/EGR1/TLR2/RORC/ABCC2/ERRFI1/TIPARP,      | 24 |
| GO:1903530 | regulation of secretion by cell                                 | 24/182 | 121/749 | 0,91614891  | 0,999954951 | 0,999954951 | HIF1A/FCER1G/TNFRSF1A/IL4R/TGFB1/SOCS1/XBP1/IL17RA/AGT/TLR4/APOE/TLR2/MAPK11/TNFRSF1B/IL1R2/CD58/ITG   | 24 |
| GO:0070661 | leukocyte proliferation                                         | 24/182 | 134/749 | 0,980246593 | 0,999954951 | 0,999954951 | BCL6/CD24/IMPDPH1/PSMB10/JAK3/TGFB1/BAX/AHR/CDKN1A/VCAM1/CD276/TLR4/KITLG/LILRB2/LST1/IL6R/SLC11A1/I   | 24 |
| GO:0032880 | regulation of protein localization                              | 24/182 | 138/749 | 0,988105389 | 0,999954951 | 0,999954951 | HIF1A/FCER1G/HDAC6/IL4R/TGFB1/SOCS1/XBP1/IL17RA/FKBP1A/TLR4/APOE/TLR2/MAPK11/TNFRSF1B/IL1R2/CD58/ITC   | 24 |
| GO:0052548 | regulation of endopeptidase activity                            | 23/182 | 69/749  | 0,048685315 | 0,999954951 | 0,999954951 | SERPINA3/S100A9/LTF/RARRES1/TIMP1/STAT3/S100A8/C3/SLPI/SERPING1/PSMB8/PSME2/BAX/AGT/MYC/TNFSF10/BIR    | 23 |
| GO:1901652 | response to peptide                                             | 23/182 | 72/749  | 0,076600226 | 0,999954951 | 0,999954951 | TIMP1/STAT3/SOCS3/COL1A1/NR4A1/ICAM1/JAK3/STAT1/TGFB1/SOCS1/XBP1/VCAM1/STAT6/AGT/EGR1/TLR4/TLR2/AI     | 23 |
| GO:0009057 | macromolecule catabolic process                                 | 23/182 | 75/749  | 0,113905697 | 0,999954951 | 0,999954951 | TIMP1/PSMB8/LYVE1/HDAC6/PSME2/PSMB10/TGFB1/XBP1/BAX/LDLR/CTSS/VCAN/MYD88/APOE/SLC11A1/TNFRSF1B/I       | 23 |
| GO:0006873 | cellular ion homeostasis                                        | 23/182 | 83/749  | 0,259959304 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/S100A8/CD24/LCN2/TGFB1/BAX/AGT/FKBP1A/SLAMF8/MT1A/APOE/SLC11A1/MYC/CMKLR1/I      | 23 |
| GO:0042060 | wound healing                                                   | 23/182 | 86/749  | 0,329079101 | 0,999954951 | 0,999954951 | HIF1A/TIMP1/S100A8/SERPING1/FCER1G/EHD3/COL1A1/COL3A1/TGFB1/XBP1/CDKN1A/CD59/TNC/TLR4/APOE/SLC11A      | 23 |
| GO:0055065 | metal ion homeostasis                                           | 23/182 | 86/749  | 0,329079101 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/S100A8/CD24/LCN2/TGFB1/BAX/AGT/SLC12A3/FKBP1A/MT1A/APOE/SLC11A1/MYC/CMKLR1/I     | 23 |
| GO:0030099 | myeloid cell differentiation                                    | 23/182 | 90/749  | 0,427863591 | 0,999954951 | 0,999954951 | HIF1A/LTF/BCL6/STAT3/FCER1G/LTBR/RELB/JAK3/STAT1/TGFB1/TLR4/KITLG/TLR2/IRF7/MYC/TRIB1/G6PD/LILRB1/TMEN | 23 |
| GO:0051253 | negative regulation of RNA metabolic process                    | 23/182 | 100/749 | 0,669171384 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/MUC1/HDAC6/MAF/RELB/STAT1/TGFB1/DNMT1/AHR/STAT6/EGR1/MYD88/IRF7/SLC11A1/RORC/MY        | 23 |
| GO:0045934 | negative regulation of nucleobase-containing compound metabo    | 23/182 | 104/749 | 0,749908017 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/MUC1/HDAC6/MAF/RELB/STAT1/TGFB1/DNMT1/AHR/STAT6/EGR1/MYD88/IRF7/SLC11A1/RORC/MY        | 23 |
| GO:0002683 | negative regulation of immune system process                    | 23/182 | 112/749 | 0,870963535 | 0,999954951 | 0,999954951 | LTF/BCL6/SERPING1/FCER1G/COL3A1/JAK3/IL4R/TGFB1/SOCS1/STAT6/CD59/LDLR/TLR4/KITLG/SLAMF8/LILRB2/LST1/M  | 23 |
| GO:0046651 | lymphocyte proliferation                                        | 23/182 | 127/749 | 0,973683455 | 0,999954951 | 0,999954951 | BCL6/CD24/IMPDPH1/PSMB10/JAK3/TGFB1/BAX/AHR/CDKN1A/VCAM1/CD276/TLR4/LILRB2/LST1/IL6R/SLC11A1/TNFRSF    | 23 |
| GO:0032943 | mononuclear cell proliferation                                  | 23/182 | 128/749 | 0,976690442 | 0,999954951 | 0,999954951 | BCL6/CD24/IMPDPH1/PSMB10/JAK3/TGFB1/BAX/AHR/CDKN1A/VCAM1/CD276/TLR4/LILRB2/LST1/IL6R/SLC11A1/TNFRSF    | 23 |
| GO:0035239 | tube morphogenesis                                              | 23/182 | 133/749 | 0,987635459 | 0,999954951 | 0,999954951 | HIF1A/JAK1/STAT3/C3/COL4A1/NR4A1/COL3A1/STAT1/TGFB1/XBP1/BAX/AGT/LDLR/TNC/APOE/MYC/TGFB1/ITGB2/TIPA    | 23 |
| GO:0007159 | leukocyte cell-cell adhesion                                    | 23/182 | 139/749 | 0,994550782 | 0,999954951 | 0,999954951 | S100A9/BCL6/S100A8/CD24/ICAM1/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/VCAM1/CD276/LILRB2/IL6R/ITGB2/LILRB1/I | 23 |
| GO:0002696 | positive regulation of leukocyte activation                     | 23/182 | 141/749 | 0,995909849 | 0,999954951 | 0,999954951 | BCL6/CD24/FCER1G/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/CDKN1A/VCAM1/STAT6/CD276/TLR4/LILRB2/IL6R/ITGB2/LI  | 23 |
| GO:0050867 | positive regulation of cell activation                          | 23/182 | 145/749 | 0,997741527 | 0,999954951 | 0,999954951 | BCL6/CD24/FCER1G/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/CDKN1A/VCAM1/STAT6/CD276/TLR4/LILRB2/IL6R/ITGB2/LI  | 23 |
| GO:0071356 | cellular response to tumor necrosis factor                      | 22/182 | 79/749  | 0,257904496 | 0,999954951 | 0,999954951 | PSMB8/TNFRSF1A/GBP2/LCN2/KRT8/LTBR/COL1A1/PSME2/ICAM1/PSMB10/STAT1/VCAM1/TNFRSF1B/ABCC2/CD58/BIF       | 22 |
| GO:0060284 | regulation of cell development                                  | 22/182 | 80/749  | 0,28071862  | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/BCL6/STAT3/TNFRSF1A/MME/COL3A1/TGFB1/AGT/LDLR/SLAMF8/APOE/TLR2/TNFRSF1B/TRIB1/G6P     | 22 |
| GO:0030003 | cellular cation homeostasis                                     | 22/182 | 82/749  | 0,328417862 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/S100A8/CD24/LCN2/TGFB1/BAX/AGT/FKBP1A/SLAMF8/MT1A/APOE/SLC11A1/MYC/CMKLR1/C      | 22 |
| GO:0006959 | humoral immune response                                         | 22/182 | 85/749  | 0,403646751 | 0,999954951 | 0,999954951 | S100A9/LTF/BCL3/C1QB/C1S/S100A8/C3/SLPI/SERPING1/C9/CFB/LCN2/C1QA/PSMB10/CD59/MASP1/CXCL1/SLC11A1/S    | 22 |
| GO:0051347 | positive regulation of transferase activity                     | 22/182 | 92/749  | 0,581460912 | 0,999954951 | 0,999954951 | LTF/PLAAT4/FPR1/CD24/FCGR1A/TGFB1/SOCS1/CDKN1A/AGT/EGR1/TLR4/KITLG/MAPK11/IL6R/SLC11A1/MYC/S100A12     | 22 |
| GO:2000113 | negative regulation of cellular macromolecule biosynthetic proc | 22/182 | 96/749  | 0,674525257 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/MUC1/HDAC6/MAF/RELB/JAK3/STAT1/TGFB1/DNMT1/AHR/STAT6/EGR1/IRF7/RORC/MYC/EPO/ATF3       | 22 |
| GO:0002449 | lymphocyte mediated immunity                                    | 22/182 | 113/749 | 0,924344271 | 0,999954951 | 0,999954951 | BCL3/C1QB/C1S/BCL6/C3/SERPING1/C9/FCER1G/IL1R1/ICAM1/C1QA/IL4R/TGFB1/STAT6/IRF7/SLC11A1/PVR/TNFRSF1B,  | 22 |
| GO:0043408 | regulation of MAPK cascade                                      | 22/182 | 117/749 | 0,950827553 | 0,999954951 | 0,999954951 | FPR1/CD24/LTBR/ICAM1/TGFB1/TLR4/KITLG/APOE/MAPK11/MYC/S100A12/FGD2/TRIB1/ERRFI1/NOX4/C5AR1/FN1/GDI     | 22 |
| GO:0051272 | positive regulation of cellular component movement              | 22/182 | 120/749 | 0,965133475 | 0,999954951 | 0,999954951 | HIF1A/SOD2/BCL6/STAT3/ADAMTS1/IL1R1/HDAC6/COL1A1/ICAM1/TGFB1/XBP1/CXCL16/AGT/KITLG/IL6R/CMKLR1/NO      | 22 |
| GO:0007167 | enzyme linked receptor protein signaling pathway                | 22/182 | 121/749 | 0,969028437 | 0,999954951 | 0,999954951 | HIF1A/STAT3/COL4A1/SOST/SOCS3/COL1A1/COL3A1/JAK3/TGFB1/SOCS1/STAT6/AGT/EGR1/FKBP1A/MAPK11/CD8B/ER      | 22 |
| GO:0070201 | regulation of establishment of protein localization             | 22/182 | 121/749 | 0,969028437 | 0,999954951 | 0,999954951 | HIF1A/HDAC6/IL4R/TGFB1/SOCS1/XBP1/IL17RA/TLR4/APOE/TLR2/MAPK11/TNFRSF1B/IL1R2/CD58/ITGB2/FN1/LILRB1/C  | 22 |
| GO:0090087 | regulation of peptide transport                                 | 22/182 | 124/749 | 0,978536902 | 0,999954951 | 0,999954951 | HIF1A/S100A8/IL4R/TGFB1/SOCS1/XBP1/IL17RA/TLR4/APOE/TLR2/MAPK11/TNFRSF1B/IL1R2/CD58/ITGB2/FN1/LILRB1/I | 22 |
| GO:0006812 | cation transport                                                | 21/182 | 79/749  | 0,352845259 | 0,999954951 | 0,999954951 | LTF/FCER1G/EHD3/LCN2/ICAM1/TGFB1/BAX/AGT/SLC12A3/FKBP1A/CTSS/LILRB2/SLC11A1/ABCC2/G6PD/LILRB1/EPO/SI   | 21 |

|            |                                                                 |        |         |             |             |             |                                                                                                          |    |
|------------|-----------------------------------------------------------------|--------|---------|-------------|-------------|-------------|----------------------------------------------------------------------------------------------------------|----|
| GO:0006875 | cellular metal ion homeostasis                                  | 21/182 | 79/749  | 0,352845259 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/FPR1/S100A8/CD24/LCN2/TGFB1/BAX/AGT/FKBP1A/MT1A/APOE/SLC11A1/MYC/CMKLR1/C5AR1/TN        | 21 |
| GO:0040007 | growth                                                          | 21/182 | 88/749  | 0,585845067 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/STAT3/S100A8/SOCS3/HDAC6/TGFB1/SOCS1/CXCL16/CDKN1A/AGT/TNC/MT1A/APOE/MAPK11/G6         | 21 |
| GO:1902679 | negative regulation of RNA biosynthetic process                 | 21/182 | 94/749  | 0,72275454  | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/MUC1/HDAC6/MAF/RELB/STAT1/TGFB1/DNMT1/AHR/STAT6/EGR1/IRF7/RORC/MYC/EPO/ATF3/GAT          | 21 |
| GO:0002791 | regulation of peptide secretion                                 | 21/182 | 105/749 | 0,89241512  | 0,999954951 | 0,999954951 | HIF1A/S100A8/IL4R/TGFB1/SOCS1/XBP1/IL17RA/TLR4/APOE/TLR2/MAPK11/TNFRSF1B/IL1R2/CD58/FN1/LILRB1/CD14/G    | 21 |
| GO:0043068 | positive regulation of programmed cell death                    | 21/182 | 107/749 | 0,911944916 | 0,999954951 | 0,999954951 | S100A9/SOD2/BCL6/S100A8/TNFRSF1A/LTBR/HDAC6/TGFB1/BAX/CDKN1A/AGT/TNFRSF1B/MYC/FGD2/TNFSF10/NOX4/         | 21 |
| GO:0002764 | immune response-regulating signaling pathway                    | 21/182 | 110/749 | 0,935809618 | 0,999954951 | 0,999954951 | FPR1/CD24/FCER1G/PSMB8/MUC1/PSME2/PSMB10/RELB/FCGR1A/NFKBIZ/BAX/FCGR2A/CD276/LILRB2/CMKLR1/C5AR:         | 21 |
| GO:0002768 | immune response-regulating cell surface receptor signaling path | 21/182 | 110/749 | 0,935809618 | 0,999954951 | 0,999954951 | FPR1/CD24/FCER1G/PSMB8/MUC1/PSME2/PSMB10/RELB/FCGR1A/NFKBIZ/BAX/FCGR2A/CD276/LILRB2/CMKLR1/C5AR:         | 21 |
| GO:0043933 | protein-containing complex subunit organization                 | 21/182 | 117/749 | 0,971393384 | 0,999954951 | 0,999954951 | SOD2/C9/FCER1G/SOST/TNFRSF1A/EHD3/LCN2/HDAC6/COL1A1/ICAM1/TGFB1/BAX/AGT/CD59/FKBP1A/TLR4/APOE/M          | 21 |
| GO:0030335 | positive regulation of cell migration                           | 21/182 | 118/749 | 0,974711546 | 0,999954951 | 0,999954951 | HIF1A/SOD2/STAT3/ADAMTS1/IL1R1/HDAC6/COL1A1/ICAM1/TGFB1/XBP1/CXCL16/AGT/KITLG/IL6R/CMKLR1/NOX4/C5        | 21 |
| GO:2000147 | positive regulation of cell motility                            | 21/182 | 119/749 | 0,977687472 | 0,999954951 | 0,999954951 | HIF1A/SOD2/STAT3/ADAMTS1/IL1R1/HDAC6/COL1A1/ICAM1/TGFB1/XBP1/CXCL16/AGT/KITLG/IL6R/CMKLR1/NOX4/C5        | 21 |
| GO:0051223 | regulation of protein transport                                 | 21/182 | 120/749 | 0,980350441 | 0,999954951 | 0,999954951 | HIF1A/IL4R/TGFB1/SOCS1/XBP1/IL17RA/TLR4/APOE/TLR2/MAPK11/TNFRSF1B/IL1R2/CD58/ITGB2/FN1/LILRB1/CD14/GA    | 21 |
| GO:0040017 | positive regulation of locomotion                               | 21/182 | 121/749 | 0,982728062 | 0,999954951 | 0,999954951 | HIF1A/SOD2/STAT3/ADAMTS1/IL1R1/HDAC6/COL1A1/ICAM1/TGFB1/XBP1/CXCL16/AGT/KITLG/IL6R/CMKLR1/NOX4/C5        | 21 |
| GO:0030098 | lymphocyte differentiation                                      | 21/182 | 125/749 | 0,989877964 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/FCER1G/RELB/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/BAX/VCAM1/STAT6/EGR1/SLAMF8/LILRB2/RO      | 21 |
| GO:1903037 | regulation of leukocyte cell-cell adhesion                      | 21/182 | 129/749 | 0,994236893 | 0,999954951 | 0,999954951 | BCL6/CD24/ICAM1/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/VCAM1/CD276/LILRB2/IL6R/ITGB2/LILRB1/EPO/GATA3/ADO     | 21 |
| GO:0051251 | positive regulation of lymphocyte activation                    | 21/182 | 131/749 | 0,995697008 | 0,999954951 | 0,999954951 | BCL6/CD24/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/CDKN1A/VCAM1/STAT6/CD276/TLR4/LILRB2/IL6R/LILRB1/EPO/GAT     | 21 |
| GO:0045785 | positive regulation of cell adhesion                            | 21/182 | 132/749 | 0,996291463 | 0,999954951 | 0,999954951 | BCL6/CD24/ICAM1/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/VCAM1/CD276/LILRB2/IL6R/ITGB2/FN1/LILRB1/EPO/GATA3/    | 21 |
| GO:0022407 | regulation of cell-cell adhesion                                | 21/182 | 143/749 | 0,999352706 | 0,999954951 | 0,999954951 | BCL6/CD24/ICAM1/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/VCAM1/CD276/LILRB2/IL6R/ITGB2/LILRB1/EPO/GATA3/ADO     | 21 |
| GO:0032870 | cellular response to hormone stimulus                           | 20/182 | 63/749  | 0,101162959 | 0,999954951 | 0,999954951 | STAT3/SOST/SOCS3/HDAC6/NR4A1/ICAM1/JAK3/STAT1/TGFB1/SOCS1/XBP1/STAT6/AGT/TNC/CTSS/RORC/ABCC2/ERRFI       | 20 |
| GO:0042742 | defense response to bacterium                                   | 20/182 | 67/749  | 0,167715127 | 0,999954951 | 0,999954951 | S100A9/LTF/BCL3/S100A8/SLPI/FCER1G/TNFRSF1A/GBP2/LCN2/TLR4/SLAMF8/MYD88/TLR2/IL6R/SLC11A1/S100A12/TB     | 20 |
| GO:0007417 | central nervous system development                              | 20/182 | 77/749  | 0,405337331 | 0,999954951 | 0,999954951 | ALDH3A2/HIF1A/STAT3/S100A8/C3/COL4A1/COL3A1/C1QA/TGFB1/BAX/LDLR/TLR4/VCAN/TLR2/TNFRSF1B/C5AR1/G6PI       | 20 |
| GO:0034341 | response to interferon-gamma                                    | 20/182 | 77/749  | 0,405337331 | 0,999954951 | 0,999954951 | JAK1/IFITM3/IFITM2/IFITM1/IFNGR2/SOCS3/GBP2/ICAM1/FCGR1A/STAT1/SOCS1/CXCL16/VCAM1/IFI30/TLR4/TLR2/IRF    | 20 |
| GO:0050663 | cytokine secretion                                              | 20/182 | 81/749  | 0,512525268 | 0,999954951 | 0,999954951 | ITGB6/IL4R/SOCS1/XBP1/IL17RA/AGT/TLR4/TLR2/MAPK11/TNFRSF1B/S100A12/IL1R2/CD58/FN1/LILRB1/CD14/GATA3/I    | 20 |
| GO:0045860 | positive regulation of protein kinase activity                  | 20/182 | 82/749  | 0,538918939 | 0,999954951 | 0,999954951 | LTF/FPR1/CD24/FCGR1A/TGFB1/SOCS1/CDKN1A/AGT/EGR1/TLR4/KITLG/MAPK11/IL6R/SLC11A1/S100A12/FGD2/NOX4/       | 20 |
| GO:0033674 | positive regulation of kinase activity                          | 20/182 | 86/749  | 0,639702389 | 0,999954951 | 0,999954951 | LTF/FPR1/CD24/FCGR1A/TGFB1/SOCS1/CDKN1A/AGT/EGR1/TLR4/KITLG/MAPK11/IL6R/SLC11A1/S100A12/FGD2/NOX4/       | 20 |
| GO:0001818 | negative regulation of cytokine production                      | 20/182 | 87/749  | 0,663267193 | 0,999954951 | 0,999954951 | LTF/BCL3/BCL6/CD24/RELB/JAK3/TGFB1/SIGIRR/TLR4/SLC11A1/IL1R2/TBK1/CMKLR1/ERRFI1/FN1/LILRB1/GATA3/NFKB1   | 20 |
| GO:0007049 | cell cycle                                                      | 20/182 | 92/749  | 0,768258798 | 0,999954951 | 0,999954951 | BCL6/STAT3/ADAMTS1/PSMB8/MUC1/MAPK13/ABCB1/NR4A1/PSME2/PSMB10/TGFB1/BAX/AHR/CDKN1A/MYC/PSME1             | 20 |
| GO:0045596 | negative regulation of cell differentiation                     | 20/182 | 92/749  | 0,768258798 | 0,999954951 | 0,999954951 | LTF/BCL6/STAT3/COL3A1/JAK3/STAT1/IL4R/TGFB1/SOCS1/XBP1/DNMT1/LDLR/TLR4/APOE/MYC/TRIB1/G6PD/LILRB1/TN     | 20 |
| GO:0045892 | negative regulation of transcription, DNA-templated             | 20/182 | 92/749  | 0,768258798 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/MUC1/HDAC6/MAF/RELB/STAT1/TGFB1/DNMT1/AHR/STAT6/EGR1/IRF7/RORC/MYC/EPO/ATF3/GAT          | 20 |
| GO:1903507 | negative regulation of nucleic acid-templated transcription     | 20/182 | 93/749  | 0,7864483   | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/MUC1/HDAC6/MAF/RELB/STAT1/TGFB1/DNMT1/AHR/STAT6/EGR1/IRF7/RORC/MYC/EPO/ATF3/GAT          | 20 |
| GO:0050708 | regulation of protein secretion                                 | 20/182 | 101/749 | 0,897648699 | 0,999954951 | 0,999954951 | HIF1A/IL4R/TGFB1/SOCS1/XBP1/IL17RA/TLR4/APOE/TLR2/MAPK11/TNFRSF1B/IL1R2/CD58/FN1/LILRB1/CD14/GATA3/IF    | 20 |
| GO:0048514 | blood vessel morphogenesis                                      | 20/182 | 107/749 | 0,94619364  | 0,999954951 | 0,999954951 | HIF1A/JAK1/STAT3/C3/COL4A1/NR4A1/COL3A1/STAT1/TGFB1/XBP1/BAX/AGT/LDLR/APOE/TGFB1/ITGB2/TIPARP/C5AR1      | 20 |
| GO:1903039 | positive regulation of leukocyte cell-cell adhesion             | 20/182 | 108/749 | 0,952013304 | 0,999954951 | 0,999954951 | BCL6/CD24/ICAM1/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/VCAM1/CD276/LILRB2/IL6R/ITGB2/LILRB1/EPO/GATA3/TNFS    | 20 |
| GO:0065003 | protein-containing complex assembly                             | 20/182 | 113/749 | 0,973730717 | 0,999954951 | 0,999954951 | SOD2/C9/FCER1G/SOST/TNFRSF1A/EHD3/LCN2/HDAC6/COL1A1/ICAM1/TGFB1/BAX/CD59/FKBP1A/TLR4/APOE/MYC/BII        | 20 |
| GO:0022409 | positive regulation of cell-cell adhesion                       | 20/182 | 114/749 | 0,97685027  | 0,999954951 | 0,999954951 | BCL6/CD24/ICAM1/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/VCAM1/CD276/LILRB2/IL6R/ITGB2/LILRB1/EPO/GATA3/TNFS    | 20 |
| GO:0006935 | chemotaxis                                                      | 20/182 | 119/749 | 0,988043463 | 0,999954951 | 0,999954951 | S100A9/FPR1/S100A8/FCER1G/NR4A1/TGFB1/CXCL16/VCAM1/IL17RA/SLAMF8/CXCL1/IL6R/S100A12/CMKLR1/ITGB2/C       | 20 |
| GO:0042330 | taxis                                                           | 20/182 | 119/749 | 0,988043463 | 0,999954951 | 0,999954951 | S100A9/FPR1/S100A8/FCER1G/NR4A1/TGFB1/CXCL16/VCAM1/IL17RA/SLAMF8/CXCL1/IL6R/S100A12/CMKLR1/ITGB2/C       | 20 |
| GO:0050863 | regulation of T cell activation                                 | 20/182 | 134/749 | 0,998742263 | 0,999954951 | 0,999954951 | BCL6/CD24/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/VCAM1/CD276/LILRB2/IL6R/TNFRSF1B/LILRB1/EPO/GATA3/ADORA2     | 20 |
| GO:0031400 | negative regulation of protein modification process             | 19/182 | 59/749  | 0,096251939 | 0,999954951 | 0,999954951 | SOCS3/TGFB1/SOCS1/DNMT1/BAX/CDKN1A/FKBP1A/TLR4/APOE/MYC/TRIB1/ERRFI1/G6PD/ATF3/ADORA2A/ISG15/RGN         | 19 |
| GO:0019752 | carboxylic acid metabolic process                               | 19/182 | 61/749  | 0,127103701 | 0,999954951 | 0,999954951 | ALDH3A2/HIF1A/STAT3/C3/PSMB8/LYVE1/TNFRSF1A/PSME2/PSMB10/TGFB1/XBP1/ALOX5/VCAN/TLR2/ABCC2/NOX4/P         | 19 |
| GO:0043436 | oxoacid metabolic process                                       | 19/182 | 61/749  | 0,127103701 | 0,999954951 | 0,999954951 | ALDH3A2/HIF1A/STAT3/C3/PSMB8/LYVE1/TNFRSF1A/PSME2/PSMB10/TGFB1/XBP1/ALOX5/VCAN/TLR2/ABCC2/NOX4/P         | 19 |
| GO:0006082 | organic acid metabolic process                                  | 19/182 | 63/749  | 0,163251105 | 0,999954951 | 0,999954951 | ALDH3A2/HIF1A/STAT3/C3/PSMB8/LYVE1/TNFRSF1A/PSME2/PSMB10/TGFB1/XBP1/ALOX5/VCAN/TLR2/ABCC2/NOX4/P         | 19 |
| GO:0032102 | negative regulation of response to external stimulus            | 19/182 | 70/749  | 0,325458046 | 0,999954951 | 0,999954951 | LTF/SERPING1/SOCS3/TNFRSF1A/CDKN1A/SIGIRR/LDLR/SLAMF8/APOE/TNFRSF1B/IL1R2/TRIB1/LILRB1/SERPINE1/GATA:    | 19 |
| GO:1901565 | organonitrogen compound catabolic process                       | 19/182 | 71/749  | 0,351926606 | 0,999954951 | 0,999954951 | TIMP1/PSMB8/LYVE1/HDAC6/PSME2/PSMB10/TGFB1/XBP1/LDLR/CTSS/VCAN/APOE/TNFRSF1B/TRIB1/TIPARP/PSME1/I        | 19 |
| GO:0009894 | regulation of catabolic process                                 | 19/182 | 75/749  | 0,46111304  | 0,999954951 | 0,999954951 | HIF1A/TIMP1/STAT3/PSMB8/HDAC6/PSME2/PSMB10/XBP1/BAX/LDLR/MYD88/APOE/SLC11A1/TNFRSF1B/TBK1/TRIB1/I        | 19 |
| GO:0018108 | peptidyl-tyrosine phosphorylation                               | 19/182 | 87/749  | 0,755749053 | 0,999954951 | 0,999954951 | JAK1/STAT3/CD24/SOCS3/TNFRSF1A/ICAM1/FCGR1A/JAK3/TGFB1/SOCS1/AGT/KITLG/IL6R/ITGB2/ERRFI1/NOX4/EPO/IL     | 19 |
| GO:0018212 | peptidyl-tyrosine modification                                  | 19/182 | 87/749  | 0,755749053 | 0,999954951 | 0,999954951 | JAK1/STAT3/CD24/SOCS3/TNFRSF1A/ICAM1/FCGR1A/JAK3/TGFB1/SOCS1/AGT/KITLG/IL6R/ITGB2/ERRFI1/NOX4/EPO/IL     | 19 |
| GO:0009615 | response to virus                                               | 19/182 | 89/749  | 0,79312567  | 0,999954951 | 0,999954951 | BCL3/IFITM3/IFITM2/IFITM1/IFNGR2/LCN2/IFNAR2/STAT1/IRF7/MAPK11/TBK1/ISG20/BIRC3/LILRB1/IL10RB/IFIT1/GATA | 19 |
| GO:1901566 | organonitrogen compound biosynthetic process                    | 19/182 | 96/749  | 0,89252379  | 0,999954951 | 0,999954951 | ALDH3A2/HIF1A/BCL3/STAT3/NNMT/MUC1/TNFRSF1A/IMPDH1/JAK3/TGFB1/EGR1/TLR4/VCAN/APOE/TBK1/EPO/GATA          | 19 |
| GO:1902105 | regulation of leukocyte differentiation                         | 19/182 | 98/749  | 0,912660228 | 0,999954951 | 0,999954951 | LTF/BCL6/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/TLR4/KITLG/SLAMF8/LILRB2/IRF7/MYC/TRIB1/LILRB1/TMEM178A/GA    | 19 |
| GO:0043065 | positive regulation of apoptotic process                        | 19/182 | 105/749 | 0,960518576 | 0,999954951 | 0,999954951 | S100A9/SOD2/BCL6/S100A8/TNFRSF1A/LTBR/TGFB1/BAX/AGT/TNFRSF1B/MYC/FGD2/TNFSF10/NOX4/LILRB1/ATF3/CAS       | 19 |
| GO:0044265 | cellular macromolecule catabolic process                        | 18/182 | 50/749  | 0,037562459 | 0,999954951 | 0,999954951 | PSMB8/HDAC6/PSME2/PSMB10/XBP1/BAX/LDLR/CTSS/MYD88/APOE/SLC11A1/TNFRSF1B/TRIB1/ISG20/PSME1/ISG15/F        | 18 |
| GO:0070647 | protein modification by small protein conjugation or removal    | 18/182 | 52/749  | 0,05505828  | 0,999954951 | 0,999954951 | HIF1A/PSMB8/SOCS3/ASB15/HDAC6/PSME2/PSMB10/SOCS1/EGR1/FKBP1A/MYC/BIRC3/PSME1/DCAF12/GATA3/KLHL1          | 18 |
| GO:0050729 | positive regulation of inflammatory response                    | 18/182 | 60/749  | 0,178625544 | 0,999954951 | 0,999954951 | OSMR/S100A9/S100A8/C3/FCER1G/MAPK13/TNFRSF1A/NFKBIZ/IL17RA/AGT/LDLR/TLR4/MYD88/TLR2/S100A12/SERPIN       | 18 |
| GO:0030001 | metal ion transport                                             | 18/182 | 66/749  | 0,324065769 | 0,999954951 | 0,999954951 | LTF/EHD3/LCN2/ICAM1/TGFB1/BAX/AGT/SLC12A3/FKBP1A/LILRB2/SLC11A1/ABCC2/G6PD/LILRB1/EPO/ADORA2A/RGN/       | 18 |
| GO:0031329 | regulation of cellular catabolic process                        | 18/182 | 66/749  | 0,324065769 | 0,999954951 | 0,999954951 | HIF1A/TIMP1/STAT3/PSMB8/HDAC6/PSME2/PSMB10/XBP1/BAX/LDLR/MYD88/APOE/SLC11A1/TNFRSF1B/TBK1/TRIB1/I        | 18 |
| GO:0040008 | regulation of growth                                            | 18/182 | 66/749  | 0,324065769 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/STAT3/S100A8/SOCS3/TGFB1/SOCS1/CXCL16/CDKN1A/AGT/MT1A/APOE/MAPK11/G6PD/FN1/GDF         | 18 |
| GO:0002819 | regulation of adaptive immune response                          | 18/182 | 77/749  | 0,626283899 | 0,999954951 | 0,999954951 | BCL6/C3/FCER1G/IL1R1/JAK3/IL4R/NFKBIZ/TGFB1/STAT6/IRF7/IL6R/SLC11A1/PVR/TNFRSF1B/LILRB1/GATA3/IL6ST/PTPN | 18 |
| GO:0010035 | response to inorganic substance                                 | 18/182 | 78/749  | 0,651331187 | 0,999954951 | 0,999954951 | HIF1A/SOD2/S100A8/MAPK13/LCN2/KRT8/HDAC6/COL1A1/ICAM1/C1QA/STAT1/VCAM1/STAT6/MT1A/ABCC2/G6PD/CI          | 18 |
| GO:0061061 | muscle structure development                                    | 18/182 | 79/749  | 0,675530939 | 0,999954951 | 0,999954951 | SOD2/KRT8/COL3A1/IL4R/TGFB1/XBP1/DNMT1/AGT/EGR1/FKBP1A/MAPK11/KRT19/NOX4/G6PD/MYOM2/GDF15/ATF3           | 18 |



|            |                                                                 |        |         |             |             |             |                                                                                                         |    |
|------------|-----------------------------------------------------------------|--------|---------|-------------|-------------|-------------|---------------------------------------------------------------------------------------------------------|----|
| GO:0071222 | cellular response to lipopolysaccharide                         | 18/182 | 80/749  | 0,698818394 | 0,999954951 | 0,999954951 | LTF/LCN2/ICAM1/TGFB1/XBP1/SIGIRR/LY96/TLR4/CXCL1/TLR2/LILRB2/TNFRSF1B/ABCC2/TRIB1/LILRB1/CD14/SERPINE1/ | 18 |
| GO:0033043 | regulation of organelle organization                            | 18/182 | 81/749  | 0,72114058  | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/S100A8/MUC1/EHD3/HDAC6/ICAM1/TGFB1/DNMT1/BAX/LILRB2/MYC/ARHGDIB/TNFSF10/NOX4/         | 18 |
| GO:0071219 | cellular response to molecule of bacterial origin               | 18/182 | 81/749  | 0,72114058  | 0,999954951 | 0,999954951 | LTF/LCN2/ICAM1/TGFB1/XBP1/SIGIRR/LY96/TLR4/CXCL1/TLR2/LILRB2/TNFRSF1B/ABCC2/TRIB1/LILRB1/CD14/SERPINE1/ | 18 |
| GO:0051090 | regulation of DNA-binding transcription factor activity         | 18/182 | 83/749  | 0,76273472  | 0,999954951 | 0,999954951 | S100A9/LTF/STAT3/S100A8/ICAM1/TGFB1/AGT/SIGIRR/NFKB2/TLR4/MYD88/TLR2/MAPK11/S100A12/CMKLR1/TRIB1/IT     | 18 |
| GO:0071216 | cellular response to biotic stimulus                            | 18/182 | 85/749  | 0,800112984 | 0,999954951 | 0,999954951 | LTF/LCN2/ICAM1/TGFB1/XBP1/SIGIRR/LY96/TLR4/CXCL1/TLR2/LILRB2/TNFRSF1B/ABCC2/TRIB1/LILRB1/CD14/SERPINE1/ | 18 |
| GO:0051047 | positive regulation of secretion                                | 18/182 | 89/749  | 0,862191039 | 0,999954951 | 0,999954951 | HIF1A/S100A8/FCER1G/IL4R/TGFB1/XBP1/IL17RA/AGT/TLR4/TLR2/MAPK11/CD58/ITGB2/CD14/GATA3/IFNGR1/ADORA      | 18 |
| GO:0002429 | immune response-activating cell surface receptor signaling path | 18/182 | 94/749  | 0,917860992 | 0,999954951 | 0,999954951 | FPR1/FCER1G/PSMB8/MUC1/PSME2/PSMB10/RELB/FCGR1A/NFKBIZ/BAX/FCGR2A/CD276/CMKLR1/C5AR1/PSME1/GAT          | 18 |
| GO:0002757 | immune response-activating signal transduction                  | 18/182 | 94/749  | 0,917860992 | 0,999954951 | 0,999954951 | FPR1/FCER1G/PSMB8/MUC1/PSME2/PSMB10/RELB/FCGR1A/NFKBIZ/BAX/FCGR2A/CD276/CMKLR1/C5AR1/PSME1/GAT          | 18 |
| GO:0050870 | positive regulation of T cell activation                        | 18/182 | 102/749 | 0,968003089 | 0,999954951 | 0,999954951 | BCL6/CD24/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/VCAM1/CD276/LILRB2/IL6R/LILRB1/EPO/GATA3/TNFSF14/IL6ST/PTF  | 18 |
| GO:0070663 | regulation of leukocyte proliferation                           | 18/182 | 111/749 | 0,990527888 | 0,999954951 | 0,999954951 | BCL6/CD24/JAK3/TGFB1/AHR/CDKN1A/VCAM1/CD276/TLR4/KITLG/LILRB2/LST1/IL6R/TNFRSF1B/LILRB1/EPO/IL6ST/PTP   | 18 |
| GO:0010563 | negative regulation of phosphorus metabolic process             | 17/182 | 53/749  | 0,116099207 | 0,999954951 | 0,999954951 | STAT3/SOCS3/TGFB1/SOCS1/BAX/CDKN1A/FKBP1A/TLR4/APOE/MYC/TRIB1/ERRFI1/ATF3/ADORA2A/RGN/RNF149/PTPN       | 17 |
| GO:0045936 | negative regulation of phosphate metabolic process              | 17/182 | 53/749  | 0,116099207 | 0,999954951 | 0,999954951 | STAT3/SOCS3/TGFB1/SOCS1/BAX/CDKN1A/FKBP1A/TLR4/APOE/MYC/TRIB1/ERRFI1/ATF3/ADORA2A/RGN/RNF149/PTPN       | 17 |
| GO:0034220 | ion transmembrane transport                                     | 17/182 | 58/749  | 0,218726482 | 0,999954951 | 0,999954951 | EHD3/ABCB1/TGFB1/BAX/AGT/APOL1/SLC12A3/FKBP1A/CTSS/SLC11A1/ABCC2/TAP2/G6PD/EPO/TAP1/RGN/PTPN6           | 17 |
| GO:0046677 | response to antibiotic                                          | 17/182 | 60/749  | 0,268685292 | 0,999954951 | 0,999954951 | JAK1/STAT3/S100A8/MAPK13/LCN2/HDAC6/COL1A1/ICAM1/STAT1/AHR/VCAM1/STAT6/TNC/EGR1/G6PD/CD14/GATA3         | 17 |
| GO:0070555 | response to interleukin-1                                       | 17/182 | 60/749  | 0,268685292 | 0,999954951 | 0,999954951 | HIF1A/PSMB8/IL1R1/MAPK13/GBP2/LCN2/PSME2/ICAM1/PSMB10/EGR1/MYD88/MAPK11/IL1R2/ABCC2/PSME1/EPO/N         | 17 |
| GO:0050878 | regulation of body fluid levels                                 | 17/182 | 61/749  | 0,295148289 | 0,999954951 | 0,999954951 | HIF1A/SERPING1/FCER1G/EHD3/COL1A1/COL3A1/XBP1/CD59/TLR4/APOE/SERPINE1/GATA3/SLC22A2/ADORA2A/THBD/       | 17 |
| GO:0071407 | cellular response to organic cyclic compound                    | 17/182 | 66/749  | 0,436512953 | 0,999954951 | 0,999954951 | STAT3/HDAC6/COL1A1/NR4A1/ICAM1/STAT1/TGFB1/AHR/TNC/EGR1/RORC/ABCC2/ERRFI1/TIPARP/NOX4/IFIT1/NFKB1       | 17 |
| GO:0046907 | intracellular transport                                         | 17/182 | 69/749  | 0,522998018 | 0,999954951 | 0,999954951 | HIF1A/STAT3/CD24/FCER1G/EHD3/HDAC6/IL4R/TGFB1/BAX/CDKN1A/AGT/CD59/LDLR/APOE/TAP2/ITGB2/TAP1             | 17 |
| GO:0002285 | lymphocyte activation involved in immune response               | 17/182 | 70/749  | 0,551209574 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/FCER1G/ICAM1/RELB/JAK3/IL4R/NFKBIZ/TGFB1/XBP1/STAT6/TLR4/SLC11A1/RORC/LILRB1/GATA3      | 17 |
| GO:0050730 | regulation of peptidyl-tyrosine phosphorylation                 | 17/182 | 70/749  | 0,551209574 | 0,999954951 | 0,999954951 | STAT3/CD24/SOCS3/TNFRSF1A/ICAM1/FCGR1A/TGFB1/SOCS1/AGT/KITLG/IL6R/ITGB2/ERRFI1/NOX4/EPO/IL6ST/PTPN6     | 17 |
| GO:0072503 | cellular divalent inorganic cation homeostasis                  | 17/182 | 70/749  | 0,551209574 | 0,999954951 | 0,999954951 | S100A9/FPR1/S100A8/CD24/TGFB1/BAX/AGT/FKBP1A/MT1A/APOE/SLC11A1/CMKLR1/C5AR1/TMEM178A/EPO/RGN/P1         | 17 |
| GO:0072507 | divalent inorganic cation homeostasis                           | 17/182 | 71/749  | 0,578893309 | 0,999954951 | 0,999954951 | S100A9/FPR1/S100A8/CD24/TGFB1/BAX/AGT/FKBP1A/MT1A/APOE/SLC11A1/CMKLR1/C5AR1/TMEM178A/EPO/RGN/P1         | 17 |
| GO:0051726 | regulation of cell cycle                                        | 17/182 | 77/749  | 0,728294671 | 0,999954951 | 0,999954951 | BCL6/STAT3/ADAMTS1/PSMB8/MUC1/NR4A1/PSME2/PSMB10/TGFB1/BAX/CDKN1A/MYC/PSME1/LILRB1/GATA3/KLHL1          | 17 |
| GO:0003006 | developmental process involved in reproduction                  | 17/182 | 80/749  | 0,789324712 | 0,999954951 | 0,999954951 | HIF1A/BCL6/ADAMTS1/SOCS3/MME/KRT8/ICAM1/TGFB1/BAX/TNC/KITLG/KRT19/TNFSF10/BIRC3/TIPARP/GATA3/RGN        | 17 |
| GO:0007169 | transmembrane receptor protein tyrosine kinase signaling pathw  | 17/182 | 80/749  | 0,789324712 | 0,999954951 | 0,999954951 | HIF1A/STAT3/COL4A1/SOCS3/COL1A1/JAK3/TGFB1/SOCS1/STAT6/AGT/MAPK11/CD8B/ERRFI1/TIPARP/GDF15/GATA3/P      | 17 |
| GO:0030182 | neuron differentiation                                          | 17/182 | 85/749  | 0,868886111 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/STAT3/C3/HDAC6/C1QA/XBP1/VCAM1/AGT/TNC/APOE/LST1/FN1/EPO/GATA3/ADORA2A                | 17 |
| GO:1903532 | positive regulation of secretion by cell                        | 17/182 | 86/749  | 0,881619707 | 0,999954951 | 0,999954951 | HIF1A/FCER1G/IL4R/TGFB1/XBP1/IL17RA/AGT/TLR4/TLR2/MAPK11/CD58/ITGB2/CD14/GATA3/IFNGR1/ADORA2A/IL17R     | 17 |
| GO:0070848 | response to growth factor                                       | 17/182 | 93/749  | 0,945749452 | 0,999954951 | 0,999954951 | HIF1A/SOST/HDAC6/COL1A1/NR4A1/COL3A1/TGFB1/VCAM1/AGT/TNC/EGR1/TNFRSF1B/MYC/ERRFI1/NOX4/GDF15/GA         | 17 |
| GO:0050670 | regulation of lymphocyte proliferation                          | 17/182 | 107/749 | 0,991688356 | 0,999954951 | 0,999954951 | BCL6/CD24/JAK3/TGFB1/AHR/CDKN1A/VCAM1/CD276/TLR4/LILRB2/LST1/IL6R/TNFRSF1B/LILRB1/EPO/IL6ST/PTPN6       | 17 |
| GO:0032944 | regulation of mononuclear cell proliferation                    | 17/182 | 108/749 | 0,992837741 | 0,999954951 | 0,999954951 | BCL6/CD24/JAK3/TGFB1/AHR/CDKN1A/VCAM1/CD276/TLR4/LILRB2/LST1/IL6R/TNFRSF1B/LILRB1/EPO/IL6ST/PTPN6       | 17 |
| GO:0042326 | negative regulation of phosphorylation                          | 16/182 | 47/749  | 0,079110846 | 0,999954951 | 0,999954951 | STAT3/SOCS3/TGFB1/SOCS1/BAX/CDKN1A/TLR4/APOE/MYC/TRIB1/ERRFI1/ATF3/ADORA2A/RGN/RNF149/PTPN6             | 16 |
| GO:0051346 | negative regulation of hydrolase activity                       | 16/182 | 50/749  | 0,127587049 | 0,999954951 | 0,999954951 | SERPINA3/LTF/RARRES1/TIMP1/C3/SLPI/SERPING1/AGT/FKBP1A/BIRC3/IFIT1/SERPINE1/ADORA2A/TNFSF14/RGN/PLAU    | 16 |
| GO:0030163 | protein catabolic process                                       | 16/182 | 54/749  | 0,213960399 | 0,999954951 | 0,999954951 | TIMP1/PSMB8/HDAC6/PSME2/PSMB10/XBP1/LDLR/CTSS/APOE/TNFRSF1B/TRIB1/TIPARP/PSME1/ISG15/RGN/RNF149         | 16 |
| GO:0071347 | cellular response to interleukin-1                              | 16/182 | 55/749  | 0,239000303 | 0,999954951 | 0,999954951 | HIF1A/PSMB8/IL1R1/MAPK13/GBP2/LCN2/PSME2/ICAM1/PSMB10/EGR1/MYD88/MAPK11/IL1R2/ABCC2/PSME1/NFKB1         | 16 |
| GO:0071496 | cellular response to external stimulus                          | 16/182 | 57/749  | 0,292402455 | 0,999954951 | 0,999954951 | TNFRSF1A/LCN2/LTBR/COL1A1/ICAM1/TGFB1/XBP1/CDKN1A/VCAM1/AGT/TNC/TLR4/MYD88/ATF3/TNFSF14/NFKB1           | 16 |
| GO:0007249 | I-kappaB kinase/NF-kappaB signaling                             | 16/182 | 59/749  | 0,349232704 | 0,999954951 | 0,999954951 | LTF/BCL3/TNFRSF1A/LTBR/RELB/STAT1/LY96/FKBP1A/TLR4/MYD88/TLR2/S100A12/TBK1/TNFSF10/BIRC3/CD14           | 16 |
| GO:1901214 | regulation of neuron death                                      | 16/182 | 59/749  | 0,349232704 | 0,999954951 | 0,999954951 | HIF1A/SOD2/STAT3/C1QA/BAX/EGR1/TLR4/APOE/TNFRSF1B/TBK1/ITGB2/C5AR1/G6PD/EPO/GATA3/ADORA2A               | 16 |
| GO:0070997 | neuron death                                                    | 16/182 | 61/749  | 0,408166897 | 0,999954951 | 0,999954951 | HIF1A/SOD2/STAT3/C1QA/BAX/EGR1/TLR4/APOE/TNFRSF1B/TBK1/ITGB2/C5AR1/G6PD/EPO/GATA3/ADORA2A               | 16 |
| GO:0043269 | regulation of ion transport                                     | 16/182 | 63/749  | 0,46783079  | 0,999954951 | 0,999954951 | EHD3/ABCB1/ICAM1/TGFB1/BAX/AGT/FKBP1A/CTSS/APOE/LILRB2/G6PD/LILRB1/EPO/ADORA2A/RGN/PTPN6                | 16 |
| GO:0050767 | regulation of neurogenesis                                      | 16/182 | 65/749  | 0,526893558 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/STAT3/MME/COL3A1/TGFB1/AGT/LDLR/APOE/TLR2/TNFRSF1B/FN1/EPO/GATA3/IL6ST                | 16 |
| GO:0051960 | regulation of nervous system development                        | 16/182 | 68/749  | 0,611765653 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/STAT3/MME/COL3A1/TGFB1/AGT/LDLR/APOE/TLR2/TNFRSF1B/FN1/EPO/GATA3/IL6ST                | 16 |
| GO:0070482 | response to oxygen levels                                       | 16/182 | 68/749  | 0,611765653 | 0,999954951 | 0,999954951 | HIF1A/CD24/PSMB8/COL1A1/PSME2/ICAM1/PSMB10/TGFB1/CDKN1A/VCAM1/EGR1/TLR2/MYC/NOX4/PSME1/EPO              | 16 |
| GO:0002822 | regulation of adaptive immune response based on somatic reco    | 16/182 | 70/749  | 0,664446054 | 0,999954951 | 0,999954951 | BCL6/C3/FCER1G/IL1R1/JAK3/IL4R/NFKBIZ/TGFB1/STAT6/IL6R/SLC11A1/PVR/TNFRSF1B/LILRB1/GATA3/PTPN6          | 16 |
| GO:2001233 | regulation of apoptotic signaling pathway                       | 16/182 | 70/749  | 0,664446054 | 0,999954951 | 0,999954951 | S100A9/HIF1A/SOD2/S100A8/MUC1/LTBR/ICAM1/XBP1/BAX/AGT/TNFSF10/EPO/ATF3/SERPINE1/ADORA2A/PLAUR           | 16 |
| GO:0071900 | regulation of protein serine/threonine kinase activity          | 16/182 | 71/749  | 0,689334125 | 0,999954951 | 0,999954951 | LTF/FPR1/CD24/TGFB1/CDKN1A/TLR4/KITLG/APOE/MAPK11/S100A12/FGD2/TRIB1/NOX4/C5AR1/GDF15/PTPN6             | 16 |
| GO:0030855 | epithelial cell differentiation                                 | 16/182 | 72/749  | 0,713162907 | 0,999954951 | 0,999954951 | HIF1A/PLAAT4/CD24/COL4A1/TNFRSF1A/KRT8/ICAM1/MAF/STAT1/TGFB1/XBP1/CDKN1A/KRT19/ERRFI1/SERPINE1/GA1      | 16 |
| GO:0048729 | tissue morphogenesis                                            | 16/182 | 72/749  | 0,713162907 | 0,999954951 | 0,999954951 | HIF1A/COL4A1/PSMB8/SOCS3/COL3A1/PSME2/PSMB10/STAT1/TGFB1/AGT/TNC/FKBP1A/MYC/PSME1/MYOM2/GATA3           | 16 |
| GO:0050707 | regulation of cytokine secretion                                | 16/182 | 72/749  | 0,713162907 | 0,999954951 | 0,999954951 | IL4R/SOCS1/XBP1/IL17RA/TLR4/TLR2/MAPK11/TNFRSF1B/IL1R2/CD58/FN1/LILRB1/CD14/GATA3/IFNGR1/IL17RB         | 16 |
| GO:0000122 | negative regulation of transcription by RNA polymerase II       | 16/182 | 74/749  | 0,757455013 | 0,999954951 | 0,999954951 | BCL6/STAT3/MAF/RELB/STAT1/TGFB1/DNMT1/STAT6/EGR1/IRF7/RORC/MYC/EPO/ATF3/GATA3/NFKB1                     | 16 |
| GO:0051704 | multi-organism process                                          | 16/182 | 76/749  | 0,797081312 | 0,999954951 | 0,999954951 | BCL6/TIMP1/STAT3/ADAMTS1/IL4R/TGFB1/BAX/AGT/APOL2/ARHGDIB/ABCC2/BIRC3/IFIT1/EPO/RGN/THBD                | 16 |
| GO:0051345 | positive regulation of hydrolase activity                       | 16/182 | 82/749  | 0,888283853 | 0,999954951 | 0,999954951 | S100A9/STAT3/S100A8/PSME2/ICAM1/BAX/AGT/MYC/ARHGDIB/TNFSF10/ERRFI1/C5AR1/PSME1/FN1/CASP4/RGN            | 16 |
| GO:0002703 | regulation of leukocyte mediated immunity                       | 16/182 | 83/749  | 0,899737349 | 0,999954951 | 0,999954951 | BCL6/C3/FCER1G/IL1R1/ICAM1/JAK3/IL4R/TGFB1/STAT6/TLR4/PVR/TNFRSF1B/ITGB2/LILRB1/GATA3/PTPN6             | 16 |
| GO:0042098 | T cell proliferation                                            | 16/182 | 93/749  | 0,970081489 | 0,999954951 | 0,999954951 | CD24/PSMB10/JAK3/TGFB1/BAX/VCAM1/CD276/LILRB2/IL6R/SLC11A1/TNFRSF1B/LILRB1/EPO/TNFSF14/IL6ST/PTPN6      | 16 |
| GO:0060326 | cell chemotaxis                                                 | 16/182 | 94/749  | 0,973809663 | 0,999954951 | 0,999954951 | S100A9/S100A8/FCER1G/NR4A1/CXCL16/VCAM1/IL17RA/SLAMF8/CXCL1/IL6R/S100A12/CMKLR1/ITGB2/C5AR1/SERPIN      | 16 |
| GO:0030217 | T cell differentiation                                          | 16/182 | 99/749  | 0,986948816 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/FCER1G/RELB/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/STAT6/EGR1/LILRB2/RORC/GATA3              | 16 |
| GO:0009314 | response to radiation                                           | 15/182 | 42/749  | 0,059786618 | 0,999954951 | 0,999954951 | HIF1A/BCL3/MAPK13/MME/COL3A1/ICAM1/TGFB1/BAX/CDKN1A/VCAM1/EGR1/MYC/NOX4/GATA3/THBD                      | 15 |
| GO:0045861 | negative regulation of proteolysis                              | 15/182 | 43/749  | 0,072485814 | 0,999954951 | 0,999954951 | SERPINA3/LTF/RARRES1/TIMP1/C3/SLPI/SERPING1/HDAC6/AGT/IL1R2/BIRC3/SERPINE1/ADORA2A/TNFSF14/PLAUR        | 15 |
| GO:0001933 | negative regulation of protein phosphorylation                  | 15/182 | 46/749  | 0,120767445 | 0,999954951 | 0,999954951 | SOCS3/TGFB1/SOCS1/BAX/CDKN1A/TLR4/APOE/MYC/TRIB1/ERRFI1/ATF3/ADORA2A/RGN/RNF149/PTPN6                   | 15 |
| GO:0031667 | response to nutrient levels                                     | 15/182 | 47/749  | 0,140293976 | 0,999954951 | 0,999954951 | LCN2/COL1A1/ICAM1/STAT1/TGFB1/XBP1/CDKN1A/VCAM1/LDLR/TNC/APOE/G6PD/GDF15/EPO/ATF3                       | 15 |

|            |                                                                     |        |        |             |             |             |                                                                                                  |    |
|------------|---------------------------------------------------------------------|--------|--------|-------------|-------------|-------------|--------------------------------------------------------------------------------------------------|----|
| GO:0009991 | response to extracellular stimulus                                  | 15/182 | 53/749 | 0,289221721 | 0,999954951 | 0,999954951 | LCN2/COL1A1/ICAM1/STAT1/TGFB1/XBP1/CDKN1A/VCAM1/LDLR/TNC/APOE/G6PD/GDF15/EPO/ATF3                | 15 |
| GO:0001655 | urogenital system development                                       | 15/182 | 56/749 | 0,378098472 | 0,999954951 | 0,999954951 | CD24/COL4A1/ADAMTS1/MME/STAT1/TGFB1/BAX/AGT/TNC/EGR1/IL6R/MYC/TIPARP/GATA3/RGN                   | 15 |
| GO:0072511 | divalent inorganic cation transport                                 | 15/182 | 57/749 | 0,408704192 | 0,999954951 | 0,999954951 | EHD3/ICAM1/TGFB1/BAX/AGT/FKBP1A/LILRB2/SLC11A1/ABCC2/G6PD/LILRB1/EPO/ADORA2A/RGN/PTPN6           | 15 |
| GO:1902532 | negative regulation of intracellular signal transduction            | 15/182 | 61/749 | 0,531042635 | 0,999954951 | 0,999954951 | HIF1A/SOD2/BCL6/MUC1/STAT1/XBP1/TLR4/APOE/MYC/ERRFI1/EPO/ATF3/RNF149/PTPN6/PLAUR                 | 15 |
| GO:0007507 | heart development                                                   | 15/182 | 62/749 | 0,560739378 | 0,999954951 | 0,999954951 | HIF1A/ADAMTS1/TNFRSF1A/COL3A1/TGFB1/CDKN1A/VCAM1/AGT/FKBP1A/MAPK11/TNFRSF1B/NOX4/G6PD/MYOM2/     | 15 |
| GO:0044703 | multi-organism reproductive process                                 | 15/182 | 67/749 | 0,696937559 | 0,999954951 | 0,999954951 | BCL6/TIMP1/STAT3/ADAMTS1/IL4R/TGFB1/BAX/AGT/APOL2/ARHGDIB/ABCC2/BIRC3/EPO/RGN/THBD               | 15 |
| GO:0071346 | cellular response to interferon-gamma                               | 15/182 | 70/749 | 0,765637674 | 0,999954951 | 0,999954951 | JAK1/IFNGR2/SOCS3/GBP2/ICAM1/FCGR1A/STAT1/SOCS1/VCAM1/IFI30/TLR4/TLR2/IRF7/CD58/IFNGR1           | 15 |
| GO:0007162 | negative regulation of cell adhesion                                | 15/182 | 73/749 | 0,823207375 | 0,999954951 | 0,999954951 | BCL6/MUC1/COL1A1/JAK3/IL4R/TGFB1/SOCS1/TNC/LILRB2/TGFB1/ARHGDIB/LILRB1/SERPINE1/ADORA2A/PTPN6    | 15 |
| GO:0002793 | positive regulation of peptide secretion                            | 15/182 | 75/749 | 0,85544048  | 0,999954951 | 0,999954951 | HIF1A/S100A8/IL4R/TGFB1/XBP1/IL17RA/TLR4/TLR2/MAPK11/CD58/CD14/GATA3/IFNGR1/ADORA2A/IL17RB       | 15 |
| GO:0030030 | cell projection organization                                        | 15/182 | 78/749 | 0,895164945 | 0,999954951 | 0,999954951 | S100A9/EHD3/LCN2/HDAC6/ICAM1/AGT/TNC/APOE/LST1/EMP3/FGD2/FN1/EPO/GATA3/ADORA2A                   | 15 |
| GO:0034613 | cellular protein localization                                       | 15/182 | 85/749 | 0,95453779  | 0,999954951 | 0,999954951 | BCL3/STAT3/CD24/FCER1G/TNFRSF1A/EHD3/GBP2/HDAC6/COL1A1/TGFB1/BAX/CDKN1A/AGT/APOE/ITGB2           | 15 |
| GO:0070727 | cellular macromolecule localization                                 | 15/182 | 85/749 | 0,95453779  | 0,999954951 | 0,999954951 | BCL3/STAT3/CD24/FCER1G/TNFRSF1A/EHD3/GBP2/HDAC6/COL1A1/TGFB1/BAX/CDKN1A/AGT/APOE/ITGB2           | 15 |
| GO:0051222 | positive regulation of protein transport                            | 15/182 | 88/749 | 0,969305071 | 0,999954951 | 0,999954951 | HIF1A/IL4R/TGFB1/XBP1/IL17RA/TLR4/TLR2/MAPK11/CD58/ITGB2/CD14/GATA3/IFNGR1/ADORA2A/IL17RB        | 15 |
| GO:1904951 | positive regulation of establishment of protein localization        | 15/182 | 88/749 | 0,969305071 | 0,999954951 | 0,999954951 | HIF1A/IL4R/TGFB1/XBP1/IL17RA/TLR4/TLR2/MAPK11/CD58/ITGB2/CD14/GATA3/IFNGR1/ADORA2A/IL17RB        | 15 |
| GO:0043410 | positive regulation of MAPK cascade                                 | 15/182 | 95/749 | 0,988613618 | 0,999954951 | 0,999954951 | FPR1/CD24/LTBR/ICAM1/TGFB1/TLR4/KITLG/APOE/MAPK11/S100A12/FGD2/NOX4/C5AR1/GDF15/EPO              | 15 |
| GO:0051092 | positive regulation of NF-kappaB transcription factor activity      | 14/182 | 44/749 | 0,154381996 | 0,999954951 | 0,999954951 | S100A9/LTF/STAT3/S100A8/ICAM1/TGFB1/AGT/NFKB2/TLR4/MYD88/TLR2/S100A12/ITGB2/NFKB1                | 14 |
| GO:0007596 | blood coagulation                                                   | 14/182 | 47/749 | 0,22885722  | 0,999954951 | 0,999954951 | SERPING1/FCER1G/EHD3/COL1A1/COL3A1/CD59/TLR4/APOE/SERPINE1/GATA3/ADORA2A/THBD/PTPN6/PLAUR        | 14 |
| GO:0007599 | hemostasis                                                          | 14/182 | 47/749 | 0,22885722  | 0,999954951 | 0,999954951 | SERPING1/FCER1G/EHD3/COL1A1/COL3A1/CD59/TLR4/APOE/SERPINE1/GATA3/ADORA2A/THBD/PTPN6/PLAUR        | 14 |
| GO:0019216 | regulation of lipid metabolic process                               | 14/182 | 47/749 | 0,22885722  | 0,999954951 | 0,999954951 | SERPINA3/C3/SOCS3/TNFRSF1A/TGFB1/SOCS1/AGT/LDLR/EGR1/APOE/RORC/NFKB1/ALAS1/RGN                   | 14 |
| GO:0050817 | coagulation                                                         | 14/182 | 48/749 | 0,25659724  | 0,999954951 | 0,999954951 | SERPING1/FCER1G/EHD3/COL1A1/COL3A1/CD59/TLR4/APOE/SERPINE1/GATA3/ADORA2A/THBD/PTPN6/PLAUR        | 14 |
| GO:1905114 | cell surface receptor signaling pathway involved in cell-cell signa | 14/182 | 51/749 | 0,346162909 | 0,999954951 | 0,999954951 | C3/CD24/SOST/PSMB8/COL1A1/PSME2/PSMB10/EGR1/APOE/TLR2/PSME1/GATA3/ADORA2A/NFKB1                  | 14 |
| GO:0002286 | T cell activation involved in immune response                       | 14/182 | 52/749 | 0,377466127 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/FCER1G/ICAM1/RELB/JAK3/IL4R/NFKBIZ/STAT6/SLC11A1/RORC/LILRB1/GATA3               | 14 |
| GO:0019882 | antigen processing and presentation                                 | 14/182 | 52/749 | 0,377466127 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/PSME2/ICAM1/PSMB10/RELB/FCGR1A/IFI30/CTSS/LILRB2/SLC11A1/TAP2/PSME1/TAP1            | 14 |
| GO:0007259 | receptor signaling pathway via JAK-STAT                             | 14/182 | 53/749 | 0,409143606 | 0,999954951 | 0,999954951 | BCL3/STAT3/SOCS3/TNFRSF1A/IFNAR2/JAK3/STAT1/SOCS1/STAT6/AGT/IL6R/IL10RB/EPO/IL6ST                | 14 |
| GO:0072001 | renal system development                                            | 14/182 | 53/749 | 0,409143606 | 0,999954951 | 0,999954951 | CD24/COL4A1/ADAMTS1/MME/STAT1/TGFB1/BAX/AGT/EGR1/IL6R/MYC/TIPARP/GATA3/RGN                       | 14 |
| GO:0019058 | viral life cycle                                                    | 14/182 | 54/749 | 0,440984935 | 0,999954951 | 0,999954951 | LTF/IFITM3/ITGB6/SLPI/IFITM2/IFITM1/HAVCR1/ICAM1/LDLR/APOE/PVR/ISG20/IFIT1/ISG15                 | 14 |
| GO:0034330 | cell junction organization                                          | 14/182 | 54/749 | 0,440984935 | 0,999954951 | 0,999954951 | C1QB/C3/COL4A1/HDAC6/C1QA/TGFB1/AGT/TNC/APOE/TLR2/LILRB2/PVR/C5AR1/FN1                           | 14 |
| GO:0042692 | muscle cell differentiation                                         | 14/182 | 54/749 | 0,440984935 | 0,999954951 | 0,999954951 | SOD2/KRT8/IL4R/TGFB1/XBP1/DNMT1/AGT/MAPK11/KRT19/NOX4/G6PD/MYOM2/GDF15/TNFSF14                   | 14 |
| GO:0044255 | cellular lipid metabolic process                                    | 14/182 | 54/749 | 0,440984935 | 0,999954951 | 0,999954951 | ALDH3A2/PLAAT4/C3/SOCS3/TNFRSF1A/TGFB1/SOCS1/XBP1/BAX/ALOX5/AGT/LDLR/APOE/RGN                    | 14 |
| GO:0072593 | reactive oxygen species metabolic process                           | 14/182 | 54/749 | 0,440984935 | 0,999954951 | 0,999954951 | HIF1A/SOD2/STAT3/HDAC6/ICAM1/TGFB1/CDKN1A/AGT/TLR4/TLR2/ITGB2/NOX4/G6PD/RGN                      | 14 |
| GO:0097696 | receptor signaling pathway via STAT                                 | 14/182 | 54/749 | 0,440984935 | 0,999954951 | 0,999954951 | BCL3/STAT3/SOCS3/TNFRSF1A/IFNAR2/JAK3/STAT1/SOCS1/STAT6/AGT/IL6R/IL10RB/EPO/IL6ST                | 14 |
| GO:0045862 | positive regulation of proteolysis                                  | 14/182 | 55/749 | 0,472784918 | 0,999954951 | 0,999954951 | S100A9/STAT3/S100A8/PSME2/BAX/APOE/TNFRSF1B/MYC/TNFSF10/TRIB1/PSME1/FN1/CASP4/RGN                | 14 |
| GO:0001501 | skeletal system development                                         | 14/182 | 56/749 | 0,504347067 | 0,999954951 | 0,999954951 | HIF1A/LTF/TIMP1/COL1A1/COL3A1/MAF/TGFB1/VCAN/TGFB1/CMKLR1/TIPARP/LILRB1/RGN/PTPN6                | 14 |
| GO:0070838 | divalent metal ion transport                                        | 14/182 | 56/749 | 0,504347067 | 0,999954951 | 0,999954951 | EHD3/ICAM1/TGFB1/BAX/AGT/FKBP1A/LILRB2/SLC11A1/G6PD/LILRB1/EPO/ADORA2A/RGN/PTPN6                 | 14 |
| GO:0050877 | nervous system process                                              | 14/182 | 57/749 | 0,535486607 | 0,999954951 | 0,999954951 | HIF1A/SOD2/MME/COL1A1/ICAM1/AGT/LDLR/APOE/TLR2/LILRB2/TNFRSF1B/TGFB1/C5AR1/ADORA2A               | 14 |
| GO:0051091 | positive regulation of DNA-binding transcription factor activity    | 14/182 | 57/749 | 0,535486607 | 0,999954951 | 0,999954951 | S100A9/LTF/STAT3/S100A8/ICAM1/TGFB1/AGT/NFKB2/TLR4/MYD88/TLR2/S100A12/ITGB2/NFKB1                | 14 |
| GO:0016064 | immunoglobulin mediated immune response                             | 14/182 | 58/749 | 0,566032975 | 0,999954951 | 0,999954951 | BCL3/C1QB/C1S/BCL6/C3/SERPING1/C9/FCER1G/C1QA/IL4R/TGFB1/STAT6/IRF7/PTPN6                        | 14 |
| GO:0048872 | homeostasis of number of cells                                      | 14/182 | 58/749 | 0,566032975 | 0,999954951 | 0,999954951 | HIF1A/BCL6/STAT3/FCER1G/JAK3/STAT1/TGFB1/BAX/KITLG/G6PD/EPO/GATA3/TNFSF14/ISG15                  | 14 |
| GO:0035690 | cellular response to drug                                           | 14/182 | 59/749 | 0,59583177  | 0,999954951 | 0,999954951 | MAPK13/LCN2/HDAC6/ICAM1/TGFB1/AHR/STAT6/EGR1/SLAMF8/MYC/ABCC2/ERRFI1/NFKB1/RNF149                | 14 |
| GO:0019724 | B cell mediated immunity                                            | 14/182 | 60/749 | 0,624746176 | 0,999954951 | 0,999954951 | BCL3/C1QB/C1S/BCL6/C3/SERPING1/C9/FCER1G/C1QA/IL4R/TGFB1/STAT6/IRF7/PTPN6                        | 14 |
| GO:0097191 | extrinsic apoptotic signaling pathway                               | 14/182 | 60/749 | 0,624746176 | 0,999954951 | 0,999954951 | TNFRSF1A/LCN2/KRT8/LTBR/ICAM1/TGFB1/BAX/AGT/KITLG/IL6R/TNFRSF1B/TNFSF10/ATF3/SERPINE1            | 14 |
| GO:0043405 | regulation of MAP kinase activity                                   | 14/182 | 61/749 | 0,65265787  | 0,999954951 | 0,999954951 | FPR1/CD24/TGFB1/TLR4/KITLG/APOE/MAPK11/S100A12/FGD2/TRIB1/NOX4/C5AR1/GDF15/PTPN6                 | 14 |
| GO:0001666 | response to hypoxia                                                 | 14/182 | 63/749 | 0,70509432  | 0,999954951 | 0,999954951 | HIF1A/CD24/PSMB8/PSME2/ICAM1/PSMB10/TGFB1/VCAM1/EGR1/TLR2/MYC/NOX4/PSME1/EPO                     | 14 |
| GO:0002573 | myeloid leukocyte differentiation                                   | 14/182 | 63/749 | 0,70509432  | 0,999954951 | 0,999954951 | LTF/FCER1G/LTBR/RELB/TGFB1/TLR4/KITLG/TLR2/IRF7/MYC/TRIB1/LILRB1/TMEM178A/GATA3                  | 14 |
| GO:0036293 | response to decreased oxygen levels                                 | 14/182 | 63/749 | 0,70509432  | 0,999954951 | 0,999954951 | HIF1A/CD24/PSMB8/PSME2/ICAM1/PSMB10/TGFB1/VCAM1/EGR1/TLR2/MYC/NOX4/PSME1/EPO                     | 14 |
| GO:0050673 | epithelial cell proliferation                                       | 14/182 | 63/749 | 0,70509432  | 0,999954951 | 0,999954951 | HIF1A/STAT3/NR4A1/STAT1/TGFB1/XBP1/BAX/STAT6/APOE/MYC/ERRFI1/C5AR1/GATA3/RGN                     | 14 |
| GO:0006979 | response to oxidative stress                                        | 14/182 | 65/749 | 0,752569557 | 0,999954951 | 0,999954951 | HIF1A/SOD2/MAPK13/LCN2/HDAC6/COL1A1/STAT1/STAT6/TLR4/APOE/ABCC2/NOX4/G6PD/RGN                    | 14 |
| GO:0007010 | cytoskeleton organization                                           | 14/182 | 66/749 | 0,774345927 | 0,999954951 | 0,999954951 | S100A9/BCL6/S100A8/KRT8/HDAC6/ICAM1/TGFB1/APOE/CXCL1/ARHGDIB/FGD2/KRT19/NOX4/MYOM2               | 14 |
| GO:0022402 | cell cycle process                                                  | 14/182 | 67/749 | 0,79479342  | 0,999954951 | 0,999954951 | BCL6/ADAMTS1/PSMB8/MUC1/ABCB1/PSME2/PSMB10/TGFB1/BAX/CDKN1A/MYC/PSME1/KLHL13/PTPN6               | 14 |
| GO:0046631 | alpha-beta T cell activation                                        | 14/182 | 69/749 | 0,831721996 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/RELB/JAK3/IL4R/NFKBIZ/SOCS1/STAT6/IL6R/RORC/LILRB1/GATA3/ADORA2A                 | 14 |
| GO:1903708 | positive regulation of hemopoiesis                                  | 14/182 | 72/749 | 0,877572098 | 0,999954951 | 0,999954951 | HIF1A/BCL6/STAT3/STAT1/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/KITLG/LILRB2/TRIB1/GATA3/ISG15               | 14 |
| GO:0050714 | positive regulation of protein secretion                            | 14/182 | 73/749 | 0,890472201 | 0,999954951 | 0,999954951 | HIF1A/IL4R/TGFB1/XBP1/IL17RA/TLR4/TLR2/MAPK11/CD58/CD14/GATA3/IFNGR1/ADORA2A/IL17RB              | 14 |
| GO:0120036 | plasma membrane bounded cell projection organization                | 14/182 | 74/749 | 0,902266764 | 0,999954951 | 0,999954951 | S100A9/EHD3/HDAC6/ICAM1/AGT/TNC/APOE/LST1/EMP3/FGD2/FN1/EPO/GATA3/ADORA2A                        | 14 |
| GO:1901342 | regulation of vasculature development                               | 14/182 | 74/749 | 0,902266764 | 0,999954951 | 0,999954951 | HIF1A/JAK1/SOD2/STAT3/C3/STAT1/XBP1/DNMT1/AGT/EGR1/IL6R/ITGB2/C5AR1/SERPINE1                     | 14 |
| GO:0002440 | production of molecular mediator of immune response                 | 14/182 | 77/749 | 0,931608556 | 0,999954951 | 0,999954951 | BCL6/FCER1G/IL1R1/JAK3/IL4R/TGFB1/XBP1/STAT6/TLR4/TLR2/SLC11A1/TNFRSF1B/LILRB1/GATA3             | 14 |
| GO:0030595 | leukocyte chemotaxis                                                | 14/182 | 79/749 | 0,946751867 | 0,999954951 | 0,999954951 | S100A9/S100A8/FCER1G/CXCL16/IL17RA/SLAMF8/CXCL1/IL6R/S100A12/CMKLR1/ITGB2/C5AR1/SERPINE1/TNFSF14 | 14 |
| GO:0071363 | cellular response to growth factor stimulus                         | 14/182 | 88/749 | 0,984591759 | 0,999954951 | 0,999954951 | HIF1A/SOST/COL1A1/NR4A1/COL3A1/TGFB1/VCAM1/AGT/EGR1/TNFRSF1B/ERRFI1/NOX4/GDF15/GATA3             | 14 |
| GO:0001525 | angiogenesis                                                        | 14/182 | 95/749 | 0,994782796 | 0,999954951 | 0,999954951 | HIF1A/JAK1/STAT3/C3/COL4A1/NR4A1/STAT1/XBP1/AGT/TGFB1/ITGB2/C5AR1/FN1/SERPINE1                   | 14 |
| GO:0044257 | cellular protein catabolic process                                  | 13/182 | 34/749 | 0,045875397 | 0,999954951 | 0,999954951 | PSMB8/HDAC6/PSME2/PSMB10/XBP1/LDLR/CTSS/APOE/TRIB1/PSME1/ISG15/RGN/RNF149                        | 13 |

|            |                                                            |        |        |             |             |             |                                                                                         |    |
|------------|------------------------------------------------------------|--------|--------|-------------|-------------|-------------|-----------------------------------------------------------------------------------------|----|
| GO:0010466 | negative regulation of peptidase activity                  | 13/182 | 36/749 | 0,071425161 | 0,999954951 | 0,999954951 | SERPINA3/LTF/RARRES1/TIMP1/C3/SLPI/SERPING1/AGT/BIRC3/SERPINE1/ADORA2A/TNFSF14/PLAUR    | 13 |
| GO:0010951 | negative regulation of endopeptidase activity              | 13/182 | 36/749 | 0,071425161 | 0,999954951 | 0,999954951 | SERPINA3/LTF/RARRES1/TIMP1/C3/SLPI/SERPING1/AGT/BIRC3/SERPINE1/ADORA2A/TNFSF14/PLAUR    | 13 |
| GO:0006898 | receptor-mediated endocytosis                              | 13/182 | 40/749 | 0,146381538 | 0,999954951 | 0,999954951 | CD163/C3/FCER1G/FCGR1A/CXCL16/APOL1/LDLR/MASP1/APOE/ITGB2/LILRB1/CD14/SERPINE1          | 13 |
| GO:0002224 | toll-like receptor signaling pathway                       | 13/182 | 42/749 | 0,195513648 | 0,999954951 | 0,999954951 | S100A9/LTF/S100A8/LY96/TLR4/CTSS/MYD88/TLR2/IRF7/TBK1/ITGB2/BIRC3/CD14                  | 13 |
| GO:0062012 | regulation of small molecule metabolic process             | 13/182 | 42/749 | 0,195513648 | 0,999954951 | 0,999954951 | HIF1A/STAT3/PSMB8/PSME2/PSMB10/TGFB1/LDLR/EGR1/APOE/RORC/PSME1/NFKB1/RGN                | 13 |
| GO:1903047 | mitotic cell cycle process                                 | 13/182 | 42/749 | 0,195513648 | 0,999954951 | 0,999954951 | BCL6/ADAMTS1/PSMB8/MUC1/ABCB1/PSME2/PSMB10/TGFB1/BAX/CDKN1A/MYC/PSME1/PTPN6             | 13 |
| GO:0033209 | tumor necrosis factor-mediated signaling pathway           | 13/182 | 44/749 | 0,251274257 | 0,999954951 | 0,999954951 | PSMB8/TNFRSF1A/KRT8/LTBR/PSME2/PSMB10/STAT1/TNFRSF1B/BIRC3/PSME1/CASP4/TNFSF14/LTB      | 13 |
| GO:0040013 | negative regulation of locomotion                          | 13/182 | 44/749 | 0,251274257 | 0,999954951 | 0,999954951 | TIMP1/STAT3/IFITM1/COL3A1/TGFB1/SLAMF8/APOE/ARHGDIB/TRIB1/SERPINE1/GATA3/ADORA2A/RGN    | 13 |
| GO:0002221 | pattern recognition receptor signaling pathway             | 13/182 | 45/749 | 0,281200909 | 0,999954951 | 0,999954951 | S100A9/LTF/S100A8/LY96/TLR4/CTSS/MYD88/TLR2/IRF7/TBK1/ITGB2/BIRC3/CD14                  | 13 |
| GO:0051924 | regulation of calcium ion transport                        | 13/182 | 45/749 | 0,281200909 | 0,999954951 | 0,999954951 | EHD3/ICAM1/TGFB1/BAX/AGT/FKBP1A/LILRB2/G6PD/LILRB1/EPO/ADORA2A/RGN/PTPN6                | 13 |
| GO:0010959 | regulation of metal ion transport                          | 13/182 | 48/749 | 0,376580449 | 0,999954951 | 0,999954951 | EHD3/ICAM1/TGFB1/BAX/AGT/FKBP1A/LILRB2/G6PD/LILRB1/EPO/ADORA2A/RGN/PTPN6                | 13 |
| GO:0017144 | drug metabolic process                                     | 13/182 | 48/749 | 0,376580449 | 0,999954951 | 0,999954951 | ALDH3A2/STAT3/HDAC6/ICAM1/TGFB1/AGT/EGR1/TLR4/VCAN/TLR2/ABCC2/ITGB2/RGN                 | 13 |
| GO:0000278 | mitotic cell cycle                                         | 13/182 | 50/749 | 0,44249503  | 0,999954951 | 0,999954951 | BCL6/ADAMTS1/PSMB8/MUC1/ABCB1/PSME2/PSMB10/TGFB1/BAX/CDKN1A/MYC/PSME1/PTPN6             | 13 |
| GO:0001101 | response to acid chemical                                  | 13/182 | 51/749 | 0,475450756 | 0,999954951 | 0,999954951 | COL4A1/KRT8/COL1A1/COL3A1/ICAM1/SOCS1/XBP1/DNMT1/LDLR/TNC/EGR1/TLR2/ABCC2               | 13 |
| GO:0001822 | kidney development                                         | 13/182 | 52/749 | 0,508112299 | 0,999954951 | 0,999954951 | CD24/ADAMTS1/MME/STAT1/TGFB1/BAX/AGT/EGR1/IL6R/MYC/TIPARP/GATA3/RGN                     | 13 |
| GO:0009612 | response to mechanical stimulus                            | 13/182 | 53/749 | 0,540277124 | 0,999954951 | 0,999954951 | SOST/TNFRSF1A/LTBR/COL1A1/COL3A1/STAT1/TGFB1/AGT/TNC/TLR4/MYD88/TNFSF14/NFKB1           | 13 |
| GO:0045637 | regulation of myeloid cell differentiation                 | 13/182 | 54/749 | 0,571760013 | 0,999954951 | 0,999954951 | HIF1A/LTF/STAT3/STAT1/TGFB1/TLR4/KITLG/IRF7/MYC/TRIB1/LILRB1/TMEM178A/ISG15             | 13 |
| GO:0045786 | negative regulation of cell cycle                          | 13/182 | 54/749 | 0,571760013 | 0,999954951 | 0,999954951 | BCL6/PSMB8/MUC1/NR4A1/PSME2/PSMB10/TGFB1/BAX/CDKN1A/MYC/PSME1/LILRB1/GATA3              | 13 |
| GO:0062197 | cellular response to chemical stress                       | 13/182 | 54/749 | 0,571760013 | 0,999954951 | 0,999954951 | HIF1A/SOD2/MAPK13/LCN2/HDAC6/RELB/STAT6/TLR4/ERRFI1/NOX4/G6PD/EPO/RGN                   | 13 |
| GO:0006816 | calcium ion transport                                      | 13/182 | 55/749 | 0,602395162 | 0,999954951 | 0,999954951 | EHD3/ICAM1/TGFB1/BAX/AGT/FKBP1A/LILRB2/G6PD/LILRB1/EPO/ADORA2A/RGN/PTPN6                | 13 |
| GO:0006909 | phagocytosis                                               | 13/182 | 55/749 | 0,602395162 | 0,999954951 | 0,999954951 | C3/FCER1G/FCGR1A/TGFB1/FCGR2A/LDLR/TLR4/MYD88/TLR2/SLC11A1/ITGB2/CD14/ADORA2A           | 13 |
| GO:0042089 | cytokine biosynthetic process                              | 13/182 | 55/749 | 0,602395162 | 0,999954951 | 0,999954951 | BCL3/STAT3/SIGIRR/CD276/EGR1/TLR4/IRF7/TBK1/ERRFI1/LILRB1/GATA3/NFKB1/LTB               | 13 |
| GO:0042107 | cytokine metabolic process                                 | 13/182 | 55/749 | 0,602395162 | 0,999954951 | 0,999954951 | BCL3/STAT3/SIGIRR/CD276/EGR1/TLR4/IRF7/TBK1/ERRFI1/LILRB1/GATA3/NFKB1/LTB               | 13 |
| GO:0010720 | positive regulation of cell development                    | 13/182 | 56/749 | 0,632037609 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/MME/TGFB1/AGT/APOE/TLR2/TNFRSF1B/TRIB1/FN1/EPO/IL6ST                  | 13 |
| GO:0050678 | regulation of epithelial cell proliferation                | 13/182 | 56/749 | 0,632037609 | 0,999954951 | 0,999954951 | HIF1A/STAT3/NR4A1/STAT1/TGFB1/XBP1/BAX/APOE/MYC/ERRFI1/C5AR1/GATA3/RGN                  | 13 |
| GO:0050731 | positive regulation of peptidyl-tyrosine phosphorylation   | 13/182 | 59/749 | 0,713884673 | 0,999954951 | 0,999954951 | STAT3/CD24/SOCS3/TNFRSF1A/ICAM1/FCGR1A/TGFB1/AGT/KITLG/IL6R/NOX4/EPO/IL6ST              | 13 |
| GO:0002009 | morphogenesis of an epithelium                             | 13/182 | 60/749 | 0,738540002 | 0,999954951 | 0,999954951 | HIF1A/COL4A1/PSMB8/SOCS3/PSME2/PSMB10/STAT1/TGFB1/AGT/TNC/MYC/PSME1/GATA3               | 13 |
| GO:0048608 | reproductive structure development                         | 13/182 | 60/749 | 0,738540002 | 0,999954951 | 0,999954951 | HIF1A/ADAMTS1/SOCS3/MME/KRT8/ICAM1/BAX/TNC/KITLG/KRT19/TNFSF10/TIPARP/GATA3             | 13 |
| GO:0051607 | defense response to virus                                  | 13/182 | 60/749 | 0,738540002 | 0,999954951 | 0,999954951 | IFITM3/IFITM2/IFITM1/IFNAR2/STAT1/IRF7/TBK1/ISG20/BIRC3/LILRB1/IL10RB/IFIT1/ISG15       | 13 |
| GO:0061458 | reproductive system development                            | 13/182 | 60/749 | 0,738540002 | 0,999954951 | 0,999954951 | HIF1A/ADAMTS1/SOCS3/MME/KRT8/ICAM1/BAX/TNC/KITLG/KRT19/TNFSF10/TIPARP/GATA3             | 13 |
| GO:0050866 | negative regulation of cell activation                     | 13/182 | 63/749 | 0,804065675 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/TGFB1/STAT3/CD24/FCER1G/ABCB1/FCGR1A/BAX/CD59/LDLR/APOE/TAP2/ITGB2/TAP1  | 13 |
| GO:0061024 | membrane organization                                      | 13/182 | 64/749 | 0,823078608 | 0,999954951 | 0,999954951 | STAT3/C3/CD24/FCER1G/ABCB1/FCGR1A/BAX/CD59/LDLR/APOE/TAP2/ITGB2/TAP1                    | 13 |
| GO:0006874 | cellular calcium ion homeostasis                           | 13/182 | 65/749 | 0,840705871 | 0,999954951 | 0,999954951 | FPR1/CD24/TGFB1/BAX/AGT/FKBP1A/APOE/CMKLR1/C5AR1/TMEM178A/EPO/RGN/PTPN6                 | 13 |
| GO:0055074 | calcium ion homeostasis                                    | 13/182 | 65/749 | 0,840705871 | 0,999954951 | 0,999954951 | FPR1/CD24/TGFB1/BAX/AGT/FKBP1A/APOE/CMKLR1/C5AR1/TMEM178A/EPO/RGN/PTPN6                 | 13 |
| GO:0006897 | endocytosis                                                | 13/182 | 67/749 | 0,871954365 | 0,999954951 | 0,999954951 | CD163/C3/FCER1G/FCGR1A/CXCL16/APOL1/LDLR/MASP1/APOE/ITGB2/LILRB1/CD14/SERPINE1          | 13 |
| GO:0048666 | neuron development                                         | 13/182 | 68/749 | 0,885673009 | 0,999954951 | 0,999954951 | S100A9/C3/HDAC6/C1QA/XBP1/AGT/TNC/APOE/LST1/FN1/EPO/GATA3/ADORA2A                       | 13 |
| GO:0070371 | ERK1 and ERK2 cascade                                      | 13/182 | 71/749 | 0,919918321 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/AGT/TLR4/APOE/MYC/ERRFI1/NOX4/C5AR1/FN1/EPO/ATF3/PTPN6                      | 13 |
| GO:0080135 | regulation of cellular response to stress                  | 13/182 | 73/749 | 0,93765045  | 0,999954951 | 0,999954951 | HIF1A/SOD2/BCL6/MUC1/LTBR/HDAC6/XBP1/BAX/TLR4/MYC/FGD2/EPO/RGN                          | 13 |
| GO:0000902 | cell morphogenesis                                         | 13/182 | 74/749 | 0,945191236 | 0,999954951 | 0,999954951 | BCL6/HDAC6/ICAM1/PSMB10/APOE/LST1/FGD2/ITGB2/NOX4/FN1/GATA3/ADORA2A/PTPN6               | 13 |
| GO:0097529 | myeloid leukocyte migration                                | 13/182 | 76/749 | 0,957956169 | 0,999954951 | 0,999954951 | S100A9/S100A8/FCER1G/IL1R1/IL17RA/SLAMF8/CXCL1/IL6R/S100A12/CMKLR1/ITGB2/C5AR1/SERPINE1 | 13 |
| GO:0002699 | positive regulation of immune effector process             | 13/182 | 85/749 | 0,98861883  | 0,999954951 | 0,999954951 | C3/FCER1G/IL1R1/IL4R/NFKBIZ/TGFB1/XBP1/STAT6/TLR4/PVR/ITGB2/LILRB1/GATA3                | 13 |
| GO:0042113 | B cell activation                                          | 13/182 | 85/749 | 0,98861883  | 0,999954951 | 0,999954951 | BCL3/BCL6/JAK3/TGFB1/XBP1/BAX/AHR/CDKN1A/VCAM1/STAT6/TLR4/SLAMF8/PTPN6                  | 13 |
| GO:0010001 | glial cell differentiation                                 | 12/182 | 30/749 | 0,038354947 | 0,999954951 | 0,999954951 | STAT3/S100A8/C1QA/TGFB1/LDLR/TLR4/TLR2/TNFRSF1B/C5AR1/IFNGR1/ADORA2A/IL6ST              | 12 |
| GO:0051603 | proteolysis involved in cellular protein catabolic process | 12/182 | 30/749 | 0,038354947 | 0,999954951 | 0,999954951 | PSMB8/HDAC6/PSME2/PSMB10/XBP1/CTSS/APOE/TRIB1/PSME1/ISG15/RGN/RNF149                    | 12 |
| GO:0044772 | mitotic cell cycle phase transition                        | 12/182 | 31/749 | 0,049508756 | 0,999954951 | 0,999954951 | ADAMTS1/PSMB8/MUC1/ABCB1/PSME2/PSMB10/TGFB1/BAX/CDKN1A/MYC/PSME1/PTPN6                  | 12 |
| GO:0044770 | cell cycle phase transition                                | 12/182 | 32/749 | 0,062703805 | 0,999954951 | 0,999954951 | ADAMTS1/PSMB8/MUC1/ABCB1/PSME2/PSMB10/TGFB1/BAX/CDKN1A/MYC/PSME1/PTPN6                  | 12 |
| GO:0008610 | lipid biosynthetic process                                 | 12/182 | 33/749 | 0,078043258 | 0,999954951 | 0,999954951 | ALDH3A2/C3/TNFRSF1A/XBP1/ALOX5/HSD11B1/LDLR/EGR1/APOE/G6PD/NFKB1/RGN                    | 12 |
| GO:0055114 | oxidation-reduction process                                | 12/182 | 33/749 | 0,078043258 | 0,999954951 | 0,999954951 | ALDH3A2/HIF1A/SOD2/IMPDH1/ALOX5/VCAM1/HSD11B1/IFI30/MYC/NOX4/G6PD/IL6ST                 | 12 |
| GO:0002262 | myeloid cell homeostasis                                   | 12/182 | 38/749 | 0,187515986 | 0,999954951 | 0,999954951 | HIF1A/BCL6/STAT3/FCER1G/JAK3/STAT1/BAX/KITLG/G6PD/EPO/GATA3/ISG15                       | 12 |
| GO:0038061 | NIK/NF-kappaB signaling                                    | 12/182 | 39/749 | 0,215463793 | 0,999954951 | 0,999954951 | BCL3/PSMB8/PSME2/PSMB10/RELB/NFKB2/TLR4/TLR2/BIRC3/PSME1/CD14/TNFSF14                   | 12 |
| GO:0010564 | regulation of cell cycle process                           | 12/182 | 40/749 | 0,245070474 | 0,999954951 | 0,999954951 | BCL6/ADAMTS1/PSMB8/MUC1/PSME2/PSMB10/TGFB1/BAX/CDKN1A/PSME1/KLHL13/PTPN6                | 12 |
| GO:2000146 | negative regulation of cell motility                       | 12/182 | 40/749 | 0,245070474 | 0,999954951 | 0,999954951 | TIMP1/STAT3/IFITM1/COL3A1/TGFB1/SLAMF8/APOE/ARHGDIB/TRIB1/SERPINE1/GATA3/RGN            | 12 |
| GO:0048880 | sensory system development                                 | 12/182 | 41/749 | 0,276115658 | 0,999954951 | 0,999954951 | HIF1A/STAT3/C3/COL4A1/MEGF11/C1QA/MAF/TGFB1/BAX/FJX1/MYOM2/GATA3                        | 12 |
| GO:0150063 | visual system development                                  | 12/182 | 41/749 | 0,276115658 | 0,999954951 | 0,999954951 | HIF1A/STAT3/C3/COL4A1/MEGF11/C1QA/MAF/TGFB1/BAX/FJX1/MYOM2/GATA3                        | 12 |
| GO:0051271 | negative regulation of cellular component movement         | 12/182 | 42/749 | 0,308356463 | 0,999954951 | 0,999954951 | TIMP1/STAT3/IFITM1/COL3A1/TGFB1/SLAMF8/APOE/ARHGDIB/TRIB1/SERPINE1/GATA3/RGN            | 12 |
| GO:0016049 | cell growth                                                | 12/182 | 44/749 | 0,375381843 | 0,999954951 | 0,999954951 | S100A9/BCL6/S100A8/HDAC6/TGFB1/CXCL16/CDKN1A/AGT/APOE/G6PD/FN1/IL17RB                   | 12 |
| GO:0034762 | regulation of transmembrane transport                      | 12/182 | 44/749 | 0,375381843 | 0,999954951 | 0,999954951 | C3/EHD3/ABCB1/TGFB1/BAX/AGT/FKBP1A/CTSS/G6PD/EPO/RGN/PTPN6                              | 12 |
| GO:0060333 | interferon-gamma-mediated signaling pathway                | 12/182 | 44/749 | 0,375381843 | 0,999954951 | 0,999954951 | JAK1/IFNGR2/SOCS3/GBP2/ICAM1/FCGR1A/STAT1/SOCS1/VCAM1/IFI30/IRF7/IFNGR1                 | 12 |
| GO:0016055 | Wnt signaling pathway                                      | 12/182 | 45/749 | 0,409629456 | 0,999954951 | 0,999954951 | CD24/SOST/PSMB8/COL1A1/PSME2/PSMB10/EGR1/APOE/TLR2/PSME1/GATA3/NFKB1                    | 12 |



|            |                                                                     |        |        |             |             |             |                                                                                    |    |
|------------|---------------------------------------------------------------------|--------|--------|-------------|-------------|-------------|------------------------------------------------------------------------------------|----|
| GO:0198738 | cell-cell signaling by wnt                                          | 12/182 | 45/749 | 0,409629456 | 0,999954951 | 0,999954951 | CD24/SOST/PSMB8/COL1A1/PSME2/PSMB10/EGR1/APOE/TLR2/PSME1/GATA3/NFKB1               | 12 |
| GO:0098655 | cation transmembrane transport                                      | 12/182 | 46/749 | 0,444011564 | 0,999954951 | 0,999954951 | EHD3/TGFB1/BAX/AGT/SLC12A3/FKBP1A/CTSS/SLC11A1/G6PD/EPO/RGN/PTPN6                  | 12 |
| GO:0031348 | negative regulation of defense response                             | 12/182 | 47/749 | 0,478272101 | 0,999954951 | 0,999954951 | SERPING1/SOCS3/TNFRSF1A/LDLR/SLAMF8/APOE/TNFRSF1B/IL1R2/LILRB1/GATA3/ADORA2A/NFKB1 | 12 |
| GO:0042063 | gliogenesis                                                         | 12/182 | 47/749 | 0,478272101 | 0,999954951 | 0,999954951 | STAT3/S100A8/C1QA/TGFB1/LDLR/TLR4/TLR2/TNFRSF1B/C5AR1/IFNGR1/ADORA2A/IL6ST         | 12 |
| GO:2000377 | regulation of reactive oxygen species metabolic process             | 12/182 | 47/749 | 0,478272101 | 0,999954951 | 0,999954951 | HIF1A/STAT3/HDAC6/ICAM1/TGFB1/CDKN1A/AGT/TLR4/ITGB2/NOX4/G6PD/RGN                  | 12 |
| GO:0042035 | regulation of cytokine biosynthetic process                         | 12/182 | 51/749 | 0,609555209 | 0,999954951 | 0,999954951 | BCL3/STAT3/SIGIRR/CD276/EGR1/TLR4/TBK1/ERRFI1/LILRB1/GATA3/NFKB1/LTB               | 12 |
| GO:0050769 | positive regulation of neurogenesis                                 | 12/182 | 51/749 | 0,609555209 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/MME/TGFB1/AGT/APOE/TLR2/TNFRSF1B/FN1/EPO/IL6ST                   | 12 |
| GO:0003013 | circulatory system process                                          | 12/182 | 52/749 | 0,639988082 | 0,999954951 | 0,999954951 | SOD2/SERPING1/EHD3/MME/ICAM1/STAT1/TGFB1/AGT/APOE/NOX4/EPO/ADORA2A                 | 12 |
| GO:0051962 | positive regulation of nervous system development                   | 12/182 | 54/749 | 0,697003709 | 0,999954951 | 0,999954951 | S100A9/HIF1A/BCL6/MME/TGFB1/AGT/APOE/TLR2/TNFRSF1B/FN1/EPO/IL6ST                   | 12 |
| GO:0071902 | positive regulation of protein serine/threonine kinase activity     | 12/182 | 55/749 | 0,723406094 | 0,999954951 | 0,999954951 | LTF/FPR1/CD24/TGFB1/TLR4/KITLG/MAPK11/S100A12/FGD2/NOX4/C5AR1/GDF15                | 12 |
| GO:0010638 | positive regulation of organelle organization                       | 12/182 | 56/749 | 0,748324772 | 0,999954951 | 0,999954951 | HIF1A/BCL6/MUC1/HDAC6/ICAM1/TGFB1/DNMT1/BAX/TNFSF10/NOX4/GATA3/PLAUR               | 12 |
| GO:0060627 | regulation of vesicle-mediated transport                            | 12/182 | 56/749 | 0,748324772 | 0,999954951 | 0,999954951 | C3/FCER1G/IL4R/TGFB1/APOE/TLR2/SLC11A1/ITGB2/LILRB1/CD14/SERPINE1/ADORA2A          | 12 |
| GO:0001667 | ameboidal-type cell migration                                       | 12/182 | 58/749 | 0,793602751 | 0,999954951 | 0,999954951 | HIF1A/TIMP1/HDAC6/NR4A1/TGFB1/AGT/KITLG/APOE/ARHGDIB/ITGB2/FN1/GATA3               | 12 |
| GO:0002833 | positive regulation of response to biotic stimulus                  | 12/182 | 59/749 | 0,813956303 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/MUC1/PSME2/PSMB10/RELB/LY96/IRF7/PVR/TBK1/PSME1/NFKB1                 | 12 |
| GO:0006259 | DNA metabolic process                                               | 12/182 | 60/749 | 0,832810378 | 0,999954951 | 0,999954951 | BCL6/TGFB1/DNMT1/BAX/CDKN1A/STAT6/MYC/ISG20/NOX4/GATA3/ISG15/RGN                   | 12 |
| GO:0051051 | negative regulation of transport                                    | 12/182 | 60/749 | 0,832810378 | 0,999954951 | 0,999954951 | TNFRSF1A/ICAM1/TGFB1/APOE/TLR2/LILRB2/TNFRSF1B/IL1R2/FN1/LILRB1/EPO/NFKB1          | 12 |
| GO:0002700 | regulation of production of molecular mediator of immune response   | 12/182 | 61/749 | 0,850200736 | 0,999954951 | 0,999954951 | BCL6/FCER1G/IL1R1/JAK3/IL4R/TGFB1/XBP1/STAT6/TLR4/TNFRSF1B/LILRB1/GATA3            | 12 |
| GO:0048589 | developmental growth                                                | 12/182 | 62/749 | 0,86617459  | 0,999954951 | 0,999954951 | STAT3/HDAC6/TGFB1/CDKN1A/AGT/TNC/APOE/MAPK11/G6PD/FN1/GDF15/GATA3                  | 12 |
| GO:0048871 | multicellular organismal homeostasis                                | 12/182 | 66/749 | 0,917133148 | 0,999954951 | 0,999954951 | SERPINA3/LTF/STAT3/LCN2/IL4R/BAX/STAT6/EGR1/TLR4/SLC11A1/CMKLR1/NOX4               | 12 |
| GO:0044087 | regulation of cellular component biogenesis                         | 12/182 | 69/749 | 0,943769671 | 0,999954951 | 0,999954951 | SOST/TNFRSF1A/HDAC6/ICAM1/TGFB1/DNMT1/BAX/AGT/TLR4/APOE/TLR2/NOX4                  | 12 |
| GO:0007186 | G protein-coupled receptor signaling pathway                        | 12/182 | 76/749 | 0,979143234 | 0,999954951 | 0,999954951 | FPR1/C3/CXCL16/AGT/APOE/CXCL1/ACKR1/CMKLR1/FGD2/C5AR1/ADORA2A/PTPN6                | 12 |
| GO:0070665 | positive regulation of leukocyte proliferation                      | 12/182 | 79/749 | 0,986829165 | 0,999954951 | 0,999954951 | BCL6/CD24/JAK3/CDKN1A/VCAM1/CD276/TLR4/KITLG/LILRB2/IL6R/EPO/IL6ST                 | 12 |
| GO:0009790 | embryo development                                                  | 12/182 | 81/749 | 0,990409744 | 0,999954951 | 0,999954951 | HIF1A/SOCS3/KRT8/COL1A1/TGFB1/DNMT1/BAX/KITLG/KRT19/ITGB2/FN1/GATA3                | 12 |
| GO:0042129 | regulation of T cell proliferation                                  | 12/182 | 84/749 | 0,994133215 | 0,999954951 | 0,999954951 | CD24/JAK3/TGFB1/VCAM1/CD276/LILRB2/IL6R/TNFRSF1B/LILRB1/EPO/IL6ST/PTPN6            | 12 |
| GO:0009410 | response to xenobiotic stimulus                                     | 11/182 | 28/749 | 0,053281593 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/AHR/EGR1/RORC/S100A12/ABCC2/ERRFI1/TIPARP/EPO/ADORA2A                  | 11 |
| GO:1901361 | organic cyclic compound catabolic process                           | 11/182 | 28/749 | 0,053281593 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/BAX/MYD88/APOE/SLC11A1/TNFRSF1B/ISG20/PSME1/RGN                 | 11 |
| GO:0034765 | regulation of ion transmembrane transport                           | 11/182 | 35/749 | 0,207083841 | 0,999954951 | 0,999954951 | EHD3/ABCB1/TGFB1/BAX/AGT/FKBP1A/CTSS/G6PD/EPO/RGN/PTPN6                            | 11 |
| GO:0044283 | small molecule biosynthetic process                                 | 11/182 | 35/749 | 0,207083841 | 0,999954951 | 0,999954951 | IMPDH1/TGFB1/XBP1/ALOX5/EGR1/VCAN/APOE/G6PD/ATF3/NFKB1/RGN                         | 11 |
| GO:2000027 | regulation of animal organ morphogenesis                            | 11/182 | 36/749 | 0,237776617 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/STAT1/TGFB1/XBP1/BAX/AGT/MYC/PSME1/GATA3                        | 11 |
| GO:0097305 | response to alcohol                                                 | 11/182 | 37/749 | 0,270082014 | 0,999954951 | 0,999954951 | STAT3/S100A8/ICAM1/TGFB1/AHR/CDKN1A/VCAM1/TNC/G6PD/CD14/GATA3                      | 11 |
| GO:0001558 | regulation of cell growth                                           | 11/182 | 39/749 | 0,338392117 | 0,999954951 | 0,999954951 | S100A9/BCL6/S100A8/TGFB1/CXCL16/CDKN1A/AGT/APOE/G6PD/FN1/IL17RB                    | 11 |
| GO:0002292 | T cell differentiation involved in immune response                  | 11/182 | 39/749 | 0,338392117 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/FCER1G/RELB/JAK3/IL4R/NFKBIZ/STAT6/RORC/GATA3                      | 11 |
| GO:0043367 | CD4-positive, alpha-beta T cell differentiation                     | 11/182 | 39/749 | 0,338392117 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/RELB/JAK3/IL4R/NFKBIZ/SOCS1/STAT6/RORC/GATA3                       | 11 |
| GO:0051235 | maintenance of location                                             | 11/182 | 39/749 | 0,338392117 | 0,999954951 | 0,999954951 | S100A9/BCL3/S100A8/C3/LCN2/TGFB1/BAX/FKBP1A/APOE/NFKB1/PTPN6                       | 11 |
| GO:0007346 | regulation of mitotic cell cycle                                    | 11/182 | 40/749 | 0,373789982 | 0,999954951 | 0,999954951 | BCL6/ADAMTS1/PSMB8/MUC1/PSME2/PSMB10/TGFB1/BAX/CDKN1A/PSME1/PTPN6                  | 11 |
| GO:0048002 | antigen processing and presentation of peptide antigen              | 11/182 | 40/749 | 0,373789982 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/PSME2/PSMB10/FCGR1A/IFI30/CTSS/SLC11A1/TAP2/PSME1/TAP1                | 11 |
| GO:0007610 | behavior                                                            | 11/182 | 42/749 | 0,44553041  | 0,999954951 | 0,999954951 | HIF1A/STAT3/MME/AGT/LDLR/EGR1/APOE/TLR2/LILRB2/GDF15/ADORA2A                       | 11 |
| GO:0046425 | regulation of receptor signaling pathway via JAK-STAT               | 11/182 | 44/749 | 0,516578141 | 0,999954951 | 0,999954951 | BCL3/STAT3/SOCS3/TNFRSF1A/JAK3/SOCS1/AGT/IL6R/IL10RB/EPO/IL6ST                     | 11 |
| GO:0051146 | striated muscle cell differentiation                                | 11/182 | 44/749 | 0,516578141 | 0,999954951 | 0,999954951 | KRT8/IL4R/TGFB1/XBP1/AGT/KRT19/NOX4/G6PD/MYOM2/GDF15/TNFSF14                       | 11 |
| GO:0097435 | supramolecular fiber organization                                   | 11/182 | 45/749 | 0,551179186 | 0,999954951 | 0,999954951 | KRT8/HDAC6/COL1A1/COL3A1/ICAM1/LDLR/FKBP1A/APOE/KRT19/NOX4/MYOM2                   | 11 |
| GO:1904892 | regulation of receptor signaling pathway via STAT                   | 11/182 | 45/749 | 0,551179186 | 0,999954951 | 0,999954951 | BCL3/STAT3/SOCS3/TNFRSF1A/JAK3/SOCS1/AGT/IL6R/IL10RB/EPO/IL6ST                     | 11 |
| GO:0007423 | sensory organ development                                           | 11/182 | 47/749 | 0,617429097 | 0,999954951 | 0,999954951 | HIF1A/C1QB/STAT3/COL4A1/MEGF11/MAF/TGFB1/BAX/FJX1/MYOM2/GATA3                      | 11 |
| GO:1901135 | carbohydrate derivative metabolic process                           | 11/182 | 47/749 | 0,617429097 | 0,999954951 | 0,999954951 | HIF1A/STAT3/LYVE1/MUC1/IMPDH1/JAK3/TGFB1/BAX/VCAN/G6PD/NFKB1                       | 11 |
| GO:0001503 | ossification                                                        | 11/182 | 48/749 | 0,648722545 | 0,999954951 | 0,999954951 | HIF1A/LTF/IFITM1/SOST/COL1A1/TGFB1/TNC/VCAN/IL6R/IL6ST/ISG15                       | 11 |
| GO:0008015 | blood circulation                                                   | 11/182 | 48/749 | 0,648722545 | 0,999954951 | 0,999954951 | SOD2/SERPING1/EHD3/MME/ICAM1/STAT1/TGFB1/AGT/APOE/EPO/ADORA2A                      | 11 |
| GO:0046632 | alpha-beta T cell differentiation                                   | 11/182 | 48/749 | 0,648722545 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/RELB/JAK3/IL4R/NFKBIZ/SOCS1/STAT6/RORC/GATA3                       | 11 |
| GO:1904018 | positive regulation of vasculature development                      | 11/182 | 48/749 | 0,648722545 | 0,999954951 | 0,999954951 | HIF1A/JAK1/SOD2/STAT3/C3/XBP1/EGR1/IL6R/ITGB2/C5AR1/SERPINE1                       | 11 |
| GO:0002367 | cytokine production involved in immune response                     | 11/182 | 49/749 | 0,678608622 | 0,999954951 | 0,999954951 | BCL6/FCER1G/IL1R1/JAK3/TGFB1/TLR4/TLR2/SLC11A1/TNFRSF1B/LILRB1/GATA3               | 11 |
| GO:0032640 | tumor necrosis factor production                                    | 11/182 | 49/749 | 0,678608622 | 0,999954951 | 0,999954951 | LTF/BCL3/FCER1G/LY96/TLR4/TLR2/ERRFI1/LILRB1/CD14/IFNGR1/PTPN6                     | 11 |
| GO:0032680 | regulation of tumor necrosis factor production                      | 11/182 | 49/749 | 0,678608622 | 0,999954951 | 0,999954951 | LTF/BCL3/FCER1G/LY96/TLR4/TLR2/ERRFI1/LILRB1/CD14/IFNGR1/PTPN6                     | 11 |
| GO:0035710 | CD4-positive, alpha-beta T cell activation                          | 11/182 | 49/749 | 0,678608622 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/RELB/JAK3/IL4R/NFKBIZ/SOCS1/STAT6/RORC/GATA3                       | 11 |
| GO:0043122 | regulation of I-kappaB kinase/NF-kappaB signaling                   | 11/182 | 49/749 | 0,678608622 | 0,999954951 | 0,999954951 | LTF/TNFRSF1A/LTBR/STAT1/FKBP1A/TLR4/MYD88/S100A12/TBK1/TNFSF10/BIRC3               | 11 |
| GO:2000116 | regulation of cysteine-type endopeptidase activity                  | 11/182 | 50/749 | 0,706985069 | 0,999954951 | 0,999954951 | S100A9/LTF/S100A8/BAX/MYC/TNFSF10/BIRC3/CASP4/ADORA2A/TNFSF14/PLAUR                | 11 |
| GO:0002821 | positive regulation of adaptive immune response                     | 11/182 | 51/749 | 0,733778281 | 0,999954951 | 0,999954951 | C3/FCER1G/IL1R1/NFKBIZ/TGFB1/STAT6/IL6R/SLC11A1/PVR/GATA3/IL6ST                    | 11 |
| GO:0043406 | positive regulation of MAP kinase activity                          | 11/182 | 51/749 | 0,733778281 | 0,999954951 | 0,999954951 | FPR1/CD24/TGFB1/TLR4/KITLG/MAPK11/S100A12/FGD2/NOX4/C5AR1/GDF15                    | 11 |
| GO:0045089 | positive regulation of innate immune response                       | 11/182 | 51/749 | 0,733778281 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/MUC1/PSME2/PSMB10/RELB/IRF7/PVR/TBK1/PSME1/NFKB1                      | 11 |
| GO:0050715 | positive regulation of cytokine secretion                           | 11/182 | 52/749 | 0,758941505 | 0,999954951 | 0,999954951 | IL4R/XBP1/IL17RA/TLR4/TLR2/MAPK11/CD58/CD14/GATA3/IFNGR1/IL17RB                    | 11 |
| GO:0060537 | muscle tissue development                                           | 11/182 | 52/749 | 0,758941505 | 0,999954951 | 0,999954951 | COL3A1/TGFB1/AGT/EGR1/FKBP1A/MAPK11/TIPARP/NOX4/G6PD/MYOM2/ATF3                    | 11 |
| GO:1903555 | regulation of tumor necrosis factor superfamily cytokine production | 11/182 | 52/749 | 0,758941505 | 0,999954951 | 0,999954951 | LTF/BCL3/FCER1G/LY96/TLR4/TLR2/ERRFI1/LILRB1/CD14/IFNGR1/PTPN6                     | 11 |

|            |                                                                   |        |        |             |             |             |                                                                           |    |
|------------|-------------------------------------------------------------------|--------|--------|-------------|-------------|-------------|---------------------------------------------------------------------------|----|
| GO:0051129 | negative regulation of cellular component organization            | 11/182 | 53/749 | 0,782452624 | 0,999954951 | 0,999954951 | SOST/TNFRSF1A/HDAC6/TGFB1/DNMT1/LDLR/APOE/TLR2/LILRB2/TNFRSF1B/LILRB1     | 11 |
| GO:0071706 | tumor necrosis factor superfamily cytokine production             | 11/182 | 53/749 | 0,782452624 | 0,999954951 | 0,999954951 | LTF/BCL3/FCER1G/LY96/TLR4/TLR2/ERRFI1/LILRB1/CD14/IFNGR1/PTPN6            | 11 |
| GO:0048545 | response to steroid hormone                                       | 11/182 | 55/749 | 0,824538038 | 0,999954951 | 0,999954951 | HDAC6/COL1A1/NR4A1/ICAM1/TGFB1/CDKN1A/TLR2/RORC/ABCC2/ERRFI1/EPO          | 11 |
| GO:0050777 | negative regulation of immune response                            | 11/182 | 55/749 | 0,824538038 | 0,999954951 | 0,999954951 | BCL6/SERPING1/COL3A1/JAK3/IL4R/TGFB1/STAT6/CD59/SLAMF8/LILRB1/PTPN6       | 11 |
| GO:0051480 | regulation of cytosolic calcium ion concentration                 | 11/182 | 56/749 | 0,843167947 | 0,999954951 | 0,999954951 | FPR1/CD24/TGFB1/BAX/AGT/FKBP1A/CMKLR1/C5AR1/TMEM178A/EPO/PTPN6            | 11 |
| GO:0097530 | granulocyte migration                                             | 11/182 | 56/749 | 0,843167947 | 0,999954951 | 0,999954951 | S100A9/S100A8/FCER1G/IL1R1/IL17RA/SLAMF8/CXCL1/S100A12/CMKLR1/ITGB2/C5AR1 | 11 |
| GO:0002695 | negative regulation of leukocyte activation                       | 11/182 | 59/749 | 0,890034149 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/TGFB1/SOCS1/LDLR/LILRB2/LST1/LILRB1/ADORA2A/PTPN6          | 11 |
| GO:0001906 | cell killing                                                      | 11/182 | 62/749 | 0,924886422 | 0,999954951 | 0,999954951 | LTF/C3/C9/ICAM1/CD59/APOL1/PVR/S100A12/LILRB1/KIR3DL1/PTPN6               | 11 |
| GO:0070372 | regulation of ERK1 and ERK2 cascade                               | 11/182 | 67/749 | 0,962301637 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/TLR4/APOE/ERRFI1/NOX4/C5AR1/FN1/EPO/ATF3/PTPN6                | 11 |
| GO:0002706 | regulation of lymphocyte mediated immunity                        | 11/182 | 69/749 | 0,971890522 | 0,999954951 | 0,999954951 | BCL6/C3/FCER1G/IL1R1/TGFB1/STAT6/PVR/TNFRSF1B/LILRB1/GATA3/PTPN6          | 11 |
| GO:0045619 | regulation of lymphocyte differentiation                          | 11/182 | 69/749 | 0,971890522 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/SLAMF8/LILRB2/GATA3/PTPN6          | 11 |
| GO:0050671 | positive regulation of lymphocyte proliferation                   | 11/182 | 76/749 | 0,990648868 | 0,999954951 | 0,999954951 | BCL6/CD24/JAK3/CDKN1A/VCAM1/CD276/TLR4/LILRB2/IL6R/EPO/IL6ST              | 11 |
| GO:0032946 | positive regulation of mononuclear cell proliferation             | 11/182 | 77/749 | 0,992079237 | 0,999954951 | 0,999954951 | BCL6/CD24/JAK3/CDKN1A/VCAM1/CD276/TLR4/LILRB2/IL6R/EPO/IL6ST              | 11 |
| GO:0034655 | nucleobase-containing compound catabolic process                  | 10/182 | 25/749 | 0,057130794 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/BAX/MYD88/SLC11A1/TNFRSF1B/ISG20/PSME1/RGN             | 10 |
| GO:0019439 | aromatic compound catabolic process                               | 10/182 | 27/749 | 0,09309822  | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/BAX/MYD88/SLC11A1/TNFRSF1B/ISG20/PSME1/RGN             | 10 |
| GO:0044270 | cellular nitrogen compound catabolic process                      | 10/182 | 27/749 | 0,09309822  | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/BAX/MYD88/SLC11A1/TNFRSF1B/ISG20/PSME1/RGN             | 10 |
| GO:0046700 | heterocycle catabolic process                                     | 10/182 | 27/749 | 0,09309822  | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/BAX/MYD88/SLC11A1/TNFRSF1B/ISG20/PSME1/RGN             | 10 |
| GO:0050808 | synapse organization                                              | 10/182 | 29/749 | 0,140040378 | 0,999954951 | 0,999954951 | C1QB/C3/COL4A1/HDAC6/C1QA/TNC/APOE/TLR2/LILRB2/C5AR1                      | 10 |
| GO:0006956 | complement activation                                             | 10/182 | 31/749 | 0,197206136 | 0,999954951 | 0,999954951 | C1QB/C1S/C3/SERPING1/C9/CFB/C1QA/CD59/MASP1/C5AR1                         | 10 |
| GO:0050728 | negative regulation of inflammatory response                      | 10/182 | 31/749 | 0,197206136 | 0,999954951 | 0,999954951 | SOCS3/TNFRSF1A/LDLR/SLAMF8/APOE/TNFRSF1B/IL1R2/GATA3/ADORA2A/NFKB1        | 10 |
| GO:0060070 | canonical Wnt signaling pathway                                   | 10/182 | 31/749 | 0,197206136 | 0,999954951 | 0,999954951 | SOST/PSMB8/COL1A1/PSME2/PSMB10/EGR1/APOE/PSME1/GATA3/NFKB1                | 10 |
| GO:1902106 | negative regulation of leukocyte differentiation                  | 10/182 | 31/749 | 0,197206136 | 0,999954951 | 0,999954951 | LTF/BCL6/JAK3/IL4R/SOCS1/TLR4/MYC/TRIB1/LILRB1/TMEM178A                   | 10 |
| GO:1904062 | regulation of cation transmembrane transport                      | 10/182 | 31/749 | 0,197206136 | 0,999954951 | 0,999954951 | EHD3/TGFB1/BAX/AGT/FKBP1A/CTSS/G6PD/EPO/RGN/PTPN6                         | 10 |
| GO:0002920 | regulation of humoral immune response                             | 10/182 | 32/749 | 0,229108078 | 0,999954951 | 0,999954951 | C1QB/C1S/C3/SERPING1/C9/CFB/C1QA/CD59/C5AR1/PTPN6                         | 10 |
| GO:0030111 | regulation of Wnt signaling pathway                               | 10/182 | 33/749 | 0,262845868 | 0,999954951 | 0,999954951 | SOST/PSMB8/COL1A1/PSME2/PSMB10/EGR1/APOE/TLR2/PSME1/NFKB1                 | 10 |
| GO:0032602 | chemokine production                                              | 10/182 | 33/749 | 0,262845868 | 0,999954951 | 0,999954951 | S100A9/HIF1A/S100A8/IL4R/SIGIRR/EGR1/TLR4/TLR2/IL6R/ACKR1                 | 10 |
| GO:0007265 | Ras protein signal transduction                                   | 10/182 | 34/749 | 0,298091491 | 0,999954951 | 0,999954951 | BCL6/COL3A1/DNMT1/CDKN1A/KITLG/APOE/MAPK11/ARHGDIB/FGD2/EPO               | 10 |
| GO:0022411 | cellular component disassembly                                    | 10/182 | 34/749 | 0,298091491 | 0,999954951 | 0,999954951 | HIF1A/C1QB/TIMP1/C3/HDAC6/C1QA/TGFB1/BAX/CTSS/MYC                         | 10 |
| GO:0042088 | T-helper 1 type immune response                                   | 10/182 | 34/749 | 0,298091491 | 0,999954951 | 0,999954951 | BCL3/IL1R1/RELB/JAK3/IL4R/STAT6/IL18BP/TLR4/IL6R/SLC11A1                  | 10 |
| GO:0050792 | regulation of viral process                                       | 10/182 | 34/749 | 0,298091491 | 0,999954951 | 0,999954951 | LTF/IFITM3/SLPI/IFITM2/IFITM1/STAT1/APOE/ISG20/IFIT1/ISG15                | 10 |
| GO:0097237 | cellular response to toxic substance                              | 10/182 | 34/749 | 0,298091491 | 0,999954951 | 0,999954951 | S100A9/SOD2/MAPK13/LCN2/HDAC6/STAT6/EGR1/APOE/NFKB1/RGN                   | 10 |
| GO:1903707 | negative regulation of hemopoiesis                                | 10/182 | 34/749 | 0,298091491 | 0,999954951 | 0,999954951 | LTF/BCL6/JAK3/IL4R/SOCS1/TLR4/MYC/TRIB1/LILRB1/TMEM178A                   | 10 |
| GO:0032787 | monocarboxylic acid metabolic process                             | 10/182 | 35/749 | 0,334494552 | 0,999954951 | 0,999954951 | ALDH3A2/HIF1A/STAT3/C3/TNFRSF1A/XBP1/ALOX5/VCAN/ABCC2/RGN                 | 10 |
| GO:0042093 | T-helper cell differentiation                                     | 10/182 | 35/749 | 0,334494552 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/RELB/JAK3/IL4R/NFKBIZ/STAT6/RORC/GATA3                    | 10 |
| GO:1901615 | organic hydroxy compound metabolic process                        | 10/182 | 35/749 | 0,334494552 | 0,999954951 | 0,999954951 | ALDH3A2/HIF1A/APOL1/LDLR/APOE/APOL2/ITGB2/G6PD/GATA3/NFKB1                | 10 |
| GO:0002294 | CD4-positive, alpha-beta T cell differentiation involved in immun | 10/182 | 36/749 | 0,371693757 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/RELB/JAK3/IL4R/NFKBIZ/STAT6/RORC/GATA3                    | 10 |
| GO:0007264 | small GTPase mediated signal transduction                         | 10/182 | 36/749 | 0,371693757 | 0,999954951 | 0,999954951 | BCL6/COL3A1/DNMT1/CDKN1A/KITLG/APOE/MAPK11/ARHGDIB/FGD2/EPO               | 10 |
| GO:0010608 | posttranscriptional regulation of gene expression                 | 10/182 | 36/749 | 0,371693757 | 0,999954951 | 0,999954951 | BCL3/STAT3/PSMB8/PSME2/PSMB10/TGFB1/MYD88/SLC11A1/TNFRSF1B/PSME1          | 10 |
| GO:0002287 | alpha-beta T cell activation involved in immune response          | 10/182 | 37/749 | 0,409327736 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/RELB/JAK3/IL4R/NFKBIZ/STAT6/RORC/GATA3                    | 10 |
| GO:0002293 | alpha-beta T cell differentiation involved in immune response     | 10/182 | 37/749 | 0,409327736 | 0,999954951 | 0,999954951 | BCL3/BCL6/STAT3/RELB/JAK3/IL4R/NFKBIZ/STAT6/RORC/GATA3                    | 10 |
| GO:0002478 | antigen processing and presentation of exogenous peptide antig    | 10/182 | 37/749 | 0,409327736 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/PSME2/PSMB10/FCGR1A/IFI30/CTSS/TAP2/PSME1/TAP1               | 10 |
| GO:0010817 | regulation of hormone levels                                      | 10/182 | 37/749 | 0,409327736 | 0,999954951 | 0,999954951 | HIF1A/MME/HSD11B1/AGT/EGR1/ABCC2/HNF1A/TIPARP/GATA3/NFKB1                 | 10 |
| GO:0030336 | negative regulation of cell migration                             | 10/182 | 37/749 | 0,409327736 | 0,999954951 | 0,999954951 | TIMP1/STAT3/IFITM1/COL3A1/TGFB1/SLAMF8/APOE/ARHGDIB/TRIB1/SERPINE1        | 10 |
| GO:0001654 | eye development                                                   | 10/182 | 38/749 | 0,447044776 | 0,999954951 | 0,999954951 | HIF1A/STAT3/COL4A1/MEGF11/MAF/TGFB1/BAX/FJX1/MYOM2/GATA3                  | 10 |
| GO:0019884 | antigen processing and presentation of exogenous antigen          | 10/182 | 38/749 | 0,447044776 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/PSME2/PSMB10/FCGR1A/IFI30/CTSS/TAP2/PSME1/TAP1               | 10 |
| GO:0043903 | regulation of interspecies interactions between organisms         | 10/182 | 39/749 | 0,48451121  | 0,999954951 | 0,999954951 | LTF/IFITM3/SLPI/IFITM2/IFITM1/STAT1/APOE/ISG20/IFIT1/ISG15                | 10 |
| GO:0061448 | connective tissue development                                     | 10/182 | 40/749 | 0,521418285 | 0,999954951 | 0,999954951 | HIF1A/TIMP1/COL1A1/MAF/TGFB1/XBP1/EGR1/IL6R/RORC/TGFB1                    | 10 |
| GO:0098660 | inorganic ion transmembrane transport                             | 10/182 | 40/749 | 0,521418285 | 0,999954951 | 0,999954951 | EHD3/TGFB1/BAX/APOL1/SLC12A3/FKBP1A/SLC11A1/G6PD/RGN/PTPN6                | 10 |
| GO:0010952 | positive regulation of peptidase activity                         | 10/182 | 41/749 | 0,557487442 | 0,999954951 | 0,999954951 | S100A9/STAT3/S100A8/PSME2/BAX/MYC/TNFSF10/PSME1/FN1/CASP4                 | 10 |
| GO:0009896 | positive regulation of catabolic process                          | 10/182 | 42/749 | 0,592474014 | 0,999954951 | 0,999954951 | HIF1A/HDAC6/BAX/LDLR/APOE/TNFRSF1B/TBK1/TRIB1/TIPARP/RGN                  | 10 |
| GO:0032675 | regulation of interleukin-6 production                            | 10/182 | 44/749 | 0,658402192 | 0,999954951 | 0,999954951 | STAT3/FCER1G/MAPK13/XBP1/TLR4/MYD88/TLR2/LILRB2/IL6R/PTPN6                | 10 |
| GO:0043123 | positive regulation of I-kappaB kinase/NF-kappaB signaling        | 10/182 | 44/749 | 0,658402192 | 0,999954951 | 0,999954951 | LTF/TNFRSF1A/LTBR/FKBP1A/TLR4/MYD88/S100A12/TBK1/TNFSF10/BIRC3            | 10 |
| GO:0051701 | interaction with host                                             | 10/182 | 45/749 | 0,689037337 | 0,999954951 | 0,999954951 | IFITM3/ITGB6/IFITM2/IFITM1/HAVCR1/ICAM1/TGFB1/LDLR/PVR/IFIT1              | 10 |
| GO:0006974 | cellular response to DNA damage stimulus                          | 10/182 | 46/749 | 0,717975364 | 0,999954951 | 0,999954951 | BCL3/BCL6/MUC1/TNFRSF1A/BAX/CDKN1A/IRF7/TNFRSF1B/MYC/ISG15                | 10 |
| GO:0032989 | cellular component morphogenesis                                  | 10/182 | 46/749 | 0,717975364 | 0,999954951 | 0,999954951 | KRT8/HDAC6/BAX/APOE/TLR2/KRT19/FN1/MYOM2/GATA3/ADORA2A                    | 10 |
| GO:0034599 | cellular response to oxidative stress                             | 10/182 | 46/749 | 0,717975364 | 0,999954951 | 0,999954951 | HIF1A/SOD2/MAPK13/LCN2/HDAC6/STAT6/TLR4/NOX4/G6PD/RGN                     | 10 |
| GO:0043281 | regulation of cysteine-type endopeptidase activity involved in ap | 10/182 | 46/749 | 0,717975364 | 0,999954951 | 0,999954951 | S100A9/S100A8/BAX/MYC/TNFSF10/BIRC3/CASP4/ADORA2A/TNFSF14/PLAUR           | 10 |
| GO:0032635 | interleukin-6 production                                          | 10/182 | 47/749 | 0,74515003  | 0,999954951 | 0,999954951 | STAT3/FCER1G/MAPK13/XBP1/TLR4/MYD88/TLR2/LILRB2/IL6R/PTPN6                | 10 |
| GO:0033002 | muscle cell proliferation                                         | 10/182 | 47/749 | 0,74515003  | 0,999954951 | 0,999954951 | SOD2/STAT3/ADAMTS1/STAT1/DNMT1/CDKN1A/AGT/MAPK11/IL6R/TRIB1               | 10 |

|            |                                                                |        |        |             |             |             |                                                                   |    |
|------------|----------------------------------------------------------------|--------|--------|-------------|-------------|-------------|-------------------------------------------------------------------|----|
| GO:0044057 | regulation of system process                                   | 10/182 | 47/749 | 0,74515003  | 0,999954951 | 0,999954951 | TNFRSF1A/EHD3/ICAM1/AGT/APOE/TNFRSF1B/ERRFI1/G6PD/ADORA2A/IL6ST   | 10 |
| GO:0051259 | protein complex oligomerization                                | 10/182 | 48/749 | 0,770525684 | 0,999954951 | 0,999954951 | SOD2/C9/FCER1G/EHD3/LCN2/HDAC6/COL1A1/BAX/APOE/BIRC3              | 10 |
| GO:0030036 | actin cytoskeleton organization                                | 10/182 | 49/749 | 0,794094162 | 0,999954951 | 0,999954951 | BCL6/KRT8/ICAM1/TGFB1/CXCL1/ARHGDIB/FGD2/KRT19/NOX4/MYOM2         | 10 |
| GO:2001234 | negative regulation of apoptotic signaling pathway             | 10/182 | 49/749 | 0,794094162 | 0,999954951 | 0,999954951 | HIF1A/SOD2/MUC1/ICAM1/XBP1/BAX/TNFSF10/EPO/SERPINE1/PLAUR         | 10 |
| GO:0002824 | positive regulation of adaptive immune response based on som   | 10/182 | 50/749 | 0,815871435 | 0,999954951 | 0,999954951 | C3/FCER1G/IL1R1/NFKBIZ/TGFB1/STAT6/IL6R/SLC11A1/PVR/GATA3         | 10 |
| GO:0019637 | organophosphate metabolic process                              | 10/182 | 51/749 | 0,835894156 | 0,999954951 | 0,999954951 | HIF1A/PLAAT4/STAT3/NNMT/SOCS3/IMPDH1/TGFB1/SOCS1/LDLR/G6PD        | 10 |
| GO:0032147 | activation of protein kinase activity                          | 10/182 | 51/749 | 0,835894156 | 0,999954951 | 0,999954951 | FPR1/SOCS1/AGT/TLR4/MAPK11/IL6R/SLC11A1/C5AR1/GDF15/EPO           | 10 |
| GO:0030029 | actin filament-based process                                   | 10/182 | 52/749 | 0,854216215 | 0,999954951 | 0,999954951 | BCL6/KRT8/ICAM1/TGFB1/CXCL1/ARHGDIB/FGD2/KRT19/NOX4/MYOM2         | 10 |
| GO:0007204 | positive regulation of cytosolic calcium ion concentration     | 10/182 | 54/749 | 0,886040371 | 0,999954951 | 0,999954951 | FPR1/CD24/TGFB1/BAX/AGT/FKBP1A/CMKLR1/C5AR1/EPO/PTPN6             | 10 |
| GO:0051250 | negative regulation of lymphocyte activation                   | 10/182 | 54/749 | 0,886040371 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/TGFB1/SOCS1/LILRB2/LST1/LILRB1/ADORA2A/PTPN6       | 10 |
| GO:0032649 | regulation of interferon-gamma production                      | 10/182 | 57/749 | 0,923008834 | 0,999954951 | 0,999954951 | BCL3/IL1R1/CD276/TLR4/IL6R/SLC11A1/LILRB1/CD14/GATA3/ISG15        | 10 |
| GO:0031175 | neuron projection development                                  | 10/182 | 58/749 | 0,932833561 | 0,999954951 | 0,999954951 | S100A9/HDAC6/AGT/TNC/APOE/LST1/FN1/EPO/GATA3/ADORA2A              | 10 |
| GO:0032609 | interferon-gamma production                                    | 10/182 | 59/749 | 0,941568135 | 0,999954951 | 0,999954951 | BCL3/IL1R1/CD276/TLR4/IL6R/SLC11A1/LILRB1/CD14/GATA3/ISG15        | 10 |
| GO:0002685 | regulation of leukocyte migration                              | 10/182 | 62/749 | 0,962145854 | 0,999954951 | 0,999954951 | IL1R1/ICAM1/TGFB1/KITLG/SLAMF8/IL6R/CMKLR1/C5AR1/SERPINE1/TNFSF14 | 10 |
| GO:0045765 | regulation of angiogenesis                                     | 10/182 | 64/749 | 0,972022629 | 0,999954951 | 0,999954951 | HIF1A/JAK1/STAT3/C3/STAT1/XBP1/AGT/ITGB2/C5AR1/SERPINE1           | 10 |
| GO:1902107 | positive regulation of leukocyte differentiation               | 10/182 | 65/749 | 0,976037214 | 0,999954951 | 0,999954951 | BCL6/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/KITLG/LILRB2/TRIB1/GATA3        | 10 |
| GO:0050851 | antigen receptor-mediated signaling pathway                    | 10/182 | 74/749 | 0,994639108 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/NFKBIZ/BAX/CD276/PSME1/GATA3/NFKB1/PTPN6       | 10 |
| GO:0060341 | regulation of cellular localization                            | 10/182 | 79/749 | 0,997831808 | 0,999954951 | 0,999954951 | HIF1A/FCER1G/IL4R/TGFB1/BAX/FKBP1A/ITGB2/EPO/ADORA2A/PTPN6        | 10 |
| GO:0048708 | astrocyte differentiation                                      | 9/182  | 21/749 | 0,045280773 | 0,999954951 | 0,999954951 | STAT3/S100A8/C1QA/LDLR/TLR4/C5AR1/IFNGR1/ADORA2A/IL6ST            | 9  |
| GO:0002532 | production of molecular mediator involved in inflammatory resp | 9/182  | 22/749 | 0,0609463   | 0,999954951 | 0,999954951 | FCER1G/IL4R/ALOX5/IL17RA/TLR4/SLAMF8/MYD88/IL1R2/SERPINE1         | 9  |
| GO:0019941 | modification-dependent protein catabolic process               | 9/182  | 22/749 | 0,0609463   | 0,999954951 | 0,999954951 | PSMB8/HDAC6/PSME2/PSMB10/XBP1/TRIB1/PSME1/ISG15/RNF149            | 9  |
| GO:0042590 | antigen processing and presentation of exogenous peptide antig | 9/182  | 22/749 | 0,0609463   | 0,999954951 | 0,999954951 | FCER1G/PSMB8/PSME2/PSMB10/FCGR1A/IFI30/TAP2/PSME1/TAP1            | 9  |
| GO:0043632 | modification-dependent macromolecule catabolic process         | 9/182  | 22/749 | 0,0609463   | 0,999954951 | 0,999954951 | PSMB8/HDAC6/PSME2/PSMB10/XBP1/TRIB1/PSME1/ISG15/RNF149            | 9  |
| GO:0002474 | antigen processing and presentation of peptide antigen via MHC | 9/182  | 23/749 | 0,079705531 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/PSME2/PSMB10/FCGR1A/IFI30/TAP2/PSME1/TAP1            | 9  |
| GO:0016071 | mRNA metabolic process                                         | 9/182  | 23/749 | 0,079705531 | 0,999954951 | 0,999954951 | HIF1A/STAT3/PSMB8/PSME2/PSMB10/MYD88/SLC11A1/C5AR1/PSME1          | 9  |
| GO:0030449 | regulation of complement activation                            | 9/182  | 25/749 | 0,126638016 | 0,999954951 | 0,999954951 | C1QB/C1S/C3/SERPING1/C9/CFB/C1QA/CD59/C5AR1                       | 9  |
| GO:0060828 | regulation of canonical Wnt signaling pathway                  | 9/182  | 25/749 | 0,126638016 | 0,999954951 | 0,999954951 | SOST/PSMB8/COL1A1/PSME2/PSMB10/EGR1/APOE/PSME1/NFKB1              | 9  |
| GO:0070498 | interleukin-1-mediated signaling pathway                       | 9/182  | 25/749 | 0,126638016 | 0,999954951 | 0,999954951 | PSMB8/IL1R1/PSME2/PSMB10/EGR1/MYD88/IL1R2/PSME1/NFKB1             | 9  |
| GO:2001242 | regulation of intrinsic apoptotic signaling pathway            | 9/182  | 25/749 | 0,126638016 | 0,999954951 | 0,999954951 | S100A9/HIF1A/SOD2/S100A8/MUC1/XBP1/BAX/EPO/PLAUR                  | 9  |
| GO:0019730 | antimicrobial humoral response                                 | 9/182  | 26/749 | 0,154643079 | 0,999954951 | 0,999954951 | S100A9/LTF/BCL3/S100A8/SLPI/LCN2/CXCL1/SLC11A1/S100A12            | 9  |
| GO:0030218 | erythrocyte differentiation                                    | 9/182  | 26/749 | 0,154643079 | 0,999954951 | 0,999954951 | HIF1A/BCL6/STAT3/JAK3/STAT1/G6PD/EPO/GATA3/ISG15                  | 9  |
| GO:0034101 | erythrocyte homeostasis                                        | 9/182  | 27/749 | 0,185415509 | 0,999954951 | 0,999954951 | HIF1A/BCL6/STAT3/JAK3/STAT1/G6PD/EPO/GATA3/ISG15                  | 9  |
| GO:0061041 | regulation of wound healing                                    | 9/182  | 27/749 | 0,185415509 | 0,999954951 | 0,999954951 | SERPING1/FCER1G/XBP1/CDKN1A/TLR4/APOE/SERPINE1/THBD/PLAUR         | 9  |
| GO:0006469 | negative regulation of protein kinase activity                 | 9/182  | 28/749 | 0,218666692 | 0,999954951 | 0,999954951 | SOCS3/SOCS1/CDKN1A/APOE/TRIB1/ERRFI1/ADORA2A/RGN/PTPN6            | 9  |
| GO:0033673 | negative regulation of kinase activity                         | 9/182  | 28/749 | 0,218666692 | 0,999954951 | 0,999954951 | SOCS3/SOCS1/CDKN1A/APOE/TRIB1/ERRFI1/ADORA2A/RGN/PTPN6            | 9  |
| GO:0045926 | negative regulation of growth                                  | 9/182  | 28/749 | 0,218666692 | 0,999954951 | 0,999954951 | HIF1A/BCL6/TGFB1/CDKN1A/AGT/MT1A/MAPK11/G6PD/GDF15                | 9  |
| GO:0045930 | negative regulation of mitotic cell cycle                      | 9/182  | 28/749 | 0,218666692 | 0,999954951 | 0,999954951 | BCL6/PSMB8/MUC1/PSME2/PSMB10/TGFB1/BAX/CDKN1A/PSME1               | 9  |
| GO:0006820 | anion transport                                                | 9/182  | 29/749 | 0,254048534 | 0,999954951 | 0,999954951 | ABCB1/AGT/APOL1/LDLR/SLC12A3/APOE/SLC11A1/ABCC2/ADORA2A           | 9  |
| GO:0048863 | stem cell differentiation                                      | 9/182  | 29/749 | 0,254048534 | 0,999954951 | 0,999954951 | HIF1A/STAT3/PSMB8/PSME2/PSMB10/KITLG/PSME1/FN1/GATA3              | 9  |
| GO:0051651 | maintenance of location in cell                                | 9/182  | 29/749 | 0,254048534 | 0,999954951 | 0,999954951 | S100A9/BCL3/S100A8/LCN2/TGFB1/BAX/FKBP1A/APOE/PTPN6               | 9  |
| GO:1903034 | regulation of response to wounding                             | 9/182  | 29/749 | 0,254048534 | 0,999954951 | 0,999954951 | SERPING1/FCER1G/XBP1/CDKN1A/TLR4/APOE/SERPINE1/THBD/PLAUR         | 9  |
| GO:0051348 | negative regulation of transferase activity                    | 9/182  | 30/749 | 0,291169046 | 0,999954951 | 0,999954951 | SOCS3/SOCS1/CDKN1A/APOE/TRIB1/ERRFI1/ADORA2A/RGN/PTPN6            | 9  |
| GO:0010876 | lipid localization                                             | 9/182  | 31/749 | 0,329608419 | 0,999954951 | 0,999954951 | C3/ABCB1/AGT/APOL1/LDLR/APOE/APOL2/ABCC2/NFKB1                    | 9  |
| GO:0036294 | cellular response to decreased oxygen levels                   | 9/182  | 31/749 | 0,329608419 | 0,999954951 | 0,999954951 | HIF1A/PSMB8/PSME2/ICAM1/PSMB10/EGR1/MYC/PSME1/EPO                 | 9  |
| GO:0071229 | cellular response to acid chemical                             | 9/182  | 31/749 | 0,329608419 | 0,999954951 | 0,999954951 | COL4A1/COL1A1/COL3A1/SOCS1/XBP1/DNMT1/LDLR/TNC/EGR1               | 9  |
| GO:0071456 | cellular response to hypoxia                                   | 9/182  | 31/749 | 0,329608419 | 0,999954951 | 0,999954951 | HIF1A/PSMB8/PSME2/ICAM1/PSMB10/EGR1/MYC/PSME1/EPO                 | 9  |
| GO:1901654 | response to ketone                                             | 9/182  | 31/749 | 0,329608419 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/AHR/CDKN1A/TNC/TLR2/ABCC2/ERRFI1/EPO                  | 9  |
| GO:2001235 | positive regulation of apoptotic signaling pathway             | 9/182  | 31/749 | 0,329608419 | 0,999954951 | 0,999954951 | S100A9/S100A8/LTBR/BAX/AGT/TNFSF10/ATF3/ADORA2A/PLAUR             | 9  |
| GO:0005975 | carbohydrate metabolic process                                 | 9/182  | 32/749 | 0,368934639 | 0,999954951 | 0,999954951 | HIF1A/STAT3/TGFB1/RORC/G6PD/ATF3/NFKB1/IL6ST/RGN                  | 9  |
| GO:0021700 | developmental maturation                                       | 9/182  | 32/749 | 0,368934639 | 0,999954951 | 0,999954951 | HIF1A/LTF/C3/C1QA/XBP1/CDKN1A/G6PD/EPO/GATA3                      | 9  |
| GO:0032755 | positive regulation of interleukin-6 production                | 9/182  | 32/749 | 0,368934639 | 0,999954951 | 0,999954951 | STAT3/FCER1G/MAPK13/XBP1/TLR4/MYD88/TLR2/LILRB2/IL6R              | 9  |
| GO:0071260 | cellular response to mechanical stimulus                       | 9/182  | 32/749 | 0,368934639 | 0,999954951 | 0,999954951 | TNFRSF1A/LTBR/COL1A1/TGFB1/AGT/TLR4/MYD88/TNFSF14/NFKB1           | 9  |
| GO:0071695 | anatomical structure maturation                                | 9/182  | 32/749 | 0,368934639 | 0,999954951 | 0,999954951 | HIF1A/LTF/C3/C1QA/XBP1/CDKN1A/G6PD/EPO/GATA3                      | 9  |
| GO:0043010 | camera-type eye development                                    | 9/182  | 33/749 | 0,408717928 | 0,999954951 | 0,999954951 | HIF1A/COL4A1/MEGF11/MAF/TGFB1/BAX/FJX1/MYOM2/GATA3                | 9  |
| GO:0010950 | positive regulation of endopeptidase activity                  | 9/182  | 34/749 | 0,448543445 | 0,999954951 | 0,999954951 | S100A9/STAT3/S100A8/PSME2/BAX/MYC/TNFSF10/PSME1/CASP4             | 9  |
| GO:0051147 | regulation of muscle cell differentiation                      | 9/182  | 34/749 | 0,448543445 | 0,999954951 | 0,999954951 | SOD2/IL4R/TGFB1/XBP1/DNMT1/MAPK11/G6PD/GDF15/TNFSF14              | 9  |
| GO:0071453 | cellular response to oxygen levels                             | 9/182  | 34/749 | 0,448543445 | 0,999954951 | 0,999954951 | HIF1A/PSMB8/PSME2/ICAM1/PSMB10/EGR1/MYC/PSME1/EPO                 | 9  |
| GO:0042116 | macrophage activation                                          | 9/182  | 35/749 | 0,488021909 | 0,999954951 | 0,999954951 | C1QA/IL4R/LDLR/TLR4/TLR2/SLC11A1/ITGB2/C5AR1/IFNGR1               | 9  |
| GO:0042176 | regulation of protein catabolic process                        | 9/182  | 35/749 | 0,488021909 | 0,999954951 | 0,999954951 | TIMP1/PSME2/LDLR/APOE/TNFRSF1B/TRIB1/TIPARP/PSME1/RGN             | 9  |

|            |                                                                  |       |        |             |             |             |                                                              |   |
|------------|------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|--------------------------------------------------------------|---|
| GO:1901215 | negative regulation of neuron death                              | 9/182 | 35/749 | 0,488021909 | 0,999954951 | 0,999954951 | HIF1A/SOD2/STAT3/BAX/APOE/TNFRSF1B/C5AR1/EPO/ADORA2A         | 9 |
| GO:0043270 | positive regulation of ion transport                             | 9/182 | 37/749 | 0,564556245 | 0,999954951 | 0,999954951 | EHD3/ABCB1/BAX/AGT/CTSS/APOE/G6PD/ADORA2A/RGN                | 9 |
| GO:0051052 | regulation of DNA metabolic process                              | 9/182 | 37/749 | 0,564556245 | 0,999954951 | 0,999954951 | BCL6/TGFB1/BAX/CDKN1A/STAT6/MYC/NOX4/GATA3/RGN               | 9 |
| GO:0098662 | inorganic cation transmembrane transport                         | 9/182 | 37/749 | 0,564556245 | 0,999954951 | 0,999954951 | EHD3/TGFB1/BAX/SLC12A3/FKBP1A/SLC11A1/G6PD/RGN/PTPN6         | 9 |
| GO:0002761 | regulation of myeloid leukocyte differentiation                  | 9/182 | 38/749 | 0,601025322 | 0,999954951 | 0,999954951 | LTF/TGFB1/TLR4/KITLG/IRF7/MYC/TRIB1/LILRB1/TMEM178A          | 9 |
| GO:0046427 | positive regulation of receptor signaling pathway via JAK-STAT   | 9/182 | 38/749 | 0,601025322 | 0,999954951 | 0,999954951 | STAT3/SOCS3/TNFRSF1A/SOCS1/AGT/IL6R/IL10RB/EPO/IL6ST         | 9 |
| GO:0010038 | response to metal ion                                            | 9/182 | 39/749 | 0,635979556 | 0,999954951 | 0,999954951 | HIF1A/S100A8/ICAM1/C1QA/VCAM1/MT1A/ABCC2/G6PD/CD14           | 9 |
| GO:0031331 | positive regulation of cellular catabolic process                | 9/182 | 39/749 | 0,635979556 | 0,999954951 | 0,999954951 | HIF1A/HDAC6/BAX/LDLR/APOE/TNFRSF1B/TBK1/TRIB1/RGN            | 9 |
| GO:0043603 | cellular amide metabolic process                                 | 9/182 | 39/749 | 0,635979556 | 0,999954951 | 0,999954951 | BCL3/PLAAT4/STAT3/TNFRSF1A/MME/APOE/ABCC2/G6PD/IFNGR1        | 9 |
| GO:1904894 | positive regulation of receptor signaling pathway via STAT       | 9/182 | 39/749 | 0,635979556 | 0,999954951 | 0,999954951 | STAT3/SOCS3/TNFRSF1A/SOCS1/AGT/IL6R/IL10RB/EPO/IL6ST         | 9 |
| GO:0002698 | negative regulation of immune effector process                   | 9/182 | 41/749 | 0,700669484 | 0,999954951 | 0,999954951 | BCL6/SERPING1/JAK3/IL4R/TGFB1/CD59/SLAMF8/LILRB1/PTPN6       | 9 |
| GO:0002718 | regulation of cytokine production involved in immune response    | 9/182 | 41/749 | 0,700669484 | 0,999954951 | 0,999954951 | BCL6/FCER1G/IL1R1/JAK3/TGFB1/TLR4/TNFRSF1B/LILRB1/GATA3      | 9 |
| GO:0002702 | positive regulation of production of molecular mediator of immu  | 9/182 | 42/749 | 0,730177339 | 0,999954951 | 0,999954951 | FCER1G/IL1R1/IL4R/TGFB1/XBP1/STAT6/TLR4/LILRB1/GATA3         | 9 |
| GO:0050868 | negative regulation of T cell activation                         | 9/182 | 45/749 | 0,806796707 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/TGFB1/SOCS1/LILRB2/LILRB1/ADORA2A/PTPN6       | 9 |
| GO:0051403 | stress-activated MAPK cascade                                    | 9/182 | 45/749 | 0,806796707 | 0,999954951 | 0,999954951 | MAPK13/LTBR/AGT/TLR4/MAPK11/MYC/FGD2/TRIB1/NFKB1             | 9 |
| GO:0031098 | stress-activated protein kinase signaling cascade                | 9/182 | 46/749 | 0,828401899 | 0,999954951 | 0,999954951 | MAPK13/LTBR/AGT/TLR4/MAPK11/MYC/FGD2/TRIB1/NFKB1             | 9 |
| GO:1990266 | neutrophil migration                                             | 9/182 | 46/749 | 0,828401899 | 0,999954951 | 0,999954951 | S100A9/S100A8/FCER1G/IL1R1/SLAMF8/CXCL1/S100A12/ITGB2/C5AR1  | 9 |
| GO:0031589 | cell-substrate adhesion                                          | 9/182 | 48/749 | 0,8660257   | 0,999954951 | 0,999954951 | BCL6/ITGB6/LYVE1/COL1A1/COL3A1/VCAM1/ITGB2/FN1/SERPINE1      | 9 |
| GO:1903038 | negative regulation of leukocyte cell-cell adhesion              | 9/182 | 48/749 | 0,8660257   | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/TGFB1/SOCS1/LILRB2/LILRB1/ADORA2A/PTPN6       | 9 |
| GO:0002687 | positive regulation of leukocyte migration                       | 9/182 | 49/749 | 0,882210296 | 0,999954951 | 0,999954951 | IL1R1/ICAM1/TGFB1/KITLG/IL6R/CMKLR1/C5AR1/SERPINE1/TNFSF14   | 9 |
| GO:0007517 | muscle organ development                                         | 9/182 | 49/749 | 0,882210296 | 0,999954951 | 0,999954951 | COL3A1/TGFB1/XBP1/EGR1/FKBP1A/MAPK11/G6PD/MYOM2/ATF3         | 9 |
| GO:0071621 | granulocyte chemotaxis                                           | 9/182 | 49/749 | 0,882210296 | 0,999954951 | 0,999954951 | S100A9/S100A8/FCER1G/IL17RA/CXCL1/S100A12/CMKLR1/ITGB2/C5AR1 | 9 |
| GO:0014706 | striated muscle tissue development                               | 9/182 | 50/749 | 0,896772485 | 0,999954951 | 0,999954951 | TGFB1/AGT/EGR1/FKBP1A/MAPK11/NOX4/G6PD/MYOM2/ATF3            | 9 |
| GO:0050852 | T cell receptor signaling pathway                                | 9/182 | 50/749 | 0,896772485 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/NFKBIZ/CD276/PSME1/GATA3/NFKB1/PTPN6      | 9 |
| GO:0000302 | response to reactive oxygen species                              | 9/182 | 51/749 | 0,909817841 | 0,999954951 | 0,999954951 | SOD2/MAPK13/LCN2/HDAC6/COL1A1/STAT1/STAT6/APOE/RGN           | 9 |
| GO:0032504 | multicellular organism reproduction                              | 9/182 | 51/749 | 0,909817841 | 0,999954951 | 0,999954951 | BCL6/ADAMTS1/IL4R/TGFB1/BAX/EGR1/APOL2/BIRC3/RGN             | 9 |
| GO:0048609 | multicellular organismal reproductive process                    | 9/182 | 51/749 | 0,909817841 | 0,999954951 | 0,999954951 | BCL6/ADAMTS1/IL4R/TGFB1/BAX/EGR1/APOL2/BIRC3/RGN             | 9 |
| GO:0046634 | regulation of alpha-beta T cell activation                       | 9/182 | 52/749 | 0,921455391 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/NFKBIZ/SOCS1/IL6R/LILRB1/GATA3/ADORA2A        | 9 |
| GO:0051098 | regulation of binding                                            | 9/182 | 54/749 | 0,940946115 | 0,999954951 | 0,999954951 | BCL3/SLPI/TGFB1/BAX/FKBP1A/APOE/IFIT1/GATA3/PLAUR            | 9 |
| GO:0022408 | negative regulation of cell-cell adhesion                        | 9/182 | 55/749 | 0,949014528 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/TGFB1/SOCS1/LILRB2/LILRB1/ADORA2A/PTPN6       | 9 |
| GO:0048732 | gland development                                                | 9/182 | 57/749 | 0,962307742 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/XBP1/BAX/STAT6/TNC/HNF1A/GATA3/RGN               | 9 |
| GO:0050864 | regulation of B cell activation                                  | 9/182 | 57/749 | 0,962307742 | 0,999954951 | 0,999954951 | BCL6/TGFB1/XBP1/AHR/CDKN1A/STAT6/TLR4/SLAMF8/PTPN6           | 9 |
| GO:0060322 | head development                                                 | 9/182 | 57/749 | 0,962307742 | 0,999954951 | 0,999954951 | HIF1A/COL4A1/COL1A1/COL3A1/TGFB1/BAX/TIPARP/C5AR1/G6PD       | 9 |
| GO:0002705 | positive regulation of leukocyte mediated immunity               | 9/182 | 60/749 | 0,976509522 | 0,999954951 | 0,999954951 | C3/FCER1G/IL1R1/IL4R/TGFB1/STAT6/PVR/ITGB2/GATA3             | 9 |
| GO:0045580 | regulation of T cell differentiation                             | 9/182 | 61/749 | 0,980035662 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/LILRB2/GATA3          | 9 |
| GO:0019932 | second-messenger-mediated signaling                              | 9/182 | 66/749 | 0,991454784 | 0,999954951 | 0,999954951 | FPR1/AHR/VCAM1/AGT/FKBP1A/APOE/CMKLR1/ADORA2A/RGN            | 9 |
| GO:0055076 | transition metal ion homeostasis                                 | 8/182 | 18/749 | 0,046859599 | 0,999954951 | 0,999954951 | S100A9/HIF1A/LTF/S100A8/LCN2/MT1A/SLC11A1/MYC                | 8 |
| GO:0090183 | regulation of kidney development                                 | 8/182 | 18/749 | 0,046859599 | 0,999954951 | 0,999954951 | CD24/STAT1/TGFB1/AGT/EGR1/IL6R/MYC/GATA3                     | 8 |
| GO:0015850 | organic hydroxy compound transport                               | 8/182 | 19/749 | 0,064537124 | 0,999954951 | 0,999954951 | FCER1G/AGT/LDLR/APOE/ABCC2/LILRB1/ADORA2A/NFKB1              | 8 |
| GO:0006511 | ubiquitin-dependent protein catabolic process                    | 8/182 | 21/749 | 0,110823899 | 0,999954951 | 0,999954951 | PSMB8/HDAC6/PSME2/PSMB10/XBP1/TRIB1/PSME1/RNF149             | 8 |
| GO:0045069 | regulation of viral genome replication                           | 8/182 | 21/749 | 0,110823899 | 0,999954951 | 0,999954951 | LTF/IFITM3/SLPI/IFITM2/IFITM1/ISG20/IFIT1/ISG15              | 8 |
| GO:1905330 | regulation of morphogenesis of an epithelium                     | 8/182 | 21/749 | 0,110823899 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/STAT1/TGFB1/AGT/PSME1/GATA3               | 8 |
| GO:0002220 | innate immune response activating cell surface receptor signalin | 8/182 | 22/749 | 0,139325384 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/MUC1/PSME2/PSMB10/RELB/PSME1/NFKB1              | 8 |
| GO:0002223 | stimulatory C-type lectin receptor signaling pathway             | 8/182 | 22/749 | 0,139325384 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/MUC1/PSME2/PSMB10/RELB/PSME1/NFKB1              | 8 |
| GO:0002758 | innate immune response-activating signal transduction            | 8/182 | 22/749 | 0,139325384 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/MUC1/PSME2/PSMB10/RELB/PSME1/NFKB1              | 8 |
| GO:0010948 | negative regulation of cell cycle process                        | 8/182 | 22/749 | 0,139325384 | 0,999954951 | 0,999954951 | BCL6/PSMB8/MUC1/PSME2/PSMB10/BAX/CDKN1A/PSME1                | 8 |
| GO:0002244 | hematopoietic progenitor cell differentiation                    | 8/182 | 23/749 | 0,171122639 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/TGFB1/KITLG/PSME1/GATA3/PTPN6             | 8 |
| GO:0043112 | receptor metabolic process                                       | 8/182 | 23/749 | 0,171122639 | 0,999954951 | 0,999954951 | HIF1A/FCER1G/EHD3/HDAC6/TGFB1/APOE/ITGB2/LILRB1              | 8 |
| GO:0016579 | protein deubiquitination                                         | 8/182 | 24/749 | 0,20587625  | 0,999954951 | 0,999954951 | HIF1A/PSMB8/PSME2/PSMB10/MYC/BIRC3/PSME1/GATA3               | 8 |
| GO:0019079 | viral genome replication                                         | 8/182 | 24/749 | 0,20587625  | 0,999954951 | 0,999954951 | LTF/IFITM3/SLPI/IFITM2/IFITM1/ISG20/IFIT1/ISG15              | 8 |
| GO:0048469 | cell maturation                                                  | 8/182 | 24/749 | 0,20587625  | 0,999954951 | 0,999954951 | HIF1A/C3/C1QA/XBP1/CDKN1A/G6PD/EPO/GATA3                     | 8 |
| GO:0070646 | protein modification by small protein removal                    | 8/182 | 24/749 | 0,20587625  | 0,999954951 | 0,999954951 | HIF1A/PSMB8/PSME2/PSMB10/MYC/BIRC3/PSME1/GATA3               | 8 |
| GO:1903900 | regulation of viral life cycle                                   | 8/182 | 24/749 | 0,20587625  | 0,999954951 | 0,999954951 | LTF/IFITM3/SLPI/IFITM2/IFITM1/ISG20/IFIT1/ISG15              | 8 |
| GO:0000082 | G1/S transition of mitotic cell cycle                            | 8/182 | 25/749 | 0,243164831 | 0,999954951 | 0,999954951 | ADAMTS1/MUC1/PSME2/BAX/CDKN1A/MYC/PSME1/PTPN6                | 8 |
| GO:0002218 | activation of innate immune response                             | 8/182 | 25/749 | 0,243164831 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/MUC1/PSME2/PSMB10/RELB/PSME1/NFKB1              | 8 |
| GO:0044843 | cell cycle G1/S phase transition                                 | 8/182 | 25/749 | 0,243164831 | 0,999954951 | 0,999954951 | ADAMTS1/MUC1/PSME2/BAX/CDKN1A/MYC/PSME1/PTPN6                | 8 |
| GO:0006869 | lipid transport                                                  | 8/182 | 26/749 | 0,282507831 | 0,999954951 | 0,999954951 | ABCB1/AGT/APOL1/LDLR/APOE/APOL2/ABCC2/NFKB1                  | 8 |
| GO:0034764 | positive regulation of transmembrane transport                   | 8/182 | 26/749 | 0,282507831 | 0,999954951 | 0,999954951 | C3/EHD3/ABCB1/BAX/AGT/CTSS/G6PD/RGN                          | 8 |
| GO:0031663 | lipopolysaccharide-mediated signaling pathway                    | 8/182 | 28/749 | 0,365277656 | 0,999954951 | 0,999954951 | LTF/TGFB1/SIGIRR/LY96/TLR4/TLR2/TRIB1/CD14                   | 8 |



|            |                                                                  |       |        |             |             |             |                                                     |   |
|------------|------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|-----------------------------------------------------|---|
| GO:0032642 | regulation of chemokine production                               | 8/182 | 28/749 | 0,365277656 | 0,999954951 | 0,999954951 | HIF1A/IL4R/SIGIRR/EGR1/TLR4/TLR2/IL6R/ACKR1         | 8 |
| GO:1901137 | carbohydrate derivative biosynthetic process                     | 8/182 | 28/749 | 0,365277656 | 0,999954951 | 0,999954951 | STAT3/MUC1/IMPDH1/JAK3/TGFB1/VCAN/G6PD/NFKB1        | 8 |
| GO:0007005 | mitochondrion organization                                       | 8/182 | 29/749 | 0,407650655 | 0,999954951 | 0,999954951 | HIF1A/SOD2/STAT3/HDAC6/BAX/TNFSF10/ALAS1/PLAUR      | 8 |
| GO:0030522 | intracellular receptor signaling pathway                         | 8/182 | 29/749 | 0,407650655 | 0,999954951 | 0,999954951 | STAT3/HDAC6/NR4A1/AHR/TLR4/IRF7/RORC/BIRC3          | 8 |
| GO:0048511 | rhythmic process                                                 | 8/182 | 29/749 | 0,407650655 | 0,999954951 | 0,999954951 | ADAMTS1/RELB/AHR/EGR1/NFKB2/RORC/SERPINE1/ADORA2A   | 8 |
| GO:0050890 | cognition                                                        | 8/182 | 29/749 | 0,407650655 | 0,999954951 | 0,999954951 | HIF1A/MME/AGT/LDLR/APOE/TLR2/LILRB2/C5AR1           | 8 |
| GO:0002455 | humoral immune response mediated by circulating immunoglob       | 8/182 | 30/749 | 0,450007603 | 0,999954951 | 0,999954951 | BCL3/C1QB/C1S/C3/SERPING1/C9/C1QA/PTPN6             | 8 |
| GO:0007565 | female pregnancy                                                 | 8/182 | 30/749 | 0,450007603 | 0,999954951 | 0,999954951 | TIMP1/TGFB1/AGT/APOL2/ARHGDIB/ABCC2/EPO/THBD        | 8 |
| GO:0031668 | cellular response to extracellular stimulus                      | 8/182 | 30/749 | 0,450007603 | 0,999954951 | 0,999954951 | LCN2/COL1A1/ICAM1/XBP1/CDKN1A/VCAM1/TNC/ATF3        | 8 |
| GO:0044706 | multi-multicellular organism process                             | 8/182 | 30/749 | 0,450007603 | 0,999954951 | 0,999954951 | TIMP1/TGFB1/AGT/APOL2/ARHGDIB/ABCC2/EPO/THBD        | 8 |
| GO:0010721 | negative regulation of cell development                          | 8/182 | 31/749 | 0,49188558  | 0,999954951 | 0,999954951 | LTF/STAT3/COL3A1/TGFB1/LDLR/APOE/G6PD/LILRB1        | 8 |
| GO:0072006 | nephron development                                              | 8/182 | 31/749 | 0,49188558  | 0,999954951 | 0,999954951 | CD24/STAT1/TGFB1/AGT/EGR1/IL6R/MYC/GATA3            | 8 |
| GO:2000379 | positive regulation of reactive oxygen species metabolic process | 8/182 | 31/749 | 0,49188558  | 0,999954951 | 0,999954951 | ICAM1/TGFB1/CDKN1A/AGT/TLR4/ITGB2/NOX4/RGN          | 8 |
| GO:0150076 | neuroinflammatory response                                       | 8/182 | 32/749 | 0,532869227 | 0,999954951 | 0,999954951 | C1QA/LDLR/TLR2/TNFRSF1B/ITGB2/C5AR1/IFNGR1/ADORA2A  | 8 |
| GO:0001505 | regulation of neurotransmitter levels                            | 8/182 | 33/749 | 0,572597643 | 0,999954951 | 0,999954951 | ICAM1/AGT/TLR4/TLR2/ITGB2/SLC22A2/ADORA2A/RGN       | 8 |
| GO:0046718 | viral entry into host cell                                       | 8/182 | 33/749 | 0,572597643 | 0,999954951 | 0,999954951 | IFITM3/ITGB6/IFITM2/IFITM1/HAVCR1/ICAM1/LDLR/PVR    | 8 |
| GO:0030278 | regulation of ossification                                       | 8/182 | 34/749 | 0,610768165 | 0,999954951 | 0,999954951 | HIF1A/LTF/IFITM1/SOST/TGFB1/IL6R/IL6ST/ISG15        | 8 |
| GO:0072657 | protein localization to membrane                                 | 8/182 | 34/749 | 0,610768165 | 0,999954951 | 0,999954951 | CD24/FCER1G/TNFRSF1A/EHD3/TGFB1/BAX/APOE/ITGB2      | 8 |
| GO:0007160 | cell-matrix adhesion                                             | 8/182 | 35/749 | 0,647137426 | 0,999954951 | 0,999954951 | BCL6/ITGB6/LYVE1/COL3A1/VCAM1/ITGB2/FN1/SERPINE1    | 8 |
| GO:0007260 | tyrosine phosphorylation of STAT protein                         | 8/182 | 35/749 | 0,647137426 | 0,999954951 | 0,999954951 | STAT3/SOCS3/TNFRSF1A/JAK3/SOCS1/IL6R/EPO/IL6ST      | 8 |
| GO:0032615 | interleukin-12 production                                        | 8/182 | 35/749 | 0,647137426 | 0,999954951 | 0,999954951 | JAK3/TLR4/TLR2/MAPK11/CMKLR1/LILRB1/NFKB1/LTB       | 8 |
| GO:0032655 | regulation of interleukin-12 production                          | 8/182 | 35/749 | 0,647137426 | 0,999954951 | 0,999954951 | JAK3/TLR4/TLR2/MAPK11/CMKLR1/LILRB1/NFKB1/LTB       | 8 |
| GO:0043523 | regulation of neuron apoptotic process                           | 8/182 | 35/749 | 0,647137426 | 0,999954951 | 0,999954951 | HIF1A/SOD2/BAX/APOE/C5AR1/G6PD/GATA3/ADORA2A        | 8 |
| GO:0030183 | B cell differentiation                                           | 8/182 | 36/749 | 0,681520131 | 0,999954951 | 0,999954951 | BCL3/BCL6/JAK3/XBP1/BAX/VCAM1/SLAMF8/PTPN6          | 8 |
| GO:0003012 | muscle system process                                            | 8/182 | 37/749 | 0,713786031 | 0,999954951 | 0,999954951 | TNFRSF1A/EHD3/AGT/TNFRSF1B/ERRFI1/G6PD/MYOM2/IL6ST  | 8 |
| GO:0044409 | entry into host                                                  | 8/182 | 37/749 | 0,713786031 | 0,999954951 | 0,999954951 | IFITM3/ITGB6/IFITM2/IFITM1/HAVCR1/ICAM1/LDLR/PVR    | 8 |
| GO:0051402 | neuron apoptotic process                                         | 8/182 | 37/749 | 0,713786031 | 0,999954951 | 0,999954951 | HIF1A/SOD2/BAX/APOE/C5AR1/G6PD/GATA3/ADORA2A        | 8 |
| GO:0052126 | movement in host environment                                     | 8/182 | 37/749 | 0,713786031 | 0,999954951 | 0,999954951 | IFITM3/ITGB6/IFITM2/IFITM1/HAVCR1/ICAM1/LDLR/PVR    | 8 |
| GO:2000106 | regulation of leukocyte apoptotic process                        | 8/182 | 37/749 | 0,713786031 | 0,999954951 | 0,999954951 | HIF1A/BCL6/FCER1G/JAK3/BAX/KITLG/IRF7/LILRB1        | 8 |
| GO:0048659 | smooth muscle cell proliferation                                 | 8/182 | 39/749 | 0,77169452  | 0,999954951 | 0,999954951 | SOD2/ADAMTS1/STAT1/DNMT1/CDKN1A/AGT/IL6R/TRIB1      | 8 |
| GO:0048660 | regulation of smooth muscle cell proliferation                   | 8/182 | 39/749 | 0,77169452  | 0,999954951 | 0,999954951 | SOD2/ADAMTS1/STAT1/DNMT1/CDKN1A/AGT/IL6R/TRIB1      | 8 |
| GO:0031344 | regulation of cell projection organization                       | 8/182 | 40/749 | 0,797308331 | 0,999954951 | 0,999954951 | S100A9/LCN2/ICAM1/AGT/APOE/FN1/EPO/GATA3            | 8 |
| GO:0038093 | Fc receptor signaling pathway                                    | 8/182 | 42/749 | 0,842043833 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/PSME2/PSMB10/FCGR1A/FCGR2A/PSME1/NFKB1 | 8 |
| GO:0045582 | positive regulation of T cell differentiation                    | 8/182 | 42/749 | 0,842043833 | 0,999954951 | 0,999954951 | BCL6/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/LILRB2/GATA3      | 8 |
| GO:0045766 | positive regulation of angiogenesis                              | 8/182 | 42/749 | 0,842043833 | 0,999954951 | 0,999954951 | HIF1A/JAK1/STAT3/C3/XBP1/ITGB2/C5AR1/SERPINE1       | 8 |
| GO:0019953 | sexual reproduction                                              | 8/182 | 43/749 | 0,861320404 | 0,999954951 | 0,999954951 | BCL6/STAT3/ADAMTS1/IL4R/TGFB1/BAX/BIRC3/RGN         | 8 |
| GO:0071887 | leukocyte apoptotic process                                      | 8/182 | 44/749 | 0,87867053  | 0,999954951 | 0,999954951 | HIF1A/BCL6/FCER1G/JAK3/BAX/KITLG/IRF7/LILRB1        | 8 |
| GO:0006886 | intracellular protein transport                                  | 8/182 | 45/749 | 0,894210816 | 0,999954951 | 0,999954951 | STAT3/CD24/HDAC6/TGFB1/BAX/CDKN1A/AGT/ITGB2         | 8 |
| GO:0045621 | positive regulation of lymphocyte differentiation                | 8/182 | 47/749 | 0,920361916 | 0,999954951 | 0,999954951 | BCL6/IL4R/NFKBIZ/TGFB1/SOCS1/XBP1/LILRB2/GATA3      | 8 |
| GO:0060249 | anatomical structure homeostasis                                 | 8/182 | 47/749 | 0,920361916 | 0,999954951 | 0,999954951 | SERPINA3/HIF1A/LTF/TGFB1/BAX/TLR4/MYC/NOX4          | 8 |
| GO:0010631 | epithelial cell migration                                        | 8/182 | 49/749 | 0,940793815 | 0,999954951 | 0,999954951 | HIF1A/HDAC6/NR4A1/TGFB1/AGT/APOE/ITGB2/GATA3        | 8 |
| GO:0090132 | epithelium migration                                             | 8/182 | 49/749 | 0,940793815 | 0,999954951 | 0,999954951 | HIF1A/HDAC6/NR4A1/TGFB1/AGT/APOE/ITGB2/GATA3        | 8 |
| GO:0044089 | positive regulation of cellular component biogenesis             | 8/182 | 50/749 | 0,94917883  | 0,999954951 | 0,999954951 | HDAC6/ICAM1/TGFB1/DNMT1/BAX/AGT/TLR4/NOX4           | 8 |
| GO:0090130 | tissue migration                                                 | 8/182 | 50/749 | 0,94917883  | 0,999954951 | 0,999954951 | HIF1A/HDAC6/NR4A1/TGFB1/AGT/APOE/ITGB2/GATA3        | 8 |
| GO:0033365 | protein localization to organelle                                | 8/182 | 51/749 | 0,956501805 | 0,999954951 | 0,999954951 | BCL3/STAT3/GBP2/COL1A1/TGFB1/BAX/CDKN1A/AGT         | 8 |
| GO:0042102 | positive regulation of T cell proliferation                      | 8/182 | 61/749 | 0,992047556 | 0,999954951 | 0,999954951 | CD24/JAK3/VCAM1/CD276/LILRB2/IL6R/EPO/IL6ST         | 8 |
| GO:0007229 | integrin-mediated signaling pathway                              | 7/182 | 15/749 | 0,047517878 | 0,999954951 | 0,999954951 | TIMP1/ITGB6/ADAMTS1/FCER1G/COL3A1/ITGB2/ISG15       | 7 |
| GO:0009620 | response to fungus                                               | 7/182 | 15/749 | 0,047517878 | 0,999954951 | 0,999954951 | S100A9/LTF/S100A8/TGFB1/IL17RA/TLR4/S100A12         | 7 |
| GO:0042445 | hormone metabolic process                                        | 7/182 | 15/749 | 0,047517878 | 0,999954951 | 0,999954951 | HIF1A/MME/HSD11B1/EGR1/TIPARP/GATA3/NFKB1           | 7 |
| GO:0090090 | negative regulation of canonical Wnt signaling pathway           | 7/182 | 15/749 | 0,047517878 | 0,999954951 | 0,999954951 | SOST/PSMB8/PSME2/PSMB10/EGR1/APOE/PSME1             | 7 |
| GO:0030178 | negative regulation of Wnt signaling pathway                     | 7/182 | 16/749 | 0,067566096 | 0,999954951 | 0,999954951 | SOST/PSMB8/PSME2/PSMB10/EGR1/APOE/PSME1             | 7 |
| GO:0060760 | positive regulation of response to cytokine stimulus             | 7/182 | 16/749 | 0,067566096 | 0,999954951 | 0,999954951 | HIF1A/IL1R1/TLR4/TLR2/IRF7/TBK1/CASP4               | 7 |
| GO:1901988 | negative regulation of cell cycle phase transition               | 7/182 | 16/749 | 0,067566096 | 0,999954951 | 0,999954951 | PSMB8/MUC1/PSME2/PSMB10/BAX/CDKN1A/PSME1            | 7 |
| GO:1901991 | negative regulation of mitotic cell cycle phase transition       | 7/182 | 16/749 | 0,067566096 | 0,999954951 | 0,999954951 | PSMB8/MUC1/PSME2/PSMB10/BAX/CDKN1A/PSME1            | 7 |
| GO:0061326 | renal tubule development                                         | 7/182 | 17/749 | 0,091984989 | 0,999954951 | 0,999954951 | CD24/COL4A1/STAT1/TGFB1/AGT/MYC/GATA3               | 7 |
| GO:0030177 | positive regulation of Wnt signaling pathway                     | 7/182 | 18/749 | 0,120701146 | 0,999954951 | 0,999954951 | PSMB8/COL1A1/PSME2/PSMB10/TLR2/PSME1/NFKB1          | 7 |
| GO:0030193 | regulation of blood coagulation                                  | 7/182 | 18/749 | 0,120701146 | 0,999954951 | 0,999954951 | SERPING1/FCER1G/TLR4/APOE/SERPINE1/THBD/PLAUR       | 7 |
| GO:0034121 | regulation of toll-like receptor signaling pathway               | 7/182 | 18/749 | 0,120701146 | 0,999954951 | 0,999954951 | LTF/LY96/TLR4/TLR2/IRF7/BIRC3/CD14                  | 7 |
| GO:0043200 | response to amino acid                                           | 7/182 | 18/749 | 0,120701146 | 0,999954951 | 0,999954951 | COL4A1/COL1A1/COL3A1/ICAM1/SOCS1/XBP1/DNMT1         | 7 |

|            |                                                                  |       |        |             |             |             |                                                   |   |
|------------|------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|---------------------------------------------------|---|
| GO:0062207 | regulation of pattern recognition receptor signaling pathway     | 7/182 | 18/749 | 0,120701146 | 0,999954951 | 0,999954951 | LTF/LY96/TLR4/TLR2/IRF7/BIRC3/CD14                | 7 |
| GO:1900046 | regulation of hemostasis                                         | 7/182 | 18/749 | 0,120701146 | 0,999954951 | 0,999954951 | SERPING1/FCER1G/TLR4/APOE/SERPINE1/THBD/PLAUR     | 7 |
| GO:1902806 | regulation of cell cycle G1/S phase transition                   | 7/182 | 18/749 | 0,120701146 | 0,999954951 | 0,999954951 | ADAMTS1/MUC1/PSME2/BAX/CDKN1A/PSME1/PTPN6         | 7 |
| GO:2000045 | regulation of G1/S transition of mitotic cell cycle              | 7/182 | 18/749 | 0,120701146 | 0,999954951 | 0,999954951 | ADAMTS1/MUC1/PSME2/BAX/CDKN1A/PSME1/PTPN6         | 7 |
| GO:0009743 | response to carbohydrate                                         | 7/182 | 19/749 | 0,153463492 | 0,999954951 | 0,999954951 | HIF1A/MAPK13/ICAM1/TGFB1/XBP1/EGR1/NOX4           | 7 |
| GO:0046486 | glycerolipid metabolic process                                   | 7/182 | 19/749 | 0,153463492 | 0,999954951 | 0,999954951 | PLAAT4/C3/SOCS3/SOCS1/LDLR/APOE/RGN               | 7 |
| GO:0046890 | regulation of lipid biosynthetic process                         | 7/182 | 19/749 | 0,153463492 | 0,999954951 | 0,999954951 | C3/TNFRSF1A/LDLR/EGR1/APOE/NFKB1/RGN              | 7 |
| GO:0050818 | regulation of coagulation                                        | 7/182 | 19/749 | 0,153463492 | 0,999954951 | 0,999954951 | SERPING1/FCER1G/TLR4/APOE/SERPINE1/THBD/PLAUR     | 7 |
| GO:0051341 | regulation of oxidoreductase activity                            | 7/182 | 19/749 | 0,153463492 | 0,999954951 | 0,999954951 | HIF1A/HDAC6/AGT/SLAMF8/APOE/NFKB1/RGN             | 7 |
| GO:0002479 | antigen processing and presentation of exogenous peptide antigen | 7/182 | 20/749 | 0,189868017 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/FCGR1A/TAP2/PSME1/TAP1         | 7 |
| GO:0002576 | platelet degranulation                                           | 7/182 | 20/749 | 0,189868017 | 0,999954951 | 0,999954951 | SERPINA3/TIMP1/SERPING1/FCER1G/TGFB1/FN1/SERPINE1 | 7 |
| GO:0046578 | regulation of Ras protein signal transduction                    | 7/182 | 20/749 | 0,189868017 | 0,999954951 | 0,999954951 | BCL6/COL3A1/KITLG/APOE/ARHGDIB/FGD2/EPO           | 7 |
| GO:1903169 | regulation of calcium ion transmembrane transport                | 7/182 | 20/749 | 0,189868017 | 0,999954951 | 0,999954951 | EHD3/TGFB1/BAX/FKBP1A/G6PD/RGN/PTPN6              | 7 |
| GO:0006066 | alcohol metabolic process                                        | 7/182 | 21/749 | 0,229390076 | 0,999954951 | 0,999954951 | ALDH3A2/APOL1/LDLR/APOE/APOL2/G6PD/NFKB1          | 7 |
| GO:0007219 | Notch signaling pathway                                          | 7/182 | 22/749 | 0,271420266 | 0,999954951 | 0,999954951 | BCL6/STAT3/STAT1/TGFB1/MYC/KRT19/IL6ST            | 7 |
| GO:0034767 | positive regulation of ion transmembrane transport               | 7/182 | 22/749 | 0,271420266 | 0,999954951 | 0,999954951 | EHD3/ABCB1/BAX/AGT/CTSS/G6PD/RGN                  | 7 |
| GO:0009416 | response to light stimulus                                       | 7/182 | 23/749 | 0,315300478 | 0,999954951 | 0,999954951 | HIF1A/BCL3/MAPK13/MME/BAX/CDKN1A/MYC              | 7 |
| GO:0031669 | cellular response to nutrient levels                             | 7/182 | 23/749 | 0,315300478 | 0,999954951 | 0,999954951 | LCN2/COL1A1/ICAM1/XBP1/CDKN1A/TNC/ATF3            | 7 |
| GO:0051056 | regulation of small GTPase mediated signal transduction          | 7/182 | 23/749 | 0,315300478 | 0,999954951 | 0,999954951 | BCL6/COL3A1/KITLG/APOE/ARHGDIB/FGD2/EPO           | 7 |
| GO:0090257 | regulation of muscle system process                              | 7/182 | 24/749 | 0,360357513 | 0,999954951 | 0,999954951 | TNFRSF1A/EHD3/AGT/TNFRSF1B/ERRFI1/G6PD/IL6ST      | 7 |
| GO:0043409 | negative regulation of MAPK cascade                              | 7/182 | 25/749 | 0,405932445 | 0,999954951 | 0,999954951 | TLR4/APOE/MYC/ERRFI1/ATF3/RNF149/PTPN6            | 7 |
| GO:0043588 | skin development                                                 | 7/182 | 25/749 | 0,405932445 | 0,999954951 | 0,999954951 | PLAAT4/KRT8/COL1A1/COL3A1/KRT19/ERRFI1/LTB        | 7 |
| GO:2000107 | negative regulation of leukocyte apoptotic process               | 7/182 | 25/749 | 0,405932445 | 0,999954951 | 0,999954951 | HIF1A/BCL6/FCER1G/JAK3/KITLG/IRF7/LILRB1          | 7 |
| GO:0007611 | learning or memory                                               | 7/182 | 26/749 | 0,451404671 | 0,999954951 | 0,999954951 | HIF1A/MME/AGT/LDLR/APOE/TLR2/LILRB2               | 7 |
| GO:0015711 | organic anion transport                                          | 7/182 | 26/749 | 0,451404671 | 0,999954951 | 0,999954951 | ABCB1/AGT/LDLR/APOE/SLC11A1/ABCC2/ADORA2A         | 7 |
| GO:0061900 | glial cell activation                                            | 7/182 | 26/749 | 0,451404671 | 0,999954951 | 0,999954951 | C1QA/LDLR/TLR2/ITGB2/C5AR1/IFNGR1/ADORA2A         | 7 |
| GO:0001659 | temperature homeostasis                                          | 7/182 | 27/749 | 0,496210222 | 0,999954951 | 0,999954951 | STAT3/LCN2/IL4R/STAT6/EGR1/TLR4/CMKLR1            | 7 |
| GO:0007584 | response to nutrient                                             | 7/182 | 27/749 | 0,496210222 | 0,999954951 | 0,999954951 | COL1A1/STAT1/TGFB1/XBP1/VCAM1/TNC/EPO             | 7 |
| GO:0030856 | regulation of epithelial cell differentiation                    | 7/182 | 27/749 | 0,496210222 | 0,999954951 | 0,999954951 | PLAAT4/CD24/TNFRSF1A/STAT1/ERRFI1/SERPINE1/GATA3  | 7 |
| GO:0071383 | cellular response to steroid hormone stimulus                    | 7/182 | 27/749 | 0,496210222 | 0,999954951 | 0,999954951 | HDAC6/NR4A1/ICAM1/TGFB1/RORC/ABCC2/ERRFI1         | 7 |
| GO:0001649 | osteoblast differentiation                                       | 7/182 | 28/749 | 0,539854411 | 0,999954951 | 0,999954951 | LTF/IFITM1/COL1A1/TNC/VCAN/IL6R/IL6ST             | 7 |
| GO:0001776 | leukocyte homeostasis                                            | 7/182 | 28/749 | 0,539854411 | 0,999954951 | 0,999954951 | HIF1A/FCER1G/JAK3/TGFB1/BAX/KITLG/TNFSF14         | 7 |
| GO:0032677 | regulation of interleukin-8 production                           | 7/182 | 28/749 | 0,539854411 | 0,999954951 | 0,999954951 | BCL3/TLR4/MYD88/TLR2/CD58/CD14/SERPINE1           | 7 |
| GO:0034504 | protein localization to nucleus                                  | 7/182 | 28/749 | 0,539854411 | 0,999954951 | 0,999954951 | BCL3/STAT3/GBP2/COL1A1/TGFB1/CDKN1A/AGT           | 7 |
| GO:0030168 | platelet activation                                              | 7/182 | 29/749 | 0,581919243 | 0,999954951 | 0,999954951 | FCER1G/COL1A1/COL3A1/TLR4/APOE/THBD/PTPN6         | 7 |
| GO:0090066 | regulation of anatomical structure size                          | 7/182 | 29/749 | 0,581919243 | 0,999954951 | 0,999954951 | SOD2/ICAM1/AGT/SLC12A3/APOE/FN1/ADORA2A           | 7 |
| GO:0008406 | gonad development                                                | 7/182 | 30/749 | 0,622066263 | 0,999954951 | 0,999954951 | ADAMTS1/ICAM1/BAX/KITLG/TNFSF10/TIPARP/GATA3      | 7 |
| GO:0032637 | interleukin-8 production                                         | 7/182 | 30/749 | 0,622066263 | 0,999954951 | 0,999954951 | BCL3/TLR4/MYD88/TLR2/CD58/CD14/SERPINE1           | 7 |
| GO:0042133 | neurotransmitter metabolic process                               | 7/182 | 30/749 | 0,622066263 | 0,999954951 | 0,999954951 | ICAM1/AGT/TLR4/TLR2/ITGB2/SLC22A2/RGN             | 7 |
| GO:0045137 | development of primary sexual characteristics                    | 7/182 | 30/749 | 0,622066263 | 0,999954951 | 0,999954951 | ADAMTS1/ICAM1/BAX/KITLG/TNFSF10/TIPARP/GATA3      | 7 |
| GO:0070588 | calcium ion transmembrane transport                              | 7/182 | 30/749 | 0,622066263 | 0,999954951 | 0,999954951 | EHD3/TGFB1/BAX/FKBP1A/G6PD/RGN/PTPN6              | 7 |
| GO:0032613 | interleukin-10 production                                        | 7/182 | 31/749 | 0,660035629 | 0,999954951 | 0,999954951 | BCL3/FCER1G/JAK3/TLR4/TLR2/LILRB1/ISG15           | 7 |
| GO:0045639 | positive regulation of myeloid cell differentiation              | 7/182 | 31/749 | 0,660035629 | 0,999954951 | 0,999954951 | HIF1A/STAT3/STAT1/TGFB1/KITLG/TRIB1/ISG15         | 7 |
| GO:1903409 | reactive oxygen species biosynthetic process                     | 7/182 | 31/749 | 0,660035629 | 0,999954951 | 0,999954951 | STAT3/ICAM1/AGT/TLR4/ITGB2/NOX4/RGN               | 7 |
| GO:0048638 | regulation of developmental growth                               | 7/182 | 33/749 | 0,728769608 | 0,999954951 | 0,999954951 | STAT3/CDKN1A/APOE/MAPK11/G6PD/FN1/GDF15           | 7 |
| GO:0048738 | cardiac muscle tissue development                                | 7/182 | 33/749 | 0,728769608 | 0,999954951 | 0,999954951 | TGFB1/AGT/FKBP1A/MAPK11/NOX4/G6PD/MYOM2           | 7 |
| GO:0051260 | protein homooligomerization                                      | 7/182 | 33/749 | 0,728769608 | 0,999954951 | 0,999954951 | SOD2/C9/FCER1G/EHD3/LCN2/BAX/APOE                 | 7 |
| GO:0031960 | response to corticosteroid                                       | 7/182 | 34/749 | 0,759362575 | 0,999954951 | 0,999954951 | COL1A1/ICAM1/TGFB1/CDKN1A/ABCC2/ERRFI1/EPO        | 7 |
| GO:0042509 | regulation of tyrosine phosphorylation of STAT protein           | 7/182 | 34/749 | 0,759362575 | 0,999954951 | 0,999954951 | STAT3/SOCS3/TNFRSF1A/SOCS1/IL6R/EPO/IL6ST         | 7 |
| GO:0043542 | endothelial cell migration                                       | 7/182 | 35/749 | 0,787418862 | 0,999954951 | 0,999954951 | HIF1A/NR4A1/TGFB1/AGT/APOE/ITGB2/GATA3            | 7 |
| GO:0006325 | chromatin organization                                           | 7/182 | 36/749 | 0,812980625 | 0,999954951 | 0,999954951 | BCL6/MUC1/HDAC6/TGFB1/DNMT1/MYC/GATA3             | 7 |
| GO:0007268 | chemical synaptic transmission                                   | 7/182 | 36/749 | 0,812980625 | 0,999954951 | 0,999954951 | STAT3/MME/AGT/APOE/LILRB2/SLC22A2/ADORA2A         | 7 |
| GO:0045664 | regulation of neuron differentiation                             | 7/182 | 36/749 | 0,812980625 | 0,999954951 | 0,999954951 | S100A9/BCL6/AGT/APOE/FN1/EPO/GATA3                | 7 |
| GO:0051493 | regulation of cytoskeleton organization                          | 7/182 | 36/749 | 0,812980625 | 0,999954951 | 0,999954951 | S100A9/S100A8/HDAC6/ICAM1/TGFB1/ARHGDIB/NOX4      | 7 |
| GO:0098916 | anterograde trans-synaptic signaling                             | 7/182 | 36/749 | 0,812980625 | 0,999954951 | 0,999954951 | STAT3/MME/AGT/APOE/LILRB2/SLC22A2/ADORA2A         | 7 |
| GO:0007548 | sex differentiation                                              | 7/182 | 37/749 | 0,83612603  | 0,999954951 | 0,999954951 | ADAMTS1/ICAM1/BAX/KITLG/TNFSF10/TIPARP/GATA3      | 7 |
| GO:0042108 | positive regulation of cytokine biosynthetic process             | 7/182 | 37/749 | 0,83612603  | 0,999954951 | 0,999954951 | BCL3/STAT3/CD276/EGR1/TLR4/TBK1/LTB               | 7 |
| GO:0043254 | regulation of protein-containing complex assembly                | 7/182 | 37/749 | 0,83612603  | 0,999954951 | 0,999954951 | SOST/HDAC6/ICAM1/TGFB1/BAX/TLR4/APOE              | 7 |
| GO:0099537 | trans-synaptic signaling                                         | 7/182 | 37/749 | 0,83612603  | 0,999954951 | 0,999954951 | STAT3/MME/AGT/APOE/LILRB2/SLC22A2/ADORA2A         | 7 |

|            |                                                                 |       |        |             |             |             |                                                 |   |
|------------|-----------------------------------------------------------------|-------|--------|-------------|-------------|-------------|-------------------------------------------------|---|
| GO:0006914 | autophagy                                                       | 7/182 | 38/749 | 0,856961299 | 0,999954951 | 0,999954951 | S100A9/HIF1A/STAT3/S100A8/HDAC6/XBP1/TBK1       | 7 |
| GO:0061919 | process utilizing autophagic mechanism                          | 7/182 | 38/749 | 0,856961299 | 0,999954951 | 0,999954951 | S100A9/HIF1A/STAT3/S100A8/HDAC6/XBP1/TBK1       | 7 |
| GO:0071674 | mononuclear cell migration                                      | 7/182 | 38/749 | 0,856961299 | 0,999954951 | 0,999954951 | TGFB1/SLAMF8/IL6R/S100A12/CMKLR1/C5AR1/SERPINE1 | 7 |
| GO:0099536 | synaptic signaling                                              | 7/182 | 38/749 | 0,856961299 | 0,999954951 | 0,999954951 | STAT3/MME/AGT/APOE/LILRB2/SLC22A2/ADORA2A       | 7 |
| GO:0060485 | mesenchyme development                                          | 7/182 | 39/749 | 0,875613407 | 0,999954951 | 0,999954951 | HIF1A/COL1A1/STAT1/TGFB1/KITLG/MYC/FN1          | 7 |
| GO:0120035 | regulation of plasma membrane bounded cell projection organiz   | 7/182 | 39/749 | 0,875613407 | 0,999954951 | 0,999954951 | S100A9/ICAM1/AGT/APOE/FN1/EPO/GATA3             | 7 |
| GO:0007276 | gamete generation                                               | 7/182 | 40/749 | 0,892223575 | 0,999954951 | 0,999954951 | BCL6/ADAMTS1/IL4R/TGFB1/BAX/BIRC3/RGN           | 7 |
| GO:0032729 | positive regulation of interferon-gamma production              | 7/182 | 40/749 | 0,892223575 | 0,999954951 | 0,999954951 | BCL3/IL1R1/CD276/TLR4/IL6R/SLC11A1/CD14         | 7 |
| GO:0060562 | epithelial tube morphogenesis                                   | 7/182 | 40/749 | 0,892223575 | 0,999954951 | 0,999954951 | HIF1A/COL4A1/TGFB1/AGT/TNC/MYC/GATA3            | 7 |
| GO:0030593 | neutrophil chemotaxis                                           | 7/182 | 41/749 | 0,90694162  | 0,999954951 | 0,999954951 | S100A9/S100A8/FCER1G/CXCL1/S100A12/ITGB2/C5AR1  | 7 |
| GO:0050679 | positive regulation of epithelial cell proliferation            | 7/182 | 42/749 | 0,919921177 | 0,999954951 | 0,999954951 | HIF1A/STAT3/NR4A1/TGFB1/XBP1/MYC/C5AR1          | 7 |
| GO:0051276 | chromosome organization                                         | 7/182 | 42/749 | 0,919921177 | 0,999954951 | 0,999954951 | BCL6/MUC1/HDAC6/TGFB1/DNMT1/MYC/GATA3           | 7 |
| GO:0048568 | embryonic organ development                                     | 7/182 | 45/749 | 0,949945526 | 0,999954951 | 0,999954951 | HIF1A/SOCS3/KRT8/TGFB1/KITLG/KRT19/GATA3        | 7 |
| GO:0048598 | embryonic morphogenesis                                         | 7/182 | 48/749 | 0,969542439 | 0,999954951 | 0,999954951 | HIF1A/SOCS3/TGFB1/BAX/ITGB2/FN1/GATA3           | 7 |
| GO:0002456 | T cell mediated immunity                                        | 7/182 | 50/749 | 0,978428883 | 0,999954951 | 0,999954951 | IL1R1/ICAM1/SLC11A1/PVR/TNFRSF1B/LILRB1/GATA3   | 7 |
| GO:0002708 | positive regulation of lymphocyte mediated immunity             | 7/182 | 51/749 | 0,981917282 | 0,999954951 | 0,999954951 | C3/FCER1G/IL1R1/TGFB1/STAT6/PVR/GATA3           | 7 |
| GO:0070374 | positive regulation of ERK1 and ERK2 cascade                    | 7/182 | 54/749 | 0,989504502 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/TLR4/APOE/NOX4/C5AR1/EPO            | 7 |
| GO:0050920 | regulation of chemotaxis                                        | 7/182 | 55/749 | 0,991286433 | 0,999954951 | 0,999954951 | TGFB1/SLAMF8/IL6R/CMKLR1/C5AR1/SERPINE1/TNFSF14 | 7 |
| GO:0009792 | embryo development ending in birth or egg hatching              | 7/182 | 58/749 | 0,995080031 | 0,999954951 | 0,999954951 | HIF1A/SOCS3/KRT8/COL1A1/TGFB1/KRT19/GATA3       | 7 |
| GO:0043009 | chordate embryonic development                                  | 7/182 | 58/749 | 0,995080031 | 0,999954951 | 0,999954951 | HIF1A/SOCS3/KRT8/COL1A1/TGFB1/KRT19/GATA3       | 7 |
| GO:0010332 | response to gamma radiation                                     | 6/182 | 12/749 | 0,04655142  | 0,999954951 | 0,999954951 | BAX/CDKN1A/EGR1/MYC/NOX4/GATA3                  | 6 |
| GO:0032608 | interferon-beta production                                      | 6/182 | 12/749 | 0,04655142  | 0,999954951 | 0,999954951 | RELB/TLR4/TLR2/IRF7/TBK1/LILRB1                 | 6 |
| GO:0032648 | regulation of interferon-beta production                        | 6/182 | 12/749 | 0,04655142  | 0,999954951 | 0,999954951 | RELB/TLR4/TLR2/IRF7/TBK1/LILRB1                 | 6 |
| GO:0044106 | cellular amine metabolic process                                | 6/182 | 12/749 | 0,04655142  | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/ABCC2/ITGB2/PSME1            | 6 |
| GO:0061013 | regulation of mRNA catabolic process                            | 6/182 | 12/749 | 0,04655142  | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/MYD88/SLC11A1/PSME1          | 6 |
| GO:0098754 | detoxification                                                  | 6/182 | 12/749 | 0,04655142  | 0,999954951 | 0,999954951 | S100A9/SOD2/MT1A/APOE/ABCC2/RGN                 | 6 |
| GO:1903311 | regulation of mRNA metabolic process                            | 6/182 | 12/749 | 0,04655142  | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/MYD88/SLC11A1/PSME1          | 6 |
| GO:0002762 | negative regulation of myeloid leukocyte differentiation        | 6/182 | 13/749 | 0,06941507  | 0,999954951 | 0,999954951 | LTF/TLR4/MYC/TRIB1/LILRB1/TMEM178A              | 6 |
| GO:0015893 | drug transport                                                  | 6/182 | 13/749 | 0,06941507  | 0,999954951 | 0,999954951 | AGT/SLC11A1/MYC/ABCC2/SLC22A2/ADORA2A           | 6 |
| GO:0043627 | response to estrogen                                            | 6/182 | 13/749 | 0,06941507  | 0,999954951 | 0,999954951 | CD24/IL4R/KRT19/ABCC2/EPO/GATA3                 | 6 |
| GO:0051186 | cofactor metabolic process                                      | 6/182 | 13/749 | 0,06941507  | 0,999954951 | 0,999954951 | STAT3/NNMT/HDAC6/G6PD/ALAS1/RGN                 | 6 |
| GO:0071230 | cellular response to amino acid stimulus                        | 6/182 | 13/749 | 0,06941507  | 0,999954951 | 0,999954951 | COL4A1/COL1A1/COL3A1/SOCS1/XBP1/DNMT1           | 6 |
| GO:0090263 | positive regulation of canonical Wnt signaling pathway          | 6/182 | 13/749 | 0,06941507  | 0,999954951 | 0,999954951 | PSMB8/COL1A1/PSME2/PSMB10/PSME1/NFKB1           | 6 |
| GO:2000736 | regulation of stem cell differentiation                         | 6/182 | 13/749 | 0,06941507  | 0,999954951 | 0,999954951 | STAT3/PSMB8/PSME2/PSMB10/PSME1/GATA3            | 6 |
| GO:0002756 | MyD88-independent toll-like receptor signaling pathway          | 6/182 | 14/749 | 0,097683986 | 0,999954951 | 0,999954951 | LY96/TLR4/IRF7/TBK1/BIRC3/CD14                  | 6 |
| GO:0006801 | superoxide metabolic process                                    | 6/182 | 14/749 | 0,097683986 | 0,999954951 | 0,999954951 | SOD2/TGFB1/AGT/ITGB2/NOX4/RGN                   | 6 |
| GO:0006970 | response to osmotic stress                                      | 6/182 | 14/749 | 0,097683986 | 0,999954951 | 0,999954951 | MAPK13/ABCB1/RELB/BAX/ERRFI1/EPO                | 6 |
| GO:0035666 | TRIF-dependent toll-like receptor signaling pathway             | 6/182 | 14/749 | 0,097683986 | 0,999954951 | 0,999954951 | LY96/TLR4/IRF7/TBK1/BIRC3/CD14                  | 6 |
| GO:0061045 | negative regulation of wound healing                            | 6/182 | 14/749 | 0,097683986 | 0,999954951 | 0,999954951 | SERPING1/CDKN1A/APOE/SERPINE1/THBD/PLAUR        | 6 |
| GO:1903035 | negative regulation of response to wounding                     | 6/182 | 14/749 | 0,097683986 | 0,999954951 | 0,999954951 | SERPING1/CDKN1A/APOE/SERPINE1/THBD/PLAUR        | 6 |
| GO:0002755 | MyD88-dependent toll-like receptor signaling pathway            | 6/182 | 15/749 | 0,131128058 | 0,999954951 | 0,999954951 | LY96/TLR4/MYD88/TLR2/IRF7/CD14                  | 6 |
| GO:0006402 | mRNA catabolic process                                          | 6/182 | 15/749 | 0,131128058 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/MYD88/SLC11A1/PSME1          | 6 |
| GO:0010611 | regulation of cardiac muscle hypertrophy                        | 6/182 | 15/749 | 0,131128058 | 0,999954951 | 0,999954951 | TNFRSF1A/AGT/TNFRSF1B/ERRFI1/G6PD/IL6ST         | 6 |
| GO:0014743 | regulation of muscle hypertrophy                                | 6/182 | 15/749 | 0,131128058 | 0,999954951 | 0,999954951 | TNFRSF1A/AGT/TNFRSF1B/ERRFI1/G6PD/IL6ST         | 6 |
| GO:0019218 | regulation of steroid metabolic process                         | 6/182 | 15/749 | 0,131128058 | 0,999954951 | 0,999954951 | AGT/LDLR/EGR1/APOE/RORC/NFKB1                   | 6 |
| GO:0033627 | cell adhesion mediated by integrin                              | 6/182 | 15/749 | 0,131128058 | 0,999954951 | 0,999954951 | ITGB6/MUC1/ICAM1/ITGB2/SERPINE1/PTPN6           | 6 |
| GO:0045598 | regulation of fat cell differentiation                          | 6/182 | 15/749 | 0,131128058 | 0,999954951 | 0,999954951 | HDAC6/TGFB1/XBP1/RORC/CMKLR1/GATA3              | 6 |
| GO:0045638 | negative regulation of myeloid cell differentiation             | 6/182 | 15/749 | 0,131128058 | 0,999954951 | 0,999954951 | LTF/TLR4/MYC/TRIB1/LILRB1/TMEM178A              | 6 |
| GO:0009749 | response to glucose                                             | 6/182 | 16/749 | 0,169265235 | 0,999954951 | 0,999954951 | HIF1A/ICAM1/TGFB1/XBP1/EGR1/NOX4                | 6 |
| GO:0032869 | cellular response to insulin stimulus                           | 6/182 | 16/749 | 0,169265235 | 0,999954951 | 0,999954951 | SOCS3/STAT1/SOCS1/XBP1/AGT/ERRFI1               | 6 |
| GO:0033500 | carbohydrate homeostasis                                        | 6/182 | 16/749 | 0,169265235 | 0,999954951 | 0,999954951 | HIF1A/STAT3/ICAM1/XBP1/HNF1A/NOX4               | 6 |
| GO:0042593 | glucose homeostasis                                             | 6/182 | 16/749 | 0,169265235 | 0,999954951 | 0,999954951 | HIF1A/STAT3/ICAM1/XBP1/HNF1A/NOX4               | 6 |
| GO:0072080 | nephron tubule development                                      | 6/182 | 16/749 | 0,169265235 | 0,999954951 | 0,999954951 | CD24/STAT1/TGFB1/AGT/MYC/GATA3                  | 6 |
| GO:2001243 | negative regulation of intrinsic apoptotic signaling pathway    | 6/182 | 16/749 | 0,169265235 | 0,999954951 | 0,999954951 | HIF1A/SOD2/MUC1/XBP1/EPO/PLAUR                  | 6 |
| GO:0008630 | intrinsic apoptotic signaling pathway in response to DNA damage | 6/182 | 17/749 | 0,211418097 | 0,999954951 | 0,999954951 | BCL3/MUC1/TNFRSF1A/BAX/CDKN1A/TNFRSF1B          | 6 |
| GO:0009746 | response to hexose                                              | 6/182 | 17/749 | 0,211418097 | 0,999954951 | 0,999954951 | HIF1A/ICAM1/TGFB1/XBP1/EGR1/NOX4                | 6 |
| GO:0032412 | regulation of ion transmembrane transporter activity            | 6/182 | 17/749 | 0,211418097 | 0,999954951 | 0,999954951 | EHD3/ABCB1/FKBP1A/CTSS/EPO/RGN                  | 6 |
| GO:0034284 | response to monosaccharide                                      | 6/182 | 17/749 | 0,211418097 | 0,999954951 | 0,999954951 | HIF1A/ICAM1/TGFB1/XBP1/EGR1/NOX4                | 6 |
| GO:0043502 | regulation of muscle adaptation                                 | 6/182 | 17/749 | 0,211418097 | 0,999954951 | 0,999954951 | TNFRSF1A/AGT/TNFRSF1B/ERRFI1/G6PD/IL6ST         | 6 |

|            |                                                                   |       |        |             |             |             |                                          |   |
|------------|-------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|------------------------------------------|---|
| GO:1901655 | cellular response to ketone                                       | 6/182 | 17/749 | 0,211418097 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/AHR/TNC/ABCC2/ERRFI1         | 6 |
| GO:0003300 | cardiac muscle hypertrophy                                        | 6/182 | 18/749 | 0,256776573 | 0,999954951 | 0,999954951 | TNFRSF1A/AGT/TNFRSF1B/ERRFI1/G6PD/IL6ST  | 6 |
| GO:0006109 | regulation of carbohydrate metabolic process                      | 6/182 | 18/749 | 0,256776573 | 0,999954951 | 0,999954951 | HIF1A/STAT3/TGFB1/RORC/NFKB1/RGN         | 6 |
| GO:0014896 | muscle hypertrophy                                                | 6/182 | 18/749 | 0,256776573 | 0,999954951 | 0,999954951 | TNFRSF1A/AGT/TNFRSF1B/ERRFI1/G6PD/IL6ST  | 6 |
| GO:0014897 | striated muscle hypertrophy                                       | 6/182 | 18/749 | 0,256776573 | 0,999954951 | 0,999954951 | TNFRSF1A/AGT/TNFRSF1B/ERRFI1/G6PD/IL6ST  | 6 |
| GO:0022898 | regulation of transmembrane transporter activity                  | 6/182 | 18/749 | 0,256776573 | 0,999954951 | 0,999954951 | EHD3/ABCB1/FKBP1A/CTSS/EPO/RGN           | 6 |
| GO:0032409 | regulation of transporter activity                                | 6/182 | 18/749 | 0,256776573 | 0,999954951 | 0,999954951 | EHD3/ABCB1/FKBP1A/CTSS/EPO/RGN           | 6 |
| GO:0090596 | sensory organ morphogenesis                                       | 6/182 | 18/749 | 0,256776573 | 0,999954951 | 0,999954951 | HIF1A/STAT3/MEGF11/BAX/FJX1/GATA3        | 6 |
| GO:1903362 | regulation of cellular protein catabolic process                  | 6/182 | 18/749 | 0,256776573 | 0,999954951 | 0,999954951 | PSME2/LDLR/APOE/TRIB1/PSME1/RGN          | 6 |
| GO:0007569 | cell aging                                                        | 6/182 | 19/749 | 0,304459533 | 0,999954951 | 0,999954951 | BCL6/MME/ICAM1/CDKN1A/NOX4/SERPINE1      | 6 |
| GO:0007623 | circadian rhythm                                                  | 6/182 | 19/749 | 0,304459533 | 0,999954951 | 0,999954951 | RELB/AHR/EGR1/RORC/SERPINE1/ADORA2A      | 6 |
| GO:0009411 | response to UV                                                    | 6/182 | 19/749 | 0,304459533 | 0,999954951 | 0,999954951 | BCL3/MAPK13/MME/BAX/CDKN1A/MYC           | 6 |
| GO:0010498 | proteasomal protein catabolic process                             | 6/182 | 19/749 | 0,304459533 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/APOE/TRIB1/PSME1      | 6 |
| GO:0014074 | response to purine-containing compound                            | 6/182 | 19/749 | 0,304459533 | 0,999954951 | 0,999954951 | COL1A1/STAT1/AHR/NOX4/ADORA2A/THBD       | 6 |
| GO:0016053 | organic acid biosynthetic process                                 | 6/182 | 19/749 | 0,304459533 | 0,999954951 | 0,999954951 | TGFB1/XBP1/ALOX5/VCAN/NFKB1/RGN          | 6 |
| GO:0018205 | peptidyl-lysine modification                                      | 6/182 | 19/749 | 0,304459533 | 0,999954951 | 0,999954951 | MUC1/HDAC6/TGFB1/DNMT1/EGR1/GATA3        | 6 |
| GO:0046394 | carboxylic acid biosynthetic process                              | 6/182 | 19/749 | 0,304459533 | 0,999954951 | 0,999954951 | TGFB1/XBP1/ALOX5/VCAN/NFKB1/RGN          | 6 |
| GO:0046636 | negative regulation of alpha-beta T cell activation               | 6/182 | 19/749 | 0,304459533 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/SOCS1/LILRB1/ADORA2A      | 6 |
| GO:0006091 | generation of precursor metabolites and energy                    | 6/182 | 20/749 | 0,353570182 | 0,999954951 | 0,999954951 | HIF1A/STAT3/MYC/NOX4/G6PD/IL6ST          | 6 |
| GO:0006631 | fatty acid metabolic process                                      | 6/182 | 20/749 | 0,353570182 | 0,999954951 | 0,999954951 | ALDH3A2/C3/TNFRSF1A/XBP1/ALOX5/RGN       | 6 |
| GO:0010565 | regulation of cellular ketone metabolic process                   | 6/182 | 20/749 | 0,353570182 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/EGR1/PSME1/RGN        | 6 |
| GO:0032757 | positive regulation of interleukin-8 production                   | 6/182 | 20/749 | 0,353570182 | 0,999954951 | 0,999954951 | TLR4/MYD88/TLR2/CD58/CD14/SERPINE1       | 6 |
| GO:0045778 | positive regulation of ossification                               | 6/182 | 20/749 | 0,353570182 | 0,999954951 | 0,999954951 | LTF/IFITM1/TGFB1/IL6R/IL6ST/ISG15        | 6 |
| GO:0048144 | fibroblast proliferation                                          | 6/182 | 20/749 | 0,353570182 | 0,999954951 | 0,999954951 | TGFB1/BAX/CDKN1A/AGT/MYC/FN1             | 6 |
| GO:0048145 | regulation of fibroblast proliferation                            | 6/182 | 20/749 | 0,353570182 | 0,999954951 | 0,999954951 | TGFB1/BAX/CDKN1A/AGT/MYC/FN1             | 6 |
| GO:1904064 | positive regulation of cation transmembrane transport             | 6/182 | 20/749 | 0,353570182 | 0,999954951 | 0,999954951 | EHD3/BAX/AGT/CTSS/G6PD/RGN               | 6 |
| GO:0003018 | vascular process in circulatory system                            | 6/182 | 21/749 | 0,403242225 | 0,999954951 | 0,999954951 | SOD2/ICAM1/TGFB1/AGT/APOE/ADORA2A        | 6 |
| GO:0008625 | extrinsic apoptotic signaling pathway via death domain receptor   | 6/182 | 21/749 | 0,403242225 | 0,999954951 | 0,999954951 | TNFRSF1A/ICAM1/BAX/TNFSF10/ATF3/SERPINE1 | 6 |
| GO:0030879 | mammary gland development                                         | 6/182 | 21/749 | 0,403242225 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/XBP1/BAX/STAT6/GATA3         | 6 |
| GO:0033044 | regulation of chromosome organization                             | 6/182 | 21/749 | 0,403242225 | 0,999954951 | 0,999954951 | BCL6/MUC1/TGFB1/DNMT1/MYC/GATA3          | 6 |
| GO:0042180 | cellular ketone metabolic process                                 | 6/182 | 21/749 | 0,403242225 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/EGR1/PSME1/RGN        | 6 |
| GO:1903556 | negative regulation of tumor necrosis factor superfamily cytokin  | 6/182 | 21/749 | 0,403242225 | 0,999954951 | 0,999954951 | LTF/BCL3/TLR4/ERRFI1/LILRB1/PTPN6        | 6 |
| GO:0001774 | microglial cell activation                                        | 6/182 | 22/749 | 0,452675459 | 0,999954951 | 0,999954951 | C1QA/LDLR/TLR2/ITGB2/C5AR1/IFNGR1        | 6 |
| GO:0002269 | leukocyte activation involved in inflammatory response            | 6/182 | 22/749 | 0,452675459 | 0,999954951 | 0,999954951 | C1QA/LDLR/TLR2/ITGB2/C5AR1/IFNGR1        | 6 |
| GO:0006958 | complement activation, classical pathway                          | 6/182 | 22/749 | 0,452675459 | 0,999954951 | 0,999954951 | C1QB/C1S/C3/SERPING1/C9/C1QA             | 6 |
| GO:0043524 | negative regulation of neuron apoptotic process                   | 6/182 | 22/749 | 0,452675459 | 0,999954951 | 0,999954951 | HIF1A/SOD2/BAX/APOE/C5AR1/ADORA2A        | 6 |
| GO:0045732 | positive regulation of protein catabolic process                  | 6/182 | 22/749 | 0,452675459 | 0,999954951 | 0,999954951 | LDLR/APOE/TNFRSF1B/TRIB1/TIPARP/RGN      | 6 |
| GO:0051149 | positive regulation of muscle cell differentiation                | 6/182 | 22/749 | 0,452675459 | 0,999954951 | 0,999954951 | SOD2/IL4R/TGFB1/MAPK11/GDF15/TNFSF14     | 6 |
| GO:0051604 | protein maturation                                                | 6/182 | 22/749 | 0,452675459 | 0,999954951 | 0,999954951 | MME/FKBP1A/CTSS/IL1R2/BIRC3/SERPINE1     | 6 |
| GO:0072009 | nephron epithelium development                                    | 6/182 | 22/749 | 0,452675459 | 0,999954951 | 0,999954951 | CD24/STAT1/TGFB1/AGT/MYC/GATA3           | 6 |
| GO:0032722 | positive regulation of chemokine production                       | 6/182 | 23/749 | 0,501160747 | 0,999954951 | 0,999954951 | HIF1A/IL4R/EGR1/TLR4/TLR2/IL6R           | 6 |
| GO:0043500 | muscle adaptation                                                 | 6/182 | 23/749 | 0,501160747 | 0,999954951 | 0,999954951 | TNFRSF1A/AGT/TNFRSF1B/ERRFI1/G6PD/IL6ST  | 6 |
| GO:0002312 | B cell activation involved in immune response                     | 6/182 | 24/749 | 0,548095158 | 0,999954951 | 0,999954951 | BCL3/BCL6/TGFB1/XBP1/STAT6/TLR4          | 6 |
| GO:0002712 | regulation of B cell mediated immunity                            | 6/182 | 24/749 | 0,548095158 | 0,999954951 | 0,999954951 | BCL6/C3/FCER1G/TGFB1/STAT6/PTPN6         | 6 |
| GO:0002889 | regulation of immunoglobulin mediated immune response             | 6/182 | 24/749 | 0,548095158 | 0,999954951 | 0,999954951 | BCL6/C3/FCER1G/TGFB1/STAT6/PTPN6         | 6 |
| GO:0051961 | negative regulation of nervous system development                 | 6/182 | 24/749 | 0,548095158 | 0,999954951 | 0,999954951 | STAT3/COL3A1/TGFB1/LDLR/APOE/TLR2        | 6 |
| GO:0110110 | positive regulation of animal organ morphogenesis                 | 6/182 | 24/749 | 0,548095158 | 0,999954951 | 0,999954951 | TGFB1/XBP1/BAX/AGT/MYC/GATA3             | 6 |
| GO:0002832 | negative regulation of response to biotic stimulus                | 6/182 | 25/749 | 0,592988647 | 0,999954951 | 0,999954951 | LTF/SERPING1/SIGIRR/SLAMF8/TRIB1/LILRB1  | 6 |
| GO:0043280 | positive regulation of cysteine-type endopeptidase activity invol | 6/182 | 25/749 | 0,592988647 | 0,999954951 | 0,999954951 | S100A9/S100A8/BAX/MYC/TNFSF10/CASP4      | 6 |
| GO:0051153 | regulation of striated muscle cell differentiation                | 6/182 | 25/749 | 0,592988647 | 0,999954951 | 0,999954951 | IL4R/TGFB1/XBP1/G6PD/GDF15/TNFSF14       | 6 |
| GO:0016570 | histone modification                                              | 6/182 | 26/749 | 0,63546384  | 0,999954951 | 0,999954951 | BCL6/MUC1/HDAC6/TGFB1/DNMT1/GATA3        | 6 |
| GO:0031099 | regeneration                                                      | 6/182 | 26/749 | 0,63546384  | 0,999954951 | 0,999954951 | NNMT/TGFB1/CDKN1A/TNC/C5AR1/RGN          | 6 |
| GO:0031346 | positive regulation of cell projection organization               | 6/182 | 26/749 | 0,63546384  | 0,999954951 | 0,999954951 | S100A9/LCN2/AGT/APOE/FN1/EPO             | 6 |
| GO:0035051 | cardiocyte differentiation                                        | 6/182 | 26/749 | 0,63546384  | 0,999954951 | 0,999954951 | TGFB1/VCAM1/AGT/NOX4/G6PD/MYOM2          | 6 |
| GO:0071236 | cellular response to antibiotic                                   | 6/182 | 26/749 | 0,63546384  | 0,999954951 | 0,999954951 | MAPK13/LCN2/HDAC6/AHR/STAT6/EGR1         | 6 |
| GO:0038095 | Fc-epsilon receptor signaling pathway                             | 6/182 | 27/749 | 0,675250588 | 0,999954951 | 0,999954951 | FCER1G/PSMB8/PSME2/PSMB10/PSME1/NFKB1    | 6 |
| GO:0043370 | regulation of CD4-positive, alpha-beta T cell differentiation     | 6/182 | 27/749 | 0,675250588 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/NFKBIZ/SOCS1/GATA3        | 6 |
| GO:0045666 | positive regulation of neuron differentiation                     | 6/182 | 27/749 | 0,675250588 | 0,999954951 | 0,999954951 | S100A9/BCL6/AGT/APOE/FN1/EPO             | 6 |
| GO:0045834 | positive regulation of lipid metabolic process                    | 6/182 | 27/749 | 0,675250588 | 0,999954951 | 0,999954951 | TNFRSF1A/TGFB1/AGT/LDLR/APOE/RGN         | 6 |



|            |                                                                   |       |        |             |             |             |                                           |   |
|------------|-------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|-------------------------------------------|---|
| GO:1903426 | regulation of reactive oxygen species biosynthetic process        | 6/182 | 27/749 | 0,675250588 | 0,999954951 | 0,999954951 | STAT3/ICAM1/AGT/TLR4/ITGB2/RGN            | 6 |
| GO:2001056 | positive regulation of cysteine-type endopeptidase activity       | 6/182 | 27/749 | 0,675250588 | 0,999954951 | 0,999954951 | S100A9/S100A8/BAX/MYC/TNFSF10/CASP4       | 6 |
| GO:0007600 | sensory perception                                                | 6/182 | 28/749 | 0,712176818 | 0,999954951 | 0,999954951 | MME/COL1A1/ICAM1/TGFB1/C5AR1/ADORA2A      | 6 |
| GO:0010975 | regulation of neuron projection development                       | 6/182 | 28/749 | 0,712176818 | 0,999954951 | 0,999954951 | S100A9/AGT/APOE/FN1/EPO/GATA3             | 6 |
| GO:0016569 | covalent chromatin modification                                   | 6/182 | 28/749 | 0,712176818 | 0,999954951 | 0,999954951 | BCL6/MUC1/HDAC6/TGFB1/DNMT1/GATA3         | 6 |
| GO:0030316 | osteoclast differentiation                                        | 6/182 | 28/749 | 0,712176818 | 0,999954951 | 0,999954951 | LTF/FCER1G/TGFB1/TLR4/LILRB1/TMEM178A     | 6 |
| GO:0046209 | nitric oxide metabolic process                                    | 6/182 | 28/749 | 0,712176818 | 0,999954951 | 0,999954951 | ICAM1/AGT/TLR4/TLR2/ITGB2/RGN             | 6 |
| GO:0051216 | cartilage development                                             | 6/182 | 28/749 | 0,712176818 | 0,999954951 | 0,999954951 | HIF1A/TIMP1/COL1A1/MAF/TGFB1/TGFB1        | 6 |
| GO:0060348 | bone development                                                  | 6/182 | 28/749 | 0,712176818 | 0,999954951 | 0,999954951 | LTF/COL1A1/TGFB1/LILRB1/RGN/PTPN6         | 6 |
| GO:2001057 | reactive nitrogen species metabolic process                       | 6/182 | 28/749 | 0,712176818 | 0,999954951 | 0,999954951 | ICAM1/AGT/TLR4/TLR2/ITGB2/RGN             | 6 |
| GO:0032760 | positive regulation of tumor necrosis factor production           | 6/182 | 29/749 | 0,746157055 | 0,999954951 | 0,999954951 | FCER1G/LY96/TLR4/TLR2/CD14/IFNGR1         | 6 |
| GO:0042136 | neurotransmitter biosynthetic process                             | 6/182 | 29/749 | 0,746157055 | 0,999954951 | 0,999954951 | ICAM1/AGT/TLR4/ITGB2/SLC22A2/RGN          | 6 |
| GO:0050804 | modulation of chemical synaptic transmission                      | 6/182 | 29/749 | 0,746157055 | 0,999954951 | 0,999954951 | STAT3/MME/AGT/APOE/LILRB2/ADORA2A         | 6 |
| GO:0051384 | response to glucocorticoid                                        | 6/182 | 29/749 | 0,746157055 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/CDKN1A/ABCC2/ERRFI1/EPO       | 6 |
| GO:0061138 | morphogenesis of a branching epithelium                           | 6/182 | 29/749 | 0,746157055 | 0,999954951 | 0,999954951 | COL4A1/SOCS3/TGFB1/AGT/TNC/MYC            | 6 |
| GO:0072073 | kidney epithelium development                                     | 6/182 | 29/749 | 0,746157055 | 0,999954951 | 0,999954951 | CD24/STAT1/TGFB1/AGT/MYC/GATA3            | 6 |
| GO:0099177 | regulation of trans-synaptic signaling                            | 6/182 | 29/749 | 0,746157055 | 0,999954951 | 0,999954951 | STAT3/MME/AGT/APOE/LILRB2/ADORA2A         | 6 |
| GO:0032653 | regulation of interleukin-10 production                           | 6/182 | 30/749 | 0,777179753 | 0,999954951 | 0,999954951 | BCL3/FCER1G/JAK3/TLR4/TLR2/LILRB1         | 6 |
| GO:0042531 | positive regulation of tyrosine phosphorylation of STAT protein   | 6/182 | 31/749 | 0,805294342 | 0,999954951 | 0,999954951 | STAT3/SOCS3/TNFRSF1A/IL6R/EPO/IL6ST       | 6 |
| GO:0042542 | response to hydrogen peroxide                                     | 6/182 | 31/749 | 0,805294342 | 0,999954951 | 0,999954951 | MAPK13/LCN2/HDAC6/COL1A1/STAT1/STAT6      | 6 |
| GO:0046637 | regulation of alpha-beta T cell differentiation                   | 6/182 | 31/749 | 0,805294342 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/NFKBIZ/SOCS1/GATA3         | 6 |
| GO:1903557 | positive regulation of tumor necrosis factor superfamily cytokine | 6/182 | 31/749 | 0,805294342 | 0,999954951 | 0,999954951 | FCER1G/LY96/TLR4/TLR2/CD14/IFNGR1         | 6 |
| GO:0001763 | morphogenesis of a branching structure                            | 6/182 | 32/749 | 0,830598678 | 0,999954951 | 0,999954951 | COL4A1/SOCS3/TGFB1/AGT/TNC/MYC            | 6 |
| GO:0006518 | peptide metabolic process                                         | 6/182 | 32/749 | 0,830598678 | 0,999954951 | 0,999954951 | BCL3/STAT3/MME/APOE/G6PD/IFNGR1           | 6 |
| GO:0022604 | regulation of cell morphogenesis                                  | 6/182 | 32/749 | 0,830598678 | 0,999954951 | 0,999954951 | ICAM1/APOE/LST1/FGD2/ITGB2/FN1            | 6 |
| GO:0043087 | regulation of GTPase activity                                     | 6/182 | 32/749 | 0,830598678 | 0,999954951 | 0,999954951 | BCL6/ICAM1/ARHGDIB/FGD2/ERRFI1/RGN        | 6 |
| GO:0048762 | mesenchymal cell differentiation                                  | 6/182 | 32/749 | 0,830598678 | 0,999954951 | 0,999954951 | HIF1A/COL1A1/STAT1/TGFB1/KITLG/FN1        | 6 |
| GO:0001935 | endothelial cell proliferation                                    | 6/182 | 35/749 | 0,891118286 | 0,999954951 | 0,999954951 | HIF1A/STAT3/NR4A1/STAT1/XBP1/APOE         | 6 |
| GO:0003007 | heart morphogenesis                                               | 6/182 | 36/749 | 0,906745818 | 0,999954951 | 0,999954951 | HIF1A/ADAMTS1/TGFB1/FKBP1A/MYOM2/GATA3    | 6 |
| GO:0034614 | cellular response to reactive oxygen species                      | 6/182 | 36/749 | 0,906745818 | 0,999954951 | 0,999954951 | SOD2/MAPK13/LCN2/HDAC6/STAT6/RGN          | 6 |
| GO:1903531 | negative regulation of secretion by cell                          | 6/182 | 36/749 | 0,906745818 | 0,999954951 | 0,999954951 | TNFRSF1A/APOE/TNFRSF1B/IL1R2/FN1/LILRB1   | 6 |
| GO:2000514 | regulation of CD4-positive, alpha-beta T cell activation          | 6/182 | 36/749 | 0,906745818 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/NFKBIZ/SOCS1/GATA3         | 6 |
| GO:0002688 | regulation of leukocyte chemotaxis                                | 6/182 | 37/749 | 0,920414164 | 0,999954951 | 0,999954951 | SLAMF8/IL6R/CMKLR1/C5AR1/SERPINE1/TNFSF14 | 6 |
| GO:0032990 | cell part morphogenesis                                           | 6/182 | 37/749 | 0,920414164 | 0,999954951 | 0,999954951 | HDAC6/BAX/APOE/FN1/GATA3/ADORA2A          | 6 |
| GO:0051048 | negative regulation of secretion                                  | 6/182 | 37/749 | 0,920414164 | 0,999954951 | 0,999954951 | TNFRSF1A/APOE/TNFRSF1B/IL1R2/FN1/LILRB1   | 6 |
| GO:2001236 | regulation of extrinsic apoptotic signaling pathway               | 6/182 | 38/749 | 0,932311576 | 0,999954951 | 0,999954951 | LTBR/ICAM1/AGT/TNFSF10/ATF3/SERPINE1      | 6 |
| GO:0018105 | peptidyl-serine phosphorylation                                   | 6/182 | 39/749 | 0,942620334 | 0,999954951 | 0,999954951 | MAPK13/HDAC6/TGFB1/BAX/TBK1/EPO           | 6 |
| GO:0018209 | peptidyl-serine modification                                      | 6/182 | 39/749 | 0,942620334 | 0,999954951 | 0,999954951 | MAPK13/HDAC6/TGFB1/BAX/TBK1/EPO           | 6 |
| GO:0034622 | cellular protein-containing complex assembly                      | 6/182 | 40/749 | 0,95151388  | 0,999954951 | 0,999954951 | HDAC6/ICAM1/TGFB1/FKBP1A/TLR4/MYOM2       | 6 |
| GO:0010632 | regulation of epithelial cell migration                           | 6/182 | 43/749 | 0,971268595 | 0,999954951 | 0,999954951 | HIF1A/HDAC6/TGFB1/AGT/APOE/GATA3          | 6 |
| GO:0048771 | tissue remodeling                                                 | 6/182 | 43/749 | 0,971268595 | 0,999954951 | 0,999954951 | HIF1A/TIMP1/TGFB1/BAX/AGT/NOX4            | 6 |
| GO:0050871 | positive regulation of B cell activation                          | 6/182 | 43/749 | 0,971268595 | 0,999954951 | 0,999954951 | BCL6/TGFB1/XBP1/CDKN1A/STAT6/TLR4         | 6 |
| GO:0007178 | transmembrane receptor protein serine/threonine kinase signal     | 6/182 | 45/749 | 0,980013363 | 0,999954951 | 0,999954951 | SOST/COL3A1/TGFB1/EGR1/FKBP1A/GDF15       | 6 |
| GO:0050921 | positive regulation of chemotaxis                                 | 6/182 | 46/749 | 0,983395995 | 0,999954951 | 0,999954951 | TGFB1/IL6R/CMKLR1/C5AR1/SERPINE1/TNFSF14  | 6 |
| GO:0007420 | brain development                                                 | 6/182 | 51/749 | 0,993665522 | 0,999954951 | 0,999954951 | HIF1A/COL4A1/COL3A1/BAX/C5AR1/G6PD        | 6 |
| GO:0006879 | cellular iron ion homeostasis                                     | 5/182 | 10/749 | 0,068878288 | 0,999954951 | 0,999954951 | HIF1A/LTF/LCN2/SLC11A1/MYC                | 5 |
| GO:0008203 | cholesterol metabolic process                                     | 5/182 | 10/749 | 0,068878288 | 0,999954951 | 0,999954951 | APOL1/LDLR/APOE/APOL2/G6PD                | 5 |
| GO:0016125 | sterol metabolic process                                          | 5/182 | 10/749 | 0,068878288 | 0,999954951 | 0,999954951 | APOL1/LDLR/APOE/APOL2/G6PD                | 5 |
| GO:0035456 | response to interferon-beta                                       | 5/182 | 10/749 | 0,068878288 | 0,999954951 | 0,999954951 | IFITM3/IFITM2/IFITM1/IFNAR2/STAT1         | 5 |
| GO:0051926 | negative regulation of calcium ion transport                      | 5/182 | 10/749 | 0,068878288 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/LILRB2/LILRB1/EPO             | 5 |
| GO:0055067 | monovalent inorganic cation homeostasis                           | 5/182 | 10/749 | 0,068878288 | 0,999954951 | 0,999954951 | AGT/SLC12A3/SLAMF8/SLC11A1/ADORA2A        | 5 |
| GO:0071322 | cellular response to carbohydrate stimulus                        | 5/182 | 10/749 | 0,068878288 | 0,999954951 | 0,999954951 | HIF1A/MAPK13/ICAM1/XBP1/NOX4              | 5 |
| GO:0071479 | cellular response to ionizing radiation                           | 5/182 | 10/749 | 0,068878288 | 0,999954951 | 0,999954951 | TGFB1/CDKN1A/EGR1/NOX4/GATA3              | 5 |
| GO:0071548 | response to dexamethasone                                         | 5/182 | 10/749 | 0,068878288 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/ABCC2/ERRFI1/EPO              | 5 |
| GO:0072111 | cell proliferation involved in kidney development                 | 5/182 | 10/749 | 0,068878288 | 0,999954951 | 0,999954951 | STAT1/EGR1/IL6R/MYC/GATA3                 | 5 |
| GO:1902652 | secondary alcohol metabolic process                               | 5/182 | 10/749 | 0,068878288 | 0,999954951 | 0,999954951 | APOL1/LDLR/APOE/APOL2/G6PD                | 5 |
| GO:0030195 | negative regulation of blood coagulation                          | 5/182 | 11/749 | 0,102085117 | 0,999954951 | 0,999954951 | SERPING1/APOE/SERPINE1/THBD/PLAUR         | 5 |
| GO:0034644 | cellular response to UV                                           | 5/182 | 11/749 | 0,102085117 | 0,999954951 | 0,999954951 | MAPK13/MME/BAX/CDKN1A/MYC                 | 5 |
| GO:0035023 | regulation of Rho protein signal transduction                     | 5/182 | 11/749 | 0,102085117 | 0,999954951 | 0,999954951 | BCL6/COL3A1/APOE/ARHGDIB/FGD2             | 5 |

|            |                                                                          |       |        |             |             |             |                                   |   |
|------------|--------------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|-----------------------------------|---|
| GO:0050819 | negative regulation of coagulation                                       | 5/182 | 11/749 | 0,102085117 | 0,999954951 | 0,999954951 | SERPING1/APOE/SERPINE1/THBD/PLAUR | 5 |
| GO:0060218 | hematopoietic stem cell differentiation                                  | 5/182 | 11/749 | 0,102085117 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/PSME1/GATA3    | 5 |
| GO:0061082 | myeloid leukocyte cytokine production                                    | 5/182 | 11/749 | 0,102085117 | 0,999954951 | 0,999954951 | BCL6/FCER1G/TGFB1/TLR4/LILRB1     | 5 |
| GO:0061180 | mammary gland epithelium development                                     | 5/182 | 11/749 | 0,102085117 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/BAX/STAT6/GATA3       | 5 |
| GO:0071482 | cellular response to light stimulus                                      | 5/182 | 11/749 | 0,102085117 | 0,999954951 | 0,999954951 | MAPK13/MME/BAX/CDKN1A/MYC         | 5 |
| GO:1900047 | negative regulation of hemostasis                                        | 5/182 | 11/749 | 0,102085117 | 0,999954951 | 0,999954951 | SERPING1/APOE/SERPINE1/THBD/PLAUR | 5 |
| GO:1900407 | regulation of cellular response to oxidative stress                      | 5/182 | 11/749 | 0,102085117 | 0,999954951 | 0,999954951 | HIF1A/SOD2/HDAC6/TLR4/RGN         | 5 |
| GO:1902882 | regulation of response to oxidative stress                               | 5/182 | 11/749 | 0,102085117 | 0,999954951 | 0,999954951 | HIF1A/SOD2/HDAC6/TLR4/RGN         | 5 |
| GO:0010575 | positive regulation of vascular endothelial growth factor production     | 5/182 | 12/749 | 0,141752044 | 0,999954951 | 0,999954951 | HIF1A/C3/TGFB1/C5AR1/IL6ST        | 5 |
| GO:0016051 | carbohydrate biosynthetic process                                        | 5/182 | 12/749 | 0,141752044 | 0,999954951 | 0,999954951 | TGFB1/G6PD/ATF3/NFKB1/RGN         | 5 |
| GO:0030258 | lipid modification                                                       | 5/182 | 12/749 | 0,141752044 | 0,999954951 | 0,999954951 | ALDH3A2/SOCS3/SOCS1/AGT/APOE      | 5 |
| GO:0048143 | astrocyte activation                                                     | 5/182 | 12/749 | 0,141752044 | 0,999954951 | 0,999954951 | C1QA/LDLR/C5AR1/IFNGR1/ADORA2A    | 5 |
| GO:0061333 | renal tubule morphogenesis                                               | 5/182 | 12/749 | 0,141752044 | 0,999954951 | 0,999954951 | COL4A1/TGFB1/AGT/MYC/GATA3        | 5 |
| GO:0072088 | nephron epithelium morphogenesis                                         | 5/182 | 12/749 | 0,141752044 | 0,999954951 | 0,999954951 | STAT1/TGFB1/AGT/MYC/GATA3         | 5 |
| GO:0006694 | steroid biosynthetic process                                             | 5/182 | 13/749 | 0,186962653 | 0,999954951 | 0,999954951 | HSD11B1/EGR1/APOE/G6PD/NFKB1      | 5 |
| GO:0010573 | vascular endothelial growth factor production                            | 5/182 | 13/749 | 0,186962653 | 0,999954951 | 0,999954951 | HIF1A/C3/TGFB1/C5AR1/IL6ST        | 5 |
| GO:0010574 | regulation of vascular endothelial growth factor production              | 5/182 | 13/749 | 0,186962653 | 0,999954951 | 0,999954951 | HIF1A/C3/TGFB1/C5AR1/IL6ST        | 5 |
| GO:0033619 | membrane protein proteolysis                                             | 5/182 | 13/749 | 0,186962653 | 0,999954951 | 0,999954951 | TIMP1/TGFB1/APOE/TNFRSF1B/NFKB1   | 5 |
| GO:0045685 | regulation of glial cell differentiation                                 | 5/182 | 13/749 | 0,186962653 | 0,999954951 | 0,999954951 | TGFB1/LDLR/TLR2/TNFRSF1B/IL6ST    | 5 |
| GO:0055072 | iron ion homeostasis                                                     | 5/182 | 13/749 | 0,186962653 | 0,999954951 | 0,999954951 | HIF1A/LTF/LCN2/SLC11A1/MYC        | 5 |
| GO:1903050 | regulation of proteolysis involved in cellular protein catabolic process | 5/182 | 13/749 | 0,186962653 | 0,999954951 | 0,999954951 | PSME2/APOE/TRIB1/PSME1/RGN        | 5 |
| GO:1904705 | regulation of vascular smooth muscle cell proliferation                  | 5/182 | 13/749 | 0,186962653 | 0,999954951 | 0,999954951 | SOD2/ADAMTS1/DNMT1/CDKN1A/AGT     | 5 |
| GO:1990874 | vascular smooth muscle cell proliferation                                | 5/182 | 13/749 | 0,186962653 | 0,999954951 | 0,999954951 | SOD2/ADAMTS1/DNMT1/CDKN1A/AGT     | 5 |
| GO:2000378 | negative regulation of reactive oxygen species metabolic process         | 5/182 | 13/749 | 0,186962653 | 0,999954951 | 0,999954951 | HIF1A/STAT3/HDAC6/G6PD/RGN        | 5 |
| GO:0001961 | positive regulation of cytokine-mediated signaling pathway               | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | HIF1A/IL1R1/IRF7/TBK1/CASP4       | 5 |
| GO:0006367 | transcription initiation from RNA polymerase II promoter                 | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | NR4A1/BAX/CDKN1A/RORC/HNF1A       | 5 |
| GO:0014910 | regulation of smooth muscle cell migration                               | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | ADAMTS1/AGT/TRIB1/NOX4/SERPINE1   | 5 |
| GO:0035150 | regulation of tube size                                                  | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | SOD2/ICAM1/AGT/APOE/ADORA2A       | 5 |
| GO:0035296 | regulation of tube diameter                                              | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | SOD2/ICAM1/AGT/APOE/ADORA2A       | 5 |
| GO:0042036 | negative regulation of cytokine biosynthetic process                     | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | BCL3/SIGIRR/ERRF1/LILRB1/NFKB1    | 5 |
| GO:0043271 | negative regulation of ion transport                                     | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/LILRB2/LILRB1/EPO     | 5 |
| GO:0061097 | regulation of protein tyrosine kinase activity                           | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | CD24/FCGR1A/AGT/ERRF1/NOX4        | 5 |
| GO:0070265 | necrotic cell death                                                      | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | BAX/LY96/TLR4/BIRC3/CD14          | 5 |
| GO:0070670 | response to interleukin-4                                                | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | JAK3/IL4R/XBP1/STAT6/GATA3        | 5 |
| GO:0071353 | cellular response to interleukin-4                                       | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | JAK3/IL4R/XBP1/STAT6/GATA3        | 5 |
| GO:0072028 | nephron morphogenesis                                                    | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | STAT1/TGFB1/AGT/MYC/GATA3         | 5 |
| GO:0097300 | programmed necrotic cell death                                           | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | BAX/LY96/TLR4/BIRC3/CD14          | 5 |
| GO:0097746 | regulation of blood vessel diameter                                      | 5/182 | 14/749 | 0,236561912 | 0,999954951 | 0,999954951 | SOD2/ICAM1/AGT/APOE/ADORA2A       | 5 |
| GO:0000209 | protein polyubiquitination                                               | 5/182 | 15/749 | 0,289278838 | 0,999954951 | 0,999954951 | PSMB8/HDAC6/PSME2/PSMB10/PSME1    | 5 |
| GO:0014909 | smooth muscle cell migration                                             | 5/182 | 15/749 | 0,289278838 | 0,999954951 | 0,999954951 | ADAMTS1/AGT/TRIB1/NOX4/SERPINE1   | 5 |
| GO:0031058 | positive regulation of histone modification                              | 5/182 | 15/749 | 0,289278838 | 0,999954951 | 0,999954951 | BCL6/MUC1/TGFB1/DNMT1/GATA3       | 5 |
| GO:0031100 | animal organ regeneration                                                | 5/182 | 15/749 | 0,289278838 | 0,999954951 | 0,999954951 | NNMT/TGFB1/CDKN1A/C5AR1/RGN       | 5 |
| GO:0048146 | positive regulation of fibroblast proliferation                          | 5/182 | 15/749 | 0,289278838 | 0,999954951 | 0,999954951 | TGFB1/CDKN1A/AGT/MYC/FN1          | 5 |
| GO:0048167 | regulation of synaptic plasticity                                        | 5/182 | 15/749 | 0,289278838 | 0,999954951 | 0,999954951 | MME/AGT/APOE/LILRB2/ADORA2A       | 5 |
| GO:0050680 | negative regulation of epithelial cell proliferation                     | 5/182 | 15/749 | 0,289278838 | 0,999954951 | 0,999954951 | STAT1/TGFB1/APOE/GATA3/RGN        | 5 |
| GO:0051591 | response to cAMP                                                         | 5/182 | 15/749 | 0,289278838 | 0,999954951 | 0,999954951 | COL1A1/STAT1/AHR/NOX4/THBD        | 5 |
| GO:0060993 | kidney morphogenesis                                                     | 5/182 | 15/749 | 0,289278838 | 0,999954951 | 0,999954951 | STAT1/TGFB1/AGT/MYC/GATA3         | 5 |
| GO:1905269 | positive regulation of chromatin organization                            | 5/182 | 15/749 | 0,289278838 | 0,999954951 | 0,999954951 | BCL6/MUC1/TGFB1/DNMT1/GATA3       | 5 |
| GO:2001252 | positive regulation of chromosome organization                           | 5/182 | 15/749 | 0,289278838 | 0,999954951 | 0,999954951 | BCL6/MUC1/TGFB1/DNMT1/GATA3       | 5 |
| GO:0006520 | cellular amino acid metabolic process                                    | 5/182 | 16/749 | 0,343830476 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/NOX4/PSME1     | 5 |
| GO:0010822 | positive regulation of mitochondrion organization                        | 5/182 | 16/749 | 0,343830476 | 0,999954951 | 0,999954951 | HIF1A/HDAC6/BAX/TNFSF10/PLAUR     | 5 |
| GO:0014812 | muscle cell migration                                                    | 5/182 | 16/749 | 0,343830476 | 0,999954951 | 0,999954951 | ADAMTS1/AGT/TRIB1/NOX4/SERPINE1   | 5 |
| GO:0048592 | eye morphogenesis                                                        | 5/182 | 16/749 | 0,343830476 | 0,999954951 | 0,999954951 | HIF1A/STAT3/MEGF11/BAX/FJX1       | 5 |
| GO:0060041 | retina development in camera-type eye                                    | 5/182 | 16/749 | 0,343830476 | 0,999954951 | 0,999954951 | HIF1A/COL4A1/MEGF11/BAX/FJX1      | 5 |
| GO:0007266 | Rho protein signal transduction                                          | 5/182 | 17/749 | 0,399002301 | 0,999954951 | 0,999954951 | BCL6/COL3A1/APOE/ARHGDIB/FGD2     | 5 |
| GO:0019693 | ribose phosphate metabolic process                                       | 5/182 | 17/749 | 0,399002301 | 0,999954951 | 0,999954951 | HIF1A/STAT3/IMPDH1/TGFB1/G6PD     | 5 |
| GO:0031330 | negative regulation of cellular catabolic process                        | 5/182 | 17/749 | 0,399002301 | 0,999954951 | 0,999954951 | TIMP1/STAT3/MYD88/SLC11A1/RGN     | 5 |
| GO:0043161 | proteasome-mediated ubiquitin-dependent protein catabolic process        | 5/182 | 17/749 | 0,399002301 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/TRIB1/PSME1    | 5 |
| GO:0050829 | defense response to Gram-negative bacterium                              | 5/182 | 17/749 | 0,399002301 | 0,999954951 | 0,999954951 | LTF/TLR4/IL6R/SLC11A1/SERPINE1    | 5 |

|            |                                                                   |       |        |             |             |             |                                    |   |
|------------|-------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|------------------------------------|---|
| GO:0120031 | plasma membrane bounded cell projection assembly                  | 5/182 | 17/749 | 0,399002301 | 0,999954951 | 0,999954951 | EHD3/HDAC6/ICAM1/EMP3/FGD2         | 5 |
| GO:0002260 | lymphocyte homeostasis                                            | 5/182 | 18/749 | 0,453704504 | 0,999954951 | 0,999954951 | HIF1A/JAK3/TGFB1/BAX/TNFSF14       | 5 |
| GO:0031056 | regulation of histone modification                                | 5/182 | 18/749 | 0,453704504 | 0,999954951 | 0,999954951 | BCL6/MUC1/TGFB1/DNMT1/GATA3        | 5 |
| GO:0046683 | response to organophosphorus                                      | 5/182 | 18/749 | 0,453704504 | 0,999954951 | 0,999954951 | COL1A1/STAT1/AHR/NOX4/THBD         | 5 |
| GO:0006352 | DNA-templated transcription, initiation                           | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | NR4A1/BAX/CDKN1A/RORC/HNF1A        | 5 |
| GO:0006919 | activation of cysteine-type endopeptidase activity involved in ap | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | S100A9/S100A8/BAX/TNFSF10/CASP4    | 5 |
| GO:0008584 | male gonad development                                            | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | ICAM1/BAX/KITLG/TNFSF10/GATA3      | 5 |
| GO:0008585 | female gonad development                                          | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | ADAMTS1/ICAM1/BAX/KITLG/TIPARP     | 5 |
| GO:0010522 | regulation of calcium ion transport into cytosol                  | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | TGFB1/BAX/FKBP1A/EPO/PTPN6         | 5 |
| GO:0010821 | regulation of mitochondrion organization                          | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | HIF1A/HDAC6/BAX/TNFSF10/PLAUR      | 5 |
| GO:0010976 | positive regulation of neuron projection development              | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | S100A9/AGT/APOE/FN1/EPO            | 5 |
| GO:0017038 | protein import                                                    | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | STAT3/TGFB1/CDKN1A/AGT/APOE        | 5 |
| GO:0030308 | negative regulation of cell growth                                | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | BCL6/TGFB1/CDKN1A/AGT/G6PD         | 5 |
| GO:0032720 | negative regulation of tumor necrosis factor production           | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | BCL3/TLR4/ERRFI1/LILRB1/PTPN6      | 5 |
| GO:0032963 | collagen metabolic process                                        | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | HIF1A/COL1A1/TGFB1/CTSS/ERRFI1     | 5 |
| GO:0046545 | development of primary female sexual characteristics              | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | ADAMTS1/ICAM1/BAX/KITLG/TIPARP     | 5 |
| GO:0046546 | development of primary male sexual characteristics                | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | ICAM1/BAX/KITLG/TNFSF10/GATA3      | 5 |
| GO:0048588 | developmental cell growth                                         | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | HDAC6/AGT/APOE/G6PD/FN1            | 5 |
| GO:0055007 | cardiac muscle cell differentiation                               | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | TGFB1/AGT/NOX4/G6PD/MYOM2          | 5 |
| GO:0071675 | regulation of mononuclear cell migration                          | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | TGFB1/SLAMF8/CMKLR1/C5AR1/SERPINE1 | 5 |
| GO:0071897 | DNA biosynthetic process                                          | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | CDKN1A/MYC/NOX4/ISG15/RGN          | 5 |
| GO:0090068 | positive regulation of cell cycle process                         | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | ADAMTS1/MUC1/TGFB1/BAX/CDKN1A      | 5 |
| GO:1902275 | regulation of chromatin organization                              | 5/182 | 19/749 | 0,50700628  | 0,999954951 | 0,999954951 | BCL6/MUC1/TGFB1/DNMT1/GATA3        | 5 |
| GO:0008360 | regulation of cell shape                                          | 5/182 | 20/749 | 0,558151645 | 0,999954951 | 0,999954951 | ICAM1/LST1/FGD2/ITGB2/FN1          | 5 |
| GO:0015849 | organic acid transport                                            | 5/182 | 20/749 | 0,558151645 | 0,999954951 | 0,999954951 | AGT/APOE/SLC11A1/ABCC2/ADORA2A     | 5 |
| GO:0046942 | carboxylic acid transport                                         | 5/182 | 20/749 | 0,558151645 | 0,999954951 | 0,999954951 | AGT/APOE/SLC11A1/ABCC2/ADORA2A     | 5 |
| GO:0050830 | defense response to Gram-positive bacterium                       | 5/182 | 20/749 | 0,558151645 | 0,999954951 | 0,999954951 | GBP2/MYD88/TLR2/TBK1/C5AR1         | 5 |
| GO:0055123 | digestive system development                                      | 5/182 | 20/749 | 0,558151645 | 0,999954951 | 0,999954951 | HIF1A/COL3A1/TGFB1/XBP1/CDKN1A     | 5 |
| GO:0060560 | developmental growth involved in morphogenesis                    | 5/182 | 20/749 | 0,558151645 | 0,999954951 | 0,999954951 | HDAC6/TGFB1/TNC/APOE/FN1           | 5 |
| GO:0072331 | signal transduction by p53 class mediator                         | 5/182 | 20/749 | 0,558151645 | 0,999954951 | 0,999954951 | BCL3/MUC1/BAX/CDKN1A/MAPK11        | 5 |
| GO:0106106 | cold-induced thermogenesis                                        | 5/182 | 20/749 | 0,558151645 | 0,999954951 | 0,999954951 | LCN2/IL4R/STAT6/TLR4/CMKLR1        | 5 |
| GO:0120161 | regulation of cold-induced thermogenesis                          | 5/182 | 20/749 | 0,558151645 | 0,999954951 | 0,999954951 | LCN2/IL4R/STAT6/TLR4/CMKLR1        | 5 |
| GO:1990845 | adaptive thermogenesis                                            | 5/182 | 20/749 | 0,558151645 | 0,999954951 | 0,999954951 | LCN2/IL4R/STAT6/TLR4/CMKLR1        | 5 |
| GO:0001890 | placenta development                                              | 5/182 | 21/749 | 0,606560839 | 0,999954951 | 0,999954951 | HIF1A/SOCS3/MME/KRT8/KRT19         | 5 |
| GO:0016485 | protein processing                                                | 5/182 | 21/749 | 0,606560839 | 0,999954951 | 0,999954951 | MME/CTSS/IL1R2/BIRC3/SERPINE1      | 5 |
| GO:0030031 | cell projection assembly                                          | 5/182 | 21/749 | 0,606560839 | 0,999954951 | 0,999954951 | EHD3/HDAC6/ICAM1/EMP3/FGD2         | 5 |
| GO:0034248 | regulation of cellular amide metabolic process                    | 5/182 | 21/749 | 0,606560839 | 0,999954951 | 0,999954951 | BCL3/STAT3/TNFRSF1A/APOE/IFNGR1    | 5 |
| GO:0097028 | dendritic cell differentiation                                    | 5/182 | 21/749 | 0,606560839 | 0,999954951 | 0,999954951 | LTBR/RELB/TGFB1/LILRB2/LILRB1      | 5 |
| GO:0002823 | negative regulation of adaptive immune response based on som      | 5/182 | 22/749 | 0,651821245 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/LILRB1/PTPN6        | 5 |
| GO:0002825 | regulation of T-helper 1 type immune response                     | 5/182 | 22/749 | 0,651821245 | 0,999954951 | 0,999954951 | IL1R1/JAK3/IL4R/IL6R/SLC11A1       | 5 |
| GO:0006753 | nucleoside phosphate metabolic process                            | 5/182 | 22/749 | 0,651821245 | 0,999954951 | 0,999954951 | HIF1A/STAT3/NNMT/IMPDH1/TGFB1      | 5 |
| GO:0009117 | nucleotide metabolic process                                      | 5/182 | 22/749 | 0,651821245 | 0,999954951 | 0,999954951 | HIF1A/STAT3/NNMT/IMPDH1/TGFB1      | 5 |
| GO:0030100 | regulation of endocytosis                                         | 5/182 | 22/749 | 0,651821245 | 0,999954951 | 0,999954951 | C3/APOE/LILRB1/CD14/SERPINE1       | 5 |
| GO:0046660 | female sex differentiation                                        | 5/182 | 22/749 | 0,651821245 | 0,999954951 | 0,999954951 | ADAMTS1/ICAM1/BAX/KITLG/TIPARP     | 5 |
| GO:0090407 | organophosphate biosynthetic process                              | 5/182 | 22/749 | 0,651821245 | 0,999954951 | 0,999954951 | STAT3/NNMT/IMPDH1/TGFB1/G6PD       | 5 |
| GO:0006470 | protein dephosphorylation                                         | 5/182 | 23/749 | 0,693671384 | 0,999954951 | 0,999954951 | TGFB1/FKBP1A/LILRB2/RGN/PTPN6      | 5 |
| GO:0042476 | odontogenesis                                                     | 5/182 | 23/749 | 0,693671384 | 0,999954951 | 0,999954951 | COL1A1/TGFB1/BAX/TNC/SERPINE1      | 5 |
| GO:0045428 | regulation of nitric oxide biosynthetic process                   | 5/182 | 23/749 | 0,693671384 | 0,999954951 | 0,999954951 | ICAM1/AGT/TLR4/ITGB2/RGN           | 5 |
| GO:0046661 | male sex differentiation                                          | 5/182 | 23/749 | 0,693671384 | 0,999954951 | 0,999954951 | ICAM1/BAX/KITLG/TNFSF10/GATA3      | 5 |
| GO:0050764 | regulation of phagocytosis                                        | 5/182 | 23/749 | 0,693671384 | 0,999954951 | 0,999954951 | C3/FCER1G/TGFB1/TLR2/SLC11A1       | 5 |
| GO:0050768 | negative regulation of neurogenesis                               | 5/182 | 23/749 | 0,693671384 | 0,999954951 | 0,999954951 | STAT3/COL3A1/TGFB1/LDLR/APOE       | 5 |
| GO:0051640 | organelle localization                                            | 5/182 | 23/749 | 0,693671384 | 0,999954951 | 0,999954951 | HIF1A/FCER1G/HDAC6/IL4R/CD59       | 5 |
| GO:0055002 | striated muscle cell development                                  | 5/182 | 23/749 | 0,693671384 | 0,999954951 | 0,999954951 | KRT8/AGT/KRT19/G6PD/MYOM2          | 5 |
| GO:2000117 | negative regulation of cysteine-type endopeptidase activity       | 5/182 | 23/749 | 0,693671384 | 0,999954951 | 0,999954951 | LTF/BIRC3/ADORA2A/TNFSF14/PLAUR    | 5 |
| GO:0003206 | cardiac chamber morphogenesis                                     | 5/182 | 24/749 | 0,731980917 | 0,999954951 | 0,999954951 | HIF1A/ADAMTS1/TGFB1/FKBP1A/GATA3   | 5 |
| GO:0007050 | cell cycle arrest                                                 | 5/182 | 24/749 | 0,731980917 | 0,999954951 | 0,999954951 | MUC1/TGFB1/BAX/CDKN1A/MYC          | 5 |
| GO:0008544 | epidermis development                                             | 5/182 | 24/749 | 0,731980917 | 0,999954951 | 0,999954951 | ALDH3A2/PLAAT4/KRT8/KRT19/ERRFI1   | 5 |
| GO:0022612 | gland morphogenesis                                               | 5/182 | 24/749 | 0,731980917 | 0,999954951 | 0,999954951 | TGFB1/XBP1/BAX/STAT6/TNC           | 5 |
| GO:0048754 | branching morphogenesis of an epithelial tube                     | 5/182 | 24/749 | 0,731980917 | 0,999954951 | 0,999954951 | COL4A1/TGFB1/AGT/TNC/MYC           | 5 |

|            |                                                                        |       |        |             |             |             |                                    |   |
|------------|------------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|------------------------------------|---|
| GO:0051054 | positive regulation of DNA metabolic process                           | 5/182 | 24/749 | 0,731980917 | 0,999954951 | 0,999954951 | TGFB1/BAX/STAT6/MYC/NOX4           | 5 |
| GO:0055086 | nucleobase-containing small molecule metabolic process                 | 5/182 | 24/749 | 0,731980917 | 0,999954951 | 0,999954951 | HIF1A/STAT3/NNMT/IMPDH1/TGFB1      | 5 |
| GO:0070925 | organelle assembly                                                     | 5/182 | 24/749 | 0,731980917 | 0,999954951 | 0,999954951 | EHD3/KRT8/HDAC6/KRT19/MYOM2        | 5 |
| GO:1901216 | positive regulation of neuron death                                    | 5/182 | 24/749 | 0,731980917 | 0,999954951 | 0,999954951 | C1QA/BAX/EGR1/TLR4/ITGB2           | 5 |
| GO:0002720 | positive regulation of cytokine production involved in immune response | 5/182 | 25/749 | 0,766728984 | 0,999954951 | 0,999954951 | FCER1G/IL1R1/TLR4/LILRB1/GATA3     | 5 |
| GO:0002820 | negative regulation of adaptive immune response                        | 5/182 | 25/749 | 0,766728984 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/LILRB1/PTPN6        | 5 |
| GO:0003205 | cardiac chamber development                                            | 5/182 | 25/749 | 0,766728984 | 0,999954951 | 0,999954951 | HIF1A/ADAMTS1/TGFB1/FKBP1A/GATA3   | 5 |
| GO:0009895 | negative regulation of catabolic process                               | 5/182 | 25/749 | 0,766728984 | 0,999954951 | 0,999954951 | TIMP1/STAT3/MYD88/SLC11A1/RGN      | 5 |
| GO:0014013 | regulation of gliogenesis                                              | 5/182 | 25/749 | 0,766728984 | 0,999954951 | 0,999954951 | TGFB1/LDLR/TLR2/TNFRSF1B/IL6ST     | 5 |
| GO:0031214 | biomineral tissue development                                          | 5/182 | 25/749 | 0,766728984 | 0,999954951 | 0,999954951 | HIF1A/LTF/COL1A1/TGFB1/ISG15       | 5 |
| GO:0035821 | modulation of process of other organism                                | 5/182 | 25/749 | 0,766728984 | 0,999954951 | 0,999954951 | S100A9/LTF/SLPI/TGFB1/APOE         | 5 |
| GO:0042092 | type 2 immune response                                                 | 5/182 | 25/749 | 0,766728984 | 0,999954951 | 0,999954951 | BCL3/BCL6/IL4R/STAT6/GATA3         | 5 |
| GO:0055001 | muscle cell development                                                | 5/182 | 25/749 | 0,766728984 | 0,999954951 | 0,999954951 | KRT8/AGT/KRT19/G6PD/MYOM2          | 5 |
| GO:0110148 | biomineralization                                                      | 5/182 | 25/749 | 0,766728984 | 0,999954951 | 0,999954951 | HIF1A/LTF/COL1A1/TGFB1/ISG15       | 5 |
| GO:1902903 | regulation of supramolecular fiber organization                        | 5/182 | 25/749 | 0,766728984 | 0,999954951 | 0,999954951 | HDAC6/ICAM1/LDLR/APOE/NOX4         | 5 |
| GO:0000187 | activation of MAPK activity                                            | 5/182 | 26/749 | 0,79798259  | 0,999954951 | 0,999954951 | FPR1/TLR4/MAPK11/C5AR1/GDF15       | 5 |
| GO:0002064 | epithelial cell development                                            | 5/182 | 27/749 | 0,825876227 | 0,999954951 | 0,999954951 | HIF1A/TNFRSF1A/ICAM1/XBP1/CDKN1A   | 5 |
| GO:0006644 | phospholipid metabolic process                                         | 5/182 | 27/749 | 0,825876227 | 0,999954951 | 0,999954951 | PLAAT4/SOCS3/TGFB1/SOCS1/LDLR      | 5 |
| GO:0006809 | nitric oxide biosynthetic process                                      | 5/182 | 27/749 | 0,825876227 | 0,999954951 | 0,999954951 | ICAM1/AGT/TLR4/ITGB2/RGN           | 5 |
| GO:0045787 | positive regulation of cell cycle                                      | 5/182 | 27/749 | 0,825876227 | 0,999954951 | 0,999954951 | ADAMTS1/MUC1/TGFB1/BAX/CDKN1A      | 5 |
| GO:0048661 | positive regulation of smooth muscle cell proliferation                | 5/182 | 28/749 | 0,850593489 | 0,999954951 | 0,999954951 | ADAMTS1/STAT1/DNMT1/AGT/IL6R       | 5 |
| GO:0060401 | cytosolic calcium ion transport                                        | 5/182 | 28/749 | 0,850593489 | 0,999954951 | 0,999954951 | TGFB1/BAX/FKBP1A/EPO/PTPN6         | 5 |
| GO:0060402 | calcium ion transport into cytosol                                     | 5/182 | 28/749 | 0,850593489 | 0,999954951 | 0,999954951 | TGFB1/BAX/FKBP1A/EPO/PTPN6         | 5 |
| GO:0009914 | hormone transport                                                      | 5/182 | 29/749 | 0,87235108  | 0,999954951 | 0,999954951 | HIF1A/AGT/ABCC2/HNF1A/GATA3        | 5 |
| GO:0051099 | positive regulation of binding                                         | 5/182 | 29/749 | 0,87235108  | 0,999954951 | 0,999954951 | TGFB1/FKBP1A/APOE/GATA3/PLAUR      | 5 |
| GO:1901222 | regulation of NIK/NF-kappaB signaling                                  | 5/182 | 29/749 | 0,87235108  | 0,999954951 | 0,999954951 | BCL3/TLR4/TLR2/CD14/TNFSF14        | 5 |
| GO:0002637 | regulation of immunoglobulin production                                | 5/182 | 30/749 | 0,891385345 | 0,999954951 | 0,999954951 | BCL6/IL4R/TGFB1/XBP1/STAT6         | 5 |
| GO:0010506 | regulation of autophagy                                                | 5/182 | 30/749 | 0,891385345 | 0,999954951 | 0,999954951 | HIF1A/STAT3/HDAC6/XBP1/TBK1        | 5 |
| GO:0010594 | regulation of endothelial cell migration                               | 5/182 | 30/749 | 0,891385345 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/AGT/APOE/GATA3         | 5 |
| GO:0016311 | dephosphorylation                                                      | 5/182 | 30/749 | 0,891385345 | 0,999954951 | 0,999954951 | TGFB1/FKBP1A/LILRB2/RGN/PTPN6      | 5 |
| GO:0001936 | regulation of endothelial cell proliferation                           | 5/182 | 31/749 | 0,907941307 | 0,999954951 | 0,999954951 | HIF1A/STAT3/NR4A1/STAT1/APOE       | 5 |
| GO:0031334 | positive regulation of protein-containing complex assembly             | 5/182 | 31/749 | 0,907941307 | 0,999954951 | 0,999954951 | HDAC6/ICAM1/TGFB1/BAX/TLR4         | 5 |
| GO:0032945 | negative regulation of mononuclear cell proliferation                  | 5/182 | 31/749 | 0,907941307 | 0,999954951 | 0,999954951 | TGFB1/LILRB2/LST1/LILRB1/PTPN6     | 5 |
| GO:0043393 | regulation of protein binding                                          | 5/182 | 31/749 | 0,907941307 | 0,999954951 | 0,999954951 | SLPI/BAX/FKBP1A/APOE/IFIT1         | 5 |
| GO:0050672 | negative regulation of lymphocyte proliferation                        | 5/182 | 31/749 | 0,907941307 | 0,999954951 | 0,999954951 | TGFB1/LILRB2/LST1/LILRB1/PTPN6     | 5 |
| GO:0061564 | axon development                                                       | 5/182 | 31/749 | 0,907941307 | 0,999954951 | 0,999954951 | HDAC6/TNC/APOE/FN1/GATA3           | 5 |
| GO:0002690 | positive regulation of leukocyte chemotaxis                            | 5/182 | 32/749 | 0,922264017 | 0,999954951 | 0,999954951 | IL6R/CMKLR1/C5AR1/SERPINE1/TNFSF14 | 5 |
| GO:0070664 | negative regulation of leukocyte proliferation                         | 5/182 | 32/749 | 0,922264017 | 0,999954951 | 0,999954951 | TGFB1/LILRB2/LST1/LILRB1/PTPN6     | 5 |
| GO:0010634 | positive regulation of epithelial cell migration                       | 5/182 | 33/749 | 0,934591991 | 0,999954951 | 0,999954951 | HIF1A/HDAC6/TGFB1/AGT/GATA3        | 5 |
| GO:0048812 | neuron projection morphogenesis                                        | 5/182 | 33/749 | 0,934591991 | 0,999954951 | 0,999954951 | HDAC6/APOE/FN1/GATA3/ADORA2A       | 5 |
| GO:0090287 | regulation of cellular response to growth factor stimulus              | 5/182 | 34/749 | 0,945152465 | 0,999954951 | 0,999954951 | HIF1A/SOST/TGFB1/AGT/GATA3         | 5 |
| GO:0048858 | cell projection morphogenesis                                          | 5/182 | 35/749 | 0,954158162 | 0,999954951 | 0,999954951 | HDAC6/APOE/FN1/GATA3/ADORA2A       | 5 |
| GO:0072594 | establishment of protein localization to organelle                     | 5/182 | 35/749 | 0,954158162 | 0,999954951 | 0,999954951 | STAT3/TGFB1/BAX/CDKN1A/AGT         | 5 |
| GO:0120039 | plasma membrane bounded cell projection morphogenesis                  | 5/182 | 35/749 | 0,954158162 | 0,999954951 | 0,999954951 | HDAC6/APOE/FN1/GATA3/ADORA2A       | 5 |
| GO:0002709 | regulation of T cell mediated immunity                                 | 5/182 | 37/749 | 0,968272681 | 0,999954951 | 0,999954951 | IL1R1/PVR/TNFRSF1B/LILRB1/GATA3    | 5 |
| GO:0001894 | tissue homeostasis                                                     | 5/182 | 38/749 | 0,973721333 | 0,999954951 | 0,999954951 | SERPINA3/LTF/BAX/TLR4/NOX4         | 5 |
| GO:0001701 | in utero embryonic development                                         | 5/182 | 39/749 | 0,978295009 | 0,999954951 | 0,999954951 | HIF1A/SOCS3/KRT8/KRT19/GATA3       | 5 |
| GO:0002377 | immunoglobulin production                                              | 5/182 | 40/749 | 0,982120885 | 0,999954951 | 0,999954951 | BCL6/IL4R/TGFB1/XBP1/STAT6         | 5 |
| GO:0042100 | B cell proliferation                                                   | 5/182 | 40/749 | 0,982120885 | 0,999954951 | 0,999954951 | BCL6/BAX/AHR/CDKN1A/TLR4           | 5 |
| GO:0071559 | response to transforming growth factor beta                            | 5/182 | 40/749 | 0,982120885 | 0,999954951 | 0,999954951 | COL1A1/COL3A1/TGFB1/NOX4/GDF15     | 5 |
| GO:0071560 | cellular response to transforming growth factor beta stimulus          | 5/182 | 40/749 | 0,982120885 | 0,999954951 | 0,999954951 | COL1A1/COL3A1/TGFB1/NOX4/GDF15     | 5 |
| GO:0045165 | cell fate commitment                                                   | 5/182 | 42/749 | 0,987961537 | 0,999954951 | 0,999954951 | STAT3/STAT6/SLAMF8/RORC/GATA3      | 5 |
| GO:0000904 | cell morphogenesis involved in differentiation                         | 5/182 | 44/749 | 0,991972548 | 0,999954951 | 0,999954951 | HDAC6/APOE/FN1/GATA3/PTPN6         | 5 |
| GO:0001909 | leukocyte mediated cytotoxicity                                        | 5/182 | 45/749 | 0,993467446 | 0,999954951 | 0,999954951 | ICAM1/PVR/LILRB1/KIR3DL1/PTPN6     | 5 |
| GO:0051897 | positive regulation of protein kinase B signaling                      | 5/182 | 47/749 | 0,99570218  | 0,999954951 | 0,999954951 | TGFB1/KITLG/NOX4/GDF15/GATA3       | 5 |
| GO:0051896 | regulation of protein kinase B signaling                               | 5/182 | 50/749 | 0,997741682 | 0,999954951 | 0,999954951 | TGFB1/KITLG/NOX4/GDF15/GATA3       | 5 |
| GO:0043491 | protein kinase B signaling                                             | 5/182 | 58/749 | 0,999625543 | 0,999954951 | 0,999954951 | TGFB1/KITLG/NOX4/GDF15/GATA3       | 5 |
| GO:0010927 | cellular component assembly involved in morphogenesis                  | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | KRT8/TLR2/KRT19/MYOM2              | 4 |
| GO:0032350 | regulation of hormone metabolic process                                | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | HIF1A/EGR1/GATA3/NFKB1             | 4 |



|            |                                                                 |       |        |             |             |             |                               |   |
|------------|-----------------------------------------------------------------|-------|--------|-------------|-------------|-------------|-------------------------------|---|
| GO:0032411 | positive regulation of transporter activity                     | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | EHD3/ABCB1/CTSS/RGN           | 4 |
| GO:0032414 | positive regulation of ion transmembrane transporter activity   | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | EHD3/ABCB1/CTSS/RGN           | 4 |
| GO:0032480 | negative regulation of type I interferon production             | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | RELB/TBK1/LILRB1/ISG15        | 4 |
| GO:0035567 | non-canonical Wnt signaling pathway                             | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | PSMB8/PSME2/PSMB10/PSME1      | 4 |
| GO:0036473 | cell death in response to oxidative stress                      | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | HIF1A/SOD2/HDAC6/TLR4         | 4 |
| GO:0042632 | cholesterol homeostasis                                         | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | CD24/XBP1/LDLR/APOE           | 4 |
| GO:0045064 | T-helper 2 cell differentiation                                 | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | BCL3/BCL6/IL4R/GATA3          | 4 |
| GO:0045671 | negative regulation of osteoclast differentiation               | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | LTF/TLR4/LILRB1/TMEM178A      | 4 |
| GO:0045687 | positive regulation of glial cell differentiation               | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | TGFB1/TLR2/TNFRSF1B/IL6ST     | 4 |
| GO:0051353 | positive regulation of oxidoreductase activity                  | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | HIF1A/AGT/APOE/RGN            | 4 |
| GO:0055092 | sterol homeostasis                                              | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | CD24/XBP1/LDLR/APOE           | 4 |
| GO:0060338 | regulation of type I interferon-mediated signaling pathway      | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | IFNAR2/IRF7/TBK1/PTPN6        | 4 |
| GO:0060675 | ureteric bud morphogenesis                                      | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | TGFB1/AGT/MYC/GATA3           | 4 |
| GO:0070757 | interleukin-35-mediated signaling pathway                       | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | JAK1/STAT3/STAT1/IL6ST        | 4 |
| GO:0072078 | nephron tubule morphogenesis                                    | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | TGFB1/AGT/MYC/GATA3           | 4 |
| GO:0072171 | mesonephric tubule morphogenesis                                | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | TGFB1/AGT/MYC/GATA3           | 4 |
| GO:0072332 | intrinsic apoptotic signaling pathway by p53 class mediator     | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | BCL3/MUC1/BAX/CDKN1A          | 4 |
| GO:0090322 | regulation of superoxide metabolic process                      | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | TGFB1/AGT/ITGB2/RGN           | 4 |
| GO:1903510 | mucopolysaccharide metabolic process                            | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | LYVE1/TGFB1/VCAN/NFKB1        | 4 |
| GO:1905314 | semi-lunar valve development                                    | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | TNFRSF1A/TGFB1/TNFRSF1B/GATA3 | 4 |
| GO:2001238 | positive regulation of extrinsic apoptotic signaling pathway    | 4/182 | 10/749 | 0,206742596 | 0,999954951 | 0,999954951 | LTBR/AGT/TNFSF10/ATF3         | 4 |
| GO:0001678 | cellular glucose homeostasis                                    | 4/182 | 11/749 | 0,26654687  | 0,999954951 | 0,999954951 | HIF1A/ICAM1/XBP1/NOX4         | 4 |
| GO:0002888 | positive regulation of myeloid leukocyte mediated immunity      | 4/182 | 11/749 | 0,26654687  | 0,999954951 | 0,999954951 | C3/FCER1G/IL4R/ITGB2          | 4 |
| GO:0006836 | neurotransmitter transport                                      | 4/182 | 11/749 | 0,26654687  | 0,999954951 | 0,999954951 | FCER1G/LILRB1/SLC22A2/ADORA2A | 4 |
| GO:0007093 | mitotic cell cycle checkpoint                                   | 4/182 | 11/749 | 0,26654687  | 0,999954951 | 0,999954951 | MUC1/TGFB1/BAX/CDKN1A         | 4 |
| GO:0030216 | keratinocyte differentiation                                    | 4/182 | 11/749 | 0,26654687  | 0,999954951 | 0,999954951 | PLAAT4/KRT8/KRT19/ERRFI1      | 4 |
| GO:0032727 | positive regulation of interferon-alpha production              | 4/182 | 11/749 | 0,26654687  | 0,999954951 | 0,999954951 | STAT1/TLR4/IRF7/TBK1          | 4 |
| GO:0035967 | cellular response to topologically incorrect protein            | 4/182 | 11/749 | 0,26654687  | 0,999954951 | 0,999954951 | HDAC6/XBP1/BAX/ATF3           | 4 |
| GO:0042446 | hormone biosynthetic process                                    | 4/182 | 11/749 | 0,26654687  | 0,999954951 | 0,999954951 | HIF1A/HSD11B1/EGR1/NFKB1      | 4 |
| GO:0045591 | positive regulation of regulatory T cell differentiation        | 4/182 | 11/749 | 0,26654687  | 0,999954951 | 0,999954951 | BCL6/TGFB1/SOCS1/LILRB2       | 4 |
| GO:0046639 | negative regulation of alpha-beta T cell differentiation        | 4/182 | 11/749 | 0,26654687  | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/SOCS1          | 4 |
| GO:0055088 | lipid homeostasis                                               | 4/182 | 11/749 | 0,26654687  | 0,999954951 | 0,999954951 | CD24/XBP1/LDLR/APOE           | 4 |
| GO:0010742 | macrophage derived foam cell differentiation                    | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | STAT1/TGFB1/AGT/NFKB1         | 4 |
| GO:0031664 | regulation of lipopolysaccharide-mediated signaling pathway     | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | LTF/SIGIRR/LY96/TRIB1         | 4 |
| GO:0033032 | regulation of myeloid cell apoptotic process                    | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | FCER1G/KITLG/IRF7/EPO         | 4 |
| GO:0038111 | interleukin-7-mediated signaling pathway                        | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | JAK1/STAT3/JAK3/SOCS1         | 4 |
| GO:0043029 | T cell homeostasis                                              | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | JAK3/TGFB1/BAX/TNFSF14        | 4 |
| GO:0044070 | regulation of anion transport                                   | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | ABCB1/AGT/APOE/ADORA2A        | 4 |
| GO:0045063 | T-helper 1 cell differentiation                                 | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | RELB/JAK3/IL4R/STAT6          | 4 |
| GO:0046889 | positive regulation of lipid biosynthetic process               | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | TNFRSF1A/LDLR/APOE/RGN        | 4 |
| GO:0048593 | camera-type eye morphogenesis                                   | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | HIF1A/MEGF11/BAX/FJX1         | 4 |
| GO:0051279 | regulation of release of sequestered calcium ion into cytosol   | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | TGFB1/BAX/FKBP1A/PTPN6        | 4 |
| GO:0061136 | regulation of proteasomal protein catabolic process             | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | PSME2/APOE/TRIB1/PSME1        | 4 |
| GO:0071385 | cellular response to glucocorticoid stimulus                    | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/ABCC2/ERRFI1      | 4 |
| GO:0090077 | foam cell differentiation                                       | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | STAT1/TGFB1/AGT/NFKB1         | 4 |
| GO:0090303 | positive regulation of wound healing                            | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | XBP1/TLR4/SERPINE1/THBD       | 4 |
| GO:0098656 | anion transmembrane transport                                   | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | ABCB1/AGT/APOL1/SLC12A3       | 4 |
| GO:1900015 | regulation of cytokine production involved in inflammatory resp | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | IL17RA/TLR4/MYD88/IL1R2       | 4 |
| GO:1903036 | positive regulation of response to wounding                     | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | XBP1/TLR4/SERPINE1/THBD       | 4 |
| GO:1904646 | cellular response to amyloid-beta                               | 4/182 | 12/749 | 0,328944283 | 0,999954951 | 0,999954951 | ICAM1/VCAM1/TLR4/CASP4        | 4 |
| GO:0000075 | cell cycle checkpoint                                           | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | MUC1/TGFB1/BAX/CDKN1A         | 4 |
| GO:0002675 | positive regulation of acute inflammatory response              | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | OSMR/C3/FCER1G/IL6ST          | 4 |
| GO:0006022 | aminoglycan metabolic process                                   | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | LYVE1/TGFB1/VCAN/NFKB1        | 4 |
| GO:0009165 | nucleotide biosynthetic process                                 | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | STAT3/NNMT/IMPDH1/TGFB1       | 4 |
| GO:0016042 | lipid catabolic process                                         | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | ALDH3A2/PLAAT4/LDLR/APOE      | 4 |
| GO:0019835 | cytolysis                                                       | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | C9/TGFB1/APOL1/LILRB1         | 4 |
| GO:0030203 | glycosaminoglycan metabolic process                             | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | LYVE1/TGFB1/VCAN/NFKB1        | 4 |
| GO:0032607 | interferon-alpha production                                     | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | STAT1/TLR4/IRF7/TBK1          | 4 |
| GO:0032647 | regulation of interferon-alpha production                       | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | STAT1/TLR4/IRF7/TBK1          | 4 |

|            |                                                                        |       |        |             |             |             |                              |   |
|------------|------------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|------------------------------|---|
| GO:0035304 | regulation of protein dephosphorylation                                | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | TGFB1/FKBP1A/LILRB2/RGN      | 4 |
| GO:0035966 | response to topologically incorrect protein                            | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | HDAC6/XBP1/BAX/ATF3          | 4 |
| GO:0048839 | inner ear development                                                  | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | C1QB/MAF/TGFB1/GATA3         | 4 |
| GO:0070266 | necroptotic process                                                    | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | LY96/TLR4/BIRC3/CD14         | 4 |
| GO:0071384 | cellular response to corticosteroid stimulus                           | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | ICAM1/TGFB1/ABCC2/ERRFI1     | 4 |
| GO:0098760 | response to interleukin-7                                              | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | JAK1/STAT3/JAK3/SOCS1        | 4 |
| GO:0098761 | cellular response to interleukin-7                                     | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | JAK1/STAT3/JAK3/SOCS1        | 4 |
| GO:1901293 | nucleoside phosphate biosynthetic process                              | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | STAT3/NNMT/IMPDH1/TGFB1      | 4 |
| GO:1904427 | positive regulation of calcium ion transmembrane transport             | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | EHD3/BAX/G6PD/RGN            | 4 |
| GO:2001257 | regulation of cation channel activity                                  | 4/182 | 13/749 | 0,39204723  | 0,999954951 | 0,999954951 | EHD3/FKBP1A/CTSS/EPO         | 4 |
| GO:0001562 | response to protozoan                                                  | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | BCL3/GBP2/IL4R/SLC11A1       | 4 |
| GO:0001836 | release of cytochrome c from mitochondria                              | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | SOD2/BAX/TNFSF10/PLAUR       | 4 |
| GO:0001892 | embryonic placenta development                                         | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | HIF1A/SOCS3/KRT8/KRT19       | 4 |
| GO:0002534 | cytokine production involved in inflammatory response                  | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | IL17RA/TLR4/MYD88/IL1R2      | 4 |
| GO:0002886 | regulation of myeloid leukocyte mediated immunity                      | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | C3/FCER1G/IL4R/ITGB2         | 4 |
| GO:0006650 | glycerophospholipid metabolic process                                  | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | PLAAT4/SOCS3/SOCS1/LDLR      | 4 |
| GO:0007173 | epidermal growth factor receptor signaling pathway                     | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | TGFB1/AGT/ERRFI1/PLAUR       | 4 |
| GO:0010830 | regulation of myotube differentiation                                  | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | IL4R/XBP1/GDF15/TNFSF14      | 4 |
| GO:0030330 | DNA damage response, signal transduction by p53 class mediator         | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | BCL3/MUC1/BAX/CDKN1A         | 4 |
| GO:0032259 | methylation                                                            | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | NNMT/DNMT1/MYC/GATA3         | 4 |
| GO:0033028 | myeloid cell apoptotic process                                         | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | FCER1G/KITLG/IRF7/EPO        | 4 |
| GO:0033273 | response to vitamin                                                    | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | COL1A1/TGFB1/TNC/EPO         | 4 |
| GO:0042533 | tumor necrosis factor biosynthetic process                             | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | BCL3/TLR4/ERRFI1/LILRB1      | 4 |
| GO:0042534 | regulation of tumor necrosis factor biosynthetic process               | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | BCL3/TLR4/ERRFI1/LILRB1      | 4 |
| GO:0042832 | defense response to protozoan                                          | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | BCL3/GBP2/IL4R/SLC11A1       | 4 |
| GO:0050806 | positive regulation of synaptic transmission                           | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | MME/APOE/LILRB2/ADORA2A      | 4 |
| GO:0072330 | monocarboxylic acid biosynthetic process                               | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | XBP1/ALOX5/VCAN/RGN          | 4 |
| GO:1903305 | regulation of regulated secretory pathway                              | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | FCER1G/IL4R/ITGB2/ADORA2A    | 4 |
| GO:1903364 | positive regulation of cellular protein catabolic process              | 4/182 | 14/749 | 0,454241357 | 0,999954951 | 0,999954951 | LDLR/APOE/TRIB1/RGN          | 4 |
| GO:0001764 | neuron migration                                                       | 4/182 | 15/749 | 0,514227727 | 0,999954951 | 0,999954951 | STAT3/COL3A1/BAX/GATA3       | 4 |
| GO:0002673 | regulation of acute inflammatory response                              | 4/182 | 15/749 | 0,514227727 | 0,999954951 | 0,999954951 | OSMR/C3/FCER1G/IL6ST         | 4 |
| GO:0002719 | negative regulation of cytokine production involved in immune response | 4/182 | 15/749 | 0,514227727 | 0,999954951 | 0,999954951 | BCL6/JAK3/TGFB1/LILRB1       | 4 |
| GO:0009913 | epidermal cell differentiation                                         | 4/182 | 15/749 | 0,514227727 | 0,999954951 | 0,999954951 | PLAAT4/KRT8/KRT19/ERRFI1     | 4 |
| GO:0042770 | signal transduction in response to DNA damage                          | 4/182 | 15/749 | 0,514227727 | 0,999954951 | 0,999954951 | BCL3/MUC1/BAX/CDKN1A         | 4 |
| GO:0045807 | positive regulation of endocytosis                                     | 4/182 | 15/749 | 0,514227727 | 0,999954951 | 0,999954951 | C3/APOE/CD14/SERPINE1        | 4 |
| GO:0072089 | stem cell proliferation                                                | 4/182 | 15/749 | 0,514227727 | 0,999954951 | 0,999954951 | HIF1A/ABCB1/TGFB1/KITLG      | 4 |
| GO:1904645 | response to amyloid-beta                                               | 4/182 | 15/749 | 0,514227727 | 0,999954951 | 0,999954951 | ICAM1/VCAM1/TLR4/CASP4       | 4 |
| GO:2000278 | regulation of DNA biosynthetic process                                 | 4/182 | 15/749 | 0,514227727 | 0,999954951 | 0,999954951 | CDKN1A/MYC/NOX4/RGN          | 4 |
| GO:0003208 | cardiac ventricle morphogenesis                                        | 4/182 | 16/749 | 0,57102681  | 0,999954951 | 0,999954951 | HIF1A/TGFB1/FKBP1A/GATA3     | 4 |
| GO:0009150 | purine ribonucleotide metabolic process                                | 4/182 | 16/749 | 0,57102681  | 0,999954951 | 0,999954951 | HIF1A/STAT3/IMPDH1/TGFB1     | 4 |
| GO:0009259 | ribonucleotide metabolic process                                       | 4/182 | 16/749 | 0,57102681  | 0,999954951 | 0,999954951 | HIF1A/STAT3/IMPDH1/TGFB1     | 4 |
| GO:0030500 | regulation of bone mineralization                                      | 4/182 | 16/749 | 0,57102681  | 0,999954951 | 0,999954951 | HIF1A/LTF/TGFB1/ISG15        | 4 |
| GO:0038127 | ERBB signaling pathway                                                 | 4/182 | 16/749 | 0,57102681  | 0,999954951 | 0,999954951 | TGFB1/AGT/ERRFI1/PLAUR       | 4 |
| GO:0043583 | ear development                                                        | 4/182 | 16/749 | 0,57102681  | 0,999954951 | 0,999954951 | C1QB/MAF/TGFB1/GATA3         | 4 |
| GO:0045669 | positive regulation of osteoblast differentiation                      | 4/182 | 16/749 | 0,57102681  | 0,999954951 | 0,999954951 | LTF/IFITM1/IL6R/IL6ST        | 4 |
| GO:0051155 | positive regulation of striated muscle cell differentiation            | 4/182 | 16/749 | 0,57102681  | 0,999954951 | 0,999954951 | IL4R/TGFB1/GDF15/TNFSF14     | 4 |
| GO:0072659 | protein localization to plasma membrane                                | 4/182 | 16/749 | 0,57102681  | 0,999954951 | 0,999954951 | FCER1G/TNFRSF1A/EHD3/TGFB1   | 4 |
| GO:1901617 | organic hydroxy compound biosynthetic process                          | 4/182 | 16/749 | 0,57102681  | 0,999954951 | 0,999954951 | APOE/G6PD/GATA3/NFKB1        | 4 |
| GO:0001656 | metanephros development                                                | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | STAT1/EGR1/MYC/GATA3         | 4 |
| GO:0002714 | positive regulation of B cell mediated immunity                        | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | C3/FCER1G/TGFB1/STAT6        | 4 |
| GO:0002891 | positive regulation of immunoglobulin mediated immune response         | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | C3/FCER1G/TGFB1/STAT6        | 4 |
| GO:0005996 | monosaccharide metabolic process                                       | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | RORC/G6PD/ATF3/RGN           | 4 |
| GO:0006006 | glucose metabolic process                                              | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | RORC/G6PD/ATF3/RGN           | 4 |
| GO:0006606 | protein import into nucleus                                            | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | STAT3/TGFB1/CDKN1A/AGT       | 4 |
| GO:0010469 | regulation of signaling receptor activity                              | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | HDAC6/IL18BP/ERRFI1/SERPINE1 | 4 |
| GO:0017157 | regulation of exocytosis                                               | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | FCER1G/IL4R/ITGB2/ADORA2A    | 4 |
| GO:0019318 | hexose metabolic process                                               | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | RORC/G6PD/ATF3/RGN           | 4 |
| GO:0032535 | regulation of cellular component size                                  | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | ICAM1/SLC12A3/APOE/FN1       | 4 |
| GO:0044262 | cellular carbohydrate metabolic process                                | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | STAT3/RORC/IL6ST/RGN         | 4 |

|            |                                                                   |       |        |             |             |             |                               |   |
|------------|-------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|-------------------------------|---|
| GO:0045429 | positive regulation of nitric oxide biosynthetic process          | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | ICAM1/AGT/TLR4/ITGB2          | 4 |
| GO:0045581 | negative regulation of T cell differentiation                     | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/SOCS1          | 4 |
| GO:0045620 | negative regulation of lymphocyte differentiation                 | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/SOCS1          | 4 |
| GO:0050688 | regulation of defense response to virus                           | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | STAT1/BIRC3/LILRB1/IFIT1      | 4 |
| GO:0060415 | muscle tissue morphogenesis                                       | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | COL3A1/TGFB1/FKBP1A/MYOM2     | 4 |
| GO:0061844 | antimicrobial humoral immune response mediated by antimicro       | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | S100A9/LTF/CXCL1/S100A12      | 4 |
| GO:0071774 | response to fibroblast growth factor                              | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | COL1A1/NR4A1/TNC/GATA3        | 4 |
| GO:0120162 | positive regulation of cold-induced thermogenesis                 | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | LCN2/IL4R/STAT6/CMKLR1        | 4 |
| GO:1902041 | regulation of extrinsic apoptotic signaling pathway via death dor | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | ICAM1/TNFSF10/ATF3/SERPINE1   | 4 |
| GO:1903428 | positive regulation of reactive oxygen species biosynthetic proce | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | ICAM1/AGT/TLR4/ITGB2          | 4 |
| GO:1904407 | positive regulation of nitric oxide metabolic process             | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | ICAM1/AGT/TLR4/ITGB2          | 4 |
| GO:1990778 | protein localization to cell periphery                            | 4/182 | 17/749 | 0,623957429 | 0,999954951 | 0,999954951 | FCER1G/TNFRSF1A/EHD3/TGFB1    | 4 |
| GO:0001657 | ureteric bud development                                          | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | TGFB1/AGT/MYC/GATA3           | 4 |
| GO:0001823 | mesonephros development                                           | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | TGFB1/AGT/MYC/GATA3           | 4 |
| GO:0002701 | negative regulation of production of molecular mediator of imm    | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | BCL6/JAK3/TGFB1/LILRB1        | 4 |
| GO:0003170 | heart valve development                                           | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | TNFRSF1A/TGFB1/TNFRSF1B/GATA3 | 4 |
| GO:0006911 | phagocytosis, engulfment                                          | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | C3/FCER1G/FCGR1A/ITGB2        | 4 |
| GO:0007283 | spermatogenesis                                                   | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | BCL6/BAX/BIRC3/RGN            | 4 |
| GO:0008637 | apoptotic mitochondrial changes                                   | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | SOD2/BAX/TNFSF10/PLAUR        | 4 |
| GO:0010324 | membrane invagination                                             | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | C3/FCER1G/FCGR1A/ITGB2        | 4 |
| GO:0031647 | regulation of protein stability                                   | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | HDAC6/XBP1/CDKN1A/RNF149      | 4 |
| GO:0048644 | muscle organ morphogenesis                                        | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | COL3A1/TGFB1/FKBP1A/MYOM2     | 4 |
| GO:0051170 | import into nucleus                                               | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | STAT3/TGFB1/CDKN1A/AGT        | 4 |
| GO:0070167 | regulation of biomineral tissue development                       | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | HIF1A/LTF/TGFB1/ISG15         | 4 |
| GO:0072163 | mesonephric epithelium development                                | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | TGFB1/AGT/MYC/GATA3           | 4 |
| GO:0072164 | mesonephric tubule development                                    | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | TGFB1/AGT/MYC/GATA3           | 4 |
| GO:0099024 | plasma membrane invagination                                      | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | C3/FCER1G/FCGR1A/ITGB2        | 4 |
| GO:0110149 | regulation of biomineralization                                   | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | HIF1A/LTF/TGFB1/ISG15         | 4 |
| GO:1903725 | regulation of phospholipid metabolic process                      | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | SOCS3/TGFB1/SOCS1/LDLR        | 4 |
| GO:1905952 | regulation of lipid localization                                  | 4/182 | 18/749 | 0,672601122 | 0,999954951 | 0,999954951 | C3/AGT/APOE/NFKB1             | 4 |
| GO:0001889 | liver development                                                 | 4/182 | 19/749 | 0,716759746 | 0,999954951 | 0,999954951 | TGFB1/XBP1/HNF1A/RGN          | 4 |
| GO:0002437 | inflammatory response to antigenic stimulus                       | 4/182 | 19/749 | 0,716759746 | 0,999954951 | 0,999954951 | C3/FCER1G/ICAM1/GATA3         | 4 |
| GO:0006163 | purine nucleotide metabolic process                               | 4/182 | 19/749 | 0,716759746 | 0,999954951 | 0,999954951 | HIF1A/STAT3/IMPDH1/TGFB1      | 4 |
| GO:0009100 | glycoprotein metabolic process                                    | 4/182 | 19/749 | 0,716759746 | 0,999954951 | 0,999954951 | HIF1A/MUC1/JAK3/VCAN          | 4 |
| GO:0031032 | actomyosin structure organization                                 | 4/182 | 19/749 | 0,716759746 | 0,999954951 | 0,999954951 | KRT8/KRT19/NOX4/MYOM2         | 4 |
| GO:0034976 | response to endoplasmic reticulum stress                          | 4/182 | 19/749 | 0,716759746 | 0,999954951 | 0,999954951 | XBP1/BAX/ATF3/CASP4           | 4 |
| GO:0035303 | regulation of dephosphorylation                                   | 4/182 | 19/749 | 0,716759746 | 0,999954951 | 0,999954951 | TGFB1/FKBP1A/LILRB2/RGN       | 4 |
| GO:0040029 | regulation of gene expression, epigenetic                         | 4/182 | 19/749 | 0,716759746 | 0,999954951 | 0,999954951 | STAT3/HDAC6/TGFB1/DNMT1       | 4 |
| GO:0048565 | digestive tract development                                       | 4/182 | 19/749 | 0,716759746 | 0,999954951 | 0,999954951 | HIF1A/COL3A1/TGFB1/CDKN1A     | 4 |
| GO:0061008 | hepaticobiliary system development                                | 4/182 | 19/749 | 0,716759746 | 0,999954951 | 0,999954951 | TGFB1/XBP1/HNF1A/RGN          | 4 |
| GO:0072521 | purine-containing compound metabolic process                      | 4/182 | 19/749 | 0,716759746 | 0,999954951 | 0,999954951 | HIF1A/STAT3/IMPDH1/TGFB1      | 4 |
| GO:0002639 | positive regulation of immunoglobulin production                  | 4/182 | 20/749 | 0,756411771 | 0,999954951 | 0,999954951 | IL4R/TGFB1/XBP1/STAT6         | 4 |
| GO:0003231 | cardiac ventricle development                                     | 4/182 | 20/749 | 0,756411771 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/FKBP1A/GATA3      | 4 |
| GO:0006968 | cellular defense response                                         | 4/182 | 20/749 | 0,756411771 | 0,999954951 | 0,999954951 | LY96/LILRB2/C5AR1/ADORA2A     | 4 |
| GO:0007519 | skeletal muscle tissue development                                | 4/182 | 20/749 | 0,756411771 | 0,999954951 | 0,999954951 | TGFB1/EGR1/MYOM2/ATF3         | 4 |
| GO:0014015 | positive regulation of gliogenesis                                | 4/182 | 20/749 | 0,756411771 | 0,999954951 | 0,999954951 | TGFB1/TLR2/TNFRSF1B/IL6ST     | 4 |
| GO:0014902 | myotube differentiation                                           | 4/182 | 20/749 | 0,756411771 | 0,999954951 | 0,999954951 | IL4R/XBP1/GDF15/TNFSF14       | 4 |
| GO:0032733 | positive regulation of interleukin-10 production                  | 4/182 | 20/749 | 0,756411771 | 0,999954951 | 0,999954951 | BCL3/FCER1G/TLR4/TLR2         | 4 |
| GO:0048232 | male gamete generation                                            | 4/182 | 20/749 | 0,756411771 | 0,999954951 | 0,999954951 | BCL6/BAX/BIRC3/RGN            | 4 |
| GO:0051208 | sequestering of calcium ion                                       | 4/182 | 20/749 | 0,756411771 | 0,999954951 | 0,999954951 | TGFB1/BAX/FKBP1A/PTPN6        | 4 |
| GO:0051209 | release of sequestered calcium ion into cytosol                   | 4/182 | 20/749 | 0,756411771 | 0,999954951 | 0,999954951 | TGFB1/BAX/FKBP1A/PTPN6        | 4 |
| GO:0051282 | regulation of sequestering of calcium ion                         | 4/182 | 20/749 | 0,756411771 | 0,999954951 | 0,999954951 | TGFB1/BAX/FKBP1A/PTPN6        | 4 |
| GO:0051283 | negative regulation of sequestering of calcium ion                | 4/182 | 20/749 | 0,756411771 | 0,999954951 | 0,999954951 | TGFB1/BAX/FKBP1A/PTPN6        | 4 |
| GO:0002828 | regulation of type 2 immune response                              | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | BCL6/IL4R/STAT6/GATA3         | 4 |
| GO:0010595 | positive regulation of endothelial cell migration                 | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/AGT/GATA3         | 4 |
| GO:0030282 | bone mineralization                                               | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | HIF1A/LTF/TGFB1/ISG15         | 4 |
| GO:0034113 | heterotypic cell-cell adhesion                                    | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | VCAM1/LILRB2/CD58/ITGB2       | 4 |
| GO:0043154 | negative regulation of cysteine-type endopeptidase activity invo  | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | BIRC3/ADORA2A/TNFSF14/PLAUR   | 4 |
| GO:0045066 | regulatory T cell differentiation                                 | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | BCL6/TGFB1/SOCS1/LILRB2       | 4 |

|            |                                                                    |       |        |             |             |             |                              |   |
|------------|--------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|------------------------------|---|
| GO:0045589 | regulation of regulatory T cell differentiation                    | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | BCL6/TGFB1/SOCS1/LILRB2      | 4 |
| GO:0045622 | regulation of T-helper cell differentiation                        | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R/NFKBIZ        | 4 |
| GO:0045667 | regulation of osteoblast differentiation                           | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | LTF/IFITM1/IL6R/IL6ST        | 4 |
| GO:0051656 | establishment of organelle localization                            | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | HIF1A/FCER1G/IL4R/CD59       | 4 |
| GO:0060538 | skeletal muscle organ development                                  | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | TGFB1/EGR1/MYOM2/ATF3        | 4 |
| GO:0070301 | cellular response to hydrogen peroxide                             | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | MAPK13/LCN2/HDAC6/STAT6      | 4 |
| GO:0090288 | negative regulation of cellular response to growth factor stimulus | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | SOST/TGFB1/AGT/GATA3         | 4 |
| GO:1903320 | regulation of protein modification by small protein conjugation    | 4/182 | 21/749 | 0,791670814 | 0,999954951 | 0,999954951 | EGR1/FKBP1A/BIRC3/ISG15      | 4 |
| GO:0030307 | positive regulation of cell growth                                 | 4/182 | 22/749 | 0,822748496 | 0,999954951 | 0,999954951 | S100A9/S100A8/CXCL16/FN1     | 4 |
| GO:0043534 | blood vessel endothelial cell migration                            | 4/182 | 22/749 | 0,822748496 | 0,999954951 | 0,999954951 | HIF1A/NR4A1/TGFB1/APOE       | 4 |
| GO:0045670 | regulation of osteoclast differentiation                           | 4/182 | 22/749 | 0,822748496 | 0,999954951 | 0,999954951 | LTF/TLR4/LILRB1/TMEM178A     | 4 |
| GO:0062013 | positive regulation of small molecule metabolic process            | 4/182 | 22/749 | 0,822748496 | 0,999954951 | 0,999954951 | HIF1A/STAT3/NFKB1/RGN        | 4 |
| GO:0070228 | regulation of lymphocyte apoptotic process                         | 4/182 | 22/749 | 0,822748496 | 0,999954951 | 0,999954951 | HIF1A/BCL6/JAK3/BAX          | 4 |
| GO:0097553 | calcium ion transmembrane import into cytosol                      | 4/182 | 22/749 | 0,822748496 | 0,999954951 | 0,999954951 | TGFB1/BAX/FKBP1A/PTPN6       | 4 |
| GO:0002704 | negative regulation of leukocyte mediated immunity                 | 4/182 | 23/749 | 0,849922625 | 0,999954951 | 0,999954951 | BCL6/JAK3/LILRB1/PTPN6       | 4 |
| GO:0006913 | nucleocytoplasmic transport                                        | 4/182 | 23/749 | 0,849922625 | 0,999954951 | 0,999954951 | STAT3/TGFB1/CDKN1A/AGT       | 4 |
| GO:0032355 | response to estradiol                                              | 4/182 | 23/749 | 0,849922625 | 0,999954951 | 0,999954951 | STAT3/COL1A1/TGFB1/AGT       | 4 |
| GO:0033135 | regulation of peptidyl-serine phosphorylation                      | 4/182 | 23/749 | 0,849922625 | 0,999954951 | 0,999954951 | HDAC6/TGFB1/BAX/TBK1         | 4 |
| GO:0051101 | regulation of DNA binding                                          | 4/182 | 23/749 | 0,849922625 | 0,999954951 | 0,999954951 | BCL3/TGFB1/GATA3/PLAUR       | 4 |
| GO:0051169 | nuclear transport                                                  | 4/182 | 23/749 | 0,849922625 | 0,999954951 | 0,999954951 | STAT3/TGFB1/CDKN1A/AGT       | 4 |
| GO:0002369 | T cell cytokine production                                         | 4/182 | 24/749 | 0,873510966 | 0,999954951 | 0,999954951 | IL1R1/SLC11A1/TNFRSF1B/GATA3 | 4 |
| GO:0044282 | small molecule catabolic process                                   | 4/182 | 24/749 | 0,873510966 | 0,999954951 | 0,999954951 | ALDH3A2/LYVE1/TGFB1/APOE     | 4 |
| GO:0071772 | response to BMP                                                    | 4/182 | 24/749 | 0,873510966 | 0,999954951 | 0,999954951 | SOST/EGR1/GDF15/GATA3        | 4 |
| GO:0071773 | cellular response to BMP stimulus                                  | 4/182 | 24/749 | 0,873510966 | 0,999954951 | 0,999954951 | SOST/EGR1/GDF15/GATA3        | 4 |
| GO:1901224 | positive regulation of NIK/NF-kappaB signaling                     | 4/182 | 24/749 | 0,873510966 | 0,999954951 | 0,999954951 | TLR4/TLR2/CD14/TNFSF14       | 4 |
| GO:0032388 | positive regulation of intracellular transport                     | 4/182 | 25/749 | 0,893850392 | 0,999954951 | 0,999954951 | FCER1G/IL4R/TGFB1/ITGB2      | 4 |
| GO:0032735 | positive regulation of interleukin-12 production                   | 4/182 | 25/749 | 0,893850392 | 0,999954951 | 0,999954951 | TLR4/TLR2/MAPK11/LTB         | 4 |
| GO:0042130 | negative regulation of T cell proliferation                        | 4/182 | 25/749 | 0,893850392 | 0,999954951 | 0,999954951 | TGFB1/LILRB2/LILRB1/PTPN6    | 4 |
| GO:0042267 | natural killer cell mediated cytotoxicity                          | 4/182 | 25/749 | 0,893850392 | 0,999954951 | 0,999954951 | PVR/LILRB1/KIR3DL1/PTPN6     | 4 |
| GO:0045123 | cellular extravasation                                             | 4/182 | 25/749 | 0,893850392 | 0,999954951 | 0,999954951 | IL1R1/ICAM1/VCAM1/ITGB2      | 4 |
| GO:0048705 | skeletal system morphogenesis                                      | 4/182 | 25/749 | 0,893850392 | 0,999954951 | 0,999954951 | LTF/COL1A1/TGFB1/TIPARP      | 4 |
| GO:0051928 | positive regulation of calcium ion transport                       | 4/182 | 25/749 | 0,893850392 | 0,999954951 | 0,999954951 | EHD3/BAX/G6PD/RGN            | 4 |
| GO:0002548 | monocyte chemotaxis                                                | 4/182 | 26/749 | 0,911280901 | 0,999954951 | 0,999954951 | SLAMF8/IL6R/S100A12/SERPINE1 | 4 |
| GO:0007409 | axonogenesis                                                       | 4/182 | 26/749 | 0,911280901 | 0,999954951 | 0,999954951 | HDAC6/APOE/FN1/GATA3         | 4 |
| GO:0043547 | positive regulation of GTPase activity                             | 4/182 | 26/749 | 0,911280901 | 0,999954951 | 0,999954951 | ICAM1/ARHGDIB/ERRFI1/RGN     | 4 |
| GO:0070227 | lymphocyte apoptotic process                                       | 4/182 | 26/749 | 0,911280901 | 0,999954951 | 0,999954951 | HIF1A/BCL6/JAK3/BAX          | 4 |
| GO:0098742 | cell-cell adhesion via plasma-membrane adhesion molecules          | 4/182 | 27/749 | 0,926133888 | 0,999954951 | 0,999954951 | ICAM1/VCAM1/PVR/ITGB2        | 4 |
| GO:0002228 | natural killer cell mediated immunity                              | 4/182 | 28/749 | 0,938723954 | 0,999954951 | 0,999954951 | PVR/LILRB1/KIR3DL1/PTPN6     | 4 |
| GO:0046879 | hormone secretion                                                  | 4/182 | 28/749 | 0,938723954 | 0,999954951 | 0,999954951 | HIF1A/AGT/HNF1A/GATA3        | 4 |
| GO:0050709 | negative regulation of protein secretion                           | 4/182 | 28/749 | 0,938723954 | 0,999954951 | 0,999954951 | APOE/IL1R2/FN1/LILRB1        | 4 |
| GO:1901343 | negative regulation of vasculature development                     | 4/182 | 28/749 | 0,938723954 | 0,999954951 | 0,999954951 | STAT1/DNMT1/AGT/SERPINE1     | 4 |
| GO:0014065 | phosphatidylinositol 3-kinase signaling                            | 4/182 | 29/749 | 0,949343614 | 0,999954951 | 0,999954951 | AGT/EPO/GATA3/PTPN6          | 4 |
| GO:0032956 | regulation of actin cytoskeleton organization                      | 4/182 | 29/749 | 0,949343614 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/ARHGDIB/NOX4     | 4 |
| GO:0048667 | cell morphogenesis involved in neuron differentiation              | 4/182 | 29/749 | 0,949343614 | 0,999954951 | 0,999954951 | HDAC6/APOE/FN1/GATA3         | 4 |
| GO:0002792 | negative regulation of peptide secretion                           | 4/182 | 30/749 | 0,958260271 | 0,999954951 | 0,999954951 | APOE/IL1R2/FN1/LILRB1        | 4 |
| GO:0030324 | lung development                                                   | 4/182 | 30/749 | 0,958260271 | 0,999954951 | 0,999954951 | MME/HSD11B1/TNC/ERRFI1       | 4 |
| GO:0030888 | regulation of B cell proliferation                                 | 4/182 | 30/749 | 0,958260271 | 0,999954951 | 0,999954951 | BCL6/AHR/CDKN1A/TLR4         | 4 |
| GO:0032652 | regulation of interleukin-1 production                             | 4/182 | 30/749 | 0,958260271 | 0,999954951 | 0,999954951 | EGR1/TLR4/IL1R2/ERRFI1       | 4 |
| GO:0048015 | phosphatidylinositol-mediated signaling                            | 4/182 | 30/749 | 0,958260271 | 0,999954951 | 0,999954951 | AGT/EPO/GATA3/PTPN6          | 4 |
| GO:0048017 | inositol lipid-mediated signaling                                  | 4/182 | 30/749 | 0,958260271 | 0,999954951 | 0,999954951 | AGT/EPO/GATA3/PTPN6          | 4 |
| GO:0051224 | negative regulation of protein transport                           | 4/182 | 30/749 | 0,958260271 | 0,999954951 | 0,999954951 | APOE/IL1R2/FN1/LILRB1        | 4 |
| GO:1904950 | negative regulation of establishment of protein localization       | 4/182 | 30/749 | 0,958260271 | 0,999954951 | 0,999954951 | APOE/IL1R2/FN1/LILRB1        | 4 |
| GO:0007254 | JNK cascade                                                        | 4/182 | 31/749 | 0,965714932 | 0,999954951 | 0,999954951 | LTBR/TLR4/FGD2/TRIB1         | 4 |
| GO:0010810 | regulation of cell-substrate adhesion                              | 4/182 | 31/749 | 0,965714932 | 0,999954951 | 0,999954951 | BCL6/COL1A1/FN1/SERPINE1     | 4 |
| GO:0030323 | respiratory tube development                                       | 4/182 | 31/749 | 0,965714932 | 0,999954951 | 0,999954951 | MME/HSD11B1/TNC/ERRFI1       | 4 |
| GO:0032970 | regulation of actin filament-based process                         | 4/182 | 31/749 | 0,965714932 | 0,999954951 | 0,999954951 | ICAM1/TGFB1/ARHGDIB/NOX4     | 4 |
| GO:1904019 | epithelial cell apoptotic process                                  | 4/182 | 31/749 | 0,965714932 | 0,999954951 | 0,999954951 | KRT8/ICAM1/SERPINE1/GATA3    | 4 |
| GO:0032872 | regulation of stress-activated MAPK cascade                        | 4/182 | 32/749 | 0,971922206 | 0,999954951 | 0,999954951 | LTBR/TLR4/MYC/FGD2           | 4 |
| GO:0070302 | regulation of stress-activated protein kinase signaling cascade    | 4/182 | 32/749 | 0,971922206 | 0,999954951 | 0,999954951 | LTBR/TLR4/MYC/FGD2           | 4 |



|            |                                                                    |       |        |             |             |             |                            |   |
|------------|--------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|----------------------------|---|
| GO:0032386 | regulation of intracellular transport                              | 4/182 | 33/749 | 0,977071201 | 0,999954951 | 0,999954951 | FCER1G/IL4R/TGFB1/ITGB2    | 4 |
| GO:0032612 | interleukin-1 production                                           | 4/182 | 33/749 | 0,977071201 | 0,999954951 | 0,999954951 | EGR1/TLR4/IL1R2/ERRFI1     | 4 |
| GO:0090092 | regulation of transmembrane receptor protein serine/threonine      | 4/182 | 33/749 | 0,977071201 | 0,999954951 | 0,999954951 | SOST/TGFB1/FKBP1A/GDF15    | 4 |
| GO:0045927 | positive regulation of growth                                      | 4/182 | 34/749 | 0,981327033 | 0,999954951 | 0,999954951 | S100A9/S100A8/CXCL16/FN1   | 4 |
| GO:0046635 | positive regulation of alpha-beta T cell activation                | 4/182 | 34/749 | 0,981327033 | 0,999954951 | 0,999954951 | IL4R/NFKBIZ/SOCS1/IL6R     | 4 |
| GO:0060541 | respiratory system development                                     | 4/182 | 34/749 | 0,981327033 | 0,999954951 | 0,999954951 | MME/HSD11B1/TNC/ERRFI1     | 4 |
| GO:0072676 | lymphocyte migration                                               | 4/182 | 39/749 | 0,993555524 | 0,999954951 | 0,999954951 | ICAM1/CXCL16/GATA3/TNFSF14 | 4 |
| GO:0070098 | chemokine-mediated signaling pathway                               | 4/182 | 40/749 | 0,99482604  | 0,999954951 | 0,999954951 | HIF1A/CXCL1/ACKR1/CMKLR1   | 4 |
| GO:1990868 | response to chemokine                                              | 4/182 | 41/749 | 0,995854735 | 0,999954951 | 0,999954951 | HIF1A/CXCL1/ACKR1/CMKLR1   | 4 |
| GO:1990869 | cellular response to chemokine                                     | 4/182 | 41/749 | 0,995854735 | 0,999954951 | 0,999954951 | HIF1A/CXCL1/ACKR1/CMKLR1   | 4 |
| GO:0019722 | calcium-mediated signaling                                         | 4/182 | 44/749 | 0,997893352 | 0,999954951 | 0,999954951 | VCAM1/FKBP1A/CMKLR1/RGN    | 4 |
| GO:0031341 | regulation of cell killing                                         | 4/182 | 48/749 | 0,999167149 | 0,999954951 | 0,999954951 | ICAM1/CD59/PVR/LILRB1      | 4 |
| GO:0000768 | syncytium formation by plasma membrane fusion                      | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | IL4R/GDF15/TNFSF14         | 3 |
| GO:0001974 | blood vessel remodeling                                            | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | TGFB1/BAX/AGT              | 3 |
| GO:0002088 | lens development in camera-type eye                                | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | MAF/TGFB1/GATA3            | 3 |
| GO:0002374 | cytokine secretion involved in immune response                     | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | TLR2/TNFRSF1B/LILRB1       | 3 |
| GO:0006164 | purine nucleotide biosynthetic process                             | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | STAT3/IMPDH1/TGFB1         | 3 |
| GO:0006475 | internal protein amino acid acetylation                            | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | MUC1/TGFB1/GATA3           | 3 |
| GO:0006476 | protein deacetylation                                              | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | BCL6/HDAC6/TGFB1           | 3 |
| GO:0006633 | fatty acid biosynthetic process                                    | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | XBP1/ALOX5/RGN             | 3 |
| GO:0006949 | syncytium formation                                                | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | IL4R/GDF15/TNFSF14         | 3 |
| GO:0007520 | myoblast fusion                                                    | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | IL4R/GDF15/TNFSF14         | 3 |
| GO:0007589 | body fluid secretion                                               | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | HIF1A/XBP1/SLC22A2         | 3 |
| GO:0016573 | histone acetylation                                                | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | MUC1/TGFB1/GATA3           | 3 |
| GO:0018393 | internal peptidyl-lysine acetylation                               | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | MUC1/TGFB1/GATA3           | 3 |
| GO:0018394 | peptidyl-lysine acetylation                                        | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | MUC1/TGFB1/GATA3           | 3 |
| GO:0032634 | interleukin-5 production                                           | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | IL17RA/GATA3/IL17RB        | 3 |
| GO:0032674 | regulation of interleukin-5 production                             | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | IL17RA/GATA3/IL17RB        | 3 |
| GO:0032736 | positive regulation of interleukin-13 production                   | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | IL17RA/GATA3/IL17RB        | 3 |
| GO:0035601 | protein deacylation                                                | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | BCL6/HDAC6/TGFB1           | 3 |
| GO:0042982 | amyloid precursor protein metabolic process                        | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | FKBP1A/APOE/IFNGR1         | 3 |
| GO:0042987 | amyloid precursor protein catabolic process                        | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | FKBP1A/APOE/IFNGR1         | 3 |
| GO:0043114 | regulation of vascular permeability                                | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | TGFB1/APOE/ADORA2A         | 3 |
| GO:0043371 | negative regulation of CD4-positive, alpha-beta T cell differentia | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R             | 3 |
| GO:0048864 | stem cell development                                              | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | HIF1A/KITLG/FN1            | 3 |
| GO:0050810 | regulation of steroid biosynthetic process                         | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | EGR1/APOE/NFKB1            | 3 |
| GO:0051057 | positive regulation of small GTPase mediated signal transductio    | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | COL3A1/KITLG/EPO           | 3 |
| GO:0060443 | mammary gland morphogenesis                                        | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | TGFB1/BAX/STAT6            | 3 |
| GO:0062208 | positive regulation of pattern recognition receptor signaling patl | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | LTF/TLR4/TLR2              | 3 |
| GO:0072522 | purine-containing compound biosynthetic process                    | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | STAT3/IMPDH1/TGFB1         | 3 |
| GO:0072606 | interleukin-8 secretion                                            | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | TLR2/CD58/CD14             | 3 |
| GO:0090199 | regulation of release of cytochrome c from mitochondria            | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | BAX/TNFSF10/PLAUR          | 3 |
| GO:0098732 | macromolecule deacylation                                          | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | BCL6/HDAC6/TGFB1           | 3 |
| GO:0140253 | cell-cell fusion                                                   | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | IL4R/GDF15/TNFSF14         | 3 |
| GO:1904036 | negative regulation of epithelial cell apoptotic process           | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | ICAM1/SERPINE1/GATA3       | 3 |
| GO:1904707 | positive regulation of vascular smooth muscle cell proliferation   | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | ADAMTS1/DNMT1/AGT          | 3 |
| GO:1905954 | positive regulation of lipid localization                          | 3/182 | 10/749 | 0,453644039 | 0,999954951 | 0,999954951 | C3/APOE/NFKB1              | 3 |
| GO:0006338 | chromatin remodeling                                               | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | DNMT1/MYC/GATA3            | 3 |
| GO:0006473 | protein acetylation                                                | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | MUC1/TGFB1/GATA3           | 3 |
| GO:0006986 | response to unfolded protein                                       | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | XBP1/BAX/ATF3              | 3 |
| GO:0007566 | embryo implantation                                                | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | TIMP1/ARHGDIB/EPO          | 3 |
| GO:0007612 | learning                                                           | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | HIF1A/AGT/TLR2             | 3 |
| GO:0008361 | regulation of cell size                                            | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | SLC12A3/APOE/FN1           | 3 |
| GO:0010758 | regulation of macrophage chemotaxis                                | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | SLAMF8/CMKLR1/C5AR1        | 3 |
| GO:0014031 | mesenchymal cell development                                       | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | HIF1A/KITLG/FN1            | 3 |
| GO:0014033 | neural crest cell differentiation                                  | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | HIF1A/KITLG/FN1            | 3 |
| GO:0015980 | energy derivation by oxidation of organic compounds                | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | HIF1A/MYC/IL6ST            | 3 |
| GO:0019915 | lipid storage                                                      | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | C3/APOE/NFKB1              | 3 |
| GO:0021987 | cerebral cortex development                                        | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | HIF1A/COL3A1/BAX           | 3 |

|            |                                                                          |       |        |             |             |             |                        |   |
|------------|--------------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|------------------------|---|
| GO:0030858 | positive regulation of epithelial cell differentiation                   | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | PLAAT4/CD24/SERPINE1   | 3 |
| GO:0032418 | lysosome localization                                                    | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | FCER1G/HDAC6/IL4R      | 3 |
| GO:0032768 | regulation of monooxygenase activity                                     | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | HIF1A/APOE/NFKB1       | 3 |
| GO:0032964 | collagen biosynthetic process                                            | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | COL1A1/TGFB1/ERRFI1    | 3 |
| GO:0033628 | regulation of cell adhesion mediated by integrin                         | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | MUC1/SERPINE1/PTPN6    | 3 |
| GO:0043011 | myeloid dendritic cell differentiation                                   | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | LTBR/RELB/TGFB1        | 3 |
| GO:0043414 | macromolecule methylation                                                | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | DNMT1/MYC/GATA3        | 3 |
| GO:0043543 | protein acylation                                                        | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | MUC1/TGFB1/GATA3       | 3 |
| GO:0045577 | regulation of B cell differentiation                                     | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | XBP1/SLAMF8/PTPN6      | 3 |
| GO:0045913 | positive regulation of carbohydrate metabolic process                    | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | HIF1A/NFKB1/RGN        | 3 |
| GO:0045921 | positive regulation of exocytosis                                        | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | FCER1G/IL4R/ITGB2      | 3 |
| GO:0048662 | negative regulation of smooth muscle cell proliferation                  | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | SOD2/CDKN1A/TRIB1      | 3 |
| GO:0051053 | negative regulation of DNA metabolic process                             | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | BCL6/GATA3/RGN         | 3 |
| GO:0070373 | negative regulation of ERK1 and ERK2 cascade                             | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | TLR4/ERRFI1/ATF3       | 3 |
| GO:0072091 | regulation of stem cell proliferation                                    | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/KITLG      | 3 |
| GO:1902807 | negative regulation of cell cycle G1/S phase transition                  | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | MUC1/BAX/CDKN1A        | 3 |
| GO:2000134 | negative regulation of G1/S transition of mitotic cell cycle             | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | MUC1/BAX/CDKN1A        | 3 |
| GO:2001244 | positive regulation of intrinsic apoptotic signaling pathway             | 3/182 | 11/749 | 0,523805477 | 0,999954951 | 0,999954951 | S100A9/S100A8/BAX      | 3 |
| GO:0001838 | embryonic epithelial tube formation                                      | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/GATA3      | 3 |
| GO:0006690 | icosanoid metabolic process                                              | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | TNFRSF1A/ALOX5/TLR2    | 3 |
| GO:0007272 | ensheathment of neurons                                                  | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | TGFB1/TLR2/TNFRSF1B    | 3 |
| GO:0008286 | insulin receptor signaling pathway                                       | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | SOCS3/SOCS1/AGT        | 3 |
| GO:0008366 | axon ensheathment                                                        | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | TGFB1/TLR2/TNFRSF1B    | 3 |
| GO:0010657 | muscle cell apoptotic process                                            | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | SOD2/DNMT1/AGT         | 3 |
| GO:0010660 | regulation of muscle cell apoptotic process                              | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | SOD2/DNMT1/AGT         | 3 |
| GO:0010812 | negative regulation of cell-substrate adhesion                           | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | BCL6/COL1A1/SERPINE1   | 3 |
| GO:0016050 | vesicle organization                                                     | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | CD59/TAP2/TAP1         | 3 |
| GO:0022617 | extracellular matrix disassembly                                         | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | TIMP1/TGFB1/CTSS       | 3 |
| GO:0030279 | negative regulation of ossification                                      | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | HIF1A/SOST/TGFB1       | 3 |
| GO:0030501 | positive regulation of bone mineralization                               | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | LTF/TGFB1/ISG15        | 3 |
| GO:0031016 | pancreas development                                                     | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | XBP1/IL6R/HNF1A        | 3 |
| GO:0031623 | receptor internalization                                                 | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | FCER1G/ITGB2/LILRB1    | 3 |
| GO:0042058 | regulation of epidermal growth factor receptor signaling pathway         | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | AGT/ERRFI1/PLAUR       | 3 |
| GO:0042552 | myelination                                                              | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | TGFB1/TLR2/TNFRSF1B    | 3 |
| GO:0043300 | regulation of leukocyte degranulation                                    | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | FCER1G/IL4R/ITGB2      | 3 |
| GO:0045576 | mast cell activation                                                     | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | FCER1G/IL4R/S100A12    | 3 |
| GO:0051148 | negative regulation of muscle cell differentiation                       | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | XBP1/DNMT1/G6PD        | 3 |
| GO:0055013 | cardiac muscle cell development                                          | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | AGT/G6PD/MYOM2         | 3 |
| GO:0060349 | bone morphogenesis                                                       | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | LTF/COL1A1/TGFB1       | 3 |
| GO:0061383 | trabecula morphogenesis                                                  | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | ADAMTS1/COL1A1/FKBP1A  | 3 |
| GO:0070169 | positive regulation of biomineral tissue development                     | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | LTF/TGFB1/ISG15        | 3 |
| GO:0070542 | response to fatty acid                                                   | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | LDLR/TNC/TLR2          | 3 |
| GO:0098657 | import into cell                                                         | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | LTF/AGT/SLC12A3        | 3 |
| GO:0110151 | positive regulation of biomineralization                                 | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | LTF/TGFB1/ISG15        | 3 |
| GO:1901568 | fatty acid derivative metabolic process                                  | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | TNFRSF1A/ALOX5/TLR2    | 3 |
| GO:1902042 | negative regulation of extrinsic apoptotic signaling pathway via caspase | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | ICAM1/TNFSF10/SERPINE1 | 3 |
| GO:1902622 | regulation of neutrophil migration                                       | 3/182 | 12/749 | 0,588759209 | 0,999954951 | 0,999954951 | IL1R1/SLAMF8/CSAR1     | 3 |
| GO:0002065 | columnar/cuboidal epithelial cell differentiation                        | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | HIF1A/CDKN1A/SERPINE1  | 3 |
| GO:0002753 | cytoplasmic pattern recognition receptor signaling pathway               | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | TLR4/IRF7/BIRC3        | 3 |
| GO:0008593 | regulation of Notch signaling pathway                                    | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | BCL6/STAT3/IL6ST       | 3 |
| GO:0009267 | cellular response to starvation                                          | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | XBP1/CDKN1A/ATF3       | 3 |
| GO:0010675 | regulation of cellular carbohydrate metabolic process                    | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | STAT3/RORC/RGN         | 3 |
| GO:0016241 | regulation of macroautophagy                                             | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | HIF1A/HDAC6/TBK1       | 3 |
| GO:0016331 | morphogenesis of embryonic epithelium                                    | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/GATA3      | 3 |
| GO:0031640 | killing of cells of other organism                                       | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | LTF/APOL1/S100A12      | 3 |
| GO:0032368 | regulation of lipid transport                                            | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | AGT/APOE/NFKB1         | 3 |
| GO:0032656 | regulation of interleukin-13 production                                  | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | IL17RA/GATA3/IL17RB    | 3 |
| GO:0042594 | response to starvation                                                   | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | XBP1/CDKN1A/ATF3       | 3 |
| GO:0043388 | positive regulation of DNA binding                                       | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | TGFB1/GATA3/PLAUR      | 3 |

|            |                                                                   |       |        |             |             |             |                      |   |
|------------|-------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|----------------------|---|
| GO:0046034 | ATP metabolic process                                             | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | HIF1A/STAT3/TGFB1    | 3 |
| GO:0050803 | regulation of synapse structure or activity                       | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | APOE/TLR2/LILRB2     | 3 |
| GO:0050807 | regulation of synapse organization                                | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | APOE/TLR2/LILRB2     | 3 |
| GO:0055006 | cardiac cell development                                          | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | AGT/G6PD/MYOM2       | 3 |
| GO:0070229 | negative regulation of lymphocyte apoptotic process               | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | HIF1A/BCL6/JAK3      | 3 |
| GO:0072175 | epithelial tube formation                                         | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/GATA3    | 3 |
| GO:1901136 | carbohydrate derivative catabolic process                         | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | LYVE1/TGFB1/VCAN     | 3 |
| GO:1901184 | regulation of ERBB signaling pathway                              | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | AGT/ERRFI1/PLAUR     | 3 |
| GO:1902895 | positive regulation of pri-miRNA transcription by RNA polymerase  | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | HIF1A/STAT3/TGFB1    | 3 |
| GO:2000241 | regulation of reproductive process                                | 3/182 | 13/749 | 0,647772803 | 0,999954951 | 0,999954951 | TIMP1/ARHGDI1B/RGN   | 3 |
| GO:0001541 | ovarian follicle development                                      | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | ICAM1/BAX/KITLG      | 3 |
| GO:0009101 | glycoprotein biosynthetic process                                 | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | MUC1/JAK3/VCAN       | 3 |
| GO:0010803 | regulation of tumor necrosis factor-mediated signaling pathway    | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | TNFRSF1A/BIRC3/CASP4 | 3 |
| GO:0016358 | dendrite development                                              | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | HDAC6/APOE/LST1      | 3 |
| GO:0016458 | gene silencing                                                    | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | STAT3/TGFB1/DNMT1    | 3 |
| GO:0032616 | interleukin-13 production                                         | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | IL17RA/GATA3/IL17RB  | 3 |
| GO:0034250 | positive regulation of cellular amide metabolic process           | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | BCL3/TNFRSF1A/IFNGR1 | 3 |
| GO:0035306 | positive regulation of dephosphorylation                          | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | TGFB1/LILRB2/RGN     | 3 |
| GO:0035722 | interleukin-12-mediated signaling pathway                         | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | JAK1/SOD2/PSME2      | 3 |
| GO:0043401 | steroid hormone mediated signaling pathway                        | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | HDAC6/NR4A1/RORC     | 3 |
| GO:0045191 | regulation of isotype switching                                   | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | BCL6/TGFB1/STAT6     | 3 |
| GO:0051145 | smooth muscle cell differentiation                                | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | SOD2/TGFB1/DNMT1     | 3 |
| GO:0051302 | regulation of cell division                                       | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | TGFB1/MYC/KLHL13     | 3 |
| GO:0051606 | detection of stimulus                                             | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | LY96/TLR4/TLR2       | 3 |
| GO:2000515 | negative regulation of CD4-positive, alpha-beta T cell activation | 3/182 | 14/749 | 0,700554106 | 0,999954951 | 0,999954951 | BCL6/JAK3/IL4R       | 3 |
| GO:0001773 | myeloid dendritic cell activation                                 | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | LTBR/RELB/TGFB1      | 3 |
| GO:0002827 | positive regulation of T-helper 1 type immune response            | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | IL1R1/IL6R/SLC11A1   | 3 |
| GO:0003014 | renal system process                                              | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | AGT/HNF1A/ADORA2A    | 3 |
| GO:0007492 | endoderm development                                              | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | TGFB1/ITGB2/FN1      | 3 |
| GO:0009755 | hormone-mediated signaling pathway                                | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | HDAC6/NR4A1/RORC     | 3 |
| GO:0010508 | positive regulation of autophagy                                  | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | HIF1A/HDAC6/TBK1     | 3 |
| GO:0030225 | macrophage differentiation                                        | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | TGFB1/TLR2/TRIB1     | 3 |
| GO:0032091 | negative regulation of protein binding                            | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | SLPI/BAX/IFIT1       | 3 |
| GO:0035850 | epithelial cell differentiation involved in kidney development    | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | CD24/STAT1/GATA3     | 3 |
| GO:0042475 | odontogenesis of dentin-containing tooth                          | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | BAX/TNC/SERPINE1     | 3 |
| GO:0043551 | regulation of phosphatidylinositol 3-kinase activity              | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | SOCS3/TGFB1/SOCS1    | 3 |
| GO:0044344 | cellular response to fibroblast growth factor stimulus            | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | COL1A1/NR4A1/GATA3   | 3 |
| GO:0048844 | artery morphogenesis                                              | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | COL3A1/LDLR/APOE     | 3 |
| GO:0061005 | cell differentiation involved in kidney development               | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | CD24/STAT1/GATA3     | 3 |
| GO:0070671 | response to interleukin-12                                        | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | JAK1/SOD2/PSME2      | 3 |
| GO:0071349 | cellular response to interleukin-12                               | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | JAK1/SOD2/PSME2      | 3 |
| GO:0071901 | negative regulation of protein serine/threonine kinase activity   | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | CDKN1A/APOE/PTPN6    | 3 |
| GO:0090150 | establishment of protein localization to membrane                 | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | CD24/BAX/ITGB2       | 3 |
| GO:1902893 | regulation of pri-miRNA transcription by RNA polymerase II        | 3/182 | 15/749 | 0,747135701 | 0,999954951 | 0,999954951 | HIF1A/STAT3/TGFB1    | 3 |
| GO:0000018 | regulation of DNA recombination                                   | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | BCL6/TGFB1/STAT6     | 3 |
| GO:0007187 | G protein-coupled receptor signaling pathway, coupled to cyclic   | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | FPR1/AGT/ADORA2A     | 3 |
| GO:0008217 | regulation of blood pressure                                      | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | SOD2/MME/AGT         | 3 |
| GO:0009791 | post-embryonic development                                        | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | BAX/TIPARP/GATA3     | 3 |
| GO:0016236 | macroautophagy                                                    | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | HIF1A/HDAC6/TBK1     | 3 |
| GO:0021543 | pallium development                                               | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | HIF1A/COL3A1/BAX     | 3 |
| GO:0042104 | positive regulation of activated T cell proliferation             | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | CD24/IL6R/EPO        | 3 |
| GO:0043550 | regulation of lipid kinase activity                               | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | SOCS3/TGFB1/SOCS1    | 3 |
| GO:0048246 | macrophage chemotaxis                                             | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | SLAMF8/CMKLR1/C5AR1  | 3 |
| GO:0055008 | cardiac muscle tissue morphogenesis                               | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | TGFB1/FKBP1A/MYOM2   | 3 |
| GO:0055024 | regulation of cardiac muscle tissue development                   | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | TGFB1/MAPK11/G6PD    | 3 |
| GO:0060840 | artery development                                                | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | COL3A1/LDLR/APOE     | 3 |
| GO:0061351 | neural precursor cell proliferation                               | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/C5AR1    | 3 |
| GO:0061756 | leukocyte adhesion to vascular endothelial cell                   | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | ICAM1/VCAM1/ITGB2    | 3 |
| GO:0071604 | transforming growth factor beta production                        | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | HIF1A/CD24/ITGB6     | 3 |

|            |                                                                               |       |        |             |             |             |                        |   |
|------------|-------------------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|------------------------|---|
| GO:0071634 | regulation of transforming growth factor beta production                      | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | HIF1A/CD24/ITGB6       | 3 |
| GO:0072539 | T-helper 17 cell differentiation                                              | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | STAT3/NFKBIZ/RORC      | 3 |
| GO:1905521 | regulation of macrophage migration                                            | 3/182 | 16/749 | 0,787776214 | 0,999954951 | 0,999954951 | SLAMF8/CMKLR1/C5AR1    | 3 |
| GO:0002062 | chondrocyte differentiation                                                   | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | MAF/TGFB1/TGFB1        | 3 |
| GO:0002495 | antigen processing and presentation of peptide antigen via MHC                | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | FCER1G/IFI30/CTSS      | 3 |
| GO:0016054 | organic acid catabolic process                                                | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | ALDH3A2/LYVE1/TGFB1    | 3 |
| GO:0019886 | antigen processing and presentation of exogenous peptide antigen              | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | FCER1G/IFI30/CTSS      | 3 |
| GO:0019935 | cyclic-nucleotide-mediated signaling                                          | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | AHR/APOE/ADORA2A       | 3 |
| GO:0031396 | regulation of protein ubiquitination                                          | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | FKBP1A/BIRC3/ISG15     | 3 |
| GO:0032689 | negative regulation of interferon-gamma production                            | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | TLR4/LILRB1/GATA3      | 3 |
| GO:0035148 | tube formation                                                                | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/GATA3      | 3 |
| GO:0045824 | negative regulation of innate immune response                                 | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | SERPINE1/SLAMF8/LILRB1 | 3 |
| GO:0046395 | carboxylic acid catabolic process                                             | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | ALDH3A2/LYVE1/TGFB1    | 3 |
| GO:0051301 | cell division                                                                 | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | TGFB1/MYC/KLHL13       | 3 |
| GO:0051702 | interaction with symbiont                                                     | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | LTF/APOE/FN1           | 3 |
| GO:0055017 | cardiac muscle tissue growth                                                  | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | AGT/MAPK11/G6PD        | 3 |
| GO:0072538 | T-helper 17 type immune response                                              | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | STAT3/NFKBIZ/RORC      | 3 |
| GO:1902905 | positive regulation of supramolecular fiber organization                      | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | ICAM1/APOE/NOX4        | 3 |
| GO:1903522 | regulation of blood circulation                                               | 3/182 | 17/749 | 0,822880239 | 0,999954951 | 0,999954951 | EHD3/ICAM1/AGT         | 3 |
| GO:0002204 | somatic recombination of immunoglobulin genes involved in immune response     | 3/182 | 18/749 | 0,852936063 | 0,999954951 | 0,999954951 | BCL6/TGFB1/STAT6       | 3 |
| GO:0002208 | somatic diversification of immunoglobulins involved in immune response        | 3/182 | 18/749 | 0,852936063 | 0,999954951 | 0,999954951 | BCL6/TGFB1/STAT6       | 3 |
| GO:0002504 | antigen processing and presentation of peptide or polysaccharide antigen      | 3/182 | 18/749 | 0,852936063 | 0,999954951 | 0,999954951 | FCER1G/IFI30/CTSS      | 3 |
| GO:0002724 | regulation of T cell cytokine production                                      | 3/182 | 18/749 | 0,852936063 | 0,999954951 | 0,999954951 | IL1R1/TNFRSF1B/GATA3   | 3 |
| GO:0006936 | muscle contraction                                                            | 3/182 | 18/749 | 0,852936063 | 0,999954951 | 0,999954951 | EHD3/AGT/MYOM2         | 3 |
| GO:0016447 | somatic recombination of immunoglobulin gene segments                         | 3/182 | 18/749 | 0,852936063 | 0,999954951 | 0,999954951 | BCL6/TGFB1/STAT6       | 3 |
| GO:0043030 | regulation of macrophage activation                                           | 3/182 | 18/749 | 0,852936063 | 0,999954951 | 0,999954951 | IL4R/LDLR/TLR4         | 3 |
| GO:0043372 | positive regulation of CD4-positive, alpha-beta T cell differentiation        | 3/182 | 18/749 | 0,852936063 | 0,999954951 | 0,999954951 | IL4R/NFKBIZ/SOCS1      | 3 |
| GO:0045190 | isotype switching                                                             | 3/182 | 18/749 | 0,852936063 | 0,999954951 | 0,999954951 | BCL6/TGFB1/STAT6       | 3 |
| GO:0050766 | positive regulation of phagocytosis                                           | 3/182 | 18/749 | 0,852936063 | 0,999954951 | 0,999954951 | C3/FCER1G/SLC11A1      | 3 |
| GO:0050848 | regulation of calcium-mediated signaling                                      | 3/182 | 18/749 | 0,852936063 | 0,999954951 | 0,999954951 | FKBP1A/CMKLR1/RGN      | 3 |
| GO:0061614 | pri-miRNA transcription by RNA polymerase II                                  | 3/182 | 18/749 | 0,852936063 | 0,999954951 | 0,999954951 | HIF1A/STAT3/TGFB1      | 3 |
| GO:0002431 | Fc receptor mediated stimulatory signaling pathway                            | 3/182 | 19/749 | 0,878469122 | 0,999954951 | 0,999954951 | FCER1G/FCGR1A/FCGR2A   | 3 |
| GO:0002707 | negative regulation of lymphocyte mediated immunity                           | 3/182 | 19/749 | 0,878469122 | 0,999954951 | 0,999954951 | BCL6/LILRB1/PTPN6      | 3 |
| GO:0003015 | heart process                                                                 | 3/182 | 19/749 | 0,878469122 | 0,999954951 | 0,999954951 | EHD3/AGT/NOX4          | 3 |
| GO:0009408 | response to heat                                                              | 3/182 | 19/749 | 0,878469122 | 0,999954951 | 0,999954951 | CDKN1A/ABCC2/CD14      | 3 |
| GO:0016445 | somatic diversification of immunoglobulins                                    | 3/182 | 19/749 | 0,878469122 | 0,999954951 | 0,999954951 | BCL6/TGFB1/STAT6       | 3 |
| GO:0038034 | signal transduction in absence of ligand                                      | 3/182 | 19/749 | 0,878469122 | 0,999954951 | 0,999954951 | LCN2/BAX/KITLG         | 3 |
| GO:0038094 | Fc-gamma receptor signaling pathway                                           | 3/182 | 19/749 | 0,878469122 | 0,999954951 | 0,999954951 | FCER1G/FCGR1A/FCGR2A   | 3 |
| GO:0045216 | cell-cell junction organization                                               | 3/182 | 19/749 | 0,878469122 | 0,999954951 | 0,999954951 | TGFB1/AGT/PVR          | 3 |
| GO:0060419 | heart growth                                                                  | 3/182 | 19/749 | 0,878469122 | 0,999954951 | 0,999954951 | AGT/MAPK11/G6PD        | 3 |
| GO:0070231 | T cell apoptotic process                                                      | 3/182 | 19/749 | 0,878469122 | 0,999954951 | 0,999954951 | HIF1A/JAK3/BAX         | 3 |
| GO:0097192 | extrinsic apoptotic signaling pathway in absence of ligand                    | 3/182 | 19/749 | 0,878469122 | 0,999954951 | 0,999954951 | LCN2/BAX/KITLG         | 3 |
| GO:2000351 | regulation of endothelial cell apoptotic process                              | 3/182 | 19/749 | 0,878469122 | 0,999954951 | 0,999954951 | ICAM1/SERPINE1/GATA3   | 3 |
| GO:0010639 | negative regulation of organelle organization                                 | 3/182 | 20/749 | 0,900008655 | 0,999954951 | 0,999954951 | HDAC6/DNMT1/LILRB2     | 3 |
| GO:0032620 | interleukin-17 production                                                     | 3/182 | 20/749 | 0,900008655 | 0,999954951 | 0,999954951 | TGFB1/TLR4/MYD88       | 3 |
| GO:0032660 | regulation of interleukin-17 production                                       | 3/182 | 20/749 | 0,900008655 | 0,999954951 | 0,999954951 | TGFB1/TLR4/MYD88       | 3 |
| GO:0032835 | glomerulus development                                                        | 3/182 | 20/749 | 0,900008655 | 0,999954951 | 0,999954951 | CD24/EGR1/IL6R         | 3 |
| GO:0042391 | regulation of membrane potential                                              | 3/182 | 20/749 | 0,900008655 | 0,999954951 | 0,999954951 | EHD3/BAX/ADORA2A       | 3 |
| GO:0002381 | immunoglobulin production involved in immunoglobulin mediated immune response | 3/182 | 21/749 | 0,918064962 | 0,999954951 | 0,999954951 | BCL6/TGFB1/STAT6       | 3 |
| GO:0030890 | positive regulation of B cell proliferation                                   | 3/182 | 21/749 | 0,918064962 | 0,999954951 | 0,999954951 | BCL6/CDKN1A/TLR4       | 3 |
| GO:0033138 | positive regulation of peptidyl-serine phosphorylation                        | 3/182 | 21/749 | 0,918064962 | 0,999954951 | 0,999954951 | HDAC6/TGFB1/TBK1       | 3 |
| GO:0043535 | regulation of blood vessel endothelial cell migration                         | 3/182 | 21/749 | 0,918064962 | 0,999954951 | 0,999954951 | HIF1A/TGFB1/APOE       | 3 |
| GO:0046330 | positive regulation of JNK cascade                                            | 3/182 | 21/749 | 0,918064962 | 0,999954951 | 0,999954951 | LTBR/TLR4/FGD2         | 3 |
| GO:0072577 | endothelial cell apoptotic process                                            | 3/182 | 21/749 | 0,918064962 | 0,999954951 | 0,999954951 | ICAM1/SERPINE1/GATA3   | 3 |
| GO:1905517 | macrophage migration                                                          | 3/182 | 21/749 | 0,918064962 | 0,999954951 | 0,999954951 | SLAMF8/CMKLR1/C5AR1    | 3 |
| GO:0016202 | regulation of striated muscle tissue development                              | 3/182 | 22/749 | 0,93311493  | 0,999954951 | 0,999954951 | TGFB1/MAPK11/G6PD      | 3 |
| GO:0034103 | regulation of tissue remodeling                                               | 3/182 | 22/749 | 0,93311493  | 0,999954951 | 0,999954951 | TGFB1/BAX/AGT          | 3 |
| GO:0046006 | regulation of activated T cell proliferation                                  | 3/182 | 22/749 | 0,93311493  | 0,999954951 | 0,999954951 | CD24/IL6R/EPO          | 3 |
| GO:0046638 | positive regulation of alpha-beta T cell differentiation                      | 3/182 | 22/749 | 0,93311493  | 0,999954951 | 0,999954951 | IL4R/NFKBIZ/SOCS1      | 3 |

|            |                                                                     |       |        |             |             |             |                        |   |
|------------|---------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|------------------------|---|
| GO:0048634 | regulation of muscle organ development                              | 3/182 | 22/749 | 0,93311493  | 0,999954951 | 0,999954951 | TGFB1/MAPK11/G6PD      | 3 |
| GO:0050710 | negative regulation of cytokine secretion                           | 3/182 | 22/749 | 0,93311493  | 0,999954951 | 0,999954951 | IL1R2/FN1/LILRB1       | 3 |
| GO:0051100 | negative regulation of binding                                      | 3/182 | 22/749 | 0,93311493  | 0,999954951 | 0,999954951 | SLPI/BAX/IFIT1         | 3 |
| GO:1901861 | regulation of muscle tissue development                             | 3/182 | 22/749 | 0,93311493  | 0,999954951 | 0,999954951 | TGFB1/MAPK11/G6PD      | 3 |
| GO:0002562 | somatic diversification of immune receptors via germline recom      | 3/182 | 23/749 | 0,945593776 | 0,999954951 | 0,999954951 | BCL6/TGFB1/STAT6       | 3 |
| GO:0002763 | positive regulation of myeloid leukocyte differentiation            | 3/182 | 23/749 | 0,945593776 | 0,999954951 | 0,999954951 | TGFB1/KITLG/TRIB1      | 3 |
| GO:0014068 | positive regulation of phosphatidylinositol 3-kinase signaling      | 3/182 | 23/749 | 0,945593776 | 0,999954951 | 0,999954951 | AGT/EPO/PTPN6          | 3 |
| GO:0016444 | somatic cell DNA recombination                                      | 3/182 | 23/749 | 0,945593776 | 0,999954951 | 0,999954951 | BCL6/TGFB1/STAT6       | 3 |
| GO:0016525 | negative regulation of angiogenesis                                 | 3/182 | 23/749 | 0,945593776 | 0,999954951 | 0,999954951 | STAT1/AGT/SERPINE1     | 3 |
| GO:0030509 | BMP signaling pathway                                               | 3/182 | 23/749 | 0,945593776 | 0,999954951 | 0,999954951 | SOST/EGR1/GDF15        | 3 |
| GO:0050798 | activated T cell proliferation                                      | 3/182 | 23/749 | 0,945593776 | 0,999954951 | 0,999954951 | CD24/IL6R/EPO          | 3 |
| GO:0051817 | modulation of process of other organism involved in symbiotic ir    | 3/182 | 23/749 | 0,945593776 | 0,999954951 | 0,999954951 | LTF/TGFB1/APOE         | 3 |
| GO:2000181 | negative regulation of blood vessel morphogenesis                   | 3/182 | 23/749 | 0,945593776 | 0,999954951 | 0,999954951 | STAT1/AGT/SERPINE1     | 3 |
| GO:2000516 | positive regulation of CD4-positive, alpha-beta T cell activation   | 3/182 | 23/749 | 0,945593776 | 0,999954951 | 0,999954951 | IL4R/NFKBIZ/SOCS1      | 3 |
| GO:0001837 | epithelial to mesenchymal transition                                | 3/182 | 24/749 | 0,95589132  | 0,999954951 | 0,999954951 | HIF1A/COL1A1/TGFB1     | 3 |
| GO:0001938 | positive regulation of endothelial cell proliferation               | 3/182 | 24/749 | 0,95589132  | 0,999954951 | 0,999954951 | HIF1A/STAT3/NR4A1      | 3 |
| GO:0002200 | somatic diversification of immune receptors                         | 3/182 | 24/749 | 0,95589132  | 0,999954951 | 0,999954951 | BCL6/TGFB1/STAT6       | 3 |
| GO:0021537 | telencephalon development                                           | 3/182 | 24/749 | 0,95589132  | 0,999954951 | 0,999954951 | HIF1A/COL3A1/BAX       | 3 |
| GO:0032874 | positive regulation of stress-activated MAPK cascade                | 3/182 | 24/749 | 0,95589132  | 0,999954951 | 0,999954951 | LTBR/TLR4/FGD2         | 3 |
| GO:0043433 | negative regulation of DNA-binding transcription factor activity    | 3/182 | 24/749 | 0,95589132  | 0,999954951 | 0,999954951 | SIGIRR/CMKLR1/TRIB1    | 3 |
| GO:0070304 | positive regulation of stress-activated protein kinase signaling ca | 3/182 | 24/749 | 0,95589132  | 0,999954951 | 0,999954951 | LTBR/TLR4/FGD2         | 3 |
| GO:1904035 | regulation of epithelial cell apoptotic process                     | 3/182 | 24/749 | 0,95589132  | 0,999954951 | 0,999954951 | ICAM1/SERPINE1/GATA3   | 3 |
| GO:0009266 | response to temperature stimulus                                    | 3/182 | 25/749 | 0,964351447 | 0,999954951 | 0,999954951 | CDKN1A/ABCC2/CD14      | 3 |
| GO:0035265 | organ growth                                                        | 3/182 | 25/749 | 0,964351447 | 0,999954951 | 0,999954951 | AGT/MAPK11/G6PD        | 3 |
| GO:0046328 | regulation of JNK cascade                                           | 3/182 | 25/749 | 0,964351447 | 0,999954951 | 0,999954951 | LTBR/TLR4/FGD2         | 3 |
| GO:0007015 | actin filament organization                                         | 3/182 | 26/749 | 0,971273692 | 0,999954951 | 0,999954951 | ICAM1/NOX4/MYOM2       | 3 |
| GO:0014066 | regulation of phosphatidylinositol 3-kinase signaling               | 3/182 | 26/749 | 0,971273692 | 0,999954951 | 0,999954951 | AGT/EPO/PTPN6          | 3 |
| GO:0032651 | regulation of interleukin-1 beta production                         | 3/182 | 26/749 | 0,971273692 | 0,999954951 | 0,999954951 | EGR1/TLR4/ERRFI1       | 3 |
| GO:0043604 | amide biosynthetic process                                          | 3/182 | 26/749 | 0,971273692 | 0,999954951 | 0,999954951 | BCL3/STAT3/TNFRSF1A    | 3 |
| GO:0072678 | T cell migration                                                    | 3/182 | 26/749 | 0,971273692 | 0,999954951 | 0,999954951 | ICAM1/CXCL16/TNFSF14   | 3 |
| GO:0002711 | positive regulation of T cell mediated immunity                     | 3/182 | 27/749 | 0,976916167 | 0,999954951 | 0,999954951 | IL1R1/PVR/GATA3        | 3 |
| GO:0006310 | DNA recombination                                                   | 3/182 | 27/749 | 0,976916167 | 0,999954951 | 0,999954951 | BCL6/TGFB1/STAT6       | 3 |
| GO:0034329 | cell junction assembly                                              | 3/182 | 27/749 | 0,976916167 | 0,999954951 | 0,999954951 | AGT/TLR2/FN1           | 3 |
| GO:0031294 | lymphocyte costimulation                                            | 3/182 | 28/749 | 0,981499233 | 0,999954951 | 0,999954951 | CD24/TNFSF14/PTPN6     | 3 |
| GO:0031295 | T cell costimulation                                                | 3/182 | 28/749 | 0,981499233 | 0,999954951 | 0,999954951 | CD24/TNFSF14/PTPN6     | 3 |
| GO:0032611 | interleukin-1 beta production                                       | 3/182 | 29/749 | 0,985209496 | 0,999954951 | 0,999954951 | EGR1/TLR4/ERRFI1       | 3 |
| GO:0007179 | transforming growth factor beta receptor signaling pathway          | 3/182 | 30/749 | 0,988203855 | 0,999954951 | 0,999954951 | COL3A1/TGFB1/GDF15     | 3 |
| GO:0032623 | interleukin-2 production                                            | 3/182 | 30/749 | 0,988203855 | 0,999954951 | 0,999954951 | FCER1G/SLC11A1/GATA3   | 3 |
| GO:0045058 | T cell selection                                                    | 3/182 | 30/749 | 0,988203855 | 0,999954951 | 0,999954951 | STAT3/STAT6/GATA3      | 3 |
| GO:1903829 | positive regulation of cellular protein localization                | 3/182 | 30/749 | 0,988203855 | 0,999954951 | 0,999954951 | FCER1G/TGFB1/ITGB2     | 3 |
| GO:2001237 | negative regulation of extrinsic apoptotic signaling pathway        | 3/182 | 30/749 | 0,988203855 | 0,999954951 | 0,999954951 | ICAM1/TNFSF10/SERPINE1 | 3 |
| GO:0030101 | natural killer cell activation                                      | 3/182 | 31/749 | 0,990613382 | 0,999954951 | 0,999954951 | IL6R/HNF1A/ITGB2       | 3 |
| GO:0007389 | pattern specification process                                       | 3/182 | 33/749 | 0,994094527 | 0,999954951 | 0,999954951 | HIF1A/C3/C1QA          | 3 |
| GO:0030900 | forebrain development                                               | 3/182 | 33/749 | 0,994094527 | 0,999954951 | 0,999954951 | HIF1A/COL3A1/BAX       | 3 |
| GO:0001910 | regulation of leukocyte mediated cytotoxicity                       | 3/182 | 38/749 | 0,998207347 | 0,999954951 | 0,999954951 | ICAM1/PVR/LILRB1       | 3 |
| GO:1903827 | regulation of cellular protein localization                         | 3/182 | 43/749 | 0,999478047 | 0,999954951 | 0,999954951 | FCER1G/TGFB1/ITGB2     | 3 |
| GO:0001782 | B cell homeostasis                                                  | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | HIF1A/BAX              | 2 |
| GO:0001841 | neural tube formation                                               | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | HIF1A/TGFB1            | 2 |
| GO:0002279 | mast cell activation involved in immune response                    | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | FCER1G/IL4R            | 2 |
| GO:0002448 | mast cell mediated immunity                                         | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | FCER1G/IL4R            | 2 |
| GO:0007405 | neuroblast proliferation                                            | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | HIF1A/TGFB1            | 2 |
| GO:0010712 | regulation of collagen metabolic process                            | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | TGFB1/ERRFI1           | 2 |
| GO:0010743 | regulation of macrophage derived foam cell differentiation          | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | AGT/NFKB1              | 2 |
| GO:0014020 | primary neural tube formation                                       | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | HIF1A/TGFB1            | 2 |
| GO:0031398 | positive regulation of protein ubiquitination                       | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | FKBP1A/BIRC3           | 2 |
| GO:0032570 | response to progesterone                                            | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | TGFB1/TLR2             | 2 |
| GO:0032700 | negative regulation of interleukin-17 production                    | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | TGFB1/TLR4             | 2 |
| GO:0033559 | unsaturated fatty acid metabolic process                            | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | TNFRSF1A/ALOX5         | 2 |
| GO:0035195 | gene silencing by miRNA                                             | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | STAT3/TGFB1            | 2 |



|            |                                                                   |       |        |             |             |             |                |   |
|------------|-------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|----------------|---|
| GO:0038110 | interleukin-2-mediated signaling pathway                          | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | JAK1/JAK3      | 2 |
| GO:0042033 | chemokine biosynthetic process                                    | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | SIGIRR/EGR1    | 2 |
| GO:0042752 | regulation of circadian rhythm                                    | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | RORC/ADORA2A   | 2 |
| GO:0043279 | response to alkaloid                                              | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | ICAM1/ADORA2A  | 2 |
| GO:0043303 | mast cell degranulation                                           | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | FCER1G/IL4R    | 2 |
| GO:0043407 | negative regulation of MAP kinase activity                        | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | APOE/PTPN6     | 2 |
| GO:0045414 | regulation of interleukin-8 biosynthetic process                  | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | BCL3/TLR4      | 2 |
| GO:0045830 | positive regulation of isotype switching                          | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | TGFB1/STAT6    | 2 |
| GO:0045911 | positive regulation of DNA recombination                          | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | TGFB1/STAT6    | 2 |
| GO:0050755 | chemokine metabolic process                                       | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | SIGIRR/EGR1    | 2 |
| GO:0060688 | regulation of morphogenesis of a branching structure              | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | TGFB1/AGT      | 2 |
| GO:0070669 | response to interleukin-2                                         | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | JAK1/JAK3      | 2 |
| GO:0071352 | cellular response to interleukin-2                                | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | JAK1/JAK3      | 2 |
| GO:0090398 | cellular senescence                                               | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | BCL6/CDKN1A    | 2 |
| GO:0097306 | cellular response to alcohol                                      | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | AHR/TNC        | 2 |
| GO:1904994 | regulation of leukocyte adhesion to vascular endothelial cell     | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | ICAM1/ITGB2    | 2 |
| GO:1990138 | neuron projection extension                                       | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | APOE/FN1       | 2 |
| GO:2000573 | positive regulation of DNA biosynthetic process                   | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | MYC/NOX4       | 2 |
| GO:2000725 | regulation of cardiac muscle cell differentiation                 | 2/182 | 10/749 | 0,741695722 | 0,999954951 | 0,999954951 | TGFB1/G6PD     | 2 |
| GO:0002483 | antigen processing and presentation of endogenous peptide ant     | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | TAP2/TAP1      | 2 |
| GO:0002544 | chronic inflammatory response                                     | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | S100A8/VCAM1   | 2 |
| GO:0002691 | regulation of cellular extravasation                              | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | IL1R1/ICAM1    | 2 |
| GO:0002726 | positive regulation of T cell cytokine production                 | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | IL1R1/GATA3    | 2 |
| GO:0008643 | carbohydrate transport                                            | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | C3/HNF1A       | 2 |
| GO:0010463 | mesenchymal cell proliferation                                    | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | STAT1/MYC      | 2 |
| GO:0010596 | negative regulation of endothelial cell migration                 | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | TGFB1/APOE     | 2 |
| GO:0010906 | regulation of glucose metabolic process                           | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | RORC/RGN       | 2 |
| GO:0015908 | fatty acid transport                                              | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | APOE/ABCC2     | 2 |
| GO:0016052 | carbohydrate catabolic process                                    | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | HIF1A/STAT3    | 2 |
| GO:0016441 | posttranscriptional gene silencing                                | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | STAT3/TGFB1    | 2 |
| GO:0019885 | antigen processing and presentation of endogenous peptide ant     | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | TAP2/TAP1      | 2 |
| GO:0030224 | monocyte differentiation                                          | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | IRF7/MYC       | 2 |
| GO:0031047 | gene silencing by RNA                                             | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | STAT3/TGFB1    | 2 |
| GO:0032692 | negative regulation of interleukin-1 production                   | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | IL1R2/ERRFI1   | 2 |
| GO:0034763 | negative regulation of transmembrane transport                    | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | TGFB1/EPO      | 2 |
| GO:0035194 | post-transcriptional gene silencing by RNA                        | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | STAT3/TGFB1    | 2 |
| GO:0035924 | cellular response to vascular endothelial growth factor stimulus  | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | NR4A1/VCAM1    | 2 |
| GO:0042228 | interleukin-8 biosynthetic process                                | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | BCL3/TLR4      | 2 |
| GO:0042698 | ovulation cycle                                                   | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | ADAMTS1/EGR1   | 2 |
| GO:0043467 | regulation of generation of precursor metabolites and energy      | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | HIF1A/STAT3    | 2 |
| GO:0045072 | regulation of interferon-gamma biosynthetic process               | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | CD276/LILRB1   | 2 |
| GO:0045661 | regulation of myoblast differentiation                            | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | TGFB1/TNFSF14  | 2 |
| GO:0045682 | regulation of epidermis development                               | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | PLAAT4/ERRFI1  | 2 |
| GO:0045931 | positive regulation of mitotic cell cycle                         | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | ADAMTS1/TGFB1  | 2 |
| GO:0046902 | regulation of mitochondrial membrane permeability                 | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | STAT3/BAX      | 2 |
| GO:0048259 | regulation of receptor-mediated endocytosis                       | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | C3/SERPINE1    | 2 |
| GO:0048260 | positive regulation of receptor-mediated endocytosis              | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | C3/SERPINE1    | 2 |
| GO:0050954 | sensory perception of mechanical stimulus                         | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | COL1A1/ICAM1   | 2 |
| GO:0055021 | regulation of cardiac muscle tissue growth                        | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | MAPK11/G6PD    | 2 |
| GO:0061025 | membrane fusion                                                   | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | TAP2/TAP1      | 2 |
| GO:0061384 | heart trabecula morphogenesis                                     | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | ADAMTS1/FKBP1A | 2 |
| GO:0061437 | renal system vasculature development                              | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | EGR1/IL6R      | 2 |
| GO:0061440 | kidney vasculature development                                    | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | EGR1/IL6R      | 2 |
| GO:0070206 | protein trimerization                                             | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | LCN2/COL1A1    | 2 |
| GO:0071677 | positive regulation of mononuclear cell migration                 | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | TGFB1/SERPINE1 | 2 |
| GO:0072012 | glomerulus vasculature development                                | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | EGR1/IL6R      | 2 |
| GO:1902624 | positive regulation of neutrophil migration                       | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | IL1R1/C5AR1    | 2 |
| GO:1903131 | mononuclear cell differentiation                                  | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | IRF7/MYC       | 2 |
| GO:1903322 | positive regulation of protein modification by small protein conj | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | FKBP1A/BIRC3   | 2 |

|            |                                                                 |       |        |             |             |             |                |   |
|------------|-----------------------------------------------------------------|-------|--------|-------------|-------------|-------------|----------------|---|
| GO:1905523 | positive regulation of macrophage migration                     | 2/182 | 11/749 | 0,790115776 | 0,999954951 | 0,999954951 | CMKLR1/C5AR1   | 2 |
| GO:0002295 | T-helper cell lineage commitment                                | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | STAT3/STAT6    | 2 |
| GO:0002577 | regulation of antigen processing and presentation               | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | LILRB2/SLC11A1 | 2 |
| GO:0002861 | regulation of inflammatory response to antigenic stimulus       | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | C3/FCER1G      | 2 |
| GO:0003229 | ventricular cardiac muscle tissue development                   | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | TGFB1/FKBP1A   | 2 |
| GO:0007006 | mitochondrial membrane organization                             | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | STAT3/BAX      | 2 |
| GO:0007017 | microtubule-based process                                       | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | HIF1A/HDAC6    | 2 |
| GO:0007188 | adenylate cyclase-modulating G protein-coupled receptor signal  | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | FPR1/ADORA2A   | 2 |
| GO:0008016 | regulation of heart contraction                                 | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | EHD3/AGT       | 2 |
| GO:0010633 | negative regulation of epithelial cell migration                | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | TGFB1/APOE     | 2 |
| GO:0010769 | regulation of cell morphogenesis involved in differentiation    | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | APOE/FN1       | 2 |
| GO:0014855 | striated muscle cell proliferation                              | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | STAT3/MAPK11   | 2 |
| GO:0015718 | monocarboxylic acid transport                                   | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | APOE/ABCC2     | 2 |
| GO:0019933 | cAMP-mediated signaling                                         | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | AHR/ADORA2A    | 2 |
| GO:0032693 | negative regulation of interleukin-10 production                | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | JAK3/LILRB1    | 2 |
| GO:0032740 | positive regulation of interleukin-17 production                | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | TGFB1/MYD88    | 2 |
| GO:0035264 | multicellular organism growth                                   | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | STAT3/GDF15    | 2 |
| GO:0035872 | nucleotide-binding domain, leucine rich repeat containing recep | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | TLR4/BIRC3     | 2 |
| GO:0036037 | CD8-positive, alpha-beta T cell activation                      | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | SOCS1/LILRB1   | 2 |
| GO:0042095 | interferon-gamma biosynthetic process                           | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | CD276/LILRB1   | 2 |
| GO:0048010 | vascular endothelial growth factor receptor signaling pathway   | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | HIF1A/MAPK11   | 2 |
| GO:0055010 | ventricular cardiac muscle tissue morphogenesis                 | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | TGFB1/FKBP1A   | 2 |
| GO:0061035 | regulation of cartilage development                             | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | MAF/TGFB1      | 2 |
| GO:0070423 | nucleotide-binding oligomerization domain containing signaling  | 2/182 | 12/749 | 0,83038709  | 0,999954951 | 0,999954951 | TLR4/BIRC3     | 2 |
| GO:0001570 | vasculogenesis                                                  | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | TGFB1/TIPARP   | 2 |
| GO:0001885 | endothelial cell development                                    | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | TNFRSF1A/ICAM1 | 2 |
| GO:0002830 | positive regulation of type 2 immune response                   | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | IL4R/GATA3     | 2 |
| GO:0006396 | RNA processing                                                  | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | TGFB1/ISG20    | 2 |
| GO:0010818 | T cell chemotaxis                                               | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | CXCL16/TNFSF14 | 2 |
| GO:0019883 | antigen processing and presentation of endogenous antigen       | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | TAP2/TAP1      | 2 |
| GO:0043373 | CD4-positive, alpha-beta T cell lineage commitment              | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | STAT3/STAT6    | 2 |
| GO:0048524 | positive regulation of viral process                            | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | APOE/IFIT1     | 2 |
| GO:0051851 | modulation by host of symbiont process                          | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | LTF/APOE       | 2 |
| GO:0060420 | regulation of heart growth                                      | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | MAPK11/G6PD    | 2 |
| GO:1901796 | regulation of signal transduction by p53 class mediator         | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | MUC1/MAPK11    | 2 |
| GO:1905207 | regulation of cardiocyte differentiation                        | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | TGFB1/G6PD     | 2 |
| GO:2000177 | regulation of neural precursor cell proliferation               | 2/182 | 13/749 | 0,863589688 | 0,999954951 | 0,999954951 | HIF1A/TGFB1    | 2 |
| GO:0001960 | negative regulation of cytokine-mediated signaling pathway      | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | SIGIRR/IL1R2   | 2 |
| GO:0002363 | alpha-beta T cell lineage commitment                            | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | STAT3/STAT6    | 2 |
| GO:0006417 | regulation of translation                                       | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | BCL3/STAT3     | 2 |
| GO:0010921 | regulation of phosphatase activity                              | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | FKBP1A/RGN     | 2 |
| GO:0021915 | neural tube development                                         | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | HIF1A/TGFB1    | 2 |
| GO:0032526 | response to retinoic acid                                       | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | COL1A1/TNC     | 2 |
| GO:0032715 | negative regulation of interleukin-6 production                 | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | TLR4/PTPN6     | 2 |
| GO:0032753 | positive regulation of interleukin-4 production                 | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | FCER1G/GATA3   | 2 |
| GO:0035270 | endocrine system development                                    | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | IL6R/GATA3     | 2 |
| GO:0043369 | CD4-positive or CD8-positive, alpha-beta T cell lineage commitm | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | STAT3/STAT6    | 2 |
| GO:0045624 | positive regulation of T-helper cell differentiation            | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | IL4R/NFKBIZ    | 2 |
| GO:0050691 | regulation of defense response to virus by host                 | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | STAT1/LILRB1   | 2 |
| GO:0070232 | regulation of T cell apoptotic process                          | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | HIF1A/JAK3     | 2 |
| GO:0090559 | regulation of membrane permeability                             | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | STAT3/BAX      | 2 |
| GO:2001020 | regulation of response to DNA damage stimulus                   | 2/182 | 14/749 | 0,890762285 | 0,999954951 | 0,999954951 | MUC1/MYC       | 2 |
| GO:0003179 | heart valve morphogenesis                                       | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | TGFB1/GATA3    | 2 |
| GO:0006839 | mitochondrial transport                                         | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | STAT3/BAX      | 2 |
| GO:0007292 | female gamete generation                                        | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | ADAMTS1/IL4R   | 2 |
| GO:0010862 | positive regulation of pathway-restricted SMAD protein phospho  | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | TGFB1/GDF15    | 2 |
| GO:0035743 | CD4-positive, alpha-beta T cell cytokine production             | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | IL1R1/GATA3    | 2 |
| GO:0043536 | positive regulation of blood vessel endothelial cell migration  | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | HIF1A/TGFB1    | 2 |
| GO:0045445 | myoblast differentiation                                        | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | TGFB1/TNFSF14  | 2 |

|            |                                                                    |       |        |             |             |             |                |   |
|------------|--------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|----------------|---|
| GO:0050704 | regulation of interleukin-1 secretion                              | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | TLR4/IL1R2     | 2 |
| GO:0060047 | heart contraction                                                  | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | EHD3/AGT       | 2 |
| GO:0060761 | negative regulation of response to cytokine stimulus               | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | SIGIRR/IL1R2   | 2 |
| GO:0071622 | regulation of granulocyte chemotaxis                               | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | CMKLR1/C5AR1   | 2 |
| GO:0090101 | negative regulation of transmembrane receptor protein serine/t     | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | SOST/TGFB1     | 2 |
| GO:0150077 | regulation of neuroinflammatory response                           | 2/182 | 15/749 | 0,912858682 | 0,999954951 | 0,999954951 | LDLR/TNFRSF1B  | 2 |
| GO:0001704 | formation of primary germ layer                                    | 2/182 | 16/749 | 0,930727606 | 0,999954951 | 0,999954951 | ITGB2/FN1      | 2 |
| GO:0030073 | insulin secretion                                                  | 2/182 | 16/749 | 0,930727606 | 0,999954951 | 0,999954951 | HIF1A/HNF1A    | 2 |
| GO:0032092 | positive regulation of protein binding                             | 2/182 | 16/749 | 0,930727606 | 0,999954951 | 0,999954951 | FKBP1A/APOE    | 2 |
| GO:0046620 | regulation of organ growth                                         | 2/182 | 16/749 | 0,930727606 | 0,999954951 | 0,999954951 | MAPK11/G6PD    | 2 |
| GO:0046849 | bone remodeling                                                    | 2/182 | 16/749 | 0,930727606 | 0,999954951 | 0,999954951 | TGFB1/NOX4     | 2 |
| GO:0051495 | positive regulation of cytoskeleton organization                   | 2/182 | 16/749 | 0,930727606 | 0,999954951 | 0,999954951 | ICAM1/NOX4     | 2 |
| GO:1905477 | positive regulation of protein localization to membrane            | 2/182 | 16/749 | 0,930727606 | 0,999954951 | 0,999954951 | TGFB1/ITGB2    | 2 |
| GO:0002360 | T cell lineage commitment                                          | 2/182 | 17/749 | 0,945107255 | 0,999954951 | 0,999954951 | STAT3/STAT6    | 2 |
| GO:0002507 | tolerance induction                                                | 2/182 | 17/749 | 0,945107255 | 0,999954951 | 0,999954951 | TGFB1/LILRB2   | 2 |
| GO:0032673 | regulation of interleukin-4 production                             | 2/182 | 17/749 | 0,945107255 | 0,999954951 | 0,999954951 | FCER1G/GATA3   | 2 |
| GO:0032731 | positive regulation of interleukin-1 beta production               | 2/182 | 17/749 | 0,945107255 | 0,999954951 | 0,999954951 | EGR1/TLR4      | 2 |
| GO:0050701 | interleukin-1 secretion                                            | 2/182 | 17/749 | 0,945107255 | 0,999954951 | 0,999954951 | TLR4/IL1R2     | 2 |
| GO:0060393 | regulation of pathway-restricted SMAD protein phosphorylation      | 2/182 | 17/749 | 0,945107255 | 0,999954951 | 0,999954951 | TGFB1/GDF15    | 2 |
| GO:0060395 | SMAD protein signal transduction                                   | 2/182 | 17/749 | 0,945107255 | 0,999954951 | 0,999954951 | TGFB1/GDF15    | 2 |
| GO:0110053 | regulation of actin filament organization                          | 2/182 | 17/749 | 0,945107255 | 0,999954951 | 0,999954951 | ICAM1/NOX4     | 2 |
| GO:0002433 | immune response-regulating cell surface receptor signaling path    | 2/182 | 18/749 | 0,956628654 | 0,999954951 | 0,999954951 | FCGR1A/FCGR2A  | 2 |
| GO:0032732 | positive regulation of interleukin-1 production                    | 2/182 | 18/749 | 0,956628654 | 0,999954951 | 0,999954951 | EGR1/TLR4      | 2 |
| GO:0038096 | Fc-gamma receptor signaling pathway involved in phagocytosis       | 2/182 | 18/749 | 0,956628654 | 0,999954951 | 0,999954951 | FCGR1A/FCGR2A  | 2 |
| GO:0060389 | pathway-restricted SMAD protein phosphorylation                    | 2/182 | 18/749 | 0,956628654 | 0,999954951 | 0,999954951 | TGFB1/GDF15    | 2 |
| GO:1901888 | regulation of cell junction assembly                               | 2/182 | 18/749 | 0,956628654 | 0,999954951 | 0,999954951 | AGT/TLR2       | 2 |
| GO:0032633 | interleukin-4 production                                           | 2/182 | 19/749 | 0,965823893 | 0,999954951 | 0,999954951 | FCER1G/GATA3   | 2 |
| GO:0090100 | positive regulation of transmembrane receptor protein serine/tt    | 2/182 | 19/749 | 0,965823893 | 0,999954951 | 0,999954951 | TGFB1/GDF15    | 2 |
| GO:1905475 | regulation of protein localization to membrane                     | 2/182 | 19/749 | 0,965823893 | 0,999954951 | 0,999954951 | TGFB1/ITGB2    | 2 |
| GO:0001952 | regulation of cell-matrix adhesion                                 | 2/182 | 20/749 | 0,973136697 | 0,999954951 | 0,999954951 | BCL6/SERPINE1  | 2 |
| GO:0030072 | peptide hormone secretion                                          | 2/182 | 20/749 | 0,973136697 | 0,999954951 | 0,999954951 | HIF1A/HNF1A    | 2 |
| GO:0042269 | regulation of natural killer cell mediated cytotoxicity            | 2/182 | 20/749 | 0,973136697 | 0,999954951 | 0,999954951 | PVR/LILRB1     | 2 |
| GO:0090316 | positive regulation of intracellular protein transport             | 2/182 | 20/749 | 0,973136697 | 0,999954951 | 0,999954951 | TGFB1/ITGB2    | 2 |
| GO:0001914 | regulation of T cell mediated cytotoxicity                         | 2/182 | 21/749 | 0,978933722 | 0,999954951 | 0,999954951 | PVR/LILRB1     | 2 |
| GO:0002040 | sprouting angiogenesis                                             | 2/182 | 21/749 | 0,978933722 | 0,999954951 | 0,999954951 | JAK1/NR4A1     | 2 |
| GO:0006412 | translation                                                        | 2/182 | 21/749 | 0,978933722 | 0,999954951 | 0,999954951 | BCL3/STAT3     | 2 |
| GO:0010717 | regulation of epithelial to mesenchymal transition                 | 2/182 | 21/749 | 0,978933722 | 0,999954951 | 0,999954951 | COL1A1/TGFB1   | 2 |
| GO:0010718 | positive regulation of epithelial to mesenchymal transition        | 2/182 | 21/749 | 0,978933722 | 0,999954951 | 0,999954951 | COL1A1/TGFB1   | 2 |
| GO:0043043 | peptide biosynthetic process                                       | 2/182 | 21/749 | 0,978933722 | 0,999954951 | 0,999954951 | BCL3/STAT3     | 2 |
| GO:0046883 | regulation of hormone secretion                                    | 2/182 | 21/749 | 0,978933722 | 0,999954951 | 0,999954951 | HIF1A/AGT      | 2 |
| GO:0002715 | regulation of natural killer cell mediated immunity                | 2/182 | 22/749 | 0,983515602 | 0,999954951 | 0,999954951 | PVR/LILRB1     | 2 |
| GO:0043368 | positive T cell selection                                          | 2/182 | 22/749 | 0,983515602 | 0,999954951 | 0,999954951 | STAT3/STAT6    | 2 |
| GO:0048562 | embryonic organ morphogenesis                                      | 2/182 | 22/749 | 0,983515602 | 0,999954951 | 0,999954951 | HIF1A/GATA3    | 2 |
| GO:0007369 | gastrulation                                                       | 2/182 | 23/749 | 0,987127204 | 0,999954951 | 0,999954951 | ITGB2/FN1      | 2 |
| GO:0033157 | regulation of intracellular protein transport                      | 2/182 | 23/749 | 0,987127204 | 0,999954951 | 0,999954951 | TGFB1/ITGB2    | 2 |
| GO:0001913 | T cell mediated cytotoxicity                                       | 2/182 | 25/749 | 0,992194254 | 0,999954951 | 0,999954951 | PVR/LILRB1     | 2 |
| GO:0003002 | regionalization                                                    | 2/182 | 25/749 | 0,992194254 | 0,999954951 | 0,999954951 | C3/C1QA        | 2 |
| GO:0022412 | cellular process involved in reproduction in multicellular organis | 2/182 | 25/749 | 0,992194254 | 0,999954951 | 0,999954951 | TGFB1/BAX      | 2 |
| GO:0045446 | endothelial cell differentiation                                   | 2/182 | 26/749 | 0,993937635 | 0,999954951 | 0,999954951 | TNFRSF1A/ICAM1 | 2 |
| GO:0048247 | lymphocyte chemotaxis                                              | 2/182 | 26/749 | 0,993937635 | 0,999954951 | 0,999954951 | CXCL16/TNFSF14 | 2 |
| GO:0003158 | endothelium development                                            | 2/182 | 29/749 | 0,99718693  | 0,999954951 | 0,999954951 | TNFRSF1A/ICAM1 | 2 |
| GO:0050853 | B cell receptor signaling pathway                                  | 2/182 | 32/749 | 0,998711459 | 0,999954951 | 0,999954951 | BAX/PTPN6      | 2 |
| GO:0001911 | negative regulation of leukocyte mediated cytotoxicity             | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | LILRB1         | 1 |
| GO:0002468 | dendritic cell antigen processing and presentation                 | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | SLC11A1        | 1 |
| GO:0002604 | regulation of dendritic cell antigen processing and presentation   | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | SLC11A1        | 1 |
| GO:0002686 | negative regulation of leukocyte migration                         | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | SLAMF8         | 1 |
| GO:0006605 | protein targeting                                                  | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | ITGB2          | 1 |
| GO:0006925 | inflammatory cell apoptotic process                                | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | IRF7           | 1 |
| GO:0006941 | striated muscle contraction                                        | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | EHD3           | 1 |

|            |                                                                 |       |        |             |             |             |        |   |
|------------|-----------------------------------------------------------------|-------|--------|-------------|-------------|-------------|--------|---|
| GO:0007088 | regulation of mitotic nuclear division                          | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | TGFB1  | 1 |
| GO:0008154 | actin polymerization or depolymerization                        | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | ICAM1  | 1 |
| GO:0009855 | determination of bilateral symmetry                             | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | HIF1A  | 1 |
| GO:0014888 | striated muscle adaptation                                      | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | ERRFI1 | 1 |
| GO:0019080 | viral gene expression                                           | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | IFITM3 | 1 |
| GO:0019083 | viral transcription                                             | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | IFITM3 | 1 |
| GO:0030038 | contractile actin filament bundle assembly                      | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | NOX4   | 1 |
| GO:0030512 | negative regulation of transforming growth factor beta receptor | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | TGFB1  | 1 |
| GO:0032231 | regulation of actin filament bundle assembly                    | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | NOX4   | 1 |
| GO:0032271 | regulation of protein polymerization                            | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | ICAM1  | 1 |
| GO:0032330 | regulation of chondrocyte differentiation                       | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | MAF    | 1 |
| GO:0042177 | negative regulation of protein catabolic process                | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | TIMP1  | 1 |
| GO:0042246 | tissue regeneration                                             | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | CDKN1A | 1 |
| GO:0043149 | stress fiber assembly                                           | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | NOX4   | 1 |
| GO:0044003 | modulation by symbiont of host process                          | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | TGFB1  | 1 |
| GO:0045727 | positive regulation of translation                              | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | BCL3   | 1 |
| GO:0046824 | positive regulation of nucleocytoplasmic transport              | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | TGFB1  | 1 |
| GO:0046887 | positive regulation of hormone secretion                        | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | HIF1A  | 1 |
| GO:0048008 | platelet-derived growth factor receptor signaling pathway       | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | TIPARP | 1 |
| GO:0048546 | digestive tract morphogenesis                                   | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | HIF1A  | 1 |
| GO:0050716 | positive regulation of interleukin-1 secretion                  | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | TLR4   | 1 |
| GO:0050718 | positive regulation of interleukin-1 beta secretion             | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | TLR4   | 1 |
| GO:0050869 | negative regulation of B cell activation                        | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | BCL6   | 1 |
| GO:0055025 | positive regulation of cardiac muscle tissue development        | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | TGFB1  | 1 |
| GO:0070585 | protein localization to mitochondrion                           | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | BAX    | 1 |
| GO:0071103 | DNA conformation change                                         | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | DNMT1  | 1 |
| GO:0071276 | cellular response to cadmium ion                                | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | MT1A   | 1 |
| GO:0072540 | T-helper 17 cell lineage commitment                             | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | STAT3  | 1 |
| GO:0072655 | establishment of protein localization to mitochondrion          | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | BAX    | 1 |
| GO:0090713 | immunological memory process                                    | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | BCL6   | 1 |
| GO:0140014 | mitotic nuclear division                                        | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | TGFB1  | 1 |
| GO:1903076 | regulation of protein localization to plasma membrane           | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | TGFB1  | 1 |
| GO:1903672 | positive regulation of sprouting angiogenesis                   | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | JAK1   | 1 |
| GO:1904375 | regulation of protein localization to cell periphery            | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | TGFB1  | 1 |
| GO:2000316 | regulation of T-helper 17 type immune response                  | 1/182 | 10/749 | 0,939388651 | 0,999954951 | 0,999954951 | NFKBIZ | 1 |
| GO:0002042 | cell migration involved in sprouting angiogenesis               | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | NR4A1  | 1 |
| GO:0002643 | regulation of tolerance induction                               | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | LILRB2 | 1 |
| GO:0002710 | negative regulation of T cell mediated immunity                 | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | LILRB1 | 1 |
| GO:0007043 | cell-cell junction assembly                                     | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | AGT    | 1 |
| GO:0007044 | cell-substrate junction assembly                                | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | FN1    | 1 |
| GO:0009799 | specification of symmetry                                       | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | HIF1A  | 1 |
| GO:0030510 | regulation of BMP signaling pathway                             | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | SOST   | 1 |
| GO:0030857 | negative regulation of epithelial cell differentiation          | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | STAT1  | 1 |
| GO:0031345 | negative regulation of cell projection organization             | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | APOE   | 1 |
| GO:0032703 | negative regulation of interleukin-2 production                 | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | GATA3  | 1 |
| GO:0032816 | positive regulation of natural killer cell activation           | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | IL6R   | 1 |
| GO:0035904 | aorta development                                               | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | COL3A1 | 1 |
| GO:0045061 | thymic T cell selection                                         | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | GATA3  | 1 |
| GO:0045665 | negative regulation of neuron differentiation                   | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | APOE   | 1 |
| GO:0045995 | regulation of embryonic development                             | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | GATA3  | 1 |
| GO:0048538 | thymus development                                              | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | GATA3  | 1 |
| GO:0050796 | regulation of insulin secretion                                 | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | HIF1A  | 1 |
| GO:0050901 | leukocyte tethering or rolling                                  | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | VCAM1  | 1 |
| GO:0050922 | negative regulation of chemotaxis                               | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | SLAMF8 | 1 |
| GO:0051017 | actin filament bundle assembly                                  | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | NOX4   | 1 |
| GO:0051289 | protein homotetramerization                                     | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | SOD2   | 1 |
| GO:0051783 | regulation of nuclear division                                  | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | TGFB1  | 1 |
| GO:0061572 | actin filament bundle organization                              | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | NOX4   | 1 |
| GO:0150115 | cell-substrate junction organization                            | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | FN1    | 1 |

|            |                                                                  |       |        |             |             |             |          |   |
|------------|------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|----------|---|
| GO:1900182 | positive regulation of protein localization to nucleus           | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:1903845 | negative regulation of cellular response to transforming growth  | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:1904888 | cranial skeletal system development                              | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:2000108 | positive regulation of leukocyte apoptotic process               | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | BAX      | 1 |
| GO:2000778 | positive regulation of interleukin-6 secretion                   | 1/182 | 11/749 | 0,954315939 | 0,999954951 | 0,999954951 | XBP1     | 1 |
| GO:0006281 | DNA repair                                                       | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | ISG15    | 1 |
| GO:0007163 | establishment or maintenance of cell polarity                    | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | GATA3    | 1 |
| GO:0010256 | endomembrane system organization                                 | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | EHD3     | 1 |
| GO:0030902 | hindbrain development                                            | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | C5AR1    | 1 |
| GO:0031342 | negative regulation of cell killing                              | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | LILRB1   | 1 |
| GO:0034105 | positive regulation of tissue remodeling                         | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | BAX      | 1 |
| GO:0034405 | response to fluid shear stress                                   | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:0034605 | cellular response to heat                                        | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | CDKN1A   | 1 |
| GO:0043552 | positive regulation of phosphatidylinositol 3-kinase activity    | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:0045844 | positive regulation of striated muscle tissue development        | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:0048636 | positive regulation of muscle organ development                  | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:0050856 | regulation of T cell receptor signaling pathway                  | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | PTPN6    | 1 |
| GO:0060021 | roof of mouth development                                        | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | TIPARP   | 1 |
| GO:0110020 | regulation of actomyosin structure organization                  | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | NOX4     | 1 |
| GO:1901623 | regulation of lymphocyte chemotaxis                              | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | TNFSF14  | 1 |
| GO:1901863 | positive regulation of muscle tissue development                 | 1/182 | 12/749 | 0,965582198 | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:0000280 | nuclear division                                                 | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:0002407 | dendritic cell chemotaxis                                        | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | SLAMF8   | 1 |
| GO:0003281 | ventricular septum development                                   | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | GATA3    | 1 |
| GO:0010524 | positive regulation of calcium ion transport into cytosol        | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | BAX      | 1 |
| GO:0030326 | embryonic limb morphogenesis                                     | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | BAX      | 1 |
| GO:0035113 | embryonic appendage morphogenesis                                | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | BAX      | 1 |
| GO:0036336 | dendritic cell migration                                         | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | SLAMF8   | 1 |
| GO:0045601 | regulation of endothelial cell differentiation                   | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | TNFRSF1A | 1 |
| GO:0046686 | response to cadmium ion                                          | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | MT1A     | 1 |
| GO:0048305 | immunoglobulin secretion                                         | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | XBP1     | 1 |
| GO:0051023 | regulation of immunoglobulin secretion                           | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | XBP1     | 1 |
| GO:0090218 | positive regulation of lipid kinase activity                     | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:1903727 | positive regulation of phospholipid metabolic process            | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:2000406 | positive regulation of T cell migration                          | 1/182 | 13/749 | 0,974081574 | 0,999954951 | 0,999954951 | TNFSF14  | 1 |
| GO:0003151 | outflow tract morphogenesis                                      | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | HIF1A    | 1 |
| GO:0019233 | sensory perception of pain                                       | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | MME      | 1 |
| GO:0035107 | appendage morphogenesis                                          | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | BAX      | 1 |
| GO:0035108 | limb morphogenesis                                               | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | BAX      | 1 |
| GO:0043525 | positive regulation of neuron apoptotic process                  | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | BAX      | 1 |
| GO:0045453 | bone resorption                                                  | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | NOX4     | 1 |
| GO:0046822 | regulation of nucleocytoplasmic transport                        | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:0048706 | embryonic skeletal system development                            | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | COL1A1   | 1 |
| GO:0048736 | appendage development                                            | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | BAX      | 1 |
| GO:0050706 | regulation of interleukin-1 beta secretion                       | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | TLR4     | 1 |
| GO:0051258 | protein polymerization                                           | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | ICAM1    | 1 |
| GO:0060173 | limb development                                                 | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | BAX      | 1 |
| GO:0072604 | interleukin-6 secretion                                          | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | XBP1     | 1 |
| GO:0090276 | regulation of peptide hormone secretion                          | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | HIF1A    | 1 |
| GO:1900180 | regulation of protein localization to nucleus                    | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:1903670 | regulation of sprouting angiogenesis                             | 1/182 | 14/749 | 0,98049075  | 0,999954951 | 0,999954951 | JAK1     | 1 |
| GO:0032088 | negative regulation of NF-kappaB transcription factor activity   | 1/182 | 15/749 | 0,985321612 | 0,999954951 | 0,999954951 | CMKLR1   | 1 |
| GO:0032814 | regulation of natural killer cell activation                     | 1/182 | 15/749 | 0,985321612 | 0,999954951 | 0,999954951 | IL6R     | 1 |
| GO:0045954 | positive regulation of natural killer cell mediated cytotoxicity | 1/182 | 15/749 | 0,985321612 | 0,999954951 | 0,999954951 | PVR      | 1 |
| GO:0051262 | protein tetramerization                                          | 1/182 | 15/749 | 0,985321612 | 0,999954951 | 0,999954951 | SOD2     | 1 |
| GO:0007411 | axon guidance                                                    | 1/182 | 16/749 | 0,988961212 | 0,999954951 | 0,999954951 | GATA3    | 1 |
| GO:0010811 | positive regulation of cell-substrate adhesion                   | 1/182 | 16/749 | 0,988961212 | 0,999954951 | 0,999954951 | FN1      | 1 |
| GO:0017015 | regulation of transforming growth factor beta receptor signaling | 1/182 | 16/749 | 0,988961212 | 0,999954951 | 0,999954951 | TGFB1    | 1 |
| GO:0048285 | organelle fission                                                | 1/182 | 16/749 | 0,988961212 | 0,999954951 | 0,999954951 | TGFB1    | 1 |



|            |                                                                    |       |        |             |             |             |         |   |
|------------|--------------------------------------------------------------------|-------|--------|-------------|-------------|-------------|---------|---|
| GO:0050702 | interleukin-1 beta secretion                                       | 1/182 | 16/749 | 0,988961212 | 0,999954951 | 0,999954951 | TLR4    | 1 |
| GO:0097485 | neuron projection guidance                                         | 1/182 | 16/749 | 0,988961212 | 0,999954951 | 0,999954951 | GATA3   | 1 |
| GO:2000403 | positive regulation of lymphocyte migration                        | 1/182 | 16/749 | 0,988961212 | 0,999954951 | 0,999954951 | TNFSF14 | 1 |
| GO:2000404 | regulation of T cell migration                                     | 1/182 | 16/749 | 0,988961212 | 0,999954951 | 0,999954951 | TNFSF14 | 1 |
| GO:0001916 | positive regulation of T cell mediated cytotoxicity                | 1/182 | 17/749 | 0,991702084 | 0,999954951 | 0,999954951 | PVR     | 1 |
| GO:0002717 | positive regulation of natural killer cell mediated immunity       | 1/182 | 17/749 | 0,991702084 | 0,999954951 | 0,999954951 | PVR     | 1 |
| GO:0072132 | mesenchyme morphogenesis                                           | 1/182 | 17/749 | 0,991702084 | 0,999954951 | 0,999954951 | MYC     | 1 |
| GO:1903844 | regulation of cellular response to transforming growth factor beta | 1/182 | 17/749 | 0,991702084 | 0,999954951 | 0,999954951 | TGFB1   | 1 |
| GO:0003279 | cardiac septum development                                         | 1/182 | 18/749 | 0,993765227 | 0,999954951 | 0,999954951 | GATA3   | 1 |
| GO:0007281 | germ cell development                                              | 1/182 | 18/749 | 0,993765227 | 0,999954951 | 0,999954951 | BAX     | 1 |
| GO:0019827 | stem cell population maintenance                                   | 1/182 | 18/749 | 0,993765227 | 0,999954951 | 0,999954951 | STAT3   | 1 |
| GO:0050854 | regulation of antigen receptor-mediated signaling pathway          | 1/182 | 20/749 | 0,996484936 | 0,999954951 | 0,999954951 | PTPN6   | 1 |
| GO:0071248 | cellular response to metal ion                                     | 1/182 | 20/749 | 0,996484936 | 0,999954951 | 0,999954951 | MT1A    | 1 |
| GO:0098727 | maintenance of cell number                                         | 1/182 | 20/749 | 0,996484936 | 0,999954951 | 0,999954951 | STAT3   | 1 |
| GO:0048639 | positive regulation of developmental growth                        | 1/182 | 21/749 | 0,997362496 | 0,999954951 | 0,999954951 | FN1     | 1 |
| GO:2000401 | regulation of lymphocyte migration                                 | 1/182 | 21/749 | 0,997362496 | 0,999954951 | 0,999954951 | TNFSF14 | 1 |
| GO:0071241 | cellular response to inorganic substance                           | 1/182 | 22/749 | 0,998021872 | 0,999954951 | 0,999954951 | MT1A    | 1 |
| GO:0033077 | T cell differentiation in thymus                                   | 1/182 | 24/749 | 0,998888835 | 0,999954951 | 0,999954951 | GATA3   | 1 |
| GO:0008037 | cell recognition                                                   | 1/182 | 25/749 | 0,999167775 | 0,999954951 | 0,999954951 | VCAN    | 1 |
| GO:0032663 | regulation of interleukin-2 production                             | 1/182 | 25/749 | 0,999167775 | 0,999954951 | 0,999954951 | GATA3   | 1 |
| GO:0046777 | protein autophosphorylation                                        | 1/182 | 27/749 | 0,999533813 | 0,999954951 | 0,999954951 | ERRFI1  | 1 |
| GO:0001912 | positive regulation of leukocyte mediated cytotoxicity             | 1/182 | 30/749 | 0,999805231 | 0,999954951 | 0,999954951 | PVR     | 1 |
| GO:0031343 | positive regulation of cell killing                                | 1/182 | 35/749 | 0,999954951 | 0,999954951 | 0,999954951 | PVR     | 1 |