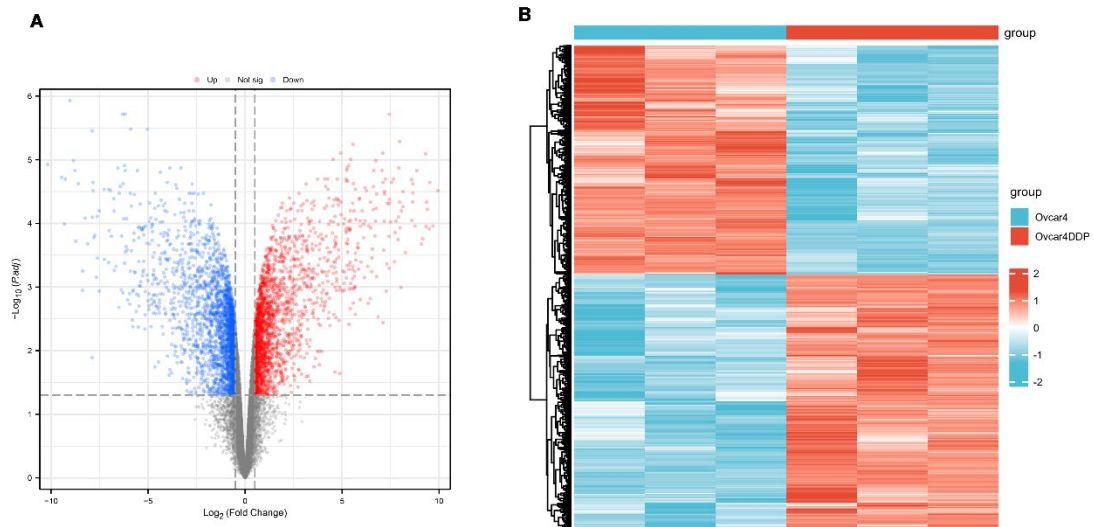
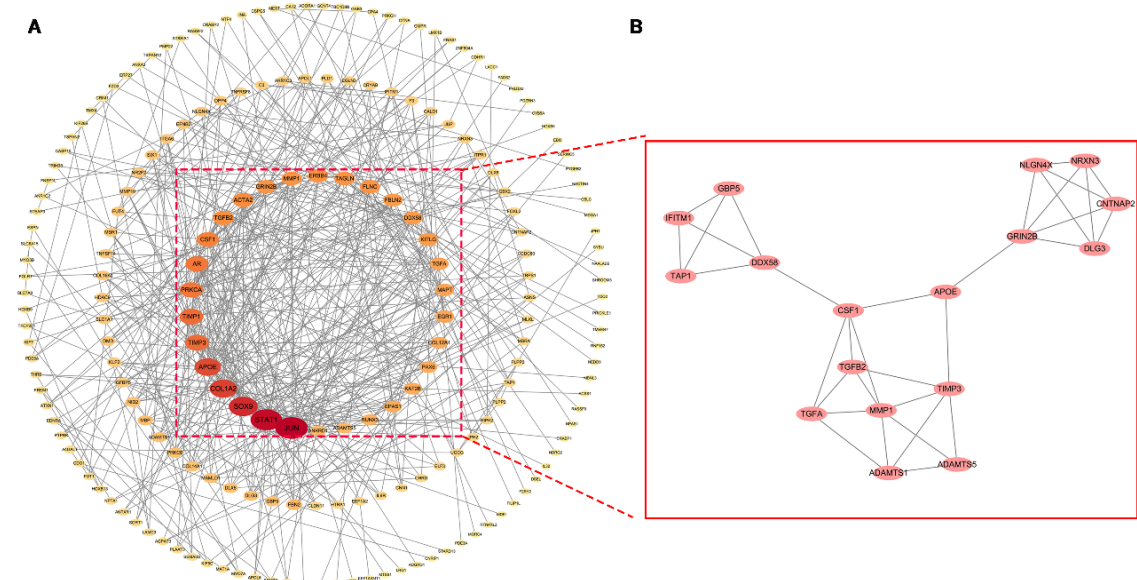


## Supplementary Figure

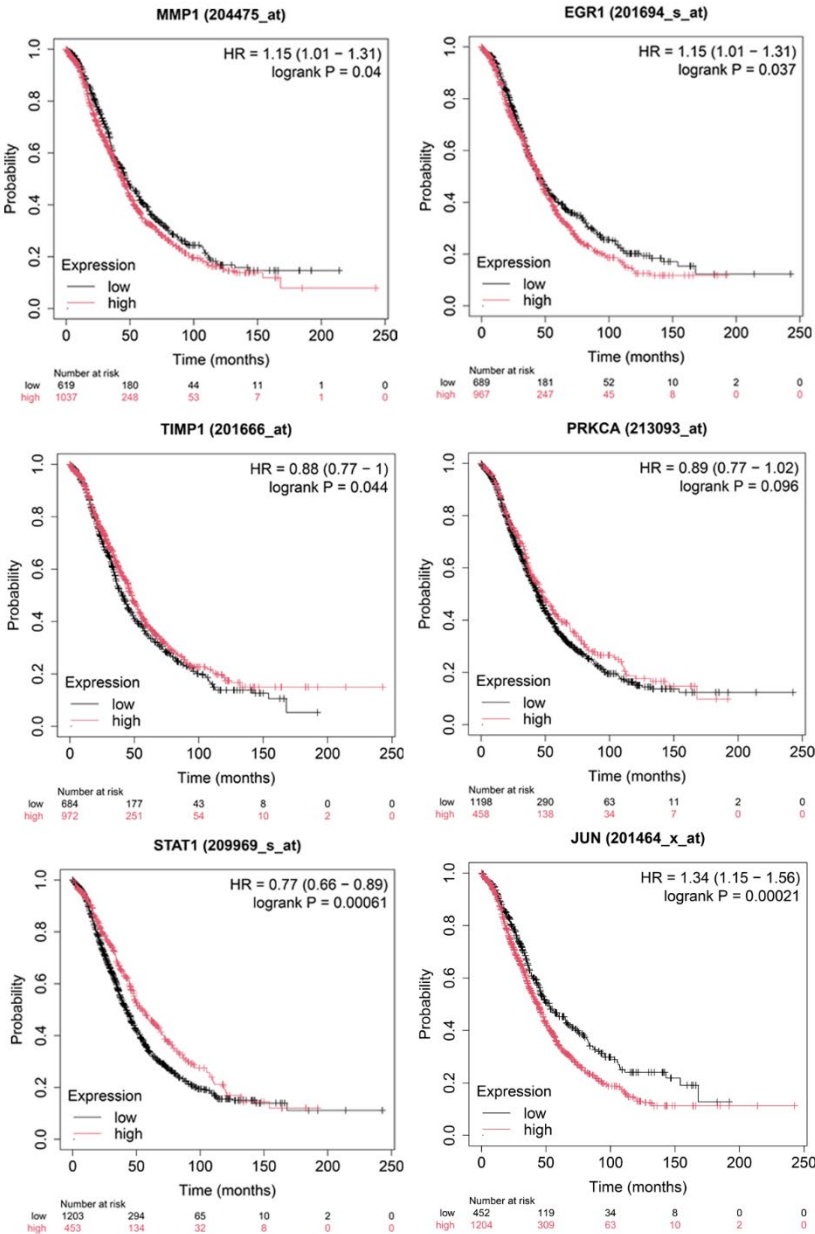


**Supplementary Figure 1. Identification of differential expressed genes (DEGs) between Ovarcar4 and Ovarcar4DDP cells.** (A) The volcano plot of DEGs between Ovarcar4 and Ovarcar4DDP cells. DEGs between Ovarcar4 and Ovarcar4DDP cells were identified using the limma package in R. Genes with a  $\log_2(\text{fold change})$  threshold of  $>0.5$  and a P value  $< 0.05$  were marked in blue (downregulated genes) or red (upregulated genes). (B) The heatmap of DEGs between Ovarcar4 and Ovarcar4DDP cells.



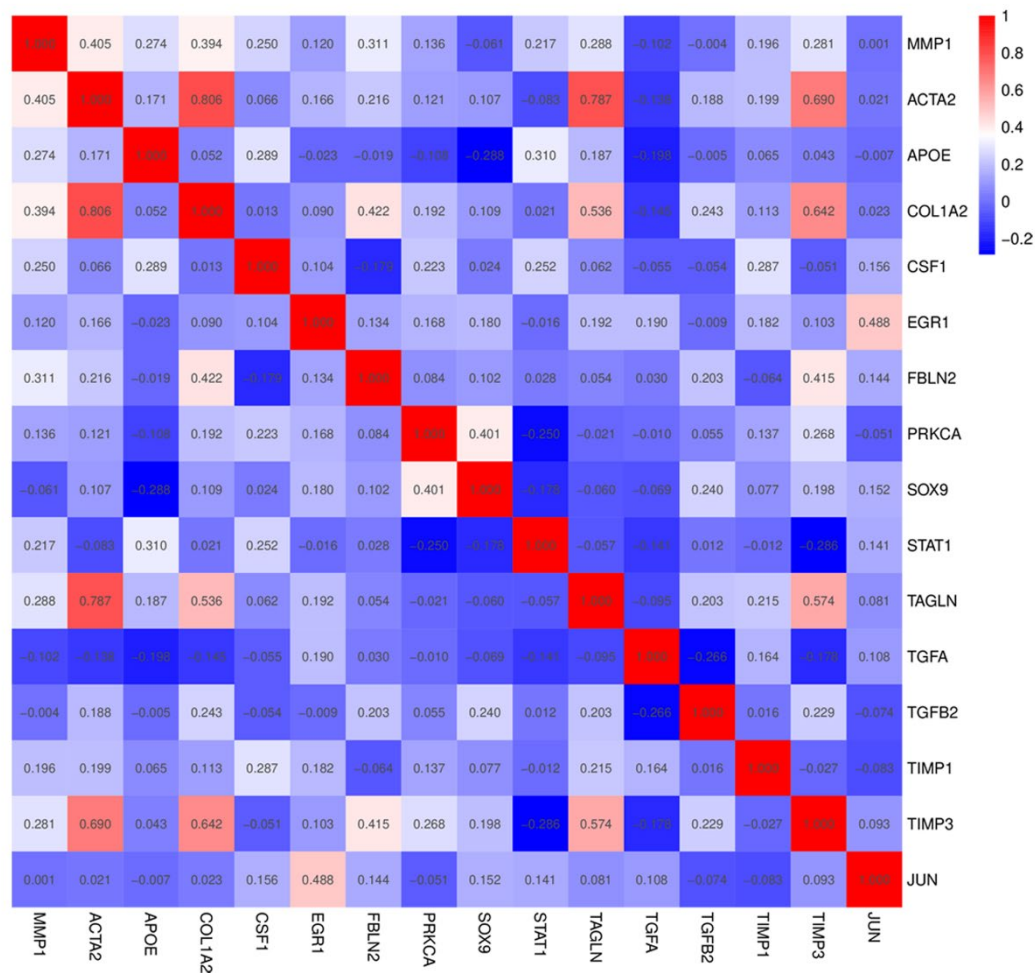
**Supplementary Figure 2. PPI network construction of cisplatin-resistance-related (CR) genes.** (A) The PPI network of DEGs was visualized using the STRING and

Cytoscape software. The color intensity and size of genes in the PPI network are determined by their DEGREE values in the PPI network. (B) MCODE plugin in Cytoscape software were performed to identified the core submodule of the PPI network. 17 genes including MMP1, IFITM1, TGFB2, TIMP3, APOE, and CSF1 were identified in the core submodule.



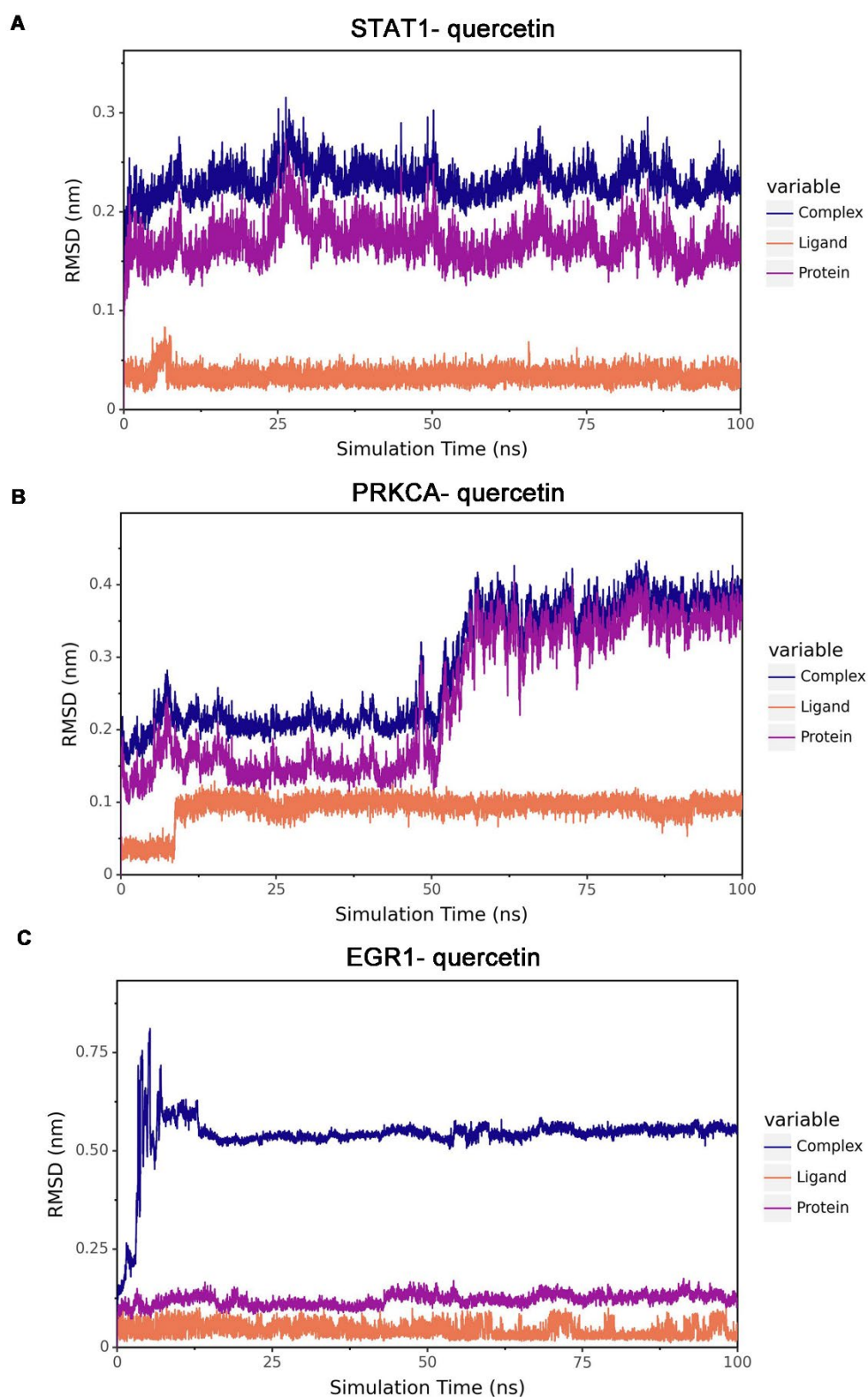
**Supplementary Figure 3. Survival curves of OC patients in different high- and low-expressed RNA groups analyzed by the Kaplan-Meier plotter. The expression of MMP1,**

EGR1, TIMP1, STAT1, and JUN is associated with overall survival (OS) in EOC patients ( $P < 0.05$ ). And High expression of MMP1 and EGR1 was found to be associated with poor OS in EOC.

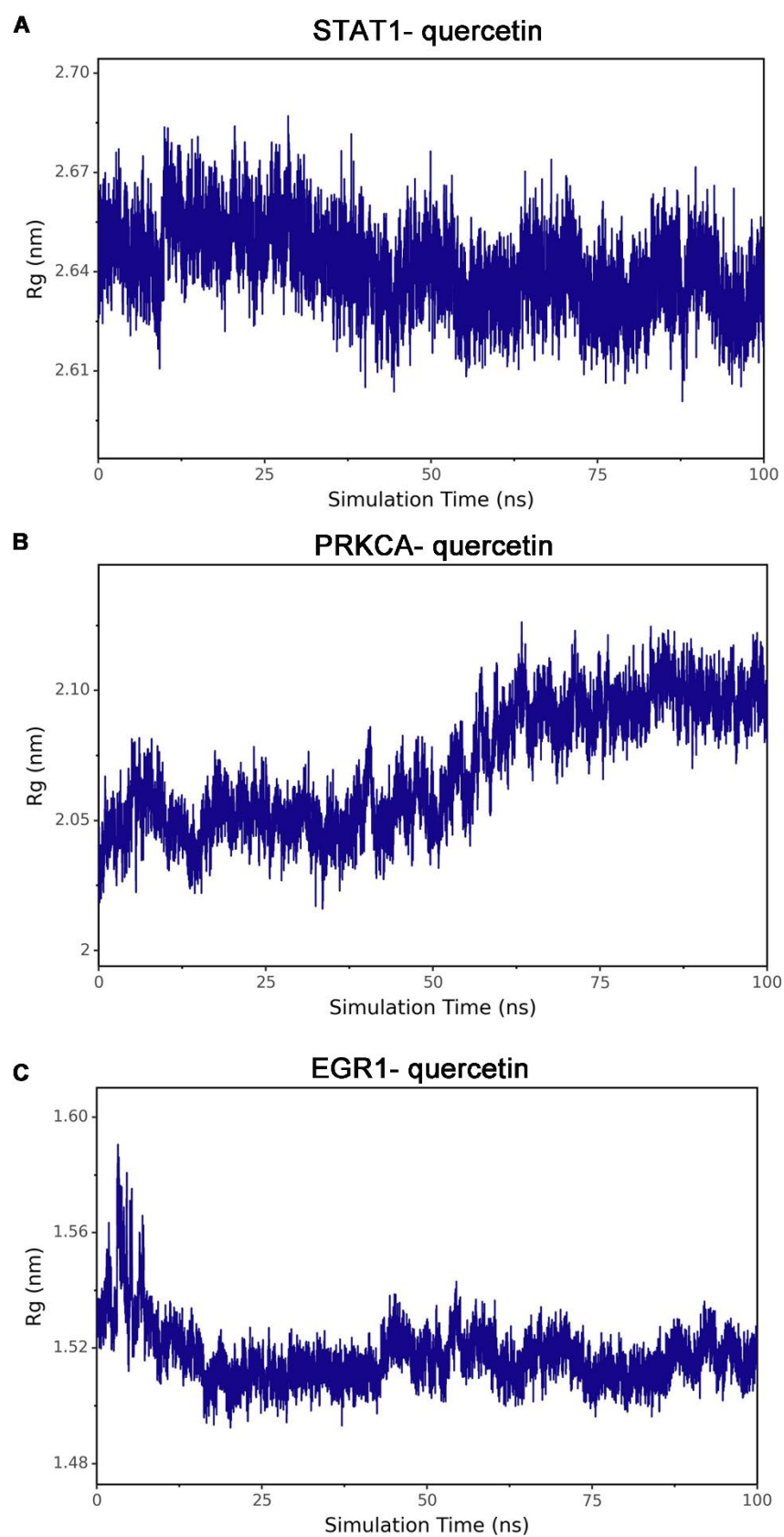


**Supplementary Figure 4. Correlation matrix of hub genes.** Spearman's method was used to analyze the correlations among hub genes, and the correlation matrix was plotted based on the Spearman correlation coefficient ( $r_s$ ). A coefficient of  $0.9 < r_s < 1$  indicates a high correlation;  $0.7 < r_s < 0.9$  indicates a strong correlation;  $0.4 < r_s < 0.7$  indicates a moderate correlation;  $0.2 < r_s < 0.4$  indicates a weak correlation; and  $0 < r_s < 0.2$  indicates a very weak correlation or no correlation.



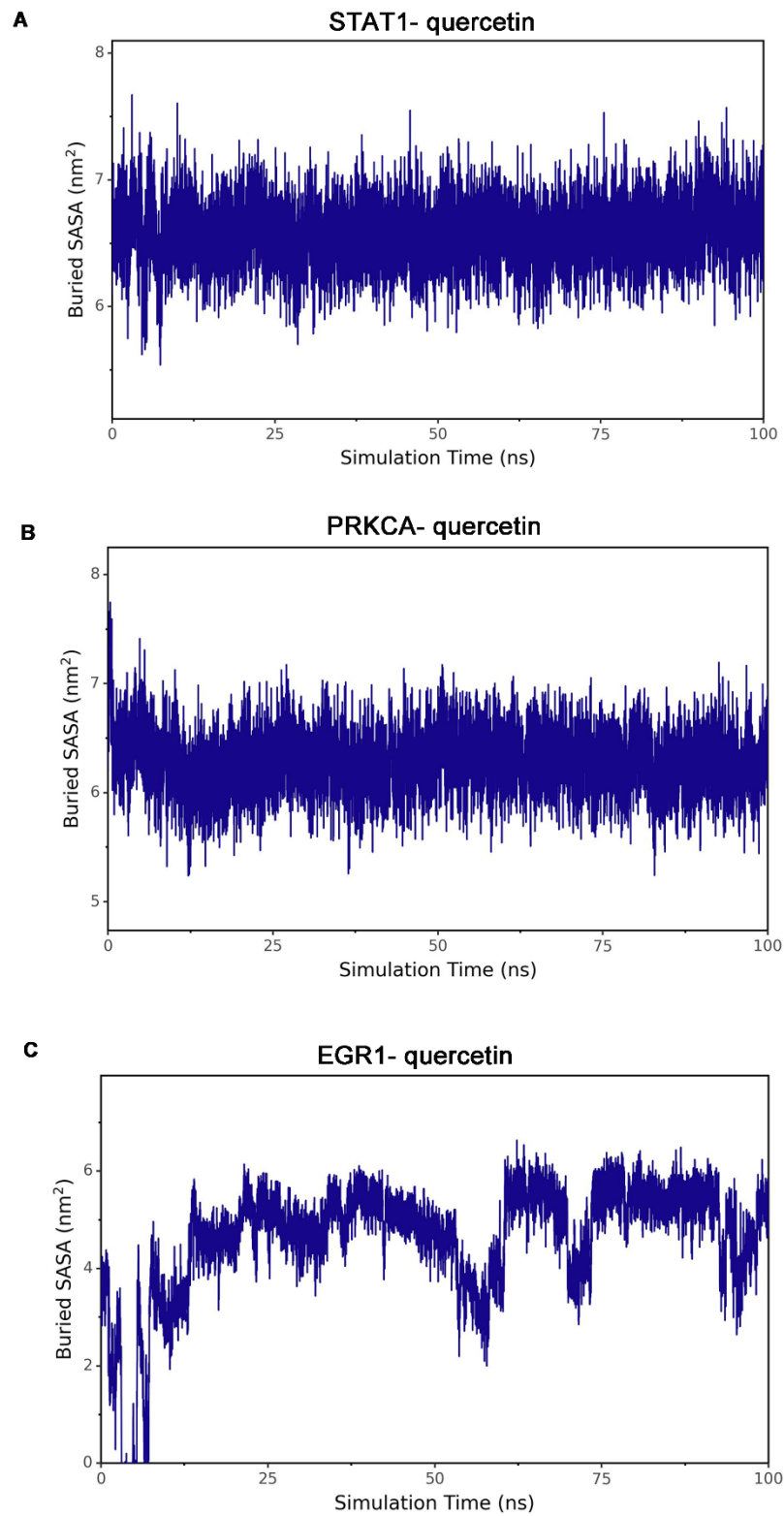


**Supplementary Figure 6. RMSD values in MD Simulations of protein–ligand complexes: STAT1- quercetin, PRKCA-quercetin, and EGR1-quercetin.** (A) RMSD values of the complexes of STAT1- quercetin. (B) RMSD values of the complexes of PRKCA-quercetin. (C) RMSD values of the complexes of EGR1-quercetin.



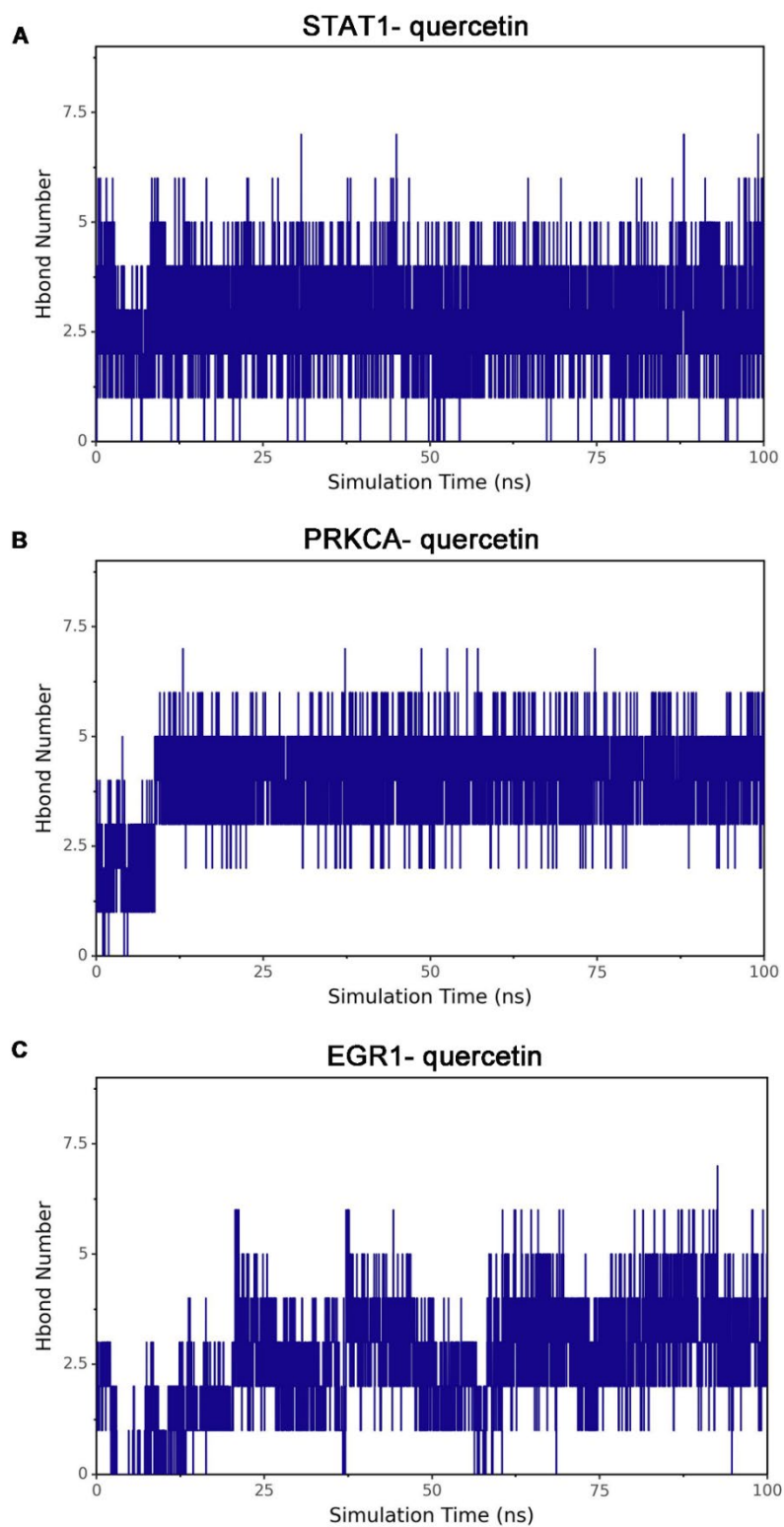
**Supplementary Figure 7. The diagram of Rg over time of protein–ligand complexes.**

(A) The diagram of Rg of STAT1- quercetin. (B) The diagram of Rg of PRKCA-quercetin.  
(C) The diagram of Rg of EGR1-quercetin.

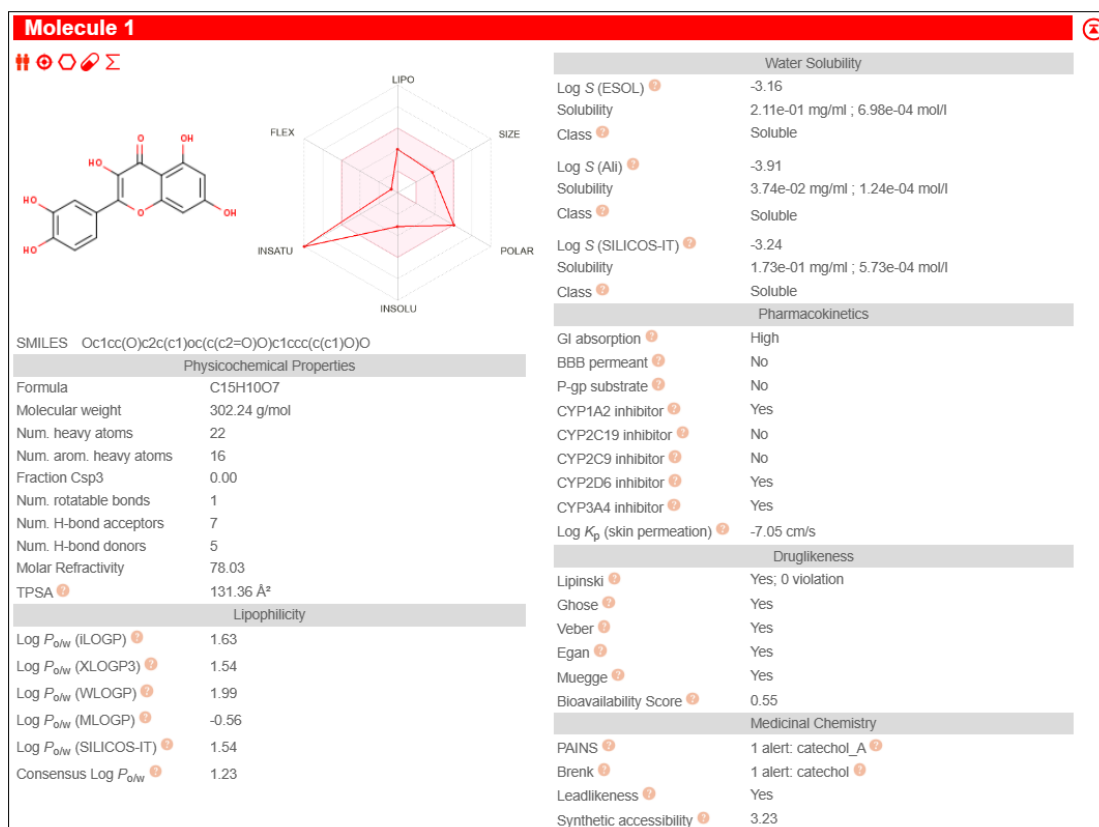


**Supplementary Figure 8. SASA values in MD Simulations of protein–ligand**

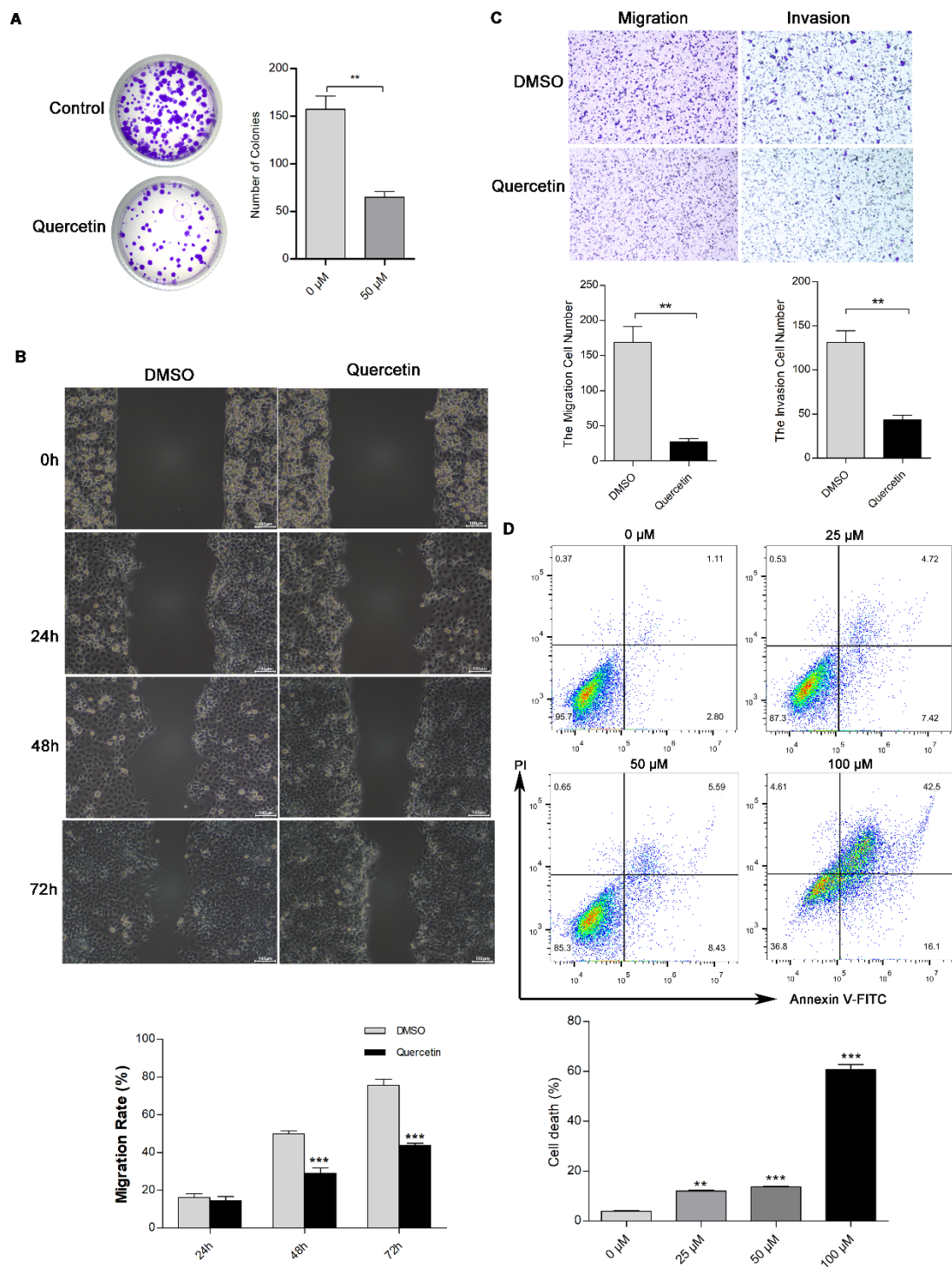
**complexes: STAT1- quercetin, PRKCA-quercetin, and EGR1-quercetin.** (A) SASA values of STAT1- quercetin complex. (B) SASA values of PRKCA-quercetin complex. (C) SASA values of EGR1-quercetin complex.



**Supplementary Figure 9. Variation in the number of hydrogen bonds within the complexes during the molecular simulation.** (A) The variation in the number of hydrogen bonds within STAT1- quercetin complex. (B) The variation in the number of hydrogen bonds within PRKCA- quercetin complex. (C) The variation in the number of hydrogen bonds within EGR1- quercetin complex.



**Supplementary Figure 10. The report of quercetin from SwissADME.** The chemical structure of quercetin was uploaded to the SwissADME to obtain its ADME properties.



**Supplementary Figure 11. Effects of quercetin on the proliferation, apoptosis, migration, and invasion of Ovar4DDP cells.** (A) Colony formation assay of Ovar4DDP cells after treated with 0 or 50  $\mu$ M of quercetin for 72 hours. (B) Wound-healing scratch assay in Ovar4DDP cells exposed to DMSO or quercetin (50  $\mu$ M) for 72 hours. The Scratch of cells treated with DMSO or quercetin were photographed at 0h, 24h, 48h, and 72h. (C) Transwell migration and invasion assay of Ovar4DDP cells

treated with 0 or 50  $\mu$ M of quercetin for 72 hours. Cells that migrated or invaded through the membrane were counted using ImageJ2 software. (D) Effect of quercetin on apoptosis in Ovar4DDP cells. Annexin V-PI double staining assay by flow cytometry were performed in cells after the treatment of 0 $\mu$ M, 25 $\mu$ M, 50 $\mu$ M, and 100 $\mu$ M quercetin for 72 hours. \*p < 0.05; \*\*p < 0.01; \*\*\*p < 0.001.

**Supplementary Table 1: qRT-PCR Primers**

| Gene  | Sequence (5' -> 3') |                        |
|-------|---------------------|------------------------|
| MMP1  | Forward             | TTTCATTTCTGTTTTCTGGCCA |
|       | Reverse             | CATCTCTGTCGGCAAATTCGT  |
| STAT1 | Forward             | CCATCCTTTGGTACAACATGC  |
|       | Reverse             | TGCACATGGTGGAGTCAGG    |
| EGR1  | Forward             | GCCTGCGACATCTGTGGAA    |
|       | Reverse             | CGCAAGTGGATCTTGGTATGC  |
| APOE  | Forward             | TGCTCAGCTCCCAGGTCAC    |
|       | Reverse             | GCCTTCAACTCCTTCATGGTCT |
| PRKCA | Forward             | ATGGCTGATGTCTTCCAGCA   |
|       | Reverse             | AAGCCCCATATAAAGTCGGT   |
| JUN   | Forward             | GAGCTGGAGCGCCTGATAAT   |
|       | Reverse             | CCCTCCTGCTCATCTGTCAC   |
| GAPDH | Forward             | GCAAAGTGGAGATTGTTGCCAT |
|       | Reverse             | CCTTGACTGTGCCGTTGAATTT |

**Supplementary Table 2: DEGs in A2780/A2780DDP**

| gene     | logFC   | AveExpr | t       | P.Value  | adj.P.Val | B       |
|----------|---------|---------|---------|----------|-----------|---------|
| INHBA    | -3.0661 | 1.5832  | -53.018 | 5.68E-14 | 6.65E-11  | 22.7814 |
| CD36     | -2.9146 | 1.65333 | -22.857 | 3.26E-10 | 3.63E-08  | 13.828  |
| TBR1     | -2.8862 | 1.78963 | -22.72  | 3.46E-10 | 3.81E-08  | 13.7628 |
| KHDRBS   | -2.7387 | 1.92803 | -36.459 | 2.71E-12 | 1.21E-09  | 18.8807 |
| PTGER3   | -2.7332 | 1.59663 | -34.602 | 4.64E-12 | 1.69E-09  | 18.322  |
| SLC4A4   | -2.7206 | 1.8817  | -31.328 | 1.29E-11 | 3.09E-09  | 17.2528 |
| PERP     | -2.7007 | 1.68926 | -24.188 | 1.83E-10 | 2.33E-08  | 14.4451 |
| GALNT14  | -2.6964 | 1.59906 | -24.422 | 1.66E-10 | 2.19E-08  | 14.5499 |
| BACE2    | -2.6849 | 1.49294 | -30.913 | 1.48E-11 | 3.44E-09  | 17.1089 |
| ST3GAL1  | -2.6096 | 1.43451 | -29.028 | 2.82E-11 | 5.64E-09  | 16.4281 |
| TDO2     | -2.5523 | 1.52702 | -20.84  | 8.33E-10 | 7.42E-08  | 12.8207 |
| RUNX3    | -2.5375 | 1.39846 | -22.629 | 3.61E-10 | 3.94E-08  | 13.7187 |
| PTPN3    | -2.5027 | 1.63191 | -20.332 | 1.07E-09 | 9.09E-08  | 12.5519 |
| PDLIM1   | -2.492  | 1.37569 | -25.823 | 9.37E-11 | 1.40E-08  | 15.1574 |
| FILIP1   | -2.469  | 2.09818 | -26.99  | 5.96E-11 | 9.62E-09  | 15.6379 |
| FAM9C    | -2.4289 | 2.69696 | -47.065 | 1.95E-13 | 1.72E-10  | 21.5648 |
| LRRTM3   | -2.3838 | 1.75529 | -26.058 | 8.54E-11 | 1.29E-08  | 15.2557 |
| DNAJC6   | -2.379  | 1.34001 | -30.645 | 1.62E-11 | 3.61E-09  | 17.0148 |
| CHST15   | -2.3572 | 1.22875 | -37.823 | 1.86E-12 | 9.11E-10  | 19.2719 |
| CAMK4    | -2.299  | 1.4165  | -17.227 | 5.71E-09 | 3.56E-07  | 10.7499 |
| CACNA1H  | -2.2963 | 1.632   | -13.87  | 4.96E-08 | 2.13E-06  | 8.41304 |
| SHTN1    | -2.282  | 1.34167 | -21.374 | 6.44E-10 | 6.10E-08  | 13.097  |
| GABRA5   | -2.2676 | 1.3932  | -22.603 | 3.65E-10 | 3.96E-08  | 13.7066 |
| LINC0088 | -2.2222 | 1.487   | -16.135 | 1.10E-08 | 6.08E-07  | 10.0402 |
| RALYL    | -2.2163 | 1.15833 | -35.222 | 3.87E-12 | 1.51E-09  | 18.5121 |
| MYO6     | -2.2147 | 1.96061 | -29.174 | 2.68E-11 | 5.44E-09  | 16.4823 |
| NFATC1   | -2.2074 | 1.25419 | -19.734 | 1.45E-09 | 1.14E-07  | 12.2267 |
| SLC4A10  | -2.2052 | 1.31181 | -21.072 | 7.44E-10 | 6.81E-08  | 12.9419 |
| SOX8     | -2.1125 | 1.66215 | -20.712 | 8.87E-10 | 7.83E-08  | 12.7538 |
| JAKMIP1  | -2.1114 | 1.0557  | -34.355 | 5.00E-12 | 1.77E-09  | 18.2451 |
| SOST     | -2.1079 | 1.28401 | -21.258 | 6.81E-10 | 6.35E-08  | 13.0374 |
| GALNT18  | -2.0961 | 1.22789 | -17.441 | 5.04E-09 | 3.23E-07  | 10.8833 |
| COL12A1  | -2.0785 | 3.13126 | -28.47  | 3.45E-11 | 6.68E-09  | 16.2176 |
| HSPA12A  | -2.0749 | 1.16714 | -22.539 | 3.76E-10 | 4.05E-08  | 13.6753 |
| MMP1     | -2.0731 | 2.97492 | -50.392 | 9.60E-14 | 9.43E-11  | 22.266  |
| CEROX1   | -2.072  | 1.41186 | -15.47  | 1.68E-08 | 8.61E-07  | 9.586   |
| PPIC     | -2.0459 | 1.52    | -18.085 | 3.50E-09 | 2.41E-07  | 11.2774 |
| HTRA1    | -2.0407 | 1.12069 | -25.589 | 1.03E-10 | 1.50E-08  | 15.0582 |
| GRID1    | -2.0364 | 1.14787 | -15.746 | 1.41E-08 | 7.54E-07  | 9.77635 |
| GNAI1    | -2.0155 | 2.49683 | -31.609 | 1.18E-11 | 2.99E-09  | 17.3491 |
| LMX1B    | -2.0118 | 1.13557 | -18.181 | 3.32E-09 | 2.31E-07  | 11.3349 |
| FAM83H   | -2.0095 | 1.3143  | -17.377 | 5.23E-09 | 3.33E-07  | 10.8436 |
| ARHGAP   | -1.9971 | 1.04872 | -27.835 | 4.34E-11 | 7.84E-09  | 15.9729 |
| NTN1     | -1.9947 | 1.57393 | -12.672 | 1.21E-07 | 4.52E-06  | 7.44994 |
| SFMBT2   | -1.9625 | 1.16113 | -20.978 | 7.79E-10 | 7.02E-08  | 12.893  |
| LRATD2   | -1.9619 | 1.39082 | -17.614 | 4.57E-09 | 2.98E-07  | 10.9905 |
| CD55     | -1.9335 | 1.37663 | -16.128 | 1.11E-08 | 6.09E-07  | 10.0358 |
| LRRK1    | -1.9023 | 1.48986 | -20.221 | 1.13E-09 | 9.47E-08  | 12.4924 |
| PLPP2    | -1.8687 | 1.3366  | -9.7653 | 1.48E-06 | 3.97E-05  | 4.73339 |
| LINC0248 | -1.8645 | 0.9824  | -31.12  | 1.38E-11 | 3.25E-09  | 17.181  |
| SYN2     | -1.8481 | 1.45641 | -14.893 | 2.45E-08 | 1.18E-06  | 9.1761  |
| TAFA4    | -1.8432 | 0.97179 | -33.082 | 7.37E-12 | 2.19E-09  | 17.8398 |
| DLX3     | -1.8327 | 1.04604 | -16.13  | 1.10E-08 | 6.09E-07  | 10.0373 |
| TLR8-AS  | -1.8287 | 1.01469 | -27.187 | 5.53E-11 | 9.15E-09  | 15.717  |
| ZC3H12C  | -1.8183 | 1.59754 | -27.124 | 5.66E-11 | 9.26E-09  | 15.692  |
| PDGFC    | -1.7999 | 2.3988  | -42.717 | 5.29E-13 | 3.65E-10  | 20.5565 |

|         |         |         |         |          |          |         |
|---------|---------|---------|---------|----------|----------|---------|
| PPARG   | -1.793  | 0.99685 | -24.205 | 1.81E-10 | 2.33E-08 | 14.4529 |
| SYT17   | -1.7833 | 1.03749 | -17.903 | 3.87E-09 | 2.59E-07 | 11.1674 |
| GALNT17 | -1.7679 | 0.88395 | -17.991 | 3.69E-09 | 2.51E-07 | 11.2205 |
| HOXB13  | -1.7668 | 0.93358 | -15.686 | 1.46E-08 | 7.77E-07 | 9.73573 |
| TRIM58  | -1.7609 | 0.93062 | -19.309 | 1.81E-09 | 1.39E-07 | 11.9897 |
| SSTR5-A | -1.7602 | 0.88701 | -14.605 | 2.97E-08 | 1.39E-06 | 8.96663 |
| ALDH1A3 | -1.7456 | 1.46258 | -19.371 | 1.75E-09 | 1.35E-07 | 12.0249 |
| FGFR2   | -1.7367 | 0.91852 | -29.748 | 2.20E-11 | 4.64E-09 | 16.6935 |
| NMU     | -1.7315 | 1.42619 | -14.458 | 3.29E-08 | 1.52E-06 | 8.85785 |
| MOCOS   | -1.7272 | 1.89736 | -15.639 | 1.50E-08 | 7.96E-07 | 9.70322 |
| PAPPA   | -1.7268 | 2.2967  | -24.786 | 1.42E-10 | 1.94E-08 | 14.7112 |
| CFAP47  | -1.7231 | 1.15793 | -14.069 | 4.31E-08 | 1.89E-06 | 8.56529 |
| TMEFF2  | -1.7204 | 1.30706 | -15.514 | 1.63E-08 | 8.46E-07 | 9.61633 |
| PRDM16  | -1.7113 | 1.16523 | -12.568 | 1.31E-07 | 4.84E-06 | 7.3626  |
| PAPPA-A | -1.7072 | 1.79902 | -21.75  | 5.40E-10 | 5.29E-08 | 13.2868 |
| BARX1   | -1.697  | 1.17887 | -10.428 | 7.96E-07 | 2.32E-05 | 5.4079  |
| ECEL1   | -1.6855 | 1.0918  | -14.359 | 3.52E-08 | 1.60E-06 | 8.78431 |
| TTC39C  | -1.6819 | 1.31204 | -13.291 | 7.56E-08 | 3.06E-06 | 7.95718 |
| GLRB    | -1.678  | 1.19873 | -14.455 | 3.30E-08 | 1.52E-06 | 8.85516 |
| NPTX2   | -1.673  | 1.37052 | -12.902 | 1.01E-07 | 3.93E-06 | 7.64105 |
| MIRLET7 | -1.6547 | 1.04703 | -11.836 | 2.35E-07 | 8.10E-06 | 6.72905 |
| EGR2    | -1.6504 | 1.5534  | -18.54  | 2.72E-09 | 1.97E-07 | 11.5478 |
| ALDH1A3 | -1.6501 | 1.31446 | -19.814 | 1.39E-09 | 1.11E-07 | 12.2708 |
| ADCY8   | -1.6499 | 0.87514 | -23.565 | 2.39E-10 | 2.87E-08 | 14.1608 |
| LSAMP   | -1.6441 | 1.54801 | -27.563 | 4.80E-11 | 8.30E-09 | 15.8663 |
| PRKCB   | -1.6409 | 1.20954 | -14.021 | 4.46E-08 | 1.95E-06 | 8.52876 |
| CA13    | -1.6397 | 1.85761 | -17.367 | 5.26E-09 | 3.33E-07 | 10.8373 |
| ADAMTS  | -1.635  | 0.86765 | -16.555 | 8.51E-09 | 4.94E-07 | 10.3181 |
| TSLP    | -1.6305 | 0.86541 | -24.744 | 1.45E-10 | 1.97E-08 | 14.6927 |
| SPATA13 | -1.623  | 1.58406 | -22.389 | 4.02E-10 | 4.28E-08 | 13.6025 |
| KIF26B  | -1.621  | 1.98533 | -14.015 | 4.48E-08 | 1.96E-06 | 8.52421 |
| EOMES   | -1.6076 | 2.39242 | -31.381 | 1.27E-11 | 3.07E-09 | 17.2712 |
| MMP3    | -1.6036 | 3.8271  | -43.342 | 4.55E-13 | 3.35E-10 | 20.7086 |
| MAP3K21 | -1.5846 | 0.84249 | -24.052 | 1.94E-10 | 2.44E-08 | 14.3835 |
| OLFM1   | -1.5789 | 0.83964 | -26.917 | 6.12E-11 | 9.77E-09 | 15.6087 |
| SGCG    | -1.5676 | 1.28082 | -10.489 | 7.53E-07 | 2.21E-05 | 5.46842 |
| DPP4    | -1.565  | 0.83269 | -21.149 | 7.18E-10 | 6.60E-08 | 12.9814 |
| VEGFC   | -1.5624 | 2.06104 | -40.173 | 9.97E-13 | 6.00E-10 | 19.9105 |
| STK32B  | -1.561  | 1.06925 | -13.72  | 5.52E-08 | 2.34E-06 | 8.29645 |
| CFAP46  | -1.5591 | 0.95941 | -14.729 | 2.73E-08 | 1.29E-06 | 9.05725 |
| FOXO1   | -1.5576 | 1.16786 | -17.101 | 6.15E-09 | 3.76E-07 | 10.6697 |
| JAK1    | -1.5513 | 3.06616 | -27.671 | 4.62E-11 | 8.12E-09 | 15.9088 |
| MLKL    | -1.5269 | 1.69087 | -14.122 | 4.15E-08 | 1.84E-06 | 8.60572 |
| EPHA6   | -1.5219 | 1.79241 | -15.629 | 1.51E-08 | 8.00E-07 | 9.69587 |
| COL11A1 | -1.5135 | 3.5145  | -26.198 | 8.08E-11 | 1.26E-08 | 15.3141 |
| HMX1    | -1.5045 | 0.80243 | -8.4068 | 5.98E-06 | 0.00013  | 3.22706 |
| DMBX1   | -1.5016 | 0.87013 | -11.38  | 3.44E-07 | 1.12E-05 | 6.31686 |
| KANK1   | -1.4915 | 2.00808 | -19.165 | 1.95E-09 | 1.48E-07 | 11.9085 |
| ADGRL3  | -1.4887 | 0.92421 | -16.937 | 6.77E-09 | 4.11E-07 | 10.5654 |
| ANKRD33 | -1.4878 | 1.21161 | -15.646 | 1.50E-08 | 7.93E-07 | 9.70793 |
| PCED1B  | -1.4749 | 1.8991  | -16.638 | 8.09E-09 | 4.74E-07 | 10.3727 |
| COL14A1 | -1.4669 | 1.20205 | -13.281 | 7.61E-08 | 3.08E-06 | 7.94966 |
| TWIST2  | -1.4633 | 1.14917 | -8.8706 | 3.65E-06 | 8.64E-05 | 3.76136 |
| RTN4RL2 | -1.4547 | 1.94446 | -7.1971 | 2.41E-05 | 0.00044  | 1.72372 |
| SSH3    | -1.4512 | 1.62936 | -10.325 | 8.75E-07 | 2.51E-05 | 5.30567 |
| DPYSL3  | -1.4421 | 1.78974 | -16.279 | 1.01E-08 | 5.66E-07 | 10.1366 |
| MNX1    | -1.4401 | 0.72005 | -14.291 | 3.69E-08 | 1.67E-06 | 8.73274 |
| GRIN2B  | -1.44   | 1.73712 | -17.174 | 5.89E-09 | 3.65E-07 | 10.7161 |

|           |         |         |         |          |          |         |
|-----------|---------|---------|---------|----------|----------|---------|
| PPP2R2C   | -1.4351 | 1.91141 | -12.821 | 1.08E-07 | 4.13E-06 | 7.57465 |
| HECA      | -1.4342 | 1.88365 | -24.414 | 1.66E-10 | 2.19E-08 | 14.5465 |
| NKX2-5    | -1.4295 | 1.29426 | -8.6182 | 4.76E-06 | 0.00011  | 3.47336 |
| FGF10     | -1.4209 | 2.46239 | -30.843 | 1.52E-11 | 3.49E-09 | 17.0843 |
| SEMA3C    | -1.4199 | 2.4768  | -26.121 | 8.33E-11 | 1.28E-08 | 15.2824 |
| LINC0120  | -1.416  | 0.80835 | -15.101 | 2.13E-08 | 1.05E-06 | 9.32531 |
| EFCAB5    | -1.4036 | 1.54424 | -24.073 | 1.92E-10 | 2.43E-08 | 14.3932 |
| PLPP3     | -1.3992 | 0.74976 | -21.617 | 5.74E-10 | 5.57E-08 | 13.22   |
| MSX2      | -1.3935 | 0.77629 | -15.355 | 1.81E-08 | 9.19E-07 | 9.50532 |
| FGF1      | -1.3867 | 1.46595 | -13.936 | 4.73E-08 | 2.05E-06 | 8.46372 |
| HSD11B2   | -1.3858 | 1.09313 | -9.0362 | 3.07E-06 | 7.45E-05 | 3.94693 |
| LRRC7     | -1.3835 | 2.23133 | -30.161 | 1.91E-11 | 4.10E-09 | 16.8425 |
| OPN5      | -1.3797 | 0.7902  | -18.798 | 2.37E-09 | 1.75E-07 | 11.6978 |
| KLHL29    | -1.3774 | 1.6287  | -21.043 | 7.55E-10 | 6.87E-08 | 12.9265 |
| NRG1      | -1.3756 | 1.20098 | -17.324 | 5.39E-09 | 3.40E-07 | 10.8106 |
| CCDC149   | -1.3736 | 1.32209 | -13.929 | 4.76E-08 | 2.06E-06 | 8.45788 |
| TLR7      | -1.3708 | 0.73559 | -17.56  | 4.71E-09 | 3.07E-07 | 10.9577 |
| DNAJC12   | -1.3692 | 2.23672 | -16.299 | 9.95E-09 | 5.62E-07 | 10.15   |
| AGPAT3    | -1.3678 | 1.85121 | -13.162 | 8.32E-08 | 3.31E-06 | 7.85334 |
| FGF10-AS1 | -1.362  | 1.43243 | -11.561 | 2.95E-07 | 9.88E-06 | 6.48215 |
| HPSE      | -1.3535 | 1.46884 | -11.055 | 4.55E-07 | 1.42E-05 | 6.0139  |
| PCDHB17   | -1.3514 | 0.77915 | -15.674 | 1.47E-08 | 7.81E-07 | 9.72734 |
| TNFSF14   | -1.3497 | 0.87556 | -11.876 | 2.27E-07 | 7.85E-06 | 6.76432 |
| MMP12     | -1.3463 | 1.76483 | -25.02  | 1.29E-10 | 1.79E-08 | 14.8133 |
| KAZN      | -1.346  | 1.77639 | -20.046 | 1.24E-09 | 1.00E-07 | 12.3976 |
| FAM225A   | -1.3369 | 1.28849 | -11.857 | 2.31E-07 | 7.96E-06 | 6.74774 |
| OSGIN1    | -1.331  | 1.26937 | -6.0249 | 0.00011  | 0.00161  | 0.09656 |
| CCPG1     | -1.3278 | 2.99945 | -25.788 | 9.50E-11 | 1.41E-08 | 15.1424 |
| FCF1P3    | -1.3246 | 0.66232 | -21.872 | 5.10E-10 | 5.08E-08 | 13.3479 |
| PDGFA     | -1.3202 | 1.7001  | -17.121 | 6.07E-09 | 3.73E-07 | 10.6824 |
| ICOSLG    | -1.319  | 1.71344 | -11.6   | 2.86E-07 | 9.60E-06 | 6.5173  |
| SLC1A1    | -1.3174 | 1.02696 | -10.022 | 1.16E-06 | 3.21E-05 | 4.99874 |
| ALPL      | -1.3166 | 2.0541  | -8.8589 | 3.69E-06 | 8.74E-05 | 3.74822 |
| CPEB2     | -1.3133 | 0.93686 | -17.932 | 3.81E-09 | 2.57E-07 | 11.1853 |
| CD226     | -1.3126 | 1.21204 | -18.043 | 3.58E-09 | 2.45E-07 | 11.2519 |
| CACNB4    | -1.3042 | 1.85762 | -33.687 | 6.12E-12 | 1.99E-09 | 18.0344 |
| WLS       | -1.3039 | 2.08069 | -22.295 | 4.19E-10 | 4.40E-08 | 13.5569 |
| SLC24A4   | -1.3031 | 1.90084 | -18.141 | 3.39E-09 | 2.35E-07 | 11.3108 |
| MAMLD1    | -1.2979 | 1.24724 | -14.407 | 3.41E-08 | 1.56E-06 | 8.81979 |
| PTPRE     | -1.296  | 1.0371  | -11.311 | 3.65E-07 | 1.18E-05 | 6.25307 |
| ARFGEF3   | -1.2954 | 0.6799  | -17.142 | 6.00E-09 | 3.71E-07 | 10.6959 |
| MICAL2    | -1.2853 | 1.86392 | -15.531 | 1.61E-08 | 8.38E-07 | 9.62828 |
| LAMC3     | -1.2817 | 2.03292 | -7.8058 | 1.17E-05 | 0.00024  | 2.5009  |
| RNF144A   | -1.2737 | 1.38361 | -8.3207 | 6.57E-06 | 0.00014  | 3.12544 |
| TOX2      | -1.2736 | 0.63681 | -12.561 | 1.32E-07 | 4.86E-06 | 7.35705 |
| GABRQ     | -1.27   | 0.73534 | -11.37  | 3.47E-07 | 1.12E-05 | 6.30721 |
| ZNF365    | -1.2627 | 1.11875 | -10.295 | 9.00E-07 | 2.58E-05 | 5.2751  |
| TBC1D30   | -1.2473 | 2.42762 | -23.033 | 3.01E-10 | 3.42E-08 | 13.912  |
| GS1-6000  | -1.2473 | 0.75333 | -14.138 | 4.10E-08 | 1.82E-06 | 8.61788 |
| FAM225B   | -1.2397 | 1.23778 | -10.853 | 5.43E-07 | 1.65E-05 | 5.82236 |
| KRT18     | -1.2371 | 1.93454 | -11.044 | 4.59E-07 | 1.43E-05 | 6.00395 |
| ARRDC4    | -1.231  | 1.03303 | -11.153 | 4.18E-07 | 1.31E-05 | 6.10632 |
| PIERCE2   | -1.2301 | 1.56193 | -17.122 | 6.07E-09 | 3.73E-07 | 10.6834 |
| ARNT2     | -1.2294 | 1.49118 | -11.582 | 2.90E-07 | 9.73E-06 | 6.50074 |
| KCNH3     | -1.2262 | 1.74058 | -6.648  | 4.80E-05 | 0.00079  | 0.98376 |
| FRRS1L    | -1.2178 | 0.78875 | -11.299 | 3.68E-07 | 1.18E-05 | 6.24242 |
| GLYATL2   | -1.2172 | 1.67574 | -16.677 | 7.91E-09 | 4.67E-07 | 10.3981 |
| MNX1-AS1  | -1.2171 | 0.60853 | -11.764 | 2.49E-07 | 8.50E-06 | 6.66457 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| ACSS1    | -1.217  | 1.58322 | -10.612 | 6.73E-07 | 2.00E-05 | 5.58932 |
| KNDC1    | -1.2143 | 0.65731 | -9.5194 | 1.89E-06 | 4.87E-05 | 4.47351 |
| DNAAF4-  | -1.2108 | 2.98462 | -23.971 | 2.00E-10 | 2.50E-08 | 14.3471 |
| ATXN3L   | -1.2096 | 0.65499 | -19.945 | 1.30E-09 | 1.05E-07 | 12.3429 |
| DEF6     | -1.2091 | 1.86807 | -8.6669 | 4.52E-06 | 0.0001   | 3.52941 |
| ADGRE2   | -1.206  | 1.60899 | -10.063 | 1.12E-06 | 3.11E-05 | 5.04089 |
| LPXN     | -1.1942 | 2.25133 | -20.259 | 1.11E-09 | 9.36E-08 | 12.5129 |
| LURAP1L  | -1.1895 | 2.55059 | -17.958 | 3.76E-09 | 2.55E-07 | 11.2008 |
| FOXF2    | -1.183  | 0.5915  | -56.382 | 3.01E-14 | 4.26E-11 | 23.3985 |
| HSPA12A  | -1.1732 | 0.58659 | -52.966 | 5.74E-14 | 6.65E-11 | 22.7716 |
| KITLG    | -1.1721 | 3.03822 | -29.721 | 2.22E-11 | 4.64E-09 | 16.6837 |
| LDAF1    | -1.1704 | 1.39329 | -12.268 | 1.66E-07 | 6.00E-06 | 7.10674 |
| TFAP2E   | -1.1683 | 1.35524 | -9.2526 | 2.46E-06 | 6.11E-05 | 4.18548 |
| COMP     | -1.1681 | 0.84342 | -6.642  | 4.84E-05 | 0.00079  | 0.97543 |
| CHD5     | -1.1636 | 2.10132 | -8.2271 | 7.28E-06 | 0.00016  | 3.01407 |
| VGLL3    | -1.1635 | 2.86778 | -24.425 | 1.65E-10 | 2.19E-08 | 14.5515 |
| OTUD1    | -1.1587 | 0.57937 | -14.479 | 3.24E-08 | 1.50E-06 | 8.87333 |
| MAPT     | -1.1579 | 1.55716 | -8.6696 | 4.51E-06 | 0.0001   | 3.53254 |
| CAMK2N   | -1.1495 | 0.90513 | -11.63  | 2.79E-07 | 9.38E-06 | 6.54413 |
| NOTUM    | -1.1492 | 1.15118 | -6.2263 | 8.35E-05 | 0.00127  | 0.38897 |
| ROR1     | -1.1485 | 0.67459 | -15.297 | 1.88E-08 | 9.47E-07 | 9.46466 |
| EPHB2    | -1.1421 | 1.58433 | -8.2796 | 6.87E-06 | 0.00015  | 3.07667 |
| SATB2    | -1.1382 | 1.06968 | -10.911 | 5.16E-07 | 1.58E-05 | 5.87716 |
| TFCP2L1  | -1.1376 | 1.54284 | -15.845 | 1.32E-08 | 7.14E-07 | 9.84404 |
| SH3RF3   | -1.1353 | 1.48539 | -14.384 | 3.46E-08 | 1.58E-06 | 8.80299 |
| ACE      | -1.1352 | 0.87718 | -8.2459 | 7.13E-06 | 0.00015  | 3.03658 |
| CCDC3    | -1.1347 | 1.61954 | -13.743 | 5.43E-08 | 2.31E-06 | 8.3145  |
| IQANK1   | -1.1333 | 0.80022 | -11.215 | 3.96E-07 | 1.25E-05 | 6.16403 |
| SOX7     | -1.1253 | 1.87092 | -14.492 | 3.21E-08 | 1.49E-06 | 8.88304 |
| RHCG     | -1.124  | 0.66233 | -13.328 | 7.35E-08 | 3.00E-06 | 7.98696 |
| STOX2    | -1.1218 | 2.12163 | -16.52  | 8.69E-09 | 5.03E-07 | 10.2956 |
| MIR9-3HC | -1.1197 | 1.23062 | -10.232 | 9.54E-07 | 2.71E-05 | 5.21179 |
| COBL     | -1.1174 | 0.84745 | -9.92   | 1.28E-06 | 3.50E-05 | 4.89415 |
| SFXN3    | -1.1172 | 1.86701 | -11.939 | 2.16E-07 | 7.52E-06 | 6.82069 |
| DENND1   | -1.1148 | 1.83655 | -22.222 | 4.34E-10 | 4.51E-08 | 13.5209 |
| CACHD1   | -1.111  | 2.25321 | -22.535 | 3.76E-10 | 4.05E-08 | 13.6736 |
| SLIT1    | -1.1095 | 1.02243 | -7.2095 | 2.37E-05 | 0.00044  | 1.74    |
| PMEPA1   | -1.1094 | 0.55471 | -21.841 | 5.17E-10 | 5.14E-08 | 13.3327 |
| PKIB     | -1.1085 | 1.18097 | -21.041 | 7.56E-10 | 6.87E-08 | 12.9258 |
| NECTIN1  | -1.1072 | 0.98431 | -12.328 | 1.58E-07 | 5.77E-06 | 7.15882 |
| VDR      | -1.1067 | 2.07133 | -12.794 | 1.10E-07 | 4.19E-06 | 7.55147 |
| PTCHD4   | -1.1063 | 1.42797 | -22.117 | 4.55E-10 | 4.67E-08 | 13.4692 |
| MAFA     | -1.1032 | 1.0325  | -6.9314 | 3.35E-05 | 0.00058  | 1.37036 |
| LINC0236 | -1.1031 | 0.60175 | -6.2483 | 8.11E-05 | 0.00124  | 0.42061 |
| NAV1     | -1.0988 | 2.45395 | -13.601 | 6.02E-08 | 2.53E-06 | 8.20334 |
| ZNF804A  | -1.0941 | 1.33839 | -16.699 | 7.80E-09 | 4.61E-07 | 10.4123 |
| AKR1C2   | -1.0914 | 1.56459 | -17.242 | 5.66E-09 | 3.54E-07 | 10.7588 |
| ARHGAP   | -1.0895 | 1.46436 | -10.577 | 6.95E-07 | 2.06E-05 | 5.55457 |
| FNDCA    | -1.0881 | 1.29842 | -11.401 | 3.38E-07 | 1.10E-05 | 6.33603 |
| PSD2     | -1.0875 | 0.54376 | -10.712 | 6.16E-07 | 1.85E-05 | 5.68612 |
| DEPTOR   | -1.0845 | 0.82245 | -10.468 | 7.67E-07 | 2.25E-05 | 5.44761 |
| LINC0273 | -1.082  | 0.541   | -27.601 | 4.74E-11 | 8.29E-09 | 15.8811 |
| KCNQ3    | -1.0791 | 0.63987 | -11.943 | 2.15E-07 | 7.51E-06 | 6.82384 |
| RIN3     | -1.079  | 1.2361  | -7.0899 | 2.75E-05 | 0.00049  | 1.58216 |
| TSHZ3    | -1.0783 | 0.5893  | -20.582 | 9.46E-10 | 8.20E-08 | 12.685  |
| TNFRSF1  | -1.0775 | 3.22797 | -20.485 | 9.92E-10 | 8.55E-08 | 12.6335 |
| ST3GAL1  | -1.0773 | 0.639   | -14.866 | 2.49E-08 | 1.20E-06 | 9.15652 |
| HOPX     | -1.0758 | 0.71778 | -11.327 | 3.60E-07 | 1.16E-05 | 6.26782 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| CDHR1    | -1.0753 | 1.00626 | -15.092 | 2.15E-08 | 1.06E-06 | 9.31942 |
| LGI3     | -1.0751 | 0.58772 | -7.8614 | 1.10E-05 | 0.00022  | 2.56985 |
| ITGA6-AS | -1.0751 | 0.76758 | -8.2776 | 6.89E-06 | 0.00015  | 3.07428 |
| GPR176   | -1.074  | 1.96863 | -19.002 | 2.12E-09 | 1.58E-07 | 11.8154 |
| C1QL4    | -1.073  | 1.64951 | -8.2454 | 7.14E-06 | 0.00015  | 3.03593 |
| TMEM26   | -1.0713 | 2.01497 | -28.499 | 3.41E-11 | 6.64E-09 | 16.2286 |
| CYP4F2   | -1.0709 | 0.76547 | -7.2142 | 2.36E-05 | 0.00043  | 1.74612 |
| HNRNPA   | -1.0654 | 0.62402 | -14.611 | 2.96E-08 | 1.39E-06 | 8.9705  |
| ZFYVE28  | -1.0654 | 1.05704 | -7.3187 | 2.08E-05 | 0.00039  | 1.88242 |
| EPIC1    | -1.0619 | 0.53096 | -15.803 | 1.36E-08 | 7.31E-07 | 9.81565 |
| GPR27    | -1.0616 | 0.58098 | -20.097 | 1.20E-09 | 9.93E-08 | 12.4252 |
| EML6     | -1.061  | 2.04176 | -20.639 | 9.19E-10 | 8.04E-08 | 12.7154 |
| MAPK15   | -1.0598 | 1.41715 | -5.0566 | 0.00044  | 0.00538  | -1.3865 |
| ASIP     | -1.0577 | 1.03443 | -8.3474 | 6.38E-06 | 0.00014  | 3.15704 |
| PRDM6    | -1.0543 | 0.75718 | -9.1569 | 2.71E-06 | 6.67E-05 | 4.08056 |
| TESC     | -1.0508 | 1.32236 | -7.4536 | 1.77E-05 | 0.00034  | 2.0566  |
| SDK2     | -1.05   | 1.57894 | -5.346  | 0.00029  | 0.00372  | -0.9298 |
| ABCA15P  | -1.0496 | 0.5248  | -19.03  | 2.09E-09 | 1.57E-07 | 11.8313 |
| PRPH     | -1.0467 | 0.77376 | -6.5442 | 5.49E-05 | 0.00088  | 0.83952 |
| PARD3B   | -1.0442 | 0.75212 | -8.659  | 4.56E-06 | 0.0001   | 3.52035 |
| TMCO4    | -1.0436 | 1.55528 | -8.9891 | 3.22E-06 | 7.75E-05 | 3.8945  |
| LRRCC1   | -1.0425 | 2.27381 | -13.384 | 7.05E-08 | 2.89E-06 | 8.03186 |
| KBTBD11  | -1.0422 | 0.88082 | -12.067 | 1.95E-07 | 6.89E-06 | 6.933   |
| TBXAS1   | -1.0409 | 0.52044 | -13.274 | 7.65E-08 | 3.09E-06 | 7.94404 |
| HLX      | -1.0388 | 0.64911 | -6.9726 | 3.18E-05 | 0.00056  | 1.42576 |
| MYORG    | -1.0312 | 2.01535 | -13.946 | 4.70E-08 | 2.04E-06 | 8.47143 |
| EEF1A2   | -1.0295 | 2.66004 | -5.5437 | 0.00022  | 0.00292  | -0.6244 |
| TRIB2    | -1.0292 | 0.81097 | -7.6913 | 1.34E-05 | 0.00027  | 2.35801 |
| MYLIP    | -1.0287 | 1.50364 | -18.081 | 3.51E-09 | 2.41E-07 | 11.275  |
| SMAGP    | -1.0264 | 1.72916 | -23.666 | 2.28E-10 | 2.78E-08 | 14.2075 |
| SYCP2    | -1.0263 | 2.27749 | -14.977 | 2.32E-08 | 1.12E-06 | 9.23695 |
| PLAC4    | -1.0262 | 0.5131  | -11.294 | 3.70E-07 | 1.19E-05 | 6.23731 |
| ANKRD34  | -1.0223 | 2.03711 | -18.5   | 2.78E-09 | 2.00E-07 | 11.5238 |
| CFAP20D  | -1.0211 | 0.79075 | -12.914 | 1.00E-07 | 3.90E-06 | 7.65114 |
| RNU7-15  | -1.021  | 0.59003 | -11.889 | 2.25E-07 | 7.78E-06 | 6.77621 |
| FGD4     | -1.0188 | 0.6581  | -8.9119 | 3.49E-06 | 8.31E-05 | 3.80787 |
| HYLS1    | -1.0184 | 1.60878 | -14.719 | 2.75E-08 | 1.30E-06 | 9.0499  |
| PRDM16   | -1.0177 | 0.50884 | -8.2796 | 6.87E-06 | 0.00015  | 3.07661 |
| AR       | -1.0151 | 1.34337 | -12.129 | 1.85E-07 | 6.61E-06 | 6.98651 |
| MIR9-1HG | -1.012  | 0.97138 | -8.0995 | 8.40E-06 | 0.00018  | 2.86078 |
| PALM2AK  | -1.0057 | 2.38077 | -13.818 | 5.15E-08 | 2.20E-06 | 8.37223 |
| CALN1    | -1.0051 | 0.50255 | -7.4788 | 1.72E-05 | 0.00033  | 2.0888  |
| FOXE1    | -1.0016 | 0.99021 | -9.9507 | 1.24E-06 | 3.41E-05 | 4.92582 |
| TRABD2B  | -1.0014 | 0.70141 | -10.467 | 7.68E-07 | 2.25E-05 | 5.44644 |
| ARC      | -1.0004 | 1.22817 | -8.2361 | 7.21E-06 | 0.00016  | 3.02483 |
| CITED2   | -0.9996 | 2.5272  | -9.7815 | 1.46E-06 | 3.92E-05 | 4.75028 |
| CPT1A    | -0.9985 | 2.54161 | -14.998 | 2.28E-08 | 1.11E-06 | 9.25185 |
| C3       | -0.9974 | 1.52845 | -10.056 | 1.12E-06 | 3.13E-05 | 5.03371 |
| FAM81A   | -0.9965 | 1.29816 | -6.1164 | 9.69E-05 | 0.00145  | 0.23009 |
| C1orf105 | -0.9941 | 0.87758 | -7.2068 | 2.38E-05 | 0.00044  | 1.73645 |
| LRRC7-A  | -0.9923 | 0.69682 | -9.2674 | 2.43E-06 | 6.03E-05 | 4.20163 |
| NPTX1    | -0.9909 | 1.07201 | -10.049 | 1.13E-06 | 3.15E-05 | 5.02683 |
| ELAPOR2  | -0.9888 | 0.61374 | -13.275 | 7.65E-08 | 3.09E-06 | 7.94414 |
| TMC3-AS  | -0.9885 | 1.08401 | -8.7618 | 4.09E-06 | 9.52E-05 | 3.63801 |
| LINC0294 | -0.9843 | 1.27677 | -5.8914 | 0.00013  | 0.00189  | -0.1003 |
| EFCC1    | -0.9842 | 0.89996 | -5.8607 | 0.00014  | 0.00196  | -0.1458 |
| LMCD1    | -0.9827 | 1.53636 | -10.308 | 8.89E-07 | 2.55E-05 | 5.28853 |
| PPIC-AS1 | -0.98   | 0.49002 | -6.965  | 3.21E-05 | 0.00056  | 1.41551 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| GUCY1A   | -0.9796 | 2.78766 | -31.442 | 1.24E-11 | 3.05E-09 | 17.292  |
| GNAT3    | -0.9755 | 0.48775 | -50.329 | 9.73E-14 | 9.43E-11 | 22.253  |
| SYNE3    | -0.9744 | 1.45602 | -13.437 | 6.78E-08 | 2.81E-06 | 8.07396 |
| MCOLN3   | -0.9743 | 1.69758 | -18.687 | 2.51E-09 | 1.84E-07 | 11.6334 |
| LAMP3    | -0.9723 | 1.3221  | -10.823 | 5.57E-07 | 1.69E-05 | 5.79367 |
| CYP4F33  | -0.9719 | 1.93998 | -11.702 | 2.63E-07 | 8.90E-06 | 6.60894 |
| ENPP7P6  | -0.9717 | 0.59982 | -9.4602 | 2.00E-06 | 5.12E-05 | 4.41023 |
| WTAPP1   | -0.9697 | 2.53024 | -17.503 | 4.86E-09 | 3.15E-07 | 10.9221 |
| FERMT1   | -0.9694 | 2.00857 | -14.348 | 3.55E-08 | 1.61E-06 | 8.77584 |
| TATDN2P  | -0.968  | 0.61369 | -8.7617 | 4.09E-06 | 9.52E-05 | 3.63788 |
| JUN      | -0.9656 | 1.03356 | -8.4747 | 5.55E-06 | 0.00012  | 3.30671 |
| AK4      | -0.9654 | 2.65487 | -20.339 | 1.07E-09 | 9.09E-08 | 12.556  |
| DERL3    | -0.9648 | 2.34797 | -7.7176 | 1.30E-05 | 0.00026  | 2.391   |
| CD70     | -0.963  | 2.30552 | -7.1652 | 2.51E-05 | 0.00046  | 1.68169 |
| TAFA1    | -0.961  | 0.4805  | -9.1753 | 2.66E-06 | 6.57E-05 | 4.10083 |
| LINC0063 | -0.9548 | 0.62793 | -10.371 | 8.39E-07 | 2.43E-05 | 5.35112 |
| SLC22A3  | -0.952  | 1.53041 | -4.2002 | 0.00169  | 0.01635  | -2.8019 |
| GPD1     | -0.9515 | 0.8968  | -5.882  | 0.00013  | 0.00191  | -0.1143 |
| C6orf141 | -0.9504 | 0.4752  | -12.268 | 1.66E-07 | 6.00E-06 | 7.10673 |
| C7orf31  | -0.9492 | 1.83319 | -15.3   | 1.87E-08 | 9.46E-07 | 9.46666 |
| DOC2B    | -0.9467 | 1.80745 | -15.772 | 1.38E-08 | 7.43E-07 | 9.79478 |
| TNFRSF2  | -0.9449 | 2.21408 | -15.08  | 2.16E-08 | 1.06E-06 | 9.31056 |
| CYP2S1   | -0.9433 | 1.36719 | -4.8461 | 0.00061  | 0.00706  | -1.726  |
| CALB1    | -0.9432 | 1.29982 | -18.22  | 3.25E-09 | 2.27E-07 | 11.3584 |
| IGFBP7-A | -0.9426 | 0.47132 | -16.587 | 8.35E-09 | 4.86E-07 | 10.339  |
| TMEM178  | -0.9414 | 0.85977 | -12.047 | 1.98E-07 | 6.97E-06 | 6.91543 |
| IL1R1    | -0.9377 | 1.81276 | -24.401 | 1.67E-10 | 2.20E-08 | 14.5408 |
| SGK3     | -0.9358 | 1.79254 | -12.919 | 9.99E-08 | 3.89E-06 | 7.65527 |
| MCC      | -0.9335 | 1.9658  | -12.179 | 1.78E-07 | 6.38E-06 | 7.0303  |
| LINC0300 | -0.9326 | 0.63002 | -12.766 | 1.12E-07 | 4.26E-06 | 7.52828 |
| RNASE4   | -0.9307 | 0.6452  | -9.1217 | 2.81E-06 | 6.88E-05 | 4.04171 |
| SNX18P3  | -0.9264 | 1.61053 | -18.184 | 3.31E-09 | 2.31E-07 | 11.3369 |
| PLCG2    | -0.9257 | 1.34989 | -8.0974 | 8.42E-06 | 0.00018  | 2.85816 |
| NKAIN1   | -0.9254 | 1.58752 | -6.7789 | 4.06E-05 | 0.00068  | 1.16362 |
| ENTPD2   | -0.9246 | 0.74251 | -5.8367 | 0.00014  | 0.00202  | -0.1816 |
| RASSF2   | -0.9239 | 2.13926 | -12.234 | 1.70E-07 | 6.14E-06 | 7.07821 |
| TSPAN9   | -0.9236 | 2.60092 | -8.9326 | 3.42E-06 | 8.16E-05 | 3.83123 |
| RMDN2    | -0.9222 | 2.51635 | -21.18  | 7.07E-10 | 6.54E-08 | 12.9977 |
| PODXL    | -0.922  | 2.14551 | -14.145 | 4.09E-08 | 1.82E-06 | 8.62289 |
| KCNIP3   | -0.9205 | 1.96754 | -7.1969 | 2.41E-05 | 0.00044  | 1.72335 |
| GPRC5A   | -0.9192 | 0.81932 | -7.0314 | 2.96E-05 | 0.00052  | 1.50438 |
| ATP8B3   | -0.9188 | 1.54549 | -5.385  | 0.00027  | 0.00354  | -0.8692 |
| TTLL7    | -0.9175 | 2.00445 | -14.505 | 3.18E-08 | 1.48E-06 | 8.89239 |
| TMEM51-  | -0.9163 | 0.60865 | -9.8632 | 1.35E-06 | 3.68E-05 | 4.83532 |
| IMPG1    | -0.916  | 0.63788 | -7.3581 | 1.98E-05 | 0.00038  | 1.93355 |
| SMPDL3A  | -0.9154 | 0.9926  | -6.3843 | 6.77E-05 | 0.00106  | 0.61452 |
| BARX1-D  | -0.9131 | 0.60706 | -7.5909 | 1.50E-05 | 0.00029  | 2.23156 |
| TPSG1    | -0.9131 | 0.50671 | -8.2909 | 6.79E-06 | 0.00015  | 3.09006 |
| USP43    | -0.9128 | 0.55676 | -9.7343 | 1.53E-06 | 4.06E-05 | 4.70091 |
| AHNAK    | -0.9117 | 3.01138 | -14.993 | 2.29E-08 | 1.11E-06 | 9.24861 |
| GAS7     | -0.9093 | 0.75101 | -5.9582 | 0.00012  | 0.00174  | -0.0015 |
| SSH2     | -0.9088 | 3.15164 | -14.324 | 3.61E-08 | 1.63E-06 | 8.75809 |
| SGMS2    | -0.9079 | 2.13292 | -17.887 | 3.91E-09 | 2.61E-07 | 11.1577 |
| NEK10    | -0.9043 | 1.42584 | -15.674 | 1.47E-08 | 7.81E-07 | 9.72691 |
| COL3A1   | -0.9043 | 4.00698 | -10.36  | 8.48E-07 | 2.45E-05 | 5.33998 |
| LGI4     | -0.9041 | 0.68206 | -5.0833 | 0.00042  | 0.0052   | -1.3439 |
| BMAL2    | -0.9032 | 2.45338 | -23.734 | 2.22E-10 | 2.72E-08 | 14.2387 |
| TRIM7    | -0.9005 | 1.60571 | -7.9109 | 1.04E-05 | 0.00021  | 2.63084 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| TSPAN13  | -0.8965 | 2.72478 | -17.507 | 4.85E-09 | 3.15E-07 | 10.9243 |
| CA7      | -0.8953 | 0.69852 | -5.7848 | 0.00015  | 0.00216  | -0.2592 |
| SLC9A2   | -0.8952 | 0.80734 | -9.6764 | 1.62E-06 | 4.26E-05 | 4.64005 |
| CCNO     | -0.8946 | 0.49749 | -6.5451 | 5.48E-05 | 0.00088  | 0.84073 |
| GBX2     | -0.8919 | 0.49611 | -8.9278 | 3.44E-06 | 8.20E-05 | 3.82581 |
| PHLDA2   | -0.8914 | 1.08566 | -4.7167 | 0.00074  | 0.00833  | -1.9373 |
| CD9      | -0.8906 | 1.92592 | -10.429 | 7.95E-07 | 2.32E-05 | 5.40873 |
| FGD3     | -0.8898 | 1.18182 | -7.2927 | 2.15E-05 | 0.0004   | 1.84863 |
| ECHDC2   | -0.8897 | 2.19046 | -11.991 | 2.07E-07 | 7.27E-06 | 6.86567 |
| HOXC12   | -0.8884 | 0.63095 | -9.0158 | 3.14E-06 | 7.58E-05 | 3.92427 |
| CPSF1P1  | -0.8884 | 0.98173 | -6.1086 | 9.79E-05 | 0.00146  | 0.21872 |
| RPS3AP2  | -0.8863 | 0.44315 | -13.323 | 7.38E-08 | 3.00E-06 | 7.98292 |
| SEMA3D   | -0.8851 | 2.93072 | -25.686 | 9.89E-11 | 1.45E-08 | 15.0997 |
| CORO6    | -0.8842 | 2.28293 | -6.0608 | 0.0001   | 0.00154  | 0.14912 |
| P2RX5    | -0.8818 | 1.98882 | -8.8232 | 3.83E-06 | 9.02E-05 | 3.70773 |
| MMP16    | -0.8813 | 2.31503 | -25.805 | 9.43E-11 | 1.40E-08 | 15.1497 |
| ITGA6    | -0.8812 | 2.85134 | -14.314 | 3.63E-08 | 1.64E-06 | 8.75055 |
| LINC0093 | -0.8804 | 0.9019  | -7.6334 | 1.43E-05 | 0.00028  | 2.28526 |
| ACSL1    | -0.8801 | 2.90945 | -24.79  | 1.42E-10 | 1.94E-08 | 14.7131 |
| ITPR3    | -0.8791 | 2.7204  | -6.1217 | 9.62E-05 | 0.00144  | 0.23788 |
| FDX1     | -0.8784 | 2.93836 | -20.456 | 1.01E-09 | 8.65E-08 | 12.6181 |
| ITGB3    | -0.8777 | 0.6689  | -6.9881 | 3.12E-05 | 0.00055  | 1.44646 |
| ENPP7P1  | -0.8767 | 0.58283 | -9.4982 | 1.93E-06 | 4.96E-05 | 4.45086 |
| CBLN2    | -0.8754 | 3.82899 | -23.711 | 2.24E-10 | 2.74E-08 | 14.2282 |
| CHMP4C   | -0.8733 | 2.5876  | -18.058 | 3.55E-09 | 2.44E-07 | 11.2609 |
| PAG1     | -0.8727 | 2.17001 | -22.339 | 4.11E-10 | 4.36E-08 | 13.578  |
| STAMBP   | -0.8722 | 1.66654 | -20.227 | 1.13E-09 | 9.47E-08 | 12.4957 |
| TMEM15   | -0.8717 | 0.72461 | -5.1192 | 0.0004   | 0.00496  | -1.2868 |
| OSTF1    | -0.8711 | 1.7824  | -11.206 | 3.99E-07 | 1.26E-05 | 6.15572 |
| ALOX12B  | -0.8691 | 0.53487 | -8.4561 | 5.67E-06 | 0.00013  | 3.28497 |
| CSRP1    | -0.869  | 1.11527 | -11.811 | 2.40E-07 | 8.22E-06 | 6.70695 |
| NDRG1    | -0.8664 | 0.74277 | -7.7215 | 1.29E-05 | 0.00026  | 2.39585 |
| FGD5     | -0.8641 | 0.90065 | -5.8583 | 0.00014  | 0.00197  | -0.1494 |
| ARHGAP   | -0.8626 | 1.74459 | -13.217 | 7.98E-08 | 3.20E-06 | 7.89761 |
| PRPH2    | -0.8612 | 1.96314 | -10.046 | 1.14E-06 | 3.15E-05 | 5.02338 |
| LNMICC   | -0.8606 | 2.54971 | -7.5288 | 1.62E-05 | 0.00032  | 2.15264 |
| OGFRL1   | -0.8595 | 1.81317 | -17.557 | 4.72E-09 | 3.07E-07 | 10.9555 |
| FOXA3    | -0.8582 | 1.19758 | -4.5308 | 0.00099  | 0.01061  | -2.2449 |
| MFSD2A   | -0.8573 | 2.13807 | -11.665 | 2.71E-07 | 9.15E-06 | 6.5759  |
| NPPC     | -0.8552 | 0.93786 | -6.5293 | 5.60E-05 | 0.0009   | 0.81866 |
| MEOX1    | -0.8546 | 2.07731 | -8.0352 | 9.02E-06 | 0.00019  | 2.78282 |
| CDH23    | -0.8514 | 1.24345 | -5.981  | 0.00012  | 0.0017   | 0.03206 |
| ITPR2    | -0.8496 | 2.25759 | -13.151 | 8.39E-08 | 3.34E-06 | 7.84426 |
| ULK4P1   | -0.8492 | 0.71796 | -14.558 | 3.07E-08 | 1.44E-06 | 8.93154 |
| KCNH4    | -0.8471 | 0.74924 | -5.3439 | 0.00029  | 0.00373  | -0.9332 |
| ANG      | -0.8466 | 0.60316 | -9.2972 | 2.36E-06 | 5.88E-05 | 4.23409 |
| ADORA1   | -0.8454 | 1.62097 | -7.5486 | 1.58E-05 | 0.00031  | 2.17785 |
| MCOLN2   | -0.8441 | 2.20179 | -18.725 | 2.46E-09 | 1.81E-07 | 11.6553 |
| H19      | -0.8439 | 1.93063 | -4.9715 | 0.0005   | 0.00599  | -1.523  |
| FABP5    | -0.8439 | 3.50596 | -15.537 | 1.61E-08 | 8.37E-07 | 9.63247 |
| TLR8     | -0.8436 | 0.47196 | -7.7948 | 1.19E-05 | 0.00024  | 2.48727 |
| NPAS1    | -0.8421 | 2.04655 | -4.7431 | 0.00071  | 0.00807  | -1.894  |
| TNFRSF1  | -0.8408 | 0.4204  | -12.988 | 9.48E-08 | 3.72E-06 | 7.71199 |
| FABP5P7  | -0.8402 | 3.05905 | -16.167 | 1.08E-08 | 5.99E-07 | 10.062  |
| USH1G    | -0.8394 | 0.9593  | -4.3606 | 0.0013   | 0.01324  | -2.5301 |
| IRAK4    | -0.8382 | 1.74748 | -10.989 | 4.82E-07 | 1.48E-05 | 5.9518  |
| AKR1C1   | -0.836  | 1.20851 | -14.616 | 2.95E-08 | 1.39E-06 | 8.9742  |
| ZYG11A   | -0.8351 | 2.24206 | -11.299 | 3.68E-07 | 1.18E-05 | 6.24231 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| P4HA2    | -0.8349 | 2.684   | -8.2033 | 7.48E-06 | 0.00016  | 2.98567 |
| MYZAP    | -0.8337 | 0.89305 | -10.104 | 1.07E-06 | 3.01E-05 | 5.08276 |
| DAZL     | -0.8332 | 0.49611 | -9.6409 | 1.68E-06 | 4.39E-05 | 4.60264 |
| CTSZ     | -0.8324 | 2.57801 | -9.743  | 1.52E-06 | 4.03E-05 | 4.71008 |
| HSD3B7   | -0.8315 | 1.86129 | -4.5229 | 0.00101  | 0.01072  | -2.2579 |
| HCAR3    | -0.8286 | 0.48208 | -7.3317 | 2.05E-05 | 0.00039  | 1.89928 |
| SLC9A7   | -0.828  | 2.27962 | -10.248 | 9.39E-07 | 2.68E-05 | 5.22849 |
| EPB41L4  | -0.8278 | 2.19326 | -16.198 | 1.06E-08 | 5.91E-07 | 10.0827 |
| FRMPD1   | -0.8276 | 0.59366 | -7.8267 | 1.14E-05 | 0.00023  | 2.52686 |
| RNF212   | -0.8266 | 2.18857 | -9.7133 | 1.56E-06 | 4.14E-05 | 4.67888 |
| ANKRD29  | -0.8259 | 0.56349 | -8.6344 | 4.68E-06 | 0.00011  | 3.49206 |
| OR2W3    | -0.8242 | 0.41212 | -13.637 | 5.87E-08 | 2.47E-06 | 8.23132 |
| PTPN6    | -0.8239 | 1.5793  | -4.8756 | 0.00058  | 0.0068   | -1.6779 |
| FAM201A  | -0.8239 | 0.94687 | -5.2998 | 0.00031  | 0.00396  | -1.002  |
| KLHDC7E  | -0.8237 | 0.59169 | -5.4294 | 0.00025  | 0.00336  | -0.8003 |
| TMEM26   | -0.8229 | 0.97836 | -5.5491 | 0.00021  | 0.0029   | -0.6161 |
| HTR1F    | -0.8221 | 2.14857 | -23.475 | 2.48E-10 | 2.94E-08 | 14.119  |
| PLD1     | -0.8213 | 1.07528 | -6.8532 | 3.69E-05 | 0.00063  | 1.26475 |
| RET      | -0.82   | 1.4207  | -6.3742 | 6.86E-05 | 0.00107  | 0.60024 |
| SYPL2    | -0.8198 | 1.63349 | -14.042 | 4.39E-08 | 1.92E-06 | 8.54445 |
| FABP5P1  | -0.8183 | 1.91157 | -11.483 | 3.15E-07 | 1.04E-05 | 6.41144 |
| PFKP     | -0.8167 | 2.79792 | -6.7369 | 4.28E-05 | 0.00072  | 1.10604 |
| VSTM4    | -0.8164 | 1.10297 | -5.0249 | 0.00046  | 0.0056   | -1.4374 |
| PRRT4    | -0.8157 | 1.15047 | -3.8707 | 0.0029   | 0.02555  | -3.3685 |
| CHRM4    | -0.8148 | 0.60343 | -5.7415 | 0.00016  | 0.00228  | -0.3242 |
| SLC27A2  | -0.8146 | 2.08992 | -16.635 | 8.11E-09 | 4.75E-07 | 10.3705 |
| CDH15    | -0.8142 | 0.78763 | -5.4213 | 0.00026  | 0.00339  | -0.8128 |
| SNX16    | -0.8137 | 3.1374  | -18.167 | 3.34E-09 | 2.32E-07 | 11.3267 |
| RTTN     | -0.8122 | 3.22196 | -15.674 | 1.47E-08 | 7.81E-07 | 9.72745 |
| SNX29P1  | -0.8117 | 0.42483 | -6.6772 | 4.62E-05 | 0.00076  | 1.02406 |
| ABCC8    | -0.811  | 1.26558 | -7.02   | 3.00E-05 | 0.00053  | 1.48917 |
| NOG      | -0.8088 | 0.50476 | -10.446 | 7.83E-07 | 2.29E-05 | 5.4255  |
| CHRFAM   | -0.8088 | 0.93013 | -9.4287 | 2.06E-06 | 5.25E-05 | 4.37636 |
| LINC0188 | -0.8087 | 0.88665 | -13.223 | 7.95E-08 | 3.19E-06 | 7.90265 |
| SGCA     | -0.8081 | 1.326   | -4.3114 | 0.00141  | 0.01415  | -2.6131 |
| GLYATL1  | -0.8077 | 1.72412 | -17.805 | 4.09E-09 | 2.72E-07 | 11.1081 |
| EPHA10   | -0.8068 | 1.4192  | -6.6182 | 4.99E-05 | 0.00081  | 0.94249 |
| SACS-AS  | -0.8066 | 1.0016  | -7.1599 | 2.52E-05 | 0.00046  | 1.6748  |
| AK4P1    | -0.8052 | 1.57815 | -11.489 | 3.14E-07 | 1.04E-05 | 6.41613 |
| INKA1    | -0.805  | 1.04891 | -4.0351 | 0.00221  | 0.02043  | -3.0845 |
| HPCAL4   | -0.8046 | 1.77647 | -11.37  | 3.47E-07 | 1.12E-05 | 6.30756 |
| KIF5C    | -0.8031 | 1.60615 | -11.486 | 3.14E-07 | 1.04E-05 | 6.41391 |
| TMEM64   | -0.8022 | 2.86661 | -17.369 | 5.26E-09 | 3.33E-07 | 10.8385 |
| SLC4A11  | -0.8021 | 2.41487 | -6.4899 | 5.89E-05 | 0.00094  | 0.76355 |
| AGTR1    | -0.8017 | 1.29181 | -8.3573 | 6.31E-06 | 0.00014  | 3.16877 |
| LINC0202 | -0.8005 | 0.40023 | -17.127 | 6.05E-09 | 3.73E-07 | 10.6864 |
| LARGE2   | -0.8001 | 1.97995 | -4.0032 | 0.00233  | 0.02136  | -3.1394 |
| ADGRD2   | -0.7997 | 0.47937 | -6.3111 | 7.46E-05 | 0.00115  | 0.51051 |
| FABP5P1  | -0.7992 | 1.25413 | -13.323 | 7.38E-08 | 3.00E-06 | 7.98288 |
| APOBEC   | -0.7991 | 1.9748  | -18.514 | 2.76E-09 | 1.99E-07 | 11.5321 |
| MAP3K5   | -0.7965 | 1.91233 | -17.915 | 3.85E-09 | 2.59E-07 | 11.1746 |
| RAPGEF4  | -0.7958 | 1.40572 | -10.95  | 4.98E-07 | 1.53E-05 | 5.91486 |
| SYT7     | -0.795  | 1.4896  | -7.8936 | 1.06E-05 | 0.00022  | 2.6095  |
| CLDN11   | -0.7939 | 1.56729 | -7.2303 | 2.32E-05 | 0.00043  | 1.76714 |
| SORBS1   | -0.7931 | 1.14756 | -6.089  | 0.0001   | 0.00149  | 0.1902  |
| LINC0139 | -0.7916 | 1.19583 | -6.9924 | 3.10E-05 | 0.00055  | 1.45229 |
| CA12     | -0.7909 | 2.78349 | -9.625  | 1.70E-06 | 4.45E-05 | 4.58578 |
| P4HA2-A  | -0.7907 | 1.67386 | -7.9457 | 9.99E-06 | 0.00021  | 2.67348 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| ALDH3B1  | -0.7899 | 1.30781 | -5.2134 | 0.00035  | 0.0044   | -1.1377 |
| FBN1     | -0.7897 | 2.75819 | -13.587 | 6.08E-08 | 2.56E-06 | 8.19233 |
| CNTF     | -0.7887 | 2.0972  | -15.946 | 1.24E-08 | 6.77E-07 | 9.9131  |
| GLYATL1  | -0.7887 | 0.44454 | -9.7015 | 1.58E-06 | 4.17E-05 | 4.66646 |
| SNAI1    | -0.7873 | 1.19279 | -4.5218 | 0.00101  | 0.01073  | -2.2598 |
| ARHGEF   | -0.7859 | 1.76286 | -9.7895 | 1.45E-06 | 3.90E-05 | 4.75867 |
| LINC0101 | -0.7856 | 0.47234 | -6.7685 | 4.11E-05 | 0.00069  | 1.14942 |
| SNHG26   | -0.7834 | 1.90496 | -15.172 | 2.04E-08 | 1.01E-06 | 9.37579 |
| SHB      | -0.7832 | 1.75861 | -8.7847 | 3.99E-06 | 9.34E-05 | 3.66404 |
| LGI2     | -0.7828 | 0.98379 | -5.0416 | 0.00045  | 0.00549  | -1.4107 |
| KCNK6    | -0.7816 | 1.74799 | -9.0676 | 2.97E-06 | 7.24E-05 | 3.98183 |
| PMP22    | -0.7809 | 1.86931 | -11.308 | 3.66E-07 | 1.18E-05 | 6.25024 |
| INHBA-AS | -0.7795 | 0.38974 | -13.322 | 7.38E-08 | 3.00E-06 | 7.98214 |
| DAPK2    | -0.7786 | 0.8899  | -5.4133 | 0.00026  | 0.00342  | -0.8253 |
| KDELR3   | -0.7777 | 2.58828 | -14.147 | 4.08E-08 | 1.82E-06 | 8.62428 |
| GLYATL1  | -0.7772 | 0.48896 | -8.241  | 7.17E-06 | 0.00015  | 3.03066 |
| DLX4     | -0.7763 | 1.04425 | -6.9046 | 3.46E-05 | 0.0006   | 1.33426 |
| DOCK5    | -0.7742 | 2.37294 | -13.335 | 7.31E-08 | 2.99E-06 | 7.9925  |
| LINC0064 | -0.7741 | 0.48738 | -7.7223 | 1.29E-05 | 0.00026  | 2.39687 |
| AK4P3    | -0.7739 | 1.38184 | -11.556 | 2.96E-07 | 9.91E-06 | 6.47725 |
| PDGFA-D  | -0.7734 | 0.43686 | -5.4835 | 0.00024  | 0.00315  | -0.7168 |
| CFTR     | -0.7729 | 0.68281 | -6.1686 | 9.03E-05 | 0.00136  | 0.30579 |
| SMOC1    | -0.772  | 0.64537 | -6.5088 | 5.75E-05 | 0.00092  | 0.79001 |
| ZNF703   | -0.7715 | 1.0753  | -4.656  | 0.00082  | 0.00902  | -2.0372 |
| ATP2A3   | -0.7714 | 1.56011 | -3.8478 | 0.00301  | 0.02636  | -3.4082 |
| KIAA0319 | -0.7708 | 1.15036 | -6.1896 | 8.78E-05 | 0.00133  | 0.33606 |
| RCN3     | -0.7698 | 1.62536 | -4.3828 | 0.00126  | 0.01284  | -2.4927 |
| ZDHHC23  | -0.7691 | 2.86582 | -17.321 | 5.40E-09 | 3.40E-07 | 10.8089 |
| DOK6     | -0.7689 | 1.72223 | -8.3918 | 6.08E-06 | 0.00013  | 3.20946 |
| FABP5P2  | -0.7686 | 1.69676 | -13.307 | 7.47E-08 | 3.03E-06 | 7.97006 |
| GATA2    | -0.7676 | 2.78646 | -7.242  | 2.28E-05 | 0.00042  | 1.7825  |
| SH2D3A   | -0.7675 | 1.05252 | -4.5237 | 0.001    | 0.01071  | -2.2566 |
| LINC0208 | -0.7674 | 1.12785 | -8.6398 | 4.65E-06 | 0.00011  | 3.49827 |
| APOBEC   | -0.7662 | 2.66244 | -11.72  | 2.59E-07 | 8.78E-06 | 6.62536 |
| OTOP2    | -0.7658 | 0.43305 | -6.7854 | 4.02E-05 | 0.00068  | 1.17248 |
| TRABD2A  | -0.7655 | 1.13715 | -8.3819 | 6.14E-06 | 0.00014  | 3.19774 |
| PTGES    | -0.7655 | 1.96009 | -5.6091 | 0.0002   | 0.00268  | -0.5245 |
| CAMK2B   | -0.7652 | 1.17192 | -6.1013 | 9.89E-05 | 0.00147  | 0.2082  |
| MSRA     | -0.7648 | 1.83102 | -7.9436 | 1.00E-05 | 0.00021  | 2.67093 |
| ANKRD18  | -0.7643 | 2.03731 | -11.956 | 2.13E-07 | 7.45E-06 | 6.83516 |
| LAMA3    | -0.7631 | 0.51126 | -7.0316 | 2.96E-05 | 0.00052  | 1.50464 |
| C1QTNF1  | -0.7608 | 0.48075 | -6.9978 | 3.08E-05 | 0.00054  | 1.45947 |
| IGFBP4   | -0.7602 | 2.17363 | -6.2441 | 8.16E-05 | 0.00125  | 0.41451 |
| DKK2     | -0.759  | 2.49627 | -20.607 | 9.34E-10 | 8.13E-08 | 12.6985 |
| APOBEC   | -0.7576 | 1.8944  | -14.329 | 3.59E-08 | 1.63E-06 | 8.76179 |
| ZNF704   | -0.7571 | 2.40365 | -15.973 | 1.22E-08 | 6.67E-07 | 9.93094 |
| NFIB     | -0.7568 | 3.3074  | -17.114 | 6.10E-09 | 3.74E-07 | 10.6781 |
| NKX3-1   | -0.7559 | 0.99971 | -6.6319 | 4.90E-05 | 0.0008   | 0.96149 |
| JAM2     | -0.7552 | 1.25486 | -7.2808 | 2.18E-05 | 0.00041  | 1.8332  |
| CMPK2    | -0.7549 | 0.8942  | -7.0886 | 2.75E-05 | 0.00049  | 1.5805  |
| GDPD5    | -0.7546 | 0.99483 | -5.2757 | 0.00032  | 0.00408  | -1.0397 |
| CYP26B1  | -0.7546 | 1.48825 | -6.5022 | 5.80E-05 | 0.00092  | 0.78079 |
| IFNLR1   | -0.7527 | 1.56687 | -6.0524 | 0.00011  | 0.00156  | 0.13688 |
| FDX1P1   | -0.7522 | 1.49889 | -14.255 | 3.78E-08 | 1.70E-06 | 8.70598 |
| TMX4     | -0.7521 | 2.75601 | -20.662 | 9.09E-10 | 7.99E-08 | 12.7276 |
| DENND1   | -0.752  | 1.84495 | -25.008 | 1.30E-10 | 1.79E-08 | 14.8084 |
| SYT12    | -0.7495 | 1.25225 | -5.6071 | 0.0002   | 0.00269  | -0.5277 |
| LURAP1L  | -0.7479 | 0.94085 | -5.48   | 0.00024  | 0.00316  | -0.7222 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| TRNP1    | -0.7478 | 1.59633 | -13.704 | 5.59E-08 | 2.36E-06 | 8.28376 |
| ANTXR1   | -0.7472 | 2.52372 | -10.389 | 8.25E-07 | 2.39E-05 | 5.36954 |
| ULK4P2   | -0.747  | 0.73239 | -9.1033 | 2.87E-06 | 7.00E-05 | 4.0214  |
| AHR      | -0.7462 | 0.42327 | -8.9679 | 3.30E-06 | 7.91E-05 | 3.87072 |
| CTSH     | -0.7457 | 1.88228 | -12.257 | 1.67E-07 | 6.05E-06 | 7.09733 |
| NKX2-3   | -0.7449 | 0.37247 | -6.9867 | 3.13E-05 | 0.00055  | 1.44455 |
| SYTL2    | -0.7444 | 2.06427 | -16.368 | 9.53E-09 | 5.42E-07 | 10.1958 |
| DENND5   | -0.7426 | 1.41726 | -14.083 | 4.27E-08 | 1.88E-06 | 8.57614 |
| WIF1     | -0.7425 | 2.82292 | -11.768 | 2.49E-07 | 8.48E-06 | 6.66815 |
| PRKAG2   | -0.7417 | 0.65108 | -6.2792 | 7.78E-05 | 0.0012   | 0.46485 |
| C1QTNF9  | -0.7402 | 0.58783 | -12.529 | 1.35E-07 | 4.98E-06 | 7.32978 |
| EPHA8    | -0.7394 | 1.68232 | -4.3854 | 0.00125  | 0.01279  | -2.4882 |
| KLF2     | -0.7391 | 1.29676 | -9.2852 | 2.38E-06 | 5.94E-05 | 4.22105 |
| BATF3    | -0.7388 | 1.14549 | -5.4482 | 0.00025  | 0.00329  | -0.7713 |
| TPBGL    | -0.7378 | 0.54878 | -7.8009 | 1.18E-05 | 0.00024  | 2.49486 |
| TMC3     | -0.7352 | 0.894   | -6.7245 | 4.35E-05 | 0.00073  | 1.08911 |
| HTRA4    | -0.7351 | 0.57676 | -6.654  | 4.76E-05 | 0.00078  | 0.99201 |
| ARL4A    | -0.7348 | 1.99766 | -23.41  | 2.55E-10 | 2.98E-08 | 14.089  |
| STAT1    | -0.7324 | 3.66481 | 15.3294 | 1.84E-08 | 9.31E-07 | 9.48733 |
| FXD5     | -0.7321 | 2.32678 | -5.9763 | 0.00012  | 0.00171  | 0.02524 |
| GMPR     | -0.7317 | 0.46621 | -6.7999 | 3.95E-05 | 0.00067  | 1.19229 |
| GNG12-A  | -0.7315 | 0.67532 | -5.7042 | 0.00017  | 0.00238  | -0.3805 |
| CTH      | -0.731  | 2.17655 | -10.41  | 8.09E-07 | 2.35E-05 | 5.39032 |
| PHOSPH   | -0.7301 | 0.91521 | -3.5476 | 0.005    | 0.04023  | -3.9326 |
| SLC16A1  | -0.7298 | 0.86192 | -4.8927 | 0.00057  | 0.00666  | -1.6502 |
| CHRNA7   | -0.7295 | 1.0508  | -9.709  | 1.57E-06 | 4.15E-05 | 4.67433 |
| ADGRG6   | -0.7281 | 2.01745 | -11.636 | 2.77E-07 | 9.35E-06 | 6.54976 |
| TMEM98   | -0.7263 | 1.86358 | -12.869 | 1.04E-07 | 4.01E-06 | 7.61384 |
| GSTM3P   | -0.7245 | 0.91299 | -4.9603 | 0.00051  | 0.00608  | -1.5411 |
| NPAS2    | -0.7244 | 1.93606 | -8.7777 | 4.02E-06 | 9.39E-05 | 3.65607 |
| TAGLN2   | -0.7242 | 2.75605 | -7.7436 | 1.26E-05 | 0.00025  | 2.42354 |
| TMEM30A  | -0.7235 | 1.07096 | -10.252 | 9.36E-07 | 2.67E-05 | 5.23248 |
| FBXL16   | -0.7209 | 1.21947 | -4.2268 | 0.00161  | 0.0158   | -2.7566 |
| GCAWK    | -0.7209 | 0.79555 | -4.3664 | 0.00129  | 0.01313  | -2.5203 |
| FOXA1    | -0.7207 | 1.23211 | -7.1046 | 2.70E-05 | 0.00049  | 1.60161 |
| PLAAT3   | -0.7206 | 2.06987 | -7.5537 | 1.57E-05 | 0.00031  | 2.18434 |
| ULK4P3   | -0.7189 | 0.60002 | -13.855 | 5.01E-08 | 2.15E-06 | 8.40149 |
| GALNT16  | -0.7185 | 2.11312 | -6.1881 | 8.79E-05 | 0.00133  | 0.33402 |
| GSTM5P   | -0.7183 | 0.35916 | -8.7919 | 3.96E-06 | 9.28E-05 | 3.67222 |
| TMEM51   | -0.7178 | 2.04689 | -8.8013 | 3.92E-06 | 9.20E-05 | 3.68299 |
| ATP8B4   | -0.7169 | 0.91684 | -5.2144 | 0.00035  | 0.00439  | -1.1362 |
| EGR1     | -0.7167 | 2.41806 | -7.1352 | 2.60E-05 | 0.00047  | 1.6421  |
| TNFRSF8  | -0.7162 | 0.52477 | -4.5731 | 0.00093  | 0.01007  | -2.1745 |
| FHIP1A   | -0.7157 | 1.04123 | -6.6116 | 5.03E-05 | 0.00082  | 0.93332 |
| CNIH3-AS | -0.7132 | 0.45692 | -6.3127 | 7.44E-05 | 0.00115  | 0.51274 |
| TUBB2A   | -0.7127 | 2.28479 | -5.5849 | 0.0002   | 0.00277  | -0.5615 |
| CLMN     | -0.7125 | 1.78699 | -7.8771 | 1.08E-05 | 0.00022  | 2.58916 |
| SHISA4   | -0.7123 | 1.79434 | -5.5187 | 0.00022  | 0.00301  | -0.6628 |
| SNORA20  | -0.7117 | 0.80568 | -4.8752 | 0.00058  | 0.0068   | -1.6787 |
| KRT8     | -0.7117 | 1.49273 | -6.0504 | 0.00011  | 0.00156  | 0.13395 |
| COL16A1  | -0.709  | 0.77202 | -3.6827 | 0.00397  | 0.03322  | -3.6959 |
| HYMAI    | -0.708  | 0.6342  | -6.9175 | 3.41E-05 | 0.00059  | 1.35166 |
| TUBBP5   | -0.7069 | 1.84324 | -5.6173 | 0.00019  | 0.00265  | -0.5121 |
| IGSF9B   | -0.7057 | 0.9881  | -4.7037 | 0.00076  | 0.00847  | -1.9587 |
| GJA3     | -0.7053 | 2.05211 | -9.1827 | 2.64E-06 | 6.53E-05 | 4.1089  |
| SNORD9   | -0.7039 | 0.79118 | -5.9942 | 0.00011  | 0.00167  | 0.05148 |
| PRPS2    | -0.7037 | 3.3145  | -15.036 | 2.23E-08 | 1.09E-06 | 9.27881 |
| DUSP9    | -0.7025 | 1.8881  | -5.0973 | 0.00041  | 0.00511  | -1.3216 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| GASK1B   | -0.7019 | 1.86982 | -14.583 | 3.02E-08 | 1.41E-06 | 8.95004 |
| SMCO2    | -0.7001 | 0.50058 | -6.687  | 4.56E-05 | 0.00076  | 1.03753 |
| ZHX2     | -0.6995 | 0.34977 | -14.08  | 4.28E-08 | 1.88E-06 | 8.57335 |
| DCLK2    | -0.699  | 1.60447 | -8.0252 | 9.13E-06 | 0.00019  | 2.77068 |
| BHLHA15  | -0.6974 | 0.77475 | -3.9104 | 0.00271  | 0.02416  | -3.2998 |
| DTX4     | -0.6972 | 2.74849 | -11.524 | 3.04E-07 | 1.01E-05 | 6.44861 |
| SLC30A3  | -0.6969 | 0.94939 | -5.148  | 0.00038  | 0.00479  | -1.2412 |
| LINC0061 | -0.6966 | 0.3483  | -12.781 | 1.11E-07 | 4.22E-06 | 7.54075 |
| RAPGEF3  | -0.6952 | 1.42815 | -5.4623 | 0.00024  | 0.00323  | -0.7496 |
| TMEM86A  | -0.695  | 0.67786 | -11.623 | 2.80E-07 | 9.43E-06 | 6.53786 |
| TMSB4X1  | -0.6947 | 1.10947 | -8.5532 | 5.10E-06 | 0.00012  | 3.39815 |
| TP73     | -0.6929 | 1.85418 | -5.3681 | 0.00028  | 0.00361  | -0.8954 |
| LINC0264 | -0.6919 | 0.34596 | -8.9836 | 3.24E-06 | 7.79E-05 | 3.88831 |
| UNC93B1  | -0.6918 | 1.72358 | -3.7903 | 0.00332  | 0.02854  | -3.5081 |
| C1R      | -0.6911 | 1.61595 | -7.6026 | 1.48E-05 | 0.00029  | 2.24626 |
| IL6R     | -0.6907 | 1.72245 | -11.457 | 3.22E-07 | 1.06E-05 | 6.3877  |
| SPATA3-1 | -0.6904 | 1.20571 | -7.6914 | 1.34E-05 | 0.00027  | 2.35819 |
| ANKRD13  | -0.6899 | 2.70827 | -4.7117 | 0.00075  | 0.00839  | -1.9455 |
| PMAIP1   | -0.6896 | 1.7456  | -12.27  | 1.65E-07 | 6.00E-06 | 7.10915 |
| DNAAF11  | -0.6894 | 0.7414  | -9.5686 | 1.80E-06 | 4.66E-05 | 4.52603 |
| HERC5    | -0.6894 | 1.87833 | -8.8714 | 3.64E-06 | 8.64E-05 | 3.76231 |
| TMEM38A  | -0.6893 | 2.1632  | -9.7997 | 1.44E-06 | 3.87E-05 | 4.76935 |
| POU6F1   | -0.689  | 1.89753 | -7.2861 | 2.16E-05 | 0.0004   | 1.84012 |
| CSPG5    | -0.6887 | 2.04535 | -6.7912 | 4.00E-05 | 0.00068  | 1.18035 |
| LINC0099 | -0.6881 | 0.34403 | -7.0719 | 2.81E-05 | 0.0005   | 1.55834 |
| HIPK2    | -0.6865 | 1.97637 | -8.8204 | 3.84E-06 | 9.04E-05 | 3.70459 |
| CARMIL1  | -0.6864 | 2.2061  | -10.302 | 8.93E-07 | 2.56E-05 | 5.28291 |
| SIRT1    | -0.686  | 3.30713 | -14.832 | 2.55E-08 | 1.22E-06 | 9.13187 |
| BMP7     | -0.6856 | 2.38579 | -6.6191 | 4.98E-05 | 0.00081  | 0.94374 |
| BMP2     | -0.6854 | 0.44306 | -6.1584 | 9.15E-05 | 0.00138  | 0.29101 |
| EGR3     | -0.6848 | 1.43499 | -6.9129 | 3.43E-05 | 0.00059  | 1.34544 |
| NPFFR2   | -0.6839 | 0.85979 | -4.4061 | 0.00121  | 0.01244  | -2.4535 |
| CHST6    | -0.6832 | 2.32989 | -9.61   | 1.73E-06 | 4.51E-05 | 4.56991 |
| SLC35D3  | -0.6804 | 0.39039 | -10.592 | 6.86E-07 | 2.03E-05 | 5.56956 |
| TIMP1    | -0.6795 | 3.41015 | -7.7147 | 1.30E-05 | 0.00026  | 2.38738 |
| MRAP2    | -0.6787 | 1.91403 | -8.9235 | 3.45E-06 | 8.22E-05 | 3.821   |
| ABHD15   | -0.6786 | 2.79187 | -8.5128 | 5.33E-06 | 0.00012  | 3.3511  |
| C1QTNF9  | -0.6782 | 1.53038 | -11.25  | 3.84E-07 | 1.22E-05 | 6.19672 |
| MBOAT1   | -0.6776 | 1.44647 | -7.6431 | 1.42E-05 | 0.00028  | 2.29742 |
| TXNIP    | -0.6771 | 1.99456 | -12.193 | 1.76E-07 | 6.33E-06 | 7.04266 |
| AHCY     | -0.676  | 3.88202 | -6.8625 | 3.65E-05 | 0.00063  | 1.2773  |
| CHRD     | -0.6758 | 0.56792 | -4.2079 | 0.00167  | 0.01619  | -2.7888 |
| FABP5P9  | -0.6749 | 0.76935 | -11.999 | 2.06E-07 | 7.23E-06 | 6.87346 |
| SRRM3    | -0.6743 | 1.37995 | -6.1716 | 8.99E-05 | 0.00136  | 0.31014 |
| FOXD2    | -0.6705 | 0.8455  | -4.4375 | 0.00115  | 0.01197  | -2.4008 |
| KIF7     | -0.6699 | 2.53046 | -4.8214 | 0.00063  | 0.00727  | -1.766  |
| RIPK2    | -0.6697 | 3.14626 | -16.193 | 1.06E-08 | 5.92E-07 | 10.0789 |
| PCDHB10  | -0.6678 | 0.69853 | -5.1599 | 0.00038  | 0.00471  | -1.2223 |
| MAMSTR   | -0.6678 | 1.64933 | -5.7359 | 0.00016  | 0.00229  | -0.3326 |
| ANO1     | -0.6672 | 0.33362 | -12.438 | 1.45E-07 | 5.32E-06 | 7.25236 |
| MIR124-1 | -0.6672 | 0.33362 | -12.438 | 1.45E-07 | 5.32E-06 | 7.25236 |
| MIR6826  | -0.6672 | 0.50029 | -7.7649 | 1.23E-05 | 0.00025  | 2.45005 |
| ABLIM1   | -0.665  | 2.76954 | -9.6498 | 1.66E-06 | 4.36E-05 | 4.61197 |
| ARHGAP   | -0.6649 | 1.3263  | -6.6525 | 4.77E-05 | 0.00078  | 0.98996 |
| ESAM     | -0.6645 | 1.14033 | -5.8884 | 0.00013  | 0.0019   | -0.1047 |
| UBE2Q2F  | -0.6632 | 0.48497 | -8.3908 | 6.08E-06 | 0.00013  | 3.20829 |
| A4GALT   | -0.6631 | 1.04543 | -3.685  | 0.00396  | 0.03312  | -3.6919 |
| PPP1R16  | -0.6627 | 0.79438 | -5.6678 | 0.00018  | 0.00249  | -0.4354 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| NFATC2   | -0.6621 | 1.81532 | -6.946  | 3.29E-05 | 0.00057  | 1.39002 |
| BMAL2-A  | -0.6619 | 0.87349 | -9.8314 | 1.39E-06 | 3.77E-05 | 4.80236 |
| PCOTH    | -0.6618 | 1.63465 | -10.285 | 9.08E-07 | 2.60E-05 | 5.26536 |
| STEAP3-  | -0.6609 | 1.75611 | -4.4787 | 0.00108  | 0.01136  | -2.3318 |
| AKR1B10  | -0.6608 | 0.33038 | -5.4013 | 0.00026  | 0.00347  | -0.8438 |
| GABBR2   | -0.6601 | 1.10115 | -7.8425 | 1.12E-05 | 0.00023  | 2.54643 |
| PLIN5    | -0.6599 | 1.45098 | -5.1589 | 0.00038  | 0.00472  | -1.2238 |
| TMEM163  | -0.6596 | 0.48032 | -7.9947 | 9.45E-06 | 0.0002   | 2.73341 |
| FRMD8    | -0.6569 | 2.53346 | -5.5039 | 0.00023  | 0.00307  | -0.6855 |
| MIR1291  | -0.6566 | 0.6795  | -4.797  | 0.00066  | 0.0075   | -1.8059 |
| RHOV     | -0.6565 | 1.59499 | -5.7716 | 0.00016  | 0.00219  | -0.279  |
| NIPAL2   | -0.6547 | 1.598   | -12.146 | 1.83E-07 | 6.53E-06 | 7.00178 |
| LINC0035 | -0.654  | 0.60719 | -5.5837 | 0.0002   | 0.00277  | -0.5633 |
| ITPR1    | -0.6536 | 2.51589 | -8.7748 | 4.03E-06 | 9.41E-05 | 3.65278 |
| NR2F2    | -0.6536 | 1.94259 | -6.4529 | 6.18E-05 | 0.00098  | 0.71144 |
| STEAP3   | -0.6534 | 2.66842 | -6.2322 | 8.29E-05 | 0.00126  | 0.39744 |
| KAT2B    | -0.653  | 2.05411 | -13.907 | 4.83E-08 | 2.08E-06 | 8.44085 |
| FABP5P1  | -0.6527 | 0.82974 | -9.3579 | 2.22E-06 | 5.58E-05 | 4.29997 |
| OR7E14F  | -0.6518 | 0.50931 | -4.5911 | 0.0009   | 0.00983  | -2.1446 |
| KRT18P4  | -0.6511 | 0.32555 | -8.1785 | 7.69E-06 | 0.00016  | 2.95594 |
| ADAMTS   | -0.651  | 1.11687 | -5.2169 | 0.00035  | 0.00438  | -1.1321 |
| PCDH10   | -0.6501 | 3.35569 | -12.016 | 2.03E-07 | 7.14E-06 | 6.88843 |
| LRAT     | -0.6498 | 0.37507 | -5.9356 | 0.00012  | 0.00179  | -0.0348 |
| MMP13    | -0.6493 | 0.92296 | -4.6591 | 0.00081  | 0.00899  | -2.0322 |
| IGFBP6   | -0.6493 | 1.8219  | -4.7399 | 0.00072  | 0.0081   | -1.8993 |
| ERFL     | -0.6492 | 0.79046 | -3.9359 | 0.0026   | 0.02333  | -3.2555 |
| CFHR1    | -0.6489 | 2.79221 | -14.382 | 3.46E-08 | 1.58E-06 | 8.80101 |
| NOS2     | -0.6484 | 1.52283 | -4.282  | 0.00148  | 0.0147   | -2.6629 |
| MOCS1    | -0.6482 | 1.79534 | -7.7921 | 1.19E-05 | 0.00024  | 2.48389 |
| DOP1B    | -0.6474 | 1.81675 | -7.7927 | 1.19E-05 | 0.00024  | 2.48465 |
| LINC0190 | -0.6448 | 0.86847 | -6.2747 | 7.83E-05 | 0.0012   | 0.45842 |
| SMKR1    | -0.6445 | 1.68393 | -10.252 | 9.36E-07 | 2.67E-05 | 5.23248 |
| TANK     | -0.6437 | 2.94117 | -16.844 | 7.15E-09 | 4.30E-07 | 10.5061 |
| TYRP1    | -0.6431 | 3.30166 | -19.055 | 2.06E-09 | 1.56E-07 | 11.8456 |
| CYBRD1   | -0.6426 | 2.96513 | -13.984 | 4.58E-08 | 1.99E-06 | 8.50014 |
| CNRIP1   | -0.6423 | 1.58985 | -11.157 | 4.16E-07 | 1.31E-05 | 6.10966 |
| ASIC5    | -0.6414 | 0.32071 | -6.3135 | 7.43E-05 | 0.00115  | 0.51391 |
| ITPKB    | -0.6393 | 2.33303 | -4.7142 | 0.00074  | 0.00836  | -1.9415 |
| GAB3     | -0.6383 | 0.92971 | -5.512  | 0.00023  | 0.00304  | -0.673  |
| SH3RF3-  | -0.6379 | 0.36912 | -3.8862 | 0.00283  | 0.02496  | -3.3416 |
| KIFC2    | -0.6379 | 2.35791 | -3.6614 | 0.00412  | 0.03419  | -3.7333 |
| SPINT2   | -0.6374 | 1.05226 | -3.5433 | 0.00503  | 0.04046  | -3.9401 |
| SRGAP1   | -0.6373 | 2.1008  | -9.1371 | 2.77E-06 | 6.79E-05 | 4.05872 |
| MAN1C1   | -0.637  | 1.33729 | -6.2429 | 8.17E-05 | 0.00125  | 0.41278 |
| CHST11   | -0.6357 | 2.08915 | -8.9836 | 3.24E-06 | 7.79E-05 | 3.88829 |
| VIP      | -0.6353 | 0.31763 | -6.8974 | 3.49E-05 | 0.0006   | 1.32456 |
| TRIM46   | -0.6352 | 1.38306 | -3.5608 | 0.00489  | 0.03955  | -3.9095 |
| LRRC73   | -0.6328 | 1.42739 | -4.7407 | 0.00071  | 0.00809  | -1.898  |
| SOWAHA   | -0.6321 | 1.19042 | -6.842  | 3.75E-05 | 0.00064  | 1.24946 |
| SMYD3    | -0.6315 | 2.68728 | -11.911 | 2.21E-07 | 7.67E-06 | 6.79525 |
| DAAM2    | -0.6311 | 0.66137 | -4.1175 | 0.00193  | 0.01825  | -2.943  |
| CABYR    | -0.6303 | 1.96991 | -8.0925 | 8.46E-06 | 0.00018  | 2.85224 |
| COL23A1  | -0.6288 | 1.89861 | -3.7106 | 0.00379  | 0.03193  | -3.6471 |
| CCDC69   | -0.6274 | 1.52048 | -6.787  | 4.02E-05 | 0.00068  | 1.1746  |
| NMRK1    | -0.627  | 1.48116 | -11.2   | 4.01E-07 | 1.26E-05 | 6.14988 |
| LMX1B-D  | -0.6267 | 0.36354 | -10.388 | 8.26E-07 | 2.39E-05 | 5.36798 |
| SEMA7A   | -0.6249 | 1.52675 | -4.3054 | 0.00142  | 0.01426  | -2.6233 |
| GPR137B  | -0.6224 | 2.26308 | -10.417 | 8.04E-07 | 2.34E-05 | 5.39723 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| ARRDC2   | -0.6224 | 2.16789 | -5.6756 | 0.00018  | 0.00246  | -0.4236 |
| MYO5A    | -0.6221 | 2.65552 | -13.461 | 6.67E-08 | 2.77E-06 | 8.09304 |
| RHAG     | -0.6221 | 0.31103 | -8.0772 | 8.61E-06 | 0.00018  | 2.83377 |
| ATOH8    | -0.6217 | 0.31087 | -6.8884 | 3.53E-05 | 0.00061  | 1.31236 |
| DBNDD2   | -0.6212 | 2.59728 | -7.7861 | 1.20E-05 | 0.00024  | 2.47652 |
| CELSR1F  | -0.6209 | 1.21854 | -5.7054 | 0.00017  | 0.00238  | -0.3786 |
| SLC41A2  | -0.6204 | 1.88191 | -10.993 | 4.80E-07 | 1.48E-05 | 5.95495 |
| LIPA     | -0.6187 | 4.03847 | -16.654 | 8.02E-09 | 4.71E-07 | 10.383  |
| C2orf88  | -0.6186 | 1.88278 | -10.228 | 9.57E-07 | 2.72E-05 | 5.20861 |
| AKR1C3   | -0.6176 | 1.73432 | -10.886 | 5.27E-07 | 1.61E-05 | 5.8537  |
| DLGAP2   | -0.6171 | 0.40888 | -6.9317 | 3.35E-05 | 0.00058  | 1.37082 |
| BARX2    | -0.6163 | 0.40665 | -6.1048 | 9.84E-05 | 0.00146  | 0.21326 |
| DCAF4    | -0.6154 | 2.11735 | -8.2359 | 7.21E-06 | 0.00016  | 3.0246  |
| HS6ST2   | -0.6153 | 2.5298  | -9.8373 | 1.38E-06 | 3.75E-05 | 4.80849 |
| KCTD12   | -0.6143 | 0.50784 | -6.4317 | 6.36E-05 | 0.001    | 0.68159 |
| MEGF11   | -0.6143 | 1.66363 | -6.6762 | 4.63E-05 | 0.00076  | 1.02268 |
| CASP10   | -0.614  | 1.74771 | -6.9481 | 3.28E-05 | 0.00057  | 1.39279 |
| LINC0131 | -0.6137 | 0.79627 | -5.9672 | 0.00012  | 0.00172  | 0.01187 |
| PRKG1-A  | -0.6137 | 1.83491 | -15.355 | 1.81E-08 | 9.19E-07 | 9.505   |
| LINGO1   | -0.6132 | 1.63338 | -4.4417 | 0.00114  | 0.01191  | -2.3937 |
| MATK     | -0.6131 | 2.26774 | -3.558  | 0.00491  | 0.0397   | -3.9144 |
| ADAMTS   | -0.6126 | 2.04062 | -3.8238 | 0.00314  | 0.02727  | -3.4499 |
| DENND2C  | -0.6088 | 1.40854 | -8.9012 | 3.53E-06 | 8.38E-05 | 3.79586 |
| SEMA3G   | -0.6079 | 1.5763  | -3.507  | 0.00535  | 0.04251  | -4.0041 |
| PSLNR    | -0.607  | 0.55526 | -5.3898 | 0.00027  | 0.00352  | -0.8617 |
| SPINK1   | -0.6059 | 0.30296 | -12.64  | 1.24E-07 | 4.61E-06 | 7.42297 |
| DUBR     | -0.6058 | 2.23164 | -11.726 | 2.57E-07 | 8.74E-06 | 6.63072 |
| GASK1B   | -0.6055 | 1.23203 | -6.1148 | 9.71E-05 | 0.00145  | 0.22778 |
| SUGCT    | -0.6053 | 2.00727 | -9.3429 | 2.25E-06 | 5.66E-05 | 4.28369 |
| FAM110A  | -0.6033 | 1.45473 | -4.6959 | 0.00077  | 0.00856  | -1.9715 |
| PLEKHA7  | -0.6033 | 1.45519 | -3.9902 | 0.00238  | 0.02174  | -3.1619 |
| GPRC5B   | -0.6028 | 2.33182 | -8.5687 | 5.02E-06 | 0.00011  | 3.41606 |
| SH3BP5   | -0.6027 | 2.33213 | -12.411 | 1.48E-07 | 5.43E-06 | 7.22937 |
| RAB27A   | -0.6024 | 2.65309 | -11.55  | 2.98E-07 | 9.93E-06 | 6.47249 |
| DMKN     | -0.602  | 2.57447 | -6.9147 | 3.42E-05 | 0.00059  | 1.3478  |
| STXBP2   | -0.6003 | 2.09584 | -4.0065 | 0.00232  | 0.02128  | -3.1338 |
| HTR7     | -0.5985 | 0.5906  | -5.4586 | 0.00024  | 0.00325  | -0.7552 |
| SYS1-DB  | -0.5984 | 2.59801 | -7.046  | 2.90E-05 | 0.00052  | 1.52382 |
| ALDH1A1  | -0.598  | 1.92715 | -11.24  | 3.87E-07 | 1.23E-05 | 6.18761 |
| MCIDAS   | -0.5974 | 0.29869 | -7.3415 | 2.02E-05 | 0.00038  | 1.91199 |
| ADAMTS   | -0.5971 | 0.96581 | -3.7101 | 0.0038   | 0.03195  | -3.6481 |
| PRNP     | -0.5971 | 3.01283 | -14.795 | 2.62E-08 | 1.25E-06 | 9.10511 |
| SPATS2L  | -0.597  | 1.35055 | -8.7476 | 4.15E-06 | 9.65E-05 | 3.62186 |
| VILL     | -0.5969 | 0.78786 | -3.4249 | 0.00616  | 0.04763  | -4.1485 |
| MCUB     | -0.5961 | 2.51701 | -11.817 | 2.39E-07 | 8.20E-06 | 6.71208 |
| MAP3K7C  | -0.5954 | 0.67823 | -4.6937 | 0.00077  | 0.00857  | -1.9752 |
| MMP10    | -0.5944 | 4.04201 | -16     | 1.20E-08 | 6.57E-07 | 9.94943 |
| SUGT1P1  | -0.594  | 1.06536 | -6.3089 | 7.48E-05 | 0.00116  | 0.50739 |
| CTNNA3   | -0.5938 | 1.51204 | -13.711 | 5.56E-08 | 2.36E-06 | 8.28967 |
| TMSB4XF  | -0.5936 | 1.9148  | -11.812 | 2.40E-07 | 8.22E-06 | 6.7077  |
| TMSB4X   | -0.593  | 4.3583  | -12.912 | 1.00E-07 | 3.90E-06 | 7.6492  |
| FAM111A  | -0.5926 | 3.37713 | -13.277 | 7.64E-08 | 3.09E-06 | 7.94594 |
| CDC42EP  | -0.5921 | 2.09913 | -12.562 | 1.31E-07 | 4.86E-06 | 7.35764 |
| YPEL2    | -0.5906 | 1.54607 | -6.6178 | 4.99E-05 | 0.00081  | 0.94192 |
| PNPLA5   | -0.5886 | 0.39465 | -5.2184 | 0.00035  | 0.00437  | -1.1299 |
| METRNL   | -0.588  | 1.42174 | -3.8082 | 0.00322  | 0.02784  | -3.4771 |
| MIR27B   | -0.5877 | 0.64392 | -4.1937 | 0.0017   | 0.01648  | -2.8129 |
| ZCCHC12  | -0.5877 | 0.42355 | -4.6026 | 0.00089  | 0.00968  | -2.1256 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| MYO7A    | -0.5871 | 1.55145 | -3.5994 | 0.00458  | 0.03739  | -3.8418 |
| C1D      | -0.5859 | 2.83069 | -11.69  | 2.65E-07 | 8.98E-06 | 6.59835 |
| TPPA     | -0.5857 | 1.51488 | -9.0083 | 3.16E-06 | 7.62E-05 | 3.9159  |
| ADAMTS   | -0.5853 | 1.56212 | -7.0604 | 2.85E-05 | 0.00051  | 1.54295 |
| EDA      | -0.5845 | 1.94709 | -7.2344 | 2.30E-05 | 0.00043  | 1.77261 |
| FUT4     | -0.5843 | 1.39733 | -6.7417 | 4.26E-05 | 0.00071  | 1.11262 |
| NEURL1   | -0.5834 | 0.72241 | -4.6664 | 0.0008   | 0.0089   | -2.0201 |
| MAP9     | -0.5828 | 3.29538 | -13.854 | 5.02E-08 | 2.15E-06 | 8.40011 |
| TLE1     | -0.5817 | 2.03796 | -5.2187 | 0.00035  | 0.00437  | -1.1293 |
| ELL2     | -0.5816 | 1.37408 | -10.656 | 6.47E-07 | 1.94E-05 | 5.63181 |
| SERINC5  | -0.5807 | 2.49826 | -11.513 | 3.07E-07 | 1.02E-05 | 6.43847 |
| TP53INP2 | -0.5802 | 2.3566  | -7.2969 | 2.14E-05 | 0.0004   | 1.85412 |
| EEPD1    | -0.58   | 1.94062 | -5.1717 | 0.00037  | 0.00465  | -1.2035 |
| SLC35E4  | -0.5799 | 1.90815 | -5.5029 | 0.00023  | 0.00307  | -0.687  |
| UBASH3B  | -0.5788 | 2.21605 | -9.6494 | 1.66E-06 | 4.36E-05 | 4.61158 |
| PLXND1   | -0.5777 | 2.39886 | -4.2773 | 0.00149  | 0.01478  | -2.6709 |
| SEPTIN3  | -0.5775 | 2.50252 | -7.2062 | 2.38E-05 | 0.00044  | 1.73565 |
| FAM222A  | -0.5774 | 1.56391 | -4.4183 | 0.00119  | 0.01223  | -2.4331 |
| FXVD6-A  | -0.5772 | 0.3681  | -4.6085 | 0.00088  | 0.0096   | -2.1157 |
| MEOX2    | -0.5753 | 3.4465  | -9.7538 | 1.50E-06 | 4.00E-05 | 4.72136 |
| CNNM2    | -0.5743 | 3.47255 | -12.951 | 9.75E-08 | 3.81E-06 | 7.68108 |
| C10orf10 | -0.5734 | 0.38704 | -5.069  | 0.00043  | 0.0053   | -1.3668 |
| ATP10A   | -0.5732 | 1.86704 | -7.2075 | 2.38E-05 | 0.00044  | 1.73726 |
| LINC0135 | -0.5731 | 0.33672 | -8.0847 | 8.54E-06 | 0.00018  | 2.84283 |
| CYP2U1   | -0.5728 | 0.95866 | -4.7852 | 0.00067  | 0.00763  | -1.8252 |
| SPATA20  | -0.5728 | 2.28982 | -4.1551 | 0.00181  | 0.01738  | -2.8788 |
| MAP9-AS  | -0.5724 | 2.43735 | -12.673 | 1.21E-07 | 4.51E-06 | 7.45137 |
| TUBB2BF  | -0.5718 | 0.95629 | -5.4392 | 0.00025  | 0.00332  | -0.7852 |
| IL27RA   | -0.5708 | 2.57761 | -6.2895 | 7.68E-05 | 0.00118  | 0.47964 |
| TUBB8B   | -0.5706 | 1.45224 | -4.8999 | 0.00056  | 0.0066   | -1.6386 |
| ZFP91-C1 | -0.5706 | 3.23379 | -11.375 | 3.45E-07 | 1.12E-05 | 6.31227 |
| HNRNPA   | -0.5704 | 1.10478 | -7.2959 | 2.14E-05 | 0.0004   | 1.85282 |
| ZBTB41   | -0.5691 | 2.91405 | -13.413 | 6.91E-08 | 2.85E-06 | 8.05443 |
| PROC     | -0.5689 | 0.41416 | -4.3026 | 0.00143  | 0.0143   | -2.628  |
| PUS7L    | -0.5677 | 2.15221 | -8.337  | 6.45E-06 | 0.00014  | 3.14474 |
| ANKH     | -0.5676 | 2.21419 | -7.513  | 1.65E-05 | 0.00032  | 2.13248 |
| ZFP91    | -0.5675 | 3.75954 | -12.833 | 1.07E-07 | 4.10E-06 | 7.58443 |
| SLC22A1  | -0.5669 | 0.52964 | -4.2348 | 0.00159  | 0.01564  | -2.7431 |
| TNNC2    | -0.5667 | 0.60054 | -3.5299 | 0.00515  | 0.04124  | -3.9638 |
| PCDHB7   | -0.5661 | 0.46774 | -4.4551 | 0.00112  | 0.01172  | -2.3713 |
| PDK1-AS  | -0.5657 | 1.29593 | -9.6521 | 1.66E-06 | 4.36E-05 | 4.61447 |
| PSD4     | -0.5648 | 0.85398 | -4.2528 | 0.00155  | 0.01528  | -2.7125 |
| CCDC113  | -0.5643 | 2.33459 | -7.9899 | 9.50E-06 | 0.0002   | 2.7276  |
| PATE2    | -0.5643 | 0.33231 | -6.2362 | 8.24E-05 | 0.00126  | 0.40318 |
| PXDC1    | -0.564  | 1.55655 | -7.3249 | 2.06E-05 | 0.00039  | 1.8905  |
| LINC0219 | -0.5638 | 0.83306 | -7.627  | 1.44E-05 | 0.00028  | 2.27711 |
| PRKCA    | -0.5633 | 2.08607 | -7.6345 | 1.43E-05 | 0.00028  | 2.28664 |
| FAM78B   | -0.5626 | 0.58235 | -4.8489 | 0.0006   | 0.00704  | -1.7213 |
| ZNF654   | -0.5615 | 2.8421  | -18.651 | 2.56E-09 | 1.87E-07 | 11.6122 |
| SH3RF1   | -0.5608 | 1.88998 | -7.1689 | 2.50E-05 | 0.00045  | 1.68658 |
| KCNC4    | -0.5607 | 1.82618 | -7.8504 | 1.11E-05 | 0.00023  | 2.55623 |
| DECR1    | -0.5597 | 2.83732 | -12.589 | 1.29E-07 | 4.77E-06 | 7.3805  |
| CCDC148  | -0.5596 | 1.3274  | -8.9556 | 3.34E-06 | 7.99E-05 | 3.85696 |
| SCN5A    | -0.5595 | 1.30094 | -4.4815 | 0.00107  | 0.01133  | -2.3272 |
| RPL23AP  | -0.5594 | 0.85514 | -6.7154 | 4.40E-05 | 0.00073  | 1.07663 |
| FSTL3    | -0.5592 | 2.2458  | -4.4021 | 0.00122  | 0.01251  | -2.4602 |
| HSF2     | -0.5589 | 3.03349 | -12.649 | 1.23E-07 | 4.59E-06 | 7.43064 |
| NT5C2    | -0.5577 | 3.7124  | -14.339 | 3.57E-08 | 1.62E-06 | 8.76883 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| ABCG4    | -0.5568 | 1.30935 | -4.5622 | 0.00094  | 0.01021  | -2.1926 |
| NIBAN1   | -0.5564 | 2.32705 | -9.4574 | 2.01E-06 | 5.13E-05 | 4.40717 |
| UBE2Q2   | -0.5563 | 2.64712 | -9.2602 | 2.44E-06 | 6.07E-05 | 4.19382 |
| ENPP7P1  | -0.5561 | 0.42858 | -4.7291 | 0.00073  | 0.00821  | -1.917  |
| B3GNT7   | -0.5561 | 0.69648 | -4.7742 | 0.00068  | 0.00773  | -1.8432 |
| IGSF11   | -0.5557 | 0.32804 | -9.6589 | 1.65E-06 | 4.33E-05 | 4.62165 |
| RN7SL68  | -0.5557 | 0.27787 | -8.0227 | 9.15E-06 | 0.00019  | 2.76754 |
| CLDN23   | -0.5531 | 0.8455  | -6.3099 | 7.47E-05 | 0.00116  | 0.50879 |
| TMEM144  | -0.5494 | 1.76331 | -6.5269 | 5.61E-05 | 0.0009   | 0.81531 |
| CADM2    | -0.5489 | 2.08015 | -8.5415 | 5.17E-06 | 0.00012  | 3.38448 |
| DYNLT3   | -0.5473 | 1.90555 | -10.25  | 9.38E-07 | 2.68E-05 | 5.2302  |
| PDE6A    | -0.5471 | 0.56388 | -5.1848 | 0.00036  | 0.00457  | -1.1829 |
| DUSP2    | -0.5462 | 2.20755 | -5.247  | 0.00033  | 0.00422  | -1.0849 |
| AOPEP    | -0.5455 | 3.16621 | -10.224 | 9.61E-07 | 2.73E-05 | 5.20383 |
| PAQR5    | -0.5452 | 1.75177 | -5.4196 | 0.00026  | 0.0034   | -0.8155 |
| OSGIN2   | -0.5451 | 3.31082 | -12.675 | 1.20E-07 | 4.51E-06 | 7.45252 |
| TMEM117  | -0.5451 | 2.17384 | -10.529 | 7.26E-07 | 2.14E-05 | 5.508   |
| ENPP7P4  | -0.5448 | 0.60277 | -4.2742 | 0.0015   | 0.01484  | -2.6761 |
| TMSB4XP  | -0.5444 | 2.98817 | -13.185 | 8.17E-08 | 3.27E-06 | 7.87228 |
| LPAL2    | -0.5425 | 0.32144 | -6.2979 | 7.59E-05 | 0.00117  | 0.49157 |
| ADGRF2   | -0.542  | 0.50103 | -6.5363 | 5.54E-05 | 0.00089  | 0.82841 |
| MTMR11   | -0.5419 | 2.60127 | -7.0422 | 2.92E-05 | 0.00052  | 1.51873 |
| ANGPT1   | -0.5419 | 2.24573 | -9.7663 | 1.48E-06 | 3.96E-05 | 4.73449 |
| TMEM30A  | -0.5403 | 3.45276 | -12.324 | 1.59E-07 | 5.79E-06 | 7.15516 |
| SLC19A3  | -0.5396 | 0.2698  | -8.3678 | 6.24E-06 | 0.00014  | 3.18121 |
| TENM2-A  | -0.5396 | 0.31997 | -4.6229 | 0.00086  | 0.00944  | -2.092  |
| ALCAM    | -0.5394 | 3.33319 | -12.968 | 9.62E-08 | 3.77E-06 | 7.69568 |
| IL17RD   | -0.5392 | 2.11422 | -7.8894 | 1.06E-05 | 0.00022  | 2.6044  |
| RIPPLY3  | -0.538  | 1.50422 | -5.7166 | 0.00017  | 0.00234  | -0.3616 |
| DLK2     | -0.538  | 1.81564 | -3.6082 | 0.00451  | 0.03695  | -3.8264 |
| EPHX2    | -0.5376 | 1.38901 | -5.2327 | 0.00034  | 0.0043   | -1.1073 |
| SERPINE1 | -0.5376 | 0.31895 | -4.0956 | 0.002    | 0.01879  | -2.9805 |
| RELL1    | -0.5368 | 1.56919 | -5.476  | 0.00024  | 0.00318  | -0.7285 |
| ZMYND10  | -0.5365 | 1.10363 | -3.8261 | 0.00312  | 0.02717  | -3.4459 |
| LYSMD2   | -0.5362 | 2.13344 | -13.453 | 6.70E-08 | 2.79E-06 | 8.08686 |
| SLC66A3  | -0.536  | 2.34019 | -11.979 | 2.09E-07 | 7.32E-06 | 6.85544 |
| RGS20    | -0.5359 | 1.88639 | -12.614 | 1.26E-07 | 4.69E-06 | 7.40116 |
| CREG2    | -0.5349 | 0.31763 | -5.2027 | 0.00035  | 0.00446  | -1.1545 |
| PAX1     | -0.5349 | 0.3678  | -5.2524 | 0.00033  | 0.0042   | -1.0763 |
| SLITRK5  | -0.5349 | 0.51832 | -7.483  | 1.71E-05 | 0.00033  | 2.09421 |
| MB21D2   | -0.534  | 0.3967  | -4.5672 | 0.00094  | 0.01015  | -2.1843 |
| LEMD3    | -0.5337 | 3.18165 | -13.855 | 5.01E-08 | 2.15E-06 | 8.40149 |
| FOXH1    | -0.5334 | 2.06459 | -3.7846 | 0.00335  | 0.02873  | -3.5182 |
| TLE2     | -0.5328 | 2.18632 | -3.4579 | 0.00582  | 0.04545  | -4.0903 |
| HSPA4L   | -0.5326 | 3.18683 | -10.374 | 8.37E-07 | 2.42E-05 | 5.35392 |
| FAS      | -0.5325 | 2.51493 | -14.905 | 2.43E-08 | 1.17E-06 | 9.18531 |
| CDO1     | -0.5322 | 1.95558 | -7.9611 | 9.81E-06 | 0.0002   | 2.69238 |
| MTND5P   | -0.5311 | 0.26553 | -10.748 | 5.96E-07 | 1.80E-05 | 5.72132 |
| MTSS1    | -0.531  | 1.84872 | -7.9451 | 9.99E-06 | 0.00021  | 2.67281 |
| MORC4    | -0.5305 | 2.51454 | -7.9034 | 1.05E-05 | 0.00022  | 2.62156 |
| FAT4     | -0.5299 | 1.61955 | -8.5852 | 4.93E-06 | 0.00011  | 3.43523 |
| NPVF     | -0.5299 | 0.26496 | -7.272  | 2.20E-05 | 0.00041  | 1.82176 |
| RHBDL3   | -0.5298 | 1.44345 | -11.831 | 2.36E-07 | 8.12E-06 | 6.72482 |
| PIWIL4-A | -0.5297 | 0.76192 | -5.448  | 0.00025  | 0.00329  | -0.7716 |
| CDC25B   | -0.5293 | 2.87533 | -4.2238 | 0.00162  | 0.01586  | -2.7616 |
| FAM20C   | -0.5287 | 2.07671 | -4.2222 | 0.00163  | 0.0159   | -2.7645 |
| ABTB2    | -0.5282 | 1.91802 | -5.8552 | 0.00014  | 0.00198  | -0.154  |
| IGDCC4   | -0.5277 | 2.15773 | -6.3039 | 7.53E-05 | 0.00116  | 0.50018 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| KLF4     | -0.5264 | 0.2632  | -6.52   | 5.66E-05 | 0.00091  | 0.80567 |
| RPRML    | -0.5264 | 0.41371 | -4.0107 | 0.0023   | 0.02115  | -3.1264 |
| OCA2     | -0.5259 | 1.79856 | -5.9973 | 0.00011  | 0.00167  | 0.05617 |
| NDRG2    | -0.5254 | 2.03104 | -6.6518 | 4.77E-05 | 0.00078  | 0.98902 |
| FBXO32   | -0.5253 | 0.41314 | -3.8931 | 0.00279  | 0.02472  | -3.3296 |
| TRAPPC6  | -0.5235 | 2.89442 | -10.69  | 6.28E-07 | 1.88E-05 | 5.66515 |
| LINC0261 | -0.5232 | 1.17497 | -6.3622 | 6.97E-05 | 0.00109  | 0.58317 |
| FXVD6    | -0.5223 | 0.65783 | -4.3911 | 0.00124  | 0.0127   | -2.4788 |
| MYLK2    | -0.5222 | 0.74848 | -3.9067 | 0.00273  | 0.02428  | -3.3061 |
| GLYATL1  | -0.5213 | 1.62624 | -5.6871 | 0.00018  | 0.00243  | -0.4062 |
| PCDHGB3  | -0.5201 | 0.5696  | -4.6141 | 0.00087  | 0.00954  | -2.1065 |
| TMEM225  | -0.5199 | 0.79398 | -4.9373 | 0.00053  | 0.00627  | -1.5782 |
| SLC39A4  | -0.5199 | 1.91482 | -3.7328 | 0.00365  | 0.03093  | -3.6085 |
| TMSB4X   | -0.5196 | 1.33668 | -8.9111 | 3.50E-06 | 8.31E-05 | 3.80702 |
| CBFA2T3  | -0.5188 | 1.22655 | -4.0816 | 0.00205  | 0.01917  | -3.0046 |
| CNIH3    | -0.5187 | 1.12999 | -4.1628 | 0.00179  | 0.01721  | -2.8656 |
| SAT1     | -0.5186 | 2.18305 | -8.6389 | 4.66E-06 | 0.00011  | 3.49721 |
| SNX29P2  | -0.5181 | 0.30739 | -5.4812 | 0.00024  | 0.00316  | -0.7203 |
| CSPG4P1  | -0.5173 | 0.78132 | -4.5942 | 0.0009   | 0.00979  | -2.1395 |
| EGILA    | -0.5167 | 0.35871 | -5.0557 | 0.00044  | 0.00538  | -1.388  |
| RNF157   | -0.5161 | 2.33368 | -4.9963 | 0.00048  | 0.00581  | -1.4832 |
| SNORA44  | -0.5149 | 1.39527 | -8.5275 | 5.25E-06 | 0.00012  | 3.36828 |
| FXVD1    | -0.5148 | 0.92966 | -3.7632 | 0.00347  | 0.02961  | -3.5555 |
| ARL4AP5  | -0.5138 | 0.68091 | -9.6883 | 1.60E-06 | 4.22E-05 | 4.65266 |
| PLAGL1   | -0.5138 | 2.51511 | -7.3676 | 1.96E-05 | 0.00037  | 1.94579 |
| EFNA2    | -0.5137 | 0.45752 | -3.6695 | 0.00406  | 0.03383  | -3.719  |
| TMEM87B  | -0.5136 | 2.67255 | -9.7503 | 1.51E-06 | 4.01E-05 | 4.71768 |
| PLIN1    | -0.5132 | 0.30677 | -3.8468 | 0.00302  | 0.02639  | -3.41   |
| SCD5     | -0.5131 | 2.49265 | -5.5026 | 0.00023  | 0.00307  | -0.6875 |
| ZFAND4   | -0.5128 | 2.23553 | -10.192 | 9.90E-07 | 2.80E-05 | 5.17207 |
| NAAA     | -0.5127 | 2.7839  | -10.194 | 9.88E-07 | 2.80E-05 | 5.1738  |
| SNORD11  | -0.5121 | 1.17225 | -6.1745 | 8.96E-05 | 0.00135  | 0.31436 |
| F11R     | -0.5114 | 2.15107 | -4.886  | 0.00057  | 0.00672  | -1.6611 |
| STOM     | -0.5109 | 2.96631 | -10.348 | 8.57E-07 | 2.47E-05 | 5.32795 |
| RFTN1    | -0.5109 | 1.90987 | -8.7181 | 4.28E-06 | 9.93E-05 | 3.58807 |
| LINC0222 | -0.5102 | 0.30529 | -9.172  | 2.67E-06 | 6.58E-05 | 4.0972  |
| TFR2     | -0.5099 | 2.33558 | -4.1725 | 0.00176  | 0.01698  | -2.8491 |
| C1DP1    | -0.5099 | 1.49302 | -8.3066 | 6.67E-06 | 0.00015  | 3.10871 |
| TCF15    | -0.5093 | 1.3788  | -8.2031 | 7.48E-06 | 0.00016  | 2.98543 |
| EMID1    | -0.509  | 1.53408 | -3.4635 | 0.00577  | 0.0451   | -4.0806 |
| PRSS23   | -0.5081 | 1.9795  | -9.853  | 1.36E-06 | 3.70E-05 | 4.82478 |
| KLF13    | -0.5079 | 2.68293 | -7.6701 | 1.37E-05 | 0.00027  | 2.33146 |
| HEBP2    | -0.5071 | 2.26229 | -8.766  | 4.07E-06 | 9.48E-05 | 3.64283 |
| IQCK     | -0.5068 | 2.1878  | -10.451 | 7.79E-07 | 2.28E-05 | 5.43107 |
| NHSL1    | -0.5058 | 1.50377 | -5.4131 | 0.00026  | 0.00342  | -0.8256 |
| REEP2    | -0.5057 | 2.51447 | -3.4136 | 0.00628  | 0.04845  | -4.1683 |
| WNT7B    | -0.5056 | 0.25279 | -4.5865 | 0.00091  | 0.00989  | -2.1523 |
| KCNT2    | -0.5053 | 1.89661 | -10.581 | 6.93E-07 | 2.05E-05 | 5.55852 |
| LARGE1   | -0.5051 | 0.862   | -4.2477 | 0.00156  | 0.01538  | -2.7211 |
| PHB1P19  | -0.5039 | 0.57691 | -3.5734 | 0.00478  | 0.03888  | -3.8875 |
| LRRC37A  | -0.5036 | 2.07122 | -8.283  | 6.85E-06 | 0.00015  | 3.08076 |
| VSTM2L   | -0.5032 | 0.85251 | -3.4957 | 0.00546  | 0.04311  | -4.0239 |
| SEPTIN4  | -0.503  | 0.86004 | -4.0806 | 0.00205  | 0.01919  | -3.0063 |
| LIN7A    | -0.5024 | 0.76028 | -4.2979 | 0.00144  | 0.0144   | -2.636  |
| ABRACL   | -0.5015 | 2.4707  | -9.34   | 2.26E-06 | 5.67E-05 | 4.28057 |
| NECTIN1  | -0.5014 | 2.57696 | -5.1262 | 0.0004   | 0.00492  | -1.2757 |
| ASZ1     | -0.5    | 0.25    | -4.3108 | 0.00141  | 0.01415  | -2.6142 |
| MEGF8    | 0.5003  | 2.19607 | 3.49846 | 0.00543  | 0.04296  | -4.019  |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| HMCN1    | 0.5009  | 0.77684 | 5.18151 | 0.00037  | 0.00459  | -1.1881 |
| STAT2    | 0.50093 | 2.61851 | 4.97607 | 0.0005   | 0.00596  | -1.5157 |
| HNRNPD   | 0.50172 | 0.25086 | 5.09313 | 0.00042  | 0.00513  | -1.3283 |
| SNORD1   | 0.5019  | 0.53116 | 4.13847 | 0.00186  | 0.01779  | -2.9072 |
| ANXA1    | 0.50204 | 2.26752 | 9.30496 | 2.34E-06 | 5.84E-05 | 4.24254 |
| RALGPS2  | 0.50228 | 0.25114 | 7.29687 | 2.14E-05 | 0.0004   | 1.85409 |
| BTBD8    | 0.5027  | 1.38971 | 5.63162 | 0.00019  | 0.0026   | -0.4903 |
| CNTNAP3  | 0.50296 | 1.39843 | 8.30516 | 6.68E-06 | 0.00015  | 3.10703 |
| EDARAD   | 0.50302 | 1.53823 | 4.45014 | 0.00113  | 0.01179  | -2.3796 |
| TRPV2    | 0.50314 | 0.85748 | 3.52937 | 0.00515  | 0.04126  | -3.9647 |
| CCDC144  | 0.50319 | 0.72859 | 6.60597 | 5.07E-05 | 0.00082  | 0.92548 |
| USP12P1  | 0.50444 | 1.00133 | 6.69063 | 4.54E-05 | 0.00075  | 1.04252 |
| SSC5D    | 0.50444 | 0.91184 | 3.76011 | 0.00349  | 0.02973  | -3.5608 |
| CACNA1D  | 0.50481 | 0.8111  | 5.45507 | 0.00024  | 0.00326  | -0.7607 |
| IFIH1    | 0.50482 | 1.80477 | 8.5915  | 4.90E-06 | 0.00011  | 3.44249 |
| BBS10    | 0.50493 | 2.15433 | 9.42527 | 2.07E-06 | 5.26E-05 | 4.37267 |
| CCDC18   | 0.50526 | 1.97319 | 5.88295 | 0.00013  | 0.00191  | -0.1128 |
| CRYAB    | 0.50557 | 0.35313 | 6.43136 | 6.36E-05 | 0.001    | 0.68111 |
| MYMX     | 0.50557 | 0.25279 | 4.58646 | 0.00091  | 0.00989  | -2.1523 |
| PPBP     | 0.50557 | 0.25279 | 6.35516 | 7.03E-05 | 0.0011   | 0.57321 |
| VNN2     | 0.50557 | 0.25279 | 4.66867 | 0.0008   | 0.00888  | -2.0164 |
| DTX3L    | 0.50562 | 2.82506 | 8.59839 | 4.86E-06 | 0.00011  | 3.45046 |
| SLC44A2  | 0.50635 | 2.3569  | 4.29184 | 0.00145  | 0.01451  | -2.6462 |
| TMED5    | 0.50708 | 2.90566 | 9.82606 | 1.40E-06 | 3.78E-05 | 4.79677 |
| STC2     | 0.50717 | 2.83105 | 5.32533 | 0.0003   | 0.00383  | -0.9621 |
| LMNB1-D  | 0.50853 | 0.35461 | 6.68836 | 4.56E-05 | 0.00076  | 1.0394  |
| LINC0044 | 0.50923 | 0.69386 | 4.45619 | 0.00112  | 0.0117   | -2.3695 |
| CPQ      | 0.50977 | 1.72376 | 7.44846 | 1.78E-05 | 0.00034  | 2.04996 |
| BNIP3P2  | 0.51024 | 0.25512 | 10.6643 | 6.42E-07 | 1.92E-05 | 5.63984 |
| CXCL6    | 0.51024 | 0.25512 | 6.76126 | 4.15E-05 | 0.0007   | 1.13946 |
| LINC0209 | 0.51024 | 0.25512 | 6.76126 | 4.15E-05 | 0.0007   | 1.13946 |
| SLITRK1  | 0.51024 | 0.25512 | 4.8445  | 0.00061  | 0.00707  | -1.7285 |
| CCDC152  | 0.51108 | 1.5991  | 9.51318 | 1.90E-06 | 4.90E-05 | 4.46692 |
| ABTB3    | 0.51136 | 0.58606 | 5.0637  | 0.00044  | 0.00533  | -1.3753 |
| SESN2    | 0.51164 | 2.64893 | 4.07896 | 0.00206  | 0.01924  | -3.0091 |
| EEF1AKM  | 0.51168 | 1.92661 | 16.6197 | 8.18E-09 | 4.77E-07 | 10.3606 |
| LINC0111 | 0.51194 | 0.26917 | 4.29613 | 0.00144  | 0.01443  | -2.639  |
| FABP4    | 0.51206 | 0.59493 | 5.67671 | 0.00018  | 0.00246  | -0.4219 |
| TSPEAR   | 0.5125  | 1.70717 | 4.025   | 0.00225  | 0.02072  | -3.1019 |
| REELD1   | 0.5132  | 0.30677 | 6.54216 | 5.50E-05 | 0.00089  | 0.83663 |
| SHROOM   | 0.5132  | 0.2566  | 4.84331 | 0.00061  | 0.00707  | -1.7304 |
| TMEM176  | 0.5132  | 0.30677 | 5.24891 | 0.00033  | 0.00421  | -1.0818 |
| TNNT2    | 0.5132  | 0.2566  | 4.24241 | 0.00157  | 0.01548  | -2.7301 |
| SNN      | 0.51326 | 2.05357 | 6.0105  | 0.00011  | 0.00164  | 0.07548 |
| NRN1     | 0.5141  | 0.25705 | 14.1622 | 4.04E-08 | 1.80E-06 | 8.63594 |
| SIGLEC1  | 0.51447 | 0.37657 | 5.95996 | 0.00012  | 0.00174  | 0.00114 |
| PPM1AP1  | 0.51469 | 0.5669  | 4.62713 | 0.00085  | 0.00938  | -2.085  |
| RHO      | 0.51483 | 1.85701 | 9.70192 | 1.58E-06 | 4.17E-05 | 4.66693 |
| MIR548X  | 0.51566 | 0.27682 | 3.76527 | 0.00346  | 0.02951  | -3.5518 |
| LINC0297 | 0.51641 | 0.56449 | 4.25731 | 0.00154  | 0.01521  | -2.7048 |
| A2MP1    | 0.51673 | 0.40888 | 6.07087 | 0.0001   | 0.00152  | 0.16382 |
| ARID3BP  | 0.51699 | 1.44837 | 3.84874 | 0.00301  | 0.02633  | -3.4066 |
| CLMP     | 0.51728 | 0.75569 | 5.30971 | 0.0003   | 0.0039   | -0.9865 |
| KIF13B   | 0.51769 | 0.98946 | 3.60153 | 0.00456  | 0.03726  | -3.838  |
| SERPINI1 | 0.51864 | 1.03543 | 5.08281 | 0.00042  | 0.0052   | -1.3448 |
| MYLK4    | 0.51877 | 0.38908 | 4.38996 | 0.00124  | 0.01272  | -2.4806 |
| HLA-C    | 0.51886 | 3.24144 | 4.64901 | 0.00082  | 0.0091   | -2.0488 |
| TMEM169  | 0.51887 | 1.56537 | 9.23934 | 2.50E-06 | 6.19E-05 | 4.171   |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| BCHE     | 0.51914 | 1.4475  | 7.52649 | 1.62E-05 | 0.00032  | 2.14971 |
| JDP2-AS  | 0.51938 | 1.26526 | 16.6737 | 7.92E-09 | 4.67E-07 | 10.3958 |
| PMCHL2   | 0.51968 | 0.31354 | 5.53943 | 0.00022  | 0.00293  | -0.631  |
| TLCD4-R  | 0.52024 | 2.20374 | 11.2208 | 3.94E-07 | 1.25E-05 | 6.16936 |
| SMARCA   | 0.52026 | 0.56116 | 5.29365 | 0.00031  | 0.00399  | -1.0116 |
| AGKP2    | 0.5214  | 0.3194  | 6.40366 | 6.60E-05 | 0.00104  | 0.64199 |
| ANKRD17  | 0.5214  | 0.39039 | 4.69548 | 0.00077  | 0.00856  | -1.9722 |
| PTH2     | 0.5214  | 0.32702 | 5.26379 | 0.00032  | 0.00415  | -1.0584 |
| ARHGAP   | 0.52172 | 0.26086 | 8.49137 | 5.46E-06 | 0.00012  | 3.32616 |
| CLTRN    | 0.52172 | 0.41138 | 4.09858 | 0.00199  | 0.01872  | -2.9755 |
| GALNTL6  | 0.52172 | 0.46155 | 4.35213 | 0.00132  | 0.01338  | -2.5443 |
| H3Y1     | 0.52172 | 0.26086 | 5.7345  | 0.00016  | 0.00229  | -0.3347 |
| GPD2     | 0.52174 | 2.92271 | 10.8671 | 5.36E-07 | 1.63E-05 | 5.83548 |
| ZNF680   | 0.52252 | 2.24845 | 9.4164  | 2.09E-06 | 5.29E-05 | 4.36312 |
| ARHGAP   | 0.52435 | 0.36252 | 5.46827 | 0.00024  | 0.00321  | -0.7403 |
| ST3GAL6  | 0.52454 | 0.91836 | 6.93204 | 3.35E-05 | 0.00058  | 1.37123 |
| GREB1    | 0.52516 | 1.67822 | 4.66053 | 0.00081  | 0.00897  | -2.0298 |
| H2BC8    | 0.52552 | 0.90065 | 3.72468 | 0.0037   | 0.03129  | -3.6226 |
| CTTNBP2  | 0.52598 | 2.23148 | 8.5392  | 5.18E-06 | 0.00012  | 3.38186 |
| LINC0245 | 0.52599 | 0.94286 | 10.2675 | 9.23E-07 | 2.64E-05 | 5.24787 |
| LEKR1    | 0.52639 | 0.2632  | 9.43553 | 2.05E-06 | 5.23E-05 | 4.3837  |
| LINC0109 | 0.52639 | 0.2632  | 9.43553 | 2.05E-06 | 5.23E-05 | 4.3837  |
| USP26    | 0.52639 | 0.2632  | 4.73855 | 0.00072  | 0.00811  | -1.9015 |
| UBE2L6   | 0.52662 | 3.07211 | 8.45556 | 5.67E-06 | 0.00013  | 3.2843  |
| SUGT1-D  | 0.52704 | 1.13257 | 5.68162 | 0.00018  | 0.00245  | -0.4145 |
| GEMIN8F  | 0.52719 | 0.97838 | 3.99986 | 0.00234  | 0.02146  | -3.1452 |
| SPATA17  | 0.5273  | 1.54659 | 6.22747 | 8.34E-05 | 0.00127  | 0.39068 |
| ICAM4-AS | 0.52735 | 1.03178 | 4.49613 | 0.00105  | 0.0111   | -2.3027 |
| VCL      | 0.52745 | 3.88936 | 10.522  | 7.31E-07 | 2.15E-05 | 5.50072 |
| CNTNAP3  | 0.5276  | 0.67485 | 5.71244 | 0.00017  | 0.00235  | -0.368  |
| ADGRE1   | 0.52808 | 1.11468 | 5.95451 | 0.00012  | 0.00175  | -0.0069 |
| CCDC144  | 0.52848 | 0.7457  | 6.21834 | 8.44E-05 | 0.00128  | 0.37754 |
| GPC3     | 0.52957 | 2.51463 | 8.79661 | 3.94E-06 | 9.24E-05 | 3.67762 |
| GPR149   | 0.52993 | 0.26496 | 7.27205 | 2.20E-05 | 0.00041  | 1.82176 |
| MIR23C   | 0.52993 | 0.36531 | 6.06873 | 0.0001   | 0.00153  | 0.16069 |
| TNS1     | 0.53007 | 0.77677 | 3.50554 | 0.00537  | 0.04258  | -4.0065 |
| MAPK8IP  | 0.53087 | 1.54366 | 3.43264 | 0.00608  | 0.04708  | -4.1348 |
| LINC0123 | 0.53103 | 2.02957 | 6.3745  | 6.86E-05 | 0.00107  | 0.60067 |
| LINC0065 | 0.53105 | 0.74642 | 4.79969 | 0.00065  | 0.00748  | -1.8015 |
| LYG2     | 0.53215 | 0.64663 | 3.71429 | 0.00377  | 0.03179  | -3.6407 |
| OLFM3    | 0.53244 | 3.12159 | 14.7687 | 2.66E-08 | 1.27E-06 | 9.08615 |
| ACVR2B   | 0.53251 | 2.4969  | 5.99823 | 0.00011  | 0.00167  | 0.05746 |
| TWF2-DT  | 0.53262 | 0.76689 | 3.78609 | 0.00334  | 0.02868  | -3.5155 |
| OR7E7P   | 0.53268 | 0.73757 | 4.29377 | 0.00145  | 0.01447  | -2.643  |
| ANKRD7   | 0.53288 | 0.31661 | 5.68975 | 0.00018  | 0.00242  | -0.4022 |
| MTF2     | 0.53345 | 2.97579 | 10.644  | 6.54E-07 | 1.95E-05 | 5.62016 |
| BCO1     | 0.53492 | 0.31763 | 7.43745 | 1.80E-05 | 0.00035  | 2.03583 |
| STARD13  | 0.53551 | 0.49779 | 5.98541 | 0.00012  | 0.00169  | 0.03861 |
| MGAT3-A  | 0.53625 | 0.46881 | 4.53249 | 0.00099  | 0.0106   | -2.242  |
| PELI1    | 0.53657 | 2.4115  | 9.84709 | 1.37E-06 | 3.72E-05 | 4.81865 |
| CYB5AP5  | 0.53697 | 0.34801 | 5.32411 | 0.0003   | 0.00383  | -0.964  |
| PARP14   | 0.53727 | 3.21589 | 11.7105 | 2.61E-07 | 8.84E-06 | 6.617   |
| RPL7AP2  | 0.53755 | 0.26878 | 6.11762 | 9.67E-05 | 0.00144  | 0.23188 |
| RTN1     | 0.53755 | 0.41929 | 4.57047 | 0.00093  | 0.0101   | -2.1789 |
| SMTNL1   | 0.53866 | 1.08578 | 4.49564 | 0.00105  | 0.01111  | -2.3035 |
| FAM167B  | 0.53909 | 0.62927 | 4.24961 | 0.00156  | 0.01535  | -2.7178 |
| LINC0030 | 0.53959 | 0.2698  | 19.6722 | 1.50E-09 | 1.18E-07 | 12.1926 |
| LINC0203 | 0.53959 | 0.2698  | 8.36785 | 6.24E-06 | 0.00014  | 3.18121 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| MT1E     | 0.53959 | 0.2698  | 8.36785 | 6.24E-06 | 0.00014  | 3.18121 |
| TRIM64E  | 0.5398  | 0.2699  | 4.91361 | 0.00055  | 0.00648  | -1.6164 |
| LINC0096 | 0.54028 | 0.75103 | 3.43683 | 0.00604  | 0.04681  | -4.1274 |
| ADH6     | 0.54092 | 0.65101 | 5.44652 | 0.00025  | 0.0033   | -0.7739 |
| H1-2     | 0.54105 | 2.06903 | 5.51011 | 0.00023  | 0.00305  | -0.6759 |
| LRCH2    | 0.54222 | 0.27111 | 6.46704 | 6.07E-05 | 0.00096  | 0.73137 |
| CYP4F22  | 0.54225 | 0.71037 | 5.36415 | 0.00028  | 0.00363  | -0.9016 |
| FAM167A  | 0.54241 | 1.16524 | 6.76758 | 4.12E-05 | 0.00069  | 1.1481  |
| CAPN6    | 0.54255 | 0.27127 | 6.37596 | 6.84E-05 | 0.00107  | 0.60274 |
| LINC0273 | 0.54255 | 0.27127 | 4.74695 | 0.00071  | 0.00803  | -1.8877 |
| PRDM1    | 0.54255 | 0.32144 | 3.74925 | 0.00355  | 0.0302   | -3.5797 |
| TMEM178  | 0.54255 | 0.37162 | 5.06287 | 0.00044  | 0.00534  | -1.3766 |
| SERPINE  | 0.54374 | 1.00748 | 5.98982 | 0.00012  | 0.00168  | 0.04511 |
| ZNF596   | 0.54397 | 1.53362 | 5.84472 | 0.00014  | 0.002    | -0.1697 |
| DST      | 0.54425 | 2.86254 | 8.95544 | 3.34E-06 | 7.99E-05 | 3.8568  |
| PPP1R9A  | 0.54435 | 0.88104 | 7.14354 | 2.57E-05 | 0.00047  | 1.65316 |
| TCP10L   | 0.54445 | 0.58178 | 4.32047 | 0.00139  | 0.01397  | -2.5978 |
| DNAJC3-  | 0.5459  | 1.30977 | 7.39255 | 1.90E-05 | 0.00036  | 1.97804 |
| RIN2     | 0.54608 | 0.32321 | 4.46957 | 0.00109  | 0.01151  | -2.3471 |
| UNC80    | 0.54608 | 0.37338 | 5.18162 | 0.00037  | 0.00459  | -1.1879 |
| ZNF880   | 0.54624 | 1.03221 | 6.05809 | 0.0001   | 0.00155  | 0.14516 |
| TMSB15A  | 0.54638 | 2.03502 | 10.4979 | 7.47E-07 | 2.20E-05 | 5.47704 |
| CPB2-AS  | 0.54722 | 0.27361 | 9.77373 | 1.47E-06 | 3.94E-05 | 4.74221 |
| PRAMEF   | 0.5474  | 0.2737  | 13.3524 | 7.22E-08 | 2.95E-06 | 8.00646 |
| ENPP1    | 0.54741 | 0.36642 | 5.64753 | 0.00019  | 0.00255  | -0.4662 |
| WDR25    | 0.54791 | 1.74865 | 5.54046 | 0.00022  | 0.00293  | -0.6294 |
| HHIP-AS  | 0.54812 | 0.27406 | 4.24868 | 0.00156  | 0.01536  | -2.7194 |
| MSRB2    | 0.54826 | 1.8873  | 7.34378 | 2.02E-05 | 0.00038  | 1.915   |
| LINC0261 | 0.54872 | 0.50439 | 3.6213  | 0.00441  | 0.03626  | -3.8034 |
| DISP2    | 0.54892 | 0.88228 | 3.82798 | 0.00311  | 0.0271   | -3.4427 |
| PLEKHH2  | 0.54948 | 1.03412 | 5.36581 | 0.00028  | 0.00362  | -0.899  |
| ZNF528   | 0.54985 | 0.7227  | 10.9839 | 4.84E-07 | 1.49E-05 | 5.94677 |
| FRG2     | 0.54995 | 0.36302 | 6.91825 | 3.40E-05 | 0.00059  | 1.35264 |
| FGF7P4   | 0.55011 | 0.44647 | 10.1773 | 1.00E-06 | 2.83E-05 | 5.15705 |
| FRG2C    | 0.55025 | 0.3253  | 4.71199 | 0.00075  | 0.00839  | -1.9451 |
| ADAMTS   | 0.55056 | 1.89575 | 11.518  | 3.06E-07 | 1.02E-05 | 6.44302 |
| C16orf96 | 0.55075 | 0.40507 | 4.35246 | 0.00132  | 0.01338  | -2.5438 |
| LINC0032 | 0.55075 | 0.45524 | 4.29865 | 0.00144  | 0.01439  | -2.6347 |
| H2AC11   | 0.55103 | 1.15352 | 4.75361 | 0.0007   | 0.00795  | -1.8768 |
| CSRNP3   | 0.55122 | 2.06401 | 13.55   | 6.25E-08 | 2.62E-06 | 8.16321 |
| RPL37A-I | 0.55128 | 1.1926  | 8.67309 | 4.49E-06 | 0.0001   | 3.53653 |
| MAP3K4-  | 0.55131 | 0.91445 | 6.88264 | 3.56E-05 | 0.00061  | 1.30457 |
| CCDC71L  | 0.55202 | 1.85494 | 6.42936 | 6.38E-05 | 0.001    | 0.67829 |
| ATP5MC1  | 0.55208 | 0.59675 | 3.89215 | 0.0028   | 0.02474  | -3.3313 |
| RBKS     | 0.55302 | 1.39881 | 6.24897 | 8.10E-05 | 0.00124  | 0.42157 |
| SALL2    | 0.55363 | 2.36541 | 4.79868 | 0.00065  | 0.00749  | -1.8031 |
| KCNK15-  | 0.5537  | 0.37719 | 6.9413  | 3.31E-05 | 0.00057  | 1.38368 |
| MRC1     | 0.5537  | 0.37719 | 6.9413  | 3.31E-05 | 0.00057  | 1.38368 |
| SORT1    | 0.55389 | 2.37898 | 10.0371 | 1.14E-06 | 3.17E-05 | 5.01451 |
| ZNF568   | 0.55426 | 0.35902 | 4.92426 | 0.00054  | 0.00638  | -1.5992 |
| ATXN1    | 0.55574 | 0.30722 | 6.65057 | 4.78E-05 | 0.00078  | 0.98725 |
| GHET1    | 0.55574 | 0.55808 | 4.8598  | 0.00059  | 0.00694  | -1.7036 |
| HNMT     | 0.55574 | 0.27787 | 8.02266 | 9.15E-06 | 0.00019  | 2.76754 |
| MAMDC2   | 0.55574 | 0.32804 | 8.08571 | 8.53E-06 | 0.00018  | 2.84406 |
| RN7SKP4  | 0.55574 | 0.27787 | 8.02266 | 9.15E-06 | 0.00019  | 2.76754 |
| TMCO5B   | 0.55647 | 0.28513 | 6.56751 | 5.32E-05 | 0.00086  | 0.872   |
| UTRN     | 0.55664 | 2.22008 | 9.791   | 1.45E-06 | 3.89E-05 | 4.76025 |
| KCNMB4   | 0.55737 | 0.4361  | 5.403   | 0.00026  | 0.00346  | -0.8412 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| TRIM38   | 0.55756 | 1.49176 | 6.88521 | 3.55E-05 | 0.00061  | 1.30804 |
| OLMALIN  | 0.55793 | 2.0795  | 4.87938 | 0.00058  | 0.00677  | -1.6719 |
| SLF2     | 0.55906 | 3.18431 | 9.68895 | 1.60E-06 | 4.22E-05 | 4.65328 |
| KRT24    | 0.55927 | 0.27964 | 6.70547 | 4.46E-05 | 0.00074  | 1.06294 |
| TMEM132  | 0.55927 | 0.37998 | 5.20583 | 0.00035  | 0.00444  | -1.1497 |
| ANKRD24  | 0.55931 | 0.7899  | 3.56248 | 0.00487  | 0.03946  | -3.9065 |
| C1orf162 | 0.5595  | 0.85985 | 3.76241 | 0.00348  | 0.02964  | -3.5568 |
| EGFEM1   | 0.56041 | 0.28021 | 5.63327 | 0.00019  | 0.0026   | -0.4878 |
| NR5A2    | 0.56041 | 0.28021 | 8.77944 | 4.01E-06 | 9.39E-05 | 3.6581  |
| IRF1-AS1 | 0.56105 | 1.62416 | 6.63775 | 4.86E-05 | 0.00079  | 0.96953 |
| CSH2     | 0.56283 | 0.28141 | 6.6877  | 4.56E-05 | 0.00076  | 1.03849 |
| APOL4    | 0.56337 | 0.38203 | 3.49628 | 0.00545  | 0.04309  | -4.0228 |
| HLA-DRA  | 0.56337 | 0.28168 | 9.22735 | 2.53E-06 | 6.25E-05 | 4.15789 |
| LINC0060 | 0.56337 | 0.33186 | 6.77657 | 4.07E-05 | 0.00069  | 1.16039 |
| ZNF30-AS | 0.56337 | 0.41138 | 6.30582 | 7.51E-05 | 0.00116  | 0.50294 |
| CRIM1    | 0.56366 | 1.13826 | 7.62566 | 1.44E-05 | 0.00028  | 2.27546 |
| DDIT4    | 0.56481 | 2.8246  | 5.4744  | 0.00024  | 0.00319  | -0.7309 |
| ZNF204P  | 0.56565 | 1.41279 | 4.05222 | 0.00215  | 0.01996  | -3.0551 |
| C2orf15  | 0.566   | 0.6219  | 5.03082 | 0.00046  | 0.00556  | -1.4278 |
| NELL1    | 0.566   | 0.39187 | 6.53389 | 5.56E-05 | 0.00089  | 0.82509 |
| ARL9     | 0.56632 | 0.41285 | 6.54643 | 5.47E-05 | 0.00088  | 0.8426  |
| LINC0259 | 0.56632 | 0.3835  | 5.17399 | 0.00037  | 0.00463  | -1.2    |
| SCOC-AS  | 0.56634 | 1.00545 | 4.84512 | 0.00061  | 0.00707  | -1.7275 |
| ASXL3-D  | 0.5669  | 0.28345 | 4.16691 | 0.00178  | 0.01711  | -2.8586 |
| CFAP58   | 0.5669  | 0.46331 | 4.81292 | 0.00064  | 0.00735  | -1.7799 |
| IMPG2    | 0.5669  | 0.41314 | 5.68242 | 0.00018  | 0.00245  | -0.4133 |
| LINC0255 | 0.5669  | 0.38379 | 6.89521 | 3.50E-05 | 0.0006   | 1.32156 |
| XK       | 0.5669  | 0.64318 | 4.48821 | 0.00106  | 0.01122  | -2.3159 |
| ZEB2-AS  | 0.5669  | 0.28345 | 7.39598 | 1.90E-05 | 0.00036  | 1.98247 |
| ABCC6    | 0.56702 | 1.94739 | 5.77148 | 0.00016  | 0.00219  | -0.2792 |
| RTN2     | 0.56823 | 2.03213 | 4.60002 | 0.00089  | 0.00971  | -2.1299 |
| GRHL3    | 0.56843 | 0.6146  | 3.88425 | 0.00284  | 0.02503  | -3.345  |
| SNRPGP   | 0.56873 | 0.30336 | 4.62094 | 0.00086  | 0.00946  | -2.0952 |
| SALRNA2  | 0.56894 | 0.33464 | 6.63284 | 4.89E-05 | 0.0008   | 0.96273 |
| NPL      | 0.5693  | 2.0931  | 10.1292 | 1.05E-06 | 2.95E-05 | 5.10832 |
| ERBB4    | 0.57147 | 1.70621 | 14.1335 | 4.12E-08 | 1.82E-06 | 8.61419 |
| TARS1-D  | 0.5716  | 0.77522 | 7.19669 | 2.41E-05 | 0.00044  | 1.72313 |
| ARHGAP   | 0.57189 | 0.38629 | 4.86053 | 0.00059  | 0.00693  | -1.7025 |
| ASIC4    | 0.57189 | 0.46581 | 4.33559 | 0.00135  | 0.01368  | -2.5723 |
| IRX6     | 0.57461 | 0.2873  | 4.74117 | 0.00071  | 0.00809  | -1.8972 |
| TRIM6-TF | 0.57461 | 1.96851 | 6.18601 | 8.82E-05 | 0.00133  | 0.33094 |
| TMEM100  | 0.57497 | 1.23494 | 7.09918 | 2.72E-05 | 0.00049  | 1.59449 |
| ZNF697   | 0.57515 | 1.82644 | 9.94215 | 1.25E-06 | 3.43E-05 | 4.917   |
| LUNAR1   | 0.57651 | 0.75595 | 4.12053 | 0.00192  | 0.01819  | -2.9379 |
| KHDC1    | 0.57657 | 0.38863 | 4.21259 | 0.00165  | 0.0161   | -2.7808 |
| KHDC1P   | 0.57657 | 0.28828 | 16.788  | 7.40E-09 | 4.42E-07 | 10.4698 |
| FAM229B  | 0.57906 | 0.91397 | 4.52484 | 0.001    | 0.01069  | -2.2548 |
| CSGALN   | 0.57919 | 1.49409 | 7.66753 | 1.38E-05 | 0.00027  | 2.3282  |
| DPYSL5   | 0.5794  | 0.35603 | 3.4416  | 0.00599  | 0.04649  | -4.119  |
| RXFP1    | 0.57952 | 0.33993 | 5.43196 | 0.00025  | 0.00335  | -0.7964 |
| MYO15A   | 0.57961 | 0.51517 | 3.49289 | 0.00548  | 0.04329  | -4.0288 |
| CP       | 0.57991 | 2.15884 | 10.6986 | 6.23E-07 | 1.87E-05 | 5.67318 |
| CDKN1A   | 0.58078 | 2.53992 | 8.3093  | 6.65E-06 | 0.00015  | 3.11195 |
| LRP1-AS  | 0.5809  | 0.61616 | 4.13739 | 0.00187  | 0.01781  | -2.9091 |
| HOXB-AS  | 0.58152 | 0.97769 | 3.39847 | 0.00645  | 0.0495   | -4.195  |
| RWDD3    | 0.58173 | 2.17935 | 11.4403 | 3.27E-07 | 1.07E-05 | 6.37201 |
| CASP5    | 0.58305 | 0.3417  | 6.09579 | 9.96E-05 | 0.00148  | 0.20014 |
| LINC0114 | 0.58305 | 0.44204 | 7.84288 | 1.12E-05 | 0.00023  | 2.54691 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| USP30-A  | 0.58365 | 0.49251 | 4.61634 | 0.00087  | 0.00951  | -2.1028 |
| UGCG     | 0.58404 | 2.93899 | 17.5007 | 4.87E-09 | 3.15E-07 | 10.9207 |
| ETS1     | 0.58419 | 0.37162 | 5.16689 | 0.00037  | 0.00467  | -1.2112 |
| ESPN     | 0.58508 | 0.71859 | 4.09399 | 0.00201  | 0.01883  | -2.9834 |
| DACH1    | 0.58509 | 0.29255 | 11.1636 | 4.14E-07 | 1.30E-05 | 6.11596 |
| SLC5A5   | 0.58642 | 0.53177 | 4.48808 | 0.00106  | 0.01122  | -2.3161 |
| DNAI3    | 0.58661 | 1.26511 | 7.008   | 3.04E-05 | 0.00054  | 1.47312 |
| NUDT10   | 0.5873  | 1.582   | 12.3    | 1.62E-07 | 5.89E-06 | 7.13468 |
| KRTAP7-  | 0.58772 | 0.29386 | 4.0926  | 0.00201  | 0.01887  | -2.9858 |
| LINC0234 | 0.58772 | 0.34403 | 6.4569  | 6.15E-05 | 0.00098  | 0.7171  |
| UNC5C-A  | 0.58805 | 0.29402 | 12.0746 | 1.93E-07 | 6.86E-06 | 6.93934 |
| STXBP5L  | 0.58945 | 1.38153 | 8.30697 | 6.67E-06 | 0.00015  | 3.10919 |
| VLDLR    | 0.59033 | 2.57735 | 9.76061 | 1.49E-06 | 3.98E-05 | 4.72848 |
| CHAC1    | 0.59034 | 2.17647 | 4.47902 | 0.00108  | 0.01136  | -2.3313 |
| KCNK12   | 0.59059 | 0.75536 | 5.78164 | 0.00015  | 0.00216  | -0.2639 |
| FAM230I  | 0.59088 | 0.49613 | 5.72325 | 0.00017  | 0.00232  | -0.3517 |
| RNASE1   | 0.59125 | 0.39597 | 5.89914 | 0.00013  | 0.00187  | -0.0888 |
| LINC0088 | 0.59258 | 0.42598 | 4.49168 | 0.00106  | 0.01117  | -2.3101 |
| STX18-A  | 0.59259 | 1.5401  | 6.02876 | 0.00011  | 0.0016   | 0.10225 |
| CD101-A  | 0.59272 | 0.3967  | 6.93835 | 3.32E-05 | 0.00058  | 1.37972 |
| PMP2     | 0.59272 | 0.32571 | 10.232  | 9.54E-07 | 2.71E-05 | 5.21226 |
| POU2AF1  | 0.59272 | 0.29636 | 8.38608 | 6.12E-06 | 0.00014  | 3.20271 |
| PYROXD   | 0.59272 | 0.47622 | 5.39079 | 0.00027  | 0.00352  | -0.8602 |
| RIT2     | 0.59272 | 0.29636 | 8.38608 | 6.12E-06 | 0.00014  | 3.20271 |
| MRPL23-  | 0.59348 | 0.37626 | 5.12131 | 0.0004   | 0.00495  | -1.2835 |
| WARS1    | 0.59462 | 3.6534  | 8.99344 | 3.21E-06 | 7.72E-05 | 3.8993  |
| GRIP1    | 0.59594 | 0.73518 | 3.44761 | 0.00593  | 0.0461   | -4.1084 |
| HOXB-AS  | 0.59659 | 1.86812 | 7.0025  | 3.06E-05 | 0.00054  | 1.46576 |
| ZNF626   | 0.59674 | 2.13889 | 15.6896 | 1.46E-08 | 7.77E-07 | 9.73793 |
| HLA-K    | 0.59696 | 0.63035 | 4.28328 | 0.00147  | 0.01467  | -2.6607 |
| SELENBF  | 0.59739 | 0.29869 | 4.74515 | 0.00071  | 0.00805  | -1.8907 |
| HLA-DPB  | 0.59808 | 0.31803 | 6.68312 | 4.59E-05 | 0.00076  | 1.03218 |
| C8orf88  | 0.59818 | 0.65882 | 4.55654 | 0.00095  | 0.01029  | -2.202  |
| LINC0228 | 0.59829 | 0.29914 | 10.1215 | 1.06E-06 | 2.97E-05 | 5.10047 |
| MISP     | 0.59829 | 0.29914 | 10.1215 | 1.06E-06 | 2.97E-05 | 5.10047 |
| DGKI     | 0.59862 | 0.37883 | 3.78853 | 0.00333  | 0.02859  | -3.5113 |
| RNASEL   | 0.59953 | 1.80483 | 7.46153 | 1.75E-05 | 0.00034  | 2.06672 |
| TMEM37   | 0.60015 | 1.93889 | 5.38775 | 0.00027  | 0.00353  | -0.8649 |
| CLPTM1L  | 0.60034 | 0.30017 | 6.1151  | 9.70E-05 | 0.00145  | 0.22823 |
| ELAVL3   | 0.60069 | 0.88544 | 6.1665  | 9.05E-05 | 0.00136  | 0.30274 |
| DLGAP1-  | 0.60119 | 1.60497 | 11.2293 | 3.91E-07 | 1.24E-05 | 6.17726 |
| C5       | 0.60136 | 2.2962  | 12.9284 | 9.92E-08 | 3.87E-06 | 7.66289 |
| AMOT     | 0.60178 | 1.85857 | 7.52172 | 1.63E-05 | 0.00032  | 2.14363 |
| RNU6-35  | 0.60257 | 0.72734 | 4.93792 | 0.00053  | 0.00627  | -1.5772 |
| DNAI7    | 0.60387 | 0.35211 | 8.62011 | 4.75E-06 | 0.00011  | 3.47554 |
| STX18    | 0.60398 | 2.9567  | 11.2365 | 3.89E-07 | 1.23E-05 | 6.18394 |
| MLIP     | 0.60429 | 0.45266 | 4.80744 | 0.00064  | 0.0074   | -1.7888 |
| MESTP4   | 0.60435 | 0.33152 | 8.54671 | 5.14E-06 | 0.00012  | 3.39058 |
| PPP1R3C  | 0.60562 | 1.60019 | 8.18717 | 7.61E-06 | 0.00016  | 2.96629 |
| ERP27    | 0.60591 | 0.30296 | 12.6395 | 1.24E-07 | 4.61E-06 | 7.42297 |
| MANCR    | 0.60591 | 0.30296 | 6.90676 | 3.45E-05 | 0.0006   | 1.33715 |
| OR5G3    | 0.60591 | 0.30296 | 8.82454 | 3.83E-06 | 9.02E-05 | 3.7093  |
| NRXN3    | 0.60623 | 0.41726 | 9.01495 | 3.14E-06 | 7.58E-05 | 3.9233  |
| FLT3LG   | 0.60626 | 1.24003 | 5.3204  | 0.0003   | 0.00385  | -0.9698 |
| SEMA3E   | 0.6066  | 1.10047 | 5.0109  | 0.00047  | 0.0057   | -1.4598 |
| GRM8     | 0.60741 | 0.50439 | 5.14681 | 0.00039  | 0.00479  | -1.243  |
| UBTFL1   | 0.60785 | 0.30392 | 6.59746 | 5.12E-05 | 0.00083  | 0.91365 |
| PDZRN3   | 0.60804 | 1.02996 | 4.58516 | 0.00091  | 0.0099   | -2.1545 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| PAN3-AS  | 0.60818 | 0.95051 | 4.79875 | 0.00065  | 0.00749  | -1.803  |
| STEAP2   | 0.60821 | 1.55706 | 11.1987 | 4.02E-07 | 1.27E-05 | 6.14875 |
| RBM17P1  | 0.60823 | 0.3231  | 6.22013 | 8.42E-05 | 0.00128  | 0.38012 |
| DNAH6    | 0.60855 | 0.48414 | 5.41495 | 0.00026  | 0.00342  | -0.8227 |
| EBI3     | 0.60887 | 0.43413 | 4.52947 | 0.00099  | 0.01063  | -2.2471 |
| GJA5     | 0.60887 | 0.35461 | 9.3917  | 2.14E-06 | 5.41E-05 | 4.33649 |
| GRM1     | 0.60945 | 0.30472 | 6.90348 | 3.47E-05 | 0.0006   | 1.33272 |
| ZFPM2    | 0.61043 | 0.80693 | 9.43178 | 2.06E-06 | 5.24E-05 | 4.37967 |
| MAGEA1   | 0.61059 | 0.30529 | 15.8513 | 1.31E-08 | 7.13E-07 | 9.84867 |
| SLC2A12  | 0.61077 | 0.86876 | 7.15029 | 2.55E-05 | 0.00046  | 1.66206 |
| HEXA-AS  | 0.61137 | 0.58589 | 5.68165 | 0.00018  | 0.00245  | -0.4145 |
| P2RX3    | 0.61148 | 0.6731  | 4.69838 | 0.00076  | 0.00853  | -1.9675 |
| TRIM51E  | 0.61198 | 0.30599 | 7.04739 | 2.90E-05 | 0.00052  | 1.52568 |
| EDNRB    | 0.61208 | 0.30604 | 7.21918 | 2.35E-05 | 0.00043  | 1.75264 |
| ERVMER   | 0.6128  | 1.62267 | 9.7067  | 1.57E-06 | 4.16E-05 | 4.67196 |
| AGAP2    | 0.61425 | 1.79621 | 4.31562 | 0.0014   | 0.01406  | -2.606  |
| B2M      | 0.61495 | 3.86927 | 12.1903 | 1.76E-07 | 6.34E-06 | 7.04    |
| LINC0183 | 0.61513 | 1.2725  | 10.8895 | 5.26E-07 | 1.60E-05 | 5.85691 |
| USP18    | 0.61534 | 2.09543 | 8.58707 | 4.92E-06 | 0.00011  | 3.43736 |
| ADGRL2   | 0.61552 | 1.73778 | 9.5235  | 1.88E-06 | 4.86E-05 | 4.47794 |
| ACTL8    | 0.6158  | 1.01496 | 5.77801 | 0.00015  | 0.00217  | -0.2694 |
| LINC0152 | 0.61605 | 1.03944 | 3.55661 | 0.00492  | 0.03976  | -3.9168 |
| STARD8   | 0.61663 | 0.83004 | 4.85546 | 0.0006   | 0.00697  | -1.7107 |
| ANXA10   | 0.61707 | 0.35871 | 8.47295 | 5.57E-06 | 0.00012  | 3.30465 |
| BCAN-AS  | 0.61707 | 0.40888 | 5.00557 | 0.00048  | 0.00574  | -1.4683 |
| DLGAP1-  | 0.61836 | 1.88513 | 8.96027 | 3.32E-06 | 7.96E-05 | 3.86221 |
| ZBTB8B   | 0.61861 | 1.15779 | 10.688  | 6.29E-07 | 1.88E-05 | 5.66292 |
| FAM226B  | 0.61895 | 0.49786 | 5.44368 | 0.00025  | 0.0033   | -0.7783 |
| ADAMTS   | 0.61911 | 0.4099  | 5.42487 | 0.00026  | 0.00338  | -0.8074 |
| LINC0039 | 0.61911 | 0.30956 | 11.4195 | 3.33E-07 | 1.09E-05 | 6.35294 |
| RGS22    | 0.61911 | 0.42605 | 6.65758 | 4.74E-05 | 0.00078  | 0.99694 |
| RINL     | 0.62042 | 0.4399  | 4.68025 | 0.00079  | 0.00873  | -1.9973 |
| EDNRA    | 0.62044 | 0.85834 | 4.04251 | 0.00218  | 0.02023  | -3.0718 |
| MPP4     | 0.62049 | 0.41748 | 7.92003 | 1.03E-05 | 0.00021  | 2.64203 |
| PRSS8    | 0.6206  | 0.46082 | 4.55284 | 0.00096  | 0.01034  | -2.2082 |
| ZBED9    | 0.62143 | 1.56749 | 6.99652 | 3.09E-05 | 0.00054  | 1.45777 |
| ASNS     | 0.62169 | 3.5385  | 14.8369 | 2.54E-08 | 1.21E-06 | 9.13573 |
| FAT3     | 0.62207 | 0.31103 | 6.98837 | 3.12E-05 | 0.00055  | 1.44686 |
| RPS17P1  | 0.62207 | 0.31103 | 12.3784 | 1.52E-07 | 5.56E-06 | 7.20186 |
| NGFR     | 0.62217 | 0.8592  | 5.96025 | 0.00012  | 0.00174  | 0.00157 |
| SEMA6A-  | 0.62263 | 1.44302 | 6.96535 | 3.21E-05 | 0.00056  | 1.41599 |
| FZD3     | 0.6228  | 2.53029 | 15.4723 | 1.67E-08 | 8.61E-07 | 9.58743 |
| S1PR3    | 0.62326 | 1.66362 | 10.1198 | 1.06E-06 | 2.97E-05 | 5.09879 |
| STK24-AS | 0.62399 | 0.69254 | 6.18473 | 8.83E-05 | 0.00134  | 0.32909 |
| TRANK1   | 0.624   | 1.25446 | 7.11348 | 2.67E-05 | 0.00048  | 1.61342 |
| NTF4     | 0.62418 | 1.37833 | 5.68897 | 0.00018  | 0.00243  | -0.4034 |
| ANKRD3   | 0.62422 | 1.11241 | 7.22484 | 2.33E-05 | 0.00043  | 1.76006 |
| C1GALT1  | 0.6249  | 0.4128  | 8.52497 | 5.26E-06 | 0.00012  | 3.36531 |
| RTL9     | 0.6256  | 0.3128  | 9.23081 | 2.52E-06 | 6.23E-05 | 4.16167 |
| CTNNA2-  | 0.62674 | 0.31337 | 15.2813 | 1.90E-08 | 9.53E-07 | 9.4535  |
| GLT1D1   | 0.62674 | 0.31337 | 7.23484 | 2.30E-05 | 0.00043  | 1.77315 |
| PCM1     | 0.62675 | 3.78587 | 14.8887 | 2.46E-08 | 1.18E-06 | 9.17322 |
| SBK1     | 0.62813 | 1.61587 | 3.68263 | 0.00397  | 0.03322  | -3.696  |
| CPHL1P   | 0.62823 | 0.41446 | 6.89323 | 3.51E-05 | 0.0006   | 1.31887 |
| NCCRP1   | 0.62823 | 0.41446 | 6.89323 | 3.51E-05 | 0.0006   | 1.31887 |
| OR5AK1F  | 0.62823 | 0.31411 | 7.31413 | 2.09E-05 | 0.00039  | 1.87653 |
| ZSCAN10  | 0.62866 | 0.56519 | 6.43868 | 6.30E-05 | 0.00099  | 0.69144 |
| ARHGAP   | 0.62871 | 0.99979 | 7.63514 | 1.43E-05 | 0.00028  | 2.28742 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| PBX3     | 0.62873 | 3.11324 | 11.8256 | 2.37E-07 | 8.15E-06 | 6.71987 |
| IRF1     | 0.62913 | 2.60359 | 8.50428 | 5.38E-06 | 0.00012  | 3.34121 |
| CD200R1  | 0.62937 | 0.3942  | 6.63229 | 4.90E-05 | 0.0008   | 0.96197 |
| PCBP3    | 0.62951 | 0.51544 | 4.46599 | 0.0011   | 0.01156  | -2.3531 |
| RSPO3    | 0.62969 | 0.31485 | 9.21902 | 2.55E-06 | 6.30E-05 | 4.14877 |
| SP110    | 0.62999 | 1.88626 | 6.33611 | 7.21E-05 | 0.00112  | 0.54613 |
| LINC0240 | 0.63027 | 0.31513 | 6.59201 | 5.16E-05 | 0.00084  | 0.90609 |
| SCTR     | 0.63027 | 0.41548 | 5.44533 | 0.00025  | 0.0033   | -0.7757 |
| NEFHP1   | 0.63064 | 0.31532 | 7.49398 | 1.69E-05 | 0.00033  | 2.10824 |
| BTN3A1   | 0.63192 | 2.26261 | 5.53402 | 0.00022  | 0.00295  | -0.6393 |
| NAB1     | 0.63193 | 2.51837 | 16.8194 | 7.26E-09 | 4.36E-07 | 10.49   |
| KCNN3    | 0.63214 | 0.64645 | 5.37156 | 0.00028  | 0.0036   | -0.8901 |
| THSD4    | 0.63296 | 1.64369 | 5.47382 | 0.00024  | 0.00319  | -0.7318 |
| GRIN1    | 0.63322 | 0.4008  | 6.22954 | 8.32E-05 | 0.00127  | 0.39365 |
| SLC7A2   | 0.63447 | 3.16532 | 13.9354 | 4.74E-08 | 2.05E-06 | 8.46305 |
| ATP1A2   | 0.63526 | 0.31763 | 5.57486 | 0.00021  | 0.0028   | -0.5768 |
| DPYS     | 0.63526 | 0.54767 | 7.35408 | 1.99E-05 | 0.00038  | 1.92834 |
| SYN3     | 0.63526 | 0.3678  | 5.66512 | 0.00018  | 0.0025   | -0.4395 |
| PKDREJ   | 0.636   | 0.76487 | 5.04762 | 0.00045  | 0.00544  | -1.401  |
| TRIM43B  | 0.63679 | 0.31839 | 6.19461 | 8.72E-05 | 0.00132  | 0.34335 |
| CPNE8    | 0.63702 | 3.07212 | 14.2711 | 3.74E-08 | 1.69E-06 | 8.71806 |
| DYNC1LI  | 0.63716 | 0.57167 | 5.02446 | 0.00046  | 0.0056   | -1.438  |
| CYP4F29  | 0.63717 | 0.35656 | 17.2222 | 5.72E-09 | 3.56E-07 | 10.7466 |
| LINC0179 | 0.63719 | 0.90369 | 9.79979 | 1.44E-06 | 3.87E-05 | 4.76941 |
| GUCY1A2  | 0.63789 | 0.41929 | 6.78834 | 4.01E-05 | 0.00068  | 1.17646 |
| SERTAD4  | 0.63789 | 0.31895 | 4.82152 | 0.00063  | 0.00727  | -1.7659 |
| TM4SF4   | 0.63789 | 0.31895 | 12.8786 | 1.03E-07 | 3.98E-06 | 7.6219  |
| LINC0037 | 0.63822 | 0.79533 | 4.8478  | 0.00061  | 0.00705  | -1.7231 |
| NECTIN4  | 0.63822 | 0.46962 | 5.78968 | 0.00015  | 0.00214  | -0.2519 |
| MBD3L5   | 0.63825 | 0.31912 | 15.3998 | 1.75E-08 | 8.97E-07 | 9.53677 |
| NUGGC    | 0.6385  | 0.52846 | 4.34691 | 0.00133  | 0.01348  | -2.5532 |
| IFI35    | 0.63864 | 2.2509  | 6.71523 | 4.40E-05 | 0.00073  | 1.07636 |
| LARP6    | 0.6399  | 2.30804 | 10.9394 | 5.03E-07 | 1.54E-05 | 5.90446 |
| AIM2     | 0.63993 | 0.31997 | 6.2582  | 8.00E-05 | 0.00123  | 0.43481 |
| RCAN1    | 0.6421  | 2.77898 | 14.2188 | 3.88E-08 | 1.74E-06 | 8.67871 |
| CASC15   | 0.64289 | 0.37162 | 10.9842 | 4.84E-07 | 1.49E-05 | 5.947   |
| CLPSL2   | 0.64289 | 0.32144 | 15.2385 | 1.95E-08 | 9.73E-07 | 9.42329 |
| GDNF-AS  | 0.64289 | 0.32144 | 15.2385 | 1.95E-08 | 9.73E-07 | 9.42329 |
| H2BC27P  | 0.64379 | 0.32189 | 5.05472 | 0.00044  | 0.00539  | -1.3896 |
| CA2      | 0.6438  | 1.83328 | 11.2789 | 3.75E-07 | 1.20E-05 | 6.2233  |
| DLG1-AS  | 0.64416 | 1.08316 | 5.58435 | 0.0002   | 0.00277  | -0.5623 |
| TMEM126  | 0.64419 | 2.6221  | 12.1152 | 1.87E-07 | 6.68E-06 | 6.97477 |
| MAGED2   | 0.64456 | 3.0225  | 8.25008 | 7.10E-06 | 0.00015  | 3.04152 |
| H2AC6    | 0.64557 | 1.55824 | 11.153  | 4.18E-07 | 1.31E-05 | 6.10603 |
| KCNE1    | 0.64571 | 0.62388 | 6.7631  | 4.14E-05 | 0.0007   | 1.14198 |
| GAB2     | 0.64623 | 1.78171 | 5.93289 | 0.00012  | 0.0018   | -0.0388 |
| EXO5-DT  | 0.64756 | 0.32378 | 11.2463 | 3.85E-07 | 1.23E-05 | 6.19312 |
| PKN2-AS  | 0.64756 | 0.32378 | 21.5978 | 5.80E-10 | 5.60E-08 | 13.2104 |
| PURPL    | 0.64901 | 2.42188 | 11.7585 | 2.50E-07 | 8.53E-06 | 6.66    |
| PANCR    | 0.64905 | 0.32453 | 5.82756 | 0.00014  | 0.00204  | -0.1953 |
| ZC2HC1C  | 0.64912 | 1.35153 | 4.93094 | 0.00053  | 0.00633  | -1.5884 |
| KDM4E    | 0.64938 | 0.32469 | 11.5231 | 3.05E-07 | 1.01E-05 | 6.4476  |
| MYLK3    | 0.64942 | 0.99195 | 6.51626 | 5.69E-05 | 0.00091  | 0.80043 |
| DMD      | 0.64944 | 3.54438 | 13.8991 | 4.86E-08 | 2.09E-06 | 8.43512 |
| THBS4    | 0.64991 | 0.53417 | 3.62488 | 0.00438  | 0.03611  | -3.7971 |
| FBLIM1   | 0.65052 | 2.03448 | 8.85846 | 3.69E-06 | 8.74E-05 | 3.74768 |
| SSC4D    | 0.65099 | 0.69375 | 6.58637 | 5.20E-05 | 0.00084  | 0.89824 |
| RGS4     | 0.65109 | 0.40507 | 7.89235 | 1.06E-05 | 0.00022  | 2.60798 |

|           |         |         |         |          |          |         |
|-----------|---------|---------|---------|----------|----------|---------|
| TRIM69    | 0.65112 | 2.42374 | 9.95413 | 1.24E-06 | 3.41E-05 | 4.92934 |
| TSPY26P   | 0.65115 | 0.83468 | 6.27477 | 7.83E-05 | 0.0012   | 0.45855 |
| RNF152    | 0.65119 | 0.79419 | 5.62266 | 0.00019  | 0.00264  | -0.5039 |
| PHF24     | 0.65141 | 0.37588 | 6.37772 | 6.83E-05 | 0.00107  | 0.60524 |
| TIGD2     | 0.65233 | 2.59905 | 11.2429 | 3.87E-07 | 1.23E-05 | 6.18995 |
| GPX3      | 0.6524  | 0.85259 | 5.18586 | 0.00036  | 0.00456  | -1.1812 |
| LCP1      | 0.65329 | 1.37556 | 13.4061 | 6.94E-08 | 2.86E-06 | 8.04929 |
| LIN28B    | 0.65377 | 3.2598  | 16.4816 | 8.90E-09 | 5.13E-07 | 10.2703 |
| CDH11     | 0.65405 | 0.32702 | 4.93961 | 0.00053  | 0.00626  | -1.5744 |
| AMPH      | 0.65412 | 0.85345 | 4.77009 | 0.00068  | 0.00777  | -1.8498 |
| DLG3      | 0.65421 | 2.44442 | 7.23708 | 2.30E-05 | 0.00042  | 1.77608 |
| LINC0202  | 0.65462 | 0.75336 | 4.1828  | 0.00173  | 0.01674  | -2.8315 |
| FAM110D   | 0.65562 | 1.43287 | 5.20239 | 0.00035  | 0.00446  | -1.1551 |
| SH2D4A    | 0.6559  | 2.7921  | 13.2686 | 7.68E-08 | 3.09E-06 | 7.93936 |
| SYNM-AS   | 0.65609 | 0.50791 | 4.69125 | 0.00077  | 0.0086   | -1.9792 |
| ZIC5      | 0.65609 | 0.32804 | 9.62186 | 1.71E-06 | 4.46E-05 | 4.58248 |
| EPHA5     | 0.65622 | 1.13153 | 12.1365 | 1.84E-07 | 6.58E-06 | 6.9933  |
| RHOT1P    | 0.65633 | 0.51347 | 7.01161 | 3.03E-05 | 0.00054  | 1.47795 |
| CACNG7    | 0.65718 | 2.12704 | 4.34343 | 0.00134  | 0.01354  | -2.559  |
| MOV10     | 0.65719 | 2.83544 | 5.68026 | 0.00018  | 0.00245  | -0.4166 |
| BTN3A2    | 0.65721 | 2.4787  | 6.55395 | 5.42E-05 | 0.00087  | 0.8531  |
| SLIT2-IT1 | 0.65904 | 0.42986 | 7.92716 | 1.02E-05 | 0.00021  | 2.65079 |
| CACNA1C   | 0.65943 | 1.29055 | 3.42111 | 0.0062   | 0.04789  | -4.1551 |
| SLC7A7    | 0.65955 | 1.45681 | 5.87175 | 0.00014  | 0.00194  | -0.1294 |
| P2RY1     | 0.66047 | 0.68996 | 6.04805 | 0.00011  | 0.00156  | 0.13048 |
| H2BC12L   | 0.6607  | 0.88199 | 9.99651 | 1.19E-06 | 3.28E-05 | 4.9729  |
| SNCA-AS   | 0.66076 | 0.33038 | 7.81394 | 1.16E-05 | 0.00024  | 2.51106 |
| ABCA6     | 0.66271 | 0.44213 | 6.97117 | 3.19E-05 | 0.00056  | 1.4238  |
| DLGAP1    | 0.66289 | 1.32653 | 7.88076 | 1.08E-05 | 0.00022  | 2.5937  |
| IGF2BP1   | 0.66359 | 3.41492 | 7.37242 | 1.95E-05 | 0.00037  | 1.95205 |
| NES       | 0.66383 | 3.51912 | 7.20048 | 2.40E-05 | 0.00044  | 1.72812 |
| RFX5-AS   | 0.66415 | 1.11228 | 6.14878 | 9.27E-05 | 0.00139  | 0.2771  |
| SLC16A4   | 0.66453 | 1.15502 | 5.28227 | 0.00032  | 0.00405  | -1.0295 |
| HAS2-AS   | 0.66461 | 0.33231 | 5.55093 | 0.00021  | 0.00289  | -0.6133 |
| CHN1      | 0.6659  | 1.89401 | 10.3267 | 8.74E-07 | 2.51E-05 | 5.30719 |
| IDO2      | 0.66667 | 0.3967  | 6.16573 | 9.06E-05 | 0.00136  | 0.30163 |
| PDGFB     | 0.66667 | 0.46303 | 6.80229 | 3.94E-05 | 0.00067  | 1.19548 |
| BRWD1P    | 0.66724 | 0.33362 | 4.98326 | 0.00049  | 0.00591  | -1.5041 |
| LINC0161  | 0.66724 | 0.33362 | 8.41728 | 5.91E-06 | 0.00013  | 3.23941 |
| DCBLD2    | 0.66778 | 2.71773 | 17.3643 | 5.27E-09 | 3.33E-07 | 10.8357 |
| SGK1      | 0.66797 | 0.45738 | 4.70677 | 0.00075  | 0.00844  | -1.9537 |
| S100A1    | 0.66801 | 1.93309 | 7.12721 | 2.63E-05 | 0.00047  | 1.63159 |
| DISP1     | 0.6685  | 1.48371 | 9.58596 | 1.77E-06 | 4.60E-05 | 4.54442 |
| TSPAN2    | 0.66928 | 0.38481 | 7.40771 | 1.87E-05 | 0.00036  | 1.99758 |
| TBX10     | 0.66951 | 0.64431 | 5.12336 | 0.0004   | 0.00493  | -1.2802 |
| COL6A5    | 0.6702  | 0.38527 | 7.57988 | 1.52E-05 | 0.0003   | 2.21756 |
| RPL10L    | 0.67022 | 0.45484 | 5.83077 | 0.00014  | 0.00203  | -0.1905 |
| BAGE2     | 0.67043 | 1.02163 | 5.26308 | 0.00032  | 0.00415  | -1.0596 |
| SOX6      | 0.67048 | 1.29325 | 11.9432 | 2.15E-07 | 7.51E-06 | 6.82401 |
| CEACAM    | 0.67151 | 1.25885 | 9.15869 | 2.71E-06 | 6.66E-05 | 4.08252 |
| CARMAL    | 0.67191 | 0.33596 | 10.1645 | 1.02E-06 | 2.86E-05 | 5.1441  |
| LINC0095  | 0.67224 | 0.33612 | 5.3707  | 0.00028  | 0.0036   | -0.8914 |
| PHOX2B    | 0.67224 | 0.33612 | 9.95007 | 1.24E-06 | 3.41E-05 | 4.92516 |
| UBAC2-A   | 0.67228 | 1.06971 | 8.67232 | 4.49E-06 | 0.0001   | 3.53565 |
| SP140     | 0.67273 | 0.87424 | 6.68297 | 4.59E-05 | 0.00076  | 1.03197 |
| ARL10     | 0.67287 | 2.59901 | 4.76195 | 0.00069  | 0.00787  | -1.8632 |
| FBXO27    | 0.67419 | 2.01721 | 6.03137 | 0.00011  | 0.0016   | 0.10608 |
| H4C8      | 0.67498 | 1.20412 | 6.96521 | 3.21E-05 | 0.00056  | 1.41581 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| LRRTM1   | 0.67508 | 0.38771 | 5.96018 | 0.00012  | 0.00174  | 0.00147 |
| ADCY10   | 0.67519 | 0.64715 | 4.08526 | 0.00203  | 0.01907  | -2.9983 |
| CPA1     | 0.67519 | 0.3376  | 8.02904 | 9.09E-06 | 0.00019  | 2.77529 |
| STAU2-A  | 0.67691 | 0.38863 | 5.75253 | 0.00016  | 0.00224  | -0.3076 |
| FOXO1B   | 0.67771 | 0.58504 | 4.8758  | 0.00058  | 0.0068   | -1.6777 |
| WWC2-A   | 0.67806 | 0.88715 | 4.42477 | 0.00117  | 0.01212  | -2.4221 |
| CRMA     | 0.6784  | 0.3392  | 11.5081 | 3.09E-07 | 1.02E-05 | 6.43401 |
| MIR130A  | 0.67861 | 1.6625  | 8.82354 | 3.83E-06 | 9.02E-05 | 3.70817 |
| BMP4     | 0.67914 | 0.43991 | 6.30675 | 7.50E-05 | 0.00116  | 0.50428 |
| FERMT2   | 0.68053 | 3.70784 | 18.1131 | 3.44E-09 | 2.38E-07 | 11.2942 |
| KHDRBS1  | 0.68076 | 0.34038 | 9.2698  | 2.42E-06 | 6.03E-05 | 4.20426 |
| OR2B6    | 0.6834  | 0.39187 | 7.70015 | 1.32E-05 | 0.00026  | 2.36915 |
| CAV1     | 0.6838  | 1.19753 | 9.55993 | 1.81E-06 | 4.70E-05 | 4.51675 |
| DISC1FP  | 0.68429 | 0.34215 | 7.43209 | 1.82E-05 | 0.00035  | 2.02894 |
| PTGER2   | 0.68429 | 0.44249 | 7.16456 | 2.51E-05 | 0.00046  | 1.68087 |
| MIR17HG  | 0.68463 | 2.13203 | 12.1015 | 1.89E-07 | 6.73E-06 | 6.96281 |
| TBC1D8E  | 0.68463 | 1.30788 | 7.8732  | 1.08E-05 | 0.00022  | 2.58437 |
| MACIR    | 0.6849  | 2.04468 | 15.0079 | 2.27E-08 | 1.10E-06 | 9.259   |
| HHLA2    | 0.68665 | 0.34332 | 13.948  | 4.69E-08 | 2.04E-06 | 8.4727  |
| DDO      | 0.68693 | 0.34346 | 10.0116 | 1.17E-06 | 3.24E-05 | 4.98837 |
| STYXL2   | 0.68693 | 0.34346 | 10.0116 | 1.17E-06 | 3.24E-05 | 4.98837 |
| HHIP     | 0.68702 | 1.02983 | 9.5609  | 1.81E-06 | 4.70E-05 | 4.51779 |
| SCIRT    | 0.68737 | 0.50273 | 5.28897 | 0.00031  | 0.00402  | -1.019  |
| LINC0185 | 0.68744 | 1.05646 | 10.605  | 6.78E-07 | 2.01E-05 | 5.58206 |
| NR3C1    | 0.68807 | 0.42355 | 6.22776 | 8.34E-05 | 0.00127  | 0.39109 |
| SHISA3   | 0.6884  | 1.98853 | 9.01887 | 3.13E-06 | 7.56E-05 | 3.92767 |
| LINC0103 | 0.69011 | 0.4454  | 5.90327 | 0.00013  | 0.00186  | -0.0827 |
| GNG11    | 0.69029 | 0.34515 | 4.81698 | 0.00064  | 0.00731  | -1.7733 |
| HEPH     | 0.69062 | 0.49582 | 5.5969  | 0.0002   | 0.00272  | -0.5431 |
| SCN2A    | 0.69092 | 2.06549 | 16.3764 | 9.49E-09 | 5.40E-07 | 10.201  |
| RBM20    | 0.69101 | 0.44585 | 5.60957 | 0.0002   | 0.00268  | -0.5238 |
| SPATA46  | 0.6916  | 0.3458  | 7.06971 | 2.82E-05 | 0.0005   | 1.55538 |
| CALD1    | 0.69183 | 3.15582 | 13.2719 | 7.66E-08 | 3.09E-06 | 7.94195 |
| GRIK2    | 0.69295 | 1.24112 | 7.88624 | 1.07E-05 | 0.00022  | 2.60046 |
| ADD3-AS1 | 0.69306 | 0.34653 | 7.38209 | 1.93E-05 | 0.00037  | 1.96455 |
| FGF21    | 0.69325 | 0.57666 | 5.71041 | 0.00017  | 0.00236  | -0.371  |
| ZNF860   | 0.69325 | 0.39193 | 7.77476 | 1.21E-05 | 0.00024  | 2.46236 |
| ERVV-1   | 0.69399 | 0.39717 | 6.46865 | 6.06E-05 | 0.00096  | 0.73364 |
| HOXB6    | 0.6941  | 1.66961 | 6.96381 | 3.22E-05 | 0.00056  | 1.41393 |
| HLA-DOA  | 0.69418 | 0.41046 | 6.15578 | 9.18E-05 | 0.00138  | 0.28724 |
| PATL2    | 0.6951  | 0.87394 | 4.44991 | 0.00113  | 0.01179  | -2.38   |
| TEX19    | 0.69575 | 1.45439 | 5.03423 | 0.00046  | 0.00554  | -1.4224 |
| PDLIM3   | 0.69922 | 0.34961 | 4.97621 | 0.0005   | 0.00596  | -1.5155 |
| RPL12P7  | 0.69955 | 0.34977 | 14.0797 | 4.28E-08 | 1.88E-06 | 8.57335 |
| HOXB4    | 0.70033 | 1.93549 | 4.58023 | 0.00092  | 0.00997  | -2.1627 |
| EPHA5-A  | 0.70126 | 0.45098 | 7.88437 | 1.07E-05 | 0.00022  | 2.59815 |
| RNU6-27  | 0.70126 | 0.35063 | 7.93245 | 1.01E-05 | 0.00021  | 2.65728 |
| LINC0127 | 0.70159 | 0.35079 | 5.4826  | 0.00024  | 0.00315  | -0.7182 |
| LAMA4    | 0.70422 | 0.35211 | 11.2735 | 3.77E-07 | 1.21E-05 | 6.21831 |
| LINC0298 | 0.70422 | 0.35211 | 11.2735 | 3.77E-07 | 1.21E-05 | 6.21831 |
| LRG1     | 0.70422 | 0.5528  | 5.93349 | 0.00012  | 0.0018   | -0.0379 |
| PAPPA2   | 0.70422 | 0.35211 | 7.34907 | 2.01E-05 | 0.00038  | 1.92185 |
| ACHE     | 0.70508 | 0.99044 | 4.70414 | 0.00076  | 0.00847  | -1.958  |
| EDIL3-DT | 0.70512 | 0.35256 | 9.0017  | 3.18E-06 | 7.67E-05 | 3.90852 |
| H3P21    | 0.70626 | 0.35313 | 12.5048 | 1.37E-07 | 5.06E-06 | 7.30945 |
| PNMA8B   | 0.70626 | 0.4033  | 7.6863  | 1.35E-05 | 0.00027  | 2.35178 |
| GRAPLD1  | 0.70679 | 0.46819 | 7.2567  | 2.24E-05 | 0.00042  | 1.80173 |
| LUM      | 0.70681 | 1.2711  | 10.8998 | 5.21E-07 | 1.59E-05 | 5.86678 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| PTBP2    | 0.70694 | 2.55952 | 15.1698 | 2.04E-08 | 1.01E-06 | 9.37458 |
| CD207    | 0.70738 | 0.40386 | 7.34286 | 2.02E-05 | 0.00038  | 1.91381 |
| SYNPO2   | 0.70802 | 1.37554 | 9.57588 | 1.79E-06 | 4.64E-05 | 4.53372 |
| CNTNAP3  | 0.7093  | 1.29631 | 11.7958 | 2.43E-07 | 8.31E-06 | 6.6933  |
| DSCAS    | 0.70979 | 0.35489 | 6.77832 | 4.06E-05 | 0.00069  | 1.16278 |
| FGF14    | 0.70979 | 0.35489 | 9.51296 | 1.90E-06 | 4.90E-05 | 4.46669 |
| NAV3     | 0.71044 | 1.76304 | 11.4845 | 3.15E-07 | 1.04E-05 | 6.41246 |
| MIR34AH  | 0.71097 | 1.01737 | 4.01006 | 0.0023   | 0.02116  | -3.1276 |
| SPARCL1  | 0.71127 | 1.22946 | 9.05685 | 3.01E-06 | 7.31E-05 | 3.96992 |
| STX1B    | 0.71225 | 1.22232 | 5.39177 | 0.00027  | 0.00351  | -0.8587 |
| H2BC11   | 0.71307 | 1.29737 | 8.58247 | 4.95E-06 | 0.00011  | 3.43204 |
| EXPH5    | 0.71354 | 0.50729 | 8.20789 | 7.44E-06 | 0.00016  | 2.99112 |
| RAB9B    | 0.71401 | 0.86258 | 11.3251 | 3.60E-07 | 1.17E-05 | 6.26613 |
| IGSF1    | 0.71448 | 0.61663 | 5.90615 | 0.00013  | 0.00186  | -0.0784 |
| PRAMEF   | 0.71478 | 0.35739 | 7.9123  | 1.04E-05 | 0.00021  | 2.63253 |
| PLCH1    | 0.71539 | 1.99301 | 8.45479 | 5.68E-06 | 0.00013  | 3.2834  |
| CNDP1    | 0.71593 | 0.83419 | 7.6394  | 1.42E-05 | 0.00028  | 2.29279 |
| CACNG6   | 0.71611 | 0.40823 | 7.05096 | 2.89E-05 | 0.00051  | 1.53044 |
| KCNC1    | 0.71628 | 0.61752 | 5.81353 | 0.00015  | 0.00208  | -0.2162 |
| FZD2     | 0.71656 | 2.19373 | 3.39311 | 0.00651  | 0.04985  | -4.2044 |
| PRTG     | 0.71738 | 3.04877 | 16.5945 | 8.31E-09 | 4.84E-07 | 10.3442 |
| ADGRF1   | 0.71742 | 0.40888 | 11.0078 | 4.74E-07 | 1.46E-05 | 5.96937 |
| CARMN    | 0.71742 | 0.45905 | 8.27116 | 6.94E-06 | 0.00015  | 3.06663 |
| LINC0162 | 0.71742 | 0.35871 | 11.9254 | 2.18E-07 | 7.60E-06 | 6.80828 |
| SYBU     | 0.71742 | 0.43823 | 6.75426 | 4.19E-05 | 0.0007   | 1.12989 |
| CBR3     | 0.71774 | 1.16433 | 10.6322 | 6.61E-07 | 1.97E-05 | 5.60865 |
| CFAP91   | 0.71774 | 0.35887 | 7.48039 | 1.71E-05 | 0.00033  | 2.09087 |
| HLA-G    | 0.71843 | 1.25039 | 4.58675 | 0.00091  | 0.00989  | -2.1519 |
| RIGI     | 0.71882 | 2.22479 | 11.4923 | 3.13E-07 | 1.03E-05 | 6.41954 |
| SLC25A2  | 0.71962 | 2.3779  | 15.489  | 1.66E-08 | 8.57E-07 | 9.59905 |
| HOXB5    | 0.71978 | 1.69713 | 6.94303 | 3.30E-05 | 0.00057  | 1.38601 |
| ZNF736   | 0.7213  | 0.41772 | 9.12209 | 2.81E-06 | 6.88E-05 | 4.04216 |
| IRF9     | 0.72172 | 2.52231 | 7.66738 | 1.38E-05 | 0.00027  | 2.32801 |
| USP41    | 0.72204 | 1.24456 | 6.77942 | 4.06E-05 | 0.00068  | 1.16428 |
| BTG4     | 0.72241 | 0.41138 | 7.73504 | 1.27E-05 | 0.00025  | 2.41283 |
| NFIA     | 0.72321 | 0.46195 | 6.95136 | 3.27E-05 | 0.00057  | 1.39721 |
| GREB1L   | 0.72577 | 0.8523  | 7.37058 | 1.95E-05 | 0.00037  | 1.94967 |
| TRIM15   | 0.72594 | 0.36297 | 11.8796 | 2.27E-07 | 7.84E-06 | 6.76782 |
| ADM      | 0.72861 | 1.76788 | 7.03835 | 2.93E-05 | 0.00052  | 1.51363 |
| DNAJA1F  | 0.72919 | 3.03076 | 13.9279 | 4.76E-08 | 2.06E-06 | 8.45729 |
| ASB9     | 0.72931 | 0.41483 | 8.02168 | 9.16E-06 | 0.00019  | 2.76634 |
| FNBP1L   | 0.73055 | 2.49658 | 17.3214 | 5.40E-09 | 3.40E-07 | 10.8089 |
| RIC3-DT  | 0.73061 | 0.36531 | 11.3863 | 3.42E-07 | 1.11E-05 | 6.3225  |
| PHGDH    | 0.73181 | 3.29877 | 8.69108 | 4.41E-06 | 0.0001   | 3.55717 |
| SCG2     | 0.73284 | 0.54628 | 8.05651 | 8.81E-06 | 0.00019  | 2.80867 |
| TRIM51B  | 0.73321 | 0.36661 | 9.03498 | 3.08E-06 | 7.46E-05 | 3.94561 |
| PTPRR    | 0.73357 | 0.41696 | 8.32783 | 6.52E-06 | 0.00014  | 3.13391 |
| CCDC160  | 0.73369 | 1.40609 | 9.04219 | 3.05E-06 | 7.41E-05 | 3.95362 |
| LINC0230 | 0.73443 | 0.84344 | 9.48824 | 1.95E-06 | 5.00E-05 | 4.44025 |
| VLDLR-A  | 0.73451 | 1.73821 | 7.4544  | 1.77E-05 | 0.00034  | 2.05757 |
| MYOF     | 0.73483 | 1.33608 | 5.84575 | 0.00014  | 0.002    | -0.1681 |
| SPTSSB   | 0.73506 | 0.36753 | 12.6282 | 1.25E-07 | 4.65E-06 | 7.41348 |
| MTMR9L   | 0.73518 | 1.51608 | 7.03585 | 2.94E-05 | 0.00052  | 1.5103  |
| BAALC-A  | 0.73536 | 0.93458 | 7.30564 | 2.11E-05 | 0.0004   | 1.8655  |
| BMF      | 0.73553 | 0.93803 | 3.54475 | 0.00502  | 0.04037  | -3.9377 |
| PPP1R3A  | 0.73561 | 0.3678  | 8.46246 | 5.63E-06 | 0.00013  | 3.29238 |
| TNC      | 0.7371  | 1.30434 | 7.22032 | 2.34E-05 | 0.00043  | 1.75414 |
| BMP5     | 0.73795 | 0.82905 | 7.77042 | 1.22E-05 | 0.00024  | 2.45695 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| FGG      | 0.73813 | 1.66787 | 16.7959 | 7.36E-09 | 4.40E-07 | 10.4749 |
| RBM11    | 0.73824 | 0.46946 | 8.03889 | 8.99E-06 | 0.00019  | 2.78727 |
| AK3P5    | 0.73904 | 0.52856 | 6.77706 | 4.07E-05 | 0.00069  | 1.16106 |
| LINC0068 | 0.73914 | 0.41974 | 5.11474 | 0.0004   | 0.00499  | -1.2939 |
| SLC6A20  | 0.73967 | 0.42001 | 8.21419 | 7.39E-06 | 0.00016  | 2.99866 |
| NTRK3    | 0.74119 | 0.3706  | 4.86636 | 0.00059  | 0.00689  | -1.693  |
| SOX2     | 0.74323 | 0.37162 | 11.6329 | 2.78E-07 | 9.37E-06 | 6.54713 |
| ASB2     | 0.74472 | 0.45188 | 8.45659 | 5.67E-06 | 0.00013  | 3.28551 |
| RUNX1    | 0.74547 | 0.83576 | 8.59548 | 4.88E-06 | 0.00011  | 3.44709 |
| PKD1L2   | 0.74572 | 0.38606 | 7.25307 | 2.25E-05 | 0.00042  | 1.79699 |
| FUT1     | 0.7466  | 1.00004 | 5.96604 | 0.00012  | 0.00173  | 0.0101  |
| TGFB2-O  | 0.74676 | 0.37338 | 22.0037 | 4.80E-10 | 4.87E-08 | 13.4134 |
| XKR5     | 0.7474  | 1.38617 | 7.31433 | 2.09E-05 | 0.00039  | 1.8768  |
| MBD3L4   | 0.74757 | 0.37378 | 14.8787 | 2.47E-08 | 1.19E-06 | 9.16594 |
| MRPL35F  | 0.74823 | 0.63509 | 6.72517 | 4.35E-05 | 0.00073  | 1.09    |
| MIX23P2  | 0.7503  | 0.37515 | 10.2334 | 9.52E-07 | 2.71E-05 | 5.21365 |
| ACOX2    | 0.75098 | 0.42566 | 10.5625 | 7.04E-07 | 2.08E-05 | 5.54045 |
| NOVA2    | 0.75106 | 1.47728 | 6.41344 | 6.51E-05 | 0.00102  | 0.65581 |
| MAML2    | 0.75123 | 0.65399 | 7.44551 | 1.79E-05 | 0.00034  | 2.04617 |
| TSPAN6   | 0.75184 | 2.96946 | 15.6017 | 1.54E-08 | 8.10E-07 | 9.67727 |
| FBXO15   | 0.75484 | 0.81667 | 7.68603 | 1.35E-05 | 0.00027  | 2.35144 |
| RGS21    | 0.75529 | 0.37764 | 9.63552 | 1.68E-06 | 4.41E-05 | 4.59693 |
| TRIM6    | 0.75551 | 2.06332 | 8.71209 | 4.31E-06 | 9.99E-05 | 3.58124 |
| MEG3     | 0.75588 | 0.37794 | 6.82712 | 3.82E-05 | 0.00065  | 1.22928 |
| PPP3R2   | 0.75643 | 0.37821 | 12.6063 | 1.27E-07 | 4.72E-06 | 7.39507 |
| LINC0180 | 0.75747 | 1.04894 | 11.4294 | 3.30E-07 | 1.08E-05 | 6.36204 |
| ITPRID2- | 0.75792 | 0.37896 | 10.041  | 1.14E-06 | 3.16E-05 | 5.0185  |
| GDAP1    | 0.75925 | 2.84837 | 20.1733 | 1.16E-09 | 9.63E-08 | 12.4667 |
| FABP9    | 0.75996 | 0.43015 | 8.90496 | 3.52E-06 | 8.36E-05 | 3.80011 |
| HNRNPC   | 0.7609  | 1.08191 | 6.98209 | 3.14E-05 | 0.00055  | 1.43844 |
| H3C6     | 0.76099 | 1.12463 | 9.68383 | 1.61E-06 | 4.24E-05 | 4.64789 |
| DSG2-AS  | 0.76259 | 0.43147 | 11.3906 | 3.41E-07 | 1.11E-05 | 6.32647 |
| RGS8     | 0.76292 | 0.38146 | 9.5932  | 1.76E-06 | 4.58E-05 | 4.55211 |
| MBD3L3   | 0.76327 | 0.38164 | 12.8114 | 1.08E-07 | 4.15E-06 | 7.56628 |
| SLC17A6  | 0.76345 | 0.69128 | 7.96954 | 9.72E-06 | 0.0002   | 2.70272 |
| NLGN1    | 0.76366 | 0.98774 | 7.82555 | 1.15E-05 | 0.00023  | 2.52545 |
| HMG5     | 0.7641  | 2.40794 | 15.5708 | 1.57E-08 | 8.23E-07 | 9.65589 |
| COBLL1   | 0.76448 | 2.12028 | 14.2345 | 3.84E-08 | 1.72E-06 | 8.69053 |
| LRRC8D-  | 0.76575 | 0.53339 | 6.57299 | 5.29E-05 | 0.00086  | 0.87963 |
| PRKN     | 0.76628 | 0.43331 | 9.90191 | 1.30E-06 | 3.55E-05 | 4.87545 |
| SLC6A15  | 0.76628 | 0.38314 | 8.62741 | 4.71E-06 | 0.00011  | 3.48396 |
| LRRK2    | 0.76715 | 1.09836 | 9.93876 | 1.26E-06 | 3.44E-05 | 4.9135  |
| ADAM12   | 0.76791 | 0.38395 | 10.0219 | 1.16E-06 | 3.21E-05 | 4.9989  |
| APOBEC   | 0.76805 | 1.42731 | 8.28595 | 6.83E-06 | 0.00015  | 3.08423 |
| CTSLP4   | 0.76929 | 0.38464 | 16.9361 | 6.77E-09 | 4.11E-07 | 10.565  |
| INHBE    | 0.76963 | 2.12433 | 8.3567  | 6.32E-06 | 0.00014  | 3.16805 |
| CACNA1B  | 0.77035 | 1.78141 | 7.23924 | 2.29E-05 | 0.00042  | 1.7789  |
| GABARA   | 0.77068 | 1.6459  | 10.187  | 9.95E-07 | 2.81E-05 | 5.16683 |
| SERP2    | 0.77258 | 0.38629 | 11.192  | 4.04E-07 | 1.27E-05 | 6.14253 |
| TNIK     | 0.77258 | 0.53681 | 7.26753 | 2.21E-05 | 0.00041  | 1.81587 |
| LOXL4    | 0.77346 | 1.0038  | 7.68668 | 1.35E-05 | 0.00027  | 2.35225 |
| TMPRSS   | 0.77367 | 1.0212  | 8.06888 | 8.69E-06 | 0.00018  | 2.82367 |
| SCN1A    | 0.77496 | 1.02021 | 14.5318 | 3.13E-08 | 1.46E-06 | 8.91239 |
| MIR8089  | 0.77521 | 0.38761 | 15.3685 | 1.79E-08 | 9.14E-07 | 9.51482 |
| KRTAP19  | 0.77611 | 0.38806 | 7.22027 | 2.34E-05 | 0.00043  | 1.75407 |
| SLC38A5  | 0.7762  | 1.10552 | 8.77178 | 4.05E-06 | 9.43E-05 | 3.64938 |
| COL6A6   | 0.77654 | 0.56813 | 5.86745 | 0.00014  | 0.00195  | -0.1358 |
| ZIC2     | 0.77665 | 0.51802 | 6.09542 | 9.97E-05 | 0.00148  | 0.1996  |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| MDM1     | 0.77668 | 2.67964 | 12.1067 | 1.89E-07 | 6.71E-06 | 6.96737 |
| CSF1     | 0.77728 | 1.89426 | 6.5664  | 5.33E-05 | 0.00086  | 0.87045 |
| MGAT4A   | 0.77838 | 0.96871 | 9.4865  | 1.95E-06 | 5.01E-05 | 4.43839 |
| KYAT3    | 0.77968 | 2.63038 | 15.4957 | 1.65E-08 | 8.54E-07 | 9.60373 |
| SP100    | 0.77971 | 1.96525 | 13.3986 | 6.98E-08 | 2.87E-06 | 8.04332 |
| OSBPL10  | 0.77979 | 1.26972 | 8.08056 | 8.58E-06 | 0.00018  | 2.83782 |
| ANO5     | 0.78061 | 1.08337 | 10.4294 | 7.95E-07 | 2.32E-05 | 5.40931 |
| FBXO39   | 0.78078 | 0.49074 | 5.73584 | 0.00016  | 0.00229  | -0.3327 |
| ZNF614   | 0.78083 | 0.39042 | 4.84094 | 0.00061  | 0.00709  | -1.7343 |
| PLOD2    | 0.78154 | 1.63162 | 15.0806 | 2.16E-08 | 1.06E-06 | 9.31102 |
| TRIM43   | 0.78281 | 0.3914  | 19.3215 | 1.79E-09 | 1.38E-07 | 11.9968 |
| EFNA5    | 0.78285 | 1.46433 | 9.84978 | 1.37E-06 | 3.71E-05 | 4.82144 |
| THRB-AS  | 0.78301 | 0.39151 | 9.18389 | 2.64E-06 | 6.53E-05 | 4.11023 |
| APLF     | 0.78372 | 0.87161 | 7.61995 | 1.45E-05 | 0.00029  | 2.26825 |
| NPY1R    | 0.78374 | 0.54238 | 9.80538 | 1.43E-06 | 3.85E-05 | 4.77524 |
| TRIM10   | 0.78415 | 0.39208 | 9.28685 | 2.38E-06 | 5.94E-05 | 4.22284 |
| LRRN3    | 0.78455 | 1.71228 | 14.6195 | 2.94E-08 | 1.38E-06 | 8.97702 |
| YPEL4    | 0.78493 | 1.81139 | 8.77888 | 4.02E-06 | 9.39E-05 | 3.65745 |
| FSIP2    | 0.7863  | 0.72799 | 5.74639 | 0.00016  | 0.00226  | -0.3168 |
| XCR1     | 0.78668 | 0.44351 | 12.839  | 1.06E-07 | 4.08E-06 | 7.5892  |
| MIR548A  | 0.78711 | 0.39355 | 7.24348 | 2.28E-05 | 0.00042  | 1.78445 |
| RASGRP   | 0.7878  | 1.1873  | 9.15869 | 2.71E-06 | 6.66E-05 | 4.08252 |
| AKAP6    | 0.78996 | 1.03024 | 8.12904 | 8.12E-06 | 0.00017  | 2.8964  |
| CERKL    | 0.79064 | 0.39532 | 7.42053 | 1.84E-05 | 0.00035  | 2.01408 |
| ARID3A   | 0.79141 | 2.63076 | 5.10767 | 0.00041  | 0.00504  | -1.3052 |
| PANTR1   | 0.79194 | 0.39597 | 18.9361 | 2.20E-09 | 1.63E-07 | 11.7775 |
| ERRFI1   | 0.79234 | 2.48185 | 14.0955 | 4.23E-08 | 1.86E-06 | 8.58541 |
| BTN3A3   | 0.79237 | 1.96847 | 9.15645 | 2.72E-06 | 6.67E-05 | 4.08006 |
| NWD2     | 0.79268 | 0.44651 | 8.02981 | 9.08E-06 | 0.00019  | 2.77623 |
| TMEM170  | 0.79386 | 1.19536 | 13.4092 | 6.92E-08 | 2.86E-06 | 8.05173 |
| RNVU1-4  | 0.7949  | 0.46377 | 9.81353 | 1.42E-06 | 3.82E-05 | 4.78374 |
| NMI      | 0.79551 | 2.29545 | 11.2711 | 3.77E-07 | 1.21E-05 | 6.21615 |
| LNC-LBC  | 0.7966  | 1.67299 | 6.14238 | 9.35E-05 | 0.0014   | 0.26782 |
| LINC0204 | 0.79694 | 0.39847 | 10.7658 | 5.87E-07 | 1.77E-05 | 5.73818 |
| FRAS1    | 0.79806 | 0.49937 | 7.24261 | 2.28E-05 | 0.00042  | 1.78331 |
| ETV1     | 0.79904 | 2.14942 | 10.1262 | 1.05E-06 | 2.96E-05 | 5.10526 |
| CSH1     | 0.79942 | 0.39971 | 9.11036 | 2.85E-06 | 6.95E-05 | 4.02921 |
| RGS3     | 0.79954 | 2.64935 | 7.47875 | 1.72E-05 | 0.00033  | 2.08876 |
| MGP      | 0.79987 | 2.32918 | 23.2543 | 2.73E-10 | 3.14E-08 | 14.016  |
| CHRNA9   | 0.79989 | 0.39995 | 17.723  | 4.29E-09 | 2.83E-07 | 11.0577 |
| GASK1A   | 0.8003  | 0.50049 | 8.91321 | 3.49E-06 | 8.30E-05 | 3.80939 |
| POTEC    | 0.80033 | 0.40017 | 11.8072 | 2.41E-07 | 8.24E-06 | 6.70341 |
| OLFML3   | 0.80353 | 0.65262 | 6.086   | 0.0001   | 0.0015   | 0.18589 |
| ADPRHL1  | 0.80358 | 1.02576 | 4.67679 | 0.00079  | 0.00877  | -2.003  |
| CBLC     | 0.80387 | 0.40193 | 8.68556 | 4.43E-06 | 0.0001   | 3.55085 |
| LINC0303 | 0.8044  | 0.53189 | 8.15568 | 7.89E-06 | 0.00017  | 2.92847 |
| FABP3    | 0.80531 | 1.44034 | 9.85756 | 1.36E-06 | 3.69E-05 | 4.82951 |
| NFE2     | 0.8054  | 1.39565 | 7.94879 | 9.95E-06 | 0.00021  | 2.67732 |
| TNS3     | 0.80594 | 1.39495 | 6.82919 | 3.81E-05 | 0.00065  | 1.2321  |
| H2BC12   | 0.8077  | 2.14511 | 6.53954 | 5.52E-05 | 0.00089  | 0.83298 |
| CLYBL    | 0.80873 | 1.18048 | 9.85549 | 1.36E-06 | 3.70E-05 | 4.82736 |
| CA14     | 0.80876 | 2.53605 | 10.6138 | 6.72E-07 | 2.00E-05 | 5.59066 |
| ZNF516-A | 0.8093  | 1.08498 | 7.46329 | 1.75E-05 | 0.00034  | 2.06898 |
| KCNK2    | 0.80956 | 0.55529 | 7.40068 | 1.89E-05 | 0.00036  | 1.98852 |
| GNG2     | 0.81013 | 0.40507 | 13.0492 | 9.05E-08 | 3.57E-06 | 7.76182 |
| NFKBIZ   | 0.81137 | 2.23157 | 14.5431 | 3.10E-08 | 1.45E-06 | 8.92075 |
| CXADRP   | 0.81199 | 0.5045  | 7.86685 | 1.09E-05 | 0.00022  | 2.57653 |
| EBF3     | 0.81423 | 0.40711 | 7.20839 | 2.38E-05 | 0.00044  | 1.73849 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| SERPINC  | 0.81488 | 2.47005 | 7.79167 | 1.19E-05 | 0.00024  | 2.4834  |
| SESN3    | 0.81499 | 0.57416 | 6.63934 | 4.85E-05 | 0.00079  | 0.97172 |
| FLG-AS1  | 0.81502 | 0.68771 | 7.54753 | 1.58E-05 | 0.00031  | 2.17649 |
| KIF25    | 0.81513 | 0.40756 | 5.39091 | 0.00027  | 0.00352  | -0.86   |
| HOXB7    | 0.81559 | 1.36219 | 7.29086 | 2.15E-05 | 0.0004   | 1.84628 |
| RNF144B  | 0.81604 | 0.45819 | 10.8695 | 5.35E-07 | 1.63E-05 | 5.83777 |
| TTYH1    | 0.81679 | 1.07538 | 5.34935 | 0.00029  | 0.0037   | -0.9246 |
| MYL7     | 0.81776 | 0.40888 | 25.2835 | 1.16E-10 | 1.64E-08 | 14.9276 |
| MYOT     | 0.81869 | 0.7644  | 7.49875 | 1.68E-05 | 0.00033  | 2.11433 |
| BCAN     | 0.81888 | 0.55996 | 5.90023 | 0.00013  | 0.00187  | -0.0872 |
| COLEC11  | 0.81907 | 0.78541 | 4.59951 | 0.00089  | 0.00972  | -2.1307 |
| SYT4     | 0.81952 | 0.97666 | 5.97182 | 0.00012  | 0.00172  | 0.01862 |
| HLA-DRB  | 0.81991 | 0.56047 | 9.86424 | 1.35E-06 | 3.67E-05 | 4.83644 |
| LINC0238 | 0.82071 | 0.41036 | 10.8838 | 5.28E-07 | 1.61E-05 | 5.8515  |
| USP51    | 0.82095 | 2.05106 | 18.4069 | 2.93E-09 | 2.09E-07 | 11.4691 |
| SLC16A4  | 0.82252 | 1.76536 | 10.0353 | 1.15E-06 | 3.17E-05 | 5.01265 |
| CNTN6    | 0.82314 | 0.96731 | 11.9688 | 2.11E-07 | 7.38E-06 | 6.84653 |
| COL9A1   | 0.82408 | 0.41204 | 11.3183 | 3.62E-07 | 1.17E-05 | 6.25984 |
| LINC0177 | 0.82433 | 0.41216 | 11.4664 | 3.20E-07 | 1.05E-05 | 6.39591 |
| ATCAY    | 0.82467 | 0.56285 | 6.50649 | 5.76E-05 | 0.00092  | 0.78675 |
| GPR84    | 0.82527 | 0.85188 | 7.30772 | 2.11E-05 | 0.0004   | 1.8682  |
| CLDN6    | 0.8255  | 0.66361 | 6.95641 | 3.25E-05 | 0.00057  | 1.404   |
| PDCD4-A  | 0.82559 | 0.83885 | 6.11056 | 9.77E-05 | 0.00145  | 0.22163 |
| IGF1R    | 0.82601 | 1.68305 | 9.49525 | 1.93E-06 | 4.97E-05 | 4.44776 |
| TEX11    | 0.82855 | 0.51462 | 9.08386 | 2.92E-06 | 7.13E-05 | 3.99987 |
| AGPAT4   | 0.8289  | 1.6934  | 7.23208 | 2.31E-05 | 0.00043  | 1.76954 |
| SIPA1L2  | 0.82962 | 0.6742  | 6.92283 | 3.38E-05 | 0.00059  | 1.35881 |
| SLC27A6  | 0.82986 | 1.08217 | 8.02988 | 9.08E-06 | 0.00019  | 2.77632 |
| H4C9     | 0.8322  | 2.25196 | 16.6274 | 8.15E-09 | 4.76E-07 | 10.3657 |
| ZSCAN4   | 0.83481 | 0.46758 | 7.27387 | 2.20E-05 | 0.00041  | 1.82413 |
| ATF3     | 0.83531 | 1.73592 | 9.9109  | 1.29E-06 | 3.53E-05 | 4.88475 |
| SPOCK2   | 0.83637 | 0.90293 | 6.67031 | 4.66E-05 | 0.00077  | 1.01451 |
| TCN2     | 0.8364  | 0.64824 | 5.44664 | 0.00025  | 0.0033   | -0.7737 |
| PDE4C    | 0.83707 | 1.37048 | 7.82654 | 1.14E-05 | 0.00023  | 2.52668 |
| BDNF-AS  | 0.83941 | 0.75304 | 6.56109 | 5.37E-05 | 0.00087  | 0.86305 |
| LINC0220 | 0.83944 | 0.54941 | 7.27418 | 2.20E-05 | 0.00041  | 1.82455 |
| LINC0260 | 0.84058 | 1.16148 | 11.6859 | 2.66E-07 | 9.00E-06 | 6.59485 |
| BEND4    | 0.84307 | 2.2779  | 17.6293 | 4.52E-09 | 2.96E-07 | 11.0002 |
| TBX15    | 0.84324 | 0.42162 | 14.6892 | 2.81E-08 | 1.33E-06 | 9.02812 |
| CABP1    | 0.84413 | 0.99863 | 7.22551 | 2.33E-05 | 0.00043  | 1.76093 |
| FCGR2A   | 0.8458  | 0.47307 | 10.393  | 8.22E-07 | 2.38E-05 | 5.37322 |
| PCDH19   | 0.84597 | 1.75866 | 11.8963 | 2.24E-07 | 7.75E-06 | 6.78256 |
| HMGB3P   | 0.84711 | 0.42355 | 12.184  | 1.77E-07 | 6.36E-06 | 7.03453 |
| TSGA10   | 0.84732 | 1.22676 | 15.2458 | 1.94E-08 | 9.72E-07 | 9.42839 |
| HOXD-AS  | 0.84754 | 0.42377 | 8.69252 | 4.40E-06 | 0.0001   | 3.55882 |
| SH3BGR   | 0.84877 | 2.01549 | 16.0285 | 1.18E-08 | 6.46E-07 | 9.96879 |
| LINC0298 | 0.84982 | 0.65495 | 5.93176 | 0.00012  | 0.0018   | -0.0405 |
| FYN      | 0.85015 | 1.20456 | 6.98764 | 3.12E-05 | 0.00055  | 1.44588 |
| MBD3L2E  | 0.85115 | 0.42557 | 14.2423 | 3.82E-08 | 1.72E-06 | 8.69642 |
| SPP1     | 0.85116 | 1.29555 | 12.2939 | 1.62E-07 | 5.92E-06 | 7.12939 |
| SCN3A    | 0.85139 | 2.22088 | 18.9403 | 2.19E-09 | 1.63E-07 | 11.7798 |
| MSRB3-A  | 0.85237 | 1.46078 | 14.8869 | 2.46E-08 | 1.18E-06 | 9.17191 |
| DCC      | 0.8538  | 0.47707 | 11.9168 | 2.20E-07 | 7.64E-06 | 6.80068 |
| SYT16    | 0.85416 | 1.35857 | 11.4803 | 3.16E-07 | 1.04E-05 | 6.40866 |
| ZBTB20   | 0.85456 | 0.86653 | 7.25082 | 2.26E-05 | 0.00042  | 1.79404 |
| ZNF781   | 0.85504 | 1.23988 | 8.81738 | 3.86E-06 | 9.06E-05 | 3.70119 |
| PAX9     | 0.85525 | 1.67188 | 8.73922 | 4.19E-06 | 9.72E-05 | 3.61225 |
| HIF3A    | 0.85627 | 0.45748 | 7.13138 | 2.61E-05 | 0.00047  | 1.6371  |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| DNAH7    | 0.8568  | 0.80428 | 7.35054 | 2.00E-05 | 0.00038  | 1.92375 |
| DISC1    | 0.85731 | 1.37814 | 5.6387  | 0.00019  | 0.00258  | -0.4796 |
| HLA-DME  | 0.85765 | 0.81586 | 6.53603 | 5.55E-05 | 0.00089  | 0.82808 |
| IFIT3    | 0.85866 | 2.5206  | 29.1605 | 2.70E-11 | 5.44E-09 | 16.4774 |
| ICA1     | 0.85894 | 0.70968 | 7.92162 | 1.03E-05 | 0.00021  | 2.64399 |
| ETV7     | 0.85973 | 0.42986 | 16.9175 | 6.85E-09 | 4.14E-07 | 10.5531 |
| ZDBF2    | 0.86069 | 0.71055 | 7.04893 | 2.89E-05 | 0.00052  | 1.52773 |
| PIFO     | 0.86152 | 0.9997  | 11.9866 | 2.08E-07 | 7.29E-06 | 6.86225 |
| RASGRP   | 0.86204 | 2.15477 | 7.6008  | 1.49E-05 | 0.00029  | 2.24404 |
| PLP1     | 0.86326 | 0.51115 | 7.38002 | 1.93E-05 | 0.00037  | 1.96187 |
| LINC0226 | 0.86358 | 0.43179 | 10.8999 | 5.21E-07 | 1.59E-05 | 5.86684 |
| MUC19    | 0.86496 | 1.20343 | 7.77463 | 1.21E-05 | 0.00024  | 2.4622  |
| MBD3L2   | 0.8651  | 0.43255 | 32.1329 | 9.95E-12 | 2.72E-09 | 17.5263 |
| ITGA2    | 0.86695 | 1.06021 | 12.7983 | 1.10E-07 | 4.18E-06 | 7.55542 |
| SLITRK6  | 0.86905 | 0.43453 | 11.2679 | 3.78E-07 | 1.21E-05 | 6.21311 |
| LINC0197 | 0.86933 | 0.64388 | 6.50966 | 5.74E-05 | 0.00092  | 0.79119 |
| IL15     | 0.87267 | 0.43634 | 10.5024 | 7.44E-07 | 2.19E-05 | 5.48147 |
| GCNT1    | 0.87405 | 0.53737 | 7.3554  | 1.99E-05 | 0.00038  | 1.93004 |
| CNKSR2   | 0.87407 | 0.71724 | 11.2784 | 3.75E-07 | 1.20E-05 | 6.22289 |
| RNU1-15  | 0.87437 | 0.43718 | 14.1027 | 4.21E-08 | 1.86E-06 | 8.59085 |
| KCNMA1   | 0.87515 | 0.48775 | 8.13778 | 8.04E-06 | 0.00017  | 2.90693 |
| PIK3CG   | 0.87646 | 0.43823 | 12.6956 | 1.19E-07 | 4.45E-06 | 7.46997 |
| ITPRID2  | 0.87732 | 2.57576 | 23.4141 | 2.55E-10 | 2.98E-08 | 14.0907 |
| PROB1    | 0.87869 | 1.33399 | 5.31774 | 0.0003   | 0.00387  | -0.974  |
| GABRB2   | 0.87982 | 0.43991 | 17.8324 | 4.03E-09 | 2.68E-07 | 11.1245 |
| ADGRG1   | 0.88021 | 0.72031 | 8.40547 | 5.99E-06 | 0.00013  | 3.22552 |
| DACT1    | 0.88115 | 0.57027 | 12.1455 | 1.83E-07 | 6.53E-06 | 7.0011  |
| PARM1    | 0.88268 | 0.74237 | 18.0278 | 3.61E-09 | 2.47E-07 | 11.243  |
| KLHL32   | 0.88335 | 0.54202 | 9.39849 | 2.13E-06 | 5.37E-05 | 4.34383 |
| JUP      | 0.88552 | 1.88124 | 4.71913 | 0.00074  | 0.00831  | -1.9334 |
| CCDC85A  | 0.88622 | 0.62297 | 9.87974 | 1.33E-06 | 3.63E-05 | 4.85252 |
| CASP4LP  | 0.88631 | 0.44315 | 16.4751 | 8.93E-09 | 5.13E-07 | 10.266  |
| MC5R     | 0.88724 | 0.49379 | 8.40624 | 5.98E-06 | 0.00013  | 3.22643 |
| PAX6     | 0.8925  | 1.7091  | 12.8554 | 1.05E-07 | 4.04E-06 | 7.60269 |
| RIOX1    | 0.89251 | 2.17453 | 9.0286  | 3.10E-06 | 7.49E-05 | 3.9385  |
| LINC0030 | 0.8928  | 0.69726 | 6.68898 | 4.55E-05 | 0.00076  | 1.04025 |
| GABRP    | 0.8928  | 0.5973  | 14.2652 | 3.76E-08 | 1.69E-06 | 8.71363 |
| SAP30-D  | 0.89324 | 0.7129  | 6.79146 | 3.99E-05 | 0.00068  | 1.18072 |
| SLC38A1  | 0.8942  | 0.87315 | 8.59533 | 4.88E-06 | 0.00011  | 3.44693 |
| XKR7     | 0.8942  | 0.54744 | 9.05104 | 3.03E-06 | 7.35E-05 | 3.96347 |
| IGFBP5   | 0.89421 | 0.54745 | 9.77928 | 1.46E-06 | 3.92E-05 | 4.748   |
| BMPRI1B  | 0.89465 | 0.44732 | 15.2283 | 1.96E-08 | 9.78E-07 | 9.41605 |
| LINC0099 | 0.89465 | 0.44732 | 12.8266 | 1.07E-07 | 4.11E-06 | 7.5789  |
| PGGT1B   | 0.89486 | 0.46642 | 9.35954 | 2.21E-06 | 5.57E-05 | 4.30174 |
| INSM2    | 0.89494 | 0.62733 | 7.92371 | 1.02E-05 | 0.00021  | 2.64654 |
| GSAP     | 0.89677 | 0.44839 | 10.4326 | 7.93E-07 | 2.31E-05 | 5.41245 |
| HEATR4   | 0.89684 | 1.17346 | 13.5626 | 6.19E-08 | 2.60E-06 | 8.17311 |
| ELAVL2   | 0.89728 | 0.44864 | 18.3063 | 3.09E-09 | 2.18E-07 | 11.4095 |
| OR5G5P   | 0.89808 | 0.44904 | 12.0584 | 1.96E-07 | 6.93E-06 | 6.92517 |
| PDE11A   | 0.89808 | 0.44904 | 10.8575 | 5.41E-07 | 1.64E-05 | 5.82632 |
| EPAS1    | 0.8984  | 0.67924 | 8.68672 | 4.43E-06 | 0.0001   | 3.55217 |
| CASZ1    | 0.89966 | 2.13022 | 6.94874 | 3.28E-05 | 0.00057  | 1.39369 |
| PLEKHA5  | 0.89983 | 2.38577 | 16.7466 | 7.58E-09 | 4.51E-07 | 10.443  |
| TOGARA   | 0.90005 | 0.55037 | 6.45062 | 6.20E-05 | 0.00098  | 0.70826 |
| SUSD1    | 0.90112 | 0.86046 | 5.44608 | 0.00025  | 0.0033   | -0.7746 |
| HLA-U    | 0.90324 | 0.65231 | 5.00521 | 0.00048  | 0.00575  | -1.4689 |
| COL1A1   | 0.90389 | 1.51239 | 4.31714 | 0.0014   | 0.01403  | -2.6034 |
| F2RL1    | 0.90418 | 0.6026  | 9.40942 | 2.10E-06 | 5.32E-05 | 4.3556  |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| GPM6A-D  | 0.9053  | 0.50282 | 12.8866 | 1.02E-07 | 3.97E-06 | 7.62849 |
| CNN3-DT  | 0.90619 | 0.92932 | 9.033   | 3.08E-06 | 7.47E-05 | 3.9434  |
| TLR3     | 0.90652 | 2.01454 | 14.0121 | 4.49E-08 | 1.96E-06 | 8.52179 |
| GIPC3    | 0.90672 | 0.78374 | 6.39695 | 6.66E-05 | 0.00104  | 0.63249 |
| KRT25    | 0.90825 | 0.53365 | 10.7761 | 5.81E-07 | 1.76E-05 | 5.74811 |
| TAGLN    | 0.91054 | 2.74918 | 9.42685 | 2.07E-06 | 5.26E-05 | 4.37437 |
| MX1      | 0.91217 | 1.26268 | 9.38973 | 2.15E-06 | 5.41E-05 | 4.33437 |
| CD24     | 0.91336 | 0.89126 | 8.4777  | 5.54E-06 | 0.00012  | 3.3102  |
| DNAH11   | 0.91343 | 0.55706 | 9.79342 | 1.44E-06 | 3.89E-05 | 4.76277 |
| GCNT4    | 0.91529 | 1.70651 | 12.8897 | 1.02E-07 | 3.96E-06 | 7.63103 |
| TRIM49B  | 0.91626 | 0.45813 | 17.715  | 4.31E-09 | 2.84E-07 | 11.0528 |
| GAD2     | 0.91627 | 0.45813 | 15.4833 | 1.66E-08 | 8.59E-07 | 9.59507 |
| RIPOR3   | 0.91913 | 0.78994 | 8.46011 | 5.64E-06 | 0.00013  | 3.28963 |
| LINC0210 | 0.91972 | 0.51003 | 11.9504 | 2.14E-07 | 7.48E-06 | 6.83034 |
| ZFP69    | 0.92003 | 1.62443 | 21.5729 | 5.86E-10 | 5.64E-08 | 13.1978 |
| GLCCI1   | 0.92116 | 1.13642 | 7.36139 | 1.98E-05 | 0.00037  | 1.9378  |
| TPTEP2   | 0.92218 | 1.40578 | 9.98492 | 1.20E-06 | 3.31E-05 | 4.961   |
| HMGB1P   | 0.92237 | 0.46118 | 17.999  | 3.67E-09 | 2.51E-07 | 11.2255 |
| FOLR1    | 0.92288 | 0.56179 | 11.1416 | 4.22E-07 | 1.32E-05 | 6.09539 |
| USP44    | 0.92453 | 0.83814 | 9.16006 | 2.71E-06 | 6.66E-05 | 4.08403 |
| LINC0169 | 0.92539 | 0.79307 | 9.12848 | 2.79E-06 | 6.84E-05 | 4.04922 |
| FGA      | 0.92628 | 0.54266 | 6.71477 | 4.40E-05 | 0.00073  | 1.07572 |
| NRROS    | 0.92802 | 1.02555 | 4.88298 | 0.00057  | 0.00675  | -1.666  |
| PPM1L    | 0.93193 | 1.5192  | 8.92572 | 3.44E-06 | 8.21E-05 | 3.82345 |
| PBX3-DT  | 0.93528 | 0.61816 | 8.21539 | 7.38E-06 | 0.00016  | 3.00009 |
| PALMD    | 0.93616 | 0.46808 | 23.2873 | 2.69E-10 | 3.11E-08 | 14.0315 |
| PTPRD-A  | 0.93683 | 0.46841 | 15.3498 | 1.81E-08 | 9.21E-07 | 9.5017  |
| RCBTB2   | 0.93693 | 2.07615 | 27.5669 | 4.80E-11 | 8.30E-09 | 15.8678 |
| FGFBP3   | 0.93719 | 2.19011 | 14.3522 | 3.54E-08 | 1.61E-06 | 8.7789  |
| TAF11L1  | 0.93741 | 0.46871 | 15.7837 | 1.37E-08 | 7.39E-07 | 9.8025  |
| FST      | 0.93871 | 0.6862  | 6.86107 | 3.66E-05 | 0.00063  | 1.27536 |
| DACT3    | 0.93912 | 2.17312 | 10.3361 | 8.66E-07 | 2.50E-05 | 5.31652 |
| FADS2B   | 0.94015 | 0.47007 | 28.4433 | 3.48E-11 | 6.71E-09 | 16.2075 |
| SKAP1    | 0.9403  | 0.47015 | 8.56057 | 5.06E-06 | 0.00011  | 3.40667 |
| NUAK2    | 0.94191 | 1.23804 | 6.80375 | 3.93E-05 | 0.00067  | 1.19747 |
| LRRC8C   | 0.94199 | 1.79328 | 17.0728 | 6.25E-09 | 3.82E-07 | 10.6521 |
| HMGN1P   | 0.94285 | 0.47143 | 21.3231 | 6.60E-10 | 6.19E-08 | 13.0708 |
| KIAA1217 | 0.94334 | 1.3201  | 10.6492 | 6.51E-07 | 1.94E-05 | 5.62516 |
| ATP1B2   | 0.94337 | 1.17591 | 9.1785  | 2.66E-06 | 6.55E-05 | 4.10431 |
| PRDM8-A  | 0.94338 | 0.47169 | 21.5775 | 5.85E-10 | 5.64E-08 | 13.2001 |
| MAP7D2   | 0.94352 | 2.29157 | 15.2721 | 1.91E-08 | 9.58E-07 | 9.447   |
| F3       | 0.94368 | 0.62235 | 8.41014 | 5.96E-06 | 0.00013  | 3.23102 |
| GNA14    | 0.94468 | 0.47234 | 23.7854 | 2.17E-10 | 2.68E-08 | 14.2622 |
| WFDC1    | 0.94468 | 0.52251 | 12.2813 | 1.64E-07 | 5.96E-06 | 7.11859 |
| DCN      | 0.94551 | 1.638   | 13.4513 | 6.71E-08 | 2.79E-06 | 8.08518 |
| SHISAL2  | 0.94605 | 1.31174 | 8.13793 | 8.04E-06 | 0.00017  | 2.90711 |
| TAMALIN  | 0.94667 | 1.3433  | 5.38701 | 0.00027  | 0.00353  | -0.8661 |
| ATP11B   | 0.94817 | 2.67639 | 21.0594 | 7.49E-10 | 6.84E-08 | 12.9352 |
| SSPN     | 0.94835 | 0.72503 | 10.9164 | 5.13E-07 | 1.57E-05 | 5.88262 |
| CD48     | 0.94857 | 0.47429 | 13.6396 | 5.85E-08 | 2.47E-06 | 8.23356 |
| RNF217   | 0.95186 | 1.00233 | 8.08786 | 8.51E-06 | 0.00018  | 2.84665 |
| SERPINB  | 0.95217 | 0.90213 | 9.41798 | 2.09E-06 | 5.29E-05 | 4.36482 |
| GDNF     | 0.95244 | 0.47622 | 54.7908 | 4.04E-14 | 5.35E-11 | 23.1124 |
| SERTM1   | 0.95377 | 0.47689 | 12.2842 | 1.64E-07 | 5.96E-06 | 7.12107 |
| CRNDE    | 0.95439 | 0.77823 | 9.43239 | 2.06E-06 | 5.24E-05 | 4.38033 |
| ONECUT   | 0.95504 | 1.77679 | 15.608  | 1.53E-08 | 8.07E-07 | 9.68165 |
| LINC0123 | 0.95598 | 0.52816 | 11.0417 | 4.60E-07 | 1.43E-05 | 6.00146 |
| EN1      | 0.9573  | 0.47865 | 9.10678 | 2.86E-06 | 6.98E-05 | 4.02524 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| SPAG6    | 0.95751 | 0.5791  | 13.0505 | 9.04E-08 | 3.57E-06 | 7.76288 |
| DYNC1I1  | 0.95824 | 0.47912 | 10.0765 | 1.10E-06 | 3.08E-05 | 5.05469 |
| PLAU     | 0.95843 | 1.7854  | 16.5714 | 8.43E-09 | 4.89E-07 | 10.3291 |
| PDZD2    | 0.95865 | 1.42374 | 8.56425 | 5.04E-06 | 0.00011  | 3.41093 |
| CDH19    | 0.95875 | 0.47938 | 19.8447 | 1.37E-09 | 1.10E-07 | 12.2877 |
| LINGO2   | 0.95891 | 0.62997 | 11.505  | 3.09E-07 | 1.02E-05 | 6.43116 |
| ACOT12   | 0.95921 | 0.4796  | 22.3964 | 4.01E-10 | 4.28E-08 | 13.6063 |
| SLC8A2   | 0.95957 | 1.03053 | 7.95237 | 9.91E-06 | 0.00021  | 2.68171 |
| ZNF516-D | 0.96263 | 0.53148 | 9.13549 | 2.77E-06 | 6.80E-05 | 4.05695 |
| PRKCH-A  | 0.96291 | 0.48145 | 13.5201 | 6.38E-08 | 2.67E-06 | 8.13963 |
| CALCB    | 0.96514 | 0.53274 | 12.0941 | 1.90E-07 | 6.77E-06 | 6.95636 |
| LINC0168 | 0.96551 | 0.48275 | 10.9493 | 4.99E-07 | 1.53E-05 | 5.91394 |
| GPR158   | 0.96732 | 1.02621 | 9.41966 | 2.08E-06 | 5.28E-05 | 4.36663 |
| CDH2     | 0.96735 | 2.34853 | 18.4623 | 2.84E-09 | 2.03E-07 | 11.5018 |
| GABRA4   | 0.96742 | 0.53388 | 10.098  | 1.08E-06 | 3.02E-05 | 5.07658 |
| TRIM64   | 0.96781 | 0.4839  | 12.7702 | 1.12E-07 | 4.25E-06 | 7.53213 |
| ENOX1    | 0.9692  | 0.53477 | 13.3857 | 7.05E-08 | 2.89E-06 | 8.03303 |
| DNM1     | 0.96988 | 2.32875 | 7.4571  | 1.76E-05 | 0.00034  | 2.06104 |
| GRAPL    | 0.9704  | 0.65993 | 8.56421 | 5.04E-06 | 0.00011  | 3.41089 |
| ANXA3    | 0.97082 | 0.48541 | 15.4804 | 1.67E-08 | 8.59E-07 | 9.59308 |
| C19orf84 | 0.97105 | 0.63604 | 7.3705  | 1.95E-05 | 0.00037  | 1.94957 |
| SLC16A1  | 0.97167 | 0.74522 | 6.77746 | 4.07E-05 | 0.00069  | 1.1616  |
| EPHB6    | 0.97251 | 0.53643 | 7.84524 | 1.12E-05 | 0.00023  | 2.54982 |
| TGFA     | 0.97266 | 0.66619 | 9.7981  | 1.44E-06 | 3.87E-05 | 4.76765 |
| MAPK10   | 0.97356 | 0.64582 | 8.45674 | 5.66E-06 | 0.00013  | 3.28569 |
| CYB5A    | 0.97426 | 0.48713 | 14.1922 | 3.95E-08 | 1.77E-06 | 8.65861 |
| MT1F     | 0.97472 | 0.81144 | 7.89465 | 1.06E-05 | 0.00022  | 2.61081 |
| VWA2     | 0.97611 | 0.48805 | 10.4549 | 7.77E-07 | 2.27E-05 | 5.43454 |
| RGS16    | 0.9779  | 2.63391 | 25.465  | 1.08E-10 | 1.56E-08 | 15.0054 |
| HGD      | 0.97899 | 0.80758 | 8.29524 | 6.76E-06 | 0.00015  | 3.09526 |
| GABRA1   | 0.97903 | 0.53968 | 12.8016 | 1.09E-07 | 4.18E-06 | 7.55819 |
| SIX3-AS1 | 0.97975 | 0.48988 | 12.6433 | 1.23E-07 | 4.61E-06 | 7.42615 |
| IRX5     | 0.9801  | 0.61974 | 8.35994 | 6.29E-06 | 0.00014  | 3.17187 |
| TSPAN12  | 0.98284 | 1.60605 | 15.472  | 1.67E-08 | 8.61E-07 | 9.58723 |
| MEF2C-A  | 0.98304 | 1.01324 | 11.1179 | 4.31E-07 | 1.34E-05 | 6.07313 |
| CBR1     | 0.98319 | 0.4916  | 24.4831 | 1.61E-10 | 2.15E-08 | 14.5772 |
| OR5E1P   | 0.98345 | 0.5419  | 11.2474 | 3.85E-07 | 1.23E-05 | 6.19415 |
| DNAJB13  | 0.98348 | 0.91779 | 11.5258 | 3.04E-07 | 1.01E-05 | 6.45006 |
| SYCP2L   | 0.98349 | 0.49175 | 18.4758 | 2.82E-09 | 2.02E-07 | 11.5098 |
| KERA     | 0.9839  | 0.84315 | 16.2833 | 1.00E-08 | 5.65E-07 | 10.1393 |
| CETP     | 0.98532 | 0.54283 | 12.8099 | 1.09E-07 | 4.15E-06 | 7.56505 |
| HCG27    | 0.98551 | 0.74361 | 8.39072 | 6.09E-06 | 0.00013  | 3.20817 |
| MAGI3    | 0.98605 | 1.59901 | 10.3589 | 8.48E-07 | 2.45E-05 | 5.33927 |
| LINC0200 | 0.98652 | 0.49326 | 20.5576 | 9.57E-10 | 8.28E-08 | 12.6723 |
| GALNT13  | 0.98665 | 0.88036 | 6.55968 | 5.38E-05 | 0.00087  | 0.86108 |
| ZIC4-AS1 | 0.98706 | 0.49353 | 9.78388 | 1.46E-06 | 3.91E-05 | 4.75281 |
| RASGEF   | 0.98745 | 0.62342 | 10.5271 | 7.27E-07 | 2.14E-05 | 5.50572 |
| HLA-H    | 0.98782 | 1.52399 | 5.0171  | 0.00047  | 0.00566  | -1.4498 |
| LINC0232 | 0.98819 | 0.49409 | 16.2893 | 1.00E-08 | 5.64E-07 | 10.1433 |
| FLNC-AS  | 0.98949 | 0.49475 | 13.7244 | 5.51E-08 | 2.34E-06 | 8.29983 |
| EHHADH   | 0.98988 | 0.7335  | 8.03146 | 9.06E-06 | 0.00019  | 2.77825 |
| RAB3IP   | 0.99218 | 1.6676  | 20.8372 | 8.34E-10 | 7.42E-08 | 12.8195 |
| SAP30    | 0.99264 | 1.62263 | 6.45926 | 6.13E-05 | 0.00097  | 0.72043 |
| TMTC2    | 0.99513 | 1.60538 | 15.2595 | 1.92E-08 | 9.64E-07 | 9.43811 |
| RFPL4AL  | 0.99521 | 0.4976  | 56.6781 | 2.85E-14 | 4.19E-11 | 23.4506 |
| CALCA    | 0.99561 | 0.49781 | 15.0663 | 2.18E-08 | 1.07E-06 | 9.30081 |
| BEND3P1  | 0.99581 | 1.14382 | 9.57491 | 1.79E-06 | 4.65E-05 | 4.53268 |
| FRZB     | 0.99665 | 0.59867 | 12.9837 | 9.51E-08 | 3.73E-06 | 7.70829 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| RGS2     | 0.99677 | 3.31662 | 24.8546 | 1.38E-10 | 1.90E-08 | 14.7413 |
| KCNH1    | 0.99722 | 0.49861 | 18.308  | 3.09E-09 | 2.18E-07 | 11.4105 |
| BACH2    | 0.99895 | 0.49948 | 27.2448 | 5.41E-11 | 9.14E-09 | 15.7402 |
| RND3     | 0.99966 | 0.9599  | 9.83727 | 1.39E-06 | 3.75E-05 | 4.80844 |
| SSU72P6  | 1.00085 | 0.50042 | 33.208  | 7.09E-12 | 2.18E-09 | 17.8805 |
| GRB14    | 1.00134 | 1.44182 | 10.9893 | 4.82E-07 | 1.48E-05 | 5.95186 |
| MGAT3    | 1.00182 | 1.90583 | 8.95506 | 3.34E-06 | 7.99E-05 | 3.85637 |
| TRIM49C  | 1.00185 | 0.50092 | 11.7702 | 2.48E-07 | 8.47E-06 | 6.67041 |
| GRIK1-AS | 1.00272 | 0.50136 | 22.7691 | 3.39E-10 | 3.77E-08 | 13.7862 |
| NR6A1    | 1.00289 | 2.72648 | 11.1761 | 4.09E-07 | 1.29E-05 | 6.12769 |
| DACT3-A  | 1.00307 | 0.75888 | 5.95116 | 0.00012  | 0.00176  | -0.0118 |
| ABCA1    | 1.00362 | 2.02829 | 21.2092 | 6.97E-10 | 6.47E-08 | 13.0124 |
| NPAS4    | 1.00383 | 0.68178 | 11.1911 | 4.04E-07 | 1.27E-05 | 6.14168 |
| SOX5     | 1.00424 | 0.68198 | 9.62544 | 1.70E-06 | 4.45E-05 | 4.58626 |
| MIR2052H | 1.00487 | 0.63213 | 10.689  | 6.28E-07 | 1.88E-05 | 5.66389 |
| RFPL4A   | 1.00873 | 0.50436 | 33.0699 | 7.40E-12 | 2.19E-09 | 17.8357 |
| ICAM1    | 1.01003 | 1.20628 | 7.42001 | 1.84E-05 | 0.00035  | 2.01341 |
| CCDC194  | 1.01104 | 0.53487 | 21.9481 | 4.92E-10 | 4.95E-08 | 13.3858 |
| JAG1     | 1.01685 | 1.68063 | 12.1141 | 1.87E-07 | 6.68E-06 | 6.9738  |
| BATF2    | 1.01797 | 1.75595 | 6.80286 | 3.94E-05 | 0.00067  | 1.19625 |
| HOXD3    | 1.01816 | 0.50908 | 19.6597 | 1.50E-09 | 1.18E-07 | 12.1857 |
| LINC0017 | 1.01922 | 0.91951 | 5.64079 | 0.00019  | 0.00258  | -0.4764 |
| SEMA6A-  | 1.01937 | 0.50968 | 27.2142 | 5.47E-11 | 9.14E-09 | 15.728  |
| MESTP3   | 1.02019 | 0.5101  | 20.3838 | 1.04E-09 | 8.91E-08 | 12.5798 |
| TRIM53C  | 1.02025 | 0.51012 | 8.68324 | 4.44E-06 | 0.0001   | 3.54818 |
| KCND2    | 1.02067 | 0.51034 | 14.6397 | 2.90E-08 | 1.37E-06 | 8.99188 |
| LAMA2    | 1.02099 | 0.61084 | 12.882  | 1.03E-07 | 3.98E-06 | 7.62465 |
| ABCA9    | 1.02132 | 0.611   | 12.0419 | 1.99E-07 | 7.00E-06 | 6.9108  |
| UBA7     | 1.02415 | 1.88701 | 7.51762 | 1.64E-05 | 0.00032  | 2.1384  |
| PELO-AS  | 1.02424 | 0.51212 | 16.1687 | 1.08E-08 | 5.99E-07 | 10.0629 |
| INPP5D   | 1.02459 | 0.98852 | 9.73415 | 1.53E-06 | 4.06E-05 | 4.70078 |
| SAA2-SA  | 1.02555 | 0.59229 | 18.8659 | 2.28E-09 | 1.69E-07 | 11.7371 |
| FBLN2    | 1.02717 | 0.56376 | 9.46173 | 2.00E-06 | 5.12E-05 | 4.41184 |
| TRIM71   | 1.0288  | 2.62254 | 15.4123 | 1.74E-08 | 8.91E-07 | 9.54554 |
| C10orf55 | 1.03038 | 0.89574 | 8.83768 | 3.77E-06 | 8.92E-05 | 3.72419 |
| PARP9    | 1.0318  | 2.67083 | 17.0071 | 6.49E-09 | 3.96E-07 | 10.6103 |
| PTH1R    | 1.03196 | 0.51598 | 14.7673 | 2.66E-08 | 1.27E-06 | 9.08514 |
| PKD2L2-L | 1.03423 | 0.91382 | 7.07445 | 2.80E-05 | 0.0005   | 1.56168 |
| ADAM19   | 1.03707 | 2.0004  | 12.2505 | 1.68E-07 | 6.07E-06 | 7.09208 |
| SAA2     | 1.03925 | 0.69949 | 16.2706 | 1.01E-08 | 5.68E-07 | 10.1309 |
| DGKK     | 1.03941 | 0.59923 | 15.3326 | 1.83E-08 | 9.30E-07 | 9.48958 |
| SP140L   | 1.04027 | 1.95081 | 14.11   | 4.19E-08 | 1.85E-06 | 8.5964  |
| IQGAP2   | 1.04131 | 1.01271 | 8.25067 | 7.10E-06 | 0.00015  | 3.04223 |
| SIX1     | 1.04241 | 2.746   | 13.8185 | 5.15E-08 | 2.20E-06 | 8.37292 |
| FAM102B  | 1.04425 | 2.07239 | 18.7611 | 2.42E-09 | 1.78E-07 | 11.6764 |
| GSG1     | 1.04549 | 1.23549 | 14.0667 | 4.32E-08 | 1.89E-06 | 8.56344 |
| PRSS35   | 1.04615 | 0.67359 | 13.1649 | 8.30E-08 | 3.31E-06 | 7.85579 |
| FAM163A  | 1.04678 | 0.52339 | 15.893  | 1.28E-08 | 6.98E-07 | 9.877   |
| NLGN4X   | 1.04744 | 2.38069 | 26.1456 | 8.25E-11 | 1.28E-08 | 15.2925 |
| HRC      | 1.04767 | 1.13887 | 6.32083 | 7.36E-05 | 0.00114  | 0.52435 |
| LRFN5-D  | 1.04812 | 0.52406 | 32.8155 | 8.01E-12 | 2.31E-09 | 17.7527 |
| ANGPTL1  | 1.04869 | 0.57452 | 13.8257 | 5.12E-08 | 2.19E-06 | 8.37849 |
| GATM     | 1.04908 | 1.37002 | 16.5432 | 8.57E-09 | 4.96E-07 | 10.3107 |
| SLC15A3  | 1.04994 | 1.62907 | 10.6514 | 6.50E-07 | 1.94E-05 | 5.62734 |
| PURG     | 1.05133 | 0.70553 | 10.3317 | 8.70E-07 | 2.50E-05 | 5.31217 |
| LINC0127 | 1.05155 | 0.52577 | 12.5216 | 1.36E-07 | 5.00E-06 | 7.32361 |
| PCGF5    | 1.05182 | 1.24332 | 14.9936 | 2.29E-08 | 1.11E-06 | 9.24879 |
| CPA4     | 1.05212 | 0.57623 | 13.4868 | 6.54E-08 | 2.73E-06 | 8.11328 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| ZNF493   | 1.05295 | 0.78272 | 11.552  | 2.97E-07 | 9.93E-06 | 6.4739  |
| SLC44A5  | 1.05498 | 0.83705 | 9.50801 | 1.91E-06 | 4.91E-05 | 4.4614  |
| INSIG2   | 1.05518 | 2.41921 | 17.4651 | 4.97E-09 | 3.20E-07 | 10.8986 |
| PTPRK    | 1.05542 | 0.6574  | 10.827  | 5.56E-07 | 1.68E-05 | 5.79707 |
| RMST     | 1.05595 | 0.69464 | 8.25586 | 7.06E-06 | 0.00015  | 3.04842 |
| EGLN3    | 1.0565  | 0.70811 | 12.2793 | 1.64E-07 | 5.97E-06 | 7.1169  |
| CD53     | 1.05831 | 0.57933 | 14.5095 | 3.17E-08 | 1.48E-06 | 8.89588 |
| PIM1     | 1.05845 | 2.11995 | 12.7345 | 1.15E-07 | 4.35E-06 | 7.50241 |
| CHST9    | 1.05858 | 0.52929 | 21.8263 | 5.21E-10 | 5.16E-08 | 13.3251 |
| DHRS2    | 1.05917 | 1.22618 | 9.54862 | 1.83E-06 | 4.74E-05 | 4.50472 |
| SHC4     | 1.06099 | 1.05689 | 10.7411 | 6.00E-07 | 1.81E-05 | 5.71429 |
| DBX2     | 1.06131 | 0.53066 | 34.5574 | 4.71E-12 | 1.70E-09 | 18.3081 |
| RFPL4B   | 1.06232 | 0.53116 | 16.2939 | 9.98E-09 | 5.63E-07 | 10.1464 |
| CCR3     | 1.06248 | 0.53124 | 10.3946 | 8.21E-07 | 2.38E-05 | 5.37479 |
| ST8SIA1  | 1.06255 | 0.81148 | 9.77962 | 1.46E-06 | 3.92E-05 | 4.74837 |
| PDGFRB   | 1.06402 | 1.27178 | 6.7954  | 3.97E-05 | 0.00067  | 1.18609 |
| SLC44A1  | 1.06647 | 2.88284 | 18.6295 | 2.59E-09 | 1.89E-07 | 11.5999 |
| PLAAT4   | 1.06766 | 1.49743 | 22.5856 | 3.68E-10 | 3.98E-08 | 13.698  |
| CHRD1    | 1.06786 | 0.66362 | 10.4718 | 7.65E-07 | 2.25E-05 | 5.4513  |
| SLITRK4  | 1.06862 | 0.664   | 11.4381 | 3.27E-07 | 1.07E-05 | 6.36999 |
| AMOTL1   | 1.06878 | 1.44487 | 13.3647 | 7.16E-08 | 2.93E-06 | 8.01626 |
| PNMA3    | 1.06897 | 0.92356 | 8.52885 | 5.24E-06 | 0.00012  | 3.36983 |
| NELL2    | 1.0706  | 1.40546 | 11.7508 | 2.52E-07 | 8.58E-06 | 6.65308 |
| TENM1    | 1.07066 | 0.53533 | 27.7952 | 4.41E-11 | 7.92E-09 | 15.9574 |
| DHRS3    | 1.07139 | 1.14924 | 9.74507 | 1.51E-06 | 4.03E-05 | 4.71222 |
| MLXP1    | 1.0717  | 0.58602 | 15.5397 | 1.60E-08 | 8.37E-07 | 9.63433 |
| LMO3     | 1.07228 | 1.21954 | 18.4461 | 2.87E-09 | 2.05E-07 | 11.4923 |
| IRX3     | 1.07315 | 0.6161  | 10.6114 | 6.74E-07 | 2.00E-05 | 5.58828 |
| LINC0103 | 1.07413 | 0.53706 | 25.1959 | 1.20E-10 | 1.69E-08 | 14.8898 |
| CPNE8-A  | 1.07547 | 0.96846 | 8.92664 | 3.44E-06 | 8.20E-05 | 3.82449 |
| LINC0182 | 1.07766 | 0.84839 | 11.3025 | 3.67E-07 | 1.18E-05 | 6.24518 |
| GABRG2   | 1.08051 | 0.59043 | 13.0684 | 8.92E-08 | 3.53E-06 | 7.77744 |
| EPDR1    | 1.0807  | 0.54035 | 12.5957 | 1.28E-07 | 4.75E-06 | 7.38619 |
| IZUMO3   | 1.08103 | 0.54051 | 20.1393 | 1.18E-09 | 9.77E-08 | 12.4483 |
| GABRA2   | 1.08153 | 0.69128 | 8.9991  | 3.19E-06 | 7.69E-05 | 3.90561 |
| FLRT2    | 1.0817  | 1.15144 | 14.1342 | 4.12E-08 | 1.82E-06 | 8.61477 |
| KCTD16   | 1.08243 | 1.66002 | 17.7449 | 4.24E-09 | 2.81E-07 | 11.0711 |
| MPZL2    | 1.08259 | 0.64164 | 13.0062 | 9.35E-08 | 3.68E-06 | 7.72667 |
| BRINP3-L | 1.08335 | 0.59184 | 13.3292 | 7.35E-08 | 3.00E-06 | 7.98795 |
| FES      | 1.08586 | 0.79379 | 7.11197 | 2.68E-05 | 0.00048  | 1.61143 |
| CAVIN2   | 1.0862  | 0.59327 | 13.3885 | 7.03E-08 | 2.89E-06 | 8.03527 |
| SPX      | 1.08658 | 0.95614 | 8.63026 | 4.70E-06 | 0.00011  | 3.48725 |
| ACTG2    | 1.08774 | 0.61735 | 13.8088 | 5.18E-08 | 2.21E-06 | 8.36541 |
| P2RY2    | 1.08789 | 0.59412 | 9.42409 | 2.07E-06 | 5.27E-05 | 4.3714  |
| TMTC1    | 1.08809 | 1.34098 | 20.9906 | 7.74E-10 | 6.99E-08 | 12.8995 |
| GPHA2    | 1.08868 | 0.92022 | 8.03167 | 9.06E-06 | 0.00019  | 2.77849 |
| TRIM49   | 1.08875 | 0.54437 | 22.2445 | 4.29E-10 | 4.48E-08 | 13.5321 |
| SUCNR1   | 1.09037 | 0.98443 | 9.74741 | 1.51E-06 | 4.02E-05 | 4.71467 |
| GRID2    | 1.09536 | 0.54768 | 23.0052 | 3.05E-10 | 3.44E-08 | 13.8987 |
| TMEM35A  | 1.09549 | 0.69826 | 9.46419 | 1.99E-06 | 5.11E-05 | 4.41449 |
| NKX2-1-A | 1.09616 | 0.54808 | 13.1495 | 8.40E-08 | 3.34E-06 | 7.84328 |
| QRFPR    | 1.09666 | 0.54833 | 35.4316 | 3.64E-12 | 1.46E-09 | 18.5756 |
| SH3BP4   | 1.09746 | 2.14998 | 16.4507 | 9.07E-09 | 5.19E-07 | 10.25   |
| DIO3OS   | 1.09781 | 0.5621  | 21.996  | 4.81E-10 | 4.87E-08 | 13.4095 |
| SHC2     | 1.09845 | 0.94593 | 6.69312 | 4.53E-05 | 0.00075  | 1.04595 |
| SOX9-AS  | 1.09874 | 0.54937 | 14.4342 | 3.34E-08 | 1.54E-06 | 8.84001 |
| TM4SF1   | 1.10116 | 0.6301  | 12.5905 | 1.29E-07 | 4.77E-06 | 7.38178 |
| LTF      | 1.10137 | 0.65103 | 11.9115 | 2.21E-07 | 7.67E-06 | 6.79606 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| THBS1-A  | 1.1015  | 0.68044 | 11.5891 | 2.88E-07 | 9.67E-06 | 6.50752 |
| TRIM49D  | 1.1015  | 0.55075 | 31.4269 | 1.25E-11 | 3.05E-09 | 17.2868 |
| CXXC4    | 1.10326 | 2.98989 | 18.5411 | 2.72E-09 | 1.97E-07 | 11.5481 |
| HOATZ    | 1.10439 | 0.5522  | 14.2288 | 3.85E-08 | 1.73E-06 | 8.68623 |
| ITGA4    | 1.10477 | 0.60256 | 16.8013 | 7.34E-09 | 4.40E-07 | 10.4784 |
| TRIM49D  | 1.10504 | 0.55252 | 33.1534 | 7.21E-12 | 2.19E-09 | 17.8628 |
| HOXB8    | 1.10604 | 1.23683 | 8.82926 | 3.81E-06 | 8.98E-05 | 3.71465 |
| CDH10    | 1.10758 | 1.8855  | 18.5296 | 2.74E-09 | 1.98E-07 | 11.5414 |
| ELOVL2   | 1.10925 | 0.68432 | 12.0893 | 1.91E-07 | 6.79E-06 | 6.95223 |
| UTS2B    | 1.11034 | 1.20262 | 12.0689 | 1.94E-07 | 6.89E-06 | 6.93439 |
| GRIN3A   | 1.11153 | 1.86876 | 15.5319 | 1.61E-08 | 8.38E-07 | 9.62888 |
| KRT28    | 1.11333 | 0.55666 | 20.0028 | 1.26E-09 | 1.02E-07 | 12.3742 |
| MEIS3    | 1.11442 | 2.34604 | 7.43993 | 1.80E-05 | 0.00034  | 2.03901 |
| RTP4     | 1.11475 | 0.65772 | 15.7014 | 1.45E-08 | 7.72E-07 | 9.74602 |
| LGR5     | 1.11585 | 1.42272 | 9.64287 | 1.67E-06 | 4.38E-05 | 4.6047  |
| TMEM74   | 1.1161  | 0.70856 | 14.6653 | 2.85E-08 | 1.35E-06 | 9.01059 |
| AQP9     | 1.11721 | 0.5586  | 16.1473 | 1.09E-08 | 6.05E-07 | 10.0486 |
| FOXL2NE  | 1.11727 | 1.59902 | 11.2702 | 3.78E-07 | 1.21E-05 | 6.21523 |
| ERVV-2   | 1.11843 | 0.65956 | 12.064  | 1.95E-07 | 6.90E-06 | 6.93009 |
| RBM47    | 1.12377 | 1.22354 | 11.8116 | 2.40E-07 | 8.22E-06 | 6.70739 |
| HLA-DPA  | 1.12387 | 0.72257 | 13.436  | 6.79E-08 | 2.81E-06 | 8.07302 |
| HNF4G    | 1.12497 | 1.67324 | 16.9862 | 6.58E-09 | 4.01E-07 | 10.597  |
| LRP2     | 1.12668 | 0.79337 | 13.1545 | 8.36E-08 | 3.33E-06 | 7.84731 |
| SYT1     | 1.12827 | 0.77334 | 10.7241 | 6.09E-07 | 1.83E-05 | 5.69789 |
| RNF180   | 1.1325  | 0.74611 | 12.2009 | 1.75E-07 | 6.30E-06 | 7.0492  |
| DPYD-AS  | 1.13311 | 0.56655 | 20.1085 | 1.20E-09 | 9.89E-08 | 12.4316 |
| S1PR1    | 1.13921 | 1.21898 | 11.9837 | 2.08E-07 | 7.30E-06 | 6.85966 |
| ANKRD30  | 1.13934 | 0.59902 | 18.3474 | 3.03E-09 | 2.15E-07 | 11.434  |
| SERPINA  | 1.13937 | 0.56969 | 9.75671 | 1.50E-06 | 3.99E-05 | 4.7244  |
| NXPH1    | 1.13958 | 0.61996 | 12.3591 | 1.54E-07 | 5.64E-06 | 7.18536 |
| MMRN2    | 1.1399  | 1.0497  | 6.6921  | 4.53E-05 | 0.00075  | 1.04454 |
| LINC0287 | 1.1407  | 0.62052 | 9.37669 | 2.17E-06 | 5.48E-05 | 4.32029 |
| LINC0279 | 1.14589 | 0.57984 | 30.8052 | 1.53E-11 | 3.50E-09 | 17.0711 |
| DIO3     | 1.15072 | 0.70505 | 11.6574 | 2.72E-07 | 9.20E-06 | 6.56926 |
| ROCR     | 1.15128 | 0.57564 | 20.68   | 9.01E-10 | 7.94E-08 | 12.737  |
| FADS2    | 1.15138 | 2.9574  | 10.5524 | 7.11E-07 | 2.10E-05 | 5.53062 |
| LIPK     | 1.1519  | 0.57595 | 20.08   | 1.21E-09 | 9.93E-08 | 12.4161 |
| CCN1     | 1.15305 | 1.97948 | 17.5089 | 4.85E-09 | 3.15E-07 | 10.9258 |
| TM4SF18  | 1.15333 | 0.57667 | 20.0809 | 1.21E-09 | 9.93E-08 | 12.4166 |
| GRIA3    | 1.15557 | 0.94047 | 8.95203 | 3.35E-06 | 8.01E-05 | 3.85298 |
| PABPC5   | 1.15686 | 0.57843 | 19.465  | 1.66E-09 | 1.29E-07 | 12.0773 |
| OR5AK2   | 1.15695 | 0.57847 | 13.5046 | 6.46E-08 | 2.70E-06 | 8.12736 |
| LINC0109 | 1.15784 | 0.57892 | 14.7347 | 2.72E-08 | 1.29E-06 | 9.06137 |
| CDH6     | 1.15842 | 0.62938 | 13.9783 | 4.59E-08 | 2.00E-06 | 8.49597 |
| LINC0115 | 1.15918 | 0.57959 | 17.4623 | 4.98E-09 | 3.20E-07 | 10.8969 |
| LGALS3B  | 1.15984 | 2.28309 | 7.89283 | 1.06E-05 | 0.00022  | 2.60856 |
| PDZRN4   | 1.16005 | 0.58002 | 36.6497 | 2.57E-12 | 1.16E-09 | 18.9365 |
| INA      | 1.16303 | 2.48044 | 22.655  | 3.56E-10 | 3.90E-08 | 13.7314 |
| GNG8     | 1.16655 | 0.58328 | 12.792  | 1.10E-07 | 4.19E-06 | 7.55025 |
| APELA    | 1.16738 | 0.58369 | 45.6051 | 2.69E-13 | 2.23E-10 | 21.2387 |
| NLR5     | 1.1681  | 2.45553 | 12.9127 | 1.00E-07 | 3.90E-06 | 7.64997 |
| IL32     | 1.16815 | 0.6636  | 11.7722 | 2.48E-07 | 8.47E-06 | 6.67221 |
| CD69     | 1.16854 | 0.73478 | 13.2435 | 7.83E-08 | 3.14E-06 | 7.9192  |
| SLC66A1  | 1.16974 | 0.63504 | 13.3812 | 7.07E-08 | 2.90E-06 | 8.02939 |
| MAOA     | 1.17202 | 0.75268 | 9.88299 | 1.33E-06 | 3.62E-05 | 4.85588 |
| MYOCOS   | 1.17437 | 1.10038 | 9.37038 | 2.19E-06 | 5.51E-05 | 4.31346 |
| MAP1LC3  | 1.1757  | 0.66737 | 9.59067 | 1.76E-06 | 4.58E-05 | 4.54943 |
| CYSLTR2  | 1.17723 | 1.36586 | 17.6656 | 4.43E-09 | 2.91E-07 | 11.0225 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| SFTA3    | 1.17841 | 0.5892  | 20.0612 | 1.23E-09 | 9.96E-08 | 12.4059 |
| TENM3    | 1.17972 | 0.76972 | 10.8202 | 5.59E-07 | 1.69E-05 | 5.79054 |
| LINC0046 | 1.18184 | 0.59092 | 25.4962 | 1.07E-10 | 1.55E-08 | 15.0188 |
| TGFB2    | 1.18343 | 0.8379  | 9.42147 | 2.08E-06 | 5.28E-05 | 4.36858 |
| CCDC80   | 1.18557 | 2.03365 | 15.5135 | 1.63E-08 | 8.46E-07 | 9.61608 |
| RFPL1    | 1.1858  | 0.62225 | 18.0917 | 3.49E-09 | 2.40E-07 | 11.2814 |
| NLGN4Y   | 1.18582 | 0.98198 | 15.4503 | 1.70E-08 | 8.71E-07 | 9.57209 |
| NID2     | 1.18649 | 1.9457  | 15.2435 | 1.94E-08 | 9.72E-07 | 9.42681 |
| PDLIM5   | 1.18738 | 2.22277 | 32.8916 | 7.82E-12 | 2.29E-09 | 17.7776 |
| SLC16A3  | 1.18837 | 1.26922 | 8.60777 | 4.81E-06 | 0.00011  | 3.4613  |
| TRIM22   | 1.18971 | 1.07108 | 16.4979 | 8.81E-09 | 5.09E-07 | 10.281  |
| TP53INP  | 1.19056 | 1.6321  | 16.2001 | 1.06E-08 | 5.91E-07 | 10.0839 |
| GFY      | 1.19228 | 1.56664 | 11.389  | 3.41E-07 | 1.11E-05 | 6.32501 |
| PDE11A   | 1.19323 | 0.89765 | 9.43583 | 2.05E-06 | 5.23E-05 | 4.38403 |
| HLA-A    | 1.19338 | 1.2328  | 4.91913 | 0.00054  | 0.00643  | -1.6075 |
| ARX      | 1.19407 | 0.59703 | 9.45323 | 2.02E-06 | 5.15E-05 | 4.40273 |
| HOXD10   | 1.19752 | 0.59876 | 15.1499 | 2.07E-08 | 1.02E-06 | 9.36046 |
| HLA-B    | 1.19772 | 3.00235 | 12.2439 | 1.69E-07 | 6.10E-06 | 7.08632 |
| SLC34A2  | 1.19928 | 0.59964 | 15.8773 | 1.29E-08 | 7.04E-07 | 9.86631 |
| ARPP21   | 1.19943 | 0.59972 | 30.6278 | 1.63E-11 | 3.61E-09 | 17.0087 |
| DSPP     | 1.20072 | 0.80105 | 15.8705 | 1.30E-08 | 7.05E-07 | 9.86169 |
| KHDC1L   | 1.20102 | 0.7302  | 13.0104 | 9.32E-08 | 3.67E-06 | 7.73012 |
| CCDC120  | 1.20233 | 1.25988 | 11.5105 | 3.08E-07 | 1.02E-05 | 6.43613 |
| TANC1    | 1.20241 | 2.31885 | 17.2551 | 5.61E-09 | 3.51E-07 | 10.7673 |
| CNTN1    | 1.20419 | 0.60209 | 45.135  | 3.00E-13 | 2.38E-10 | 21.1311 |
| NKX3-2   | 1.20505 | 0.65269 | 10.6519 | 6.50E-07 | 1.94E-05 | 5.6278  |
| FIRRE    | 1.20682 | 1.27565 | 15.1334 | 2.09E-08 | 1.03E-06 | 9.34867 |
| CNTN4-A  | 1.20834 | 0.60417 | 43.0156 | 4.93E-13 | 3.49E-10 | 20.6294 |
| GOLGA8   | 1.21053 | 1.17109 | 17.9013 | 3.88E-09 | 2.59E-07 | 11.1664 |
| LRRTM4   | 1.21143 | 2.14219 | 20.8536 | 8.28E-10 | 7.39E-08 | 12.8281 |
| ZNF385D  | 1.21153 | 1.05617 | 9.92987 | 1.27E-06 | 3.47E-05 | 4.90434 |
| CAPS2    | 1.21208 | 0.65621 | 21.3387 | 6.55E-10 | 6.15E-08 | 13.0788 |
| INPP1    | 1.21266 | 0.60633 | 19.6092 | 1.54E-09 | 1.21E-07 | 12.1577 |
| TNMD     | 1.21642 | 0.86759 | 12.5156 | 1.36E-07 | 5.02E-06 | 7.31853 |
| KCNJ2    | 1.21732 | 1.50626 | 19.6049 | 1.55E-09 | 1.21E-07 | 12.1553 |
| SH2D2A   | 1.21835 | 0.70952 | 10.2572 | 9.32E-07 | 2.66E-05 | 5.23755 |
| FBN2     | 1.2195  | 2.7221  | 19.0431 | 2.08E-09 | 1.56E-07 | 11.8388 |
| DGKB     | 1.22353 | 0.79853 | 10.8975 | 5.22E-07 | 1.59E-05 | 5.86458 |
| RERGL    | 1.22393 | 1.04917 | 9.54349 | 1.84E-06 | 4.76E-05 | 4.49926 |
| PTX3     | 1.22439 | 0.66237 | 19.2192 | 1.89E-09 | 1.45E-07 | 11.939  |
| MSR1     | 1.22531 | 0.98001 | 16.4779 | 8.92E-09 | 5.13E-07 | 10.2679 |
| PRKCH    | 1.22565 | 2.18142 | 16.9159 | 6.85E-09 | 4.14E-07 | 10.552  |
| SOCS3-D  | 1.22755 | 0.66395 | 14.3486 | 3.55E-08 | 1.61E-06 | 8.77619 |
| OSTN     | 1.22795 | 2.38552 | 31.4379 | 1.25E-11 | 3.05E-09 | 17.2906 |
| FLG      | 1.22873 | 0.9154  | 8.52084 | 5.29E-06 | 0.00012  | 3.36051 |
| DSEL     | 1.2302  | 2.01474 | 30.7447 | 1.57E-11 | 3.53E-09 | 17.0498 |
| MYO3B    | 1.23147 | 0.61573 | 10.764  | 5.88E-07 | 1.77E-05 | 5.73645 |
| CTTNBP2  | 1.23176 | 0.79574 | 13.444  | 6.75E-08 | 2.80E-06 | 8.07939 |
| LINC0166 | 1.23377 | 1.18128 | 13.4396 | 6.77E-08 | 2.81E-06 | 8.07589 |
| LINC0127 | 1.2338  | 0.6169  | 15.1514 | 2.06E-08 | 1.02E-06 | 9.36146 |
| PLAG1    | 1.23382 | 1.57289 | 17.7227 | 4.29E-09 | 2.83E-07 | 11.0575 |
| IL21R-AS | 1.23524 | 1.08885 | 6.85463 | 3.69E-05 | 0.00063  | 1.26663 |
| LGR4     | 1.23582 | 2.80342 | 29.7314 | 2.21E-11 | 4.64E-09 | 16.6874 |
| UACA     | 1.23596 | 3.39315 | 27.725  | 4.52E-11 | 8.02E-09 | 15.9299 |
| SULT2A1  | 1.23677 | 0.66856 | 21.8227 | 5.22E-10 | 5.16E-08 | 13.3233 |
| TECRL    | 1.23701 | 0.92806 | 14.2193 | 3.88E-08 | 1.74E-06 | 8.67909 |
| MBP      | 1.23891 | 0.79932 | 10.307  | 8.90E-07 | 2.55E-05 | 5.28753 |
| BEX4     | 1.24055 | 0.62028 | 19.516  | 1.62E-09 | 1.26E-07 | 12.1058 |

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|----------|---------|---------|---------|----------|----------|---------|
| CXXC4-A  | 1.24169 | 1.27693 | 10.0925 | 1.09E-06 | 3.04E-05 | 5.07104 |
| MPPED2   | 1.24649 | 0.86018 | 12.7094 | 1.17E-07 | 4.42E-06 | 7.48149 |
| CPXM1    | 1.24743 | 0.62371 | 16.2335 | 1.04E-08 | 5.80E-07 | 10.1062 |
| MPZ      | 1.24821 | 0.72445 | 11.5614 | 2.95E-07 | 9.88E-06 | 6.48246 |
| BMPR1B   | 1.2484  | 0.6242  | 35.2586 | 3.83E-12 | 1.51E-09 | 18.5232 |
| FOLH1    | 1.24855 | 1.07968 | 10.795  | 5.72E-07 | 1.73E-05 | 5.7663  |
| OLFML1   | 1.24954 | 1.83069 | 15.2847 | 1.89E-08 | 9.52E-07 | 9.45585 |
| ALX4     | 1.25052 | 1.08533 | 12.8574 | 1.05E-07 | 4.03E-06 | 7.60435 |
| XAF1     | 1.2517  | 1.96964 | 14.1446 | 4.09E-08 | 1.82E-06 | 8.62267 |
| LBX1-AS  | 1.25301 | 0.6265  | 12.6943 | 1.19E-07 | 4.45E-06 | 7.46888 |
| ACTA2    | 1.25547 | 2.32756 | 36.9188 | 2.38E-12 | 1.11E-09 | 19.0145 |
| BCL6     | 1.25664 | 1.35357 | 7.48099 | 1.71E-05 | 0.00033  | 2.09163 |
| ZDHHC2   | 1.25716 | 2.6513  | 30.8324 | 1.52E-11 | 3.49E-09 | 17.0806 |
| VANGL2   | 1.25763 | 2.04017 | 9.77493 | 1.47E-06 | 3.94E-05 | 4.74346 |
| NHSL2    | 1.26102 | 2.10021 | 16.3468 | 9.66E-09 | 5.48E-07 | 10.1814 |
| PDE4DIP  | 1.26676 | 0.77707 | 14.4153 | 3.39E-08 | 1.56E-06 | 8.82598 |
| ATP6V0D  | 1.26692 | 0.83415 | 11.9099 | 2.21E-07 | 7.67E-06 | 6.79464 |
| LBX1     | 1.26864 | 0.63432 | 11.1364 | 4.24E-07 | 1.32E-05 | 6.09049 |
| APOL1    | 1.27019 | 1.90175 | 13.6759 | 5.70E-08 | 2.41E-06 | 8.26199 |
| GBP2     | 1.27193 | 0.73631 | 12.9692 | 9.62E-08 | 3.77E-06 | 7.69639 |
| RPA4     | 1.27429 | 1.51829 | 15.8458 | 1.32E-08 | 7.14E-07 | 9.84487 |
| RARB     | 1.27942 | 1.18783 | 18.2252 | 3.24E-09 | 2.27E-07 | 11.3613 |
| ZFP42    | 1.28024 | 0.81999 | 13.497  | 6.49E-08 | 2.71E-06 | 8.12136 |
| MIR222H  | 1.28038 | 0.9204  | 15.9763 | 1.22E-08 | 6.66E-07 | 9.9335  |
| ACTA2-A  | 1.28165 | 1.91157 | 20.2367 | 1.12E-09 | 9.45E-08 | 12.5008 |
| TCIM     | 1.2826  | 0.6413  | 22.7536 | 3.41E-10 | 3.78E-08 | 13.7788 |
| ABCD2    | 1.28285 | 0.79194 | 12.3614 | 1.54E-07 | 5.63E-06 | 7.18737 |
| SALRNA1  | 1.28294 | 0.988   | 9.87563 | 1.33E-06 | 3.64E-05 | 4.84825 |
| MARCKS   | 1.28384 | 0.74226 | 13.324  | 7.37E-08 | 3.00E-06 | 7.98376 |
| VSNL1    | 1.284   | 0.74234 | 15.2005 | 2.00E-08 | 9.95E-07 | 9.39637 |
| PRAL     | 1.28857 | 1.77139 | 11.1677 | 4.12E-07 | 1.30E-05 | 6.11979 |
| ELF3     | 1.28882 | 0.82428 | 11.0721 | 4.48E-07 | 1.40E-05 | 6.03014 |
| DDX60    | 1.28971 | 2.2388  | 23.5653 | 2.39E-10 | 2.87E-08 | 14.1609 |
| LINC0191 | 1.29111 | 0.64555 | 23.5238 | 2.43E-10 | 2.91E-08 | 14.1417 |
| ANKRD1   | 1.29228 | 0.90552 | 13.2004 | 8.08E-08 | 3.23E-06 | 7.88441 |
| CACNA1C  | 1.2923  | 1.17608 | 10.0246 | 1.16E-06 | 3.21E-05 | 5.00164 |
| LINC0037 | 1.29325 | 0.64662 | 35.1478 | 3.95E-12 | 1.52E-09 | 18.4895 |
| DLC1     | 1.29374 | 0.84756 | 10.866  | 5.37E-07 | 1.63E-05 | 5.83441 |
| LINC0038 | 1.29458 | 0.64729 | 21.9962 | 4.81E-10 | 4.87E-08 | 13.4096 |
| CSF2RA   | 1.29614 | 0.70836 | 16.3263 | 9.78E-09 | 5.54E-07 | 10.1679 |
| TMEM156  | 1.29783 | 0.82878 | 12.8609 | 1.04E-07 | 4.03E-06 | 7.60724 |
| CARTPT   | 1.29847 | 0.64924 | 24.3652 | 1.70E-10 | 2.22E-08 | 14.5246 |
| NUPR1    | 1.29864 | 1.80136 | 9.32086 | 2.30E-06 | 5.75E-05 | 4.25981 |
| IKZF3    | 1.30024 | 1.07617 | 14.3873 | 3.45E-08 | 1.58E-06 | 8.80506 |
| FGB      | 1.30066 | 0.86717 | 11.061  | 4.52E-07 | 1.41E-05 | 6.0196  |
| OTOL1    | 1.30075 | 0.70055 | 20.0665 | 1.22E-09 | 9.96E-08 | 12.4088 |
| QPCT     | 1.30404 | 0.80253 | 17.9789 | 3.71E-09 | 2.52E-07 | 11.2134 |
| UBBP2    | 1.30539 | 1.10261 | 13.0032 | 9.37E-08 | 3.68E-06 | 7.72427 |
| PSMB8    | 1.30704 | 1.24624 | 14.4309 | 3.35E-08 | 1.54E-06 | 8.83758 |
| ACTG1P2  | 1.3091  | 0.98026 | 10.9418 | 5.02E-07 | 1.54E-05 | 5.90674 |
| POF1B    | 1.31008 | 0.80556 | 16.8767 | 7.02E-09 | 4.22E-07 | 10.5269 |
| SUN3     | 1.31206 | 1.18386 | 19.1969 | 1.92E-09 | 1.46E-07 | 11.9264 |
| PINCR    | 1.31254 | 0.99517 | 15.4726 | 1.67E-08 | 8.61E-07 | 9.5876  |
| IQCJ-SCF | 1.31299 | 0.70667 | 18.3897 | 2.96E-09 | 2.10E-07 | 11.459  |
| OSTN-AS  | 1.3157  | 1.15489 | 13.9932 | 4.55E-08 | 1.98E-06 | 8.50736 |
| PRICKLE  | 1.31675 | 1.0181  | 21.2134 | 6.96E-10 | 6.47E-08 | 13.0146 |
| SAMD10   | 1.32056 | 0.8108  | 10.2996 | 8.96E-07 | 2.57E-05 | 5.28006 |
| CRISPLD  | 1.32142 | 2.08709 | 15.9189 | 1.26E-08 | 6.88E-07 | 9.89459 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| RGL1     | 1.32153 | 1.67676 | 21.7071 | 5.51E-10 | 5.38E-08 | 13.2654 |
| EPS8     | 1.32303 | 1.3009  | 9.17276 | 2.67E-06 | 6.58E-05 | 4.098   |
| TNIP3    | 1.32464 | 0.66232 | 49.8829 | 1.07E-13 | 1.01E-10 | 22.1622 |
| FAM241A  | 1.3275  | 0.83249 | 16.3043 | 9.92E-09 | 5.61E-07 | 10.1532 |
| GBP1P1   | 1.33087 | 0.76578 | 19.8413 | 1.37E-09 | 1.10E-07 | 12.2859 |
| DTNA     | 1.33134 | 1.12574 | 20.2921 | 1.09E-09 | 9.25E-08 | 12.5306 |
| RPS6KA6  | 1.3324  | 1.23514 | 21.9128 | 5.00E-10 | 5.02E-08 | 13.3682 |
| ZNF66    | 1.33413 | 0.77284 | 25.9206 | 9.01E-11 | 1.36E-08 | 15.1984 |
| B3GALT1  | 1.33542 | 0.66771 | 23.3065 | 2.67E-10 | 3.09E-08 | 14.0405 |
| SGCE     | 1.33675 | 0.66837 | 23.0419 | 3.00E-10 | 3.42E-08 | 13.916  |
| HOXD8    | 1.3371  | 0.66855 | 19.7537 | 1.43E-09 | 1.14E-07 | 12.2377 |
| ENO2     | 1.3373  | 1.70403 | 13.2652 | 7.70E-08 | 3.10E-06 | 7.93659 |
| KCNJ3    | 1.3422  | 0.75062 | 13.1118 | 8.64E-08 | 3.43E-06 | 7.8127  |
| ITM2A    | 1.34437 | 1.28722 | 12.1689 | 1.79E-07 | 6.42E-06 | 7.02148 |
| CCRL2    | 1.34679 | 0.72357 | 21.157  | 7.15E-10 | 6.60E-08 | 12.9856 |
| CARD17F  | 1.34852 | 0.67426 | 25.6493 | 1.00E-10 | 1.47E-08 | 15.0839 |
| CXCL10   | 1.35266 | 0.7265  | 19.2147 | 1.90E-09 | 1.45E-07 | 11.9364 |
| C3orf70  | 1.35267 | 0.7265  | 21.3479 | 6.52E-10 | 6.15E-08 | 13.0835 |
| HTATIP2  | 1.35378 | 0.67689 | 21.2611 | 6.80E-10 | 6.35E-08 | 13.0391 |
| SLC7A8   | 1.35543 | 0.84438 | 11.5994 | 2.86E-07 | 9.60E-06 | 6.5169  |
| SULF1    | 1.35601 | 0.77835 | 12.2768 | 1.65E-07 | 5.98E-06 | 7.11473 |
| PDE3A    | 1.35713 | 1.38949 | 21.4218 | 6.30E-10 | 6.00E-08 | 13.1212 |
| HFM1     | 1.35824 | 0.67912 | 21.0351 | 7.58E-10 | 6.88E-08 | 12.9225 |
| TMCC3    | 1.36013 | 1.56151 | 17.8574 | 3.98E-09 | 2.65E-07 | 11.1397 |
| IFITM1   | 1.36338 | 2.68484 | 11.7311 | 2.56E-07 | 8.71E-06 | 6.63549 |
| KCNJ16   | 1.36456 | 0.73245 | 23.1814 | 2.82E-10 | 3.23E-08 | 13.9818 |
| CDCA7L   | 1.36594 | 0.73314 | 19.1537 | 1.96E-09 | 1.49E-07 | 11.9018 |
| IRF8     | 1.36847 | 0.73441 | 22.3945 | 4.01E-10 | 4.28E-08 | 13.6053 |
| PCDH9    | 1.37007 | 2.3861  | 31.1359 | 1.38E-11 | 3.25E-09 | 17.1864 |
| ABCA10   | 1.37098 | 0.81051 | 18.6671 | 2.54E-09 | 1.86E-07 | 11.6218 |
| SCRG1    | 1.373   | 0.7003  | 22.3486 | 4.09E-10 | 4.35E-08 | 13.5829 |
| SIX6     | 1.37651 | 0.68825 | 20.6451 | 9.17E-10 | 8.04E-08 | 12.7186 |
| PSMB8-A  | 1.37783 | 2.14312 | 15.0342 | 2.23E-08 | 1.09E-06 | 9.27784 |
| TRIM53B  | 1.37792 | 0.68896 | 65.0072 | 6.89E-15 | 1.82E-11 | 24.7904 |
| CCR5     | 1.37857 | 0.68928 | 27.5863 | 4.76E-11 | 8.30E-09 | 15.8755 |
| THSD7B   | 1.38013 | 0.69006 | 14.4116 | 3.39E-08 | 1.56E-06 | 8.8232  |
| TFPI2    | 1.38073 | 0.79071 | 17.1262 | 6.05E-09 | 3.73E-07 | 10.686  |
| GIMAP2   | 1.38091 | 1.29138 | 12.9454 | 9.79E-08 | 3.82E-06 | 7.67686 |
| TFEC     | 1.38163 | 0.82051 | 13.0861 | 8.80E-08 | 3.48E-06 | 7.79182 |
| LINC0300 | 1.38165 | 1.26272 | 25.4468 | 1.09E-10 | 1.56E-08 | 14.9976 |
| NEDD9    | 1.38509 | 0.90939 | 16.2264 | 1.04E-08 | 5.82E-07 | 10.1014 |
| GABRB1   | 1.38778 | 0.74406 | 20.1365 | 1.18E-09 | 9.77E-08 | 12.4468 |
| LINC0138 | 1.38795 | 0.69397 | 23.4038 | 2.56E-10 | 2.98E-08 | 14.0859 |
| IL26     | 1.38943 | 0.74488 | 26.1833 | 8.13E-11 | 1.27E-08 | 15.3081 |
| NOS1AP   | 1.38994 | 0.84548 | 11.9256 | 2.18E-07 | 7.60E-06 | 6.80849 |
| ACTN3    | 1.39016 | 2.21397 | 10.2023 | 9.80E-07 | 2.78E-05 | 5.18231 |
| PPP1R3B  | 1.39251 | 1.44992 | 16.4433 | 9.11E-09 | 5.21E-07 | 10.2451 |
| LINC0057 | 1.39288 | 0.69644 | 28.1418 | 3.88E-11 | 7.31E-09 | 16.0919 |
| APOE     | -1.3951 | 1.91431 | 8.51791 | 5.30E-06 | 0.00012  | 3.3571  |
| OAS1     | 1.39529 | 0.74781 | 16.4808 | 8.90E-09 | 5.13E-07 | 10.2698 |
| JPH1     | 1.39537 | 1.62381 | 16.9167 | 6.85E-09 | 4.14E-07 | 10.5526 |
| CDH12    | 1.39555 | 1.22479 | 12.7963 | 1.10E-07 | 4.19E-06 | 7.55379 |
| GBP7     | 1.39616 | 0.69808 | 17.9821 | 3.71E-09 | 2.52E-07 | 11.2154 |
| ADAMTS   | 1.39906 | 0.82922 | 12.7202 | 1.16E-07 | 4.39E-06 | 7.49047 |
| FOXN4    | 1.39923 | 1.40253 | 10.2367 | 9.50E-07 | 2.70E-05 | 5.21698 |
| MAP2     | 1.41216 | 1.72828 | 15.6217 | 1.52E-08 | 8.03E-07 | 9.69109 |
| TRIM64B  | 1.41368 | 0.70684 | 23.4335 | 2.53E-10 | 2.97E-08 | 14.0997 |
| HOXD4    | 1.41399 | 0.75717 | 19.0315 | 2.09E-09 | 1.57E-07 | 11.8322 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| SAMD9    | 1.4144  | 0.85772 | 17.453  | 5.01E-09 | 3.21E-07 | 10.891  |
| ZNF516   | 1.4145  | 2.14718 | 12.7312 | 1.15E-07 | 4.35E-06 | 7.49966 |
| PDE4DIP  | 1.42195 | 0.84067 | 13.7781 | 5.30E-08 | 2.26E-06 | 8.3416  |
| B3GALNT  | 1.4241  | 0.71205 | 27.4696 | 4.97E-11 | 8.52E-09 | 15.8294 |
| CTSF     | 1.42425 | 0.74147 | 22.2003 | 4.38E-10 | 4.53E-08 | 13.5104 |
| CDH7     | 1.43194 | 0.81631 | 21.3421 | 6.54E-10 | 6.15E-08 | 13.0805 |
| CRADD-A  | 1.43748 | 0.76891 | 24.5544 | 1.57E-10 | 2.11E-08 | 14.6089 |
| DNAJC15  | 1.44028 | 0.72014 | 54.1278 | 4.58E-14 | 5.87E-11 | 22.9902 |
| LRRTM4-  | 1.44245 | 0.72122 | 41.6442 | 6.88E-13 | 4.48E-10 | 20.2895 |
| PIK3C2G  | 1.44256 | 0.82162 | 20.0797 | 1.21E-09 | 9.93E-08 | 12.416  |
| PCLO     | 1.4447  | 1.01108 | 15.1735 | 2.03E-08 | 1.01E-06 | 9.37716 |
| MIR100H  | 1.4504  | 0.87572 | 19.0943 | 2.02E-09 | 1.53E-07 | 11.868  |
| LINC0171 | 1.45131 | 0.8329  | 17.1841 | 5.85E-09 | 3.63E-07 | 10.7226 |
| POU4F1   | 1.45366 | 0.72683 | 27.8802 | 4.27E-11 | 7.75E-09 | 15.9905 |
| CCN2     | 1.45435 | 1.18257 | 12.2463 | 1.69E-07 | 6.09E-06 | 7.08845 |
| BEX1     | 1.45481 | 1.26528 | 23.788  | 2.17E-10 | 2.68E-08 | 14.2634 |
| TAP1     | 1.45519 | 2.73568 | 14.1713 | 4.01E-08 | 1.79E-06 | 8.64286 |
| NEO1     | 1.45529 | 2.21937 | 18.3128 | 3.08E-09 | 2.18E-07 | 11.4134 |
| TRIM9    | 1.45751 | 0.90862 | 15.3156 | 1.85E-08 | 9.38E-07 | 9.47763 |
| SORCS1   | 1.45794 | 0.72897 | 27.0631 | 5.79E-11 | 9.43E-09 | 15.6675 |
| LINC0086 | 1.45857 | 1.47666 | 20.8712 | 8.21E-10 | 7.34E-08 | 12.8373 |
| RBPMS    | 1.46307 | 2.4015  | 19.7797 | 1.42E-09 | 1.13E-07 | 12.252  |
| GAREM1   | 1.46372 | 1.38591 | 17.1584 | 5.94E-09 | 3.68E-07 | 10.7064 |
| JPH2     | 1.46427 | 0.78231 | 23.0108 | 3.04E-10 | 3.44E-08 | 13.9013 |
| PALLD    | 1.46526 | 1.77162 | 13.2366 | 7.87E-08 | 3.16E-06 | 7.91359 |
| THRB     | 1.46621 | 0.73311 | 22.9089 | 3.18E-10 | 3.56E-08 | 13.8529 |
| ZNF835   | 1.46709 | 0.78372 | 18.5882 | 2.65E-09 | 1.93E-07 | 11.5757 |
| CDH9     | 1.46805 | 0.7842  | 22.2741 | 4.24E-10 | 4.43E-08 | 13.5465 |
| BDNF     | 1.47153 | 0.87235 | 14.7204 | 2.75E-08 | 1.30E-06 | 9.05092 |
| APOL6    | 1.47656 | 2.42762 | 32.9615 | 7.66E-12 | 2.25E-09 | 17.8004 |
| LZTS1    | 1.47925 | 1.25282 | 9.95322 | 1.24E-06 | 3.41E-05 | 4.92841 |
| C1orf21  | 1.48539 | 1.07307 | 12.79   | 1.10E-07 | 4.19E-06 | 7.54857 |
| ZFHx4-A  | 1.48732 | 0.74366 | 88.0112 | 2.99E-16 | 2.29E-12 | 27.5398 |
| RGS18    | 1.48736 | 0.74368 | 28.0532 | 4.01E-11 | 7.44E-09 | 16.0577 |
| TRPS1    | 1.49107 | 2.09901 | 26.9413 | 6.07E-11 | 9.72E-09 | 15.6184 |
| HAND2-A  | 1.49156 | 0.74578 | 14.852  | 2.52E-08 | 1.20E-06 | 9.14664 |
| DOCK10   | 1.49423 | 1.10684 | 16.436  | 9.15E-09 | 5.22E-07 | 10.2403 |
| SLC1A3   | 1.49463 | 1.07769 | 12.7345 | 1.15E-07 | 4.35E-06 | 7.50237 |
| CYP1B1   | 1.49571 | 2.88906 | 27.6672 | 4.62E-11 | 8.12E-09 | 15.9073 |
| COLEC12  | 1.49791 | 1.18543 | 11.4011 | 3.38E-07 | 1.10E-05 | 6.33612 |
| F2RL2    | 1.49878 | 1.0296  | 10.1574 | 1.02E-06 | 2.88E-05 | 5.13694 |
| SCHIP1   | 1.49946 | 0.85007 | 20.3356 | 1.07E-09 | 9.09E-08 | 12.554  |
| EPM2AIP  | 1.49986 | 0.76312 | 35.0362 | 4.08E-12 | 1.56E-09 | 18.4555 |
| LINC0155 | 1.50108 | 0.9373  | 15.0855 | 2.16E-08 | 1.06E-06 | 9.31457 |
| TRIM53A  | 1.50423 | 0.75211 | 33.9044 | 5.73E-12 | 1.93E-09 | 18.1035 |
| LRP1B    | 1.50452 | 1.01164 | 16.3931 | 9.39E-09 | 5.35E-07 | 10.212  |
| CCDC33   | 1.50492 | 0.75246 | 15.8371 | 1.33E-08 | 7.16E-07 | 9.83898 |
| BMPER    | 1.5053  | 1.00351 | 14.8482 | 2.52E-08 | 1.21E-06 | 9.14392 |
| HOXB9    | 1.5057  | 1.8692  | 21.6835 | 5.57E-10 | 5.42E-08 | 13.2535 |
| ZNF439   | 1.50775 | 1.526   | 37.3431 | 2.12E-12 | 1.00E-09 | 19.1361 |
| USH2A    | 1.5117  | 1.26405 | 14.9089 | 2.42E-08 | 1.17E-06 | 9.18782 |
| LINC0085 | 1.51296 | 0.836   | 21.7826 | 5.32E-10 | 5.23E-08 | 13.3033 |
| COL2A1   | 1.51506 | 0.96674 | 11.0216 | 4.68E-07 | 1.45E-05 | 5.98242 |
| OVCH2    | 1.51587 | 0.83745 | 15.6179 | 1.52E-08 | 8.03E-07 | 9.68849 |
| MLLT3    | 1.51587 | 0.9378  | 15.7412 | 1.41E-08 | 7.55E-07 | 9.77334 |
| DEPDC7   | 1.51595 | 0.80815 | 23.7566 | 2.20E-10 | 2.70E-08 | 14.249  |
| ADRB1    | 1.51632 | 0.80833 | 17.3001 | 5.47E-09 | 3.44E-07 | 10.7956 |
| RIC3     | 1.52246 | 1.47978 | 21.7034 | 5.52E-10 | 5.38E-08 | 13.2636 |

|         |         |         |         |          |          |         |
|---------|---------|---------|---------|----------|----------|---------|
| NEFL    | 1.52276 | 1.76966 | 12.6146 | 1.26E-07 | 4.69E-06 | 7.40209 |
| CHODL   | 1.52287 | 0.91195 | 17.7123 | 4.32E-09 | 2.84E-07 | 11.0512 |
| LMO4    | 1.52721 | 2.42332 | 24.3805 | 1.69E-10 | 2.21E-08 | 14.5315 |
| MDGA1   | 1.5302  | 1.58172 | 18.3339 | 3.05E-09 | 2.16E-07 | 11.4259 |
| MESTP1  | 1.53035 | 0.76517 | 31.6167 | 1.17E-11 | 2.99E-09 | 17.3517 |
| KCTD14  | 1.53137 | 0.95245 | 16.4549 | 9.04E-09 | 5.18E-07 | 10.2528 |
| VCAN-AS | 1.53399 | 0.91751 | 20.0701 | 1.22E-09 | 9.96E-08 | 12.4108 |
| ADAMTS  | 1.53465 | 1.65331 | 27.1552 | 5.60E-11 | 9.19E-09 | 15.7044 |
| FCGRT   | 1.539   | 1.09988 | 15.3601 | 1.80E-08 | 9.18E-07 | 9.50895 |
| DSG3    | 1.53923 | 0.76961 | 38.5546 | 1.52E-12 | 7.86E-10 | 19.4754 |
| VEPH1   | 1.53987 | 0.82011 | 28.5638 | 3.33E-11 | 6.52E-09 | 16.2533 |
| KRT222  | 1.54031 | 1.29655 | 13.1008 | 8.71E-08 | 3.45E-06 | 7.80378 |
| MLH1    | 1.5407  | 0.97104 | 14.5267 | 3.14E-08 | 1.46E-06 | 8.90862 |
| PHOX2B  | 1.54254 | 0.77127 | 19.7671 | 1.42E-09 | 1.13E-07 | 12.2451 |
| TRHDE-A | 1.54419 | 1.25684 | 13.7057 | 5.58E-08 | 2.36E-06 | 8.28524 |
| AGT     | 1.54523 | 0.77262 | 36.0589 | 3.04E-12 | 1.30E-09 | 18.7631 |
| BHLHE41 | 1.54733 | 0.92418 | 15.7592 | 1.39E-08 | 7.48E-07 | 9.78572 |
| RERG    | 1.5485  | 1.325   | 19.0271 | 2.10E-09 | 1.57E-07 | 11.8297 |
| FGF5    | 1.55142 | 1.40147 | 12.7916 | 1.10E-07 | 4.19E-06 | 7.54985 |
| PLCB4   | 1.55172 | 0.77586 | 46.3688 | 2.27E-13 | 1.92E-10 | 21.4108 |
| ADD3    | 1.55424 | 1.9396  | 24.2903 | 1.75E-10 | 2.27E-08 | 14.4911 |
| MYH15   | 1.55524 | 1.47421 | 25.2006 | 1.20E-10 | 1.69E-08 | 14.8918 |
| UCHL1   | 1.55644 | 2.45832 | 25.2987 | 1.16E-10 | 1.64E-08 | 14.9341 |
| PRTFDC1 | 1.55885 | 0.77943 | 44.3731 | 3.57E-13 | 2.73E-10 | 20.9539 |
| DSG2    | 1.55922 | 1.22123 | 23.0295 | 3.02E-10 | 3.42E-08 | 13.9102 |
| ANTXR2  | 1.56181 | 1.04029 | 14.434  | 3.34E-08 | 1.54E-06 | 8.83991 |
| POU3F4  | 1.56302 | 0.78151 | 22.0743 | 4.64E-10 | 4.75E-08 | 13.4483 |
| HAS2    | 1.56466 | 0.99154 | 15.1954 | 2.00E-08 | 9.97E-07 | 9.39275 |
| ZNF354C | 1.5699  | 1.46978 | 19.575  | 1.57E-09 | 1.22E-07 | 12.1387 |
| PGPEP1L | 1.5778  | 0.7889  | 29.902  | 2.08E-11 | 4.45E-09 | 16.7493 |
| HOXD9   | 1.57811 | 0.78905 | 22.0254 | 4.75E-10 | 4.84E-08 | 13.4241 |
| RBPMS-A | 1.58495 | 0.84265 | 19.0149 | 2.11E-09 | 1.57E-07 | 11.8226 |
| UGT3A2  | 1.58805 | 1.22475 | 15.5894 | 1.55E-08 | 8.14E-07 | 9.66875 |
| GBP3    | 1.59051 | 0.94577 | 22.7413 | 3.43E-10 | 3.79E-08 | 13.7729 |
| FRRS1   | 1.59156 | 1.09681 | 13.0914 | 8.77E-08 | 3.47E-06 | 7.79617 |
| PRL     | 1.59199 | 0.796   | 36.3656 | 2.78E-12 | 1.23E-09 | 18.8535 |
| ABCA5   | 1.59389 | 1.72843 | 22.0257 | 4.75E-10 | 4.84E-08 | 13.4243 |
| RADX    | 1.59856 | 0.89962 | 21.1543 | 7.16E-10 | 6.60E-08 | 12.9842 |
| NEGR1   | 1.60071 | 0.80035 | 36.6875 | 2.54E-12 | 1.16E-09 | 18.9475 |
| TMEM47  | 1.60172 | 1.87597 | 22.3076 | 4.17E-10 | 4.38E-08 | 13.5629 |
| GAD1    | 1.60706 | 1.59063 | 17.2736 | 5.55E-09 | 3.48E-07 | 10.7789 |
| GCNT2   | 1.609   | 1.14136 | 17.3713 | 5.25E-09 | 3.33E-07 | 10.8401 |
| VMO1    | 1.60977 | 1.4686  | 7.458   | 1.76E-05 | 0.00034  | 2.06219 |
| FOXL2   | 1.60998 | 0.95551 | 11.24   | 3.88E-07 | 1.23E-05 | 6.18727 |
| RFPL1S  | 1.61123 | 0.96465 | 17.7085 | 4.32E-09 | 2.84E-07 | 11.0488 |
| CYP4F35 | 1.613   | 0.91821 | 17.2934 | 5.49E-09 | 3.45E-07 | 10.7914 |
| MDFI    | 1.6133  | 0.93634 | 13.5744 | 6.14E-08 | 2.58E-06 | 8.18242 |
| EPB41L3 | 1.61416 | 1.1668  | 16.716  | 7.72E-09 | 4.57E-07 | 10.4232 |
| OR5AO1F | 1.62041 | 0.86038 | 26.2048 | 8.06E-11 | 1.26E-08 | 15.3171 |
| SLIT2   | 1.62263 | 2.50238 | 16.7355 | 7.63E-09 | 4.53E-07 | 10.4359 |
| QPRT    | 1.6258  | 2.00266 | 17.4942 | 4.89E-09 | 3.15E-07 | 10.9166 |
| SCIN    | 1.62957 | 0.86496 | 22.308  | 4.17E-10 | 4.38E-08 | 13.5631 |
| IFNG    | 1.63055 | 0.86545 | 25.482  | 1.07E-10 | 1.55E-08 | 15.0127 |
| EFNB2   | 1.63102 | 0.99537 | 16.1412 | 1.10E-08 | 6.07E-07 | 10.0445 |
| NIPAL4  | 1.63376 | 1.12643 | 20.4088 | 1.03E-09 | 8.82E-08 | 12.5931 |
| TARID   | 1.63661 | 0.81831 | 92.19   | 1.85E-16 | 2.29E-12 | 27.9294 |
| ANK3    | 1.63734 | 2.54049 | 27.2012 | 5.50E-11 | 9.14E-09 | 15.7228 |
| IFI16   | 1.63758 | 0.94848 | 18.3292 | 3.06E-09 | 2.16E-07 | 11.4231 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| MGAT4C   | 1.63798 | 0.92623 | 23.9341 | 2.04E-10 | 2.53E-08 | 14.3301 |
| DLK1     | 1.64105 | 0.82053 | 29.1699 | 2.69E-11 | 5.44E-09 | 16.4809 |
| LMO1     | 1.6428  | 1.2049  | 12.8794 | 1.03E-07 | 3.98E-06 | 7.62252 |
| SAA1     | 1.64292 | 0.9805  | 18.6911 | 2.51E-09 | 1.84E-07 | 11.6357 |
| PCDH20   | 1.65135 | 1.32625 | 19.2969 | 1.82E-09 | 1.40E-07 | 11.9829 |
| MMP8     | 1.6581  | 1.55146 | 21.3708 | 6.45E-10 | 6.10E-08 | 13.0952 |
| SRPX2    | 1.65908 | 1.19689 | 12.6994 | 1.18E-07 | 4.45E-06 | 7.47311 |
| LINC0259 | 1.65986 | 0.84892 | 27.7726 | 4.45E-11 | 7.95E-09 | 15.9486 |
| TPH2     | 1.66373 | 0.83186 | 58.9988 | 1.88E-14 | 3.39E-11 | 23.8478 |
| TRG-AS1  | 1.66754 | 0.93411 | 16.9497 | 6.72E-09 | 4.09E-07 | 10.5737 |
| NR2E1    | 1.6678  | 0.8339  | 28.1248 | 3.91E-11 | 7.32E-09 | 16.0853 |
| SHC3     | 1.6689  | 0.83445 | 31.0372 | 1.42E-11 | 3.32E-09 | 17.1521 |
| SEMA6A   | 1.67352 | 2.20829 | 17.9475 | 3.78E-09 | 2.55E-07 | 11.1944 |
| CCSER1   | 1.67483 | 0.85061 | 33.3531 | 6.78E-12 | 2.13E-09 | 17.9274 |
| SHROOM   | 1.67592 | 1.62786 | 21.6349 | 5.70E-10 | 5.53E-08 | 13.2291 |
| MAP2K6   | 1.68059 | 2.15246 | 45.2693 | 2.91E-13 | 2.36E-10 | 21.1619 |
| PREX2    | 1.68075 | 0.89055 | 26.1151 | 8.35E-11 | 1.28E-08 | 15.2798 |
| MAT1A    | 1.68199 | 1.09185 | 15.2889 | 1.89E-08 | 9.51E-07 | 9.45887 |
| KIF25-AS | 1.68296 | 0.84148 | 16.1757 | 1.07E-08 | 5.97E-07 | 10.0676 |
| DDAH1    | 1.6853  | 1.6619  | 22.4434 | 3.92E-10 | 4.21E-08 | 13.6291 |
| PYGM     | 1.68729 | 1.33306 | 15.0759 | 2.17E-08 | 1.06E-06 | 9.30773 |
| HAND2    | 1.68765 | 0.84383 | 15.8752 | 1.30E-08 | 7.04E-07 | 9.8649  |
| SNCG     | 1.69081 | 1.27145 | 12.0568 | 1.96E-07 | 6.93E-06 | 6.92377 |
| NAALAD2  | 1.6944  | 2.39649 | 24.0504 | 1.94E-10 | 2.44E-08 | 14.383  |
| NKX2-1   | 1.69911 | 0.84955 | 22.9783 | 3.08E-10 | 3.47E-08 | 13.8859 |
| ALDH1A2  | 1.70145 | 1.21045 | 17.9034 | 3.87E-09 | 2.59E-07 | 11.1677 |
| LINC0109 | 1.70231 | 1.55741 | 23.4929 | 2.46E-10 | 2.93E-08 | 14.1273 |
| POU3F3   | 1.70386 | 0.85193 | 30.3524 | 1.79E-11 | 3.90E-09 | 16.911  |
| TAC1     | 1.71385 | 0.85693 | 60.3728 | 1.48E-14 | 2.94E-11 | 24.0739 |
| GLUL     | 1.7141  | 1.74095 | 33.9872 | 5.59E-12 | 1.90E-09 | 18.1296 |
| BOC      | 1.719   | 1.81176 | 16.7345 | 7.64E-09 | 4.53E-07 | 10.4352 |
| NRP1     | 1.72054 | 1.23615 | 17.4478 | 5.02E-09 | 3.22E-07 | 10.8878 |
| PDGFRL   | 1.72081 | 1.62263 | 14.9842 | 2.30E-08 | 1.12E-06 | 9.242   |
| RIPOR2   | 1.7247  | 1.04222 | 17.1937 | 5.82E-09 | 3.62E-07 | 10.7286 |
| DCLK1    | 1.72543 | 0.86272 | 36.0722 | 3.03E-12 | 1.30E-09 | 18.767  |
| NETO1    | 1.72657 | 1.09332 | 21.1304 | 7.24E-10 | 6.64E-08 | 12.9718 |
| METTL7B  | 1.72893 | 1.44456 | 13.4761 | 6.59E-08 | 2.75E-06 | 8.10481 |
| LINC0255 | 1.73097 | 0.86548 | 57.0693 | 2.65E-14 | 4.07E-11 | 23.5189 |
| ARL4C    | 1.73168 | 0.91601 | 20.8741 | 8.20E-10 | 7.34E-08 | 12.8388 |
| MME-AS1  | 1.73532 | 0.86766 | 58.3512 | 2.11E-14 | 3.64E-11 | 23.7389 |
| TMEM200  | 1.73846 | 0.86923 | 43.0917 | 4.84E-13 | 3.49E-10 | 20.6479 |
| PDGFRA   | 1.73908 | 2.51641 | 34.8941 | 4.26E-12 | 1.60E-09 | 18.412  |
| ZNF737   | 1.74472 | 1.24554 | 24.5156 | 1.59E-10 | 2.14E-08 | 14.5917 |
| OAS2     | 1.7476  | 1.56981 | 33.3326 | 6.82E-12 | 2.13E-09 | 17.9208 |
| IKZF2    | 1.75488 | 0.92761 | 26.4917 | 7.21E-11 | 1.14E-08 | 15.4355 |
| SLC2A10  | 1.76042 | 0.88021 | 32.4075 | 9.11E-12 | 2.53E-09 | 17.618  |
| ANO3-AS  | 1.7632  | 0.8816  | 40.0825 | 1.02E-12 | 6.05E-10 | 19.8868 |
| D21S208  | 1.76734 | 0.93384 | 32.4266 | 9.06E-12 | 2.53E-09 | 17.6243 |
| SIX3     | 1.77456 | 0.93745 | 24.6314 | 1.52E-10 | 2.05E-08 | 14.643  |
| RNLS     | 1.78385 | 0.99227 | 25.9001 | 9.09E-11 | 1.36E-08 | 15.1898 |
| KLHDC8A  | 1.78751 | 0.94393 | 22.6533 | 3.57E-10 | 3.90E-08 | 13.7306 |
| CDK6     | 1.78765 | 1.12386 | 19.0419 | 2.08E-09 | 1.56E-07 | 11.8381 |
| BRINP3   | 1.7891  | 1.53744 | 18.2206 | 3.24E-09 | 2.27E-07 | 11.3585 |
| ZNF432   | 1.79335 | 0.99702 | 24.205  | 1.81E-10 | 2.33E-08 | 14.4527 |
| FGF18    | 1.79503 | 1.42686 | 20.9997 | 7.71E-10 | 6.98E-08 | 12.9042 |
| CD40     | 1.79942 | 0.94988 | 24.1406 | 1.86E-10 | 2.37E-08 | 14.4237 |
| FRMD7    | 1.80128 | 0.90064 | 63.1337 | 9.32E-15 | 2.20E-11 | 24.5089 |
| CLDN17   | 1.80211 | 0.95123 | 28.343  | 3.61E-11 | 6.93E-09 | 16.1692 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| ZNF841   | 1.80536 | 0.9759  | 25.7753 | 9.55E-11 | 1.41E-08 | 15.1373 |
| DCDC1    | 1.80556 | 1.34965 | 16.7664 | 7.49E-09 | 4.47E-07 | 10.4558 |
| TBX18    | 1.80687 | 0.90344 | 40.2767 | 9.71E-13 | 5.96E-10 | 19.9378 |
| THBS1    | 1.80863 | 1.81717 | 30.472  | 1.72E-11 | 3.77E-09 | 16.9535 |
| KCNS1    | 1.80987 | 0.90493 | 80.5654 | 7.46E-16 | 3.29E-12 | 26.7725 |
| CNTNAP2  | 1.8108  | 0.96247 | 31.9374 | 1.06E-11 | 2.82E-09 | 17.4605 |
| FILIP1L  | 1.8176  | 2.08518 | 38.6813 | 1.47E-12 | 7.80E-10 | 19.5102 |
| OTOAP1   | 1.82026 | 1.23937 | 21.9607 | 4.89E-10 | 4.93E-08 | 13.392  |
| SHROOM   | 1.82377 | 0.98105 | 26.4075 | 7.45E-11 | 1.17E-08 | 15.4009 |
| NBEA     | 1.8257  | 2.08157 | 25.141  | 1.23E-10 | 1.72E-08 | 14.866  |
| ITGA8    | 1.82571 | 1.0132  | 23.5121 | 2.44E-10 | 2.92E-08 | 14.1362 |
| PCYT1B   | 1.82864 | 1.37439 | 24.4926 | 1.61E-10 | 2.15E-08 | 14.5814 |
| ANKRD30  | 1.82873 | 1.04405 | 28.0264 | 4.05E-11 | 7.48E-09 | 16.0473 |
| GPR85    | 1.83107 | 0.91553 | 43.8852 | 4.01E-13 | 3.00E-10 | 20.8386 |
| CER1     | 1.83825 | 0.9693  | 33.2628 | 6.97E-12 | 2.16E-09 | 17.8983 |
| TLX3     | 1.83927 | 1.01998 | 15.5888 | 1.55E-08 | 8.14E-07 | 9.66835 |
| CNN1     | 1.84117 | 1.49601 | 16.751  | 7.56E-09 | 4.50E-07 | 10.4459 |
| RASSF9   | 1.84178 | 1.2011  | 17.9495 | 3.77E-09 | 2.55E-07 | 11.1956 |
| LRRC55   | 1.8451  | 0.97272 | 23.6307 | 2.32E-10 | 2.82E-08 | 14.1911 |
| CASP4    | 1.85107 | 1.34659 | 15.7375 | 1.41E-08 | 7.56E-07 | 9.77083 |
| MBNL3    | 1.85259 | 1.10616 | 20.1799 | 1.16E-09 | 9.62E-08 | 12.4702 |
| LACC1    | 1.85463 | 0.97749 | 30.6505 | 1.62E-11 | 3.61E-09 | 17.0167 |
| C1orf226 | 1.855   | 1.07802 | 14.925  | 2.40E-08 | 1.16E-06 | 9.19941 |
| ARMCX4   | 1.85534 | 0.92767 | 17.6257 | 4.53E-09 | 2.96E-07 | 10.9979 |
| IL21R    | 1.85716 | 1.23814 | 11.021  | 4.68E-07 | 1.45E-05 | 5.98186 |
| APOL3    | 1.8586  | 1.19631 | 13.1774 | 8.22E-08 | 3.28E-06 | 7.86589 |
| LINC0238 | 1.86041 | 1.00972 | 22.163  | 4.46E-10 | 4.60E-08 | 13.492  |
| CRABP2   | 1.86207 | 2.18279 | 16.6464 | 8.05E-09 | 4.73E-07 | 10.378  |
| EDIL3    | 1.86806 | 1.16406 | 14.7637 | 2.67E-08 | 1.27E-06 | 9.08253 |
| CCR5AS   | 1.86909 | 0.93454 | 31.6255 | 1.17E-11 | 2.99E-09 | 17.3547 |
| COL4A6   | 1.87204 | 0.98619 | 22.6028 | 3.65E-10 | 3.96E-08 | 13.7063 |
| FOXG1    | 1.87458 | 0.93729 | 30.26   | 1.84E-11 | 3.98E-09 | 16.878  |
| ZNF85    | 1.87562 | 1.22934 | 23.2834 | 2.70E-10 | 3.11E-08 | 14.0297 |
| BISPR    | 1.87907 | 1.16957 | 18.626  | 2.60E-09 | 1.89E-07 | 11.5978 |
| PRDM8    | 1.88377 | 1.47531 | 18.183  | 3.31E-09 | 2.31E-07 | 11.3361 |
| FREM1    | 1.88881 | 1.09492 | 22.3114 | 4.16E-10 | 4.38E-08 | 13.5648 |
| PRR16    | 1.89218 | 1.26327 | 19.8279 | 1.38E-09 | 1.11E-07 | 12.2785 |
| DSC2     | 1.89513 | 1.09808 | 23.4529 | 2.50E-10 | 2.96E-08 | 14.1088 |
| LINC0165 | 1.89524 | 0.94762 | 55.2062 | 3.74E-14 | 5.12E-11 | 23.188  |
| LINC0021 | 1.89722 | 0.94861 | 38.4229 | 1.58E-12 | 7.94E-10 | 19.4391 |
| MME      | 1.89983 | 2.20929 | 35.9361 | 3.15E-12 | 1.32E-09 | 18.7266 |
| CRABP1   | 1.89986 | 0.94993 | 26.1318 | 8.29E-11 | 1.28E-08 | 15.2867 |
| ISL1-DT  | 1.90036 | 1.00035 | 31.8184 | 1.10E-11 | 2.90E-09 | 17.4203 |
| PIP5K1B  | 1.90825 | 1.05447 | 28.9269 | 2.93E-11 | 5.79E-09 | 16.3903 |
| MIR7-3HC | 1.90954 | 1.00494 | 34.0922 | 5.41E-12 | 1.89E-09 | 18.1628 |
| DPYD     | 1.91303 | 1.42511 | 41.0866 | 7.91E-13 | 4.99E-10 | 20.1477 |
| ZEB2     | 1.91677 | 1.00856 | 24.0968 | 1.90E-10 | 2.41E-08 | 14.404  |
| MEF2C-A  | 1.92206 | 0.96103 | 39.3172 | 1.25E-12 | 6.90E-10 | 19.6829 |
| LRFN5    | 1.92305 | 1.17074 | 18.9475 | 2.19E-09 | 1.63E-07 | 11.784  |
| LINC0113 | 1.92833 | 0.96417 | 34.748  | 4.45E-12 | 1.65E-09 | 18.367  |
| BICC1    | 1.93378 | 1.44664 | 14.3793 | 3.47E-08 | 1.58E-06 | 8.7991  |
| ARHGDI3  | 1.93624 | 1.01829 | 30.2831 | 1.83E-11 | 3.97E-09 | 16.8863 |
| FGL1     | 1.937   | 0.9685  | 52.5702 | 6.20E-14 | 6.68E-11 | 22.6958 |
| GPC6     | 1.94219 | 1.67459 | 16.6727 | 7.93E-09 | 4.67E-07 | 10.3951 |
| PPP2R2B  | 1.94699 | 1.10318 | 21.7835 | 5.31E-10 | 5.23E-08 | 13.3037 |
| GPC5     | 1.95887 | 1.1593  | 20.8792 | 8.17E-10 | 7.34E-08 | 12.8415 |
| SOCS3    | 1.96362 | 1.6853  | 14.4452 | 3.32E-08 | 1.53E-06 | 8.84819 |
| EXO5     | 1.96374 | 1.08221 | 19.6652 | 1.50E-09 | 1.18E-07 | 12.1887 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| LINC0062 | 1.96471 | 1.01171 | 34.6098 | 4.63E-12 | 1.69E-09 | 18.3243 |
| IGFN1    | 1.96821 | 1.43394 | 13.9625 | 4.65E-08 | 2.02E-06 | 8.48382 |
| CYB5R2   | 1.97406 | 1.24641 | 20.6207 | 9.28E-10 | 8.10E-08 | 12.7057 |
| GRIK1    | 1.97578 | 1.73112 | 20.4326 | 1.02E-09 | 8.74E-08 | 12.6058 |
| PITX2    | 1.97746 | 1.0389  | 25.4012 | 1.11E-10 | 1.58E-08 | 14.9781 |
| USP53    | 1.97903 | 1.42876 | 23.9533 | 2.02E-10 | 2.51E-08 | 14.3389 |
| MESTIT1  | 1.98249 | 0.99124 | 62.4202 | 1.05E-14 | 2.31E-11 | 24.3988 |
| PPP1R1C  | 1.98266 | 1.0547  | 38.4383 | 1.57E-12 | 7.94E-10 | 19.4433 |
| L1TD1    | 1.98269 | 1.16937 | 36.1847 | 2.93E-12 | 1.28E-09 | 18.8003 |
| ISL1     | 1.98299 | 1.64758 | 18.1776 | 3.32E-09 | 2.31E-07 | 11.3328 |
| SAMD9L   | 1.98474 | 1.04254 | 34.0495 | 5.48E-12 | 1.89E-09 | 18.1493 |
| KANK4    | 1.98543 | 1.46131 | 17.8426 | 4.01E-09 | 2.67E-07 | 11.1307 |
| RGS13    | 1.98825 | 1.0443  | 28.9707 | 2.88E-11 | 5.73E-09 | 16.4067 |
| NRK      | 1.99416 | 2.29643 | 45.0096 | 3.08E-13 | 2.40E-10 | 21.1021 |
| IFI27    | 1.99782 | 1.60745 | 16.9146 | 6.86E-09 | 4.14E-07 | 10.5512 |
| PSMB9    | 2.00192 | 1.88321 | 19.809  | 1.39E-09 | 1.11E-07 | 12.2681 |
| LINC0219 | 2.00232 | 1.00116 | 95.8967 | 1.23E-16 | 2.29E-12 | 28.2529 |
| A1CF     | 2.00617 | 1.32027 | 18.1958 | 3.29E-09 | 2.30E-07 | 11.3438 |
| GBP1     | 2.01008 | 2.25354 | 35.8325 | 3.24E-12 | 1.34E-09 | 18.6958 |
| PTPRO    | 2.01012 | 1.05523 | 27.7587 | 4.47E-11 | 7.96E-09 | 15.9431 |
| LINC0114 | 2.01161 | 1.10432 | 26.9789 | 5.98E-11 | 9.62E-09 | 15.6336 |
| ROBO2    | 2.01248 | 1.55699 | 22.9496 | 3.12E-10 | 3.51E-08 | 13.8723 |
| ZIC4     | 2.01291 | 1.05663 | 28.7304 | 3.14E-11 | 6.17E-09 | 16.3164 |
| SLC7A3   | 2.02055 | 1.16079 | 25.317  | 1.15E-10 | 1.63E-08 | 14.942  |
| PXMP4    | 2.0242  | 1.06546 | 26.9797 | 5.98E-11 | 9.62E-09 | 15.6339 |
| CD248    | 2.02599 | 1.2932  | 13.4655 | 6.64E-08 | 2.77E-06 | 8.0964  |
| KCNMA1   | 2.02931 | 1.14435 | 20.2203 | 1.13E-09 | 9.47E-08 | 12.492  |
| FLRT3    | 2.03569 | 1.76814 | 33.5784 | 6.33E-12 | 2.04E-09 | 17.9997 |
| PDE4DIP  | 2.03787 | 1.10425 | 27.9019 | 4.24E-11 | 7.72E-09 | 15.999  |
| ANKRD20  | 2.03808 | 1.19423 | 20.2863 | 1.10E-09 | 9.26E-08 | 12.5275 |
| CTNNA2   | 2.03922 | 1.29982 | 17.4165 | 5.11E-09 | 3.27E-07 | 10.8683 |
| MUC15    | 2.03959 | 1.32935 | 19.204  | 1.91E-09 | 1.46E-07 | 11.9304 |
| FRY      | 2.04546 | 1.0729  | 33.1016 | 7.33E-12 | 2.19E-09 | 17.846  |
| EBF2     | 2.04661 | 1.0233  | 48.7546 | 1.35E-13 | 1.25E-10 | 21.9279 |
| MMRN1    | 2.05064 | 1.46457 | 39.301  | 1.25E-12 | 6.90E-10 | 19.6786 |
| DTX3     | 2.05334 | 1.12701 | 20.5004 | 9.84E-10 | 8.50E-08 | 12.6419 |
| FMN1     | 2.06252 | 1.03126 | 37.6223 | 1.96E-12 | 9.50E-10 | 19.2154 |
| ZNF521   | 2.06778 | 1.39362 | 32.774  | 8.12E-12 | 2.32E-09 | 17.739  |
| RUNX2    | 2.06997 | 1.39471 | 21.4815 | 6.12E-10 | 5.85E-08 | 13.1515 |
| TRPM3    | 2.07462 | 1.03731 | 59.431  | 1.74E-14 | 3.30E-11 | 23.9196 |
| OR5AK4F  | 2.086   | 1.24369 | 29.3338 | 2.54E-11 | 5.22E-09 | 16.5416 |
| PSD3     | 2.08749 | 1.71598 | 27.5317 | 4.86E-11 | 8.36E-09 | 15.8539 |
| GPM6A    | 2.09087 | 2.2568  | 41.1838 | 7.72E-13 | 4.95E-10 | 20.1726 |
| NTS      | 2.09938 | 2.98774 | 42.6226 | 5.41E-13 | 3.65E-10 | 20.5333 |
| CACNA2D  | 2.1105  | 1.31463 | 19.6084 | 1.55E-09 | 1.21E-07 | 12.1572 |
| NEFH     | 2.11217 | 2.2831  | 22.7343 | 3.44E-10 | 3.80E-08 | 13.7695 |
| SCN7A    | 2.1126  | 1.40283 | 21.551  | 5.93E-10 | 5.69E-08 | 13.1867 |
| TDRD1    | 2.12832 | 1.06416 | 57.0412 | 2.66E-14 | 4.07E-11 | 23.5141 |
| HAPLN1   | 2.1296  | 1.81099 | 50.4599 | 9.47E-14 | 9.43E-11 | 22.2796 |
| INPP4B   | 2.1351  | 1.48597 | 19.1889 | 1.92E-09 | 1.46E-07 | 11.9218 |
| MIR137H  | 2.13705 | 1.21904 | 20.804  | 8.48E-10 | 7.50E-08 | 12.8022 |
| ZNF738   | 2.1435  | 1.20144 | 21.8714 | 5.10E-10 | 5.08E-08 | 13.3476 |
| SCN1A-A  | 2.14446 | 1.48657 | 21.5361 | 5.97E-10 | 5.71E-08 | 13.1792 |
| DSC1     | 2.14683 | 1.08031 | 61.667  | 1.19E-14 | 2.49E-11 | 24.2809 |
| CNTN4    | 2.15401 | 1.17735 | 29.4717 | 2.42E-11 | 5.00E-09 | 16.5924 |
| SOX9     | 2.15641 | 1.0782  | 27.2645 | 5.37E-11 | 9.12E-09 | 15.748  |
| IDO1     | 2.15641 | 1.07821 | 70.3952 | 3.02E-15 | 1.09E-11 | 25.544  |
| CLDN8    | 2.15806 | 1.07903 | 65.7668 | 6.11E-15 | 1.82E-11 | 24.9016 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| RSPO2    | 2.15933 | 1.33052 | 21.8809 | 5.08E-10 | 5.08E-08 | 13.3524 |
| GBP5     | 2.16906 | 1.16405 | 26.1748 | 8.16E-11 | 1.27E-08 | 15.3046 |
| PEG10    | 2.16978 | 1.26475 | 21.4131 | 6.33E-10 | 6.01E-08 | 13.1167 |
| VCAN     | 2.1708  | 1.80577 | 51.2843 | 8.01E-14 | 8.37E-11 | 22.4446 |
| FOLH1B   | 2.17263 | 1.16584 | 38.8253 | 1.42E-12 | 7.61E-10 | 19.5496 |
| BAALC    | 2.17765 | 1.33501 | 17.4087 | 5.14E-09 | 3.28E-07 | 10.8635 |
| PWWP3B   | 2.18802 | 1.40356 | 19.7457 | 1.44E-09 | 1.14E-07 | 12.2333 |
| POSTN    | 2.18889 | 2.99337 | 63.0838 | 9.40E-15 | 2.20E-11 | 24.5013 |
| FGF20    | 2.19496 | 1.14765 | 33.8663 | 5.79E-12 | 1.93E-09 | 18.0914 |
| RORB     | 2.20097 | 1.28035 | 29.2721 | 2.59E-11 | 5.31E-09 | 16.5188 |
| TRHDE    | 2.20538 | 1.20303 | 31.7355 | 1.13E-11 | 2.95E-09 | 17.3922 |
| NDNF     | 2.21019 | 1.15527 | 33.8446 | 5.83E-12 | 1.93E-09 | 18.0845 |
| STRA6    | 2.21067 | 1.25585 | 19.5913 | 1.56E-09 | 1.21E-07 | 12.1478 |
| CEMIP2   | 2.22212 | 2.20273 | 38.3081 | 1.63E-12 | 8.09E-10 | 19.4073 |
| PDE1A    | 2.2276  | 1.39401 | 22.2002 | 4.38E-10 | 4.53E-08 | 13.5103 |
| ASS1     | 2.26444 | 1.13222 | 40.2593 | 9.75E-13 | 5.96E-10 | 19.9332 |
| UNC5C    | 2.26837 | 1.18436 | 31.3392 | 1.29E-11 | 3.09E-09 | 17.2566 |
| SHOX2    | 2.26995 | 2.4106  | 34.4146 | 4.91E-12 | 1.76E-09 | 18.2637 |
| SLC30A8  | 2.28019 | 1.34078 | 22.119  | 4.55E-10 | 4.67E-08 | 13.4704 |
| PDGFD    | 2.28122 | 1.47099 | 15.0448 | 2.21E-08 | 1.08E-06 | 9.28546 |
| LINC0233 | 2.29998 | 1.21915 | 39.0971 | 1.32E-12 | 7.18E-10 | 19.6235 |
| CASP1P2  | 2.30911 | 1.2549  | 32.6479 | 8.45E-12 | 2.38E-09 | 17.6975 |
| MAML3    | 2.30977 | 1.21063 | 23.5666 | 2.38E-10 | 2.87E-08 | 14.1615 |
| VAV3     | 2.31137 | 1.20586 | 35.2419 | 3.85E-12 | 1.51E-09 | 18.5181 |
| POU3F2   | 2.3147  | 1.25769 | 27.9593 | 4.15E-11 | 7.60E-09 | 16.0213 |
| L3MBTL4  | 2.31866 | 1.2095  | 31.5749 | 1.19E-11 | 2.99E-09 | 17.3375 |
| RALGPS2  | 2.32267 | 1.78044 | 24.0319 | 1.95E-10 | 2.45E-08 | 14.3745 |
| B3GALT1  | 2.33287 | 1.30656 | 25.9045 | 9.07E-11 | 1.36E-08 | 15.1917 |
| PCDH15   | 2.3528  | 1.35626 | 27.3299 | 5.24E-11 | 8.94E-09 | 15.7741 |
| NTNG1    | 2.36775 | 1.18388 | 52.8606 | 5.86E-14 | 6.65E-11 | 22.7514 |
| NRXN1    | 2.37117 | 1.62279 | 16.0867 | 1.13E-08 | 6.24E-07 | 10.0079 |
| CPA2     | 2.37391 | 1.2873  | 34.9001 | 4.25E-12 | 1.60E-09 | 18.4138 |
| NOX4     | 2.37493 | 1.18747 | 84.146  | 4.76E-16 | 2.36E-12 | 27.154  |
| SEMA6D   | 2.37564 | 1.28816 | 33.1164 | 7.30E-12 | 2.19E-09 | 17.8508 |
| TLE4     | 2.37822 | 1.59434 | 20.6051 | 9.35E-10 | 8.13E-08 | 12.6975 |
| CCDC178  | 2.37936 | 1.52006 | 28.2317 | 3.76E-11 | 7.14E-09 | 16.1265 |
| XIRP2    | 2.38055 | 1.19027 | 89.0592 | 2.64E-16 | 2.29E-12 | 27.6401 |
| TMEM30B  | 2.39255 | 1.34679 | 31.5317 | 1.21E-11 | 3.01E-09 | 17.3227 |
| SLC5A12  | 2.39892 | 1.19946 | 65.2483 | 6.63E-15 | 1.82E-11 | 24.8259 |
| ZIC1     | 2.40455 | 1.61217 | 23.4374 | 2.52E-10 | 2.97E-08 | 14.1016 |
| CNNM1    | 2.40846 | 1.2544  | 32.1197 | 9.99E-12 | 2.72E-09 | 17.5219 |
| ZNF826P  | 2.41521 | 1.26751 | 53.8295 | 4.85E-14 | 6.02E-11 | 22.9346 |
| SDC2     | 2.42101 | 2.17411 | 34.0289 | 5.52E-12 | 1.89E-09 | 18.1428 |
| SNX7     | 2.42724 | 1.31396 | 32.8236 | 7.99E-12 | 2.31E-09 | 17.7553 |
| IL1RAPL2 | 2.44113 | 1.5216  | 31.2705 | 1.32E-11 | 3.13E-09 | 17.2329 |
| KRT8P48  | 2.44488 | 1.27261 | 34.2206 | 5.21E-12 | 1.83E-09 | 18.2031 |
| TIMP3    | 2.44583 | 2.08434 | 32.074  | 1.01E-11 | 2.74E-09 | 17.5066 |
| CPED1    | 2.45018 | 1.88925 | 41.6632 | 6.85E-13 | 4.48E-10 | 20.2943 |
| ME1      | 2.45175 | 1.22587 | 52.5489 | 6.23E-14 | 6.68E-11 | 22.6916 |
| PTPRD    | 2.46249 | 1.51145 | 23.5005 | 2.45E-10 | 2.93E-08 | 14.1308 |
| ALX1     | 2.46679 | 1.33374 | 32.1477 | 9.90E-12 | 2.72E-09 | 17.5313 |
| GBP4     | 2.4688  | 1.28457 | 38.6356 | 1.49E-12 | 7.80E-10 | 19.4976 |
| FLNC     | 2.47813 | 1.48879 | 17.9319 | 3.81E-09 | 2.57E-07 | 11.185  |
| GRIA4    | 2.48065 | 1.67105 | 24.2143 | 1.81E-10 | 2.33E-08 | 14.457  |
| ANO3     | 2.48197 | 1.86772 | 27.1707 | 5.56E-11 | 9.17E-09 | 15.7106 |
| LAMA1    | 2.49218 | 1.60935 | 25.1213 | 1.24E-10 | 1.72E-08 | 14.8575 |
| PI15     | 2.50284 | 3.30793 | 46.9179 | 2.01E-13 | 1.73E-10 | 21.5325 |
| MFAP2    | 2.50417 | 1.30226 | 24.3592 | 1.70E-10 | 2.22E-08 | 14.522  |

|         |         |         |         |          |          |         |
|---------|---------|---------|---------|----------|----------|---------|
| MSX1    | 2.51642 | 1.76378 | 20.1865 | 1.15E-09 | 9.61E-08 | 12.4738 |
| MARCHF  | 2.52448 | 1.31241 | 27.9641 | 4.14E-11 | 7.60E-09 | 16.0231 |
| TWIST1  | 2.52937 | 1.57424 | 24.6405 | 1.51E-10 | 2.05E-08 | 14.647  |
| PBX1    | 2.53539 | 1.2677  | 31.5256 | 1.21E-11 | 3.01E-09 | 17.3206 |
| PRRX1   | 2.5363  | 1.31832 | 39.6644 | 1.14E-12 | 6.55E-10 | 19.776  |
| CASP1   | 2.5407  | 1.43702 | 31.6984 | 1.14E-11 | 2.97E-09 | 17.3796 |
| LAYN    | 2.57207 | 1.28604 | 85.497  | 4.03E-16 | 2.29E-12 | 27.2918 |
| LHX8    | 2.57382 | 1.76313 | 28.2474 | 3.74E-11 | 7.14E-09 | 16.1325 |
| GPRIN3  | 2.58333 | 2.26979 | 33.4122 | 6.66E-12 | 2.12E-09 | 17.9464 |
| FIBIN   | 2.59261 | 1.92453 | 26.725  | 6.59E-11 | 1.05E-08 | 15.5308 |
| ZFHX4   | 2.59627 | 1.44865 | 31.586  | 1.19E-11 | 2.99E-09 | 17.3412 |
| MTUS1   | 2.61179 | 2.04862 | 47.5544 | 1.75E-13 | 1.58E-10 | 21.6716 |
| CEP41   | 2.61274 | 1.35654 | 37.4747 | 2.04E-12 | 9.78E-10 | 19.1736 |
| TRPC4   | 2.61585 | 1.68848 | 27.221  | 5.46E-11 | 9.14E-09 | 15.7307 |
| KLHL14  | 2.62739 | 1.36386 | 42.6362 | 5.40E-13 | 3.65E-10 | 20.5366 |
| EPHA3   | 2.64302 | 1.98522 | 69.1444 | 3.64E-15 | 1.20E-11 | 25.3761 |
| ITGA1   | 2.66499 | 1.68256 | 20.0884 | 1.21E-09 | 9.93E-08 | 12.4207 |
| ESRRG   | 2.66813 | 1.33406 | 86.2653 | 3.68E-16 | 2.29E-12 | 27.3687 |
| MEF2C   | 2.6767  | 1.94445 | 36.8503 | 2.43E-12 | 1.12E-09 | 18.9947 |
| FIGN    | 2.70219 | 1.65212 | 33.6933 | 6.11E-12 | 1.99E-09 | 18.0364 |
| ALPK2   | 2.71258 | 1.35629 | 88.5537 | 2.80E-16 | 2.29E-12 | 27.592  |
| UCP2    | 2.71796 | 1.35898 | 35.5324 | 3.53E-12 | 1.43E-09 | 18.6059 |
| CCR1    | 2.72541 | 1.83893 | 35.81   | 3.26E-12 | 1.34E-09 | 18.6891 |
| SCN9A   | 2.72625 | 2.36415 | 58.0318 | 2.23E-14 | 3.69E-11 | 23.6847 |
| EPHA7   | 2.75326 | 1.8822  | 33.4057 | 6.67E-12 | 2.12E-09 | 17.9443 |
| COL1A2  | 2.75575 | 1.42805 | 28.143  | 3.88E-11 | 7.31E-09 | 16.0924 |
| OTOA    | 2.76119 | 1.65114 | 30.7672 | 1.55E-11 | 3.53E-09 | 17.0577 |
| CARD16  | 2.79307 | 1.80939 | 18.499  | 2.78E-09 | 2.00E-07 | 11.5234 |
| PAX2    | 2.82281 | 1.41141 | 36.0015 | 3.09E-12 | 1.30E-09 | 18.7461 |
| EYA4    | 2.84035 | 1.62938 | 28.0821 | 3.97E-11 | 7.40E-09 | 16.0688 |
| MAB21L2 | 2.84061 | 1.55    | 26.0942 | 8.42E-11 | 1.28E-08 | 15.271  |
| DLX6    | 2.85458 | 1.47746 | 39.8514 | 1.08E-12 | 6.33E-10 | 19.8257 |
| SNCA    | 2.85548 | 1.42774 | 70.6459 | 2.91E-15 | 1.09E-11 | 25.5772 |
| FREM2   | 2.85992 | 1.74714 | 23.3435 | 2.63E-10 | 3.05E-08 | 14.0578 |
| DLX5    | 2.88101 | 1.49068 | 30.564  | 1.66E-11 | 3.67E-09 | 16.9861 |
| ASXL3   | 2.89764 | 1.66566 | 25.14   | 1.23E-10 | 1.72E-08 | 14.8656 |
| HDAC9   | 2.90642 | 1.63545 | 31.8406 | 1.09E-11 | 2.89E-09 | 17.4278 |
| RGS1    | 2.91223 | 1.87717 | 24.204  | 1.82E-10 | 2.33E-08 | 14.4523 |
| ZPLD1   | 3.02114 | 1.76143 | 31.9455 | 1.06E-11 | 2.82E-09 | 17.4633 |
| LIN28A  | 3.06842 | 2.00544 | 29.614  | 2.30E-11 | 4.79E-09 | 16.6446 |
| COL6A3  | 3.13261 | 2.1402  | 29.0414 | 2.81E-11 | 5.64E-09 | 16.4331 |
| BST2    | 3.14792 | 1.7908  | 20.8161 | 8.43E-10 | 7.48E-08 | 12.8085 |
| TSIX    | 3.15647 | 2.18495 | 39.3488 | 1.24E-12 | 6.90E-10 | 19.6914 |
| MAB21L1 | 3.21882 | 1.78927 | 32.6813 | 8.36E-12 | 2.37E-09 | 17.7086 |
| ARHGAP  | 3.3571  | 1.97491 | 29.8408 | 2.13E-11 | 4.52E-09 | 16.7272 |
| MEST    | 3.35992 | 3.12374 | 20.008  | 1.26E-09 | 1.02E-07 | 12.377  |
| XIST    | 3.46291 | 2.2822  | 27.211  | 5.48E-11 | 9.14E-09 | 15.7267 |
| DLX6-AS | 3.46959 | 2.18167 | 25.6946 | 9.86E-11 | 1.45E-08 | 15.1032 |

**Supplementary Table 3: DEGs in Ovsc4/OVsc4DDP**

| gene      | logFC   | AveExpr | t       | P.Value  | adj.P.Val | B       |
|-----------|---------|---------|---------|----------|-----------|---------|
| HOXD1     | -10.173 | -1.3863 | -41.581 | 1.31E-08 | 1.19E-05  | 10.7679 |
| TSPAN7    | -9.4485 | -2.3856 | -34.431 | 4.03E-08 | 1.89E-05  | 9.78066 |
| CALCR     | -9.3055 | -2.0875 | -19.083 | 1.35E-06 | 0.0001    | 6.25245 |
| HAGLR     | -9.2626 | -2.0709 | -32.978 | 5.21E-08 | 2.01E-05  | 9.54311 |
| ZNF385D   | -9.0295 | -1.4137 | -98.318 | 7.55E-11 | 1.17E-06  | 13.8582 |
| EN2       | -8.8515 | -1.9057 | -43.016 | 1.07E-08 | 1.03E-05  | 10.9355 |
| ANO3      | -8.769  | -2.1016 | -36.255 | 2.96E-08 | 1.48E-05  | 10.0597 |
| HAGLRO    | -8.7275 | -0.0828 | -15.701 | 4.25E-06 | 0.00019   | 5.00276 |
| PRKCB     | -8.6017 | -0.387  | -30.842 | 7.77E-08 | 2.36E-05  | 9.16591 |
| NOSTRIN   | -8.3844 | -1.502  | -9.4934 | 7.81E-05 | 0.00113   | 1.74492 |
| VNN1      | -8.3745 | -1.5396 | -11.627 | 2.45E-05 | 0.00056   | 3.05438 |
| HAVCR1    | -8.2385 | -2.6159 | -20.596 | 8.57E-07 | 8.30E-05  | 6.73395 |
| TDGF1     | -8.1169 | -2.2972 | -15.345 | 4.86E-06 | 0.00021   | 4.85468 |
| TSHR      | -7.8788 | -3.1941 | -59.14  | 1.59E-09 | 3.51E-06  | 12.3338 |
| SST       | -7.8749 | 0.70746 | -4.8073 | 0.00298  | 0.01286   | -2.3811 |
| NR1H4     | -7.8689 | -3.7827 | -20.77  | 8.16E-07 | 8.01E-05  | 6.78687 |
| TMEM252   | -7.8328 | -2.7456 | -31.266 | 7.16E-08 | 2.27E-05  | 9.24365 |
| HOXD8     | -7.8258 | -2.6653 | -28.161 | 1.34E-07 | 3.07E-05  | 8.64006 |
| TDGF1P3   | -7.7825 | -1.8779 | -16.391 | 3.30E-06 | 0.00017   | 5.28006 |
| PLCL1     | -7.7619 | -1.1879 | -16.854 | 2.80E-06 | 0.00015   | 5.45928 |
| HP        | -7.6633 | -1.2506 | -10.914 | 3.52E-05 | 0.0007    | 2.64423 |
| TNIK      | -7.6267 | -2.273  | -20.953 | 7.74E-07 | 7.77E-05  | 6.84183 |
| FEZ1      | -7.6058 | -0.7938 | -13.252 | 1.15E-05 | 0.00035   | 3.90401 |
| ANGPTL1   | -7.512  | -2.5922 | -21.855 | 6.03E-07 | 6.38E-05  | 7.10486 |
| CLEC4E    | -7.5051 | -2.843  | -9.4337 | 8.10E-05 | 0.00116   | 1.70448 |
| PAK3      | -7.2682 | -2.8121 | -28.587 | 1.22E-07 | 2.92E-05  | 8.72787 |
| CA4       | -7.2551 | -3.6281 | -13.093 | 1.23E-05 | 0.00037   | 3.82568 |
| FAM13C    | -7.0368 | -4.1126 | -28.638 | 1.21E-07 | 2.92E-05  | 8.73817 |
| GJA5      | -7.0319 | 0.4473  | -12.66  | 1.50E-05 | 0.00041   | 3.60724 |
| TDRD10    | -7.0054 | -3.4487 | -17.605 | 2.17E-06 | 0.00013   | 5.73879 |
| HOXD-AS1  | -6.9379 | -4.0247 | -28.108 | 1.35E-07 | 3.07E-05  | 8.62887 |
| RGS5      | -6.8892 | -0.7319 | -16.609 | 3.05E-06 | 0.00016   | 5.36526 |
| LINC01111 | -6.7658 | -3.4708 | -25.612 | 2.35E-07 | 4.10E-05  | 8.0761  |
| SPATA18   | -6.7463 | -3.8611 | -21.846 | 6.05E-07 | 6.38E-05  | 7.10234 |
| NRG2      | -6.7385 | -2.9444 | -11.705 | 2.35E-05 | 0.00055   | 3.09793 |
| A2ML1     | -6.6442 | -3.144  | -12.236 | 1.82E-05 | 0.00047   | 3.38616 |
| KCND2     | -6.5555 | -3.2722 | -38.841 | 1.96E-08 | 1.35E-05  | 10.4219 |
| SHE       | -6.5055 | -0.4622 | -7.9995 | 0.0002   | 0.00209   | 0.65564 |
| ZIC2      | -6.4859 | -2.7312 | -26.943 | 1.74E-07 | 3.37E-05  | 8.37906 |
| AADAC     | -6.4299 | -3.6388 | -29.706 | 9.72E-08 | 2.63E-05  | 8.95082 |
| CHGA      | -6.3775 | -0.2723 | -9.5541 | 7.53E-05 | 0.00111   | 1.78586 |
| BMX       | -6.3683 | -3.7747 | -16.731 | 2.93E-06 | 0.00016   | 5.41235 |
| TMEM252   | -6.3022 | -4.5397 | -71.821 | 4.95E-10 | 1.92E-06  | 13.02   |
| MMP1      | -6.2907 | -0.4557 | -9.2762 | 8.91E-05 | 0.00123   | 1.59654 |
| PTPRD     | -6.2852 | 3.22814 | -30.655 | 8.06E-08 | 2.40E-05  | 9.13138 |
| C12orf75  | -6.2644 | -1.8584 | -20.382 | 9.12E-07 | 8.47E-05  | 6.66843 |
| HBE1      | -6.2213 | -3.6259 | -40.742 | 1.47E-08 | 1.24E-05  | 10.6658 |
| TM4SF18   | -6.2069 | 0.27011 | -12.601 | 1.54E-05 | 0.00042   | 3.57686 |
| GATA4     | -6.1892 | -4.7458 | -72.596 | 4.65E-10 | 1.92E-06  | 13.0541 |
| TWIST1    | -6.1816 | -2.7629 | -36.363 | 2.91E-08 | 1.48E-05  | 10.0755 |
| THBS2     | -6.1611 | -3.8599 | -14.079 | 8.05E-06 | 0.00028   | 4.29686 |
| CECR2     | -6.1243 | -1.2746 | -14.907 | 5.76E-06 | 0.00023   | 4.66736 |
| FOXR2     | -6.107  | -2.8135 | -20.458 | 8.92E-07 | 8.44E-05  | 6.69175 |
| HLF       | -6.0734 | -1.4792 | -14.408 | 7.04E-06 | 0.00026   | 4.44676 |
| MIR3142H  | -6.0578 | -1.4491 | -8.6382 | 0.00013  | 0.00159   | 1.14169 |
| SPAG17    | -5.96   | -1.556  | -9.1967 | 9.35E-05 | 0.00127   | 1.54143 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| FLG      | -5.9456 | -3.983  | -8.2914 | 0.00017  | 0.00184  | 0.88183 |
| ZIC5     | -5.9187 | -3.8138 | -27.029 | 1.71E-07 | 3.37E-05 | 8.39799 |
| TNFAIP6  | -5.9041 | -2.2786 | -11.613 | 2.46E-05 | 0.00056  | 3.04682 |
| PTPRD-A  | -5.892  | -3.716  | -61.319 | 1.28E-09 | 3.30E-06 | 12.4715 |
| CHST1    | -5.8675 | -2.3072 | -23.158 | 4.28E-07 | 5.35E-05 | 7.46298 |
| SYTL5    | -5.8613 | -4.3661 | -14.241 | 7.53E-06 | 0.00027  | 4.37117 |
| GRAMD1   | -5.8066 | -0.6264 | -7.0055 | 0.00042  | 0.00332  | -0.1709 |
| DPP4     | -5.7923 | 0.15617 | -9.403  | 8.25E-05 | 0.00117  | 1.68352 |
| CLDN2    | -5.7852 | -3.7854 | -6.5617 | 0.0006   | 0.00419  | -0.5712 |
| VNN2     | -5.7515 | -3.4184 | -9.5383 | 7.61E-05 | 0.00111  | 1.77523 |
| SPARC    | -5.7332 | 4.17337 | -15.838 | 4.04E-06 | 0.00019  | 5.05881 |
| LINC0253 | -5.727  | -3.031  | -17.21  | 2.48E-06 | 0.00014  | 5.59345 |
| ZC4H2    | -5.7066 | -2.9583 | -26.538 | 1.90E-07 | 3.51E-05 | 8.28883 |
| POU6F2-  | -5.6913 | -2.3851 | -11.549 | 2.54E-05 | 0.00057  | 3.01114 |
| CALHM6   | -5.6828 | -2.9266 | -11.395 | 2.75E-05 | 0.00059  | 2.92403 |
| AADACP   | -5.6114 | -3.1969 | -7.6644 | 0.00026  | 0.00243  | 0.38707 |
| CALHM5   | -5.5956 | -2.0542 | -9.1527 | 9.61E-05 | 0.00129  | 1.51072 |
| DGKG     | -5.5527 | -4.1079 | -36.865 | 2.68E-08 | 1.48E-05 | 10.1484 |
| RBM20    | -5.5087 | -2.3177 | -18.234 | 1.76E-06 | 0.00012  | 5.96293 |
| LINC0230 | -5.5058 | -0.7776 | -6.5294 | 0.00062  | 0.00427  | -0.6012 |
| NAV3     | -5.4883 | -2.4282 | -9.0168 | 0.0001   | 0.00137  | 1.41511 |
| LINC0093 | -5.4782 | -3.7923 | -12.789 | 1.41E-05 | 0.0004   | 3.6733  |
| LINC0216 | -5.4779 | 1.22737 | -16.338 | 3.37E-06 | 0.00017  | 5.25907 |
| PHACTR   | -5.4686 | 1.39632 | -8.1172 | 0.00019  | 0.00198  | 0.7477  |
| LINC0059 | -5.4513 | -2.6259 | -9.9716 | 5.91E-05 | 0.00096  | 2.06097 |
| SEPTIN4  | -5.4456 | -1.9236 | -18.428 | 1.66E-06 | 0.00011  | 6.03056 |
| SLC8A3   | -5.3972 | -3.2131 | -23.75  | 3.68E-07 | 4.97E-05 | 7.61779 |
| RASGRF   | -5.3929 | -2.1088 | -9.9365 | 6.03E-05 | 0.00097  | 2.03826 |
| C6orf141 | -5.3763 | -2.2971 | -10.426 | 4.58E-05 | 0.00082  | 2.34845 |
| TIE1     | -5.3384 | 2.85083 | -18.077 | 1.85E-06 | 0.00012  | 5.90779 |
| NKX2-4   | -5.3378 | -3.8625 | -17.875 | 1.98E-06 | 0.00012  | 5.83622 |
| TBXA2R   | -5.2996 | -4.0087 | -17.68  | 2.11E-06 | 0.00013  | 5.76591 |
| LINC0185 | -5.2869 | -2.9626 | -11.063 | 3.26E-05 | 0.00067  | 2.73228 |
| CFP      | -5.2576 | -1.3424 | -11.507 | 2.60E-05 | 0.00058  | 2.98707 |
| AR       | -5.2471 | -3.3898 | -17.931 | 1.95E-06 | 0.00012  | 5.85596 |
| ACSM1    | -5.2241 | -4.1142 | -12.841 | 1.38E-05 | 0.00039  | 3.69946 |
| SHISA3   | -5.2201 | -1.0623 | -18.365 | 1.69E-06 | 0.00011  | 6.00855 |
| NKX2-1   | -5.2186 | -0.341  | -11.784 | 2.26E-05 | 0.00054  | 3.14173 |
| ELMO1    | -5.2138 | -1.2258 | -16.942 | 2.72E-06 | 0.00015  | 5.49256 |
| GJA4     | -5.1603 | 1.89036 | -6.3977 | 0.00069  | 0.00458  | -0.7245 |
| ST8SIA4  | -5.1531 | -1.8373 | -7.4038 | 0.00031  | 0.00271  | 0.17132 |
| ADAM33   | -5.1467 | -3.1394 | -9.3833 | 8.35E-05 | 0.00118  | 1.67008 |
| STAT4    | -5.1407 | -2.4444 | -18.605 | 1.56E-06 | 0.00011  | 6.09136 |
| C2CD4C   | -5.0707 | -4.0375 | -15.443 | 4.69E-06 | 0.00021  | 4.89587 |
| SRGN     | -5.061  | 0.45058 | -11.136 | 3.14E-05 | 0.00065  | 2.7749  |
| CLEC18B  | -5.0301 | -3.1285 | -62.944 | 1.09E-09 | 3.30E-06 | 12.5683 |
| SHC2     | -5.0073 | -4.6676 | -10.539 | 4.31E-05 | 0.00079  | 2.41782 |
| LRRTM2   | -4.9922 | -3.1284 | -8.5793 | 0.00014  | 0.00164  | 1.09826 |
| SIRPB2   | -4.9654 | -3.3455 | -7.7982 | 0.00024  | 0.00228  | 0.49547 |
| FAM83A   | -4.9619 | -4.1714 | -9.1654 | 9.53E-05 | 0.00128  | 1.51961 |
| FXD2     | -4.9574 | -3.9789 | -8.1249 | 0.00019  | 0.00198  | 0.75366 |
| MRAP2    | -4.9302 | -3.621  | -19.57  | 1.16E-06 | 9.37E-05 | 6.41208 |
| SLC25A1  | -4.9297 | -1.7288 | -15.244 | 5.06E-06 | 0.00021  | 4.81218 |
| JAKMIP3  | -4.9252 | -2.3068 | -24.315 | 3.20E-07 | 4.77E-05 | 7.7614  |
| PKHD1    | -4.8639 | -3.2029 | -20.673 | 8.39E-07 | 8.18E-05 | 6.75732 |
| MCOLN2   | -4.8418 | -3.5129 | -6.5623 | 0.0006   | 0.00419  | -0.5706 |
| BTBD16   | -4.8204 | -4.0588 | -8.7068 | 0.00013  | 0.00156  | 1.19206 |
| ST8SIA5  | -4.8149 | -3.6875 | -18.342 | 1.70E-06 | 0.00012  | 6.00049 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| ADAMTS   | -4.8054 | -3.1842 | -8.2475 | 0.00017  | 0.00188  | 0.84825 |
| UNC80    | -4.7961 | -3.5451 | -18.959 | 1.40E-06 | 0.0001   | 6.21094 |
| TUBAL3   | -4.796  | -3.9413 | -15.878 | 3.98E-06 | 0.00018  | 5.07502 |
| AOAH     | -4.78   | -1.1313 | -10.167 | 5.29E-05 | 0.00089  | 2.18629 |
| STK32B   | -4.7729 | 1.54743 | -17.481 | 2.26E-06 | 0.00013  | 5.69337 |
| LINC0233 | -4.7626 | -2.6502 | -18.886 | 1.43E-06 | 0.0001   | 6.18667 |
| INSYN2B  | -4.7527 | -3.3077 | -13.42  | 1.07E-05 | 0.00034  | 3.98576 |
| CHP2     | -4.7464 | -4.2223 | -11.137 | 3.14E-05 | 0.00065  | 2.77528 |
| DIRAS2   | -4.7279 | -3.9336 | -9.0321 | 0.0001   | 0.00136  | 1.42593 |
| SIX3-AS1 | -4.7237 | -1.9972 | -7.5527 | 0.00028  | 0.00255  | 0.29534 |
| CRYM     | -4.7169 | -3.7696 | -11.213 | 3.02E-05 | 0.00064  | 2.81919 |
| EFNA3    | -4.7066 | 0.76417 | -11.763 | 2.29E-05 | 0.00054  | 3.12984 |
| AMOT     | -4.6978 | -0.3656 | -10.585 | 4.20E-05 | 0.00078  | 2.44598 |
| SELENOF  | -4.6861 | -1.9022 | -8.5456 | 0.00014  | 0.00166  | 1.07324 |
| TAL1     | -4.6811 | -3.6233 | -8.4032 | 0.00016  | 0.00177  | 0.96663 |
| SPARCL1  | -4.6774 | -4.1942 | -9.1259 | 9.77E-05 | 0.00131  | 1.49196 |
| ROBO3    | -4.6697 | -1.4843 | -13.952 | 8.49E-06 | 0.00029  | 4.23846 |
| TMEM100  | -4.658  | 0.3588  | -4.3606 | 0.00477  | 0.01797  | -2.9083 |
| GLI3     | -4.6556 | 1.21576 | -22.641 | 4.89E-07 | 5.80E-05 | 7.3238  |
| FFAR4    | -4.6262 | -4.0108 | -26.97  | 1.73E-07 | 3.37E-05 | 8.38483 |
| CCDC181  | -4.6232 | -2.1595 | -10.854 | 3.64E-05 | 0.00071  | 2.60857 |
| MAGEC1   | -4.6037 | -1.1624 | -7.5021 | 0.00029  | 0.00261  | 0.25338 |
| HOXA11   | -4.5929 | 1.71326 | -20.302 | 9.34E-07 | 8.61E-05 | 6.64367 |
| CA3      | -4.5835 | -2.259  | -8.0981 | 0.00019  | 0.00201  | 0.73284 |
| MAOB     | -4.5692 | 0.59191 | -8.082  | 0.00019  | 0.00202  | 0.72024 |
| GLIS1    | -4.5637 | -3.7531 | -10.729 | 3.89E-05 | 0.00074  | 2.53341 |
| ADGRE1   | -4.5388 | -4.3215 | -9.0463 | 0.0001   | 0.00135  | 1.43597 |
| ZNF804A  | -4.5228 | -3.3038 | -10.181 | 5.25E-05 | 0.00089  | 2.19466 |
| ZPLD1    | -4.4829 | -2.5913 | -7.8382 | 0.00023  | 0.00223  | 0.5276  |
| PPP4R4   | -4.4705 | -4.1642 | -23.341 | 4.08E-07 | 5.30E-05 | 7.51131 |
| MMP10    | -4.4531 | 0.53539 | -4.5898 | 0.00374  | 0.01511  | -2.6342 |
| PPP1R16  | -4.4521 | 0.02614 | -15.065 | 5.42E-06 | 0.00022  | 4.73567 |
| PHYHIPL  | -4.4433 | -0.5697 | -10.203 | 5.18E-05 | 0.00088  | 2.20862 |
| SLC23A1  | -4.4244 | -2.0068 | -8.3768 | 0.00016  | 0.00178  | 0.94671 |
| LINC0150 | -4.4239 | -2.0965 | -8.048  | 0.0002   | 0.00205  | 0.69368 |
| LINC0196 | -4.4175 | -2.8037 | -8.6588 | 0.00013  | 0.00159  | 1.15685 |
| AOX1     | -4.416  | -1.0718 | -7.548  | 0.00028  | 0.00255  | 0.29146 |
| GALNT16  | -4.3869 | -3.934  | -13.267 | 1.14E-05 | 0.00035  | 3.91156 |
| LRRK2    | -4.3779 | -4.0313 | -12.958 | 1.31E-05 | 0.00038  | 3.75837 |
| SCN3A    | -4.373  | -3.5514 | -19.415 | 1.22E-06 | 9.53E-05 | 6.36178 |
| LINC0106 | -4.3676 | -2.8092 | -35.719 | 3.24E-08 | 1.57E-05 | 9.97983 |
| ADRA2A   | -4.3639 | 1.50122 | -9.192  | 9.38E-05 | 0.00127  | 1.53817 |
| CDO1     | -4.3577 | -2.6612 | -12.538 | 1.58E-05 | 0.00043  | 3.54437 |
| COL4A6   | -4.3422 | -3.3692 | -10.499 | 4.40E-05 | 0.00081  | 2.39372 |
| LINC0136 | -4.3383 | -2.2432 | -17.107 | 2.57E-06 | 0.00015  | 5.55488 |
| RMST     | -4.3289 | -5.0243 | -25.119 | 2.64E-07 | 4.31E-05 | 7.95875 |
| KCNJ16   | -4.301  | -0.203  | -13.865 | 8.81E-06 | 0.00029  | 4.19748 |
| FAM133A  | -4.2652 | -2.0645 | -6.5593 | 0.0006   | 0.00419  | -0.5734 |
| TDO2     | -4.2414 | -3.5012 | -19.467 | 1.20E-06 | 9.43E-05 | 6.37877 |
| CASC19   | -4.2373 | -2.797  | -9.1482 | 9.63E-05 | 0.00129  | 1.50762 |
| P2RX6    | -4.2165 | -3.1937 | -23.3   | 4.12E-07 | 5.30E-05 | 7.50069 |
| RBFOX3   | -4.2164 | -2.666  | -6.094  | 0.00089  | 0.00551  | -1.0163 |
| PITX2    | -4.1997 | -2.3193 | -11.397 | 2.75E-05 | 0.00059  | 2.92477 |
| APBB1    | -4.1972 | 0.02742 | -16.617 | 3.05E-06 | 0.00016  | 5.36828 |
| CECR7    | -4.1678 | -0.1493 | -17.32  | 2.39E-06 | 0.00014  | 5.63425 |
| ST8SIA2  | -4.1587 | -0.8468 | -10.262 | 5.02E-05 | 0.00087  | 2.24589 |
| SORBS2   | -4.1497 | 2.9296  | -10.953 | 3.45E-05 | 0.00069  | 2.66745 |
| LINC0135 | -4.1492 | -4.1803 | -13.88  | 8.75E-06 | 0.00029  | 4.20458 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| GEM      | -4.1484 | -1.0773 | -7.8672 | 0.00022  | 0.00221  | 0.5508  |
| GAB3     | -4.1361 | -2.0761 | -21.907 | 5.95E-07 | 6.37E-05 | 7.11965 |
| MAGEA3   | -4.1244 | 2.61389 | -23.992 | 3.47E-07 | 4.82E-05 | 7.67974 |
| SLC22A1  | -4.1236 | -3.6019 | -14.11  | 7.95E-06 | 0.00028  | 4.31111 |
| MMRN2    | -4.1047 | -0.3653 | -7.4356 | 0.00031  | 0.00269  | 0.19798 |
| PKDCC    | -4.095  | -2.0116 | -13.16  | 1.19E-05 | 0.00036  | 3.85899 |
| F2       | -4.0921 | -2.9683 | -7.5566 | 0.00028  | 0.00254  | 0.29859 |
| RAD21L1  | -4.073  | -3.8613 | -9.8386 | 6.38E-05 | 0.001    | 1.97449 |
| LINC0144 | -4.0691 | -1.3314 | -11.896 | 2.14E-05 | 0.00052  | 3.20311 |
| BCAN-AS  | -4.0361 | -3.5595 | -15.726 | 4.21E-06 | 0.00019  | 5.01308 |
| PTX3     | -4.0299 | 5.23821 | -21.767 | 6.18E-07 | 6.47E-05 | 7.07963 |
| CUBN     | -4.023  | -2.9736 | -17.161 | 2.52E-06 | 0.00014  | 5.57491 |
| PKIA     | -4.0198 | -4.2402 | -13.153 | 1.20E-05 | 0.00036  | 3.85517 |
| LNCRNA-  | -4.0072 | -3.6437 | -12.998 | 1.28E-05 | 0.00037  | 3.77846 |
| RTN4RL2  | -4.0052 | -3.0428 | -10.398 | 4.65E-05 | 0.00083  | 2.33119 |
| WSCD1    | -4.003  | 0.64801 | -31.254 | 7.18E-08 | 2.27E-05 | 9.24152 |
| RASSF2   | -3.9988 | -0.2799 | -4.8831 | 0.00276  | 0.01216  | -2.2945 |
| KCNMB4   | -3.9888 | -0.6326 | -12.926 | 1.33E-05 | 0.00038  | 3.74211 |
| SLC13A5  | -3.9845 | -2.5479 | -15.929 | 3.91E-06 | 0.00018  | 5.09604 |
| IGSF1    | -3.9822 | -3.2314 | -16.845 | 2.81E-06 | 0.00015  | 5.45576 |
| LINC0144 | -3.976  | -3.8306 | -9.6306 | 7.20E-05 | 0.00108  | 1.83706 |
| NINJ2    | -3.9314 | -3.7774 | -17.749 | 2.07E-06 | 0.00013  | 5.79086 |
| DIO2     | -3.9203 | -4.2517 | -9.4048 | 8.24E-05 | 0.00117  | 1.6848  |
| NAP1L2   | -3.9072 | -0.2414 | -3.9955 | 0.00716  | 0.02436  | -3.361  |
| ABCA13   | -3.8922 | -2.6466 | -15.146 | 5.25E-06 | 0.00022  | 4.77035 |
| LINC0204 | -3.8849 | -3.0711 | -13.218 | 1.16E-05 | 0.00035  | 3.88747 |
| ADAM12   | -3.8826 | -2.3519 | -4.2379 | 0.00546  | 0.01985  | -3.0582 |
| CXXC4    | -3.8813 | -2.8805 | -38.5   | 2.07E-08 | 1.35E-05 | 10.3761 |
| HHIP     | -3.8739 | -2.5917 | -6.9932 | 0.00043  | 0.00334  | -0.1818 |
| CLDN14-  | -3.8417 | -1.7304 | -15.221 | 5.10E-06 | 0.00021  | 4.80216 |
| CASC6    | -3.8323 | -4.349  | -8.361  | 0.00016  | 0.00179  | 0.93474 |
| PPM1E    | -3.7978 | -2.7578 | -4.1008 | 0.00636  | 0.02234  | -3.2284 |
| HNF1A-A  | -3.7932 | -2.9166 | -7.8155 | 0.00023  | 0.00226  | 0.50936 |
| GALNT5   | -3.7901 | -3.2089 | -8.6395 | 0.00013  | 0.00159  | 1.14267 |
| IMPG2    | -3.7851 | -3.1693 | -5.489  | 0.00153  | 0.00806  | -1.631  |
| ZNF233   | -3.7572 | -1.6766 | -6.4545 | 0.00066  | 0.00444  | -0.671  |
| SHC3     | -3.746  | -3.1922 | -7.4511 | 0.0003   | 0.00267  | 0.21096 |
| CCDC198  | -3.7288 | 0.42352 | -6.1578 | 0.00084  | 0.00532  | -0.9541 |
| DLGAP1   | -3.7282 | 1.31406 | -11.478 | 2.64E-05 | 0.00058  | 2.97096 |
| ATP8A1   | -3.7218 | 3.03311 | -11.976 | 2.06E-05 | 0.00051  | 3.24632 |
| ANKRD18  | -3.71   | -3.9823 | -7.9879 | 0.00021  | 0.0021   | 0.64648 |
| FAM124A  | -3.703  | -4.4724 | -10.055 | 5.63E-05 | 0.00093  | 2.11462 |
| SIX3     | -3.7001 | -0.0536 | -8.3759 | 0.00016  | 0.00178  | 0.94606 |
| CLDN11   | -3.6816 | 3.60225 | -14.525 | 6.71E-06 | 0.00026  | 4.49944 |
| MLPH     | -3.6744 | 0.33158 | -7.3642 | 0.00032  | 0.00275  | 0.13795 |
| NEBL     | -3.6643 | 2.97044 | -7.408  | 0.00031  | 0.00271  | 0.17481 |
| RTP4     | -3.6596 | -1.7963 | -9.7034 | 6.90E-05 | 0.00105  | 1.88546 |
| GCNT3    | -3.6584 | 0.47419 | -11.212 | 3.02E-05 | 0.00064  | 2.81862 |
| ACTN2    | -3.6574 | -5.0678 | -9.2767 | 8.90E-05 | 0.00123  | 1.59686 |
| PLSCR4   | -3.6445 | -3.783  | -12.667 | 1.49E-05 | 0.00041  | 3.61082 |
| ELAPOR1  | -3.6439 | -3.7392 | -7.1397 | 0.00038  | 0.0031   | -0.0539 |
| COL14A1  | -3.6368 | -3.776  | -8.8337 | 0.00012  | 0.00148  | 1.28423 |
| CA8      | -3.6329 | 0.41492 | -4.9178 | 0.00267  | 0.01186  | -2.2552 |
| DPYSL4   | -3.6253 | -2.4009 | -5.4273 | 0.00162  | 0.0084   | -1.6963 |
| ENTREP2  | -3.6244 | 1.3853  | -21.258 | 7.11E-07 | 7.30E-05 | 6.93215 |
| TSPEAR-  | -3.6003 | -4.4439 | -7.9049 | 0.00022  | 0.00217  | 0.58079 |
| LUCAT1   | -3.5906 | -4.6119 | -5.0986 | 0.00223  | 0.01041  | -2.0527 |
| COL15A1  | -3.5863 | -3.2523 | -6.4551 | 0.00066  | 0.00444  | -0.6705 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| MYH3     | -3.5741 | -2.5324 | -9.8334 | 6.40E-05 | 0.001    | 1.97112 |
| BCO1     | -3.5723 | 0.33754 | -30.11  | 8.97E-08 | 2.48E-05 | 9.0286  |
| KLF2     | -3.5694 | 2.22079 | -11.66  | 2.41E-05 | 0.00056  | 3.0732  |
| WT1      | -3.5589 | -3.295  | -5.3766 | 0.0017   | 0.00867  | -1.7502 |
| OAS1     | -3.5316 | -0.0261 | -14.296 | 7.36E-06 | 0.00026  | 4.3962  |
| C1orf127 | -3.521  | -0.8127 | -29.047 | 1.11E-07 | 2.82E-05 | 8.82086 |
| AKR1C3   | -3.5167 | 1.049   | -11.588 | 2.50E-05 | 0.00057  | 3.03265 |
| MYO1B-A  | -3.5159 | -3.4493 | -16.385 | 3.31E-06 | 0.00017  | 5.27763 |
| JPH3     | -3.5103 | -1.4172 | -12.031 | 2.01E-05 | 0.0005   | 3.27649 |
| SOX6     | -3.4986 | 2.2814  | -4.5642 | 0.00384  | 0.0154   | -2.6643 |
| CNRIP1   | -3.4898 | -1.8839 | -4.85   | 0.00286  | 0.01246  | -2.3322 |
| SPX      | -3.4884 | -2.1522 | -12.685 | 1.48E-05 | 0.00041  | 3.62012 |
| SH2D1B   | -3.4802 | -4.2033 | -7.4422 | 0.0003   | 0.00268  | 0.20351 |
| FAAHP1   | -3.4749 | -2.0277 | -6.4646 | 0.00065  | 0.00442  | -0.6616 |
| GREB1    | -3.4456 | -0.8647 | -17.639 | 2.14E-06 | 0.00013  | 5.75122 |
| AMBP     | -3.4421 | -2.0646 | -9.2177 | 9.23E-05 | 0.00126  | 1.55606 |
| TLR6     | -3.4369 | -3.7116 | -9.7698 | 6.64E-05 | 0.00103  | 1.92932 |
| MAJIN    | -3.4364 | -3.7178 | -16.809 | 2.85E-06 | 0.00016  | 5.44216 |
| SLC22A1  | -3.4352 | -1.3638 | -12.446 | 1.65E-05 | 0.00045  | 3.49664 |
| EPDR1    | -3.415  | 0.84577 | -8.5065 | 0.00014  | 0.0017   | 1.04409 |
| NKD2     | -3.3963 | -1.7378 | -6.5216 | 0.00062  | 0.00428  | -0.6083 |
| STAC     | -3.3808 | 1.19221 | -25.392 | 2.47E-07 | 4.17E-05 | 8.0242  |
| HSD17B1  | -3.3795 | 0.51608 | -6.8984 | 0.00046  | 0.00349  | -0.2657 |
| SRPX2    | -3.376  | -1.7898 | -9.6077 | 7.30E-05 | 0.00109  | 1.82181 |
| HSPA12B  | -3.3647 | -3.1669 | -12.723 | 1.45E-05 | 0.00041  | 3.63975 |
| PLCD4    | -3.3365 | -3.014  | -13.03  | 1.26E-05 | 0.00037  | 3.79462 |
| GNG4     | -3.3286 | -2.6654 | -8.1262 | 0.00019  | 0.00198  | 0.75467 |
| TRIM9    | -3.3274 | -1.7914 | -13.673 | 9.55E-06 | 0.00031  | 4.10697 |
| DTX1     | -3.313  | -3.6632 | -38.438 | 2.09E-08 | 1.35E-05 | 10.3678 |
| MMP19    | -3.3123 | -1.7398 | -4.596  | 0.00371  | 0.01504  | -2.6269 |
| LINC0184 | -3.3103 | -2.3214 | -6.4719 | 0.00065  | 0.0044   | -0.6548 |
| LDLRAD4  | -3.3089 | 0.85611 | -21.555 | 6.55E-07 | 6.80E-05 | 7.01857 |
| DAPL1    | -3.3027 | -4.7908 | -5.4349 | 0.00161  | 0.00837  | -1.6882 |
| LINC0183 | -3.2997 | 0.31069 | -10.012 | 5.77E-05 | 0.00095  | 2.08708 |
| DUSP6    | -3.2878 | 2.96797 | -10.93  | 3.49E-05 | 0.0007   | 2.65368 |
| KCNE3    | -3.2595 | -0.4579 | -6.3598 | 0.00071  | 0.00469  | -0.7603 |
| HABP2    | -3.2558 | 1.68372 | -6.3953 | 0.00069  | 0.00459  | -0.7267 |
| MAN1C1   | -3.2505 | -2.5553 | -8.4833 | 0.00015  | 0.00171  | 1.02679 |
| LINC0270 | -3.2499 | -2.4355 | -9.6689 | 7.04E-05 | 0.00107  | 1.86258 |
| APLN     | -3.2461 | 0.09926 | -5.2792 | 0.00187  | 0.00923  | -1.855  |
| ADAMTS   | -3.2407 | -1.3176 | -4.5783 | 0.00378  | 0.01524  | -2.6478 |
| MORC4    | -3.2373 | 2.44931 | -14.482 | 6.83E-06 | 0.00026  | 4.47994 |
| ENTPD1   | -3.2371 | 1.26713 | -11.864 | 2.18E-05 | 0.00053  | 3.18578 |
| HLA-DPB  | -3.2336 | 0.20371 | -15.394 | 4.77E-06 | 0.00021  | 4.8751  |
| PTGS2    | -3.2293 | -4.5246 | -11.306 | 2.88E-05 | 0.00061  | 2.87294 |
| PDZD4    | -3.2247 | -2.8087 | -12.594 | 1.54E-05 | 0.00042  | 3.57326 |
| LINC0064 | -3.2203 | -3.2794 | -3.8579 | 0.00839  | 0.02734  | -3.5365 |
| TRIM6    | -3.2178 | 0.01597 | -12.128 | 1.92E-05 | 0.00049  | 3.32849 |
| PCDH12   | -3.209  | -4.4816 | -6.0944 | 0.00089  | 0.00551  | -1.0159 |
| LINC0048 | -3.2021 | -5.1861 | -7.6265 | 0.00027  | 0.00246  | 0.35607 |
| ACVRL1   | -3.1948 | 1.22388 | -13.058 | 1.25E-05 | 0.00037  | 3.80809 |
| GRIK4    | -3.191  | -0.5421 | -4.9825 | 0.0025   | 0.01128  | -2.1821 |
| FAM43A   | -3.1874 | 2.5625  | -9.0082 | 0.00011  | 0.00137  | 1.40904 |
| FAM66C   | -3.1765 | -2.1805 | -9.886  | 6.21E-05 | 0.00098  | 2.00545 |
| TMEM10   | -3.1721 | 3.05417 | -5.7481 | 0.00121  | 0.00684  | -1.3621 |
| WNK4     | -3.1699 | -0.0416 | -5.8505 | 0.0011   | 0.00641  | -1.2582 |
| ADAMTS   | -3.1579 | 0.344   | -20.776 | 8.14E-07 | 8.01E-05 | 6.78858 |
| TRPV2    | -3.154  | -2.5146 | -10.491 | 4.42E-05 | 0.00081  | 2.38878 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| SAMD5    | -3.1509 | 1.81215 | -16.615 | 3.05E-06 | 0.00016  | 5.36732 |
| OPRD1    | -3.1429 | -0.3021 | -11.551 | 2.54E-05 | 0.00057  | 3.01176 |
| SAMD14   | -3.1427 | -2.1104 | -11.178 | 3.07E-05 | 0.00064  | 2.79933 |
| LINC0051 | -3.1356 | -0.2293 | -21.538 | 6.58E-07 | 6.80E-05 | 7.01379 |
| AQP5     | -3.1339 | -1.231  | -10.273 | 4.98E-05 | 0.00087  | 2.25302 |
| RGS11    | -3.1205 | -1.0699 | -5.1859 | 0.00205  | 0.00982  | -1.9566 |
| PLIN2    | -3.117  | 3.36262 | -5.872  | 0.00108  | 0.00632  | -1.2366 |
| CDH13    | -3.1148 | 2.06008 | -8.7598 | 0.00012  | 0.00152  | 1.23069 |
| ROR2     | -3.1126 | 0.40658 | -10.179 | 5.25E-05 | 0.00089  | 2.19361 |
| KLRG1    | -3.108  | -3.7197 | -11.135 | 3.14E-05 | 0.00065  | 2.77406 |
| ARL14EP  | -3.1073 | -4.7065 | -5.2153 | 0.00199  | 0.00962  | -1.9245 |
| ARHGAP   | -3.1036 | 1.41536 | -24.053 | 3.41E-07 | 4.82E-05 | 7.69541 |
| CHST9    | -3.0986 | 0.68694 | -18.453 | 1.64E-06 | 0.00011  | 6.03912 |
| IFI44L   | -3.0965 | 1.05558 | -6.0784 | 0.0009   | 0.00555  | -1.0316 |
| GPR173   | -3.0913 | -1.3257 | -5.0687 | 0.00229  | 0.01061  | -2.0858 |
| SLC4A5   | -3.0829 | -2.4277 | -10.781 | 3.78E-05 | 0.00073  | 2.56516 |
| DOCK2    | -3.079  | 0.46167 | -13.95  | 8.50E-06 | 0.00029  | 4.23736 |
| GPR55    | -3.0749 | -1.8401 | -6.3362 | 0.00072  | 0.00476  | -0.7827 |
| METTL7A  | -3.0748 | 1.91253 | -19.809 | 1.08E-06 | 9.18E-05 | 6.48869 |
| SAMD9L   | -3.071  | 1.02685 | -8.3889 | 0.00016  | 0.00178  | 0.95589 |
| LINC0064 | -3.0672 | -2.1196 | -8.1219 | 0.00019  | 0.00198  | 0.75134 |
| ZNF610   | -3.0602 | -0.482  | -17.689 | 2.11E-06 | 0.00013  | 5.76918 |
| IRAK3    | -3.0602 | 1.13032 | -6.928  | 0.00045  | 0.00344  | -0.2393 |
| CFAP70   | -3.0464 | -2.8969 | -10.054 | 5.64E-05 | 0.00093  | 2.11408 |
| B4GALNT  | -3.041  | 5.09731 | -8.8343 | 0.00012  | 0.00148  | 1.28465 |
| SESN3    | -3.0398 | 2.76503 | -9.3367 | 8.58E-05 | 0.0012   | 1.63818 |
| IGFBP1   | -3.0116 | -3.2902 | -3.7162 | 0.00991  | 0.03086  | -3.7203 |
| CD247    | -3.0103 | -2.7496 | -3.8106 | 0.00887  | 0.02844  | -3.5976 |
| KIF19    | -2.9994 | -1.7242 | -3.641  | 0.01083  | 0.03305  | -3.819  |
| FOSB     | -2.9985 | 4.09134 | -3.3643 | 0.01516  | 0.04261  | -4.1887 |
| RHBDL3   | -2.9968 | -4.7021 | -6.7071 | 0.00053  | 0.00387  | -0.4378 |
| RIMKLA   | -2.9884 | -2.8224 | -6.637  | 0.00057  | 0.00403  | -0.5018 |
| HLA-DPA  | -2.9878 | -2.4123 | -7.9805 | 0.00021  | 0.0021   | 0.64064 |
| DCHS1    | -2.9857 | -2.1318 | -6.0452 | 0.00093  | 0.00566  | -1.0642 |
| TIGD4    | -2.9823 | -3.4719 | -8.5019 | 0.00015  | 0.0017   | 1.04069 |
| MIR646H  | -2.9746 | -3.4609 | -6.5138 | 0.00063  | 0.00429  | -0.6156 |
| DMRTA1   | -2.971  | -1.3173 | -10.366 | 4.73E-05 | 0.00084  | 2.31118 |
| OAS2     | -2.9657 | -0.0305 | -7.4053 | 0.00031  | 0.00271  | 0.17257 |
| ADAMTS   | -2.9605 | -2.5805 | -6.2335 | 0.00079  | 0.00506  | -0.8809 |
| B3GALT5  | -2.9416 | -1.748  | -4.1268 | 0.00618  | 0.02186  | -3.1959 |
| ABCC2    | -2.9368 | -1.2096 | -8.7464 | 0.00012  | 0.00153  | 1.22096 |
| CHRNA6   | -2.9364 | -3.3949 | -5.7695 | 0.00119  | 0.00675  | -1.3403 |
| LMO1     | -2.9304 | -4.3763 | -15.193 | 5.16E-06 | 0.00021  | 4.79013 |
| LINC0097 | -2.9253 | 0.15409 | -4.2988 | 0.00511  | 0.01888  | -2.9835 |
| GRAP     | -2.9181 | -2.4362 | -11.968 | 2.07E-05 | 0.00051  | 3.24203 |
| STEAP1   | -2.9168 | 2.3765  | -12.532 | 1.59E-05 | 0.00043  | 3.54121 |
| MCC      | -2.9066 | 3.05261 | -9.2631 | 8.98E-05 | 0.00124  | 1.58749 |
| SLC16A2  | -2.903  | -0.6059 | -12.718 | 1.46E-05 | 0.00041  | 3.63686 |
| EFHB     | -2.9025 | -3.0183 | -10.958 | 3.44E-05 | 0.00069  | 2.67055 |
| TG       | -2.8967 | -3.8602 | -5.5238 | 0.00148  | 0.00791  | -1.5944 |
| PPM1L    | -2.8913 | -0.9391 | -7.121  | 0.00039  | 0.00313  | -0.0701 |
| ECSCR    | -2.8824 | 3.96573 | -22.145 | 5.58E-07 | 6.36E-05 | 7.18676 |
| DNAAF11  | -2.8805 | -2.3762 | -5.8251 | 0.00113  | 0.00652  | -1.2839 |
| CFAP95   | -2.876  | -1.6945 | -4.0823 | 0.00649  | 0.02271  | -3.2515 |
| PFN2     | -2.8742 | 4.64291 | -27.126 | 1.67E-07 | 3.37E-05 | 8.41922 |
| AATK     | -2.872  | -3.7916 | -15.367 | 4.82E-06 | 0.00021  | 4.86377 |
| NPNT     | -2.8686 | -0.6837 | -9.4659 | 7.94E-05 | 0.00115  | 1.72632 |
| TRIM22   | -2.8663 | -1.8358 | -3.2805 | 0.01683  | 0.04599  | -4.3025 |

|         |         |         |         |          |          |         |
|---------|---------|---------|---------|----------|----------|---------|
| CDH2    | -2.8609 | 4.6356  | -8.2985 | 0.00017  | 0.00184  | 0.88722 |
| NPTX1   | -2.86   | -3.1985 | -3.76   | 0.00941  | 0.0297   | -3.6632 |
| ALDH1L1 | -2.8573 | -1.7003 | -13.264 | 1.14E-05 | 0.00035  | 3.91003 |
| SKAP1   | -2.8558 | -1.0465 | -9.8216 | 6.44E-05 | 0.00101  | 1.96336 |
| NALF2   | -2.855  | -4.1654 | -7.3977 | 0.00031  | 0.00271  | 0.16619 |
| FAR2    | -2.8519 | -0.4156 | -4.9036 | 0.00271  | 0.01198  | -2.2712 |
| SLC44A5 | -2.8431 | -2.0447 | -10.74  | 3.87E-05 | 0.00074  | 2.54004 |
| RASGRP  | -2.8343 | -3.299  | -15.339 | 4.88E-06 | 0.00021  | 4.85206 |
| LMX1B   | -2.8301 | -5.0339 | -8.8344 | 0.00012  | 0.00148  | 1.2847  |
| SLC1A1  | -2.8296 | 0.95968 | -12.031 | 2.01E-05 | 0.0005   | 3.27625 |
| ZNF429  | -2.8282 | -1.3859 | -16.232 | 3.50E-06 | 0.00017  | 5.2173  |
| SMILR   | -2.8229 | -3.3503 | -9.926  | 6.06E-05 | 0.00097  | 2.03143 |
| DNAI3   | -2.8177 | -3.8428 | -11.159 | 3.10E-05 | 0.00065  | 2.78835 |
| ZP1     | -2.8176 | -3.938  | -5.1899 | 0.00204  | 0.0098   | -1.9523 |
| HGD     | -2.8162 | 5.32908 | -18.482 | 1.63E-06 | 0.00011  | 6.04892 |
| ARL9    | -2.8148 | -2.0373 | -7.9157 | 0.00022  | 0.00216  | 0.58936 |
| TESC    | -2.8064 | -2.4745 | -4.7627 | 0.00312  | 0.01327  | -2.4324 |
| SENCR   | -2.8019 | 3.07548 | -17.312 | 2.39E-06 | 0.00014  | 5.63113 |
| PCBP3   | -2.7916 | -3.872  | -5.8156 | 0.00114  | 0.00657  | -1.2935 |
| LANCL3  | -2.7905 | -3.0833 | -16.652 | 3.01E-06 | 0.00016  | 5.38157 |
| PLXNB3  | -2.7839 | -1.6238 | -9.8244 | 6.43E-05 | 0.00101  | 1.96519 |
| NHSL2   | -2.7778 | 2.89797 | -19.182 | 1.31E-06 | 0.0001   | 6.2854  |
| CASC15  | -2.7708 | -1.5549 | -14.54  | 6.67E-06 | 0.00025  | 4.50598 |
| WNT10B  | -2.7643 | -0.2729 | -7.4947 | 0.00029  | 0.00262  | 0.24729 |
| LGI2    | -2.7627 | 0.11538 | -19.625 | 1.14E-06 | 9.31E-05 | 6.42984 |
| SPEF2   | -2.7581 | -1.9454 | -8.5697 | 0.00014  | 0.00164  | 1.0911  |
| MAPK11  | -2.7566 | 1.94981 | -14.183 | 7.71E-06 | 0.00027  | 4.34468 |
| TNFRSF8 | -2.751  | -3.9928 | -3.328  | 0.01586  | 0.04408  | -4.2379 |
| HOXA10  | -2.7474 | 1.45229 | -27.336 | 1.60E-07 | 3.37E-05 | 8.46478 |
| STEAP2  | -2.7414 | 1.28983 | -15.359 | 4.84E-06 | 0.00021  | 4.86072 |
| SNPH    | -2.738  | 0.45493 | -24.01  | 3.45E-07 | 4.82E-05 | 7.68442 |
| CXCR4   | -2.7324 | -1.8654 | -3.2056 | 0.01848  | 0.04944  | -4.4051 |
| DNAH6   | -2.7304 | -2.8401 | -30.361 | 8.54E-08 | 2.41E-05 | 9.07609 |
| NKX3-2  | -2.7189 | -0.9918 | -13.457 | 1.05E-05 | 0.00034  | 4.00361 |
| ENG     | -2.7188 | 3.33685 | -10.707 | 3.93E-05 | 0.00074  | 2.52012 |
| NEBL-AS | -2.7137 | -1.3186 | -5.0023 | 0.00245  | 0.01112  | -2.16   |
| GRK5    | -2.7134 | 1.34374 | -9.1472 | 9.64E-05 | 0.00129  | 1.50691 |
| SDK2    | -2.7121 | -2.8352 | -5.1321 | 0.00216  | 0.0102   | -2.0157 |
| KDM2B-D | -2.7104 | -2.9908 | -9.1735 | 9.48E-05 | 0.00128  | 1.52528 |
| CCDC180 | -2.7099 | -2.8933 | -6.4861 | 0.00064  | 0.00436  | -0.6415 |
| SLC47A2 | -2.7091 | -3.231  | -7.9502 | 0.00021  | 0.00212  | 0.61675 |
| LAMA2   | -2.6978 | 1.12562 | -19.853 | 1.07E-06 | 9.18E-05 | 6.5026  |
| MTSS1   | -2.6954 | -0.0149 | -6.7366 | 0.00052  | 0.00383  | -0.411  |
| LIPC    | -2.6952 | 0.52943 | -10.203 | 5.18E-05 | 0.00088  | 2.2086  |
| AQP4    | -2.6934 | -3.3554 | -6.9375 | 0.00045  | 0.00342  | -0.2309 |
| NLGN3   | -2.6883 | -2.8784 | -6.2765 | 0.00076  | 0.00493  | -0.8397 |
| PODNL1  | -2.6879 | -3.3223 | -9.3869 | 8.33E-05 | 0.00118  | 1.67256 |
| MMP17   | -2.6763 | -2.1791 | -5.4394 | 0.00161  | 0.00835  | -1.6834 |
| F2RL2   | -2.6707 | 1.52281 | -9.4988 | 7.79E-05 | 0.00113  | 1.74861 |
| CDH5    | -2.6667 | 3.79636 | -21.983 | 5.83E-07 | 6.37E-05 | 7.14119 |
| PLCH1   | -2.6615 | -2.8364 | -5.5187 | 0.00149  | 0.00794  | -1.5997 |
| PINLYP  | -2.6611 | -1.7832 | -5.9897 | 0.00098  | 0.00585  | -1.119  |
| EFEMP1  | -2.654  | 3.31316 | -12.334 | 1.74E-05 | 0.00046  | 3.43762 |
| TTLL7   | -2.6515 | 2.2482  | -14.317 | 7.30E-06 | 0.00026  | 4.40581 |
| EMILIN3 | -2.6434 | -2.3782 | -3.9069 | 0.00793  | 0.0262   | -3.4737 |
| ID2-AS1 | -2.6378 | -2.0212 | -16.994 | 2.67E-06 | 0.00015  | 5.5122  |
| ST3GAL5 | -2.6203 | 0.32363 | -8.9298 | 0.00011  | 0.00142  | 1.35318 |
| TNFRSF1 | -2.6187 | -0.2584 | -27.152 | 1.66E-07 | 3.37E-05 | 8.42483 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| CPP      | -2.6158 | 5.47949 | -20.009 | 1.02E-06 | 9.07E-05 | 6.55219 |
| HSPA12A  | -2.6091 | 1.31315 | -11.145 | 3.12E-05 | 0.00065  | 2.78011 |
| SLC44A4  | -2.6048 | -2.5642 | -7.201  | 0.00036  | 0.00299  | -0.0011 |
| CD22     | -2.6007 | -4.7186 | -3.4495 | 0.01365  | 0.03954  | -4.0737 |
| THSD1    | -2.5997 | -2.0736 | -7.3946 | 0.00031  | 0.00271  | 0.16356 |
| B4GALT6  | -2.5966 | 2.06116 | -20.426 | 9.01E-07 | 8.46E-05 | 6.68195 |
| RCAN2    | -2.5897 | -0.7124 | -5.4182 | 0.00164  | 0.00845  | -1.7059 |
| STX18    | -2.586  | 4.04216 | -13.25  | 1.15E-05 | 0.00035  | 3.90298 |
| FTCD     | -2.577  | -3.0493 | -7.0554 | 0.00041  | 0.00323  | -0.1272 |
| IGF2     | -2.5763 | -2.6503 | -9.7599 | 6.68E-05 | 0.00103  | 1.92283 |
| SPAAR    | -2.5739 | -0.7046 | -11.026 | 3.32E-05 | 0.00067  | 2.71063 |
| CNTFR    | -2.5687 | -2.728  | -10.991 | 3.39E-05 | 0.00068  | 2.68959 |
| ADGRG4   | -2.5626 | -3.8895 | -6.5688 | 0.0006   | 0.00417  | -0.5646 |
| LAMB4    | -2.5564 | -2.3283 | -7.3523 | 0.00032  | 0.00276  | 0.12793 |
| RAB3B    | -2.5553 | 2.13636 | -4.8572 | 0.00284  | 0.0124   | -2.3239 |
| FLI1     | -2.55   | 3.94352 | -14.304 | 7.34E-06 | 0.00026  | 4.40008 |
| IGFN1    | -2.5464 | -3.0049 | -3.2419 | 0.01766  | 0.04772  | -4.3553 |
| MEGF11   | -2.5463 | -2.2045 | -18.605 | 1.56E-06 | 0.00011  | 6.09139 |
| CD34     | -2.5418 | 0.28065 | -5.5181 | 0.00149  | 0.00794  | -1.6004 |
| CYTIP    | -2.538  | -3.6167 | -5.7483 | 0.00121  | 0.00684  | -1.3619 |
| SCOC-AS  | -2.5377 | -2.8937 | -5.1613 | 0.0021   | 0.00999  | -1.9836 |
| TNFSF14  | -2.5371 | -1.9207 | -3.3157 | 0.0161   | 0.04464  | -4.2545 |
| FAM53A   | -2.5307 | -1.3954 | -5.6838 | 0.00128  | 0.00715  | -1.428  |
| ADAMTS   | -2.53   | 1.37848 | -8.0462 | 0.0002   | 0.00205  | 0.69227 |
| SCN2A    | -2.5245 | -4.6576 | -5.3777 | 0.0017   | 0.00866  | -1.7491 |
| ZNF345   | -2.5216 | -1.5015 | -7.4856 | 0.00029  | 0.00263  | 0.23969 |
| SLC7A10  | -2.5151 | -2.7213 | -4.1143 | 0.00626  | 0.0221   | -3.2115 |
| HHEX     | -2.5138 | 4.14047 | -10.401 | 4.64E-05 | 0.00083  | 2.33274 |
| FAM110D  | -2.5076 | -0.4387 | -9.4194 | 8.17E-05 | 0.00116  | 1.69476 |
| TAGLN3   | -2.4972 | -1.4979 | -4.0557 | 0.00669  | 0.02322  | -3.285  |
| TPK1     | -2.4916 | 4.73224 | -14.02  | 8.25E-06 | 0.00029  | 4.26973 |
| TMEM229  | -2.4905 | -2.7863 | -7.0096 | 0.00042  | 0.00331  | -0.1673 |
| EFR3B    | -2.4904 | -0.0068 | -4.3181 | 0.005    | 0.0186   | -2.96   |
| BAHCC1   | -2.4829 | -3.3288 | -5.4066 | 0.00166  | 0.00851  | -1.7183 |
| RNASEL   | -2.4813 | -0.4795 | -10.554 | 4.27E-05 | 0.00079  | 2.42727 |
| SLC26A1  | -2.4769 | -0.555  | -9.9288 | 6.05E-05 | 0.00097  | 2.03324 |
| ITGB1-D1 | -2.4754 | -2.1596 | -6.1914 | 0.00082  | 0.0052   | -0.9216 |
| MMP2     | -2.4676 | 4.70552 | -14.426 | 6.98E-06 | 0.00026  | 4.45481 |
| CMKLR2   | -2.4619 | -2.4381 | -14.12  | 7.92E-06 | 0.00028  | 4.3159  |
| CYP27A1  | -2.4611 | -1.4993 | -6.764  | 0.00051  | 0.00376  | -0.3862 |
| CUX2     | -2.4561 | -5.4739 | -4.8098 | 0.00298  | 0.01284  | -2.3783 |
| FAM149A  | -2.4521 | -0.73   | -9.7526 | 6.70E-05 | 0.00103  | 1.91799 |
| HDX      | -2.4502 | -0.6421 | -5.5008 | 0.00152  | 0.00801  | -1.6185 |
| NR2F2-A  | -2.4464 | -2.134  | -4.1916 | 0.00575  | 0.02064  | -3.1154 |
| SAMD13   | -2.4443 | -3.3822 | -11.646 | 2.42E-05 | 0.00056  | 3.06525 |
| TECTA    | -2.4438 | -1.5181 | -17.3   | 2.40E-06 | 0.00014  | 5.62678 |
| PRDM16   | -2.4435 | -3.7711 | -4.7459 | 0.00318  | 0.01341  | -2.4518 |
| ARHGDIC  | -2.4407 | -3.5763 | -4.6081 | 0.00367  | 0.0149   | -2.6126 |
| LINC0134 | -2.4398 | -3.3593 | -8.3726 | 0.00016  | 0.00178  | 0.94355 |
| HOXA11-  | -2.4375 | 1.85741 | -11.823 | 2.22E-05 | 0.00053  | 3.16317 |
| TGM5     | -2.4338 | -1.3351 | -8.1269 | 0.00019  | 0.00198  | 0.75525 |
| CDH26    | -2.4292 | -2.7913 | -7.4893 | 0.00029  | 0.00263  | 0.24275 |
| PRKD1    | -2.4284 | -0.8163 | -4.7762 | 0.00308  | 0.01315  | -2.4169 |
| ZFP92    | -2.4276 | -2.6026 | -5.3635 | 0.00173  | 0.00873  | -1.7643 |
| TCAF2    | -2.4216 | -4.4741 | -10.484 | 4.44E-05 | 0.00081  | 2.3841  |
| SLC40A1  | -2.4212 | 0.49893 | -11.475 | 2.64E-05 | 0.00058  | 2.96908 |
| CRHBP    | -2.4208 | -2.8382 | -6.1138 | 0.00088  | 0.00545  | -0.997  |
| EFCAB6-  | -2.4205 | -2.6178 | -5.4056 | 0.00166  | 0.00851  | -1.7194 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| AQP5-AS  | -2.4199 | 0.99211 | -8.546  | 0.00014  | 0.00166  | 1.07352 |
| EFCAB10  | -2.4173 | -1.0396 | -8.8865 | 0.00011  | 0.00144  | 1.32219 |
| SLC16A4  | -2.4163 | 1.06999 | -15.13  | 5.28E-06 | 0.00022  | 4.76343 |
| CP       | -2.4114 | 6.027   | -26.792 | 1.80E-07 | 3.44E-05 | 8.34545 |
| RELN     | -2.4112 | 3.30711 | -8.1857 | 0.00018  | 0.00193  | 0.80077 |
| RASGRP   | -2.4076 | -4.3047 | -13.949 | 8.50E-06 | 0.00029  | 4.23665 |
| S1PR1    | -2.4063 | 0.93588 | -7.4872 | 0.00029  | 0.00263  | 0.24102 |
| PPFIBP2  | -2.4029 | 1.51446 | -19.71  | 1.11E-06 | 9.23E-05 | 6.45701 |
| EGF      | -2.4024 | -0.7113 | -10.154 | 5.33E-05 | 0.0009   | 2.17792 |
| MOV10L1  | -2.4018 | -0.0335 | -4.5416 | 0.00393  | 0.01564  | -2.6911 |
| LONRF2   | -2.4009 | 2.10434 | -9.6686 | 7.04E-05 | 0.00107  | 1.8624  |
| MAP3K15  | -2.3992 | -0.9796 | -7.6424 | 0.00026  | 0.00244  | 0.36911 |
| TTYH2    | -2.3881 | 1.06274 | -11.998 | 2.04E-05 | 0.00051  | 3.25827 |
| CXCL5    | -2.3854 | 4.49612 | -8.4401 | 0.00015  | 0.00174  | 0.99442 |
| COX7A1   | -2.3807 | -2.9549 | -3.489  | 0.01301  | 0.03807  | -4.0207 |
| PARP11   | -2.38   | -1.3644 | -6.7337 | 0.00052  | 0.00383  | -0.4136 |
| CTSS     | -2.3743 | 1.81607 | -19.075 | 1.35E-06 | 0.0001   | 6.24981 |
| BNC1     | -2.3667 | -1.8053 | -5.2362 | 0.00195  | 0.00949  | -1.9018 |
| SLC16A6  | -2.3578 | -1.0712 | -8.8303 | 0.00012  | 0.00148  | 1.28173 |
| VAT1     | -2.3556 | 5.31481 | -15.727 | 4.21E-06 | 0.00019  | 5.01336 |
| CLMP     | -2.3547 | 0.19621 | -6.3222 | 0.00073  | 0.0048   | -0.796  |
| DPYD     | -2.3394 | 4.65738 | -12.169 | 1.88E-05 | 0.00048  | 3.3505  |
| MAP2K6   | -2.339  | 1.33506 | -19.021 | 1.37E-06 | 0.0001   | 6.23171 |
| MAGEA6   | -2.3369 | 0.70658 | -13.742 | 9.27E-06 | 0.00031  | 4.13999 |
| GABRP    | -2.3337 | 0.09742 | -10.845 | 3.66E-05 | 0.00071  | 2.60302 |
| OLFML3   | -2.3274 | 2.62497 | -11.519 | 2.58E-05 | 0.00058  | 2.99409 |
| LCTL     | -2.3274 | 0.59192 | -9.9878 | 5.85E-05 | 0.00095  | 2.07143 |
| GGT1     | -2.3263 | 0.00472 | -6.4629 | 0.00065  | 0.00442  | -0.6632 |
| ZSCAN18  | -2.3226 | 2.39233 | -11.048 | 3.29E-05 | 0.00067  | 2.7234  |
| ITGAX    | -2.3182 | -4.1369 | -4.5247 | 0.004    | 0.01584  | -2.7113 |
| LHFPL3-A | -2.3157 | -1.0532 | -4.0979 | 0.00638  | 0.02239  | -3.232  |
| MLLT11   | -2.3134 | 4.06388 | -19.945 | 1.04E-06 | 9.09E-05 | 6.53181 |
| MICE     | -2.3048 | -2.9191 | -5.8062 | 0.00115  | 0.00661  | -1.3031 |
| EPHX4    | -2.3047 | 0.89541 | -7.6466 | 0.00026  | 0.00244  | 0.3725  |
| NLRP1    | -2.3045 | 0.42573 | -6.0646 | 0.00091  | 0.00559  | -1.0451 |
| FHOD3    | -2.3008 | 1.41579 | -7.4401 | 0.0003   | 0.00268  | 0.20175 |
| ST6GAL1  | -2.2996 | 0.72693 | -6.3156 | 0.00074  | 0.00482  | -0.8023 |
| HACD4    | -2.291  | 0.38123 | -9.7658 | 6.65E-05 | 0.00103  | 1.92672 |
| HHIP-AS1 | -2.2873 | -1.9373 | -6.8091 | 0.00049  | 0.00368  | -0.3455 |
| ZNF19    | -2.2859 | -3.3321 | -9.9379 | 6.02E-05 | 0.00097  | 2.03915 |
| AHRR     | -2.2809 | -0.681  | -6.6489 | 0.00056  | 0.00401  | -0.4909 |
| KLHDC7A  | -2.28   | 1.07536 | -5.0147 | 0.00242  | 0.01103  | -2.1461 |
| ADGRA2   | -2.2748 | 0.29333 | -11.622 | 2.45E-05 | 0.00056  | 3.05152 |
| SMTNL2   | -2.2745 | -3.9009 | -3.64   | 0.01085  | 0.03309  | -3.8203 |
| LINC0158 | -2.2696 | 0.48441 | -4.4315 | 0.00442  | 0.01701  | -2.8226 |
| EEF1A2   | -2.2682 | 4.99345 | -4.3693 | 0.00473  | 0.01788  | -2.8978 |
| FGF13    | -2.2646 | 1.5278  | -5.0858 | 0.00226  | 0.0105   | -2.067  |
| IL6-AS1  | -2.2545 | -1.0773 | -10.061 | 5.61E-05 | 0.00093  | 2.1188  |
| SLC26A7  | -2.2545 | -1.3343 | -3.8039 | 0.00894  | 0.02861  | -3.6062 |
| PDLIM4   | -2.2425 | 2.40277 | -5.1    | 0.00223  | 0.0104   | -2.0512 |
| GALNT14  | -2.2358 | 3.32545 | -11.067 | 3.25E-05 | 0.00067  | 2.73465 |
| ULBP2    | -2.2346 | -0.5449 | -3.8922 | 0.00807  | 0.02652  | -3.4925 |
| LINC0303 | -2.2327 | -0.0395 | -4.169  | 0.00589  | 0.02106  | -3.1434 |
| NEK10    | -2.2297 | -1.7665 | -7.1251 | 0.00039  | 0.00312  | -0.0666 |
| ZNF790   | -2.2184 | -1.6322 | -5.1791 | 0.00206  | 0.00986  | -1.964  |
| PDIA2    | -2.2178 | -3.7487 | -4.0494 | 0.00674  | 0.0233   | -3.2928 |
| PLPP3    | -2.2167 | 3.43551 | -11.856 | 2.19E-05 | 0.00053  | 3.18088 |
| CD79B    | -2.2141 | -3.422  | -4.3324 | 0.00492  | 0.0184   | -2.9426 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| CPEB1    | -2.213  | -1.6878 | -11.642 | 2.43E-05 | 0.00056  | 3.06268 |
| THBS4    | -2.2099 | -2.4596 | -5.9879 | 0.00098  | 0.00585  | -1.1208 |
| LRRRC17  | -2.2026 | 0.35093 | -13.447 | 1.05E-05 | 0.00034  | 3.99891 |
| PDE2A    | -2.2016 | -0.3385 | -6.413  | 0.00068  | 0.00454  | -0.7101 |
| SLC3A1   | -2.2013 | 0.12433 | -6.2146 | 0.0008   | 0.00512  | -0.8991 |
| MPZ      | -2.2001 | -3.3448 | -4.1962 | 0.00572  | 0.02056  | -3.1097 |
| LINC0181 | -2.1973 | 0.12035 | -8.7647 | 0.00012  | 0.00152  | 1.23423 |
| LY6G5C   | -2.1969 | -2.6047 | -16.318 | 3.39E-06 | 0.00017  | 5.25128 |
| LIMD2    | -2.194  | 3.02908 | -8.9743 | 0.00011  | 0.00139  | 1.38493 |
| TSPAN18  | -2.1922 | 0.81415 | -7.4869 | 0.00029  | 0.00263  | 0.24076 |
| JCAD     | -2.1909 | 2.91869 | -9.6948 | 6.93E-05 | 0.00106  | 1.87981 |
| TBXAS1   | -2.188  | 1.7924  | -15.229 | 5.09E-06 | 0.00021  | 4.80554 |
| APPBP2   | -2.1828 | -2.635  | -11.984 | 2.06E-05 | 0.00051  | 3.25067 |
| LMO2     | -2.1769 | 0.62487 | -5.531  | 0.00147  | 0.00788  | -1.5867 |
| ARSL     | -2.1727 | 2.06984 | -13.995 | 8.34E-06 | 0.00029  | 4.25807 |
| CXCL6    | -2.1696 | 0.60822 | -7.32   | 0.00033  | 0.0028   | 0.10053 |
| SLC47A1  | -2.1685 | -0.2209 | -5.0621 | 0.00231  | 0.01067  | -2.0933 |
| ACSM3    | -2.1643 | 3.03519 | -5.3677 | 0.00172  | 0.00871  | -1.7598 |
| GCAWK    | -2.1566 | -1.9816 | -5.5954 | 0.00139  | 0.00758  | -1.5195 |
| COCH     | -2.1559 | 0.11995 | -7.9308 | 0.00021  | 0.00214  | 0.60138 |
| SLC2A5   | -2.1519 | -1.4622 | -3.4136 | 0.01427  | 0.04077  | -4.1221 |
| ITIH5    | -2.1515 | 1.5923  | -4.7594 | 0.00313  | 0.0133   | -2.4362 |
| S100Z    | -2.1472 | -1.9346 | -5.3545 | 0.00174  | 0.00877  | -1.7739 |
| RPA4     | -2.1457 | -1.0318 | -3.6868 | 0.01026  | 0.03171  | -3.7588 |
| ASB9     | -2.1454 | 0.42813 | -6.7327 | 0.00052  | 0.00383  | -0.4145 |
| NMRAL2   | -2.1445 | -1.0923 | -4.0047 | 0.00709  | 0.02416  | -3.3493 |
| NRGN     | -2.144  | 4.05455 | -26.97  | 1.73E-07 | 3.37E-05 | 8.3848  |
| LGR6     | -2.1399 | -2.0058 | -3.3339 | 0.01574  | 0.04384  | -4.2298 |
| BHLHE41  | -2.1383 | 1.46676 | -10.461 | 4.49E-05 | 0.00081  | 2.36987 |
| HORMAD   | -2.1281 | -1.3987 | -4.4067 | 0.00454  | 0.01731  | -2.8525 |
| VAV3     | -2.1274 | -0.2371 | -4.4575 | 0.0043   | 0.01667  | -2.7915 |
| ARHGAP   | -2.1263 | 1.93199 | -9.742  | 6.75E-05 | 0.00104  | 1.91099 |
| COL24A1  | -2.1236 | -0.5409 | -5.4317 | 0.00162  | 0.00838  | -1.6916 |
| DYNLT4   | -2.1179 | -1.4298 | -11.491 | 2.62E-05 | 0.00058  | 2.97805 |
| LINC0132 | -2.1034 | 0.34662 | -7.3398 | 0.00033  | 0.00277  | 0.11736 |
| ARHGEF   | -2.0999 | -0.6044 | -10.312 | 4.88E-05 | 0.00086  | 2.27762 |
| SCARF2   | -2.0983 | 3.68576 | -7.5947 | 0.00027  | 0.0025   | 0.33    |
| RASL10A  | -2.096  | -2.1406 | -7.2632 | 0.00035  | 0.00289  | 0.05223 |
| TP53AIP1 | -2.0959 | -1.3204 | -6.605  | 0.00058  | 0.00409  | -0.5312 |
| RNLS     | -2.0882 | -1.064  | -4.1462 | 0.00604  | 0.02149  | -3.1717 |
| B3GNT9   | -2.0871 | 2.22254 | -10.048 | 5.66E-05 | 0.00094  | 2.11034 |
| CXCL12   | -2.0788 | 0.73346 | -3.7813 | 0.00918  | 0.02918  | -3.6355 |
| LAMA4    | -2.077  | -2.2129 | -6.7434 | 0.00052  | 0.00381  | -0.4048 |
| MAPK12   | -2.0749 | 2.82117 | -15.122 | 5.30E-06 | 0.00022  | 4.76006 |
| USHBP1   | -2.071  | -0.8943 | -8.182  | 0.00018  | 0.00194  | 0.79785 |
| PLAAT4   | -2.0652 | 1.66512 | -8.6597 | 0.00013  | 0.00159  | 1.15753 |
| ITGA5    | -2.0645 | 4.79576 | -8.721  | 0.00013  | 0.00154  | 1.20242 |
| OGFRL1   | -2.0628 | 4.36662 | -9.6685 | 7.04E-05 | 0.00107  | 1.86235 |
| RAMP2    | -2.0616 | 1.18438 | -10.402 | 4.64E-05 | 0.00083  | 2.33345 |
| ACHE     | -2.0606 | 0.54781 | -7.0997 | 0.00039  | 0.00315  | -0.0886 |
| PCDHB9   | -2.0583 | -1.3664 | -4.9803 | 0.00251  | 0.0113   | -2.1846 |
| BTNL9    | -2.0574 | 1.0202  | -15.267 | 5.01E-06 | 0.00021  | 4.82164 |
| SOX5     | -2.0572 | 3.306   | -3.7658 | 0.00934  | 0.02956  | -3.6557 |
| PDE4D    | -2.0564 | 1.77794 | -7.9979 | 0.0002   | 0.00209  | 0.6544  |
| SH2B3    | -2.0557 | 2.87021 | -14.711 | 6.23E-06 | 0.00024  | 4.58173 |
| ZNF382   | -2.0493 | 0.63738 | -12.308 | 1.76E-05 | 0.00046  | 3.42417 |
| IFI44    | -2.0463 | 0.78221 | -7.781  | 0.00024  | 0.0023   | 0.4816  |
| ABTB3    | -2.046  | 1.21336 | -7.1356 | 0.00038  | 0.00311  | -0.0575 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| GDPD1    | -2.0448 | -0.8873 | -3.3188 | 0.01604  | 0.04451 | -4.2504 |
| TOB1-AS  | -2.0447 | -2.9928 | -16.393 | 3.30E-06 | 0.00017 | 5.28104 |
| MSX1     | -2.0441 | 3.49305 | -10.172 | 5.27E-05 | 0.00089 | 2.18949 |
| CCNB3    | -2.0415 | -2.784  | -5.2388 | 0.00194  | 0.00948 | -1.8989 |
| TLR1     | -2.0413 | -2.6902 | -5.757  | 0.0012   | 0.0068  | -1.353  |
| XKR4     | -2.037  | 1.6676  | -4.5769 | 0.00379  | 0.01525 | -2.6494 |
| CARD16   | -2.0328 | -1.343  | -16.1   | 3.67E-06 | 0.00018 | 5.16475 |
| CFAP69   | -2.0175 | -0.9501 | -7.7077 | 0.00025  | 0.00238 | 0.42235 |
| RRAGD    | -2.0155 | 3.2429  | -10.041 | 5.68E-05 | 0.00094 | 2.1059  |
| PKIG     | -2.0098 | 2.56998 | -10.078 | 5.56E-05 | 0.00093 | 2.12934 |
| CEACAM   | -2.0034 | 1.61158 | -5.4679 | 0.00156  | 0.00818 | -1.6533 |
| RARB     | -1.9964 | -0.6371 | -7.5395 | 0.00028  | 0.00257 | 0.28444 |
| DNM1     | -1.9932 | 3.01745 | -9.3796 | 8.36E-05 | 0.00118 | 1.66755 |
| ECM1     | -1.9921 | 0.48436 | -8.3998 | 0.00016  | 0.00178 | 0.9641  |
| ZNF280A  | -1.9898 | -0.2634 | -7.0922 | 0.0004   | 0.00316 | -0.0951 |
| VEPH1    | -1.9832 | 2.44178 | -9.9017 | 6.15E-05 | 0.00098 | 2.01568 |
| B3GALNT  | -1.9825 | 4.18651 | -16.905 | 2.75E-06 | 0.00015 | 5.47868 |
| OASL     | -1.9771 | 0.61592 | -4.4107 | 0.00452  | 0.01727 | -2.8477 |
| TMEM154  | -1.9751 | 0.36121 | -6.5074 | 0.00063  | 0.0043  | -0.6216 |
| KIAA1549 | -1.9747 | -0.7038 | -5.4225 | 0.00163  | 0.00842 | -1.7014 |
| MMD      | -1.9735 | 3.0389  | -12.689 | 1.48E-05 | 0.00041 | 3.62192 |
| ESPNL    | -1.9705 | -3.0488 | -11.304 | 2.88E-05 | 0.00061 | 2.87194 |
| PHETA2   | -1.9705 | 2.84797 | -12.849 | 1.37E-05 | 0.00039 | 3.70376 |
| CD7      | -1.9673 | -4.3353 | -6.4634 | 0.00065  | 0.00442 | -0.6627 |
| SIPA1L2  | -1.9649 | 4.09705 | -12.014 | 2.03E-05 | 0.00051 | 3.26732 |
| PIK3CD-A | -1.9638 | -2.6332 | -8.7145 | 0.00013  | 0.00155 | 1.1977  |
| LINC0298 | -1.963  | -0.6175 | -15.918 | 3.92E-06 | 0.00018 | 5.09152 |
| ITGA10   | -1.9619 | -2.3333 | -12.035 | 2.01E-05 | 0.0005  | 3.27832 |
| DPY19L1  | -1.954  | -1.1104 | -6.5674 | 0.0006   | 0.00418 | -0.5659 |
| ZNF547   | -1.9532 | -1.5966 | -3.8374 | 0.00859  | 0.02781 | -3.5629 |
| LINC0141 | -1.946  | -2.0389 | -3.5354 | 0.0123   | 0.03641 | -3.9588 |
| OTUB2    | -1.9427 | 0.94161 | -6.9765 | 0.00043  | 0.00336 | -0.1965 |
| SERPINA  | -1.9422 | 2.04094 | -3.6787 | 0.01036  | 0.03195 | -3.7694 |
| TBX1     | -1.938  | -1.4025 | -3.5653 | 0.01186  | 0.03542 | -3.919  |
| GAS1     | -1.9368 | 1.93774 | -5.3241 | 0.00179  | 0.00895 | -1.8066 |
| RHO      | -1.9352 | 1.78404 | -5.5292 | 0.00148  | 0.00789 | -1.5887 |
| PNPLA7   | -1.9341 | -2.7713 | -8.1252 | 0.00019  | 0.00198 | 0.75387 |
| TMEM37   | -1.9313 | 2.18292 | -8.1839 | 0.00018  | 0.00194 | 0.79933 |
| PLEKHG4  | -1.93   | 0.63505 | -9.0845 | 0.0001   | 0.00133 | 1.46291 |
| PRSS35   | -1.9262 | -2.7251 | -3.5036 | 0.01278  | 0.03759 | -4.0012 |
| AGAP2-A  | -1.9175 | 1.46006 | -8.9461 | 0.00011  | 0.00141 | 1.36488 |
| STARD8   | -1.9129 | 2.01374 | -9.2148 | 9.25E-05 | 0.00126 | 1.55403 |
| DNASE1L  | -1.9113 | -1.5942 | -8.9161 | 0.00011  | 0.00143 | 1.34343 |
| ALDH6A1  | -1.9087 | 4.94402 | -15.411 | 4.74E-06 | 0.00021 | 4.88238 |
| CGNL1    | -1.9075 | 3.63934 | -10.223 | 5.12E-05 | 0.00088 | 2.22167 |
| HOGA1    | -1.9063 | -0.4016 | -5.7843 | 0.00117  | 0.00668 | -1.3252 |
| SYT16    | -1.9048 | -1.7612 | -5.0265 | 0.00239  | 0.01095 | -2.1329 |
| PAPLN    | -1.891  | -0.5472 | -7.3826 | 0.00032  | 0.00273 | 0.15343 |
| PLA2G4C  | -1.8909 | -4.2492 | -4.0284 | 0.0069   | 0.02372 | -3.3193 |
| FTCDNL1  | -1.8852 | -2.2275 | -4.4536 | 0.00432  | 0.01671 | -2.7961 |
| LINC0141 | -1.885  | 0.73984 | -7.0718 | 0.0004   | 0.0032  | -0.1129 |
| CHST10   | -1.884  | 2.30973 | -7.9263 | 0.00021  | 0.00215 | 0.59777 |
| LBX2-AS  | -1.8811 | -0.3676 | -6.1494 | 0.00085  | 0.00534 | -0.9623 |
| TEKT4P2  | -1.8778 | -0.1951 | -8.7463 | 0.00012  | 0.00153 | 1.22087 |
| SCAT1    | -1.8776 | -1.8016 | -3.2468 | 0.01755  | 0.04755 | -4.3486 |
| TTC28    | -1.8761 | 5.65888 | -15.852 | 4.02E-06 | 0.00018 | 5.0646  |
| PLEKHG4  | -1.8758 | 3.99122 | -13.863 | 8.81E-06 | 0.00029 | 4.19685 |
| PAXBP1-  | -1.8757 | -2.1178 | -4.3071 | 0.00506  | 0.01876 | -2.9733 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| TBX2-AS  | -1.8757 | -2.0994 | -6.1216 | 0.00087  | 0.00543  | -0.9893 |
| PIR      | -1.8734 | 3.96055 | -15.81  | 4.08E-06 | 0.00019  | 5.04744 |
| CYP1B1   | -1.8732 | 1.46456 | -10.012 | 5.77E-05 | 0.00095  | 2.08727 |
| RAB6B    | -1.8686 | 1.61775 | -18.985 | 1.39E-06 | 0.0001   | 6.21976 |
| ENTPD8   | -1.8658 | -1.5707 | -18.171 | 1.80E-06 | 0.00012  | 5.94086 |
| ISM1     | -1.8657 | -1.8149 | -3.3492 | 0.01545  | 0.04321  | -4.2091 |
| FAM102B  | -1.8637 | 0.0699  | -8.8833 | 0.00011  | 0.00145  | 1.31988 |
| SYNE1    | -1.8592 | 1.10052 | -11.009 | 3.35E-05 | 0.00068  | 2.70047 |
| LY96     | -1.8582 | -4.5551 | -7.1475 | 0.00038  | 0.00309  | -0.0472 |
| PRAME    | -1.8532 | 5.16877 | -11.994 | 2.05E-05 | 0.00051  | 3.25618 |
| PGBD5    | -1.8492 | 0.29759 | -8.8963 | 0.00011  | 0.00144  | 1.32922 |
| TGFB1    | -1.8448 | 4.973   | -20.027 | 1.01E-06 | 9.07E-05 | 6.55791 |
| EGFL7    | -1.843  | 2.0706  | -5.6709 | 0.0013   | 0.0072   | -1.4413 |
| SLC9A9   | -1.8422 | -5.1231 | -5.1071 | 0.00221  | 0.01035  | -2.0434 |
| FHAD1    | -1.8389 | 0.19294 | -6.2136 | 0.0008   | 0.00512  | -0.9001 |
| KIF5C    | -1.837  | -3.4462 | -4.6361 | 0.00356  | 0.0146   | -2.5797 |
| KITLG    | -1.8336 | -0.4931 | -15.783 | 4.12E-06 | 0.00019  | 5.03661 |
| NFKBIZ   | -1.8302 | 3.6289  | -6.2867 | 0.00076  | 0.0049   | -0.8299 |
| ZNF223   | -1.8293 | -2.0483 | -6.0296 | 0.00094  | 0.00572  | -1.0796 |
| SULT4A1  | -1.8292 | -0.5651 | -10.006 | 5.79E-05 | 0.00095  | 2.08335 |
| ASRGL1   | -1.8285 | 5.49519 | -9.2214 | 9.21E-05 | 0.00126  | 1.55859 |
| LINC0031 | -1.8279 | -0.4159 | -3.4274 | 0.01403  | 0.04031  | -4.1034 |
| CFAP54   | -1.8278 | -0.1248 | -5.4134 | 0.00165  | 0.00848  | -1.711  |
| EEF1A1P  | -1.8257 | -0.8933 | -5.3682 | 0.00172  | 0.00871  | -1.7592 |
| OAS3     | -1.8215 | 2.89493 | -4.1762 | 0.00585  | 0.02093  | -3.1345 |
| GPR162   | -1.8206 | -1.2518 | -7.7292 | 0.00025  | 0.00236  | 0.43977 |
| FBXL9P   | -1.8191 | -2.1594 | -4.7066 | 0.00331  | 0.01385  | -2.4974 |
| CFAP418  | -1.819  | 1.24927 | -13.013 | 1.27E-05 | 0.00037  | 3.78607 |
| SYNE3    | -1.8181 | -0.2659 | -10.239 | 5.08E-05 | 0.00088  | 2.23141 |
| CASP1    | -1.8174 | -0.662  | -5.4886 | 0.00153  | 0.00806  | -1.6314 |
| ANGPTL2  | -1.8169 | 2.35076 | -6.1771 | 0.00083  | 0.00525  | -0.9354 |
| IGFL2-AS | -1.8151 | 0.59081 | -7.5574 | 0.00028  | 0.00254  | 0.29925 |
| SERINC5  | -1.8118 | 3.13322 | -6.3034 | 0.00075  | 0.00485  | -0.8139 |
| PLAAT3   | -1.8102 | 3.2587  | -14.624 | 6.45E-06 | 0.00025  | 4.54314 |
| LINC0127 | -1.8096 | -0.0416 | -12.344 | 1.73E-05 | 0.00046  | 3.44312 |
| MTCL1    | -1.8071 | 4.02902 | -13.364 | 1.09E-05 | 0.00034  | 3.95891 |
| CCL5     | -1.8064 | -2.3467 | -3.309  | 0.01624  | 0.04488  | -4.2637 |
| SPATA20  | -1.8062 | 3.86595 | -16.532 | 3.14E-06 | 0.00016  | 5.33517 |
| TCN2     | -1.8031 | 2.69906 | -13.285 | 1.13E-05 | 0.00035  | 3.92019 |
| FOS      | -1.7996 | 5.81679 | -3.4207 | 0.01414  | 0.04053  | -4.1125 |
| HOXA4    | -1.7891 | -0.318  | -5.1809 | 0.00206  | 0.00985  | -1.9621 |
| RASSF8-  | -1.7873 | 0.62822 | -18.424 | 1.66E-06 | 0.00011  | 6.02915 |
| LINC0227 | -1.7866 | -0.8748 | -5.647  | 0.00133  | 0.00732  | -1.466  |
| AMIGO2   | -1.7851 | 6.35711 | -7.5542 | 0.00028  | 0.00255  | 0.29662 |
| BCHE     | -1.7848 | 1.27607 | -7.696  | 0.00025  | 0.00239  | 0.41281 |
| TMCC1-D  | -1.7842 | 0.66159 | -7.3443 | 0.00033  | 0.00277  | 0.12114 |
| MLLT3    | -1.7837 | 0.79519 | -7.643  | 0.00026  | 0.00244  | 0.36956 |
| SULT1C2  | -1.7836 | 0.65575 | -4.4147 | 0.0045   | 0.01721  | -2.8428 |
| TMEM64   | -1.7826 | 2.90301 | -6.8903 | 0.00046  | 0.00351  | -0.2729 |
| AP1S2    | -1.7809 | 4.58092 | -6.9707 | 0.00043  | 0.00337  | -0.2016 |
| TNRC6C   | -1.7807 | 1.50797 | -7.4366 | 0.00031  | 0.00269  | 0.19875 |
| SLC52A1  | -1.7803 | -2.8877 | -6.014  | 0.00095  | 0.00578  | -1.095  |
| AKR1C2   | -1.7789 | -4.3804 | -6.8468 | 0.00048  | 0.0036   | -0.3117 |
| FRMD4A   | -1.7782 | 4.05401 | -9.4497 | 8.02E-05 | 0.00115  | 1.71533 |
| CFI      | -1.7779 | 3.89923 | -7.0753 | 0.0004   | 0.0032   | -0.1098 |
| RBM24    | -1.7758 | 0.43762 | -9.7258 | 6.81E-05 | 0.00104  | 1.9003  |
| CLU      | -1.7742 | 5.38319 | -5.8653 | 0.00109  | 0.00635  | -1.2434 |
| MFAP3L   | -1.7715 | -0.0056 | -6.6603 | 0.00056  | 0.00398  | -0.4804 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| EVC      | -1.7714 | 1.82031 | -8.6922 | 0.00013  | 0.00156  | 1.18134 |
| FOLH1    | -1.7706 | 0.42306 | -3.4341 | 0.01391  | 0.04007  | -4.0944 |
| KAT2B    | -1.767  | 2.87757 | -8.1976 | 0.00018  | 0.00192  | 0.80988 |
| PLEKHD1  | -1.7652 | -1.2118 | -4.2709 | 0.00526  | 0.01933  | -3.0176 |
| MAPT     | -1.7641 | -3.9705 | -5.7117 | 0.00125  | 0.00703  | -1.3994 |
| IFI27L2  | -1.7638 | 3.92904 | -11.351 | 2.81E-05 | 0.0006   | 2.89857 |
| GLRX     | -1.7634 | 1.25759 | -23.606 | 3.82E-07 | 5.10E-05 | 7.58058 |
| LINC0066 | -1.763  | 1.32414 | -20.498 | 8.82E-07 | 8.39E-05 | 6.7042  |
| LINC0092 | -1.7629 | -2.3862 | -5.1641 | 0.00209  | 0.00997  | -1.9805 |
| SALL1    | -1.7619 | 3.39962 | -10.449 | 4.52E-05 | 0.00082  | 2.36263 |
| TNFRSF1  | -1.7584 | -2.8952 | -5.1554 | 0.00211  | 0.01003  | -1.9901 |
| SIGLEC9  | -1.7491 | -3.7688 | -5.0644 | 0.0023   | 0.01065  | -2.0907 |
| SLC37A2  | -1.748  | -0.3731 | -5.4155 | 0.00164  | 0.00846  | -1.7088 |
| TMEM91   | -1.7453 | -1.575  | -4.865  | 0.00281  | 0.01235  | -2.3151 |
| ZNF589   | -1.7377 | 2.13245 | -18.662 | 1.54E-06 | 0.00011  | 6.11068 |
| NCR3LG1  | -1.7348 | -1.504  | -3.3016 | 0.01639  | 0.04516  | -4.2737 |
| ANXA2R   | -1.7322 | 0.52002 | -9.1551 | 9.59E-05 | 0.00129  | 1.51244 |
| DAPK2    | -1.731  | -2.8587 | -9.2423 | 9.09E-05 | 0.00125  | 1.5731  |
| THNSL2   | -1.7287 | 0.09788 | -13.014 | 1.27E-05 | 0.00037  | 3.78663 |
| THPO     | -1.7249 | -2.7259 | -4.5281 | 0.00399  | 0.01582  | -2.7072 |
| PLAAT1   | -1.7239 | -1.0001 | -6.9029 | 0.00046  | 0.00349  | -0.2616 |
| SMPD1    | -1.7227 | 3.68189 | -8.1307 | 0.00019  | 0.00198  | 0.75815 |
| RPGRIP1  | -1.7221 | -2.0062 | -3.992  | 0.00719  | 0.02444  | -3.3654 |
| MAMLD1   | -1.7199 | 0.17196 | -4.6408 | 0.00354  | 0.01454  | -2.5742 |
| RGL1     | -1.7175 | 2.94889 | -7.8696 | 0.00022  | 0.00221  | 0.55266 |
| UAP1L1   | -1.7163 | 3.63867 | -17.956 | 1.93E-06 | 0.00012  | 5.8648  |
| WNT3     | -1.7129 | 0.61521 | -10.244 | 5.07E-05 | 0.00088  | 2.23447 |
| ITPR1    | -1.7125 | 1.90991 | -9.0905 | 9.98E-05 | 0.00133  | 1.46714 |
| SCUBE1   | -1.7124 | -5.6886 | -6.6868 | 0.00054  | 0.00392  | -0.4563 |
| STEAP1B  | -1.7087 | 0.99773 | -18.003 | 1.90E-06 | 0.00012  | 5.88147 |
| FABP3    | -1.7077 | 3.17926 | -10.405 | 4.63E-05 | 0.00083  | 2.3353  |
| CAPN5    | -1.7077 | 2.01713 | -7.5571 | 0.00028  | 0.00254  | 0.29895 |
| LINC0092 | -1.7074 | -2.4565 | -8.09   | 0.00019  | 0.00201  | 0.72649 |
| ADAM11   | -1.7073 | 0.29504 | -10.87  | 3.61E-05 | 0.00071  | 2.6184  |
| MGAT5B   | -1.7025 | 2.79968 | -10.531 | 4.33E-05 | 0.00079  | 2.41322 |
| RAMP2-A  | -1.7018 | -0.4197 | -6.699  | 0.00054  | 0.00389  | -0.4451 |
| RASL12   | -1.6957 | 0.70855 | -6.6036 | 0.00058  | 0.00409  | -0.5325 |
| SPATA7   | -1.6953 | -0.9384 | -5.9119 | 0.00104  | 0.00616  | -1.1966 |
| SLC4A8   | -1.694  | -1.5329 | -4.9876 | 0.00249  | 0.01125  | -2.1765 |
| KIAA1614 | -1.6938 | -1.7984 | -3.3786 | 0.0149   | 0.04205  | -4.1693 |
| MVB12B   | -1.6891 | -0.4673 | -3.4925 | 0.01296  | 0.03797  | -4.0161 |
| ZNF320   | -1.6826 | 1.22314 | -7.9064 | 0.00022  | 0.00217  | 0.58203 |
| PLA1A    | -1.6814 | -1.0066 | -6.9122 | 0.00045  | 0.00347  | -0.2534 |
| SH3PXD2  | -1.6805 | -0.1968 | -10.626 | 4.11E-05 | 0.00077  | 2.47146 |
| ZEB1     | -1.6797 | 2.91436 | -10.817 | 3.71E-05 | 0.00072  | 2.58649 |
| HAP1     | -1.6796 | -2.9669 | -8.3525 | 0.00016  | 0.0018   | 0.92827 |
| MSRA     | -1.6787 | 1.43467 | -8.4546 | 0.00015  | 0.00173  | 1.00533 |
| C8orf88  | -1.6766 | 1.73554 | -17.227 | 2.46E-06 | 0.00014  | 5.59958 |
| AK9      | -1.6766 | -1.621  | -9.4863 | 7.84E-05 | 0.00114  | 1.74016 |
| GSG1L    | -1.6765 | -1.6338 | -7.0493 | 0.00041  | 0.00325  | -0.1326 |
| ZNF423   | -1.6744 | 1.32453 | -4.4139 | 0.00451  | 0.01722  | -2.8438 |
| ZNF502   | -1.6744 | -2.7372 | -5.3554 | 0.00174  | 0.00877  | -1.773  |
| LINC0085 | -1.6688 | -2.5354 | -10.43  | 4.57E-05 | 0.00082  | 2.35119 |
| NR2F2    | -1.6683 | 4.6518  | -11.685 | 2.38E-05 | 0.00055  | 3.08702 |
| HOXA3    | -1.668  | 2.34905 | -9.5842 | 7.40E-05 | 0.0011   | 1.80607 |
| FOXN3-A  | -1.6635 | 1.55674 | -7.4462 | 0.0003   | 0.00268  | 0.20686 |
| MEIOC    | -1.6607 | 0.82906 | -3.4792 | 0.01317  | 0.03846  | -4.0339 |
| SSPOP    | -1.659  | 0.06997 | -5.3545 | 0.00174  | 0.00877  | -1.7739 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| APBB1IP  | -1.6582 | -2.2227 | -5.9733 | 0.00099  | 0.00591 | -1.1353 |
| RASGRF   | -1.6541 | 3.59641 | -19.127 | 1.33E-06 | 0.0001  | 6.2669  |
| CEP126   | -1.6515 | 1.0169  | -18.484 | 1.63E-06 | 0.00011 | 6.04987 |
| LPCAT2   | -1.6487 | 3.04616 | -4.7068 | 0.00331  | 0.01385 | -2.4972 |
| SLC30A3  | -1.6485 | -5.0045 | -4.4559 | 0.00431  | 0.01668 | -2.7934 |
| LRRC24   | -1.6471 | 0.83188 | -11.093 | 3.21E-05 | 0.00066 | 2.74948 |
| PLA2G4A  | -1.644  | -0.0271 | -8.0235 | 0.0002   | 0.00207 | 0.67453 |
| MIAT     | -1.6416 | -2.1    | -13.561 | 1.00E-05 | 0.00032 | 4.05383 |
| ONECUT   | -1.639  | -1.3584 | -7.5792 | 0.00028  | 0.00252 | 0.31718 |
| HCLS1    | -1.6372 | 1.06995 | -7.34   | 0.00033  | 0.00277 | 0.11749 |
| GLT8D2   | -1.6355 | 2.00716 | -13.717 | 9.37E-06 | 0.00031 | 4.1282  |
| CYP39A1  | -1.6322 | -1.4593 | -7.3556 | 0.00032  | 0.00276 | 0.13067 |
| ADORA1   | -1.6312 | 4.04958 | -7.4039 | 0.00031  | 0.00271 | 0.17134 |
| FLRT3    | -1.6284 | 2.01173 | -11.472 | 2.64E-05 | 0.00058 | 2.96736 |
| CXCL1    | -1.6271 | 5.98818 | -4.6144 | 0.00364  | 0.01483 | -2.6052 |
| BRPF3-A  | -1.6271 | -3.5159 | -4.3244 | 0.00497  | 0.01851 | -2.9523 |
| SCNN1D   | -1.6263 | -0.9573 | -7.531  | 0.00028  | 0.00257 | 0.27737 |
| GAREM2   | -1.6262 | 0.55949 | -16.847 | 2.81E-06 | 0.00015 | 5.45647 |
| BATF2    | -1.6246 | -2.2408 | -3.5376 | 0.01227  | 0.03636 | -3.956  |
| TRABD2A  | -1.6222 | -0.4504 | -5.6504 | 0.00132  | 0.00731 | -1.4625 |
| CACNA2D  | -1.6212 | 0.1854  | -8.252  | 0.00017  | 0.00188 | 0.85171 |
| DND1     | -1.621  | -0.0191 | -4.7371 | 0.00321  | 0.01351 | -2.4621 |
| TSHZ1    | -1.62   | 0.94569 | -4.8893 | 0.00274  | 0.01211 | -2.2875 |
| NXPE3    | -1.6198 | 3.96407 | -14.801 | 6.01E-06 | 0.00024 | 4.62117 |
| DGCR6    | -1.6197 | 2.12504 | -12.15  | 1.90E-05 | 0.00048 | 3.34017 |
| CAMK1G   | -1.6193 | -4.0062 | -3.7581 | 0.00943  | 0.02975 | -3.6657 |
| ZBTB20   | -1.6186 | 1.82992 | -4.8849 | 0.00276  | 0.01214 | -2.2925 |
| TEX19    | -1.6183 | -1.0745 | -3.9821 | 0.00727  | 0.02465 | -3.3779 |
| CFH      | -1.6165 | 4.39899 | -4.3581 | 0.00479  | 0.01799 | -2.9114 |
| SELENBF  | -1.6162 | 2.72125 | -13.892 | 8.70E-06 | 0.00029 | 4.21046 |
| LBX2     | -1.6105 | -1.1024 | -5.0764 | 0.00228  | 0.01057 | -2.0773 |
| MYO7A    | -1.6085 | -0.2405 | -11.622 | 2.45E-05 | 0.00056 | 3.05155 |
| SLC49A3  | -1.6058 | -4.5113 | -4.9087 | 0.00269  | 0.01193 | -2.2654 |
| MERTK    | -1.6057 | 1.25835 | -16.232 | 3.50E-06 | 0.00017 | 5.2174  |
| VWDE     | -1.6038 | -3.3586 | -3.2657 | 0.01714  | 0.04666 | -4.3228 |
| MAP3K7C  | -1.6036 | -0.3159 | -10.484 | 4.44E-05 | 0.00081 | 2.38419 |
| CPM      | -1.6036 | 5.05357 | -7.9544 | 0.00021  | 0.00212 | 0.62007 |
| RUNDC3   | -1.5911 | -1.8755 | -4.7121 | 0.00329  | 0.01379 | -2.4911 |
| OPRL1    | -1.5894 | -1.7145 | -4.75   | 0.00316  | 0.01337 | -2.4472 |
| METTL27  | -1.5862 | -1.8627 | -3.2675 | 0.0171   | 0.04659 | -4.3202 |
| FIBCD1   | -1.5853 | -4.8963 | -3.6659 | 0.01052  | 0.03233 | -3.7862 |
| LINC0293 | -1.5852 | -1.2912 | -4.3134 | 0.00503  | 0.01868 | -2.9657 |
| TOR4A    | -1.582  | 3.56824 | -15.929 | 3.91E-06 | 0.00018 | 5.09605 |
| UCHL1    | -1.5804 | 5.92525 | -9.9716 | 5.91E-05 | 0.00096 | 2.06094 |
| PRUNE2   | -1.5764 | 2.90095 | -8.0263 | 0.0002   | 0.00207 | 0.67669 |
| PROCR    | -1.575  | 4.08908 | -10.808 | 3.73E-05 | 0.00072 | 2.58095 |
| RIMKLB   | -1.5748 | 4.5065  | -3.3604 | 0.01524  | 0.04277 | -4.1939 |
| KIF26B   | -1.5747 | 3.32574 | -3.6631 | 0.01055  | 0.0324  | -3.7899 |
| MARCHF   | -1.5714 | -0.3544 | -10.587 | 4.20E-05 | 0.00078 | 2.44725 |
| PRKAR2B  | -1.5681 | 2.88633 | -12.238 | 1.82E-05 | 0.00047 | 3.387   |
| PPM1F    | -1.5679 | 4.73261 | -11.367 | 2.79E-05 | 0.0006  | 2.90797 |
| HOXB13   | -1.5668 | 1.39389 | -10.911 | 3.53E-05 | 0.0007  | 2.64277 |
| PHLDA1   | -1.5653 | 2.81333 | -4.5202 | 0.00402  | 0.01591 | -2.7166 |
| RGS2     | -1.5649 | 2.76584 | -7.1652 | 0.00037  | 0.00306 | -0.0319 |
| FAM222A  | -1.5598 | 1.22513 | -4.5046 | 0.00409  | 0.01607 | -2.7352 |
| GPAT3    | -1.5593 | 0.61869 | -3.754  | 0.00948  | 0.02984 | -3.671  |
| HOXA-AS  | -1.5483 | 1.68317 | -14.104 | 7.97E-06 | 0.00028 | 4.30877 |
| CACHD1   | -1.5465 | 4.41918 | -4.8837 | 0.00276  | 0.01216 | -2.2938 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| MACC1-D  | -1.5458 | 0.23635 | -8.2004 | 0.00018  | 0.00192 | 0.81206 |
| COL5A2   | -1.5457 | 1.5484  | -15.385 | 4.79E-06 | 0.00021 | 4.87143 |
| FAM89A   | -1.5449 | 0.43488 | -7.5256 | 0.00029  | 0.00258 | 0.27294 |
| TP53TG1  | -1.5436 | 0.88769 | -7.1016 | 0.00039  | 0.00315 | -0.087  |
| TMEM98   | -1.5419 | 0.74745 | -5.4109 | 0.00165  | 0.00849 | -1.7137 |
| MAP1B    | -1.539  | 5.25654 | -7.3814 | 0.00032  | 0.00273 | 0.15242 |
| SNHG25   | -1.5383 | 1.50117 | -5.2233 | 0.00197  | 0.00956 | -1.9158 |
| UBAP1L   | -1.5326 | -2.6205 | -6.3119 | 0.00074  | 0.00483 | -0.8059 |
| ARHGEF   | -1.5314 | 2.97519 | -9.6501 | 7.12E-05 | 0.00107 | 1.85009 |
| HOMER3   | -1.5288 | -1.8476 | -5.3225 | 0.00179  | 0.00896 | -1.8083 |
| DAB2     | -1.5283 | 1.16849 | -11.139 | 3.13E-05 | 0.00065 | 2.77637 |
| GNG2     | -1.525  | -0.4007 | -7.2815 | 0.00034  | 0.00286 | 0.06782 |
| SLC19A3  | -1.5248 | -1.023  | -3.4624 | 0.01344  | 0.03909 | -4.0564 |
| TLR5     | -1.5245 | -1.158  | -15.262 | 5.02E-06 | 0.00021 | 4.81983 |
| ETFBKM   | -1.5228 | -0.8257 | -11.534 | 2.56E-05 | 0.00058 | 3.00222 |
| SNX10    | -1.5215 | 2.3694  | -13.074 | 1.24E-05 | 0.00037 | 3.81639 |
| NECAB2   | -1.5205 | -1.7069 | -4.5922 | 0.00373  | 0.01509 | -2.6313 |
| PTK6     | -1.5196 | -2.4505 | -5.6834 | 0.00128  | 0.00715 | -1.4284 |
| DYNC1I1  | -1.5194 | 1.86672 | -7.0241 | 0.00042  | 0.00329 | -0.1546 |
| RIPK2    | -1.5193 | 5.0929  | -14.322 | 7.29E-06 | 0.00026 | 4.40788 |
| APOBEC   | -1.519  | -2.2905 | -3.7918 | 0.00906  | 0.02891 | -3.622  |
| LINC0051 | -1.5175 | 1.70556 | -9.9036 | 6.14E-05 | 0.00098 | 2.01688 |
| PDK1-AS  | -1.5132 | -2.0868 | -4.3596 | 0.00478  | 0.01798 | -2.9095 |
| RAB27B   | -1.5131 | -3.2025 | -9.0473 | 0.0001   | 0.00135 | 1.4367  |
| ICAM2    | -1.513  | -2.2594 | -3.6634 | 0.01055  | 0.0324  | -3.7895 |
| SNHG26   | -1.512  | -1.72   | -3.6453 | 0.01078  | 0.03294 | -3.8134 |
| RBPMS-A  | -1.5105 | -0.5652 | -7.3646 | 0.00032  | 0.00275 | 0.13831 |
| GABRE    | -1.5101 | 3.44431 | -6.1147 | 0.00087  | 0.00545 | -0.9961 |
| SPP1     | -1.5052 | 7.14264 | -6.0662 | 0.00091  | 0.00558 | -1.0436 |
| CFL1P1   | -1.5038 | -2.6148 | -5.5697 | 0.00142  | 0.0077  | -1.5463 |
| ZNF667   | -1.4998 | 0.69009 | -8.6393 | 0.00013  | 0.00159 | 1.14257 |
| MYLK     | -1.4992 | 6.24114 | -7.7166 | 0.00025  | 0.00237 | 0.42952 |
| CLDN15   | -1.4965 | 2.65596 | -9.1759 | 9.47E-05 | 0.00128 | 1.52691 |
| RFFL     | -1.4964 | 1.90814 | -9.646  | 7.14E-05 | 0.00107 | 1.84737 |
| KCNAB2   | -1.4962 | 3.29645 | -8.8925 | 0.00011  | 0.00144 | 1.32649 |
| SEMA6B   | -1.4947 | 3.61795 | -4.0685 | 0.00659  | 0.02298 | -3.2688 |
| SLC38A4  | -1.4927 | -2.0932 | -3.316  | 0.0161   | 0.04463 | -4.2542 |
| PLB1     | -1.4914 | -1.5271 | -3.8431 | 0.00854  | 0.02766 | -3.5556 |
| PNMA2    | -1.4877 | 0.89218 | -8.9617 | 0.00011  | 0.0014  | 1.37594 |
| TMEM140  | -1.4874 | -0.8325 | -6.0133 | 0.00096  | 0.00578 | -1.0957 |
| FMO4     | -1.4869 | -1.1747 | -10.619 | 4.12E-05 | 0.00077 | 2.46727 |
| STUM     | -1.4867 | -2.0252 | -4.4582 | 0.0043   | 0.01666 | -2.7906 |
| EIF5A2   | -1.4863 | 1.72625 | -9.8614 | 6.29E-05 | 0.00099 | 1.98937 |
| PREX1    | -1.4849 | 4.47122 | -3.8599 | 0.00837  | 0.0273  | -3.534  |
| DENND3   | -1.482  | -0.6003 | -6.6056 | 0.00058  | 0.00409 | -0.5307 |
| SARDH    | -1.4812 | -1.1342 | -5.3907 | 0.00168  | 0.00859 | -1.7353 |
| CEP112   | -1.4803 | 1.54623 | -8.0555 | 0.0002   | 0.00204 | 0.69955 |
| CACNA1D  | -1.4761 | -0.2311 | -5.7006 | 0.00126  | 0.00708 | -1.4108 |
| KCNH3    | -1.4741 | 1.46233 | -4.8294 | 0.00292  | 0.01265 | -2.3558 |
| DNMBP    | -1.4741 | 2.39904 | -7.5794 | 0.00027  | 0.00252 | 0.31734 |
| LAMA1    | -1.473  | 4.71993 | -4.6998 | 0.00333  | 0.01391 | -2.5054 |
| ANKRD6   | -1.4691 | 3.38793 | -7.543  | 0.00028  | 0.00256 | 0.28736 |
| NID1     | -1.4656 | 3.3137  | -8.7727 | 0.00012  | 0.00151 | 1.24007 |
| TAMALIN  | -1.4652 | 2.49539 | -7.5653 | 0.00028  | 0.00254 | 0.30578 |
| CDK5R1   | -1.4631 | 1.13535 | -4.9141 | 0.00268  | 0.01189 | -2.2593 |
| CYP2D6   | -1.4562 | -1.7118 | -4.8352 | 0.0029   | 0.0126  | -2.3491 |
| RESF1    | -1.4559 | 5.29387 | -8.2655 | 0.00017  | 0.00187 | 0.86206 |
| RFX5-AS  | -1.4553 | 0.17378 | -10.317 | 4.86E-05 | 0.00086 | 2.28049 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| PCTP     | -1.4551 | 2.71224 | -6.8608 | 0.00047  | 0.00357 | -0.2992 |
| C1orf226 | -1.455  | 1.4535  | -11.94  | 2.10E-05 | 0.00051 | 3.22703 |
| IFI35    | -1.4543 | 2.49006 | -12.746 | 1.44E-05 | 0.0004  | 3.65114 |
| HOXA13   | -1.4504 | 0.83679 | -4.5172 | 0.00404  | 0.01595 | -2.7201 |
| NDUFA6   | -1.4482 | -1.3439 | -6.5298 | 0.00062  | 0.00427 | -0.6008 |
| LIPH     | -1.4466 | -2.0522 | -4.3068 | 0.00506  | 0.01876 | -2.9737 |
| ADAM8    | -1.4464 | 0.10104 | -9.1056 | 9.89E-05 | 0.00132 | 1.47772 |
| MPP1     | -1.4456 | 3.13609 | -9.295  | 8.80E-05 | 0.00123 | 1.60952 |
| PRODH    | -1.4455 | 0.88784 | -3.3101 | 0.01622  | 0.04483 | -4.2623 |
| CAMK1    | -1.445  | 1.27519 | -13.298 | 1.12E-05 | 0.00035 | 3.9268  |
| NWD1     | -1.4449 | -0.4104 | -6.9706 | 0.00043  | 0.00337 | -0.2016 |
| FOXF2    | -1.4439 | 1.42907 | -6.2057 | 0.00081  | 0.00514 | -0.9077 |
| MCIDAS   | -1.4438 | -2.1152 | -3.402  | 0.01447  | 0.04118 | -4.1376 |
| CYP2J2   | -1.439  | 1.41588 | -7.9654 | 0.00021  | 0.00212 | 0.62878 |
| SCARB1   | -1.4385 | 4.74674 | -13.109 | 1.22E-05 | 0.00037 | 3.83353 |
| TBC1D8   | -1.4361 | 4.12393 | -7.6198 | 0.00027  | 0.00247 | 0.35055 |
| ZNF114   | -1.4357 | 2.36777 | -4.4843 | 0.00418  | 0.01634 | -2.7594 |
| GLI4     | -1.4331 | 2.67108 | -7.2038 | 0.00036  | 0.00298 | 0.00138 |
| SDSL     | -1.4327 | 1.95496 | -8.3419 | 0.00016  | 0.00181 | 0.92023 |
| SLC25A4  | -1.4326 | 0.14138 | -4.1894 | 0.00576  | 0.02068 | -3.1181 |
| DCBLD2   | -1.4319 | 6.0452  | -9.9394 | 6.02E-05 | 0.00097 | 2.0401  |
| PTGIS    | -1.4314 | 1.54275 | -10.257 | 5.03E-05 | 0.00087 | 2.24301 |
| CACNA1C  | -1.43   | -1.5057 | -4.4848 | 0.00418  | 0.01634 | -2.7588 |
| SLC6A20  | -1.43   | -2.4571 | -4.7043 | 0.00332  | 0.01387 | -2.5001 |
| APBA2    | -1.4299 | 3.18967 | -18.109 | 1.84E-06 | 0.00012 | 5.91902 |
| CTHRC1   | -1.4288 | 2.17529 | -7.5345 | 0.00028  | 0.00257 | 0.28027 |
| DUSP19   | -1.4263 | -0.4958 | -9.6127 | 7.28E-05 | 0.00109 | 1.82514 |
| ZBTB47   | -1.4225 | 1.19126 | -7.016  | 0.00042  | 0.0033  | -0.1618 |
| SNRPA1   | -1.422  | -3.0138 | -3.1948 | 0.01874  | 0.04987 | -4.4199 |
| SNRK     | -1.4189 | 2.31385 | -11.462 | 2.66E-05 | 0.00058 | 2.96194 |
| PMP22    | -1.4169 | 0.96478 | -6.4553 | 0.00066  | 0.00444 | -0.6703 |
| KCNJ5-A  | -1.4159 | 1.16948 | -8.083  | 0.00019  | 0.00202 | 0.72102 |
| CAPS2    | -1.4152 | -1.2118 | -11.401 | 2.74E-05 | 0.00059 | 2.92745 |
| ZNF134   | -1.415  | 0.44326 | -14.297 | 7.36E-06 | 0.00026 | 4.39671 |
| FGFR4    | -1.4143 | 5.2216  | -15.539 | 4.52E-06 | 0.0002  | 4.93576 |
| ELOVL2   | -1.4107 | 2.35879 | -8.5786 | 0.00014  | 0.00164 | 1.09775 |
| BTBD19   | -1.4104 | 1.70249 | -6.3734 | 0.0007   | 0.00465 | -0.7474 |
| AKAP1-D  | -1.4082 | -1.3672 | -3.2965 | 0.01649  | 0.04536 | -4.2807 |
| BRSK2    | -1.4076 | -2.5842 | -7.4942 | 0.00029  | 0.00262 | 0.24687 |
| KIF26A   | -1.4074 | 0.83568 | -4.0251 | 0.00693  | 0.02379 | -3.3235 |
| RUNX3    | -1.4072 | 1.67318 | -12.78  | 1.42E-05 | 0.0004  | 3.6687  |
| MAST4    | -1.4072 | 2.23874 | -8.5561 | 0.00014  | 0.00165 | 1.08104 |
| PAPSS2   | -1.4068 | 4.32726 | -7.9616 | 0.00021  | 0.00212 | 0.62577 |
| LINC0115 | -1.4059 | 0.13023 | -3.3441 | 0.01555  | 0.04341 | -4.216  |
| PSMG3-A  | -1.4058 | -1.0176 | -3.806  | 0.00891  | 0.02855 | -3.6035 |
| SGMS1-A  | -1.4043 | -0.6179 | -4.4423 | 0.00437  | 0.01685 | -2.8097 |
| TNKS2-D  | -1.4013 | -2.0024 | -6.3263 | 0.00073  | 0.00479 | -0.7921 |
| C17orf58 | -1.3974 | 3.44686 | -10.094 | 5.51E-05 | 0.00092 | 2.13991 |
| SEPTIN4  | -1.3968 | 1.11289 | -8.5265 | 0.00014  | 0.00168 | 1.059   |
| DNAAF8   | -1.3962 | -2.9185 | -3.2158 | 0.01825  | 0.04897 | -4.391  |
| ZNF667-A | -1.3931 | 0.66807 | -11.446 | 2.68E-05 | 0.00059 | 2.95284 |
| BNIP3    | -1.3925 | 3.74144 | -7.8258 | 0.00023  | 0.00225 | 0.51765 |
| HOXA2    | -1.3916 | 0.85424 | -4.3476 | 0.00484  | 0.01814 | -2.9241 |
| ARHGAP   | -1.3905 | 3.51277 | -9.266  | 8.96E-05 | 0.00124 | 1.58947 |
| LHFPL2   | -1.3891 | 3.39489 | -10.468 | 4.48E-05 | 0.00081 | 2.37424 |
| SYTL4    | -1.3888 | 0.63002 | -17.037 | 2.63E-06 | 0.00015 | 5.5286  |
| KCNC4    | -1.3885 | 0.83164 | -9.0397 | 0.0001   | 0.00135 | 1.43134 |
| BMERB1   | -1.3864 | -1.2691 | -6.2595 | 0.00077  | 0.00498 | -0.8559 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| RHCE     | -1.3819 | -1.0121 | -11.068 | 3.25E-05 | 0.00067 | 2.73511 |
| ARHGAP   | -1.3811 | -2.9158 | -4.4805 | 0.0042   | 0.01638 | -2.764  |
| POMGNT   | -1.3802 | 2.51669 | -11.401 | 2.74E-05 | 0.00059 | 2.92695 |
| SMIM6    | -1.3778 | -0.0596 | -4.9406 | 0.00261  | 0.01164 | -2.2293 |
| PDGFRL   | -1.3734 | 0.03696 | -7.4007 | 0.00031  | 0.00271 | 0.16872 |
| FLT4     | -1.3733 | -2.5436 | -3.5792 | 0.01167  | 0.03503 | -3.9007 |
| CATSPEP  | -1.3728 | -1.3219 | -5.3083 | 0.00182  | 0.00904 | -1.8236 |
| GRIN2B   | -1.3721 | -0.0304 | -3.4291 | 0.014    | 0.04026 | -4.1011 |
| ANXA2R   | -1.3716 | 0.72962 | -10.903 | 3.54E-05 | 0.0007  | 2.63781 |
| SEMA3G   | -1.3704 | 0.65214 | -3.643  | 0.01081  | 0.03299 | -3.8164 |
| NLGN1    | -1.3681 | 1.95408 | -5.1788 | 0.00206  | 0.00986 | -1.9644 |
| APH1B    | -1.3672 | 0.75683 | -6.1225 | 0.00087  | 0.00543 | -0.9884 |
| TPBG     | -1.3666 | 2.91574 | -10.315 | 4.87E-05 | 0.00086 | 2.27913 |
| ABCA1    | -1.3663 | 1.96445 | -3.4848 | 0.01308  | 0.03823 | -4.0263 |
| MGST3    | -1.3662 | 4.68972 | -12.623 | 1.52E-05 | 0.00042 | 3.58816 |
| SCIRT    | -1.3652 | -1.2371 | -6.7413 | 0.00052  | 0.00382 | -0.4067 |
| RAB31    | -1.3645 | 3.25271 | -9.3824 | 8.35E-05 | 0.00118 | 1.66946 |
| XAF1     | -1.3636 | 0.69141 | -6.8583 | 0.00047  | 0.00357 | -0.3014 |
| THBS2-A  | -1.3617 | -2.4383 | -3.4274 | 0.01403  | 0.04031 | -4.1035 |
| KDM4A-A  | -1.3602 | -1.9779 | -4.735  | 0.00321  | 0.01353 | -2.4645 |
| PPP1R3C  | -1.3584 | -0.7386 | -7.5465 | 0.00028  | 0.00256 | 0.29024 |
| CMTM3    | -1.3579 | 2.11372 | -8.2309 | 0.00017  | 0.00189 | 0.83554 |
| RPS6KA5  | -1.3571 | 3.37557 | -14.59  | 6.54E-06 | 0.00025 | 4.52835 |
| CCDC116  | -1.3541 | -0.8978 | -4.7043 | 0.00332  | 0.01387 | -2.5001 |
| LAMC3    | -1.3527 | 1.61777 | -6.7674 | 0.00051  | 0.00376 | -0.3831 |
| OSGIN1   | -1.3517 | 1.75014 | -15.062 | 5.43E-06 | 0.00022 | 4.7342  |
| NPEPL1   | -1.3515 | 0.09826 | -7.6747 | 0.00026  | 0.00242 | 0.39547 |
| CA12     | -1.3472 | 5.3835  | -6.5597 | 0.0006   | 0.00419 | -0.573  |
| WIPF1    | -1.3467 | 3.74853 | -17.005 | 2.66E-06 | 0.00015 | 5.51644 |
| PTPRB    | -1.3458 | 1.59508 | -4.4131 | 0.00451  | 0.01723 | -2.8448 |
| PCDHB5   | -1.3452 | 1.12758 | -8.0953 | 0.00019  | 0.00201 | 0.73063 |
| PYROXD   | -1.3426 | 0.47781 | -9.2146 | 9.25E-05 | 0.00126 | 1.55387 |
| SHBG     | -1.3399 | -2.5588 | -8.8425 | 0.00012  | 0.00148 | 1.29052 |
| LPAR3    | -1.3392 | 1.75119 | -9.9965 | 5.82E-05 | 0.00095 | 2.077   |
| ABCA5    | -1.3377 | 1.39349 | -11.125 | 3.16E-05 | 0.00065 | 2.7682  |
| FAM21EF  | -1.3365 | -2.5669 | -3.6374 | 0.01088  | 0.03316 | -3.8237 |
| GPR153   | -1.3321 | 1.68791 | -11.791 | 2.26E-05 | 0.00054 | 3.14568 |
| GPRIN3   | -1.331  | -0.0117 | -4.46   | 0.00429  | 0.01664 | -2.7885 |
| HEYL     | -1.3306 | -0.445  | -5.9232 | 0.00103  | 0.00611 | -1.1852 |
| SDCBP2   | -1.3286 | -0.6724 | -9.413  | 8.20E-05 | 0.00116 | 1.69036 |
| OSBPL5   | -1.3249 | 1.3271  | -8.1488 | 0.00018  | 0.00196 | 0.77217 |
| LINC0066 | -1.3247 | -1.6546 | -8.0088 | 0.0002   | 0.00208 | 0.66293 |
| SLC16A7  | -1.3243 | 3.07593 | -5.8599 | 0.00109  | 0.00637 | -1.2488 |
| GALNT1   | -1.3214 | 3.89875 | -7.0501 | 0.00041  | 0.00325 | -0.1319 |
| ARL4D    | -1.3188 | 3.3542  | -6.0132 | 0.00096  | 0.00578 | -1.0958 |
| SLC7A2   | -1.3186 | 3.27327 | -8.1191 | 0.00019  | 0.00198 | 0.74915 |
| MAPK10   | -1.3158 | -0.5014 | -5.9042 | 0.00105  | 0.00619 | -1.2042 |
| MCOLN3   | -1.314  | 1.34648 | -13.328 | 1.11E-05 | 0.00035 | 3.94143 |
| TMEM44   | -1.3138 | 2.4318  | -13.805 | 9.03E-06 | 0.0003  | 4.16966 |
| SLC9A5   | -1.3136 | -0.6194 | -5.5869 | 0.0014   | 0.00761 | -1.5284 |
| HOXA5    | -1.3118 | 1.7972  | -6.5399 | 0.00061  | 0.00424 | -0.5914 |
| GTF2H2C  | -1.311  | -1.4484 | -4.4164 | 0.00449  | 0.01719 | -2.8408 |
| ASB2     | -1.3071 | -3.4539 | -3.3099 | 0.01622  | 0.04484 | -4.2625 |
| KIAA1614 | -1.306  | 0.06185 | -8.6645 | 0.00013  | 0.00158 | 1.16103 |
| CROT     | -1.3017 | 2.3037  | -6.3303 | 0.00073  | 0.00478 | -0.7883 |
| TLR3     | -1.3013 | -0.0136 | -7.2752 | 0.00034  | 0.00287 | 0.06244 |
| ST3GAL4  | -1.3001 | 3.67921 | -6.574  | 0.0006   | 0.00417 | -0.5598 |
| ZNF284   | -1.2984 | 0.17615 | -6.9804 | 0.00043  | 0.00335 | -0.1931 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| NKX2-8   | -1.2972 | 0.54193 | -7.2418 | 0.00035  | 0.00293 | 0.03399 |
| TGFB1    | -1.2968 | 4.41852 | -3.2466 | 0.01756  | 0.04756 | -4.3488 |
| LRRRC63  | -1.2947 | -2.4677 | -4.0123 | 0.00703  | 0.02403 | -3.3396 |
| ENTPD3   | -1.2938 | -1.7835 | -5.8778 | 0.00108  | 0.0063  | -1.2307 |
| PCOLCE   | -1.292  | 2.86639 | -6.4082 | 0.00068  | 0.00456 | -0.7145 |
| SH3TC1   | -1.2903 | 1.00417 | -6.075  | 0.00091  | 0.00556 | -1.035  |
| SEMA6C   | -1.2888 | 2.0318  | -9.2407 | 9.10E-05 | 0.00125 | 1.57195 |
| NAGLU    | -1.2875 | 2.88536 | -11.126 | 3.15E-05 | 0.00065 | 2.76907 |
| KANSL1   | -1.2856 | 1.16642 | -9.5797 | 7.42E-05 | 0.0011  | 1.80306 |
| TMED2-D  | -1.2854 | 0.47293 | -6.7208 | 0.00053  | 0.00385 | -0.4253 |
| INPP1    | -1.2831 | 2.68799 | -12.378 | 1.70E-05 | 0.00045 | 3.46099 |
| CFAP20D  | -1.2784 | 0.9314  | -6.8305 | 0.00048  | 0.00363 | -0.3263 |
| ZNF567-D | -1.2763 | 0.78789 | -4.8174 | 0.00295  | 0.01279 | -2.3695 |
| PIK3R3   | -1.2744 | 3.96186 | -7.2757 | 0.00034  | 0.00287 | 0.06294 |
| BCYRN1   | -1.2712 | 2.64825 | -6.4563 | 0.00066  | 0.00444 | -0.6694 |
| RBM11    | -1.2678 | -1.1862 | -4.46   | 0.00429  | 0.01664 | -2.7884 |
| ISL1     | -1.2677 | 0.08132 | -3.8194 | 0.00878  | 0.02825 | -3.5862 |
| PDCD4-A  | -1.2651 | -0.0301 | -4.8372 | 0.00289  | 0.01258 | -2.3469 |
| IL6R     | -1.2647 | 2.87176 | -11.378 | 2.77E-05 | 0.0006  | 2.91384 |
| TRANK1   | -1.2632 | -0.2983 | -6.7392 | 0.00052  | 0.00382 | -0.4086 |
| TTLL1    | -1.2619 | -0.5774 | -5.0226 | 0.0024   | 0.01098 | -2.1372 |
| SARNP    | -1.2613 | -2.4967 | -4.0865 | 0.00646  | 0.02263 | -3.2462 |
| PHLDA2   | -1.2611 | 3.38714 | -5.5603 | 0.00144  | 0.00774 | -1.5562 |
| GPX3     | -1.2604 | 7.86441 | -4.2288 | 0.00551  | 0.02    | -3.0695 |
| SAMD9    | -1.2603 | 1.626   | -4.484  | 0.00418  | 0.01634 | -2.7597 |
| RIN1     | -1.26   | 2.04015 | -7.6021 | 0.00027  | 0.0025  | 0.33601 |
| ZBTB44-D | -1.2594 | -2.5238 | -5.5464 | 0.00145  | 0.0078  | -1.5706 |
| C9orf43  | -1.2589 | -1.7111 | -3.7459 | 0.00957  | 0.03004 | -3.6815 |
| CCDC17   | -1.2581 | -0.8238 | -6.2875 | 0.00076  | 0.00489 | -0.8291 |
| GDPD5    | -1.2578 | 5.07643 | -3.7692 | 0.00931  | 0.02947 | -3.6513 |
| CFAP74   | -1.2559 | -3.0885 | -3.8357 | 0.00861  | 0.02785 | -3.5652 |
| SCN8A    | -1.2555 | -0.7607 | -5.1136 | 0.0022   | 0.0103  | -2.0362 |
| FBLN1    | -1.2552 | 6.04467 | -8.6258 | 0.00013  | 0.0016  | 1.13263 |
| GMPR     | -1.2543 | 2.45125 | -8.2549 | 0.00017  | 0.00188 | 0.85392 |
| DACT3    | -1.2538 | 0.61902 | -11.701 | 2.36E-05 | 0.00055 | 3.09582 |
| SYT3     | -1.2537 | -0.4259 | -7.5666 | 0.00028  | 0.00254 | 0.30682 |
| CCDC137  | -1.2532 | 0.73624 | -6.2602 | 0.00077  | 0.00498 | -0.8553 |
| HLA-F-AS | -1.252  | -1.7349 | -8.6436 | 0.00013  | 0.00159 | 1.14573 |
| TMOD1    | -1.2499 | 2.49393 | -9.3798 | 8.36E-05 | 0.00118 | 1.66768 |
| DNAJC27  | -1.2487 | -2.6354 | -3.4967 | 0.01289  | 0.03781 | -4.0105 |
| COLQ     | -1.2474 | -2.5575 | -5.851  | 0.0011   | 0.00641 | -1.2577 |
| OSGIN2   | -1.2431 | 5.31222 | -12.985 | 1.29E-05 | 0.00038 | 3.77182 |
| ALDH2    | -1.2422 | 4.39446 | -8.4344 | 0.00015  | 0.00175 | 0.99015 |
| HMGN5    | -1.2412 | 2.01331 | -8.0363 | 0.0002   | 0.00206 | 0.68453 |
| OSBPL7   | -1.2406 | 2.59208 | -9.8859 | 6.21E-05 | 0.00098 | 2.00538 |
| ASIC1    | -1.2388 | 2.13242 | -4.3925 | 0.00461  | 0.01751 | -2.8697 |
| GLYCTK   | -1.2376 | 1.32486 | -6.5422 | 0.00061  | 0.00424 | -0.5892 |
| PIK3R1   | -1.2363 | 3.88681 | -5.5465 | 0.00145  | 0.0078  | -1.5705 |
| PLEKHB1  | -1.2359 | 0.33961 | -8.2363 | 0.00017  | 0.00189 | 0.83963 |
| STAT1    | -1.2356 | 5.29868 | -5.857  | 0.0011   | 0.00638 | -1.2517 |
| SLC12A5  | -1.2351 | -0.3004 | -5.3538 | 0.00174  | 0.00877 | -1.7747 |
| GPSM1    | -1.233  | 2.38459 | -13.29  | 1.13E-05 | 0.00035 | 3.92259 |
| LINC0261 | -1.2328 | 0.39393 | -6.527  | 0.00062  | 0.00427 | -0.6034 |
| CD44     | -1.2325 | 4.8721  | -5.1638 | 0.00209  | 0.00997 | -1.9809 |
| PDGFRB   | -1.2321 | -2.1217 | -4.3966 | 0.00459  | 0.01746 | -2.8647 |
| BNIP3P1  | -1.2307 | 5.01562 | -7.1883 | 0.00037  | 0.00301 | -0.0119 |
| A4GALT   | -1.2302 | 3.37956 | -4.6084 | 0.00366  | 0.0149  | -2.6122 |
| PAXIP1-A | -1.2277 | -1.8348 | -3.7833 | 0.00916  | 0.02914 | -3.633  |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| ZNF234   | -1.227  | 2.02391 | -12.172 | 1.88E-05 | 0.00048 | 3.35205 |
| MR1      | -1.227  | 2.9465  | -13.88  | 8.75E-06 | 0.00029 | 4.20458 |
| MTA1-DT  | -1.2242 | 1.67195 | -3.5561 | 0.012    | 0.03573 | -3.9313 |
| LINC0108 | -1.2242 | 1.77299 | -5.7193 | 0.00124  | 0.00699 | -1.3916 |
| WASF1    | -1.2212 | 2.95797 | -11.985 | 2.05E-05 | 0.00051 | 3.25142 |
| IKBIP    | -1.2205 | 3.9705  | -10.662 | 4.03E-05 | 0.00076 | 2.49295 |
| DRAXIN   | -1.2196 | -1.303  | -6.8726 | 0.00047  | 0.00354 | -0.2887 |
| CYCSP6   | -1.2174 | -1.4759 | -3.282  | 0.0168   | 0.04595 | -4.3006 |
| DLK2     | -1.2164 | -0.6897 | -5.3652 | 0.00172  | 0.00872 | -1.7625 |
| GNAL     | -1.2145 | -0.0271 | -9.4064 | 8.23E-05 | 0.00117 | 1.68587 |
| CASC8    | -1.2115 | 1.76699 | -5.2359 | 0.00195  | 0.00949 | -1.9021 |
| HMX1     | -1.2065 | 3.49721 | -8.299  | 0.00017  | 0.00184 | 0.8876  |
| MOCS2-D  | -1.2043 | 0.97006 | -8.4171 | 0.00015  | 0.00176 | 0.9771  |
| BTD      | -1.2037 | 0.77985 | -6.5    | 0.00063  | 0.00432 | -0.6285 |
| TNFSF10  | -1.2027 | 2.66282 | -3.223  | 0.01808  | 0.04862 | -4.3812 |
| GRAMD1   | -1.2025 | 0.25673 | -3.7844 | 0.00914  | 0.02911 | -3.6315 |
| VASH1    | -1.2015 | 0.10889 | -5.9496 | 0.00101  | 0.006   | -1.1589 |
| SPAG4    | -1.1995 | 1.34695 | -3.4467 | 0.0137   | 0.03963 | -4.0775 |
| DZIP1L   | -1.1992 | 0.86942 | -5.6044 | 0.00138  | 0.00755 | -1.5101 |
| CLDN16   | -1.1989 | 3.84753 | -4.7404 | 0.0032   | 0.01348 | -2.4582 |
| LRRC4B   | -1.1985 | 0.25136 | -3.3797 | 0.01488  | 0.04201 | -4.1678 |
| GBX2     | -1.1977 | -0.0519 | -6.1864 | 0.00082  | 0.00521 | -0.9263 |
| SEPTIN5  | -1.197  | 1.15784 | -9.414  | 8.19E-05 | 0.00116 | 1.69103 |
| SLC15A1  | -1.1963 | -2.5054 | -3.3404 | 0.01562  | 0.04357 | -4.2211 |
| SRD5A3   | -1.1955 | 2.84649 | -7.5359 | 0.00028  | 0.00257 | 0.28146 |
| CHRD     | -1.1924 | 1.48278 | -4.3653 | 0.00475  | 0.01791 | -2.9026 |
| TNFRSF1  | -1.1903 | -4.1054 | -3.954  | 0.00751  | 0.02523 | -3.4136 |
| HOXC6    | -1.1889 | 0.10391 | -8.9629 | 0.00011  | 0.0014  | 1.37683 |
| COA3     | -1.1871 | 5.56553 | -12.345 | 1.73E-05 | 0.00046 | 3.44358 |
| TMEM108  | -1.1864 | -0.2016 | -11.049 | 3.28E-05 | 0.00067 | 2.72419 |
| C20orf20 | -1.185  | -0.6606 | -3.2    | 0.01861  | 0.04966 | -4.4127 |
| GRK3     | -1.1846 | 1.81734 | -11.855 | 2.19E-05 | 0.00053 | 3.18045 |
| CCDC15   | -1.1823 | 0.40579 | -5.3859 | 0.00169  | 0.00862 | -1.7404 |
| CAPN14   | -1.1823 | -2.3373 | -5.344  | 0.00176  | 0.00884 | -1.7852 |
| HOXA6    | -1.182  | -0.6454 | -4.1681 | 0.0059   | 0.02107 | -3.1445 |
| ZEB1-AS  | -1.1787 | 0.08543 | -6.9872 | 0.00043  | 0.00334 | -0.1871 |
| IFTAP    | -1.1781 | -0.0391 | -8.2909 | 0.00017  | 0.00184 | 0.88148 |
| TGFB3    | -1.1772 | 0.70971 | -3.7709 | 0.00929  | 0.02942 | -3.6491 |
| IL11RA   | -1.1761 | 0.65819 | -7.3652 | 0.00032  | 0.00275 | 0.13879 |
| PFKM     | -1.1747 | 5.14579 | -13.154 | 1.20E-05 | 0.00036 | 3.85585 |
| SLC9A3-A | -1.1728 | 2.25273 | -6.9169 | 0.00045  | 0.00347 | -0.2492 |
| SHC1P2   | -1.1726 | 0.87456 | -5.2253 | 0.00197  | 0.00955 | -1.9135 |
| LINC0094 | -1.1721 | 1.36351 | -5.9684 | 0.00099  | 0.00593 | -1.1402 |
| CEACAM   | -1.172  | -0.9099 | -4.7577 | 0.00314  | 0.01332 | -2.4382 |
| AARSD1   | -1.1709 | -1.2872 | -6.4843 | 0.00064  | 0.00436 | -0.6432 |
| TTN-AS1  | -1.1692 | 0.72716 | -11.437 | 2.69E-05 | 0.00059 | 2.9475  |
| USP44    | -1.1692 | 1.39567 | -5.4239 | 0.00163  | 0.00841 | -1.6999 |
| GAL3ST4  | -1.169  | -2.3243 | -5.0137 | 0.00242  | 0.01103 | -2.1472 |
| PLOD2    | -1.1688 | 4.26195 | -11.201 | 3.03E-05 | 0.00064 | 2.81263 |
| KCNMA1   | -1.1674 | 0.36423 | -5.0783 | 0.00227  | 0.01056 | -2.0753 |
| LPP-AS2  | -1.1673 | 1.84031 | -5.0441 | 0.00235  | 0.01082 | -2.1132 |
| COL12A1  | -1.1671 | 5.81158 | -3.873  | 0.00825  | 0.02697 | -3.5171 |
| SRP54-A  | -1.1652 | -2.5131 | -4.1143 | 0.00626  | 0.0221  | -3.2115 |
| SNX22    | -1.1648 | -1.5177 | -5.3385 | 0.00177  | 0.00887 | -1.7912 |
| ZNF155   | -1.1635 | 1.03517 | -6.96   | 0.00044  | 0.00339 | -0.211  |
| SULF1    | -1.162  | -1.6114 | -3.6165 | 0.01116  | 0.03382 | -3.8513 |
| TFCP2L1  | -1.1618 | -0.4631 | -5.7665 | 0.00119  | 0.00676 | -1.3433 |
| C2orf72  | -1.1616 | -0.0163 | -5.6913 | 0.00127  | 0.00712 | -1.4203 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| JUN      | -1.1611 | 6.5585  | -6.068  | 0.00091  | 0.00558 | -1.0418 |
| HOXB-AS  | -1.1611 | 0.6366  | -4.8602 | 0.00283  | 0.01238 | -2.3206 |
| SH3TC2   | -1.1605 | 0.64477 | -3.6947 | 0.01016  | 0.03145 | -3.7484 |
| UBE2L6   | -1.1591 | 3.79901 | -6.7838 | 0.0005   | 0.00372 | -0.3683 |
| ANKRD44  | -1.1591 | 1.69842 | -4.4517 | 0.00433  | 0.01674 | -2.7984 |
| COQ10A   | -1.158  | 2.59809 | -9.3686 | 8.42E-05 | 0.00118 | 1.66007 |
| TMEM218  | -1.1569 | 2.24785 | -12.205 | 1.85E-05 | 0.00048 | 3.36945 |
| ZNF542P  | -1.1552 | 1.08509 | -7.0773 | 0.0004   | 0.0032  | -0.1081 |
| DIPK1B   | -1.152  | 3.98343 | -7.4273 | 0.00031  | 0.00269 | 0.19098 |
| SLC15A2  | -1.1518 | -2.1803 | -8.3287 | 0.00016  | 0.00182 | 0.91025 |
| SORD2P   | -1.1484 | -2.6279 | -7.5892 | 0.00027  | 0.00251 | 0.32541 |
| CHST2    | -1.1441 | 3.83229 | -3.9749 | 0.00733  | 0.02479 | -3.3871 |
| SP5      | -1.1439 | 0.21315 | -5.1694 | 0.00208  | 0.00993 | -1.9747 |
| PDE6A    | -1.1435 | -0.8512 | -4.2059 | 0.00566  | 0.02038 | -3.0977 |
| CRYGS    | -1.1413 | -1.4057 | -3.9245 | 0.00777  | 0.02583 | -3.4512 |
| LHX2     | -1.1394 | -0.4405 | -8.0629 | 0.0002   | 0.00204 | 0.70535 |
| PITPNM2  | -1.1392 | 3.04914 | -4.2518 | 0.00538  | 0.01965 | -3.0412 |
| IDH1-AS1 | -1.1387 | 0.66933 | -3.5369 | 0.01228  | 0.03636 | -3.9569 |
| MOXD1    | -1.1385 | -1.0202 | -5.9087 | 0.00105  | 0.00617 | -1.1997 |
| HIVEP3   | -1.138  | 2.18641 | -5.2894 | 0.00185  | 0.00917 | -1.844  |
| ARSG     | -1.1372 | 0.43856 | -7.3695 | 0.00032  | 0.00274 | 0.14245 |
| TIMP2    | -1.1369 | 6.85846 | -13.669 | 9.57E-06 | 0.00031 | 4.1053  |
| ZNF702P  | -1.1363 | 0.46558 | -4.3284 | 0.00494  | 0.01845 | -2.9474 |
| ZNF569   | -1.1358 | 1.2594  | -11.271 | 2.93E-05 | 0.00062 | 2.85298 |
| CCDC88B  | -1.1352 | 0.15749 | -5.3038 | 0.00183  | 0.00907 | -1.8285 |
| AQP11    | -1.129  | -0.7593 | -5.4346 | 0.00161  | 0.00837 | -1.6885 |
| RSAD1    | -1.1276 | 4.16055 | -9.1364 | 9.70E-05 | 0.0013  | 1.49931 |
| NUDT14   | -1.1271 | 2.96279 | -6.1999 | 0.00081  | 0.00517 | -0.9133 |
| ZNF235   | -1.1268 | 0.43075 | -8.1803 | 0.00018  | 0.00194 | 0.79656 |
| SYNPO    | -1.125  | 6.01483 | -5.017  | 0.00242  | 0.01101 | -2.1435 |
| THAP7-A  | -1.1247 | 0.23555 | -8.5716 | 0.00014  | 0.00164 | 1.09256 |
| ZNF420   | -1.124  | 1.05634 | -10.769 | 3.81E-05 | 0.00073 | 2.55768 |
| STRADA   | -1.1238 | -0.7108 | -3.2199 | 0.01816  | 0.04876 | -4.3855 |
| PDCD6IP  | -1.1208 | -0.7616 | -3.6838 | 0.0103   | 0.03179 | -3.7628 |
| PRTG     | -1.1206 | 1.44422 | -6.736  | 0.00052  | 0.00383 | -0.4115 |
| KCNIP2   | -1.1184 | -1.2135 | -4.0114 | 0.00704  | 0.02404 | -3.3408 |
| FMNL2    | -1.1169 | 5.6408  | -11.726 | 2.33E-05 | 0.00055 | 3.1098  |
| MIR130A  | -1.1167 | -0.4519 | -5.5878 | 0.0014   | 0.00761 | -1.5274 |
| TNS2     | -1.1149 | 3.99478 | -4.4034 | 0.00456  | 0.01736 | -2.8565 |
| NOS1AP   | -1.1137 | -0.0143 | -5.7865 | 0.00117  | 0.00667 | -1.323  |
| GFRA3    | -1.1133 | -1.6989 | -6.2491 | 0.00078  | 0.00501 | -0.8659 |
| LINC0091 | -1.1133 | -0.3537 | -4.0092 | 0.00705  | 0.02409 | -3.3436 |
| ACOT1    | -1.1113 | 0.59092 | -8.5385 | 0.00014  | 0.00167 | 1.06799 |
| HYPK     | -1.1102 | -1.8759 | -3.2005 | 0.0186   | 0.04965 | -4.4121 |
| RAI2     | -1.1101 | 3.39919 | -5.9661 | 0.001    | 0.00593 | -1.1424 |
| EGR1     | -1.1099 | 6.54992 | -3.2308 | 0.01791  | 0.04828 | -4.3705 |
| SULT1A1  | -1.1096 | 2.85648 | -7.8278 | 0.00023  | 0.00225 | 0.51923 |
| TCF12    | -1.1082 | 5.12411 | -7.205  | 0.00036  | 0.00298 | 0.00242 |
| TMEM121  | -1.1061 | -1.6326 | -3.4892 | 0.01301  | 0.03807 | -4.0205 |
| SLC46A3  | -1.1058 | -1.7396 | -4.0535 | 0.00671  | 0.02324 | -3.2877 |
| FBF1     | -1.1041 | 0.6586  | -11.65  | 2.42E-05 | 0.00056 | 3.06763 |
| GDF11    | -1.1024 | 4.45795 | -4.6494 | 0.00351  | 0.01446 | -2.5641 |
| ADAP2    | -1.1018 | -0.3791 | -3.4423 | 0.01377  | 0.03977 | -4.0834 |
| PRR7     | -1.1006 | 3.57763 | -14.186 | 7.70E-06 | 0.00027 | 4.34633 |
| COG1     | -1.1006 | 3.6095  | -14.482 | 6.83E-06 | 0.00026 | 4.47993 |
| ANXA4    | -1.0991 | 6.53214 | -11.307 | 2.88E-05 | 0.00061 | 2.87351 |
| RPL39L   | -1.0975 | 3.04282 | -10.847 | 3.65E-05 | 0.00071 | 2.60466 |
| PLEKHA7  | -1.0941 | 2.36152 | -7.9241 | 0.00022  | 0.00215 | 0.59608 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| BNC2     | -1.0938 | 4.01659 | -12.245 | 1.81E-05 | 0.00047 | 3.39055 |
| RBPMS    | -1.0933 | 3.91697 | -4.0498 | 0.00674  | 0.0233  | -3.2924 |
| C3orf18  | -1.0929 | -0.1028 | -6.6226 | 0.00057  | 0.00406 | -0.5151 |
| MBLAC1   | -1.0919 | 2.32539 | -4.4632 | 0.00427  | 0.01661 | -2.7846 |
| TRNP1    | -1.0909 | 5.42367 | -6.0463 | 0.00093  | 0.00566 | -1.0632 |
| TECPR1   | -1.0905 | 3.29866 | -9.4408 | 8.06E-05 | 0.00116 | 1.70927 |
| CRLF1    | -1.0888 | 1.0888  | -4.8932 | 0.00273  | 0.01207 | -2.2831 |
| RNFT1    | -1.0886 | 0.7374  | -11.159 | 3.10E-05 | 0.00065 | 2.78794 |
| FTSJ3    | -1.0879 | 5.1328  | -6.7692 | 0.00051  | 0.00375 | -0.3814 |
| SELENOI  | -1.0871 | 3.85788 | -7.7159 | 0.00025  | 0.00237 | 0.42896 |
| CA2      | -1.087  | 3.32927 | -3.3927 | 0.01464  | 0.04151 | -4.1502 |
| GPR158   | -1.0865 | 1.96184 | -7.3169 | 0.00033  | 0.00281 | 0.09795 |
| ADGRB2   | -1.085  | 2.60545 | -7.5944 | 0.00027  | 0.0025  | 0.32976 |
| CCDC137  | -1.0831 | 4.86565 | -8.0047 | 0.0002   | 0.00208 | 0.65973 |
| GIHCG    | -1.083  | 2.45484 | -5.7108 | 0.00125  | 0.00703 | -1.4003 |
| DYSF     | -1.082  | 4.01698 | -5.2858 | 0.00186  | 0.00918 | -1.8479 |
| GPER1    | -1.0808 | -1.1632 | -4.6297 | 0.00358  | 0.01466 | -2.5873 |
| MGST1    | -1.0805 | 4.92188 | -9.2933 | 8.81E-05 | 0.00123 | 1.60833 |
| TBX2     | -1.0803 | 0.43875 | -5.238  | 0.00195  | 0.00948 | -1.8998 |
| ATXN2-A  | -1.0791 | -0.1886 | -4.5615 | 0.00385  | 0.01541 | -2.6676 |
| EDA      | -1.0779 | 1.2824  | -3.207  | 0.01845  | 0.04938 | -4.4031 |
| LRP4     | -1.0765 | 0.01354 | -4.8595 | 0.00283  | 0.01239 | -2.3214 |
| EIF1P5   | -1.0764 | 1.46288 | -3.9025 | 0.00797  | 0.02628 | -3.4793 |
| ABCB6    | -1.0764 | 0.25835 | -9.52   | 7.69E-05 | 0.00112 | 1.76288 |
| MCRIP1   | -1.075  | 3.83838 | -6.1927 | 0.00082  | 0.0052  | -0.9203 |
| TUBA8    | -1.0733 | -0.3138 | -3.9359 | 0.00767  | 0.02562 | -3.4366 |
| PHETA1   | -1.0722 | 3.56843 | -8.9267 | 0.00011  | 0.00142 | 1.35096 |
| ZNF697   | -1.0717 | 1.64801 | -5.4006 | 0.00167  | 0.00853 | -1.7247 |
| IFIT1    | -1.0674 | 1.84069 | -3.4811 | 0.01314  | 0.03839 | -4.0314 |
| FBXO10   | -1.0668 | -0.1447 | -3.6776 | 0.01037  | 0.03198 | -3.7709 |
| PASD1    | -1.0667 | 3.05907 | -6.0353 | 0.00094  | 0.0057  | -1.074  |
| GPR135   | -1.0665 | 0.95973 | -9.7024 | 6.90E-05 | 0.00105 | 1.8848  |
| TRAF5    | -1.0657 | 1.1091  | -7.7095 | 0.00025  | 0.00238 | 0.42383 |
| ANKHD1-  | -1.0644 | -2.2876 | -5.579  | 0.00141  | 0.00765 | -1.5366 |
| HHAT     | -1.0641 | -0.0155 | -3.6998 | 0.0101   | 0.03132 | -3.7418 |
| ZNF222   | -1.0623 | 0.74102 | -8.8145 | 0.00012  | 0.00149 | 1.27032 |
| ITGA6    | -1.0621 | 3.22131 | -5.1248 | 0.00217  | 0.01024 | -2.0237 |
| B3GALT9  | -1.0617 | -0.54   | -3.9333 | 0.00769  | 0.02567 | -3.4399 |
| IFI16    | -1.0602 | 3.85355 | -8.7497 | 0.00012  | 0.00153 | 1.22332 |
| OSTM1    | -1.057  | 3.66871 | -8.9497 | 0.00011  | 0.0014  | 1.36739 |
| ASIC3    | -1.0564 | -1.7191 | -4.8778 | 0.00278  | 0.01221 | -2.3005 |
| ZNRF2    | -1.0544 | 3.32405 | -7.27   | 0.00035  | 0.00288 | 0.05809 |
| MIR3677f | -1.0534 | -1.5916 | -13.66  | 9.60E-06 | 0.00031 | 4.10104 |
| STXBP4   | -1.0531 | 1.53095 | -5.3775 | 0.0017   | 0.00866 | -1.7493 |
| MALINC1  | -1.053  | -0.5908 | -3.2777 | 0.01688  | 0.0461  | -4.3063 |
| GPC4     | -1.0509 | 5.45067 | -3.2102 | 0.01838  | 0.04925 | -4.3988 |
| CBFA2T2  | -1.0504 | 5.10728 | -6.7486 | 0.00052  | 0.0038  | -0.4001 |
| DSE      | -1.0492 | 0.9002  | -5.0565 | 0.00232  | 0.01072 | -2.0994 |
| NMNAT3   | -1.0485 | 0.13083 | -7.5016 | 0.00029  | 0.00261 | 0.25304 |
| GSAP     | -1.0484 | -1.0173 | -9.1882 | 9.40E-05 | 0.00127 | 1.53554 |
| FAM241A  | -1.0477 | 1.61352 | -6.4929 | 0.00064  | 0.00434 | -0.6351 |
| LRMDA    | -1.047  | 3.42952 | -6.6165 | 0.00058  | 0.00406 | -0.5206 |
| SLFN12   | -1.0458 | 1.95866 | -3.9326 | 0.0077   | 0.02568 | -3.4409 |
| PLEKHM   | -1.0443 | 2.55173 | -7.2473 | 0.00035  | 0.00292 | 0.03869 |
| TMEM63C  | -1.0438 | 2.82259 | -6.3336 | 0.00073  | 0.00477 | -0.7852 |
| CDKN1C   | -1.0427 | 1.81297 | -4.7961 | 0.00302  | 0.01297 | -2.394  |
| ZNF396   | -1.0427 | -2.7277 | -3.3652 | 0.01515  | 0.04258 | -4.1875 |
| NT5C3B   | -1.0395 | 3.20549 | -7.5304 | 0.00028  | 0.00257 | 0.27688 |

|            |         |         |         |          |         |         |
|------------|---------|---------|---------|----------|---------|---------|
| ZNF227     | -1.0394 | 2.50036 | -6.6775 | 0.00055  | 0.00394 | -0.4648 |
| BLVRB      | -1.0393 | 5.40539 | -4.3103 | 0.00504  | 0.01872 | -2.9695 |
| ADORA2L    | -1.0373 | 0.9254  | -8.9978 | 0.00011  | 0.00138 | 1.40163 |
| VCAN       | -1.0372 | 6.43985 | -5.787  | 0.00117  | 0.00667 | -1.3225 |
| CD177      | -1.0364 | -2.6655 | -5.7056 | 0.00126  | 0.00706 | -1.4056 |
| SLC25A2    | -1.0347 | 1.61119 | -10.26  | 5.02E-05 | 0.00087 | 2.24487 |
| SH3RF2     | -1.0345 | 3.86489 | -6.7305 | 0.00052  | 0.00383 | -0.4165 |
| SLC10A4    | -1.0337 | -0.4606 | -4.3156 | 0.00501  | 0.01864 | -2.963  |
| HMOX2      | -1.0333 | 4.2287  | -6.2568 | 0.00077  | 0.00498 | -0.8585 |
| BRSK1      | -1.0333 | 2.33616 | -4.6815 | 0.0034   | 0.01409 | -2.5267 |
| JAZF1      | -1.0332 | 4.24727 | -13.638 | 9.70E-06 | 0.00032 | 4.09045 |
| FAM104A    | -1.0305 | 3.584   | -13.36  | 1.09E-05 | 0.00034 | 3.95693 |
| NRROS      | -1.0303 | -0.2797 | -9.074  | 0.0001   | 0.00134 | 1.4555  |
| INPP4B     | -1.0292 | 3.61451 | -5.4406 | 0.0016   | 0.00835 | -1.6822 |
| HIGD1A     | -1.0229 | 4.47925 | -7.9908 | 0.00021  | 0.0021  | 0.64881 |
| CRADD      | -1.0229 | 0.37258 | -9.1136 | 9.84E-05 | 0.00131 | 1.48334 |
| KLHL3      | -1.0224 | 0.20468 | -8.206  | 0.00018  | 0.00191 | 0.81634 |
| OXLD1      | -1.0221 | 4.83295 | -4.8567 | 0.00284  | 0.01241 | -2.3245 |
| LINC0257   | -1.022  | 1.52231 | -7.3701 | 0.00032  | 0.00274 | 0.1429  |
| COLEC12    | -1.0215 | 0.54904 | -3.4369 | 0.01387  | 0.03996 | -4.0907 |
| EXTL3-AS1  | -1.0202 | -1.4692 | -7.7714 | 0.00024  | 0.0023  | 0.47392 |
| PDZK1IP    | -1.0194 | 1.71415 | -3.2108 | 0.01836  | 0.04923 | -4.3979 |
| ARMCX1     | -1.0191 | 4.04332 | -7.0227 | 0.00042  | 0.00329 | -0.1558 |
| MDH1B      | -1.019  | -2.5748 | -3.38   | 0.01487  | 0.042   | -4.1674 |
| TTC21B-AS1 | -1.0189 | -6.3443 | -5.3283 | 0.00178  | 0.00893 | -1.8021 |
| ZNF45      | -1.0186 | 2.34159 | -6.1335 | 0.00086  | 0.00539 | -0.9778 |
| STYK1      | -1.018  | 0.65531 | -3.98   | 0.00729  | 0.02468 | -3.3806 |
| PPP1R9B    | -1.0175 | 4.65396 | -10.511 | 4.37E-05 | 0.0008  | 2.40093 |
| INTS2      | -1.0168 | 1.4708  | -8.6683 | 0.00013  | 0.00158 | 1.16384 |
| MHENCRA    | -1.0163 | 3.0813  | -3.8385 | 0.00858  | 0.0278  | -3.5615 |
| CASP4      | -1.016  | 2.8178  | -9.1217 | 9.79E-05 | 0.00131 | 1.48907 |
| AJM1       | -1.0138 | 1.21028 | -4.0258 | 0.00692  | 0.02377 | -3.3226 |
| HTRA1      | -1.0134 | 2.42748 | -5.0898 | 0.00225  | 0.01047 | -2.0625 |
| STK39      | -1.0126 | 2.65199 | -7.3415 | 0.00033  | 0.00277 | 0.11874 |
| PRKCA      | -1.012  | 3.5875  | -10.06  | 5.62E-05 | 0.00093 | 2.1181  |
| C2orf74-D  | -1.0097 | 2.03077 | -7.3139 | 0.00033  | 0.00281 | 0.09538 |
| LINC0269   | -1.0094 | 0.879   | -3.4419 | 0.01378  | 0.03977 | -4.084  |
| PLCXD2     | -1.0085 | -1.4619 | -5.4731 | 0.00156  | 0.00815 | -1.6477 |
| HMGCR      | -1.0078 | 6.4851  | -10.867 | 3.61E-05 | 0.00071 | 2.61619 |
| ARSJ       | -1.0077 | 1.69207 | -3.5643 | 0.01188  | 0.03545 | -3.9205 |
| ARL4C      | -1.0074 | 5.03225 | -10.727 | 3.89E-05 | 0.00074 | 2.53237 |
| DGCR6L     | -1.0044 | 4.05489 | -7.3306 | 0.00033  | 0.00279 | 0.10954 |
| BICD1      | -1.0034 | 4.06504 | -7.9573 | 0.00021  | 0.00212 | 0.62232 |
| ATP5MC1    | -1.0031 | 1.34317 | -7.2301 | 0.00036  | 0.00294 | 0.02398 |
| SLC35E3    | -1.0028 | 2.63939 | -6.7118 | 0.00053  | 0.00386 | -0.4335 |
| NRP1       | -1.0027 | 4.90125 | -3.8941 | 0.00805  | 0.02648 | -3.4901 |
| ASPHD2     | -1.0017 | -0.3706 | -4.2453 | 0.00542  | 0.01975 | -3.0491 |
| METTL7B    | -1.0005 | 1.44425 | -8.0666 | 0.00019  | 0.00204 | 0.70824 |
| LINC0245   | -1      | -0.9835 | -4.7174 | 0.00327  | 0.01374 | -2.4848 |
| SETX       | -0.9978 | 4.15968 | -9.0317 | 0.0001   | 0.00136 | 1.42563 |
| DPY19L1    | -0.9975 | 3.58636 | -8.3802 | 0.00016  | 0.00178 | 0.94931 |
| PLCB2      | -0.9951 | -1.4367 | -6.3972 | 0.00069  | 0.00458 | -0.7249 |
| PRKACB     | -0.9946 | 3.77467 | -4.9896 | 0.00248  | 0.01123 | -2.1743 |
| HCFC2      | -0.99   | 2.09693 | -12.015 | 2.02E-05 | 0.00051 | 3.26776 |
| PLD1       | -0.9871 | 1.94636 | -9.5438 | 7.58E-05 | 0.00111 | 1.77891 |
| FGGY       | -0.987  | 1.88877 | -11.727 | 2.33E-05 | 0.00055 | 3.11008 |
| PAQR6      | -0.9869 | 1.28738 | -3.6089 | 0.01126  | 0.03407 | -3.8613 |
| LMF1       | -0.9867 | 0.81795 | -5.1407 | 0.00214  | 0.01015 | -2.0063 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| BAZ2B-A  | -0.9852 | 0.84676 | -8.982  | 0.00011  | 0.00139 | 1.39042 |
| BCL2L13  | -0.9849 | 4.80183 | -9.5236 | 7.67E-05 | 0.00112 | 1.76529 |
| INTS6L   | -0.9849 | 1.94749 | -4.749  | 0.00317  | 0.01338 | -2.4483 |
| ZNF226   | -0.9846 | 2.81501 | -7.0407 | 0.00041  | 0.00326 | -0.14   |
| LINC0046 | -0.9843 | 0.26578 | -7.6416 | 0.00026  | 0.00244 | 0.36847 |
| EIF4E3   | -0.9841 | 1.63279 | -6.3081 | 0.00074  | 0.00484 | -0.8095 |
| MGST2    | -0.984  | 3.77758 | -12.013 | 2.03E-05 | 0.00051 | 3.26682 |
| CHKB-DT  | -0.9825 | 1.80881 | -9.0535 | 0.0001   | 0.00135 | 1.44108 |
| TMEM144  | -0.9817 | 0.87636 | -6.5605 | 0.0006   | 0.00419 | -0.5723 |
| MILIP    | -0.9803 | 2.37266 | -7.9854 | 0.00021  | 0.0021  | 0.64452 |
| NDRG2    | -0.9796 | 1.8309  | -8.436  | 0.00015  | 0.00174 | 0.99133 |
| PRR7-AS  | -0.9782 | 0.49255 | -3.8118 | 0.00885  | 0.02843 | -3.5961 |
| WDR86-A  | -0.978  | 1.80251 | -7.0018 | 0.00042  | 0.00333 | -0.1742 |
| FRMD4B   | -0.9774 | 2.48514 | -5.2613 | 0.0019   | 0.00935 | -1.8745 |
| EXOC7    | -0.9756 | 5.08644 | -10.003 | 5.80E-05 | 0.00095 | 2.08091 |
| AGA      | -0.9755 | 1.96337 | -7.8683 | 0.00022  | 0.00221 | 0.55166 |
| SHC1     | -0.9746 | 6.33478 | -7.472  | 0.0003   | 0.00264 | 0.22839 |
| DPM3     | -0.9733 | 5.28189 | -5.1915 | 0.00204  | 0.00979 | -1.9505 |
| PIGHP1   | -0.973  | 1.52095 | -7.3847 | 0.00032  | 0.00273 | 0.15526 |
| TK2      | -0.9724 | 1.63604 | -5.3195 | 0.0018   | 0.00898 | -1.8115 |
| GABARA   | -0.9723 | 2.83428 | -7.0404 | 0.00041  | 0.00326 | -0.1403 |
| HOMER3   | -0.9722 | 3.58895 | -4.9356 | 0.00262  | 0.01168 | -2.235  |
| EHHADH   | -0.9714 | 2.18973 | -6.7999 | 0.0005   | 0.00369 | -0.3538 |
| IL10RB   | -0.9698 | 1.95589 | -7.6454 | 0.00026  | 0.00244 | 0.37156 |
| COPZ2    | -0.9695 | 0.40903 | -8.4438 | 0.00015  | 0.00174 | 0.99716 |
| PCSK1N   | -0.9694 | 3.40612 | -8.5573 | 0.00014  | 0.00165 | 1.08191 |
| CDHR1    | -0.969  | 2.0624  | -4.9083 | 0.00269  | 0.01193 | -2.2658 |
| PSMB3P1  | -0.9689 | 2.44144 | -3.5399 | 0.01223  | 0.03627 | -3.9529 |
| CARD6    | -0.9682 | 2.04208 | -10.107 | 5.47E-05 | 0.00092 | 2.14804 |
| EME2     | -0.9674 | 2.20037 | -8.1764 | 0.00018  | 0.00194 | 0.79358 |
| RAB5CP2  | -0.9669 | -0.3084 | -4.277  | 0.00523  | 0.01924 | -3.0102 |
| ZFHX2    | -0.9667 | -0.2369 | -3.8769 | 0.00821  | 0.02687 | -3.5121 |
| SLC26A1  | -0.9657 | -3.6215 | -3.4204 | 0.01415  | 0.04054 | -4.1129 |
| NF2      | -0.9649 | 5.8246  | -5.013  | 0.00242  | 0.01103 | -2.1479 |
| TEX9     | -0.9648 | -0.3352 | -5.7865 | 0.00117  | 0.00667 | -1.323  |
| SNCB     | -0.9642 | -0.9464 | -3.2483 | 0.01752  | 0.04749 | -4.3465 |
| PLD6     | -0.9634 | 1.23316 | -5.3804 | 0.0017   | 0.00865 | -1.7462 |
| GAMT     | -0.9627 | 2.3712  | -12.898 | 1.34E-05 | 0.00039 | 3.72808 |
| CRYZL2F  | -0.9625 | 2.37213 | -4.7609 | 0.00313  | 0.01329 | -2.4345 |
| G6PC3    | -0.9621 | 4.21811 | -10.08  | 5.56E-05 | 0.00093 | 2.13036 |
| DNAH17-  | -0.9617 | 0.06248 | -5.7665 | 0.00119  | 0.00676 | -1.3434 |
| SLC38A1  | -0.9604 | 4.81214 | -9.4049 | 8.24E-05 | 0.00117 | 1.68486 |
| DENND5B  | -0.9604 | 4.12505 | -10.53  | 4.33E-05 | 0.00079 | 2.41274 |
| SFXN5    | -0.96   | 2.87524 | -4.2445 | 0.00542  | 0.01976 | -3.05   |
| KRT8P12  | -0.9583 | 2.71927 | -4.5574 | 0.00387  | 0.01544 | -2.6725 |
| GPR27    | -0.9577 | 3.56343 | -6.31   | 0.00074  | 0.00483 | -0.8077 |
| IL17RA   | -0.9566 | 3.30246 | -8.7007 | 0.00013  | 0.00156 | 1.18759 |
| NRIP3    | -0.9564 | 1.16365 | -5.2873 | 0.00186  | 0.00917 | -1.8463 |
| CD302    | -0.9564 | 2.65725 | -4.5099 | 0.00407  | 0.016   | -2.7289 |
| BBS4     | -0.9563 | 1.5116  | -8.7457 | 0.00012  | 0.00153 | 1.22042 |
| CCDC88A  | -0.9523 | 4.62925 | -10.889 | 3.57E-05 | 0.00071 | 2.62955 |
| PHYHD1   | -0.9513 | 0.14986 | -4.4794 | 0.0042   | 0.01639 | -2.7653 |
| HSD17B1  | -0.9513 | 2.68566 | -6.6036 | 0.00058  | 0.00409 | -0.5325 |
| ARHGEF2  | -0.9506 | -0.6078 | -4.6318 | 0.00358  | 0.01465 | -2.5848 |
| CBLL1-AS | -0.9503 | 1.46606 | -3.559  | 0.01195  | 0.03564 | -3.9274 |
| PPM1M    | -0.9499 | 2.63354 | -3.9034 | 0.00796  | 0.02627 | -3.4782 |
| NKIRAS2  | -0.9487 | 4.70052 | -10.946 | 3.47E-05 | 0.00069 | 2.66328 |
| RTL6     | -0.9482 | 4.33954 | -5.069  | 0.00229  | 0.01061 | -2.0856 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| LINC0260 | -0.947  | 1.11885 | -6.6181 | 0.00057  | 0.00406 | -0.5192 |
| DAPK1    | -0.9462 | 3.75326 | -7.9647 | 0.00021  | 0.00212 | 0.62819 |
| SLC35G2  | -0.9452 | 2.23188 | -7.4584 | 0.0003   | 0.00266 | 0.21698 |
| EVA1B    | -0.9447 | 3.06968 | -7.6432 | 0.00026  | 0.00244 | 0.36974 |
| ARMCX4   | -0.9443 | 2.42409 | -8.7725 | 0.00012  | 0.00151 | 1.23992 |
| NBR2     | -0.9437 | -0.6178 | -4.9167 | 0.00267  | 0.01187 | -2.2564 |
| TMEM104  | -0.9429 | 2.82185 | -5.2009 | 0.00202  | 0.00972 | -1.9402 |
| B3GNTL1  | -0.9421 | 2.49627 | -5.4755 | 0.00155  | 0.00814 | -1.6452 |
| INPP5F   | -0.9419 | 2.51143 | -11.653 | 2.42E-05 | 0.00056 | 3.06931 |
| ABHD4    | -0.9409 | 2.58139 | -8.9963 | 0.00011  | 0.00138 | 1.40056 |
| ZNF225   | -0.9405 | 0.83565 | -7.228  | 0.00036  | 0.00294 | 0.02211 |
| HDAC10   | -0.9391 | -0.6127 | -5.3253 | 0.00179  | 0.00894 | -1.8054 |
| ALPK1    | -0.9387 | 1.82568 | -3.8523 | 0.00845  | 0.02747 | -3.5437 |
| ANK2     | -0.9384 | 2.20183 | -3.5372 | 0.01227  | 0.03636 | -3.9564 |
| HTATIP2  | -0.9355 | 3.72582 | -9.4464 | 8.03E-05 | 0.00115 | 1.71306 |
| ZNF285   | -0.9355 | 0.30236 | -7.3455 | 0.00033  | 0.00277 | 0.12216 |
| HDHD5    | -0.9352 | 3.78767 | -5.9475 | 0.00101  | 0.00601 | -1.161  |
| ATP5MC1  | -0.935  | -0.2087 | -3.4026 | 0.01446  | 0.04118 | -4.1368 |
| GALK1    | -0.9341 | 2.68637 | -7.7243 | 0.00025  | 0.00236 | 0.43579 |
| ZNF850   | -0.9332 | -1.2423 | -5.129  | 0.00216  | 0.01022 | -2.0191 |
| PRRX2    | -0.9324 | 2.21036 | -4.085  | 0.00647  | 0.02266 | -3.2481 |
| GSTT2B   | -0.9323 | 0.15596 | -6.1193 | 0.00087  | 0.00544 | -0.9916 |
| NME4     | -0.932  | 4.22913 | -5.5682 | 0.00142  | 0.0077  | -1.5479 |
| ZNF225-A | -0.9314 | -0.0843 | -4.528  | 0.00399  | 0.01582 | -2.7073 |
| SH3RF3   | -0.9307 | 2.48113 | -5.822  | 0.00113  | 0.00654 | -1.287  |
| NUDT17   | -0.9305 | 1.35266 | -5.6908 | 0.00127  | 0.00712 | -1.4208 |
| ZNF112   | -0.9296 | 0.3456  | -9.5969 | 7.35E-05 | 0.00109 | 1.81459 |
| CCDC110  | -0.9294 | -1.6829 | -4.7148 | 0.00328  | 0.01377 | -2.4879 |
| TXNRD2   | -0.9283 | 3.55324 | -5.4094 | 0.00165  | 0.00849 | -1.7153 |
| DPP3-DT  | -0.928  | 0.42931 | -7.3363 | 0.00033  | 0.00278 | 0.11441 |
| SNCA     | -0.928  | 2.57215 | -9.5766 | 7.43E-05 | 0.0011  | 1.80097 |
| THRA     | -0.9274 | 2.60505 | -8.2698 | 0.00017  | 0.00186 | 0.86536 |
| SLC38A6  | -0.927  | 2.02713 | -6.2401 | 0.00079  | 0.00504 | -0.8746 |
| COX20P1  | -0.9265 | 4.13101 | -4.3361 | 0.0049   | 0.01833 | -2.938  |
| NEK6     | -0.926  | 3.83158 | -4.2767 | 0.00523  | 0.01924 | -3.0105 |
| PHKA1    | -0.9245 | 0.16285 | -6.4869 | 0.00064  | 0.00436 | -0.6408 |
| CHD1L    | -0.9234 | 4.12387 | -9.2352 | 9.13E-05 | 0.00125 | 1.56816 |
| KLHL22   | -0.9222 | 2.61837 | -9.0725 | 0.0001   | 0.00134 | 1.45446 |
| CYB5D2   | -0.9217 | 0.88769 | -4.5917 | 0.00373  | 0.01509 | -2.6319 |
| FAM166C  | -0.9201 | 0.1397  | -4.2286 | 0.00552  | 0.02    | -3.0697 |
| ZNF85    | -0.9199 | -0.0927 | -4.3593 | 0.00478  | 0.01798 | -2.9099 |
| PIK3CG   | -0.9199 | 1.76778 | -6.9674 | 0.00044  | 0.00337 | -0.2045 |
| MRPL10   | -0.9194 | 3.14294 | -8.3964 | 0.00016  | 0.00178 | 0.96154 |
| MKS1     | -0.9185 | 2.05453 | -8.9914 | 0.00011  | 0.00138 | 1.39708 |
| STARD3   | -0.9182 | 3.10782 | -11.128 | 3.15E-05 | 0.00065 | 2.76986 |
| SNF8     | -0.9176 | 4.17707 | -9.3766 | 8.38E-05 | 0.00118 | 1.66549 |
| TTLL12   | -0.917  | 5.88605 | -5.9855 | 0.00098  | 0.00586 | -1.1232 |
| FXYD6    | -0.9167 | 1.50649 | -5.495  | 0.00152  | 0.00804 | -1.6246 |
| MFSD11   | -0.9166 | 2.83095 | -6.1373 | 0.00086  | 0.00538 | -0.974  |
| ZNFX1    | -0.9165 | 4.602   | -6.1569 | 0.00084  | 0.00532 | -0.955  |
| SIRT2    | -0.9155 | 4.48797 | -10.162 | 5.30E-05 | 0.0009  | 2.18318 |
| ZNF529   | -0.9147 | 1.91125 | -6.7807 | 0.0005   | 0.00372 | -0.3711 |
| PCDHB12  | -0.9141 | -0.0807 | -5.8039 | 0.00115  | 0.00661 | -1.3053 |
| DOCK4    | -0.9133 | 4.4662  | -3.3503 | 0.01543  | 0.04316 | -4.2076 |
| CEP290   | -0.9131 | 3.63786 | -8.8508 | 0.00012  | 0.00147 | 1.29656 |
| CCDC47   | -0.9127 | 4.88294 | -6.9228 | 0.00045  | 0.00345 | -0.244  |
| MXD4     | -0.9127 | 3.45105 | -4.0498 | 0.00674  | 0.0233  | -3.2924 |
| CPQ      | -0.9119 | 2.65108 | -5.3429 | 0.00176  | 0.00884 | -1.7864 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| ABHD14E  | -0.9116 | 4.19591 | -3.8458 | 0.00851  | 0.02762 | -3.5521 |
| SNF8P1   | -0.9114 | 1.59729 | -9.9082 | 6.13E-05 | 0.00098 | 2.01989 |
| JAK2     | -0.9111 | 1.37225 | -8.7814 | 0.00012  | 0.00151 | 1.24635 |
| LRRC20   | -0.909  | 3.36683 | -6.1036 | 0.00088  | 0.00548 | -1.0069 |
| MIRLET7  | -0.9083 | 0.47963 | -4.5106 | 0.00406  | 0.016   | -2.728  |
| XYLT2    | -0.9082 | 3.25522 | -6.9479 | 0.00044  | 0.00341 | -0.2217 |
| GAL3ST1  | -0.9077 | 1.53018 | -6.5114 | 0.00063  | 0.00429 | -0.6178 |
| RAB38    | -0.9073 | 0.80291 | -5.8023 | 0.00115  | 0.00662 | -1.3069 |
| SNAP25   | -0.9071 | 1.23068 | -3.4568 | 0.01353  | 0.03927 | -4.0639 |
| ANXA6    | -0.9071 | 5.99892 | -6.6375 | 0.00057  | 0.00403 | -0.5014 |
| OGDHL    | -0.9062 | 4.12354 | -4.4878 | 0.00416  | 0.0163  | -2.7553 |
| LINC0102 | -0.9058 | 0.90327 | -6.1367 | 0.00086  | 0.00538 | -0.9746 |
| BNC2-AS  | -0.9037 | -0.1325 | -5.3981 | 0.00167  | 0.00853 | -1.7273 |
| THAP7    | -0.903  | 4.44154 | -12.146 | 1.90E-05 | 0.00048 | 3.33826 |
| PCDHB6   | -0.9005 | -0.2343 | -3.8581 | 0.00839  | 0.02734 | -3.5363 |
| ABHD14A  | -0.9002 | 1.75381 | -12.191 | 1.86E-05 | 0.00048 | 3.36208 |
| PRXL2AF  | -0.9    | 3.04657 | -9.043  | 0.0001   | 0.00135 | 1.43366 |
| ACOT2    | -0.8998 | 1.75652 | -7.1517 | 0.00038  | 0.00308 | -0.0435 |
| CNP      | -0.8997 | 5.18258 | -6.6798 | 0.00055  | 0.00394 | -0.4627 |
| DPYSL2   | -0.8987 | 4.29336 | -3.253  | 0.01741  | 0.04728 | -4.34   |
| AKR7A3   | -0.898  | -1.488  | -3.9903 | 0.00721  | 0.02447 | -3.3674 |
| MPP2     | -0.8979 | 2.33681 | -9.5993 | 7.34E-05 | 0.00109 | 1.81615 |
| P4HA1    | -0.8979 | 4.53254 | -8.2854 | 0.00017  | 0.00185 | 0.87725 |
| LDLRAD3  | -0.8978 | 2.6675  | -7.1582 | 0.00038  | 0.00307 | -0.0379 |
| CCNY-AS  | -0.8978 | -0.773  | -4.4269 | 0.00444  | 0.01708 | -2.8282 |
| SHF      | -0.8966 | 0.07507 | -6.2401 | 0.00079  | 0.00504 | -0.8746 |
| YPEL2    | -0.8963 | -0.5201 | -3.3713 | 0.01503  | 0.04236 | -4.1792 |
| FLJ20021 | -0.8955 | 0.715   | -4.3194 | 0.00499  | 0.01858 | -2.9584 |
| SCRN3    | -0.8955 | 2.08395 | -6.8879 | 0.00046  | 0.00351 | -0.275  |
| ZNF595   | -0.895  | -1.0935 | -4.424  | 0.00446  | 0.01711 | -2.8317 |
| NHS      | -0.8936 | 2.34369 | -4.4304 | 0.00443  | 0.01703 | -2.824  |
| PSMC5    | -0.8936 | 6.26777 | -11.18  | 3.07E-05 | 0.00064 | 2.80016 |
| MAP3K12  | -0.8936 | 3.19829 | -5.1347 | 0.00215  | 0.01019 | -2.0128 |
| PRKCQ-A  | -0.8933 | 0.90226 | -5.7659 | 0.00119  | 0.00676 | -1.344  |
| ARHGAP   | -0.8924 | 2.32622 | -8.447  | 0.00015  | 0.00174 | 0.99962 |
| NIPAL2   | -0.8908 | 1.15217 | -4.1469 | 0.00604  | 0.02148 | -3.1708 |
| PPP1R3E  | -0.8905 | 1.9445  | -4.4234 | 0.00446  | 0.01711 | -2.8324 |
| RAB30    | -0.8879 | 2.15779 | -4.8496 | 0.00286  | 0.01246 | -2.3326 |
| PIP4P2   | -0.8876 | 2.87764 | -8.7216 | 0.00013  | 0.00154 | 1.20288 |
| HS1BP3   | -0.8875 | 2.71206 | -9.7692 | 6.64E-05 | 0.00103 | 1.92895 |
| CDPF1    | -0.8854 | 2.36676 | -7.0831 | 0.0004   | 0.00318 | -0.1031 |
| TGFB2    | -0.8853 | 6.192   | -3.9645 | 0.00742  | 0.02501 | -3.4003 |
| ARL17A   | -0.8851 | -1.3243 | -4.2306 | 0.0055   | 0.01997 | -3.0673 |
| ZNF492   | -0.8827 | -0.8178 | -3.5857 | 0.01158  | 0.0348  | -3.8921 |
| MTMR8    | -0.8826 | -1.4848 | -3.9906 | 0.0072   | 0.02446 | -3.3671 |
| LTBP4    | -0.8826 | 5.34371 | -5.1217 | 0.00218  | 0.01026 | -2.0272 |
| NUDT16   | -0.8821 | 5.28167 | -11.579 | 2.51E-05 | 0.00057 | 3.02799 |
| PEX12    | -0.8818 | 1.5967  | -5.6727 | 0.00129  | 0.0072  | -1.4394 |
| PPP1R12  | -0.8813 | -1.2804 | -3.7996 | 0.00898  | 0.02872 | -3.6119 |
| PLL      | -0.881  | 2.1139  | -8.6103 | 0.00014  | 0.00162 | 1.12119 |
| GTF3C6F  | -0.8798 | 4.73094 | -4.5779 | 0.00378  | 0.01524 | -2.6481 |
| PFKFB3   | -0.8792 | 3.97553 | -4.5559 | 0.00387  | 0.01546 | -2.6742 |
| CHST14   | -0.8789 | 4.09197 | -5.8115 | 0.00114  | 0.00659 | -1.2977 |
| ZNF662   | -0.878  | 1.5871  | -5.0474 | 0.00234  | 0.0108  | -2.1096 |
| ZDHHC8   | -0.8779 | 3.76394 | -9.8752 | 6.24E-05 | 0.00099 | 1.99843 |
| STOML1   | -0.8772 | 1.62518 | -7.6909 | 0.00025  | 0.0024  | 0.40864 |
| RASSF10  | -0.8771 | 2.07364 | -3.3935 | 0.01462  | 0.04148 | -4.1491 |
| C17orf80 | -0.8769 | 3.41569 | -6.6198 | 0.00057  | 0.00406 | -0.5176 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| TRABD-A  | -0.8754 | 0.84521 | -4.1544 | 0.00599  | 0.02132 | -3.1615 |
| ABCD1    | -0.8751 | 3.80023 | -6.4279 | 0.00067  | 0.0045  | -0.696  |
| GASAL1   | -0.8743 | -0.9133 | -3.9021 | 0.00797  | 0.02629 | -3.4799 |
| KMT2E-A  | -0.8738 | 2.96256 | -5.85   | 0.0011   | 0.00641 | -1.2587 |
| TMX4     | -0.8736 | 3.07458 | -4.584  | 0.00376  | 0.01518 | -2.641  |
| SIPA1    | -0.8714 | 4.42097 | -9.2911 | 8.82E-05 | 0.00123 | 1.60681 |
| HEXB     | -0.8711 | 4.78891 | -7.6344 | 0.00026  | 0.00245 | 0.36256 |
| STARD9   | -0.8698 | 0.84835 | -5.9728 | 0.00099  | 0.00591 | -1.1358 |
| TEDC2    | -0.8696 | 2.51355 | -6.1185 | 0.00087  | 0.00544 | -0.9924 |
| TTC34    | -0.8691 | -2.141  | -5.399  | 0.00167  | 0.00853 | -1.7264 |
| COX11    | -0.8681 | 3.81342 | -9.4199 | 8.16E-05 | 0.00116 | 1.69505 |
| SIGLEC1  | -0.8678 | -0.6531 | -7.9548 | 0.00021  | 0.00212 | 0.62038 |
| GSTT2    | -0.8661 | -0.4173 | -3.3671 | 0.01511  | 0.04252 | -4.1849 |
| TTF1     | -0.8655 | 3.3454  | -9.4536 | 8.00E-05 | 0.00115 | 1.71796 |
| PROS1    | -0.8645 | 0.32006 | -5.2878 | 0.00185  | 0.00917 | -1.8457 |
| IER5     | -0.8643 | 5.79171 | -5.5435 | 0.00146  | 0.00781 | -1.5737 |
| ATP6V1E  | -0.8638 | 5.01532 | -6.5304 | 0.00062  | 0.00427 | -0.6002 |
| ABHD6    | -0.8614 | 0.95725 | -5.8006 | 0.00115  | 0.00662 | -1.3087 |
| PSMD11   | -0.8605 | 5.69953 | -10.735 | 3.88E-05 | 0.00074 | 2.53713 |
| SPR      | -0.8604 | 3.69182 | -6.9379 | 0.00045  | 0.00342 | -0.2306 |
| ORMDL3   | -0.8591 | 3.48172 | -8.3793 | 0.00016  | 0.00178 | 0.94859 |
| SLC25A2  | -0.8589 | 0.82958 | -3.5984 | 0.0114   | 0.0344  | -3.8752 |
| SLC46A1  | -0.8586 | 1.96292 | -3.7278 | 0.00977  | 0.03055 | -3.7052 |
| HOXB4    | -0.8586 | 3.9507  | -4.3666 | 0.00474  | 0.0179  | -2.901  |
| WDR41    | -0.8582 | 2.46199 | -6.3978 | 0.00069  | 0.00458 | -0.7243 |
| MLX      | -0.8576 | 4.49348 | -10.933 | 3.49E-05 | 0.0007  | 2.65566 |
| PON2     | -0.8564 | 5.64353 | -8.8291 | 0.00012  | 0.00148 | 1.28086 |
| RNASE1   | -0.8556 | -0.0179 | -4.2836 | 0.00519  | 0.01915 | -3.0021 |
| ADIRF-A9 | -0.8549 | 1.66819 | -4.0898 | 0.00644  | 0.02256 | -3.2421 |
| MRPS23   | -0.8545 | 4.41314 | -8.5533 | 0.00014  | 0.00166 | 1.07897 |
| CPNE7    | -0.8538 | 1.00142 | -4.7856 | 0.00305  | 0.01306 | -2.4061 |
| FICD     | -0.8535 | 0.78272 | -10.409 | 4.62E-05 | 0.00083 | 2.33774 |
| C22orf39 | -0.8528 | 2.00905 | -8.6769 | 0.00013  | 0.00158 | 1.17016 |
| FBXO43   | -0.8522 | 1.70416 | -7.5927 | 0.00027  | 0.0025  | 0.32829 |
| CTSC     | -0.8519 | 6.46972 | -8.3477 | 0.00016  | 0.0018  | 0.92469 |
| SCPEP1   | -0.8513 | 4.60952 | -6.9153 | 0.00045  | 0.00347 | -0.2506 |
| CCPG1    | -0.8511 | 1.39462 | -7.1206 | 0.00039  | 0.00313 | -0.0704 |
| EEA1     | -0.8502 | 3.97152 | -10.354 | 4.77E-05 | 0.00084 | 2.30375 |
| POLR3H   | -0.8495 | 4.61155 | -4.3396 | 0.00488  | 0.01827 | -2.9338 |
| ZNF337-A | -0.8495 | -0.3218 | -5.2311 | 0.00196  | 0.00951 | -1.9072 |
| DNAH1    | -0.8495 | 1.44232 | -4.5732 | 0.0038   | 0.01529 | -2.6538 |
| LDAF1    | -0.8494 | 1.27465 | -3.906  | 0.00794  | 0.02621 | -3.4749 |
| MAPRE3   | -0.8478 | 1.48205 | -9.8018 | 6.51E-05 | 0.00101 | 1.95035 |
| EPB41L5  | -0.8475 | 2.97825 | -6.5517 | 0.00061  | 0.00421 | -0.5804 |
| NUDT19-  | -0.8469 | -0.643  | -4.1727 | 0.00587  | 0.02099 | -3.1388 |
| ALG12    | -0.8463 | 3.30059 | -7.7734 | 0.00024  | 0.0023  | 0.47552 |
| RNF43    | -0.845  | 2.10636 | -3.5026 | 0.0128   | 0.03761 | -4.0026 |
| ANKMY2   | -0.8446 | 2.42619 | -9.1069 | 9.88E-05 | 0.00132 | 1.47865 |
| CAT      | -0.8443 | 2.50516 | -5.1212 | 0.00218  | 0.01026 | -2.0277 |
| GIT2     | -0.844  | 3.69522 | -9.5909 | 7.37E-05 | 0.0011  | 1.81052 |
| CDK17    | -0.842  | 3.34609 | -6.3471 | 0.00072  | 0.00473 | -0.7723 |
| STAG3L1  | -0.8418 | -1.9866 | -6.3431 | 0.00072  | 0.00474 | -0.7761 |
| PDZK1    | -0.8411 | -1.5775 | -3.3684 | 0.01508  | 0.04248 | -4.183  |
| BASP1    | -0.8411 | 5.35098 | -7.8518 | 0.00023  | 0.00222 | 0.53849 |
| PANX2    | -0.8394 | 2.47594 | -4.7923 | 0.00303  | 0.013   | -2.3983 |
| COL25A1  | -0.8393 | 1.14842 | -6.5216 | 0.00062  | 0.00428 | -0.6084 |
| RAD51D   | -0.8392 | 2.33301 | -8.2261 | 0.00017  | 0.0019  | 0.83183 |
| RNF157   | -0.8392 | 3.79416 | -3.8156 | 0.00882  | 0.02834 | -3.5912 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| RBMX2    | -0.8381 | 3.54991 | -5.8119 | 0.00114  | 0.00659 | -1.2973 |
| ENTPD1   | -0.8368 | 1.83831 | -4.0233 | 0.00694  | 0.02382 | -3.3258 |
| DIP2C    | -0.8355 | 3.42946 | -3.9911 | 0.0072   | 0.02446 | -3.3665 |
| MSI2     | -0.8352 | 5.15663 | -6.8112 | 0.00049  | 0.00368 | -0.3436 |
| TMEM175  | -0.8343 | 2.73091 | -7.9706 | 0.00021  | 0.00211 | 0.63287 |
| MECOM    | -0.8341 | 6.96949 | -5.8814 | 0.00107  | 0.00628 | -1.2271 |
| RIBC2    | -0.8338 | 0.36052 | -4.4573 | 0.0043   | 0.01667 | -2.7917 |
| C3       | -0.8331 | 7.04513 | -4.0658 | 0.00662  | 0.02303 | -3.2723 |
| METAP1D  | -0.8319 | 0.69743 | -5.7891 | 0.00117  | 0.00666 | -1.3203 |
| SRSF9P1  | -0.8315 | -0.1076 | -3.2323 | 0.01787  | 0.04822 | -4.3684 |
| CHST12   | -0.8313 | 2.05568 | -5.5475 | 0.00145  | 0.0078  | -1.5695 |
| RXYLT1   | -0.8307 | 3.33808 | -6.5964 | 0.00058  | 0.00411 | -0.5391 |
| HPS4     | -0.8301 | 3.36506 | -8.8296 | 0.00012  | 0.00148 | 1.28123 |
| KCND1    | -0.83   | -0.0239 | -3.2589 | 0.01729  | 0.04699 | -4.3321 |
| PRXL2A   | -0.8299 | 6.20073 | -6.1691 | 0.00084  | 0.00527 | -0.9432 |
| NAT9     | -0.8289 | 3.89475 | -6.7397 | 0.00052  | 0.00382 | -0.4082 |
| PLPP2    | -0.8287 | 3.40546 | -5.1652 | 0.00209  | 0.00997 | -1.9793 |
| ACVR1B   | -0.8287 | 3.88675 | -6.1357 | 0.00086  | 0.00538 | -0.9756 |
| RASSF3   | -0.8278 | 4.15079 | -7.1245 | 0.00039  | 0.00312 | -0.067  |
| C17orf75 | -0.8267 | 1.91621 | -7.5011 | 0.00029  | 0.00261 | 0.2526  |
| PRR5     | -0.8264 | 2.02288 | -8.298  | 0.00017  | 0.00184 | 0.88686 |
| PANK2-A  | -0.8252 | 0.95312 | -3.2204 | 0.01814  | 0.04873 | -4.3847 |
| CALCOC   | -0.8248 | 3.87606 | -3.6017 | 0.01135  | 0.03429 | -3.8708 |
| CGAS     | -0.8245 | 2.7916  | -3.6607 | 0.01058  | 0.03247 | -3.7931 |
| PDCD6    | -0.824  | 3.09659 | -6.6915 | 0.00054  | 0.00391 | -0.452  |
| AFMID    | -0.8236 | 3.25736 | -9.6567 | 7.09E-05 | 0.00107 | 1.85444 |
| DLG4     | -0.8235 | 2.07458 | -4.1219 | 0.00621  | 0.02195 | -3.202  |
| SBK3     | -0.8228 | -2.2407 | -6.7938 | 0.0005   | 0.0037  | -0.3593 |
| SGCB     | -0.8228 | 2.29183 | -4.6416 | 0.00354  | 0.01454 | -2.5733 |
| CAVIN3   | -0.8228 | 2.84314 | -6.8526 | 0.00048  | 0.00359 | -0.3065 |
| MRPL40   | -0.8224 | 4.67317 | -8.2294 | 0.00017  | 0.00189 | 0.83435 |
| NBN      | -0.8211 | 5.17814 | -6.9937 | 0.00043  | 0.00334 | -0.1813 |
| CHMP6    | -0.8207 | 2.64535 | -5.9199 | 0.00104  | 0.00612 | -1.1885 |
| RBMXP4   | -0.8198 | -0.5137 | -4.5962 | 0.00371  | 0.01504 | -2.6267 |
| ABCC3    | -0.8195 | 1.49394 | -5.7427 | 0.00121  | 0.00687 | -1.3676 |
| TMEM17   | -0.8194 | -0.0955 | -5.8757 | 0.00108  | 0.00631 | -1.2328 |
| CABYR    | -0.8194 | 2.27511 | -8.0178 | 0.0002   | 0.00207 | 0.67004 |
| SMG9     | -0.8191 | 3.87418 | -4.1948 | 0.00573  | 0.02059 | -3.1114 |
| STEAP3   | -0.8187 | 1.48522 | -3.7779 | 0.00921  | 0.02925 | -3.6399 |
| ENOSF1   | -0.8184 | 3.53225 | -5.602  | 0.00138  | 0.00756 | -1.5126 |
| FAM81A   | -0.8179 | -0.5068 | -4.0693 | 0.00659  | 0.02296 | -3.2679 |
| CC2D1B   | -0.8176 | 4.21198 | -8.001  | 0.0002   | 0.00209 | 0.65678 |
| FLCN     | -0.816  | 2.32291 | -8.9854 | 0.00011  | 0.00138 | 1.3928  |
| SLC19A1  | -0.8156 | 3.97054 | -3.5868 | 0.01156  | 0.03476 | -3.8906 |
| ELK3     | -0.8153 | 4.0769  | -4.5338 | 0.00397  | 0.01574 | -2.7005 |
| ENDOV    | -0.8141 | 2.22489 | -4.7556 | 0.00315  | 0.01333 | -2.4406 |
| RIPK2-D1 | -0.8137 | 1.84147 | -9.535  | 7.62E-05 | 0.00111 | 1.77299 |
| PARP10   | -0.8133 | 4.21446 | -5.4711 | 0.00156  | 0.00816 | -1.6499 |
| ANKRD7   | -0.8127 | -0.7626 | -3.4251 | 0.01407  | 0.04038 | -4.1065 |
| DYRK4    | -0.8119 | -0.128  | -8.4827 | 0.00015  | 0.00171 | 1.02633 |
| PIGH     | -0.8118 | 1.44924 | -6.443  | 0.00066  | 0.00447 | -0.6818 |
| NDUFAF8  | -0.8116 | 5.06832 | -7.5924 | 0.00027  | 0.0025  | 0.32809 |
| NFE2L1-D | -0.8115 | -0.4072 | -3.306  | 0.0163   | 0.04497 | -4.2678 |
| ERG      | -0.8106 | 2.87495 | -3.4129 | 0.01428  | 0.04078 | -4.123  |
| DUSP3    | -0.8105 | 4.84635 | -6.1701 | 0.00083  | 0.00527 | -0.9422 |
| GOLGA1   | -0.8104 | 2.03265 | -9.3584 | 8.47E-05 | 0.00118 | 1.65306 |
| CUEDC1   | -0.8102 | 3.50198 | -10.219 | 5.14E-05 | 0.00088 | 2.21902 |
| AMDHD2   | -0.8098 | 3.02677 | -7.0588 | 0.00041  | 0.00323 | -0.1242 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| ATP1A3   | -0.8088 | 1.06045 | -4.0434 | 0.00679  | 0.0234  | -3.3005 |
| STAT5B   | -0.8079 | 4.49424 | -5.8006 | 0.00115  | 0.00662 | -1.3087 |
| UPRT     | -0.8078 | 1.66209 | -9.1974 | 9.34E-05 | 0.00127 | 1.54192 |
| SPATC1L  | -0.8064 | 1.64613 | -6.6265 | 0.00057  | 0.00405 | -0.5115 |
| URB1-AS  | -0.8057 | 2.6882  | -6.004  | 0.00096  | 0.0058  | -1.1049 |
| SCRN2    | -0.8045 | 4.1817  | -3.3282 | 0.01585  | 0.04408 | -4.2375 |
| DUS1L    | -0.8035 | 5.68254 | -11.161 | 3.10E-05 | 0.00065 | 2.78949 |
| ACSS3    | -0.8032 | -6.3856 | -6.562  | 0.0006   | 0.00419 | -0.5709 |
| TRMT2A   | -0.8032 | 5.11874 | -10.355 | 4.76E-05 | 0.00084 | 2.30432 |
| GNS      | -0.8031 | 6.83506 | -7.2206 | 0.00036  | 0.00296 | 0.01582 |
| DTX3     | -0.8031 | 4.05667 | -4.9027 | 0.00271  | 0.01199 | -2.2723 |
| CDHR3    | -0.8023 | -0.6383 | -4.3059 | 0.00507  | 0.01876 | -2.9748 |
| FKBP11   | -0.8022 | 3.58232 | -3.2983 | 0.01646  | 0.04527 | -4.2782 |
| FAM234B  | -0.802  | 0.79634 | -5.6116 | 0.00137  | 0.00751 | -1.5027 |
| AOC2     | -0.8018 | 0.63329 | -3.359  | 0.01526  | 0.04281 | -4.1959 |
| METTL23  | -0.8017 | 3.577   | -6.7237 | 0.00053  | 0.00385 | -0.4227 |
| HOXA1    | -0.8008 | 1.79901 | -6.2983 | 0.00075  | 0.00487 | -0.8188 |
| NFU1     | -0.7987 | 2.64992 | -8.3619 | 0.00016  | 0.00179 | 0.93543 |
| EEPD1    | -0.7985 | 0.98029 | -5.0309 | 0.00238  | 0.01091 | -2.128  |
| ZFH4     | -0.7982 | 2.96434 | -3.9633 | 0.00743  | 0.02502 | -3.4018 |
| GRB14    | -0.7981 | 1.80471 | -3.5019 | 0.01281  | 0.03763 | -4.0035 |
| RAPGEF   | -0.798  | 1.13889 | -4.8497 | 0.00286  | 0.01246 | -2.3326 |
| FAM3C    | -0.7977 | 5.14845 | -6.0785 | 0.0009   | 0.00555 | -1.0315 |
| FAM174B  | -0.7973 | 2.63399 | -3.5148 | 0.01261  | 0.03721 | -3.9864 |
| DHX40    | -0.7965 | 3.10746 | -10.296 | 4.92E-05 | 0.00086 | 2.26724 |
| BPTF     | -0.7964 | 4.46289 | -8.8731 | 0.00011  | 0.00145 | 1.31257 |
| DSC2     | -0.7964 | 1.38854 | -3.3112 | 0.01619  | 0.04478 | -4.2607 |
| SYNJ1    | -0.7961 | 2.96106 | -8.4783 | 0.00015  | 0.00171 | 1.02309 |
| PAK1     | -0.7959 | 3.39833 | -7.3536 | 0.00032  | 0.00276 | 0.12902 |
| B3GAT3F  | -0.7949 | 2.87715 | -7.5044 | 0.00029  | 0.00261 | 0.25531 |
| ZNF219   | -0.7949 | 2.40835 | -6.0119 | 0.00096  | 0.00578 | -1.097  |
| ZC3HAV1  | -0.7947 | 4.69955 | -6.1551 | 0.00085  | 0.00532 | -0.9567 |
| RBMX2P4  | -0.7947 | 2.00493 | -7.3896 | 0.00032  | 0.00272 | 0.15938 |
| BDH2P1   | -0.7945 | 4.17239 | -4.8851 | 0.00276  | 0.01214 | -2.2922 |
| SLC20A1  | -0.7944 | 1.13253 | -4.7103 | 0.0033   | 0.01381 | -2.4932 |
| BECN1    | -0.7942 | 4.02724 | -11.067 | 3.25E-05 | 0.00067 | 2.73442 |
| TBKBP1   | -0.7942 | 2.34236 | -7.6598 | 0.00026  | 0.00243 | 0.3833  |
| MINPP1   | -0.7939 | 3.81647 | -7.8814 | 0.00022  | 0.00219 | 0.5621  |
| MIF4GD-I | -0.7925 | -0.6321 | -3.1986 | 0.01865  | 0.04972 | -4.4147 |
| SLC25A1  | -0.7918 | 2.07684 | -9.9896 | 5.85E-05 | 0.00095 | 2.0726  |
| FSD1L    | -0.7916 | 2.36188 | -4.8959 | 0.00273  | 0.01205 | -2.28   |
| ZNF512B  | -0.7912 | 5.59132 | -5.6833 | 0.00128  | 0.00715 | -1.4286 |
| SPATA24  | -0.7901 | 0.93666 | -5.5631 | 0.00143  | 0.00773 | -1.5532 |
| GRN      | -0.7882 | 6.02922 | -7.7386 | 0.00025  | 0.00235 | 0.4474  |
| ENKD1    | -0.7882 | 0.87776 | -3.4118 | 0.0143   | 0.04081 | -4.1245 |
| GTF3C6   | -0.7868 | 2.93188 | -7.1119 | 0.00039  | 0.00314 | -0.078  |
| RNF144A  | -0.7861 | 2.60358 | -5.7357 | 0.00122  | 0.00691 | -1.3748 |
| TEX264   | -0.7861 | 3.35313 | -7.878  | 0.00022  | 0.0022  | 0.55941 |
| LINC0260 | -0.7839 | 0.76191 | -4.4802 | 0.0042   | 0.01638 | -2.7643 |
| CSPG5    | -0.7836 | 1.91238 | -3.222  | 0.01811  | 0.04866 | -4.3826 |
| TUBG1P   | -0.783  | 2.23037 | -7.4331 | 0.00031  | 0.00269 | 0.19588 |
| ZHX1     | -0.7828 | 3.79829 | -6.353  | 0.00071  | 0.00471 | -0.7667 |
| FUOM     | -0.7819 | 3.20416 | -4.8219 | 0.00294  | 0.01274 | -2.3643 |
| RECQL5   | -0.7817 | 2.82412 | -7.2987 | 0.00034  | 0.00283 | 0.08251 |
| TERF1P4  | -0.7808 | 4.2841  | -8.3465 | 0.00016  | 0.0018  | 0.92376 |
| ARFRP1   | -0.7805 | 4.22983 | -9.8307 | 6.41E-05 | 0.001   | 1.96932 |
| SLC9A1   | -0.7804 | 3.93569 | -7.8242 | 0.00023  | 0.00225 | 0.51635 |
| TRABD    | -0.7802 | 5.09396 | -8.7218 | 0.00013  | 0.00154 | 1.20296 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| ZFP41    | -0.78   | 2.29092 | -4.0079 | 0.00706  | 0.02411 | -3.3452 |
| WDR31    | -0.7797 | -1.497  | -3.5153 | 0.0126   | 0.03719 | -3.9856 |
| LONRF3   | -0.7797 | 1.13685 | -6.1785 | 0.00083  | 0.00524 | -0.9341 |
| C12orf75 | -0.7795 | 6.39153 | -5.8894 | 0.00107  | 0.00625 | -1.2191 |
| DYNC2H   | -0.7793 | 4.44405 | -8.2048 | 0.00018  | 0.00191 | 0.81542 |
| TNFAIP8  | -0.7789 | 1.43471 | -6.3973 | 0.00069  | 0.00458 | -0.7248 |
| UBR7     | -0.7788 | 4.15901 | -8.3776 | 0.00016  | 0.00178 | 0.94734 |
| DGLUCY   | -0.7785 | 4.51362 | -7.2276 | 0.00036  | 0.00294 | 0.02182 |
| TIGD7    | -0.7777 | 1.44334 | -6.5908 | 0.00059  | 0.00412 | -0.5443 |
| TOM1L1   | -0.7769 | 3.1198  | -6.8229 | 0.00049  | 0.00365 | -0.3331 |
| FAM117A  | -0.7763 | 3.47213 | -8.1602 | 0.00018  | 0.00195 | 0.78107 |
| SV2A     | -0.7762 | 4.81286 | -5.1507 | 0.00212  | 0.01006 | -1.9953 |
| NRG4     | -0.7755 | 0.28933 | -5.2051 | 0.00201  | 0.0097  | -1.9356 |
| GALM     | -0.7754 | 3.26448 | -8.2178 | 0.00018  | 0.0019  | 0.82547 |
| SPACA9   | -0.7749 | -0.2264 | -5.2901 | 0.00185  | 0.00916 | -1.8433 |
| MIEN1    | -0.7748 | 4.80056 | -6.1917 | 0.00082  | 0.0052  | -0.9213 |
| LCMT1-A  | -0.7744 | -2.7662 | -3.872  | 0.00826  | 0.027   | -3.5184 |
| HEXD     | -0.7739 | 2.35167 | -5.9927 | 0.00097  | 0.00584 | -1.116  |
| PNPO     | -0.7738 | 3.62494 | -8.7766 | 0.00012  | 0.00151 | 1.2429  |
| TYSND1   | -0.773  | 4.29112 | -7.076  | 0.0004   | 0.0032  | -0.1092 |
| PSD3     | -0.7715 | 2.96895 | -4.8363 | 0.0029   | 0.01259 | -2.3478 |
| PRDX5    | -0.7713 | 6.70408 | -5.4226 | 0.00163  | 0.00842 | -1.7012 |
| TAF15    | -0.7711 | 5.2672  | -9.0538 | 0.0001   | 0.00135 | 1.44131 |
| FSD1     | -0.7709 | 2.59173 | -6.9452 | 0.00044  | 0.00342 | -0.2241 |
| FAM13A   | -0.7707 | 2.27954 | -4.1153 | 0.00626  | 0.02209 | -3.2102 |
| POC1B    | -0.7687 | 1.42105 | -3.4458 | 0.01372  | 0.03966 | -4.0787 |
| KIF3C    | -0.7685 | 2.88575 | -7.966  | 0.00021  | 0.00212 | 0.62923 |
| HK2-DT   | -0.7682 | 2.34863 | -4.4089 | 0.00453  | 0.01729 | -2.8499 |
| VPS25    | -0.7676 | 5.34188 | -4.3672 | 0.00474  | 0.0179  | -2.9003 |
| ZNF471   | -0.7673 | -0.7935 | -3.5195 | 0.01254  | 0.03703 | -3.98   |
| ADD2     | -0.7659 | 2.43947 | -3.1929 | 0.01878  | 0.04996 | -4.4226 |
| CTNS     | -0.7656 | 2.53005 | -5.9441 | 0.00102  | 0.00602 | -1.1644 |
| ACAP3    | -0.765  | 3.67283 | -5.0846 | 0.00226  | 0.0105  | -2.0683 |
| CADM1    | -0.7649 | 4.23162 | -4.8692 | 0.0028   | 0.01231 | -2.3103 |
| C10orf88 | -0.7641 | -0.1604 | -4.0699 | 0.00658  | 0.02296 | -3.267  |
| SAP30BP  | -0.7626 | 3.74612 | -9.5713 | 7.46E-05 | 0.0011  | 1.79737 |
| DOCK10   | -0.7621 | 0.17312 | -3.573  | 0.01175  | 0.03519 | -3.9088 |
| PRKACB   | -0.7619 | 1.2969  | -4.8753 | 0.00278  | 0.01224 | -2.3034 |
| CHCHD1   | -0.7613 | 6.86479 | -6.4858 | 0.00064  | 0.00436 | -0.6418 |
| PTER     | -0.7602 | 3.28787 | -7.3616 | 0.00032  | 0.00275 | 0.13576 |
| COX11P1  | -0.7597 | 2.00785 | -5.3781 | 0.0017   | 0.00866 | -1.7487 |
| CYSTM1   | -0.7586 | 4.27921 | -4.3932 | 0.00461  | 0.01751 | -2.8689 |
| JPT1     | -0.7585 | 5.38758 | -6.6936 | 0.00054  | 0.00391 | -0.4501 |
| LIMCH1   | -0.7584 | 6.3171  | -6.297  | 0.00075  | 0.00487 | -0.82   |
| ARHGEF   | -0.7578 | 4.0726  | -5.3759 | 0.00171  | 0.00867 | -1.751  |
| GPR137   | -0.7578 | 3.71563 | -4.8577 | 0.00283  | 0.0124  | -2.3235 |
| CLTCL1   | -0.7576 | 2.15049 | -8.0766 | 0.00019  | 0.00203 | 0.71608 |
| RSPO4    | -0.7568 | 1.75926 | -3.7814 | 0.00917  | 0.02918 | -3.6354 |
| SH3BGR   | -0.7564 | 4.16853 | -8.6037 | 0.00014  | 0.00162 | 1.11628 |
| ASB16-A  | -0.7562 | 2.40371 | -6.3233 | 0.00073  | 0.0048  | -0.795  |
| IDUA     | -0.7558 | 2.65096 | -8.1125 | 0.00019  | 0.00199 | 0.74403 |
| TMEM106  | -0.7554 | 6.14303 | -4.803  | 0.003    | 0.01291 | -2.3861 |
| CYTOR    | -0.7538 | 1.80527 | -5.0754 | 0.00228  | 0.01057 | -2.0784 |
| PYGB     | -0.7534 | 5.57866 | -6.109  | 0.00088  | 0.00546 | -1.0016 |
| ZNF605   | -0.7529 | -0.0771 | -3.7734 | 0.00926  | 0.02936 | -3.6457 |
| DNAJC24  | -0.7521 | 1.28488 | -8.0605 | 0.0002   | 0.00204 | 0.70352 |
| BTBD6    | -0.7517 | 5.20728 | -4.025  | 0.00693  | 0.02379 | -3.3236 |
| ZNF570   | -0.7517 | 1.16699 | -6.31   | 0.00074  | 0.00483 | -0.8077 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| LUC7L3   | -0.7514 | 5.27912 | -5.4087 | 0.00165  | 0.0085  | -1.7161 |
| GJC1     | -0.7514 | 3.59813 | -6.5806 | 0.00059  | 0.00415 | -0.5537 |
| TCTN2    | -0.7511 | 2.87844 | -7.0649 | 0.0004   | 0.00321 | -0.1189 |
| SLC35B4  | -0.751  | 3.80598 | -5.1518 | 0.00212  | 0.01006 | -1.994  |
| TOP3B    | -0.7508 | 3.53225 | -5.6287 | 0.00135  | 0.00742 | -1.485  |
| ZDHHC12  | -0.7506 | 0.14146 | -3.243  | 0.01764  | 0.04768 | -4.3538 |
| ENGASE   | -0.7496 | 3.8651  | -5.275  | 0.00188  | 0.00925 | -1.8596 |
| SHISA8   | -0.7488 | -0.8987 | -3.2071 | 0.01845  | 0.04938 | -4.403  |
| PRR19    | -0.7484 | 0.77967 | -5.2213 | 0.00198  | 0.00958 | -1.9179 |
| TMUB2    | -0.7484 | 3.87711 | -8.91   | 0.00011  | 0.00143 | 1.33906 |
| WDR54    | -0.7483 | 3.31222 | -3.5227 | 0.01249  | 0.03691 | -3.9757 |
| TUBG1    | -0.7478 | 5.09547 | -8.7424 | 0.00012  | 0.00153 | 1.21805 |
| ZNF529-A | -0.7477 | -0.0731 | -3.8979 | 0.00801  | 0.02639 | -3.4852 |
| ATP5MC2  | -0.7467 | 5.04337 | -7.0937 | 0.00039  | 0.00316 | -0.0938 |
| FAM3C2F  | -0.7461 | 7.20263 | -5.4211 | 0.00163  | 0.00843 | -1.7028 |
| POLG2    | -0.7455 | 1.86189 | -5.6005 | 0.00138  | 0.00756 | -1.5142 |
| ORAI2    | -0.7451 | 5.48833 | -7.5348 | 0.00028  | 0.00257 | 0.2805  |
| C2CD2    | -0.7445 | 3.00067 | -7.3771 | 0.00032  | 0.00273 | 0.14883 |
| VIM      | -0.7439 | 8.39134 | -4.1282 | 0.00617  | 0.02183 | -3.1942 |
| TRAF7    | -0.7438 | 5.11381 | -8.3915 | 0.00016  | 0.00178 | 0.95782 |
| SNHG20   | -0.7436 | 2.5248  | -5.1316 | 0.00216  | 0.0102  | -2.0163 |
| C12orf43 | -0.7435 | 2.61175 | -9.6628 | 7.07E-05 | 0.00107 | 1.85853 |
| GHDC     | -0.7434 | 3.23807 | -6.3311 | 0.00073  | 0.00478 | -0.7875 |
| MSH5     | -0.7433 | -0.6138 | -3.5562 | 0.01199  | 0.03573 | -3.9312 |
| SH2B2    | -0.7427 | 4.07604 | -7.4414 | 0.0003   | 0.00268 | 0.20279 |
| IGFBP7   | -0.7406 | 6.43464 | -6.4635 | 0.00065  | 0.00442 | -0.6626 |
| NCK1-DT  | -0.7402 | 1.07468 | -7.3764 | 0.00032  | 0.00273 | 0.14824 |
| HEG1     | -0.7388 | 4.26749 | -3.7545 | 0.00947  | 0.02983 | -3.6703 |
| RAD51C   | -0.738  | 3.33625 | -4.6806 | 0.0034   | 0.0141  | -2.5277 |
| GXYLT2   | -0.7378 | 2.9108  | -6.9131 | 0.00045  | 0.00347 | -0.2526 |
| KIAA0930 | -0.7359 | 4.7361  | -7.0106 | 0.00042  | 0.00331 | -0.1664 |
| CD63-AS  | -0.7358 | 3.0415  | -5.2093 | 0.002    | 0.00966 | -1.931  |
| SRRD     | -0.7354 | 3.32804 | -9.3287 | 8.63E-05 | 0.0012  | 1.63269 |
| BRCA1    | -0.7353 | 2.68714 | -5.3993 | 0.00167  | 0.00853 | -1.7261 |
| MAFG     | -0.7351 | 5.14568 | -7.7362 | 0.00025  | 0.00235 | 0.4454  |
| CCDC102  | -0.7348 | 1.79126 | -5.5496 | 0.00145  | 0.0078  | -1.5673 |
| TRIM37   | -0.7346 | 3.64961 | -9.235  | 9.13E-05 | 0.00125 | 1.56803 |
| GTF2IP20 | -0.7341 | 1.29397 | -4.1129 | 0.00627  | 0.02211 | -3.2132 |
| VLDLR    | -0.7339 | 4.81977 | -6.7825 | 0.0005   | 0.00372 | -0.3694 |
| RRAS2    | -0.7333 | 4.65286 | -8.3013 | 0.00017  | 0.00184 | 0.88939 |
| RNF166   | -0.7322 | 2.56575 | -8.0131 | 0.0002   | 0.00208 | 0.66636 |
| RASSF8   | -0.7319 | 2.62649 | -6.9077 | 0.00046  | 0.00348 | -0.2574 |
| APLP1    | -0.7316 | 4.73305 | -3.8906 | 0.00808  | 0.02654 | -3.4946 |
| EXTL3    | -0.7313 | 4.53262 | -9.6035 | 7.32E-05 | 0.00109 | 1.81899 |
| TBC1D8-  | -0.7313 | -0.5236 | -4.0782 | 0.00652  | 0.02279 | -3.2567 |
| CA13     | -0.731  | 1.03588 | -3.695  | 0.01016  | 0.03144 | -3.7481 |
| RAB5C    | -0.7306 | 3.57574 | -7.2745 | 0.00034  | 0.00287 | 0.06188 |
| MTERF2   | -0.7292 | 2.27506 | -7.8956 | 0.00022  | 0.00218 | 0.5734  |
| PTRH2    | -0.7286 | 3.05641 | -5.9997 | 0.00097  | 0.00582 | -1.1091 |
| KLHL35   | -0.7272 | 1.75995 | -7.2183 | 0.00036  | 0.00296 | 0.01385 |
| C1orf216 | -0.7271 | 3.06279 | -3.812  | 0.00885  | 0.02842 | -3.5957 |
| C1QBPP2  | -0.7264 | 3.17355 | -6.5516 | 0.00061  | 0.00421 | -0.5805 |
| CHPT1    | -0.7261 | 1.94947 | -5.1722 | 0.00207  | 0.00991 | -1.9716 |
| EPB41L4  | -0.7255 | 4.0378  | -6.4556 | 0.00066  | 0.00444 | -0.67   |
| CHIC2    | -0.7247 | 1.24564 | -3.4023 | 0.01447  | 0.04118 | -4.1372 |
| TOMM40   | -0.7245 | 4.14448 | -6.5043 | 0.00063  | 0.00431 | -0.6244 |
| LINC0278 | -0.7245 | 0.5985  | -4.2279 | 0.00552  | 0.02001 | -3.0706 |
| CFAP44   | -0.7241 | -0.2394 | -5.9532 | 0.00101  | 0.00599 | -1.1553 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| TMEM115  | -0.7239 | 3.85152 | -6.3988 | 0.00069  | 0.00458 | -0.7234 |
| RTKL1-TM | -0.7237 | 0.17129 | -4.6557 | 0.00349  | 0.01438 | -2.5567 |
| GATD1    | -0.7233 | 4.04601 | -7.807  | 0.00023  | 0.00227 | 0.50256 |
| ARRDC1   | -0.723  | 3.07303 | -6.8037 | 0.0005   | 0.00369 | -0.3504 |
| NEIL2    | -0.7229 | 1.48611 | -6.6327 | 0.00057  | 0.00404 | -0.5057 |
| RPP25    | -0.7228 | 4.74615 | -5.9897 | 0.00098  | 0.00585 | -1.1191 |
| TRAPPC1  | -0.7227 | 4.40351 | -8.1003 | 0.00019  | 0.002   | 0.73456 |
| RGS19    | -0.7226 | 3.65339 | -5.7896 | 0.00116  | 0.00666 | -1.3199 |
| IQSEC1   | -0.7216 | 3.93642 | -6.6709 | 0.00055  | 0.00396 | -0.4708 |
| LKAAEAF  | -0.7215 | 0.17556 | -4.1524 | 0.006    | 0.02137 | -3.164  |
| C22orf46 | -0.7213 | 2.11131 | -5.4474 | 0.00159  | 0.0083  | -1.6749 |
| NFU1P1   | -0.7212 | 1.51228 | -4.4566 | 0.0043   | 0.01667 | -2.7925 |
| GEMIN6   | -0.7211 | 2.93169 | -4.5916 | 0.00373  | 0.01509 | -2.632  |
| ARAP3    | -0.7209 | 5.11131 | -8.6053 | 0.00014  | 0.00162 | 1.11749 |
| ZNF32    | -0.7209 | 2.76796 | -4.7557 | 0.00315  | 0.01333 | -2.4406 |
| PCED1A   | -0.7204 | 4.14827 | -5.2592 | 0.00191  | 0.00936 | -1.8767 |
| TIMP1    | -0.72   | 5.64303 | -3.8136 | 0.00884  | 0.02839 | -3.5938 |
| GPRASP   | -0.7199 | 2.05158 | -5.0219 | 0.0024   | 0.01098 | -2.1381 |
| ACVR1    | -0.7189 | 2.3853  | -8.0679 | 0.00019  | 0.00203 | 0.70929 |
| SGSH     | -0.7185 | 4.24708 | -7.6808 | 0.00026  | 0.00241 | 0.40044 |
| ANTXR1   | -0.7184 | 3.89992 | -3.1991 | 0.01864  | 0.0497  | -4.414  |
| ANKRD37  | -0.7184 | -0.512  | -3.676  | 0.01039  | 0.03203 | -3.7729 |
| MOB3C    | -0.7179 | 1.44678 | -4.3308 | 0.00493  | 0.01841 | -2.9445 |
| HYAL2    | -0.7175 | 3.84207 | -8.1504 | 0.00018  | 0.00196 | 0.77344 |
| PPIL2    | -0.7165 | 4.2062  | -8.9793 | 0.00011  | 0.00139 | 1.38849 |
| NMT1     | -0.7154 | 6.63969 | -9.6943 | 6.94E-05 | 0.00106 | 1.87944 |
| SEPTIN6  | -0.7138 | 3.21733 | -6.2328 | 0.00079  | 0.00506 | -0.8816 |
| C4orf48  | -0.7134 | 3.08138 | -5.8006 | 0.00115  | 0.00662 | -1.3087 |
| SPOP     | -0.7132 | 3.53891 | -8.7068 | 0.00013  | 0.00156 | 1.19202 |
| ZNF461   | -0.7131 | 0.56886 | -8.2593 | 0.00017  | 0.00187 | 0.85734 |
| VMP1     | -0.7127 | 6.18584 | -3.9051 | 0.00795  | 0.02623 | -3.476  |
| RPL19P1  | -0.7123 | 0.47266 | -4.2463 | 0.00541  | 0.01974 | -3.0479 |
| PDK2     | -0.7119 | 2.47242 | -8.1638 | 0.00018  | 0.00195 | 0.78381 |
| TRMU     | -0.7117 | 4.5153  | -6.8935 | 0.00046  | 0.0035  | -0.27   |
| CAPN15   | -0.7116 | 4.48178 | -4.7515 | 0.00316  | 0.01336 | -2.4454 |
| GSTO3P   | -0.7113 | 0.88979 | -4.9785 | 0.00251  | 0.01131 | -2.1866 |
| FCGRT    | -0.7104 | 3.0949  | -5.1379 | 0.00214  | 0.01016 | -2.0094 |
| ZNF703   | -0.7103 | 4.64437 | -5.8022 | 0.00115  | 0.00662 | -1.3071 |
| ZNF530   | -0.7096 | 1.5298  | -4.4836 | 0.00418  | 0.01635 | -2.7603 |
| ZFPM1    | -0.7095 | 0.71787 | -6.5708 | 0.0006   | 0.00417 | -0.5628 |
| SNX29    | -0.7094 | 2.62127 | -5.6584 | 0.00131  | 0.00727 | -1.4542 |
| NPAS1    | -0.709  | -1.0198 | -4.6848 | 0.00338  | 0.01405 | -2.5228 |
| LGALS3B  | -0.7089 | 7.74306 | -7.0135 | 0.00042  | 0.00331 | -0.1639 |
| ARHGAP   | -0.7075 | 1.6762  | -3.4808 | 0.01314  | 0.0384  | -4.0318 |
| CCDC85B  | -0.7073 | 6.02282 | -4.9975 | 0.00246  | 0.01116 | -2.1653 |
| GPRC5C   | -0.7071 | 3.6159  | -3.6499 | 0.01072  | 0.0328  | -3.8072 |
| MANSC1   | -0.7071 | 1.97159 | -5.1604 | 0.0021   | 0.00999 | -1.9846 |
| DMPK     | -0.7062 | 3.75027 | -7.1413 | 0.00038  | 0.0031  | -0.0525 |
| SUPT4H1  | -0.7057 | 1.50888 | -7.9275 | 0.00021  | 0.00215 | 0.59874 |
| KLHL20   | -0.7056 | 2.43516 | -5.5417 | 0.00146  | 0.00782 | -1.5756 |
| EIF2B1   | -0.7054 | 4.96173 | -8.122  | 0.00019  | 0.00198 | 0.75145 |
| MOCS2    | -0.7054 | 3.62955 | -7.8903 | 0.00022  | 0.00218 | 0.56918 |
| GNG11    | -0.705  | 6.61268 | -7.319  | 0.00033  | 0.0028  | 0.09971 |
| MINDY1   | -0.7047 | 2.20255 | -4.5074 | 0.00408  | 0.01603 | -2.7318 |
| SPRED1   | -0.704  | 2.72815 | -8.4115 | 0.00015  | 0.00177 | 0.97291 |
| SQOR     | -0.7037 | 0.45381 | -5.1378 | 0.00214  | 0.01016 | -2.0095 |
| TKFC     | -0.7035 | 2.62171 | -6.4423 | 0.00066  | 0.00447 | -0.6825 |
| BCAR1    | -0.7009 | 5.08135 | -3.7051 | 0.01004  | 0.03116 | -3.7348 |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| RBMX2P3  | -0.7003 | 0.60964 | -5.3182 | 0.0018  | 0.00898 | -1.813  |
| NECAB3   | -0.6998 | 3.87883 | -7.3763 | 0.00032 | 0.00273 | 0.14819 |
| WASHC3   | -0.6993 | 0.80605 | -7.4211 | 0.00031 | 0.00269 | 0.1858  |
| TPI1P2   | -0.6993 | 0.95275 | -4.2247 | 0.00554 | 0.02007 | -3.0745 |
| USP18    | -0.6992 | 0.54651 | -3.8615 | 0.00836 | 0.02726 | -3.532  |
| ZNF83    | -0.6986 | 3.27554 | -3.56   | 0.01194 | 0.03561 | -3.9262 |
| STX11    | -0.6984 | -1.5623 | -3.8693 | 0.00828 | 0.02707 | -3.5219 |
| CD63     | -0.6983 | 7.7841  | -4.6371 | 0.00356 | 0.01459 | -2.5786 |
| BID      | -0.6981 | 4.02081 | -4.3884 | 0.00463 | 0.01755 | -2.8746 |
| SQSTM1   | -0.698  | 7.5654  | -4.351  | 0.00482 | 0.01809 | -2.92   |
| ERCC6L2  | -0.6976 | 1.61445 | -7.6502 | 0.00026 | 0.00244 | 0.37547 |
| SYN1     | -0.6973 | -0.0589 | -3.4177 | 0.0142  | 0.04062 | -4.1165 |
| CACNB3   | -0.6963 | 2.91338 | -7.1284 | 0.00038 | 0.00312 | -0.0637 |
| INO80D-A | -0.6961 | 0.70058 | -3.5844 | 0.01159 | 0.03484 | -3.8938 |
| SBF1     | -0.6956 | 5.89305 | -5.7472 | 0.00121 | 0.00685 | -1.363  |
| DUSP8P5  | -0.6946 | 0.55406 | -5.2701 | 0.00189 | 0.00928 | -1.8649 |
| ILRUN-AS | -0.6939 | -0.2982 | -3.2743 | 0.01696 | 0.04623 | -4.311  |
| SLC4A2   | -0.6932 | 6.40187 | -5.0362 | 0.00237 | 0.01087 | -2.1221 |
| IAH1     | -0.6929 | 2.0771  | -5.5027 | 0.00151 | 0.00801 | -1.6165 |
| SH3GL1P  | -0.6927 | -1.132  | -4.4053 | 0.00455 | 0.01734 | -2.8542 |
| KCTD2    | -0.692  | 2.74339 | -8.6175 | 0.00013 | 0.00161 | 1.1265  |
| ZNF276   | -0.6919 | 2.78885 | -5.5928 | 0.00139 | 0.00759 | -1.5222 |
| SLC18B1  | -0.6918 | 2.54786 | -6.0736 | 0.00091 | 0.00556 | -1.0363 |
| MXRA7    | -0.6916 | 6.19545 | -5.1834 | 0.00205 | 0.00984 | -1.9593 |
| GPR75    | -0.6912 | -0.9722 | -5.6896 | 0.00127 | 0.00713 | -1.4221 |
| ZNF830   | -0.6909 | 3.30354 | -5.2273 | 0.00197 | 0.00953 | -1.9114 |
| PALS2    | -0.6908 | 3.2395  | -3.8954 | 0.00804 | 0.02645 | -3.4884 |
| NUDT4    | -0.6905 | 3.26255 | -6.28   | 0.00076 | 0.00492 | -0.8363 |
| NGLY1    | -0.6902 | 3.37372 | -5.7919 | 0.00116 | 0.00666 | -1.3175 |
| SPAG9    | -0.6892 | 4.67666 | -6.6451 | 0.00056 | 0.00401 | -0.4944 |
| CASP8    | -0.689  | 3.93508 | -4.0541 | 0.0067  | 0.02324 | -3.2869 |
| LINC0020 | -0.6887 | 2.95032 | -8.5953 | 0.00014 | 0.00162 | 1.11011 |
| TOP2A    | -0.6879 | 7.07455 | -9.0617 | 0.0001  | 0.00134 | 1.44685 |
| CTSF     | -0.6877 | 3.66921 | -5.4881 | 0.00153 | 0.00806 | -1.6319 |
| NDUFV2P  | -0.6857 | 6.78193 | -8.6571 | 0.00013 | 0.00159 | 1.15563 |
| BICC1    | -0.6855 | 6.28622 | -7.5271 | 0.00029 | 0.00258 | 0.27419 |
| RNASEH1  | -0.6855 | 4.86407 | -5.0347 | 0.00237 | 0.01088 | -2.1237 |
| GBP2     | -0.6849 | 3.3795  | -6.9863 | 0.00043 | 0.00334 | -0.1879 |
| MPG      | -0.6847 | 2.87622 | -7.0249 | 0.00042 | 0.00329 | -0.1539 |
| SHC1P1   | -0.6846 | 0.69817 | -4.5691 | 0.00382 | 0.01535 | -2.6586 |
| OGFOD2   | -0.6829 | -0.2198 | -3.4101 | 0.01433 | 0.04086 | -4.1268 |
| CHIC1    | -0.6827 | 2.24733 | -7.2775 | 0.00034 | 0.00287 | 0.06446 |
| SYNGR1   | -0.6826 | 2.81955 | -7.4182 | 0.00031 | 0.00269 | 0.18341 |
| SMIM10   | -0.6824 | 2.24248 | -4.49   | 0.00415 | 0.01627 | -2.7525 |
| TRIM5    | -0.6823 | 2.90802 | -6.5252 | 0.00062 | 0.00427 | -0.605  |
| ESS2     | -0.6822 | 3.14529 | -8.6753 | 0.00013 | 0.00158 | 1.16898 |
| RAB35    | -0.682  | 4.11249 | -4.6728 | 0.00343 | 0.01419 | -2.5367 |
| MAP3K10  | -0.682  | 3.04562 | -3.3068 | 0.01628 | 0.04495 | -4.2667 |
| MTMR4    | -0.6817 | 3.88588 | -6.8581 | 0.00047 | 0.00357 | -0.3016 |
| PCDHGB   | -0.6811 | -2.5635 | -3.3532 | 0.01537 | 0.04303 | -4.2037 |
| MED27    | -0.6807 | 1.97808 | -6.8486 | 0.00048 | 0.0036  | -0.3101 |
| PPP6R2   | -0.6802 | 4.41902 | -8.2132 | 0.00018 | 0.00191 | 0.8219  |
| LINC0096 | -0.6797 | 3.30725 | -3.2826 | 0.01678 | 0.04594 | -4.2997 |
| SCMH1    | -0.6795 | 3.40703 | -6.0374 | 0.00094 | 0.00569 | -1.0719 |
| TACC1    | -0.6792 | 4.43816 | -4.2598 | 0.00533 | 0.01951 | -3.0312 |
| ZNF316   | -0.6789 | 3.46937 | -5.4327 | 0.00162 | 0.00838 | -1.6905 |
| ATOSA    | -0.6789 | 1.64271 | -4.0121 | 0.00703 | 0.02403 | -3.3399 |
| ZC3HC1   | -0.6787 | 3.37555 | -5.6046 | 0.00138 | 0.00755 | -1.51   |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| TRAPPC2  | -0.6775 | 3.72948 | -8.0237 | 0.0002  | 0.00207 | 0.67467 |
| NEU1     | -0.6772 | 6.0125  | -5.3356 | 0.00177 | 0.00888 | -1.7942 |
| HSPA1A   | -0.6772 | 5.0531  | -4.9411 | 0.00261 | 0.01164 | -2.2288 |
| NAPEPLD  | -0.677  | 2.72253 | -3.5016 | 0.01281 | 0.03764 | -4.0039 |
| EA2F2    | -0.6761 | -0.7081 | -3.9462 | 0.00758 | 0.02539 | -3.4235 |
| TBC1D32  | -0.676  | 0.26582 | -4.7013 | 0.00333 | 0.01389 | -2.5036 |
| TOX      | -0.6759 | 3.09505 | -4.7185 | 0.00327 | 0.01373 | -2.4836 |
| EPB41L2  | -0.675  | 5.87025 | -6.7158 | 0.00053 | 0.00386 | -0.4298 |
| AGMAT    | -0.6741 | 0.69236 | -4.5354 | 0.00396 | 0.01572 | -2.6985 |
| AGPAT3   | -0.674  | 4.17579 | -6.1273 | 0.00087 | 0.00541 | -0.9838 |
| PRR34-A  | -0.6738 | 1.48699 | -6.6976 | 0.00054 | 0.00389 | -0.4464 |
| GOSR2    | -0.6738 | 2.46963 | -6.6565 | 0.00056 | 0.00399 | -0.484  |
| LIPE-AS1 | -0.6736 | -1.2541 | -4.8074 | 0.00298 | 0.01286 | -2.381  |
| CDC42EP  | -0.6727 | 3.90273 | -6.2605 | 0.00077 | 0.00498 | -0.855  |
| C3orf62  | -0.6723 | 0.85526 | -5.097  | 0.00223 | 0.01042 | -2.0545 |
| DNM3     | -0.6715 | 3.02719 | -4.5259 | 0.004   | 0.01583 | -2.7098 |
| TMEM43   | -0.6712 | 4.40002 | -4.0566 | 0.00668 | 0.0232  | -3.2838 |
| AGPAT2   | -0.6709 | 3.48804 | -5.5116 | 0.0015  | 0.00796 | -1.6071 |
| NMD3     | -0.6707 | 5.4507  | -7.9624 | 0.00021 | 0.00212 | 0.62641 |
| TRPM2    | -0.6707 | 3.35319 | -7.1047 | 0.00039 | 0.00315 | -0.0842 |
| TERF1P5  | -0.67   | 2.5177  | -6.6404 | 0.00056 | 0.00402 | -0.4987 |
| CEP128   | -0.6699 | 3.41066 | -6.5776 | 0.00059 | 0.00416 | -0.5565 |
| KLF10    | -0.6694 | 4.89858 | -4.0003 | 0.00712 | 0.02426 | -3.3548 |
| PCNX2    | -0.6691 | 3.51369 | -7.5822 | 0.00027 | 0.00252 | 0.31971 |
| DNAJA2-  | -0.669  | -1.6457 | -4.7137 | 0.00328 | 0.01377 | -2.4892 |
| CDK11A   | -0.6688 | -2.119  | -3.5068 | 0.01273 | 0.03749 | -3.997  |
| NRCAM    | -0.6686 | 7.35523 | -4.1778 | 0.00583 | 0.0209  | -3.1324 |
| PBLD     | -0.6686 | 0.841   | -5.3143 | 0.00181 | 0.00901 | -1.8171 |
| MED24    | -0.6661 | 3.90853 | -5.9117 | 0.00104 | 0.00616 | -1.1968 |
| C11orf1  | -0.6652 | 1.98876 | -7.4498 | 0.0003  | 0.00267 | 0.20983 |
| DTWD2    | -0.6645 | 1.93959 | -5.268  | 0.00189 | 0.0093  | -1.8671 |
| PDE9A    | -0.6641 | 2.37866 | -3.8467 | 0.0085  | 0.02762 | -3.551  |
| CDC6     | -0.6639 | 5.1167  | -4.3105 | 0.00504 | 0.01872 | -2.9692 |
| RARA     | -0.6639 | 2.42423 | -7.6196 | 0.00027 | 0.00247 | 0.3504  |
| RNF126P  | -0.6638 | 0.59957 | -3.9732 | 0.00735 | 0.02481 | -3.3892 |
| AMZ2     | -0.6635 | 4.47665 | -8.372  | 0.00016 | 0.00178 | 0.94309 |
| ATP6V1E  | -0.6631 | 3.37833 | -5.0121 | 0.00243 | 0.01104 | -2.149  |
| UHMK1    | -0.663  | 5.99164 | -8.812  | 0.00012 | 0.00149 | 1.26851 |
| C1QTNF6  | -0.6627 | 2.09373 | -6.1871 | 0.00082 | 0.00521 | -0.9257 |
| BIN1     | -0.6627 | 4.25435 | -6.5159 | 0.00062 | 0.00429 | -0.6137 |
| ZCCHC12  | -0.6624 | -2.205  | -5.0671 | 0.0023  | 0.01063 | -2.0877 |
| PSMD12   | -0.6622 | 4.53363 | -6.7296 | 0.00053 | 0.00384 | -0.4173 |
| PRRG1    | -0.6618 | 3.82038 | -7.7792 | 0.00024 | 0.0023  | 0.48021 |
| SNX8     | -0.6616 | 2.68292 | -6.4282 | 0.00067 | 0.0045  | -0.6957 |
| POLR2L   | -0.6615 | 5.59771 | -7.3663 | 0.00032 | 0.00275 | 0.13976 |
| RAC2     | -0.6613 | 1.75275 | -5.1114 | 0.0022  | 0.01032 | -2.0385 |
| ZNF875   | -0.6606 | 2.47888 | -4.3051 | 0.00507 | 0.01877 | -2.9758 |
| THAP3    | -0.6593 | 1.7178  | -8.7885 | 0.00012 | 0.00151 | 1.25152 |
| CENPM    | -0.6593 | 4.42686 | -3.5951 | 0.01145 | 0.0345  | -3.8796 |
| MLKL     | -0.6588 | 0.97456 | -3.9633 | 0.00743 | 0.02502 | -3.4018 |
| PSMD3    | -0.6586 | 6.04626 | -7.9539 | 0.00021 | 0.00212 | 0.6197  |
| SBF2-AS  | -0.6583 | 0.61626 | -5.0172 | 0.00241 | 0.01101 | -2.1433 |
| TERF1P2  | -0.6577 | 0.34409 | -4.1324 | 0.00614 | 0.02175 | -3.1889 |
| HEXIM2   | -0.6571 | 2.57693 | -8.4651 | 0.00015 | 0.00173 | 1.0132  |
| CRYZ     | -0.6567 | 5.21134 | -5.5686 | 0.00142 | 0.0077  | -1.5475 |
| UTP18    | -0.6564 | 2.90735 | -5.9157 | 0.00104 | 0.00614 | -1.1928 |
| ZNF138   | -0.6561 | 1.61134 | -5.5484 | 0.00145 | 0.0078  | -1.5685 |
| BMT2     | -0.6555 | 2.5305  | -6.5397 | 0.00061 | 0.00424 | -0.5915 |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| HIGD1AP  | -0.6554 | 5.17427 | -5.1622 | 0.00209 | 0.00998 | -1.9826 |
| PMM1     | -0.6552 | 3.35328 | -6.1666 | 0.00084 | 0.00528 | -0.9456 |
| DOK1     | -0.6551 | 2.38237 | -5.7668 | 0.00119 | 0.00676 | -1.3431 |
| FBXW5    | -0.6546 | 4.94776 | -5.755  | 0.0012  | 0.00681 | -1.3551 |
| HEATR6   | -0.6543 | 1.81313 | -6.0784 | 0.0009  | 0.00555 | -1.0316 |
| LRFN1    | -0.653  | 2.45562 | -4.295  | 0.00513 | 0.01894 | -2.9882 |
| ZNF546   | -0.6528 | -1.0878 | -4.3063 | 0.00506 | 0.01876 | -2.9743 |
| WWTR1    | -0.6527 | 5.48041 | -3.4128 | 0.01428 | 0.04078 | -4.1231 |
| METTL1F  | -0.6527 | 0.98599 | -3.4698 | 0.01332 | 0.03882 | -4.0465 |
| APPBP2   | -0.6502 | 3.59252 | -6.9823 | 0.00043 | 0.00335 | -0.1914 |
| LINC0046 | -0.6502 | 0.45015 | -3.7908 | 0.00907 | 0.02894 | -3.6232 |
| LMF2     | -0.6491 | 5.68259 | -5.4067 | 0.00166 | 0.00851 | -1.7181 |
| PCNX4    | -0.649  | 4.04813 | -6.5119 | 0.00063 | 0.00429 | -0.6174 |
| SOWAHC   | -0.6489 | 6.02651 | -8.3107 | 0.00017 | 0.00183 | 0.89651 |
| STK32C   | -0.6488 | 2.4847  | -5.9563 | 0.001   | 0.00597 | -1.1522 |
| TRIM52   | -0.6485 | 2.77492 | -4.5138 | 0.00405 | 0.01597 | -2.7243 |
| NIFK-AS1 | -0.6479 | -0.3753 | -5.4527 | 0.00159 | 0.00827 | -1.6693 |
| PAX9     | -0.6477 | -0.8027 | -7.746  | 0.00024 | 0.00234 | 0.45339 |
| DNAJC7   | -0.6476 | 4.76468 | -8.0418 | 0.0002  | 0.00205 | 0.68883 |
| LRFN3    | -0.6475 | 2.62681 | -4.6465 | 0.00352 | 0.01449 | -2.5675 |
| RPS6KC1  | -0.6471 | 2.69389 | -5.4878 | 0.00154 | 0.00806 | -1.6322 |
| ABTB2    | -0.6471 | 2.42817 | -5.9748 | 0.00099 | 0.00591 | -1.1339 |
| WDCP     | -0.647  | 2.60766 | -4.3064 | 0.00506 | 0.01876 | -2.9742 |
| DRAM1    | -0.647  | 3.04539 | -6.4554 | 0.00066 | 0.00444 | -0.6702 |
| OSTCP4   | -0.647  | 0.87721 | -4.7628 | 0.00312 | 0.01327 | -2.4323 |
| LIX1L    | -0.6463 | 4.16648 | -8.1481 | 0.00018 | 0.00196 | 0.7717  |
| TTC26    | -0.6455 | 2.78901 | -6.9765 | 0.00043 | 0.00336 | -0.1965 |
| SFXN3    | -0.6454 | 3.0699  | -7.867  | 0.00022 | 0.00221 | 0.55059 |
| MIATNB   | -0.645  | -0.8874 | -6.4189 | 0.00068 | 0.00453 | -0.7045 |
| NKIRAS1  | -0.645  | 2.29123 | -6.4494 | 0.00066 | 0.00446 | -0.6758 |
| ATP6V1E  | -0.645  | 5.30635 | -5.6096 | 0.00137 | 0.00752 | -1.5047 |
| CRYBB2P  | -0.6445 | 2.22593 | -6.5124 | 0.00063 | 0.00429 | -0.6169 |
| HSPA4L   | -0.6444 | 3.60108 | -4.7909 | 0.00303 | 0.01301 | -2.3999 |
| BBS5     | -0.6441 | 0.82052 | -3.7746 | 0.00925 | 0.02933 | -3.6443 |
| SOX12    | -0.6429 | 5.78476 | -7.2161 | 0.00036 | 0.00296 | 0.01196 |
| VPS16    | -0.6416 | 3.67352 | -7.4291 | 0.00031 | 0.00269 | 0.19254 |
| SUMF2    | -0.6413 | 5.49257 | -4.7783 | 0.00307 | 0.01313 | -2.4144 |
| RPL38    | -0.6411 | 5.90671 | -3.3581 | 0.01528 | 0.04284 | -4.197  |
| USP51    | -0.6408 | 2.14602 | -3.4469 | 0.0137  | 0.03962 | -4.0772 |
| PSMD12P  | -0.6404 | 4.26058 | -4.6879 | 0.00337 | 0.01401 | -2.5192 |
| FAM229A  | -0.6404 | 2.17528 | -3.8485 | 0.00848 | 0.02757 | -3.5487 |
| COPRS    | -0.6397 | 3.91919 | -6.4318 | 0.00067 | 0.0045  | -0.6923 |
| SPIRE2   | -0.6396 | 1.16994 | -3.8226 | 0.00874 | 0.02818 | -3.5821 |
| SDHAP3   | -0.6396 | -1.7924 | -3.6102 | 0.01124 | 0.03403 | -3.8597 |
| LRRC37B  | -0.6395 | 0.48855 | -3.4208 | 0.01414 | 0.04053 | -4.1123 |
| YDJC     | -0.6392 | 5.9285  | -7.6835 | 0.00026 | 0.00241 | 0.40266 |
| ADRM1    | -0.6391 | 6.31045 | -6.888  | 0.00046 | 0.00351 | -0.2749 |
| TRIM68   | -0.6391 | 1.18959 | -5.1489 | 0.00212 | 0.01008 | -1.9973 |
| NT5C     | -0.639  | 3.34541 | -4.583  | 0.00376 | 0.01519 | -2.6422 |
| PKNOX1   | -0.639  | 4.3367  | -4.8881 | 0.00275 | 0.01212 | -2.2888 |
| NRSN2    | -0.6382 | 3.9804  | -6.1107 | 0.00088 | 0.00546 | -1      |
| ZNF107   | -0.638  | 2.23734 | -3.344  | 0.01555 | 0.04341 | -4.2161 |
| KIF18B   | -0.6377 | 4.54788 | -4.9087 | 0.00269 | 0.01193 | -2.2654 |
| SMG8     | -0.6374 | 3.25738 | -7.6591 | 0.00026 | 0.00243 | 0.38274 |
| NNT-AS1  | -0.6366 | 2.29829 | -6.5393 | 0.00061 | 0.00424 | -0.5919 |
| SNX11    | -0.6361 | 2.17778 | -6.501  | 0.00063 | 0.00432 | -0.6276 |
| B3GAT3   | -0.6361 | 4.03042 | -8.0657 | 0.0002  | 0.00204 | 0.70752 |
| DESI1    | -0.6352 | 5.08908 | -6.7955 | 0.0005  | 0.0037  | -0.3578 |

|           |         |         |         |         |         |         |
|-----------|---------|---------|---------|---------|---------|---------|
| TEPSIN    | -0.6349 | 2.96476 | -5.3668 | 0.00172 | 0.00871 | -1.7608 |
| SNHG9     | -0.6346 | 2.52191 | -3.6194 | 0.01112 | 0.03375 | -3.8475 |
| CCDC117   | -0.6345 | 4.21874 | -6.6328 | 0.00057 | 0.00404 | -0.5057 |
| FAM107B   | -0.6329 | 4.27048 | -3.6833 | 0.0103  | 0.0318  | -3.7634 |
| PSEN2     | -0.6327 | 1.3891  | -4.5425 | 0.00393 | 0.01563 | -2.6901 |
| ALKBH8    | -0.6326 | 1.16766 | -5.4313 | 0.00162 | 0.00838 | -1.692  |
| MYOF      | -0.6322 | 6.97603 | -3.9212 | 0.0078  | 0.02588 | -3.4554 |
| GPC2      | -0.6321 | 1.81753 | -5.188  | 0.00204 | 0.00981 | -1.9543 |
| ARSA      | -0.6318 | 4.09381 | -5.1638 | 0.00209 | 0.00997 | -1.9808 |
| PURA      | -0.6316 | 4.37723 | -7.8371 | 0.00023 | 0.00223 | 0.52673 |
| MRPS7     | -0.6313 | 5.40241 | -8.6537 | 0.00013 | 0.00159 | 1.15315 |
| PARVB     | -0.6313 | 3.65446 | -8.4049 | 0.00016 | 0.00177 | 0.96791 |
| SMARCE1   | -0.631  | 3.49135 | -6.0587 | 0.00092 | 0.00561 | -1.0509 |
| SECTM1    | -0.6307 | 0.34995 | -5.8435 | 0.00111 | 0.00643 | -1.2653 |
| RAB11FIP1 | -0.6302 | 3.76243 | -7.0288 | 0.00042 | 0.00328 | -0.1505 |
| SELENOO   | -0.6295 | 4.05167 | -6.6056 | 0.00058 | 0.00409 | -0.5307 |
| B4GALT7   | -0.629  | 4.12496 | -6.5181 | 0.00062 | 0.00429 | -0.6116 |
| L3MBTL3   | -0.6284 | 1.32582 | -3.204  | 0.01852 | 0.04949 | -4.4073 |
| PSMB3P2   | -0.6284 | 3.02892 | -6.8958 | 0.00046 | 0.0035  | -0.268  |
| SLC25A1   | -0.628  | 3.94405 | -3.9253 | 0.00776 | 0.02582 | -3.4502 |
| CTIF      | -0.6279 | 4.57556 | -5.7034 | 0.00126 | 0.00707 | -1.4078 |
| PHB1P21   | -0.6277 | 3.25484 | -6.2149 | 0.0008  | 0.00512 | -0.8988 |
| WDR5B-D   | -0.6274 | -1.9421 | -3.9816 | 0.00728 | 0.02466 | -3.3785 |
| LINC0142  | -0.6274 | 0.04699 | -4.3808 | 0.00467 | 0.01768 | -2.8839 |
| PNISR-A9  | -0.6272 | -0.119  | -6.9515 | 0.00044 | 0.00341 | -0.2186 |
| TRPM2-A   | -0.6271 | 0.33497 | -4.7886 | 0.00304 | 0.01303 | -2.4026 |
| RILPL2    | -0.6267 | 1.84983 | -5.993  | 0.00097 | 0.00584 | -1.1157 |
| LSM10     | -0.6267 | 3.7821  | -6.3562 | 0.00071 | 0.0047  | -0.7637 |
| CENPP     | -0.6266 | 1.97171 | -6.376  | 0.0007  | 0.00465 | -0.7449 |
| SEC61A2   | -0.6262 | 1.73957 | -7.801  | 0.00023 | 0.00228 | 0.49777 |
| REEP2     | -0.626  | 1.55657 | -3.2434 | 0.01763 | 0.04767 | -4.3532 |
| UBE2O     | -0.6251 | 4.51842 | -5.9739 | 0.00099 | 0.00591 | -1.1347 |
| SGCE      | -0.6251 | 4.75263 | -6.0689 | 0.00091 | 0.00558 | -1.0409 |
| PLEKHM1   | -0.6248 | 0.5855  | -4.1625 | 0.00594 | 0.02116 | -3.1515 |
| MSRB2     | -0.6247 | 2.62466 | -3.8035 | 0.00894 | 0.02862 | -3.6067 |
| MRPL12    | -0.6247 | 3.37172 | -5.5082 | 0.00151 | 0.00798 | -1.6107 |
| INO80C    | -0.6238 | 0.64777 | -3.3147 | 0.01612 | 0.04467 | -4.256  |
| SORD      | -0.6236 | 3.1067  | -4.7059 | 0.00331 | 0.01386 | -2.4982 |
| MPHOSP    | -0.6234 | 3.46308 | -4.9322 | 0.00263 | 0.01171 | -2.2388 |
| TOR2A     | -0.6232 | 2.36472 | -6.8869 | 0.00046 | 0.00351 | -0.2759 |
| RMDN3     | -0.6227 | 3.45423 | -6.4351 | 0.00067 | 0.00449 | -0.6892 |
| GTF2IP13  | -0.6221 | 2.35923 | -3.5732 | 0.01175 | 0.03519 | -3.9087 |
| INSIG1-D  | -0.622  | 1.14964 | -3.444  | 0.01375 | 0.03972 | -4.0811 |
| PIGB      | -0.6216 | 1.40875 | -7.1335 | 0.00038 | 0.00311 | -0.0593 |
| RPP25L    | -0.6216 | 3.23789 | -4.1041 | 0.00634 | 0.02227 | -3.2242 |
| ANAPC7    | -0.6208 | 4.40756 | -7.1749 | 0.00037 | 0.00304 | -0.0235 |
| AP2B1     | -0.6202 | 5.82519 | -7.9719 | 0.00021 | 0.00211 | 0.63385 |
| RPS24P1   | -0.62   | 0.86879 | -3.3077 | 0.01626 | 0.04493 | -4.2654 |
| CSGALN1   | -0.62   | -0.1068 | -4.5105 | 0.00406 | 0.016   | -2.7282 |
| PNPLA3    | -0.6197 | 2.73994 | -3.5896 | 0.01152 | 0.03466 | -3.8869 |
| KSR1      | -0.6191 | 2.10001 | -7.3196 | 0.00033 | 0.0028  | 0.10024 |
| FAM219A   | -0.618  | 2.91581 | -4.9535 | 0.00257 | 0.01153 | -2.2148 |
| EFTUD2    | -0.6175 | 5.68122 | -5.2126 | 0.00199 | 0.00964 | -1.9275 |
| DYRK3     | -0.6167 | 0.53859 | -4.0628 | 0.00664 | 0.02309 | -3.276  |
| ATP5MC2   | -0.6167 | 4.98406 | -5.4634 | 0.00157 | 0.00821 | -1.658  |
| ZSWIM8    | -0.6167 | 4.34002 | -6.3449 | 0.00072 | 0.00473 | -0.7745 |
| GRINA     | -0.6167 | 7.5193  | -7.8594 | 0.00023 | 0.00222 | 0.54453 |
| DYNLT3    | -0.6167 | 3.2836  | -5.5268 | 0.00148 | 0.00791 | -1.5912 |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| SLC12A5  | -0.6166 | 1.04678 | -3.5194 | 0.01254 | 0.03703 | -3.9802 |
| SLC25A1  | -0.6164 | 1.34668 | -3.5375 | 0.01227 | 0.03636 | -3.9561 |
| ADPRM    | -0.6161 | 0.02765 | -7.7203 | 0.00025 | 0.00237 | 0.43259 |
| MAP3K3   | -0.6157 | 2.96447 | -6.6431 | 0.00056 | 0.00402 | -0.4962 |
| SKA2     | -0.6154 | 3.87965 | -6.5529 | 0.00061 | 0.00421 | -0.5793 |
| PEX26    | -0.6153 | 4.97817 | -7.0345 | 0.00041 | 0.00327 | -0.1455 |
| FAM151B  | -0.6152 | 0.52216 | -3.2053 | 0.01849 | 0.04944 | -4.4054 |
| NCAPH2   | -0.6152 | 4.87166 | -5.4818 | 0.00154 | 0.00809 | -1.6386 |
| FAM241B  | -0.6152 | 3.54207 | -4.3489 | 0.00483 | 0.01812 | -2.9224 |
| TMEM135  | -0.6145 | 2.90861 | -3.2323 | 0.01787 | 0.04822 | -4.3684 |
| OSBPL1A  | -0.6143 | 3.64025 | -7.9842 | 0.00021 | 0.0021  | 0.64358 |
| WWC3     | -0.6141 | 4.19881 | -7.3823 | 0.00032 | 0.00273 | 0.15325 |
| TP53I3   | -0.614  | 2.61175 | -3.7136 | 0.00994 | 0.03091 | -3.7237 |
| FAM114A  | -0.6134 | 2.6568  | -4.9637 | 0.00255 | 0.01144 | -2.2034 |
| IFNAR2   | -0.6133 | 2.69971 | -7.1001 | 0.00039 | 0.00315 | -0.0883 |
| PLD3     | -0.6133 | 6.56345 | -5.1231 | 0.00218 | 0.01025 | -2.0256 |
| TMEM59L  | -0.6131 | -0.0954 | -3.4108 | 0.01432 | 0.04084 | -4.1259 |
| VMA21    | -0.6131 | 4.77865 | -5.9368 | 0.00102 | 0.00605 | -1.1716 |
| CLMN     | -0.613  | 1.68142 | -4.7501 | 0.00316 | 0.01337 | -2.447  |
| ZC3H10   | -0.6129 | 1.79964 | -4.6264 | 0.0036  | 0.0147  | -2.5911 |
| UNKL     | -0.6119 | 2.88904 | -3.9785 | 0.0073  | 0.02471 | -3.3825 |
| MAN1B1   | -0.6115 | 3.74097 | -5.7737 | 0.00118 | 0.00674 | -1.336  |
| ZNF91    | -0.6114 | 1.40408 | -3.5166 | 0.01258 | 0.03714 | -3.984  |
| ARHGDI   | -0.6111 | 7.59207 | -4.4422 | 0.00437 | 0.01685 | -2.8098 |
| ATP5MC1  | -0.611  | 5.26412 | -4.7351 | 0.00321 | 0.01353 | -2.4643 |
| IMPACT   | -0.6107 | 2.74029 | -4.7726 | 0.00309 | 0.01319 | -2.421  |
| SGPP1    | -0.61   | 2.76784 | -4.6393 | 0.00355 | 0.01456 | -2.576  |
| TSPAN10  | -0.6099 | 0.9179  | -4.4212 | 0.00447 | 0.01713 | -2.8351 |
| C19orf33 | -0.6097 | 1.12308 | -3.3288 | 0.01584 | 0.04406 | -4.2368 |
| EOGT     | -0.6091 | 1.79471 | -4.5589 | 0.00386 | 0.01543 | -2.6706 |
| C8orf76  | -0.609  | -1.3277 | -6.7573 | 0.00051 | 0.00378 | -0.3922 |
| CDKL2    | -0.6087 | -2.6046 | -3.8914 | 0.00807 | 0.02654 | -3.4935 |
| RRAS2P1  | -0.6085 | 5.85998 | -7.3419 | 0.00033 | 0.00277 | 0.11911 |
| LAGE3    | -0.6085 | 5.06132 | -7.4738 | 0.0003  | 0.00264 | 0.22984 |
| TCTN1    | -0.6084 | 2.39828 | -6.4353 | 0.00067 | 0.00449 | -0.689  |
| UBTF     | -0.6074 | 5.25949 | -3.5502 | 0.01208 | 0.03594 | -3.9391 |
| IQSEC2   | -0.6067 | 2.52884 | -3.7311 | 0.00973 | 0.03046 | -3.7008 |
| RBM19    | -0.6063 | 3.32846 | -6.6535 | 0.00056 | 0.00399 | -0.4867 |
| PNMA8A   | -0.6063 | 2.82415 | -5.79   | 0.00116 | 0.00666 | -1.3195 |
| MYO1B    | -0.6062 | 5.2115  | -4.4453 | 0.00436 | 0.01681 | -2.8061 |
| TAF9B    | -0.606  | 3.9662  | -5.6529 | 0.00132 | 0.0073  | -1.4599 |
| NFE2L1   | -0.6054 | 5.77021 | -5.1811 | 0.00206 | 0.00985 | -1.9618 |
| ATP5PD   | -0.6048 | 4.53401 | -5.2176 | 0.00198 | 0.0096  | -1.922  |
| CDK12    | -0.6046 | 4.3927  | -3.5456 | 0.01215 | 0.03609 | -3.9453 |
| EXOGE    | -0.6042 | 2.67801 | -4.3136 | 0.00502 | 0.01868 | -2.9655 |
| C8orf58  | -0.6041 | 1.46464 | -4.8514 | 0.00285 | 0.01245 | -2.3307 |
| MRPL27   | -0.6037 | 3.60561 | -6.4472 | 0.00066 | 0.00446 | -0.6779 |
| C1orf56  | -0.6037 | 2.00965 | -4.9213 | 0.00266 | 0.01182 | -2.2511 |
| DCTN6-D  | -0.6035 | -0.0933 | -3.7131 | 0.00994 | 0.03092 | -3.7244 |
| WASHC4   | -0.6033 | 4.69288 | -7.4279 | 0.00031 | 0.00269 | 0.19151 |
| RAB3IL1  | -0.6032 | 1.78395 | -3.2859 | 0.01671 | 0.0458  | -4.2952 |
| L3HYPDH  | -0.6025 | 1.77062 | -4.6301 | 0.00358 | 0.01466 | -2.5867 |
| MAP3K11  | -0.6025 | 5.09978 | -6.0132 | 0.00096 | 0.00578 | -1.0958 |
| PHB1P11  | -0.602  | 1.33684 | -3.9899 | 0.00721 | 0.02447 | -3.3679 |
| KCTD21   | -0.6009 | 0.04527 | -4.6985 | 0.00334 | 0.01391 | -2.5069 |
| NCK1     | -0.6005 | 3.40659 | -5.6851 | 0.00128 | 0.00715 | -1.4267 |
| PGGT1B   | -0.6002 | 0.67376 | -4.2827 | 0.0052  | 0.01916 | -3.0032 |
| FAAP24   | -0.6    | 2.04888 | -4.7569 | 0.00314 | 0.01332 | -2.4391 |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| ATP6V0A  | -0.5997 | 3.30722 | -3.5077 | 0.01272 | 0.03745 | -3.9958 |
| SCLY     | -0.5992 | -0.822  | -3.2434 | 0.01763 | 0.04767 | -4.3532 |
| PARVG    | -0.5991 | 0.50903 | -3.2994 | 0.01643 | 0.04524 | -4.2768 |
| TERF2IP  | -0.5982 | 3.57021 | -8.1446 | 0.00018 | 0.00196 | 0.76892 |
| HELZ     | -0.598  | 3.50227 | -7.4302 | 0.00031 | 0.00269 | 0.19342 |
| SEPTIN7  | -0.5972 | -1.1816 | -5.1717 | 0.00207 | 0.00992 | -1.9722 |
| TRDMT1   | -0.5971 | 1.57682 | -4.6725 | 0.00343 | 0.0142  | -2.5372 |
| COMMD5   | -0.5965 | 3.58534 | -7.4757 | 0.0003  | 0.00264 | 0.23144 |
| TWF2     | -0.596  | 4.35246 | -7.1857 | 0.00037 | 0.00302 | -0.0142 |
| DSTYK    | -0.5958 | 2.56606 | -7.6714 | 0.00026 | 0.00242 | 0.39281 |
| NME2P1   | -0.5958 | 7.27653 | -4.6029 | 0.00369 | 0.01497 | -2.6187 |
| NBR1     | -0.5956 | 4.36515 | -5.0133 | 0.00242 | 0.01103 | -2.1476 |
| ZNF780B  | -0.5956 | 1.97238 | -5.1507 | 0.00212 | 0.01006 | -1.9953 |
| ZNF566-A | -0.5953 | -0.3309 | -4.4574 | 0.0043  | 0.01667 | -2.7916 |
| SRP68    | -0.5934 | 4.71809 | -7.381  | 0.00032 | 0.00273 | 0.1521  |
| DCP1B    | -0.5933 | 0.24544 | -3.5724 | 0.01176 | 0.03521 | -3.9097 |
| ZNF280C  | -0.5928 | 2.16818 | -5.4412 | 0.0016  | 0.00834 | -1.6815 |
| GLMP     | -0.5927 | 5.32106 | -6.6472 | 0.00056 | 0.00401 | -0.4924 |
| ACTR3C   | -0.5925 | -0.1209 | -3.9121 | 0.00788 | 0.02607 | -3.4671 |
| HSP90AA  | -0.5923 | 2.99237 | -4.4307 | 0.00443 | 0.01702 | -2.8236 |
| FAM86C1  | -0.592  | 0.85218 | -3.6681 | 0.01049 | 0.03228 | -3.7834 |
| SLC22A4  | -0.5919 | -0.096  | -4.2639 | 0.00531 | 0.01945 | -3.0262 |
| FRMD8    | -0.5918 | 3.33872 | -4.2811 | 0.00521 | 0.01918 | -3.0052 |
| MATCAP   | -0.5916 | 1.8573  | -6.1124 | 0.00088 | 0.00546 | -0.9983 |
| BTN3A2   | -0.5914 | 2.60067 | -5.3758 | 0.00171 | 0.00867 | -1.7511 |
| COL16A1  | -0.5913 | -0.0236 | -3.3307 | 0.01581 | 0.04397 | -4.2343 |
| IPO13    | -0.5905 | 4.07391 | -3.5712 | 0.01178 | 0.03524 | -3.9112 |
| IFT46    | -0.5901 | 2.96437 | -5.1214 | 0.00218 | 0.01026 | -2.0275 |
| GCFC2    | -0.5887 | 2.45179 | -5.283  | 0.00186 | 0.0092  | -1.8509 |
| PDE7B    | -0.5884 | 1.52507 | -3.2907 | 0.01661 | 0.04558 | -4.2887 |
| JMJD6    | -0.5878 | 4.24501 | -4.7477 | 0.00317 | 0.01339 | -2.4497 |
| UROD     | -0.5865 | 5.83744 | -6.9015 | 0.00046 | 0.00349 | -0.2629 |
| TUBB6    | -0.5864 | 5.6534  | -5.804  | 0.00115 | 0.00661 | -1.3052 |
| TBC1D13  | -0.5863 | 3.23277 | -4.6014 | 0.00369 | 0.01498 | -2.6205 |
| UCK1     | -0.5861 | 3.62048 | -5.424  | 0.00163 | 0.00841 | -1.6997 |
| MIER2    | -0.5856 | 2.22965 | -6.5825 | 0.00059 | 0.00415 | -0.5519 |
| MRPL38   | -0.5855 | -0.5115 | -6.3616 | 0.00071 | 0.00469 | -0.7586 |
| LAMP2    | -0.5854 | 5.9502  | -5.7323 | 0.00123 | 0.00692 | -1.3783 |
| DHX8     | -0.5852 | 3.97542 | -4.0159 | 0.007   | 0.02396 | -3.335  |
| PRELID1  | -0.5851 | 3.67014 | -5.769  | 0.00119 | 0.00675 | -1.3408 |
| UBE2Z    | -0.5848 | 5.30256 | -8.1455 | 0.00018 | 0.00196 | 0.76961 |
| TCIRG1   | -0.5843 | 2.61933 | -3.8106 | 0.00887 | 0.02844 | -3.5976 |
| DYNLT3F  | -0.5843 | 0.32486 | -7.8307 | 0.00023 | 0.00224 | 0.52159 |
| LRIF1    | -0.5836 | 2.87167 | -6.1691 | 0.00084 | 0.00527 | -0.9432 |
| NMD3P2   | -0.5827 | 1.18418 | -3.8289 | 0.00868 | 0.02801 | -3.5739 |
| UFL1     | -0.5822 | 3.7326  | -4.2842 | 0.00519 | 0.01914 | -3.0013 |
| PHF20L1  | -0.582  | 5.4468  | -5.9445 | 0.00101 | 0.00602 | -1.164  |
| CCDC40   | -0.5815 | 1.02496 | -4.8113 | 0.00297 | 0.01283 | -2.3765 |
| TACO1    | -0.5808 | 2.98914 | -6.6701 | 0.00055 | 0.00396 | -0.4715 |
| CDC27    | -0.5808 | 4.71595 | -6.8293 | 0.00049 | 0.00363 | -0.3274 |
| MT1X     | -0.5804 | 1.15305 | -3.577  | 0.0117  | 0.03507 | -3.9035 |
| ALAD     | -0.5802 | 2.88647 | -5.7309 | 0.00123 | 0.00693 | -1.3797 |
| TMEM106  | -0.58   | -0.1227 | -4.2784 | 0.00522 | 0.01922 | -3.0085 |
| HENMT1   | -0.5797 | 2.02587 | -6.3063 | 0.00074 | 0.00484 | -0.8112 |
| SMN1     | -0.5795 | -0.3388 | -5.668  | 0.0013  | 0.00722 | -1.4443 |
| NDUFA12  | -0.5791 | 3.87423 | -4.4137 | 0.00451 | 0.01722 | -2.8441 |
| DCAF7    | -0.579  | 5.07671 | -7.0008 | 0.00042 | 0.00333 | -0.1751 |
| GREB1L   | -0.5788 | 2.91541 | -5.988  | 0.00098 | 0.00585 | -1.1207 |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| BLOC1S1  | -0.5785 | 1.99347 | -5.2345 | 0.00195 | 0.0095  | -1.9036 |
| COILP1   | -0.5783 | 0.62237 | -6.8338 | 0.00048 | 0.00363 | -0.3234 |
| SLC25A4  | -0.5777 | 2.00815 | -3.4293 | 0.014   | 0.04026 | -4.1009 |
| TMEM45A  | -0.5776 | 2.19805 | -3.6884 | 0.01024 | 0.03167 | -3.7567 |
| GSTA4    | -0.5776 | 1.59202 | -4.8978 | 0.00272 | 0.01203 | -2.2778 |
| DEPDC1B  | -0.5772 | 4.00405 | -4.4196 | 0.00448 | 0.01715 | -2.837  |
| LSM12    | -0.5771 | 1.45934 | -7.4222 | 0.00031 | 0.00269 | 0.18676 |
| MED15    | -0.5771 | 5.39451 | -6.6641 | 0.00055 | 0.00397 | -0.477  |
| PEX11G   | -0.576  | -2.0288 | -3.2135 | 0.0183  | 0.0491  | -4.3943 |
| GAD1     | -0.5755 | 1.44063 | -3.3062 | 0.0163  | 0.04497 | -4.2676 |
| SNAI3-AS | -0.5753 | -0.1697 | -3.5435 | 0.01218 | 0.03615 | -3.948  |
| GUCD1    | -0.575  | 5.64089 | -5.202  | 0.00201 | 0.00972 | -1.939  |
| MFSD1    | -0.5743 | 3.83395 | -6.4369 | 0.00067 | 0.00449 | -0.6876 |
| LAMC1    | -0.5739 | 7.53578 | -5.0737 | 0.00228 | 0.01058 | -2.0803 |
| SPATS2   | -0.5734 | 4.70496 | -4.656  | 0.00349 | 0.01438 | -2.5564 |
| C19orf44 | -0.5723 | 1.58306 | -5.4568 | 0.00158 | 0.00825 | -1.6649 |
| HEXA     | -0.572  | 3.17369 | -7.1383 | 0.00038 | 0.0031  | -0.0551 |
| QPRT     | -0.5716 | 6.1697  | -6.8537 | 0.00048 | 0.00359 | -0.3055 |
| TSPAN4   | -0.5716 | 3.92265 | -5.987  | 0.00098 | 0.00586 | -1.1218 |
| JMJD4    | -0.5715 | 3.6809  | -3.7504 | 0.00952 | 0.02994 | -3.6757 |
| NEIL3    | -0.5715 | 2.04286 | -4.6904 | 0.00336 | 0.014   | -2.5163 |
| MT1F     | -0.5704 | 3.48047 | -3.942  | 0.00762 | 0.02548 | -3.4288 |
| TYMS     | -0.5702 | 6.1604  | -3.9555 | 0.0075  | 0.0252  | -3.4117 |
| TMEM126  | -0.5699 | 2.77771 | -7.2524 | 0.00035 | 0.00291 | 0.043   |
| JRK      | -0.5697 | 3.57367 | -3.6206 | 0.0111  | 0.03372 | -3.8458 |
| SLC23A2  | -0.5688 | 3.44512 | -5.0828 | 0.00226 | 0.01051 | -2.0702 |
| UFD1     | -0.5681 | 4.06168 | -5.5911 | 0.00139 | 0.00759 | -1.524  |
| CASP10   | -0.5673 | 1.95134 | -3.6707 | 0.01046 | 0.03219 | -3.78   |
| KPNB1    | -0.5668 | 7.09658 | -5.6181 | 0.00136 | 0.00748 | -1.4959 |
| TYMSOS   | -0.5668 | -0.4038 | -4.7371 | 0.00321 | 0.01351 | -2.462  |
| NPLOC4   | -0.5668 | 6.36951 | -7.7047 | 0.00025 | 0.00238 | 0.41991 |
| SLC25A4  | -0.5667 | 3.10212 | -6.6564 | 0.00056 | 0.00399 | -0.484  |
| CYBC1    | -0.566  | 5.179   | -6.5724 | 0.0006  | 0.00417 | -0.5613 |
| PODXL2   | -0.5656 | 4.01762 | -4.6289 | 0.00359 | 0.01467 | -2.5882 |
| NLE1     | -0.5651 | 3.07462 | -3.8266 | 0.0087  | 0.02808 | -3.5769 |
| GNPDA2   | -0.5651 | 2.86303 | -5.1111 | 0.0022  | 0.01032 | -2.0389 |
| ARHGAP   | -0.5648 | 3.85066 | -3.8897 | 0.00809 | 0.02656 | -3.4958 |
| TLCD5    | -0.5645 | 2.0091  | -5.8109 | 0.00114 | 0.00659 | -1.2983 |
| ZNF652   | -0.5645 | 2.76441 | -3.4816 | 0.01313 | 0.03838 | -4.0307 |
| PRPS1P2  | -0.5645 | 1.3756  | -3.7784 | 0.00921 | 0.02925 | -3.6394 |
| SLC66A1  | -0.5644 | 3.00049 | -6.7555 | 0.00051 | 0.00378 | -0.3939 |
| ZNF70    | -0.5641 | 2.0414  | -6.1095 | 0.00088 | 0.00546 | -1.0011 |
| EME1     | -0.5638 | 2.60196 | -4.2417 | 0.00544 | 0.01979 | -3.0535 |
| AMMECR   | -0.5637 | 4.01077 | -5.9942 | 0.00097 | 0.00584 | -1.1146 |
| TXNDC15  | -0.5634 | 3.34896 | -3.444  | 0.01375 | 0.03972 | -4.0811 |
| IQCG     | -0.563  | 1.53457 | -5.6309 | 0.00134 | 0.00741 | -1.4827 |
| PHB1P10  | -0.5629 | 2.48395 | -6.4403 | 0.00066 | 0.00448 | -0.6844 |
| C19orf25 | -0.5627 | 1.77563 | -4.4625 | 0.00428 | 0.01662 | -2.7855 |
| NSF      | -0.5626 | 3.98461 | -5.5915 | 0.00139 | 0.00759 | -1.5235 |
| FAM131A  | -0.5621 | 1.96229 | -3.7403 | 0.00963 | 0.03019 | -3.6888 |
| GNPDA1   | -0.5621 | 5.55955 | -5.26   | 0.0019  | 0.00935 | -1.8758 |
| ACAA2P1  | -0.5618 | 3.35378 | -5.0446 | 0.00235 | 0.01082 | -2.1127 |
| SLC35B1  | -0.5618 | 4.37768 | -6.6783 | 0.00055 | 0.00394 | -0.464  |
| FGF18    | -0.5617 | 4.48011 | -4.2644 | 0.0053  | 0.01944 | -3.0256 |
| SLC16A1  | -0.561  | 1.5449  | -5.797  | 0.00116 | 0.00664 | -1.3123 |
| C1GALT1  | -0.5606 | 0.96075 | -3.7925 | 0.00906 | 0.0289  | -3.6211 |
| TERF1    | -0.5606 | 3.64282 | -3.9491 | 0.00755 | 0.02533 | -3.4199 |
| CASP7    | -0.5603 | 3.24613 | -6.3941 | 0.00069 | 0.00459 | -0.7278 |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| MIDEAS-  | -0.56   | 0.51339 | -4.0304 | 0.00689 | 0.02368 | -3.3168 |
| WAS      | -0.5595 | -2.0434 | -3.8456 | 0.00851 | 0.02762 | -3.5525 |
| PYGO1    | -0.5594 | 1.81502 | -3.4231 | 0.0141  | 0.04045 | -4.1093 |
| CMTM8    | -0.5593 | 1.6045  | -3.428  | 0.01402 | 0.0403  | -4.1027 |
| ADGRL2   | -0.5588 | 7.15882 | -5.1043 | 0.00222 | 0.01037 | -2.0465 |
| TBX3     | -0.5588 | 0.22144 | -6.938  | 0.00045 | 0.00342 | -0.2305 |
| VAMP1    | -0.5579 | 2.21869 | -3.9735 | 0.00735 | 0.02481 | -3.3888 |
| TRIM65   | -0.5577 | 2.55834 | -4.2523 | 0.00537 | 0.01964 | -3.0406 |
| DPM2     | -0.5567 | 4.36734 | -4.6367 | 0.00356 | 0.0146  | -2.5791 |
| ENTPD5   | -0.556  | 2.23711 | -3.8858 | 0.00812 | 0.02665 | -3.5007 |
| TCEAL1   | -0.5556 | 3.0625  | -3.9217 | 0.0078  | 0.02588 | -3.4548 |
| PXN-AS1  | -0.5556 | 0.85941 | -3.8242 | 0.00873 | 0.02814 | -3.58   |
| NCKAP5L  | -0.5555 | 4.17819 | -6.4336 | 0.00067 | 0.00449 | -0.6906 |
| TOLLIP   | -0.5555 | 3.40098 | -3.9387 | 0.00765 | 0.02557 | -3.4331 |
| ACO1     | -0.5555 | 4.3833  | -3.5542 | 0.01202 | 0.03579 | -3.9339 |
| LINC0088 | -0.5554 | -0.7447 | -4.251  | 0.00538 | 0.01966 | -3.0421 |
| SSNA1    | -0.5551 | 5.11074 | -5.4012 | 0.00167 | 0.00853 | -1.724  |
| RPTOR    | -0.555  | 4.85294 | -5.5928 | 0.00139 | 0.00759 | -1.5222 |
| TRPC1    | -0.555  | 1.79695 | -4.5577 | 0.00387 | 0.01544 | -2.6721 |
| SLC25A1  | -0.5543 | 6.65793 | -4.7878 | 0.00304 | 0.01303 | -2.4036 |
| FAAP100  | -0.5542 | 4.47025 | -4.1147 | 0.00626 | 0.0221  | -3.211  |
| TMEM92   | -0.554  | 1.68958 | -3.834  | 0.00863 | 0.0279  | -3.5674 |
| MIF4GD   | -0.554  | 1.91524 | -4.0982 | 0.00638 | 0.02239 | -3.2316 |
| THOC1    | -0.5538 | 3.46491 | -5.628  | 0.00135 | 0.00742 | -1.4856 |
| CENPX    | -0.5536 | 5.56067 | -4.3489 | 0.00483 | 0.01812 | -2.9225 |
| GPS1     | -0.5536 | 6.34431 | -7.4323 | 0.00031 | 0.00269 | 0.19522 |
| UBA6     | -0.5528 | 4.64273 | -4.2722 | 0.00526 | 0.0193  | -3.0161 |
| NOL9     | -0.5528 | 3.54133 | -3.5474 | 0.01212 | 0.03604 | -3.9428 |
| RBM33-D  | -0.5527 | 1.298   | -5.1069 | 0.00221 | 0.01035 | -2.0435 |
| UTP6     | -0.5524 | 3.77664 | -6.1153 | 0.00087 | 0.00545 | -0.9955 |
| POP5     | -0.5523 | 4.48561 | -6.8017 | 0.0005  | 0.00369 | -0.3521 |
| APOBEC   | -0.5521 | 3.86012 | -3.2855 | 0.01672 | 0.04581 | -4.2956 |
| TLE3     | -0.5517 | 3.45998 | -7.4782 | 0.0003  | 0.00264 | 0.23354 |
| HDHD2    | -0.5516 | 2.55766 | -6.7196 | 0.00053 | 0.00385 | -0.4264 |
| FAM174C  | -0.5515 | 2.78762 | -3.8684 | 0.00829 | 0.02708 | -3.5231 |
| ARL16    | -0.5514 | 5.131   | -5.544  | 0.00146 | 0.00781 | -1.5732 |
| SNHG8    | -0.551  | 5.42082 | -3.372  | 0.01502 | 0.04234 | -4.1783 |
| BEX3     | -0.5508 | 7.48032 | -6.9006 | 0.00046 | 0.00349 | -0.2637 |
| GSTO1    | -0.5507 | 3.68911 | -3.9124 | 0.00788 | 0.02606 | -3.4667 |
| CCDC148  | -0.5504 | -2.2805 | -4.6409 | 0.00354 | 0.01454 | -2.574  |
| ATP5PDF  | -0.55   | 5.54215 | -4.646  | 0.00352 | 0.01449 | -2.5682 |
| NUDT1    | -0.5499 | 2.6305  | -4.4827 | 0.00419 | 0.01635 | -2.7613 |
| AP5S1    | -0.5499 | 2.97603 | -3.2902 | 0.01662 | 0.04558 | -4.2893 |
| ATPAF2   | -0.5497 | 1.29461 | -3.8863 | 0.00812 | 0.02664 | -3.5    |
| ZNF566   | -0.5493 | 1.60049 | -4.4186 | 0.00448 | 0.01716 | -2.8382 |
| MT1XP1   | -0.548  | 0.8965  | -4.723  | 0.00325 | 0.01367 | -2.4784 |
| C11orf71 | -0.5474 | 2.04301 | -3.5418 | 0.0122  | 0.0362  | -3.9504 |
| GNA13    | -0.546  | 4.35608 | -5.5213 | 0.00149 | 0.00793 | -1.5969 |
| ELP6     | -0.5449 | 2.82867 | -7.4746 | 0.0003  | 0.00264 | 0.23056 |
| ZNF426   | -0.544  | 1.51879 | -4.0434 | 0.00678 | 0.0234  | -3.3003 |
| TUBD1    | -0.5433 | 1.51054 | -5.5606 | 0.00143 | 0.00774 | -1.5558 |
| NCBP2    | -0.5432 | 5.04172 | -6.3721 | 0.0007  | 0.00466 | -0.7486 |
| MRPL17   | -0.5423 | 5.37582 | -6.2513 | 0.00078 | 0.005   | -0.8638 |
| AK1      | -0.5422 | -0.0098 | -4.4249 | 0.00445 | 0.0171  | -2.8306 |
| CCDC34   | -0.5419 | 2.98899 | -4.0593 | 0.00666 | 0.02315 | -3.2804 |
| PSTK     | -0.5416 | 0.91678 | -3.7991 | 0.00899 | 0.02873 | -3.6124 |
| MFSD5    | -0.5415 | 4.27257 | -7.3365 | 0.00033 | 0.00278 | 0.11455 |
| NOL11    | -0.5414 | 3.80176 | -3.2952 | 0.01652 | 0.04541 | -4.2825 |

|         |         |         |         |         |         |         |
|---------|---------|---------|---------|---------|---------|---------|
| TMCO1   | -0.5414 | 4.91377 | -5.56   | 0.00144 | 0.00774 | -1.5565 |
| NINL    | -0.5409 | 2.3315  | -4.8463 | 0.00287 | 0.01249 | -2.3364 |
| ASB8    | -0.5402 | 3.3535  | -6.0631 | 0.00091 | 0.00559 | -1.0466 |
| SEC31B  | -0.54   | 0.53459 | -3.3452 | 0.01552 | 0.04338 | -4.2145 |
| RUSC2   | -0.5399 | 2.97184 | -4.3238 | 0.00497 | 0.01852 | -2.953  |
| NT5DC1  | -0.5399 | 2.92154 | -5.1398 | 0.00214 | 0.01015 | -2.0072 |
| NFS1    | -0.5394 | 3.47599 | -4.5287 | 0.00399 | 0.01582 | -2.7065 |
| PWWP3A  | -0.5391 | 1.95657 | -5.4303 | 0.00162 | 0.00838 | -1.693  |
| NMD3P1  | -0.5388 | 4.39092 | -5.6543 | 0.00132 | 0.00729 | -1.4585 |
| PWP1    | -0.5385 | 4.72237 | -5.4978 | 0.00152 | 0.00803 | -1.6216 |
| F2RL3   | -0.5381 | 0.53584 | -5.1146 | 0.00219 | 0.0103  | -2.0351 |
| KANSL1  | -0.5379 | 3.53481 | -6.9439 | 0.00044 | 0.00342 | -0.2253 |
| NUP50   | -0.5375 | 5.33736 | -5.7457 | 0.00121 | 0.00685 | -1.3646 |
| VEZT    | -0.5374 | 3.35715 | -4.107  | 0.00632 | 0.02223 | -3.2206 |
| WFS1    | -0.5371 | 3.69542 | -5.1959 | 0.00203 | 0.00976 | -1.9457 |
| SH3BP5- | -0.537  | 0.33711 | -4.4291 | 0.00443 | 0.01704 | -2.8255 |
| LIMS1   | -0.537  | 5.71192 | -6.371  | 0.0007  | 0.00466 | -0.7497 |
| RNF138  | -0.5363 | 3.31618 | -5.5117 | 0.0015  | 0.00796 | -1.6071 |
| MPV17   | -0.536  | 3.88633 | -4.0078 | 0.00706 | 0.02411 | -3.3454 |
| PINX1   | -0.5359 | 0.85867 | -4.9421 | 0.0026  | 0.01163 | -2.2277 |
| DUXAP8  | -0.5359 | 1.97107 | -3.431  | 0.01397 | 0.0402  | -4.0985 |
| GGA3    | -0.5357 | 3.60655 | -6.2226 | 0.0008  | 0.0051  | -0.8914 |
| HIGD2AP | -0.5354 | 1.16279 | -3.8099 | 0.00887 | 0.02845 | -3.5985 |
| FAM229B | -0.5354 | 1.51644 | -4.2427 | 0.00543 | 0.01977 | -3.0523 |
| NCALD   | -0.5353 | 1.37882 | -3.2904 | 0.01662 | 0.04558 | -4.289  |
| TIPARP  | -0.5352 | 3.26163 | -3.6556 | 0.01065 | 0.03264 | -3.7997 |
| SNX17   | -0.5351 | 5.56754 | -5.355  | 0.00174 | 0.00877 | -1.7734 |
| PPP3CB- | -0.535  | 0.10973 | -3.9326 | 0.0077  | 0.02568 | -3.4408 |
| ZFYVE16 | -0.5346 | 3.6859  | -5.4473 | 0.00159 | 0.0083  | -1.6751 |
| KRCC1   | -0.5343 | 3.59188 | -5.0455 | 0.00235 | 0.01082 | -2.1117 |
| SUOX    | -0.5341 | 3.74779 | -3.9133 | 0.00787 | 0.02604 | -3.4655 |
| APPL2   | -0.5341 | 2.91233 | -5.8753 | 0.00108 | 0.00631 | -1.2332 |
| TMEM177 | -0.534  | 2.37449 | -5.2338 | 0.00195 | 0.0095  | -1.9043 |
| ACAA2   | -0.5336 | 2.19946 | -7.2284 | 0.00036 | 0.00294 | 0.02247 |
| ACACB   | -0.5335 | 1.57888 | -3.3969 | 0.01456 | 0.04138 | -4.1445 |
| CAMK2N  | -0.5334 | 4.62986 | -3.5942 | 0.01146 | 0.03452 | -3.8808 |
| SNHG7   | -0.5334 | 3.17032 | -4.3457 | 0.00485 | 0.01817 | -2.9264 |
| RNF216P | -0.5329 | 1.24405 | -4.1863 | 0.00578 | 0.02074 | -3.1219 |
| DEPDC7  | -0.5328 | 1.45492 | -5.6487 | 0.00132 | 0.00732 | -1.4643 |
| NPHP3   | -0.5322 | 1.3944  | -5.9068 | 0.00105 | 0.00618 | -1.2017 |
| OGFOD3  | -0.532  | 3.89762 | -5.2783 | 0.00187 | 0.00923 | -1.8561 |
| LAMB1   | -0.5319 | 7.46431 | -4.3581 | 0.00479 | 0.01799 | -2.9113 |
| METTL2A | -0.5309 | 1.84155 | -6.4465 | 0.00066 | 0.00446 | -0.6785 |
| EHD3    | -0.5307 | 2.11857 | -3.2993 | 0.01644 | 0.04524 | -4.2769 |
| PHLDB1  | -0.5306 | 5.46756 | -3.751  | 0.00951 | 0.02992 | -3.6749 |
| COG2    | -0.5306 | 2.4627  | -5.6294 | 0.00135 | 0.00741 | -1.4842 |
| SNRPD3  | -0.5305 | 5.50093 | -6.6462 | 0.00056 | 0.00401 | -0.4933 |
| CTBP1   | -0.5304 | 4.96789 | -5.7536 | 0.0012  | 0.00682 | -1.3565 |
| PPIAP22 | -0.5304 | 9.36523 | -5.7203 | 0.00124 | 0.00698 | -1.3905 |
| ZFP28   | -0.5301 | 1.59052 | -3.2046 | 0.01851 | 0.04947 | -4.4065 |
| NDUFC1  | -0.5301 | 3.48249 | -4.5333 | 0.00397 | 0.01574 | -2.701  |
| MRGBP   | -0.53   | 5.2536  | -6.0851 | 0.0009  | 0.00554 | -1.0251 |
| GALNT10 | -0.528  | 6.34235 | -3.2994 | 0.01643 | 0.04524 | -4.2767 |
| PSMC4   | -0.5277 | 6.54231 | -5.1388 | 0.00214 | 0.01016 | -2.0083 |
| CAMSAP  | -0.5271 | 5.11626 | -4.088  | 0.00645 | 0.0226  | -3.2444 |
| RASA3   | -0.527  | 3.21096 | -4.4381 | 0.00439 | 0.01692 | -2.8148 |
| PSAP    | -0.5268 | 7.76646 | -4.281  | 0.00521 | 0.01918 | -3.0054 |
| COL27A1 | -0.5267 | 2.6177  | -3.3088 | 0.01624 | 0.04488 | -4.264  |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| ACOT4    | -0.5266 | 0.72975 | -4.0069 | 0.00707 | 0.02412 | -3.3464 |
| FBXL20   | -0.5264 | 1.69314 | -3.4433 | 0.01376 | 0.03974 | -4.0821 |
| SLC2A4R  | -0.5261 | 6.65121 | -3.997  | 0.00715 | 0.02433 | -3.359  |
| CERS5    | -0.5259 | 3.50558 | -4.1293 | 0.00616 | 0.02182 | -3.1928 |
| GSTM2    | -0.5258 | 0.38268 | -3.569  | 0.01181 | 0.03531 | -3.9142 |
| ERP29P1  | -0.5256 | 3.09472 | -5.3046 | 0.00183 | 0.00906 | -1.8276 |
| FAM217B  | -0.5248 | 3.03808 | -4.2445 | 0.00542 | 0.01976 | -3.0501 |
| LARP4    | -0.5247 | 5.02346 | -7.0254 | 0.00042 | 0.00329 | -0.1535 |
| C18orf32 | -0.5237 | 1.22615 | -3.9064 | 0.00793 | 0.02621 | -3.4743 |
| ATXN7L1  | -0.5236 | 1.77544 | -5.4886 | 0.00153 | 0.00806 | -1.6313 |
| MRPL41   | -0.5234 | 5.11779 | -5.2918 | 0.00185 | 0.00915 | -1.8415 |
| RETREG   | -0.5229 | 3.31585 | -6.7824 | 0.0005  | 0.00372 | -0.3695 |
| ZNF197   | -0.5229 | 1.13574 | -4.7029 | 0.00332 | 0.01388 | -2.5017 |
| RMDN1    | -0.5227 | 3.44868 | -5.8621 | 0.00109 | 0.00636 | -1.2465 |
| MTHFS    | -0.5224 | -0.8398 | -3.4703 | 0.01331 | 0.0388  | -4.0458 |
| DNAJC9-  | -0.5218 | 1.35683 | -5.6679 | 0.0013  | 0.00722 | -1.4445 |
| PPP1R14  | -0.5215 | 0.60739 | -5.0982 | 0.00223 | 0.01041 | -2.0531 |
| DDX55    | -0.5215 | 3.60472 | -5.314  | 0.00181 | 0.00901 | -1.8175 |
| C15orf40 | -0.5214 | 1.7104  | -5.2659 | 0.00189 | 0.00932 | -1.8694 |
| ZBTB17   | -0.5214 | 2.95879 | -6.3687 | 0.00071 | 0.00467 | -0.7518 |
| ACSS1    | -0.5208 | 2.35382 | -6.408  | 0.00068 | 0.00456 | -0.7147 |
| SSTR2    | -0.5201 | 1.14098 | -3.2426 | 0.01764 | 0.04769 | -4.3543 |
| KCTD7    | -0.5201 | 1.59624 | -4.3575 | 0.00479 | 0.018   | -2.912  |
| LZTS3    | -0.5197 | 4.77539 | -4.6465 | 0.00352 | 0.01449 | -2.5676 |
| ZNF503   | -0.5195 | 5.50624 | -4.4238 | 0.00446 | 0.01711 | -2.8319 |
| POLR2H   | -0.519  | 5.10425 | -4.5424 | 0.00393 | 0.01563 | -2.6903 |
| KLHL14   | -0.5188 | 3.24456 | -3.7603 | 0.00941 | 0.0297  | -3.6628 |
| TPGS1    | -0.5187 | 1.81381 | -5.5491 | 0.00145 | 0.0078  | -1.5678 |
| ATP7A    | -0.5186 | 1.86841 | -4.9839 | 0.0025  | 0.01127 | -2.1806 |
| VAV2     | -0.5186 | 3.37372 | -4.0506 | 0.00673 | 0.0233  | -3.2914 |
| PI4KAP2  | -0.5183 | 0.61642 | -4.8444 | 0.00287 | 0.01251 | -2.3386 |
| TRMT112  | -0.5181 | 4.77344 | -5.6167 | 0.00136 | 0.00748 | -1.4974 |
| STAG3L3  | -0.5179 | 0.28704 | -3.8817 | 0.00816 | 0.02675 | -3.506  |
| ABCD4    | -0.5169 | 3.4991  | -5.2549 | 0.00191 | 0.00938 | -1.8814 |
| WDR82    | -0.5166 | 6.02945 | -4.4665 | 0.00426 | 0.01657 | -2.7806 |
| REX1BD   | -0.5165 | 4.92345 | -6.0642 | 0.00091 | 0.00559 | -1.0455 |
| ALDH7A1  | -0.5165 | 6.52515 | -5.1277 | 0.00217 | 0.01022 | -2.0206 |
| KIAA1328 | -0.5163 | 0.62171 | -5.045  | 0.00235 | 0.01082 | -2.1123 |
| BAG3     | -0.5163 | 4.49243 | -3.737  | 0.00967 | 0.03029 | -3.6932 |
| DIABLO   | -0.5158 | 0.72682 | -4.3338 | 0.00491 | 0.01837 | -2.9408 |
| ZNF264   | -0.5155 | 2.77151 | -3.4139 | 0.01426 | 0.04076 | -4.1216 |
| HIBCH    | -0.5153 | 2.72094 | -3.734  | 0.0097  | 0.03037 | -3.6971 |
| NT5DC1F  | -0.5152 | 2.98871 | -3.2246 | 0.01805 | 0.04855 | -4.379  |
| TNIP2    | -0.5146 | 3.28565 | -5.4049 | 0.00166 | 0.00851 | -1.7201 |
| COQ2     | -0.5146 | 2.66754 | -4.9798 | 0.00251 | 0.0113  | -2.1852 |
| FUT4     | -0.5143 | 3.29419 | -4.4746 | 0.00422 | 0.01645 | -2.7709 |
| GINM1    | -0.5142 | 3.22171 | -4.693  | 0.00336 | 0.01397 | -2.5133 |
| LPGAT1   | -0.5135 | 3.47651 | -5.0495 | 0.00234 | 0.01079 | -2.1073 |
| RCCD1    | -0.513  | 3.13739 | -5.4349 | 0.00161 | 0.00837 | -1.6882 |
| IMPA1    | -0.5129 | 3.08826 | -5.4661 | 0.00157 | 0.00819 | -1.6551 |
| DNAJB4   | -0.5126 | 3.03956 | -6.2543 | 0.00078 | 0.00499 | -0.8609 |
| ZNF503-A | -0.5119 | 1.72918 | -4.3203 | 0.00499 | 0.01857 | -2.9572 |
| CCDC159  | -0.5117 | 0.47535 | -6.6077 | 0.00058 | 0.00409 | -0.5287 |
| CPE      | -0.5115 | 2.74862 | -4.0218 | 0.00695 | 0.02385 | -3.3276 |
| SFR1     | -0.5111 | 1.67432 | -6.103  | 0.00088 | 0.00548 | -1.0075 |
| SLC30A4  | -0.5106 | 1.20096 | -4.5481 | 0.00391 | 0.01557 | -2.6835 |
| UBE2L4   | -0.5106 | 1.10698 | -3.458  | 0.01351 | 0.03924 | -4.0623 |
| APRT     | -0.5104 | 5.63806 | -4.8907 | 0.00274 | 0.0121  | -2.2859 |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| STUB1    | -0.5102 | 5.44735 | -5.9082 | 0.00105 | 0.00617 | -1.2003 |
| SGTB     | -0.5101 | 2.00494 | -4.4748 | 0.00422 | 0.01645 | -2.7708 |
| MTRES1   | -0.5098 | 1.45112 | -5.7633 | 0.00119 | 0.00677 | -1.3466 |
| ABL1     | -0.5094 | 4.56223 | -4.1504 | 0.00602 | 0.0214  | -3.1665 |
| ZMYM6    | -0.5091 | 2.19546 | -4.9758 | 0.00252 | 0.01133 | -2.1897 |
| KIF7     | -0.5086 | 0.74469 | -3.9976 | 0.00715 | 0.02432 | -3.3582 |
| EID2B    | -0.5086 | 1.91579 | -6.8033 | 0.0005  | 0.00369 | -0.3507 |
| NME1     | -0.5083 | 4.47389 | -4.5649 | 0.00384 | 0.01539 | -2.6636 |
| RPS6KB1  | -0.5079 | 3.0626  | -4.047  | 0.00676 | 0.02334 | -3.2959 |
| BRF1     | -0.5078 | 3.22532 | -3.2814 | 0.01681 | 0.04597 | -4.3013 |
| GALNS    | -0.5077 | 3.04161 | -5.039  | 0.00236 | 0.01086 | -2.1189 |
| SIRT4    | -0.5073 | -1.0309 | -3.7995 | 0.00898 | 0.02872 | -3.6119 |
| NAPG     | -0.5066 | 3.183   | -3.602  | 0.01135 | 0.03429 | -3.8704 |
| YBEY     | -0.5065 | 2.13706 | -3.5401 | 0.01223 | 0.03626 | -3.9525 |
| LSG1     | -0.5063 | 4.39708 | -5.0219 | 0.0024  | 0.01098 | -2.1381 |
| HSP90AA  | -0.5063 | 8.6569  | -3.9598 | 0.00746 | 0.0251  | -3.4062 |
| NR3C1    | -0.5062 | 4.42105 | -3.7435 | 0.00959 | 0.03011 | -3.6847 |
| TRIQQ    | -0.5062 | 1.40289 | -4.2348 | 0.00548 | 0.01991 | -3.0621 |
| CSGALN   | -0.506  | 2.6224  | -4.2739 | 0.00525 | 0.01928 | -3.014  |
| OGFR     | -0.5059 | 4.29533 | -4.2558 | 0.00535 | 0.01958 | -3.0362 |
| USF1     | -0.5059 | 4.68905 | -6.3944 | 0.00069 | 0.00459 | -0.7275 |
| KRT10-A  | -0.5053 | 2.32909 | -3.7573 | 0.00944 | 0.02976 | -3.6667 |
| MDM1     | -0.5048 | 1.85265 | -3.6811 | 0.01033 | 0.03188 | -3.7663 |
| PAXX     | -0.5044 | 4.59485 | -5.5587 | 0.00144 | 0.00774 | -1.5577 |
| TMEM138  | -0.5043 | 4.20133 | -5.5966 | 0.00139 | 0.00758 | -1.5182 |
| ANAPC5   | -0.5041 | 5.3593  | -6.0259 | 0.00095 | 0.00573 | -1.0833 |
| MRPL28   | -0.504  | 4.8732  | -4.5574 | 0.00387 | 0.01544 | -2.6724 |
| EZH1     | -0.5031 | 2.36844 | -3.7242 | 0.00981 | 0.03064 | -3.7099 |
| SAMM50   | -0.5031 | 4.45536 | -6.0573 | 0.00092 | 0.00561 | -1.0523 |
| CRELD2   | -0.5028 | 4.31046 | -5.0026 | 0.00245 | 0.01112 | -2.1596 |
| SLC39A6  | -0.5027 | 4.74445 | -4.6985 | 0.00334 | 0.01391 | -2.5069 |
| PPIA     | -0.5023 | 6.3798  | -5.023  | 0.0024  | 0.01098 | -2.1368 |
| ARMC7    | -0.5008 | 2.07384 | -5.501  | 0.00152 | 0.00801 | -1.6183 |
| NUP85    | -0.5005 | 4.15236 | -6.1492 | 0.00085 | 0.00534 | -0.9625 |
| MIEF1    | 0.50032 | 4.44185 | 3.71567 | 0.00991 | 0.03086 | -3.721  |
| TAP2     | 0.50048 | 3.31387 | 3.63542 | 0.01091 | 0.03323 | -3.8263 |
| NAAA     | 0.501   | 1.62692 | 3.81996 | 0.00877 | 0.02824 | -3.5855 |
| ZBTB45   | 0.50113 | 2.83098 | 3.78497 | 0.00914 | 0.0291  | -3.6308 |
| SIRPAP1  | 0.50169 | 0.80957 | 4.10604 | 0.00632 | 0.02225 | -3.2218 |
| PIP4K2C  | 0.50203 | 4.99829 | 5.0936  | 0.00224 | 0.01044 | -2.0583 |
| WDTC1    | 0.50221 | 4.17941 | 4.95968 | 0.00256 | 0.01147 | -2.2078 |
| NSD3     | 0.50235 | 4.29676 | 5.48394 | 0.00154 | 0.00809 | -1.6363 |
| CREB3L4  | 0.50256 | 2.38285 | 5.51177 | 0.0015  | 0.00796 | -1.607  |
| UBE2H    | 0.50358 | 6.49009 | 5.12585 | 0.00217 | 0.01024 | -2.0226 |
| SLC39A1  | 0.50374 | 3.88069 | 5.69623 | 0.00127 | 0.0071  | -1.4153 |
| WDFY1    | 0.50375 | 2.86507 | 5.00074 | 0.00245 | 0.01114 | -2.1617 |
| DLGAP5   | 0.50409 | 4.98296 | 4.43887 | 0.00439 | 0.01691 | -2.8138 |
| FEM1C    | 0.50417 | 4.04512 | 6.32184 | 0.00073 | 0.0048  | -0.7964 |
| KLRA1P   | 0.50423 | -0.673  | 4.85503 | 0.00284 | 0.01242 | -2.3265 |
| TRAF3IP2 | 0.50424 | 2.33091 | 4.32606 | 0.00496 | 0.01848 | -2.9503 |
| VPS4B    | 0.50443 | 2.54817 | 6.25624 | 0.00078 | 0.00498 | -0.8591 |
| FNBP1L   | 0.5049  | 4.48104 | 5.90614 | 0.00105 | 0.00618 | -1.2023 |
| DFFB     | 0.50605 | 0.64839 | 4.03475 | 0.00685 | 0.02359 | -3.3113 |
| NBEAL1   | 0.507   | 2.19686 | 5.35154 | 0.00175 | 0.00878 | -1.7771 |
| COTL1    | 0.50728 | 6.52261 | 3.57622 | 0.01171 | 0.03509 | -3.9046 |
| RPL12P1  | 0.50743 | 0.9621  | 4.07814 | 0.00652 | 0.02279 | -3.2567 |
| TRAM1L1  | 0.50807 | 0.31009 | 4.21676 | 0.00559 | 0.02022 | -3.0843 |
| STK38L   | 0.5082  | 2.97225 | 4.78934 | 0.00304 | 0.01302 | -2.4017 |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| DCAF4    | 0.50843 | 2.50605 | 4.58529 | 0.00376 | 0.01517 | -2.6395 |
| COMMD7   | 0.5086  | 4.32903 | 3.96858 | 0.00739 | 0.02492 | -3.3951 |
| ATIC     | 0.50888 | 5.08539 | 5.31181 | 0.00181 | 0.00902 | -1.8198 |
| ZNRF3    | 0.50963 | 2.95371 | 4.18188 | 0.00581 | 0.02082 | -3.1274 |
| HNRNPU   | 0.50978 | 4.76634 | 6.34004 | 0.00072 | 0.00475 | -0.779  |
| FKBP5    | 0.50997 | 3.2328  | 3.95279 | 0.00752 | 0.02524 | -3.4151 |
| KCNIP3   | 0.5102  | 1.35288 | 3.7409  | 0.00962 | 0.03019 | -3.6881 |
| PTPRK    | 0.51074 | 4.44868 | 5.98343 | 0.00098 | 0.00587 | -1.1253 |
| OSTF1    | 0.51132 | 2.25699 | 4.99612 | 0.00247 | 0.01117 | -2.1669 |
| ZNF487   | 0.51143 | -0.3903 | 4.54323 | 0.00393 | 0.01563 | -2.6892 |
| SNX25    | 0.51199 | 1.80024 | 5.11033 | 0.0022  | 0.01032 | -2.0397 |
| FARSB    | 0.51214 | 3.82711 | 4.78401 | 0.00306 | 0.01307 | -2.4079 |
| ZRANB3   | 0.51393 | 1.9745  | 5.31178 | 0.00181 | 0.00902 | -1.8199 |
| ZNF432   | 0.51473 | 2.187   | 4.06841 | 0.0066  | 0.02298 | -3.269  |
| EPM2AIP  | 0.5159  | 3.07289 | 6.59902 | 0.00058 | 0.0041  | -0.5367 |
| RITA1    | 0.51601 | 4.60904 | 5.2283  | 0.00196 | 0.00953 | -1.9103 |
| MRPL48F  | 0.51613 | 1.76885 | 5.51293 | 0.0015  | 0.00796 | -1.6058 |
| TPMT     | 0.51647 | 4.37674 | 4.958   | 0.00256 | 0.01149 | -2.2097 |
| MEF2A    | 0.51648 | 3.41919 | 3.20519 | 0.01849 | 0.04944 | -4.4056 |
| MRTFB    | 0.51677 | 3.13506 | 4.58993 | 0.00374 | 0.01511 | -2.634  |
| TRAK1    | 0.51698 | 4.90672 | 4.7574  | 0.00314 | 0.01332 | -2.4386 |
| CARM1    | 0.51783 | 5.07026 | 5.79815 | 0.00116 | 0.00663 | -1.3112 |
| MMUT     | 0.51806 | 3.66626 | 5.36356 | 0.00173 | 0.00873 | -1.7642 |
| MAN2A2   | 0.51814 | 3.04396 | 5.21798 | 0.00198 | 0.0096  | -1.9216 |
| PCNT     | 0.51827 | 4.49205 | 3.73063 | 0.00974 | 0.03047 | -3.7015 |
| RPL12P1  | 0.51857 | 0.19911 | 3.24941 | 0.01749 | 0.04744 | -4.345  |
| ZNF766   | 0.5196  | 2.98315 | 4.50416 | 0.00409 | 0.01607 | -2.7357 |
| MAPK14   | 0.51985 | 4.45961 | 6.91186 | 0.00045 | 0.00347 | -0.2537 |
| LRRRC49  | 0.51986 | 0.24563 | 3.92239 | 0.00779 | 0.02586 | -3.4539 |
| AKR1A1   | 0.51998 | 3.559   | 3.84654 | 0.0085  | 0.02762 | -3.5512 |
| REXO2    | 0.52061 | 5.17821 | 6.70669 | 0.00053 | 0.00387 | -0.4381 |
| CPT1A    | 0.52119 | 4.50335 | 5.64488 | 0.00133 | 0.00733 | -1.4682 |
| PNPLA6   | 0.52137 | 4.65749 | 6.0325  | 0.00094 | 0.00571 | -1.0767 |
| GOLGA2   | 0.52164 | 4.36776 | 3.28293 | 0.01678 | 0.04593 | -4.2992 |
| CSNK2B   | 0.52179 | 3.01397 | 3.97204 | 0.00736 | 0.02484 | -3.3907 |
| NOSIP    | 0.52282 | 4.97146 | 5.9896  | 0.00098 | 0.00585 | -1.1192 |
| LARP1B   | 0.523   | 3.17209 | 3.76623 | 0.00934 | 0.02955 | -3.6551 |
| CCDC149  | 0.52349 | 1.55356 | 4.03633 | 0.00684 | 0.02356 | -3.3093 |
| NOP9     | 0.52364 | 2.66066 | 3.36393 | 0.01517 | 0.04261 | -4.1891 |
| SHTN1    | 0.52378 | 4.09253 | 4.92772 | 0.00264 | 0.01175 | -2.2439 |
| DPP3P2   | 0.52416 | 0.01893 | 3.4867  | 0.01305 | 0.03817 | -4.0238 |
| PLA2G12  | 0.52497 | 1.97623 | 3.51145 | 0.01266 | 0.03731 | -3.9908 |
| EIF4BP7  | 0.52508 | 4.7267  | 4.71304 | 0.00329 | 0.01378 | -2.4899 |
| SMIM13   | 0.52545 | 4.37968 | 4.32771 | 0.00495 | 0.01846 | -2.9483 |
| NEK2     | 0.52548 | 2.30904 | 3.23964 | 0.01771 | 0.04783 | -4.3584 |
| ZNF770   | 0.52553 | 4.02555 | 5.88681 | 0.00107 | 0.00626 | -1.2217 |
| MAST3    | 0.52566 | 2.12434 | 5.35879 | 0.00173 | 0.00876 | -1.7694 |
| ASL      | 0.52578 | 2.48559 | 5.5484  | 0.00145 | 0.0078  | -1.5686 |
| GALNT7   | 0.52578 | 3.53581 | 6.15516 | 0.00085 | 0.00532 | -0.9567 |
| FCHO1    | 0.52595 | 2.28344 | 6.09412 | 0.00089 | 0.00551 | -1.0162 |
| RPS6KL1  | 0.52597 | 1.75204 | 5.58373 | 0.0014  | 0.00763 | -1.5317 |
| ZNF468   | 0.52634 | 2.72989 | 5.29645 | 0.00184 | 0.00912 | -1.8364 |
| CUL7     | 0.52666 | 3.63348 | 5.99658 | 0.00097 | 0.00583 | -1.1122 |
| RPS5     | 0.52669 | 7.1771  | 6.05134 | 0.00092 | 0.00564 | -1.0582 |
| LINC0298 | 0.52679 | 1.3591  | 3.37911 | 0.01489 | 0.04203 | -4.1686 |
| KCMF1    | 0.52727 | 4.89639 | 5.29368 | 0.00184 | 0.00914 | -1.8394 |
| GABPAP   | 0.52744 | 3.05804 | 3.84453 | 0.00852 | 0.02763 | -3.5538 |
| RPS11P5  | 0.52771 | 7.79749 | 6.02313 | 0.00095 | 0.00574 | -1.086  |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| ARL3     | 0.52783 | 2.17019 | 4.23709 | 0.00546 | 0.01986 | -3.0592 |
| SGMS2    | 0.52816 | 2.38298 | 3.703   | 0.01006 | 0.03122 | -3.7376 |
| PTGES3L  | 0.52821 | -2.2797 | 3.58912 | 0.01153 | 0.03467 | -3.8875 |
| ACTR3    | 0.52827 | 6.09254 | 5.59425 | 0.00139 | 0.00758 | -1.5207 |
| MAD2L1E  | 0.52836 | 3.03325 | 5.66157 | 0.00131 | 0.00725 | -1.4509 |
| GPANK1   | 0.52887 | 2.70293 | 4.60198 | 0.00369 | 0.01498 | -2.6198 |
| SNHG12   | 0.52895 | 3.73016 | 5.15617 | 0.00211 | 0.01002 | -1.9892 |
| SLC35F5  | 0.52898 | 3.97875 | 4.37872 | 0.00468 | 0.0177  | -2.8863 |
| HERPUD   | 0.52994 | 3.18529 | 6.36636 | 0.00071 | 0.00467 | -0.7541 |
| PPP1R3C  | 0.53016 | 0.30586 | 3.4249  | 0.01407 | 0.04038 | -4.1068 |
| TMCO4    | 0.53095 | 2.68461 | 4.40912 | 0.00453 | 0.01729 | -2.8496 |
| SMCHD1   | 0.53099 | 4.12306 | 5.13533 | 0.00215 | 0.01018 | -2.0122 |
| C10orf95 | 0.53103 | 1.40867 | 4.21312 | 0.00561 | 0.02027 | -3.0888 |
| UBA2     | 0.53237 | 5.39016 | 6.70249 | 0.00054 | 0.00388 | -0.442  |
| ADAM10   | 0.53256 | 5.11752 | 5.78838 | 0.00117 | 0.00666 | -1.3211 |
| TJP1     | 0.53288 | 5.25277 | 5.80926 | 0.00114 | 0.00659 | -1.2999 |
| PHF11    | 0.53294 | 0.76891 | 3.24441 | 0.0176  | 0.04765 | -4.3518 |
| EIF3LP3  | 0.53308 | 2.23145 | 3.66373 | 0.01054 | 0.03239 | -3.7891 |
| NCOA4    | 0.53327 | 6.51763 | 5.86836 | 0.00109 | 0.00634 | -1.2402 |
| ACTN4    | 0.53331 | 8.10627 | 3.30016 | 0.01642 | 0.04523 | -4.2757 |
| MRPL14   | 0.53354 | 3.92106 | 6.70604 | 0.00054 | 0.00387 | -0.4387 |
| MED25    | 0.53398 | 4.48958 | 7.09931 | 0.00039 | 0.00315 | -0.0889 |
| BAG5     | 0.53417 | 4.86619 | 6.94284 | 0.00044 | 0.00342 | -0.2262 |
| GXYLT1   | 0.53489 | 3.50341 | 6.33037 | 0.00073 | 0.00478 | -0.7882 |
| HMGB3    | 0.53507 | 4.86984 | 4.99035 | 0.00248 | 0.01123 | -2.1734 |
| WSB2     | 0.53538 | 4.74827 | 3.76234 | 0.00938 | 0.02965 | -3.6602 |
| OFD1     | 0.53573 | 2.39352 | 4.59984 | 0.0037  | 0.015   | -2.6223 |
| SIRT5    | 0.53636 | 2.81865 | 3.96694 | 0.0074  | 0.02495 | -3.3971 |
| GTPBP1   | 0.53649 | 2.57361 | 3.72498 | 0.0098  | 0.03061 | -3.7088 |
| LENG8-A  | 0.53672 | 1.01029 | 5.19046 | 0.00204 | 0.0098  | -1.9516 |
| OXR1     | 0.53719 | 4.77242 | 5.03669 | 0.00237 | 0.01087 | -2.1215 |
| ARHGAP   | 0.53744 | 4.47389 | 6.24063 | 0.00079 | 0.00504 | -0.8741 |
| UBAP1    | 0.53799 | 3.82381 | 6.35626 | 0.00071 | 0.0047  | -0.7636 |
| QTRT1    | 0.53822 | 4.31422 | 5.86445 | 0.00109 | 0.00635 | -1.2442 |
| LINC0113 | 0.53843 | 0.46137 | 5.1338  | 0.00215 | 0.01019 | -2.0138 |
| PTGFRN   | 0.53845 | 3.72848 | 3.35704 | 0.0153  | 0.04288 | -4.1985 |
| ANKLE2   | 0.53848 | 4.29451 | 6.67668 | 0.00055 | 0.00394 | -0.4655 |
| ERI2     | 0.53878 | 2.28502 | 4.51028 | 0.00407 | 0.016   | -2.7284 |
| CHST15   | 0.53911 | 2.91739 | 4.12808 | 0.00617 | 0.02183 | -3.1943 |
| SRD5A1F  | 0.53918 | 1.78516 | 5.09502 | 0.00224 | 0.01043 | -2.0567 |
| MYH10    | 0.53934 | 6.11206 | 5.33688 | 0.00177 | 0.00887 | -1.7929 |
| USP33    | 0.53937 | 5.36565 | 6.87585 | 0.00047 | 0.00354 | -0.2857 |
| KRBOX5   | 0.54092 | 2.09435 | 5.28397 | 0.00186 | 0.00919 | -1.8499 |
| SEMA4C   | 0.5411  | 3.29044 | 4.1876  | 0.00577 | 0.02072 | -3.1203 |
| GOT1     | 0.54128 | 4.67295 | 3.60384 | 0.01133 | 0.03424 | -3.868  |
| DEGS1    | 0.54135 | 5.43154 | 5.25527 | 0.00191 | 0.00938 | -1.881  |
| SCD      | 0.54152 | 6.51997 | 3.68514 | 0.01028 | 0.03175 | -3.761  |
| RANBP9   | 0.54178 | 5.04576 | 4.68875 | 0.00337 | 0.01401 | -2.5182 |
| EPN1     | 0.54185 | 6.4421  | 6.54441 | 0.00061 | 0.00423 | -0.5872 |
| NFKBIL1  | 0.54207 | 2.62447 | 5.24428 | 0.00193 | 0.00945 | -1.8929 |
| USP4     | 0.54208 | 3.26571 | 4.1447  | 0.00605 | 0.02152 | -3.1736 |
| TMEM30A  | 0.54249 | 6.29422 | 3.80876 | 0.00889 | 0.02848 | -3.6    |
| ZNRF2P2  | 0.54258 | -1.4669 | 3.4363  | 0.01388 | 0.03997 | -4.0915 |
| SNX18    | 0.54278 | 3.09938 | 4.39143 | 0.00462 | 0.01752 | -2.871  |
| ZNF436   | 0.54282 | 1.75567 | 6.09033 | 0.00089 | 0.00552 | -1.0199 |
| ARL6IP1F | 0.54406 | 1.23047 | 4.70261 | 0.00332 | 0.01388 | -2.5021 |
| COPS7A   | 0.5444  | 3.54585 | 6.24684 | 0.00078 | 0.00502 | -0.8681 |
| BAIAP2L  | 0.54451 | 5.08474 | 4.6626  | 0.00346 | 0.0143  | -2.5487 |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| ARID2    | 0.54472 | 4.00216 | 6.92573 | 0.00045 | 0.00345 | -0.2414 |
| OARD1    | 0.54501 | 1.58496 | 5.18569 | 0.00205 | 0.00982 | -1.9568 |
| SPOPL    | 0.54676 | 2.72292 | 6.27243 | 0.00076 | 0.00494 | -0.8435 |
| KIF22    | 0.54788 | 5.46023 | 6.59911 | 0.00058 | 0.0041  | -0.5366 |
| TMSB4X   | 0.54808 | 2.47682 | 5.0721  | 0.00229 | 0.01059 | -2.0821 |
| PTENP1   | 0.5487  | 4.31742 | 5.52504 | 0.00148 | 0.00791 | -1.593  |
| SIMC1    | 0.55021 | 3.03981 | 6.09626 | 0.00089 | 0.00551 | -1.0141 |
| ZNF283   | 0.55059 | 1.35956 | 5.09561 | 0.00223 | 0.01043 | -2.056  |
| CNOT9    | 0.55067 | 4.16468 | 5.54347 | 0.00146 | 0.00781 | -1.5737 |
| ZBTB42   | 0.55097 | 1.79243 | 3.59704 | 0.01142 | 0.03444 | -3.877  |
| PBX2P1   | 0.55118 | 3.06604 | 4.07788 | 0.00653 | 0.02279 | -3.2571 |
| RPL28    | 0.55138 | 7.70594 | 6.11556 | 0.00087 | 0.00545 | -0.9952 |
| DNAI4    | 0.55147 | 0.13134 | 3.99607 | 0.00716 | 0.02434 | -3.3602 |
| MRPL48   | 0.55168 | 1.87025 | 5.57337 | 0.00142 | 0.00768 | -1.5425 |
| PABIR2   | 0.55192 | 4.67414 | 5.38025 | 0.0017  | 0.00865 | -1.7464 |
| CRY1     | 0.55239 | 3.06937 | 6.31189 | 0.00074 | 0.00483 | -0.8058 |
| SNRPC    | 0.55275 | 3.96002 | 3.66672 | 0.01051 | 0.03232 | -3.7851 |
| KATNIP   | 0.55277 | 3.06362 | 7.11783 | 0.00039 | 0.00313 | -0.0728 |
| PRR14L   | 0.55313 | 3.60205 | 7.03965 | 0.00041 | 0.00326 | -0.141  |
| PPP2R1A  | 0.5536  | 7.00048 | 6.80584 | 0.00049 | 0.00368 | -0.3484 |
| NSUN5P1  | 0.55413 | 2.61934 | 3.72675 | 0.00978 | 0.03057 | -3.7065 |
| OSTF1P1  | 0.55437 | 1.91728 | 5.41298 | 0.00165 | 0.00848 | -1.7115 |
| SKIC2    | 0.55566 | 4.92752 | 5.58541 | 0.0014  | 0.00762 | -1.5299 |
| C18orf25 | 0.55608 | 4.30203 | 4.27366 | 0.00525 | 0.01928 | -3.0143 |
| KAZN     | 0.55627 | 5.02268 | 3.85158 | 0.00845 | 0.02749 | -3.5447 |
| EXOC4    | 0.55645 | 6.37607 | 4.538   | 0.00395 | 0.01568 | -2.6954 |
| UBE2J1   | 0.55658 | 4.60489 | 5.24674 | 0.00193 | 0.00943 | -1.8903 |
| PCDHGC   | 0.55683 | 2.91508 | 4.36719 | 0.00474 | 0.0179  | -2.9003 |
| ACTN1    | 0.55685 | 6.88373 | 4.44788 | 0.00435 | 0.01678 | -2.803  |
| NPDC1    | 0.5569  | 2.94268 | 7.09961 | 0.00039 | 0.00315 | -0.0887 |
| ARSK     | 0.55753 | 1.47504 | 6.2617  | 0.00077 | 0.00498 | -0.8538 |
| TBC1D14  | 0.55758 | 3.29715 | 5.8483  | 0.00111 | 0.00641 | -1.2604 |
| GSTP1    | 0.55777 | 8.57304 | 4.00501 | 0.00709 | 0.02416 | -3.3489 |
| FBLIM1   | 0.55869 | 5.63982 | 5.92654 | 0.00103 | 0.0061  | -1.1819 |
| RCOR1    | 0.55919 | 4.42409 | 5.9003  | 0.00106 | 0.0062  | -1.2082 |
| PRR12    | 0.55921 | 3.84662 | 3.22419 | 0.01806 | 0.04857 | -4.3795 |
| HLCS     | 0.55944 | 3.927   | 6.04928 | 0.00093 | 0.00565 | -1.0602 |
| MED20    | 0.55944 | 3.0894  | 4.78272 | 0.00306 | 0.01308 | -2.4094 |
| PTPN18   | 0.55996 | 2.92095 | 7.01111 | 0.00042 | 0.00331 | -0.166  |
| ROGDI    | 0.56031 | 1.99426 | 6.67653 | 0.00055 | 0.00394 | -0.4656 |
| MRPS18A  | 0.56086 | 3.41319 | 5.50489 | 0.00151 | 0.008   | -1.6142 |
| ST7-AS1  | 0.56116 | 0.45069 | 3.46923 | 0.01333 | 0.03884 | -4.0473 |
| UPF3AP2  | 0.56146 | 1.94488 | 3.79589 | 0.00902 | 0.02881 | -3.6166 |
| C6orf62  | 0.5617  | 6.21414 | 7.00045 | 0.00042 | 0.00333 | -0.1754 |
| MAP4K5   | 0.56208 | 4.01532 | 6.14628 | 0.00085 | 0.00535 | -0.9653 |
| MCUR1P   | 0.56286 | 4.08564 | 5.33374 | 0.00178 | 0.00889 | -1.7962 |
| ABCF1    | 0.5632  | 5.17902 | 5.48873 | 0.00153 | 0.00806 | -1.6312 |
| PDCD2L   | 0.56452 | 2.15425 | 5.2179  | 0.00198 | 0.0096  | -1.9216 |
| ARPC2    | 0.56503 | 5.96423 | 6.51522 | 0.00062 | 0.00429 | -0.6143 |
| TES      | 0.56519 | 6.11597 | 4.02844 | 0.0069  | 0.02372 | -3.3193 |
| CSNK1E   | 0.56556 | 4.77032 | 4.91402 | 0.00268 | 0.01189 | -2.2594 |
| AK3      | 0.56637 | 4.2787  | 4.54903 | 0.0039  | 0.01556 | -2.6824 |
| CARMIL1  | 0.56704 | 4.90186 | 4.52683 | 0.00399 | 0.01583 | -2.7087 |
| RPS11    | 0.56903 | 6.88094 | 4.83302 | 0.00291 | 0.01262 | -2.3516 |
| TMEM168  | 0.57071 | 3.2192  | 4.17254 | 0.00587 | 0.02099 | -3.139  |
| HSPB1P1  | 0.57087 | 3.70261 | 3.67865 | 0.01036 | 0.03195 | -3.7695 |
| HIVEP1   | 0.57114 | 3.46971 | 6.99078 | 0.00043 | 0.00334 | -0.1839 |
| ZNF618   | 0.57117 | 3.95243 | 4.7625  | 0.00312 | 0.01327 | -2.4327 |

|          |         |         |         |         |         |         |
|----------|---------|---------|---------|---------|---------|---------|
| TTC3     | 0.57138 | 5.54247 | 5.43366 | 0.00161 | 0.00837 | -1.6895 |
| ELF4     | 0.57213 | 3.93532 | 5.99931 | 0.00097 | 0.00582 | -1.1095 |
| LDLR     | 0.57219 | 5.89226 | 5.57172 | 0.00142 | 0.00769 | -1.5442 |
| NIBAN2   | 0.57243 | 6.10382 | 5.8103  | 0.00114 | 0.00659 | -1.2989 |
| LHX6     | 0.57252 | 0.02532 | 3.5118  | 0.01266 | 0.0373  | -3.9903 |
| COBLL1   | 0.57262 | 2.46171 | 7.15961 | 0.00038 | 0.00307 | -0.0367 |
| CCNA2    | 0.57283 | 5.06453 | 4.46054 | 0.00429 | 0.01664 | -2.7878 |
| GCDH     | 0.57313 | 3.20519 | 4.91015 | 0.00269 | 0.01193 | -2.2638 |
| GOLPH3   | 0.57349 | 4.66457 | 5.37764 | 0.0017  | 0.00866 | -1.7492 |
| ZNF544   | 0.57418 | 3.00897 | 5.13095 | 0.00216 | 0.0102  | -2.017  |
| STRAP    | 0.57487 | 5.38552 | 6.20831 | 0.00081 | 0.00514 | -0.9052 |
| EEF1E1P  | 0.57577 | 1.60527 | 4.10515 | 0.00633 | 0.02226 | -3.2229 |
| ALDH4A1  | 0.57591 | 1.36471 | 3.89512 | 0.00804 | 0.02645 | -3.4888 |
| LIN54    | 0.57678 | 2.73523 | 6.65969 | 0.00056 | 0.00398 | -0.481  |
| FLII     | 0.57693 | 5.62507 | 4.87357 | 0.00279 | 0.01226 | -2.3053 |
| YWHAZP   | 0.57797 | 3.30658 | 4.9368  | 0.00262 | 0.01167 | -2.2336 |
| NCS1     | 0.57841 | 4.19454 | 5.54109 | 0.00146 | 0.00782 | -1.5762 |
| LEMD2    | 0.57844 | 4.73868 | 4.88801 | 0.00275 | 0.01212 | -2.2889 |
| YWHAH    | 0.57863 | 5.73408 | 4.45515 | 0.00431 | 0.01669 | -2.7943 |
| ARRDC2   | 0.57879 | 1.74135 | 5.39898 | 0.00167 | 0.00853 | -1.7264 |
| MRS2     | 0.57884 | 4.64488 | 6.0066  | 0.00096 | 0.00579 | -1.1023 |
| PPFIA3   | 0.57931 | 2.80015 | 4.76786 | 0.00311 | 0.01324 | -2.4265 |
| OPN3     | 0.57981 | 2.50998 | 4.07124 | 0.00657 | 0.02294 | -3.2654 |
| CITED2   | 0.58004 | 4.79224 | 5.15928 | 0.0021  | 0.01    | -1.9858 |
| DSTNP2   | 0.58133 | 3.24431 | 3.81431 | 0.00883 | 0.02837 | -3.5928 |
| DRG1P1   | 0.58152 | 3.83866 | 3.50423 | 0.01277 | 0.03757 | -4.0004 |
| TAGLN2P  | 0.58157 | 6.67335 | 4.35653 | 0.0048  | 0.01802 | -2.9132 |
| SLC4A7   | 0.58159 | 3.53811 | 3.22561 | 0.01802 | 0.04852 | -4.3776 |
| CTSH     | 0.58176 | 2.25417 | 4.31975 | 0.00499 | 0.01858 | -2.958  |
| BYSL     | 0.58334 | 3.56984 | 3.54209 | 0.0122  | 0.0362  | -3.9499 |
| YWHAZP   | 0.58593 | 5.13055 | 4.79943 | 0.00301 | 0.01293 | -2.3901 |
| SLC25A2  | 0.58632 | 2.57096 | 3.59201 | 0.01149 | 0.03458 | -3.8837 |
| EIF3LP1  | 0.5865  | 3.81586 | 5.0615  | 0.00231 | 0.01067 | -2.0939 |
| ERV3-1   | 0.58669 | 0.00141 | 3.67064 | 0.01046 | 0.03219 | -3.78   |
| ZCCHC2   | 0.58673 | 0.81882 | 3.82214 | 0.00875 | 0.02819 | -3.5827 |
| PRKCIP1  | 0.58687 | 5.09882 | 5.10299 | 0.00222 | 0.01038 | -2.0479 |
| TBC1D23  | 0.58696 | 3.33657 | 8.04386 | 0.0002  | 0.00205 | 0.69046 |
| XRCC5    | 0.58752 | 6.5061  | 5.47642 | 0.00155 | 0.00813 | -1.6442 |
| LINC0298 | 0.58845 | 0.45745 | 3.28059 | 0.01682 | 0.04599 | -4.3024 |
| OSER1    | 0.58986 | 4.5406  | 6.07588 | 0.0009  | 0.00556 | -1.0341 |
| GOLGA2   | 0.59    | 0.52876 | 5.42615 | 0.00163 | 0.0084  | -1.6975 |
| PRPF4BP  | 0.59009 | 1.64403 | 5.80326 | 0.00115 | 0.00662 | -1.306  |
| CRIM1    | 0.5907  | 6.04314 | 4.35431 | 0.00481 | 0.01805 | -2.9159 |
| CAPN2    | 0.59118 | 5.5728  | 3.36771 | 0.0151  | 0.0425  | -4.184  |
| LRRK1    | 0.59126 | 1.44723 | 3.36395 | 0.01517 | 0.04261 | -4.1891 |
| ANAPC15  | 0.59143 | 3.79774 | 6.0234  | 0.00095 | 0.00574 | -1.0857 |
| WDR25    | 0.59188 | 1.5426  | 3.8318  | 0.00865 | 0.02796 | -3.5702 |
| GIPC1    | 0.59198 | 5.91851 | 7.41959 | 0.00031 | 0.00269 | 0.18455 |
| LINC0066 | 0.59199 | 1.87682 | 3.31127 | 0.01619 | 0.04478 | -4.2606 |
| ZFAND3   | 0.59201 | 5.1013  | 4.10439 | 0.00633 | 0.02227 | -3.2239 |
| NT5E     | 0.59232 | 4.21457 | 4.47825 | 0.00421 | 0.01641 | -2.7666 |
| SLC38A1  | 0.59247 | 7.29854 | 4.99006 | 0.00248 | 0.01123 | -2.1737 |
| PSPC1    | 0.5929  | 3.6039  | 6.83118 | 0.00048 | 0.00363 | -0.3257 |
| RPS5P8   | 0.59379 | 4.4995  | 6.25616 | 0.00078 | 0.00498 | -0.8591 |
| RANBP6   | 0.59387 | 4.86103 | 5.20121 | 0.00202 | 0.00972 | -1.9399 |
| FOXP4    | 0.59422 | 3.69235 | 4.23424 | 0.00548 | 0.01991 | -3.0627 |
| LSM2     | 0.59459 | 3.73169 | 6.27876 | 0.00076 | 0.00492 | -0.8375 |
| MRPS18B  | 0.59511 | 4.22725 | 5.35791 | 0.00173 | 0.00876 | -1.7703 |

|         |         |         |         |         |         |         |
|---------|---------|---------|---------|---------|---------|---------|
| AGAP1   | 0.59577 | 4.25127 | 6.6398  | 0.00056 | 0.00402 | -0.4992 |
| TBCC    | 0.59801 | 3.56973 | 5.99714 | 0.00097 | 0.00583 | -1.1117 |
| RPL13AP | 0.59807 | 1.46623 | 4.12151 | 0.00621 | 0.02196 | -3.2025 |
| FBXW9   | 0.59853 | 2.29606 | 4.4098  | 0.00453 | 0.01728 | -2.8488 |
| WVOX    | 0.59963 | 2.89886 | 5.10029 | 0.00222 | 0.0104  | -2.0508 |
| ABHD17C | 0.59963 | 1.57655 | 5.45652 | 0.00158 | 0.00825 | -1.6653 |
| ENAH    | 0.59965 | 6.06883 | 6.99362 | 0.00043 | 0.00334 | -0.1814 |
| ACTR3B  | 0.60003 | 2.2507  | 4.57991 | 0.00378 | 0.01523 | -2.6458 |
| FBXO46  | 0.60038 | 3.25421 | 6.95843 | 0.00044 | 0.00339 | -0.2124 |
| TBC1D7  | 0.60168 | 4.41915 | 4.22565 | 0.00553 | 0.02005 | -3.0733 |
| ARHGEF  | 0.6017  | 4.5095  | 5.55416 | 0.00144 | 0.00777 | -1.5625 |
| PBX2    | 0.6031  | 3.32317 | 4.24711 | 0.0054  | 0.01973 | -3.0469 |
| RFX3    | 0.60342 | 2.27425 | 3.85858 | 0.00839 | 0.02733 | -3.5357 |
| PAX6    | 0.60423 | 1.39249 | 4.85042 | 0.00286 | 0.01246 | -2.3317 |
| ZYX     | 0.60437 | 6.8094  | 4.76726 | 0.00311 | 0.01324 | -2.4272 |
| DCDC2   | 0.6044  | 5.81796 | 3.45759 | 0.01352 | 0.03926 | -4.0629 |
| SEPTIN7 | 0.60495 | 0.55436 | 3.33115 | 0.0158  | 0.04396 | -4.2336 |
| BDH1    | 0.60523 | 3.42472 | 4.63353 | 0.00357 | 0.01463 | -2.5827 |
| SLC35E1 | 0.60686 | 4.60461 | 7.45649 | 0.0003  | 0.00266 | 0.21543 |
| KDM1B   | 0.60755 | 3.75336 | 3.7171  | 0.0099  | 0.03085 | -3.7191 |
| UBE2MP  | 0.60759 | 6.46326 | 7.21699 | 0.00036 | 0.00296 | 0.0127  |
| DAG1    | 0.60784 | 5.097   | 6.44825 | 0.00066 | 0.00446 | -0.6769 |
| DEPDC5  | 0.60792 | 1.80926 | 5.04884 | 0.00234 | 0.01079 | -2.108  |
| RPL10AP | 0.60865 | 3.97317 | 6.91215 | 0.00045 | 0.00347 | -0.2534 |
| TRAF4   | 0.609   | 4.64599 | 7.2424  | 0.00035 | 0.00293 | 0.03447 |
| SPART   | 0.60974 | 3.81853 | 6.58885 | 0.00059 | 0.00413 | -0.5461 |
| ZBTB33  | 0.60992 | 3.95905 | 5.50166 | 0.00152 | 0.00801 | -1.6176 |
| WWC1    | 0.61034 | 6.04531 | 3.39891 | 0.01453 | 0.04128 | -4.1418 |
| LAPTM4B | 0.61117 | 3.93046 | 4.76895 | 0.0031  | 0.01323 | -2.4252 |
| IL6STP1 | 0.6112  | 0.98584 | 3.34462 | 0.01554 | 0.04341 | -4.2153 |
| B3GNT7  | 0.61233 | 0.37874 | 3.42544 | 0.01406 | 0.04037 | -4.1061 |
| LSM14A  | 0.61249 | 5.68313 | 6.66777 | 0.00055 | 0.00396 | -0.4736 |
| MAP3K14 | 0.61399 | -0.6172 | 3.92149 | 0.0078  | 0.02588 | -3.4551 |
| GNL1    | 0.61418 | 4.5517  | 7.70485 | 0.00025 | 0.00238 | 0.42001 |
| FGFR10B | 0.6142  | 2.97235 | 5.54372 | 0.00146 | 0.00781 | -1.5735 |
| GAB1    | 0.61481 | 1.37771 | 4.04548 | 0.00677 | 0.02338 | -3.2978 |
| HSPBP1  | 0.61512 | 5.02741 | 5.8958  | 0.00106 | 0.00622 | -1.2127 |
| FBXO41  | 0.61518 | 0.78546 | 4.02693 | 0.00691 | 0.02375 | -3.3212 |
| GCAT    | 0.61571 | 3.499   | 6.96892 | 0.00043 | 0.00337 | -0.2031 |
| PEX6    | 0.61589 | 3.4971  | 6.98401 | 0.00043 | 0.00335 | -0.1898 |
| ZNF765  | 0.61591 | 2.54453 | 5.64713 | 0.00133 | 0.00732 | -1.4659 |
| HMGNA4  | 0.61594 | 4.5652  | 5.16411 | 0.00209 | 0.00997 | -1.9805 |
| PLXNA3  | 0.61688 | 3.02345 | 6.62118 | 0.00057 | 0.00406 | -0.5163 |
| RNF5P1  | 0.61712 | 4.47269 | 3.70543 | 0.01003 | 0.03116 | -3.7344 |
| NBL1    | 0.61728 | 1.1914  | 3.69493 | 0.01016 | 0.03144 | -3.7481 |
| ZNF554  | 0.61729 | 0.64972 | 4.57635 | 0.00379 | 0.01525 | -2.65   |
| SEPTIN8 | 0.61931 | 5.37531 | 3.25625 | 0.01734 | 0.04712 | -4.3357 |
| DERL3   | 0.61955 | 0.60566 | 3.93776 | 0.00765 | 0.02559 | -3.4343 |
| LRRC8B  | 0.61965 | 2.75436 | 6.99924 | 0.00042 | 0.00333 | -0.1764 |
| PHF21B  | 0.61969 | -1.1112 | 3.53145 | 0.01236 | 0.03656 | -3.9641 |
| PUS7L   | 0.61976 | 3.31243 | 7.16835 | 0.00037 | 0.00305 | -0.0291 |
| UTP14C  | 0.62    | 3.27992 | 8.29039 | 0.00017 | 0.00184 | 0.88106 |
| MEMO1   | 0.62085 | -0.0317 | 4.20926 | 0.00564 | 0.02033 | -3.0935 |
| BRME1   | 0.62087 | 1.30681 | 3.54349 | 0.01218 | 0.03615 | -3.9481 |
| MRPL57  | 0.6216  | 4.33543 | 6.82722 | 0.00049 | 0.00364 | -0.3292 |
| FBXW11B | 0.62175 | 2.99519 | 6.97573 | 0.00043 | 0.00336 | -0.1971 |
| TINAGL1 | 0.62294 | 6.15409 | 3.79032 | 0.00908 | 0.02894 | -3.6238 |
| DLG3    | 0.6231  | 2.72499 | 4.48688 | 0.00417 | 0.01631 | -2.7563 |

|         |         |         |         |         |         |         |
|---------|---------|---------|---------|---------|---------|---------|
| PRKCI   | 0.62423 | 4.70124 | 5.35431 | 0.00174 | 0.00877 | -1.7742 |
| BAG6    | 0.62527 | 6.29979 | 8.37278 | 0.00016 | 0.00178 | 0.94367 |
| PCDHB13 | 0.62542 | 1.17104 | 4.13212 | 0.00614 | 0.02176 | -3.1892 |
| GNAZ    | 0.62562 | 1.30151 | 3.22622 | 0.01801 | 0.0485  | -4.3768 |
| PHLDB2  | 0.62577 | 5.3773  | 3.7456  | 0.00957 | 0.03005 | -3.682  |
| WDFY2   | 0.62608 | 1.24322 | 3.97364 | 0.00735 | 0.02481 | -3.3886 |
| SCD5    | 0.62774 | 3.03488 | 3.72817 | 0.00977 | 0.03054 | -3.7047 |
| USP49   | 0.62858 | 1.68535 | 6.0955  | 0.00089 | 0.00551 | -1.0148 |
| CARS2   | 0.62859 | 4.15214 | 4.51381 | 0.00405 | 0.01597 | -2.7242 |
| EEF1E1  | 0.62861 | 2.84995 | 5.36808 | 0.00172 | 0.00871 | -1.7594 |
| FCSK    | 0.6289  | 1.90444 | 7.85102 | 0.00023 | 0.00222 | 0.53784 |
| RPL7P22 | 0.62892 | 1.56997 | 3.24312 | 0.01763 | 0.04768 | -4.3536 |
| FOXO3   | 0.62903 | 3.08628 | 5.59994 | 0.00138 | 0.00756 | -1.5148 |
| COMMD6  | 0.62941 | 2.44393 | 7.79521 | 0.00024 | 0.00228 | 0.49308 |
| TRIM38  | 0.62953 | 4.22143 | 3.29021 | 0.01662 | 0.04558 | -4.2893 |
| SEPTIN2 | 0.62979 | 0.96378 | 3.85947 | 0.00838 | 0.02731 | -3.5346 |
| PIK3AP1 | 0.63072 | 2.4948  | 4.0701  | 0.00658 | 0.02296 | -3.2668 |
| MRPL44  | 0.63075 | 2.18107 | 7.4187  | 0.00031 | 0.00269 | 0.1838  |
| EXT1    | 0.63212 | 4.48242 | 5.62027 | 0.00136 | 0.00746 | -1.4937 |
| FKBP4   | 0.6328  | 5.77147 | 6.09168 | 0.00089 | 0.00552 | -1.0186 |
| UBE4B   | 0.63341 | 4.75208 | 7.78738 | 0.00024 | 0.00229 | 0.48677 |
| SPRY1   | 0.63375 | 3.1891  | 4.51291 | 0.00405 | 0.01598 | -2.7253 |
| ZSCAN22 | 0.63455 | 1.57643 | 7.23964 | 0.00035 | 0.00293 | 0.03211 |
| TRIM8   | 0.63469 | 3.04581 | 4.55543 | 0.00388 | 0.01547 | -2.6748 |
| ZNF451  | 0.63534 | 3.49023 | 5.07087 | 0.00229 | 0.0106  | -2.0835 |
| MPST    | 0.63624 | 4.06939 | 6.97798 | 0.00043 | 0.00336 | -0.1952 |
| DLX6    | 0.63646 | 2.76926 | 4.25646 | 0.00535 | 0.01957 | -3.0354 |
| ZNF613  | 0.63676 | 0.80017 | 5.48813 | 0.00153 | 0.00806 | -1.6319 |
| DBT     | 0.63717 | 2.29755 | 6.79245 | 0.0005  | 0.0037  | -0.3605 |
| ARHGAP  | 0.63727 | 2.02901 | 4.54801 | 0.00391 | 0.01557 | -2.6836 |
| CEP20   | 0.63728 | 4.43656 | 7.11895 | 0.00039 | 0.00313 | -0.0719 |
| C6orf89 | 0.63729 | 4.07287 | 8.01369 | 0.0002  | 0.00208 | 0.6668  |
| CDYL    | 0.63767 | 4.16974 | 8.69382 | 0.00013 | 0.00156 | 1.18255 |
| EIF3D   | 0.63782 | 5.94588 | 6.98641 | 0.00043 | 0.00334 | -0.1877 |
| FBXO7   | 0.63783 | 4.72727 | 7.88609 | 0.00022 | 0.00219 | 0.56583 |
| SGPL1   | 0.63846 | 4.92254 | 5.70158 | 0.00126 | 0.00708 | -1.4098 |
| PASK    | 0.63865 | 1.7299  | 6.73496 | 0.00052 | 0.00383 | -0.4125 |
| UBE2HP1 | 0.63924 | 3.31723 | 4.14808 | 0.00603 | 0.02145 | -3.1694 |
| PWWP2A  | 0.63946 | 3.44077 | 8.3925  | 0.00016 | 0.00178 | 0.95857 |
| TRIM47  | 0.63993 | 3.80806 | 3.40748 | 0.01438 | 0.04098 | -4.1303 |
| SOS2    | 0.64004 | 3.09565 | 6.66251 | 0.00055 | 0.00398 | -0.4784 |
| TCF7    | 0.64061 | 0.62799 | 3.38762 | 0.01473 | 0.0417  | -4.1571 |
| ZDHHC7  | 0.6408  | 4.08117 | 8.13297 | 0.00019 | 0.00198 | 0.75993 |
| BICRA   | 0.64081 | 1.39044 | 6.83009 | 0.00048 | 0.00363 | -0.3267 |
| ALKBH7  | 0.64144 | 4.7874  | 3.9284  | 0.00774 | 0.02575 | -3.4462 |
| SFT2D2  | 0.64162 | 5.47023 | 6.07957 | 0.0009  | 0.00555 | -1.0305 |
| SLC44A3 | 0.64292 | 0.48569 | 4.71615 | 0.00328 | 0.01375 | -2.4863 |
| ANKRD13 | 0.64305 | 3.42421 | 4.39019 | 0.00462 | 0.01753 | -2.8725 |
| C1QL1   | 0.64311 | 1.76073 | 4.9975  | 0.00246 | 0.01116 | -2.1653 |
| METRNL  | 0.64317 | 3.02482 | 6.26036 | 0.00077 | 0.00498 | -0.8551 |
| TPM4    | 0.64321 | 7.6333  | 5.50441 | 0.00151 | 0.008   | -1.6147 |
| YAF2    | 0.64345 | 2.61565 | 6.70655 | 0.00054 | 0.00387 | -0.4383 |
| FADS2   | 0.64395 | 3.54044 | 3.88932 | 0.00809 | 0.02656 | -3.4962 |
| ARID3BP | 0.64434 | 0.43406 | 6.07273 | 0.00091 | 0.00556 | -1.0372 |
| ZNF318  | 0.64452 | 3.016   | 5.76432 | 0.00119 | 0.00677 | -1.3456 |
| KLC4    | 0.64452 | 2.49201 | 6.09606 | 0.00089 | 0.00551 | -1.0143 |
| LRATD2  | 0.6447  | 5.90657 | 3.3571  | 0.0153  | 0.04288 | -4.1984 |
| G2E3    | 0.64511 | 3.41233 | 5.97324 | 0.00099 | 0.00591 | -1.1354 |

|         |         |         |         |         |         |         |
|---------|---------|---------|---------|---------|---------|---------|
| TSNARE1 | 0.64521 | 1.90208 | 6.40036 | 0.00069 | 0.00458 | -0.7219 |
| PHKA2   | 0.64614 | 3.02791 | 4.55896 | 0.00386 | 0.01543 | -2.6706 |
| OTUD6B  | 0.64614 | 3.78919 | 7.48292 | 0.0003  | 0.00264 | 0.23747 |
| TRNAU1A | 0.64637 | 1.68744 | 6.29974 | 0.00075 | 0.00486 | -0.8174 |
| TENT4B  | 0.64689 | 4.49411 | 7.97895 | 0.00021 | 0.00211 | 0.63944 |
| CC2D1A  | 0.64757 | 4.55523 | 6.40113 | 0.00069 | 0.00458 | -0.7212 |
| PAPOLB  | 0.64771 | 1.02489 | 5.29289 | 0.00185 | 0.00915 | -1.8403 |
| NUFIP1P | 0.64776 | 2.39051 | 4.83333 | 0.00291 | 0.01262 | -2.3513 |
| SETDB2  | 0.64865 | 0.99788 | 6.11749 | 0.00087 | 0.00544 | -0.9934 |
| CLCN2   | 0.65016 | 1.95829 | 3.65676 | 0.01063 | 0.0326  | -3.7982 |
| HPGD    | 0.65059 | -6.3062 | 3.40148 | 0.01448 | 0.04118 | -4.1384 |
| PLS1    | 0.6517  | 4.53997 | 7.60129 | 0.00027 | 0.0025  | 0.33538 |
| SORBS3  | 0.65175 | 3.59462 | 6.34455 | 0.00072 | 0.00473 | -0.7748 |
| PKP4    | 0.6525  | 5.05914 | 5.26344 | 0.0019  | 0.00933 | -1.8721 |
| BEND6   | 0.65276 | 1.41445 | 3.37229 | 0.01501 | 0.04233 | -4.1778 |
| AKAP12  | 0.65351 | 3.20702 | 3.57058 | 0.01179 | 0.03526 | -3.9121 |
| SNRNP48 | 0.65371 | 4.04502 | 5.6001  | 0.00138 | 0.00756 | -1.5146 |
| JADE3   | 0.65417 | 3.04778 | 4.82484 | 0.00293 | 0.0127  | -2.361  |
| VAR51   | 0.65424 | 5.7816  | 7.09978 | 0.00039 | 0.00315 | -0.0885 |
| ICE2P2  | 0.65462 | -0.4966 | 4.69306 | 0.00336 | 0.01397 | -2.5132 |
| LTBP3   | 0.65538 | 3.54955 | 3.72201 | 0.00984 | 0.0307  | -3.7127 |
| NBPF3   | 0.65555 | 1.10628 | 8.68371 | 0.00013 | 0.00157 | 1.17515 |
| ITGAV   | 0.6557  | 5.93504 | 4.56694 | 0.00383 | 0.01537 | -2.6612 |
| ZNF813  | 0.65767 | 2.21413 | 5.35742 | 0.00174 | 0.00876 | -1.7708 |
| NCOA4P4 | 0.65824 | 1.93485 | 4.42109 | 0.00447 | 0.01713 | -2.8352 |
| MTCH1   | 0.65867 | 6.00764 | 6.76657 | 0.00051 | 0.00376 | -0.3838 |
| CDK19   | 0.65876 | 2.47641 | 5.9263  | 0.00103 | 0.0061  | -1.1821 |
| PLAGL2  | 0.65915 | 3.87348 | 4.57975 | 0.00378 | 0.01523 | -2.646  |
| FBXO44  | 0.65972 | 2.74367 | 4.26295 | 0.00531 | 0.01946 | -3.0274 |
| KLHDC3  | 0.66086 | 5.45602 | 8.23208 | 0.00017 | 0.00189 | 0.83643 |
| CDR2    | 0.66109 | 3.6678  | 4.80749 | 0.00298 | 0.01286 | -2.3809 |
| CYB5A   | 0.66111 | 2.79271 | 4.94209 | 0.0026  | 0.01163 | -2.2277 |
| FRAT1   | 0.66146 | 0.61183 | 5.17584 | 0.00207 | 0.00988 | -1.9676 |
| RPS18   | 0.6625  | 5.20599 | 3.38447 | 0.01479 | 0.04181 | -4.1613 |
| NUDT19  | 0.6634  | 3.63239 | 7.67289 | 0.00026 | 0.00242 | 0.394   |
| SLC39A7 | 0.66364 | 6.31992 | 7.39854 | 0.00031 | 0.00271 | 0.16687 |
| ACTR3P2 | 0.66365 | 4.2207  | 6.61804 | 0.00057 | 0.00406 | -0.5192 |
| MFSD13A | 0.66368 | -0.1814 | 4.39436 | 0.0046  | 0.0175  | -2.8674 |
| CTAGE1  | 0.66434 | 0.4312  | 3.3934  | 0.01463 | 0.04148 | -4.1493 |
| POMP    | 0.66439 | 4.53324 | 5.87109 | 0.00108 | 0.00633 | -1.2375 |
| ZBTB8B  | 0.66465 | -2.1395 | 3.22698 | 0.01799 | 0.04847 | -4.3757 |
| SYT14   | 0.66537 | 2.01484 | 6.88907 | 0.00046 | 0.00351 | -0.2739 |
| RBM7P1  | 0.66671 | 3.44645 | 5.73389 | 0.00122 | 0.00691 | -1.3766 |
| GNAI1   | 0.66674 | 3.77744 | 4.61949 | 0.00362 | 0.01477 | -2.5992 |
| CTBP2P4 | 0.66744 | 3.56534 | 4.83193 | 0.00291 | 0.01263 | -2.3529 |
| TMEM183 | 0.66759 | 3.5517  | 6.43296 | 0.00067 | 0.00449 | -0.6912 |
| SPRYD7  | 0.66835 | 2.27938 | 7.41523 | 0.00031 | 0.0027  | 0.18089 |
| WDR46   | 0.66868 | 4.81563 | 5.58066 | 0.00141 | 0.00764 | -1.5349 |
| SLC25A3 | 0.66873 | 2.7108  | 8.37798 | 0.00016 | 0.00178 | 0.9476  |
| SPIN1   | 0.66874 | 4.60206 | 8.21053 | 0.00018 | 0.00191 | 0.81986 |
| ETHE1   | 0.66936 | 3.54203 | 5.27603 | 0.00188 | 0.00924 | -1.8585 |
| NAT14   | 0.66965 | 4.86448 | 3.58034 | 0.01165 | 0.03499 | -3.8991 |
| ARFGEF1 | 0.66989 | 5.17552 | 8.76178 | 0.00012 | 0.00152 | 1.23212 |
| GYG2    | 0.67082 | 2.39567 | 3.50114 | 0.01282 | 0.03764 | -4.0045 |
| PRICKLE | 0.67112 | 3.21432 | 5.84305 | 0.00111 | 0.00643 | -1.2657 |
| ZNF579  | 0.67137 | 5.03207 | 5.89897 | 0.00106 | 0.00621 | -1.2095 |
| RAB27A  | 0.67148 | 2.98279 | 5.62484 | 0.00135 | 0.00744 | -1.4889 |
| FZD6    | 0.6716  | 4.3173  | 6.21355 | 0.0008  | 0.00512 | -0.9001 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| TRMT12   | 0.67198 | 1.4257  | 7.74964 | 0.00024  | 0.00234 | 0.45632 |
| SPECC1   | 0.67198 | 4.66632 | 6.60533 | 0.00058  | 0.00409 | -0.5309 |
| SAMD4A   | 0.67231 | 3.95554 | 3.31249 | 0.01617  | 0.04474 | -4.2589 |
| VPS52    | 0.67247 | 3.96305 | 7.31113 | 0.00034  | 0.00281 | 0.09304 |
| RNF115   | 0.6738  | 4.66635 | 4.80358 | 0.00299  | 0.0129  | -2.3854 |
| MTMR6    | 0.67447 | 2.60201 | 5.03703 | 0.00237  | 0.01087 | -2.1211 |
| TP53BP2  | 0.67566 | 3.8016  | 7.83802 | 0.00023  | 0.00223 | 0.52743 |
| SLC43A1  | 0.67636 | -0.1267 | 3.42266 | 0.01411  | 0.04046 | -4.1098 |
| MCU      | 0.67706 | 4.8     | 4.51498 | 0.00404  | 0.01597 | -2.7228 |
| TNFAIP8  | 0.67842 | 2.17782 | 4.62408 | 0.00361  | 0.01472 | -2.5938 |
| TPMTP1   | 0.67857 | 5.09367 | 6.045   | 0.00093  | 0.00566 | -1.0644 |
| ANXA11   | 0.67902 | 5.93957 | 6.29163 | 0.00075  | 0.00488 | -0.8252 |
| ZNF584   | 0.67935 | 3.18735 | 7.84868 | 0.00023  | 0.00223 | 0.53597 |
| KCTD20   | 0.68022 | 4.38614 | 9.43259 | 8.10E-05 | 0.00116 | 1.7037  |
| PRKCD    | 0.68126 | 3.38355 | 5.23666 | 0.00195  | 0.00949 | -1.9012 |
| SMURF2   | 0.68131 | -1.0711 | 3.46697 | 0.01337  | 0.03891 | -4.0503 |
| HERC3    | 0.68138 | 1.33882 | 5.18052 | 0.00206  | 0.00986 | -1.9625 |
| MYO9A    | 0.68186 | 2.9941  | 5.84726 | 0.00111  | 0.00642 | -1.2615 |
| FAM171A  | 0.68186 | 3.19642 | 6.06021 | 0.00092  | 0.0056  | -1.0495 |
| PRMT1    | 0.68245 | 5.73792 | 6.71884 | 0.00053  | 0.00385 | -0.4271 |
| ZNF761   | 0.68268 | 3.58884 | 7.94897 | 0.00021  | 0.00212 | 0.61576 |
| SPEG     | 0.6827  | 2.0649  | 4.81773 | 0.00295  | 0.01279 | -2.3691 |
| SAP30    | 0.68365 | 2.13758 | 5.58833 | 0.0014   | 0.00761 | -1.5269 |
| DM1-AS   | 0.68527 | -1.4021 | 3.93072 | 0.00772  | 0.02572 | -3.4433 |
| PABPC4L  | 0.68597 | -0.1149 | 3.31313 | 0.01616  | 0.04473 | -4.2581 |
| HLA-E    | 0.68609 | 5.04009 | 4.01693 | 0.00699  | 0.02395 | -3.3338 |
| LRP5     | 0.68697 | 4.1752  | 5.50758 | 0.00151  | 0.00798 | -1.6114 |
| KIAA1522 | 0.68758 | 5.8832  | 4.89001 | 0.00274  | 0.0121  | -2.2866 |
| PPARD    | 0.68826 | 3.23827 | 3.98394 | 0.00726  | 0.02461 | -3.3756 |
| SAP18P2  | 0.68859 | 2.32656 | 4.09693 | 0.00639  | 0.02241 | -3.2332 |
| ITPRIPL2 | 0.68868 | 4.74698 | 5.01844 | 0.00241  | 0.01101 | -2.1419 |
| HERPUD   | 0.6888  | 4.58288 | 4.25997 | 0.00533  | 0.01951 | -3.0311 |
| BCL7A    | 0.6889  | 2.17328 | 4.05389 | 0.0067   | 0.02324 | -3.2872 |
| INKA2    | 0.68906 | 0.04473 | 3.51979 | 0.01253  | 0.03703 | -3.9796 |
| TUBGCP   | 0.69    | 3.82923 | 6.22951 | 0.00079  | 0.00507 | -0.8848 |
| LITAF    | 0.69073 | 5.10921 | 4.30963 | 0.00505  | 0.01873 | -2.9703 |
| ZNF627   | 0.69085 | 1.85487 | 6.5659  | 0.0006   | 0.00418 | -0.5673 |
| BMP1     | 0.69181 | 2.2823  | 4.08619 | 0.00646  | 0.02263 | -3.2466 |
| VAV1     | 0.69274 | 2.6758  | 3.32145 | 0.01599  | 0.04439 | -4.2468 |
| DLEU1    | 0.69276 | 3.34604 | 4.06767 | 0.0066   | 0.02299 | -3.2699 |
| PLA2G12  | 0.69411 | 3.22988 | 6.12879 | 0.00086  | 0.00541 | -0.9823 |
| POLD1    | 0.69414 | 5.81296 | 7.95053 | 0.00021  | 0.00212 | 0.61699 |
| DIAPH1   | 0.69445 | 6.9261  | 7.46643 | 0.0003   | 0.00265 | 0.22372 |
| OSBPL6   | 0.69534 | 0.97047 | 3.70104 | 0.01009  | 0.03128 | -3.7401 |
| FOXO6    | 0.69592 | -0.9275 | 4.40462 | 0.00455  | 0.01735 | -2.855  |
| LPP      | 0.69638 | 6.20568 | 4.01732 | 0.00699  | 0.02394 | -3.3333 |
| LINC0130 | 0.69649 | 0.20287 | 7.93328 | 0.00021  | 0.00214 | 0.60333 |
| RPL13AP  | 0.69724 | -0.0118 | 4.16772 | 0.0059   | 0.02108 | -3.145  |
| LIPE     | 0.6975  | 0.52505 | 7.51286 | 0.00029  | 0.0026  | 0.26236 |
| CAB39    | 0.69786 | 3.4783  | 7.02521 | 0.00042  | 0.00329 | -0.1536 |
| KCTD9P3  | 0.69874 | 0.53303 | 5.39463 | 0.00168  | 0.00856 | -1.731  |
| IGF2BP2  | 0.69896 | 4.63263 | 4.25845 | 0.00534  | 0.01953 | -3.0329 |
| EIF2AK3  | 0.6992  | 2.5061  | 7.95662 | 0.00021  | 0.00212 | 0.62181 |
| PKN3     | 0.69939 | 1.7153  | 4.36222 | 0.00477  | 0.01795 | -2.9063 |
| CD82     | 0.70036 | 0.37038 | 5.9029  | 0.00105  | 0.00619 | -1.2056 |
| THAP10   | 0.70167 | 0.77893 | 4.54075 | 0.00394  | 0.01564 | -2.6922 |
| RXRB     | 0.70202 | 3.79927 | 8.22305 | 0.00018  | 0.0019  | 0.82949 |
| ATF6B    | 0.70207 | 4.67465 | 7.30606 | 0.00034  | 0.00282 | 0.08874 |

|         |         |         |         |          |         |         |
|---------|---------|---------|---------|----------|---------|---------|
| KCTD9P6 | 0.70255 | 0.49583 | 5.55731 | 0.00144  | 0.00775 | -1.5592 |
| CTBP2   | 0.70268 | 4.65888 | 9.47442 | 7.90E-05 | 0.00114 | 1.73209 |
| RPS10   | 0.70289 | 0.69332 | 3.74763 | 0.00955  | 0.03    | -3.6793 |
| RNF24   | 0.70441 | 2.67077 | 4.05119 | 0.00673  | 0.02329 | -3.2906 |
| TNS2-AS | 0.70714 | 1.41715 | 4.09906 | 0.00637  | 0.02237 | -3.2305 |
| P2RY2   | 0.70885 | 1.40269 | 4.78585 | 0.00305  | 0.01306 | -2.4058 |
| PPP2R5D | 0.70904 | 4.24491 | 7.28874 | 0.00034  | 0.00285 | 0.07401 |
| NFYA    | 0.71007 | 3.34307 | 7.63024 | 0.00027  | 0.00246 | 0.35914 |
| PRMT1P1 | 0.71146 | 4.19044 | 7.42226 | 0.00031  | 0.00269 | 0.18679 |
| SYT13   | 0.71158 | 2.57077 | 3.19713 | 0.01868  | 0.04978 | -4.4167 |
| KIF13A  | 0.71262 | 4.64518 | 4.37257 | 0.00471  | 0.01782 | -2.8938 |
| EPRS1   | 0.71364 | 5.49973 | 5.63561 | 0.00134  | 0.00738 | -1.4778 |
| DCLRE1C | 0.71456 | 1.07655 | 8.17299 | 0.00018  | 0.00194 | 0.79092 |
| MATK    | 0.71514 | -0.4199 | 6.23075 | 0.00079  | 0.00507 | -0.8836 |
| USP12   | 0.71583 | 2.35281 | 7.30272 | 0.00034  | 0.00283 | 0.0859  |
| CEBPG   | 0.71624 | 5.32107 | 3.21607 | 0.01824  | 0.04896 | -4.3907 |
| MCUR1   | 0.71674 | 4.64769 | 8.0549  | 0.0002   | 0.00204 | 0.69911 |
| FCHO2   | 0.71716 | 2.6707  | 7.13218 | 0.00038  | 0.00311 | -0.0604 |
| ADPRHL1 | 0.71758 | -0.2257 | 3.27979 | 0.01684  | 0.04602 | -4.3035 |
| BHLHE40 | 0.71767 | 5.83927 | 5.58967 | 0.0014   | 0.0076  | -1.5255 |
| SCDP1   | 0.71826 | 5.39287 | 7.47043 | 0.0003   | 0.00264 | 0.22706 |
| EFCAB5  | 0.71928 | -1.6835 | 3.40234 | 0.01447  | 0.04118 | -4.1372 |
| SEC24D  | 0.71983 | 3.81576 | 5.14229 | 0.00213  | 0.01013 | -2.0045 |
| DSP-AS1 | 0.71996 | 1.92487 | 3.47451 | 0.01324  | 0.03863 | -4.0402 |
| ATP11A  | 0.72041 | 5.14494 | 6.53478 | 0.00061  | 0.00425 | -0.5961 |
| DHX16   | 0.7207  | 4.11504 | 7.88886 | 0.00022  | 0.00219 | 0.56804 |
| CDKN2D  | 0.72224 | 2.51844 | 5.38873 | 0.00168  | 0.0086  | -1.7373 |
| MTRF1   | 0.72237 | 1.00826 | 4.19282 | 0.00574  | 0.02063 | -3.1139 |
| JARID2  | 0.72257 | 3.97128 | 6.53712 | 0.00061  | 0.00425 | -0.594  |
| THADA   | 0.72265 | 3.92493 | 7.74112 | 0.00024  | 0.00234 | 0.44942 |
| TRIM45  | 0.72297 | 0.99924 | 3.74835 | 0.00954  | 0.02999 | -3.6784 |
| TTC39A  | 0.72332 | -0.6166 | 3.62923 | 0.01099  | 0.03343 | -3.8345 |
| PRCD    | 0.72453 | 1.5477  | 5.50754 | 0.00151  | 0.00798 | -1.6114 |
| EMSLR   | 0.72468 | 2.85767 | 5.91579 | 0.00104  | 0.00614 | -1.1926 |
| MYD88   | 0.72475 | 3.52054 | 5.23399 | 0.00195  | 0.0095  | -1.9041 |
| RHPN2   | 0.72681 | 5.32544 | 5.71765 | 0.00124  | 0.00699 | -1.3933 |
| CLDND2  | 0.72698 | -0.0788 | 4.06537 | 0.00662  | 0.02304 | -3.2728 |
| PIWIL4  | 0.72738 | 0.44584 | 5.03855 | 0.00236  | 0.01086 | -2.1194 |
| HIPK3   | 0.72939 | 3.86379 | 7.14475 | 0.00038  | 0.00309 | -0.0495 |
| TTC3P1  | 0.72966 | 5.19858 | 7.61661 | 0.00027  | 0.00248 | 0.34796 |
| INTS6   | 0.73188 | 2.18665 | 6.21722 | 0.0008   | 0.00511 | -0.8966 |
| LMO4    | 0.73248 | 4.93362 | 4.7978  | 0.00301  | 0.01295 | -2.392  |
| RGL2    | 0.73294 | 3.74869 | 7.47244 | 0.0003   | 0.00264 | 0.22874 |
| MRPS31  | 0.73368 | 1.56428 | 6.93767 | 0.00045  | 0.00342 | -0.2308 |
| BARD1   | 0.73663 | 2.72421 | 6.89844 | 0.00046  | 0.00349 | -0.2656 |
| FAM86B1 | 0.7369  | -0.6048 | 6.09411 | 0.00089  | 0.00551 | -1.0162 |
| ZBED6   | 0.73708 | 0.9114  | 4.34183 | 0.00487  | 0.01823 | -2.9311 |
| C9orf72 | 0.73714 | 0.97565 | 6.00814 | 0.00096  | 0.00579 | -1.1008 |
| KIF27   | 0.73771 | -1.1355 | 4.23171 | 0.0055   | 0.01996 | -3.0658 |
| CILK1   | 0.73861 | 1.13128 | 9.64679 | 7.13E-05 | 0.00107 | 1.84787 |
| ZMYM5   | 0.73867 | 1.60224 | 6.82224 | 0.00049  | 0.00365 | -0.3337 |
| FHL2    | 0.7405  | 3.05893 | 4.66745 | 0.00345  | 0.01425 | -2.543  |
| RBM7    | 0.74105 | 3.73055 | 9.67796 | 7.00E-05 | 0.00106 | 1.86861 |
| ZNF845  | 0.74174 | 2.19192 | 6.06646 | 0.00091  | 0.00558 | -1.0433 |
| NCOA4P3 | 0.74303 | 2.98238 | 7.39512 | 0.00031  | 0.00271 | 0.164   |
| TMEM63B | 0.74375 | 2.67207 | 5.34376 | 0.00176  | 0.00884 | -1.7855 |
| TAPBP   | 0.74379 | 5.58797 | 7.12099 | 0.00039  | 0.00313 | -0.0701 |
| LMBRD1  | 0.7462  | 2.28388 | 5.40025 | 0.00167  | 0.00853 | -1.725  |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| CEACAM   | 0.74691 | -0.3508 | 8.89694 | 0.00011  | 0.00144 | 1.32968 |
| DANCR    | 0.74712 | 4.8398  | 7.16354 | 0.00037  | 0.00306 | -0.0333 |
| SPRY4    | 0.74724 | 3.89305 | 3.47194 | 0.01328  | 0.03874 | -4.0436 |
| MRPS10   | 0.74827 | 3.52896 | 5.57651 | 0.00141  | 0.00766 | -1.5392 |
| ZNF738   | 0.7492  | 1.11628 | 7.65799 | 0.00026  | 0.00243 | 0.38184 |
| DNM2     | 0.74967 | 6.16186 | 8.07361 | 0.00019  | 0.00203 | 0.71373 |
| DNAJC3-  | 0.75149 | -1.9588 | 3.62518 | 0.01104  | 0.03355 | -3.8398 |
| PKP4P1   | 0.75169 | 2.49205 | 6.52726 | 0.00062  | 0.00427 | -0.6031 |
| ALG5     | 0.75172 | 1.91356 | 6.91771 | 0.00045  | 0.00347 | -0.2485 |
| GYS1     | 0.75257 | 4.49736 | 5.23879 | 0.00194  | 0.00948 | -1.8989 |
| FBLIM1P  | 0.75266 | 1.29565 | 4.21127 | 0.00562  | 0.0203  | -3.091  |
| SERAC1   | 0.75295 | 1.3788  | 5.99602 | 0.00097  | 0.00583 | -1.1128 |
| POLR1H   | 0.75309 | 3.06213 | 6.29299 | 0.00075  | 0.00488 | -0.8239 |
| SYT17    | 0.75324 | 1.21062 | 3.36783 | 0.0151   | 0.0425  | -4.1839 |
| TPT1P9   | 0.7545  | 6.27045 | 3.87418 | 0.00824  | 0.02694 | -3.5156 |
| CAVIN4   | 0.75461 | -0.4725 | 3.31098 | 0.0162   | 0.04479 | -4.261  |
| C18orf54 | 0.75525 | 1.45005 | 5.60356 | 0.00138  | 0.00755 | -1.511  |
| SRPK1    | 0.75593 | 5.07499 | 9.38688 | 8.33E-05 | 0.00118 | 1.67255 |
| ITPKC    | 0.75614 | 2.1095  | 7.12384 | 0.00039  | 0.00312 | -0.0676 |
| TXNDC16  | 0.75629 | 2.41063 | 5.24643 | 0.00193  | 0.00943 | -1.8906 |
| GTF2F2   | 0.7566  | 2.78017 | 7.08404 | 0.0004   | 0.00318 | -0.1022 |
| CCDC80   | 0.75708 | 4.13296 | 6.49549 | 0.00064  | 0.00434 | -0.6327 |
| THOC5    | 0.75781 | 3.62784 | 4.68894 | 0.00337  | 0.01401 | -2.518  |
| LRRC8E   | 0.75848 | 3.06896 | 7.9067  | 0.00022  | 0.00217 | 0.58224 |
| CDC5L    | 0.76132 | 4.19638 | 7.71182 | 0.00025  | 0.00238 | 0.42567 |
| CA5B     | 0.76267 | 1.41045 | 3.27859 | 0.01687  | 0.04607 | -4.3051 |
| MROH1    | 0.76335 | 2.62823 | 6.4588  | 0.00065  | 0.00444 | -0.667  |
| AGFG1    | 0.76336 | 3.86508 | 8.03011 | 0.0002   | 0.00206 | 0.67968 |
| CHD7     | 0.76456 | 4.71333 | 5.36959 | 0.00172  | 0.00871 | -1.7578 |
| USP2-AS  | 0.76495 | -0.6108 | 5.73428 | 0.00122  | 0.00691 | -1.3762 |
| SIX4     | 0.76528 | 2.73967 | 6.41856 | 0.00068  | 0.00453 | -0.7048 |
| FBXO27   | 0.76532 | 3.52022 | 4.65507 | 0.00349  | 0.01439 | -2.5575 |
| PLP2     | 0.76573 | 6.07621 | 7.15575 | 0.00038  | 0.00307 | -0.04   |
| DOCK7    | 0.76683 | 4.32182 | 5.41432 | 0.00164  | 0.00847 | -1.7101 |
| HCG11    | 0.7669  | 1.86769 | 8.15175 | 0.00018  | 0.00196 | 0.77449 |
| SIPA1L1  | 0.76705 | 4.45797 | 6.71514 | 0.00053  | 0.00386 | -0.4304 |
| CTTNBP2  | 0.76715 | 2.46389 | 10.073  | 5.58E-05 | 0.00093 | 2.12614 |
| STXBP5   | 0.76853 | 2.07342 | 9.506   | 7.75E-05 | 0.00113 | 1.75344 |
| LEMD3    | 0.76881 | 3.23208 | 6.78595 | 0.0005   | 0.00372 | -0.3663 |
| ZNF311   | 0.76937 | -0.2005 | 5.03368 | 0.00238  | 0.01089 | -2.1249 |
| PITX1    | 0.76944 | 3.7486  | 3.82966 | 0.00867  | 0.028   | -3.573  |
| TMEM184  | 0.77007 | 4.43501 | 5.11592 | 0.00219  | 0.01029 | -2.0336 |
| SLC25A1  | 0.77025 | 1.54268 | 3.95458 | 0.00751  | 0.02522 | -3.4129 |
| HACD2    | 0.77265 | 4.7189  | 6.69255 | 0.00054  | 0.00391 | -0.451  |
| SPTLC2   | 0.77287 | 3.58662 | 7.94073 | 0.00021  | 0.00213 | 0.60924 |
| PCDHGB   | 0.77325 | -1.1883 | 3.93002 | 0.00772  | 0.02573 | -3.4442 |
| MYBPC2   | 0.77327 | -1.1583 | 8.95442 | 0.00011  | 0.0014  | 1.37078 |
| ALG11    | 0.7734  | 0.51627 | 4.42608 | 0.00445  | 0.01709 | -2.8292 |
| FAAH     | 0.77358 | 0.93831 | 3.41893 | 0.01418  | 0.04057 | -4.1148 |
| BLTP3A   | 0.77366 | 3.59114 | 5.32535 | 0.00179  | 0.00894 | -1.8053 |
| FBXO25   | 0.77573 | 1.16105 | 4.02679 | 0.00691  | 0.02375 | -3.3214 |
| SEC14L2  | 0.77599 | 1.55851 | 6.54404 | 0.00061  | 0.00423 | -0.5875 |
| TSPAN12  | 0.77606 | 2.53329 | 3.91555 | 0.00785  | 0.02601 | -3.4626 |
| CLIC1    | 0.7761  | 6.28588 | 9.6483  | 7.13E-05 | 0.00107 | 1.84888 |
| SNHG32   | 0.77619 | 4.27408 | 3.86836 | 0.00829  | 0.02708 | -3.5231 |
| PTPRF    | 0.7765  | 5.00511 | 4.24061 | 0.00544  | 0.0198  | -3.0549 |
| MCF2L-A  | 0.7777  | 1.53414 | 4.95588 | 0.00257  | 0.0115  | -2.2121 |
| MMP14    | 0.77777 | 2.88687 | 4.28778 | 0.00517  | 0.01908 | -2.997  |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| PRR14    | 0.77807 | 4.18344 | 6.62327 | 0.00057  | 0.00406 | -0.5144 |
| RBM47    | 0.77941 | 3.71129 | 4.0552  | 0.00669  | 0.02322 | -3.2856 |
| TCEAL8   | 0.77965 | 3.65119 | 7.66424 | 0.00026  | 0.00243 | 0.38694 |
| HNRNPH   | 0.78153 | 4.68089 | 9.19768 | 9.34E-05 | 0.00127 | 1.54211 |
| SYNGAP   | 0.78186 | 1.95038 | 3.84548 | 0.00851  | 0.02762 | -3.5526 |
| GPHN     | 0.78209 | 3.09277 | 6.57107 | 0.0006   | 0.00417 | -0.5625 |
| UGCG     | 0.78265 | 3.74645 | 3.99671 | 0.00715  | 0.02433 | -3.3594 |
| PDXDC1   | 0.78272 | 5.59787 | 10.1532 | 5.33E-05 | 0.0009  | 2.17733 |
| PWWP2E   | 0.78295 | 2.44387 | 8.82068 | 0.00012  | 0.00149 | 1.2748  |
| BCL2L11  | 0.7832  | 2.44621 | 4.26185 | 0.00532  | 0.01947 | -3.0288 |
| DDX47    | 0.78485 | -1.9814 | 4.09083 | 0.00643  | 0.02255 | -3.2408 |
| SMAGP    | 0.78494 | 1.51453 | 4.85471 | 0.00284  | 0.01242 | -2.3268 |
| CIART    | 0.78515 | 1.66542 | 6.10893 | 0.00088  | 0.00546 | -1.0017 |
| ZNF48    | 0.78522 | 2.83236 | 6.38301 | 0.0007   | 0.00462 | -0.7383 |
| CD55     | 0.7853  | 2.11597 | 4.67046 | 0.00343  | 0.01422 | -2.5395 |
| THAP9    | 0.78584 | 0.02819 | 6.84666 | 0.00048  | 0.0036  | -0.3118 |
| TESMIN   | 0.78671 | 2.23946 | 7.81584 | 0.00023  | 0.00226 | 0.50965 |
| C6orf136 | 0.78709 | 2.59048 | 7.84317 | 0.00023  | 0.00223 | 0.53156 |
| ZNF524   | 0.78745 | 2.96276 | 5.19622 | 0.00203  | 0.00976 | -1.9453 |
| USPL1    | 0.78818 | 1.55882 | 6.72256 | 0.00053  | 0.00385 | -0.4237 |
| BAG1     | 0.78837 | 2.94833 | 5.07508 | 0.00228  | 0.01057 | -2.0788 |
| CXXC5    | 0.78875 | 4.81037 | 7.64511 | 0.00026  | 0.00244 | 0.37131 |
| AMPD3    | 0.78899 | -0.9699 | 3.98907 | 0.00722  | 0.02449 | -3.3691 |
| THSD4    | 0.78949 | 3.95187 | 5.77236 | 0.00118  | 0.00674 | -1.3374 |
| MED4     | 0.79037 | 2.51578 | 9.15176 | 9.61E-05 | 0.00129 | 1.51008 |
| SHANK2   | 0.79063 | 1.94391 | 4.43357 | 0.00441  | 0.01699 | -2.8202 |
| TMEM143  | 0.79081 | -0.101  | 4.50227 | 0.0041   | 0.01609 | -2.7379 |
| MAPKAP   | 0.79107 | 4.57522 | 9.66257 | 7.07E-05 | 0.00107 | 1.85838 |
| DIP2A    | 0.79117 | 4.36132 | 7.71044 | 0.00025  | 0.00238 | 0.42456 |
| STMN3    | 0.79124 | 1.30097 | 4.9646  | 0.00254  | 0.01143 | -2.2023 |
| VPS36    | 0.79147 | 2.76989 | 9.05031 | 0.0001   | 0.00135 | 1.43881 |
| GLCE     | 0.792   | 1.72959 | 7.32237 | 0.00033  | 0.0028  | 0.10257 |
| USP2     | 0.79243 | 0.73771 | 5.7553  | 0.0012   | 0.00681 | -1.3548 |
| TEX30    | 0.79247 | 2.24647 | 9.27078 | 8.93E-05 | 0.00124 | 1.59279 |
| CHMP2B   | 0.79326 | 3.7456  | 8.1754  | 0.00018  | 0.00194 | 0.79278 |
| ITGB8    | 0.79475 | 5.49409 | 3.95338 | 0.00752  | 0.02523 | -3.4144 |
| SH3BP4   | 0.79499 | 4.84534 | 3.3461  | 0.01551  | 0.04335 | -4.2133 |
| N4BP2L2  | 0.79528 | 3.02665 | 4.61556 | 0.00364  | 0.01482 | -2.6038 |
| RPL21    | 0.79605 | 1.05477 | 5.01281 | 0.00243  | 0.01103 | -2.1482 |
| EIF3C    | 0.79646 | -0.0025 | 5.74892 | 0.00121  | 0.00684 | -1.3613 |
| PANK1    | 0.79693 | 2.15084 | 7.93523 | 0.00021  | 0.00214 | 0.60488 |
| CAMKMT   | 0.79718 | 2.17645 | 5.6941  | 0.00127  | 0.00711 | -1.4174 |
| RFC3     | 0.79777 | 3.66126 | 7.88538 | 0.00022  | 0.00219 | 0.56527 |
| NTN1     | 0.79784 | 2.72749 | 6.35939 | 0.00071  | 0.00469 | -0.7607 |
| WDR90    | 0.79885 | 2.65224 | 9.88934 | 6.19E-05 | 0.00098 | 2.00761 |
| ILRUNP1  | 0.79889 | -0.0161 | 4.00993 | 0.00705  | 0.02407 | -3.3426 |
| TGDS     | 0.79961 | 0.92334 | 7.44206 | 0.0003   | 0.00268 | 0.20336 |
| KLHL5    | 0.80171 | 3.60306 | 9.96452 | 5.93E-05 | 0.00096 | 2.05639 |
| ANKRD10  | 0.80196 | 1.7633  | 3.49225 | 0.01296  | 0.03797 | -4.0164 |
| LIPG     | 0.80245 | 4.86983 | 4.95185 | 0.00258  | 0.01154 | -2.2167 |
| PTPRU    | 0.80279 | 2.11028 | 5.19265 | 0.00203  | 0.00978 | -1.9492 |
| NEK3     | 0.80308 | -0.6817 | 7.56254 | 0.00028  | 0.00254 | 0.30347 |
| GSTM3    | 0.8031  | 4.062   | 5.56368 | 0.00143  | 0.00773 | -1.5526 |
| RNASEH1  | 0.80339 | 2.28519 | 5.25665 | 0.00191  | 0.00938 | -1.8795 |
| DSTN     | 0.80339 | 5.68882 | 9.76484 | 6.66E-05 | 0.00103 | 1.92608 |
| DCUN1D1  | 0.8039  | 2.49894 | 6.7632  | 0.00051  | 0.00376 | -0.3869 |
| GMDS     | 0.80539 | 5.23816 | 5.43668 | 0.00161  | 0.00836 | -1.6863 |
| LETM2    | 0.80584 | 1.81037 | 5.85792 | 0.0011   | 0.00638 | -1.2507 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| IQCK     | 0.80676 | 1.30646 | 4.36591 | 0.00475  | 0.01791 | -2.9018 |
| H2AC25   | 0.80697 | 0.7697  | 3.22317 | 0.01808  | 0.04861 | -4.3809 |
| EBPL     | 0.80719 | 2.20868 | 9.90192 | 6.15E-05 | 0.00098 | 2.0158  |
| NRL      | 0.80731 | -2.0144 | 4.86401 | 0.00282  | 0.01235 | -2.3162 |
| RNF5     | 0.80755 | 3.12417 | 6.26916 | 0.00077  | 0.00495 | -0.8467 |
| PICK1    | 0.80813 | 2.54666 | 8.23612 | 0.00017  | 0.00189 | 0.83953 |
| WEE1     | 0.80964 | 3.08595 | 4.79444 | 0.00302  | 0.01298 | -2.3959 |
| ZNF581   | 0.80968 | 3.46912 | 10.6578 | 4.04E-05 | 0.00076 | 2.49061 |
| H1-10-AS | 0.80998 | -0.8005 | 4.51517 | 0.00404  | 0.01597 | -2.7226 |
| F12      | 0.81013 | 1.03001 | 8.34051 | 0.00016  | 0.00181 | 0.91921 |
| MZF1     | 0.81061 | 3.09266 | 6.56873 | 0.0006   | 0.00417 | -0.5647 |
| MPND     | 0.81106 | 1.95649 | 8.61349 | 0.00014  | 0.00161 | 1.12352 |
| PRKX     | 0.81346 | 3.56827 | 8.31959 | 0.00016  | 0.00182 | 0.90331 |
| ZNF823   | 0.81395 | 1.18808 | 4.63154 | 0.00358  | 0.01465 | -2.5851 |
| PIBF1    | 0.81473 | 1.42415 | 8.12575 | 0.00019  | 0.00198 | 0.75433 |
| MTHFD2   | 0.81489 | 5.33761 | 3.31295 | 0.01616  | 0.04474 | -4.2583 |
| MYO18A   | 0.81578 | 3.38456 | 7.61509 | 0.00027  | 0.00248 | 0.34672 |
| LIG4     | 0.81718 | 2.6467  | 6.23158 | 0.00079  | 0.00506 | -0.8828 |
| FNDC3A   | 0.8173  | 3.75057 | 10.8044 | 3.73E-05 | 0.00072 | 2.57897 |
| IFFO2    | 0.81738 | 2.02779 | 6.29072 | 0.00075  | 0.00488 | -0.826  |
| AKNA     | 0.81744 | 1.80244 | 3.60749 | 0.01128  | 0.03412 | -3.8632 |
| RAB11FIP | 0.81759 | 4.45651 | 6.83373 | 0.00048  | 0.00363 | -0.3234 |
| BCL2L12  | 0.8179  | 3.74639 | 8.76666 | 0.00012  | 0.00152 | 1.23566 |
| CAPN1    | 0.81825 | 5.59295 | 9.58923 | 7.38E-05 | 0.0011  | 1.80942 |
| DCAF11   | 0.81871 | 3.80751 | 6.64328 | 0.00056  | 0.00402 | -0.496  |
| HMGB1P   | 0.81878 | 6.72216 | 9.83928 | 6.37E-05 | 0.001   | 1.97494 |
| MRPS24   | 0.81891 | -0.4277 | 5.72593 | 0.00123  | 0.00696 | -1.3848 |
| STX5     | 0.81935 | 3.45634 | 8.57817 | 0.00014  | 0.00164 | 1.0974  |
| DEK      | 0.81991 | 6.99915 | 7.78911 | 0.00024  | 0.00229 | 0.48817 |
| MCAM     | 0.82019 | 5.16661 | 4.86742 | 0.00281  | 0.01233 | -2.3123 |
| USP12Px  | 0.82207 | 0.61386 | 4.13706 | 0.00611  | 0.02166 | -3.1831 |
| ESYT2    | 0.82226 | 4.78984 | 11.0976 | 3.20E-05 | 0.00066 | 2.75237 |
| PPP1R11  | 0.82243 | -0.5001 | 3.41632 | 0.01422  | 0.04068 | -4.1184 |
| IQCA1    | 0.8234  | -2.0106 | 5.18427 | 0.00205  | 0.00983 | -1.9584 |
| LARP1BF  | 0.82346 | 0.00623 | 3.68594 | 0.01027  | 0.03173 | -3.7599 |
| KLF13    | 0.82408 | 3.85059 | 9.12341 | 9.78E-05 | 0.00131 | 1.49023 |
| ZNF844   | 0.82444 | 0.38928 | 7.641   | 0.00026  | 0.00244 | 0.36795 |
| ZNF836   | 0.82497 | 0.38018 | 4.36328 | 0.00476  | 0.01794 | -2.905  |
| RPL7L1P  | 0.82543 | 1.0739  | 6.20847 | 0.00081  | 0.00514 | -0.905  |
| PSTPIP2  | 0.82616 | 0.37131 | 7.66002 | 0.00026  | 0.00243 | 0.3835  |
| INPP5J   | 0.82792 | 0.58763 | 5.68363 | 0.00128  | 0.00715 | -1.4282 |
| SPRY2    | 0.82936 | 2.54187 | 5.8517  | 0.0011   | 0.0064  | -1.257  |
| STPG1    | 0.83104 | 1.56558 | 5.94504 | 0.00101  | 0.00602 | -1.1634 |
| TMEM102  | 0.83135 | 2.82348 | 9.21125 | 9.27E-05 | 0.00126 | 1.55154 |
| HABP4    | 0.83161 | 2.22465 | 6.78416 | 0.0005   | 0.00372 | -0.368  |
| YIPF3    | 0.83215 | 4.86501 | 9.44677 | 8.03E-05 | 0.00115 | 1.71333 |
| PPP1R15  | 0.83278 | 4.17605 | 3.64496 | 0.01078  | 0.03294 | -3.8138 |
| GAS6-DT  | 0.83451 | -0.2778 | 3.78306 | 0.00916  | 0.02914 | -3.6333 |
| INAFM1   | 0.83563 | 2.19197 | 3.37435 | 0.01498  | 0.04225 | -4.175  |
| MMP7     | 0.83583 | 5.77097 | 4.36363 | 0.00476  | 0.01794 | -2.9046 |
| PRICKLE  | 0.83605 | 4.30711 | 5.37189 | 0.00171  | 0.0087  | -1.7553 |
| KLHL24   | 0.83643 | 2.24105 | 3.80736 | 0.0089   | 0.02851 | -3.6018 |
| CCDC9    | 0.83645 | 1.45721 | 9.25364 | 9.03E-05 | 0.00124 | 1.58093 |
| ISOC2    | 0.83791 | 5.66759 | 9.43221 | 8.10E-05 | 0.00116 | 1.70344 |
| USP53    | 0.83841 | 2.16066 | 6.27154 | 0.00077  | 0.00494 | -0.8444 |
| TMCC3    | 0.83949 | 1.78432 | 4.67775 | 0.00341  | 0.01413 | -2.531  |
| LGALS8   | 0.83957 | 3.1601  | 3.65814 | 0.01061  | 0.03256 | -3.7964 |
| PLAGL1   | 0.83965 | 3.64639 | 4.65007 | 0.00351  | 0.01445 | -2.5634 |

|         |         |         |         |          |         |         |
|---------|---------|---------|---------|----------|---------|---------|
| FIZ1    | 0.83981 | 3.34586 | 7.43273 | 0.00031  | 0.00269 | 0.19556 |
| H4C3    | 0.83993 | -0.2378 | 5.28881 | 0.00185  | 0.00917 | -1.8447 |
| WNK2    | 0.84113 | 2.6483  | 6.79864 | 0.0005   | 0.00369 | -0.3549 |
| BMPR1A  | 0.84302 | 3.45224 | 5.59913 | 0.00138  | 0.00756 | -1.5156 |
| MYLK4   | 0.84407 | -1.2859 | 3.81781 | 0.00879  | 0.02829 | -3.5883 |
| PROC    | 0.84493 | -2.1512 | 3.87756 | 0.0082   | 0.02686 | -3.5113 |
| ZSWIM9  | 0.84586 | 0.83237 | 8.39476 | 0.00016  | 0.00178 | 0.96027 |
| NFE2L3  | 0.84611 | 3.92903 | 7.46131 | 0.0003   | 0.00266 | 0.21945 |
| S100A3  | 0.84637 | 1.28727 | 3.41806 | 0.01419  | 0.0406  | -4.116  |
| KLLN    | 0.84658 | -0.8627 | 4.97304 | 0.00252  | 0.01136 | -2.1928 |
| DCTPP1  | 0.848   | 5.05563 | 6.87477 | 0.00047  | 0.00354 | -0.2867 |
| RAB6A   | 0.84876 | 5.02942 | 5.48206 | 0.00154  | 0.00809 | -1.6383 |
| PRDX2P4 | 0.84894 | 2.14188 | 4.47687 | 0.00421  | 0.01643 | -2.7683 |
| ARID5A  | 0.84897 | 1.40299 | 5.41921 | 0.00164  | 0.00844 | -1.7048 |
| ELF1    | 0.84942 | 2.90267 | 9.83387 | 6.39E-05 | 0.001   | 1.9714  |
| TMEM63A | 0.84948 | 2.28057 | 6.62381 | 0.00057  | 0.00406 | -0.5139 |
| SHISA9  | 0.8498  | 2.60313 | 3.2876  | 0.01668  | 0.04571 | -4.2928 |
| SUGT1   | 0.85049 | 2.94002 | 6.41728 | 0.00068  | 0.00453 | -0.706  |
| RBM26   | 0.85079 | 4.13769 | 9.2594  | 9.00E-05 | 0.00124 | 1.58492 |
| LAYN    | 0.85142 | 1.63475 | 3.49833 | 0.01286  | 0.03774 | -4.0083 |
| ABHD16A | 0.85191 | -1.6149 | 6.98899 | 0.00043  | 0.00334 | -0.1855 |
| RAP1GA  | 0.85385 | 1.52293 | 3.63483 | 0.01091  | 0.03325 | -3.8271 |
| COL9A2  | 0.85385 | 3.93206 | 4.61237 | 0.00365  | 0.01485 | -2.6076 |
| TSPAN5  | 0.85413 | 0.43542 | 5.77138 | 0.00118  | 0.00675 | -1.3384 |
| FCF1P8  | 0.85426 | 1.21075 | 6.49748 | 0.00063  | 0.00433 | -0.6308 |
| MICU2   | 0.85434 | 2.26427 | 10.2852 | 4.95E-05 | 0.00086 | 2.26066 |
| PHEX    | 0.85495 | -2.4923 | 3.75708 | 0.00944  | 0.02976 | -3.667  |
| MED21   | 0.85575 | 2.74065 | 8.95568 | 0.00011  | 0.0014  | 1.37168 |
| STK11IP | 0.85589 | 2.3761  | 8.00153 | 0.0002   | 0.00209 | 0.65723 |
| PLEKHG3 | 0.85628 | 3.95492 | 5.3684  | 0.00172  | 0.00871 | -1.7591 |
| KHK     | 0.85874 | -0.5978 | 3.56175 | 0.01191  | 0.03554 | -3.9238 |
| FUZ     | 0.85919 | 2.54588 | 7.64366 | 0.00026  | 0.00244 | 0.37012 |
| RSPH3   | 0.8596  | 1.89938 | 8.74743 | 0.00012  | 0.00153 | 1.22168 |
| ZNF385B | 0.86047 | -1.9346 | 6.52492 | 0.00062  | 0.00427 | -0.6053 |
| ANKS6   | 0.86189 | 3.49551 | 10.9985 | 3.37E-05 | 0.00068 | 2.69425 |
| NKD1    | 0.86291 | -1.4425 | 6.91142 | 0.00045  | 0.00347 | -0.2541 |
| TPT1    | 0.86323 | 7.2719  | 5.26358 | 0.0019   | 0.00933 | -1.872  |
| MRPL2   | 0.86381 | 4.31975 | 7.25765 | 0.00035  | 0.0029  | 0.0475  |
| STAP2   | 0.86474 | 2.16892 | 5.32162 | 0.0018   | 0.00896 | -1.8093 |
| ANKRD10 | 0.86522 | 3.73998 | 8.93819 | 0.00011  | 0.00141 | 1.3592  |
| NIPAL3  | 0.86561 | 3.50917 | 4.80134 | 0.003    | 0.01292 | -2.3879 |
| NUFIP1  | 0.86591 | 0.94696 | 6.41688 | 0.00068  | 0.00453 | -0.7064 |
| CLN5    | 0.86695 | 1.28159 | 6.93463 | 0.00045  | 0.00343 | -0.2335 |
| ZNF460  | 0.8676  | 0.1142  | 4.05934 | 0.00666  | 0.02315 | -3.2804 |
| SACS    | 0.86855 | 3.74572 | 7.35456 | 0.00032  | 0.00276 | 0.12981 |
| DLEU2   | 0.86889 | 0.45228 | 6.77354 | 0.00051  | 0.00374 | -0.3775 |
| NIPSNAP | 0.86915 | 4.68227 | 5.27782 | 0.00187  | 0.00923 | -1.8566 |
| ACSL3   | 0.86953 | 4.20981 | 10.9861 | 3.39E-05 | 0.00068 | 2.687   |
| NFKB2   | 0.87042 | 3.2546  | 3.62529 | 0.01104  | 0.03355 | -3.8397 |
| ADAM19  | 0.87074 | 0.67701 | 4.56231 | 0.00385  | 0.0154  | -2.6666 |
| TTC7A   | 0.87113 | 3.39152 | 9.1239  | 9.78E-05 | 0.00131 | 1.49058 |
| CCDC186 | 0.87118 | 3.62118 | 8.78682 | 0.00012  | 0.00151 | 1.25029 |
| NHLRC3  | 0.87129 | 2.18286 | 5.48913 | 0.00153  | 0.00806 | -1.6308 |
| ZBED9   | 0.87232 | 0.46432 | 4.98709 | 0.00249  | 0.01125 | -2.177  |
| ZMYM2   | 0.87271 | 4.00031 | 5.67864 | 0.00129  | 0.00717 | -1.4333 |
| UPK2    | 0.8736  | -0.9118 | 3.72225 | 0.00984  | 0.0307  | -3.7124 |
| MYO1E   | 0.87387 | 3.52673 | 8.29281 | 0.00017  | 0.00184 | 0.88291 |
| CORO2A  | 0.87391 | 1.45801 | 7.69259 | 0.00025  | 0.0024  | 0.41004 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| SIX2     | 0.87612 | 0.87408 | 4.10354 | 0.00634  | 0.02228 | -3.2249 |
| NAA16    | 0.87742 | 1.73886 | 11.6025 | 2.48E-05 | 0.00056 | 3.04087 |
| MAMSTR   | 0.87942 | -1.0002 | 3.22835 | 0.01796  | 0.04841 | -4.3738 |
| NOP53    | 0.87947 | 2.9497  | 5.80976 | 0.00114  | 0.00659 | -1.2994 |
| ANO8     | 0.88009 | 1.97504 | 4.56493 | 0.00384  | 0.01539 | -2.6635 |
| TENM3    | 0.88022 | 5.19484 | 5.92426 | 0.00103  | 0.00611 | -1.1842 |
| TBC1D4   | 0.88102 | 1.64128 | 3.27446 | 0.01695  | 0.04623 | -4.3108 |
| C15orf39 | 0.88248 | 3.83771 | 4.13829 | 0.0061   | 0.02164 | -3.1816 |
| EGLN3    | 0.88549 | 4.12478 | 6.38525 | 0.0007   | 0.00462 | -0.7362 |
| TP53     | 0.88592 | 4.65045 | 6.80577 | 0.00049  | 0.00368 | -0.3485 |
| SLC37A1  | 0.88618 | 2.0982  | 7.14668 | 0.00038  | 0.00309 | -0.0479 |
| SUGT1P2  | 0.88882 | 2.6706  | 4.91452 | 0.00268  | 0.01189 | -2.2588 |
| ZNF69    | 0.88999 | -1.5316 | 4.75303 | 0.00315  | 0.01335 | -2.4436 |
| LCA5     | 0.89097 | 0.4302  | 7.00307 | 0.00042  | 0.00332 | -0.1731 |
| TLE1     | 0.89099 | 4.59575 | 4.33193 | 0.00492  | 0.0184  | -2.9431 |
| TMC7     | 0.89159 | -0.8571 | 4.08352 | 0.00648  | 0.02269 | -3.25   |
| INTS13   | 0.89223 | 4.48514 | 8.08273 | 0.00019  | 0.00202 | 0.72085 |
| ICA1L    | 0.89251 | -0.3072 | 4.81158 | 0.00297  | 0.01283 | -2.3762 |
| IRAK4    | 0.8932  | 2.17745 | 7.86417 | 0.00022  | 0.00221 | 0.54835 |
| GPSM2    | 0.89325 | 2.61802 | 6.51478 | 0.00063  | 0.00429 | -0.6147 |
| ABCC4    | 0.89347 | 3.14068 | 5.52083 | 0.00149  | 0.00793 | -1.5975 |
| DLG1     | 0.89437 | 4.50711 | 5.68337 | 0.00128  | 0.00715 | -1.4285 |
| HMGB1P   | 0.89467 | 5.21541 | 10.3641 | 4.74E-05 | 0.00084 | 2.31002 |
| SELENOV  | 0.89534 | -0.0656 | 3.78889 | 0.0091   | 0.02898 | -3.6257 |
| STK19    | 0.89573 | 1.34967 | 9.57075 | 7.46E-05 | 0.0011  | 1.79703 |
| GPT2     | 0.89612 | 5.33285 | 3.89722 | 0.00802  | 0.0264  | -3.4861 |
| RIGI     | 0.89621 | 2.36051 | 5.14014 | 0.00214  | 0.01015 | -2.0069 |
| SOX18    | 0.89651 | -1.0605 | 4.85147 | 0.00285  | 0.01245 | -2.3305 |
| STK3     | 0.89683 | 4.37444 | 4.58143 | 0.00377  | 0.01521 | -2.644  |
| PPP1R11  | 0.89709 | 4.94077 | 11.9885 | 2.05E-05 | 0.00051 | 3.25328 |
| RPL13A   | 0.89758 | 5.20985 | 10.3011 | 4.91E-05 | 0.00086 | 2.27064 |
| MYH9     | 0.89777 | 8.02871 | 3.77787 | 0.00921  | 0.02925 | -3.64   |
| FAM110A  | 0.90046 | 1.55236 | 7.45425 | 0.0003   | 0.00267 | 0.21355 |
| REV3L    | 0.90175 | 3.76907 | 7.23048 | 0.00036  | 0.00294 | 0.02427 |
| MTCH1P   | 0.90246 | 4.32749 | 6.28132 | 0.00076  | 0.00491 | -0.835  |
| RBMS2    | 0.90528 | 4.02835 | 5.93566 | 0.00102  | 0.00605 | -1.1728 |
| SOGA1    | 0.90582 | 4.44724 | 6.42185 | 0.00067  | 0.00453 | -0.7017 |
| PLCB1    | 0.90653 | 2.88167 | 8.32844 | 0.00016  | 0.00182 | 0.91004 |
| UPK3B    | 0.907   | 5.81996 | 3.67212 | 0.01044  | 0.03215 | -3.778  |
| NFE2L3P  | 0.90702 | 0.66587 | 5.22805 | 0.00196  | 0.00953 | -1.9106 |
| UGDH     | 0.90712 | 4.07471 | 6.07729 | 0.0009   | 0.00556 | -1.0327 |
| LATS2    | 0.90759 | 2.67357 | 8.45823 | 0.00015  | 0.00173 | 1.00802 |
| PNPLA4   | 0.90956 | 1.11166 | 6.35386 | 0.00071  | 0.00471 | -0.7659 |
| MTMR12   | 0.91094 | 3.42538 | 10.7399 | 3.86E-05 | 0.00074 | 2.54022 |
| METRNL   | 0.91215 | 3.75157 | 3.9638  | 0.00743  | 0.02501 | -3.4011 |
| LINC0267 | 0.91239 | -2.719  | 3.74048 | 0.00963  | 0.03019 | -3.6886 |
| ZBTB22   | 0.91247 | 3.25052 | 5.27831 | 0.00187  | 0.00923 | -1.856  |
| POLH     | 0.91265 | 3.19669 | 7.40128 | 0.00031  | 0.00271 | 0.16918 |
| ZSCAN12  | 0.91364 | 1.39736 | 10.5854 | 4.20E-05 | 0.00078 | 2.44654 |
| PHLPP1   | 0.91414 | 0.32838 | 10.3433 | 4.79E-05 | 0.00084 | 2.29701 |
| TRPM4    | 0.9142  | 2.34268 | 7.29448 | 0.00034  | 0.00284 | 0.07889 |
| TST      | 0.91435 | 2.96965 | 5.89983 | 0.00106  | 0.0062  | -1.2086 |
| AFAP1    | 0.91451 | 3.96379 | 10.4236 | 4.59E-05 | 0.00082 | 2.34699 |
| SMTN     | 0.9149  | 2.8991  | 8.0838  | 0.00019  | 0.00202 | 0.72168 |
| BRCA2    | 0.91663 | 1.88524 | 7.23235 | 0.00036  | 0.00294 | 0.02587 |
| EYA3     | 0.91669 | 3.27912 | 6.18591 | 0.00082  | 0.00522 | -0.9269 |
| TIAM2    | 0.91705 | 1.36292 | 3.38455 | 0.01479  | 0.04181 | -4.1612 |
| PLXNB1   | 0.91709 | 4.22169 | 6.13526 | 0.00086  | 0.00538 | -0.976  |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| MINAR1   | 0.91838 | -1.2423 | 3.66972 | 0.01047  | 0.03222 | -3.7812 |
| PDXK     | 0.91852 | 5.86865 | 7.11779 | 0.00039  | 0.00313 | -0.0729 |
| ZNF649   | 0.91882 | 1.44957 | 8.32459 | 0.00016  | 0.00182 | 0.90712 |
| COG3     | 0.92059 | 2.01467 | 6.30041 | 0.00075  | 0.00486 | -0.8168 |
| YIPF2    | 0.92145 | 4.40043 | 7.23223 | 0.00036  | 0.00294 | 0.02576 |
| TPCN1    | 0.9216  | 4.72214 | 4.48343 | 0.00418  | 0.01635 | -2.7604 |
| APOL1    | 0.92238 | 5.05509 | 4.26785 | 0.00528  | 0.01938 | -3.0214 |
| CDKAL1   | 0.92451 | 5.22773 | 11.7374 | 2.32E-05 | 0.00055 | 3.11589 |
| TERC     | 0.92492 | -0.1289 | 7.89036 | 0.00022  | 0.00218 | 0.56923 |
| MEGF6    | 0.92547 | 1.55275 | 3.8494  | 0.00848  | 0.02755 | -3.5475 |
| C1QTNF1  | 0.92617 | -1.3507 | 4.49463 | 0.00413  | 0.0162  | -2.7471 |
| PRDX2    | 0.92673 | 6.4503  | 8.48148 | 0.00015  | 0.00171 | 1.02544 |
| OBI1     | 0.92768 | 1.86589 | 8.87307 | 0.00011  | 0.00145 | 1.31255 |
| SPATA13  | 0.92893 | 2.04974 | 8.43661 | 0.00015  | 0.00174 | 0.99179 |
| RHOBTB1  | 0.93026 | 6.14183 | 8.21554 | 0.00018  | 0.00191 | 0.82372 |
| PTPN6    | 0.93039 | 1.67418 | 8.17588 | 0.00018  | 0.00194 | 0.79315 |
| NUDT3    | 0.931   | 4.08004 | 9.21534 | 9.24E-05 | 0.00126 | 1.55438 |
| STING1   | 0.93203 | 5.69263 | 4.96085 | 0.00255  | 0.01146 | -2.2065 |
| TMBIM1   | 0.93282 | 4.64253 | 6.59169 | 0.00059  | 0.00412 | -0.5435 |
| KIFC1    | 0.93285 | 4.90246 | 6.01337 | 0.00096  | 0.00578 | -1.0956 |
| SUPT20H  | 0.93352 | 3.34673 | 11.0045 | 3.36E-05 | 0.00068 | 2.6978  |
| HACD1    | 0.93359 | 3.27647 | 11.7299 | 2.33E-05 | 0.00055 | 3.11176 |
| RFXANK   | 0.93599 | 5.08564 | 4.75149 | 0.00316  | 0.01336 | -2.4454 |
| ING1     | 0.93688 | 3.52434 | 8.83354 | 0.00012  | 0.00148 | 1.28408 |
| PSORS10  | 0.93806 | -0.4125 | 6.86297 | 0.00047  | 0.00357 | -0.2972 |
| MINDY2   | 0.93863 | 2.8407  | 5.67508 | 0.00129  | 0.00718 | -1.437  |
| TBC1D2   | 0.93867 | 2.93254 | 6.47808 | 0.00064  | 0.00438 | -0.6489 |
| UBR2     | 0.94126 | 3.58261 | 12.3651 | 1.71E-05 | 0.00046 | 3.45414 |
| WBP4     | 0.94132 | 1.33139 | 8.64961 | 0.00013  | 0.00159 | 1.15012 |
| APOBEC1  | 0.94218 | 2.74655 | 4.89704 | 0.00272  | 0.01204 | -2.2787 |
| ITGB5    | 0.94232 | 4.81358 | 6.90481 | 0.00046  | 0.00348 | -0.2599 |
| BTBD3    | 0.94334 | 4.12799 | 6.93781 | 0.00045  | 0.00342 | -0.2307 |
| FLOT1    | 0.94345 | 5.69036 | 7.24484 | 0.00035  | 0.00293 | 0.03655 |
| EMP2     | 0.94383 | 2.91784 | 6.40367 | 0.00069  | 0.00457 | -0.7188 |
| MDC1     | 0.94407 | 4.20547 | 10.0043 | 5.80E-05 | 0.00095 | 2.08203 |
| GPALPP1  | 0.94456 | 2.34068 | 10.644  | 4.07E-05 | 0.00076 | 2.48223 |
| ILRUN    | 0.94701 | 5.00396 | 10.2464 | 5.06E-05 | 0.00088 | 2.23624 |
| IDH2     | 0.94828 | 5.47175 | 4.66559 | 0.00345  | 0.01426 | -2.5452 |
| NUP58    | 0.95043 | 4.01325 | 9.91    | 6.12E-05 | 0.00098 | 2.02105 |
| RAI14    | 0.95205 | 6.39007 | 10.1526 | 5.33E-05 | 0.0009  | 2.17693 |
| RHBDD1   | 0.95208 | 1.50006 | 10.368  | 4.73E-05 | 0.00084 | 2.31241 |
| TPT1P6   | 0.95388 | 1.30568 | 3.97998 | 0.00729  | 0.02468 | -3.3806 |
| BICRAL   | 0.95461 | 2.599   | 7.34814 | 0.00033  | 0.00277 | 0.12439 |
| SHROOM   | 0.9548  | 6.07066 | 4.06201 | 0.00664  | 0.0231  | -3.277  |
| SRF      | 0.95484 | 4.70968 | 4.70396 | 0.00332  | 0.01387 | -2.5005 |
| MESP1    | 0.95585 | -1.1493 | 3.29385 | 0.01655  | 0.04546 | -4.2843 |
| NR2F6    | 0.95695 | 5.72178 | 10.2412 | 5.07E-05 | 0.00088 | 2.23297 |
| CUL3     | 0.95812 | 3.76451 | 9.91261 | 6.11E-05 | 0.00098 | 2.02274 |
| ZNF132-D | 0.95928 | -0.5543 | 5.56744 | 0.00143  | 0.00771 | -1.5487 |
| ABAT     | 0.95959 | -2.0502 | 5.58156 | 0.00141  | 0.00764 | -1.5339 |
| LRRC61   | 0.9618  | 3.61365 | 5.33452 | 0.00177  | 0.00889 | -1.7954 |
| NFIX     | 0.96197 | 3.72562 | 6.51595 | 0.00062  | 0.00429 | -0.6136 |
| ATXN1    | 0.96246 | 3.79914 | 4.4924  | 0.00414  | 0.01623 | -2.7497 |
| SLC1A4   | 0.96259 | 1.93355 | 5.23703 | 0.00195  | 0.00949 | -1.9008 |
| AIFM3    | 0.96356 | 0.33408 | 6.31917 | 0.00074  | 0.00481 | -0.7989 |
| ARHGEF   | 0.96413 | -0.0948 | 3.70101 | 0.01009  | 0.03128 | -3.7402 |
| FKBP4P1  | 0.96475 | 1.3839  | 3.41982 | 0.01416  | 0.04056 | -4.1136 |
| HYI      | 0.96495 | 2.44174 | 4.99471 | 0.00247  | 0.01119 | -2.1685 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| HECTD1   | 0.96521 | 5.64231 | 8.64998 | 0.00013  | 0.00159 | 1.15039 |
| ABHD11   | 0.96538 | 4.41807 | 7.02947 | 0.00041  | 0.00328 | -0.1499 |
| CAMK1D   | 0.9671  | 0.66456 | 4.84977 | 0.00286  | 0.01246 | -2.3325 |
| POU5F1   | 0.9684  | 0.42749 | 4.18379 | 0.0058   | 0.0208  | -3.125  |
| MTHFD2   | 0.97012 | 3.94706 | 4.93032 | 0.00263  | 0.01173 | -2.241  |
| SLC29A2  | 0.97126 | 4.53821 | 6.94618 | 0.00044  | 0.00342 | -0.2232 |
| POGLUT1  | 0.97171 | 0.60088 | 10.3102 | 4.88E-05 | 0.00086 | 2.27634 |
| UCHL3    | 0.97205 | 0.29295 | 8.66707 | 0.00013  | 0.00158 | 1.16295 |
| INTS6P1  | 0.97234 | 1.70416 | 6.79501 | 0.0005   | 0.0037  | -0.3582 |
| HM13-IT1 | 0.97315 | 0.20073 | 4.41533 | 0.0045   | 0.01721 | -2.8421 |
| LGALS3   | 0.97329 | 3.86573 | 8.59938 | 0.00014  | 0.00162 | 1.1131  |
| STK24    | 0.97384 | 3.93519 | 10.4537 | 4.51E-05 | 0.00082 | 2.36561 |
| OTUD3    | 0.97654 | 3.08049 | 5.51223 | 0.0015   | 0.00796 | -1.6065 |
| IL17RB   | 0.97668 | 0.39152 | 5.08474 | 0.00226  | 0.0105  | -2.0681 |
| MCF2L    | 0.97821 | 1.49671 | 8.9965  | 0.00011  | 0.00138 | 1.40071 |
| CLIP2    | 0.97878 | 2.36178 | 3.57769 | 0.01169  | 0.03506 | -3.9027 |
| BCAR3    | 0.97886 | 3.51787 | 5.65093 | 0.00132  | 0.00731 | -1.4619 |
| FBXL3    | 0.97926 | 2.39216 | 7.44795 | 0.0003   | 0.00268 | 0.20829 |
| TACC2    | 0.9798  | 2.17448 | 7.45685 | 0.0003   | 0.00266 | 0.21572 |
| LTBP1    | 0.9803  | 2.02873 | 4.36813 | 0.00474  | 0.01789 | -2.8992 |
| EGFR     | 0.98044 | 5.06577 | 3.4544  | 0.01357  | 0.03934 | -4.0671 |
| LRCH1    | 0.98135 | 2.27102 | 9.21851 | 9.22E-05 | 0.00126 | 1.55659 |
| TPT1P4   | 0.98172 | 4.8329  | 4.32136 | 0.00498  | 0.01856 | -2.956  |
| EBF4     | 0.98183 | 1.1488  | 3.79157 | 0.00907  | 0.02892 | -3.6222 |
| KBTBD6   | 0.98261 | 2.48552 | 4.72751 | 0.00324  | 0.01361 | -2.4731 |
| ZNF556   | 0.98371 | 0.6668  | 5.25235 | 0.00192  | 0.0094  | -1.8842 |
| CSRP1    | 0.98501 | 6.60661 | 7.37016 | 0.00032  | 0.00274 | 0.14298 |
| PNKD     | 0.98719 | 4.43057 | 6.23369 | 0.00079  | 0.00506 | -0.8807 |
| KRT18P3  | 0.98764 | 2.95746 | 3.87462 | 0.00823  | 0.02693 | -3.5151 |
| NCOA3    | 0.98771 | 4.84624 | 3.55839 | 0.01196  | 0.03566 | -3.9283 |
| RAB4A    | 0.98844 | 2.71572 | 11.391  | 2.76E-05 | 0.0006  | 2.92152 |
| ZNF185   | 0.98904 | 2.51906 | 4.96299 | 0.00255  | 0.01144 | -2.2041 |
| SMIM14   | 0.98969 | 2.25205 | 5.20235 | 0.00201  | 0.00972 | -1.9386 |
| SLC25A2  | 0.99001 | 5.09003 | 8.77847 | 0.00012  | 0.00151 | 1.24424 |
| ZNF331   | 0.99016 | 3.59165 | 5.13131 | 0.00216  | 0.0102  | -2.0166 |
| ACTG1P2  | 0.9923  | -1.5981 | 4.62518 | 0.0036   | 0.01472 | -2.5925 |
| HRH1     | 0.99248 | 1.76418 | 7.7129  | 0.00025  | 0.00238 | 0.42655 |
| B4GALNT1 | 0.99287 | 2.44288 | 7.56479 | 0.00028  | 0.00254 | 0.30532 |
| HOXB5    | 0.99288 | 2.80138 | 5.23011 | 0.00196  | 0.00952 | -1.9083 |
| MAL      | 0.99438 | -0.2498 | 4.27516 | 0.00524  | 0.01926 | -3.0125 |
| ERCC5    | 0.99525 | 0.7143  | 7.94973 | 0.00021  | 0.00212 | 0.61636 |
| ARHGEF4  | 0.99614 | 0.66028 | 5.01855 | 0.00241  | 0.01101 | -2.1418 |
| CERS4    | 0.99639 | 2.63789 | 3.89848 | 0.00801  | 0.02639 | -3.4845 |
| ADCY10F  | 0.99842 | -1.0205 | 7.40672 | 0.00031  | 0.00271 | 0.17375 |
| STK38    | 0.99842 | 4.01053 | 12.3298 | 1.74E-05 | 0.00046 | 3.43558 |
| GPC1     | 0.9992  | 2.96087 | 4.5142  | 0.00405  | 0.01597 | -2.7237 |
| SNN      | 1.00179 | 3.12775 | 5.39306 | 0.00168  | 0.00857 | -1.7327 |
| TAP1     | 1.00219 | 2.30349 | 3.58263 | 0.01162  | 0.03491 | -3.8961 |
| MFF      | 1.00256 | 3.1181  | 9.98197 | 5.87E-05 | 0.00096 | 2.06766 |
| EPAS1    | 1.00377 | 4.75416 | 4.43158 | 0.00442  | 0.01701 | -2.8226 |
| CENPJ    | 1.00409 | 2.32045 | 10.815  | 3.71E-05 | 0.00072 | 2.58534 |
| FAM172A  | 1.00531 | 1.72351 | 8.5954  | 0.00014  | 0.00162 | 1.11016 |
| IFT88    | 1.00563 | 0.33472 | 6.89706 | 0.00046  | 0.0035  | -0.2668 |
| AKAP11   | 1.00586 | 3.38447 | 8.79907 | 0.00012  | 0.0015  | 1.25917 |
| CCNE1    | 1.00645 | 5.82798 | 3.76022 | 0.00941  | 0.0297  | -3.6629 |
| RNF6     | 1.00683 | 2.82857 | 12.6049 | 1.53E-05 | 0.00042 | 3.57893 |
| S1PR2    | 1.00939 | 1.83276 | 8.50868 | 0.00014  | 0.00169 | 1.04576 |
| ARSI     | 1.00978 | -1.8338 | 3.72596 | 0.00979  | 0.03059 | -3.7076 |

|         |         |         |         |          |         |         |
|---------|---------|---------|---------|----------|---------|---------|
| KRT18P1 | 1.01098 | 3.02952 | 4.90958 | 0.00269  | 0.01193 | -2.2644 |
| PRDX2P1 | 1.01225 | 2.62847 | 10.9513 | 3.46E-05 | 0.00069 | 2.66641 |
| DOCK5   | 1.01242 | 2.27862 | 6.28208 | 0.00076  | 0.00491 | -0.8343 |
| RHBDD2  | 1.01262 | 3.26119 | 5.34259 | 0.00176  | 0.00884 | -1.7867 |
| SAP18   | 1.01398 | 4.46774 | 8.79722 | 0.00012  | 0.0015  | 1.25783 |
| EML2    | 1.01402 | 3.53982 | 3.36889 | 0.01508  | 0.04247 | -4.1824 |
| LRCH2   | 1.01455 | 2.28524 | 4.55495 | 0.00388  | 0.01547 | -2.6754 |
| DLX5    | 1.01573 | 1.99913 | 4.58001 | 0.00378  | 0.01523 | -2.6457 |
| PM20D2  | 1.01641 | 3.77204 | 7.56433 | 0.00028  | 0.00254 | 0.30495 |
| PORCN   | 1.01672 | 4.22744 | 3.96437 | 0.00742  | 0.02501 | -3.4004 |
| ANKDD1A | 1.01768 | -0.2222 | 5.56543 | 0.00143  | 0.00772 | -1.5507 |
| TBC1D22 | 1.01913 | 1.97944 | 6.26892 | 0.00077  | 0.00495 | -0.8469 |
| EDNRA   | 1.01931 | -1.2451 | 3.95555 | 0.0075   | 0.0252  | -3.4116 |
| AP1S3   | 1.02073 | 0.46398 | 4.8313  | 0.00291  | 0.01263 | -2.3536 |
| DMC1    | 1.0235  | -1.0863 | 5.31889 | 0.0018   | 0.00898 | -1.8122 |
| HECA    | 1.02375 | 1.86294 | 8.33046 | 0.00016  | 0.00182 | 0.91158 |
| KHDRBS  | 1.0239  | 1.72153 | 4.12306 | 0.0062   | 0.02193 | -3.2005 |
| MZT1    | 1.02508 | 3.29944 | 10.0711 | 5.58E-05 | 0.00093 | 2.12494 |
| NACC2   | 1.02574 | 2.50613 | 4.74232 | 0.00319  | 0.01346 | -2.456  |
| ANKRD24 | 1.02642 | -2.3205 | 10.2268 | 5.11E-05 | 0.00088 | 2.22388 |
| NKX1-2  | 1.02672 | 1.73393 | 4.1611  | 0.00594  | 0.02118 | -3.1532 |
| GATA5   | 1.02702 | -1.6218 | 3.22636 | 0.01801  | 0.0485  | -4.3766 |
| DLX6-AS | 1.02839 | 1.56517 | 10.6856 | 3.98E-05 | 0.00075 | 2.50747 |
| MYH14   | 1.02925 | 5.68872 | 7.9475  | 0.00021  | 0.00212 | 0.61459 |
| TBC1D19 | 1.03149 | 0.77298 | 6.99734 | 0.00043  | 0.00333 | -0.1781 |
| LAMA5   | 1.03181 | 6.74172 | 5.51726 | 0.00149  | 0.00795 | -1.6012 |
| CSPG4   | 1.03329 | -0.7046 | 3.31256 | 0.01617  | 0.04474 | -4.2589 |
| PROSER  | 1.03552 | 1.66361 | 4.71412 | 0.00328  | 0.01377 | -2.4887 |
| TMEM23  | 1.03682 | 0.79301 | 6.83801 | 0.00048  | 0.00362 | -0.3196 |
| DNASE2  | 1.03711 | 4.6857  | 4.59902 | 0.0037   | 0.01501 | -2.6233 |
| CRYL1   | 1.03802 | 0.7598  | 4.813   | 0.00297  | 0.01282 | -2.3746 |
| DNAJC3  | 1.03803 | 3.40524 | 12.3026 | 1.77E-05 | 0.00046 | 3.42122 |
| PBX4    | 1.03976 | -0.1552 | 8.65349 | 0.00013  | 0.00159 | 1.15297 |
| ABLIM1  | 1.04091 | 5.55354 | 4.88713 | 0.00275  | 0.01212 | -2.2899 |
| HSD3B7  | 1.04148 | 0.51257 | 10.1849 | 5.24E-05 | 0.00089 | 2.19743 |
| DSTNP3  | 1.04255 | 1.87608 | 5.62268 | 0.00136  | 0.00745 | -1.4912 |
| PLXNA2  | 1.04286 | 1.21895 | 3.26835 | 0.01708  | 0.04655 | -4.3191 |
| DHRS1   | 1.04319 | 1.14319 | 5.01804 | 0.00241  | 0.01101 | -2.1423 |
| NFKBID  | 1.0448  | 1.12552 | 5.526   | 0.00148  | 0.00791 | -1.592  |
| APOLD1  | 1.04592 | 0.47448 | 6.73362 | 0.00052  | 0.00383 | -0.4137 |
| MST1    | 1.04595 | -1.5377 | 3.31343 | 0.01615  | 0.04473 | -4.2577 |
| NOTCH3  | 1.04678 | 4.02338 | 4.50869 | 0.00407  | 0.01601 | -2.7303 |
| RNF8    | 1.04693 | 2.63337 | 10.7392 | 3.87E-05 | 0.00074 | 2.5398  |
| BMPR1A  | 1.04792 | 3.18371 | 6.23976 | 0.00079  | 0.00504 | -0.8749 |
| ATP2B4  | 1.04803 | 4.95588 | 8.80408 | 0.00012  | 0.0015  | 1.26279 |
| CDK8    | 1.04944 | 2.06349 | 10.2263 | 5.12E-05 | 0.00088 | 2.22358 |
| NEDD9   | 1.04982 | 6.00226 | 4.93821 | 0.00261  | 0.01166 | -2.232  |
| SERINC2 | 1.05079 | 3.7929  | 4.7807  | 0.00307  | 0.0131  | -2.4117 |
| RDH13   | 1.05136 | 3.20015 | 9.47629 | 7.89E-05 | 0.00114 | 1.73336 |
| NEK9    | 1.05175 | 2.55098 | 5.4622  | 0.00157  | 0.00821 | -1.6593 |
| TNK1    | 1.05281 | 1.09114 | 7.60615 | 0.00027  | 0.00249 | 0.33938 |
| POLR1D  | 1.05283 | 3.75401 | 13.485  | 1.04E-05 | 0.00033 | 4.01728 |
| PDS5B   | 1.0533  | 3.26245 | 13.4138 | 1.07E-05 | 0.00034 | 3.98293 |
| PAN3    | 1.05639 | 2.48548 | 7.72734 | 0.00025  | 0.00236 | 0.43826 |
| PRKCH   | 1.0569  | 1.9388  | 4.93862 | 0.00261  | 0.01166 | -2.2316 |
| HMGB1   | 1.05697 | 5.53408 | 11.4381 | 2.69E-05 | 0.00059 | 2.94828 |
| IFNLR1  | 1.05873 | 0.86404 | 7.76888 | 0.00024  | 0.00231 | 0.47186 |
| MAP9    | 1.05985 | 1.83082 | 5.00801 | 0.00244  | 0.01107 | -2.1536 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| LRRC8D   | 1.05985 | 3.58221 | 6.95296 | 0.00044  | 0.0034  | -0.2172 |
| MYCL     | 1.0604  | -0.4434 | 3.20854 | 0.01842  | 0.04932 | -4.401  |
| ENDOD1   | 1.06661 | 3.16607 | 6.63137 | 0.00057  | 0.00404 | -0.507  |
| MIPEP    | 1.0671  | 1.4153  | 7.78492 | 0.00024  | 0.00229 | 0.48479 |
| TOGARA   | 1.06729 | 0.39029 | 6.72402 | 0.00053  | 0.00385 | -0.4224 |
| PARP4    | 1.06912 | 3.73467 | 8.79099 | 0.00012  | 0.00151 | 1.25332 |
| PRECSIT  | 1.06935 | 1.26811 | 4.37979 | 0.00468  | 0.01769 | -2.885  |
| OPLAH    | 1.06984 | 3.46554 | 4.40096 | 0.00457  | 0.01739 | -2.8595 |
| TDRD3    | 1.07001 | -0.9683 | 6.04907 | 0.00093  | 0.00565 | -1.0604 |
| VPREB3   | 1.07313 | -1.0785 | 3.92897 | 0.00773  | 0.02575 | -3.4455 |
| MAT1A    | 1.07555 | -2.0101 | 9.76117 | 6.67E-05 | 0.00103 | 1.92366 |
| LINC0298 | 1.07585 | 1.24935 | 4.2075  | 0.00565  | 0.02036 | -3.0957 |
| PXK      | 1.0764  | 3.34996 | 3.57788 | 0.01168  | 0.03506 | -3.9024 |
| CD2AP    | 1.07904 | 5.23028 | 13.5746 | 9.96E-06 | 0.00032 | 4.0603  |
| COLGALT  | 1.07945 | -1.1974 | 5.10761 | 0.00221  | 0.01035 | -2.0428 |
| ATP7B    | 1.08142 | 0.16239 | 4.87942 | 0.00277  | 0.0122  | -2.2987 |
| ZNF93    | 1.08288 | -1.1708 | 5.09259 | 0.00224  | 0.01045 | -2.0594 |
| RPL21P1  | 1.08313 | 3.7425  | 7.85099 | 0.00023  | 0.00222 | 0.53782 |
| CD99P1   | 1.08598 | -0.6849 | 10.0661 | 5.60E-05 | 0.00093 | 2.12174 |
| MEST     | 1.08606 | 4.58582 | 13.3847 | 1.08E-05 | 0.00034 | 3.96881 |
| VEGFA    | 1.08662 | 4.82553 | 3.60509 | 0.01131  | 0.03421 | -3.8664 |
| ERMP1    | 1.08698 | 4.86718 | 7.47088 | 0.0003   | 0.00264 | 0.22743 |
| ATF4P4   | 1.089   | 1.9951  | 4.19982 | 0.00569  | 0.0205  | -3.1052 |
| IRF3     | 1.09017 | 4.68673 | 14.4134 | 7.02E-06 | 0.00026 | 4.44927 |
| MYLK3    | 1.09114 | -0.6693 | 6.28883 | 0.00075  | 0.00489 | -0.8279 |
| LYN      | 1.09347 | 3.23142 | 6.78486 | 0.0005   | 0.00372 | -0.3673 |
| HPDL     | 1.09396 | 1.62542 | 5.35191 | 0.00174  | 0.00878 | -1.7767 |
| MESTP3   | 1.09554 | 1.65597 | 8.03315 | 0.0002   | 0.00206 | 0.68207 |
| RAB3D    | 1.09656 | 3.86101 | 6.49443 | 0.00064  | 0.00434 | -0.6337 |
| CDR2L    | 1.09689 | 4.83933 | 4.57781 | 0.00378  | 0.01524 | -2.6483 |
| WHRN     | 1.09757 | 0.83996 | 4.36057 | 0.00477  | 0.01797 | -2.9083 |
| DIS3     | 1.10398 | 3.12899 | 8.28729 | 0.00017  | 0.00185 | 0.87869 |
| PMEL     | 1.10483 | 0.56019 | 6.35124 | 0.00072  | 0.00472 | -0.7684 |
| OSR2     | 1.10511 | 0.63427 | 8.33034 | 0.00016  | 0.00182 | 0.91149 |
| CD2AP-D  | 1.10569 | 0.23697 | 6.00878 | 0.00096  | 0.00579 | -1.1002 |
| PPARGC   | 1.10688 | 1.76443 | 3.35968 | 0.01525  | 0.04278 | -4.1949 |
| SIM1     | 1.10886 | -2.1191 | 3.42182 | 0.01412  | 0.04049 | -4.111  |
| RBMS2P   | 1.10892 | 3.78516 | 5.67602 | 0.00129  | 0.00718 | -1.436  |
| BMPR1A   | 1.11052 | 2.98452 | 5.49336 | 0.00153  | 0.00805 | -1.6264 |
| MIR3936  | 1.11134 | -0.5419 | 9.02657 | 0.0001   | 0.00136 | 1.42203 |
| THOC3    | 1.11176 | 4.30241 | 6.32533 | 0.00073  | 0.00479 | -0.793  |
| HEY2     | 1.1129  | 2.4179  | 4.42183 | 0.00447  | 0.01713 | -2.8343 |
| PELI2    | 1.11342 | 1.12402 | 4.21552 | 0.0056   | 0.02024 | -3.0858 |
| CEMIP2   | 1.11462 | 4.57758 | 7.67517 | 0.00026  | 0.00242 | 0.39585 |
| DDX39B   | 1.11569 | 3.99758 | 10.4229 | 4.59E-05 | 0.00082 | 2.34652 |
| MYCBP2   | 1.11686 | 3.68186 | 11.4972 | 2.61E-05 | 0.00058 | 2.98171 |
| DGKH     | 1.11912 | 3.62514 | 9.26269 | 8.98E-05 | 0.00124 | 1.58719 |
| ZNF778   | 1.1193  | 3.01236 | 13.0082 | 1.28E-05 | 0.00037 | 3.78351 |
| GALNT18  | 1.12117 | 0.16192 | 4.02219 | 0.00695  | 0.02384 | -3.3272 |
| P4HTM    | 1.12179 | 1.76739 | 6.64159 | 0.00056  | 0.00402 | -0.4976 |
| PDLIM7   | 1.12215 | 5.98481 | 10.3649 | 4.74E-05 | 0.00084 | 2.31051 |
| RBMS3    | 1.1225  | 3.87706 | 6.41733 | 0.00068  | 0.00453 | -0.7059 |
| COL9A3   | 1.12259 | -1.511  | 6.37816 | 0.0007   | 0.00464 | -0.7429 |
| CYP1A1   | 1.12531 | -0.7289 | 3.25472 | 0.01738  | 0.04719 | -4.3377 |
| GRB7     | 1.12929 | 0.48154 | 3.49193 | 0.01297  | 0.03798 | -4.0169 |
| ARHGEF   | 1.13033 | 2.97966 | 10.4261 | 4.58E-05 | 0.00082 | 2.34853 |
| MESTP1   | 1.13047 | 3.98592 | 11.3305 | 2.84E-05 | 0.00061 | 2.88699 |
| FARP1    | 1.1314  | 5.07079 | 9.91796 | 6.09E-05 | 0.00098 | 2.02622 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| P2RY6    | 1.13459 | 0.83116 | 4.52657 | 0.004    | 0.01583 | -2.709  |
| GTF2F2P  | 1.13479 | -0.167  | 4.81449 | 0.00296  | 0.01281 | -2.3728 |
| UFM1P2   | 1.13598 | 1.01478 | 5.06884 | 0.00229  | 0.01061 | -2.0857 |
| SORL1    | 1.13818 | 3.2191  | 8.42117 | 0.00015  | 0.00176 | 0.98018 |
| MIEF2    | 1.13965 | 1.60847 | 5.84533 | 0.00111  | 0.00642 | -1.2634 |
| FAM20C   | 1.14048 | 2.26168 | 3.23687 | 0.01777  | 0.04798 | -4.3622 |
| S100A2   | 1.14159 | 2.34766 | 8.23605 | 0.00017  | 0.00189 | 0.83948 |
| LRRC56   | 1.14234 | -1.0323 | 6.8586  | 0.00047  | 0.00357 | -0.3011 |
| JDP2     | 1.14318 | 2.63554 | 5.31109 | 0.00181  | 0.00902 | -1.8206 |
| RB1      | 1.1434  | 4.07632 | 10.8478 | 3.65E-05 | 0.00071 | 2.60491 |
| ARRDC1   | 1.14387 | 2.94171 | 10.9276 | 3.50E-05 | 0.0007  | 2.65242 |
| RCBTB2   | 1.14419 | 1.43387 | 6.80256 | 0.0005   | 0.00369 | -0.3514 |
| CMTM4    | 1.14587 | 3.34216 | 11.9947 | 2.04E-05 | 0.00051 | 3.25667 |
| C11orf80 | 1.14688 | 0.67182 | 7.95789 | 0.00021  | 0.00212 | 0.62281 |
| SEMA3F   | 1.14901 | 2.66759 | 7.07375 | 0.0004   | 0.0032  | -0.1112 |
| MFFP2    | 1.14958 | 3.0703  | 9.58537 | 7.40E-05 | 0.0011  | 1.80683 |
| MUC3A    | 1.15049 | -1.3504 | 5.31652 | 0.0018   | 0.00899 | -1.8148 |
| ALPK3    | 1.15168 | -1.9338 | 5.64497 | 0.00133  | 0.00733 | -1.4681 |
| PRSS36   | 1.15277 | -1.8833 | 5.20131 | 0.00202  | 0.00972 | -1.9398 |
| CD9      | 1.15285 | 5.26668 | 6.60315 | 0.00058  | 0.00409 | -0.5329 |
| SORT1    | 1.15366 | 3.63343 | 5.33792 | 0.00177  | 0.00887 | -1.7917 |
| CDKN2A1  | 1.15494 | 4.13953 | 12.4145 | 1.68E-05 | 0.00045 | 3.48008 |
| ADHFE1   | 1.15537 | -1.3069 | 6.19508 | 0.00082  | 0.00519 | -0.918  |
| TMEM19   | 1.15675 | -0.5689 | 5.56418 | 0.00143  | 0.00772 | -1.5521 |
| SPNS2    | 1.15691 | 2.63559 | 8.94945 | 0.00011  | 0.0014  | 1.36724 |
| ALDH1B1  | 1.1573  | 4.38714 | 12.0831 | 1.96E-05 | 0.0005  | 3.30435 |
| CALD1    | 1.15792 | 6.98405 | 4.86244 | 0.00282  | 0.01237 | -2.318  |
| IL22RA1  | 1.15823 | -0.3552 | 6.08401 | 0.0009   | 0.00554 | -1.0261 |
| IL3RA    | 1.15841 | -1.6793 | 4.21805 | 0.00558  | 0.0202  | -3.0827 |
| RHOV     | 1.15865 | 0.12253 | 5.87499 | 0.00108  | 0.00631 | -1.2336 |
| XPO4     | 1.15964 | 3.15559 | 9.50867 | 7.74E-05 | 0.00113 | 1.75525 |
| SLC43A2  | 1.15997 | 0.811   | 5.857   | 0.0011   | 0.00638 | -1.2517 |
| MIR193B  | 1.16062 | -1.8144 | 3.71375 | 0.00994  | 0.03091 | -3.7235 |
| PPP1R13  | 1.16265 | 3.13112 | 8.46763 | 0.00015  | 0.00172 | 1.01507 |
| SKA3     | 1.16341 | 3.10319 | 6.1255  | 0.00087  | 0.00542 | -0.9855 |
| KSR2     | 1.16369 | 0.39755 | 8.38198 | 0.00016  | 0.00178 | 0.95062 |
| TM9SF2   | 1.16491 | 4.81829 | 12.8392 | 1.38E-05 | 0.00039 | 3.69858 |
| MORN3    | 1.16588 | -1.6834 | 5.10203 | 0.00222  | 0.01039 | -2.0489 |
| RAB17-D  | 1.16634 | -1.6054 | 3.73973 | 0.00964  | 0.0302  | -3.6896 |
| EPB41L4  | 1.16648 | -0.3355 | 4.56216 | 0.00385  | 0.0154  | -2.6668 |
| CCSER1   | 1.16778 | 0.17069 | 4.79561 | 0.00302  | 0.01297 | -2.3945 |
| GLIS2    | 1.16804 | 1.79584 | 7.97186 | 0.00021  | 0.00211 | 0.63385 |
| TLCD4    | 1.17008 | 2.09048 | 7.16952 | 0.00037  | 0.00305 | -0.0281 |
| SLC22A5  | 1.17119 | 2.51994 | 13.1298 | 1.21E-05 | 0.00036 | 3.84393 |
| ASAP3    | 1.17154 | 2.05675 | 8.59777 | 0.00014  | 0.00162 | 1.1119  |
| CLDN1    | 1.17155 | 4.62249 | 4.16306 | 0.00593  | 0.02116 | -3.1507 |
| EEF1AKM  | 1.17255 | -0.1065 | 11.4385 | 2.69E-05 | 0.00059 | 2.94854 |
| RAB6C    | 1.17339 | 0.52608 | 7.41045 | 0.00031  | 0.0027  | 0.17688 |
| TMEM25   | 1.17368 | 2.28383 | 11.4731 | 2.64E-05 | 0.00058 | 2.96809 |
| FBN1     | 1.17398 | -1.2917 | 3.22334 | 0.01808  | 0.04861 | -4.3807 |
| KRT18P1  | 1.17436 | 3.20862 | 6.47924 | 0.00064  | 0.00438 | -0.6479 |
| SLC10A5  | 1.17471 | -0.4064 | 7.61114 | 0.00027  | 0.00248 | 0.34348 |
| ESD      | 1.17582 | 4.12277 | 13.6349 | 9.71E-06 | 0.00032 | 4.08903 |
| OLFML2A  | 1.17688 | 0.53526 | 3.7991  | 0.00899  | 0.02873 | -3.6125 |
| CDK2AP2  | 1.17824 | 5.78035 | 8.2419  | 0.00017  | 0.00189 | 0.84397 |
| CPAMD8   | 1.17863 | 1.87122 | 3.55408 | 0.01202  | 0.03579 | -3.934  |
| KBTBD7   | 1.18008 | 0.98536 | 7.59955 | 0.00027  | 0.0025  | 0.33396 |
| PIK3IP1  | 1.18132 | 0.24113 | 3.44401 | 0.01375  | 0.03972 | -4.0811 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| TNFRSF2  | 1.18167 | 3.81373 | 4.16454 | 0.00592  | 0.02113 | -3.1489 |
| TSC22D1  | 1.1822  | 3.97018 | 14.7298 | 6.18E-06 | 0.00024 | 4.58995 |
| APLF     | 1.18362 | -0.497  | 7.06202 | 0.0004   | 0.00322 | -0.1214 |
| IL12RB2  | 1.18415 | -0.9023 | 4.5256  | 0.004    | 0.01583 | -2.7102 |
| LHFPL6   | 1.18477 | 0.59504 | 3.39603 | 0.01458  | 0.0414  | -4.1457 |
| PDE4DIP  | 1.18493 | 3.40211 | 12.4662 | 1.64E-05 | 0.00044 | 3.50706 |
| HMGA2    | 1.18565 | 4.77063 | 6.71265 | 0.00053  | 0.00386 | -0.4327 |
| SLC7A5   | 1.1882  | 5.47853 | 8.3698  | 0.00016  | 0.00179 | 0.94141 |
| AJAP1    | 1.18831 | 4.71691 | 9.95239 | 5.97E-05 | 0.00096 | 2.04854 |
| TUBB3P1  | 1.18892 | -1.0833 | 3.21003 | 0.01838  | 0.04925 | -4.399  |
| GLG1     | 1.1908  | 4.01331 | 11.2823 | 2.91E-05 | 0.00062 | 2.85934 |
| TRAPPC9  | 1.19124 | 4.7873  | 12.387  | 1.70E-05 | 0.00045 | 3.46566 |
| TMC6     | 1.19133 | 3.5745  | 3.61851 | 0.01113  | 0.03377 | -3.8486 |
| ZDHHC8B  | 1.19209 | -0.8558 | 3.35128 | 0.01541  | 0.04312 | -4.2063 |
| IPO5     | 1.19262 | 5.13648 | 7.5514  | 0.00028  | 0.00255 | 0.29427 |
| MTURN    | 1.19289 | 0.99011 | 11.4888 | 2.62E-05 | 0.00058 | 2.97697 |
| KPNA3    | 1.1946  | 3.7635  | 12.2082 | 1.85E-05 | 0.00048 | 3.37123 |
| DACT2    | 1.1946  | 1.63748 | 5.46893 | 0.00156  | 0.00817 | -1.6521 |
| RHOD     | 1.19478 | 2.49    | 12.0627 | 1.98E-05 | 0.0005  | 3.29336 |
| COG6     | 1.19552 | 2.22069 | 6.18205 | 0.00083  | 0.00523 | -0.9306 |
| RNF165   | 1.19632 | 1.08381 | 5.60872 | 0.00137  | 0.00752 | -1.5057 |
| MICAL2   | 1.19689 | 4.18378 | 7.89367 | 0.00022  | 0.00218 | 0.57187 |
| GPR180   | 1.19984 | 1.95311 | 12.301  | 1.77E-05 | 0.00046 | 3.42039 |
| KRT18P6  | 1.20045 | 0.26494 | 6.50929 | 0.00063  | 0.0043  | -0.6198 |
| KRT18    | 1.20128 | 6.925   | 7.5133  | 0.00029  | 0.0026  | 0.26272 |
| AJUBA-D  | 1.20151 | -1.1286 | 8.92741 | 0.00011  | 0.00142 | 1.3515  |
| SSH3     | 1.20179 | 3.07716 | 6.15128 | 0.00085  | 0.00533 | -0.9604 |
| BIVM     | 1.20248 | 0.4873  | 6.63206 | 0.00057  | 0.00404 | -0.5063 |
| MITF     | 1.2028  | 2.94026 | 11.8088 | 2.24E-05 | 0.00053 | 3.15527 |
| LINC0148 | 1.20322 | -1.9179 | 4.15787 | 0.00597  | 0.02125 | -3.1572 |
| MIR186   | 1.20366 | -1.5376 | 4.24651 | 0.00541  | 0.01974 | -3.0476 |
| HEY1     | 1.20447 | 0.55926 | 3.20807 | 0.01843  | 0.04934 | -4.4017 |
| AVPI1    | 1.2052  | 2.63052 | 5.41038 | 0.00165  | 0.00849 | -1.7142 |
| YPEL1    | 1.20623 | -1.5058 | 6.80992 | 0.00049  | 0.00368 | -0.3448 |
| RAB6D    | 1.20857 | 1.57487 | 7.92202 | 0.00022  | 0.00215 | 0.5944  |
| HOMER2   | 1.20927 | 2.17551 | 9.43316 | 8.10E-05 | 0.00116 | 1.70409 |
| POR      | 1.20999 | 4.57716 | 10.5839 | 4.20E-05 | 0.00078 | 2.44559 |
| DMRT2    | 1.21012 | -1.913  | 4.76393 | 0.00312  | 0.01327 | -2.431  |
| LEPR     | 1.21012 | 1.3397  | 8.00412 | 0.0002   | 0.00208 | 0.65927 |
| COL5A1   | 1.21037 | 2.9698  | 3.5026  | 0.0128   | 0.03761 | -4.0026 |
| ANKS1A   | 1.21141 | 3.67611 | 7.53132 | 0.00028  | 0.00257 | 0.27766 |
| DOP1B    | 1.21197 | 2.34457 | 7.10555 | 0.00039  | 0.00315 | -0.0835 |
| DCAF12L  | 1.21318 | 4.083   | 5.48225 | 0.00154  | 0.00809 | -1.6381 |
| FHDC1    | 1.21437 | 2.08644 | 4.09048 | 0.00643  | 0.02255 | -3.2413 |
| NDFIP2   | 1.21499 | 2.88913 | 13.7991 | 9.05E-06 | 0.0003  | 4.16673 |
| LONRF1   | 1.21582 | 0.97333 | 4.79981 | 0.00301  | 0.01293 | -2.3897 |
| MTIF3    | 1.21654 | 1.5724  | 10.7326 | 3.88E-05 | 0.00074 | 2.53583 |
| SLC20A2  | 1.21753 | 3.60514 | 7.35559 | 0.00032  | 0.00276 | 0.13068 |
| TSPAN13  | 1.21782 | 3.48461 | 11.7987 | 2.25E-05 | 0.00054 | 3.14969 |
| EFNB1    | 1.21811 | 2.57539 | 7.58737 | 0.00027  | 0.00251 | 0.32394 |
| SOWAHD   | 1.22324 | 0.73731 | 4.51393 | 0.00405  | 0.01597 | -2.7241 |
| MFGE8    | 1.22482 | 6.21782 | 7.2928  | 0.00034  | 0.00284 | 0.07746 |
| PPM1J    | 1.22707 | -1.7616 | 5.595   | 0.00139  | 0.00758 | -1.5199 |
| PITPNM1  | 1.22898 | 5.04414 | 4.81534 | 0.00296  | 0.0128  | -2.3719 |
| CCDC153  | 1.22913 | 0.59454 | 4.27958 | 0.00521  | 0.0192  | -3.007  |
| KBTBD11  | 1.23115 | -0.3283 | 4.84092 | 0.00288  | 0.01254 | -2.3426 |
| SLC7A5P  | 1.23188 | -0.0073 | 6.0829  | 0.0009   | 0.00555 | -1.0272 |
| GDA      | 1.23565 | 4.90849 | 5.68807 | 0.00128  | 0.00713 | -1.4236 |

|         |         |         |         |          |         |         |
|---------|---------|---------|---------|----------|---------|---------|
| RNF208  | 1.23797 | 0.9295  | 4.03232 | 0.00687  | 0.02364 | -3.3144 |
| MBNL2   | 1.23861 | 2.81251 | 5.68314 | 0.00128  | 0.00715 | -1.4287 |
| RDH10   | 1.2394  | 3.86525 | 8.17184 | 0.00018  | 0.00194 | 0.79003 |
| OR2A1-A | 1.23976 | 0.54387 | 3.72848 | 0.00976  | 0.03054 | -3.7043 |
| PLEKHA4 | 1.24031 | 2.38088 | 5.51675 | 0.00149  | 0.00795 | -1.6017 |
| ZNF117  | 1.24212 | -0.1936 | 5.21041 | 0.002    | 0.00966 | -1.9298 |
| STARD13 | 1.24539 | 1.81815 | 7.41026 | 0.00031  | 0.0027  | 0.17671 |
| LYPD3   | 1.24585 | 0.10383 | 4.65324 | 0.0035   | 0.01441 | -2.5596 |
| NT5DC2  | 1.25207 | 5.35801 | 14.0125 | 8.28E-06 | 0.00029 | 4.26631 |
| GARRE1  | 1.25211 | 3.41245 | 11.7149 | 2.34E-05 | 0.00055 | 3.10346 |
| REP15   | 1.25383 | 0.58563 | 8.33183 | 0.00016  | 0.00182 | 0.91262 |
| RAP2A   | 1.25389 | 2.77345 | 12.8946 | 1.34E-05 | 0.00039 | 3.72653 |
| AUTS2   | 1.25407 | 1.80773 | 4.21908 | 0.00557  | 0.02018 | -3.0814 |
| RIPPLY3 | 1.25463 | -0.3142 | 4.49146 | 0.00415  | 0.01625 | -2.7508 |
| FAIM    | 1.25519 | 0.88    | 4.72805 | 0.00324  | 0.01361 | -2.4725 |
| ADAMTS  | 1.25542 | 0.57714 | 7.87058 | 0.00022  | 0.00221 | 0.55347 |
| IER5L   | 1.256   | 4.62225 | 6.78943 | 0.0005   | 0.00371 | -0.3632 |
| TEAD2   | 1.25763 | 4.43348 | 11.2189 | 3.01E-05 | 0.00064 | 2.82284 |
| ARHGAP  | 1.25801 | 0.01552 | 5.05892 | 0.00232  | 0.0107  | -2.0967 |
| ELFN2   | 1.25919 | 2.42179 | 4.62408 | 0.00361  | 0.01472 | -2.5938 |
| FAT1    | 1.25937 | 3.91894 | 6.0767  | 0.0009   | 0.00556 | -1.0333 |
| EXOSC8  | 1.2619  | 3.36295 | 7.28647 | 0.00034  | 0.00285 | 0.07208 |
| MAGIX   | 1.26197 | 1.76395 | 10.33   | 4.83E-05 | 0.00085 | 2.2887  |
| MICB    | 1.26439 | 2.69086 | 14.6111 | 6.48E-06 | 0.00025 | 4.53752 |
| ZNF525  | 1.26442 | 2.54084 | 10.4639 | 4.49E-05 | 0.00081 | 2.37189 |
| ACBD7   | 1.26845 | 0.29796 | 7.20808 | 0.00036  | 0.00298 | 0.00506 |
| KRT18P2 | 1.26939 | -0.2333 | 6.68549 | 0.00054  | 0.00392 | -0.4574 |
| CASZ1   | 1.26961 | 0.41142 | 4.56283 | 0.00385  | 0.0154  | -2.666  |
| FUCA1   | 1.27172 | 2.95602 | 7.7433  | 0.00024  | 0.00234 | 0.45119 |
| DDN     | 1.27232 | -0.2068 | 5.96998 | 0.00099  | 0.00592 | -1.1386 |
| GSTO2   | 1.27299 | 1.45027 | 7.50673 | 0.00029  | 0.00261 | 0.25726 |
| HDAC9   | 1.27365 | 5.66941 | 5.80937 | 0.00114  | 0.00659 | -1.2998 |
| CYP2S1  | 1.27379 | 1.97966 | 9.97203 | 5.91E-05 | 0.00096 | 2.06124 |
| CKAP2   | 1.27409 | 4.16509 | 8.46844 | 0.00015  | 0.00172 | 1.01567 |
| SIX1    | 1.27548 | 0.51203 | 5.71567 | 0.00124  | 0.007   | -1.3953 |
| CENPV   | 1.27657 | 1.45107 | 7.72776 | 0.00025  | 0.00236 | 0.4386  |
| TPT1-AS | 1.27961 | -0.0861 | 7.09838 | 0.00039  | 0.00315 | -0.0897 |
| SLC17A5 | 1.28028 | 2.5513  | 5.11674 | 0.00219  | 0.01029 | -2.0327 |
| SDC4    | 1.28218 | 5.37638 | 7.04333 | 0.00041  | 0.00326 | -0.1378 |
| ANXA3   | 1.28252 | 5.18536 | 4.77038 | 0.0031   | 0.01321 | -2.4236 |
| UFM1    | 1.28314 | 3.45317 | 11.8502 | 2.19E-05 | 0.00053 | 3.17797 |
| SMIM24  | 1.28342 | 0.38188 | 3.65793 | 0.01062  | 0.03257 | -3.7967 |
| ARID3A  | 1.28399 | 1.67851 | 5.97767 | 0.00099  | 0.0059  | -1.131  |
| SERTAD4 | 1.2849  | 1.67939 | 9.00462 | 0.00011  | 0.00138 | 1.40647 |
| SOX8    | 1.28581 | -1.9944 | 3.50578 | 0.01275  | 0.03752 | -3.9983 |
| MXRA5   | 1.28581 | 3.93612 | 3.58055 | 0.01165  | 0.03499 | -3.8989 |
| KDM6A   | 1.28606 | 3.78468 | 14.3731 | 7.14E-06 | 0.00026 | 4.43108 |
| TGFA    | 1.28617 | 0.57675 | 3.93361 | 0.00769  | 0.02567 | -3.4396 |
| FGFR3   | 1.28721 | 1.50085 | 6.57997 | 0.00059  | 0.00415 | -0.5543 |
| NELL2   | 1.28783 | 3.32747 | 3.76215 | 0.00938  | 0.02966 | -3.6604 |
| UBL3    | 1.28948 | 1.65531 | 12.3981 | 1.69E-05 | 0.00045 | 3.47145 |
| CELSR3  | 1.29209 | -0.2258 | 6.72806 | 0.00053  | 0.00384 | -0.4187 |
| GAS6    | 1.29239 | 2.78196 | 9.68061 | 6.99E-05 | 0.00106 | 1.87037 |
| TMTC4   | 1.29243 | 2.73177 | 5.85285 | 0.0011   | 0.0064  | -1.2559 |
| IFIT5   | 1.29303 | 0.55224 | 4.73951 | 0.0032   | 0.01348 | -2.4592 |
| CDC42EP | 1.29303 | 4.01706 | 6.67012 | 0.00055  | 0.00396 | -0.4715 |
| VASH2   | 1.29314 | -1.9806 | 14.3666 | 7.15E-06 | 0.00026 | 4.42817 |
| WNT5A   | 1.29325 | 3.10508 | 5.07664 | 0.00228  | 0.01057 | -2.0771 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| ULK2     | 1.29971 | -0.7015 | 6.80419 | 0.00049  | 0.00369 | -0.3499 |
| DEPTOR   | 1.30293 | 1.94315 | 8.12974 | 0.00019  | 0.00198 | 0.75743 |
| VWA7     | 1.30403 | -1.5452 | 8.11746 | 0.00019  | 0.00198 | 0.74789 |
| ATF4P3   | 1.30451 | 2.36053 | 3.89374 | 0.00805  | 0.02648 | -3.4905 |
| ARID1B   | 1.3086  | 4.30792 | 12.0681 | 1.97E-05 | 0.0005  | 3.29625 |
| CENPBD   | 1.30877 | 3.0248  | 10.4828 | 4.44E-05 | 0.00081 | 2.38359 |
| TTC39B   | 1.30991 | 1.19147 | 4.50958 | 0.00407  | 0.01601 | -2.7292 |
| MYT1     | 1.31074 | -1.4357 | 7.32857 | 0.00033  | 0.00279 | 0.10782 |
| RNF144B  | 1.31264 | 5.4114  | 5.48279 | 0.00154  | 0.00809 | -1.6375 |
| SYT15-A  | 1.31471 | -0.534  | 6.57556 | 0.00059  | 0.00416 | -0.5584 |
| STK24P1  | 1.31486 | 0.6424  | 14.6784 | 6.31E-06 | 0.00024 | 4.56729 |
| TBX19    | 1.31626 | 0.19221 | 6.51482 | 0.00063  | 0.00429 | -0.6147 |
| MT1L     | 1.31831 | 1.73378 | 4.42103 | 0.00447  | 0.01713 | -2.8353 |
| GCH1     | 1.31931 | 0.70113 | 8.80575 | 0.00012  | 0.0015  | 1.264   |
| ZC3H13   | 1.31973 | 4.43203 | 16.3455 | 3.36E-06 | 0.00017 | 5.2622  |
| BORA     | 1.32023 | 1.8274  | 9.06382 | 0.0001   | 0.00134 | 1.44834 |
| RAB20    | 1.3228  | 1.37833 | 8.05781 | 0.0002   | 0.00204 | 0.70139 |
| CADM4    | 1.32295 | 2.77842 | 14.3149 | 7.31E-06 | 0.00026 | 4.40478 |
| RELB     | 1.32359 | 1.83011 | 3.77469 | 0.00925  | 0.02933 | -3.6441 |
| DUSP9    | 1.33224 | 1.71232 | 8.28435 | 0.00017  | 0.00185 | 0.87645 |
| ZDHHC20  | 1.33746 | 3.92367 | 14.2619 | 7.47E-06 | 0.00027 | 4.38073 |
| MPZL3    | 1.33794 | 1.45837 | 6.94351 | 0.00044  | 0.00342 | -0.2256 |
| ARHGEF   | 1.33929 | 1.60991 | 8.01598 | 0.0002   | 0.00208 | 0.6686  |
| THBS3-A  | 1.34219 | -1.2211 | 6.01305 | 0.00096  | 0.00578 | -1.0959 |
| BEX2     | 1.34297 | 2.54458 | 5.25329 | 0.00192  | 0.00939 | -1.8831 |
| SH3BGR   | 1.34813 | 1.98874 | 10.1138 | 5.45E-05 | 0.00091 | 2.15225 |
| MCTP2    | 1.35002 | -0.2771 | 8.49719 | 0.00015  | 0.0017  | 1.03718 |
| HAPLN3   | 1.35128 | 3.01433 | 8.49261 | 0.00015  | 0.0017  | 1.03376 |
| PDK3     | 1.3547  | 0.49578 | 6.99215 | 0.00043  | 0.00334 | -0.1827 |
| KRT18P4  | 1.35665 | -0.198  | 4.3278  | 0.00495  | 0.01846 | -2.9482 |
| CHST6    | 1.35747 | 1.95472 | 6.82401 | 0.00049  | 0.00365 | -0.3321 |
| RNF122   | 1.35914 | -0.0485 | 4.06613 | 0.00661  | 0.02303 | -3.2718 |
| GALNT12  | 1.36072 | 0.85698 | 6.51191 | 0.00063  | 0.00429 | -0.6174 |
| GFOD1    | 1.36184 | 4.67548 | 10.675  | 4.00E-05 | 0.00075 | 2.50104 |
| CTXN1    | 1.36313 | 4.81935 | 10.6147 | 4.13E-05 | 0.00077 | 2.46442 |
| FGFBP1   | 1.368   | -1.4542 | 4.8922  | 0.00274  | 0.01208 | -2.2842 |
| DAPP1    | 1.36902 | 0.0713  | 7.31305 | 0.00033  | 0.00281 | 0.09467 |
| KRT18P1  | 1.36937 | 1.96339 | 10.5691 | 4.24E-05 | 0.00078 | 2.43657 |
| LARGE2   | 1.37067 | 1.34506 | 8.51346 | 0.00014  | 0.00169 | 1.04932 |
| SH3YL1   | 1.37111 | 2.41165 | 7.48226 | 0.0003   | 0.00264 | 0.23691 |
| KLK14    | 1.37423 | -1.3317 | 4.53401 | 0.00396  | 0.01574 | -2.7002 |
| CD74     | 1.37477 | 3.96681 | 9.83656 | 6.38E-05 | 0.001   | 1.97316 |
| PCSK9    | 1.37504 | 4.05475 | 5.53189 | 0.00147  | 0.00788 | -1.5859 |
| GTF3A    | 1.37559 | 4.25616 | 16.0017 | 3.80E-06 | 0.00018 | 5.12525 |
| RAB11FIP | 1.37618 | 3.04462 | 10.4674 | 4.48E-05 | 0.00081 | 2.37404 |
| FRG1BP   | 1.37718 | -1.2268 | 11.2819 | 2.91E-05 | 0.00062 | 2.85914 |
| TSPAN2   | 1.3776  | 0.52481 | 4.80259 | 0.003    | 0.01291 | -2.3865 |
| MAB21L3  | 1.37788 | -0.8814 | 6.16801 | 0.00084  | 0.00528 | -0.9442 |
| PTCH1    | 1.38025 | 1.2244  | 6.03392 | 0.00094  | 0.0057  | -1.0753 |
| SHISA2   | 1.38082 | -0.7945 | 3.35416 | 0.01535  | 0.04299 | -4.2024 |
| HMGA1    | 1.38105 | 6.7898  | 7.91149 | 0.00022  | 0.00216 | 0.58604 |
| ZNF585B  | 1.38181 | -1.3636 | 6.14896 | 0.00085  | 0.00534 | -0.9627 |
| BCAM     | 1.38446 | 6.56344 | 10.8496 | 3.65E-05 | 0.00071 | 2.60601 |
| SUCLA2   | 1.38579 | 3.22347 | 16.3834 | 3.31E-06 | 0.00017 | 5.27713 |
| KLC3     | 1.38738 | 1.58156 | 4.96091 | 0.00255  | 0.01146 | -2.2064 |
| DENND1C  | 1.38818 | -0.0247 | 4.31319 | 0.00503  | 0.01868 | -2.966  |
| KCNIP1   | 1.38857 | 3.81808 | 5.24986 | 0.00192  | 0.00941 | -1.8869 |
| KRT18P1  | 1.39035 | 0.76155 | 8.49711 | 0.00015  | 0.0017  | 1.03712 |

|          |         |         |         |          |         |         |
|----------|---------|---------|---------|----------|---------|---------|
| HSPA2    | 1.39058 | 2.94888 | 5.60147 | 0.00138  | 0.00756 | -1.5132 |
| ACTRT3   | 1.3919  | 1.17017 | 7.84358 | 0.00023  | 0.00223 | 0.53189 |
| CLUHP3   | 1.39338 | 1.40533 | 14.7701 | 6.08E-06 | 0.00024 | 4.60761 |
| TMEM169  | 1.39822 | -0.5456 | 7.1552  | 0.00038  | 0.00307 | -0.0405 |
| CCN5     | 1.3988  | -1.2806 | 4.50364 | 0.00409  | 0.01607 | -2.7363 |
| RNF207   | 1.39918 | 1.84146 | 4.81388 | 0.00296  | 0.01281 | -2.3735 |
| MBP      | 1.40121 | 2.40329 | 6.15048 | 0.00085  | 0.00534 | -0.9612 |
| GPR176   | 1.4014  | 1.9619  | 13.7475 | 9.25E-06 | 0.00031 | 4.14245 |
| EPHB3    | 1.40188 | -1.3392 | 4.41894 | 0.00448  | 0.01716 | -2.8378 |
| HOXC9    | 1.40272 | -1.8456 | 7.42595 | 0.00031  | 0.00269 | 0.18988 |
| SERTM1   | 1.40472 | -1.6104 | 4.97077 | 0.00253  | 0.01138 | -2.1954 |
| TMSB15A  | 1.40577 | -0.3081 | 3.43665 | 0.01387  | 0.03996 | -4.091  |
| GGT5     | 1.41075 | -1.4751 | 3.50048 | 0.01283  | 0.03767 | -4.0054 |
| PCOTH    | 1.41156 | -1.1734 | 4.40725 | 0.00454  | 0.01731 | -2.8519 |
| KLF12    | 1.41232 | 2.17802 | 18.7756 | 1.48E-06 | 0.00011 | 6.14931 |
| SCHIP1   | 1.41492 | -1.4426 | 5.86584 | 0.00109  | 0.00635 | -1.2428 |
| LINC0163 | 1.41835 | -1.5782 | 6.41977 | 0.00068  | 0.00453 | -0.7036 |
| LDB3     | 1.41866 | -1.1003 | 3.70768 | 0.01001  | 0.03108 | -3.7314 |
| LRRC1    | 1.41994 | 1.66512 | 7.70116 | 0.00025  | 0.00238 | 0.41701 |
| SRSF12   | 1.42159 | -0.1871 | 7.58245 | 0.00027  | 0.00252 | 0.31988 |
| CDK8P2   | 1.42298 | -0.4286 | 5.24734 | 0.00193  | 0.00943 | -1.8896 |
| KRT18P2  | 1.42424 | 0.72191 | 7.35036 | 0.00033  | 0.00276 | 0.12626 |
| ZDHHC20  | 1.42672 | 2.24493 | 9.75998 | 6.68E-05 | 0.00103 | 1.92287 |
| EFNB2    | 1.4311  | 4.32957 | 4.34765 | 0.00484  | 0.01814 | -2.924  |
| KRT18P2  | 1.432   | -0.2018 | 7.35334 | 0.00032  | 0.00276 | 0.12878 |
| SLC6A8   | 1.43966 | 2.11048 | 7.77817 | 0.00024  | 0.0023  | 0.47935 |
| GALNT6   | 1.44035 | 2.52415 | 8.79177 | 0.00012  | 0.00151 | 1.25388 |
| CBR3-AS  | 1.441   | 0.00277 | 9.59211 | 7.37E-05 | 0.0011  | 1.81135 |
| IQC�     | 1.44207 | 0.43663 | 6.71806 | 0.00053  | 0.00385 | -0.4278 |
| UGGT2    | 1.44417 | 2.58118 | 9.37718 | 8.38E-05 | 0.00118 | 1.66591 |
| S100A1   | 1.44692 | 2.305   | 4.14276 | 0.00607  | 0.02154 | -3.176  |
| SPTBN2   | 1.45014 | 2.78079 | 7.37757 | 0.00032  | 0.00273 | 0.14923 |
| PLK2     | 1.45049 | 6.17293 | 5.50169 | 0.00152  | 0.00801 | -1.6176 |
| VWA8     | 1.45467 | 2.86631 | 18.192  | 1.79E-06 | 0.00012 | 5.94829 |
| PTK7     | 1.45608 | 5.15536 | 11.9173 | 2.12E-05 | 0.00052 | 3.21464 |
| HES4     | 1.45784 | 3.35447 | 6.81708 | 0.00049  | 0.00366 | -0.3383 |
| PPP2R3A  | 1.46002 | 3.86778 | 11.5818 | 2.50E-05 | 0.00057 | 3.02931 |
| AP1M2    | 1.46018 | 5.32091 | 12.3954 | 1.69E-05 | 0.00045 | 3.47003 |
| GAL      | 1.46072 | -0.2238 | 6.44946 | 0.00066  | 0.00446 | -0.6757 |
| KRT8P36  | 1.4609  | -0.5435 | 9.27459 | 8.91E-05 | 0.00123 | 1.59542 |
| TPP2     | 1.46103 | 3.39431 | 18.0827 | 1.85E-06 | 0.00012 | 5.90983 |
| GJB3     | 1.46176 | 1.20316 | 7.28214 | 0.00034  | 0.00286 | 0.06839 |
| CRABP2   | 1.46249 | 4.31449 | 7.36357 | 0.00032  | 0.00275 | 0.13742 |
| WNT7A    | 1.46401 | 5.32619 | 8.63032 | 0.00013  | 0.0016  | 1.13592 |
| REM1     | 1.46423 | -1.8535 | 6.65411 | 0.00056  | 0.00399 | -0.4861 |
| PPP1R14  | 1.46638 | 0.86252 | 10.4201 | 4.60E-05 | 0.00082 | 2.34477 |
| TUBA5P   | 1.46779 | 0.74921 | 6.59492 | 0.00059  | 0.00411 | -0.5405 |
| APOL6    | 1.46797 | 2.42971 | 5.09389 | 0.00224  | 0.01044 | -2.0579 |
| PARD3B   | 1.46866 | 3.28332 | 3.58524 | 0.01158  | 0.03481 | -3.8926 |
| CDA      | 1.46924 | 0.82443 | 3.29222 | 0.01658  | 0.04552 | -4.2865 |
| ERFE     | 1.47052 | 2.61893 | 9.96338 | 5.94E-05 | 0.00096 | 2.05565 |
| SPON1    | 1.47074 | 6.30607 | 7.07577 | 0.0004   | 0.0032  | -0.1094 |
| PROSER   | 1.47164 | 3.57418 | 16.6139 | 3.05E-06 | 0.00016 | 5.36701 |
| ELL2     | 1.47176 | 0.46662 | 11.9867 | 2.05E-05 | 0.00051 | 3.25234 |
| LRRC8D   | 1.47719 | 0.23606 | 5.29269 | 0.00185  | 0.00915 | -1.8405 |
| MEOX1    | 1.47768 | 2.56591 | 3.45588 | 0.01355  | 0.03929 | -4.0652 |
| USP43    | 1.47975 | 0.51824 | 7.21122 | 0.00036  | 0.00297 | 0.00775 |
| TMEM52   | 1.47988 | 0.36191 | 10.7122 | 3.92E-05 | 0.00074 | 2.52353 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| RASAL1   | 1.48091 | 2.39183 | 5.95483 | 0.00101  | 0.00598  | -1.1537 |
| MREG     | 1.48116 | 0.8381  | 5.26314 | 0.0019   | 0.00933  | -1.8725 |
| HMGA1P   | 1.48353 | 0.874   | 7.42787 | 0.00031  | 0.00269  | 0.19148 |
| VWA1     | 1.48578 | 1.8742  | 6.1401  | 0.00086  | 0.00537  | -0.9713 |
| SLC4A11  | 1.49134 | 3.0834  | 14.3917 | 7.08E-06 | 0.00026  | 4.43949 |
| ARHGEF   | 1.49594 | 2.59364 | 8.4254  | 0.00015  | 0.00175  | 0.98336 |
| PRSS23   | 1.5024  | 3.83535 | 3.30271 | 0.01637  | 0.04514  | -4.2723 |
| DTX4     | 1.50464 | 0.90816 | 5.97335 | 0.00099  | 0.00591  | -1.1353 |
| MAP1LC3  | 1.50566 | 0.42874 | 3.21404 | 0.01829  | 0.04907  | -4.3935 |
| RFXAP    | 1.50809 | 0.698   | 10.014  | 5.77E-05 | 0.00095  | 2.08833 |
| ELL2P1   | 1.51075 | 0.36791 | 7.23251 | 0.00036  | 0.00294  | 0.026   |
| ZNNT1    | 1.51158 | -0.4296 | 3.47735 | 0.0132   | 0.03853  | -4.0364 |
| TENT5B   | 1.51168 | 2.75314 | 6.29735 | 0.00075  | 0.00487  | -0.8197 |
| ITPR3    | 1.51169 | 5.34544 | 12.488  | 1.62E-05 | 0.00044  | 3.51841 |
| MYADM    | 1.51415 | 6.14696 | 13.5052 | 1.03E-05 | 0.00033  | 4.02699 |
| DUSP8    | 1.51957 | 0.73606 | 10.1907 | 5.22E-05 | 0.00089  | 2.20111 |
| PRRT2    | 1.52212 | -1.5976 | 9.58287 | 7.41E-05 | 0.0011   | 1.80516 |
| TUT7     | 1.52438 | 3.30345 | 11.7374 | 2.32E-05 | 0.00055  | 3.11591 |
| MPZL2    | 1.52463 | 4.18515 | 7.78049 | 0.00024  | 0.0023   | 0.48122 |
| SUCLA2P  | 1.52635 | 2.54803 | 13.0658 | 1.24E-05 | 0.00037  | 3.81221 |
| SLC4A3   | 1.52715 | 1.51136 | 10.6181 | 4.13E-05 | 0.00077  | 2.46648 |
| SVIP     | 1.5274  | 1.31302 | 10.5567 | 4.27E-05 | 0.00079  | 2.42899 |
| MMP15    | 1.53287 | 2.25155 | 8.92843 | 0.00011  | 0.00142  | 1.35223 |
| CCL26    | 1.53321 | -1.1306 | 3.97473 | 0.00734  | 0.02479  | -3.3872 |
| FAM107A  | 1.54233 | 2.47144 | 3.89728 | 0.00802  | 0.0264   | -3.486  |
| EYA1     | 1.54417 | -5.8595 | 4.54427 | 0.00392  | 0.01562  | -2.688  |
| KCNK1    | 1.54556 | 0.97288 | 8.36124 | 0.00016  | 0.00179  | 0.93493 |
| CERCAM   | 1.55113 | 3.40319 | 10.8268 | 3.69E-05 | 0.00072  | 2.59241 |
| SMIM10L  | 1.55214 | -0.7269 | 6.20902 | 0.00081  | 0.00514  | -0.9045 |
| FERMT1   | 1.55721 | 0.95701 | 5.96258 | 0.001    | 0.00595  | -1.146  |
| ARHGEF   | 1.55928 | 2.36884 | 17.6362 | 2.15E-06 | 0.00013  | 5.75008 |
| MAFF     | 1.56653 | 0.38189 | 7.00841 | 0.00042  | 0.00331  | -0.1684 |
| LINC0150 | 1.56748 | -3.2496 | 4.14075 | 0.00608  | 0.02159  | -3.1785 |
| CCDC122  | 1.56836 | -0.7295 | 6.53679 | 0.00061  | 0.00425  | -0.5943 |
| RAB32    | 1.57149 | 3.53058 | 15.9002 | 3.95E-06 | 0.00018  | 5.08418 |
| FSCN2    | 1.57194 | -1.5946 | 6.79826 | 0.0005   | 0.00369  | -0.3553 |
| P3H2     | 1.57574 | 4.36646 | 8.6012  | 0.00014  | 0.00162  | 1.11444 |
| LIMS2    | 1.57593 | 0.84569 | 4.4861  | 0.00417  | 0.01632  | -2.7572 |
| NAV2     | 1.57738 | 3.67288 | 8.34257 | 0.00016  | 0.00181  | 0.92078 |
| RYR2     | 1.57838 | -0.3932 | 5.93955 | 0.00102  | 0.00604  | -1.1689 |
| PDE1C    | 1.57958 | 0.98556 | 3.37286 | 0.015    | 0.04231  | -4.177  |
| HES6     | 1.58246 | 2.19872 | 10.1892 | 5.22E-05 | 0.00089  | 2.20014 |
| PLEKHO   | 1.58465 | 3.30546 | 12.9184 | 1.33E-05 | 0.00038  | 3.73852 |
| MAPRE2   | 1.58474 | -1.4647 | 3.54336 | 0.01218  | 0.03615  | -3.9482 |
| PRTFDC   | 1.58908 | -0.1698 | 19.9087 | 1.05E-06 | 9.09E-05 | 6.5204  |
| DOCK9    | 1.59117 | 2.60613 | 14.3869 | 7.10E-06 | 0.00026  | 4.43733 |
| RALGPS   | 1.59225 | 0.07035 | 7.56443 | 0.00028  | 0.00254  | 0.30503 |
| LIMK2    | 1.5964  | 4.00606 | 7.69213 | 0.00025  | 0.0024   | 0.40967 |
| SEMA7A   | 1.59653 | 1.40743 | 14.2314 | 7.56E-06 | 0.00027  | 4.36685 |
| FZD3     | 1.59906 | 0.94233 | 9.20329 | 9.31E-05 | 0.00127  | 1.54601 |
| ALPL     | 1.60317 | 1.31376 | 15.9271 | 3.91E-06 | 0.00018  | 5.0951  |
| HMGA1P   | 1.60722 | 1.804   | 13.4303 | 1.06E-05 | 0.00034  | 3.99089 |
| EBI3     | 1.60926 | -0.4896 | 5.06942 | 0.00229  | 0.01061  | -2.0851 |
| KCNH2    | 1.61157 | -2.676  | 4.84376 | 0.00287  | 0.01251  | -2.3393 |
| ZSWIM4   | 1.61421 | 1.44537 | 4.19764 | 0.00571  | 0.02054  | -3.1079 |
| FILIP1L  | 1.61602 | 0.8226  | 4.16705 | 0.00591  | 0.02109  | -3.1458 |
| ARID5B   | 1.62447 | 4.52521 | 14.2107 | 7.63E-06 | 0.00027  | 4.3574  |
| TMPRSS   | 1.62469 | -2.0943 | 5.32611 | 0.00179  | 0.00894  | -1.8044 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| NXNL2    | 1.62647 | -1.1595 | 7.78845 | 0.00024  | 0.00229  | 0.48763 |
| PATJ     | 1.62719 | 4.8406  | 10.8579 | 3.63E-05 | 0.00071  | 2.61095 |
| PAC SIN1 | 1.62807 | 2.18999 | 9.28011 | 8.88E-05 | 0.00123  | 1.59923 |
| HDAC5    | 1.63075 | 0.95092 | 5.3243  | 0.00179  | 0.00895  | -1.8064 |
| CELSR2   | 1.63095 | 3.33855 | 7.64943 | 0.00026  | 0.00244  | 0.37484 |
| OCLN     | 1.63195 | 1.03362 | 9.65123 | 7.11E-05 | 0.00107  | 1.85083 |
| SLC9A2   | 1.63323 | 1.87959 | 8.89815 | 0.00011  | 0.00144  | 1.33056 |
| KLK1     | 1.63337 | -1.2894 | 4.01312 | 0.00702  | 0.02402  | -3.3386 |
| FBLN2    | 1.63359 | 2.03198 | 5.36915 | 0.00172  | 0.00871  | -1.7583 |
| ATP6V1B  | 1.63363 | -1.5022 | 4.90549 | 0.0027   | 0.01196  | -2.2691 |
| AKR1E2   | 1.63439 | -1.9179 | 4.81568 | 0.00296  | 0.0128   | -2.3715 |
| CYFIP2   | 1.63613 | 1.46756 | 5.54268 | 0.00146  | 0.00782  | -1.5745 |
| WFDC2    | 1.63808 | 4.13201 | 5.51409 | 0.0015   | 0.00796  | -1.6045 |
| IGDCC4   | 1.63978 | 0.57595 | 5.24053 | 0.00194  | 0.00947  | -1.897  |
| NXPH4    | 1.63989 | 1.88444 | 8.02558 | 0.0002   | 0.00207  | 0.67613 |
| TENM1    | 1.64254 | -0.6969 | 3.23561 | 0.0178   | 0.04805  | -4.3639 |
| LBP      | 1.64617 | -2.5786 | 3.34276 | 0.01557  | 0.04347  | -4.2178 |
| LRRC34   | 1.64715 | -1.7343 | 10.0166 | 5.76E-05 | 0.00095  | 2.08996 |
| SLC7A1   | 1.64808 | 4.16437 | 15.344  | 4.87E-06 | 0.00021  | 4.85425 |
| SLC6A15  | 1.649   | -5.0497 | 7.3874  | 0.00032  | 0.00273  | 0.1575  |
| NFKBIE   | 1.65126 | 1.105   | 5.65296 | 0.00132  | 0.0073   | -1.4598 |
| RTKN2    | 1.65179 | 3.61297 | 6.43623 | 0.00067  | 0.00449  | -0.6882 |
| ALS2CL   | 1.65404 | 1.82749 | 6.0444  | 0.00093  | 0.00566  | -1.065  |
| BCL2L15  | 1.65707 | -1.1893 | 8.04262 | 0.0002   | 0.00205  | 0.6895  |
| INSR     | 1.66006 | 2.80942 | 7.78686 | 0.00024  | 0.00229  | 0.48635 |
| PCDH1    | 1.66472 | 1.50406 | 6.51855 | 0.00062  | 0.00429  | -0.6112 |
| SUCLA2F  | 1.66889 | 0.36863 | 9.93396 | 6.04E-05 | 0.00097  | 2.0366  |
| ST8SIA1  | 1.67019 | 0.21885 | 4.60389 | 0.00368  | 0.01496  | -2.6176 |
| GPR39    | 1.67934 | -0.3748 | 5.5373  | 0.00147  | 0.00784  | -1.5802 |
| BMAL2    | 1.67964 | 2.05132 | 9.25293 | 9.03E-05 | 0.00124  | 1.58045 |
| OR2A7    | 1.68131 | 0.71284 | 8.27204 | 0.00017  | 0.00186  | 0.86705 |
| CRISPLD  | 1.68424 | -0.0879 | 5.03099 | 0.00238  | 0.01091  | -2.1279 |
| SERPINA  | 1.69112 | 0.5961  | 5.76831 | 0.00119  | 0.00676  | -1.3415 |
| INA      | 1.69258 | 2.50374 | 4.97952 | 0.00251  | 0.0113   | -2.1855 |
| TESK2    | 1.69579 | -0.7626 | 9.06972 | 0.0001   | 0.00134  | 1.4525  |
| MPP7     | 1.70343 | 2.06322 | 5.03805 | 0.00237  | 0.01086  | -2.12   |
| FOXL2NE  | 1.70446 | -1.3399 | 8.69888 | 0.00013  | 0.00156  | 1.18625 |
| PHLDA3   | 1.70973 | 4.26343 | 12.7719 | 1.42E-05 | 0.0004   | 3.6644  |
| ZSCAN5L  | 1.71856 | -3.3454 | 3.6342  | 0.01092  | 0.03326  | -3.8279 |
| KLF5     | 1.72023 | 3.90046 | 21.1612 | 7.30E-07 | 7.40E-05 | 6.90362 |
| PTGER2   | 1.72081 | -0.4769 | 8.00873 | 0.0002   | 0.00208  | 0.6629  |
| SP6      | 1.72309 | -3.1906 | 9.88936 | 6.19E-05 | 0.00098  | 2.00762 |
| CYP26A1  | 1.73015 | -2.0926 | 4.1906  | 0.00575  | 0.02066  | -3.1166 |
| RASL11B  | 1.73235 | -1.1677 | 7.60447 | 0.00027  | 0.00249  | 0.338   |
| MDGA1    | 1.73568 | -0.7664 | 8.16362 | 0.00018  | 0.00195  | 0.78368 |
| SMIM10L  | 1.73865 | -1.1336 | 5.67814 | 0.00129  | 0.00717  | -1.4339 |
| FBLN5    | 1.74409 | 2.20243 | 4.34753 | 0.00484  | 0.01814  | -2.9242 |
| MOB3B    | 1.74491 | 2.14032 | 4.42498 | 0.00445  | 0.0171   | -2.8305 |
| PNMA3    | 1.74786 | 1.00682 | 8.96485 | 0.00011  | 0.0014   | 1.37821 |
| OPHN1    | 1.75243 | 3.94951 | 7.83723 | 0.00023  | 0.00223  | 0.5268  |
| MSI1     | 1.75384 | 0.86396 | 6.34797 | 0.00072  | 0.00473  | -0.7715 |
| CLDN3    | 1.76199 | 3.22233 | 7.68772 | 0.00025  | 0.0024   | 0.40608 |
| FOXI3    | 1.763   | -1.9506 | 4.46052 | 0.00429  | 0.01664  | -2.7878 |
| IL17D    | 1.76475 | -2.0366 | 4.4669  | 0.00426  | 0.01657  | -2.7802 |
| KRT18P1  | 1.76703 | -0.5849 | 9.70598 | 6.89E-05 | 0.00105  | 1.88719 |
| TNS1     | 1.77156 | 2.17938 | 9.40576 | 8.23E-05 | 0.00117  | 1.68543 |
| PCK2     | 1.7732  | 2.43569 | 3.66131 | 0.01057  | 0.03246  | -3.7922 |
| SYTL1    | 1.77358 | 2.67088 | 6.08067 | 0.0009   | 0.00555  | -1.0294 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| FHIP1A   | 1.77418 | -0.1707 | 8.81246 | 0.00012  | 0.00149  | 1.26886 |
| SIM2     | 1.77507 | 2.61587 | 12.7998 | 1.40E-05 | 0.0004   | 3.67857 |
| LOXL1-A  | 1.77859 | 1.78233 | 6.94886 | 0.00044  | 0.00341  | -0.2209 |
| SDCBP2   | 1.7814  | -2.336  | 6.0811  | 0.0009   | 0.00555  | -1.029  |
| DMKN     | 1.7885  | 4.89673 | 10.2029 | 5.18E-05 | 0.00088  | 2.2088  |
| PRSS16   | 1.78968 | 1.84821 | 11.7352 | 2.32E-05 | 0.00055  | 3.11467 |
| HMGA1P   | 1.7965  | 2.85494 | 15.2197 | 5.10E-06 | 0.00021  | 4.80166 |
| CDKN2B   | 1.79667 | 3.20355 | 10.2331 | 5.10E-05 | 0.00088  | 2.22787 |
| N4BP3    | 1.79768 | 1.99689 | 13.3892 | 1.08E-05 | 0.00034  | 3.97101 |
| ROBO1    | 1.80475 | -0.7136 | 4.85833 | 0.00283  | 0.0124   | -2.3227 |
| VASN     | 1.80643 | 3.09305 | 9.49769 | 7.79E-05 | 0.00113  | 1.74783 |
| TGFB2    | 1.80704 | 0.39801 | 5.49803 | 0.00152  | 0.00803  | -1.6214 |
| OBSL1    | 1.80707 | 3.53999 | 13.4588 | 1.05E-05 | 0.00034  | 4.00467 |
| PCP4L1   | 1.81068 | -3.4075 | 9.56083 | 7.50E-05 | 0.00111  | 1.79037 |
| PRR15-D  | 1.81377 | -2.1428 | 4.76709 | 0.00311  | 0.01324  | -2.4274 |
| SMAD9    | 1.81848 | 0.18023 | 6.31588 | 0.00074  | 0.00482  | -0.802  |
| CHCHD7   | 1.82001 | 4.04606 | 22.6323 | 4.90E-07 | 5.80E-05 | 7.32141 |
| HOXA10-  | 1.82078 | 0.95098 | 10.6224 | 4.12E-05 | 0.00077  | 2.46907 |
| EMX2     | 1.82235 | 4.24687 | 9.10055 | 9.92E-05 | 0.00132  | 1.47419 |
| MSR1     | 1.82908 | -2.8584 | 4.10361 | 0.00634  | 0.02228  | -3.2248 |
| CRABP1   | 1.82983 | -0.717  | 4.98215 | 0.0025   | 0.01128  | -2.1826 |
| IL18R1   | 1.83265 | -1.2092 | 16.3293 | 3.38E-06 | 0.00017  | 5.25584 |
| EPS8L2   | 1.83879 | 4.42603 | 16.335  | 3.37E-06 | 0.00017  | 5.25807 |
| MBNL1-A  | 1.84213 | 0.20996 | 4.39102 | 0.00462  | 0.01752  | -2.8715 |
| CSF1     | 1.84314 | 1.05123 | 4.13972 | 0.00609  | 0.02161  | -3.1798 |
| TMEM86A  | 1.84529 | -0.258  | 9.99436 | 5.83E-05 | 0.00095  | 2.07565 |
| DES      | 1.84678 | -1.5693 | 4.00205 | 0.00711  | 0.02422  | -3.3526 |
| AK7      | 1.84823 | -1.2869 | 3.72556 | 0.0098   | 0.0306   | -3.7081 |
| FRY      | 1.84876 | -1.9827 | 4.98601 | 0.00249  | 0.01126  | -2.1782 |
| LLGL2    | 1.85221 | 2.82165 | 12.8118 | 1.40E-05 | 0.0004   | 3.68469 |
| CYP24A1  | 1.85353 | -1.6218 | 5.54179 | 0.00146  | 0.00782  | -1.5755 |
| HOXC10   | 1.86014 | -0.5577 | 8.44722 | 0.00015  | 0.00174  | 0.99976 |
| MBOAT1   | 1.86183 | 0.86963 | 13.7457 | 9.26E-06 | 0.00031  | 4.14157 |
| TMEM51-  | 1.8647  | -1.8348 | 7.77835 | 0.00024  | 0.0023   | 0.4795  |
| TBC1D8E  | 1.86595 | -1.271  | 10.4703 | 4.47E-05 | 0.00081  | 2.37588 |
| NYNRIN   | 1.86646 | -1.7339 | 3.89606 | 0.00803  | 0.02643  | -3.4876 |
| ANKRD1   | 1.87097 | 6.08716 | 4.11176 | 0.00628  | 0.02214  | -3.2147 |
| QSOX1    | 1.87181 | 6.38821 | 13.3941 | 1.08E-05 | 0.00034  | 3.97336 |
| MYO6     | 1.87209 | 3.48754 | 8.99571 | 0.00011  | 0.00138  | 1.40015 |
| JPH1     | 1.87767 | 2.09124 | 14.9168 | 5.74E-06 | 0.00023  | 4.6716  |
| MYL2     | 1.88022 | -2.6696 | 4.68975 | 0.00337  | 0.014    | -2.517  |
| MYO5B    | 1.88721 | 0.23578 | 4.21734 | 0.00558  | 0.02021  | -3.0836 |
| IL17RE   | 1.88811 | -0.6032 | 15.628  | 4.37E-06 | 0.00019  | 4.97276 |
| TBC1D30  | 1.88969 | 1.08399 | 13.8592 | 8.83E-06 | 0.00029  | 4.19497 |
| NRAD1    | 1.89071 | -2.9947 | 4.05789 | 0.00667  | 0.02318  | -3.2822 |
| C1orf116 | 1.89765 | 0.01065 | 11.516  | 2.59E-05 | 0.00058  | 2.99231 |
| SYT12    | 1.89814 | -2.0908 | 3.77475 | 0.00925  | 0.02933  | -3.644  |
| C1orf198 | 1.90009 | 3.44224 | 19.5346 | 1.17E-06 | 9.42E-05 | 6.40059 |
| HOOK2    | 1.9073  | 3.34396 | 22.922  | 4.55E-07 | 5.60E-05 | 7.3999  |
| LPAR2    | 1.908   | 2.17717 | 14.4192 | 7.00E-06 | 0.00026  | 4.45184 |
| ACKR2    | 1.90915 | 0.19307 | 13.6302 | 9.73E-06 | 0.00032  | 4.08682 |
| TTC9     | 1.91259 | -1.3612 | 8.24624 | 0.00017  | 0.00188  | 0.84729 |
| RIPK4    | 1.91786 | 3.33496 | 5.71875 | 0.00124  | 0.00699  | -1.3921 |
| TEAD3    | 1.92    | 2.75878 | 24.1971 | 3.30E-07 | 4.82E-05 | 7.73182 |
| DOK5     | 1.92147 | 0.41632 | 7.0484  | 0.00041  | 0.00325  | -0.1333 |
| LRRC32   | 1.9218  | -2.0405 | 6.88454 | 0.00046  | 0.00352  | -0.278  |
| FAM169A  | 1.92773 | -0.795  | 6.93901 | 0.00045  | 0.00342  | -0.2296 |
| PHOSPH   | 1.93268 | 0.2868  | 3.91477 | 0.00786  | 0.02602  | -3.4636 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| ST6GALN  | 1.93833 | 0.86913 | 3.74065 | 0.00963  | 0.03019  | -3.6884 |
| NLRP4    | 1.93873 | -2.0504 | 3.85527 | 0.00842  | 0.02741  | -3.5399 |
| LOXL3    | 1.94054 | -0.2467 | 9.80904 | 6.49E-05 | 0.00101  | 1.95513 |
| SLC9A3R  | 1.94165 | 2.54947 | 12.8171 | 1.39E-05 | 0.0004   | 3.68737 |
| HES2     | 1.94725 | -0.4985 | 10.6375 | 4.08E-05 | 0.00076  | 2.47824 |
| SLITRK5  | 1.95122 | 1.42345 | 11.6538 | 2.42E-05 | 0.00056  | 3.06952 |
| CCDC3    | 1.95149 | 2.38788 | 7.11664 | 0.00039  | 0.00313  | -0.0739 |
| HMGA1P   | 1.95214 | 4.00193 | 17.3436 | 2.37E-06 | 0.00014  | 5.64296 |
| JPH2     | 1.953   | 1.82313 | 16.0662 | 3.71E-06 | 0.00018  | 5.15116 |
| HCP5     | 1.95468 | -0.724  | 4.63319 | 0.00357  | 0.01463  | -2.5831 |
| PODXL    | 1.95498 | 4.55345 | 9.08917 | 9.99E-05 | 0.00133  | 1.46619 |
| RAB11FIP | 1.95962 | 3.59067 | 4.77161 | 0.00309  | 0.0132   | -2.4222 |
| CHMP4C   | 1.96635 | 1.86578 | 12.7376 | 1.44E-05 | 0.0004   | 3.64696 |
| PRR36    | 1.9664  | 0.78902 | 10.8764 | 3.59E-05 | 0.00071  | 2.62196 |
| DIAPH3   | 1.96918 | 4.58635 | 12.8401 | 1.38E-05 | 0.00039  | 3.69901 |
| IL6      | 1.97159 | 1.82705 | 3.7643  | 0.00936  | 0.02959  | -3.6576 |
| ICAM5    | 1.97439 | 2.63238 | 5.42779 | 0.00162  | 0.0084   | -1.6957 |
| APOE     | -1.976  | 3.02986 | 4.49553 | 0.00413  | 0.01619  | -2.746  |
| NAALAD2  | 1.97647 | -5.027  | 7.41702 | 0.00031  | 0.0027   | 0.18239 |
| NMU      | 1.97969 | 2.71333 | 6.37495 | 0.0007   | 0.00465  | -0.7459 |
| MAP7     | 1.98166 | 2.60136 | 8.18318 | 0.00018  | 0.00194  | 0.79879 |
| DUTP6    | 1.98252 | -0.8193 | 3.99824 | 0.00714  | 0.02431  | -3.3574 |
| NME3     | 1.98438 | 0.93357 | 13.5067 | 1.03E-05 | 0.00033  | 4.02771 |
| TRIL     | 1.98717 | -1.5749 | 10.221  | 5.13E-05 | 0.00088  | 2.22023 |
| ZNF711   | 1.9936  | -0.9504 | 5.44814 | 0.00159  | 0.0083   | -1.6741 |
| FBXO2    | 1.99433 | 3.6382  | 9.54585 | 7.57E-05 | 0.00111  | 1.7803  |
| HCAR1    | 1.99604 | -1.6297 | 12.2492 | 1.81E-05 | 0.00047  | 3.393   |
| SMPD5    | 1.99962 | -0.5211 | 6.75269 | 0.00052  | 0.00379  | -0.3964 |
| GPR20    | 2.00462 | -4.17   | 3.61966 | 0.01111  | 0.03375  | -3.8471 |
| B4GALNT  | 2.00502 | 1.51693 | 5.82109 | 0.00113  | 0.00654  | -1.2879 |
| FGD3     | 2.00551 | -0.5411 | 13.2774 | 1.13E-05 | 0.00035  | 3.91656 |
| BBC3     | 2.0065  | -1.21   | 4.56762 | 0.00383  | 0.01536  | -2.6603 |
| NUDT16L  | 2.01099 | -0.6557 | 4.56504 | 0.00384  | 0.01539  | -2.6634 |
| SULT1A2  | 2.01198 | -0.4099 | 10.8    | 3.74E-05 | 0.00072  | 2.57634 |
| CILP2    | 2.01553 | -0.7853 | 10.1575 | 5.32E-05 | 0.0009   | 2.18005 |
| NUDT15   | 2.01982 | 3.89596 | 17.9669 | 1.92E-06 | 0.00012  | 5.86882 |
| WNT7B    | 2.02349 | 1.29655 | 9.66584 | 7.05E-05 | 0.00107  | 1.86055 |
| FREM1    | 2.02407 | -1.4726 | 7.58671 | 0.00027  | 0.00251  | 0.32339 |
| SYNGR3   | 2.02573 | -0.1017 | 8.30721 | 0.00017  | 0.00183  | 0.89388 |
| TMEM117  | 2.028   | 1.12065 | 16.2692 | 3.45E-06 | 0.00017  | 5.23208 |
| MUC20    | 2.03078 | -0.0508 | 7.83482 | 0.00023  | 0.00224  | 0.52487 |
| ALDH1L2  | 2.03381 | 2.98783 | 3.19767 | 0.01867  | 0.04976  | -4.4159 |
| PDLIM2   | 2.0501  | 0.2214  | 13.2407 | 1.15E-05 | 0.00035  | 3.89856 |
| DDR1     | 2.05436 | 3.53908 | 14.8736 | 5.84E-06 | 0.00023  | 4.65284 |
| BEX4     | 2.06007 | 0.22171 | 5.68554 | 0.00128  | 0.00715  | -1.4262 |
| ERVMER   | 2.06231 | -0.4851 | 8.46054 | 0.00015  | 0.00173  | 1.00975 |
| SMPDL3B  | 2.06815 | 1.55844 | 14.821  | 5.96E-06 | 0.00024  | 4.6299  |
| GRTP1    | 2.07155 | 0.01654 | 4.648   | 0.00352  | 0.01448  | -2.5658 |
| ID4      | 2.07239 | 5.51413 | 6.90614 | 0.00046  | 0.00348  | -0.2588 |
| IQCD     | 2.07312 | 0.10291 | 5.66608 | 0.0013   | 0.00723  | -1.4463 |
| XDH      | 2.07792 | -0.6622 | 18.1539 | 1.81E-06 | 0.00012  | 5.93488 |
| CGN      | 2.08111 | 3.80509 | 20.5345 | 8.73E-07 | 8.36E-05 | 6.71522 |
| ARTN     | 2.08255 | 0.44454 | 4.2819  | 0.0052   | 0.01917  | -3.0042 |
| PMEPA1   | 2.08568 | 1.54029 | 6.18068 | 0.00083  | 0.00523  | -0.9319 |
| NANOS1   | 2.08644 | 2.56101 | 7.0654  | 0.0004   | 0.00321  | -0.1185 |
| MYO1D    | 2.0897  | 3.47719 | 7.91079 | 0.00022  | 0.00216  | 0.58549 |
| RND3     | 2.09368 | 4.35534 | 7.36446 | 0.00032  | 0.00275  | 0.13817 |
| LNX2     | 2.09371 | 1.51621 | 14.3798 | 7.12E-06 | 0.00026  | 4.43411 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| SBK2     | 2.0983  | -2.4162 | 4.21961 | 0.00557  | 0.02018  | -3.0807 |
| SOX9     | 2.10122 | 0.10075 | 9.36532 | 8.44E-05 | 0.00118  | 1.6578  |
| RCN3     | 2.1066  | 2.46805 | 5.20156 | 0.00202  | 0.00972  | -1.9395 |
| CHPF     | 2.11223 | 3.57098 | 19.3701 | 1.23E-06 | 9.61E-05 | 6.34705 |
| SUSD3    | 2.12058 | -1.8337 | 3.82924 | 0.00868  | 0.028    | -3.5735 |
| MDFIC    | 2.12764 | -2.6232 | 11.9369 | 2.10E-05 | 0.00051  | 3.2253  |
| JUP      | 2.12844 | 4.84654 | 8.86437 | 0.00012  | 0.00146  | 1.3063  |
| ENTPD2   | 2.13032 | -2.3079 | 7.79215 | 0.00024  | 0.00229  | 0.49061 |
| IRS1     | 2.13603 | 2.01264 | 9.80399 | 6.51E-05 | 0.00101  | 1.95182 |
| SUSD2    | 2.13617 | 2.96463 | 7.43132 | 0.00031  | 0.00269  | 0.19437 |
| SELENO1  | 2.14029 | 0.09387 | 15.8308 | 4.05E-06 | 0.00019  | 5.05597 |
| ZP3      | 2.14317 | -3.0083 | 5.64484 | 0.00133  | 0.00733  | -1.4682 |
| L1CAM    | 2.14914 | 5.52542 | 8.57572 | 0.00014  | 0.00164  | 1.09559 |
| ESPN     | 2.15283 | -1.7058 | 21.9085 | 5.95E-07 | 6.37E-05 | 7.11996 |
| C21orf91 | 2.15428 | 1.68939 | 13.859  | 8.83E-06 | 0.00029  | 4.19487 |
| KCNK6    | 2.15461 | 1.10007 | 8.44275 | 0.00015  | 0.00174  | 0.99641 |
| ZNF204P  | 2.16388 | 0.0556  | 5.03917 | 0.00236  | 0.01086  | -2.1188 |
| NEXN     | 2.16736 | 3.16094 | 7.85018 | 0.00023  | 0.00222  | 0.53717 |
| ACTL8    | 2.17094 | -0.7457 | 6.01194 | 0.00096  | 0.00578  | -1.097  |
| RINL     | 2.17307 | 0.44547 | 8.51254 | 0.00014  | 0.00169  | 1.04863 |
| WNT6     | 2.17468 | -1.4166 | 4.60921 | 0.00366  | 0.01489  | -2.6113 |
| GLS2     | 2.18702 | -1.7645 | 7.63875 | 0.00026  | 0.00245  | 0.3661  |
| TMEM198  | 2.1874  | -0.4443 | 9.19132 | 9.38E-05 | 0.00127  | 1.53768 |
| FER1L4   | 2.19255 | 0.36875 | 3.91925 | 0.00782  | 0.02592  | -3.4579 |
| DTNA     | 2.199   | -2.9071 | 6.00296 | 0.00096  | 0.00581  | -1.1059 |
| ERBB4    | 2.20299 | 4.20879 | 5.05706 | 0.00232  | 0.01071  | -2.0988 |
| MUC1     | 2.20543 | 2.26506 | 11.4807 | 2.63E-05 | 0.00058  | 2.97243 |
| ADGRF1   | 2.20978 | -1.5962 | 7.4795  | 0.0003   | 0.00264  | 0.23462 |
| ADA      | 2.21342 | 2.69728 | 8.32453 | 0.00016  | 0.00182  | 0.90707 |
| LINC0123 | 2.22206 | -1.3286 | 7.98072 | 0.00021  | 0.0021   | 0.64084 |
| MYEF2    | 2.2233  | -1.0977 | 18.2788 | 1.74E-06 | 0.00012  | 5.97862 |
| ERICH5   | 2.22601 | -2.1505 | 7.97685 | 0.00021  | 0.00211  | 0.63779 |
| SLC44A2  | 2.23272 | 5.10956 | 16.0824 | 3.69E-06 | 0.00018  | 5.15766 |
| SFRP1    | 2.23294 | 2.13345 | 7.0333  | 0.00041  | 0.00327  | -0.1465 |
| CACNG6   | 2.23725 | -0.9757 | 6.13083 | 0.00086  | 0.0054   | -0.9804 |
| GBP5     | 2.24374 | 1.11149 | 8.38876 | 0.00016  | 0.00178  | 0.95574 |
| ARHGEF3  | 2.2438  | 0.94164 | 16.4969 | 3.18E-06 | 0.00016  | 5.32155 |
| CLDN10   | 2.24861 | -0.033  | 4.94333 | 0.0026   | 0.01163  | -2.2263 |
| BICDL1   | 2.25667 | 0.50679 | 5.61074 | 0.00137  | 0.00752  | -1.5036 |
| FABP5    | 2.25914 | -0.8723 | 13.9611 | 8.46E-06 | 0.00029  | 4.24247 |
| ZNF853   | 2.26023 | 0.34675 | 6.11058 | 0.00088  | 0.00546  | -1.0001 |
| COL7A1   | 2.26675 | 0.48797 | 9.43936 | 8.07E-05 | 0.00116  | 1.7083  |
| RPS6KA2  | 2.27594 | 3.79655 | 10.7735 | 3.80E-05 | 0.00073  | 2.56046 |
| LBH      | 2.27604 | 1.61989 | 5.12559 | 0.00217  | 0.01024  | -2.0229 |
| EPSTI1   | 2.27656 | 0.81748 | 5.92963 | 0.00103  | 0.00608  | -1.1788 |
| SH2D3A   | 2.27704 | 2.96531 | 16.3009 | 3.41E-06 | 0.00017  | 5.2446  |
| NOTUM    | 2.27811 | 2.02436 | 5.79485 | 0.00116  | 0.00664  | -1.3145 |
| LURAP1   | 2.279   | -2.5751 | 4.98441 | 0.00249  | 0.01127  | -2.18   |
| IL1R1    | 2.28401 | 4.59531 | 8.67053 | 0.00013  | 0.00158  | 1.16548 |
| MYEOV    | 2.28567 | -3.3561 | 5.59921 | 0.00138  | 0.00756  | -1.5155 |
| KRT8P13  | 2.28866 | -0.4263 | 8.48356 | 0.00015  | 0.00171  | 1.02699 |
| HPSE     | 2.29073 | 0.69027 | 14.4948 | 6.79E-06 | 0.00026  | 4.48572 |
| SCARA3   | 2.29089 | 2.37059 | 16.762  | 2.89E-06 | 0.00016  | 5.42406 |
| LACC1    | 2.29133 | -1.2969 | 8.89498 | 0.00011  | 0.00144  | 1.32828 |
| THEMIS2  | 2.29477 | 1.36244 | 6.04353 | 0.00093  | 0.00566  | -1.0659 |
| CLIC3    | 2.29527 | 1.92401 | 11.0301 | 3.32E-05 | 0.00067  | 2.71286 |
| LRRC41   | 2.29683 | 2.76821 | 25.9191 | 2.19E-07 | 4.00E-05 | 8.14767 |
| KRT80    | 2.31903 | 4.68286 | 6.88306 | 0.00047  | 0.00352  | -0.2793 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| DNAJC15  | 2.32584 | -1.5647 | 14.6859 | 6.29E-06 | 0.00024  | 4.57059 |
| ELF3     | 2.32996 | 3.41751 | 11.0308 | 3.31E-05 | 0.00067  | 2.71329 |
| FGF1     | 2.33079 | -1.4908 | 3.56635 | 0.01185  | 0.03539  | -3.9177 |
| RIMS4    | 2.33673 | 0.28055 | 5.639   | 0.00133  | 0.00737  | -1.4743 |
| TSPOAP   | 2.33702 | -1.4692 | 10.6723 | 4.01E-05 | 0.00075  | 2.49937 |
| CAPS     | 2.33987 | 1.83734 | 22.3687 | 5.26E-07 | 6.04E-05 | 7.24893 |
| KRT86    | 2.34005 | -1.9924 | 7.66477 | 0.00026  | 0.00243  | 0.38738 |
| C1orf115 | 2.34258 | -2.8485 | 11.6441 | 2.43E-05 | 0.00056  | 3.06409 |
| ADGRG1   | 2.34363 | 4.35612 | 19.6561 | 1.13E-06 | 9.28E-05 | 6.43977 |
| IFITM1   | 2.34437 | 1.69491 | 7.75565 | 0.00024  | 0.00233  | 0.46118 |
| SSC5D    | 2.36254 | -0.6397 | 12.1183 | 1.93E-05 | 0.00049  | 3.32322 |
| PRSS21   | 2.36503 | 2.07228 | 11.4666 | 2.65E-05 | 0.00058  | 2.96443 |
| LMTK3    | 2.36994 | -0.2657 | 12.9731 | 1.30E-05 | 0.00038  | 3.76594 |
| EMB      | 2.37025 | -2.4016 | 4.77888 | 0.00307  | 0.01312  | -2.4138 |
| DENND2L  | 2.37104 | 0.48489 | 22.7544 | 4.75E-07 | 5.80E-05 | 7.35464 |
| MYCN     | 2.37112 | -1.2299 | 7.42053 | 0.00031  | 0.00269  | 0.18533 |
| PRKCG    | 2.3727  | -0.3938 | 5.19557 | 0.00203  | 0.00976  | -1.946  |
| HMGA1P   | 2.38414 | 0.17616 | 8.35151 | 0.00016  | 0.0018   | 0.92755 |
| IL17RD   | 2.39496 | 1.4957  | 7.1152  | 0.00039  | 0.00313  | -0.0751 |
| ASNS     | 2.39872 | 4.621   | 3.2992  | 0.01644  | 0.04524  | -4.277  |
| NEURL1B  | 2.40117 | 1.50347 | 8.70127 | 0.00013  | 0.00156  | 1.188   |
| SLC35F3  | 2.40253 | -3.8557 | 5.40516 | 0.00166  | 0.00851  | -1.7198 |
| UNC5B    | 2.40364 | -0.2005 | 6.11886 | 0.00087  | 0.00544  | -0.992  |
| IL32     | 2.40721 | 1.27381 | 9.1042  | 9.90E-05 | 0.00132  | 1.47675 |
| TIMP3    | 2.40902 | 4.14408 | 9.70064 | 6.91E-05 | 0.00105  | 1.88366 |
| ATP8B1   | 2.42288 | 1.1121  | 15.6386 | 4.35E-06 | 0.00019  | 4.97715 |
| FAR2P1   | 2.42863 | -2.7469 | 4.28618 | 0.00518  | 0.0191   | -2.999  |
| BMF      | 2.43656 | -1.5646 | 8.78722 | 0.00012  | 0.00151  | 1.25058 |
| STARD10  | 2.43869 | 1.67772 | 10.36   | 4.75E-05 | 0.00084  | 2.30747 |
| HOXC4    | 2.43951 | -2.7566 | 7.80063 | 0.00023  | 0.00228  | 0.49743 |
| RBP7     | 2.44002 | -0.9146 | 6.4182  | 0.00068  | 0.00453  | -0.7051 |
| CKMT1B   | 2.4479  | -2.3388 | 7.3136  | 0.00033  | 0.00281  | 0.09514 |
| HOXC8    | 2.45331 | -2.3014 | 5.70695 | 0.00125  | 0.00705  | -1.4042 |
| C2orf15  | 2.45603 | -1.469  | 9.27719 | 8.90E-05 | 0.00123  | 1.59722 |
| SMOC2    | 2.46427 | 1.00151 | 6.08508 | 0.0009   | 0.00554  | -1.0251 |
| SCNN1A   | 2.47284 | 0.89576 | 5.24393 | 0.00193  | 0.00945  | -1.8933 |
| FABP5P7  | 2.48073 | 3.4928  | 8.54161 | 0.00014  | 0.00166  | 1.07028 |
| TACSTD2  | 2.48252 | 5.49001 | 13.4474 | 1.05E-05 | 0.00034  | 3.99913 |
| PTK2B    | 2.48581 | 0.22342 | 10.6965 | 3.96E-05 | 0.00075  | 2.51402 |
| SLC27A3  | 2.49159 | 2.64785 | 9.79194 | 6.55E-05 | 0.00102  | 1.9439  |
| SPDEF    | 2.49912 | -2.6973 | 5.47003 | 0.00156  | 0.00817  | -1.651  |
| ARHGAP   | 2.50601 | 0.30019 | 24.0937 | 3.38E-07 | 4.82E-05 | 7.70568 |
| S100A9   | 2.5062  | 0.5269  | 5.47234 | 0.00156  | 0.00815  | -1.6485 |
| NPR3     | 2.50961 | 1.00855 | 3.99718 | 0.00715  | 0.02433  | -3.3588 |
| PLEKHS1  | 2.51856 | -1.6751 | 4.85432 | 0.00284  | 0.01242  | -2.3273 |
| TUNAR    | 2.52535 | -1.82   | 4.50568 | 0.00409  | 0.01606  | -2.7339 |
| PLEKHN1  | 2.52675 | -0.4    | 9.96051 | 5.95E-05 | 0.00096  | 2.0538  |
| RBP1     | 2.53013 | 2.88941 | 13.0979 | 1.23E-05 | 0.00037  | 3.82815 |
| CATSPEP  | 2.53629 | -1.9209 | 9.20183 | 9.32E-05 | 0.00127  | 1.54499 |
| PRRG4    | 2.53972 | 0.85227 | 13.0551 | 1.25E-05 | 0.00037  | 3.80686 |
| ITGB4    | 2.54315 | 1.37595 | 12.3557 | 1.72E-05 | 0.00046  | 3.44919 |
| MYO3B    | 2.54456 | 1.22395 | 15.2055 | 5.13E-06 | 0.00021  | 4.79563 |
| ZNF165   | 2.54488 | 0.31565 | 10.598  | 4.17E-05 | 0.00077  | 2.45422 |
| LINC0070 | 2.54994 | -3.0693 | 3.78713 | 0.00911  | 0.02904  | -3.628  |
| CILP     | 2.55036 | 2.75271 | 3.94269 | 0.00761  | 0.02548  | -3.428  |
| SLC22A3  | 2.55433 | 0.03882 | 12.1701 | 1.88E-05 | 0.00048  | 3.35094 |
| DNAAF3   | 2.55466 | -0.2789 | 8.2819  | 0.00017  | 0.00185  | 0.87458 |
| KRT8P33  | 2.56396 | 2.6967  | 20.2866 | 9.38E-07 | 8.61E-05 | 6.63888 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| MFSD6    | 2.5654  | 0.43026 | 9.41711 | 8.18E-05 | 0.00116  | 1.69317 |
| C17orf10 | 2.56914 | -0.1047 | 7.40351 | 0.00031  | 0.00271  | 0.17105 |
| ARMCX2   | 2.5708  | 1.81544 | 14.8761 | 5.83E-06 | 0.00023  | 4.65391 |
| RAP1GA   | 2.57213 | 1.88222 | 5.88651 | 0.00107  | 0.00626  | -1.222  |
| KRT8P3   | 2.57915 | 5.71132 | 16.7245 | 2.93E-06 | 0.00016  | 5.40967 |
| SPSB4    | 2.58321 | -2.0502 | 6.21857 | 0.0008   | 0.00511  | -0.8953 |
| KRT8     | 2.58379 | 5.79433 | 16.4906 | 3.19E-06 | 0.00016  | 5.3191  |
| THRB     | 2.59387 | 2.23837 | 13.0965 | 1.23E-05 | 0.00037  | 3.82743 |
| FUT1     | 2.60781 | -0.1999 | 14.1731 | 7.74E-06 | 0.00027  | 4.34023 |
| NTF4     | 2.60917 | -2.1085 | 10.0933 | 5.51E-05 | 0.00092  | 2.13914 |
| CCNA1    | 2.63408 | 1.86495 | 4.93899 | 0.00261  | 0.01166  | -2.2312 |
| INAVA    | 2.63447 | 1.95844 | 8.99899 | 0.00011  | 0.00138  | 1.40248 |
| SIGLEC1  | 2.63626 | -2.9805 | 5.72445 | 0.00124  | 0.00696  | -1.3863 |
| ARFGEF3  | 2.64052 | -0.3465 | 16.1771 | 3.57E-06 | 0.00017  | 5.19552 |
| GLB1L2   | 2.64584 | -1.6569 | 6.08754 | 0.0009   | 0.00553  | -1.0226 |
| ACTA2    | 2.66646 | 0.4018  | 8.24429 | 0.00017  | 0.00188  | 0.8458  |
| FOXL2    | 2.6698  | -0.5564 | 15.9147 | 3.93E-06 | 0.00018  | 5.09007 |
| DNAJC6   | 2.68806 | 1.14718 | 6.46617 | 0.00065  | 0.00442  | -0.6601 |
| HOXB9    | 2.69842 | 4.22348 | 10.6628 | 4.03E-05 | 0.00076  | 2.49364 |
| MYO5C    | 2.70641 | 1.10939 | 13.1709 | 1.19E-05 | 0.00036  | 3.86424 |
| GRHL1    | 2.70717 | -1.1535 | 12.2721 | 1.79E-05 | 0.00047  | 3.4051  |
| ELAPOR2  | 2.71276 | -3.6291 | 5.79584 | 0.00116  | 0.00664  | -1.3135 |
| PDE3A    | 2.71398 | -1.9756 | 6.4071  | 0.00068  | 0.00456  | -0.7156 |
| FABP5P1  | 2.71596 | -0.7306 | 9.5302  | 7.64E-05 | 0.00112  | 1.76977 |
| KCNQ3    | 2.72006 | -0.6983 | 21.9039 | 5.95E-07 | 6.37E-05 | 7.11866 |
| SAMD12   | 2.72364 | -0.008  | 14.0074 | 8.30E-06 | 0.00029  | 4.26398 |
| IL2RG    | 2.7294  | -3.8081 | 3.5136  | 0.01263  | 0.03725  | -3.9879 |
| GCNT4    | 2.73388 | 0.13533 | 5.12314 | 0.00218  | 0.01025  | -2.0256 |
| DHDH     | 2.73621 | -2.3571 | 6.29157 | 0.00075  | 0.00488  | -0.8252 |
| KRT23    | 2.75015 | 1.34456 | 4.2433  | 0.00543  | 0.01976  | -3.0516 |
| LMO7     | 2.75745 | 2.3519  | 7.66618 | 0.00026  | 0.00243  | 0.38853 |
| HRK      | 2.75748 | -3.3806 | 6.95878 | 0.00044  | 0.00339  | -0.2121 |
| RPSAP52  | 2.76967 | -0.684  | 9.6727  | 7.02E-05 | 0.00107  | 1.86511 |
| DSP      | 2.77476 | 6.29478 | 16.278  | 3.44E-06 | 0.00017  | 5.23557 |
| S100A4   | 2.77903 | 3.94127 | 27.2893 | 1.61E-07 | 3.37E-05 | 8.45469 |
| SEMA4A   | 2.78093 | 0.81497 | 7.30122 | 0.00034  | 0.00283  | 0.08462 |
| PCDHGC   | 2.78267 | -1.8899 | 11.1841 | 3.06E-05 | 0.00064  | 2.80269 |
| MLXIPL   | 2.78546 | -1.3744 | 5.69517 | 0.00127  | 0.00711  | -1.4163 |
| LRRN2    | 2.79458 | -1.9595 | 5.46225 | 0.00157  | 0.00821  | -1.6592 |
| RND2     | 2.79477 | -3.8791 | 4.21645 | 0.00559  | 0.02022  | -3.0846 |
| SLC8A1   | 2.8008  | 2.85264 | 13.056  | 1.25E-05 | 0.00037  | 3.80731 |
| POU2F3   | 2.81016 | -3.5761 | 6.72151 | 0.00053  | 0.00385  | -0.4247 |
| COL4A4   | 2.81877 | -0.6251 | 9.87085 | 6.26E-05 | 0.00099  | 1.99556 |
| CREG2    | 2.81906 | -4.2455 | 5.23913 | 0.00194  | 0.00948  | -1.8985 |
| KRT8P32  | 2.81943 | -0.086  | 16.7523 | 2.90E-06 | 0.00016  | 5.42032 |
| KRT8P45  | 2.83216 | 2.92408 | 17.6045 | 2.17E-06 | 0.00013  | 5.73855 |
| NAPSB    | 2.84863 | -2.396  | 5.5144  | 0.0015   | 0.00796  | -1.6042 |
| CACNA2D  | 2.85435 | -0.7366 | 6.31493 | 0.00074  | 0.00482  | -0.8029 |
| SYNDIG1  | 2.85521 | -3.1401 | 4.85557 | 0.00284  | 0.01242  | -2.3259 |
| SYT5     | 2.8554  | -2.2175 | 6.61823 | 0.00057  | 0.00406  | -0.519  |
| TMEM45B  | 2.85917 | -2.5504 | 12.3278 | 1.74E-05 | 0.00046  | 3.43454 |
| XKR8     | 2.8783  | -0.0981 | 11.5378 | 2.56E-05 | 0.00058  | 3.00458 |
| MARVELL  | 2.88323 | 0.82105 | 10.737  | 3.87E-05 | 0.00074  | 2.53852 |
| PRRG2    | 2.8877  | -0.1838 | 23.2255 | 4.20E-07 | 5.30E-05 | 7.4809  |
| ABCG4    | 2.89027 | -1.9796 | 6.02499 | 0.00095  | 0.00573  | -1.0841 |
| SLC7A8   | 2.89028 | -1.2813 | 5.96686 | 0.001    | 0.00593  | -1.1417 |
| F3       | 2.89042 | 2.18137 | 12.4914 | 1.62E-05 | 0.00044  | 3.52018 |
| NPTX2    | 2.89568 | 4.94594 | 18.9656 | 1.40E-06 | 0.0001   | 6.21328 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| COL8A1   | 2.89802 | 1.29373 | 9.56072 | 7.50E-05 | 0.00111  | 1.7903  |
| IL11     | 2.90161 | -1.0521 | 5.92301 | 0.00103  | 0.00611  | -1.1854 |
| EMILIN2  | 2.90724 | 1.27109 | 4.04428 | 0.00678  | 0.02339  | -3.2993 |
| RGCC     | 2.92343 | -0.9849 | 7.71623 | 0.00025  | 0.00237  | 0.42925 |
| C10orf82 | 2.92346 | -4.1823 | 7.19212 | 0.00037  | 0.00301  | -0.0087 |
| RASIP1   | 2.9297  | -0.3217 | 7.4765  | 0.0003   | 0.00264  | 0.23212 |
| TMEM238  | 2.93207 | 1.9469  | 14.5616 | 6.61E-06 | 0.00025  | 4.51553 |
| IGSF9    | 2.93284 | -0.9896 | 6.71368 | 0.00053  | 0.00386  | -0.4318 |
| CRYBG1   | 2.93756 | -0.407  | 22.0411 | 5.74E-07 | 6.37E-05 | 7.15744 |
| EVPL     | 2.93972 | -0.4139 | 11.8331 | 2.21E-05 | 0.00053  | 3.1686  |
| KRT8P10  | 2.94502 | 1.78985 | 13.36   | 1.09E-05 | 0.00034  | 3.95683 |
| MYB      | 2.96247 | -1.7758 | 16.813  | 2.84E-06 | 0.00016  | 5.44358 |
| PNCK     | 2.97271 | -1.8179 | 15.1746 | 5.19E-06 | 0.00021  | 4.78247 |
| COL26A1  | 2.97971 | 3.4194  | 16.6728 | 2.99E-06 | 0.00016  | 5.38975 |
| NOXO1    | 2.99146 | -2.0267 | 10.8224 | 3.70E-05 | 0.00072  | 2.58974 |
| LAMA3    | 2.99624 | 6.17623 | 10.3607 | 4.75E-05 | 0.00084  | 2.30787 |
| CRYBG2   | 2.99658 | 1.20334 | 23.8002 | 3.64E-07 | 4.95E-05 | 7.6308  |
| PLAG1    | 3.00189 | 0.97814 | 7.40193 | 0.00031  | 0.00271  | 0.16972 |
| IRS2     | 3.01328 | 1.73502 | 11.911  | 2.13E-05 | 0.00052  | 3.21119 |
| ELMO3    | 3.02393 | 1.46742 | 15.7866 | 4.12E-06 | 0.00019  | 5.03793 |
| RNF152   | 3.03647 | -1.8694 | 11.7945 | 2.25E-05 | 0.00054  | 3.14737 |
| LINC0304 | 3.04293 | 2.71907 | 8.60628 | 0.00014  | 0.00162  | 1.11819 |
| ATP10A   | 3.04988 | -1.6649 | 7.44484 | 0.0003   | 0.00268  | 0.20569 |
| LINC0111 | 3.0522  | -3.9544 | 4.79086 | 0.00303  | 0.01301  | -2.4    |
| MDFI     | 3.06518 | -1.6509 | 10.127  | 5.41E-05 | 0.00091  | 2.16063 |
| COL8A2   | 3.0824  | -0.4903 | 15.6545 | 4.33E-06 | 0.00019  | 4.98371 |
| IGFBP2   | 3.08603 | 4.5238  | 11.3335 | 2.84E-05 | 0.00061  | 2.8887  |
| TMPRSS   | 3.09016 | -2.4419 | 8.05779 | 0.0002   | 0.00204  | 0.70136 |
| ZDHHC2   | 3.09959 | -0.0101 | 8.04648 | 0.0002   | 0.00205  | 0.69252 |
| RGL3     | 3.09967 | 2.57321 | 11.7592 | 2.29E-05 | 0.00054  | 3.12791 |
| KIF1A    | 3.11405 | 1.0843  | 10.9497 | 3.46E-05 | 0.00069  | 2.6655  |
| ELOVL3   | 3.12707 | -0.8684 | 10.2858 | 4.95E-05 | 0.00086  | 2.26101 |
| IL1RL2   | 3.14226 | -0.6651 | 30.4576 | 8.37E-08 | 2.41E-05 | 9.09438 |
| CLDN9    | 3.16056 | -0.9538 | 14.7602 | 6.11E-06 | 0.00024  | 4.60328 |
| UPK1B    | 3.16123 | -0.5402 | 3.92519 | 0.00776  | 0.02582  | -3.4503 |
| TNF      | 3.1623  | 0.01354 | 7.68019 | 0.00026  | 0.00241  | 0.39995 |
| TACR1    | 3.16625 | 0.64507 | 5.74197 | 0.00122  | 0.00687  | -1.3684 |
| EXPH5    | 3.16961 | -0.2256 | 9.86059 | 6.30E-05 | 0.00099  | 1.98887 |
| HMX2     | 3.17038 | -1.6222 | 14.2058 | 7.64E-06 | 0.00027  | 4.35519 |
| AMN      | 3.18324 | -0.3198 | 15.894  | 3.96E-06 | 0.00018  | 5.08166 |
| HPD      | 3.18404 | -1.1507 | 14.3766 | 7.13E-06 | 0.00026  | 4.4327  |
| ASIC2    | 3.1876  | 0.31079 | 5.00797 | 0.00244  | 0.01107  | -2.1536 |
| GPR15LC  | 3.19414 | -2.1214 | 24.9295 | 2.76E-07 | 4.41E-05 | 7.91301 |
| BAGE2    | 3.19848 | -5.9528 | 5.54052 | 0.00146  | 0.00782  | -1.5768 |
| CAMSAP   | 3.19854 | 1.14352 | 15.005  | 5.55E-06 | 0.00022  | 4.70976 |
| MX2      | 3.19891 | -3.0271 | 11.686  | 2.38E-05 | 0.00055  | 3.08738 |
| TSPAN1   | 3.20935 | 1.74428 | 9.8378  | 6.38E-05 | 0.001    | 1.97397 |
| NOS3     | 3.21111 | -1.578  | 10.031  | 5.71E-05 | 0.00094  | 2.09924 |
| FOXA1    | 3.21737 | 0.34548 | 7.03154 | 0.00041  | 0.00328  | -0.1481 |
| PITPNM3  | 3.22074 | 0.27273 | 20.5794 | 8.62E-07 | 8.30E-05 | 6.72893 |
| STC2     | 3.23375 | 3.88435 | 6.39274 | 0.00069  | 0.00459  | -0.7291 |
| FOLR1    | 3.23651 | 0.56046 | 11.0435 | 3.29E-05 | 0.00067  | 2.72071 |
| AMZ1     | 3.23872 | -1.8731 | 14.4914 | 6.80E-06 | 0.00026  | 4.48422 |
| GPR143   | 3.24617 | -0.5478 | 14.0323 | 8.21E-06 | 0.00028  | 4.2755  |
| FAAH2    | 3.24919 | -2.5841 | 11.0969 | 3.20E-05 | 0.00066  | 2.75195 |
| MIR4664  | 3.2517  | -3.6806 | 3.96823 | 0.00739  | 0.02493  | -3.3955 |
| TENM2    | 3.27781 | -1.0659 | 8.63141 | 0.00013  | 0.0016   | 1.13673 |
| DSEL     | 3.27881 | -2.6046 | 11.973  | 2.07E-05 | 0.00051  | 3.2449  |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| EFHD1    | 3.29312 | 2.13168 | 16.6517 | 3.01E-06 | 0.00016  | 5.38161 |
| KRT8P35  | 3.29618 | -0.3414 | 12.5203 | 1.59E-05 | 0.00043  | 3.53518 |
| ARHGEF   | 3.30033 | -0.0421 | 19.4659 | 1.20E-06 | 9.43E-05 | 6.3783  |
| LINC0259 | 3.30547 | -1.6379 | 18.9557 | 1.40E-06 | 0.0001   | 6.20994 |
| CFTR     | 3.31232 | -2.216  | 19.7779 | 1.09E-06 | 9.19E-05 | 6.47881 |
| GNGT2    | 3.31323 | -3.0249 | 5.38261 | 0.00169  | 0.00864  | -1.7439 |
| MARCHF   | 3.34734 | -0.8071 | 3.7485  | 0.00954  | 0.02999  | -3.6782 |
| RD3      | 3.34919 | -1.6758 | 11.886  | 2.16E-05 | 0.00052  | 3.19757 |
| SCGB2A1  | 3.34991 | -0.5415 | 9.78846 | 6.57E-05 | 0.00102  | 1.94162 |
| LRG1     | 3.35305 | 1.82715 | 5.76153 | 0.00119  | 0.00678  | -1.3484 |
| ANKRD2   | 3.37164 | -1.0674 | 10.7201 | 3.91E-05 | 0.00074  | 2.52833 |
| ITGB6    | 3.38067 | 1.25768 | 17.5442 | 2.21E-06 | 0.00013  | 5.71659 |
| HS3ST3A  | 3.38914 | -3.1034 | 10.1769 | 5.26E-05 | 0.00089  | 2.19237 |
| NPFFR1   | 3.39018 | -2.1823 | 8.64006 | 0.00013  | 0.00159  | 1.1431  |
| CPA4     | 3.41815 | 1.63309 | 11.4357 | 2.69E-05 | 0.00059  | 2.94692 |
| SOWAHA   | 3.42022 | 1.20635 | 9.95322 | 5.97E-05 | 0.00096  | 2.04908 |
| SGIP1    | 3.42825 | 2.00933 | 19.9548 | 1.03E-06 | 9.09E-05 | 6.53497 |
| MAGI2-A3 | 3.43477 | -1.9937 | 23.9801 | 3.48E-07 | 4.82E-05 | 7.67685 |
| PNPLA5   | 3.44154 | -3.4512 | 14.6874 | 6.29E-06 | 0.00024  | 4.57126 |
| ADAP1    | 3.44865 | -1.3008 | 15.3014 | 4.95E-06 | 0.00021  | 4.83627 |
| TMEM47   | 3.45752 | 1.17875 | 22.3954 | 5.22E-07 | 6.04E-05 | 7.25633 |
| TTC22    | 3.46651 | -1.3495 | 10.8507 | 3.64E-05 | 0.00071  | 2.60666 |
| PID1     | 3.47489 | -1.6411 | 8.29965 | 0.00017  | 0.00184  | 0.88813 |
| MST1R    | 3.47533 | -0.0705 | 10.8024 | 3.74E-05 | 0.00072  | 2.57778 |
| PRR15    | 3.48142 | 1.60444 | 7.51062 | 0.00029  | 0.0026   | 0.26049 |
| NPR1     | 3.48958 | 2.02768 | 11.7549 | 2.30E-05 | 0.00054  | 3.12556 |
| PDE5A    | 3.49458 | -2.4164 | 7.53252 | 0.00028  | 0.00257  | 0.27866 |
| SAMD11   | 3.50503 | -0.5598 | 14.4174 | 7.01E-06 | 0.00026  | 4.45106 |
| GPRIN2   | 3.50784 | -0.973  | 9.3595  | 8.47E-05 | 0.00118  | 1.65381 |
| DEPP1    | 3.51854 | -0.7231 | 7.76744 | 0.00024  | 0.00231  | 0.47069 |
| SMIM5    | 3.53602 | -3.4679 | 7.20731 | 0.00036  | 0.00298  | 0.00439 |
| SEMA3B   | 3.53684 | 1.59564 | 18.0796 | 1.85E-06 | 0.00012  | 5.90874 |
| C8orf34  | 3.53772 | 0.02138 | 11.9786 | 2.06E-05 | 0.00051  | 3.24794 |
| B4GALNT  | 3.54971 | -1.3583 | 10.7592 | 3.83E-05 | 0.00074  | 2.55185 |
| TMTC2    | 3.55121 | -0.052  | 24.836  | 2.82E-07 | 4.47E-05 | 7.89024 |
| GPR87    | 3.5541  | -4.7213 | 4.36647 | 0.00474  | 0.0179   | -2.9012 |
| FAM83H   | 3.56796 | 4.53717 | 23.2237 | 4.21E-07 | 5.30E-05 | 7.48042 |
| FOXS1    | 3.57478 | -1.1003 | 11.3619 | 2.80E-05 | 0.0006   | 2.90494 |
| TJP3     | 3.58494 | 0.04692 | 8.38286 | 0.00016  | 0.00178  | 0.95129 |
| MAP7-AS  | 3.6159  | -0.8552 | 17.2929 | 2.41E-06 | 0.00014  | 5.62418 |
| HR       | 3.62224 | 1.02485 | 4.76645 | 0.00311  | 0.01324  | -2.4281 |
| FSTL1    | 3.63762 | 5.1551  | 9.53683 | 7.61E-05 | 0.00111  | 1.77423 |
| ZNF439   | 3.66059 | -2.2577 | 15.0179 | 5.52E-06 | 0.00022  | 4.71533 |
| LYPD6B   | 3.70523 | -0.1042 | 8.42482 | 0.00015  | 0.00175  | 0.98292 |
| B3GALT4  | 3.7172  | -2.7029 | 8.83213 | 0.00012  | 0.00148  | 1.28307 |
| BLNK     | 3.72035 | -3.799  | 5.1129  | 0.0022   | 0.0103   | -2.0369 |
| SLC12A8  | 3.74418 | 0.96803 | 33.5289 | 4.72E-08 | 2.01E-05 | 9.63484 |
| IL1R2    | 3.74529 | 2.38565 | 11.2065 | 3.03E-05 | 0.00064  | 2.81564 |
| MROH2A   | 3.75774 | -3.1347 | 7.0924  | 0.0004   | 0.00316  | -0.0949 |
| KLK10    | 3.76066 | 2.5152  | 12.3802 | 1.70E-05 | 0.00045  | 3.46206 |
| IGFBP3   | 3.78272 | 4.5006  | 16.5644 | 3.10E-06 | 0.00016  | 5.34782 |
| RASSF9   | 3.79665 | -2.3724 | 6.74363 | 0.00052  | 0.00381  | -0.4046 |
| PGAP4    | 3.82584 | -3.9407 | 4.45695 | 0.0043   | 0.01667  | -2.7921 |
| CARD14   | 3.829   | -1.8474 | 10.0301 | 5.71E-05 | 0.00094  | 2.09867 |
| KLK7     | 3.82942 | -2.3733 | 5.12849 | 0.00216  | 0.01022  | -2.0197 |
| ANXA9    | 3.83481 | 0.09875 | 14.4512 | 6.91E-06 | 0.00026  | 4.46623 |
| EMX2OS   | 3.84234 | 3.46773 | 19.596  | 1.15E-06 | 9.35E-05 | 6.42043 |
| MGAT3    | 3.8525  | 0.21736 | 15.3197 | 4.91E-06 | 0.00021  | 4.84401 |

|         |         |         |         |          |          |         |
|---------|---------|---------|---------|----------|----------|---------|
| TMC4    | 3.86128 | 1.62136 | 13.1595 | 1.19E-05 | 0.00036  | 3.85863 |
| EHF     | 3.88981 | -1.9044 | 8.15637 | 0.00018  | 0.00196  | 0.77807 |
| GJB6    | 3.89738 | -1.0042 | 6.64443 | 0.00056  | 0.00401  | -0.495  |
| ANO9    | 3.91422 | 0.56382 | 17.0725 | 2.60E-06 | 0.00015  | 5.54194 |
| NR3C2   | 3.93259 | -1.2828 | 8.74868 | 0.00012  | 0.00153  | 1.22259 |
| EGFL6   | 3.95016 | -3.067  | 11.6183 | 2.46E-05 | 0.00056  | 3.0497  |
| ADAMTS  | 3.95139 | -2.711  | 5.11556 | 0.00219  | 0.01029  | -2.034  |
| PAK6    | 3.95251 | -2.0749 | 9.28103 | 8.88E-05 | 0.00123  | 1.59987 |
| STK26   | 3.96397 | 0.95517 | 16.1935 | 3.55E-06 | 0.00017  | 5.20201 |
| KRT81   | 3.98782 | -1.078  | 11.4441 | 2.68E-05 | 0.00059  | 2.95168 |
| FNDC1   | 4.001   | 2.83077 | 8.46359 | 0.00015  | 0.00173  | 1.01204 |
| PDZRN3  | 4.01381 | -2.8692 | 10.2943 | 4.93E-05 | 0.00086  | 2.26638 |
| GPRC5A  | 4.01867 | 3.01088 | 16.0003 | 3.80E-06 | 0.00018  | 5.12468 |
| SUN3    | 4.03692 | -2.3206 | 7.73429 | 0.00025  | 0.00235  | 0.4439  |
| FBN3    | 4.03783 | -0.891  | 9.54213 | 7.59E-05 | 0.00111  | 1.7778  |
| MAPK15  | 4.08771 | -2.2311 | 8.04101 | 0.0002   | 0.00205  | 0.68823 |
| SYBU    | 4.09356 | -1.7891 | 22.7252 | 4.78E-07 | 5.80E-05 | 7.34672 |
| LSR     | 4.09602 | 2.97842 | 13.3216 | 1.11E-05 | 0.00035  | 3.93813 |
| CDC42BP | 4.10792 | 0.72773 | 33.3455 | 4.88E-08 | 2.01E-05 | 9.6045  |
| EHD2    | 4.11079 | -3.807  | 8.20907 | 0.00018  | 0.00191  | 0.81874 |
| SIGIRR  | 4.13325 | 0.0259  | 11.4619 | 2.66E-05 | 0.00058  | 2.96176 |
| INHBB   | 4.15702 | 0.15235 | 8.4965  | 0.00015  | 0.0017   | 1.03666 |
| PROM1   | 4.1581  | 2.86652 | 29.6386 | 9.85E-08 | 2.63E-05 | 8.93766 |
| MSLN    | 4.17593 | -0.1995 | 16.6721 | 2.99E-06 | 0.00016  | 5.38947 |
| EDNRB   | 4.1824  | -3.3933 | 9.19154 | 9.38E-05 | 0.00127  | 1.53783 |
| HID1    | 4.2058  | -0.1036 | 23.2653 | 4.16E-07 | 5.30E-05 | 7.49142 |
| ERP27   | 4.21243 | -0.1515 | 11.0711 | 3.25E-05 | 0.00067  | 2.73688 |
| OVOL2   | 4.22658 | -0.9776 | 12.8294 | 1.38E-05 | 0.00039  | 3.69362 |
| COL1A2  | 4.23635 | -0.7268 | 14.7184 | 6.21E-06 | 0.00024  | 4.58494 |
| SYK     | 4.24145 | -2.1812 | 9.18327 | 9.43E-05 | 0.00127  | 1.53207 |
| CNGB1   | 4.25255 | 0.30214 | 33.1796 | 5.03E-08 | 2.01E-05 | 9.57687 |
| PALM3   | 4.26173 | 0.64908 | 10.4774 | 4.45E-05 | 0.00081  | 2.38025 |
| MARVELL | 4.27128 | -0.5026 | 28.6091 | 1.22E-07 | 2.92E-05 | 8.73238 |
| KLRG2   | 4.28935 | 1.84561 | 13.026  | 1.27E-05 | 0.00037  | 3.79237 |
| BARX1   | 4.3062  | -0.0718 | 7.12205 | 0.00039  | 0.00313  | -0.0692 |
| MTARC2  | 4.30745 | -1.323  | 11.574  | 2.51E-05 | 0.00057  | 3.02494 |
| SOWAHE  | 4.31453 | -3.0336 | 19.0109 | 1.38E-06 | 0.0001   | 6.22841 |
| TRIM17  | 4.32196 | -1.9975 | 14.036  | 8.20E-06 | 0.00028  | 4.27722 |
| FLNC    | 4.3328  | 1.56321 | 25.8165 | 2.24E-07 | 4.02E-05 | 8.12386 |
| GJB1    | 4.33357 | -2.5251 | 7.57955 | 0.00027  | 0.00252  | 0.31749 |
| KCNK15  | 4.35023 | 0.15073 | 8.78344 | 0.00012  | 0.00151  | 1.24784 |
| EPHB1   | 4.37901 | -1.7208 | 6.63073 | 0.00057  | 0.00404  | -0.5076 |
| NLGN4X  | 4.40393 | 0.02709 | 19.7473 | 1.10E-06 | 9.21E-05 | 6.46903 |
| LAMB3   | 4.42789 | 0.86052 | 14.0384 | 8.19E-06 | 0.00028  | 4.27829 |
| ESRP2   | 4.45554 | 1.21957 | 12.2257 | 1.83E-05 | 0.00047  | 3.38051 |
| CYP26C1 | 4.49454 | -2.867  | 10.1413 | 5.37E-05 | 0.0009   | 2.16976 |
| CARMN   | 4.49888 | -3.0568 | 17.2373 | 2.45E-06 | 0.00014  | 5.60352 |
| RNF180  | 4.5345  | -3.0971 | 44.3191 | 8.91E-09 | 9.87E-06 | 11.08   |
| LAMC2   | 4.53601 | 2.25165 | 23.3378 | 4.09E-07 | 5.30E-05 | 7.51052 |
| DLX3    | 4.553   | -0.1841 | 19.4864 | 1.19E-06 | 9.43E-05 | 6.38495 |
| PRDM5   | 4.55837 | -3.0938 | 11.3252 | 2.85E-05 | 0.00061  | 2.88397 |
| NUP210L | 4.5688  | -3.503  | 12.7583 | 1.43E-05 | 0.0004   | 3.65749 |
| TMEM178 | 4.57555 | -1.6955 | 7.4051  | 0.00031  | 0.00271  | 0.17238 |
| CRACDL  | 4.58966 | -0.7244 | 25.2123 | 2.58E-07 | 4.27E-05 | 7.98123 |
| CHSY3   | 4.60975 | -1.8711 | 14.822  | 5.96E-06 | 0.00024  | 4.63036 |
| CXCL16  | 4.61767 | 1.47757 | 15.7707 | 4.14E-06 | 0.00019  | 5.03143 |
| NPPB    | 4.61911 | -1.8115 | 12.0803 | 1.96E-05 | 0.0005   | 3.30282 |
| ZBED2   | 4.62579 | -0.2442 | 4.13538 | 0.00612  | 0.0217   | -3.1852 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| GPX7     | 4.64106 | -1.6681 | 20.9448 | 7.76E-07 | 7.77E-05 | 6.8393  |
| SLC6A12  | 4.64434 | -1.2294 | 12.6835 | 1.48E-05 | 0.00041  | 3.61928 |
| CALHM2   | 4.64876 | -2.4942 | 9.80479 | 6.50E-05 | 0.00101  | 1.95234 |
| KLHL30   | 4.65299 | -1.9009 | 15.0393 | 5.47E-06 | 0.00022  | 4.72454 |
| MSLNL    | 4.66993 | -2.1236 | 16.515  | 3.16E-06 | 0.00016  | 5.32861 |
| NCF2     | 4.68106 | -2.1228 | 15.3301 | 4.89E-06 | 0.00021  | 4.84842 |
| LMOD1    | 4.69452 | -0.6622 | 15.478  | 4.62E-06 | 0.0002   | 4.91047 |
| FUT3     | 4.69544 | -2.2764 | 7.17911 | 0.00037  | 0.00303  | -0.0199 |
| LCK      | 4.69846 | -2.1309 | 11.4524 | 2.67E-05 | 0.00059  | 2.95642 |
| XG       | 4.70365 | -3.2774 | 25.7171 | 2.29E-07 | 4.04E-05 | 8.10068 |
| SLC35G6  | 4.71068 | -2.2155 | 13.1148 | 1.22E-05 | 0.00037  | 3.83649 |
| RASD2    | 4.72484 | -3.7281 | 9.48247 | 7.86E-05 | 0.00114  | 1.73754 |
| COL4A3   | 4.72789 | -3.8568 | 10.709  | 3.93E-05 | 0.00074  | 2.52158 |
| CD164L2  | 4.73151 | -3.4932 | 10.4043 | 4.64E-05 | 0.00083  | 2.33502 |
| UNC13D   | 4.75143 | 0.57679 | 33.0471 | 5.15E-08 | 2.01E-05 | 9.55466 |
| GLDC     | 4.77373 | 0.66805 | 25.2048 | 2.59E-07 | 4.27E-05 | 7.97943 |
| CNN1     | 4.79763 | -0.5545 | 18.8793 | 1.43E-06 | 0.0001   | 6.18432 |
| EPCAM    | 4.80893 | 3.57741 | 23.5421 | 3.88E-07 | 5.14E-05 | 7.56403 |
| LINC0162 | 4.82292 | -2.0746 | 14.3672 | 7.15E-06 | 0.00026  | 4.42844 |
| ZNF469   | 4.83051 | -2.7197 | 13.3892 | 1.08E-05 | 0.00034  | 3.971   |
| PLEKHG6  | 4.83751 | -1.4373 | 25.0633 | 2.67E-07 | 4.32E-05 | 7.9454  |
| IGFL1    | 4.8395  | 0.07514 | 6.98205 | 0.00043  | 0.00335  | -0.1916 |
| EMC10    | 4.87941 | 3.33254 | 9.82655 | 6.42E-05 | 0.00101  | 1.96661 |
| INHBE    | 4.88577 | -1.9268 | 4.08018 | 0.00651  | 0.02275  | -3.2542 |
| SFTA1P   | 4.90752 | -2.6515 | 9.52052 | 7.69E-05 | 0.00112  | 1.76324 |
| SEC14L4  | 4.92669 | -3.9882 | 47.9263 | 5.58E-09 | 7.87E-06 | 11.4464 |
| PTGS1    | 4.95088 | 3.30525 | 21.2361 | 7.15E-07 | 7.30E-05 | 6.92569 |
| GLDCP1   | 4.95743 | 2.55853 | 24.4956 | 3.06E-07 | 4.65E-05 | 7.80647 |
| KLK5     | 5.03427 | -3.3337 | 9.42481 | 8.14E-05 | 0.00116  | 1.6984  |
| RNF39    | 5.04711 | -2.4908 | 11.6316 | 2.44E-05 | 0.00056  | 3.05713 |
| IQANK1   | 5.08443 | -0.8207 | 19.1513 | 1.32E-06 | 0.0001   | 6.27508 |
| FUT2     | 5.10781 | -3.0757 | 10.2233 | 5.12E-05 | 0.00088  | 2.22172 |
| PTGER4   | 5.11827 | -3.3134 | 11.4813 | 2.63E-05 | 0.00058  | 2.97275 |
| ERBB3    | 5.12166 | 1.36957 | 9.54166 | 7.59E-05 | 0.00111  | 1.77748 |
| LTB      | 5.13865 | -1.6052 | 20.4085 | 9.05E-07 | 8.46E-05 | 6.67655 |
| KRT5     | 5.19518 | -3.3864 | 32.8823 | 5.30E-08 | 2.01E-05 | 9.52685 |
| DOK7     | 5.20886 | -2.0655 | 17.2901 | 2.41E-06 | 0.00014  | 5.62315 |
| PTAFR    | 5.21427 | -1.3134 | 17.6116 | 2.16E-06 | 0.00013  | 5.74113 |
| CRB3     | 5.21924 | 1.15771 | 32.0672 | 6.16E-08 | 2.17E-05 | 9.38647 |
| SYT7     | 5.22196 | -0.9157 | 15.4502 | 4.67E-06 | 0.00021  | 4.89882 |
| COBL     | 5.22509 | -2.418  | 10.8206 | 3.70E-05 | 0.00072  | 2.58869 |
| SBK1     | 5.23011 | -1.893  | 18.2081 | 1.78E-06 | 0.00012  | 5.95389 |
| CRYAB    | 5.23659 | 3.05786 | 12.3403 | 1.73E-05 | 0.00046  | 3.44113 |
| CNKSR1   | 5.23846 | 0.03306 | 37.668  | 2.36E-08 | 1.46E-05 | 10.2621 |
| PPL      | 5.26253 | 0.41275 | 38.6249 | 2.03E-08 | 1.35E-05 | 10.393  |
| NYAP2    | 5.28552 | -1.8605 | 16.0102 | 3.79E-06 | 0.00018  | 5.12867 |
| ALDH3B2  | 5.29203 | -3.9573 | 15.2908 | 4.97E-06 | 0.00021  | 4.83182 |
| GARIN5A  | 5.29232 | -1.007  | 14.0556 | 8.13E-06 | 0.00028  | 4.28624 |
| CAND2    | 5.3045  | -2.1413 | 32.2737 | 5.93E-08 | 2.14E-05 | 9.42249 |
| LAD1     | 5.34264 | 2.49869 | 40.5576 | 1.51E-08 | 1.24E-05 | 10.6429 |
| KRT13    | 5.34759 | -2.5403 | 11.8326 | 2.21E-05 | 0.00053  | 3.1683  |
| CLDN7    | 5.35768 | 2.6032  | 19.6633 | 1.13E-06 | 9.28E-05 | 6.4421  |
| KRTAP2-  | 5.35874 | -0.5257 | 6.72822 | 0.00053  | 0.00384  | -0.4186 |
| SORCS2   | 5.36405 | 0.54814 | 12.4044 | 1.68E-05 | 0.00045  | 3.47476 |
| KRTCAP3  | 5.36666 | 0.98209 | 17.7801 | 2.04E-06 | 0.00013  | 5.80204 |
| MAP1LC3  | 5.36819 | -1.2182 | 18.2582 | 1.75E-06 | 0.00012  | 5.97143 |
| NECTIN4  | 5.37034 | -2.7899 | 9.64327 | 7.15E-05 | 0.00107  | 1.84553 |
| SPINT1   | 5.3809  | 1.79245 | 17.7743 | 2.05E-06 | 0.00013  | 5.79993 |

|           |         |         |         |          |          |         |
|-----------|---------|---------|---------|----------|----------|---------|
| MTARC1    | 5.41861 | -2.516  | 12.6881 | 1.48E-05 | 0.00041  | 3.62164 |
| C8orf34-A | 5.42297 | -2.4131 | 7.89898 | 0.00022  | 0.00218  | 0.57609 |
| FGF9      | 5.4241  | -1.9962 | 22.1058 | 5.64E-07 | 6.37E-05 | 7.17564 |
| C6orf132  | 5.43344 | 1.37988 | 20.0732 | 9.98E-07 | 9.00E-05 | 6.5723  |
| CDH3      | 5.4354  | 1.59149 | 17.896  | 1.97E-06 | 0.00012  | 5.84354 |
| LCP1      | 5.44755 | 4.13276 | 44.5154 | 8.68E-09 | 9.87E-06 | 11.1012 |
| CALB1     | 5.44831 | -1.6172 | 10.2354 | 5.09E-05 | 0.00088  | 2.22933 |
| NUP62CL   | 5.48977 | -3.5801 | 9.65185 | 7.11E-05 | 0.00107  | 1.85124 |
| HSH2D     | 5.53977 | -3.5845 | 11.8601 | 2.18E-05 | 0.00053  | 3.18341 |
| KRT6A     | 5.54639 | -3.2108 | 24.2286 | 3.27E-07 | 4.82E-05 | 7.73974 |
| NLRP7     | 5.54817 | -3.982  | 10.7314 | 3.88E-05 | 0.00074  | 2.53512 |
| PLA2G3    | 5.55456 | -1.542  | 12.2372 | 1.82E-05 | 0.00047  | 3.38662 |
| CDCP1     | 5.56117 | 1.3483  | 52.2513 | 3.33E-09 | 5.74E-06 | 11.8288 |
| PTN       | 5.57521 | -4.1185 | 8.38702 | 0.00016  | 0.00178  | 0.95443 |
| TMEM184   | 5.58624 | 0.00126 | 30.909  | 7.67E-08 | 2.36E-05 | 9.17836 |
| SYNE4     | 5.61155 | -0.0314 | 22.0685 | 5.69E-07 | 6.37E-05 | 7.16518 |
| GRAMD2    | 5.61772 | -3.2707 | 9.71006 | 6.87E-05 | 0.00105  | 1.88989 |
| MAB21L4   | 5.6411  | -2.9643 | 11.0204 | 3.33E-05 | 0.00068  | 2.70716 |
| ADAMTS    | 5.64615 | -2.928  | 11.5821 | 2.50E-05 | 0.00057  | 3.02947 |
| ADGRG5    | 5.65496 | -3.5514 | 9.75965 | 6.68E-05 | 0.00103  | 1.92265 |
| CST6      | 5.67223 | -0.8817 | 9.94251 | 6.01E-05 | 0.00097  | 2.04214 |
| TNNC1     | 5.68753 | 4.3575  | 13.9044 | 8.66E-06 | 0.00029  | 4.21609 |
| FXD3      | 5.69066 | -3.2488 | 28.8039 | 1.17E-07 | 2.92E-05 | 8.77195 |
| SLC6A9    | 5.69201 | -0.8344 | 7.42923 | 0.00031  | 0.00269  | 0.19262 |
| SPINT1-A  | 5.71133 | -1.5114 | 12.9706 | 1.30E-05 | 0.00038  | 3.76471 |
| VGLL1     | 5.72368 | -3.5642 | 20.2253 | 9.55E-07 | 8.71E-05 | 6.61981 |
| EPN3      | 5.79135 | -2.0922 | 14.7996 | 6.01E-06 | 0.00024  | 4.62057 |
| PROM2     | 5.81793 | -1.2011 | 15.4224 | 4.72E-06 | 0.00021  | 4.88722 |
| VEGFC     | 5.82956 | -3.2013 | 14.7151 | 6.22E-06 | 0.00024  | 4.58347 |
| B3GNT3    | 5.85531 | -0.6163 | 11.8903 | 2.15E-05 | 0.00052  | 3.19988 |
| TC2N      | 5.89023 | 0.7196  | 25.4052 | 2.47E-07 | 4.17E-05 | 8.02721 |
| CLDN22    | 5.91164 | -2.3792 | 25.7921 | 2.25E-07 | 4.02E-05 | 8.11818 |
| ADAMTS    | 5.93051 | -2.6906 | 19.9611 | 1.03E-06 | 9.09E-05 | 6.53699 |
| CLIC5     | 5.94508 | -1.8976 | 8.68044 | 0.00013  | 0.00157  | 1.17275 |
| CNTNAP2   | 5.9455  | -0.6721 | 18.5766 | 1.58E-06 | 0.00011  | 6.08156 |
| KLK6      | 5.97943 | -1.5242 | 12.7372 | 1.44E-05 | 0.0004   | 3.64674 |
| RARRES    | 6.04214 | -1.3702 | 21.9972 | 5.80E-07 | 6.37E-05 | 7.14505 |
| PLD5      | 6.11261 | -2.8346 | 18.9313 | 1.41E-06 | 0.0001   | 6.20178 |
| LXN       | 6.1162  | -3.1122 | 16.3169 | 3.39E-06 | 0.00017  | 5.25094 |
| ALOX12F   | 6.16109 | -3.0926 | 10.8523 | 3.64E-05 | 0.00071  | 2.60765 |
| MAL2      | 6.18108 | 2.3454  | 29.2719 | 1.06E-07 | 2.74E-05 | 8.86563 |
| LOXL1     | 6.1904  | 1.74281 | 19.9069 | 1.05E-06 | 9.09E-05 | 6.51983 |
| CAPN13    | 6.26806 | -0.5769 | 28.2447 | 1.31E-07 | 3.07E-05 | 8.65738 |
| MUC16     | 6.32437 | 1.43352 | 12.2294 | 1.83E-05 | 0.00047  | 3.38249 |
| LRRN1     | 6.35287 | -3.298  | 8.36328 | 0.00016  | 0.00179  | 0.93647 |
| NTNG1     | 6.37264 | -2.6397 | 18.7063 | 1.52E-06 | 0.00011  | 6.12581 |
| UCA1      | 6.45541 | -1.1202 | 8.76427 | 0.00012  | 0.00152  | 1.23392 |
| PKP3      | 6.46335 | 0.7696  | 24.4641 | 3.09E-07 | 4.65E-05 | 7.79865 |
| VIL1      | 6.48597 | -3.8998 | 18.1862 | 1.79E-06 | 0.00012  | 5.94625 |
| ACP7      | 6.52997 | -2.9716 | 11.5525 | 2.54E-05 | 0.00057  | 3.01288 |
| NID2      | 6.54146 | 1.20651 | 13.2802 | 1.13E-05 | 0.00035  | 3.91793 |
| KRT19P1   | 6.55758 | -0.8765 | 14.5733 | 6.58E-06 | 0.00025  | 4.52074 |
| CDS1      | 6.6048  | -0.5249 | 22.3867 | 5.23E-07 | 6.04E-05 | 7.25392 |
| ADAMTS    | 6.62206 | 1.61336 | 29.5292 | 1.01E-07 | 2.65E-05 | 8.9163  |
| IRF6      | 6.63776 | -0.5083 | 37.2086 | 2.54E-08 | 1.48E-05 | 10.1976 |
| EYA2      | 6.69195 | 1.03045 | 16.763  | 2.89E-06 | 0.00016  | 5.42442 |
| TAGLN     | 6.72792 | 4.78319 | 19.7969 | 1.08E-06 | 9.18E-05 | 6.48487 |
| BSPRY     | 6.74568 | -1.8815 | 43.2629 | 1.03E-08 | 1.03E-05 | 10.9634 |

|          |         |         |         |          |          |         |
|----------|---------|---------|---------|----------|----------|---------|
| SPINT2   | 6.75734 | 3.46937 | 22.6649 | 4.86E-07 | 5.80E-05 | 7.33029 |
| SLCO3A1  | 6.77774 | -1.1681 | 10.9757 | 3.41E-05 | 0.00069  | 2.68083 |
| STXBP6   | 6.78408 | -2.827  | 26.6604 | 1.85E-07 | 3.46E-05 | 8.31624 |
| MUC4     | 6.86024 | -2.3865 | 7.22912 | 0.00036  | 0.00294  | 0.0231  |
| MISP     | 7.06281 | -0.7813 | 36.5636 | 2.81E-08 | 1.48E-05 | 10.1049 |
| ST14     | 7.0987  | 2.07416 | 48.1631 | 5.42E-09 | 7.87E-06 | 11.4689 |
| TRIM29   | 7.11968 | -1.6952 | 6.83809 | 0.00048  | 0.00362  | -0.3195 |
| RBBP8NL  | 7.12053 | -3.8965 | 31.3487 | 7.05E-08 | 2.27E-05 | 9.25859 |
| BICDL2   | 7.14518 | -2.0536 | 14.333  | 7.25E-06 | 0.00026  | 4.41298 |
| OVOL1    | 7.17481 | -2.1677 | 19.7333 | 1.10E-06 | 9.21E-05 | 6.46454 |
| SCEL     | 7.18121 | -3.9597 | 26.6636 | 1.85E-07 | 3.46E-05 | 8.31696 |
| NRXN3    | 7.18717 | -0.6313 | 27.7859 | 1.45E-07 | 3.16E-05 | 8.56117 |
| EPHA1    | 7.23251 | 0.36142 | 32.9367 | 5.25E-08 | 2.01E-05 | 9.53606 |
| TRPS1    | 7.26961 | -0.6329 | 9.44567 | 8.04E-05 | 0.00115  | 1.71259 |
| TMEM125  | 7.31076 | -0.9905 | 12.5157 | 1.60E-05 | 0.00043  | 3.53278 |
| SFTA2    | 7.34025 | -0.1458 | 23.972  | 3.48E-07 | 4.82E-05 | 7.67478 |
| MYL9     | 7.42118 | 2.74844 | 23.908  | 3.54E-07 | 4.86E-05 | 7.65845 |
| KDF1     | 7.42646 | -1.2855 | 16.5886 | 3.08E-06 | 0.00016  | 5.35719 |
| SFN      | 7.43593 | 2.01942 | 77.4811 | 3.14E-10 | 1.92E-06 | 13.2524 |
| IGFBP5   | 7.43596 | -0.6941 | 11.9668 | 2.07E-05 | 0.00051  | 3.24155 |
| DMD      | 7.44446 | 1.197   | 25.4145 | 2.46E-07 | 4.17E-05 | 8.02942 |
| PCDH7    | 7.50198 | -2.0913 | 19.5063 | 1.18E-06 | 9.43E-05 | 6.3914  |
| MBNL3    | 7.55085 | -1.6782 | 31.5198 | 6.83E-08 | 2.27E-05 | 9.2894  |
| TRHDE-A  | 7.65579 | -2.696  | 33.8593 | 4.45E-08 | 2.01E-05 | 9.6889  |
| FRAS1    | 7.70387 | -0.5007 | 12.7641 | 1.43E-05 | 0.0004   | 3.66044 |
| TNS4     | 7.73514 | -0.4927 | 17.3567 | 2.36E-06 | 0.00014  | 5.64779 |
| COL11A1  | 7.78026 | -1.5086 | 19.8008 | 1.08E-06 | 9.18E-05 | 6.48612 |
| VTCN1    | 7.88982 | 0.14775 | 16.03   | 3.76E-06 | 0.00018  | 5.13663 |
| HS6ST2   | 7.90469 | -1.2788 | 20.8397 | 8.00E-07 | 7.95E-05 | 6.8078  |
| SMIM22   | 7.9332  | -2.0721 | 39.2201 | 1.85E-08 | 1.35E-05 | 10.4719 |
| C1orf210 | 7.96365 | -1.6455 | 54.2549 | 2.66E-09 | 5.15E-06 | 11.9877 |
| CLDN4    | 7.97093 | 1.25588 | 24.4596 | 3.09E-07 | 4.65E-05 | 7.79752 |
| FAT3     | 7.98889 | -0.7488 | 18.2338 | 1.76E-06 | 0.00012  | 5.96289 |
| ATP2C2   | 8.03789 | -1.5556 | 9.80344 | 6.51E-05 | 0.00101  | 1.95146 |
| FLRT2    | 8.06204 | -3.0104 | 21.9675 | 5.85E-07 | 6.37E-05 | 7.13667 |
| CDH1     | 8.14383 | 0.55488 | 27.8471 | 1.43E-07 | 3.16E-05 | 8.57412 |
| PRSS8    | 8.14414 | 1.52795 | 23.0457 | 4.40E-07 | 5.46E-05 | 7.43307 |
| HEPHL1   | 8.25991 | -3.2519 | 13.9855 | 8.37E-06 | 0.00029  | 4.2538  |
| RAB25    | 8.58665 | -1.8008 | 32.655  | 5.53E-08 | 2.04E-05 | 9.48819 |
| S100A14  | 8.59818 | 1.84034 | 20.1015 | 9.90E-07 | 8.98E-05 | 6.58116 |
| MACC1    | 8.6308  | -2.1613 | 24.6781 | 2.93E-07 | 4.59E-05 | 7.85155 |
| KRT19    | 8.65323 | 1.87885 | 27.5001 | 1.54E-07 | 3.32E-05 | 8.50018 |
| TRHDE    | 8.65662 | -1.0487 | 30.5738 | 8.19E-08 | 2.40E-05 | 9.11614 |
| PRSS22   | 8.75649 | -0.9823 | 18.6359 | 1.55E-06 | 0.00011  | 6.10184 |
| KRT7     | 8.84897 | 3.85686 | 36.5066 | 2.84E-08 | 1.48E-05 | 10.0966 |
| KRT17    | 9.09994 | -0.2889 | 15.2523 | 5.04E-06 | 0.00021  | 4.8155  |
| TMPRSS   | 9.15818 | -1.2147 | 16.1543 | 3.60E-06 | 0.00017  | 5.1864  |
| EPS8L1   | 9.30901 | 0.00459 | 47.0582 | 6.23E-09 | 8.05E-06 | 11.3625 |
| GALNT3   | 9.32962 | -1.2198 | 18.5165 | 1.61E-06 | 0.00011  | 6.06092 |
| TMEM30B  | 9.35363 | -0.6607 | 24.5468 | 3.03E-07 | 4.65E-05 | 7.81916 |
| ESRP1    | 9.39537 | 0.41541 | 22.4245 | 5.18E-07 | 6.04E-05 | 7.26437 |
| CBLC     | 9.49805 | -0.8881 | 17.9647 | 1.92E-06 | 0.00012  | 5.86804 |
| GRHL2    | 9.51914 | -1.3309 | 31.4876 | 6.87E-08 | 2.27E-05 | 9.28362 |
| EPPK1    | 9.69086 | 0.09465 | 18.6716 | 1.53E-06 | 0.00011  | 6.114   |
| FBN2     | 9.93886 | 0.83574 | 28.0628 | 1.36E-07 | 3.07E-05 | 8.61947 |

**Supplementary Table 4: Overlapped gene in GSE98230 and GSE141630**

| Up-regulated overlapped gene | Down-regulated overlapped gene |
|------------------------------|--------------------------------|
| GALNT14                      | SSC5D                          |
| TDO2                         | CRYAB                          |
| RUNX3                        | SLC44A2                        |
| LINC00882                    | STC2                           |
| COL12A1                      | EEF1AKMT1                      |
| HSPA12A                      | SNN                            |
| MMP1                         | ARID3BP1                       |
| HTRA1                        | MYLK4                          |
| LMX1B                        | TMEM169                        |
| PLPP2                        | CTTNBP2NL                      |
| HOXB13                       | TNS1                           |
| PRDM16                       | STARD13                        |
| MIRLET7BHG                   | LRCH2                          |
| PRKCB                        | DNAJC3-DT                      |
| CA13                         | TMSB15A                        |
| KIF26B                       | WDR25                          |
| DPP4                         | ADAMTS1                        |
| STK32B                       | SORT1                          |
| MLKL                         | ATXN1                          |
| HMX1                         | TRIM38                         |
| COL14A1                      | ANKRD24                        |
| RTN4RL2                      | CRIM1                          |
| GRIN2B                       | ZNF204P                        |
| PLPP3                        | C2orf15                        |
| AGPAT3                       | ERBB4                          |
| TNFSF14                      | UGCG                           |
| OSGIN1                       | ESPN                           |
| CCPG1                        | MISP                           |
| SLC1A1                       | ERP27                          |
| MAMLD1                       | NRXN3                          |
| LAMC3                        | PDZRN3                         |
| RNF144A                      | EBI3                           |
| KCNH3                        | EDNRB                          |
| ACSS1                        | ERVMER34-1                     |
| FOXF2                        | ACTL8                          |
| KITLG                        | ZBTB8B                         |
| LDAF1                        | RINL                           |
| MAPT                         | EDNRA                          |
| CAMK2N1                      | PRSS8                          |
| TFCP2L1                      | ZBED9                          |
| SH3RF3                       | ASNS                           |
| SFXN3                        | FAT3                           |
| CACHD1                       | FZD3                           |
| ZNF804A                      | NTF4                           |
| AKR1C2                       | SBK1                           |
| CDHR1                        | THSD4                          |
| GPR27                        | SERTAD4                        |
| TESC                         | NECTIN4                        |
| SDK2                         | MYLK3                          |
| TBXAS1                       | DMD                            |
| EEF1A2                       | FBLIM1                         |
| CFAP20DC                     | RNF152                         |
| AR                           | LCP1                           |
| C3                           | DLG3                           |
| FAM81A                       | S100A1                         |
| NPTX1                        | TSPAN2                         |

|           |           |
|-----------|-----------|
| SYNE3     | BAGE2     |
| MCOLN3    | FBXO27    |
| JUN       | PTGER2    |
| C6orf141  | TBC1D8B   |
| MCC       | CALD1     |
| RASSF2    | LRG1      |
| TTLL7     | EXPH5     |
| NEK10     | CACNG6    |
| GBX2      | ADGRF1    |
| PHLDA2    | CARMN     |
| ITGA6     | LINC01629 |
| OGFRL1    | SYBU      |
| ADORA1    | RIGI      |
| MCOLN2    | HOXB5     |
| NPAS1     | FNBP1L    |
| PLD1      | BMF       |
| KIF5C     | FUT1      |
| TMEM64    | COBLL1    |
| CLDN11    | LRRC8D-DT |
| CA12      | SLC6A15   |
| SNHG26    | INHBE     |
| LGI2      | CSF1      |
| PMP22     | APLF      |
| DAPK2     | ARID3A    |
| LINC00645 | FRAS1     |
| ZNF703    | ADPRHL1   |
| TRABD2A   | CBLC      |
| MSRA      | RNF144B   |
| GDPD5     | SH3BGRL2  |
| TMX4      | ADGRG1    |
| TRNP1     | JUP       |
| ANTXR1    | PAX6      |
| KLF2      | IGFBP5    |
| STAT1     | EPAS1     |
| GMPR      | CASZ1     |
| TMEM98    | TAGLN     |
| GCAWKR    | GCNT4     |
| PLAAT3    | FOLR1     |
| GALNT16   | RCBTB2    |
| EGR1      | F3        |
| TNFRSF8   | SERTM1    |
| CLMN      | LINC01234 |
| COL16A1   | ANXA3     |
| SLC30A3   | TGFA      |
| IL6R      | CYB5A     |
| DNAAF11   | TSPAN12   |
| CSPG5     | SAP30     |
| TIMP1     | TMTC2     |
| MRAP2     | RND3      |
| CHRD      | MGAT3     |
| KIF7      | MESTP3    |
| RIPK2     | FBLN2     |
| ARHGAP31  | ADAM19    |
| A4GALT    | SIX1      |
| PPP1R16B  | NLGN4X    |
| FRMD8     | CPA4      |
| NIPAL2    | PTPRK     |
| ITPR1     | EGLN3     |

|          |           |
|----------|-----------|
| NR2F2    | ST8SIA1   |
| STEAP3   | PNMA3     |
| KAT2B    | NELL2     |
| CNRIP1   | TENM1     |
| GAB3     | FLRT2     |
| MAN1C1   | MPZL2     |
| CABYR    | P2RY2     |
| AKR1C3   | SH3BP4    |
| MEGF11   | FOXL2NB   |
| CASP10   | RBM47     |
| SEMA3G   | RNF180    |
| PLEKHA7  | FADS2     |
| MCIDAS   | INA       |
| MAP3K7CL | IL32      |
| MMP10    | MAP1LC3A  |
| YPEL2    | TENM3     |
| ZCCHC12  | TGFB2     |
| MYO7A    | CCDC80    |
| EDA      | NID2      |
| FUT4     | FBN2      |
| SERINC5  | MSR1      |
| EEPD1    | PRKCH     |
| SPATA20  | DSEL      |
| PDK1-AS1 | MYO3B     |
| PRKCA    | PLAG1     |
| KCNC4    | MBP       |
| CCDC148  | BEX4      |
| TMEM144  | ACTA2     |
| DYNLT3   | ZDHHC2    |
| PDE6A    | APOL1     |
| OSGIN2   | ELF3      |
| SLC19A3  | ANKRD1    |
| DLK2     | SUN3      |
| HSPA4L   | PRICKLE1  |
| CDO1     | DTNA      |
| MTSS1    | SLC7A8    |
| MORC4    | PDE3A     |
| RHBDL3   | TMCC3     |
| ABTB2    | IFITM1    |
| NDRG2    | NEDD9     |
| FXVD6    | APOE      |
| RNF157   | JPH1      |
| REEP2    | ADAMTS5   |
| SEPTIN4  | DNAJC15   |
|          | TAP1      |
|          | JPH2      |
|          | THRB      |
|          | APOL6     |
|          | TRPS1     |
|          | SCHIP1    |
|          | EPM2AIP1  |
|          | HOXB9     |
|          | ZNF439    |
|          | LMO4      |
|          | MDGA1     |
|          | MESTP1    |
|          | TRHDE-AS1 |
|          | PRTFDC1   |

|  |          |
|--|----------|
|  | TMEM47   |
|  | FOXL2    |
|  | MDF1     |
|  | EFNB2    |
|  | CCSER1   |
|  | SHROOM3  |
|  | MAT1A    |
|  | NAALAD2  |
|  | ZNF432   |
|  | CNTNAP2  |
|  | FILIP1L  |
|  | CNN1     |
|  | RASSF9   |
|  | MBNL3    |
|  | LACC1    |
|  | CRABP2   |
|  | FREM1    |
|  | CRABP1   |
|  | USP53    |
|  | FRY      |
|  | ZNF738   |
|  | SOX9     |
|  | GBP5     |
|  | TRHDE    |
|  | CEMIP2   |
|  | NTNG1    |
|  | TMEM30B  |
|  | TIMP3    |
|  | FLNC     |
|  | LAYN     |
|  | COL1A2   |
|  | DLX6     |
|  | DLX5     |
|  | HDAC9    |
|  | MEST     |
|  | DLX6-AS1 |

Supplementary Table 5: The result of GO analysis

| id                                                                  | num | pvalue   | per    | ratio | class      | ID         | Description                                              | Pvalue   | Qvalue   | Up | Down | fg num | bg num |
|---------------------------------------------------------------------|-----|----------|--------|-------|------------|------------|----------------------------------------------------------|----------|----------|----|------|--------|--------|
| GO:0048731 system development                                       | 158 | 9.21E-16 | 48.916 | 0.032 | Biological | GO:0048731 | system development                                       | 9.21E-16 | 4.37E-12 | 0  | 0    | 158    | 4869   |
| GO:000653 anatomical structure morphogenesis                        | 107 | 1.75E-15 | 33.127 | 0.039 | Biological | GO:000653  | anatomical structure morphogenesis                       | 1.75E-15 | 4.37E-12 | 0  | 0    | 107    | 2749   |
| GO:0048856 anatomical structure development                         | 176 | 3.17E-15 | 54.489 | 0.03  | Biological | GO:0048856 | anatomical structure development                         | 3.17E-15 | 5.29E-12 | 0  | 0    | 176    | 5916   |
| GO:0007275 multicellular organism development                       | 160 | 5.28E-14 | 49.536 | 0.03  | Biological | GO:0007275 | multicellular organism development                       | 5.28E-14 | 6.59E-11 | 0  | 0    | 160    | 5283   |
| GO:0032502 developmental process                                    | 183 | 2.50E-13 | 56.656 | 0.028 | Biological | GO:0032502 | developmental process                                    | 2.50E-13 | 2.50E-10 | 0  | 0    | 183    | 6532   |
| GO:0008888 tissue development                                       | 82  | 7.31E-13 | 25.387 | 0.041 | Biological | GO:0008888 | tissue development                                       | 7.31E-13 | 8.38E-10 | 0  | 0    | 82     | 1997   |
| GO:0009887 animal organ morphogenesis                               | 65  | 2.33E-12 | 17.028 | 0.051 | Biological | GO:0009887 | animal organ morphogenesis                               | 2.33E-12 | 1.67E-09 | 0  | 0    | 65     | 1070   |
| GO:0048513 animal organ development                                 | 120 | 2.86E-12 | 37.152 | 0.033 | Biological | GO:0048513 | animal organ development                                 | 2.86E-12 | 1.79E-09 | 0  | 0    | 120    | 3637   |
| GO:0048646 anatomical structure formation involved in morphogenesis | 56  | 2.73E-11 | 17.337 | 0.048 | Biological | GO:0048646 | anatomical structure formation involved in morphogenesis | 2.73E-11 | 1.52E-08 | 0  | 0    | 56     | 1174   |
| GO:0016477 cell migration                                           | 65  | 3.80E-11 | 20.124 | 0.043 | Biological | GO:0016477 | cell migration                                           | 3.80E-11 | 1.90E-08 | 0  | 0    | 65     | 1504   |
| GO:0032501 multicellular organismal process                         | 148 | 4.97E-11 | 49.768 | 0.032 | Biological | GO:0032501 | multicellular organismal process                         | 4.97E-11 | 1.20E-08 | 0  | 0    | 148    | 7687   |
| GO:0030154 cell differentiation                                     | 131 | 5.25E-11 | 40.557 | 0.059 | Biological | GO:0030154 | cell differentiation                                     | 5.25E-11 | 2.02E-08 | 0  | 0    | 131    | 4301   |
| GO:0001568 blood vessel development                                 | 41  | 5.27E-11 | 12.693 | 0.058 | Biological | GO:0001568 | blood vessel development                                 | 5.27E-11 | 2.02E-08 | 0  | 0    | 41     | 706    |
| GO:0048869 cellular developmental process                           | 131 | 1.81E-10 | 40.557 | 0.03  | Biological | GO:0048869 | cellular developmental process                           | 1.81E-10 | 6.44E-08 | 0  | 0    | 131    | 4376   |
| GO:0001944 vasculature development                                  | 41  | 1.95E-10 | 12.693 | 0.058 | Biological | GO:0001944 | vasculature development                                  | 1.95E-10 | 6.51E-08 | 0  | 0    | 41     | 737    |
| GO:0004249 epithelium development                                   | 55  | 3.51E-10 | 17.028 | 0.049 | Biological | GO:0004249 | epithelium development                                   | 3.51E-10 | 1.10E-07 | 0  | 0    | 55     | 1220   |
| GO:0001755 cell adhesion                                            | 63  | 5.88E-10 | 19.505 | 0.041 | Biological | GO:0001755 | cell adhesion                                            | 5.88E-10 | 1.64E-07 | 0  | 0    | 63     | 1530   |
| GO:0030334 regulation of cell migration                             | 46  | 5.91E-10 | 14.241 | 0.05  | Biological | GO:0030334 | regulation of cell migration                             | 5.91E-10 | 1.64E-07 | 0  | 0    | 46     | 927    |
| GO:0022610 biological adhesion                                      | 63  | 7.06E-10 | 19.505 | 0.041 | Biological | GO:0022610 | biological adhesion                                      | 7.06E-10 | 1.86E-07 | 0  | 0    | 63     | 1537   |
| GO:0006928 movement of cell or subcellular component                | 78  | 9.94E-10 | 24.149 | 0.038 | Biological | GO:0006928 | movement of cell or subcellular component                | 9.94E-10 | 2.48E-07 | 0  | 0    | 78     | 2138   |
| GO:0072359 circulatory system development                           | 51  | 1.30E-09 | 17.028 | 0.039 | Biological | GO:0072359 | circulatory system development                           | 1.30E-09 | 3.17E-07 | 0  | 0    | 51     | 1123   |
| GO:0032879 regulation of localization                               | 93  | 1.90E-09 | 28.793 | 0.033 | Biological | GO:0032879 | regulation of localization                               | 1.90E-09 | 4.31E-07 | 0  | 0    | 93     | 2798   |
| GO:0071944 cell periphery                                           | 164 | 1.98E-09 | 48.665 | 0.026 | Cellular   | GO:0071944 | cell periphery                                           | 1.98E-09 | 1.06E-06 | 0  | 0    | 164    | 6197   |
| GO:0035239 tube morphogenesis                                       | 43  | 2.34E-09 | 13.313 | 0.05  | Biological | GO:0035239 | tube morphogenesis                                       | 2.34E-09 | 4.83E-07 | 0  | 0    | 43     | 867    |
| GO:0048870 cell motility                                            | 66  | 2.42E-09 | 20.433 | 0.039 | Biological | GO:0048870 | cell motility                                            | 2.42E-09 | 4.83E-07 | 0  | 0    | 66     | 1701   |
| GO:0051674 localization of cell                                     | 66  | 2.42E-09 | 20.433 | 0.039 | Biological | GO:0051674 | localization of cell                                     | 2.42E-09 | 4.83E-07 | 0  | 0    | 66     | 1701   |
| GO:0035295 tube development                                         | 49  | 3.04E-09 | 15.17  | 0.045 | Biological | GO:0035295 | tube development                                         | 3.04E-09 | 5.65E-07 | 0  | 0    | 49     | 1080   |
| GO:0042127 regulation of cell population proliferation              | 65  | 3.05E-09 | 20.124 | 0.039 | Biological | GO:0042127 | regulation of cell population proliferation              | 3.05E-09 | 5.65E-07 | 0  | 0    | 65     | 1672   |
| GO:2000145 regulation of cell motility                              | 46  | 4.05E-09 | 14.241 | 0.047 | Biological | GO:2000145 | regulation of cell motility                              | 4.05E-09 | 7.22E-07 | 0  | 0    | 46     | 985    |
| GO:0040011 locomotion                                               | 70  | 4.77E-09 | 21.872 | 0.037 | Biological | GO:0040011 | locomotion                                               | 4.77E-09 | 8.21E-07 | 0  | 0    | 70     | 1888   |
| GO:0050678 regulation of epithelial cell proliferation              | 26  | 5.53E-09 | 8.05   | 0.048 | Biological | GO:0050678 | regulation of epithelial cell proliferation              | 5.53E-09 | 8.99E-07 | 0  | 0    | 26     | 1030   |
| GO:0040012 regulation of locomotion                                 | 47  | 5.59E-09 | 14.551 | 0.048 | Biological | GO:0040012 | regulation of locomotion                                 | 5.59E-09 | 8.99E-07 | 0  | 0    | 47     | 1030   |
| GO:0022008 neurogenesis                                             | 65  | 5.76E-09 | 20.124 | 0.038 | Biological | GO:0022008 | neurogenesis                                             | 5.76E-09 | 8.99E-07 | 0  | 0    | 65     | 1699   |
| GO:0007399 nervous system development                               | 85  | 8.85E-09 | 26.316 | 0.033 | Biological | GO:0007399 | nervous system development                               | 8.85E-09 | 1.34E-06 | 0  | 0    | 85     | 2538   |
| GO:0048699 generation of neurons                                    | 61  | 9.71E-09 | 18.885 | 0.039 | Biological | GO:0048699 | generation of neurons                                    | 9.71E-09 | 1.43E-06 | 0  | 0    | 61     | 1566   |
| GO:0030855 epithelial cell differentiation                          | 37  | 1.40E-08 | 11.455 | 0.051 | Biological | GO:0030855 | epithelial cell differentiation                          | 1.40E-08 | 2.30E-06 | 0  | 0    | 37     | 721    |
| GO:0048518 positive regulation of biological process                | 164 | 1.45E-08 | 50.774 | 0.028 | Biological | GO:0048518 | positive regulation of biological process                | 1.45E-08 | 1.02E-06 | 0  | 0    | 164    | 6318   |
| GO:0034330 cell junction organization                               | 37  | 2.76E-08 | 11.455 | 0.05  | Biological | GO:0034330 | cell junction organization                               | 2.76E-08 | 3.73E-06 | 0  | 0    | 37     | 740    |
| GO:0051270 regulation of cellular component movement                | 46  | 3.21E-08 | 14.241 | 0.044 | Biological | GO:0051270 | regulation of cellular component movement                | 3.21E-08 | 4.22E-06 | 0  | 0    | 46     | 1054   |
| GO:0048514 blood vessel morphogenesis                               | 33  | 3.67E-08 | 10.217 | 0.053 | Biological | GO:0048514 | blood vessel morphogenesis                               | 3.67E-08 | 4.70E-06 | 0  | 0    | 33     | 619    |
| GO:0048522 positive regulation of cellular process                  | 42  | 4.59E-08 | 17.028 | 0.048 | Biological | GO:0048522 | positive regulation of cellular process                  | 4.59E-08 | 5.72E-06 | 0  | 0    | 42     | 976    |
| GO:0051239 regulation of multicellular organismal process           | 88  | 4.98E-08 | 27.245 | 0.032 | Biological | GO:0051239 | regulation of multicellular organismal process           | 4.98E-08 | 6.07E-06 | 0  | 0    | 88     | 2765   |
| GO:0050673 epithelial cell proliferation                            | 27  | 5.40E-08 | 8.359  | 0.061 | Biological | GO:0050673 | epithelial cell proliferation                            | 5.40E-08 | 6.42E-06 | 0  | 0    | 27     | 446    |
| GO:0030182 neuron differentiation                                   | 55  | 5.58E-08 | 17.028 | 0.039 | Biological | GO:0030182 | neuron differentiation                                   | 5.58E-08 | 6.49E-06 | 0  | 0    | 55     | 1409   |
| GO:0006283 cell population proliferation                            | 69  | 6.18E-08 | 21.362 | 0.035 | Biological | GO:0006283 | cell population proliferation                            | 6.18E-08 | 9.26E-06 | 0  | 0    | 69     | 1994   |
| GO:0016871 anatomical structure morphogenesis                       | 28  | 9.41E-08 | 8.05   | 0.061 | Biological | GO:0016871 | anatomical structure morphogenesis                       | 9.41E-08 | 1.04E-05 | 0  | 0    | 28     | 428    |
| GO:0030198 extracellular matrix organization                        | 22  | 1.36E-07 | 6.811  | 0.068 | Biological | GO:0030198 | extracellular matrix organization                        | 1.36E-07 | 1.47E-05 | 0  | 0    | 22     | 324    |
| GO:0040362 extracellular structure organization                     | 22  | 1.43E-07 | 6.811  | 0.068 | Biological | GO:0040362 | extracellular structure organization                     | 1.43E-07 | 1.52E-05 | 0  | 0    | 22     | 325    |
| GO:0045229 external encapsulating structure organization            | 22  | 1.59E-07 | 6.811  | 0.067 | Biological | GO:0045229 | external encapsulating structure organization            | 1.59E-07 | 1.66E-05 | 0  | 0    | 22     | 327    |
| GO:0050596 sensory organ morphogenesis                              | 20  | 2.40E-07 | 6.192  | 0.071 | Biological | GO:0050596 | sensory organ morphogenesis                              | 2.40E-07 | 2.45E-05 | 0  | 0    | 20     | 281    |
| GO:0050793 collagen-containing extracellular matrix                 | 25  | 2.40E-07 | 6.192  | 0.071 | Biological | GO:0050793 | collagen-containing extracellular matrix                 | 2.40E-07 | 2.45E-05 | 0  | 0    | 25     | 338    |
| GO:0031012 extracellular matrix                                     | 29  | 4.96E-07 | 8.605  | 0.051 | Cellular   | GO:0031012 | extracellular matrix                                     | 4.96E-07 | 6.88E-05 | 0  | 0    | 29     | 567    |
| GO:0001525 angiogenesis                                             | 28  | 5.04E-07 | 8.669  | 0.053 | Biological | GO:0001525 | angiogenesis                                             | 5.04E-07 | 5.03E-05 | 0  | 0    | 28     | 530    |
| GO:0030312 external encapsulating structure                         | 29  | 5.14E-07 | 8.605  | 0.051 | Cellular   | GO:0030312 | external encapsulating structure                         | 5.14E-07 | 6.88E-05 | 0  | 0    | 29     | 568    |
| GO:0050793 regulation of developmental process                      | 79  | 6.61E-07 | 24.438 | 0.031 | Biological | GO:0050793 | regulation of developmental process                      | 6.61E-07 | 6.36E-05 | 0  | 0    | 79     | 2528   |
| GO:0048498 cell development                                         | 15  | 1.62E-06 | 21.981 | 0.041 | Biological | GO:0048498 | cell development                                         | 1.62E-06 | 1.07E-04 | 0  | 0    | 15     | 2182   |
| GO:0008284 positive regulation of cell population proliferation     | 39  | 1.60E-06 | 12.074 | 0.041 | Biological | GO:0008284 | positive regulation of cell population proliferation     | 1.60E-06 | 0.00015  | 0  | 0    | 39     | 945    |
| GO:0009719 response to endogenous stimulus                          | 56  | 1.61E-06 | 17.337 | 0.035 | Biological | GO:0009719 | response to endogenous stimulus                          | 1.61E-06 | 0.00015  | 0  | 0    | 56     | 1605   |
| GO:0007423 sensory organ development                                | 29  | 1.66E-06 | 8.978  | 0.049 | Biological | GO:0007423 | sensory organ development                                | 1.66E-06 | 0.00015  | 0  | 0    | 29     | 566    |
| GO:0050699 cell-cell adhesion                                       | 39  | 1.82E-06 | 12.074 | 0.041 | Biological | GO:0050699 | cell-cell adhesion                                       | 1.82E-06 | 0.00016  | 0  | 0    | 39     | 950    |
| GO:0048866 neuron development                                       | 44  | 1.89E-06 | 13.622 | 0.039 | Biological | GO:0048866 | neuron development                                       | 1.89E-06 | 0.00016  | 0  | 0    | 44     | 1139   |
| GO:0051240 positive regulation of multicellular organismal process  | 53  | 2.92E-06 | 16.409 | 0.035 | Biological | GO:0051240 | positive regulation of multicellular organismal process  | 2.92E-06 | 0.00025  | 0  | 0    | 53     | 1514   |
| GO:0010033 response to organic substance                            | 88  | 3.62E-06 | 27.245 | 0.029 | Biological | GO:0010033 | response to organic substance                            | 3.62E-06 | 0.00031  | 0  | 0    | 88     | 3047   |
| GO:0051179 localization                                             | 155 | 5.02E-06 | 47.988 | 0.024 | Biological | GO:0051179 | localization                                             | 5.02E-06 | 0.00042  | 0  | 0    | 155    | 6369   |
| GO:0009686 regulation of signal transduction                        | 86  | 6.87E-06 | 26.625 | 0.029 | Biological | GO:0009686 | regulation of signal transduction                        | 6.87E-06 | 0.00056  | 0  | 0    | 86     | 3003   |
| GO:0050808 response to chemical                                     | 24  | 6.95E-06 | 7.43   | 0.051 | Biological | GO:0050808 | response to chemical                                     | 6.95E-06 | 0.00056  | 0  | 0    | 24     | 474    |
| GO:0045785 positive regulation of cell adhesion                     | 24  | 7.73E-06 | 7.43   | 0.05  | Biological | GO:0045785 | positive regulation of cell adhesion                     | 7.73E-06 | 0.00061  | 0  | 0    | 24     | 477    |
| GO:0048592 eye morphogenesis                                        | 13  | 9.38E-06 | 4.025  | 0.08  | Biological | GO:0048592 | eye morphogenesis                                        | 9.38E-06 | 0.00073  | 0  | 0    | 13     | 163    |
| GO:0010646 regulation of cell communication                         | 94  | 9.86E-06 | 29.102 | 0.028 | Biological | GO:0010646 | regulation of cell communication                         | 9.86E-06 | 0.00075  | 0  | 0    | 94     | 3403   |
| GO:0050880 negative regulation of epithelial cell proliferation     | 12  | 9.98E-06 | 3.715  | 0.086 | Biological | GO:0050880 | negative regulation of epithelial cell proliferation     | 9.98E-06 | 0.00075  | 0  | 0    | 12     | 140    |
| GO:0050886 plasma membrane morphogenesis                            | 140 | 1.07E-05 | 41.543 | 0.021 | Cellular   | GO:0050886 | plasma membrane morphogenesis                            | 1.07E-05 | 0.00114  | 0  | 0    | 140    | 5438   |
| GO:0023051 regulation of signaling                                  | 94  | 1.13E-05 | 29.102 | 0.028 | Biological | GO:0023051 | regulation of signaling                                  | 1.13E-05 | 0.00084  | 0  | 0    | 94     | 3414   |
| GO:0001655 urogenital system development                            | 20  | 1.27E-05 | 6.192  | 0.055 | Biological | GO:0001655 | urogenital system development                            | 1.27E-05 | 0.00094  | 0  | 0    | 20     | 364    |
| GO:0005604 basement membrane                                        | 10  | 1.30E-05 | 2.967  | 0.1   | Cellular   | GO:0005604 | basement membrane                                        | 1.30E-05 | 0.00116  | 0  | 0    | 10     | 100    |
| GO:0048568 embryonic organ development                              | 23  | 1.42E-05 | 7.121  | 0.06  | Biological | GO:0048568 | embryonic organ development                              | 1.42E-05 | 0.00103  | 0  | 0    | 23     | 462    |
| GO:0030054 cell junction                                            | 67  | 1.63E-05 | 19.881 | 0.03  | Cellular   | GO:0030054 | cell junction                                            | 1.63E-05 | 0.00124  | 0  | 0    | 67     | 2281   |
| GO:0048729 tissue morphogenesis                                     | 28  | 1.64E-05 | 8.669  | 0.044 | Biological | GO:0048729 | tissue morphogenesis                                     | 1.64E-05 | 0.00117  | 0  | 0    | 28     | 636    |
| GO:0060485 mesenchyme development                                   | 18  | 1.66E-05 | 5.573  | 0.058 | Biological | GO:0060485 | mesenchyme development                                   | 1.66E-05 | 0.00117  | 0  | 0    | 18     | 310    |
| GO:0150063 visual system development                                | 21  | 1.72E-05 | 6.502  | 0.052 | Biological | GO:0150063 | visual system development                                | 1.72E-05 | 0.00119  | 0  | 0    | 21     | 403    |
| GO:0001300 tissue migration                                         | 18  | 1.74E-05 | 5.573  | 0.058 | Biological | GO:0001300 | tissue migration                                         | 1.74E-05 | 0.00119  | 0  | 0    | 18     | 311    |
| GO:0030902 cell morphogenesis                                       | 39  | 1.85E-05 | 12.074 | 0.037 | Biological | GO:0030902 | cell morphogenesis                                       | 1.85E-05 | 0.00125  | 0  | 0    | 39     | 1049   |
| GO:0022612 gland morphogenesis                                      | 11  | 1.96E-05 | 3.406  | 0.087 | Biological | GO:0022612 | gland morphogenesis                                      | 1.96E-05 | 0.00131  | 0  | 0    | 11     | 126    |
| GO:0048880 sensory system development                               | 21  | 2.14E-05 | 6.502  | 0.051 | Biological | GO:0048880 | sensory system development                               | 2.14E-05 | 0.00141  | 0  | 0    | 21     | 409    |
| GO:1902952 positive regulation of dendritic spine maintenance       |     |          |        |       |            |            |                                                          |          |          |    |      |        |        |

|                                                                                    |     |         |        |       |            |                                                                                    |         |         |   |   |     |       |
|------------------------------------------------------------------------------------|-----|---------|--------|-------|------------|------------------------------------------------------------------------------------|---------|---------|---|---|-----|-------|
| GO:0007165 signal transduction                                                     | 139 | 0.00029 | 43.034 | 0.023 | Biological | GO:0007165 signal transduction                                                     | 0.00029 | 0.01031 | 0 | 0 | 139 | 5982  |
| GO:012036 plasma membrane bounded cell projection organization                     | 47  | 0.0003  | 14.551 | 0.031 | Biological | GO:012036 plasma membrane bounded cell projection organization                     | 0.0003  | 0.01044 | 0 | 0 | 47  | 1535  |
| GO:003719 actin binding                                                            | 20  | 0.00031 | 5.848  | 0.04  | Molecular  | GO:003719 actin binding                                                            | 0.00031 | 0.09831 | 0 | 0 | 20  | 451   |
| GO:0006972 positive regulation of signal transduction                              | 2   | 0.00031 | 14.551 | 0.031 | Biological | GO:0006972 positive regulation of signal transduction                              | 0.00031 | 0.01082 | 0 | 0 | 2   | 1538  |
| GO:0050896 response to stimulus                                                    | 194 | 0.00031 | 60.062 | 0.022 | Biological | GO:0050896 response to stimulus                                                    | 0.00031 | 0.01082 | 0 | 0 | 194 | 8949  |
| GO:0030424 axon                                                                    | 25  | 0.00031 | 7.418  | 0.039 | Cellular   | GO:0030424 axon                                                                    | 0.00031 | 0.01518 | 0 | 0 | 25  | 648   |
| GO:0060599 type I pneumocyte differentiation                                       | 3   | 0.00031 | 0.929  | 0.375 | Biological | GO:0060599 type I pneumocyte differentiation                                       | 0.00031 | 0.01082 | 0 | 0 | 3   | 8     |
| GO:0030335 positive regulation of cell migration                                   | 22  | 0.00031 | 14.551 | 0.041 | Biological | GO:0030335 positive regulation of cell migration                                   | 0.00031 | 0.01102 | 0 | 0 | 22  | 532   |
| GO:007382 specification of segmental identity, maxillary segment                   | 2   | 0.00033 | 0.619  | 1     | Biological | GO:007382 specification of segmental identity, maxillary segment                   | 0.00033 | 0.01118 | 0 | 0 | 2   | 2     |
| GO:0018993 somatic sex determination                                               | 2   | 0.00033 | 0.619  | 1     | Biological | GO:0018993 somatic sex determination                                               | 0.00033 | 0.01118 | 0 | 0 | 2   | 2     |
| GO:0004962 endothelin receptor activity                                            | 2   | 0.00034 | 0.585  | 1     | Molecular  | GO:0004962 endothelin receptor activity                                            | 0.00034 | 0.09031 | 0 | 0 | 2   | 2     |
| GO:0035403 histone kinase activity (H3-T6 specific)                                | 2   | 0.00034 | 0.585  | 1     | Molecular  | GO:0035403 histone kinase activity (H3-T6 specific)                                | 0.00034 | 0.09031 | 0 | 0 | 2   | 2     |
| GO:0007416 synapse assembly                                                        | 12  | 0.00033 | 3.715  | 0.059 | Biological | GO:0007416 synapse assembly                                                        | 0.00033 | 0.01161 | 0 | 0 | 12  | 202   |
| GO:0006915 apoptotic process                                                       | 55  | 0.00036 | 17.028 | 0.023 | Biological | GO:0006915 apoptotic process                                                       | 0.00036 | 0.012   | 0 | 0 | 55  | 1901  |
| GO:0010647 positive regulation of cell communication                               | 51  | 0.00038 | 15.789 | 0.03  | Biological | GO:0010647 positive regulation of cell communication                               | 0.00038 | 0.01252 | 0 | 0 | 51  | 1727  |
| GO:0070887 cellular response to chemical stimulus                                  | 80  | 0.00038 | 24.768 | 0.026 | Biological | GO:0070887 cellular response to chemical stimulus                                  | 0.00038 | 0.01252 | 0 | 0 | 80  | 3063  |
| GO:0043954 cellular component maintenance                                          | 7   | 0.0004  | 2.167  | 0.095 | Biological | GO:0043954 cellular component maintenance                                          | 0.0004  | 0.01287 | 0 | 0 | 7   | 74    |
| GO:0019514 cell surface receptor signaling pathway involved in cell-cell signaling | 23  | 0.0004  | 7.121  | 0.04  | Biological | GO:0019514 cell surface receptor signaling pathway involved in cell-cell signaling | 0.0004  | 0.01287 | 0 | 0 | 23  | 577   |
| GO:0220356 positive regulation of signaling                                        | 51  | 0.0004  | 15.789 | 0.023 | Biological | GO:0220356 positive regulation of signaling                                        | 0.0004  | 0.01287 | 0 | 0 | 51  | 1731  |
| GO:0003008 system process                                                          | 63  | 0.00041 | 19.505 | 0.028 | Biological | GO:0003008 system process                                                          | 0.00041 | 0.01299 | 0 | 0 | 63  | 2273  |
| GO:0097062 dendritic spine maintenance                                             | 4   | 0.00042 | 1.238  | 0.2   | Biological | GO:0097062 dendritic spine maintenance                                             | 0.00042 | 0.01326 | 0 | 0 | 4   | 20    |
| GO:0012501 programmed cell death                                                   | 56  | 0.00042 | 17.337 | 0.029 | Biological | GO:0012501 programmed cell death                                                   | 0.00042 | 0.01332 | 0 | 0 | 56  | 1958  |
| GO:0031589 cell-substrate adhesion                                                 | 17  | 0.00043 | 5.263  | 0.049 | Biological | GO:0031589 cell-substrate adhesion                                                 | 0.00043 | 0.01365 | 0 | 0 | 17  | 367   |
| GO:0046872 metal ion binding                                                       | 107 | 0.00046 | 31.287 | 0.025 | Molecular  | GO:0046872 metal ion binding                                                       | 0.00046 | 0.09031 | 0 | 0 | 107 | 4317  |
| GO:2000146 negative regulation of cell motility                                    | 15  | 0.00047 | 4.644  | 0.05  | Biological | GO:2000146 negative regulation of cell motility                                    | 0.00047 | 0.01474 | 0 | 0 | 15  | 303   |
| GO:0010811 positive regulation of cell-substrate adhesion                          | 9   | 0.00051 | 2.786  | 0.071 | Biological | GO:0010811 positive regulation of cell-substrate adhesion                          | 0.00051 | 0.01564 | 0 | 0 | 9   | 126   |
| GO:0000043 regulation of tubulin deacetylation                                     | 4   | 0.00051 | 1.238  | 0.19  | Biological | GO:0000043 regulation of tubulin deacetylation                                     | 0.00051 | 0.01564 | 0 | 0 | 4   | 21    |
| GO:0000030 cell projection organization                                            | 47  | 0.00051 | 14.551 | 0.031 | Biological | GO:0000030 cell projection organization                                            | 0.00051 | 0.01564 | 0 | 0 | 47  | 1535  |
| GO:0060562 epithelial tube morphogenesis                                           | 16  | 0.00052 | 4.954  | 0.047 | Biological | GO:0060562 epithelial tube morphogenesis                                           | 0.00052 | 0.01583 | 0 | 0 | 16  | 338   |
| GO:0051271 negative regulation of cellular component movement                      | 15  | 0.00052 | 4.644  | 0.049 | Biological | GO:0051271 negative regulation of cellular component movement                      | 0.00052 | 0.01583 | 0 | 0 | 15  | 306   |
| GO:1903670 regulation of sprouting angiogenesis                                    | 5   | 0.00053 | 1.548  | 0.135 | Biological | GO:1903670 regulation of sprouting angiogenesis                                    | 0.00053 | 0.01583 | 0 | 0 | 5   | 37    |
| GO:0000537 muscle tissue development                                               | 18  | 0.00053 | 5.573  | 0.044 | Biological | GO:0000537 muscle tissue development                                               | 0.00053 | 0.01583 | 0 | 0 | 18  | 408   |
| GO:0045687 regulation of cellular component differentiation                        | 9   | 0.00054 | 2.786  | 0.071 | Biological | GO:0045687 regulation of cellular component differentiation                        | 0.00054 | 0.01588 | 0 | 0 | 9   | 126   |
| GO:0040013 positive regulation of locomotion                                       | 16  | 0.00054 | 4.954  | 0.047 | Biological | GO:0040013 positive regulation of locomotion                                       | 0.00054 | 0.01588 | 0 | 0 | 16  | 340   |
| GO:0010942 positive regulation of cell death                                       | 23  | 0.00055 | 7.121  | 0.039 | Biological | GO:0010942 positive regulation of cell death                                       | 0.00055 | 0.01626 | 0 | 0 | 23  | 591   |
| GO:2000147 positive regulation of cell motility                                    | 22  | 0.00057 | 6.811  | 0.04  | Biological | GO:2000147 positive regulation of cell motility                                    | 0.00057 | 0.01666 | 0 | 0 | 22  | 555   |
| GO:0042471 ear morphogenesis                                                       | 9   | 0.0006  | 2.786  | 0.07  | Biological | GO:0042471 ear morphogenesis                                                       | 0.0006  | 0.01742 | 0 | 0 | 9   | 129   |
| GO:0016055 Wnt signaling pathway                                                   | 19  | 0.0006  | 5.882  | 0.042 | Biological | GO:0016055 Wnt signaling pathway                                                   | 0.0006  | 0.01742 | 0 | 0 | 19  | 448   |
| GO:0198738 cell-cell signaling by wnt                                              | 19  | 0.00064 | 5.882  | 0.042 | Biological | GO:0198738 cell-cell signaling by wnt                                              | 0.00064 | 0.01824 | 0 | 0 | 19  | 450   |
| GO:0002763 positive regulation of myeloid leukocyte differentiation                | 6   | 0.00064 | 1.858  | 0.103 | Biological | GO:0002763 positive regulation of myeloid leukocyte differentiation                | 0.00064 | 0.01824 | 0 | 0 | 6   | 58    |
| GO:0097366 all cell projection                                                     | 5   | 0.00064 | 1.484  | 0.128 | Cellular   | GO:0097366 all cell projection                                                     | 0.00064 | 0.02592 | 0 | 0 | 5   | 39    |
| GO:0043169 cation binding                                                          | 108 | 0.00065 | 31.579 | 0.025 | Molecular  | GO:0043169 cation binding                                                          | 0.00065 | 0.09031 | 0 | 0 | 108 | 4406  |
| GO:0061626 phenylethanolamine transporter activity                                 | 3   | 0.00065 | 0.929  | 0.3   | Biological | GO:0061626 phenylethanolamine transporter activity                                 | 0.00065 | 0.01848 | 0 | 0 | 3   | 10    |
| GO:0086100 endothelin receptor signaling pathway                                   | 3   | 0.00065 | 0.529  | 0.03  | Biological | GO:0086100 endothelin receptor signaling pathway                                   | 0.00065 | 0.01848 | 0 | 0 | 3   | 10    |
| GO:0019899 enzyme binding                                                          | 59  | 0.00066 | 17.251 | 0.028 | Molecular  | GO:0019899 enzyme binding                                                          | 0.00066 | 0.09031 | 0 | 0 | 59  | 2092  |
| GO:0003013 circulatory system process                                              | 23  | 0.00066 | 7.121  | 0.039 | Biological | GO:0003013 circulatory system process                                              | 0.00066 | 0.01865 | 0 | 0 | 23  | 599   |
| GO:1902533 positive regulation of intracellular signal transduction                | 33  | 0.0007  | 10.217 | 0.033 | Biological | GO:1902533 positive regulation of intracellular signal transduction                | 0.0007  | 0.01961 | 0 | 0 | 33  | 988   |
| GO:0032895 cellular component morphogenesis                                        | 28  | 0.0007  | 8.698  | 0.033 | Biological | GO:0032895 cellular component morphogenesis                                        | 0.0007  | 0.01961 | 0 | 0 | 28  | 795   |
| GO:0090042 tubulin deacetylation                                                   | 4   | 0.00073 | 1.238  | 0.174 | Biological | GO:0090042 tubulin deacetylation                                                   | 0.00073 | 0.02014 | 0 | 0 | 4   | 23    |
| GO:0051272 positive regulation of cellular component movement                      | 22  | 0.00074 | 6.811  | 0.039 | Biological | GO:0051272 positive regulation of cellular component movement                      | 0.00074 | 0.02029 | 0 | 0 | 22  | 566   |
| GO:0023052 signaling                                                               | 146 | 0.00077 | 45.201 | 0.023 | Biological | GO:0023052 signaling                                                               | 0.00077 | 0.02106 | 0 | 0 | 146 | 6474  |
| GO:0042472 inner ear morphogenesis                                                 | 8   | 0.00081 | 2.477  | 0.074 | Biological | GO:0042472 inner ear morphogenesis                                                 | 0.00081 | 0.02203 | 0 | 0 | 8   | 108   |
| GO:0000631 positive regulation of locomotion                                       | 22  | 0.00083 | 6.811  | 0.039 | Biological | GO:0000631 positive regulation of locomotion                                       | 0.00083 | 0.02238 | 0 | 0 | 22  | 571   |
| GO:0060322 head development                                                        | 29  | 0.00084 | 8.978  | 0.034 | Biological | GO:0060322 head development                                                        | 0.00084 | 0.02252 | 0 | 0 | 29  | 845   |
| GO:0005883 neurofilament                                                           | 3   | 0.00086 | 0.89   | 0.273 | Cellular   | GO:0005883 neurofilament                                                           | 0.00086 | 0.02592 | 0 | 0 | 3   | 11    |
| GO:0034992 microtubule organizing center attachment site                           | 3   | 0.00086 | 0.89   | 0.273 | Cellular   | GO:0034992 microtubule organizing center attachment site                           | 0.00086 | 0.02592 | 0 | 0 | 3   | 11    |
| GO:0034953 meiotic nuclear membrane microtubule tethering complex                  | 3   | 0.00086 | 0.89   | 0.273 | Cellular   | GO:0034953 meiotic nuclear membrane microtubule tethering complex                  | 0.00086 | 0.02592 | 0 | 0 | 3   | 11    |
| GO:0106033 nuclear membrane protein complex                                        | 3   | 0.00086 | 0.89   | 0.273 | Cellular   | GO:0106033 nuclear membrane protein complex                                        | 0.00086 | 0.02592 | 0 | 0 | 3   | 11    |
| GO:0106034 nuclear membrane microtubule tethering complex                          | 3   | 0.00086 | 0.89   | 0.273 | Cellular   | GO:0106034 nuclear membrane microtubule tethering complex                          | 0.00086 | 0.02592 | 0 | 0 | 3   | 11    |
| GO:0016020 membrane                                                                | 205 | 0.00087 | 60.831 | 0.021 | Cellular   | GO:0016020 membrane                                                                | 0.00087 | 0.02592 | 0 | 0 | 205 | 9774  |
| GO:0030397 membrane disassembly                                                    | 3   | 0.00089 | 0.929  | 0.273 | Biological | GO:0030397 membrane disassembly                                                    | 0.00089 | 0.0236  | 0 | 0 | 3   | 11    |
| GO:0060736 prostate gland growth                                                   | 3   | 0.00089 | 0.929  | 0.273 | Biological | GO:0060736 prostate gland growth                                                   | 0.00089 | 0.0236  | 0 | 0 | 3   | 11    |
| GO:0014070 response to organic cyclic compound                                     | 31  | 0.00091 | 8.698  | 0.033 | Biological | GO:0014070 response to organic cyclic compound                                     | 0.00091 | 0.02453 | 0 | 0 | 31  | 998   |
| GO:0045862 positive regulation of proteolysis                                      | 16  | 0.00096 | 4.954  | 0.045 | Biological | GO:0045862 positive regulation of proteolysis                                      | 0.00096 | 0.02521 | 0 | 0 | 16  | 359   |
| GO:0030934 anchoring collagen complex                                              | 2   | 0.00096 | 0.593  | 0.667 | Cellular   | GO:0030934 anchoring collagen complex                                              | 0.00096 | 0.02704 | 0 | 0 | 2   | 3     |
| GO:0045726 positive regulation of integrin biosynthetic process                    | 2   | 0.00098 | 0.619  | 0.667 | Biological | GO:0045726 positive regulation of integrin biosynthetic process                    | 0.00098 | 0.02558 | 0 | 0 | 2   | 3     |
| GO:0009590 embryo development                                                      | 36  | 0.00098 | 11.446 | 0.031 | Biological | GO:0009590 embryo development                                                      | 0.00098 | 0.02558 | 0 | 0 | 36  | 1144  |
| GO:0008083 protein factor activity                                                 | 10  | 0.00098 | 2.924  | 0.061 | Molecular  | GO:0008083 protein factor activity                                                 | 0.00098 | 0.02631 | 0 | 0 | 10  | 104   |
| GO:0001191 regulation of Wnt signaling pathway                                     | 15  | 0.001   | 4.644  | 0.046 | Biological | GO:0001191 regulation of Wnt signaling pathway                                     | 0.001   | 0.02583 | 0 | 0 | 15  | 326   |
| GO:0002053 positive regulation of mesenchymal cell proliferation                   | 4   | 0.00101 | 1.238  | 0.18  | Biological | GO:0002053 positive regulation of mesenchymal cell proliferation                   | 0.00101 | 0.02608 | 0 | 0 | 4   | 25    |
| GO:0018636 phenanthrene 9,10-monooxygenase activity                                | 2   | 0.00102 | 0.585  | 0.667 | Molecular  | GO:0018636 phenanthrene 9,10-monooxygenase activity                                | 0.00102 | 0.09031 | 0 | 0 | 2   | 3     |
| GO:0016235 ceramide-1-phosphate phosphatase activity                               | 2   | 0.00102 | 0.585  | 0.667 | Molecular  | GO:0016235 ceramide-1-phosphate phosphatase activity                               | 0.00102 | 0.09031 | 0 | 0 | 2   | 3     |
| GO:2000269 regulation of organometallic process                                    | 4   | 0.00103 | 1.043  | 0.03  | Biological | GO:2000269 regulation of organometallic process                                    | 0.00103 | 0.02668 | 0 | 0 | 4   | 1406  |
| GO:0001936 regulation of endothelial cell proliferation                            | 9   | 0.00108 | 2.786  | 0.064 | Biological | GO:0001936 regulation of endothelial cell proliferation                            | 0.00108 | 0.02751 | 0 | 0 | 9   | 140   |
| GO:0005102 signaling receptor binding                                              | 46  | 0.00109 | 13.45  | 0.03  | Molecular  | GO:0005102 signaling receptor binding                                              | 0.00109 | 0.09031 | 0 | 0 | 46  | 1557  |
| GO:0042981 regulation of apoptotic process                                         | 43  | 0.00112 | 13.313 | 0.03  | Biological | GO:0042981 regulation of apoptotic process                                         | 0.00112 | 0.02836 | 0 | 0 | 43  | 1455  |
| GO:0065038 regulation of biological quality                                        | 95  | 0.00115 | 29.412 | 0.024 | Biological | GO:0065038 regulation of biological quality                                        | 0.00115 | 0.02892 | 0 | 0 | 95  | 3911  |
| GO:0015175 neutral amino acid transmembrane transporter activity                   | 5   | 0.00115 | 1.482  | 0.116 | Molecular  | GO:0015175 neutral amino acid transmembrane transporter activity                   | 0.00115 | 0.09163 | 0 | 0 | 5   | 11    |
| GO:0010604 positive regulation of macromolecule metabolic process                  | 21  | 0.00118 | 6.811  | 0.039 | Biological | GO:0010604 positive regulation of macromolecule metabolic process                  | 0.00118 | 0.02972 | 0 | 0 | 21  | 571   |
| GO:0099604 ligand-gated calcium channel activity                                   | 4   | 0.00126 | 1.17   | 0.154 | Molecular  | GO:0099604 ligand-gated calcium channel activity                                   | 0.00126 | 0.09062 | 0 | 0 | 4   | 26    |
| GO:0065007 biological regulation                                                   | 250 | 0.00126 | 77.399 | 0.02  | Biological | GO:0065007 biological regulation                                                   | 0.00126 | 0.03153 | 0 | 0 | 250 | 12363 |
| GO:0046530 photoreceptor cell differentiation                                      | 6   | 0.00127 | 1.858  | 0.091 | Biological | GO:0046530 photoreceptor cell differentiation                                      | 0.00127 | 0.03156 | 0 | 0 | 6   | 66    |
| GO:0035272 exocrine system development                                             | 5   | 0.00131 | 1.548  | 0.11  | Biological | GO:0035272 exocrine system development                                             | 0.00131 | 0.03243 | 0 | 0 | 5   | 68    |
| GO:0010941 regulation of cell death                                                | 47  | 0.00132 | 14.551 | 0.029 | Biological | GO:0010941 regulation of cell death                                                | 0.00132 | 0.03244 | 0 | 0 | 47  | 1645  |
| GO:0033002 muscle cell proliferation                                               | 11  | 0.00134 | 3.406  | 0.054 | Biological | GO:0033002 muscle cell proliferation                                               | 0.00134 | 0.03279 | 0 | 0 | 11  | 204   |
| GO:0045745 positive regulation of G protein-coupled receptor signaling pathway     | 4   | 0.00137 | 1.238  | 0.148 | Biological | GO:0045745 positive regulation of G protein-coupled receptor signaling pathway     | 0.00137 | 0.03323 | 0 | 0 | 4   | 27    |
| GO:0006004 cell morphogenesis involved in differentiation                          | 26  | 0.00137 | 8.035  | 0.03  | Biological | GO:0006004 cell morphogenesis involved in differentiation                          | 0.00137 | 0.03323 | 0 | 0 | 26  | 751   |
| GO:0007389 pattern specification process                                           | 19  | 0.00139 | 5.486  | 0.04  | Biological | GO:0007389 pattern specification process                                           | 0.00139 | 0.03362 | 0 | 0 | 19  | 481   |
| GO:0048583 regulation of response to stimulus                                      | 97  | 0.00144 | 30.031 | 0.024 |            |                                                                                    |         |         |   |   |     |       |

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|-----------------------------------------------------------------------|-----|---------|--------|-------|------------|---------|---------------------------------------------------------------------|---------|---------|---|---|-----|-------|
| GO:0060173 limb development                                           | 10  | 0.00233 | 3.096  | 0.053 | Biological | GO:0060 | limb development                                                    | 0.00233 | 0.045   | 0 | 0 | 10  | 187   |
| GO:0009612 response to mechanical stimulus                            | 11  | 0.00235 | 3.406  | 0.05  | Biological | GO:0009 | response to mechanical stimulus                                     | 0.00235 | 0.045   | 0 | 0 | 11  | 219   |
| GO:0045639 positive regulation of myeloid cell differentiation        | 7   | 0.00236 | 2.167  | 0.07  | Biological | GO:0045 | positive regulation of myeloid cell differentiation                 | 0.00236 | 0.045   | 0 | 0 | 7   | 100   |
| GO:0060940 artery development                                         | 7   | 0.00236 | 2.167  | 0.07  | Biological | GO:0060 | artery development                                                  | 0.00236 | 0.045   | 0 | 0 | 7   | 100   |
| GO:0060993 kidney morphogenesis                                       | 7   | 0.00236 | 2.167  | 0.07  | Biological | GO:0060 | kidney morphogenesis                                                | 0.00236 | 0.045   | 0 | 0 | 7   | 100   |
| GO:0043005 neuron protection                                          | 40  | 0.00237 | 11.869 | 0.029 | Cellular   | GO:0043 | neuron protection                                                   | 0.00237 | 0.046   | 0 | 0 | 40  | 1394  |
| GO:0016331 morphogenesis of embryonic epithelium                      | 9   | 0.00239 | 2.786  | 0.057 | Biological | GO:0016 | morphogenesis of embryonic epithelium                               | 0.00239 | 0.04529 | 0 | 0 | 9   | 157   |
| GO:0009612 suprarenal gland morphogenesis                             | 32  | 0.00241 | 8.911  | 0.07  | Biological | GO:0009 | suprarenal gland morphogenesis                                      | 0.00241 | 0.04166 | 0 | 0 | 32  | 1044  |
| GO:0031624 ubiquitin-conjugating enzyme binding                       | 4   | 0.00246 | 1.17   | 0.125 | Molecular  | GO:0031 | ubiquitin-conjugating enzyme binding                                | 0.00246 | 0.12518 | 0 | 0 | 4   | 131   |
| GO:0001935 endothelial cell proliferation                             | 9   | 0.0026  | 2.786  | 0.057 | Biological | GO:0001 | endothelial cell proliferation                                      | 0.0026  | 0.04892 | 0 | 0 | 9   | 159   |
| GO:0003338 metanephros morphogenesis                                  | 4   | 0.00261 | 1.238  | 0.125 | Biological | GO:0003 | metanephros morphogenesis                                           | 0.00261 | 0.04892 | 0 | 0 | 4   | 32    |
| GO:0010464 regulation of mesenchymal cell proliferation               | 4   | 0.00261 | 1.238  | 0.125 | Biological | GO:0010 | regulation of mesenchymal cell proliferation                        | 0.00261 | 0.04892 | 0 | 0 | 4   | 32    |
| GO:0001838 embryonic spiral tube formation                            | 8   | 0.00264 | 2.478  | 0.114 | Biological | GO:0001 | embryonic spiral tube formation                                     | 0.00264 | 0.04898 | 0 | 0 | 8   | 137   |
| GO:0090981 supramolecular polymer                                     | 32  | 0.00275 | 9.496  | 0.03  | Cellular   | GO:0090 | supramolecular polymer                                              | 0.00275 | 0.04603 | 0 | 0 | 32  | 1053  |
| GO:0072109 glomerular mesangium development                           | 3   | 0.00282 | 0.929  | 0.188 | Biological | GO:0072 | glomerular mesangium development                                    | 0.00282 | 0.05252 | 0 | 0 | 3   | 16    |
| GO:0006935 chemotaxis                                                 | 22  | 0.00285 | 6.811  | 0.035 | Biological | GO:0006 | chemotaxis                                                          | 0.00285 | 0.05283 | 0 | 0 | 22  | 630   |
| GO:0012505 endomembrane system                                        | 109 | 0.00285 | 32.344 | 0.023 | Cellular   | GO:0012 | endomembrane system                                                 | 0.00285 | 0.04619 | 0 | 0 | 109 | 4776  |
| GO:0051015 actin filament binding                                     | 11  | 0.00286 | 3.216  | 0.05  | Molecular  | GO:0051 | actin filament binding                                              | 0.00286 | 0.13324 | 0 | 0 | 11  | 221   |
| GO:0048858 cell projection morphogenesis                              | 23  | 0.0029  | 7.121  | 0.034 | Biological | GO:0048 | cell projection morphogenesis                                       | 0.0029  | 0.05364 | 0 | 0 | 23  | 671   |
| GO:0007431 salivary gland development                                 | 4   | 0.00292 | 1.238  | 0.121 | Molecular  | GO:0007 | salivary gland development                                          | 0.00292 | 0.05387 | 0 | 0 | 4   | 33    |
| GO:0004698 calcium-dependent protein kinase C activity                | 3   | 0.00295 | 0.877  | 0.188 | Molecular  | GO:0004 | calcium-dependent protein kinase C activity                         | 0.00295 | 0.13324 | 0 | 0 | 3   | 16    |
| GO:0009893 positive regulation of metabolic process                   | 91  | 0.00297 | 28.173 | 0.024 | Biological | GO:0009 | positive regulation of metabolic process                            | 0.00297 | 0.05451 | 0 | 0 | 91  | 3828  |
| GO:0042327 positive regulation of phosphorylation                     | 26  | 0.00299 | 8.05   | 0.033 | Biological | GO:0042 | positive regulation of phosphorylation                              | 0.00299 | 0.05471 | 0 | 0 | 26  | 785   |
| GO:0044669 cell maturation                                            | 10  | 0.00303 | 3.096  | 0.052 | Biological | GO:0044 | cell maturation                                                     | 0.00303 | 0.05516 | 0 | 0 | 10  | 194   |
| GO:0003007 heart morphogenesis                                        | 12  | 0.00304 | 3.715  | 0.046 | Biological | GO:0003 | heart morphogenesis                                                 | 0.00304 | 0.05516 | 0 | 0 | 12  | 260   |
| GO:0003270 positive regulation of cellular protein metabolic process  | 39  | 0.00305 | 12.074 | 0.029 | Biological | GO:0003 | positive regulation of cellular protein metabolic process           | 0.00305 | 0.05516 | 0 | 0 | 39  | 1355  |
| GO:0003002 regionalization                                            | 15  | 0.00307 | 4.844  | 0.041 | Biological | GO:0003 | regionalization                                                     | 0.00307 | 0.05535 | 0 | 0 | 15  | 366   |
| GO:0042330 laws                                                       | 23  | 0.00313 | 8.811  | 0.03  | Biological | GO:0042 | laws                                                                | 0.00313 | 0.05598 | 0 | 0 | 23  | 681   |
| GO:0033674 positive regulation of kinase activity                     | 17  | 0.00315 | 5.263  | 0.039 | Biological | GO:0033 | positive regulation of kinase activity                              | 0.00315 | 0.05598 | 0 | 0 | 17  | 441   |
| GO:0120035 regulation of plasma membrane bounded cell projection or   | 22  | 0.00319 | 6.811  | 0.035 | Biological | GO:0120 | regulation of plasma membrane bounded cell projection organization  | 0.00319 | 0.05598 | 0 | 0 | 22  | 636   |
| GO:0003151 outflow tract morphogenesis                                | 6   | 0.00319 | 1.858  | 0.076 | Biological | GO:0003 | outflow tract morphogenesis                                         | 0.00319 | 0.05598 | 0 | 0 | 6   | 79    |
| GO:0034343 type III interlaminar production                           | 2   | 0.00319 | 0.819  | 0.4   | Biological | GO:0034 | type III interlaminar production                                    | 0.00319 | 0.05598 | 0 | 0 | 2   | 5     |
| GO:0034344 regulation of type III interferon production               | 2   | 0.00319 | 0.819  | 0.4   | Biological | GO:0034 | regulation of type III interferon production                        | 0.00319 | 0.05598 | 0 | 0 | 2   | 5     |
| GO:0045113 regulation of integrin biosynthetic process                | 2   | 0.00319 | 0.819  | 0.4   | Biological | GO:0045 | regulation of integrin biosynthetic process                         | 0.00319 | 0.05598 | 0 | 0 | 2   | 5     |
| GO:0071504 cellular response to heparin                               | 2   | 0.00319 | 0.819  | 0.4   | Biological | GO:0071 | cellular response to heparin                                        | 0.00319 | 0.05598 | 0 | 0 | 2   | 5     |
| GO:0030175 filopodium                                                 | 7   | 0.00325 | 2.077  | 0.065 | Cellular   | GO:0030 | filopodium                                                          | 0.00325 | 0.05116 | 0 | 0 | 7   | 107   |
| GO:0047086 ketosteroid monooxygenase activity                         | 2   | 0.0033  | 0.585  | 0.4   | Molecular  | GO:0047 | ketosteroid monooxygenase activity                                  | 0.0033  | 0.13324 | 0 | 0 | 2   | 5     |
| GO:0072345 NAD(P)-dependent protein metabolic channel activity        | 50  | 0.00331 | 15.48  | 0.027 | Biological | GO:0072 | NAD(P)-dependent protein metabolic channel activity                 | 0.00331 | 0.05324 | 0 | 0 | 50  | 1861  |
| GO:0042592 homeostatic process                                        | 9   | 0.00333 | 2.786  | 0.055 | Biological | GO:0042 | homeostatic process                                                 | 0.00333 | 0.0577  | 0 | 0 | 9   | 165   |
| GO:0045766 positive regulation of angiogenesis                        | 9   | 0.00333 | 2.786  | 0.055 | Biological | GO:0045 | positive regulation of angiogenesis                                 | 0.00333 | 0.0577  | 0 | 0 | 9   | 165   |
| GO:1904018 positive regulation of vasculature development             | 9   | 0.00333 | 2.786  | 0.055 | Biological | GO:1904 | positive regulation of vasculature development                      | 0.00333 | 0.0577  | 0 | 0 | 9   | 165   |
| GO:0042448 progesterone metabolic process                             | 3   | 0.00338 | 0.929  | 0.176 | Biological | GO:0042 | progesterone metabolic process                                      | 0.00338 | 0.05834 | 0 | 0 | 3   | 17    |
| GO:0010971 neuron development                                         | 15  | 0.0034  | 4.844  | 0.041 | Biological | GO:0010 | neuron development                                                  | 0.0034  | 0.05834 | 0 | 0 | 15  | 370   |
| GO:0001954 positive regulation of cell-matrix adhesion                | 3   | 0.00349 | 1.548  | 0.089 | Biological | GO:0001 | positive regulation of cell-matrix adhesion                         | 0.00349 | 0.05982 | 0 | 0 | 3   | 56    |
| GO:0004697 protein kinase C activity                                  | 3   | 0.00354 | 0.877  | 0.176 | Molecular  | GO:0004 | protein kinase C activity                                           | 0.00354 | 0.13324 | 0 | 0 | 3   | 17    |
| GO:0012578 calcium-release channel activity                           | 3   | 0.00354 | 0.877  | 0.176 | Molecular  | GO:0012 | calcium-release channel activity                                    | 0.00354 | 0.13324 | 0 | 0 | 3   | 17    |
| GO:0003018 vascular process in circulatory system                     | 12  | 0.00354 | 3.715  | 0.045 | Biological | GO:0003 | vascular process in circulatory system                              | 0.00354 | 0.06062 | 0 | 0 | 12  | 265   |
| GO:0051247 positive regulation of protein metabolic process           | 41  | 0.00357 | 12.933 | 0.025 | Biological | GO:0051 | positive regulation of protein metabolic process                    | 0.00357 | 0.06062 | 0 | 0 | 41  | 1457  |
| GO:0010594 regulation of endothelial cell migration                   | 9   | 0.0036  | 2.786  | 0.054 | Biological | GO:0010 | regulation of endothelial cell migration                            | 0.0036  | 0.06092 | 0 | 0 | 9   | 167   |
| GO:0010950 positive regulation of endopeptidase activity              | 9   | 0.0036  | 2.786  | 0.054 | Biological | GO:0010 | positive regulation of endopeptidase activity                       | 0.0036  | 0.06092 | 0 | 0 | 9   | 167   |
| GO:0035418 protein localization to synapse                            | 6   | 0.00362 | 1.858  | 0.074 | Biological | GO:0035 | protein localization to synapse                                     | 0.00362 | 0.06092 | 0 | 0 | 6   | 81    |
| GO:0050794 regulation of cellular process                             | 228 | 0.00363 | 70.588 | 0.02  | Biological | GO:0050 | regulation of cellular process                                      | 0.00363 | 0.06092 | 0 | 0 | 228 | 11233 |
| GO:0004618 embryonic eye morphogenesis                                | 4   | 0.00368 | 1.238  | 0.114 | Biological | GO:0004 | embryonic eye morphogenesis                                         | 0.00368 | 0.06092 | 0 | 0 | 4   | 35    |
| GO:0008046 gonad development                                          | 11  | 0.00365 | 3.406  | 0.047 | Biological | GO:0008 | gonad development                                                   | 0.00365 | 0.06092 | 0 | 0 | 11  | 232   |
| GO:0008544 epidermis development                                      | 15  | 0.00366 | 4.844  | 0.04  | Biological | GO:0008 | epidermis development                                               | 0.00366 | 0.06096 | 0 | 0 | 15  | 373   |
| GO:0021915 neural tube development                                    | 9   | 0.00375 | 2.786  | 0.054 | Biological | GO:0021 | neural tube development                                             | 0.00375 | 0.06189 | 0 | 0 | 9   | 168   |
| GO:0006584 catecholamine metabolic process                            | 5   | 0.00376 | 1.548  | 0.088 | Biological | GO:0006 | catecholamine metabolic process                                     | 0.00376 | 0.06189 | 0 | 0 | 5   | 57    |
| GO:0009712 catechol-containing compound metabolic process             | 11  | 0.00376 | 3.406  | 0.047 | Biological | GO:0009 | catechol-containing compound metabolic process                      | 0.00376 | 0.06189 | 0 | 0 | 11  | 233   |
| GO:0043583 ear development                                            | 11  | 0.00377 | 3.406  | 0.047 | Biological | GO:0043 | ear development                                                     | 0.00377 | 0.06189 | 0 | 0 | 11  | 233   |
| GO:0007173 epidermal growth factor receptor signaling pathway         | 7   | 0.00383 | 2.167  | 0.064 | Molecular  | GO:0007 | epidermal growth factor receptor signaling pathway                  | 0.00383 | 0.06266 | 0 | 0 | 7   | 109   |
| GO:0043177 organic acid binding                                       | 8   | 0.00388 | 2.339  | 0.059 | Biological | GO:0043 | organic acid binding                                                | 0.00388 | 0.14001 | 0 | 0 | 8   | 136   |
| GO:0030027 lamellipodium                                              | 10  | 0.00388 | 2.967  | 0.049 | Cellular   | GO:0030 | lamellipodium                                                       | 0.00388 | 0.05931 | 0 | 0 | 10  | 203   |
| GO:0030178 positive regulation of Wnt signaling pathway               | 9   | 0.00389 | 12.933 | 0.029 | Biological | GO:0030 | positive regulation of Wnt signaling pathway                        | 0.00389 | 0.05923 | 0 | 0 | 9   | 169   |
| GO:0010744 positive regulation of macrophage derived foam cell differ | 3   | 0.004   | 0.929  | 0.167 | Biological | GO:0010 | positive regulation of macrophage derived foam cell differentiation | 0.004   | 0.06454 | 0 | 0 | 3   | 18    |
| GO:0072077 renal vesicle morphogenesis                                | 3   | 0.004   | 0.929  | 0.167 | Biological | GO:0072 | renal vesicle morphogenesis                                         | 0.004   | 0.06454 | 0 | 0 | 3   | 18    |
| GO:0010573 vascular endothelial growth factor production              | 4   | 0.00403 | 1.238  | 0.111 | Biological | GO:0010 | vascular endothelial growth factor production                       | 0.00403 | 0.06454 | 0 | 0 | 4   | 36    |
| GO:0010742 macrophage derived foam cell differentiation               | 4   | 0.00403 | 1.238  | 0.111 | Biological | GO:0010 | macrophage derived foam cell differentiation                        | 0.00403 | 0.06454 | 0 | 0 | 4   | 36    |
| GO:0009077 foam cell differentiation                                  | 4   | 0.00403 | 1.238  | 0.111 | Biological | GO:0009 | foam cell differentiation                                           | 0.00403 | 0.06454 | 0 | 0 | 4   | 36    |
| GO:0110110 positive regulation of animal organ morphogenesis          | 4   | 0.00403 | 1.238  | 0.111 | Biological | GO:0110 | positive regulation of animal organ morphogenesis                   | 0.00403 | 0.06454 | 0 | 0 | 4   | 36    |
| GO:0031344 regulation of cell projection organization                 | 22  | 0.00412 | 6.811  | 0.034 | Biological | GO:0031 | regulation of cell projection organization                          | 0.00412 | 0.06558 | 0 | 0 | 22  | 650   |
| GO:0048812 neuron protection morphogenesis                            | 22  | 0.00412 | 6.811  | 0.034 | Biological | GO:0048 | neuron protection morphogenesis                                     | 0.00412 | 0.06558 | 0 | 0 | 22  | 650   |
| GO:0032860 cell part morphogenesis                                    | 23  | 0.00415 | 7.121  | 0.033 | Biological | GO:0032 | cell part morphogenesis                                             | 0.00415 | 0.06578 | 0 | 0 | 23  | 691   |
| GO:0040571 regulation of system process                               | 21  | 0.00421 | 6.192  | 0.034 | Biological | GO:0040 | regulation of system process                                        | 0.00421 | 0.06589 | 0 | 0 | 21  | 571   |
| GO:0048589 developmental growth                                       | 22  | 0.00427 | 6.811  | 0.034 | Biological | GO:0048 | developmental growth                                                | 0.00427 | 0.06722 | 0 | 0 | 22  | 652   |
| GO:0045137 development of primary sexual characteristics              | 11  | 0.00428 | 3.406  | 0.046 | Biological | GO:0045 | development of primary sexual characteristics                       | 0.00428 | 0.06722 | 0 | 0 | 11  | 237   |
| GO:0048660 regulation of smooth muscle cell proliferation             | 8   | 0.00436 | 2.477  | 0.057 | Biological | GO:0048 | regulation of smooth muscle cell proliferation                      | 0.00436 | 0.06779 | 0 | 0 | 8   | 141   |
| GO:0015804 neutral amino acid transport                               | 5   | 0.00437 | 1.548  | 0.085 | Biological | GO:0015 | neutral amino acid transport                                        | 0.00437 | 0.06779 | 0 | 0 | 5   | 59    |
| GO:0035914 acida development                                          | 5   | 0.00437 | 1.548  | 0.085 | Biological | GO:0035 | acida development                                                   | 0.00437 | 0.06779 | 0 | 0 | 5   | 59    |
| GO:0061005 cell differentiation involved in kidney development        | 5   | 0.00437 | 1.548  | 0.085 | Biological | GO:0061 | cell differentiation involved in kidney development                 | 0.00437 | 0.06779 | 0 | 0 | 5   | 59    |
| GO:0048839 inner ear development                                      | 10  | 0.00448 | 3.096  | 0.049 | Biological | GO:0048 | inner ear development                                               | 0.00448 | 0.06933 | 0 | 0 | 10  | 205   |
| GO:0048708 astrocyte differentiation                                  | 6   | 0.00459 | 1.858  | 0.071 | Biological | GO:0048 | astrocyte differentiation                                           | 0.00459 | 0.06974 | 0 | 0 | 6   | 85    |
| GO:0030314 junctional membrane complex                                | 2   | 0.00463 | 0.593  | 0.333 | Cellular   | GO:0030 | junctional membrane complex                                         | 0.00463 | 0.06883 | 0 | 0 | 2   | 6     |
| GO:0008016 regulation of heart contraction                            | 10  | 0.00463 | 3.096  | 0.049 | Biological | GO:0008 | regulation of heart contraction                                     | 0.00463 | 0.06974 | 0 | 0 | 10  | 206   |
| GO:0051235 maintenance of location                                    | 14  | 0.00466 | 4.334  | 0.04  | Biological | GO:0051 | maintenance of location                                             | 0.00466 | 0.06974 | 0 | 0 | 14  | 346   |
| GO:0043473 pigmentation                                               | 7   | 0.00467 | 2.167  | 0.062 | Biological | GO:0043 | pigmentation                                                        | 0.00467 | 0.06974 | 0 | 0 | 7   | 113   |
| GO:0071625 vocalization behavior                                      | 3   | 0.00468 | 0.929  | 0.158 | Biological | GO:0071 | vocalization behavior                                               | 0.00468 | 0.06974 | 0 | 0 | 3   | 19    |
| GO:0072087 renal vesicle development                                  | 3   | 0.00468 | 0.929  | 0.158 | Biological | GO:0072 | renal vesicle development                                           | 0.00468 | 0.06974 | 0 | 0 | 3   | 19    |
| GO:0008237 metalloproteinase activity                                 | 10  | 0.00471 | 3.224  | 0.05  | Molecular  | GO:0008 | metalloproteinase activity                                          | 0.00471 | 0.15397 | 0 | 0 | 10  | 203   |
| GO:004390 ubiquitin-like protein conjugating enzyme binding           | 4   | 0.0     |        |       |            |         |                                                                     |         |         |   |   |     |       |

|                                                                                    |     |         |        |       |            |                                                                                    |         |         |   |   |     |      |
|------------------------------------------------------------------------------------|-----|---------|--------|-------|------------|------------------------------------------------------------------------------------|---------|---------|---|---|-----|------|
| GO:0007077 mitotic nuclear membrane disassembly                                    | 2   | 0.00655 | 0.619  | 0.286 | Biological | GO:0007077 mitotic nuclear membrane disassembly                                    | 0.00655 | 0.08434 | 0 | 0 | 2   | 7    |
| GO:0021780 glial cell fate specification                                           | 2   | 0.00655 | 0.619  | 0.286 | Biological | GO:0021780 glial cell fate specification                                           | 0.00655 | 0.08434 | 0 | 0 | 2   | 7    |
| GO:0021796 cerebral cortex regionalization                                         | 2   | 0.00655 | 0.619  | 0.286 | Biological | GO:0021796 cerebral cortex regionalization                                         | 0.00655 | 0.08434 | 0 | 0 | 2   | 7    |
| GO:0032808 lacrimal gland development                                              | 2   | 0.00655 | 0.619  | 0.286 | Biological | GO:0032808 lacrimal gland development                                              | 0.00655 | 0.08434 | 0 | 0 | 2   | 7    |
| GO:0034334 adherens junction maintenance                                           | 2   | 0.00655 | 0.619  | 0.286 | Biological | GO:0034334 adherens junction maintenance                                           | 0.00655 | 0.08434 | 0 | 0 | 2   | 7    |
| GO:0071503 response to heparin                                                     | 2   | 0.00655 | 0.619  | 0.286 | Biological | GO:0071503 response to heparin                                                     | 0.00655 | 0.08434 | 0 | 0 | 2   | 7    |
| GO:0071226 positive regulation of glomerular mesangial cell proliferation          | 2   | 0.00655 | 0.619  | 0.286 | Biological | GO:0071226 positive regulation of glomerular mesangial cell proliferation          | 0.00655 | 0.08434 | 0 | 0 | 2   | 7    |
| GO:0090717 renal protein absorption                                                | 2   | 0.00655 | 0.619  | 0.286 | Biological | GO:0090717 renal protein absorption                                                | 0.00655 | 0.08434 | 0 | 0 | 2   | 7    |
| GO:1904683 regulation of metalloendopeptidase activity                             | 2   | 0.00655 | 0.619  | 0.286 | Biological | GO:1904683 regulation of metalloendopeptidase activity                             | 0.00655 | 0.08434 | 0 | 0 | 2   | 7    |
| GO:1905049 negative regulation of metalloendopeptidase activity                    | 2   | 0.00655 | 0.619  | 0.286 | Biological | GO:1905049 negative regulation of metalloendopeptidase activity                    | 0.00655 | 0.08434 | 0 | 0 | 2   | 7    |
| GO:0035107 appendage morphogenesis                                                 | 8   | 0.00655 | 2.477  | 0.053 | Biological | GO:0035107 appendage morphogenesis                                                 | 0.00655 | 0.08434 | 0 | 0 | 8   | 151  |
| GO:0035108 limb morphogenesis                                                      | 8   | 0.00655 | 2.477  | 0.053 | Biological | GO:0035108 limb morphogenesis                                                      | 0.00655 | 0.08434 | 0 | 0 | 8   | 151  |
| GO:0007548 sex differentiation                                                     | 12  | 0.00662 | 3.715  | 0.033 | Molecular  | GO:0007548 sex differentiation                                                     | 0.00662 | 0.15397 | 0 | 0 | 12  | 287  |
| GO:0030545 signaling receptor regulator activity                                   | 19  | 0.00667 | 5.556  | 0.035 | Molecular  | GO:0030545 signaling receptor regulator activity                                   | 0.00667 | 0.15397 | 0 | 0 | 19  | 546  |
| GO:0022407 regulation of cell-cell adhesion                                        | 17  | 0.00668 | 5.263  | 0.036 | Biological | GO:0022407 regulation of cell-cell adhesion                                        | 0.00668 | 0.08548 | 0 | 0 | 17  | 476  |
| GO:1901214 regulation of neuron death                                              | 13  | 0.00673 | 4.025  | 0.04  | Biological | GO:1901214 regulation of neuron death                                              | 0.00673 | 0.08594 | 0 | 0 | 13  | 324  |
| GO:0002761 regulation of myeloid leukocyte differentiation                         | 7   | 0.00675 | 2.167  | 0.058 | Biological | GO:0002761 regulation of myeloid leukocyte differentiation                         | 0.00675 | 0.08597 | 0 | 0 | 7   | 121  |
| GO:0031406 carboxylic acid binding                                                 | 9   | 0.00676 | 2.832  | 0.05  | Molecular  | GO:0031406 carboxylic acid binding                                                 | 0.00676 | 0.15397 | 0 | 0 | 9   | 187  |
| GO:0043292 sphingosine 1-phosphate phosphatase activity                            | 2   | 0.00676 | 0.585  | 0.286 | Molecular  | GO:0043292 sphingosine 1-phosphate phosphatase activity                            | 0.00676 | 0.15397 | 0 | 0 | 2   | 7    |
| GO:0043167 ion binding                                                             | 135 | 0.0068  | 39.474 | 0.022 | Molecular  | GO:0043167 ion binding                                                             | 0.0068  | 0.15397 | 0 | 0 | 135 | 6096 |
| GO:0007610 behavior                                                                | 21  | 0.00683 | 6.502  | 0.033 | Biological | GO:0007610 behavior                                                                | 0.00683 | 0.08677 | 0 | 0 | 21  | 638  |
| GO:0030020 extracellular matrix structural constituent conferring tensile strength | 4   | 0.00684 | 1.17   | 0.098 | Molecular  | GO:0030020 extracellular matrix structural constituent conferring tensile strength | 0.00684 | 0.15397 | 0 | 0 | 4   | 41   |
| GO:0052548 regulation of endopeptidase activity                                    | 13  | 0.0069  | 4.025  | 0.04  | Biological | GO:0052548 regulation of endopeptidase activity                                    | 0.0069  | 0.08742 | 0 | 0 | 13  | 325  |
| GO:1903522 regulation of blood circulation                                         | 11  | 0.00691 | 3.406  | 0.043 | Biological | GO:1903522 regulation of blood circulation                                         | 0.00691 | 0.08742 | 0 | 0 | 11  | 253  |
| GO:0086858 actin-based cell projection                                             | 10  | 0.00698 | 2.967  | 0.045 | Cellular   | GO:0086858 actin-based cell projection                                             | 0.00698 | 0.08116 | 0 | 0 | 10  | 221  |
| GO:0001656 metanephros development                                                 | 6   | 0.00709 | 1.858  | 0.065 | Biological | GO:0001656 metanephros development                                                 | 0.00709 | 0.08939 | 0 | 0 | 6   | 93   |
| GO:0001228 DNA-binding transcription activator activity, RNA polymerase II-spec    | 17  | 0.0071  | 4.971  | 0.036 | Molecular  | GO:0001228 DNA-binding transcription activator activity, RNA polymerase II-spec    | 0.0071  | 0.15397 | 0 | 0 | 17  | 471  |
| GO:0030548 signaling receptor activator activity                                   | 18  | 0.00711 | 5.929  | 0.033 | Molecular  | GO:0030548 signaling receptor activator activity                                   | 0.00711 | 0.15397 | 0 | 0 | 18  | 510  |
| GO:0007530 sex determination                                                       | 3   | 0.00715 | 0.929  | 0.136 | Biological | GO:0007530 sex determination                                                       | 0.00715 | 0.08971 | 0 | 0 | 3   | 22   |
| GO:0071379 cellular response to prostaglandin stimulus                             | 3   | 0.00715 | 0.929  | 0.136 | Biological | GO:0071379 cellular response to prostaglandin stimulus                             | 0.00715 | 0.08971 | 0 | 0 | 3   | 22   |
| GO:0043296 apical junction complex                                                 | 8   | 0.00716 | 2.374  | 0.052 | Cellular   | GO:0043296 apical junction complex                                                 | 0.00716 | 0.08155 | 0 | 0 | 8   | 155  |
| GO:0030326 embryonic limb morphogenesis                                            | 7   | 0.00736 | 2.167  | 0.057 | Biological | GO:0030326 embryonic limb morphogenesis                                            | 0.00736 | 0.09192 | 0 | 0 | 7   | 123  |
| GO:0001813 embryonic appendage morphogenesis                                       | 7   | 0.00736 | 2.167  | 0.057 | Biological | GO:0001813 embryonic appendage morphogenesis                                       | 0.00736 | 0.09192 | 0 | 0 | 7   | 123  |
| GO:0004383 neural tube closure                                                     | 6   | 0.00746 | 1.858  | 0.064 | Biological | GO:0004383 neural tube closure                                                     | 0.00746 | 0.09277 | 0 | 0 | 6   | 94   |
| GO:0050501 muscle cell development                                                 | 9   | 0.00747 | 2.786  | 0.048 | Biological | GO:0050501 muscle cell development                                                 | 0.00747 | 0.09277 | 0 | 0 | 9   | 187  |
| GO:0010633 negative regulation of epithelial cell migration                        | 5   | 0.0075  | 1.548  | 0.075 | Biological | GO:0010633 negative regulation of epithelial cell migration                        | 0.0075  | 0.09289 | 0 | 0 | 5   | 67   |
| GO:0021700 developmental maturation                                                | 13  | 0.00761 | 4.025  | 0.04  | Biological | GO:0021700 developmental maturation                                                | 0.00761 | 0.09404 | 0 | 0 | 13  | 329  |
| GO:0007613 memory                                                                  | 7   | 0.00768 | 2.167  | 0.057 | Biological | GO:0007613 memory                                                                  | 0.00768 | 0.09468 | 0 | 0 | 7   | 164  |
| GO:0001216 DNA-binding transcription activator activity                            | 17  | 0.0077  | 4.971  | 0.036 | Molecular  | GO:0001216 DNA-binding transcription activator activity                            | 0.0077  | 0.15736 | 0 | 0 | 17  | 475  |
| GO:0043068 positive regulation of programmed cell death                            | 18  | 0.0077  | 5.573  | 0.034 | Biological | GO:0043068 positive regulation of programmed cell death                            | 0.0077  | 0.09468 | 0 | 0 | 18  | 523  |
| GO:0071695 anatomical structure maturation                                         | 11  | 0.00774 | 3.406  | 0.043 | Biological | GO:0071695 anatomical structure maturation                                         | 0.00774 | 0.09495 | 0 | 0 | 11  | 257  |
| GO:0060606 tube closure                                                            | 6   | 0.00784 | 1.858  | 0.063 | Biological | GO:0060606 tube closure                                                            | 0.00784 | 0.096   | 0 | 0 | 6   | 95   |
| GO:0007267 cell-cell signaling                                                     | 44  | 0.00797 | 13.822 | 0.037 | Biological | GO:0007267 cell-cell signaling                                                     | 0.00797 | 0.10021 | 0 | 0 | 44  | 1666 |
| GO:1902893 regulation of pri-miRNA transcription by RNA polymerase II              | 5   | 0.00797 | 1.548  | 0.074 | Biological | GO:1902893 regulation of pri-miRNA transcription by RNA polymerase II              | 0.00797 | 0.097   | 0 | 0 | 5   | 68   |
| GO:0018209 peptidyl-serine modification                                            | 13  | 0.00798 | 4.025  | 0.039 | Biological | GO:0018209 peptidyl-serine modification                                            | 0.00798 | 0.097   | 0 | 0 | 13  | 331  |
| GO:0043085 positive regulation of catalytic activity                               | 32  | 0.008   | 9.907  | 0.029 | Biological | GO:0043085 positive regulation of catalytic activity                               | 0.008   | 0.09701 | 0 | 0 | 32  | 1121 |
| GO:0006509 membrane protein ectodomain proteolysis                                 | 4   | 0.00829 | 1.238  | 0.091 | Biological | GO:0006509 membrane protein ectodomain proteolysis                                 | 0.00829 | 0.10021 | 0 | 0 | 4   | 44   |
| GO:0051173 positive regulation of nitrogen compound metabolic process              | 7   | 0.00832 | 2.31   | 0.051 | Biological | GO:0051173 positive regulation of nitrogen compound metabolic process              | 0.00832 | 0.10021 | 0 | 0 | 7   | 131  |
| GO:0038127 ERBB signaling pathway                                                  | 7   | 0.00836 | 2.167  | 0.056 | Biological | GO:0038127 ERBB signaling pathway                                                  | 0.00836 | 0.10021 | 0 | 0 | 7   | 126  |
| GO:0009968 negative regulation of signal transduction                              | 35  | 0.00837 | 10.836 | 0.028 | Biological | GO:0009968 negative regulation of signal transduction                              | 0.00837 | 0.10021 | 0 | 0 | 35  | 1259 |
| GO:0042325 regulation of phosphorylation                                           | 34  | 0.00837 | 10.526 | 0.028 | Biological | GO:0042325 regulation of phosphorylation                                           | 0.00837 | 0.10021 | 0 | 0 | 34  | 1214 |
| GO:0061673 mitotic spindle astral microtubule                                      | 2   | 0.00844 | 0.593  | 0.25  | Cellular   | GO:0061673 mitotic spindle astral microtubule                                      | 0.00844 | 0.09409 | 0 | 0 | 2   | 8    |
| GO:0081134 transcription factor binding                                            | 20  | 0.00849 | 5.948  | 0.033 | Molecular  | GO:0081134 transcription factor binding                                            | 0.00849 | 0.15736 | 0 | 0 | 20  | 548  |
| GO:0002573 myeloid leukocyte differentiation                                       | 10  | 0.00847 | 3.096  | 0.044 | Biological | GO:0002573 myeloid leukocyte differentiation                                       | 0.00847 | 0.10073 | 0 | 0 | 10  | 225  |
| GO:0061614 pri-miRNA transcription by RNA polymerase II                            | 5   | 0.00847 | 1.548  | 0.072 | Biological | GO:0061614 pri-miRNA transcription by RNA polymerase II                            | 0.00847 | 0.10073 | 0 | 0 | 5   | 69   |
| GO:0097120 receptor localization to synapse                                        | 5   | 0.00847 | 1.548  | 0.072 | Biological | GO:0097120 receptor localization to synapse                                        | 0.00847 | 0.10073 | 0 | 0 | 5   | 69   |
| GO:0006951 calcium-dependent protein serine/threonine kinase activity              | 3   | 0.00849 | 0.877  | 0.13  | Molecular  | GO:0006951 calcium-dependent protein serine/threonine kinase activity              | 0.00849 | 0.15736 | 0 | 0 | 3   | 23   |
| GO:0035035 histone deacetyltransferase binding                                     | 9   | 0.00849 | 0.877  | 0.13  | Molecular  | GO:0035035 histone deacetyltransferase binding                                     | 0.00849 | 0.15736 | 0 | 0 | 9   | 237  |
| GO:0098917 postsynapse organization                                                | 9   | 0.00852 | 2.786  | 0.047 | Biological | GO:0098917 postsynapse organization                                                | 0.00852 | 0.1009  | 0 | 0 | 9   | 191  |
| GO:0010243 response to organonitrogen compound                                     | 30  | 0.00858 | 9.288  | 0.029 | Biological | GO:0010243 response to organonitrogen compound                                     | 0.00858 | 0.1009  | 0 | 0 | 30  | 1038 |
| GO:0008656 cytoskeleton                                                            | 59  | 0.00862 | 17.507 | 0.024 | Cellular   | GO:0008656 cytoskeleton                                                            | 0.00862 | 0.09411 | 0 | 0 | 59  | 2411 |
| GO:0007207 phospholipase C-activating G protein-coupled acetylcholine receptor     | 2   | 0.00863 | 0.619  | 0.25  | Biological | GO:0007207 phospholipase C-activating G protein-coupled acetylcholine receptor     | 0.00863 | 0.1009  | 0 | 0 | 2   | 8    |
| GO:0050861 positive regulation of B cell receptor signaling pathway                | 2   | 0.00863 | 0.619  | 0.25  | Biological | GO:0050861 positive regulation of B cell receptor signaling pathway                | 0.00863 | 0.1009  | 0 | 0 | 2   | 8    |
| GO:0051045 negative regulation of membrane protein ectodomain proteolysis          | 2   | 0.00863 | 0.619  | 0.25  | Biological | GO:0051045 negative regulation of membrane protein ectodomain proteolysis          | 0.00863 | 0.1009  | 0 | 0 | 2   | 8    |
| GO:0070255 regulation of mucus secretion                                           | 2   | 0.00863 | 0.619  | 0.25  | Biological | GO:0070255 regulation of mucus secretion                                           | 0.00863 | 0.1009  | 0 | 0 | 2   | 8    |
| GO:0072033 renal vesicle formation                                                 | 2   | 0.00863 | 0.619  | 0.25  | Biological | GO:0072033 renal vesicle formation                                                 | 0.00863 | 0.1009  | 0 | 0 | 2   | 8    |
| GO:0071724 SH3 domain binding                                                      | 7   | 0.00875 | 2.047  | 0.056 | Molecular  | GO:0071724 SH3 domain binding                                                      | 0.00875 | 0.15736 | 0 | 0 | 7   | 125  |
| GO:0035184 histone threonine kinase activity                                       | 2   | 0.00881 | 0.585  | 0.286 | Molecular  | GO:0035184 histone threonine kinase activity                                       | 0.00881 | 0.15736 | 0 | 0 | 2   | 8    |
| GO:0047023 androsterone dehydrogenase activity                                     | 2   | 0.00891 | 0.585  | 0.25  | Molecular  | GO:0047023 androsterone dehydrogenase activity                                     | 0.00891 | 0.15736 | 0 | 0 | 2   | 8    |
| GO:0010463 mesenchymal cell proliferation                                          | 4   | 0.00898 | 1.238  | 0.089 | Biological | GO:0010463 mesenchymal cell proliferation                                          | 0.00898 | 0.10417 | 0 | 0 | 4   | 45   |
| GO:0043620 regulation of DNA-templated transcription in response to stress         | 4   | 0.00898 | 1.238  | 0.089 | Biological | GO:0043620 regulation of DNA-templated transcription in response to stress         | 0.00898 | 0.10417 | 0 | 0 | 4   | 45   |
| GO:0061086 positive regulation of protein tyrosine kinase activity                 | 4   | 0.00898 | 1.238  | 0.089 | Biological | GO:0061086 positive regulation of protein tyrosine kinase activity                 | 0.00898 | 0.10417 | 0 | 0 | 4   | 45   |
| GO:0032772 positive regulation of cytokine production                              | 5   | 0.00898 | 1.548  | 0.072 | Biological | GO:0032772 positive regulation of cytokine production                              | 0.00898 | 0.10417 | 0 | 0 | 5   | 748  |
| GO:0051128 regulation of cellular component organization                           | 59  | 0.00902 | 18.266 | 0.025 | Biological | GO:0051128 regulation of cellular component organization                           | 0.00902 | 0.10426 | 0 | 0 | 59  | 2392 |
| GO:1901699 cellular response to nitrogen compound                                  | 22  | 0.00909 | 6.811  | 0.032 | Biological | GO:1901699 cellular response to nitrogen compound                                  | 0.00909 | 0.10481 | 0 | 0 | 22  | 697  |
| GO:0040222 metalloendopeptidase activity                                           | 7   | 0.00912 | 2.047  | 0.056 | Molecular  | GO:0040222 metalloendopeptidase activity                                           | 0.00912 | 0.15736 | 0 | 0 | 7   | 126  |
| GO:0002070 epithelial cell maturation                                              | 3   | 0.00919 | 0.929  | 0.125 | Biological | GO:0002070 epithelial cell maturation                                              | 0.00919 | 0.10502 | 0 | 0 | 3   | 24   |
| GO:0051043 regulation of membrane protein ectodomain proteolysis                   | 2   | 0.00915 | 0.929  | 0.125 | Biological | GO:0051043 regulation of membrane protein ectodomain proteolysis                   | 0.00915 | 0.10502 | 0 | 0 | 2   | 8    |
| GO:0001649 osteoblast differentiation                                              | 10  | 0.00924 | 3.096  | 0.044 | Biological | GO:0001649 osteoblast differentiation                                              | 0.00924 | 0.10588 | 0 | 0 | 10  | 228  |
| GO:0044297 cell body                                                               | 19  | 0.00927 | 5.638  | 0.033 | Cellular   | GO:0044297 cell body                                                               | 0.00927 | 0.09923 | 0 | 0 | 19  | 580  |
| GO:0003032 response to reactive oxygen species                                     | 9   | 0.00939 | 2.786  | 0.046 | Biological | GO:0003032 response to reactive oxygen species                                     | 0.00939 | 0.10726 | 0 | 0 | 9   | 194  |
| GO:0001503 ossification                                                            | 15  | 0.00948 | 4.824  | 0.036 | Biological | GO:0001503 ossification                                                            | 0.00948 | 0.10807 | 0 | 0 | 15  | 414  |
| GO:0040897 regulation of cellular component biogenesis                             | 29  | 0.00953 | 8.978  | 0.027 | Biological | GO:0040897 regulation of cellular component biogenesis                             | 0.00953 | 0.10838 | 0 | 0 | 29  | 1002 |
| GO:0010857 calcium-dependent protein kinase activity                               | 3   | 0.00957 | 0.877  | 0.125 | Molecular  | GO:0010857 calcium-dependent protein kinase activity                               | 0.00957 | 0.15736 | 0 | 0 | 3   | 24   |
| GO:0070412 R-SMAD binding                                                          | 3   | 0.00957 | 0.877  | 0.125 | Molecular  | GO:0070412 R-SMAD binding                                                          | 0.00957 | 0.15736 | 0 | 0 | 3   | 24   |
| GO:0050790 regulation of catalytic activity                                        | 48  | 0.00967 | 14.861 | 0.026 | Biological | GO:0050790 regulation of catalytic activity                                        | 0.00967 | 0.10951 | 0 | 0 | 48  | 1874 |
| GO:0021762 substance nrg1a development                                             | 4   | 0.00969 | 1.238  | 0.087 | Biological | GO:0021762 substance nrg1a development                                             | 0.00969 | 0.10851 | 0 | 0 | 4   | 46   |
| GO:0042551 neuron maturation                                                       | 23  | 0.00969 | 7.121  | 0.031 | Biological | GO:0042551 neuron maturation                                                       | 0.00969 | 0.10945 | 0 | 0 | 23  | 745  |
| GO:000                                                                             |     |         |        |       |            |                                                                                    |         |         |   |   |     |      |

|                                                                                           |     |           |        |       |            |                                                                                           |         |         |   |   |     |      |
|-------------------------------------------------------------------------------------------|-----|-----------|--------|-------|------------|-------------------------------------------------------------------------------------------|---------|---------|---|---|-----|------|
| GO:0043009 chordate embryonic development                                                 | 21  | 0.01222   | 6.502  | 0.031 | Biological | GO:0043009 chordate embryonic development                                                 | 0.01222 | 0.12376 | 0 | 0 | 21  | 674  |
| GO:007160 cell-matrix adhesion                                                            | 10  | 0.01224   | 3.096  | 0.042 | Biological | GO:007160 cell-matrix adhesion                                                            | 0.01224 | 0.12376 | 0 | 0 | 10  | 238  |
| GO:0007169 transmembrane receptor protein tyrosine kinase signaling                       | 20  | 0.01224   | 6.132  | 0.032 | Biological | GO:0007169 transmembrane receptor protein tyrosine kinase signaling                       | 0.01224 | 0.12376 | 0 | 0 | 20  | 632  |
| GO:0009090 negative regulation of canonical Wnt signaling pathway                         | 7   | 0.01241   | 2.167  | 0.051 | Biological | GO:0009090 negative regulation of canonical Wnt signaling pathway                         | 0.01241 | 0.12503 | 0 | 0 | 7   | 136  |
| GO:0009092 regulation of transmembrane receptor protein serine/threonine kinase           | 11  | 0.01243   | 3.406  | 0.04  | Biological | GO:0009092 regulation of transmembrane receptor protein serine/threonine kinase           | 0.01243 | 0.12503 | 0 | 0 | 11  | 275  |
| GO:0007519 skeletal muscle tissue development                                             | 8   | 0.01247   | 2.477  | 0.047 | Biological | GO:0007519 skeletal muscle tissue development                                             | 0.01247 | 0.12503 | 0 | 0 | 8   | 169  |
| GO:0046661 male sex differentiation                                                       | 8   | 0.01247   | 2.477  | 0.047 | Biological | GO:0046661 male sex differentiation                                                       | 0.01247 | 0.12503 | 0 | 0 | 8   | 169  |
| GO:018105 peptidyl-serine phosphorylation                                                 | 12  | 0.01283   | 3.715  | 0.038 | Biological | GO:018105 peptidyl-serine phosphorylation                                                 | 0.01283 | 0.12634 | 0 | 0 | 12  | 313  |
| GO:006314 regulation of cytosolic calcium-release channel                                 | 3   | 0.0127    | 0.929  | 0.111 | Biological | GO:006314 regulation of cytosolic calcium-release channel                                 | 0.0127  | 0.12634 | 0 | 0 | 3   | 27   |
| GO:0060384 innervation                                                                    | 3   | 0.0127    | 0.929  | 0.111 | Biological | GO:0060384 innervation                                                                    | 0.0127  | 0.12634 | 0 | 0 | 3   | 27   |
| GO:0060740 prostate gland epithelium morphogenesis                                        | 3   | 0.0127    | 0.929  | 0.111 | Biological | GO:0060740 prostate gland epithelium morphogenesis                                        | 0.0127  | 0.12634 | 0 | 0 | 3   | 27   |
| GO:0032813 tumor necrosis factor receptor superfamily binding                             | 4   | 0.01276   | 1.17   | 0.082 | Molecular  | GO:0032813 tumor necrosis factor receptor superfamily binding                             | 0.01276 | 0.15736 | 0 | 0 | 4   | 19   |
| GO:0007507 heart development                                                              | 19  | 0.01301   | 5.882  | 0.05  | Biological | GO:0007507 heart development                                                              | 0.01301 | 0.12875 | 0 | 0 | 19  | 584  |
| GO:0014701 junctional sarcoplasmic reticulum membrane                                     | 2   | 0.01325   | 0.593  | 0.2   | Cellular   | GO:0014701 junctional sarcoplasmic reticulum membrane                                     | 0.01325 | 0.1162  | 0 | 0 | 2   | 10   |
| GO:0071813 lipoprotein particle binding                                                   | 3   | 0.01328   | 0.877  | 0.111 | Molecular  | GO:0071813 lipoprotein particle binding                                                   | 0.01328 | 0.15736 | 0 | 0 | 3   | 27   |
| GO:0071814 protein-lipid complex binding                                                  | 3   | 0.01328   | 0.877  | 0.111 | Molecular  | GO:0071814 protein-lipid complex binding                                                  | 0.01328 | 0.15736 | 0 | 0 | 3   | 27   |
| GO:0048717 tissue remodeling                                                              | 8   | 0.01331   | 2.477  | 0.047 | Biological | GO:0048717 tissue remodeling                                                              | 0.01331 | 0.12875 | 0 | 0 | 8   | 171  |
| GO:0042803 protein homodimerization activity                                              | 22  | 0.01332   | 6.433  | 0.031 | Molecular  | GO:0042803 protein homodimerization activity                                              | 0.01332 | 0.15736 | 0 | 0 | 22  | 710  |
| GO:0034599 cellular response to oxidative stress                                          | 11  | 0.01339   | 3.406  | 0.04  | Biological | GO:0034599 cellular response to oxidative stress                                          | 0.01339 | 0.12875 | 0 | 0 | 11  | 278  |
| GO:0043549 regulation of kinase activity                                                  | 22  | 0.01346   | 6.811  | 0.03  | Biological | GO:0043549 regulation of kinase activity                                                  | 0.01346 | 0.12875 | 0 | 0 | 22  | 723  |
| GO:0090287 regulation of cellular response to growth factor stimulus                      | 12  | 0.01353   | 3.715  | 0.038 | Biological | GO:0090287 regulation of cellular response to growth factor stimulus                      | 0.01353 | 0.12875 | 0 | 0 | 12  | 316  |
| GO:0002138 retinoic acid biosynthetic process                                             | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0002138 retinoic acid biosynthetic process                                             | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0002934 desmosome organization                                                         | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0002934 desmosome organization                                                         | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0003253 cardiac neural crest cell migration involved in outflow tract morphogenesis    | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0003253 cardiac neural crest cell migration involved in outflow tract morphogenesis    | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0015820 leucine transport                                                              | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0015820 leucine transport                                                              | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0030638 polyketide metabolic process                                                   | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0030638 polyketide metabolic process                                                   | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0030647 aminoglycoside antibiotic metabolic process                                    | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0030647 aminoglycoside antibiotic metabolic process                                    | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0042341 fusogenic cell development                                                     | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0042341 fusogenic cell development                                                     | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0043653 mitochondrial fragmentation involved in apoptotic process                      | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0043653 mitochondrial fragmentation involved in apoptotic process                      | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0044598 doxorubicin metabolic process                                                  | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0044598 doxorubicin metabolic process                                                  | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0048865 stem cell fate commitment                                                      | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0048865 stem cell fate commitment                                                      | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0051081 nuclear membrane disassembly                                                   | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0051081 nuclear membrane disassembly                                                   | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0000056 mammary gland involution                                                       | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0000056 mammary gland involution                                                       | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0007094 renal sodium ion absorption                                                    | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0007094 renal sodium ion absorption                                                    | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0071214 regulation of glomerular mesangial cell proliferation                          | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0071214 regulation of glomerular mesangial cell proliferation                          | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0072203 cell proliferation involved in metanephros development                         | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0072203 cell proliferation involved in metanephros development                         | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0097113 AMPA glutamate receptor clustering                                             | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0097113 AMPA glutamate receptor clustering                                             | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0097698 glutamate receptor clustering                                                  | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0097698 glutamate receptor clustering                                                  | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0013054 negative regulation of extracellular matrix organization                       | 2   | 0.01354   | 0.819  | 0.2   | Biological | GO:0013054 negative regulation of extracellular matrix organization                       | 0.01354 | 0.12875 | 0 | 0 | 2   | 10   |
| GO:0060047 heart contraction                                                              | 10  | 0.01362   | 3.096  | 0.041 | Biological | GO:0060047 heart contraction                                                              | 0.01362 | 0.12932 | 0 | 0 | 10  | 242  |
| GO:0045165 cell fate commitment                                                           | 11  | 0.01372   | 3.406  | 0.039 | Biological | GO:0045165 cell fate commitment                                                           | 0.01372 | 0.13    | 0 | 0 | 11  | 279  |
| GO:0034332 adherens junction organization                                                 | 4   | 0.01383   | 1.238  | 0.078 | Biological | GO:0034332 adherens junction organization                                                 | 0.01383 | 0.13032 | 0 | 0 | 4   | 51   |
| GO:0042461 photoreceptor cell development                                                 | 4   | 0.01383   | 1.238  | 0.078 | Biological | GO:0042461 photoreceptor cell development                                                 | 0.01383 | 0.13032 | 0 | 0 | 4   | 51   |
| GO:0028955 positive regulation of pri-miRNA transcription by RNA polymerase II            | 4   | 0.01383   | 1.238  | 0.078 | Biological | GO:0028955 positive regulation of pri-miRNA transcription by RNA polymerase II            | 0.01383 | 0.13032 | 0 | 0 | 4   | 51   |
| GO:0071417 cellular response to organonitrogen compound                                   | 20  | 0.01387   | 6.192  | 0.031 | Biological | GO:0071417 cellular response to organonitrogen compound                                   | 0.01387 | 0.13047 | 0 | 0 | 20  | 640  |
| GO:0008239 dipeptidyl-peptidase activity                                                  | 2   | 0.01397   | 0.585  | 0.2   | Molecular  | GO:0008239 dipeptidyl-peptidase activity                                                  | 0.01397 | 0.15736 | 0 | 0 | 2   | 10   |
| GO:0060479 lung cell differentiation                                                      | 3   | 0.01404   | 0.929  | 0.107 | Biological | GO:0060479 lung cell differentiation                                                      | 0.01404 | 0.13102 | 0 | 0 | 3   | 28   |
| GO:0060487 lung epithelial cell differentiation                                           | 3   | 0.01404   | 0.929  | 0.107 | Biological | GO:0060487 lung epithelial cell differentiation                                           | 0.01404 | 0.13102 | 0 | 0 | 3   | 28   |
| GO:0099633 protein localization to postsynaptic specialization membrane                   | 3   | 0.01404   | 0.929  | 0.107 | Biological | GO:0099633 protein localization to postsynaptic specialization membrane                   | 0.01404 | 0.13102 | 0 | 0 | 3   | 28   |
| GO:0099645 neurotransmitter receptor localization to postsynaptic specialization membrane | 3   | 0.01404   | 0.929  | 0.107 | Biological | GO:0099645 neurotransmitter receptor localization to postsynaptic specialization membrane | 0.01404 | 0.13102 | 0 | 0 | 3   | 28   |
| GO:0001841 neural tube formation                                                          | 6   | 0.01421   | 1.858  | 0.056 | Biological | GO:0001841 neural tube formation                                                          | 0.01421 | 0.13242 | 0 | 0 | 6   | 108  |
| GO:0010977 negative regulation of neuron projection development                           | 7   | 0.01437   | 2.167  | 0.05  | Biological | GO:0010977 negative regulation of neuron projection development                           | 0.01437 | 0.13337 | 0 | 0 | 7   | 140  |
| GO:0016115 regulation of protein growth factor beta receptor signaling pathway            | 4   | 0.01437   | 2.167  | 0.05  | Biological | GO:0016115 regulation of protein growth factor beta receptor signaling pathway            | 0.01437 | 0.13337 | 0 | 0 | 4   | 140  |
| GO:0072503 cellular divalent inorganic cation homeostasis                                 | 17  | 0.01456   | 5.263  | 0.033 | Biological | GO:0072503 cellular divalent inorganic cation homeostasis                                 | 0.01456 | 0.13495 | 0 | 0 | 17  | 518  |
| GO:0000165 MAPK cascade                                                                   | 23  | 0.01464   | 7.121  | 0.03  | Biological | GO:0000165 MAPK cascade                                                                   | 0.01464 | 0.13537 | 0 | 0 | 23  | 772  |
| GO:0045499 chemorepellent activity                                                        | 3   | 0.01467   | 0.877  | 0.107 | Molecular  | GO:0045499 chemorepellent activity                                                        | 0.01467 | 0.15736 | 0 | 0 | 3   | 28   |
| GO:0010596 negative regulation of endothelial cell migration                              | 4   | 0.01477   | 1.238  | 0.077 | Biological | GO:0010596 negative regulation of endothelial cell migration                              | 0.01477 | 0.13612 | 0 | 0 | 4   | 52   |
| GO:0051489 regulation of lipoprotein assembly                                             | 4   | 0.01477   | 1.238  | 0.077 | Biological | GO:0051489 regulation of lipoprotein assembly                                             | 0.01477 | 0.13612 | 0 | 0 | 4   | 52   |
| GO:0019220 regulation of phosphate metabolic process                                      | 36  | 0.01488   | 11.146 | 0.027 | Biological | GO:0019220 regulation of phosphate metabolic process                                      | 0.01488 | 0.13868 | 0 | 0 | 36  | 1357 |
| GO:0051174 regulation of phosphorus metabolic process                                     | 36  | 0.01504   | 11.146 | 0.027 | Biological | GO:0051174 regulation of phosphorus metabolic process                                     | 0.01504 | 0.13752 | 0 | 0 | 36  | 1358 |
| GO:0001819 positive regulation of cytokine production                                     | 16  | 0.01533   | 4.954  | 0.033 | Biological | GO:0001819 positive regulation of cytokine production                                     | 0.01533 | 0.13752 | 0 | 0 | 16  | 480  |
| GO:0057435 supramolecular fiber organization                                              | 24  | 0.01535   | 7.43   | 0.029 | Biological | GO:0057435 supramolecular fiber organization                                              | 0.01535 | 0.13752 | 0 | 0 | 24  | 819  |
| GO:0021414 protein localization to cell junction                                          | 6   | 0.01544   | 1.858  | 0.056 | Biological | GO:0021414 protein localization to cell junction                                          | 0.01544 | 0.13752 | 0 | 0 | 6   | 168  |
| GO:0003094 glomerular filtration                                                          | 3   | 0.01545   | 0.929  | 0.103 | Biological | GO:0003094 glomerular filtration                                                          | 0.01545 | 0.13752 | 0 | 0 | 3   | 29   |
| GO:0005012 prostate gland morphogenesis                                                   | 3   | 0.01545   | 0.929  | 0.103 | Biological | GO:0005012 prostate gland morphogenesis                                                   | 0.01545 | 0.13752 | 0 | 0 | 3   | 29   |
| GO:0016043 cellular component organization                                                | 136 | 0.01547   | 42.105 | 0.021 | Biological | GO:0016043 cellular component organization                                                | 0.01547 | 0.13752 | 0 | 0 | 136 | 6412 |
| GO:0030864 cortical actin cytoskeleton                                                    | 5   | 0.01552   | 1.484  | 0.062 | Cellular   | GO:0030864 cortical actin cytoskeleton                                                    | 0.01552 | 0.13058 | 0 | 0 | 5   | 81   |
| GO:0002020 proteasome binding                                                             | 7   | 0.01562   | 2.047  | 0.05  | Molecular  | GO:0002020 proteasome binding                                                             | 0.01562 | 0.13058 | 0 | 0 | 7   | 147  |
| GO:0000139 Golgi membrane                                                                 | 20  | 0.01567   | 5.935  | 0.031 | Biological | GO:0000139 Golgi membrane                                                                 | 0.01567 | 0.13058 | 0 | 0 | 20  | 655  |
| GO:0019844 regulation of cellular response to transforming growth factor beta stimulus    | 7   | 0.01598   | 2.167  | 0.049 | Biological | GO:0019844 regulation of cellular response to transforming growth factor beta stimulus    | 0.01598 | 0.13752 | 0 | 0 | 7   | 143  |
| GO:0000235 astral microtubule                                                             | 2   | 0.016     | 0.593  | 0.182 | Cellular   | GO:0000235 astral microtubule                                                             | 0.016   | 0.13058 | 0 | 0 | 2   | 11   |
| GO:0005818 aster                                                                          | 2   | 0.016     | 0.593  | 0.182 | Cellular   | GO:0005818 aster                                                                          | 0.016   | 0.13058 | 0 | 0 | 2   | 11   |
| GO:0034310 positive regulation of MAPK cascade                                            | 16  | 0.01616   | 4.954  | 0.033 | Biological | GO:0034310 positive regulation of MAPK cascade                                            | 0.01616 | 0.13752 | 0 | 0 | 16  | 483  |
| GO:0045178 basal part of cell                                                             | 11  | 0.01616   | 3.264  | 0.038 | Cellular   | GO:0045178 basal part of cell                                                             | 0.01616 | 0.13058 | 0 | 0 | 11  | 289  |
| GO:0061097 regulation of protein tyrosine kinase activity                                 | 5   | 0.01621   | 1.548  | 0.062 | Biological | GO:0061097 regulation of protein tyrosine kinase activity                                 | 0.01621 | 0.13752 | 0 | 0 | 5   | 81   |
| GO:0046914 transition metal ion binding                                                   | 31  | 0.01634   | 9.064  | 0.028 | Molecular  | GO:0046914 transition metal ion binding                                                   | 0.01634 | 0.15736 | 0 | 0 | 31  | 1117 |
| GO:0009950 dorsal/ventral axis specification                                              | 2   | 0.01635   | 0.819  | 0.182 | Biological | GO:0009950 dorsal/ventral axis specification                                              | 0.01635 | 0.13752 | 0 | 0 | 2   | 11   |
| GO:0016102 divergent bicellular cleavage                                                  | 2   | 0.01635   | 0.819  | 0.182 | Biological | GO:0016102 divergent bicellular cleavage                                                  | 0.01635 | 0.13752 | 0 | 0 | 2   | 11   |
| GO:0021889 olfactory bulb interneuron differentiation                                     | 2   | 0.01635   | 0.819  | 0.182 | Biological | GO:0021889 olfactory bulb interneuron differentiation                                     | 0.01635 | 0.13752 | 0 | 0 | 2   | 11   |
| GO:0021903 rostrocaudal neural tube patterning                                            | 2   | 0.01635   | 0.819  | 0.182 | Biological | GO:0021903 rostrocaudal neural tube patterning                                            | 0.01635 | 0.13752 | 0 | 0 | 2   | 11   |
| GO:0033210 lepton-mediated signaling pathway                                              | 2   | 0.01635   | 0.819  | 0.182 | Biological | GO:0033210 lepton-mediated signaling pathway                                              | 0.01635 | 0.13752 | 0 | 0 | 2   | 11   |
| GO:0034350 regulation of glial cell apoptotic process                                     | 2   | 0.01635   | 0.819  | 0.182 | Biological | GO:0034350 regulation of glial cell apoptotic process                                     | 0.01635 | 0.13752 | 0 | 0 | 2   | 11   |
| GO:0035378 nail development                                                               | 2   | 0.01635   | 0.819  | 0.182 | Biological | GO:0035378 nail development                                                               | 0.01635 | 0.13752 | 0 | 0 | 2   | 11   |
| GO:0042045 epithelial fluid transport                                                     | 2   | 0.01635   | 0.819  | 0.182 | Biological | GO:0042045 epithelial fluid transport                                                     | 0.01635 | 0.13752 | 0 | 0 | 2   | 11   |
| GO:0046689 response to mercury ion                                                        | 2   | 0.01635   | 0.819  | 0.182 | Biological | GO:0046689 response to mercury ion                                                        | 0.01635 | 0.13752 | 0 | 0 | 2   | 11   |
| GO:0060742 epithelial cell differentiation involved in prostate gland development         | 2   | 0.01635   | 0.819  | 0.182 | Biological | GO:0060742 epithelial cell differentiation involved in prostate gland development         | 0.01635 | 0.13752 | 0 | 0 | 2   | 11   |
| GO:0060757 epithelial cell proliferation involved in prostate gland development           | 2   | 0.01635   | 0.819  | 0.182 | Biological | GO:0060757 epithelial cell proliferation involved in prostate gland development           | 0.01635 | 0.13752 | 0 | 0 | 2   | 11   |
| GO:0071492 cellular response to UV-A                                                      | 2   | 0.01635   | 0.819  | 0.182 | Biological | GO:0071492 cellular response to UV-A                                                      | 0.01635 | 0.13752 | 0 | 0 | 2   | 11   |
| GO:0072110 glomerular mesangial cell proliferation                                        | 2   | 0.01635</ |        |       |            |                                                                                           |         |         |   |   |     |      |

|                                                                                                             |    |         |       |       |            |                                                                                                             |         |         |     |   |    |     |
|-------------------------------------------------------------------------------------------------------------|----|---------|-------|-------|------------|-------------------------------------------------------------------------------------------------------------|---------|---------|-----|---|----|-----|
| GO:0021629 olfactory nerve structural organization                                                          | 1  | 0.01823 | 0.31  | 1     | Biological | GO:00221 olfactory nerve structural organization                                                            | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0021905 forebrain-midbrain boundary formation                                                            | 1  | 0.01823 | 0.31  | 1     | Biological | GO:00221 olfactory nerve structural organization                                                            | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0021919 BMP signaling pathway involved in spinal cord dorsal/ventral pattern formation                   | 1  | 0.01823 | 0.31  | 1     | Biological | GO:00221 olfactory nerve structural organization                                                            | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0030334 microvillus bundle assembly                                                                      | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0030334 microvillus bundle assembly                                                                      | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0032244 positive regulation of nucleoside transport                                                      | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0032244 positive regulation of nucleoside transport                                                      | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0032900 negative regulation of neurotrophin production                                                   | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0032900 negative regulation of neurotrophin production                                                   | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0033026 negative regulation of mast cell apoptotic process                                               | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0033026 negative regulation of mast cell apoptotic process                                               | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0033645 enteric smooth muscle cell differentiation                                                       | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0033645 enteric smooth muscle cell differentiation                                                       | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0038167 epidermal growth factor receptor signaling pathway via positive regulation of cell proliferation | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0038167 epidermal growth factor receptor signaling pathway via positive regulation of cell proliferation | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0038168 epidermal growth factor receptor signaling pathway via I-kappaB kinase                           | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0038168 epidermal growth factor receptor signaling pathway via I-kappaB kinase                           | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0042323 negative regulation of circadian sleep/wake cycle, non-REM sleep                                 | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0042323 negative regulation of circadian sleep/wake cycle, non-REM sleep                                 | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0060514 prostate induction                                                                               | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0060514 prostate induction                                                                               | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0060515 prostate field specification                                                                     | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0060515 prostate field specification                                                                     | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0060517 epithelial cell proliferation involved in prostatic bud elongation                               | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0060517 epithelial cell proliferation involved in prostatic bud elongation                               | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0060520 activation of prostate induction by androgen receptor signaling pathway                          | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0060520 activation of prostate induction by androgen receptor signaling pathway                          | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0060611 mammary gland fat development                                                                    | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0060611 mammary gland fat development                                                                    | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0060721 regulation of spongiotrophoblast cell proliferation                                              | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0060721 regulation of spongiotrophoblast cell proliferation                                              | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0060723 regulation of cell proliferation involved in embryonic placenta development                      | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0060723 regulation of cell proliferation involved in embryonic placenta development                      | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0060754 regulation of cell proliferation involved in tissue homeostasis                                  | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0060754 regulation of cell proliferation involved in tissue homeostasis                                  | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0061193 taste bud development                                                                            | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0061193 taste bud development                                                                            | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0061864 basement membrane constituent secretion                                                          | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0061864 basement membrane constituent secretion                                                          | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0061865 polarized secretion of basement membrane proteins in epithelium                                  | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0061865 polarized secretion of basement membrane proteins in epithelium                                  | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0061872 hepatic stellate cell contraction                                                                | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0061872 hepatic stellate cell contraction                                                                | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0061874 positive regulation of hepatic stellate cell contraction                                         | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0061874 positive regulation of hepatic stellate cell contraction                                         | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0070208 protein heterotrimerization                                                                      | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0070208 protein heterotrimerization                                                                      | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0070981 L-asparagine biosynthetic process                                                                | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0070981 L-asparagine biosynthetic process                                                                | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0071831 intermediate filament particle clearance                                                         | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0071831 intermediate filament particle clearance                                                         | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0072303 positive regulation of glomerular mesangial cell proliferation                                   | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0072303 positive regulation of glomerular mesangial cell proliferation                                   | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0072308 negative regulation of mesangial epithelial cell proliferation                                   | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0072308 negative regulation of mesangial epithelial cell proliferation                                   | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0072347 response to anesthetic                                                                           | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0072347 response to anesthetic                                                                           | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0075731 cellular response to very-low-density lipoprotein particle stimulus                              | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0075731 cellular response to very-low-density lipoprotein particle stimulus                              | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0120116 glucocorticoid receptor signaling pathway                                                        | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0120116 glucocorticoid receptor signaling pathway                                                        | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0150200 regulation of transport across blood-brain barrier                                               | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0150200 regulation of transport across blood-brain barrier                                               | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0150201 positive regulation of transport across blood-brain barrier                                      | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0150201 positive regulation of transport across blood-brain barrier                                      | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190120 negative regulation of extracellular matrix assembly                                             | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190120 negative regulation of extracellular matrix assembly                                             | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190175 positive regulation of post-translational protein modification                                   | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190175 positive regulation of post-translational protein modification                                   | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190228 positive regulation of macrophage colony-stimulating factor signaling                            | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190228 positive regulation of macrophage colony-stimulating factor signaling                            | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190300 regulation of lipid transport across blood-brain barrier                                         | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190300 regulation of lipid transport across blood-brain barrier                                         | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190302 positive regulation of lipid transport across blood-brain barrier                                | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190302 positive regulation of lipid transport across blood-brain barrier                                | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190371 substantia nigra development                                                                     | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190371 substantia nigra development                                                                     | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190405 negative regulation of skeletal muscle hypertrophy                                               | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190405 negative regulation of skeletal muscle hypertrophy                                               | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190570 anterior ventral ectoderm cell migration                                                         | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190570 anterior ventral ectoderm cell migration                                                         | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190587 regulation of diacylglycerol kinase activity                                                     | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190587 regulation of diacylglycerol kinase activity                                                     | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190589 positive regulation of diacylglycerol kinase activity                                            | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190589 positive regulation of diacylglycerol kinase activity                                            | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190583 regulation of heparan sulfate binding                                                            | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190583 regulation of heparan sulfate binding                                                            | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190585 positive regulation of heparan sulfate binding                                                   | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190585 positive regulation of heparan sulfate binding                                                   | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190589 regulation of heparan sulfate proteoglycan binding                                               | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190589 regulation of heparan sulfate proteoglycan binding                                               | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190580 positive regulation of heparan sulfate proteoglycan binding                                      | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190580 positive regulation of heparan sulfate proteoglycan binding                                      | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190590 regulation of cellular response to very-low-density lipoprotein particle                         | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190590 regulation of cellular response to very-low-density lipoprotein particle                         | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0190678 histone H4-K16 deacetylation                                                                     | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0190678 histone H4-K16 deacetylation                                                                     | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0200690 regulation of cardiac muscle cell myoblast differentiation                                       | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0200690 regulation of cardiac muscle cell myoblast differentiation                                       | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0200691 negative regulation of cardiac muscle cell myoblast differentiation                              | 1  | 0.01823 | 0.31  | 1     | Biological | GO:0200691 negative regulation of cardiac muscle cell myoblast differentiation                              | 0.01823 | 0.13752 | 0   | 0 | 1  | 1   |
| GO:0003015 heart process                                                                                    | 10 | 0.01848 | 3.096 | 0.039 | Biological | GO:0003015 heart process                                                                                    | 0.01848 | 0.13813 | 0   | 0 | 10 | 254 |
| GO:0007435 salivary gland morphogenesis                                                                     | 3  | 0.0185  | 0.929 | 0.097 | Biological | GO:0007435 salivary gland morphogenesis                                                                     | 0.0185  | 0.13813 | 0   | 0 | 3  | 31  |
| GO:0010743 regulation of macrophage derived foam cell differentiation                                       | 3  | 0.0185  | 0.929 | 0.097 | Biological | GO:0010743 regulation of macrophage derived foam cell differentiation                                       | 0.0185  | 0.13813 | 0   | 0 | 3  | 31  |
| GO:0032607 interferon-alpha production                                                                      | 3  | 0.0185  | 0.929 | 0.097 | Biological | GO:0032607 interferon-alpha production                                                                      | 0.0185  | 0.13813 | 0   | 0 | 3  | 31  |
| GO:0032617 interferon-beta production                                                                       | 3  | 0.0185  | 0.929 | 0.097 | Biological | GO:0032617 interferon-beta production                                                                       | 0.0185  | 0.13813 | 0   | 0 | 3  | 31  |
| GO:0051491 positive regulation of filopodium assembly                                                       | 3  | 0.0185  | 0.929 | 0.097 | Biological | GO:0051491 positive regulation of filopodium assembly                                                       | 0.0185  | 0.13813 | 0   | 0 | 3  | 31  |
| GO:007205 renal filtration                                                                                  | 3  | 0.0185  | 0.929 | 0.097 | Biological | GO:007205 renal filtration                                                                                  | 0.0185  | 0.13813 | 0   | 0 | 3  | 31  |
| GO:0003830 beta-1.4-mannosylglucosyltransferase                                                             | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0003830 beta-1.4-mannosylglucosyltransferase                                                             | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0008120 ceramide glucosyltransferase activity                                                            | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0008120 ceramide glucosyltransferase activity                                                            | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0011712 cysteine diogenesis                                                                              | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0011712 cysteine diogenesis                                                                              | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0030379 neurotensin receptor activity, non-G protein-coupled                                             | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0030379 neurotensin receptor activity, non-G protein-coupled                                             | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0031078 histone deacetylase activity (H3-K14 specific)                                                   | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0031078 histone deacetylase activity (H3-K14 specific)                                                   | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0031714 C5a anaphylatoxin chemotactic receptor binding                                                   | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0031714 C5a anaphylatoxin chemotactic receptor binding                                                   | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0031715 C5L2 anaphylatoxin chemotactic receptor binding                                                  | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0031715 C5L2 anaphylatoxin chemotactic receptor binding                                                  | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0031717 cannabinoid receptor binding                                                                     | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0031717 cannabinoid receptor binding                                                                     | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0031718 type 1 cannabinoid receptor binding                                                              | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0031718 type 1 cannabinoid receptor binding                                                              | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0031883 taste receptor binding                                                                           | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0031883 taste receptor binding                                                                           | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0033744 L-methionine-thioester-disulfide S-oxidoreductase activity                                       | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0033744 L-methionine-thioester-disulfide S-oxidoreductase activity                                       | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0036151 prostaglandin D2 11-ketoreductase activity                                                       | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0036151 prostaglandin D2 11-ketoreductase activity                                                       | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0036466 L-methionine-S-oxide reductase activity                                                          | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0036466 L-methionine-S-oxide reductase activity                                                          | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0038177 death receptor agonist activity                                                                  | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0038177 death receptor agonist activity                                                                  | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0042943 D-amino acid transmembrane transporter activity                                                  | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0042943 D-amino acid transmembrane transporter activity                                                  | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0045703 ketoreductase activity                                                                           | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0045703 ketoreductase activity                                                                           | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0046911 metal chelating activity                                                                         | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0046911 metal chelating activity                                                                         | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0050512 lactoylserine 4-epi-alpha-galactosyltransferase activity                                         | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0050512 lactoylserine 4-epi-alpha-galactosyltransferase activity                                         | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0070119 ciliary neurotrophic factor binding                                                              | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0070119 ciliary neurotrophic factor binding                                                              | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0070974 POU domain binding                                                                               | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0070974 POU domain binding                                                                               | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0096959 inositol 1,4,5-trisphosphate receptor activity involved in regulation of cell proliferation      | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0096959 inositol 1,4,5-trisphosphate receptor activity involved in regulation of cell proliferation      | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0096977 histone-dependent DNA binding                                                                    | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0096977 histone-dependent DNA binding                                                                    | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0096980 estrogen binding                                                                                 | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0096980 estrogen binding                                                                                 | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0096989 microtubule lateral binding                                                                      | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0096989 microtubule lateral binding                                                                      | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0102769 dihydroceramide glucosyltransferase activity                                                     | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0102769 dihydroceramide glucosyltransferase activity                                                     | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0140010 D-aspartate transmembrane transporter activity                                                   | 1  | 0.01853 | 0.292 | 1     | Molecular  | GO:0140010 D-aspartate transmembrane transporter activity                                                   | 0.01853 | 0.15736 | 0   | 0 | 1  | 1   |
| GO:0046861 positive regulation of smooth muscle cell proliferation                                          | 4  | 0.01869 | 1.548 | 0.06  | Biological | GO:0046861 positive regulation of smooth muscle cell proliferation                                          | 0.01869 | 0.13813 | 0   | 0 | 4  | 84  |
| GO:0060538 skeletal muscle organ development                                                                | 6  | 0.01893 | 2.477 | 0.044 | Biological | GO:0060538 skeletal muscle organ development                                                                | 0.01893 | 0.13992 | 0   | 0 | 6  | 115 |
| GO:0043534 blood vessel endothelial cell migration                                                          | 6  | 0.01893 | 1.558 | 0.052 | Biological | GO:0043534 blood vessel endothelial cell migration                                                          | 0.01893 | 0.13992 | 0   | 0 | 6  | 115 |
| GO:0031102 neuron projection regeneration                                                                   | 4  | 0.01895 | 1.238 | 0.071 | Biological | GO:0031102 neuron projection regeneration                                                                   | 0.01895 | 0.14038 | 0</ |   |    |     |

|                                                                                        |     |         |        |       |            |                                                                                        |         |         |   |   |    |      |
|----------------------------------------------------------------------------------------|-----|---------|--------|-------|------------|----------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0060788 ectodermal placode formation                                                | 2   | 0.02263 | 0.619  | 0.154 | Biological | GO:0060788 ectodermal placode formation                                                | 0.02263 | 0.15595 | 0 | 0 | 2  | 13   |
| GO:0070254 mucus secretion                                                             | 2   | 0.02263 | 0.619  | 0.154 | Biological | GO:0070254 mucus secretion                                                             | 0.02263 | 0.15595 | 0 | 0 | 2  | 13   |
| GO:0071697 ectodermal placode morphogenesis                                            | 2   | 0.02263 | 0.619  | 0.154 | Biological | GO:0071697 ectodermal placode morphogenesis                                            | 0.02263 | 0.15595 | 0 | 0 | 2  | 13   |
| GO:1904754 positive regulation of vascular associated smooth muscle cell migration     | 2   | 0.02263 | 0.619  | 0.154 | Biological | GO:1904754 positive regulation of vascular associated smooth muscle cell migration     | 0.02263 | 0.15595 | 0 | 0 | 2  | 13   |
| GO:1905209 positive regulation of cardiocyte differentiation                           | 2   | 0.02263 | 0.619  | 0.154 | Biological | GO:1905209 positive regulation of cardiocyte differentiation                           | 0.02263 | 0.15595 | 0 | 0 | 2  | 13   |
| GO:0001932 regulation of protein phosphorylation                                       | 29  | 0.02264 | 8.978  | 0.027 | Biological | GO:0001932 regulation of protein phosphorylation                                       | 0.02264 | 0.15595 | 0 | 0 | 29 | 1075 |
| GO:0032589 neuron projection membrane                                                  | 4   | 0.02294 | 1.187  | 0.067 | Cellular   | GO:0032589 neuron projection membrane                                                  | 0.02294 | 0.15153 | 0 | 0 | 4  | 60   |
| GO:0001501 skeletal system development                                                 | 17  | 0.02283 | 5.263  | 0.031 | Biological | GO:0001501 skeletal system development                                                 | 0.02283 | 0.15599 | 0 | 0 | 17 | 546  |
| GO:0006464 cellular protein modification process                                       | 81  | 0.02333 | 25.077 | 0.022 | Biological | GO:0006464 cellular protein modification process                                       | 0.02333 | 0.15989 | 0 | 0 | 81 | 3618 |
| GO:0048871 multicellular organismal homeostasis                                        | 17  | 0.02334 | 5.263  | 0.031 | Biological | GO:0048871 multicellular organismal homeostasis                                        | 0.02334 | 0.15989 | 0 | 0 | 17 | 547  |
| GO:0008417 lucosyltransferase activity                                                 | 2   | 0.02335 | 0.585  | 0.154 | Molecular  | GO:0008417 lucosyltransferase activity                                                 | 0.02335 | 0.17892 | 0 | 0 | 2  | 13   |
| GO:0031994 insulin-like growth factor I binding                                        | 2   | 0.02335 | 0.585  | 0.154 | Molecular  | GO:0031994 insulin-like growth factor I binding                                        | 0.02335 | 0.17892 | 0 | 0 | 2  | 13   |
| GO:0007589 body fluid electrolyte balance                                              | 5   | 0.02337 | 1.548  | 0.059 | Biological | GO:0007589 body fluid electrolyte balance                                              | 0.02337 | 0.15989 | 0 | 0 | 5  | 89   |
| GO:0043535 regulation of blood vessel endothelial cell migration                       | 5   | 0.02337 | 1.548  | 0.059 | Biological | GO:0043535 regulation of blood vessel endothelial cell migration                       | 0.02337 | 0.15989 | 0 | 0 | 5  | 89   |
| GO:0031345 negative regulation of cell projection organization                         | 8   | 0.02348 | 2.477  | 0.042 | Biological | GO:0031345 negative regulation of cell projection organization                         | 0.02348 | 0.15997 | 0 | 0 | 8  | 190  |
| GO:0006688 glycosphingolipid biosynthetic process                                      | 3   | 0.02367 | 0.929  | 0.088 | Biological | GO:0006688 glycosphingolipid biosynthetic process                                      | 0.02367 | 0.15997 | 0 | 0 | 3  | 34   |
| GO:0010765 positive regulation of sodium ion transport                                 | 3   | 0.02367 | 0.929  | 0.088 | Biological | GO:0010765 positive regulation of sodium ion transport                                 | 0.02367 | 0.15997 | 0 | 0 | 3  | 34   |
| GO:0021172 effactory bulb development                                                  | 3   | 0.02367 | 0.929  | 0.088 | Biological | GO:0021172 effactory bulb development                                                  | 0.02367 | 0.15997 | 0 | 0 | 3  | 34   |
| GO:0034694 response to prostaglandin                                                   | 3   | 0.02367 | 0.929  | 0.088 | Biological | GO:0034694 response to prostaglandin                                                   | 0.02367 | 0.15997 | 0 | 0 | 3  | 34   |
| GO:0042573 retinoic acid metabolic process                                             | 3   | 0.02367 | 0.929  | 0.088 | Biological | GO:0042573 retinoic acid metabolic process                                             | 0.02367 | 0.15997 | 0 | 0 | 3  | 34   |
| GO:0043537 negative regulation of blood vessel endothelial cell migration              | 3   | 0.02367 | 0.929  | 0.088 | Biological | GO:0043537 negative regulation of blood vessel endothelial cell migration              | 0.02367 | 0.15997 | 0 | 0 | 3  | 34   |
| GO:0070533 transepithelial transport                                                   | 3   | 0.02367 | 0.929  | 0.088 | Biological | GO:0070533 transepithelial transport                                                   | 0.02367 | 0.15997 | 0 | 0 | 3  | 34   |
| GO:0001833 regulation of kidney development                                            | 3   | 0.02367 | 0.929  | 0.088 | Biological | GO:0001833 regulation of kidney development                                            | 0.02367 | 0.15997 | 0 | 0 | 3  | 34   |
| GO:0051338 regulation of transesterase activity                                        | 24  | 0.02396 | 7.43   | 0.028 | Biological | GO:0051338 regulation of transesterase activity                                        | 0.02396 | 0.16171 | 0 | 0 | 24 | 854  |
| GO:0031099 regeneration                                                                | 8   | 0.02414 | 2.477  | 0.042 | Biological | GO:0031099 regeneration                                                                | 0.02414 | 0.16267 | 0 | 0 | 8  | 191  |
| GO:0042802 identical protein binding                                                   | 52  | 0.02415 | 15.205 | 0.024 | Molecular  | GO:0042802 identical protein binding                                                   | 0.02415 | 0.18346 | 0 | 0 | 52 | 2136 |
| GO:0048872 homeostasis of number of cells                                              | 11  | 0.02417 | 3.406  | 0.038 | Biological | GO:0048872 homeostasis of number of cells                                              | 0.02417 | 0.16269 | 0 | 0 | 11 | 304  |
| GO:0049444 positive regulation of transcription by RNA polymerase II                   | 33  | 0.02424 | 10.217 | 0.039 | Biological | GO:0049444 positive regulation of transcription by RNA polymerase II                   | 0.02424 | 0.16269 | 0 | 0 | 33 | 1266 |
| GO:0002685 regulation of leukocyte migration                                           | 9   | 0.02435 | 2.786  | 0.039 | Biological | GO:0002685 regulation of leukocyte migration                                           | 0.02435 | 0.16301 | 0 | 0 | 9  | 228  |
| GO:0006486 protein glycosylation                                                       | 9   | 0.02435 | 2.786  | 0.039 | Biological | GO:0006486 protein glycosylation                                                       | 0.02435 | 0.16301 | 0 | 0 | 9  | 228  |
| GO:0043413 macromolecule glycosylation                                                 | 9   | 0.02435 | 2.786  | 0.039 | Biological | GO:0043413 macromolecule glycosylation                                                 | 0.02435 | 0.16301 | 0 | 0 | 9  | 228  |
| GO:0005154 epidermal growth factor receptor binding                                    | 3   | 0.02471 | 0.877  | 0.088 | Molecular  | GO:0005154 epidermal growth factor receptor binding                                    | 0.02471 | 0.18586 | 0 | 0 | 3  | 34   |
| GO:0042562 hormone release                                                             | 5   | 0.02496 | 1.462  | 0.056 | Biological | GO:0042562 hormone release                                                             | 0.02496 | 0.18586 | 0 | 0 | 5  | 89   |
| GO:0048588 developmental cell growth                                                   | 9   | 0.02496 | 2.786  | 0.039 | Biological | GO:0048588 developmental cell growth                                                   | 0.02496 | 0.18586 | 0 | 0 | 9  | 229  |
| GO:0051145 smooth muscle cell differentiation                                          | 4   | 0.0251  | 1.238  | 0.066 | Biological | GO:0051145 smooth muscle cell differentiation                                          | 0.0251  | 0.16755 | 0 | 0 | 4  | 61   |
| GO:0009925 basal plasma membrane                                                       | 10  | 0.0251  | 2.967  | 0.037 | Cellular   | GO:0009925 basal plasma membrane                                                       | 0.0251  | 0.16374 | 0 | 0 | 10 | 270  |
| GO:0140096 catalytic activity, acting on a protein                                     | 56  | 0.02514 | 16.374 | 0.024 | Molecular  | GO:0140096 catalytic activity, acting on a protein                                     | 0.02514 | 0.18607 | 0 | 0 | 56 | 2334 |
| GO:0008212 regulation of kidney pressure                                               | 8   | 0.02582 | 2.477  | 0.041 | Biological | GO:0008212 regulation of kidney pressure                                               | 0.02582 | 0.16939 | 0 | 0 | 8  | 193  |
| GO:0019934 cGMP-mediated signaling                                                     | 3   | 0.02555 | 0.929  | 0.088 | Biological | GO:0019934 cGMP-mediated signaling                                                     | 0.02555 | 0.16939 | 0 | 0 | 3  | 35   |
| GO:0035633 maintenance of blood-brain barrier                                          | 3   | 0.02555 | 0.929  | 0.088 | Biological | GO:0035633 maintenance of blood-brain barrier                                          | 0.02555 | 0.16939 | 0 | 0 | 3  | 35   |
| GO:0048665 neuron fate specification                                                   | 3   | 0.02555 | 0.929  | 0.088 | Biological | GO:0048665 neuron fate specification                                                   | 0.02555 | 0.16939 | 0 | 0 | 3  | 35   |
| GO:0070528 protein kinase C signaling                                                  | 3   | 0.02555 | 0.929  | 0.088 | Biological | GO:0070528 protein kinase C signaling                                                  | 0.02555 | 0.16939 | 0 | 0 | 3  | 35   |
| GO:0043218 compact myelin                                                              | 13  | 0.02555 | 3.993  | 0.043 | Cellular   | GO:0043218 compact myelin                                                              | 0.02555 | 0.16467 | 0 | 0 | 13 | 14   |
| GO:0051651 maintenance of location in cell                                             | 9   | 0.02557 | 2.786  | 0.039 | Biological | GO:0051651 maintenance of location in cell                                             | 0.02557 | 0.16939 | 0 | 0 | 9  | 230  |
| GO:0008081 phosphoric diester hydrolase activity                                       | 5   | 0.02597 | 1.462  | 0.056 | Biological | GO:0008081 phosphoric diester hydrolase activity                                       | 0.02597 | 0.19062 | 0 | 0 | 5  | 90   |
| GO:0098978 glutamatergic synapse                                                       | 14  | 0.026   | 4.154  | 0.032 | Cellular   | GO:0098978 glutamatergic synapse                                                       | 0.026   | 0.16557 | 0 | 0 | 14 | 433  |
| GO:0003084 positive regulation of systemic arterial blood pressure                     | 2   | 0.02609 | 0.619  | 0.143 | Biological | GO:0003084 positive regulation of systemic arterial blood pressure                     | 0.02609 | 0.17077 | 0 | 0 | 2  | 14   |
| GO:0016322 neuron retraction                                                           | 2   | 0.02609 | 0.619  | 0.143 | Biological | GO:0016322 neuron retraction                                                           | 0.02609 | 0.17077 | 0 | 0 | 2  | 14   |
| GO:0030238 male sex determination                                                      | 2   | 0.02609 | 0.619  | 0.143 | Biological | GO:0030238 male sex determination                                                      | 0.02609 | 0.17077 | 0 | 0 | 2  | 14   |
| GO:0061029 eyelid development in camera-type eye                                       | 2   | 0.02609 | 0.619  | 0.143 | Biological | GO:0061029 eyelid development in camera-type eye                                       | 0.02609 | 0.17077 | 0 | 0 | 2  | 14   |
| GO:0070141 response to UV-A                                                            | 2   | 0.02609 | 0.619  | 0.143 | Biological | GO:0070141 response to UV-A                                                            | 0.02609 | 0.17077 | 0 | 0 | 2  | 14   |
| GO:0071696 ectodermal placode development                                              | 2   | 0.02609 | 0.619  | 0.143 | Biological | GO:0071696 ectodermal placode development                                              | 0.02609 | 0.17077 | 0 | 0 | 2  | 14   |
| GO:0010770 regulation of adenylate cyclase-activating G protein-coupled receptor       | 2   | 0.02609 | 0.619  | 0.143 | Biological | GO:0010770 regulation of adenylate cyclase-activating G protein-coupled receptor       | 0.02609 | 0.17077 | 0 | 0 | 2  | 14   |
| GO:1900452 regulation of long-term synaptic depression                                 | 2   | 0.02609 | 0.619  | 0.143 | Biological | GO:1900452 regulation of long-term synaptic depression                                 | 0.02609 | 0.17077 | 0 | 0 | 2  | 14   |
| GO:1901722 regulation of cell proliferation involved in kidney development             | 2   | 0.02609 | 0.619  | 0.143 | Biological | GO:1901722 regulation of cell proliferation involved in kidney development             | 0.02609 | 0.17077 | 0 | 0 | 2  | 14   |
| GO:0030029 actin filament-based process                                                | 23  | 0.0263  | 7.121  | 0.028 | Biological | GO:0030029 actin filament-based process                                                | 0.0263  | 0.17189 | 0 | 0 | 23 | 817  |
| GO:0060021 roof of mouth development                                                   | 5   | 0.02651 | 1.548  | 0.054 | Biological | GO:0060021 roof of mouth development                                                   | 0.02651 | 0.17308 | 0 | 0 | 5  | 92   |
| GO:0008105 phosphatidate catabolic activity                                            | 2   | 0.02681 | 0.585  | 0.143 | Molecular  | GO:0008105 phosphatidate catabolic activity                                            | 0.02681 | 0.191   | 0 | 0 | 2  | 14   |
| GO:0042577 lipid phosphatase activity                                                  | 2   | 0.02681 | 0.585  | 0.143 | Molecular  | GO:0042577 lipid phosphatase activity                                                  | 0.02681 | 0.191   | 0 | 0 | 2  | 14   |
| GO:0044594 17-beta-hydroxysteroid dehydrogenase (NAD+) activity                        | 2   | 0.02691 | 0.585  | 0.143 | Molecular  | GO:0044594 17-beta-hydroxysteroid dehydrogenase (NAD+) activity                        | 0.02691 | 0.191   | 0 | 0 | 2  | 14   |
| GO:0071837 HMG box domain binding                                                      | 2   | 0.02691 | 0.585  | 0.143 | Molecular  | GO:0071837 HMG box domain binding                                                      | 0.02691 | 0.191   | 0 | 0 | 2  | 14   |
| GO:0002688 regulation of leukocyte chemotaxis                                          | 6   | 0.02705 | 1.858  | 0.048 | Biological | GO:0002688 regulation of leukocyte chemotaxis                                          | 0.02705 | 0.17614 | 0 | 0 | 6  | 125  |
| GO:0043290 positive regulation of cysteine-type endopeptidase activity                 | 3   | 0.02705 | 1.858  | 0.048 | Biological | GO:0043290 positive regulation of cysteine-type endopeptidase activity                 | 0.02705 | 0.17614 | 0 | 0 | 3  | 36   |
| GO:0007616 long-term memory                                                            | 3   | 0.02751 | 0.929  | 0.088 | Biological | GO:0007616 long-term memory                                                            | 0.02751 | 0.17771 | 0 | 0 | 3  | 36   |
| GO:0021988 olfactory lobe development                                                  | 3   | 0.02751 | 0.929  | 0.088 | Biological | GO:0021988 olfactory lobe development                                                  | 0.02751 | 0.17771 | 0 | 0 | 3  | 36   |
| GO:0031128 developmental induction                                                     | 3   | 0.02751 | 0.929  | 0.088 | Biological | GO:0031128 developmental induction                                                     | 0.02751 | 0.17771 | 0 | 0 | 3  | 36   |
| GO:0042462 eye photoreceptor cell development                                          | 3   | 0.02751 | 0.929  | 0.088 | Biological | GO:0042462 eye photoreceptor cell development                                          | 0.02751 | 0.17771 | 0 | 0 | 3  | 36   |
| GO:1904707 positive regulation of vascular associated smooth muscle cell proliferation | 3   | 0.02751 | 0.929  | 0.088 | Biological | GO:1904707 positive regulation of vascular associated smooth muscle cell proliferation | 0.02751 | 0.17771 | 0 | 0 | 3  | 36   |
| GO:1905144 response to acetylcholine                                                   | 3   | 0.02751 | 0.929  | 0.088 | Biological | GO:1905144 response to acetylcholine                                                   | 0.02751 | 0.17771 | 0 | 0 | 3  | 36   |
| GO:0045684 regulation of neuron differentiation                                        | 8   | 0.0276  | 2.477  | 0.041 | Biological | GO:0045684 regulation of neuron differentiation                                        | 0.0276  | 0.17773 | 0 | 0 | 8  | 196  |
| GO:0030901 midbrain development                                                        | 5   | 0.02762 | 1.548  | 0.054 | Biological | GO:0030901 midbrain development                                                        | 0.02762 | 0.17773 | 0 | 0 | 5  | 93   |
| GO:0090792 regulation of postsynaptic membrane neurotransmitter receptor level         | 5   | 0.02762 | 1.548  | 0.054 | Biological | GO:0090792 regulation of postsynaptic membrane neurotransmitter receptor level         | 0.02762 | 0.17773 | 0 | 0 | 5  | 93   |
| GO:0048878 chemical synapse                                                            | 6   | 0.02777 | 1.907  | 0.027 | Cellular   | GO:0048878 chemical synapse                                                            | 0.02777 | 0.1802  | 0 | 0 | 6  | 123  |
| GO:0003014 renal system process                                                        | 6   | 0.02799 | 1.858  | 0.048 | Biological | GO:0003014 renal system process                                                        | 0.02799 | 0.17965 | 0 | 0 | 6  | 126  |
| GO:0005178 integrin binding                                                            | 7   | 0.02809 | 2.047  | 0.044 | Molecular  | GO:0005178 integrin binding                                                            | 0.02809 | 0.19512 | 0 | 0 | 7  | 158  |
| GO:0018337 epithelial to mesenchymal transition                                        | 7   | 0.02838 | 2.167  | 0.043 | Biological | GO:0018337 epithelial to mesenchymal transition                                        | 0.02838 | 0.18168 | 0 | 0 | 7  | 161  |
| GO:0007605 sensory perception of sound                                                 | 7   | 0.02838 | 2.167  | 0.043 | Biological | GO:0007605 sensory perception of sound                                                 | 0.02838 | 0.18168 | 0 | 0 | 7  | 161  |
| GO:1900778 protein localization to cell periphery                                      | 12  | 0.02854 | 3.715  | 0.034 | Biological | GO:1900778 protein localization to cell periphery                                      | 0.02854 | 0.18349 | 0 | 0 | 12 | 361  |
| GO:0032436 positive regulation of proteasomal ubiquitin-dependent proteolysis          | 5   | 0.02875 | 1.548  | 0.053 | Biological | GO:0032436 positive regulation of proteasomal ubiquitin-dependent proteolysis          | 0.02875 | 0.18313 | 0 | 0 | 5  | 94   |
| GO:0032602 chemokine production                                                        | 5   | 0.02875 | 1.548  | 0.053 | Biological | GO:0032602 chemokine production                                                        | 0.02875 | 0.18313 | 0 | 0 | 5  | 94   |
| GO:0032642 regulation of chemokine production                                          | 5   | 0.02875 | 1.548  | 0.053 | Biological | GO:0032642 regulation of chemokine production                                          | 0.02875 | 0.18313 | 0 | 0 | 5  | 94   |
| GO:0042175 nuclear outer membrane-endoplasmic reticulum membrane                       | 31  | 0.02876 | 9.199  | 0.028 | Cellular   | GO:0042175 nuclear outer membrane-endoplasmic reticulum membrane                       | 0.02876 | 0.18999 | 0 | 0 | 31 | 1203 |
| GO:0010011 glial cell differentiation                                                  | 32  | 0.02883 | 9.907  | 0.028 | Biological | GO:0010011 glial cell differentiation                                                  | 0.02883 | 0.18338 | 0 | 0 | 32 | 123  |
| GO:0014902 myotube differentiation                                                     | 6   | 0.02894 | 1.858  | 0.047 | Biological | GO:0014902 myotube differentiation                                                     | 0.02894 | 0.18366 | 0 | 0 | 6  | 127  |
| GO:0051290 release of sequestered calcium ion into cytosol                             | 6   | 0.02894 | 1.858  | 0.047 | Biological | GO:0051290 release of sequestered calcium ion into cytosol                             | 0.02894 | 0.18366 | 0 | 0 | 6  | 127  |
| GO:0030199 collagen fibril organization                                                | 4   | 0.0293  | 1.238  | 0.062 | Biological | GO:0030199 collagen fibril organization                                                | 0.0293  | 0.18447 | 0 | 0 | 4  | 64   |
| GO:0060341 regulation of cellular localization                                         | 23  | 0.02931 | 7.121  | 0.028 | Biological | GO:0060341 regulation of cellular localization                                         | 0.02931 | 0.18447 | 0 | 0 | 23 | 826  |
| GO:0001941 postsynaptic membrane organization                                          | 3   | 0.02954 | 0.929  | 0.088 | Biological | GO:0001941 postsynaptic membrane organization                                          | 0.02954 | 0.18447 | 0 | 0 | 3  | 37   |
| GO:0097242 amyloid-beta clearance                                                      | 3</ |         |        |       |            |                                                                                        |         |         |   |   |    |      |

|                                                                                    |    |         |       |       |            |                                                                                  |         |         |   |   |    |     |
|------------------------------------------------------------------------------------|----|---------|-------|-------|------------|----------------------------------------------------------------------------------|---------|---------|---|---|----|-----|
| GO:2000341 regulation of chemokine (C-X-C motif) ligand 2 production               | 2  | 0.03359 | 0.619 | 0.125 | Biological | GO:20001 regulation of chemokine (C-X-C motif) ligand 2 production               | 0.03359 | 0.18597 | 0 | 0 | 2  | 16  |
| GO:0097553 calcium ion transmembrane import into cytosol                           | 7  | 0.03365 | 2.167 | 0.042 | Biological | GO:00971 calcium ion transmembrane import into cytosol                           | 0.03365 | 0.18597 | 0 | 0 | 7  | 167 |
| GO:0032570 response to progesterone                                                | 3  | 0.03364 | 0.928 | 0.071 | Biological | GO:00321 response to progesterone                                                | 0.03364 | 0.18597 | 0 | 0 | 3  | 339 |
| GO:0011885 endothelial cell development                                            | 4  | 0.03339 | 1.238 | 0.06  | Biological | GO:0011885 endothelial cell development                                          | 0.03339 | 0.18597 | 0 | 0 | 4  | 67  |
| GO:0048857 neural nucleus development                                              | 4  | 0.03339 | 1.238 | 0.06  | Biological | GO:00488 neural nucleus development                                              | 0.03339 | 0.18597 | 0 | 0 | 4  | 67  |
| GO:0042176 regulation of protein catabolic process                                 | 13 | 0.03417 | 4.025 | 0.032 | Biological | GO:00421 regulation of protein catabolic process                                 | 0.03417 | 0.18597 | 0 | 0 | 13 | 403 |
| GO:0045859 regulation of protein kinase activity                                   | 18 | 0.0344  | 5.573 | 0.029 | Biological | GO:00458 regulation of protein kinase activity                                   | 0.0344  | 0.18597 | 0 | 0 | 18 | 617 |
| GO:0048191 metalloproteinase inhibitor activity                                    | 2  | 0.03433 | 0.585 | 0.125 | Molecular  | GO:00481 metalloproteinase inhibitor activity                                    | 0.03433 | 0.19512 | 0 | 0 | 2  | 16  |
| GO:0019841 retinol binding                                                         | 2  | 0.03463 | 0.585 | 0.125 | Molecular  | GO:00198 retinol binding                                                         | 0.03463 | 0.19512 | 0 | 0 | 2  | 2   |
| GO:0047555 3',5'-cyclic-GMP phosphodiesterase activity                             | 2  | 0.03463 | 0.585 | 0.125 | Molecular  | GO:00474 3',5'-cyclic-GMP phosphodiesterase activity                             | 0.03463 | 0.19512 | 0 | 0 | 2  | 16  |
| GO:0072080 nephron tubule development                                              | 5  | 0.03485 | 1.548 | 0.051 | Biological | GO:00722 nephron tubule development                                              | 0.03485 | 0.18597 | 0 | 0 | 5  | 99  |
| GO:0017171 serine hydrolase activity                                               | 8  | 0.03502 | 2.339 | 0.04  | Molecular  | GO:00177 serine hydrolase activity                                               | 0.03502 | 0.19512 | 0 | 0 | 8  | 202 |
| GO:0005126 cytokine receptor binding                                               | 10 | 0.03509 | 2.924 | 0.036 | Biological | GO:00051 cytokine receptor binding                                               | 0.03509 | 0.19512 | 0 | 0 | 10 | 278 |
| GO:000873 cellular ion homeostasis                                                 | 20 | 0.03519 | 6.192 | 0.028 | Biological | GO:00086 cellular ion homeostasis                                                | 0.03519 | 0.18597 | 0 | 0 | 20 | 707 |
| GO:0042445 hormone metabolic process                                               | 9  | 0.03539 | 2.786 | 0.037 | Biological | GO:00424 hormone metabolic process                                               | 0.03539 | 0.18597 | 0 | 0 | 9  | 244 |
| GO:0030239 myofibril assembly                                                      | 4  | 0.03552 | 1.238 | 0.059 | Biological | GO:00302 myofibril assembly                                                      | 0.03552 | 0.18597 | 0 | 0 | 4  | 68  |
| GO:0002449 anatomical structure homeostasis                                        | 12 | 0.03553 | 3.715 | 0.033 | Biological | GO:00024 anatomical structure homeostasis                                        | 0.03553 | 0.18597 | 0 | 0 | 12 | 364 |
| GO:0009611 response to wounding                                                    | 17 | 0.03565 | 5.263 | 0.03  | Biological | GO:00096 response to wounding                                                    | 0.03565 | 0.18597 | 0 | 0 | 17 | 576 |
| GO:0005584 collagen type 1 trimer                                                  | 1  | 0.03573 | 0.297 | 0.5   | Cellular   | GO:00055 collagen type 1 trimer                                                  | 0.03573 | 0.19705 | 0 | 0 | 1  | 2   |
| GO:0034365 discoidal high-density lipoprotein particle                             | 1  | 0.03573 | 0.297 | 0.5   | Cellular   | GO:00344 discoidal high-density lipoprotein particle                             | 0.03573 | 0.19705 | 0 | 0 | 1  | 2   |
| GO:0150002 distal dendrite                                                         | 1  | 0.03573 | 0.297 | 0.5   | Cellular   | GO:01500 distal dendrite                                                         | 0.03573 | 0.19705 | 0 | 0 | 1  | 2   |
| GO:1902580 GMP reductase complex                                                   | 1  | 0.03573 | 0.297 | 0.5   | Cellular   | GO:19025 GMP reductase complex                                                   | 0.03573 | 0.19705 | 0 | 0 | 1  | 2   |
| GO:1900682 CSF1-CSF1R complex                                                      | 1  | 0.03573 | 0.297 | 0.5   | Cellular   | GO:19006 CSF1-CSF1R complex                                                      | 0.03573 | 0.19705 | 0 | 0 | 1  | 2   |
| GO:0001894 tissue homeostasis                                                      | 10 | 0.03602 | 3.096 | 0.035 | Biological | GO:00018 tissue homeostasis                                                      | 0.03602 | 0.18597 | 0 | 0 | 10 | 284 |
| GO:0001662 behavioral fear response                                                | 3  | 0.0361  | 0.929 | 0.075 | Biological | GO:00016 behavioral fear response                                                | 0.0361  | 0.18597 | 0 | 0 | 3  | 40  |
| GO:0032350 regulation of hormone metabolic process                                 | 3  | 0.0361  | 0.929 | 0.075 | Biological | GO:00323 regulation of hormone metabolic process                                 | 0.0361  | 0.18597 | 0 | 0 | 3  | 40  |
| GO:1903115 regulation of actin filament-based movement                             | 3  | 0.0361  | 0.929 | 0.075 | Biological | GO:19033 regulation of actin filament-based movement                             | 0.0361  | 0.18597 | 0 | 0 | 3  | 40  |
| GO:1900000 amyloid fibril formation                                                | 3  | 0.0361  | 0.929 | 0.075 | Biological | GO:19000 amyloid fibril formation                                                | 0.0361  | 0.18597 | 0 | 0 | 3  | 40  |
| GO:0001575 globoside biosynthetic process                                          | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00015 globoside biosynthetic process                                          | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0001970 positive regulation of activation of membrane attack complex            | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00019 positive regulation of activation of membrane attack complex            | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0000212 anti-male aggressive behavior                                           | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00002 anti-male aggressive behavior                                           | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0002384 heparin metabolic process                                               | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00023 heparin metabolic process                                               | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0002479 antigen processing and presentation of exogenous peptide                | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00022 antigen processing and presentation of exogenous peptide antigen via    | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0002543 activation of blood coagulation via clotting cascade                    | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00022 activation of blood coagulation via clotting cascade                    | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0003340 negative regulation of mesenchymal to epithelial transition             | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00033 negative regulation of mesenchymal to epithelial transition involved in | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0006063 acetate metabolic process                                               | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00066 acetate metabolic process                                               | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0005529 aspartate biosynthetic process                                          | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00056 aspartate biosynthetic process                                          | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0007402 ganglion mother cell fate determination                                 | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00077 ganglion mother cell fate determination                                 | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0007497 posterior midgut development                                            | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00077 posterior midgut development                                            | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0007542 primary sex determination, germ-line                                    | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00077 primary sex determination, germ-line                                    | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0008050 female courtship behavior                                               | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00088 female courtship behavior                                               | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0010871 lipid transport involved in lipid storage                               | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00108 lipid transport involved in lipid storage                               | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0014036 neural crest cell fate specification                                    | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00144 neural crest cell fate specification                                    | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0016107 sesquiterpene catabolic process                                         | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00166 sesquiterpene catabolic process                                         | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0016487 farnesol metabolic process                                              | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00166 farnesol metabolic process                                              | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0016488 farnesol catabolic process                                              | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00166 farnesol catabolic process                                              | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0018992 germline sex determination                                              | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00189 germline sex determination                                              | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0019100 male germ-line sex determination                                        | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00196 male germ-line sex determination                                        | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0019427 acetyl-CoA biosynthetic process from acetate                            | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00199 acetyl-CoA biosynthetic process from acetate                            | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0021568 rhombomere 2 development                                                | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00221 rhombomere 2 development                                                | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0030237 female sex determination                                                | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00300 female sex determination                                                | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0032142 regulation of nucleoside transport                                      | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00323 regulation of nucleoside transport                                      | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0032639 TRAIL production                                                        | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00322 TRAIL production                                                        | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0032679 regulation of TRAIL production                                          | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00322 regulation of TRAIL production                                          | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0032759 positive regulation of TRAIL production                                 | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00322 positive regulation of TRAIL production                                 | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0034346 positive regulation of type III interferon production                   | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00344 positive regulation of type III interferon production                   | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0035026 leading edge cell differentiation                                       | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00355 leading edge cell differentiation                                       | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0035622 intrahaptic bile duct development                                       | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00359 intrahaptic bile duct development                                       | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0036515 serotonergic neuron axon guidance                                       | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00366 serotonergic neuron axon guidance                                       | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0042488 positive regulation of odontogenesis of dentin-containing tooth         | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00422 positive regulation of odontogenesis of dentin-containing tooth         | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0042704 uterine wall breakdown                                                  | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00422 uterine wall breakdown                                                  | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0044751 cellular response to human chorionic gonadotropin stimulus              | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00446 cellular response to human chorionic gonadotropin stimulus              | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0045213 neurotransmitter receptor metabolic process                             | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00455 neurotransmitter receptor metabolic process                             | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0045720 negative regulation of integrin biosynthetic process                    | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00445 negative regulation of integrin biosynthetic process                    | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0045827 negative regulation of isoprenoid metabolic process                     | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00445 negative regulation of isoprenoid metabolic process                     | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0045976 negative regulation of mitotic cell cycle, embryonic                    | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00445 negative regulation of mitotic cell cycle, embryonic                    | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0046725 negative regulation of viral protein levels in host cell                | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00445 negative regulation of viral protein levels in host cell                | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0051892 negative regulation of cardioblast differentiation                      | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00511 negative regulation of cardioblast differentiation                      | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0052312 modulation of transcription in other organism involved in symbiotic int | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00522 modulation of transcription in other organism involved in symbiotic int | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0052472 modulation by host of symbiont transcription                            | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00522 modulation by host of symbiont transcription                            | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0060014 granulosa cell differentiation                                          | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00600 granulosa cell differentiation                                          | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0060282 positive regulation of oocyte development                               | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00600 positive regulation of oocyte development                               | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0060516 primary prostatic bud elongation                                        | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00600 primary prostatic bud elongation                                        | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0060532 bronchus cartilage development                                          | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00600 bronchus cartilage development                                          | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0060599 lateral sprouting involved in mammary gland duct morphogenesis          | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00600 lateral sprouting involved in mammary gland duct morphogenesis          | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0060720 spongiorhoblast cell proliferation                                      | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00600 spongiorhoblast cell proliferation                                      | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0060722 cell proliferation involved in embryonic placenta development           | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00600 cell proliferation involved in embryonic placenta development           | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0060857 establishment of glial blood-brain barrier                              | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00600 establishment of glial blood-brain barrier                              | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0060974 cell migration involved in heart formation                              | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00600 cell migration involved in heart formation                              | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0061145 lung smooth muscle development                                          | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00601 lung smooth muscle development                                          | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0061152 trachea submucosa development                                           | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00601 trachea submucosa development                                           | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0061153 tracheal gland development                                              | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00601 tracheal gland development                                              | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0061159 establishment of bipolar cell polarity involved in cell morphogenesis   | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00601 establishment of bipolar cell polarity involved in cell morphogenesis   | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0061868 hepatic stellate cell migration                                         | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00601 hepatic stellate cell migration                                         | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0061869 regulation of hepatic stellate cell migration                           | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00601 regulation of hepatic stellate cell migration                           | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0061870 positive regulation of hepatic stellate cell migration                  | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00601 positive regulation of hepatic stellate cell migration                  | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0062044 negative regulation of cardiac epithelial to mesenchymal transition     | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00605 negative regulation of cardiac epithelial to mesenchymal transition     | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0070256 negative regulation of mucus secretion                                  | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00700 negative regulation of mucus secretion                                  | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0070982 L-asparagine metabolic process                                          | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00700 L-asparagine metabolic process                                          | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0071109 superior temporal gyrus development                                     | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:00701 superior temporal gyrus development                                     | 0.03613 | 0.18597 | 0 | 0 | 1  | 2   |
| GO:0071231 cellular response to folate acid                                        | 1  | 0.03613 | 0.31  | 0.5   | Biological | GO:007                                                                           |         |         |   |   |    |     |

|                                                                                |     |         |        |       |            |                                                                              |         |         |   |   |     |       |
|--------------------------------------------------------------------------------|-----|---------|--------|-------|------------|------------------------------------------------------------------------------|---------|---------|---|---|-----|-------|
| GO:0008113 peptide-methionine (S)-S-oxide reductase activity                   | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0008 peptide-methionine (S)-S-oxide reductase activity                    | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0010465 nerve growth factor receptor activity                               | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0010 nerve growth factor receptor activity                                | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0015657 branched-chain amino acid sodium symporter activity                 | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0015 branched-chain amino acid sodium symporter activity                  | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0016213 linoleate desaturase activity                                       | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0016 linoleate desaturase activity                                        | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0019981 interleukin-6 binding                                               | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0019 interleukin-6 binding                                                | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0031127 alpha-(1,2)-fucosyltransferase activity                             | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0031 alpha-(1,2)-fucosyltransferase activity                              | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0031686 A1 adenosine receptor binding                                       | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0031 A1 adenosine receptor binding                                        | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0031780 corticotropin hormone receptor binding                              | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0031 corticotropin hormone receptor binding                               | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0031783 type 5 melanocortin receptor binding                                | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0031 type 5 melanocortin receptor binding                                 | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0036130 prostaglandin H2 endoperoxidase reductase activity                  | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0036 prostaglandin H2 endoperoxidase reductase activity                   | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0043992 histone acetyltransferase activity (H3-K9 specific)                 | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0043 histone acetyltransferase activity (H3-K9 specific)                  | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0045523 interleukin-27 receptor binding                                     | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0045 interleukin-27 receptor binding                                      | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0045550 geranylgeranyl reductase activity                                   | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0045 geranylgeranyl reductase activity                                    | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0047017 prostaglandin-F synthase activity                                   | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0047 prostaglandin-F synthase activity                                    | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0047020 15-hydroxyprostaglandin-D dehydrogenase (NADP+) activity            | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0047 15-hydroxyprostaglandin-D dehydrogenase (NADP+) activity             | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0047389 glycerophosphocholine phosphodiesterase activity                    | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0047 glycerophosphocholine phosphodiesterase activity                     | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0047787 delta4-3-oxosteroid 5beta-reductase activity                        | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0047 delta4-3-oxosteroid 5beta-reductase activity                         | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0047975 quanosine phosphorylase activity                                    | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0047 quanosine phosphorylase activity                                     | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0067114 folic acid receptor activity                                        | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0067 folic acid receptor activity                                         | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0140625 opioid growth factor receptor activity                              | 1   | 0.03673 | 0.292  | 0.5   | Molecular  | GO:0140 opioid growth factor receptor activity                               | 0.03673 | 0.19512 | 0 | 0 | 1   | 2     |
| GO:0001666 response to hypoxia                                                 | 10  | 0.03675 | 3.096  | 0.035 | Biological | GO:0001 response to hypoxia                                                  | 0.03675 | 0.18825 | 0 | 0 | 10  | 285   |
| GO:0030356 macromolecule localization                                          | 67  | 0.03682 | 20.743 | 0.022 | Biological | GO:0030 macromolecule localization                                           | 0.03682 | 0.18842 | 0 | 0 | 67  | 2582  |
| GO:0005669 dyadon complex                                                      | 2   | 0.03686 | 0.593  | 0.118 | Cellular   | GO:0005 dyadon complex                                                       | 0.03686 | 0.19752 | 0 | 0 | 2   | 17    |
| GO:0043034 costamere                                                           | 2   | 0.03686 | 0.593  | 0.118 | Cellular   | GO:0043 costamere                                                            | 0.03686 | 0.19752 | 0 | 0 | 2   | 17    |
| GO:0045121 membrane raft                                                       | 11  | 0.03697 | 3.264  | 0.033 | Cellular   | GO:0045 membrane raft                                                        | 0.03697 | 0.19752 | 0 | 0 | 11  | 329   |
| GO:0045670 regulation of osteoclast differentiation                            | 4   | 0.03718 | 1.238  | 0.058 | Biological | GO:0045 regulation of osteoclast differentiation                             | 0.03718 | 0.18922 | 0 | 0 | 4   | 69    |
| GO:0048645 animal organ formation                                              | 4   | 0.03718 | 1.238  | 0.058 | Biological | GO:0048 animal organ formation                                               | 0.03718 | 0.18922 | 0 | 0 | 4   | 69    |
| GO:0050012 striatal muscle cell development                                    | 4   | 0.03718 | 1.238  | 0.058 | Biological | GO:0050 striatal muscle cell development                                     | 0.03718 | 0.18922 | 0 | 0 | 4   | 69    |
| GO:0016114 regulation of cellular protein localization                         | 16  | 0.03737 | 4.954  | 0.033 | Biological | GO:0016 regulation of cellular protein localization                          | 0.03737 | 0.18922 | 0 | 0 | 16  | 536   |
| GO:0032994 protein-lipid complex                                               | 3   | 0.03738 | 0.89   | 0.073 | Cellular   | GO:0032 protein-lipid complex                                                | 0.03738 | 0.19752 | 0 | 0 | 3   | 41    |
| GO:0071772 response to BMP                                                     | 7   | 0.03751 | 2.167  | 0.041 | Biological | GO:0071 response to BMP                                                      | 0.03751 | 0.18922 | 0 | 0 | 7   | 171   |
| GO:0071773 cellular response to BMP stimulus                                   | 7   | 0.03751 | 2.167  | 0.041 | Biological | GO:0071 cellular response to BMP stimulus                                    | 0.03751 | 0.18922 | 0 | 0 | 7   | 171   |
| GO:0010586 regulation of biosynthetic process                                  | 2   | 0.03762 | 0.619  | 0.118 | Biological | GO:0010 regulation of biosynthetic process                                   | 0.03762 | 0.18922 | 0 | 0 | 2   | 17    |
| GO:0016114 terpenoid biosynthetic process                                      | 2   | 0.03762 | 0.619  | 0.118 | Biological | GO:0016 terpenoid biosynthetic process                                       | 0.03762 | 0.18922 | 0 | 0 | 2   | 17    |
| GO:0030202 heparin metabolic process                                           | 2   | 0.03762 | 0.619  | 0.118 | Biological | GO:0030 heparin metabolic process                                            | 0.03762 | 0.18922 | 0 | 0 | 2   | 17    |
| GO:0036331 cell-cell adhesion mediated by integrin                             | 2   | 0.03762 | 0.619  | 0.118 | Biological | GO:0033 cell-cell adhesion mediated by integrin                              | 0.03762 | 0.18922 | 0 | 0 | 2   | 17    |
| GO:0036065 fucosylation                                                        | 2   | 0.03762 | 0.619  | 0.118 | Biological | GO:0036 fucosylation                                                         | 0.03762 | 0.18922 | 0 | 0 | 2   | 17    |
| GO:0042653 lipoprotein transport                                               | 2   | 0.03762 | 0.619  | 0.118 | Biological | GO:0042 lipoprotein transport                                                | 0.03762 | 0.18922 | 0 | 0 | 2   | 17    |
| GO:0043117 positive regulation of vascular permeability                        | 2   | 0.03762 | 0.619  | 0.118 | Biological | GO:0043 positive regulation of vascular permeability                         | 0.03762 | 0.18922 | 0 | 0 | 2   | 17    |
| GO:0045217 cell-cell junction maintenance                                      | 2   | 0.03762 | 0.619  | 0.118 | Biological | GO:0045 cell-cell junction maintenance                                       | 0.03762 | 0.18922 | 0 | 0 | 2   | 17    |
| GO:0061548 anion channel development                                           | 2   | 0.03762 | 0.619  | 0.118 | Biological | GO:0061 anion channel development                                            | 0.03762 | 0.18922 | 0 | 0 | 2   | 17    |
| GO:0072578 neurotransmitter-gated ion channel clustering                       | 2   | 0.03762 | 0.619  | 0.118 | Biological | GO:0072 neurotransmitter-gated ion channel clustering                        | 0.03762 | 0.18922 | 0 | 0 | 2   | 17    |
| GO:200051 positive regulation of sodium ion transmembrane transporter activity | 11  | 0.03766 | 3.264  | 0.033 | Cellular   | GO:2000 positive regulation of sodium ion transmembrane transporter activity | 0.03766 | 0.19752 | 0 | 0 | 11  | 330   |
| GO:0098857 membrane microdomain                                                | 9   | 0.03779 | 2.786  | 0.036 | Biological | GO:0098 membrane microdomain                                                 | 0.03779 | 0.18985 | 0 | 0 | 9   | 247   |
| GO:0070085 glycosylation                                                       | 9   | 0.03779 | 2.786  | 0.036 | Biological | GO:0070 glycosylation                                                        | 0.03779 | 0.18985 | 0 | 0 | 9   | 247   |
| GO:0002209 behavioral defense response                                         | 3   | 0.03844 | 0.929  | 0.073 | Biological | GO:0002 behavioral defense response                                          | 0.03844 | 0.19219 | 0 | 0 | 3   | 41    |
| GO:0003203 endocardial cushion morphogenesis                                   | 3   | 0.03844 | 0.929  | 0.073 | Biological | GO:0003 endocardial cushion morphogenesis                                    | 0.03844 | 0.19219 | 0 | 0 | 3   | 41    |
| GO:0014002 astrocyte development                                               | 3   | 0.03844 | 0.929  | 0.073 | Biological | GO:0014 astrocyte development                                                | 0.03844 | 0.19219 | 0 | 0 | 3   | 41    |
| GO:0032941 secretion by tissue                                                 | 3   | 0.03844 | 0.929  | 0.073 | Biological | GO:0032 secretion by tissue                                                  | 0.03844 | 0.19219 | 0 | 0 | 3   | 41    |
| GO:0090968 postsynapse assembly                                                | 3   | 0.03844 | 0.929  | 0.073 | Biological | GO:0090 postsynapse assembly                                                 | 0.03844 | 0.19219 | 0 | 0 | 3   | 41    |
| GO:0048663 neuron fate commitment                                              | 4   | 0.03889 | 1.238  | 0.057 | Biological | GO:0048 neuron fate commitment                                               | 0.03889 | 0.19422 | 0 | 0 | 4   | 70    |
| GO:0048594 positive regulation of response to stimulus                         | 52  | 0.0393  | 16.999 | 0.023 | Biological | GO:0048 positive regulation of response to stimulus                          | 0.0393  | 0.19605 | 0 | 0 | 52  | 2241  |
| GO:0042176 osteogenic commitment                                               | 6   | 0.03989 | 1.858  | 0.044 | Biological | GO:0042 osteogenic commitment                                                | 0.03989 | 0.19782 | 0 | 0 | 6   | 137   |
| GO:0104297 DNA-binding transcription factor binding                            | 15  | 0.03985 | 4.386  | 0.031 | Molecular  | GO:0104 DNA-binding transcription factor binding                             | 0.03985 | 0.21044 | 0 | 0 | 15  | 489   |
| GO:0045637 regulation of myeloid cell differentiation                          | 8   | 0.04002 | 2.477  | 0.038 | Biological | GO:0045 regulation of myeloid cell differentiation                           | 0.04002 | 0.19904 | 0 | 0 | 8   | 211   |
| GO:1901654 response to ketone                                                  | 8   | 0.04002 | 2.477  | 0.038 | Biological | GO:1901 response to ketone                                                   | 0.04002 | 0.19904 | 0 | 0 | 8   | 211   |
| GO:0070709 plasma membrane organization                                        | 7   | 0.04059 | 2.167  | 0.04  | Biological | GO:0070 plasma membrane organization                                         | 0.04059 | 0.20177 | 0 | 0 | 7   | 174   |
| GO:0046817 lipoprotein assembly                                                | 4   | 0.04064 | 1.238  | 0.056 | Biological | GO:0046 lipoprotein assembly                                                 | 0.04064 | 0.20178 | 0 | 0 | 4   | 71    |
| GO:0051480 regulation of cytosolic calcium ion concentration                   | 12  | 0.04083 | 3.715  | 0.032 | Biological | GO:0051 regulation of cytosolic calcium ion concentration                    | 0.04083 | 0.20244 | 0 | 0 | 12  | 372   |
| GO:0003351 epithelial cilium movement involved in extracellular fluid movement | 3   | 0.04086 | 0.929  | 0.071 | Biological | GO:0003 epithelial cilium movement involved in extracellular fluid movement  | 0.04086 | 0.20244 | 0 | 0 | 3   | 42    |
| GO:0005518 collagen binding                                                    | 4   | 0.04094 | 1.17   | 0.057 | Molecular  | GO:0005 collagen binding                                                     | 0.04094 | 0.21485 | 0 | 0 | 4   | 70    |
| GO:0070588 calcium ion transmembrane transport                                 | 11  | 0.04097 | 3.406  | 0.033 | Biological | GO:0070 calcium ion transmembrane transport                                  | 0.04097 | 0.20278 | 0 | 0 | 11  | 331   |
| GO:0031527 lipoprotein transport                                               | 2   | 0.04098 | 0.619  | 0.118 | Biological | GO:0031 lipoprotein transport                                                | 0.04098 | 0.20278 | 0 | 0 | 2   | 18    |
| GO:0034613 cellular protein localization                                       | 41  | 0.04134 | 12.993 | 0.024 | Biological | GO:0034 cellular protein localization                                        | 0.04134 | 0.20439 | 0 | 0 | 41  | 1708  |
| GO:0019896 axonal transport of mitochondrion                                   | 2   | 0.04183 | 0.619  | 0.111 | Biological | GO:0019 axonal transport of mitochondrion                                    | 0.04183 | 0.20439 | 0 | 0 | 2   | 18    |
| GO:0030050 vesicle transport along actin filament                              | 2   | 0.04183 | 0.619  | 0.111 | Biological | GO:0030 vesicle transport along actin filament                               | 0.04183 | 0.20439 | 0 | 0 | 2   | 18    |
| GO:0038128 ERBB2 signaling pathway                                             | 2   | 0.04183 | 0.619  | 0.111 | Biological | GO:0038 ERBB2 signaling pathway                                              | 0.04183 | 0.20439 | 0 | 0 | 2   | 18    |
| GO:0044320 cellular response to antigen stimulus                               | 2   | 0.04183 | 0.619  | 0.111 | Biological | GO:0044 cellular response to antigen stimulus                                | 0.04183 | 0.20439 | 0 | 0 | 2   | 18    |
| GO:0044872 lipoprotein localization                                            | 2   | 0.04183 | 0.619  | 0.111 | Biological | GO:0044 lipoprotein localization                                             | 0.04183 | 0.20439 | 0 | 0 | 2   | 18    |
| GO:0051004 regulation of lipoprotein lipase activity                           | 2   | 0.04183 | 0.619  | 0.111 | Biological | GO:0051 regulation of lipoprotein lipase activity                            | 0.04183 | 0.20439 | 0 | 0 | 2   | 18    |
| GO:0060252 positive regulation of glial cell proliferation                     | 2   | 0.04183 | 0.619  | 0.111 | Biological | GO:0060 positive regulation of glial cell proliferation                      | 0.04183 | 0.20439 | 0 | 0 | 2   | 18    |
| GO:0060644 mammary gland epithelial cell differentiation                       | 2   | 0.04183 | 0.619  | 0.111 | Biological | GO:0060 mammary gland epithelial cell differentiation                        | 0.04183 | 0.20439 | 0 | 0 | 2   | 18    |
| GO:0070206 protein transport                                                   | 2   | 0.04183 | 0.619  | 0.111 | Biological | GO:0070 protein transport                                                    | 0.04183 | 0.20439 | 0 | 0 | 2   | 18    |
| GO:0072189 ureter development                                                  | 2   | 0.04183 | 0.619  | 0.111 | Biological | GO:0072 ureter development                                                   | 0.04183 | 0.20439 | 0 | 0 | 2   | 18    |
| GO:0090136 epithelial cell-cell adhesion                                       | 2   | 0.04183 | 0.619  | 0.111 | Biological | GO:0090 epithelial cell-cell adhesion                                        | 0.04183 | 0.20439 | 0 | 0 | 2   | 18    |
| GO:2000136 regulation of cell proliferation involved in heart morphogenesis    | 2   | 0.04183 | 0.619  | 0.111 | Biological | GO:2000 regulation of cell proliferation involved in heart morphogenesis     | 0.04183 | 0.20439 | 0 | 0 | 2   | 18    |
| GO:0043254 regulation of protein-containing complex assembly                   | 14  | 0.04198 | 4.334  | 0.031 | Biological | GO:0043 regulation of protein-containing complex assembly                    | 0.04198 | 0.20495 | 0 | 0 | 14  | 458   |
| GO:0036477 commitment                                                          | 23  | 0.04204 | 6.839  | 0.027 | Cellular   | GO:0036 commitment                                                           | 0.04204 | 0.21524 | 0 | 0 | 23  | 867   |
| GO:0035914 skeletal muscle cell differentiation                                | 4   | 0.04244 | 1.238  | 0.056 | Biological | GO:0035 skeletal muscle cell differentiation                                 | 0.04244 | 0.20678 | 0 | 0 | 4   | 72    |
| GO:0061180 mammary gland epithelium development                                | 4   | 0.04244 | 1.238  | 0.056 | Biological | GO:0061 mammary gland epithelium development                                 | 0.04244 | 0.20678 | 0 | 0 | 4   | 72    |
| GO:0005488 binding                                                             | 322 | 0.04254 | 94.152 | 0.019 | Molecular  | GO:0005 binding                                                              | 0.04254 | 0.22088 | 0 | 0 | 322 | 16887 |
| GO:0006031 heparin binding                                                     | 7   | 0.04263 | 2.047  | 0.04  | Molecular  | GO:0006 heparin binding                                                      | 0.04263 | 0.22088 | 0 | 0 | 7   | 173   |
| GO:0016529 sarcoplasmic reticulum                                              | 1   | 0.0428  | 1.187  | 0.055 | Cellular   | GO:0016 sarcoplasmic reticulum                                               | 0.0428  | 0.21739 | 0 | 0 | 1   | 13    |
| GO:0060541 respiratory system development                                      | 8   | 0.04288 | 2.477  | 0.037 | Biological | GO:0060 respiratory system development                                       | 0.04288 | 0.20673 | 0 | 0 | 8   | 214   |
| GO:0010595 positive regulation of endothelial cell migration                   | 5   | 0.04316 | 1.548  | 0.048 | Biological | GO:0010 positive regulation of endothelial cell migration                    | 0.04316 | 0.20985 | 0 | 0 | 5   | 105   |
| GO:0071840 cellular component organization or biogenesis                       | 136 | 0.04327 | 42.105 | 0.021 | Biological | GO:0071 cellular component organization or biogenesis                        | 0.04327 | 0.20999 | 0 | 0 | 136 | 6619  |
| GO:0001937 negative regulation of endothelial cell proliferation               | 3   | 0.04335 | 0.929  | 0.07  | Biological | GO:0001 negative regulation of endothelial cell proliferation                | 0.04335 | 0.20999 | 0 | 0 | 3   | 43    |
| GO:0015695 organic cation transport                                            | 3   | 0.04335 | 0.929  | 0.07  | Biological | GO:0015 organic cation transport                                             | 0.04335 | 0.20999 | 0 | 0 | 3   | 43    |
| GO:0060428 lung epithelium development                                         | 3   | 0.04335 | 0.929  | 0.07  | Biological | GO:0060 lung epithelium development                                          | 0.04335 | 0.20999 | 0 | 0 | 3   | 43    |
| GO:0009986 cell surface                                                        | 25  | 0.04337 | 7.418  | 0.026 | Cellular   | GO:0009 cell surface                                                         | 0.04337 | 0.21739 | 0 | 0 | 25  | 963   |
| GO:0014069 postsynaptic density                                                | 11  | 0.04348 | 3.264  | 0.0   |            |                                                                              |         |         |   |   |     |       |

|                                                                                                   |     |         |        |       |            |                                                                                                   |         |         |   |   |     |      |
|---------------------------------------------------------------------------------------------------|-----|---------|--------|-------|------------|---------------------------------------------------------------------------------------------------|---------|---------|---|---|-----|------|
| GO:0036342 post-anal tail morphogenesis                                                           | 2   | 0.05073 | 0.619  | 0.1   | Biological | GO:0036342 post-anal tail morphogenesis                                                           | 0.05073 | 0.22168 | 0 | 0 | 2   | 20   |
| GO:0042474 middle ear morphogenesis                                                               | 2   | 0.05073 | 0.619  | 0.1   | Biological | GO:0042474 middle ear morphogenesis                                                               | 0.05073 | 0.22168 | 0 | 0 | 2   | 20   |
| GO:0043586 tongue development                                                                     | 2   | 0.05073 | 0.619  | 0.1   | Biological | GO:0043586 tongue development                                                                     | 0.05073 | 0.22168 | 0 | 0 | 2   | 20   |
| GO:0055054 chloride ion homeostasis                                                               | 2   | 0.05073 | 0.619  | 0.1   | Biological | GO:0055054 chloride ion homeostasis                                                               | 0.05073 | 0.22168 | 0 | 0 | 2   | 20   |
| GO:0055083 monovalent inorganic anion homeostasis                                                 | 2   | 0.05073 | 0.619  | 0.1   | Biological | GO:0055083 monovalent inorganic anion homeostasis                                                 | 0.05073 | 0.22168 | 0 | 0 | 2   | 20   |
| GO:0060973 cell migration involved in heart development                                           | 2   | 0.05073 | 0.619  | 0.1   | Biological | GO:0060973 cell migration involved in heart development                                           | 0.05073 | 0.22168 | 0 | 0 | 2   | 20   |
| GO:0071498 cellular response to fluid shear stress                                                | 2   | 0.05073 | 0.619  | 0.1   | Biological | GO:0071498 cellular response to fluid shear stress                                                | 0.05073 | 0.22168 | 0 | 0 | 2   | 20   |
| GO:0072079 nephron tubule formation                                                               | 2   | 0.05073 | 0.619  | 0.1   | Biological | GO:0072079 nephron tubule formation                                                               | 0.05073 | 0.22168 | 0 | 0 | 2   | 20   |
| GO:009515 actin filament-based transport                                                          | 2   | 0.05073 | 0.619  | 0.1   | Biological | GO:009515 actin filament-based transport                                                          | 0.05073 | 0.22168 | 0 | 0 | 2   | 20   |
| GO:0060402 calcium ion transport into cytosol                                                     | 7   | 0.05079 | 2.167  | 0.038 | Biological | GO:0060402 calcium ion transport into cytosol                                                     | 0.05079 | 0.22168 | 0 | 0 | 7   | 183  |
| GO:0050804 modulation of chemical synaptic transmission                                           | 14  | 0.05082 | 4.334  | 0.031 | Biological | GO:0050804 modulation of chemical synaptic transmission                                           | 0.05082 | 0.22168 | 0 | 0 | 14  | 471  |
| GO:0004252 serine-type endopeptidase activity                                                     | 7   | 0.05083 | 2.047  | 0.039 | Molecular  | GO:0004252 serine-type endopeptidase activity                                                     | 0.05083 | 0.22088 | 0 | 0 | 7   | 180  |
| GO:0060939 smooth muscle contraction                                                              | 5   | 0.05091 | 1.548  | 0.343 | Biological | GO:0060939 smooth muscle contraction                                                              | 0.05091 | 0.22168 | 0 | 0 | 5   | 148  |
| GO:1901655 cellular response to ketone                                                            | 5   | 0.05091 | 1.548  | 0.045 | Biological | GO:1901655 cellular response to ketone                                                            | 0.05091 | 0.22168 | 0 | 0 | 5   | 110  |
| GO:0014075 response to amine                                                                      | 3   | 0.05127 | 0.929  | 0.065 | Biological | GO:0014075 response to amine                                                                      | 0.05127 | 0.22168 | 0 | 0 | 3   | 46   |
| GO:0014904 myotube cell development                                                               | 3   | 0.05127 | 0.929  | 0.065 | Biological | GO:0014904 myotube cell development                                                               | 0.05127 | 0.22168 | 0 | 0 | 3   | 46   |
| GO:0042596 fear response                                                                          | 3   | 0.05127 | 0.929  | 0.065 | Biological | GO:0042596 fear response                                                                          | 0.05127 | 0.22168 | 0 | 0 | 3   | 46   |
| GO:1900271 regulation of long-term synaptic potentiation                                          | 3   | 0.05127 | 0.929  | 0.065 | Biological | GO:1900271 regulation of long-term synaptic potentiation                                          | 0.05127 | 0.22168 | 0 | 0 | 3   | 46   |
| GO:1900090 cellular response to nerve growth factor stimulus                                      | 3   | 0.05127 | 0.929  | 0.065 | Biological | GO:1900090 cellular response to nerve growth factor stimulus                                      | 0.05127 | 0.22168 | 0 | 0 | 3   | 46   |
| GO:0006865 amino acid transport                                                                   | 6   | 0.05128 | 1.858  | 0.041 | Biological | GO:0006865 amino acid transport                                                                   | 0.05128 | 0.22168 | 0 | 0 | 6   | 146  |
| GO:0007272 ensheathment of neurons                                                                | 6   | 0.05128 | 1.858  | 0.041 | Biological | GO:0007272 ensheathment of neurons                                                                | 0.05128 | 0.22168 | 0 | 0 | 6   | 146  |
| GO:0006366 axon ensheathment                                                                      | 6   | 0.05128 | 1.858  | 0.041 | Biological | GO:0006366 axon ensheathment                                                                      | 0.05128 | 0.22168 | 0 | 0 | 6   | 146  |
| GO:0090101 negative regulation of transmembrane receptor protein serine/threonine kinase activity | 6   | 0.05128 | 1.858  | 0.041 | Biological | GO:0090101 negative regulation of transmembrane receptor protein serine/threonine kinase activity | 0.05128 | 0.22168 | 0 | 0 | 6   | 146  |
| GO:0091777 regulation of trans-synaptic signaling                                                 | 14  | 0.05155 | 4.334  | 0.03  | Biological | GO:0091777 regulation of trans-synaptic signaling                                                 | 0.05155 | 0.22168 | 0 | 0 | 14  | 472  |
| GO:0019538 protein metabolic process                                                              | 113 | 0.05161 | 34.985 | 0.021 | Biological | GO:0019538 protein metabolic process                                                              | 0.05161 | 0.22168 | 0 | 0 | 113 | 5432 |
| GO:0050954 sensory perception of mechanical stimulus                                              | 7   | 0.05202 | 2.167  | 0.038 | Biological | GO:0050954 sensory perception of mechanical stimulus                                              | 0.05202 | 0.22168 | 0 | 0 | 7   | 184  |
| GO:0043412 macromolecule modification                                                             | 83  | 0.05223 | 25.697 | 0.021 | Biological | GO:0043412 macromolecule modification                                                             | 0.05223 | 0.22168 | 0 | 0 | 83  | 3863 |
| GO:0004653 polyketide N-acyltransferase activity                                                  | 2   | 0.05225 | 0.585  | 0.1   | Molecular  | GO:0004653 polyketide N-acyltransferase activity                                                  | 0.05225 | 0.22088 | 0 | 0 | 2   | 20   |
| GO:0005123 death receptor binding                                                                 | 2   | 0.05225 | 0.585  | 0.1   | Molecular  | GO:0005123 death receptor binding                                                                 | 0.05225 | 0.22088 | 0 | 0 | 2   | 20   |
| GO:0005283 amino acid:sodium symporter activity                                                   | 2   | 0.05225 | 0.585  | 0.1   | Molecular  | GO:0005283 amino acid:sodium symporter activity                                                   | 0.05225 | 0.22088 | 0 | 0 | 2   | 20   |
| GO:0001708 cell fate specification                                                                | 5   | 0.05255 | 1.548  | 0.045 | Biological | GO:0001708 cell fate specification                                                                | 0.05255 | 0.22168 | 0 | 0 | 5   | 111  |
| GO:0007200 phospholipase C-activating G protein-coupled receptor signaling pathway                | 5   | 0.05255 | 1.548  | 0.045 | Biological | GO:0007200 phospholipase C-activating G protein-coupled receptor signaling pathway                | 0.05255 | 0.22168 | 0 | 0 | 5   | 111  |
| GO:0030148 sphingomyelinase activity                                                              | 5   | 0.05255 | 1.548  | 0.045 | Biological | GO:0030148 sphingomyelinase activity                                                              | 0.05255 | 0.22168 | 0 | 0 | 5   | 111  |
| GO:0034446 substrate adhesion-dependent cell spreading                                            | 5   | 0.05255 | 1.548  | 0.045 | Biological | GO:0034446 substrate adhesion-dependent cell spreading                                            | 0.05255 | 0.22168 | 0 | 0 | 5   | 111  |
| GO:0000122 negative regulation of transcription by RNA polymerase II                              | 25  | 0.05262 | 7.74   | 0.026 | Biological | GO:0000122 negative regulation of transcription by RNA polymerase II                              | 0.05262 | 0.22168 | 0 | 0 | 25  | 972  |
| GO:0014074 response to purine-containing compound                                                 | 6   | 0.05268 | 1.858  | 0.041 | Biological | GO:0014074 response to purine-containing compound                                                 | 0.05268 | 0.22168 | 0 | 0 | 6   | 147  |
| GO:0005896 interleukin-6 receptor complex                                                         | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:0005896 interleukin-6 receptor complex                                                         | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:0016513 core-binding factor complex                                                            | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:0016513 core-binding factor complex                                                            | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:0030485 smooth muscle contractile fiber                                                        | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:0030485 smooth muscle contractile fiber                                                        | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:0035866 alpha-beta3 integrin-PKCalpha complex                                                  | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:0035866 alpha-beta3 integrin-PKCalpha complex                                                  | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:0042825 TAP complex                                                                            | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:0042825 TAP complex                                                                            | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:0046269 methionine adenosyltransferase complex                                                 | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:0046269 methionine adenosyltransferase complex                                                 | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:0070110 ciliary neurotrophic factor receptor complex                                           | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:0070110 ciliary neurotrophic factor receptor complex                                           | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:0007021 ISGF3 complex                                                                          | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:0007021 ISGF3 complex                                                                          | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:0090651 apical cytoplasm                                                                       | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:0090651 apical cytoplasm                                                                       | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:0097451 alial limiting end-foot                                                                | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:0097451 alial limiting end-foot                                                                | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:0098644 perisynaptic space                                                                     | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:0098644 perisynaptic space                                                                     | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:1901589 dendritic microtubule                                                                  | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:1901589 dendritic microtubule                                                                  | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:1905721 mitotic spindle astral microtubule end                                                 | 1   | 0.05311 | 0.297  | 0.333 | Cellular   | GO:1905721 mitotic spindle astral microtubule end                                                 | 0.05311 | 0.2189  | 0 | 0 | 1   | 3    |
| GO:0007565 female pregnancy                                                                       | 7   | 0.05326 | 2.167  | 0.038 | Biological | GO:0007565 female pregnancy                                                                       | 0.05326 | 0.22168 | 0 | 0 | 7   | 185  |
| GO:0008194 UDP-glucosyltransferase activity                                                       | 6   | 0.05333 | 1.754  | 0.041 | Molecular  | GO:0008194 UDP-glucosyltransferase activity                                                       | 0.05333 | 0.22088 | 0 | 0 | 6   | 145  |
| GO:0001555 oocyte growth                                                                          | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0001555 oocyte growth                                                                          | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0001908 positive regulation of type II hypersensitivity                                        | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0001908 positive regulation of type II hypersensitivity                                        | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0001905 activation of membrane attack complex                                                  | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0001905 activation of membrane attack complex                                                  | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0001969 regulation of activation of membrane attack complex                                    | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0001969 regulation of activation of membrane attack complex                                    | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0002074 extracellular skeletal muscle development                                              | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0002074 extracellular skeletal muscle development                                              | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0002157 positive regulation of thyroid hormone mediated signaling pathway                      | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0002157 positive regulation of thyroid hormone mediated signaling pathway                      | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0002541 activation of caspase cascade process                                                  | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0002541 activation of caspase cascade process                                                  | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0002894 positive regulation of type II hypersensitivity                                        | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0002894 positive regulation of type II hypersensitivity                                        | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0003220 left ventricular cardiac muscle tissue morphogenesis                                   | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0003220 left ventricular cardiac muscle tissue morphogenesis                                   | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0003275 apoptotic process involved in outflow tract morphogenesis                              | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0003275 apoptotic process involved in outflow tract morphogenesis                              | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0003430 growth plate cartilage chondrocyte growth                                              | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0003430 growth plate cartilage chondrocyte growth                                              | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0006799 glucocorticoid biosynthetic process                                                    | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0006799 glucocorticoid biosynthetic process                                                    | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0006714 sesquiterpene metabolic process                                                        | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0006714 sesquiterpene metabolic process                                                        | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0007538 primary sex determination                                                              | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0007538 primary sex determination                                                              | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0007619 courtship behavior                                                                     | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0007619 courtship behavior                                                                     | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0010693 negative regulation of alkaline phosphatase activity                                   | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0010693 negative regulation of alkaline phosphatase activity                                   | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0010716 negative regulation of extracellular matrix disassembly                                | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0010716 negative regulation of extracellular matrix disassembly                                | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0014043 negative regulation of neuron maturation                                               | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0014043 negative regulation of neuron maturation                                               | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0014734 skeletal muscle hypertrophy                                                            | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0014734 skeletal muscle hypertrophy                                                            | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0021538 epithalamus development                                                                | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0021538 epithalamus development                                                                | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0021551 central nervous system morphogenesis                                                   | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0021551 central nervous system morphogenesis                                                   | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0021555 midbrain boundary morphogenesis                                                        | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0021555 midbrain boundary morphogenesis                                                        | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0021627 olfactory nerve morphogenesis                                                          | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0021627 olfactory nerve morphogenesis                                                          | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0021986 habenula development                                                                   | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0021986 habenula development                                                                   | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0030910 olfactory placode formation                                                            | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0030910 olfactory placode formation                                                            | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0032805 positive regulation of low-density lipoprotein particle receptor catabolic process     | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0032805 positive regulation of low-density lipoprotein particle receptor catabolic process     | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0032899 regulation of neurotrophin production                                                  | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0032899 regulation of neurotrophin production                                                  | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0033024 mast cell apoptotic process                                                            | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0033024 mast cell apoptotic process                                                            | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0033025 regulation of mast cell apoptotic process                                              | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0033025 regulation of mast cell apoptotic process                                              | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0035702 monocyte homeostasis                                                                   | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0035702 monocyte homeostasis                                                                   | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0035846 ovicud epithelium development                                                          | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0035846 ovicud epithelium development                                                          | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0036514 dopaminergic neuron axon guidance                                                      | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0036514 dopaminergic neuron axon guidance                                                      | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0038154 interleukin-11-mediated signaling pathway                                              | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0038154 interleukin-11-mediated signaling pathway                                              | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0042305 specification of segmental identity, mandibular segment                                | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0042305 specification of segmental identity, mandibular segment                                | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0042863 cysteine transport                                                                     | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0042863 cysteine transport                                                                     | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0045218 zonula adherens maintenance                                                            | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0045218 zonula adherens maintenance                                                            | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0048769 sarcomeres                                                                             | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0048769 sarcomeres                                                                             | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0051790 short-chain fatty acid biosynthetic process                                            | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0051790 short-chain fatty acid biosynthetic process                                            | 0.0537  | 0.22168 | 0 | 0 | 1   | 3    |
| GO:0051795 positive regulation of timing of catagen                                               | 1   | 0.0537  | 0.31   | 0.333 | Biological | GO:0051795 positive regulation of timing of catagen                                               | 0.0537  | 0.22168 | 0 | 0 | 1   |      |

|                                                                                                          |    |         |        |       |            |                                                                                                          |         |        |       |   |   |    |      |
|----------------------------------------------------------------------------------------------------------|----|---------|--------|-------|------------|----------------------------------------------------------------------------------------------------------|---------|--------|-------|---|---|----|------|
| GO:0050919 negative chemotaxis                                                                           | 3  | 0.05405 | 0.929  | 0.064 | Biological | GO:0050919 negative chemotaxis                                                                           | 0.05405 | 0.929  | 0.064 | 0 | 0 | 3  | 47   |
| GO:1902622 regulation of neutrophil migration                                                            | 3  | 0.05405 | 0.929  | 0.064 | Biological | GO:1902622 regulation of neutrophil migration                                                            | 0.05405 | 0.929  | 0.064 | 0 | 0 | 3  | 47   |
| GO:1905314 semi-lunar valve development                                                                  | 3  | 0.05405 | 0.929  | 0.064 | Biological | GO:1905314 semi-lunar valve development                                                                  | 0.05405 | 0.929  | 0.064 | 0 | 0 | 3  | 47   |
| GO:2001222 region of neuron migration                                                                    | 3  | 0.05405 | 0.929  | 0.064 | Biological | GO:2001222 region of neuron migration                                                                    | 0.05405 | 0.929  | 0.064 | 0 | 0 | 3  | 47   |
| GO:0030534 adult behavior                                                                                | 6  | 0.05411 | 1.858  | 0.041 | Biological | GO:0030534 adult behavior                                                                                | 0.05411 | 1.858  | 0.041 | 0 | 0 | 6  | 148  |
| GO:1903364 positive regulation of cellular protein catabolic process                                     | 6  | 0.05411 | 1.858  | 0.041 | Biological | GO:1903364 positive regulation of cellular protein catabolic process                                     | 0.05411 | 1.858  | 0.041 | 0 | 0 | 6  | 148  |
| GO:0045445 myoblast differentiation                                                                      | 5  | 0.05423 | 1.548  | 0.045 | Biological | GO:0045445 myoblast differentiation                                                                      | 0.05423 | 1.548  | 0.045 | 0 | 0 | 5  | 112  |
| GO:2000060 positive regulation of ubiquitin-dependent protein catabolic process                          | 5  | 0.05423 | 1.548  | 0.045 | Biological | GO:2000060 positive regulation of ubiquitin-dependent protein catabolic process                          | 0.05423 | 1.548  | 0.045 | 0 | 0 | 5  | 112  |
| GO:0043066 negative regulation of apoptotic process                                                      | 23 | 0.05428 | 7.121  | 0.028 | Biological | GO:0043066 negative regulation of apoptotic process                                                      | 0.05428 | 7.121  | 0.028 | 0 | 0 | 23 | 882  |
| GO:0034361 very-low-density lipoprotein particle                                                         | 2  | 0.05431 | 0.593  | 0.095 | Cellular   | GO:0034361 very-low-density lipoprotein particle                                                         | 0.05431 | 0.593  | 0.095 | 0 | 0 | 2  | 21   |
| GO:0034385 triacylglyceride-rich plasma lipoprotein particle                                             | 2  | 0.05431 | 0.593  | 0.095 | Cellular   | GO:0034385 triacylglyceride-rich plasma lipoprotein particle                                             | 0.05431 | 0.593  | 0.095 | 0 | 0 | 2  | 21   |
| GO:0042827 platelet dense granule                                                                        | 2  | 0.05431 | 0.593  | 0.095 | Cellular   | GO:0042827 platelet dense granule                                                                        | 0.05431 | 0.593  | 0.095 | 0 | 0 | 2  | 21   |
| GO:0032432 actin filament bundle                                                                         | 4  | 0.05442 | 1.187  | 0.051 | Cellular   | GO:0032432 actin filament bundle                                                                         | 0.05442 | 1.187  | 0.051 | 0 | 0 | 4  | 79   |
| GO:0042641 actomyosin                                                                                    | 4  | 0.05442 | 1.187  | 0.051 | Cellular   | GO:0042641 actomyosin                                                                                    | 0.05442 | 1.187  | 0.051 | 0 | 0 | 4  | 79   |
| GO:0000293 ferric-chelate reductase activity                                                             | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0000293 ferric-chelate reductase activity                                                             | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0003829 beta-1.3-galactosyl-O-glycosyl-glycoprotein beta-1.6-N-acetylglucosaminyltransferase activity | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0003829 beta-1.3-galactosyl-O-glycosyl-glycoprotein beta-1.6-N-acetylglucosaminyltransferase activity | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0004145 diamine N-acetyltransferase activity                                                          | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0004145 diamine N-acetyltransferase activity                                                          | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0004689 calcium-independent protein kinase C activity                                                 | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0004689 calcium-independent protein kinase C activity                                                 | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0004768 stearyl-CoA 9-desaturase activity                                                             | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0004768 stearyl-CoA 9-desaturase activity                                                             | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0004833 tryptophan 2,3-dioxygenase activity                                                           | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0004833 tryptophan 2,3-dioxygenase activity                                                           | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0004921 interleukin-11 receptor activity                                                              | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0004921 interleukin-11 receptor activity                                                              | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0005006 epidermal growth factor-activated receptor activity                                           | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0005006 epidermal growth factor-activated receptor activity                                           | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0005010 insulin-like growth factor-activated receptor activity                                        | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0005010 insulin-like growth factor-activated receptor activity                                        | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0005157 macrophage colony-stimulating factor receptor binding                                         | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0005157 macrophage colony-stimulating factor receptor binding                                         | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0005220 inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity                       | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0005220 inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity                       | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0008109 N-acetylglucosaminidase beta-1.6-N-acetylglucosaminyltransferase activity                     | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0008109 N-acetylglucosaminidase beta-1.6-N-acetylglucosaminyltransferase activity                     | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0008427 calcium-dependent protein kinase inhibitor activity                                           | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0008427 calcium-dependent protein kinase inhibitor activity                                           | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0008623 cuproplasma reductase activity                                                                | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0008623 cuproplasma reductase activity                                                                | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0010858 calcium-dependent protein kinase regulator activity                                           | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0010858 calcium-dependent protein kinase regulator activity                                           | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0016151 nickel cation binding                                                                         | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0016151 nickel cation binding                                                                         | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0016657 oxidoreductase activity, acting on NAD(P)H, nitrogenous group as oxidant                      | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0016657 oxidoreductase activity, acting on NAD(P)H, nitrogenous group as oxidant                      | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0016920 pyroglyutamyl-peptidase activity                                                              | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0016920 pyroglyutamyl-peptidase activity                                                              | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0017020 myosin phosphatase (NADPH) activity                                                           | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0017020 myosin phosphatase (NADPH) activity                                                           | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0017061 S-methyl-5-hydroxymethylphosphorylase activity                                                | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0017061 S-methyl-5-hydroxymethylphosphorylase activity                                                | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0019970 interleukin-11 binding                                                                        | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0019970 interleukin-11 binding                                                                        | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0031229 histone deacetylase activity (H3-K9 specific)                                                 | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0031229 histone deacetylase activity (H3-K9 specific)                                                 | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0032923 cysteine transmembrane transporter activity                                                   | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0032923 cysteine transmembrane transporter activity                                                   | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0034714 type III transforming growth factor beta receptor binding                                     | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0034714 type III transforming growth factor beta receptor binding                                     | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0036314 12-hydroxyheptadecatrienoic acid synthase activity                                            | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0036314 12-hydroxyheptadecatrienoic acid synthase activity                                            | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0038131 neuregulin receptor activity                                                                  | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0038131 neuregulin receptor activity                                                                  | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0044729 hemi-methylated DNA-binding                                                                   | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0044729 hemi-methylated DNA-binding                                                                   | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0045030 G protein-coupled UTP receptor activity                                                       | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0045030 G protein-coupled UTP receptor activity                                                       | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0046979 TAP2 binding                                                                                  | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0046979 TAP2 binding                                                                                  | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0047115 trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity                                      | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0047115 trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity                                      | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0047690 aspartyltransferase activity                                                                  | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0047690 aspartyltransferase activity                                                                  | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0047718 indanol dehydrogenase activity                                                                | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0047718 indanol dehydrogenase activity                                                                | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0047757 chondroitin-glucuronate 5-epimerase activity                                                  | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0047757 chondroitin-glucuronate 5-epimerase activity                                                  | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0052851 ferric-chelate reductase (NADPH) activity                                                     | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0052851 ferric-chelate reductase (NADPH) activity                                                     | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0070290 N-acetylphosphatidylethanolamine-specific phospholipase D activity                            | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0070290 N-acetylphosphatidylethanolamine-specific phospholipase D activity                            | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0099184 structural constituent of postsynaptic intermediate filament cytoskeleton                     | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0099184 structural constituent of postsynaptic intermediate filament cytoskeleton                     | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0106130 purine phosphoribosyltransferase activity                                                     | 1  | 0.05458 | 0.292  | 0.333 | Molecular  | GO:0106130 purine phosphoribosyltransferase activity                                                     | 0.05458 | 0.292  | 0.333 | 0 | 0 | 1  | 3    |
| GO:0006491 N-glycan processing                                                                           | 2  | 0.05541 | 0.819  | 0.095 | Biological | GO:0006491 N-glycan processing                                                                           | 0.05541 | 0.819  | 0.095 | 0 | 0 | 2  | 21   |
| GO:0006704 endoplasmic reticulum metabolic process                                                       | 2  | 0.05541 | 0.819  | 0.095 | Biological | GO:0006704 endoplasmic reticulum metabolic process                                                       | 0.05541 | 0.819  | 0.095 | 0 | 0 | 2  | 21   |
| GO:0007213 G protein-coupled acetylcholine receptor signaling pathway                                    | 2  | 0.05541 | 0.819  | 0.095 | Biological | GO:0007213 G protein-coupled acetylcholine receptor signaling pathway                                    | 0.05541 | 0.819  | 0.095 | 0 | 0 | 2  | 21   |
| GO:0007379 segment specification                                                                         | 2  | 0.05541 | 0.819  | 0.095 | Biological | GO:0007379 segment specification                                                                         | 0.05541 | 0.819  | 0.095 | 0 | 0 | 2  | 21   |
| GO:0050855 regulation of B cell receptor signaling pathway                                               | 2  | 0.05541 | 0.819  | 0.095 | Biological | GO:0050855 regulation of B cell receptor signaling pathway                                               | 0.05541 | 0.819  | 0.095 | 0 | 0 | 2  | 21   |
| GO:0051000 positive regulation of nitric-oxide synthase activity                                         | 2  | 0.05541 | 0.819  | 0.095 | Biological | GO:0051000 positive regulation of nitric-oxide synthase activity                                         | 0.05541 | 0.819  | 0.095 | 0 | 0 | 2  | 21   |
| GO:0072234 methanone reductase activity                                                                  | 2  | 0.05541 | 0.819  | 0.095 | Biological | GO:0072234 methanone reductase activity                                                                  | 0.05541 | 0.819  | 0.095 | 0 | 0 | 2  | 21   |
| GO:0140131 positive regulation of lymphocyte chemotaxis                                                  | 2  | 0.05541 | 0.819  | 0.095 | Biological | GO:0140131 positive regulation of lymphocyte chemotaxis                                                  | 0.05541 | 0.819  | 0.095 | 0 | 0 | 2  | 21   |
| GO:1902307 positive regulation of sodium ion transmembrane transport                                     | 2  | 0.05541 | 0.819  | 0.095 | Biological | GO:1902307 positive regulation of sodium ion transmembrane transport                                     | 0.05541 | 0.819  | 0.095 | 0 | 0 | 2  | 21   |
| GO:1903672 positive regulation of sprouting angiogenesis                                                 | 2  | 0.05541 | 0.819  | 0.095 | Biological | GO:1903672 positive regulation of sprouting angiogenesis                                                 | 0.05541 | 0.819  | 0.095 | 0 | 0 | 2  | 21   |
| GO:2000738 positive regulation of stem cell differentiation                                              | 2  | 0.05541 | 0.819  | 0.095 | Biological | GO:2000738 positive regulation of stem cell differentiation                                              | 0.05541 | 0.819  | 0.095 | 0 | 0 | 2  | 21   |
| GO:0005789 endoplasmic reticulum membrane                                                                | 29 | 0.05591 | 8.005  | 0.025 | Biological | GO:0005789 endoplasmic reticulum membrane                                                                | 0.05591 | 8.005  | 0.025 | 0 | 0 | 29 | 1185 |
| GO:0022607 cellular component assembly                                                                   | 67 | 0.05592 | 20.743 | 0.022 | Biological | GO:0022607 cellular component assembly                                                                   | 0.05592 | 20.743 | 0.022 | 0 | 0 | 67 | 3053 |
| GO:0033116 endoplasmic reticulum-Golgi intermediate compartment membrane                                 | 4  | 0.05651 | 1.187  | 0.05  | Cellular   | GO:0033116 endoplasmic reticulum-Golgi intermediate compartment membrane                                 | 0.05651 | 1.187  | 0.05  | 0 | 0 | 4  | 80   |
| GO:0006875 cellular metal ion homeostasis                                                                | 17 | 0.05685 | 5.263  | 0.028 | Biological | GO:0006875 cellular metal ion homeostasis                                                                | 0.05685 | 5.263  | 0.028 | 0 | 0 | 17 | 612  |
| GO:0046332 SMAD binding                                                                                  | 4  | 0.05689 | 1.727  | 0.051 | Molecular  | GO:0046332 SMAD binding                                                                                  | 0.05689 | 1.727  | 0.051 | 0 | 0 | 4  | 78   |
| GO:0043114 regulation of vascular permeability                                                           | 3  | 0.05691 | 0.929  | 0.062 | Biological | GO:0043114 regulation of vascular permeability                                                           | 0.05691 | 0.929  | 0.062 | 0 | 0 | 3  | 48   |
| GO:0048089 insulin-like growth factor receptor signaling pathway                                         | 3  | 0.05691 | 0.929  | 0.062 | Biological | GO:0048089 insulin-like growth factor receptor signaling pathway                                         | 0.05691 | 0.929  | 0.062 | 0 | 0 | 3  | 48   |
| GO:0050581 anion homeostasis                                                                             | 3  | 0.05691 | 0.929  | 0.062 | Biological | GO:0050581 anion homeostasis                                                                             | 0.05691 | 0.929  | 0.062 | 0 | 0 | 3  | 48   |
| GO:0061383 trabecula morphogenesis                                                                       | 3  | 0.05691 | 0.929  | 0.062 | Biological | GO:0061383 trabecula morphogenesis                                                                       | 0.05691 | 0.929  | 0.062 | 0 | 0 | 3  | 48   |
| GO:1900839 response to nerve growth factor                                                               | 3  | 0.05691 | 0.929  | 0.062 | Biological | GO:1900839 response to nerve growth factor                                                               | 0.05691 | 0.929  | 0.062 | 0 | 0 | 3  | 48   |
| GO:0070433 cell junction assembly                                                                        | 6  | 0.05701 | 1.858  | 0.041 | Biological | GO:0070433 cell junction assembly                                                                        | 0.05701 | 1.858  | 0.041 | 0 | 0 | 6  | 158  |
| GO:0061138 morphogenesis of a branching epithelium                                                       | 7  | 0.0571  | 2.167  | 0.037 | Biological | GO:0061138 morphogenesis of a branching epithelium                                                       | 0.0571  | 2.167  | 0.037 | 0 | 0 | 7  | 188  |
| GO:0031346 positive regulation of cell projection organization                                           | 11 | 0.05773 | 3.406  | 0.031 | Biological | GO:0031346 positive regulation of cell projection organization                                           | 0.05773 | 3.406  | 0.031 | 0 | 0 | 11 | 351  |
| GO:0098827 endoplasmic reticulum subcompartment                                                          | 29 | 0.05787 | 8.605  | 0.024 | Cellular   | GO:0098827 endoplasmic reticulum subcompartment                                                          | 0.05787 | 8.605  | 0.024 | 0 | 0 | 29 | 1184 |
| GO:0072038 neptunium morphogenesis                                                                       | 4  | 0.0584  | 1.238  | 0.05  | Biological | GO:0072038 neptunium morphogenesis                                                                       | 0.0584  | 1.238  | 0.05  | 0 | 0 | 4  | 80   |
| GO:0070761 dendritic spine organization                                                                  | 4  | 0.0584  | 1.238  | 0.05  | Biological | GO:0070761 dendritic spine organization                                                                  | 0.0584  | 1.238  | 0.05  | 0 | 0 | 4  | 80   |
| GO:0031644 regulation of nervous system process                                                          | 6  | 0.05853 | 1.858  | 0.04  | Biological | GO:0031644 regulation of nervous system process                                                          | 0.05853 | 1.858  | 0.04  | 0 | 0 | 6  | 151  |
| GO:0031258 lamellipodium membrane                                                                        | 2  | 0.05905 | 0.593  | 0.091 | Cellular   | GO:0031258 lamellipodium membrane                                                                        | 0.05905 | 0.593  | 0.091 | 0 | 0 | 2  | 22   |
| GO:0098644 complex of collagen trimers                                                                   | 2  | 0.05905 | 0.593  | 0.091 | Cellular   | GO:0098644 complex of collagen trimers                                                                   | 0.05905 | 0.593  | 0.091 | 0 | 0 | 2  | 22   |
| GO:004589                                                                                                |    |         |        |       |            |                                                                                                          |         |        |       |   |   |    |      |

|                                                                                          |     |         |       |       |            |                                                                                          |         |         |   |   |    |     |
|------------------------------------------------------------------------------------------|-----|---------|-------|-------|------------|------------------------------------------------------------------------------------------|---------|---------|---|---|----|-----|
| GO:0034219 carbohydrate transmembrane transport                                          | 5   | 0.06872 | 1.548 | 0.042 | Biological | GO:0034219 carbohydrate transmembrane transport                                          | 0.06872 | 0.25078 | 0 | 0 | 5  | 120 |
| GO:0042303 molting cycle                                                                 | 5   | 0.06872 | 1.548 | 0.042 | Biological | GO:0042303 molting cycle                                                                 | 0.06872 | 0.25078 | 0 | 0 | 5  | 120 |
| GO:0042633 hair cycle                                                                    | 5   | 0.06872 | 1.548 | 0.042 | Biological | GO:0042633 hair cycle                                                                    | 0.06872 | 0.25078 | 0 | 0 | 5  | 120 |
| GO:0003197 endocardial cushion development                                               | 3   | 0.06902 | 0.929 | 0.058 | Biological | GO:0003197 endocardial cushion development                                               | 0.06902 | 0.25078 | 0 | 0 | 3  | 52  |
| GO:0060688 regulation of morphogenesis of a branching structure                          | 3   | 0.06902 | 0.929 | 0.058 | Biological | GO:0060688 regulation of morphogenesis of a branching structure                          | 0.06902 | 0.25078 | 0 | 0 | 3  | 52  |
| GO:0071622 regulation of granulocyte chemotaxis                                          | 3   | 0.06902 | 0.929 | 0.058 | Biological | GO:0071622 regulation of granulocyte chemotaxis                                          | 0.06902 | 0.25078 | 0 | 0 | 3  | 52  |
| GO:0061136 regulation of proteasomal protein catabolic process                           | 7   | 0.06964 | 2.167 | 0.036 | Biological | GO:0061136 regulation of proteasomal protein catabolic process                           | 0.06964 | 0.25078 | 0 | 0 | 7  | 197 |
| GO:0032637 interleukin-8 production                                                      | 4   | 0.06979 | 1.238 | 0.047 | Biological | GO:0032637 interleukin-8 production                                                      | 0.06979 | 0.25078 | 0 | 0 | 4  | 85  |
| GO:0032677 regulation of interleukin-8 production                                        | 4   | 0.06979 | 1.238 | 0.047 | Biological | GO:0032677 regulation of interleukin-8 production                                        | 0.06979 | 0.25078 | 0 | 0 | 4  | 85  |
| GO:0008324 cation transmembrane transporter activity                                     | 18  | 0.06992 | 5.263 | 0.027 | Molecular  | GO:0008324 cation transmembrane transporter activity                                     | 0.06992 | 0.25163 | 0 | 0 | 18 | 664 |
| GO:0005588 collagen type V trimer                                                        | 1   | 0.07018 | 0.297 | 0.25  | Cellular   | GO:0005588 collagen type V trimer                                                        | 0.07018 | 0.24865 | 0 | 0 | 1  | 4   |
| GO:0005853 eukaryotic translation elongation factor 1 complex                            | 1   | 0.07018 | 0.297 | 0.25  | Cellular   | GO:0005853 eukaryotic translation elongation factor 1 complex                            | 0.07018 | 0.24865 | 0 | 0 | 1  | 4   |
| GO:0016013 synaptobin complex                                                            | 1   | 0.07018 | 0.297 | 0.25  | Cellular   | GO:0016013 synaptobin complex                                                            | 0.07018 | 0.24865 | 0 | 0 | 1  | 4   |
| GO:0030478 actin cap                                                                     | 1   | 0.07018 | 0.297 | 0.25  | Cellular   | GO:0030478 actin cap                                                                     | 0.07018 | 0.24865 | 0 | 0 | 1  | 4   |
| GO:0033269 intermedial region of axon                                                    | 1   | 0.07018 | 0.297 | 0.25  | Cellular   | GO:0033269 intermedial region of axon                                                    | 0.07018 | 0.24865 | 0 | 0 | 1  | 4   |
| GO:0034363 intermediate-density lipoprotein particle                                     | 1   | 0.07018 | 0.297 | 0.25  | Cellular   | GO:0034363 intermediate-density lipoprotein particle                                     | 0.07018 | 0.24865 | 0 | 0 | 1  | 4   |
| GO:0042567 insulin-like growth factor ternary complex                                    | 1   | 0.07018 | 0.297 | 0.25  | Cellular   | GO:0042567 insulin-like growth factor ternary complex                                    | 0.07018 | 0.24865 | 0 | 0 | 1  | 4   |
| GO:0071664 catenin-TCTFL2 complex                                                        | 1   | 0.07018 | 0.297 | 0.25  | Cellular   | GO:0071664 catenin-TCTFL2 complex                                                        | 0.07018 | 0.24865 | 0 | 0 | 1  | 4   |
| GO:0089893 symmetric, GABA-ergic, inhibitory synapse                                     | 1   | 0.07018 | 0.297 | 0.25  | Cellular   | GO:0089893 symmetric, GABA-ergic, inhibitory synapse                                     | 0.07018 | 0.24865 | 0 | 0 | 1  | 4   |
| GO:0099160 postsynaptic intermediate filament cytoskeleton                               | 1   | 0.07018 | 0.297 | 0.25  | Cellular   | GO:0099160 postsynaptic intermediate filament cytoskeleton                               | 0.07018 | 0.24865 | 0 | 0 | 1  | 4   |
| GO:0007097 nuclear migration                                                             | 2   | 0.07029 | 0.619 | 0.083 | Biological | GO:0007097 nuclear migration                                                             | 0.07029 | 0.25078 | 0 | 0 | 2  | 24  |
| GO:0010884 positive regulation of lipid storage                                          | 2   | 0.07029 | 0.619 | 0.083 | Biological | GO:0010884 positive regulation of lipid storage                                          | 0.07029 | 0.25078 | 0 | 0 | 2  | 24  |
| GO:0021871 forebrain regionalization                                                     | 2   | 0.07029 | 0.619 | 0.083 | Biological | GO:0021871 forebrain regionalization                                                     | 0.07029 | 0.25078 | 0 | 0 | 2  | 24  |
| GO:0032528 microvillus organization                                                      | 2   | 0.07029 | 0.619 | 0.083 | Biological | GO:0032528 microvillus organization                                                      | 0.07029 | 0.25078 | 0 | 0 | 2  | 24  |
| GO:0042430 indole-containing compound metabolic process                                  | 2   | 0.07029 | 0.619 | 0.083 | Biological | GO:0042430 indole-containing compound metabolic process                                  | 0.07029 | 0.25078 | 0 | 0 | 2  | 24  |
| GO:0048745 smooth muscle tissue development                                              | 2   | 0.07029 | 0.619 | 0.083 | Biological | GO:0048745 smooth muscle tissue development                                              | 0.07029 | 0.25078 | 0 | 0 | 2  | 24  |
| GO:0050857 positive regulation of antigen receptor-mediated signaling pathway            | 2   | 0.07029 | 0.619 | 0.083 | Biological | GO:0050857 positive regulation of antigen receptor-mediated signaling pathway            | 0.07029 | 0.25078 | 0 | 0 | 2  | 24  |
| GO:0006005 uterine development                                                           | 2   | 0.07029 | 0.619 | 0.083 | Biological | GO:0006005 uterine development                                                           | 0.07029 | 0.25078 | 0 | 0 | 2  | 24  |
| GO:0061484 hematopoietic stem cell homeostasis                                           | 2   | 0.07029 | 0.619 | 0.083 | Biological | GO:0061484 hematopoietic stem cell homeostasis                                           | 0.07029 | 0.25078 | 0 | 0 | 2  | 24  |
| GO:0072170 metanephric tubule development                                                | 2   | 0.07029 | 0.619 | 0.083 | Biological | GO:0072170 metanephric tubule development                                                | 0.07029 | 0.25078 | 0 | 0 | 2  | 24  |
| GO:0072243 metanephric nephron epithelium development                                    | 2   | 0.07029 | 0.619 | 0.083 | Biological | GO:0072243 metanephric nephron epithelium development                                    | 0.07029 | 0.25078 | 0 | 0 | 2  | 24  |
| GO:0001952 regulation of cell-matrix adhesion                                            | 5   | 0.07066 | 1.548 | 0.041 | Biological | GO:0001952 regulation of cell-matrix adhesion                                            | 0.07066 | 0.25078 | 0 | 0 | 5  | 121 |
| GO:0001796 regulation of type II hypersensitivity                                        | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0001796 regulation of type II hypersensitivity                                        | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0002528 regulation of vascular permeability involved in acute inflammation            | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0002528 regulation of vascular permeability involved in acute inflammation            | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0002892 regulation of type II hypersensitivity                                        | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0002892 regulation of type II hypersensitivity                                        | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0003241 growth involved in heart morphogenesis                                        | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0003241 growth involved in heart morphogenesis                                        | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0006556 S-adenosylmethionine biosynthetic process                                     | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0006556 S-adenosylmethionine biosynthetic process                                     | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0007621 negative regulation of female receptivity                                     | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0007621 negative regulation of female receptivity                                     | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0008065 establishment of blood-nerve barrier                                          | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0008065 establishment of blood-nerve barrier                                          | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0009093 cysteine catabolic process                                                    | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0009093 cysteine catabolic process                                                    | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0009794 regulation of mitotic cell cycle, embryonic                                   | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0009794 regulation of mitotic cell cycle, embryonic                                   | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0014005 microglia development                                                         | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0014005 microglia development                                                         | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0014809 regulation of skeletal muscle contraction by regulation of release of calcium | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0014809 regulation of skeletal muscle contraction by regulation of release of calcium | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0014824 vein smooth muscle contraction                                                | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0014824 vein smooth muscle contraction                                                | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0015829 valine transport                                                              | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0015829 valine transport                                                              | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0016095 polyprenol catabolic process                                                  | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0016095 polyprenol catabolic process                                                  | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0018076 N-terminal peptidyl-lysine acetylation                                        | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0018076 N-terminal peptidyl-lysine acetylation                                        | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0019448 L-cysteine catabolic process                                                  | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0019448 L-cysteine catabolic process                                                  | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0019541 propionate metabolic process                                                  | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0019541 propionate metabolic process                                                  | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0019747 regulation of isoprenoid metabolic process                                    | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0019747 regulation of isoprenoid metabolic process                                    | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0021778 oligodendrocyte cell fate specification                                       | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0021778 oligodendrocyte cell fate specification                                       | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0021779 oligodendrocyte cell fate commitment                                          | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0021779 oligodendrocyte cell fate commitment                                          | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0030623 mast cell homeostasis                                                         | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0030623 mast cell homeostasis                                                         | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0033696 positive regulation of luteinizing hormone secretion                          | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0033696 positive regulation of luteinizing hormone secretion                          | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0035583 sequestering of TGFbeta1 in extracellular matrix                              | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0035583 sequestering of TGFbeta1 in extracellular matrix                              | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0035814 negative regulation of renal sodium excretion                                 | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0035814 negative regulation of renal sodium excretion                                 | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0035860 embryonic nail plate morphogenesis                                            | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0035860 embryonic nail plate morphogenesis                                            | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0035910 ascending aorta morphogenesis                                                 | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0035910 ascending aorta morphogenesis                                                 | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0036343 psychomotor behavior                                                          | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0036343 psychomotor behavior                                                          | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0042321 negative regulation of circadian sleep/wake cycle, sleep                      | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0042321 negative regulation of circadian sleep/wake cycle, sleep                      | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0044212 taurine biosynthetic process                                                  | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0044212 taurine biosynthetic process                                                  | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0042637 catagen                                                                       | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0042637 catagen                                                                       | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0045183 clustering of voltage-gated potassium channels                                | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0045183 clustering of voltage-gated potassium channels                                | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0045448 mitotic cell cycle, embryonic                                                 | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0045448 mitotic cell cycle, embryonic                                                 | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0046305 alkanesulfonate biosynthetic process                                          | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0046305 alkanesulfonate biosynthetic process                                          | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0046439 L-cysteine metabolic process                                                  | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0046439 L-cysteine metabolic process                                                  | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0046967 cytosol to endoplasmic reticulum transport                                    | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0046967 cytosol to endoplasmic reticulum transport                                    | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0048808 male genital morphogenesis                                                    | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0048808 male genital morphogenesis                                                    | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0051794 regulation of timing of catagen                                               | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0051794 regulation of timing of catagen                                               | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0051891 positive regulation of cardioblast differentiation                            | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0051891 positive regulation of cardioblast differentiation                            | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0060018 astrocyte fate commitment                                                     | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0060018 astrocyte fate commitment                                                     | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0060298 positive regulation of sarcomere organization                                 | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0060298 positive regulation of sarcomere organization                                 | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0060465 pharynx development                                                           | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0060465 pharynx development                                                           | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0060737 prostate gland morphogenetic growth                                           | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0060737 prostate gland morphogenetic growth                                           | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0060763 mammary duct terminal end bud growth                                          | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0060763 mammary duct terminal end bud growth                                          | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0061055 myotome development                                                           | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0061055 myotome development                                                           | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0061551 trigeminal ganglion development                                               | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0061551 trigeminal ganglion development                                               | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0070394 Harderian gland development                                                   | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0070394 Harderian gland development                                                   | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0070668 positive regulation of mast cell proliferation                                | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0070668 positive regulation of mast cell proliferation                                | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0071205 protein localization to juxtaparanode region of axon                          | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0071205 protein localization to juxtaparanode region of axon                          | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0071603 endothelial cell-cell adhesion                                                | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0071603 endothelial cell-cell adhesion                                                | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0071623 negative regulation of granulocyte chemotaxis                                 | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0071623 negative regulation of granulocyte chemotaxis                                 | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0072011 glomerular endothelium development                                            | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0072011 glomerular endothelium development                                            | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0072093 metanephric renal vesicle formation                                           | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0072093 metanephric renal vesicle formation                                           | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0072095 regulation of branch elongation involved in ureteric bud branching            | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0072095 regulation of branch elongation involved in ureteric bud branching            | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0072106 regulation of ureteric bud formation                                          | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0072106 regulation of ureteric bud formation                                          | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0072107 positive regulation of ureteric bud formation                                 | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0072107 positive regulation of ureteric bud formation                                 | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0072289 metanephric nephron tubule formation                                          | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0072289 metanephric nephron tubule formation                                          | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0072739 response to anisomycin                                                        | 1   | 0.07096 | 0.31  | 0.25  | Biological | GO:0072739 response to anisomycin                                                        | 0.07096 | 0.25078 | 0 | 0 | 1  | 4   |
| GO:0090024 negative regulation of neutrophil chemotaxis                                  | 1</ |         |       |       |            |                                                                                          |         |         |   |   |    |     |

|                                                                                                                   |    |         |        |       |            |                                                                                                                   |         |         |   |   |    |      |
|-------------------------------------------------------------------------------------------------------------------|----|---------|--------|-------|------------|-------------------------------------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0061448 connective tissue development                                                                          | 9  | 0.07294 | 2.786  | 0.032 | Biological | GO:0061448 connective tissue development                                                                          | 0.07294 | 0.25697 | 0 | 0 | 9  | 281  |
| GO:0030509 BMP signaling pathway                                                                                  | 6  | 0.07304 | 1.858  | 0.037 | Biological | GO:0030509 BMP signaling pathway                                                                                  | 0.07304 | 0.25615 | 0 | 0 | 6  | 160  |
| GO:0010817 regulation of hormone levels                                                                           | 15 | 0.07326 | 4.844  | 0.028 | Biological | GO:0010817 regulation of hormone levels                                                                           | 0.07326 | 0.25674 | 0 | 0 | 15 | 543  |
| GO:0015849 organic acid transport                                                                                 | 10 | 0.07361 | 3.096  | 0.031 | Biological | GO:0015849 organic acid transport                                                                                 | 0.07361 | 0.25885 | 0 | 0 | 10 | 324  |
| GO:0051336 regulation of hydrolase activity                                                                       | 25 | 0.07412 | 7.74   | 0.025 | Biological | GO:0051336 regulation of hydrolase activity                                                                       | 0.07412 | 0.25938 | 0 | 0 | 25 | 1009 |
| GO:0016247 channel regulator activity                                                                             | 6  | 0.07416 | 1.754  | 0.038 | Molecular  | GO:0016247 channel regulator activity                                                                             | 0.07416 | 0.25669 | 0 | 0 | 6  | 158  |
| GO:0005125 cytokine activity                                                                                      | 8  | 0.07482 | 2.339  | 0.034 | Molecular  | GO:0005125 cytokine activity                                                                                      | 0.07482 | 0.25816 | 0 | 0 | 8  | 237  |
| GO:0089772 molecular function regulator                                                                           | 47 | 0.07522 | 13.743 | 0.023 | Molecular  | GO:0089772 molecular function regulator                                                                           | 0.07522 | 0.25848 | 0 | 0 | 47 | 2055 |
| GO:0020242 cell migration involved in sprouting angiogenesis                                                      | 3  | 0.07547 | 0.929  | 0.056 | Biological | GO:0020242 cell migration involved in sprouting angiogenesis                                                      | 0.07547 | 0.26152 | 0 | 0 | 3  | 54   |
| GO:0007157 heterophilic cell-cell adhesion via plasma membrane cell adhesion molecule                             | 3  | 0.07547 | 0.929  | 0.056 | Biological | GO:0007157 heterophilic cell-cell adhesion via plasma membrane cell adhesion molecule                             | 0.07547 | 0.26152 | 0 | 0 | 3  | 54   |
| GO:0010718 positive regulation of epithelial to mesenchymal transition                                            | 3  | 0.07547 | 0.929  | 0.056 | Biological | GO:0010718 positive regulation of epithelial to mesenchymal transition                                            | 0.07547 | 0.26152 | 0 | 0 | 3  | 54   |
| GO:0014009 glial cell proliferation                                                                               | 3  | 0.07547 | 0.929  | 0.056 | Biological | GO:0014009 glial cell proliferation                                                                               | 0.07547 | 0.26152 | 0 | 0 | 3  | 54   |
| GO:0099172 presynaptic terminal organization                                                                      | 2  | 0.07551 | 0.619  | 0.08  | Biological | GO:0099172 presynaptic terminal organization                                                                      | 0.07551 | 0.26152 | 0 | 0 | 2  | 25   |
| GO:0001759 organ induction                                                                                        | 2  | 0.07551 | 0.619  | 0.08  | Biological | GO:0001759 organ induction                                                                                        | 0.07551 | 0.26152 | 0 | 0 | 2  | 25   |
| GO:0003071 renal system process involved in regulation of systemic arterial blood pressure                        | 2  | 0.07551 | 0.619  | 0.08  | Biological | GO:0003071 renal system process involved in regulation of systemic arterial blood pressure                        | 0.07551 | 0.26152 | 0 | 0 | 2  | 25   |
| GO:0030318 melanocyte differentiation                                                                             | 2  | 0.07551 | 0.619  | 0.08  | Biological | GO:0030318 melanocyte differentiation                                                                             | 0.07551 | 0.26152 | 0 | 0 | 2  | 25   |
| GO:0035330 regulation of hippo signaling                                                                          | 2  | 0.07551 | 0.619  | 0.08  | Biological | GO:0035330 regulation of hippo signaling                                                                          | 0.07551 | 0.26152 | 0 | 0 | 2  | 25   |
| GO:0046641 positive regulation of alpha-beta T cell proliferation                                                 | 2  | 0.07551 | 0.619  | 0.08  | Biological | GO:0046641 positive regulation of alpha-beta T cell proliferation                                                 | 0.07551 | 0.26152 | 0 | 0 | 2  | 25   |
| GO:0046885 regulation of hormone biosynthetic process                                                             | 2  | 0.07551 | 0.619  | 0.08  | Biological | GO:0046885 regulation of hormone biosynthetic process                                                             | 0.07551 | 0.26152 | 0 | 0 | 2  | 25   |
| GO:0070423 nucleotide-binding oligomerization domain containing signaling pathway                                 | 2  | 0.07551 | 0.619  | 0.08  | Biological | GO:0070423 nucleotide-binding oligomerization domain containing signaling pathway                                 | 0.07551 | 0.26152 | 0 | 0 | 2  | 25   |
| GO:0120255 olefinic compound biosynthetic process                                                                 | 2  | 0.07551 | 0.619  | 0.08  | Biological | GO:0120255 olefinic compound biosynthetic process                                                                 | 0.07551 | 0.26152 | 0 | 0 | 2  | 25   |
| GO:1904752 regulation of vascular associated smooth muscle cell migration                                         | 2  | 0.07551 | 0.619  | 0.08  | Biological | GO:1904752 regulation of vascular associated smooth muscle cell migration                                         | 0.07551 | 0.26152 | 0 | 0 | 2  | 25   |
| GO:200679 positive regulation of transcription regulatory region DNA binding                                      | 2  | 0.07551 | 0.619  | 0.08  | Biological | GO:200679 positive regulation of transcription regulatory region DNA binding                                      | 0.07551 | 0.26152 | 0 | 0 | 2  | 25   |
| GO:0060401 cytosolic calcium ion transport                                                                        | 7  | 0.0757  | 2.167  | 0.035 | Biological | GO:0060401 cytosolic calcium ion transport                                                                        | 0.0757  | 0.26197 | 0 | 0 | 7  | 201  |
| GO:0061572 actin filament bundle organization                                                                     | 6  | 0.07652 | 1.858  | 0.037 | Biological | GO:0061572 actin filament bundle organization                                                                     | 0.07652 | 0.26464 | 0 | 0 | 6  | 162  |
| GO:0010927 cellular component assembly involved in morphogenesis                                                  | 5  | 0.07669 | 1.548  | 0.04  | Biological | GO:0010927 cellular component assembly involved in morphogenesis                                                  | 0.07669 | 0.26504 | 0 | 0 | 5  | 124  |
| GO:0034230 sterocilin organization                                                                                | 3  | 0.07677 | 0.89   | 0.055 | Cellular   | GO:0034230 sterocilin organization                                                                                | 0.07677 | 0.27019 | 0 | 0 | 3  | 55   |
| GO:0030036 actin cytoskeleton organization                                                                        | 19 | 0.07719 | 5.882  | 0.028 | Biological | GO:0030036 actin cytoskeleton organization                                                                        | 0.07719 | 0.27032 | 0 | 0 | 19 | 731  |
| GO:0001091 RNA polymerase II general transcription initiation factor binding                                      | 2  | 0.07771 | 0.585  | 0.08  | Molecular  | GO:0001091 RNA polymerase II general transcription initiation factor binding                                      | 0.07771 | 0.26494 | 0 | 0 | 2  | 25   |
| GO:0016701 oxidoreductase activity, acting on single donors with incorporation of inorganic nitrogen into organic | 2  | 0.07771 | 0.585  | 0.08  | Molecular  | GO:0016701 oxidoreductase activity, acting on single donors with incorporation of inorganic nitrogen into organic | 0.07771 | 0.26494 | 0 | 0 | 2  | 25   |
| GO:0010469 regulation of signaling receptor activity                                                              | 6  | 0.0783  | 1.858  | 0.037 | Biological | GO:0010469 regulation of signaling receptor activity                                                              | 0.0783  | 0.27022 | 0 | 0 | 6  | 163  |
| GO:0007566 embryo implantation                                                                                    | 3  | 0.0788  | 0.929  | 0.055 | Biological | GO:0007566 embryo implantation                                                                                    | 0.0788  | 0.27134 | 0 | 0 | 3  | 55   |
| GO:0019833 cAMP-mediated signaling                                                                                | 3  | 0.0788  | 0.929  | 0.055 | Biological | GO:0019833 cAMP-mediated signaling                                                                                | 0.0788  | 0.27134 | 0 | 0 | 3  | 55   |
| GO:0050873 brown fat cell differentiation                                                                         | 3  | 0.0788  | 0.929  | 0.055 | Biological | GO:0050873 brown fat cell differentiation                                                                         | 0.0788  | 0.27134 | 0 | 0 | 3  | 55   |
| GO:0001763 morphogenesis of a branching structure                                                                 | 7  | 0.07884 | 2.167  | 0.034 | Biological | GO:0001763 morphogenesis of a branching structure                                                                 | 0.07884 | 0.27134 | 0 | 0 | 7  | 203  |
| GO:0051050 positive regulation of transport                                                                       | 23 | 0.07894 | 7.121  | 0.025 | Biological | GO:0051050 positive regulation of transport                                                                       | 0.07894 | 0.27149 | 0 | 0 | 23 | 921  |
| GO:0051641 cellular localization                                                                                  | 65 | 0.07961 | 20.124 | 0.022 | Biological | GO:0051641 cellular localization                                                                                  | 0.07961 | 0.27362 | 0 | 0 | 65 | 3016 |
| GO:200243 positive regulation of reproductive process                                                             | 4  | 0.07969 | 1.238  | 0.044 | Biological | GO:200243 positive regulation of reproductive process                                                             | 0.07969 | 0.27362 | 0 | 0 | 4  | 90   |
| GO:0016528 sarcoplasm                                                                                             | 4  | 0.07968 | 1.187  | 0.044 | Cellular   | GO:0016528 sarcoplasm                                                                                             | 0.07968 | 0.2786  | 0 | 0 | 4  | 90   |
| GO:1904951 positive regulation of establishment of protein localization                                           | 10 | 0.07994 | 3.096  | 0.03  | Biological | GO:1904951 positive regulation of establishment of protein localization                                           | 0.07994 | 0.27437 | 0 | 0 | 10 | 329  |
| GO:0006655 sphingolipid metabolic process                                                                         | 6  | 0.08009 | 1.858  | 0.037 | Biological | GO:0006655 sphingolipid metabolic process                                                                         | 0.08009 | 0.27472 | 0 | 0 | 6  | 164  |
| GO:0044089 positive regulation of cellular component biogenesis                                                   | 15 | 0.08059 | 4.844  | 0.027 | Biological | GO:0044089 positive regulation of cellular component biogenesis                                                   | 0.08059 | 0.27505 | 0 | 0 | 15 | 551  |
| GO:0010815 positive regulation of cholesterol efflux                                                              | 2  | 0.08085 | 0.619  | 0.077 | Biological | GO:0010815 positive regulation of cholesterol efflux                                                              | 0.08085 | 0.27505 | 0 | 0 | 2  | 26   |
| GO:0033622 integrin activation                                                                                    | 2  | 0.08085 | 0.619  | 0.077 | Biological | GO:0033622 integrin activation                                                                                    | 0.08085 | 0.27505 | 0 | 0 | 2  | 26   |
| GO:0035872 nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway                   | 2  | 0.08085 | 0.619  | 0.077 | Biological | GO:0035872 nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway                   | 0.08085 | 0.27505 | 0 | 0 | 2  | 26   |
| GO:0042659 regulation of cell fate specification                                                                  | 2  | 0.08085 | 0.619  | 0.077 | Biological | GO:0042659 regulation of cell fate specification                                                                  | 0.08085 | 0.27505 | 0 | 0 | 2  | 26   |
| GO:0048596 embryonic camera-type eye morphogenesis                                                                | 2  | 0.08085 | 0.619  | 0.077 | Biological | GO:0048596 embryonic camera-type eye morphogenesis                                                                | 0.08085 | 0.27505 | 0 | 0 | 2  | 26   |
| GO:0050897 negative regulation of defense response to virus                                                       | 2  | 0.08085 | 0.619  | 0.077 | Biological | GO:0050897 negative regulation of defense response to virus                                                       | 0.08085 | 0.27505 | 0 | 0 | 2  | 26   |
| GO:0060343 trabecula formation                                                                                    | 2  | 0.08085 | 0.619  | 0.077 | Biological | GO:0060343 trabecula formation                                                                                    | 0.08085 | 0.27505 | 0 | 0 | 2  | 26   |
| GO:0072010 glomerular epithelium development                                                                      | 2  | 0.08085 | 0.619  | 0.077 | Biological | GO:0072010 glomerular epithelium development                                                                      | 0.08085 | 0.27505 | 0 | 0 | 2  | 26   |
| GO:1901623 regulation of lymphocyte chemotaxis                                                                    | 2  | 0.08085 | 0.619  | 0.077 | Biological | GO:1901623 regulation of lymphocyte chemotaxis                                                                    | 0.08085 | 0.27505 | 0 | 0 | 2  | 26   |
| GO:1903901 negative regulation of viral life cycle                                                                | 2  | 0.08085 | 0.619  | 0.077 | Biological | GO:1903901 negative regulation of viral life cycle                                                                | 0.08085 | 0.27505 | 0 | 0 | 2  | 26   |
| GO:1901206 negative regulation of vascular associated smooth muscle cell proliferation                            | 2  | 0.08085 | 0.619  | 0.077 | Biological | GO:1901206 negative regulation of vascular associated smooth muscle cell proliferation                            | 0.08085 | 0.27505 | 0 | 0 | 2  | 26   |
| GO:0038024 cargo receptor activity                                                                                | 4  | 0.08086 | 1.17   | 0.045 | Molecular  | GO:0038024 cargo receptor activity                                                                                | 0.08086 | 0.27043 | 0 | 0 | 4  | 88   |
| GO:0071496 cellular response to external stimulus                                                                 | 10 | 0.08118 | 3.096  | 0.03  | Biological | GO:0071496 cellular response to external stimulus                                                                 | 0.08118 | 0.27598 | 0 | 0 | 10 | 330  |
| GO:0030003 cellular cation homeostasis                                                                            | 18 | 0.08176 | 5.573  | 0.026 | Biological | GO:0030003 cellular cation homeostasis                                                                            | 0.08176 | 0.27737 | 0 | 0 | 18 | 690  |
| GO:0050580 protein kinase C binding                                                                               | 3  | 0.08189 | 0.877  | 0.055 | Molecular  | GO:0050580 protein kinase C binding                                                                               | 0.08189 | 0.27043 | 0 | 0 | 3  | 55   |
| GO:0032608 interferon-beta production                                                                             | 3  | 0.08218 | 0.929  | 0.054 | Biological | GO:0032608 interferon-beta production                                                                             | 0.08218 | 0.27737 | 0 | 0 | 3  | 56   |
| GO:0032648 regulation of interferon-beta production                                                               | 3  | 0.08218 | 0.929  | 0.054 | Biological | GO:0032648 regulation of interferon-beta production                                                               | 0.08218 | 0.27737 | 0 | 0 | 3  | 56   |
| GO:0043616 keratinocyte proliferation                                                                             | 3  | 0.08218 | 0.929  | 0.054 | Biological | GO:0043616 keratinocyte proliferation                                                                             | 0.08218 | 0.27737 | 0 | 0 | 3  | 56   |
| GO:0050788 sodium ion homeostasis                                                                                 | 3  | 0.08218 | 0.929  | 0.054 | Biological | GO:0050788 sodium ion homeostasis                                                                                 | 0.08218 | 0.27737 | 0 | 0 | 3  | 56   |
| GO:1903535 regulation of extracellular matrix organization                                                        | 3  | 0.08218 | 0.929  | 0.054 | Biological | GO:1903535 regulation of extracellular matrix organization                                                        | 0.08218 | 0.27737 | 0 | 0 | 3  | 56   |
| GO:2001719 positive regulation of neural precursor cell proliferation                                             | 4  | 0.08218 | 1.238  | 0.044 | Biological | GO:2001719 positive regulation of neural precursor cell proliferation                                             | 0.08218 | 0.27737 | 0 | 0 | 4  | 90   |
| GO:0001892 embryonic placenta development                                                                         | 4  | 0.08223 | 1.238  | 0.044 | Biological | GO:0001892 embryonic placenta development                                                                         | 0.08223 | 0.27737 | 0 | 0 | 4  | 90   |
| GO:0043367 CD4-positive, alpha-beta T cell differentiation                                                        | 4  | 0.08223 | 1.238  | 0.044 | Biological | GO:0043367 CD4-positive, alpha-beta T cell differentiation                                                        | 0.08223 | 0.27737 | 0 | 0 | 4  | 90   |
| GO:0106027 neuron protection organization                                                                         | 4  | 0.08223 | 1.238  | 0.044 | Biological | GO:0106027 neuron protection organization                                                                         | 0.08223 | 0.27737 | 0 | 0 | 4  | 90   |
| GO:0004114 3',5'-cyclic-nucleotide phosphodiesterase activity                                                     | 2  | 0.08319 | 0.585  | 0.077 | Molecular  | GO:0004114 3',5'-cyclic-nucleotide phosphodiesterase activity                                                     | 0.08319 | 0.27043 | 0 | 0 | 2  | 26   |
| GO:0004435 phosphatidylcholine phospholipase C activity                                                           | 2  | 0.08319 | 0.585  | 0.077 | Molecular  | GO:0004435 phosphatidylcholine phospholipase C activity                                                           | 0.08319 | 0.27043 | 0 | 0 | 2  | 26   |
| GO:0005164 amino acid:cation symporter activity                                                                   | 2  | 0.08319 | 0.585  | 0.077 | Molecular  | GO:0005164 amino acid:cation symporter activity                                                                   | 0.08319 | 0.27043 | 0 | 0 | 2  | 26   |
| GO:0007249 I-kappaB kinase/NF-kappaB signaling                                                                    | 9  | 0.08343 | 2.786  | 0.031 | Biological | GO:0007249 I-kappaB kinase/NF-kappaB signaling                                                                    | 0.08343 | 0.27737 | 0 | 0 | 9  | 289  |
| GO:0016459 myosin complex                                                                                         | 3  | 0.08345 | 0.89   | 0.053 | Cellular   | GO:0016459 myosin complex                                                                                         | 0.08345 | 0.28363 | 0 | 0 | 3  | 57   |
| GO:0007204 positive regulation of cytosolic calcium ion concentration                                             | 10 | 0.0837  | 3.096  | 0.03  | Biological | GO:0007204 positive regulation of cytosolic calcium ion concentration                                             | 0.0837  | 0.27737 | 0 | 0 | 10 | 332  |
| GO:0005059 calcium ion binding                                                                                    | 19 | 0.08418 | 5.556  | 0.026 | Molecular  | GO:0005059 calcium ion binding                                                                                    | 0.08418 | 0.27737 | 0 | 0 | 19 | 727  |
| GO:0005923 bicellular tight junction                                                                              | 5  | 0.08422 | 1.444  | 0.039 | Cellular   | GO:0005923 bicellular tight junction                                                                              | 0.08422 | 0.28363 | 0 | 0 | 5  | 129  |
| GO:0072657 protein localization to membrane                                                                       | 16 | 0.08469 | 4.954  | 0.027 | Biological | GO:0072657 protein localization to membrane                                                                       | 0.08469 | 0.27737 | 0 | 0 | 16 | 601  |
| GO:0006493 protein O-linked glycosylation                                                                         | 4  | 0.08484 | 1.238  | 0.044 | Biological | GO:0006493 protein O-linked glycosylation                                                                         | 0.08484 | 0.27737 | 0 | 0 | 4  | 91   |
| GO:0051262 protein tetramerization                                                                                | 4  | 0.08484 | 1.238  | 0.044 | Biological | GO:0051262 protein tetramerization                                                                                | 0.08484 | 0.27737 | 0 | 0 | 4  | 91   |
| GO:0045926 negative regulation of growth                                                                          | 8  | 0.08497 | 2.471  | 0.037 | Biological | GO:0045926 negative regulation of growth                                                                          | 0.08497 | 0.27737 | 0 | 0 | 8  | 244  |
| GO:0005539 glycosaminoglycan binding                                                                              | 8  | 0.08514 | 2.339  | 0.033 | Molecular  | GO:0005539 glycosaminoglycan binding                                                                              | 0.08514 | 0.27043 | 0 | 0 | 8  | 244  |
| GO:0035601 protein deacylation                                                                                    | 5  | 0.08514 | 1.548  | 0.039 | Biological | GO:0035601 protein deacylation                                                                                    | 0.08514 | 0.27737 | 0 | 0 | 5  | 128  |
| GO:0043687 post-translational protein modification                                                                | 3  | 0.08563 | 0.929  | 0.053 | Biological | GO:0043687 post-translational protein modification                                                                | 0.08563 | 0.27737 | 0 | 0 | 3  | 57   |
| GO:0048168 regulation of neuronal signaling plasticity                                                            | 3  | 0.08563 | 0.929  | 0.053 | Biological | GO:0048168 regulation of neuronal signaling plasticity                                                            | 0.08563 | 0.27737 | 0 | 0 | 3  | 57   |
| GO:0031324 negative regulation of cellular metabolic process                                                      | 55 | 0.08618 | 17.028 | 0.021 | Biological | GO:0031324 negative regulation of cellular metabolic process                                                      | 0.08618 | 0.27737 | 0 | 0 | 55 | 257  |
| GO:0001702 gastrulation with mouth forming second                                                                 | 2  | 0.0863  | 0.619  | 0.074 | Biological | GO:0001702 gastrulation with mouth forming second                                                                 | 0.0863  | 0.27737 | 0 | 0 | 2  | 27   |
| GO:0019098 reproductive behavior                                                                                  | 2  | 0.0863  | 0.619  | 0.074 | Biological | GO:0019098 reproductive behavior                                                                                  | 0.0863  | 0.27737 | 0 | 0 | 2  | 27   |
| GO:0034643 establishment of mitochondrion localization, microtubule-mediated                                      | 2  | 0.0863  | 0.619  | 0.074 | Biological | GO:0034643 establishment of mitochondrion localization, microtubule-mediated                                      | 0.0863  | 0.27737 | 0 | 0 | 2  | 27   |
| GO:0047497 mitochondrion transport along microtubule                                                              | 2  | 0.0863  | 0.619  | 0.074 | Biological | GO:0047497 mitochondrion transport along microtubule                                                              | 0.0863  | 0.27737 | 0 | 0 | 2  | 27   |
| GO:0051291 protein heterodimerization                                                                             | 2  | 0.0863  | 0.619  | 0.074 | Biological | GO:0051291 protein heterodimerization                                                                             | 0.0863  | 0.27737 | 0 | 0 | 2  | 27   |
| GO:0006051 apoptotic process involved in morphogenesis                                                            | 2  | 0.0863  | 0.619  | 0.074 | Biological | GO:0006051 apoptotic process involved in morphogenesis                                                            | 0.      |         |   |   |    |      |

|                                                                                              |    |         |        |       |            |                                                                                              |         |         |   |   |    |      |
|----------------------------------------------------------------------------------------------|----|---------|--------|-------|------------|----------------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0070257 positive regulation of mucus secretion                                            | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0070257 positive regulation of mucus secretion                                            | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0070777 D-aspartate transport                                                             | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0070777 D-aspartate transport                                                             | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0070779 D-aspartate import across plasma membrane                                         | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0070779 D-aspartate import across plasma membrane                                         | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0071242 cellular response to ammonium ion                                                 | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0071242 cellular response to ammonium ion                                                 | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0071681 cellular response to indole-3-methanol                                            | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0071681 cellular response to indole-3-methanol                                            | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0072144 clomerenal mesenchymal cell development                                           | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0072144 clomerenal mesenchymal cell development                                           | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0072162 melanephric mesenchymal cell differentiation                                      | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0072162 melanephric mesenchymal cell differentiation                                      | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0072223 melanephric mesenchymal mesangium development                                     | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0072223 melanephric mesenchymal mesangium development                                     | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:008089 regulation of ribosome biogenesis                                                  | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:008089 regulation of ribosome biogenesis                                                  | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0090131 mesenchyme migration                                                              | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0090131 mesenchyme migration                                                              | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0090185 negative regulation of kidney development                                         | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0090185 negative regulation of kidney development                                         | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0090206 negative regulation of cholesterol metabolic process                              | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0090206 negative regulation of cholesterol metabolic process                              | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0094051 glutamate receptor clustering                                                     | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0094051 glutamate receptor clustering                                                     | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0095714 NMDA glutamate receptor clustering                                                | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0095714 NMDA glutamate receptor clustering                                                | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0098596 imitative learning                                                                | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0098596 imitative learning                                                                | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0098713 leucine import across plasma membrane                                             | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0098713 leucine import across plasma membrane                                             | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0098971 anterograde dendritic transport of neurotransmitter receptor complex              | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0098971 anterograde dendritic transport of neurotransmitter receptor complex              | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0106119 negative regulation of steroid biosynthetic process                               | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:0106119 negative regulation of steroid biosynthetic process                               | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1900736 regulation of phospholipase C-activating G protein-coupled receptor               | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1900736 regulation of phospholipase C-activating G protein-coupled receptor               | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1902463 protein localization to cell leading edge                                         | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1902463 protein localization to cell leading edge                                         | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1902623 negative regulation of neutrophil migration                                       | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1902623 negative regulation of neutrophil migration                                       | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1902956 regulation of mitochondrial electron transport, NADH to ubiquinone                | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1902956 regulation of mitochondrial electron transport, NADH to ubiquinone                | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1903801 L-leucine import across plasma membrane                                           | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1903801 L-leucine import across plasma membrane                                           | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1904351 negative regulation of protein catabolic process in the vacuole                   | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1904351 negative regulation of protein catabolic process in the vacuole                   | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1904447 folate import across plasma membrane                                              | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1904447 folate import across plasma membrane                                              | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1904557 L-alanine transmembrane transport                                                 | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1904557 L-alanine transmembrane transport                                                 | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1904906 positive regulation of endothelial cell-matrix adhesion via fibronectin           | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1904906 positive regulation of endothelial cell-matrix adhesion via fibronectin           | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1905007 positive regulation of mesenchymal transition involved in                         | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1905007 positive regulation of mesenchymal transition involved in                         | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1905166 negative regulation of lysosomal protein catabolic process                        | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1905166 negative regulation of lysosomal protein catabolic process                        | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1905636 positive regulation of RNA polymerase II regulatory region sequence               | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1905636 positive regulation of RNA polymerase II regulatory region sequence               | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1905651 regulation of artery morphogenesis                                                | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1905651 regulation of artery morphogenesis                                                | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1905653 positive regulation of artery morphogenesis                                       | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1905653 positive regulation of artery morphogenesis                                       | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1905749 regulation of endosome to plasma membrane protein transport                       | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1905749 regulation of endosome to plasma membrane protein transport                       | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:1905908 positive regulation of amyloid fibril formation                                   | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:1905908 positive regulation of amyloid fibril formation                                   | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:2000467 positive regulation of glycogen (starch) synthase activity                        | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:2000467 positive regulation of glycogen (starch) synthase activity                        | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:2000491 positive regulation of hepatic stellate cell activation                           | 1  | 0.0879  | 0.31   | 0.2   | Biological | GO:2000491 positive regulation of hepatic stellate cell activation                           | 0.0879  | 0.27737 | 0 | 0 | 1  | 5    |
| GO:0050877 nervous system process                                                            | 35 | 0.0879  | 10.836 | 0.023 | Biological | GO:0050877 nervous system process                                                            | 0.0879  | 0.27737 | 0 | 0 | 35 | 1517 |
| GO:0050878 nervous system process                                                            | 35 | 0.0879  | 10.836 | 0.023 | Biological | GO:0050878 nervous system process                                                            | 0.0879  | 0.27737 | 0 | 0 | 35 | 1517 |
| GO:0001961 positive regulation of cytokine-mediated signaling pathway                        | 3  | 0.0814  | 0.929  | 0.052 | Biological | GO:0001961 positive regulation of cytokine-mediated signaling pathway                        | 0.0814  | 0.2807  | 0 | 0 | 3  | 58   |
| GO:0030514 negative regulation of BMP signaling pathway                                      | 3  | 0.0814  | 0.929  | 0.052 | Biological | GO:0030514 negative regulation of BMP signaling pathway                                      | 0.0814  | 0.2807  | 0 | 0 | 3  | 58   |
| GO:0043113 receptor clustering                                                               | 3  | 0.0814  | 0.929  | 0.052 | Biological | GO:0043113 receptor clustering                                                               | 0.0814  | 0.2807  | 0 | 0 | 3  | 58   |
| GO:0010893 TFIIIB-class transcription factor binding                                         | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0010893 TFIIIB-class transcription factor binding                                         | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:001609 G protein-coupled adenosine receptor activity                                      | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:001609 G protein-coupled adenosine receptor activity                                      | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0004468 tyrosine N-acetyltransferase activity, acting on acetyl phosphate as donor        | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0004468 tyrosine N-acetyltransferase activity, acting on acetyl phosphate as donor        | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0004630 phospholipase D activity                                                          | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0004630 phospholipase D activity                                                          | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0004957 prostaglandin E receptor activity                                                 | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0004957 prostaglandin E receptor activity                                                 | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0005030 neurotrophin receptor activity                                                    | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0005030 neurotrophin receptor activity                                                    | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0005163 nerve growth factor receptor binding                                              | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0005163 nerve growth factor receptor binding                                              | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0005298 prolinsodium symporter activity                                                   | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0005298 prolinsodium symporter activity                                                   | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0005314 high-affinity glutamate transmembrane transporter activity                        | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0005314 high-affinity glutamate transmembrane transporter activity                        | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0005497 androgen binding                                                                  | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0005497 androgen binding                                                                  | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:000889 glycerophosphodiester phosphodiesterase activity                                   | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:000889 glycerophosphodiester phosphodiesterase activity                                   | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:001543 ABC-type peptide transporter activity                                              | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:001543 ABC-type peptide transporter activity                                              | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0015440 ABC-type peptide transporter activity                                             | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0015440 ABC-type peptide transporter activity                                             | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0015501 glutamate sodium symporter activity                                               | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0015501 glutamate sodium symporter activity                                               | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0016723 oxidoreductase activity, acting on metal ions, NAD or NADP as acceptor            | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0016723 oxidoreductase activity, acting on metal ions, NAD or NADP as acceptor            | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0019834 phospholipase A2 inhibitor activity                                               | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0019834 phospholipase A2 inhibitor activity                                               | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:002849 glutamate calcium channel activity                                                 | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:002849 glutamate calcium channel activity                                                 | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0031779 melanocortin receptor binding                                                     | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0031779 melanocortin receptor binding                                                     | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0038132 neuregulin binding                                                                | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0038132 neuregulin binding                                                                | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0080603 cell adhesive protein binding involved in bundle of His cell-Purkinje myelination | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0080603 cell adhesive protein binding involved in bundle of His cell-Purkinje myelination | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0097109 neuregulin family protein binding                                                 | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:0097109 neuregulin family protein binding                                                 | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:014044 cytoskeleton-nuclear membrane anchor activity                                      | 1  | 0.0831  | 0.292  | 0.2   | Molecular  | GO:014044 cytoskeleton-nuclear membrane anchor activity                                      | 0.0831  | 0.27043 | 0 | 0 | 1  | 5    |
| GO:0048706 embryonic skeletal system development                                             | 5  | 0.0854  | 1.548  | 0.038 | Biological | GO:0048706 embryonic skeletal system development                                             | 0.0854  | 0.28146 | 0 | 0 | 5  | 130  |
| GO:1900266 neutrophil migration                                                              | 5  | 0.0854  | 1.548  | 0.038 | Biological | GO:1900266 neutrophil migration                                                              | 0.0854  | 0.28146 | 0 | 0 | 5  | 130  |
| GO:1903362 regulation of cellular protein catabolic process                                  | 8  | 0.0855  | 2.477  | 0.032 | Biological | GO:1903362 regulation of cellular protein catabolic process                                  | 0.0855  | 0.28146 | 0 | 0 | 8  | 251  |
| GO:0009553 dorsal/ventral pattern formation                                                  | 4  | 0.0919  | 1.238  | 0.043 | Biological | GO:0009553 dorsal/ventral pattern formation                                                  | 0.0919  | 0.28309 | 0 | 0 | 4  | 93   |
| GO:0034644 cellular response to UV                                                           | 4  | 0.0919  | 1.238  | 0.043 | Biological | GO:0034644 cellular response to UV                                                           | 0.0919  | 0.28309 | 0 | 0 | 4  | 93   |
| GO:0060284 regulation of cell development                                                    | 14 | 0.0918  | 4.334  | 0.027 | Biological | GO:0060284 regulation of cell development                                                    | 0.0918  | 0.28571 | 0 | 0 | 14 | 516  |
| GO:0003012 muscle system process                                                             | 12 | 0.09123 | 3.715  | 0.028 | Biological | GO:0003012 muscle system process                                                             | 0.09123 | 0.28601 | 0 | 0 | 12 | 426  |
| GO:0019904 protein domain specific binding                                                   | 18 | 0.09124 | 5.263  | 0.026 | Molecular  | GO:0019904 protein domain specific binding                                                   | 0.09124 | 0.27531 | 0 | 0 | 18 | 689  |
| GO:0007156 homophilic cell adhesion via plasma membrane adhesion molecules                   | 6  | 0.09137 | 1.858  | 0.035 | Biological | GO:0007156 homophilic cell adhesion via plasma membrane adhesion molecules                   | 0.09137 | 0.28625 | 0 | 0 | 6  | 170  |
| GO:0035770 late endosome                                                                     | 9  | 0.09148 | 2.871  | 0.031 | Biological | GO:0035770 late endosome                                                                     | 0.09148 | 0.28439 | 0 | 0 | 9  | 298  |
| GO:0010996 response to auditory stimulus                                                     | 2  | 0.09186 | 0.619  | 0.071 | Biological | GO:0010996 response to auditory stimulus                                                     | 0.09186 | 0.28637 | 0 | 0 | 2  | 28   |
| GO:0014072 response to isquinoline alkaloid                                                  | 2  | 0.09186 | 0.619  | 0.071 | Biological | GO:0014072 response to isquinoline alkaloid                                                  | 0.09186 | 0.28637 | 0 | 0 | 2  | 28   |
| GO:0031954 positive regulation of protein autophosphorylation                                | 2  | 0.09186 | 0.619  | 0.071 | Biological | GO:0031954 positive regulation of protein autophosphorylation                                | 0.09186 | 0.28637 | 0 | 0 | 2  | 28   |
| GO:0043278 response to morphine                                                              | 2  | 0.09186 | 0.619  | 0.071 | Biological | GO:0043278 response to morphine                                                              | 0.09186 | 0.28637 | 0 | 0 | 2  | 28   |
| GO:0043331 cell adhesion mediated by cadherin                                                | 2  | 0.09186 | 0.619  | 0.071 | Biological | GO:0043331 cell adhesion mediated by cadherin                                                | 0.09186 | 0.28637 | 0 | 0 | 2  | 28   |
| GO:0071577 zinc ion transmembrane transport                                                  | 2  | 0.09186 | 0.619  | 0.071 | Biological | GO:0071577 zinc ion transmembrane transport                                                  | 0.09186 | 0.28637 | 0 | 0 | 2  | 28   |
| GO:0072207 melanephric epithelium development                                                | 2  | 0.09186 | 0.619  | 0.071 | Biological | GO:0072207 melanephric epithelium development                                                | 0.09186 | 0.28637 | 0 | 0 | 2  | 28   |
| GO:0150146 cell junction disassembly                                                         | 2  | 0.09186 | 0.619  | 0.071 | Biological | GO:0150146 cell junction disassembly                                                         | 0.09186 | 0.28637 | 0 | 0 | 2  | 28   |
| GO:008793 presynapse                                                                         | 15 | 0.09223 | 4.451  | 0.026 | Cellular   | GO:008793 presynapse                                                                         | 0.09223 | 0.28439 | 0 | 0 | 15 | 569  |
| GO:0005687 transcription regulator complex                                                   | 14 | 0.09244 | 1.154  | 0.027 | Cellular   | GO:0005687 transcription regulator complex                                                   | 0.09244 | 0.28309 | 0 | 0 | 14 | 523  |
| GO:0097305 response to alcohol                                                               | 8  | 0.09269 | 2.477  | 0.032 | Biological | GO:0097305 response to alcohol                                                               | 0.09269 | 0.28812 | 0 | 0 | 8  | 253  |
| GO:0008347 glial cell migration                                                              | 3  | 0.09271 | 0.929  | 0.051 | Biological | GO:0008347 glial cell migration                                                              | 0.09271 | 0.28812 | 0 | 0 | 3  | 59   |
| GO:0048599 oocyte development                                                                | 3  | 0.09271 | 0.929  | 0.051 | Biological | GO:0048599 oocyte development                                                                | 0.09271 | 0.28812 | 0 | 0 | 3  | 59   |
| GO:0051289 protein homeostasis                                                               | 3  | 0.09271 | 0.929  | 0.051 | Biological | GO:0051289 protein homeostasis                                                               | 0.09271 | 0.28812 | 0 | 0 | 3  | 59   |
| GO:005008 cardiac muscle tissue morphogenesis                                                | 13 | 0.09338 | 3.858  | 0.027 | Cellular   | GO:005008 cardiac muscle tissue morphogenesis                                                | 0.09338 | 0.28812 | 0 | 0 | 13 | 478  |
| GO:0005874 microtubule                                                                       | 16 | 0.0934  | 4.954  | 0.028 | Biological | GO:0005874 microtubule                                                                       | 0.0934  | 0.29008 | 0 | 0 | 16 | 610  |
| GO:0002521 leukocyte differentiation                                                         | 5  | 0.09406 | 1.548  | 0.038 | Biological | GO:0002521 leukocyte differentiation                                                         | 0.09406 | 0.29176 | 0 | 0 | 5  | 132  |
| GO:0046                                                                                      |    |         |        |       |            |                                                                                              |         |         |   |   |    |      |

|                                                                                           |    |         |        |       |                |                                                                                           |         |         |   |   |    |      |
|-------------------------------------------------------------------------------------------|----|---------|--------|-------|----------------|-------------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0031229 intrinsic component of nuclear inner membrane                                  | 1  | 0.10341 | 0.297  | 0.167 | Cellular C     | GO:0031229 intrinsic component of nuclear inner membrane                                  | 0.10341 | 0.30174 | 0 | 0 | 1  | 6    |
| GO:0031285 CD95 death-inducing signaling complex                                          | 1  | 0.10341 | 0.297  | 0.167 | Cellular C     | GO:0031285 CD95 death-inducing signaling complex                                          | 0.10341 | 0.30174 | 0 | 0 | 1  | 6    |
| GO:0043032 dentate gyrus mossy fiber                                                      | 1  | 0.10341 | 0.297  | 0.167 | Cellular C     | GO:0043032 dentate gyrus mossy fiber                                                      | 0.10341 | 0.30174 | 0 | 0 | 1  | 6    |
| GO:0057342 liposome                                                                       | 1  | 0.10341 | 0.297  | 0.167 | Cellular C     | GO:0057342 liposome                                                                       | 0.10341 | 0.30174 | 0 | 0 | 1  | 6    |
| GO:0097487 multivesicular body, internal vesicle                                          | 1  | 0.10341 | 0.297  | 0.167 | Cellular C     | GO:0097487 multivesicular body, internal vesicle                                          | 0.10341 | 0.30174 | 0 | 0 | 1  | 6    |
| GO:0061659 ubiquitin-like protein ligase activity                                         | 10 | 0.10373 | 2.924  | 0.029 | Molecular C    | GO:0061659 ubiquitin-like protein ligase activity                                         | 0.10373 | 0.29666 | 0 | 0 | 10 | 341  |
| GO:0006998 nuclear envelope organization                                                  | 3  | 0.10377 | 0.929  | 0.048 | Biological C   | GO:0006998 nuclear envelope organization                                                  | 0.10377 | 0.29698 | 0 | 0 | 3  | 62   |
| GO:0016836 hydro-lyase activity                                                           | 3  | 0.10381 | 0.977  | 0.049 | Molecular C    | GO:0016836 hydro-lyase activity                                                           | 0.10381 | 0.29698 | 0 | 0 | 3  | 61   |
| GO:0031982 vesicle                                                                        | 82 | 0.10414 | 24.332 | 0.021 | Cellular C     | GO:0031982 vesicle                                                                        | 0.10414 | 0.30174 | 0 | 0 | 82 | 3998 |
| GO:0010717 regulation of epithelial to mesenchymal transition                             | 4  | 0.10423 | 1.238  | 0.041 | Biological C   | GO:0010717 regulation of epithelial to mesenchymal transition                             | 0.10423 | 0.29898 | 0 | 0 | 4  | 98   |
| GO:0032755 positive regulation of interleukin-6 production                                | 4  | 0.10423 | 1.238  | 0.041 | Biological C   | GO:0032755 positive regulation of interleukin-6 production                                | 0.10423 | 0.29898 | 0 | 0 | 4  | 98   |
| GO:0001794 type Ila hypersensitivity                                                      | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0001794 type Ila hypersensitivity                                                      | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0019599 renal response to blood flow involved in circulatory renin-angiotensin         | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0019599 renal response to blood flow involved in circulatory renin-angiotensin         | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0002001 renin secretion into blood stream                                              | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0002001 renin secretion into blood stream                                              | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0002155 regulation of thyroid hormone mediated signaling pathway                       | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0002155 regulation of thyroid hormone mediated signaling pathway                       | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0002248 connective tissue replacement involved in inflammatory response                | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0002248 connective tissue replacement involved in inflammatory response                | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0002372 myeloid dendritic cell cytokine production                                     | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0002372 myeloid dendritic cell cytokine production                                     | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0002445 type II hypersensitivity                                                       | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0002445 type II hypersensitivity                                                       | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0002733 regulation of myeloid dendritic cell cytokine production                       | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0002733 regulation of myeloid dendritic cell cytokine production                       | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0002735 positive regulation of myeloid dendritic cell cytokine production              | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0002735 positive regulation of myeloid dendritic cell cytokine production              | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0002855 positive regulation of hypersensitivity                                        | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0002855 positive regulation of hypersensitivity                                        | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0003278 apoptotic process involved in heart morphogenesis                              | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0003278 apoptotic process involved in heart morphogenesis                              | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0003402 planar cell polarity pathway involved in axis elongation                       | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0003402 planar cell polarity pathway involved in axis elongation                       | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0003415 chondrocyte hypertrophy                                                        | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0003415 chondrocyte hypertrophy                                                        | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0006564 L-serine biosynthetic process                                                  | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0006564 L-serine biosynthetic process                                                  | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0006678 glucosylceramide metabolic process                                             | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0006678 glucosylceramide metabolic process                                             | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0006852 regulation of synaptic assembly at neuromuscular junction                      | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0006852 regulation of synaptic assembly at neuromuscular junction                      | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0010040 response to hypoxia                                                            | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0010040 response to hypoxia                                                            | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0010688 ectodermal cell differentiation                                                | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0010688 ectodermal cell differentiation                                                | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0015677 copper ion import                                                              | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0015677 copper ion import                                                              | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0015827 tryptophan transport                                                           | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0015827 tryptophan transport                                                           | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0021902 commitment of neuronal cell to specific neuron type in forebrain               | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0021902 commitment of neuronal cell to specific neuron type in forebrain               | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0032229 negative regulation of synaptic transmission, GABAergic                        | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0032229 negative regulation of synaptic transmission, GABAergic                        | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0032241 positive regulation of nucleobase-containing compound transport                | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0032241 positive regulation of nucleobase-containing compound transport                | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0032534 regulation of microvillus assembly                                             | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0032534 regulation of microvillus assembly                                             | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0032799 low-density lipoprotein receptor particle metabolic process                    | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0032799 low-density lipoprotein receptor particle metabolic process                    | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0032802 low-density lipoprotein particle receptor catabolic process                    | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0032802 low-density lipoprotein particle receptor catabolic process                    | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0032803 regulation of low-density lipoprotein particle receptor catabolic process      | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0032803 regulation of low-density lipoprotein particle receptor catabolic process      | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0033091 positive regulation of immature T cell proliferation                           | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0033091 positive regulation of immature T cell proliferation                           | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0033092 positive regulation of immature T cell proliferation in thymus                 | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0033092 positive regulation of immature T cell proliferation in thymus                 | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0033684 regulation of luteinizing hormone secretion                                    | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0033684 regulation of luteinizing hormone secretion                                    | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0034382 chylomicron remnant clearance                                                  | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0034382 chylomicron remnant clearance                                                  | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0034417 very-low-density lipoprotein particle clearance                                | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0034417 very-low-density lipoprotein particle clearance                                | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0038138 ERBB4-ERBB4 signaling pathway                                                  | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0038138 ERBB4-ERBB4 signaling pathway                                                  | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0042482 positive regulation of odontogenesis                                           | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0042482 positive regulation of odontogenesis                                           | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0045188 regulation of circadian sleep/wake cycle, non-REM sleep                        | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0045188 regulation of circadian sleep/wake cycle, non-REM sleep                        | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0045627 positive regulation of T-helper 1 cell differentiation                         | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0045627 positive regulation of T-helper 1 cell differentiation                         | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0045834 regulation of melanocyte differentiation                                       | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0045834 regulation of melanocyte differentiation                                       | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0046532 regulation of photoreceptor cell differentiation                               | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0046532 regulation of photoreceptor cell differentiation                               | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0046533 negative regulation of photoreceptor cell differentiation                      | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0046533 negative regulation of photoreceptor cell differentiation                      | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0046880 regulation of follicle-stimulating hormone secretion                           | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0046880 regulation of follicle-stimulating hormone secretion                           | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0046881 positive regulation of follicle-stimulating hormone secretion                  | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0046881 positive regulation of follicle-stimulating hormone secretion                  | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0046825 myoblast cell fate specification                                               | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0046825 myoblast cell fate specification                                               | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0048666 stem cell fate specification                                                   | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0048666 stem cell fate specification                                                   | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0051105 regulation of DNA ligation                                                     | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0051105 regulation of DNA ligation                                                     | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0051725 protein de-ADP-ribosylation                                                    | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0051725 protein de-ADP-ribosylation                                                    | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0060359 response to ammonium ion                                                       | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0060359 response to ammonium ion                                                       | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0060626 prostate gland morphogenesis                                                   | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0060626 prostate gland morphogenesis                                                   | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0060657 prostate epithelial cell arborization involved in prostate gland morphogenesis | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0060657 prostate epithelial cell arborization involved in prostate gland morphogenesis | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0060685 regulation of prostatic bud formation                                          | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0060685 regulation of prostatic bud formation                                          | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0060718 chorionic trophoblast cell differentiation                                     | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0060718 chorionic trophoblast cell differentiation                                     | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0060789 hair follicle placode formation                                                | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0060789 hair follicle placode formation                                                | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0061028 cardiac muscle tissue regeneration                                             | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0061028 cardiac muscle tissue regeneration                                             | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0061046 regulation of branching involved in lung morphogenesis                         | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0061046 regulation of branching involved in lung morphogenesis                         | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0061196 fungiform papilla development                                                  | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0061196 fungiform papilla development                                                  | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0070427 nucleotide-binding oligomerization domain containing 1 signaling pathway       | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0070427 nucleotide-binding oligomerization domain containing 1 signaling pathway       | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0071737 cellular response to luteinizing hormone stimulus                              | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0071737 cellular response to luteinizing hormone stimulus                              | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0071808 macrophage inflammatory protein-1 alpha production                             | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0071808 macrophage inflammatory protein-1 alpha production                             | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0071640 regulation of macrophage inflammatory protein 1 alpha production               | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0071640 regulation of macrophage inflammatory protein 1 alpha production               | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0071680 response to indole-3-methanol                                                  | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0071680 response to indole-3-methanol                                                  | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0071830 triglyceride-rich lipoprotein particle clearance                               | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0071830 triglyceride-rich lipoprotein particle clearance                               | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0072038 glomerular mesangial cell differentiation                                      | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0072038 glomerular mesangial cell differentiation                                      | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0072143 mesangial cell development                                                     | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0072143 mesangial cell development                                                     | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0072174 metanephric tubule formation                                                   | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0072174 metanephric tubule formation                                                   | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0086073 bundle of His cell-Purkinje myocyte adhesion involved in cell communication    | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0086073 bundle of His cell-Purkinje myocyte adhesion involved in cell communication    | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0090674 endothelial cell-matrix adhesion via fibronectin                               | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0090674 endothelial cell-matrix adhesion via fibronectin                               | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0097402 neuroblast migration                                                           | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0097402 neuroblast migration                                                           | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0098597 observational learning                                                         | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0098597 observational learning                                                         | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0120041 positive regulation of macrophage proliferation                                | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0120041 positive regulation of macrophage proliferation                                | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0140009 L-aspartate import across plasma membrane                                      | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0140009 L-aspartate import across plasma membrane                                      | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:0116404 negative regulation of trophoblast cell migration                              | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:0116404 negative regulation of trophoblast cell migration                              | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:1901534 positive regulation of hematopoietic progenitor cell differentiation           | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:1901534 positive regulation of hematopoietic progenitor cell differentiation           | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:1901713 regulation of post-translational protein modification                          | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:1901713 regulation of post-translational protein modification                          | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:1902083 negative regulation of peptidyl-cysteine S-nitrosylation                       | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:1902083 negative regulation of peptidyl-cysteine S-nitrosylation                       | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:1902474 positive regulation of protein localization to synapse                         | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:1902474 positive regulation of protein localization to synapse                         | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:1902949 positive regulation of tau-protein kinase activity                             | 1  | 0.10453 | 0.31   | 0.167 | Biological C   | GO:1902949 positive regulation of tau-protein kinase activity                             | 0.10453 | 0.29898 | 0 | 0 | 1  | 6    |
| GO:1903537 meiotic cell cycle process involved in oocyte maturation                       | 1  | 0.10453 | 0.31   | 0.167 | Biological C</ |                                                                                           |         |         |   |   |    |      |

|                                                                                         |    |         |        |       |            |                                                                                                |         |         |   |   |    |      |
|-----------------------------------------------------------------------------------------|----|---------|--------|-------|------------|------------------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0031965 nuclear membrane                                                             | 9  | 0.11271 | 2.671  | 0.029 | Cellular C | GO:0031965 nuclear membrane                                                                    | 0.11271 | 0.31736 | 0 | 0 | 9  | 312  |
| GO:0051090 regulation of DNA-binding transcription factor activity                      | 12 | 0.11272 | 3.715  | 0.027 | Biological | GO:0051090 regulation of DNA-binding transcription factor activity                             | 0.11272 | 0.31661 | 0 | 0 | 12 | 443  |
| GO:0032760 positive regulation of tumor necrosis factor production                      | 4  | 0.1131  | 1.238  | 0.04  | Biological | GO:0032760 positive regulation of tumor necrosis factor production                             | 0.1131  | 0.31731 | 0 | 0 | 4  | 101  |
| GO:0046709 oligodendrocyte differentiation                                              | 4  | 0.11311 | 1.238  | 0.04  | Biological | GO:0046709 oligodendrocyte differentiation                                                     | 0.1131  | 0.31731 | 0 | 0 | 4  | 101  |
| GO:0006812 cation transport                                                             | 29 | 0.1132  | 8.978  | 0.023 | Biological | GO:0006812 cation transport                                                                    | 0.1132  | 0.31741 | 0 | 0 | 29 | 1257 |
| GO:0042157 lipoprotein metabolic process                                                | 5  | 0.11326 | 1.548  | 0.036 | Biological | GO:0042157 lipoprotein metabolic process                                                       | 0.11326 | 0.31741 | 0 | 0 | 5  | 140  |
| GO:0041757 apical part of cell                                                          | 12 | 0.11415 | 3.561  | 0.027 | Cellular C | GO:0041757 apical part of cell                                                                 | 0.11415 | 0.31974 | 0 | 0 | 12 | 443  |
| GO:0030522 intracellular receptor signaling pathway                                     | 8  | 0.11433 | 2.477  | 0.033 | Biological | GO:0030522 intracellular receptor signaling pathway                                            | 0.11433 | 0.31944 | 0 | 0 | 8  | 286  |
| GO:0010574 regulation of vascular endothelial growth factor production                  | 2  | 0.11506 | 0.619  | 0.062 | Biological | GO:0010574 regulation of vascular endothelial growth factor production                         | 0.11506 | 0.3194  | 0 | 0 | 2  | 32   |
| GO:0048364 retinoic acid receptor signaling pathway                                     | 2  | 0.11506 | 0.619  | 0.062 | Biological | GO:0048364 retinoic acid receptor signaling pathway                                            | 0.11506 | 0.3194  | 0 | 0 | 2  | 32   |
| GO:0048873 homeostasis of number of cells within a tissue                               | 2  | 0.11506 | 0.619  | 0.062 | Biological | GO:0048873 homeostasis of number of cells within a tissue                                      | 0.11506 | 0.3194  | 0 | 0 | 2  | 32   |
| GO:0060292 long-term synaptic depression                                                | 2  | 0.11506 | 0.619  | 0.062 | Biological | GO:0060292 long-term synaptic depression                                                       | 0.11506 | 0.3194  | 0 | 0 | 2  | 32   |
| GO:0060325 face morphogenesis                                                           | 2  | 0.11506 | 0.619  | 0.062 | Biological | GO:0060325 face morphogenesis                                                                  | 0.11506 | 0.3194  | 0 | 0 | 2  | 32   |
| GO:0010720 positive regulation of cell development                                      | 9  | 0.11507 | 2.786  | 0.025 | Biological | GO:0010720 positive regulation of cell development                                             | 0.11507 | 0.3194  | 0 | 0 | 9  | 310  |
| GO:0098930 axonal transport                                                             | 3  | 0.11531 | 0.929  | 0.046 | Biological | GO:0098930 axonal transport                                                                    | 0.11531 | 0.3194  | 0 | 0 | 3  | 65   |
| GO:1905330 regulation of morphogenesis of an epithelium                                 | 3  | 0.11531 | 0.929  | 0.046 | Biological | GO:1905330 regulation of morphogenesis of an epithelium                                        | 0.11531 | 0.3194  | 0 | 0 | 3  | 65   |
| GO:0032101 regulation of response to external stimulus                                  | 23 | 0.11569 | 7.121  | 0.024 | Biological | GO:0032101 regulation of response to external stimulus                                         | 0.11569 | 0.3194  | 0 | 0 | 23 | 966  |
| GO:0058111 lipid droplet                                                                | 4  | 0.11569 | 1.187  | 0.039 | Cellular C | GO:0058111 lipid droplet                                                                       | 0.11569 | 0.32238 | 0 | 0 | 4  | 103  |
| GO:0003333 amino acid transmembrane transport                                           | 4  | 0.11613 | 1.238  | 0.039 | Biological | GO:0003333 amino acid transmembrane transport                                                  | 0.11613 | 0.3194  | 0 | 0 | 4  | 102  |
| GO:0032479 regulation of type I interferon production                                   | 4  | 0.11613 | 1.238  | 0.039 | Biological | GO:0032479 regulation of type I interferon production                                          | 0.11613 | 0.3194  | 0 | 0 | 4  | 102  |
| GO:0032606 type I interferon production                                                 | 4  | 0.11613 | 1.238  | 0.039 | Biological | GO:0032606 type I interferon production                                                        | 0.11613 | 0.3194  | 0 | 0 | 4  | 102  |
| GO:0098175 regulation of postsynapse organization                                       | 4  | 0.11613 | 1.238  | 0.039 | Biological | GO:0098175 regulation of postsynapse organization                                              | 0.11613 | 0.3194  | 0 | 0 | 4  | 102  |
| GO:0059653 sensory perception of light stimulus                                         | 7  | 0.1163  | 2.167  | 0.031 | Biological | GO:0059653 sensory perception of light stimulus                                                | 0.1163  | 0.3194  | 0 | 0 | 7  | 224  |
| GO:0046873 metal ion transmembrane transporter activity                                 | 12 | 0.11738 | 3.509  | 0.027 | Molecular  | GO:0046873 metal ion transmembrane transporter activity                                        | 0.11738 | 0.32217 | 0 | 0 | 12 | 439  |
| GO:0008238 exopeptidase activity                                                        | 4  | 0.11823 | 1.17   | 0.04  | Molecular  | GO:0008238 exopeptidase activity                                                               | 0.11823 | 0.32217 | 0 | 0 | 4  | 101  |
| GO:0033764 steroid dehydrogenase activity, acting on the CH-OH group                    | 2  | 0.11825 | 0.585  | 0.062 | Molecular  | GO:0033764 steroid dehydrogenase activity, acting on the CH-OH group of donors                 | 0.11825 | 0.32217 | 0 | 0 | 2  | 32   |
| GO:0097181 extrinsic apoptotic signaling pathway                                        | 7  | 0.11829 | 2.167  | 0.031 | Biological | GO:0097181 extrinsic apoptotic signaling pathway                                               | 0.11829 | 0.3194  | 0 | 0 | 7  | 225  |
| GO:0031325 regulation of peptide-serine phosphorylation                                 | 5  | 0.11834 | 1.548  | 0.035 | Biological | GO:0031325 regulation of peptide-serine phosphorylation                                        | 0.11834 | 0.3194  | 0 | 0 | 5  | 142  |
| GO:0032701 endocrine system development                                                 | 5  | 0.11834 | 1.548  | 0.035 | Biological | GO:0032701 endocrine system development                                                        | 0.11834 | 0.3194  | 0 | 0 | 5  | 142  |
| GO:0007010 cytoskeleton organization                                                    | 34 | 0.11896 | 10.526 | 0.022 | Biological | GO:0007010 cytoskeleton organization                                                           | 0.11896 | 0.3194  | 0 | 0 | 34 | 1513 |
| GO:0030900 forebrain development                                                        | 11 | 0.11898 | 3.406  | 0.027 | Biological | GO:0030900 forebrain development                                                               | 0.11898 | 0.3194  | 0 | 0 | 11 | 402  |
| GO:0016525 negative regulation of angiogenesis                                          | 4  | 0.11919 | 1.238  | 0.039 | Biological | GO:0016525 negative regulation of angiogenesis                                                 | 0.11919 | 0.3194  | 0 | 0 | 4  | 103  |
| GO:0032963 collagen biosynthetic process                                                | 4  | 0.11919 | 1.238  | 0.039 | Biological | GO:0032963 collagen biosynthetic process                                                       | 0.11919 | 0.3194  | 0 | 0 | 4  | 103  |
| GO:0015115 cell-substrate junction organization                                         | 4  | 0.11919 | 1.238  | 0.039 | Biological | GO:0015115 cell-substrate junction organization                                                | 0.11919 | 0.3194  | 0 | 0 | 4  | 103  |
| GO:0009311 oligosaccharide metabolic process                                            | 3  | 0.11927 | 0.929  | 0.045 | Biological | GO:0009311 oligosaccharide metabolic process                                                   | 0.11927 | 0.3194  | 0 | 0 | 3  | 66   |
| GO:0044458 motile cilium assembly                                                       | 3  | 0.11927 | 0.929  | 0.045 | Biological | GO:0044458 motile cilium assembly                                                              | 0.11927 | 0.3194  | 0 | 0 | 3  | 66   |
| GO:0071806 protein transmembrane transport                                              | 3  | 0.11927 | 0.929  | 0.045 | Biological | GO:0071806 protein transmembrane transport                                                     | 0.11927 | 0.3194  | 0 | 0 | 3  | 66   |
| GO:0035896 spermatogenesis                                                              | 1  | 0.11957 | 0.297  | 0.143 | Cellular C | GO:0035896 spermatogenesis                                                                     | 0.11957 | 0.32473 | 0 | 0 | 1  | 7    |
| GO:0046581 intercellular canalculus                                                     | 1  | 0.11957 | 0.297  | 0.143 | Cellular C | GO:0046581 intercellular canalculus                                                            | 0.11957 | 0.32473 | 0 | 0 | 1  | 7    |
| GO:0097512 cardiac myofibril                                                            | 1  | 0.11957 | 0.297  | 0.143 | Cellular C | GO:0097512 cardiac myofibril                                                                   | 0.11957 | 0.32473 | 0 | 0 | 1  | 7    |
| GO:0150053 cerebellar climbing fiber to Purkinje cell synapse                           | 1  | 0.11957 | 0.297  | 0.143 | Cellular C | GO:0150053 cerebellar climbing fiber to Purkinje cell synapse                                  | 0.11957 | 0.32473 | 0 | 0 | 1  | 7    |
| GO:1990635 proximal dendrite                                                            | 1  | 0.11957 | 0.297  | 0.143 | Cellular C | GO:1990635 proximal dendrite                                                                   | 0.11957 | 0.32473 | 0 | 0 | 1  | 7    |
| GO:1903039 positive regulation of leukocyte cell-cell adhesion                          | 8  | 0.11968 | 2.477  | 0.033 | Biological | GO:1903039 positive regulation of leukocyte cell-cell adhesion                                 | 0.11968 | 0.3194  | 0 | 0 | 8  | 269  |
| GO:0002684 positive regulation of immune system process                                 | 23 | 0.12034 | 7.121  | 0.024 | Biological | GO:0002684 positive regulation of immune system process                                        | 0.12034 | 0.3194  | 0 | 0 | 23 | 971  |
| GO:0046983 protein dimerization activity                                                | 26 | 0.12036 | 7.802  | 0.024 | Molecular  | GO:0046983 protein dimerization activity                                                       | 0.12036 | 0.32217 | 0 | 0 | 26 | 1099 |
| GO:0034305 regulation of MAP kinase activity                                            | 6  | 0.1208  | 1.858  | 0.033 | Biological | GO:0034305 regulation of MAP kinase activity                                                   | 0.1208  | 0.3194  | 0 | 0 | 6  | 184  |
| GO:0002154 thyroid hormone mediated signaling pathway                                   | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0002154 thyroid hormone mediated signaling pathway                                          | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0003339 regulation of mechanosensory epithelial transition involved in metastasis    | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0003339 regulation of mechanosensory epithelial transition involved in metastasis           | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0006166 purine ribonucleoside salvage                                                | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0006166 purine ribonucleoside salvage                                                       | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0006071 progesterone biosynthetic process                                            | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0006071 progesterone biosynthetic process                                                   | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0009624 response to nematode                                                         | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0009624 response to nematode                                                                | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0010536 positive regulation of activation of Janus kinase activity                   | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0010536 positive regulation of activation of Janus kinase activity                          | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0006096 positive regulation of cholesterol storage                                   | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0006096 positive regulation of cholesterol storage                                          | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0021546 homomere development                                                         | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0021546 homomere development                                                                | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0021798 forebrain dorsal/ventral pattern formation                                   | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0021798 forebrain dorsal/ventral pattern formation                                          | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0021877 forebrain neuron fate commitment                                             | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0021877 forebrain neuron fate commitment                                                    | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0030046 parallel actin filament bundle assembly                                      | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0030046 parallel actin filament bundle assembly                                             | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0030091 protein response                                                             | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0030091 protein response                                                                    | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0030917 midbrain-hindbrain boundary development                                      | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0030917 midbrain-hindbrain boundary development                                             | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0032278 positive regulation of gonadotropin secretion                                | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0032278 positive regulation of gonadotropin secretion                                       | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0032415 regulation of sodium/proton antiporter activity                              | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0032415 regulation of sodium/proton antiporter activity                                     | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0032594 protein transport within lipid bilayer                                       | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0032594 protein transport within lipid bilayer                                              | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0032741 positive regulation of interleukin-18 production                             | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0032741 positive regulation of interleukin-18 production                                    | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0038145 macrophage colony-stimulating factor signaling pathway                       | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0038145 macrophage colony-stimulating factor signaling pathway                              | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0042723 thiamine-containing compound metabolic process                               | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0042723 thiamine-containing compound metabolic process                                      | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0042748 circadian sleep/wake cycle, non-REM sleep                                    | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0042748 circadian sleep/wake cycle, non-REM sleep                                           | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0042940 D-amino acid transport                                                       | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0042940 D-amino acid transport                                                              | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0043589 negative regulation of insulin-like growth factor receptor signaling pathway | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0043589 negative regulation of insulin-like growth factor receptor signaling pathway        | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0043619 regulation of transcription from RNA polymerase II promoter                  | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0043619 regulation of transcription from RNA polymerase II promoter in response to stimulus | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0044691 tooth eruption                                                               | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0044691 tooth eruption                                                                      | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0045924 regulation of female receptivity                                             | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0045924 regulation of female receptivity                                                    | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0046133 negative regulation of vitamin metabolic process                             | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0046133 negative regulation of vitamin metabolic process                                    | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0046600 negative regulation of ceramide replication                                  | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0046600 negative regulation of ceramide replication                                         | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0046813 receptor-mediated virion attachment to host cell                             | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0046813 receptor-mediated virion attachment to host cell                                    | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0048312 intracellular distribution of mitochondria                                   | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0048312 intracellular distribution of mitochondria                                          | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0050882 voluntary musculoskeletal movement                                           | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0050882 voluntary musculoskeletal movement                                                  | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0050916 sensory perception of sweet taste                                            | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0050916 sensory perception of sweet taste                                                   | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0050942 positive regulation of cement cell differentiation                           | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0050942 positive regulation of cement cell differentiation                                  | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0060087 relaxation of vascular associated smooth muscle                              | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0060087 relaxation of vascular associated smooth muscle                                     | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0060180 female mating behavior                                                       | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0060180 female mating behavior                                                              | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0060297 regulation of sarcomere organization                                         | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0060297 regulation of sarcomere organization                                                | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0060405 regulation of penis erection                                                 | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0060405 regulation of penis erection                                                        | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0060534 tracheal cartilage development                                               | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0060534 tracheal cartilage development                                                      | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0060676 ureteric bud formation                                                       | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0060676 ureteric bud formation                                                              | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0060729 intestinal epithelial structure maintenance                                  | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0060729 intestinal epithelial structure maintenance                                         | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0060745 mammary gland branching involved in pregnancy                                | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0060745 mammary gland branching involved in pregnancy                                       | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0061370 testosterone biosynthetic process                                            | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0061370 testosterone biosynthetic process                                                   | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0071018 interleukin-27-mediated signaling pathway                                    | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0071018 interleukin-27-mediated signaling pathway                                           | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0070671 response to interleukin-12                                                   | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:0070671 response to interleukin-12                                                          | 0.12086 | 0.3194  | 0 | 0 | 1  | 7    |
| GO:0070933 histone H4 deacetylation                                                     | 1  | 0.12086 | 0.31   | 0.143 | Biological | GO:                                                                                            |         |         |   |   |    |      |

|                                                                                         |     |         |        |       |            |                                                                                         |         |         |   |   |     |       |
|-----------------------------------------------------------------------------------------|-----|---------|--------|-------|------------|-----------------------------------------------------------------------------------------|---------|---------|---|---|-----|-------|
| GO:0016627 oxidoreductase activity, acting on the CH-CH group of donor                  | 3   | 0.12367 | 0.877  | 0.045 | Molecular  | GO:0016627 oxidoreductase activity, acting on the CH-CH group of donors                 | 0.12367 | 0.32356 | 0 | 0 | 3   | 66    |
| GO:000343 organic acid sodium symporter activity                                        | 2   | 0.1244  | 0.585  | 0.061 | Molecular  | GO:000343 organic acid sodium symporter activity                                        | 0.1244  | 0.32379 | 0 | 0 | 2   | 33    |
| GO:0070851 growth factor receptor binding                                               | 5   | 0.12451 | 1.462  | 0.035 | Molecular  | GO:0070851 growth factor receptor binding                                               | 0.12451 | 0.32379 | 0 | 0 | 5   | 142   |
| GO:002241 cellular component disassembly                                                | 13  | 0.12488 | 4.025  | 0.028 | Biological | GO:002241 cellular component disassembly                                                | 0.12488 | 0.32771 | 0 | 0 | 13  | 496   |
| GO:009066 regulation of anatomical structure size                                       | 14  | 0.12541 | 4.334  | 0.026 | Biological | GO:009066 regulation of anatomical structure size                                       | 0.12541 | 0.32847 | 0 | 0 | 14  | 545   |
| GO:000685 female ovid development                                                       | 4   | 0.12543 | 1.238  | 0.038 | Biological | GO:000685 female ovid development                                                       | 0.12543 | 0.32847 | 0 | 0 | 4   | 105   |
| GO:1901343 negative regulation of vasculature development                               | 4   | 0.12543 | 1.238  | 0.038 | Biological | GO:1901343 negative regulation of vasculature development                               | 0.12543 | 0.32847 | 0 | 0 | 4   | 105   |
| GO:1903557 positive regulation of tumor necrosis factor superfamily cytokine production | 4   | 0.12543 | 1.238  | 0.038 | Biological | GO:1903557 positive regulation of tumor necrosis factor superfamily cytokine production | 0.12543 | 0.32847 | 0 | 0 | 4   | 105   |
| GO:004472 sulfur compound biosynthetic process                                          | 5   | 0.12615 | 1.548  | 0.034 | Biological | GO:004472 sulfur compound biosynthetic process                                          | 0.12615 | 0.33017 | 0 | 0 | 5   | 145   |
| GO:0060326 cell chemotaxis                                                              | 9   | 0.12691 | 2.786  | 0.028 | Biological | GO:0060326 cell chemotaxis                                                              | 0.12691 | 0.33057 | 0 | 0 | 9   | 317   |
| GO:1902105 regulation of leukocyte differentiation                                      | 9   | 0.12691 | 2.786  | 0.028 | Biological | GO:1902105 regulation of leukocyte differentiation                                      | 0.12691 | 0.33057 | 0 | 0 | 9   | 317   |
| GO:0001569 branching involved in blood vessel morphogenesis                             | 2   | 0.12716 | 0.619  | 0.059 | Biological | GO:0001569 branching involved in blood vessel morphogenesis                             | 0.12716 | 0.33057 | 0 | 0 | 2   | 34    |
| GO:0034405 response to fluid shear stress                                               | 2   | 0.12716 | 0.619  | 0.059 | Biological | GO:0034405 response to fluid shear stress                                               | 0.12716 | 0.33057 | 0 | 0 | 2   | 34    |
| GO:0035590 purine nucleotide receptor signaling pathway                                 | 2   | 0.12716 | 0.619  | 0.059 | Biological | GO:0035590 purine nucleotide receptor signaling pathway                                 | 0.12716 | 0.33057 | 0 | 0 | 2   | 34    |
| GO:0060914 heart formation                                                              | 2   | 0.12716 | 0.619  | 0.059 | Biological | GO:0060914 heart formation                                                              | 0.12716 | 0.33057 | 0 | 0 | 2   | 34    |
| GO:0061081 positive regulation of myeloid leukocyte cytokine production                 | 2   | 0.12716 | 0.619  | 0.059 | Biological | GO:0061081 positive regulation of myeloid leukocyte cytokine production                 | 0.12716 | 0.33057 | 0 | 0 | 2   | 34    |
| GO:0070873 regulation of glycerol metabolic process                                     | 2   | 0.12716 | 0.619  | 0.059 | Biological | GO:0070873 regulation of glycerol metabolic process                                     | 0.12716 | 0.33057 | 0 | 0 | 2   | 34    |
| GO:008604 regulation of cardiac muscle cell contraction                                 | 2   | 0.12716 | 0.619  | 0.059 | Biological | GO:008604 regulation of cardiac muscle cell contraction                                 | 0.12716 | 0.33057 | 0 | 0 | 2   | 34    |
| GO:0089801 regulation of renal system process                                           | 2   | 0.12716 | 0.619  | 0.059 | Biological | GO:0089801 regulation of renal system process                                           | 0.12716 | 0.33057 | 0 | 0 | 2   | 34    |
| GO:1904861 excitatory synapse assembly                                                  | 2   | 0.12716 | 0.619  | 0.059 | Biological | GO:1904861 excitatory synapse assembly                                                  | 0.12716 | 0.33057 | 0 | 0 | 2   | 34    |
| GO:0007268 chemical synaptic transmission                                               | 18  | 0.12716 | 5.573  | 0.024 | Biological | GO:0007268 chemical synaptic transmission                                               | 0.12716 | 0.33057 | 0 | 0 | 18  | 736   |
| GO:0089161 anterograde trans-synaptic signaling                                         | 18  | 0.12716 | 5.573  | 0.024 | Biological | GO:0089161 anterograde trans-synaptic signaling                                         | 0.12716 | 0.33057 | 0 | 0 | 18  | 736   |
| GO:0045699 positive regulation of osteoblast differentiation                            | 3   | 0.12732 | 0.929  | 0.044 | Biological | GO:0045699 positive regulation of osteoblast differentiation                            | 0.12732 | 0.33081 | 0 | 0 | 3   | 68    |
| GO:0021543 pallium development                                                          | 6   | 0.12785 | 1.858  | 0.032 | Biological | GO:0021543 pallium development                                                          | 0.12785 | 0.3315  | 0 | 0 | 6   | 197   |
| GO:0008235 metalloprotease activity                                                     | 3   | 0.12779 | 0.877  | 0.045 | Molecular  | GO:0008235 metalloprotease activity                                                     | 0.12779 | 0.33135 | 0 | 0 | 3   | 67    |
| GO:0043232 intracellular non-membrane-bounded organelle                                 | 105 | 0.12785 | 31.157 | 0.02  | Cellular   | GO:0043232 intracellular non-membrane-bounded organelle                                 | 0.12785 | 0.34324 | 0 | 0 | 105 | 5280  |
| GO:0045596 negative regulation of cell differentiation                                  | 7   | 0.1281  | 5.263  | 0.025 | Biological | GO:0045596 negative regulation of cell differentiation                                  | 0.1281  | 0.33249 | 0 | 0 | 7   | 689   |
| GO:0043228 non-membrane-bounded organelle                                               | 105 | 0.1283  | 31.157 | 0.02  | Cellular   | GO:0043228 non-membrane-bounded organelle                                               | 0.1283  | 0.33249 | 0 | 0 | 105 | 5281  |
| GO:0001776 leukocyte homeostasis                                                        | 4   | 0.1286  | 1.238  | 0.038 | Biological | GO:0001776 leukocyte homeostasis                                                        | 0.1286  | 0.33362 | 0 | 0 | 4   | 106   |
| GO:0005737 cytoplasm                                                                    | 229 | 0.13004 | 67.953 | 0.019 | Cellular   | GO:0005737 cytoplasm                                                                    | 0.13004 | 0.34614 | 0 | 0 | 229 | 12135 |
| GO:0051049 regulation of transport                                                      | 39  | 0.13029 | 12.074 | 0.022 | Biological | GO:0051049 regulation of transport                                                      | 0.13029 | 0.33783 | 0 | 0 | 39  | 1780  |
| GO:0003766 acetylglucosaminyltransferase activity                                       | 2   | 0.13063 | 0.585  | 0.059 | Molecular  | GO:0003766 acetylglucosaminyltransferase activity                                       | 0.13063 | 0.33669 | 0 | 0 | 2   | 34    |
| GO:0030296 protein kinase activity                                                      | 2   | 0.13063 | 0.585  | 0.059 | Molecular  | GO:0030296 protein kinase activity                                                      | 0.13063 | 0.33669 | 0 | 0 | 2   | 34    |
| GO:0014855 striated muscle cell proliferation                                           | 3   | 0.13141 | 0.929  | 0.043 | Biological | GO:0014855 striated muscle cell proliferation                                           | 0.13141 | 0.33849 | 0 | 0 | 3   | 69    |
| GO:0042093 T-helper cell differentiation                                                | 3   | 0.13141 | 0.929  | 0.043 | Biological | GO:0042093 T-helper cell differentiation                                                | 0.13141 | 0.33849 | 0 | 0 | 3   | 69    |
| GO:0060675 ureteric bud morphogenesis                                                   | 3   | 0.13141 | 0.929  | 0.043 | Biological | GO:0060675 ureteric bud morphogenesis                                                   | 0.13141 | 0.33849 | 0 | 0 | 3   | 69    |
| GO:0006954 inflammatory response                                                        | 19  | 0.13152 | 5.882  | 0.024 | Biological | GO:0006954 inflammatory response                                                        | 0.13152 | 0.33849 | 0 | 0 | 19  | 788   |
| GO:004072 protein kinase activity                                                       | 15  | 0.13172 | 4.386  | 0.028 | Biological | GO:004072 protein kinase activity                                                       | 0.13172 | 0.33849 | 0 | 0 | 15  | 587   |
| GO:0046776 regulation of protein localization to plasma membrane                        | 4   | 0.1318  | 1.238  | 0.037 | Biological | GO:0046776 regulation of protein localization to plasma membrane                        | 0.1318  | 0.33849 | 0 | 0 | 4   | 107   |
| GO:0003777 microtubule motor activity                                                   | 3   | 0.13197 | 0.877  | 0.044 | Molecular  | GO:0003777 microtubule motor activity                                                   | 0.13197 | 0.33812 | 0 | 0 | 3   | 68    |
| GO:0150034 distal axon                                                                  | 8   | 0.13294 | 2.374  | 0.029 | Cellular   | GO:0150034 distal axon                                                                  | 0.13294 | 0.34924 | 0 | 0 | 8   | 279   |
| GO:0048534 hematopoietic or lymphoid organ development                                  | 23  | 0.13297 | 7.121  | 0.023 | Biological | GO:0048534 hematopoietic or lymphoid organ development                                  | 0.13297 | 0.33849 | 0 | 0 | 23  | 984   |
| GO:001893 maternal placenta development                                                 | 2   | 0.13311 | 0.619  | 0.057 | Biological | GO:001893 maternal placenta development                                                 | 0.13311 | 0.33849 | 0 | 0 | 2   | 35    |
| GO:0048730 epidermis morphogenesis                                                      | 2   | 0.13331 | 0.619  | 0.057 | Biological | GO:0048730 epidermis morphogenesis                                                      | 0.13331 | 0.33849 | 0 | 0 | 2   | 35    |
| GO:0060251 regulation of glial cell proliferation                                       | 2   | 0.13331 | 0.619  | 0.057 | Biological | GO:0060251 regulation of glial cell proliferation                                       | 0.13331 | 0.33849 | 0 | 0 | 2   | 35    |
| GO:0071398 cellular response to fatty acid                                              | 2   | 0.13331 | 0.619  | 0.057 | Biological | GO:0071398 cellular response to fatty acid                                              | 0.13331 | 0.33849 | 0 | 0 | 2   | 35    |
| GO:0096171 presynaptic modulation of chemical synaptic transmission                     | 2   | 0.13331 | 0.619  | 0.057 | Biological | GO:0096171 presynaptic modulation of chemical synaptic transmission                     | 0.13331 | 0.33849 | 0 | 0 | 2   | 35    |
| GO:1902624 positive regulation of neutrophil migration                                  | 2   | 0.13331 | 0.619  | 0.057 | Biological | GO:1902624 positive regulation of neutrophil migration                                  | 0.13331 | 0.33849 | 0 | 0 | 2   | 35    |
| GO:0004175 endopeptidase activity                                                       | 12  | 0.13334 | 3.509  | 0.027 | Molecular  | GO:0004175 endopeptidase activity                                                       | 0.13334 | 0.33916 | 0 | 0 | 12  | 450   |
| GO:0097190 apoptotic signaling pathway                                                  | 15  | 0.13436 | 4.644  | 0.025 | Biological | GO:0097190 apoptotic signaling pathway                                                  | 0.13436 | 0.33849 | 0 | 0 | 15  | 599   |
| GO:0030308 negative regulation of cell growth                                           | 6   | 0.13469 | 1.858  | 0.032 | Biological | GO:0030308 negative regulation of cell growth                                           | 0.13469 | 0.33849 | 0 | 0 | 6   | 190   |
| GO:0034308 primary alcohol metabolic process                                            | 4   | 0.13503 | 1.238  | 0.037 | Biological | GO:0034308 primary alcohol metabolic process                                            | 0.13503 | 0.33849 | 0 | 0 | 4   | 108   |
| GO:0036173 trans-synaptic signaling                                                     | 18  | 0.13516 | 5.573  | 0.024 | Biological | GO:0036173 trans-synaptic signaling                                                     | 0.13516 | 0.33849 | 0 | 0 | 18  | 733   |
| GO:0000976 transcription cis-regulatory region binding                                  | 34  | 0.13536 | 9.942  | 0.023 | Molecular  | GO:0000976 transcription cis-regulatory region binding                                  | 0.13536 | 0.33916 | 0 | 0 | 34  | 1508  |
| GO:0033010 paranodal junction                                                           | 1   | 0.13545 | 0.297  | 0.125 | Cellular   | GO:0033010 paranodal junction                                                           | 0.13545 | 0.34924 | 0 | 0 | 1   | 8     |
| GO:0036454 growth factor complex                                                        | 1   | 0.13545 | 0.297  | 0.125 | Cellular   | GO:0036454 growth factor complex                                                        | 0.13545 | 0.34924 | 0 | 0 | 1   | 8     |
| GO:0097450 astrocyte end-foot                                                           | 1   | 0.13545 | 0.297  | 0.125 | Cellular   | GO:0097450 astrocyte end-foot                                                           | 0.13545 | 0.34924 | 0 | 0 | 1   | 8     |
| GO:0098837 positive regulation of endosome                                              | 1   | 0.13545 | 0.297  | 0.125 | Cellular   | GO:0098837 positive regulation of endosome                                              | 0.13545 | 0.34924 | 0 | 0 | 1   | 8     |
| GO:0045934 negative regulation of nucleosome-containing compound m                      | 34  | 0.13545 | 10.525 | 0.022 | Biological | GO:0045934 negative regulation of nucleosome-containing compound metabolic pr           | 0.13545 | 0.33849 | 0 | 0 | 34  | 1534  |
| GO:0106310 protein serine kinase activity                                               | 10  | 0.13549 | 2.924  | 0.028 | Molecular  | GO:0106310 protein serine kinase activity                                               | 0.13549 | 0.33916 | 0 | 0 | 10  | 361   |
| GO:0046835 positive regulation of alpha-beta T cell activation                          | 3   | 0.13556 | 0.929  | 0.043 | Biological | GO:0046835 positive regulation of alpha-beta T cell activation                          | 0.13556 | 0.33849 | 0 | 0 | 3   | 70    |
| GO:0050810 regulation of steroid biosynthetic process                                   | 3   | 0.13556 | 0.929  | 0.043 | Biological | GO:0050810 regulation of steroid biosynthetic process                                   | 0.13556 | 0.33849 | 0 | 0 | 3   | 70    |
| GO:006415 muscle tissue morphogenesis                                                   | 3   | 0.13556 | 0.929  | 0.043 | Biological | GO:006415 muscle tissue morphogenesis                                                   | 0.13556 | 0.33849 | 0 | 0 | 3   | 70    |
| GO:0072171 mesonephric tubule morphogenesis                                             | 3   | 0.13556 | 0.929  | 0.043 | Biological | GO:0072171 mesonephric tubule morphogenesis                                             | 0.13556 | 0.33849 | 0 | 0 | 3   | 70    |
| GO:0042677 cellular protein metabolic process                                           | 96  | 0.13643 | 29.721 | 0.02  | Biological | GO:0042677 cellular protein metabolic process                                           | 0.13643 | 0.33849 | 0 | 0 | 96  | 4763  |
| GO:0001725 stress fiber                                                                 | 3   | 0.13643 | 0.89   | 0.042 | Cellular   | GO:0001725 stress fiber                                                                 | 0.13643 | 0.34924 | 0 | 0 | 3   | 71    |
| GO:0016328 lateral plasma membrane                                                      | 3   | 0.13643 | 0.89   | 0.042 | Cellular   | GO:0016328 lateral plasma membrane                                                      | 0.13643 | 0.34924 | 0 | 0 | 3   | 71    |
| GO:0097517 contractile actin filament bundle                                            | 1   | 0.13643 | 0.89   | 0.042 | Cellular   | GO:0097517 contractile actin filament bundle                                            | 0.13643 | 0.34924 | 0 | 0 | 1   | 8     |
| GO:0002118 aggressive behavior                                                          | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0002118 aggressive behavior                                                          | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0002246 wound healing involved in inflammatory response                              | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0002246 wound healing involved in inflammatory response                              | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0002866 positive regulation of acute inflammatory response to antigenic stimulus     | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0002866 positive regulation of acute inflammatory response to antigenic stimulus     | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0003149 mammalian septum morphogenesis                                               | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0003149 mammalian septum morphogenesis                                               | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0003380 brainstem development                                                        | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0003380 brainstem development                                                        | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0003433 chondrocyte development involved in endochondral bone morphogenesis          | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0003433 chondrocyte development involved in endochondral bone morphogenesis          | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0009414 response to water deprivation                                                | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0009414 response to water deprivation                                                | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:014004 microglia differentiation                                                     | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:014004 microglia differentiation                                                     | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0014041 regulation of neuron maturation                                              | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0014041 regulation of neuron maturation                                              | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:015888 thiamine transport                                                            | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:015888 thiamine transport                                                            | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0021553 olfactory nerve development                                                  | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0021553 olfactory nerve development                                                  | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0030854 positive regulation of granulocyte differentiation                           | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0030854 positive regulation of granulocyte differentiation                           | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0030916 otic vesicle formation                                                       | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0030916 otic vesicle formation                                                       | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0032119 sequestering of zinc ion                                                     | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0032119 sequestering of zinc ion                                                     | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0032489 regulation of Cdc42 protein signal transduction                              | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0032489 regulation of Cdc42 protein signal transduction                              | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0032493 response to bacterial lipoprotein                                            | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0032493 response to bacterial lipoprotein                                            | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0032778 cell proliferation in midbrain                                               | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0032778 cell proliferation in midbrain                                               | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0033601 positive regulation of mammary gland epithelial cell proliferation           | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0033601 positive regulation of mammary gland epithelial cell proliferation           | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0034689 response to luteinizing hormone                                              | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0034689 response to luteinizing hormone                                              | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0034983 neptunium desorption                                                         | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0034983 neptunium desorption                                                         | 0.13689 | 0.33849 | 0 | 0 | 1   | 8     |
| GO:0038134 ERBB2-EGFR signaling pathway                                                 | 1   | 0.13689 | 0.31   | 0.125 | Biological | GO:0038134 ERBB2                                                                        |         |         |   |   |     |       |

|                                                                                    |    |         |        |       |            |          |                                                                         |         |         |   |   |    |      |
|------------------------------------------------------------------------------------|----|---------|--------|-------|------------|----------|-------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0004415 hyalurononoglucosaminidase activity                                     | 1  | 0.13903 | 0.292  | 0.125 | Molecular  | GO:00044 | hyalurononoglucosaminidase activity                                     | 0.13903 | 0.33916 | 0 | 0 | 1  | 8    |
| GO:0004897 ciliary neurotrophic factor receptor activity                           | 1  | 0.13903 | 0.292  | 0.125 | Molecular  | GO:00048 | ciliary neurotrophic factor receptor activity                           | 0.13903 | 0.33916 | 0 | 0 | 1  | 8    |
| GO:0004972 NMDA glutamate receptor activity                                        | 1  | 0.13903 | 0.292  | 0.125 | Molecular  | GO:00049 | NMDA glutamate receptor activity                                        | 0.13903 | 0.33916 | 0 | 0 | 1  | 8    |
| GO:0016717 oxidoreductase activity, acting on paired donors, with oxidation of a p | 1  | 0.13903 | 0.292  | 0.125 | Molecular  | GO:00016 | oxidoreductase activity, acting on paired donors, with oxidation of a p | 0.13903 | 0.33916 | 0 | 0 | 1  | 8    |
| GO:0019534 toxin transmembrane transporter activity                                | 1  | 0.13903 | 0.292  | 0.125 | Molecular  | GO:00019 | toxin transmembrane transporter activity                                | 0.13903 | 0.33916 | 0 | 0 | 1  | 8    |
| GO:0031995 insulin-like growth factor II binding                                   | 1  | 0.13903 | 0.292  | 0.125 | Molecular  | GO:00031 | insulin-like growth factor II binding                                   | 0.13903 | 0.33916 | 0 | 0 | 1  | 8    |
| GO:0034046 poly(G) binding                                                         | 1  | 0.13903 | 0.292  | 0.125 | Molecular  | GO:00034 | poly(G) binding                                                         | 0.13903 | 0.33916 | 0 | 0 | 1  | 8    |
| GO:0046820 alpha-1,3-galactosyltransferase activity                                | 0  | 0.13903 | 0.292  | 0.125 | Molecular  | GO:00046 | alpha-1,3-galactosyltransferase activity                                | 0.13903 | 0.33916 | 0 | 0 | 1  | 8    |
| GO:0047035 testosterone dehydrogenase (NAD+) activity                              | 1  | 0.13903 | 0.292  | 0.125 | Molecular  | GO:00047 | testosterone dehydrogenase (NAD+) activity                              | 0.13903 | 0.33916 | 0 | 0 | 1  | 8    |
| GO:0099107 ion channel regulator activity involved in G protein-coupled            | 1  | 0.13903 | 0.292  | 0.125 | Molecular  | GO:00099 | ion channel regulator activity involved in G protein-coupled receptor s | 0.13903 | 0.33916 | 0 | 0 | 1  | 8    |
| GO:0071478 cellular response to radiation                                          | 6  | 0.13948 | 1.858  | 0.031 | Biological | GO:00071 | cellular response to radiation                                          | 0.13948 | 0.34243 | 0 | 0 | 6  | 192  |
| GO:0000132 establishment of mitotic spindle orientation                            | 2  | 0.13954 | 0.619  | 0.056 | Biological | GO:00000 | establishment of mitotic spindle orientation                            | 0.13954 | 0.34243 | 0 | 0 | 2  | 36   |
| GO:0010934 macrophage cytokine production                                          | 2  | 0.13954 | 0.619  | 0.056 | Biological | GO:00010 | macrophage cytokine production                                          | 0.13954 | 0.34243 | 0 | 0 | 2  | 36   |
| GO:0010935 regulation of macrophage cytokine production                            | 2  | 0.13954 | 0.619  | 0.056 | Biological | GO:00010 | regulation of macrophage cytokine production                            | 0.13954 | 0.34243 | 0 | 0 | 2  | 36   |
| GO:0030224 monocyte differentiation                                                | 2  | 0.13954 | 0.619  | 0.056 | Biological | GO:00030 | monocyte differentiation                                                | 0.13954 | 0.34243 | 0 | 0 | 2  | 36   |
| GO:0043276 anoikis                                                                 | 2  | 0.13954 | 0.619  | 0.056 | Biological | GO:00043 | anoikis                                                                 | 0.13954 | 0.34243 | 0 | 0 | 2  | 36   |
| GO:0045777 positive regulation of blood pressure                                   | 2  | 0.13954 | 0.619  | 0.056 | Biological | GO:00045 | positive regulation of blood pressure                                   | 0.13954 | 0.34243 | 0 | 0 | 2  | 36   |
| GO:0059831 pigment cell differentiation                                            | 2  | 0.13954 | 0.619  | 0.056 | Biological | GO:00059 | pigment cell differentiation                                            | 0.13954 | 0.34243 | 0 | 0 | 2  | 36   |
| GO:0071276 cellular response to cadmium ion                                        | 2  | 0.13954 | 0.619  | 0.056 | Biological | GO:00071 | cellular response to cadmium ion                                        | 0.13954 | 0.34243 | 0 | 0 | 2  | 36   |
| GO:0046467 membrane lipid biosynthetic process                                     | 5  | 0.13967 | 1.548  | 0.033 | Biological | GO:00046 | membrane lipid biosynthetic process                                     | 0.13967 | 0.34243 | 0 | 0 | 5  | 150  |
| GO:0002294 CD4-positive, alpha-beta T cell differentiation involved in immune res  | 3  | 0.13974 | 0.929  | 0.042 | Biological | GO:00022 | CD4-positive, alpha-beta T cell differentiation involved in immune res  | 0.13974 | 0.34243 | 0 | 0 | 3  | 71   |
| GO:0015807 L-aminic acid transport                                                 | 3  | 0.13974 | 0.929  | 0.042 | Biological | GO:00015 | L-aminic acid transport                                                 | 0.13974 | 0.34243 | 0 | 0 | 3  | 71   |
| GO:0096113 polymeric cytoskeletal fiber                                            | 19 | 0.14076 | 5.538  | 0.024 | Cellular   | GO:00096 | polymeric cytoskeletal fiber                                            | 0.14076 | 0.35623 | 0 | 0 | 19 | 805  |
| GO:0014066 regulation of phosphatidylinositol 3-kinase signaling                   | 4  | 0.14159 | 1.238  | 0.036 | Biological | GO:00014 | regulation of phosphatidylinositol 3-kinase signaling                   | 0.14159 | 0.34663 | 0 | 0 | 4  | 110  |
| GO:1904659 glucose transmembrane transport                                         | 4  | 0.14159 | 1.238  | 0.036 | Biological | GO:00190 | glucose transmembrane transport                                         | 0.14159 | 0.34663 | 0 | 0 | 4  | 110  |
| GO:0048167 regulation of synaptic plasticity                                       | 6  | 0.14191 | 1.858  | 0.031 | Biological | GO:00048 | regulation of synaptic plasticity                                       | 0.14191 | 0.34722 | 0 | 0 | 6  | 193  |
| GO:0005675 lysosomal membrane                                                      | 11 | 0.14268 | 3.264  | 0.028 | Cellular   | GO:00005 | lysosomal membrane                                                      | 0.14268 | 0.35671 | 0 | 0 | 11 | 422  |
| GO:0098852 lysosomal membrane                                                      | 11 | 0.14268 | 3.264  | 0.028 | Cellular   | GO:00098 | lysosomal membrane                                                      | 0.14268 | 0.35671 | 0 | 0 | 11 | 422  |
| GO:0005250 immune system development                                               | 24 | 0.14286 | 7.43   | 0.023 | Biological | GO:00005 | immune system development                                               | 0.14286 | 0.34939 | 0 | 0 | 24 | 1003 |
| GO:0003700 DNA-binding transcription factor activity                               | 32 | 0.14303 | 9.357  | 0.023 | Molecular  | GO:00003 | DNA-binding transcription factor activity                               | 0.14303 | 0.34793 | 0 | 0 | 32 | 1418 |
| GO:0018108 peptidyl-tyrosine phosphorylation                                       | 10 | 0.14386 | 3.096  | 0.027 | Biological | GO:00018 | peptidyl-tyrosine phosphorylation                                       | 0.14386 | 0.35062 | 0 | 0 | 10 | 372  |
| GO:0002287 alpha-beta T cell activation involved in immune response                | 3  | 0.14397 | 0.929  | 0.042 | Biological | GO:00022 | alpha-beta T cell activation involved in immune response                | 0.14397 | 0.35062 | 0 | 0 | 3  | 72   |
| GO:0002293 alpha-beta T cell activation involved in immune response                | 3  | 0.14397 | 0.929  | 0.042 | Biological | GO:00022 | alpha-beta T cell activation involved in immune response                | 0.14397 | 0.35062 | 0 | 0 | 3  | 72   |
| GO:0032732 positive regulation of interleukin-1 production                         | 3  | 0.14397 | 0.929  | 0.042 | Biological | GO:00032 | positive regulation of interleukin-1 production                         | 0.14397 | 0.35062 | 0 | 0 | 3  | 72   |
| GO:0042058 regulation of epidermal growth factor receptor signaling path           | 3  | 0.14397 | 0.929  | 0.042 | Biological | GO:00042 | regulation of epidermal growth factor receptor signaling pathway        | 0.14397 | 0.35062 | 0 | 0 | 3  | 72   |
| GO:0051057 positive regulation of small GTPase mediated signal transduction        | 3  | 0.14397 | 0.929  | 0.042 | Biological | GO:00051 | positive regulation of small GTPase mediated signal transduction        | 0.14397 | 0.35062 | 0 | 0 | 3  | 72   |
| GO:0002763 positive regulation of peptide secretion                                | 4  | 0.14492 | 1.238  | 0.036 | Biological | GO:00002 | positive regulation of peptide secretion                                | 0.14492 | 0.35062 | 0 | 0 | 4  | 111  |
| GO:0055007 cardiac muscle cell differentiation                                     | 2  | 0.14575 | 1.238  | 0.036 | Cellular   | GO:00055 | cardiac muscle cell differentiation                                     | 0.14575 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0031333 negative regulation of protein-containing complex assembly              | 5  | 0.14525 | 1.548  | 0.033 | Biological | GO:00031 | negative regulation of protein-containing complex assembly              | 0.14525 | 0.35062 | 0 | 0 | 5  | 152  |
| GO:0046718 viral entry into host cell                                              | 5  | 0.14525 | 1.548  | 0.033 | Biological | GO:00046 | viral entry into host cell                                              | 0.14525 | 0.35062 | 0 | 0 | 5  | 152  |
| GO:1905039 carboxylic acid transmembrane transport                                 | 5  | 0.14525 | 1.548  | 0.033 | Biological | GO:00190 | carboxylic acid transmembrane transport                                 | 0.14525 | 0.35062 | 0 | 0 | 5  | 152  |
| GO:0071682 protein localization to extracellular region                            | 10 | 0.1456  | 3.096  | 0.027 | Biological | GO:00071 | protein localization to extracellular region                            | 0.1456  | 0.35062 | 0 | 0 | 10 | 373  |
| GO:0051024 membrane organization                                                   | 21 | 0.14564 | 6.502  | 0.023 | Cellular   | GO:00051 | membrane organization                                                   | 0.14564 | 0.35062 | 0 | 0 | 21 | 898  |
| GO:0051254 positive regulation of RNA metabolic process                            | 40 | 0.14569 | 12.384 | 0.027 | Biological | GO:00051 | positive regulation of RNA metabolic process                            | 0.14569 | 0.35062 | 0 | 0 | 40 | 1851 |
| GO:0010035 response to inorganic substance                                         | 14 | 0.14573 | 4.334  | 0.025 | Biological | GO:00010 | response to inorganic substance                                         | 0.14573 | 0.35062 | 0 | 0 | 14 | 560  |
| GO:1901615 organic hydroxy compound metabolic process                              | 14 | 0.14573 | 4.334  | 0.025 | Biological | GO:00190 | organic hydroxy compound metabolic process                              | 0.14573 | 0.35062 | 0 | 0 | 14 | 560  |
| GO:0031224 intrinsic component of membrane                                         | 49 | 0.14574 | 14.54  | 0.021 | Cellular   | GO:00031 | intrinsic component of membrane                                         | 0.14574 | 0.36074 | 0 | 0 | 49 | 2338 |
| GO:0007075 cardiac muscle cell differentiation                                     | 29 | 0.14575 | 8.036  | 0.027 | Cellular   | GO:00070 | cardiac muscle cell differentiation                                     | 0.14575 | 0.36074 | 0 | 0 | 29 | 1305 |
| GO:0000446 neutrophil mediated immunity                                            | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00000 | neutrophil mediated immunity                                            | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0007588 excretion                                                               | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00007 | excretion                                                               | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0010874 regulation of cholesterol efflux                                        | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00010 | regulation of cholesterol efflux                                        | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0014911 positive regulation of smooth muscle cell migration                     | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00014 | positive regulation of smooth muscle cell migration                     | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0021799 cerebral cortex radially oriented cell migration                        | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00021 | cerebral cortex radially oriented cell migration                        | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0031076 embryonic camera-type eye development                                   | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00031 | embryonic camera-type eye development                                   | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0045742 positive regulation of epidermal growth factor receptor sign            | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00045 | positive regulation of epidermal growth factor receptor signaling path  | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0046473 phosphatidic acid metabolic process                                     | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00046 | phosphatidic acid metabolic process                                     | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0050999 regulation of nitric-oxide synthase activity                            | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00050 | regulation of nitric-oxide synthase activity                            | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0051930 regulation of sensory perception of pain                                | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00051 | regulation of sensory perception of pain                                | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0051931 regulation of sensory perception                                        | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00051 | regulation of sensory perception                                        | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0050590 acylglycerol homeostasis                                                | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00050 | acylglycerol homeostasis                                                | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0070328 triacylglyceride homeostasis                                            | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00070 | triacylglyceride homeostasis                                            | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0050218 positive regulation of lipid kinase activity                            | 2  | 0.14582 | 0.619  | 0.054 | Biological | GO:00050 | positive regulation of lipid kinase activity                            | 0.14582 | 0.35062 | 0 | 0 | 2  | 37   |
| GO:0018212 peptidyl-tyrosine modification                                          | 10 | 0.14735 | 3.096  | 0.027 | Cellular   | GO:00018 | peptidyl-tyrosine modification                                          | 0.14735 | 0.35062 | 0 | 0 | 10 | 374  |
| GO:0002013 negative regulation of cellular macromolecule biosynthetic              | 34 | 0.14805 | 10.526 | 0.022 | Biological | GO:00020 | negative regulation of cellular macromolecule biosynthetic process      | 0.14805 | 0.35062 | 0 | 0 | 34 | 1549 |
| GO:0008643 carbohydrate transport                                                  | 5  | 0.14808 | 1.548  | 0.033 | Biological | GO:00008 | carbohydrate transport                                                  | 0.14808 | 0.35062 | 0 | 0 | 5  | 153  |
| GO:0032635 interleukin-6 production                                                | 5  | 0.14808 | 1.548  | 0.033 | Biological | GO:00032 | interleukin-6 production                                                | 0.14808 | 0.35062 | 0 | 0 | 5  | 153  |
| GO:0032675 regulation of interleukin-6 production                                  | 5  | 0.14808 | 1.548  | 0.033 | Biological | GO:00032 | regulation of interleukin-6 production                                  | 0.14808 | 0.35062 | 0 | 0 | 5  | 153  |
| GO:0050805 positive regulation of synaptic transmission                            | 5  | 0.14808 | 1.548  | 0.033 | Biological | GO:00050 | positive regulation of synaptic transmission                            | 0.14808 | 0.35062 | 0 | 0 | 5  | 153  |
| GO:1903825 organic acid transmembrane transport                                    | 5  | 0.14808 | 1.548  | 0.033 | Biological | GO:00190 | organic acid transmembrane transport                                    | 0.14808 | 0.35062 | 0 | 0 | 5  | 153  |
| GO:0003170 heart valve development                                                 | 3  | 0.14825 | 0.929  | 0.041 | Biological | GO:00003 | heart valve development                                                 | 0.14825 | 0.35062 | 0 | 0 | 3  | 73   |
| GO:0009247 glycolipid biosynthetic process                                         | 3  | 0.14825 | 0.929  | 0.041 | Biological | GO:00009 | glycolipid biosynthetic process                                         | 0.14825 | 0.35062 | 0 | 0 | 3  | 73   |
| GO:0010827 regulation of glucose transmembrane transport                           | 3  | 0.14825 | 0.929  | 0.041 | Biological | GO:00010 | regulation of glucose transmembrane transport                           | 0.14825 | 0.35062 | 0 | 0 | 3  | 73   |
| GO:0070733 negative regulation of ERK1 and ERK2 cascade                            | 3  | 0.14825 | 0.929  | 0.041 | Biological | GO:00070 | negative regulation of ERK1 and ERK2 cascade                            | 0.14825 | 0.35062 | 0 | 0 | 3  | 73   |
| GO:0033559 unsaturated fatty acid metabolic process                                | 4  | 0.14828 | 1.238  | 0.036 | Biological | GO:00033 | unsaturated fatty acid metabolic process                                | 0.14828 | 0.35062 | 0 | 0 | 4  | 112  |
| GO:0051897 positive regulation of protein kinase B signaling                       | 4  | 0.14828 | 1.238  | 0.036 | Biological | GO:00051 | positive regulation of protein kinase B signaling                       | 0.14828 | 0.35062 | 0 | 0 | 4  | 112  |
| GO:0061387 regulation of extent of cell growth                                     | 4  | 0.14828 | 1.238  | 0.036 | Biological | GO:00061 | regulation of extent of cell growth                                     | 0.14828 | 0.35062 | 0 | 0 | 4  | 112  |
| GO:0031968 organelle outer membrane                                                | 7  | 0.14855 | 2.077  | 0.029 | Cellular   | GO:00031 | organelle outer membrane                                                | 0.14855 | 0.36074 | 0 | 0 | 7  | 242  |
| GO:0031260 protein homeostasis                                                     | 6  | 0.14913 | 1.858  | 0.031 | Biological | GO:00031 | protein homeostasis                                                     | 0.14913 | 0.35062 | 0 | 0 | 6  | 193  |
| GO:0043198 dendritic shaft                                                         | 2  | 0.14947 | 0.593  | 0.053 | Cellular   | GO:00043 | dendritic shaft                                                         | 0.14947 | 0.36074 | 0 | 0 | 2  | 38   |
| GO:0019903 protein phosphatase binding                                             | 5  | 0.14958 | 1.462  | 0.033 | Molecular  | GO:00019 | protein phosphatase binding                                             | 0.14958 | 0.36017 | 0 | 0 | 5  | 151  |
| GO:0022843 voltage-gated cation channel activity                                   | 5  | 0.14958 | 1.462  | 0.033 | Molecular  | GO:00022 | voltage-gated cation channel activity                                   | 0.14958 | 0.36017 | 0 | 0 | 5  | 151  |
| GO:0000146 microfilament motor activity                                            | 2  | 0.14973 | 0.585  | 0.025 | Molecular  | GO:00000 | microfilament motor activity                                            | 0.14973 | 0.36017 | 0 | 0 | 2  | 37   |
| GO:0016229 steroid dehydrogenase activity                                          | 5  | 0.14973 | 0.585  | 0.025 | Molecular  | GO:00016 | steroid dehydrogenase activity                                          | 0.14973 | 0.36017 | 0 | 0 | 5  | 151  |
| GO:0050807 regulation of synapse organization                                      | 7  | 0.15008 | 2.167  | 0.029 | Biological | GO:00050 | regulation of synapse organization                                      | 0.15008 | 0.35062 | 0 | 0 | 7  | 240  |
| GO:0043524 negative regulation of neuron apoptotic process                         | 5  | 0.15093 | 1.548  | 0.032 | Biological | GO:00043 | negative regulation of neuron apoptotic process                         | 0.15093 | 0.35062 | 0 | 0 | 5  | 154  |
| GO:0010557 positive regulation of macromolecule biosynthetic process               | 42 | 0.15098 | 13.003 | 0.021 | Biological | GO:00010 | positive regulation of macromolecule biosynthetic process               | 0.15098 |         |   |   |    |      |

|                                                                                   |    |         |        |       |            |                                                                                       |         |         |   |   |    |      |
|-----------------------------------------------------------------------------------|----|---------|--------|-------|------------|---------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0070305 response to cGMP                                                       | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:0070305 response to cGMP                                                           | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:0071225 cellular response to muramyl dipeptide                                 | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:0071225 cellular response to muramyl dipeptide                                     | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:0072102 glomerulus morphogenesis                                               | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:0072102 glomerulus morphogenesis                                                   | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:0072239 melanocyte glomerular vasculature development                          | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:0072239 melanocyte glomerular vasculature development                              | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:0090394 negative regulation of excitatory postsynaptic potential               | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:0090394 negative regulation of excitatory postsynaptic potential                   | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:0098937 anterograde dendritic transport                                        | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:0098937 anterograde dendritic transport                                            | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:0098912 protein localization to axon                                           | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:0098912 protein localization to axon                                               | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:0098941 anterograde axonal protein transport                                   | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:0098941 anterograde axonal protein transport                                       | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:0010118 negative regulation of execution phase of apoptosis                    | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:0010118 negative regulation of execution phase of apoptosis                        | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:1902035 positive regulation of hematopoietic stem cell proliferation           | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:1902035 positive regulation of hematopoietic stem cell proliferation               | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:1902732 positive regulation of chondrocyte proliferation                       | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:1902732 positive regulation of chondrocyte proliferation                           | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:1902965 regulation of protein localization to early endosome                   | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:1902965 regulation of protein localization to early endosome                       | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:1902966 positive regulation of protein localization to early endosome          | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:1902966 positive regulation of protein localization to early endosome              | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:1903044 protein localization to membrane raft                                  | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:1903044 protein localization to membrane raft                                      | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:1903251 multi-ciliated epithelial cell differentiation                         | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:1903251 multi-ciliated epithelial cell differentiation                             | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:1903589 positive regulation of blood vessel endothelial cell proliferation     | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:1903589 positive regulation of blood vessel endothelial cell proliferation involve | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:1904776 regulation of protein localization to cell cortex                      | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:1904776 regulation of protein localization to cell cortex                          | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:1905276 regulation of epithelial tube formation                                | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:1905276 regulation of epithelial tube formation                                    | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:1905278 positive regulation of epithelial tube formation                       | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:1905278 positive regulation of epithelial tube formation                           | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:1905941 positive regulation of gonad development                               | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:1905941 positive regulation of gonad development                                   | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:1908006 liquid-gated ion channel signaling pathway                             | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:1908006 liquid-gated ion channel signaling pathway                                 | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:2000018 regulation of male gonad development                                   | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:2000018 regulation of male gonad development                                       | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:2001059 regulation of peptidyl-cysteine S-nitrosylation                        | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:2001059 regulation of peptidyl-cysteine S-nitrosylation                            | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:2004065 regulation of glycogen (starch) synthase activity                      | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:2004065 regulation of glycogen (starch) synthase activity                          | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:2001187 positive regulation of CD8-positive, alpha-beta T cell activation      | 1  | 0.15263 | 0.31   | 0.111 | Biological | GO:2001187 positive regulation of CD8-positive, alpha-beta T cell activation          | 0.15263 | 0.35062 | 0 | 0 | 1  | 9    |
| GO:0019867 outer membrane                                                         | 7  | 0.153   | 2.077  | 0.029 | Cellular   | GO:0019867 outer membrane                                                             | 0.153   | 0.36284 | 0 | 0 | 7  | 244  |
| GO:0016234 inclusion body                                                         | 3  | 0.15327 | 0.89   | 0.04  | Cellular   | GO:0016234 inclusion body                                                             | 0.15327 | 0.36284 | 0 | 0 | 3  | 75   |
| GO:0004860 protein kinase inhibitor activity                                      | 5  | 0.15351 | 0.877  | 0.041 | Molecular  | GO:0004860 protein kinase inhibitor activity                                          | 0.15351 | 0.36277 | 0 | 0 | 5  | 155  |
| GO:0007612 learning                                                               | 5  | 0.1538  | 1.548  | 0.032 | Biological | GO:0007612 learning                                                                   | 0.1538  | 0.35314 | 0 | 0 | 5  | 155  |
| GO:0120032 regulation of plasma membrane bounded cell projection assembly         | 6  | 0.15432 | 1.858  | 0.03  | Biological | GO:0120032 regulation of plasma membrane bounded cell projection assembly             | 0.15432 | 0.35418 | 0 | 0 | 6  | 198  |
| GO:0015194 L-serine transmembrane transporter activity                            | 1  | 0.155   | 0.292  | 0.111 | Molecular  | GO:0015194 L-serine transmembrane transporter activity                                | 0.155   | 0.36277 | 0 | 0 | 1  | 9    |
| GO:0015924 mannosyl-oligosaccharide mannosidase activity                          | 1  | 0.155   | 0.292  | 0.111 | Molecular  | GO:0015924 mannosyl-oligosaccharide mannosidase activity                              | 0.155   | 0.36277 | 0 | 0 | 1  | 9    |
| GO:0016671 oxidoreductase activity, acting on a sulfur group of donors, disulfide | 1  | 0.155   | 0.292  | 0.111 | Molecular  | GO:0016671 oxidoreductase activity, acting on a sulfur group of donors, disulfide     | 0.155   | 0.36277 | 0 | 0 | 1  | 9    |
| GO:0031545 peptidyl-proline 4-dioxygenase activity                                | 1  | 0.155   | 0.292  | 0.111 | Molecular  | GO:0031545 peptidyl-proline 4-dioxygenase activity                                    | 0.155   | 0.36277 | 0 | 0 | 1  | 9    |
| GO:0046977 TAP binding                                                            | 1  | 0.155   | 0.292  | 0.111 | Molecular  | GO:0046977 TAP binding                                                                | 0.155   | 0.36277 | 0 | 0 | 1  | 9    |
| GO:0047045 testosterone 17-beta-dehydrogenase (NADP+) activity                    | 1  | 0.155   | 0.292  | 0.111 | Molecular  | GO:0047045 testosterone 17-beta-dehydrogenase (NADP+) activity                        | 0.155   | 0.36277 | 0 | 0 | 1  | 9    |
| GO:0097200 cysteine-type endopeptidase activity involved in execution phase of a  | 1  | 0.155   | 0.292  | 0.111 | Molecular  | GO:0097200 cysteine-type endopeptidase activity involved in execution phase of a      | 0.155   | 0.36277 | 0 | 0 | 1  | 9    |
| GO:1905384 retrograde endosome maturation                                         | 2  | 0.156   | 0.292  | 0.111 | Molecular  | GO:1905384 retrograde endosome maturation                                             | 0.156   | 0.36277 | 0 | 0 | 2  | 39   |
| GO:0008645 hexose transmembrane transport                                         | 4  | 0.15609 | 1.238  | 0.035 | Biological | GO:0008645 hexose transmembrane transport                                             | 0.15609 | 0.35577 | 0 | 0 | 4  | 114  |
| GO:1902532 negative regulation of intracellular signal transduction               | 13 | 0.15517 | 4.025  | 0.025 | Biological | GO:1902532 negative regulation of intracellular signal transduction                   | 0.15517 | 0.3558  | 0 | 0 | 13 | 519  |
| GO:0031672 A band                                                                 | 2  | 0.15577 | 0.593  | 0.051 | Cellular   | GO:0031672 A band                                                                     | 0.15577 | 0.36712 | 0 | 0 | 2  | 39   |
| GO:0043028 cysteine-type endopeptidase regulator activity involved in apoptotic p | 2  | 0.15621 | 0.585  | 0.053 | Molecular  | GO:0043028 cysteine-type endopeptidase regulator activity involved in apoptotic p     | 0.15621 | 0.36463 | 0 | 0 | 2  | 38   |
| GO:0010558 negative regulation of macromolecule biosynthetic process              | 34 | 0.15683 | 1.238  | 0.023 | Biological | GO:0010558 negative regulation of macromolecule biosynthetic process                  | 0.15683 | 0.35324 | 0 | 0 | 34 | 1559 |
| GO:1901605 alpha-amino acid metabolic process                                     | 6  | 0.15686 | 1.858  | 0.03  | Biological | GO:1901605 alpha-amino acid metabolic process                                         | 0.15686 | 0.35934 | 0 | 0 | 6  | 199  |
| GO:0042581 specific granule                                                       | 5  | 0.15741 | 1.484  | 0.032 | Cellular   | GO:0042581 specific granule                                                           | 0.15741 | 0.36935 | 0 | 0 | 5  | 158  |
| GO:0043406 positive regulation of MAP kinase activity                             | 4  | 0.15854 | 1.238  | 0.035 | Biological | GO:0043406 positive regulation of MAP kinase activity                                 | 0.15854 | 0.36208 | 0 | 0 | 4  | 115  |
| GO:0071901 negative regulation of protein serine/threonine kinase activity        | 4  | 0.15854 | 1.238  | 0.035 | Biological | GO:0071901 negative regulation of protein serine/threonine kinase activity            | 0.15854 | 0.36208 | 0 | 0 | 4  | 115  |
| GO:0007618 mating                                                                 | 2  | 0.15856 | 0.619  | 0.051 | Biological | GO:0007618 mating                                                                     | 0.15856 | 0.36208 | 0 | 0 | 2  | 39   |
| GO:0044273 sulfur compound catabolic process                                      | 2  | 0.15856 | 0.619  | 0.051 | Biological | GO:0044273 sulfur compound catabolic process                                          | 0.15856 | 0.36208 | 0 | 0 | 2  | 39   |
| GO:0045823 positive regulation of heart contraction                               | 2  | 0.15856 | 0.619  | 0.051 | Biological | GO:0045823 positive regulation of heart contraction                                   | 0.15856 | 0.36208 | 0 | 0 | 2  | 39   |
| GO:0098926 postsynaptic signal transduction                                       | 2  | 0.15856 | 0.619  | 0.051 | Biological | GO:0098926 postsynaptic signal transduction                                           | 0.15856 | 0.36208 | 0 | 0 | 2  | 39   |
| GO:1901186 positive regulation of ERBB signaling pathway                          | 2  | 0.15856 | 0.619  | 0.051 | Biological | GO:1901186 positive regulation of ERBB signaling pathway                              | 0.15856 | 0.36208 | 0 | 0 | 2  | 39   |
| GO:0008113 epidermal cell differentiation                                         | 7  | 0.15918 | 2.167  | 0.029 | Biological | GO:0008113 epidermal cell differentiation                                             | 0.15918 | 0.36354 | 0 | 0 | 7  | 244  |
| GO:0007585 respiratory gaseous exchange by respiratory system                     | 8  | 0.15937 | 2.477  | 0.028 | Biological | GO:0007585 respiratory gaseous exchange by respiratory system                         | 0.15937 | 0.36354 | 0 | 0 | 8  | 289  |
| GO:0016324 apical plasma membrane                                                 | 10 | 0.1594  | 2.967  | 0.026 | Cellular   | GO:0016324 apical plasma membrane                                                     | 0.1594  | 0.37241 | 0 | 0 | 10 | 385  |
| GO:0060491 regulation of cell projection assembly                                 | 6  | 0.15942 | 1.858  | 0.03  | Biological | GO:0060491 regulation of cell projection assembly                                     | 0.15942 | 0.36354 | 0 | 0 | 6  | 200  |
| GO:0007189 adenylate cyclase-activating G protein-coupled receptor signaling pa   | 5  | 0.15961 | 1.548  | 0.032 | Biological | GO:0007189 adenylate cyclase-activating G protein-coupled receptor signaling pa       | 0.15961 | 0.36365 | 0 | 0 | 5  | 157  |
| GO:0013515 neuronal crest cell proliferation                                      | 6  | 0.1601  | 1.858  | 0.03  | Biological | GO:0013515 neuronal crest cell proliferation                                          | 0.1601  | 0.36365 | 0 | 0 | 6  | 197  |
| GO:0019002 phosphatase binding                                                    | 6  | 0.1602  | 1.754  | 0.03  | Molecular  | GO:0019002 phosphatase binding                                                        | 0.1602  | 0.37294 | 0 | 0 | 6  | 197  |
| GO:0007585 respiratory gaseous exchange by respiratory system                     | 3  | 0.1613  | 0.929  | 0.039 | Biological | GO:0007585 respiratory gaseous exchange by respiratory system                         | 0.1613  | 0.36666 | 0 | 0 | 3  | 76   |
| GO:0050013 cardiac muscle cell development                                        | 3  | 0.1613  | 0.929  | 0.039 | Biological | GO:0050013 cardiac muscle cell development                                            | 0.1613  | 0.36666 | 0 | 0 | 3  | 76   |
| GO:0055117 regulation of cardiac muscle contraction                               | 3  | 0.1613  | 0.929  | 0.039 | Biological | GO:0055117 regulation of cardiac muscle contraction                                   | 0.1613  | 0.36666 | 0 | 0 | 3  | 76   |
| GO:0098337 type I interferon signaling pathway                                    | 3  | 0.1613  | 0.929  | 0.039 | Biological | GO:0098337 type I interferon signaling pathway                                        | 0.1613  | 0.36666 | 0 | 0 | 3  | 76   |
| GO:0097194 execution phase of apoptosis                                           | 3  | 0.1613  | 0.929  | 0.039 | Biological | GO:0097194 execution phase of apoptosis                                               | 0.1613  | 0.36666 | 0 | 0 | 3  | 76   |
| GO:0032414 positive regulation of ion transmembrane transporter activity          | 4  | 0.16201 | 1.238  | 0.034 | Biological | GO:0032414 positive regulation of ion transmembrane transporter activity              | 0.16201 | 0.3681  | 0 | 0 | 4  | 116  |
| GO:0008328 ionotropic glutamate receptor complex                                  | 2  | 0.16212 | 0.593  | 0.05  | Cellular   | GO:0008328 ionotropic glutamate receptor complex                                      | 0.16212 | 0.37711 | 0 | 0 | 2  | 40   |
| GO:0004177 aminopeptidase activity                                                | 2  | 0.16275 | 0.585  | 0.051 | Molecular  | GO:0004177 aminopeptidase activity                                                    | 0.16275 | 0.3769  | 0 | 0 | 2  | 39   |
| GO:0146110 transition state stabilization                                         | 4  | 0.16332 | 1.238  | 0.034 | Biological | GO:0146110 transition state stabilization                                             | 0.16332 | 0.3769  | 0 | 0 | 4  | 117  |
| GO:0007188 adenylate cyclase-modulating G protein-coupled receptor signaling p    | 7  | 0.16382 | 2.167  | 0.028 | Biological | GO:0007188 adenylate cyclase-modulating G protein-coupled receptor signaling p        | 0.16382 | 0.36817 | 0 | 0 | 7  | 246  |
| GO:0050803 regulation of synapse structure or activity                            | 7  | 0.16382 | 2.167  | 0.028 | Biological | GO:0050803 regulation of synapse structure or activity                                | 0.16382 | 0.36817 | 0 | 0 | 7  | 246  |
| GO:0050870 positive regulation of T cell activation                               | 7  | 0.16382 | 2.167  | 0.028 | Biological | GO:0050870 positive regulation of T cell activation                                   | 0.16382 | 0.36817 | 0 | 0 | 7  | 246  |
| GO:0031327 negative regulation of cellular biosynthetic process                   | 35 | 0.16415 | 10.836 | 0.022 | Biological | GO:0031327 negative regulation of cellular biosynthetic process                       | 0.16415 | 0.36817 | 0 | 0 | 35 | 1618 |
| GO:0010453 regulation of cell fate commitment                                     | 2  | 0.16501 | 0.619  | 0.05  | Biological | GO:0010453 regulation of cell fate commitment                                         | 0.16501 | 0.36817 | 0 | 0 | 2  | 40   |
| GO:0010907 positive regulation of glucose metabolic process                       | 2  | 0.16501 | 0.619  | 0.05  | Biological | GO:0010907 positive regulation of glucose metabolic process                           | 0.16501 | 0.36817 | 0 | 0 | 2  | 40   |
| GO:0032728 positive regulation of interferon-beta production                      | 2  | 0.16501 | 0.619  | 0.05  | Biological | GO:0032728 positive regulation of interferon-beta production                          | 0.16501 | 0.36817 | 0 | 0 | 2  | 40   |
| GO:0034381 plasma lipoprotein particle clearance                                  | 2  | 0.16501 | 0.619  | 0.05  | Biological | GO:0034381 plasma lipoprotein particle clearance                                      | 0.16501 | 0.36817 | 0 | 0 | 2  | 40   |
| GO:0008207 regulation of triglyceride metabolic process                           | 2  | 0.16501 | 0.619  | 0.05  | Biological | GO:0008207 regulation of triglyceride metabolic process                               | 0.16501 | 0.36817 | 0 | 0 | 2  | 40   |
| GO:0097106 postsynaptic density organization                                      | 2  | 0.16501 | 0.619  | 0.05  | Biological | GO:0097106 postsynaptic density organization                                          | 0.16501 | 0.36817 | 0 | 0 | 2  | 40   |
| GO:1901661 quinine metabolic process                                              | 2  | 0.16501 | 0.619  | 0.05  | Biological | GO:1901661 quinine metabolic process                                                  | 0.16501 | 0.36817 | 0 | 0 | 2  | 40   |
| GO:1903524 positive regulation of blood circulation                               | 2  | 0.16501 | 0.619  | 0.05  | Biological | GO:1903524 positive regulation of blood circulation                                   | 0.16501 | 0.36817 | 0 | 0 | 2  | 40   |
| GO:0002367 cytokine production involved in immune response                        | 4  | 0.16552 | 1.238  | 0.034 | Biological | GO:0002367 cytokine production involved in immune response                            | 0.16552 | 0.36817 | 0 | 0 | 4  | 117  |
| GO:0002718 regulation of cytokine production involved in immune response          | 4  | 0.16552 | 1.238  | 0.034 | Biological | GO:0002718 regulation of cytokine production involved in immune response              | 0.16552 | 0.36817 | 0 | 0 | 4  | 117  |
| GO:0015749 monosaccharide transmembrane transport                                 | 4  | 0.16552 | 1.238  | 0.034 | Biological | GO:0015749 monosaccharide transmembrane transport                                     | 0.16552 | 0.36817 | 0 | 0 | 4  | 117  |
| GO:0035710 CD4-positive, alpha-beta T cell activation                             | 4  | 0.16552 | 1.238  | 0.034 | Biological | GO:0035710 CD4-positive, alpha-beta T cell activation                                 | 0.16552 | 0.36817 | 0 | 0 | 4  | 117  |
| GO:0044409 entry into host                                                        | 5  | 0.16552 | 1.548  | 0.031 | Biological | GO:0044409 entry into host                                                            | 0.16552 | 0.36817 | 0 | 0 | 5  | 159  |
| GO:0048644 muscle organ morphogenesis                                             | 3  | 0.16573 | 0.929  | 0.039 | Biological | GO:0048644 muscle organ morphogenesis                                                 | 0.16573 | 0.36817 | 0 | 0 | 3  | 77   |
| GO:0031902 late endosome membrane                                                 | 5  | 0.16614 | 1.484  | 0.031 | Cellular   | GO:0031902 late endosome membrane                                                     | 0.16614 | 0.36817 | 0 | 0 | 5  | 161  |
| GO:0042424 Lysate degradation region of axon                                      | 1  | 0.16635 | 0.297  | 0.1   | Cellular   | GO:0042424 Lysate degradation region of                                               |         |         |   |   |    |      |

|                                                                                         |    |         |        |       |            |                                                                                      |         |         |   |   |    |      |
|-----------------------------------------------------------------------------------------|----|---------|--------|-------|------------|--------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:2001064 negative regulation of mesenchymal cell apoptotic process                    | 1  | 0.16809 | 0.31   | 0.1   | Biological | GO:2001 negative regulation of mesenchymal cell apoptotic process                    | 0.16809 | 0.36817 | 0 | 0 | 1  | 10   |
| GO:0030139 endocytic vesicle                                                            | 9  | 0.1685  | 2.671  | 0.028 | Cellular   | GO:0030 endocytic vesicle                                                            | 0.1685  | 0.38365 | 0 | 0 | 9  | 343  |
| GO:0030140 trans-Golgi network transport vesicle                                        | 2  | 0.16852 | 0.593  | 0.049 | Cellular   | GO:0030 trans-Golgi network transport vesicle                                        | 0.16852 | 0.38365 | 0 | 0 | 2  | 41   |
| GO:0071345 cellular response to cytokine stimulus                                       | 19 | 0.16854 | 5.882  | 0.023 | Biological | GO:0071 cellular response to cytokine stimulus                                       | 0.16854 | 0.36852 | 0 | 0 | 19 | 819  |
| GO:0019901 protein kinase binding                                                       | 17 | 0.1686  | 4.971  | 0.024 | Molecular  | GO:0019 protein kinase binding                                                       | 0.1686  | 0.3769  | 0 | 0 | 17 | 709  |
| GO:0090904 ligand-gated cation channel activity                                         | 4  | 0.16883 | 1.17   | 0.034 | Molecular  | GO:0090 ligand-gated cation channel activity                                         | 0.16883 | 0.3769  | 0 | 0 | 4  | 116  |
| GO:0002286 T cell activation involved in immune response                                | 4  | 0.16905 | 1.238  | 0.034 | Biological | GO:0002 T cell activation involved in immune response                                | 0.16905 | 0.36978 | 0 | 0 | 4  | 118  |
| GO:0030203 glycosaminoglycan metabolic process                                          | 1  | 0.17006 | 0.292  | 0.039 | Molecular  | GO:0030 glycosaminoglycan metabolic process                                          | 0.17006 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0019216 regulation of lipid metabolic process                                        | 9  | 0.17011 | 2.786  | 0.026 | Biological | GO:0019 regulation of lipid metabolic process                                        | 0.17011 | 0.37132 | 0 | 0 | 9  | 340  |
| GO:0008088 axo-dendritic transport                                                      | 3  | 0.1702  | 0.929  | 0.038 | Biological | GO:0008 axo-dendritic transport                                                      | 0.1702  | 0.37132 | 0 | 0 | 3  | 78   |
| GO:0021536 diencephalon development                                                     | 3  | 0.1702  | 0.929  | 0.038 | Biological | GO:0021 diencephalon development                                                     | 0.1702  | 0.37132 | 0 | 0 | 3  | 78   |
| GO:0071357 cellular response to type I interferon                                       | 3  | 0.1702  | 0.929  | 0.038 | Biological | GO:0071 cellular response to type I interferon                                       | 0.1702  | 0.37132 | 0 | 0 | 3  | 78   |
| GO:0072078 nephrocyte morphogenesis                                                     | 1  | 0.17026 | 0.292  | 0.1   | Molecular  | GO:0072 nephrocyte morphogenesis                                                     | 0.17026 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:2000736 regulation of stem cell differentiation                                      | 3  | 0.1702  | 0.929  | 0.038 | Biological | GO:2000 regulation of stem cell differentiation                                      | 0.1702  | 0.37132 | 0 | 0 | 3  | 78   |
| GO:0000099 sulfur amino acid transmembrane transporter activity                         | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0000 sulfur amino acid transmembrane transporter activity                         | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0003680 minor groove of adenine-thymine-rich DNA binding                             | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0003 minor groove of adenine-thymine-rich DNA binding                             | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0004655 prostaglandin receptor activity                                              | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0004 prostaglandin receptor activity                                              | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0015180 L-alanine transmembrane transporter activity                                 | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0015 L-alanine transmembrane transporter activity                                 | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0015183 L-aspartate transmembrane transporter activity                               | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0015 L-aspartate transmembrane transporter activity                               | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0015187 glycine transmembrane transporter activity                                   | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0015 glycine transmembrane transporter activity                                   | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0015643 toxic substance binding                                                      | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0015 toxic substance binding                                                      | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0019911 structural constituent of myelin sheath                                      | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0019 structural constituent of myelin sheath                                      | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0034713 type I transforming growth factor beta receptor binding                      | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0034 type I transforming growth factor beta receptor binding                      | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0043121 neurotrophin binding                                                         | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0043 neurotrophin binding                                                         | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0046974 histone methyltransferase activity (H3-K9 specific)                          | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0046 histone methyltransferase activity (H3-K9 specific)                          | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0052740 1-acyl-2-hydroxyphosphatidylserine acylhydrolase activity                    | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0052 1-acyl-2-hydroxyphosphatidylserine acylhydrolase activity                    | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0007039 protein-glutamic acid ligase activity                                        | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0007 protein-glutamic acid ligase activity                                        | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0070740 tubulin-glutamic acid ligase activity                                        | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0070 tubulin-glutamic acid ligase activity                                        | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0057199 cysteine-type endopeptidase activity involved in apoptotic signaling pathway | 1  | 0.17066 | 0.292  | 0.1   | Molecular  | GO:0057 cysteine-type endopeptidase activity involved in apoptotic signaling pathway | 0.17066 | 0.3769  | 0 | 0 | 1  | 10   |
| GO:0001618 virus receptor activity                                                      | 3  | 0.17147 | 0.877  | 0.039 | Molecular  | GO:0001 virus receptor activity                                                      | 0.17147 | 0.3769  | 0 | 0 | 3  | 77   |
| GO:0016835 carbon-oxygen lyase activity                                                 | 3  | 0.17147 | 0.877  | 0.039 | Molecular  | GO:0016 carbon-oxygen lyase activity                                                 | 0.17147 | 0.3769  | 0 | 0 | 3  | 77   |
| GO:0019210 kinase inhibitor activity                                                    | 3  | 0.17147 | 0.877  | 0.039 | Molecular  | GO:0019 kinase inhibitor activity                                                    | 0.17147 | 0.3769  | 0 | 0 | 3  | 77   |
| GO:0003016 respiratory chain complex                                                    | 2  | 0.1715  | 0.619  | 0.049 | Biological | GO:0003 respiratory chain complex                                                    | 0.1715  | 0.37271 | 0 | 0 | 2  | 41   |
| GO:0006882 cellular zinc ion homeostasis                                                | 2  | 0.1715  | 0.619  | 0.049 | Biological | GO:0006 cellular zinc ion homeostasis                                                | 0.1715  | 0.37271 | 0 | 0 | 2  | 41   |
| GO:0009069 serine family amino acid metabolic process                                   | 2  | 0.1715  | 0.619  | 0.049 | Biological | GO:0009 serine family amino acid metabolic process                                   | 0.1715  | 0.37271 | 0 | 0 | 2  | 41   |
| GO:0021532 neural tube patterning                                                       | 2  | 0.1715  | 0.619  | 0.049 | Biological | GO:0021 neural tube patterning                                                       | 0.1715  | 0.37271 | 0 | 0 | 2  | 41   |
| GO:0032881 regulation of polysaccharide metabolic process                               | 2  | 0.1715  | 0.619  | 0.049 | Biological | GO:0032 regulation of polysaccharide metabolic process                               | 0.1715  | 0.37271 | 0 | 0 | 2  | 41   |
| GO:0042417 dopamine metabolic process                                                   | 2  | 0.1715  | 0.619  | 0.049 | Biological | GO:0042 dopamine metabolic process                                                   | 0.1715  | 0.37271 | 0 | 0 | 2  | 41   |
| GO:0048471 skeletal muscle fiber development                                            | 2  | 0.1715  | 0.619  | 0.049 | Biological | GO:0048 skeletal muscle fiber development                                            | 0.1715  | 0.37271 | 0 | 0 | 2  | 41   |
| GO:1902742 apoptotic process involved in development                                    | 2  | 0.1715  | 0.619  | 0.049 | Biological | GO:1902 apoptotic process involved in development                                    | 0.1715  | 0.37271 | 0 | 0 | 2  | 41   |
| GO:0050905 neuromuscular process                                                        | 5  | 0.1715  | 1.548  | 0.031 | Biological | GO:0050 neuromuscular process                                                        | 0.1715  | 0.37271 | 0 | 0 | 5  | 161  |
| GO:0042734 presynaptic membrane                                                         | 5  | 0.17207 | 1.484  | 0.031 | Cellular   | GO:0042 presynaptic membrane                                                         | 0.17207 | 0.39006 | 0 | 0 | 5  | 163  |
| GO:0019221 cytokine-mediated cytokine signaling pathway                                 | 7  | 0.17232 | 3.115  | 0.028 | Biological | GO:0019 cytokine-mediated cytokine signaling pathway                                 | 0.17232 | 0.37378 | 0 | 0 | 7  | 259  |
| GO:0000029 protein polyubiquitination                                                   | 7  | 0.17328 | 2.167  | 0.028 | Biological | GO:0000 protein polyubiquitination                                                   | 0.17328 | 0.37609 | 0 | 0 | 7  | 250  |
| GO:0031334 positive regulation of protein-containing complex assembly                   | 7  | 0.17328 | 2.167  | 0.028 | Biological | GO:0031 positive regulation of protein-containing complex assembly                   | 0.17328 | 0.37609 | 0 | 0 | 7  | 250  |
| GO:0048471 perinuclear region of cytoplasm                                              | 17 | 0.17328 | 2.167  | 0.028 | Cellular   | GO:0048 perinuclear region of cytoplasm                                              | 0.17328 | 0.37609 | 0 | 0 | 17 | 733  |
| GO:0048639 positive regulation of developmental growth                                  | 5  | 0.17453 | 1.548  | 0.031 | Biological | GO:0048 positive regulation of developmental growth                                  | 0.17453 | 0.37832 | 0 | 0 | 5  | 162  |
| GO:0002270 positive regulation of cytokine production involved in immune response       | 3  | 0.17469 | 0.929  | 0.038 | Biological | GO:0002 positive regulation of cytokine production involved in immune response       | 0.17469 | 0.37832 | 0 | 0 | 3  | 79   |
| GO:0000890 embryonic pattern specification                                              | 3  | 0.17469 | 0.929  | 0.038 | Biological | GO:0000 embryonic pattern specification                                              | 0.17469 | 0.37832 | 0 | 0 | 3  | 79   |
| GO:0043502 regulation of muscle adaptation                                              | 3  | 0.17469 | 0.929  | 0.038 | Biological | GO:0043 regulation of muscle adaptation                                              | 0.17469 | 0.37832 | 0 | 0 | 3  | 79   |
| GO:1901184 regulation of ERBB signaling pathway                                         | 3  | 0.17469 | 0.929  | 0.038 | Biological | GO:1901 regulation of ERBB signaling pathway                                         | 0.17469 | 0.37832 | 0 | 0 | 3  | 79   |
| GO:0030317 sarcoplasmic reticulum membrane                                              | 2  | 0.17496 | 0.593  | 0.048 | Cellular   | GO:0030 sarcoplasmic reticulum membrane                                              | 0.17496 | 0.39328 | 0 | 0 | 2  | 42   |
| GO:0001071 integral component of membrane                                               | 48 | 0.17803 | 12.423 | 0.021 | Cellular   | GO:0001 integral component of membrane                                               | 0.17803 | 0.38182 | 0 | 0 | 48 | 2343 |
| GO:0140272 exogenous protein binding                                                    | 3  | 0.17806 | 0.877  | 0.038 | Cellular   | GO:0140 exogenous protein binding                                                    | 0.17806 | 0.38589 | 0 | 0 | 3  | 78   |
| GO:0046632 alpha-beta T cell differentiation                                            | 4  | 0.17818 | 1.238  | 0.033 | Biological | GO:0046 alpha-beta T cell differentiation                                            | 0.17818 | 0.38139 | 0 | 0 | 4  | 120  |
| GO:0049643 carboxylic acid transmembrane transporter activity                           | 5  | 0.17659 | 1.462  | 0.031 | Molecular  | GO:0049 carboxylic acid transmembrane transporter activity                           | 0.17659 | 0.38619 | 0 | 0 | 5  | 160  |
| GO:0007595 lactation                                                                    | 2  | 0.17803 | 0.518  | 0.048 | Biological | GO:0007 lactation                                                                    | 0.17803 | 0.38182 | 0 | 0 | 2  | 42   |
| GO:0019320 hexose catabolic process                                                     | 2  | 0.17803 | 0.518  | 0.048 | Biological | GO:0019 hexose catabolic process                                                     | 0.17803 | 0.38182 | 0 | 0 | 2  | 42   |
| GO:0040001 establishment of mitotic spindle localization                                | 2  | 0.17803 | 0.518  | 0.048 | Biological | GO:0040 establishment of mitotic spindle localization                                | 0.17803 | 0.38182 | 0 | 0 | 2  | 42   |
| GO:0048246 macrophage chemotaxis                                                        | 2  | 0.17803 | 0.518  | 0.048 | Biological | GO:0048 macrophage chemotaxis                                                        | 0.17803 | 0.38182 | 0 | 0 | 2  | 42   |
| GO:0051155 positive regulation of striated muscle cell differentiation                  | 2  | 0.17803 | 0.518  | 0.048 | Biological | GO:0051 positive regulation of striated muscle cell differentiation                  | 0.17803 | 0.38182 | 0 | 0 | 2  | 42   |
| GO:0050569 zinc ion homeostasis                                                         | 2  | 0.17803 | 0.518  | 0.048 | Biological | GO:0050 zinc ion homeostasis                                                         | 0.17803 | 0.38182 | 0 | 0 | 2  | 42   |
| GO:1901908 town transport                                                               | 2  | 0.17803 | 0.518  | 0.048 | Biological | GO:1901 town transport                                                               | 0.17803 | 0.38182 | 0 | 0 | 2  | 42   |
| GO:2000403 positive regulation of lymphocyte migration                                  | 2  | 0.17803 | 0.518  | 0.048 | Biological | GO:2000 positive regulation of lymphocyte migration                                  | 0.17803 | 0.38182 | 0 | 0 | 2  | 42   |
| GO:0001664 G protein-coupled receptor binding                                           | 8  | 0.1787  | 2.339  | 0.027 | Molecular  | GO:0001 G protein-coupled receptor binding                                           | 0.1787  | 0.3898  | 0 | 0 | 8  | 293  |
| GO:0002292 T cell differentiation involved in immune response                           | 3  | 0.17922 | 0.929  | 0.037 | Biological | GO:0002 T cell differentiation involved in immune response                           | 0.17922 | 0.38182 | 0 | 0 | 3  | 80   |
| GO:0014068 positive regulation of phosphatidylinositol 3-kinase signaling               | 3  | 0.17922 | 0.929  | 0.037 | Biological | GO:0014 positive regulation of phosphatidylinositol 3-kinase signaling               | 0.17922 | 0.38182 | 0 | 0 | 3  | 80   |
| GO:0053142 organic anion transmembrane transporter activity                             | 1  | 0.17979 | 1.238  | 0.033 | Biological | GO:0053 organic anion transmembrane transporter activity                             | 0.17979 | 0.38182 | 0 | 0 | 1  | 11   |
| GO:0018210 peptidyl-threonine modification                                              | 4  | 0.17979 | 1.238  | 0.033 | Biological | GO:0018 peptidyl-threonine modification                                              | 0.17979 | 0.38182 | 0 | 0 | 4  | 121  |
| GO:0045931 positive regulation of mitotic cell cycle                                    | 4  | 0.17979 | 1.238  | 0.033 | Biological | GO:0045 positive regulation of mitotic cell cycle                                    | 0.17979 | 0.38182 | 0 | 0 | 4  | 121  |
| GO:0051101 regulation of DNA binding                                                    | 4  | 0.17979 | 1.238  | 0.033 | Biological | GO:0051 regulation of DNA binding                                                    | 0.17979 | 0.38182 | 0 | 0 | 4  | 121  |
| GO:0005635 nuclear envelope                                                             | 12 | 0.17986 | 3.551  | 0.024 | Cellular   | GO:0005 nuclear envelope                                                             | 0.17986 | 0.39759 | 0 | 0 | 12 | 482  |
| GO:0030705 cytoskeletal-dependent intracellular transport                               | 6  | 0.18027 | 1.858  | 0.029 | Cellular   | GO:0030 cytoskeletal-dependent intracellular transport                               | 0.18027 | 0.38182 | 0 | 0 | 6  | 238  |
| GO:0031094 platelet dense tubular network                                               | 1  | 0.18138 | 0.297  | 0.091 | Cellular   | GO:0031 platelet dense tubular network                                               | 0.18138 | 0.39759 | 0 | 0 | 1  | 11   |
| GO:0032280 symmetric synapse                                                            | 1  | 0.18138 | 0.297  | 0.091 | Cellular   | GO:0032 symmetric synapse                                                            | 0.18138 | 0.39759 | 0 | 0 | 1  | 11   |
| GO:0098981 cholinergic synapse                                                          | 1  | 0.18138 | 0.297  | 0.091 | Cellular   | GO:0098 cholinergic synapse                                                          | 0.18138 | 0.39759 | 0 | 0 | 1  | 11   |
| GO:0097060 synaptic membrane                                                            | 10 | 0.18176 | 2.567  | 0.025 | Cellular   | GO:0097 synaptic membrane                                                            | 0.18176 | 0.39759 | 0 | 0 | 10 | 397  |
| GO:0096634 postsynaptic specialization membrane                                         | 4  | 0.18207 | 1.187  | 0.031 | Cellular   | GO:0096 postsynaptic specialization membrane                                         | 0.18207 | 0.39759 | 0 | 0 | 4  | 123  |
| GO:1903230 regulation of protein modification by small protein conjugation or removal   | 7  | 0.18298 | 2.167  | 0.028 | Biological | GO:1903 regulation of protein modification by small protein conjugation or removal   | 0.18298 | 0.38182 | 0 | 0 | 7  | 254  |
| GO:2000241 regulation of reproductive process                                           | 6  | 0.18323 | 1.858  | 0.029 | Biological | GO:2000 regulation of reproductive process                                           | 0.18323 | 0.38182 | 0 | 0 | 6  | 209  |
| GO:0001660 fever generation                                                             | 1  | 0.18326 | 0.31   | 0.091 | Biological | GO:0001 fever generation                                                             | 0.18326 | 0.38182 | 0 | 0 | 1  | 11   |
| GO:0002158 osteoclast proliferation                                                     | 1  | 0.18326 | 0.31   | 0.091 | Biological | GO:0002 osteoclast proliferation                                                     | 0.18326 | 0.38182 | 0 | 0 | 1  | 11   |
| GO:0002732 positive regulation of dendritic cell cytokine production                    | 1  | 0.18326 | 0.31   | 0.091 | Biological | GO:0002 positive regulation of dendritic cell cytokine production                    | 0.18326 | 0.38182 | 0 | 0 | 1  | 11   |
| GO:0003357 noradrenergic neuron differentiation                                         | 1  | 0.18326 | 0.31   | 0.091 | Biological | GO:0003 noradrenergic neuron differentiation                                         | 0.18326 | 0.38182 | 0 | 0 | 1  | 11   |
| GO:0006568 tryptophan metabolic process                                                 | 1  | 0.18326 | 0.31   | 0.091 | Biological | GO:0006 tryptophan metabolic process                                                 | 0.18326 | 0.38182 | 0 | 0 | 1  | 11   |
| GO:0006995 cellular response to nitrogen starvation                                     | 1  | 0.18326 | 0.31   | 0.091 | Biological | GO:0006 cellular response to nitrogen starvation                                     | 0.18326 | 0.38182 | 0 | 0 | 1  | 11   |
| GO:0007406 negative regulation of neuroblast proliferation                              | 1  | 0.18326 | 0.31   | 0.091 | Biological | GO:0007 negative regulation of neuroblast proliferation                              | 0.18326 | 0.38182 | 0 | 0 | 1  | 11   |
| GO:0007494 midgut development                                                           | 1  | 0.18326 | 0.31   | 0.091 | Biological | GO:0007 midgut development                                                           | 0.18326 | 0.38182 | 0 | 0 | 1  | 11   |
| GO:0010936 negative regulation of macrophage cytokine production                        | 1  | 0.18326 | 0.31   | 0.091 | Biological | GO:0010 negative regulation of macrophage cytokine production                        | 0.18326 | 0.38182 | 0 | 0 | 1  | 11   |
| GO:0014820 tonic smooth muscle contraction                                              | 1  | 0.18326 | 0.31   | 0.091 | Biological | GO:0014 tonic smooth muscle contraction                                              | 0.18326 | 0.38182 | 0 | 0 | 1  | 11   |
| GO:0018401 peptidyl-proline hydroxylation to 4-hydroxy-L-proline                        | 1  | 0.      |        |       |            |                                                                                      |         |         |   |   |    |      |

|                                                                                        |    |         |        |       |            |                                                                                      |           |         |   |   |    |      |
|----------------------------------------------------------------------------------------|----|---------|--------|-------|------------|--------------------------------------------------------------------------------------|-----------|---------|---|---|----|------|
| GO:200644 regulation of receptor catabolic process                                     | 1  | 0.18326 | 0.31   | 0.091 | Biological | GO:20001 regulation of receptor catabolic process                                    | 0.18326   | 0.38182 | 0 | 0 | 1  | 11   |
| GO:200123 negative regulation of neuron migration                                      | 1  | 0.18326 | 0.31   | 0.091 | Biological | GO:20011 negative regulation of neuron migration                                     | 0.18326   | 0.38182 | 0 | 0 | 1  | 11   |
| GO:1830262 bone mineralization                                                         | 4  | 0.18342 | 1.238  | 0.033 | Biological | GO:00302 bone mineralization                                                         | 0.18342   | 0.38183 | 0 | 0 | 4  | 122  |
| GO:0031398 positive regulation of protein ubiquitination                               | 4  | 0.18342 | 1.238  | 0.033 | Biological | GO:00351 positive regulation of protein ubiquitination                               | 0.18342   | 0.38183 | 0 | 0 | 4  | 122  |
| GO:1901657 glycosyl compound metabolic process                                         | 3  | 0.18379 | 0.929  | 0.037 | Biological | GO:19011 glycosyl compound metabolic process                                         | 0.18379   | 0.38243 | 0 | 0 | 3  | 81   |
| GO:0051234 establishment of localization                                               | 95 | 0.18407 | 29.412 | 0.02  | Biological | GO:00511 establishment of localization                                               | 0.18407   | 0.38286 | 0 | 0 | 95 | 4794 |
| GO:0001974 blood vessel remodeling                                                     | 2  | 0.1846  | 0.819  | 0.047 | Biological | GO:00011 blood vessel remodeling                                                     | 0.1846    | 0.383   | 0 | 0 | 2  | 43   |
| GO:1903176 aortic valve development                                                    | 2  | 0.1846  | 0.819  | 0.047 | Biological | GO:00013 aortic valve development                                                    | 0.1846    | 0.383   | 0 | 0 | 2  | 43   |
| GO:0016286 O-glycan processing                                                         | 2  | 0.1846  | 0.819  | 0.047 | Biological | GO:00161 O-glycan processing                                                         | 0.1846    | 0.383   | 0 | 0 | 2  | 43   |
| GO:0033574 response to testosterone                                                    | 2  | 0.1846  | 0.819  | 0.047 | Biological | GO:00333 response to testosterone                                                    | 0.1846    | 0.383   | 0 | 0 | 2  | 43   |
| GO:0051294 establishment of spindle orientation                                        | 2  | 0.1846  | 0.819  | 0.047 | Biological | GO:00511 establishment of spindle orientation                                        | 0.1846    | 0.383   | 0 | 0 | 2  | 43   |
| GO:0071364 cellular response to epidermal growth factor stimulus                       | 2  | 0.1846  | 0.819  | 0.047 | Biological | GO:00711 cellular response to epidermal growth factor stimulus                       | 0.1846    | 0.383   | 0 | 0 | 2  | 43   |
| GO:0002376 immune system process                                                       | 59 | 0.18593 | 18.266 | 0.02  | Biological | GO:00023 immune system process                                                       | 0.18593   | 0.38502 | 0 | 0 | 59 | 2888 |
| GO:0002162 dystroglycan binding                                                        | 1  | 0.18604 | 0.292  | 0.091 | Molecular  | GO:00022 dystroglycan binding                                                        | 0.18604   | 0.39414 | 0 | 0 | 1  | 11   |
| GO:0004954 prostanoind receptor activity                                               | 1  | 0.18604 | 0.292  | 0.091 | Molecular  | GO:00044 prostanoind receptor activity                                               | 0.18604   | 0.39414 | 0 | 0 | 1  | 11   |
| GO:0016884 carbon-nitrogen ligase activity, with glutamine as amido-N-                 | 1  | 0.18604 | 0.292  | 0.091 | Molecular  | GO:00166 carbon-nitrogen ligase activity, with glutamine as amido-N-donor            | 0.18604   | 0.39414 | 0 | 0 | 1  | 11   |
| GO:0019107 myristoyltransferase activity                                               | 1  | 0.18604 | 0.292  | 0.091 | Molecular  | GO:00199 myristoyltransferase activity                                               | 0.18604   | 0.39414 | 0 | 0 | 1  | 11   |
| GO:0030283 testosterone dehydrogenase [NAD(P)] activity                                | 1  | 0.18604 | 0.292  | 0.091 | Molecular  | GO:00302 testosterone dehydrogenase [NAD(P)] activity                                | 0.18604   | 0.39414 | 0 | 0 | 1  | 11   |
| GO:0045294 alpha-catenin binding                                                       | 1  | 0.18604 | 0.292  | 0.091 | Molecular  | GO:00455 alpha-catenin binding                                                       | 0.18604   | 0.39414 | 0 | 0 | 1  | 11   |
| GO:0048407 platelet-derived growth factor binding                                      | 1  | 0.18604 | 0.292  | 0.091 | Molecular  | GO:00488 platelet-derived growth factor binding                                      | 0.18604   | 0.39414 | 0 | 0 | 1  | 11   |
| GO:0052739 phosphatidyserine 1-acylhydrolase activity                                  | 1  | 0.18604 | 0.292  | 0.091 | Molecular  | GO:00528 phosphatidyserine 1-acylhydrolase activity                                  | 0.18604   | 0.39414 | 0 | 0 | 1  | 11   |
| GO:0070037 delta-catenin binding                                                       | 1  | 0.18604 | 0.292  | 0.091 | Molecular  | GO:00700 delta-catenin binding                                                       | 0.18604   | 0.39414 | 0 | 0 | 1  | 11   |
| GO:0070410 co-SMAD binding                                                             | 1  | 0.18604 | 0.292  | 0.091 | Molecular  | GO:00706 co-SMAD binding                                                             | 0.18604   | 0.39414 | 0 | 0 | 1  | 11   |
| GO:0042542 response to hydrogen peroxide                                               | 4  | 0.18708 | 1.238  | 0.033 | Biological | GO:00424 response to hydrogen peroxide                                               | 0.18708   | 0.38783 | 0 | 0 | 4  | 123  |
| GO:0003713 transcription coactivator activity                                          | 8  | 0.18783 | 2.339  | 0.027 | Molecular  | GO:00033 transcription coactivator activity                                          | 0.18783   | 0.39414 | 0 | 0 | 8  | 297  |
| GO:0006898 receptor-mediated endocytosis                                               | 7  | 0.18791 | 2.167  | 0.027 | Biological | GO:00066 receptor-mediated endocytosis                                               | 0.18791   | 0.38922 | 0 | 0 | 7  | 256  |
| GO:0043122 regulation of I-kappaB kinase/NF-kappaB signaling                           | 7  | 0.18791 | 2.167  | 0.027 | Biological | GO:00434 regulation of I-kappaB kinase/NF-kappaB signaling                           | 0.18791   | 0.38922 | 0 | 0 | 7  | 256  |
| GO:005006 cardiac chamber morphogenesis                                                | 3  | 0.18838 | 0.928  | 0.037 | Biological | GO:00500 cardiac chamber morphogenesis                                               | 0.18838   | 0.39414 | 0 | 0 | 3  | 82   |
| GO:1908337 sequence-specific double-stranded DNA binding                               | 34 | 0.18862 | 9.942  | 0.022 | Biological | GO:19083 sequence-specific double-stranded DNA binding                               | 0.18862   | 0.39414 | 0 | 0 | 34 | 1556 |
| GO:0010506 regulation of autophagy                                                     | 9  | 0.18868 | 2.786  | 0.026 | Biological | GO:00100 regulation of autophagy                                                     | 0.18868   | 0.39004 | 0 | 0 | 9  | 349  |
| GO:0003690 double-stranded DNA binding                                                 | 36 | 0.18871 | 10.526 | 0.022 | Molecular  | GO:00033 double-stranded DNA binding                                                 | 0.18871   | 0.39414 | 0 | 0 | 36 | 1667 |
| GO:0006643 membrane lipid metabolic process                                            | 6  | 0.18871 | 1.858  | 0.028 | Biological | GO:00066 membrane lipid metabolic process                                            | 0.18871   | 0.39004 | 0 | 0 | 6  | 211  |
| GO:0007626 locomotor behavior                                                          | 6  | 0.18871 | 1.858  | 0.028 | Biological | GO:00076 locomotor behavior                                                          | 0.18871   | 0.39004 | 0 | 0 | 6  | 211  |
| GO:0009911 microtubule-based transport                                                 | 6  | 0.18871 | 1.858  | 0.028 | Biological | GO:00099 microtubule-based transport                                                 | 0.18871   | 0.39004 | 0 | 0 | 6  | 211  |
| GO:0032269 negative regulation of cellular protein metabolic process                   | 21 | 0.18877 | 6.502  | 0.022 | Biological | GO:00322 negative regulation of cellular protein metabolic process                   | 0.18877   | 0.39004 | 0 | 0 | 21 | 934  |
| GO:0005245 voltage-gated calcium channel activity                                      | 2  | 0.18933 | 0.585  | 0.047 | Molecular  | GO:00055 voltage-gated calcium channel activity                                      | 0.18933   | 0.39414 | 0 | 0 | 2  | 43   |
| GO:0008307 structural constituent of muscle                                            | 2  | 0.18933 | 0.585  | 0.047 | Molecular  | GO:00088 structural constituent of muscle                                            | 0.18933   | 0.39414 | 0 | 0 | 2  | 43   |
| GO:0008375 acetylcholinesterase activity                                               | 2  | 0.18933 | 0.585  | 0.047 | Molecular  | GO:00088 acetylcholinesterase activity                                               | 0.18933   | 0.39414 | 0 | 0 | 2  | 43   |
| GO:0016709 oxidoreductase activity, acting on paired donors, with incorporation        | 2  | 0.18933 | 0.585  | 0.047 | Molecular  | GO:00166 oxidoreductase activity, acting on paired donors, with incorporation of     | 0.18933   | 0.39414 | 0 | 0 | 2  | 43   |
| GO:0043014 alpha-tubulin binding                                                       | 2  | 0.18933 | 0.585  | 0.047 | Molecular  | GO:00433 alpha-tubulin binding                                                       | 0.18933   | 0.39414 | 0 | 0 | 2  | 43   |
| GO:1903561 extracellular vesicle                                                       | 44 | 0.18971 | 13.056 | 0.021 | Cellular   | GO:19033 extracellular vesicle                                                       | 0.18971   | 0.40782 | 0 | 0 | 44 | 2133 |
| GO:0004874 protein serine/threonine kinase activity                                    | 11 | 0.18995 | 3.216  | 0.025 | Biological | GO:00044 protein serine/threonine kinase activity                                    | 0.18995   | 0.39447 | 0 | 0 | 11 | 437  |
| GO:0030426 growth cone morphogenesis                                                   | 5  | 0.19033 | 1.484  | 0.03  | Cellular   | GO:00303 growth cone morphogenesis                                                   | 0.19033   | 0.39447 | 0 | 0 | 5  | 169  |
| GO:0050878 regulation of body fluid levels                                             | 10 | 0.1904  | 3.096  | 0.025 | Biological | GO:00500 regulation of body fluid levels                                             | 0.1904    | 0.39325 | 0 | 0 | 10 | 397  |
| GO:0030136 clathrin-coated vesicle                                                     | 6  | 0.19041 | 1.78   | 0.028 | Cellular   | GO:00303 clathrin-coated vesicle                                                     | 0.19041   | 0.40782 | 0 | 0 | 6  | 214  |
| GO:0043230 extracellular organelle                                                     | 44 | 0.19057 | 13.056 | 0.021 | Cellular   | GO:00433 extracellular organelle                                                     | 0.19057   | 0.40782 | 0 | 0 | 44 | 2134 |
| GO:0065010 extracellular membrane-bounded organelle                                    | 44 | 0.19057 | 13.056 | 0.021 | Cellular   | GO:00650 extracellular membrane-bounded organelle                                    | 0.19057   | 0.40782 | 0 | 0 | 44 | 2134 |
| GO:0003205 cardiac chamber morphogenesis                                               | 4  | 0.19073 | 1.238  | 0.033 | Biological | GO:00033 cardiac chamber morphogenesis                                               | 0.19073   | 0.39366 | 0 | 0 | 4  | 124  |
| GO:0046660 female sex differentiation                                                  | 4  | 0.19076 | 1.238  | 0.033 | Biological | GO:00466 female sex differentiation                                                  | 0.19076   | 0.39366 | 0 | 0 | 4  | 124  |
| GO:0045124 regulation of bone resorption                                               | 2  | 0.1912  | 0.619  | 0.045 | Biological | GO:00454 regulation of bone resorption                                               | 0.1912    | 0.39392 | 0 | 0 | 2  | 44   |
| GO:0050691 regulation of defense response to virus by host                             | 2  | 0.1912  | 0.619  | 0.045 | Biological | GO:00500 regulation of defense response to virus by host                             | 0.1912    | 0.39392 | 0 | 0 | 2  | 44   |
| GO:1900026 positive regulation of substrate adhesion-dependent cell spreading          | 2  | 0.1912  | 0.619  | 0.045 | Biological | GO:19001 positive regulation of substrate adhesion-dependent cell spreading          | 0.1912    | 0.39392 | 0 | 0 | 2  | 44   |
| GO:0003000 regulation of neuroblast exocytosis                                         | 2  | 0.1912  | 0.619  | 0.045 | Biological | GO:00030 regulation of neuroblast exocytosis                                         | 0.1912    | 0.39392 | 0 | 0 | 2  | 44   |
| GO:004085 cellular component biogenesis                                                | 67 | 0.19236 | 20.743 | 0.02  | Biological | GO:00404 cellular component biogenesis                                               | 0.19236   | 0.39443 | 0 | 0 | 67 | 3318 |
| GO:0031016 pancreas development                                                        | 3  | 0.193   | 0.929  | 0.036 | Biological | GO:00311 pancreas development                                                        | 0.193     | 0.39443 | 0 | 0 | 3  | 83   |
| GO:0051153 regulation of striated muscle cell differentiation                          | 3  | 0.193   | 0.929  | 0.036 | Biological | GO:00511 regulation of striated muscle cell differentiation                          | 0.193     | 0.39443 | 0 | 0 | 3  | 83   |
| GO:0051668 localization within membrane                                                | 16 | 0.19301 | 4.954  | 0.023 | Biological | GO:00511 localization within membrane                                                | 0.19301   | 0.39443 | 0 | 0 | 16 | 689  |
| GO:0003205 cardiac chamber morphogenesis                                               | 5  | 0.19309 | 1.484  | 0.03  | Cellular   | GO:00033 cardiac chamber morphogenesis                                               | 0.19309   | 0.39366 | 0 | 0 | 5  | 169  |
| GO:0070374 positive regulation of ERK1 and ERK2 cascade                                | 6  | 0.19425 | 1.858  | 0.028 | Biological | GO:00700 positive regulation of ERK1 and ERK2 cascade                                | 0.19425   | 0.39443 | 0 | 0 | 6  | 213  |
| GO:0098878 neurotransmitter receptor complex                                           | 2  | 0.19449 | 0.93   | 0.044 | Cellular   | GO:00988 neurotransmitter receptor complex                                           | 0.19449   | 0.41153 | 0 | 0 | 2  | 45   |
| GO:0042405 nuclear inclusion body                                                      | 1  | 0.19615 | 0.297  | 0.093 | Cellular   | GO:00422 nuclear inclusion body                                                      | 0.19615   | 0.41153 | 0 | 0 | 1  | 12   |
| GO:0043256 laminin complex                                                             | 1  | 0.19615 | 0.297  | 0.093 | Cellular   | GO:00433 laminin complex                                                             | 0.19615   | 0.41153 | 0 | 0 | 1  | 12   |
| GO:004754 autophagosome                                                                | 1  | 0.19615 | 0.297  | 0.093 | Cellular   | GO:00475 autophagosome                                                               | 0.19615   | 0.41153 | 0 | 0 | 1  | 12   |
| GO:1900454 L-type voltage-gated calcium channel complex                                | 1  | 0.19615 | 0.297  | 0.093 | Cellular   | GO:19001 L-type voltage-gated calcium channel complex                                | 0.19615   | 0.41153 | 0 | 0 | 1  | 12   |
| GO:1901888 regulation of cell junction assembly                                        | 6  | 0.19704 | 1.858  | 0.028 | Biological | GO:19011 regulation of cell junction assembly                                        | 0.19704   | 0.39443 | 0 | 0 | 6  | 214  |
| GO:0098655 cation transmembrane transport                                              | 22 | 0.19758 | 6.811  | 0.022 | Biological | GO:00988 cation transmembrane transport                                              | 0.19758   | 0.39443 | 0 | 0 | 22 | 991  |
| GO:0032024 positive regulation of insulin secretion                                    | 3  | 0.19765 | 0.928  | 0.036 | Biological | GO:00322 positive regulation of insulin secretion                                    | 0.19765   | 0.39443 | 0 | 0 | 3  | 84   |
| GO:0034340 response to type I interferon                                               | 3  | 0.19765 | 0.928  | 0.036 | Biological | GO:00342 response to type I interferon                                               | 0.19765   | 0.39443 | 0 | 0 | 3  | 84   |
| GO:0051279 regulation of release of sequestered calcium ion into cytosol               | 3  | 0.19765 | 0.928  | 0.036 | Biological | GO:00511 regulation of release of sequestered calcium ion into cytosol               | 0.19765   | 0.39443 | 0 | 0 | 3  | 84   |
| GO:0060419 heart growth                                                                | 3  | 0.19765 | 0.928  | 0.036 | Biological | GO:00600 heart growth                                                                | 0.19765   | 0.39443 | 0 | 0 | 3  | 84   |
| GO:1901606 alpha-amino acid catabolic process                                          | 3  | 0.19765 | 0.928  | 0.036 | Biological | GO:19011 alpha-amino acid catabolic process                                          | 0.19765   | 0.39443 | 0 | 0 | 3  | 84   |
| GO:0007109 cell fate determination                                                     | 2  | 0.19784 | 0.819  | 0.044 | Biological | GO:00071 cell fate determination                                                     | 0.19784   | 0.39443 | 0 | 0 | 2  | 45   |
| GO:0021879 forebrain neuron differentiation                                            | 2  | 0.19784 | 0.819  | 0.044 | Biological | GO:00218 forebrain neuron differentiation                                            | 0.19784   | 0.39443 | 0 | 0 | 2  | 45   |
| GO:0030574 collagen catabolic process                                                  | 2  | 0.19784 | 0.819  | 0.044 | Biological | GO:00300 collagen catabolic process                                                  | 0.19784   | 0.39443 | 0 | 0 | 2  | 45   |
| GO:0035239 hippo signaling                                                             | 2  | 0.19784 | 0.819  | 0.044 | Biological | GO:00353 hippo signaling                                                             | 0.19784   | 0.39443 | 0 | 0 | 2  | 45   |
| GO:0042181 ketone biosynthetic process                                                 | 2  | 0.19784 | 0.819  | 0.044 | Biological | GO:00422 ketone biosynthetic process                                                 | 0.19784   | 0.39443 | 0 | 0 | 2  | 45   |
| GO:0048839 phospholipid dephosphorylation                                              | 2  | 0.19784 | 0.819  | 0.044 | Biological | GO:00486 phospholipid dephosphorylation                                              | 0.19784   | 0.39443 | 0 | 0 | 2  | 45   |
| GO:0048112 circadian behavior                                                          | 2  | 0.19784 | 0.819  | 0.044 | Biological | GO:00484 circadian behavior                                                          | 0.19784   | 0.39443 | 0 | 0 | 2  | 45   |
| GO:0051602 response to electrical stimulus                                             | 2  | 0.19784 | 0.819  | 0.044 | Biological | GO:00511 response to electrical stimulus                                             | 0.19784   | 0.39443 | 0 | 0 | 2  | 45   |
| GO:0071526 semaphorin-plexin signaling pathway                                         | 2  | 0.19784 | 0.819  | 0.044 | Biological | GO:00711 semaphorin-plexin signaling pathway                                         | 0.19784   | 0.39443 | 0 | 0 | 2  | 45   |
| GO:0071763 nuclear membrane organization                                               | 2  | 0.19784 | 0.819  | 0.044 | Biological | GO:00711 nuclear membrane organization                                               | 0.19784   | 0.39443 | 0 | 0 | 2  | 45   |
| GO:0098815 modulation of excitatory postsynaptic potential                             | 2  | 0.19784 | 0.819  | 0.044 | Biological | GO:00988 modulation of excitatory postsynaptic potential                             | 0.19784   | 0.39443 | 0 | 0 | 2  | 45   |
| GO:1902692 regulation of neuroblast proliferation                                      | 2  | 0.19784 | 0.819  | 0.044 | Biological | GO:19024 regulation of neuroblast proliferation                                      | 0.19784   | 0.39443 | 0 | 0 | 2  | 45   |
| GO:0051345 positive regulation of hydrolase activity                                   | 14 | 0.19791 | 4.334  | 0.024 | Biological | GO:00511 positive regulation of hydrolase activity                                   | 0.19791   | 0.39443 | 0 | 0 | 14 | 594  |
| GO:0045927 positive regulation of growth                                               | 7  | 0.19793 | 2.167  | 0.027 | Biological | GO:00455 positive regulation of growth                                               | 0.19793   | 0.39443 | 0 | 0 | 7  | 260  |
| GO:0002674 negative regulation of acute inflammatory response                          | 1  | 0.19816 | 0.31   | 0.083 | Biological | GO:00026 negative regulation of acute inflammatory response                          | 0.19816   | 0.39443 | 0 | 0 | 1  | 12   |
| GO:0003334 keratinocyte development                                                    | 1  | 0.19816 | 0.31   | 0.083 | Biological | GO:00033 keratinocyte development                                                    | 0.19816   | 0.39443 | 0 | 0 | 1  | 12   |
| GO:0003337 keratinocyte to epithelial transition involved in metanephros morphogenesis | 1  | 0.19816 | 0.31   | 0.083 | Biological | GO:00033 keratinocyte to epithelial transition involved in metanephros morphogenesis | 0.19816   | 0.39443 | 0 | 0 | 1  | 12   |
| GO:0006534 cysteine metabolic process                                                  | 1  | 0.19816 | 0.31   | 0.083 | Biological | GO:00066 cysteine metabolic process                                                  | 0.19816   | 0.39443 | 0 | 0 | 1  | 12   |
| GO:0006563 L-serine metabolic process                                                  | 1  | 0.19816 | 0.31   | 0.083 | Biological | GO:00066 L-serine metabolic process                                                  | 0.19816</ |         |   |   |    |      |

|            |                                                                          |    |         |        |       |            |            |                                                                          |         |         |   |   |    |      |
|------------|--------------------------------------------------------------------------|----|---------|--------|-------|------------|------------|--------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0016857 | racemase and epimerase activity, acting on carbohydrates                 | 1  | 0.20114 | 0.292  | 0.083 | Molecular  | GO:0016857 | racemase and epimerase activity, acting on carbohydrates and deriv       | 0.20114 | 0.40603 | 0 | 0 | 1  | 12   |
| GO:0017166 | vinculin binding                                                         | 1  | 0.20114 | 0.292  | 0.083 | Molecular  | GO:0017166 | vinculin binding                                                         | 0.20114 | 0.40603 | 0 | 0 | 1  | 12   |
| GO:034452  | dynamitin binding                                                        | 1  | 0.20114 | 0.292  | 0.083 | Molecular  | GO:034452  | dynamitin binding                                                        | 0.20114 | 0.40603 | 0 | 0 | 1  | 12   |
| GO:035251  | UDP-glucose 4-epimerase activity                                         | 1  | 0.20114 | 0.292  | 0.083 | Molecular  | GO:035251  | UDP-glucose 4-epimerase activity                                         | 0.20114 | 0.40603 | 0 | 0 | 1  | 12   |
| GO:0086080 | protein binding involved in heterotypic cell-cell adhesion               | 1  | 0.20114 | 0.292  | 0.083 | Molecular  | GO:0086080 | protein binding involved in heterotypic cell-cell adhesion               | 0.20114 | 0.40603 | 0 | 0 | 1  | 12   |
| GO:0089720 | casease binding                                                          | 1  | 0.20114 | 0.292  | 0.083 | Molecular  | GO:0089720 | casease binding                                                          | 0.20114 | 0.40603 | 0 | 0 | 1  | 12   |
| GO:0032411 | positive regulation of transporter activity                              | 4  | 0.20193 | 1.238  | 0.031 | Biological | GO:0032411 | positive regulation of transporter activity                              | 0.20193 | 0.40114 | 0 | 0 | 4  | 127  |
| GO:0032874 | positive regulation of stress-activated MAPK cascade                     | 4  | 0.20193 | 1.238  | 0.031 | Biological | GO:0032874 | positive regulation of stress-activated MAPK cascade                     | 0.20193 | 0.40114 | 0 | 0 | 4  | 127  |
| GO:004875  | axon extension                                                           | 4  | 0.20193 | 1.238  | 0.031 | Biological | GO:004875  | axon extension                                                           | 0.20193 | 0.40114 | 0 | 0 | 4  | 127  |
| GO:0005198 | structural molecule activity                                             | 19 | 0.20211 | 5.556  | 0.023 | Molecular  | GO:0005198 | structural molecule activity                                             | 0.20211 | 0.40704 | 0 | 0 | 19 | 830  |
| GO:0010468 | regulation of gene expression                                            | 96 | 0.20215 | 29.721 | 0.02  | Biological | GO:0010468 | regulation of gene expression                                            | 0.20215 | 0.40141 | 0 | 0 | 96 | 4876 |
| GO:0020228 | regulation of sodium ion transport                                       | 3  | 0.20233 | 0.929  | 0.035 | Biological | GO:0020228 | regulation of sodium ion transport                                       | 0.20233 | 0.40161 | 0 | 0 | 3  | 85   |
| GO:0042180 | cellular ketone metabolic process                                        | 6  | 0.20267 | 1.938  | 0.028 | Molecular  | GO:0042180 | cellular ketone metabolic process                                        | 0.20267 | 0.40211 | 0 | 0 | 6  | 128  |
| GO:0004842 | ubiquitin-protein transferase activity                                   | 11 | 0.20346 | 3.216  | 0.025 | Molecular  | GO:0004842 | ubiquitin-protein transferase activity                                   | 0.20346 | 0.40882 | 0 | 0 | 11 | 444  |
| GO:0001774 | microglial cell activation                                               | 2  | 0.2045  | 0.619  | 0.043 | Biological | GO:0001774 | microglial cell activation                                               | 0.2045  | 0.4043  | 0 | 0 | 2  | 46   |
| GO:0021517 | ventral spinal cord development                                          | 2  | 0.2045  | 0.619  | 0.043 | Biological | GO:0021517 | ventral spinal cord development                                          | 0.2045  | 0.4043  | 0 | 0 | 2  | 46   |
| GO:0043655 | monosaccharide catabolic process                                         | 2  | 0.2045  | 0.619  | 0.043 | Biological | GO:0043655 | monosaccharide catabolic process                                         | 0.2045  | 0.4043  | 0 | 0 | 2  | 46   |
| GO:0046840 | regulation of alpha-beta T cell proliferation                            | 2  | 0.2045  | 0.619  | 0.043 | Biological | GO:0046840 | regulation of alpha-beta T cell proliferation                            | 0.2045  | 0.4043  | 0 | 0 | 2  | 46   |
| GO:0055010 | ventricular cardiac muscle tissue morphogenesis                          | 2  | 0.2045  | 0.619  | 0.043 | Biological | GO:0055010 | ventricular cardiac muscle tissue morphogenesis                          | 0.2045  | 0.4043  | 0 | 0 | 2  | 46   |
| GO:0098534 | centriole assembly                                                       | 2  | 0.2045  | 0.619  | 0.043 | Biological | GO:0098534 | centriole assembly                                                       | 0.2045  | 0.4043  | 0 | 0 | 2  | 46   |
| GO:0090804 | postsynaptic specialization organization                                 | 2  | 0.2045  | 0.619  | 0.043 | Biological | GO:0090804 | postsynaptic specialization organization                                 | 0.2045  | 0.4043  | 0 | 0 | 2  | 46   |
| GO:0002073 | positive regulation of signaling receptor activity                       | 2  | 0.2045  | 0.619  | 0.043 | Biological | GO:0002073 | positive regulation of signaling receptor activity                       | 0.2045  | 0.4043  | 0 | 0 | 2  | 46   |
| GO:200648  | positive regulation of stem cell proliferation                           | 2  | 0.2045  | 0.619  | 0.043 | Biological | GO:200648  | positive regulation of stem cell proliferation                           | 0.2045  | 0.4043  | 0 | 0 | 2  | 46   |
| GO:1901215 | negative regulation of neuron death                                      | 6  | 0.2055  | 1.858  | 0.028 | Biological | GO:1901215 | negative regulation of neuron death                                      | 0.2055  | 0.40612 | 0 | 0 | 6  | 217  |
| GO:0031503 | protein-containing complex localization                                  | 7  | 0.20558 | 2.167  | 0.027 | Biological | GO:0031503 | protein-containing complex localization                                  | 0.20558 | 0.40612 | 0 | 0 | 7  | 263  |
| GO:0071482 | cellular response to light stimulus                                      | 4  | 0.2057  | 1.238  | 0.031 | Biological | GO:0071482 | cellular response to light stimulus                                      | 0.2057  | 0.4062  | 0 | 0 | 4  | 128  |
| GO:0002831 | regulation of response to biotic stimulus                                | 9  | 0.2059  | 2.786  | 0.025 | Biological | GO:0002831 | regulation of response to biotic stimulus                                | 0.2059  | 0.4063  | 0 | 0 | 9  | 357  |
| GO:0043086 | negative regulation of catalytic activity                                | 15 | 0.20592 | 4.292  | 0.023 | Molecular  | GO:0043086 | negative regulation of catalytic activity                                | 0.20592 | 0.4063  | 0 | 0 | 15 | 648  |
| GO:0042826 | histone deacetylase binding                                              | 4  | 0.2061  | 1.17   | 0.032 | Molecular  | GO:0042826 | histone deacetylase binding                                              | 0.2061  | 0.41316 | 0 | 0 | 4  | 126  |
| GO:0022604 | regulation of cell morphogenesis                                         | 8  | 0.2064  | 2.477  | 0.026 | Biological | GO:0022604 | regulation of cell morphogenesis                                         | 0.2064  | 0.40697 | 0 | 0 | 8  | 310  |
| GO:0007015 | actin filament organization                                              | 11 | 0.20642 | 3.406  | 0.024 | Biological | GO:0007015 | actin filament organization                                              | 0.20642 | 0.40697 | 0 | 0 | 11 | 453  |
| GO:0001523 | retinoid metabolic process                                               | 3  | 0.20703 | 0.929  | 0.035 | Biological | GO:0001523 | retinoid metabolic process                                               | 0.20703 | 0.40786 | 0 | 0 | 3  | 86   |
| GO:0003095 | SMAD protein signal transduction                                         | 3  | 0.20703 | 0.929  | 0.035 | Biological | GO:0003095 | SMAD protein signal transduction                                         | 0.20703 | 0.40786 | 0 | 0 | 3  | 86   |
| GO:0048786 | presynaptic active zone                                                  | 3  | 0.20717 | 0.89   | 0.034 | Cellular   | GO:0048786 | presynaptic active zone                                                  | 0.20717 | 0.43062 | 0 | 0 | 3  | 87   |
| GO:0005891 | voltage-gated calcium channel complex                                    | 2  | 0.20766 | 0.593  | 0.043 | Cellular   | GO:0005891 | voltage-gated calcium channel complex                                    | 0.20766 | 0.43062 | 0 | 0 | 2  | 47   |
| GO:0006029 | lipid metabolic process                                                  | 30 | 0.20892 | 9.288  | 0.021 | Biological | GO:0006029 | lipid metabolic process                                                  | 0.20892 | 0.40872 | 0 | 0 | 30 | 1407 |
| GO:0030165 | PDZ domain binding                                                       | 3  | 0.20902 | 0.877  | 0.035 | Molecular  | GO:0030165 | PDZ domain binding                                                       | 0.20902 | 0.41803 | 0 | 0 | 3  | 85   |
| GO:0030216 | keratinocyte differentiation                                             | 5  | 0.20907 | 1.548  | 0.028 | Biological | GO:0030216 | keratinocyte differentiation                                             | 0.20907 | 0.40872 | 0 | 0 | 5  | 173  |
| GO:0006022 | amniomycin metabolic process                                             | 4  | 0.20949 | 1.238  | 0.031 | Biological | GO:0006022 | amniomycin metabolic process                                             | 0.20949 | 0.40872 | 0 | 0 | 4  | 129  |
| GO:0070304 | positive regulation of stress-activated protein kinase signaling cascade | 4  | 0.20949 | 1.238  | 0.031 | Biological | GO:0070304 | positive regulation of stress-activated protein kinase signaling cascade | 0.20949 | 0.40872 | 0 | 0 | 4  | 129  |
| GO:0061629 | RNA polymerase II-specific DNA-binding transcription factor              | 9  | 0.21015 | 2.632  | 0.025 | Molecular  | GO:0061629 | RNA polymerase II-specific DNA-binding transcription factor              | 0.21015 | 0.41934 | 0 | 0 | 9  | 353  |
| GO:0052533 | ciliary rootlet                                                          | 1  | 0.21065 | 0.297  | 0.07  | Cellular   | GO:0052533 | ciliary rootlet                                                          | 0.21065 | 0.43345 | 0 | 0 | 1  | 13   |
| GO:0095923 | presynaptic cytosol                                                      | 1  | 0.21065 | 0.297  | 0.07  | Cellular   | GO:0095923 | presynaptic cytosol                                                      | 0.21065 | 0.43345 | 0 | 0 | 1  | 13   |
| GO:0050708 | regulation of protein secretion                                          | 7  | 0.21074 | 2.167  | 0.026 | Biological | GO:0050708 | regulation of protein secretion                                          | 0.21074 | 0.40872 | 0 | 0 | 7  | 265  |
| GO:0007622 | rhythmic behavior                                                        | 2  | 0.21119 | 0.619  | 0.043 | Biological | GO:0007622 | rhythmic behavior                                                        | 0.21119 | 0.40872 | 0 | 0 | 2  | 47   |
| GO:0046427 | positive regulation of receptor signaling pathway via JAK-STAT           | 2  | 0.21119 | 0.619  | 0.043 | Biological | GO:0046427 | positive regulation of receptor signaling pathway via JAK-STAT           | 0.21119 | 0.40872 | 0 | 0 | 2  | 47   |
| GO:0061756 | leukocyte adhesion to vascular endothelial cell                          | 2  | 0.21119 | 0.619  | 0.043 | Biological | GO:0061756 | leukocyte adhesion to vascular endothelial cell                          | 0.21119 | 0.40872 | 0 | 0 | 2  | 47   |
| GO:0070849 | response to external stimulus                                            | 2  | 0.21119 | 0.619  | 0.043 | Biological | GO:0070849 | response to external stimulus                                            | 0.21119 | 0.40872 | 0 | 0 | 2  | 47   |
| GO:0019861 | regulation of muscle tissue development                                  | 2  | 0.21119 | 0.619  | 0.043 | Biological | GO:0019861 | regulation of muscle tissue development                                  | 0.21119 | 0.40872 | 0 | 0 | 2  | 47   |
| GO:0006112 | energy reserve metabolic process                                         | 3  | 0.21176 | 0.929  | 0.034 | Biological | GO:0006112 | energy reserve metabolic process                                         | 0.21176 | 0.40872 | 0 | 0 | 3  | 87   |
| GO:0010232 | vascular transport                                                       | 3  | 0.21176 | 0.929  | 0.034 | Biological | GO:0010232 | vascular transport                                                       | 0.21176 | 0.40872 | 0 | 0 | 3  | 87   |
| GO:0014812 | muscle cell migration                                                    | 3  | 0.21176 | 0.929  | 0.034 | Biological | GO:0014812 | muscle cell migration                                                    | 0.21176 | 0.40872 | 0 | 0 | 3  | 87   |
| GO:0010404 | transport across blood-brain barrier                                     | 3  | 0.21176 | 0.929  | 0.034 | Biological | GO:0010404 | transport across blood-brain barrier                                     | 0.21176 | 0.40872 | 0 | 0 | 3  | 87   |
| GO:0000012 | single strand break repair                                               | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0000012 | single strand break repair                                               | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0000011 | sulfur amino acid transport                                              | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0000011 | sulfur amino acid transport                                              | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0001973 | G protein-coupled adenosine receptor signaling pathway                   | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0001973 | G protein-coupled adenosine receptor signaling pathway                   | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0002087 | regulation of respiratory gaseous exchange by nervous system             | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0002087 | regulation of respiratory gaseous exchange by nervous system             | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0002893 | positive regulation of interferon response to antigenic stimulus         | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0002893 | positive regulation of interferon response to antigenic stimulus         | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0005656 | indolylamine metabolic process                                           | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0005656 | indolylamine metabolic process                                           | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0007638 | mechanosensory behavior                                                  | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0007638 | mechanosensory behavior                                                  | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0014854 | response to inactivity                                                   | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0014854 | response to inactivity                                                   | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0015801 | aromatic amino acid transport                                            | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0015801 | aromatic amino acid transport                                            | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0015824 | proline transport                                                        | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0015824 | proline transport                                                        | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0016024 | CDP-diacylglycerol biosynthetic process                                  | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0016024 | CDP-diacylglycerol biosynthetic process                                  | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0018095 | protein polyglutamylation                                                | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0018095 | protein polyglutamylation                                                | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0019885 | antigen processing and presentation of endogenous peptide                | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0019885 | antigen processing and presentation of endogenous peptide                | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0021514 | ventral spinal cord interneuron differentiation                          | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0021514 | ventral spinal cord interneuron differentiation                          | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0032341 | adipocyte metabolic process                                              | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0032341 | adipocyte metabolic process                                              | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0032530 | regulation of microvillus organization                                   | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0032530 | regulation of microvillus organization                                   | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0033083 | regulation of immature T cell proliferation                              | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0033083 | regulation of immature T cell proliferation                              | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0033084 | regulation of immature T cell proliferation in thymus                    | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0033084 | regulation of immature T cell proliferation in thymus                    | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0033148 | positive regulation of intracellular estrogen receptor signaling pathway | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0033148 | positive regulation of intracellular estrogen receptor signaling pathway | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0034333 | adenosine assembly                                                       | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0034333 | adenosine assembly                                                       | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0035588 | G protein-coupled purinergic receptor signaling pathway                  | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0035588 | G protein-coupled purinergic receptor signaling pathway                  | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0035815 | positive regulation of renal sodium excretion                            | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0035815 | positive regulation of renal sodium excretion                            | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0035865 | cellular response to potassium ion                                       | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0035865 | cellular response to potassium ion                                       | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0036036 | cellular response to macrophage colony-stimulating factor                | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0036036 | cellular response to macrophage colony-stimulating factor                | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0040115 | negative regulation of multicellular organism growth                     | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0040115 | negative regulation of multicellular organism growth                     | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0042363 | fat-soluble vitamin catabolic process                                    | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0042363 | fat-soluble vitamin catabolic process                                    | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0042670 | retinal cone cell differentiation                                        | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0042670 | retinal cone cell differentiation                                        | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0044650 | adhesion of symbiont to host cell                                        | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0044650 | adhesion of symbiont to host cell                                        | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0048742 | regulation of skeletal muscle fiber development                          | 1  | 0.21279 | 0.31   | 0.077 | Biological | GO:0048742 | regulation of skeletal muscle fiber development                          | 0.21279 | 0.40872 | 0 | 0 | 1  | 13   |
| GO:0050655 | dermatan sulfate proteoglycan metabolic process                          | 1  | 0.21279 | 0.3    |       |            |            |                                                                          |         |         |   |   |    |      |

|                                                                                                         |    |         |       |       |              |          |                                                                                              |         |         |   |   |    |     |
|---------------------------------------------------------------------------------------------------------|----|---------|-------|-------|--------------|----------|----------------------------------------------------------------------------------------------|---------|---------|---|---|----|-----|
| GO:0005940 septin ring                                                                                  | 1  | 0.22489 | 0.297 | 0.071 | Cellular C   | GO:00005 | septin ring                                                                                  | 0.22489 | 0.43967 | 0 | 0 | 1  | 14  |
| GO:0031089 platelet dense granule lumen                                                                 | 1  | 0.22489 | 0.297 | 0.071 | Cellular C   | GO:00331 | platelet dense granule lumen                                                                 | 0.22489 | 0.43967 | 0 | 0 | 1  | 14  |
| GO:0031105 septin complex                                                                               | 1  | 0.22489 | 0.297 | 0.071 | Cellular C   | GO:00331 | septin complex                                                                               | 0.22489 | 0.43967 | 0 | 0 | 1  | 14  |
| GO:0031254 cell trailing edge                                                                           | 1  | 0.22489 | 0.297 | 0.071 | Cellular C   | GO:00331 | cell trailing edge                                                                           | 0.22489 | 0.43967 | 0 | 0 | 1  | 14  |
| GO:0042627 chylomicron                                                                                  | 1  | 0.22489 | 0.297 | 0.071 | Cellular C   | GO:00442 | chylomicron                                                                                  | 0.22489 | 0.43967 | 0 | 0 | 1  | 14  |
| GO:0098574 cytoplasmic side of lysosomal membrane                                                       | 1  | 0.22489 | 0.297 | 0.071 | Cellular C   | GO:00988 | cytoplasmic side of lysosomal membrane                                                       | 0.22489 | 0.43967 | 0 | 0 | 1  | 14  |
| GO:0098902 postsynaptic density, intracellular component                                                | 1  | 0.22489 | 0.297 | 0.071 | Cellular C   | GO:00989 | postsynaptic density, intracellular component                                                | 0.22489 | 0.43967 | 0 | 0 | 1  | 14  |
| GO:0140672 ATAC complex                                                                                 | 1  | 0.22489 | 0.297 | 0.071 | Cellular C   | GO:01406 | ATAC complex                                                                                 | 0.22489 | 0.43967 | 0 | 0 | 1  | 14  |
| GO:1990531 phospholipid-translocating ATPase complex                                                    | 1  | 0.22489 | 0.297 | 0.071 | Cellular C   | GO:19905 | phospholipid-translocating ATPase complex                                                    | 0.22489 | 0.43967 | 0 | 0 | 1  | 14  |
| GO:0032580 Golgi cisterna membrane                                                                      | 3  | 0.226   | 0.89  | 0.033 | Cellular C   | GO:00332 | Golgi cisterna membrane                                                                      | 0.226   | 0.43967 | 0 | 0 | 3  | 91  |
| GO:0120111 neuron protection cytoplasm                                                                  | 3  | 0.226   | 0.89  | 0.033 | Cellular C   | GO:01202 | neuron protection cytoplasm                                                                  | 0.226   | 0.43967 | 0 | 0 | 3  | 91  |
| GO:0035592 establishment of protein localization to extracellular region                                | 9  | 0.22601 | 2.786 | 0.029 | Biological P | GO:00355 | establishment of protein localization to extracellular region                                | 0.22601 | 0.4236  | 0 | 0 | 9  | 366 |
| GO:0032686 response to insulin                                                                          | 1  | 0.22652 | 1.167 | 0.028 | Biological P | GO:00326 | response to insulin                                                                          | 0.22652 | 0.4236  | 0 | 0 | 1  | 271 |
| GO:0002524 hypersensitivity                                                                             | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00025 | hypersensitivity                                                                             | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0003207 cardiac chamber formation                                                                    | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00032 | cardiac chamber formation                                                                    | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0003222 ventricular trabecula myocardium morphogenesis                                               | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00032 | ventricular trabecula myocardium morphogenesis                                               | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0001715 negative regulation of epidermal growth factor-activated receptor activity                   | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00017 | negative regulation of epidermal growth factor-activated receptor activity                   | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0008212 mineralocorticoid metabolic process                                                          | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00082 | mineralocorticoid metabolic process                                                          | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0107175 regulation of extracellular matrix disassembly                                               | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:01071 | regulation of extracellular matrix disassembly                                               | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0010838 positive regulation of keratinocyte proliferation                                            | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00108 | positive regulation of keratinocyte proliferation                                            | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0014841 skeletal muscle satellite cell proliferation                                                 | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00148 | skeletal muscle satellite cell proliferation                                                 | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0014874 response to stimulus involved in regulation of muscle adaptation                             | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00148 | response to stimulus involved in regulation of muscle adaptation                             | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0018158 protein oxidation                                                                            | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00181 | protein oxidation                                                                            | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0030949 positive regulation of vascular endothelial growth factor receptor signaling pathway         | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00309 | positive regulation of vascular endothelial growth factor receptor signaling pathway         | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0032494 response to peptidoglycan                                                                    | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00324 | response to peptidoglycan                                                                    | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0033079 immature T cell proliferation                                                                | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00330 | immature T cell proliferation                                                                | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0033380 immature T cell proliferation in thymus                                                      | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00333 | immature T cell proliferation in thymus                                                      | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0033145 positive regulation of intracellular steroid hormone receptor signaling pathway              | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00331 | positive regulation of intracellular steroid hormone receptor signaling pathway              | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0033700 phospholipid efflux                                                                          | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00337 | phospholipid efflux                                                                          | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0034111 negative regulation of homotypic cell-cell adhesion                                          | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00341 | negative regulation of homotypic cell-cell adhesion                                          | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0034380 high-density lipoprotein particle assembly                                                   | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00343 | high-density lipoprotein particle assembly                                                   | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0034616 response to laminar fluid shear stress                                                       | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00346 | response to laminar fluid shear stress                                                       | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0035589 G protein-coupled purinergic nucleotide receptor signaling pathway                           | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00355 | G protein-coupled purinergic nucleotide receptor signaling pathway                           | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0035845 photoreceptor cell outer segment organization                                                | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00358 | photoreceptor cell outer segment organization                                                | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0042117 monocyte activation                                                                          | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00421 | monocyte activation                                                                          | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0042754 negative regulation of circadian rhythm                                                      | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00427 | negative regulation of circadian rhythm                                                      | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0043101 purine-containing compound salvage                                                           | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00431 | purine-containing compound salvage                                                           | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0046341 GDP-GTP exchange factor metabolic process                                                    | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00463 | GDP-GTP exchange factor metabolic process                                                    | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0046655 folate acid metabolic process                                                                | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00466 | folate acid metabolic process                                                                | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0048715 negative regulation of oligodendrocyte differentiation                                       | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00487 | negative regulation of oligodendrocyte differentiation                                       | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0051764 actin crosslink formation                                                                    | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00517 | actin crosslink formation                                                                    | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0060100 positive regulation of phagocytosis, engulfment                                              | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00601 | positive regulation of phagocytosis, engulfment                                              | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0060221 retinal rod differentiation                                                                  | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00602 | retinal rod differentiation                                                                  | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0060712 spongioroblast layer development                                                             | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00607 | spongioroblast layer development                                                             | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0071639 positive regulation of monocyte chemotactic protein-1 production                             | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00716 | positive regulation of monocyte chemotactic protein-1 production                             | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0072540 T-helper 17 cell lineage commitment                                                          | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00725 | T-helper 17 cell lineage commitment                                                          | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0094745 motor neuron migration                                                                       | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00947 | motor neuron migration                                                                       | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0098893 regulation of synaptic vesicle cycle                                                         | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00988 | regulation of synaptic vesicle cycle                                                         | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0091160 primary amino compound metabolic process                                                     | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00911 | primary amino compound metabolic process                                                     | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0092033 regulation of hematopoietic stem cell proliferation                                          | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00920 | regulation of hematopoietic stem cell proliferation                                          | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0092043 positive regulation of extrinsic apoptotic signaling pathway                                 | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00920 | positive regulation of extrinsic apoptotic signaling pathway via death                       | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0092267 semaphorin-plexin signaling pathway involved in axon guidance                                | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00922 | semaphorin-plexin signaling pathway involved in axon guidance                                | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0092514 regulation of potassium ion transmembrane transport via high voltage-gated potassium channel | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00925 | regulation of potassium ion transmembrane transport via high voltage-gated potassium channel | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0095155 positive regulation of membrane invagination                                                 | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00951 | positive regulation of membrane invagination                                                 | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0095866 regulation of protein localization to endosome                                               | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:00958 | regulation of protein localization to endosome                                               | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:2001140 positive regulation of phospholipid transport                                                | 1  | 0.22715 | 0.31  | 0.071 | Biological P | GO:20011 | positive regulation of phospholipid transport                                                | 0.22715 | 0.4236  | 0 | 0 | 1  | 14  |
| GO:0032970 regulation of actin filament-based process                                                   | 10 | 0.22757 | 3.996 | 0.024 | Biological P | GO:00329 | regulation of actin filament-based process                                                   | 0.22757 | 0.42423 | 0 | 0 | 10 | 415 |
| GO:0009852 anteroposterior pattern specification                                                        | 6  | 0.22869 | 1.858 | 0.027 | Biological P | GO:00098 | anteroposterior pattern specification                                                        | 0.22869 | 0.42415 | 0 | 0 | 6  | 225 |
| GO:0021953 central nervous system neuron differentiation                                                | 5  | 0.22879 | 1.548 | 0.028 | Biological P | GO:00219 | central nervous system neuron differentiation                                                | 0.22879 | 0.42617 | 0 | 0 | 5  | 179 |
| GO:0005504 fatty acid binding                                                                           | 2  | 0.23014 | 0.585 | 0.041 | Molecular F  | GO:00055 | fatty acid binding                                                                           | 0.23014 | 0.43774 | 0 | 0 | 2  | 49  |
| GO:0005313 L-glutamate transmembrane transporter activity                                               | 1  | 0.2305  | 0.292 | 0.071 | Molecular F  | GO:00053 | L-glutamate transmembrane transporter activity                                               | 0.2305  | 0.43774 | 0 | 0 | 1  | 14  |
| GO:0010484 H3 histone acetyltransferase activity                                                        | 1  | 0.2305  | 0.292 | 0.071 | Molecular F  | GO:00104 | H3 histone acetyltransferase activity                                                        | 0.2305  | 0.43774 | 0 | 0 | 1  | 14  |
| GO:0018855 calcium channel inhibitor activity                                                           | 1  | 0.2305  | 0.292 | 0.071 | Molecular F  | GO:00188 | calcium channel inhibitor activity                                                           | 0.2305  | 0.43774 | 0 | 0 | 1  | 14  |
| GO:0031005 flammilin binding                                                                            | 1  | 0.2305  | 0.292 | 0.071 | Molecular F  | GO:00310 | flammilin binding                                                                            | 0.2305  | 0.43774 | 0 | 0 | 1  | 14  |
| GO:0031404 chloride ion binding                                                                         | 1  | 0.2305  | 0.292 | 0.071 | Molecular F  | GO:00314 | chloride ion binding                                                                         | 0.2305  | 0.43774 | 0 | 0 | 1  | 14  |
| GO:0042043 neurexin family protein binding                                                              | 1  | 0.2305  | 0.292 | 0.071 | Molecular F  | GO:00420 | neurexin family protein binding                                                              | 0.2305  | 0.43774 | 0 | 0 | 1  | 14  |
| GO:0044548 S100 protein binding                                                                         | 1  | 0.2305  | 0.292 | 0.071 | Molecular F  | GO:00444 | S100 protein binding                                                                         | 0.2305  | 0.43774 | 0 | 0 | 1  | 14  |
| GO:0045295 paracrine signaling                                                                          | 1  | 0.2305  | 0.292 | 0.071 | Molecular F  | GO:00452 | paracrine signaling                                                                          | 0.2305  | 0.43774 | 0 | 0 | 1  | 14  |
| GO:0052650 NADP-retinol dehydrogenase activity                                                          | 1  | 0.2305  | 0.292 | 0.071 | Molecular F  | GO:00526 | NADP-retinol dehydrogenase activity                                                          | 0.2305  | 0.43774 | 0 | 0 | 1  | 14  |
| GO:1901474 azole transmembrane transporter activity                                                     | 1  | 0.2305  | 0.292 | 0.071 | Molecular F  | GO:19014 | azole transmembrane transporter activity                                                     | 0.2305  | 0.43774 | 0 | 0 | 1  | 14  |
| GO:0005793 endoplasmic reticulum-Golgi intermediate compartment                                         | 4  | 0.23059 | 1.187 | 0.029 | Cellular C   | GO:00057 | endoplasmic reticulum-Golgi intermediate compartment                                         | 0.23059 | 0.44697 | 0 | 0 | 4  | 136 |
| GO:0046849 bone remodeling                                                                              | 3  | 0.2309  | 0.928 | 0.033 | Biological P | GO:00468 | bone remodeling                                                                              | 0.2309  | 0.42921 | 0 | 0 | 3  | 91  |
| GO:0051591 response to calcium ion                                                                      | 1  | 0.2309  | 0.928 | 0.033 | Biological P | GO:00515 | response to calcium ion                                                                      | 0.2309  | 0.42921 | 0 | 0 | 1  | 14  |
| GO:0006953 acute-phase response                                                                         | 2  | 0.23136 | 0.619 | 0.04  | Biological P | GO:00069 | acute-phase response                                                                         | 0.23136 | 0.42921 | 0 | 0 | 2  | 50  |
| GO:0007520 myoblast fusion                                                                              | 2  | 0.23136 | 0.619 | 0.04  | Biological P | GO:00075 | myoblast fusion                                                                              | 0.23136 | 0.42921 | 0 | 0 | 2  | 50  |
| GO:0007528 neuromuscular junction development                                                           | 2  | 0.23136 | 0.619 | 0.04  | Biological P | GO:00075 | neuromuscular junction development                                                           | 0.23136 | 0.42921 | 0 | 0 | 2  | 50  |
| GO:0010171 body morphogenesis                                                                           | 2  | 0.23136 | 0.619 | 0.04  | Biological P | GO:00101 | body morphogenesis                                                                           | 0.23136 | 0.42921 | 0 | 0 | 2  | 50  |
| GO:0010883 regulation of lipid storage                                                                  | 2  | 0.23136 | 0.619 | 0.04  | Biological P | GO:00108 | regulation of lipid storage                                                                  | 0.23136 | 0.42921 | 0 | 0 | 2  | 50  |
| GO:0032768 regulation of monoxygenase activity                                                          | 2  | 0.23136 | 0.619 | 0.04  | Biological P | GO:00327 | regulation of monoxygenase activity                                                          | 0.23136 | 0.42921 | 0 | 0 | 2  | 50  |
| GO:0043330 response to exogenous dsRNA                                                                  | 2  | 0.23136 | 0.619 | 0.04  | Biological P | GO:00433 | response to exogenous dsRNA                                                                  | 0.23136 | 0.42921 | 0 | 0 | 2  | 50  |
| GO:0060338 cardiac muscle cell proliferation                                                            | 2  | 0.23136 | 0.619 | 0.04  | Biological P | GO:00603 | cardiac muscle cell proliferation                                                            | 0.23136 | 0.42921 | 0 | 0 | 2  | 50  |
| GO:0046844 positive regulation of receptor signaling pathway via STAT                                   | 2  | 0.23136 | 0.619 | 0.04  | Biological P | GO:00468 | positive regulation of receptor signaling pathway via STAT                                   | 0.23136 | 0.42921 | 0 | 0 | 2  | 50  |
| GO:0043309 neuron spine                                                                                 | 5  | 0.23212 | 1.484 | 0.027 | Cellular C   | GO:00433 | neuron spine                                                                                 | 0.23212 | 0.44813 | 0 | 0 | 5  | 184 |
| GO:0048017 inositol lipid-mediated signaling                                                            | 5  | 0.23213 | 1.548 | 0.028 | Biological P | GO:00480 | inositol lipid-mediated signaling                                                            | 0.23213 | 0.43048 | 0 | 0 | 5  | 180 |
| GO:0048565 digestive tract development                                                                  | 4  | 0.23261 | 1.238 | 0.03  | Biological P | GO:00484 | digestive tract development                                                                  | 0.23261 | 0.43121 | 0 | 0 | 4  | 135 |
| GO:0016053 organic acid biosynthetic process                                                            | 8  | 0.23301 | 2.477 | 0.029 | Biological P | GO:00160 | organic acid biosynthetic process                                                            | 0.23301 | 0.43179 | 0 | 0 | 8  | 321 |
| GO:0016681 sulfur compound binding                                                                      |    |         |       |       |              |          |                                                                                              |         |         |   |   |    |     |

|                                                                             |    |         |        |       |            |                                                                                   |         |         |   |   |    |      |
|-----------------------------------------------------------------------------|----|---------|--------|-------|------------|-----------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0060009 Sertoli cell development                                         | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:006001 Sertoli cell development                                                | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0003437 heart trabecula formation                                        | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0003437 heart trabecula formation                                              | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0060413 atrial septum morphogenesis                                      | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0060413 atrial septum morphogenesis                                            | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0070282 peptidyl-serine dephosphorylation                                | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0070282 peptidyl-serine dephosphorylation                                      | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0070278 extracellular matrix constituent secretion                       | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0070278 extracellular matrix constituent secretion                             | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0070831 basement membrane assembly                                       | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0070831 basement membrane assembly                                             | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0071107 response to parathyroid hormone                                  | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0071107 response to parathyroid hormone                                        | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0072531 pyrimidine-containing compound transmembrane transport           | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0072531 pyrimidine-containing compound transmembrane transport                 | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0075294 positive regulation by symbiont of entry into host               | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0075294 positive regulation by symbiont of entry into host                     | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0080609 bundle of His cell to Purkinje myocyte communication             | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0080609 bundle of His cell to Purkinje myocyte communication                   | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0086103 G protein-coupled receptor signaling pathway involved in heart h | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0086103 G protein-coupled receptor signaling pathway involved in heart proce   | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0090051 negative regulation of cell migration involved in sprouting a    | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0090051 negative regulation of cell migration involved in sprouting angiogenes | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0090650 cerebrospinal fluid circulation                                  | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0090650 cerebrospinal fluid circulation                                        | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0097531 mast cell migration                                              | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0097531 mast cell migration                                                    | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0098840 protein transport along microtubule                              | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0098840 protein transport along microtubule                                    | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0098883 synapse pruning                                                  | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0098883 synapse pruning                                                        | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0098918 microtubule-based protein transport                              | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0098918 microtubule-based protein transport                                    | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0120365 regulation of pigmentation                                       | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0120365 regulation of pigmentation                                             | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:0160011 regulation of neuron projection arborization                     | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:0160011 regulation of neuron projection arborization                           | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:1901163 regulation of trophoblast cell migration                         | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:1901163 regulation of trophoblast cell migration                               | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:1903025 regulation of RNA polymerase II regulatory region sequenc        | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:1903025 regulation of RNA polymerase II regulatory region sequence-specific    | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:2000725 regulation of cardiac muscle cell differentiation                | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:2000725 regulation of cardiac muscle cell differentiation                      | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:2001138 regulation of phospholipid transport                             | 1  | 0.24125 | 0.31   | 0.067 | Biological | GO:2001138 regulation of phospholipid transport                                   | 0.24125 | 0.43495 | 0 | 0 | 1  | 15   |
| GO:1905475 regulation of protein localization to membrane                   | 5  | 0.24222 | 1.548  | 0.027 | Biological | GO:1905475 regulation of protein localization to membrane                         | 0.24222 | 0.43654 | 0 | 0 | 5  | 183  |
| GO:0031328 positive regulation of cellular biosynthetic process             | 42 | 0.24318 | 13.003 | 0.02  | Biological | GO:0031328 positive regulation of cellular biosynthetic process                   | 0.24318 | 0.43811 | 0 | 0 | 42 | 2062 |
| GO:0008013 beta-catenin binding                                             | 3  | 0.24319 | 0.877  | 0.033 | Molecular  | GO:0008013 beta-catenin binding                                                   | 0.24319 | 0.44009 | 0 | 0 | 3  | 92   |
| GO:0016651 oxidoreductase activity, acting on NAD(P)H                       | 3  | 0.24319 | 0.877  | 0.033 | Molecular  | GO:0016651 oxidoreductase activity, acting on NAD(P)H                             | 0.24319 | 0.44009 | 0 | 0 | 3  | 92   |
| GO:0031984 ornithine decarboxylase activity                                 | 31 | 0.24438 | 8.188  | 0.03  | Molecular  | GO:0031984 ornithine decarboxylase activity                                       | 0.24438 | 0.44009 | 0 | 0 | 31 | 1508 |
| GO:0004129 cytochrome-c oxidase activity                                    | 1  | 0.24477 | 0.292  | 0.067 | Molecular  | GO:0004129 cytochrome-c oxidase activity                                          | 0.24477 | 0.44009 | 0 | 0 | 1  | 15   |
| GO:0004953 icotanol receptor activity                                       | 1  | 0.24477 | 0.292  | 0.067 | Molecular  | GO:0004953 icotanol receptor activity                                             | 0.24477 | 0.44009 | 0 | 0 | 1  | 15   |
| GO:016208 AMP binding                                                       | 1  | 0.24477 | 0.292  | 0.067 | Molecular  | GO:016208 AMP binding                                                             | 0.24477 | 0.44009 | 0 | 0 | 1  | 15   |
| GO:0042813 Wnt-activated receptor activity                                  | 1  | 0.24477 | 0.292  | 0.067 | Molecular  | GO:0042813 Wnt-activated receptor activity                                        | 0.24477 | 0.44009 | 0 | 0 | 1  | 15   |
| GO:0045028 G protein-coupled putative nucleotide receptor activity          | 1  | 0.24477 | 0.292  | 0.067 | Molecular  | GO:0045028 G protein-coupled putative nucleotide receptor activity                | 0.24477 | 0.44009 | 0 | 0 | 1  | 15   |
| GO:0097153 cysteine-type endopeptidase activity involved in apoptotic       | 1  | 0.24477 | 0.292  | 0.067 | Molecular  | GO:0097153 cysteine-type endopeptidase activity involved in apoptotic process     | 0.24477 | 0.44009 | 0 | 0 | 1  | 15   |
| GO:0099103 channel activator activity                                       | 1  | 0.24477 | 0.292  | 0.067 | Molecular  | GO:0099103 channel activator activity                                             | 0.24477 | 0.44009 | 0 | 0 | 1  | 15   |
| GO:0007215 glutamate receptor signaling pathway                             | 2  | 0.24488 | 0.619  | 0.038 | Biological | GO:0007215 glutamate receptor signaling pathway                                   | 0.24488 | 0.43969 | 0 | 0 | 2  | 52   |
| GO:0022602 ovulation cycle process                                          | 2  | 0.24488 | 0.619  | 0.038 | Biological | GO:0022602 ovulation cycle process                                                | 0.24488 | 0.43969 | 0 | 0 | 2  | 52   |
| GO:0032007 regulation of TOR signaling                                      | 2  | 0.24488 | 0.619  | 0.038 | Biological | GO:0032007 regulation of TOR signaling                                            | 0.24488 | 0.43969 | 0 | 0 | 2  | 52   |
| GO:0043536 positive regulation of blood vessel endothelial cell migratio    | 2  | 0.24488 | 0.619  | 0.038 | Biological | GO:0043536 positive regulation of blood vessel endothelial cell migration         | 0.24488 | 0.43969 | 0 | 0 | 2  | 52   |
| GO:0050435 amyloid-beta metabolic process                                   | 2  | 0.24488 | 0.619  | 0.038 | Biological | GO:0050435 amyloid-beta metabolic process                                         | 0.24488 | 0.43969 | 0 | 0 | 2  | 52   |
| GO:0089718 amino acid import across plasma membrane                         | 2  | 0.24488 | 0.619  | 0.038 | Biological | GO:0089718 amino acid import across plasma membrane                               | 0.24488 | 0.43969 | 0 | 0 | 2  | 52   |
| GO:1990828 response to amino acid starvation                                | 2  | 0.24488 | 0.619  | 0.038 | Biological | GO:1990828 response to amino acid starvation                                      | 0.24488 | 0.43969 | 0 | 0 | 2  | 52   |
| GO:2000649 regulation of sodium ion transmembrane transporter activi        | 2  | 0.24488 | 0.619  | 0.038 | Biological | GO:2000649 regulation of sodium ion transmembrane transporter activity            | 0.24488 | 0.43969 | 0 | 0 | 2  | 52   |
| GO:2000677 regulation of transcription regulatory region DNA binding        | 2  | 0.24488 | 0.619  | 0.038 | Biological | GO:2000677 regulation of transcription regulatory region DNA binding              | 0.24488 | 0.43969 | 0 | 0 | 2  | 52   |
| GO:0007018 microtubule-based movement                                       | 10 | 0.24494 | 3.096  | 0.024 | Biological | GO:0007018 microtubule-based movement                                             | 0.24494 | 0.43969 | 0 | 0 | 10 | 423  |
| GO:0008835 dicarboxylic acid transport                                      | 3  | 0.24545 | 0.929  | 0.032 | Biological | GO:0008835 dicarboxylic acid transport                                            | 0.24545 | 0.44043 | 0 | 0 | 3  | 94   |
| GO:0019218 regulation of steroid metabolic process                          | 3  | 0.24545 | 0.929  | 0.032 | Biological | GO:0019218 regulation of steroid metabolic process                                | 0.24545 | 0.44043 | 0 | 0 | 3  | 94   |
| GO:0006950 response to hypoxia                                              | 78 | 0.24613 | 24.149 | 0.02  | Biological | GO:0006950 response to hypoxia                                                    | 0.24613 | 0.44138 | 0 | 0 | 78 | 3974 |
| GO:0043565 sequence-specific DNA binding                                    | 35 | 0.24783 | 10.234 | 0.021 | Molecular  | GO:0043565 sequence-specific DNA binding                                          | 0.24783 | 0.45375 | 0 | 0 | 35 | 1672 |
| GO:0007266 Rho protein signal transduction                                  | 4  | 0.24836 | 1.238  | 0.029 | Biological | GO:0007266 Rho protein signal transduction                                        | 0.24836 | 0.44504 | 0 | 0 | 4  | 139  |
| GO:0071456 cellular response to hypoxia                                     | 4  | 0.24836 | 1.238  | 0.029 | Biological | GO:0071456 cellular response to hypoxia                                           | 0.24836 | 0.44504 | 0 | 0 | 4  | 139  |
| GO:0031869 cellular response to nutrient levels                             | 6  | 0.24963 | 1.858  | 0.026 | Biological | GO:0031869 cellular response to nutrient levels                                   | 0.24963 | 0.44715 | 0 | 0 | 6  | 232  |
| GO:0008017 microtubule-based movement                                       | 7  | 0.24982 | 2.047  | 0.029 | Biological | GO:0008017 microtubule-based movement                                             | 0.24982 | 0.45457 | 0 | 0 | 7  | 275  |
| GO:0006942 regulation of striated muscle contraction                        | 3  | 0.25034 | 0.929  | 0.032 | Biological | GO:0006942 regulation of striated muscle contraction                              | 0.25034 | 0.44724 | 0 | 0 | 3  | 95   |
| GO:0032611 interleukin-1 beta production                                    | 3  | 0.25034 | 0.929  | 0.032 | Biological | GO:0032611 interleukin-1 beta production                                          | 0.25034 | 0.44724 | 0 | 0 | 3  | 95   |
| GO:0032651 regulation of interleukin-1 beta production                      | 3  | 0.25034 | 0.929  | 0.032 | Biological | GO:0032651 regulation of interleukin-1 beta production                            | 0.25034 | 0.44724 | 0 | 0 | 3  | 95   |
| GO:0016763 peptidyltransferase activity                                     | 2  | 0.25076 | 0.585  | 0.038 | Molecular  | GO:0016763 peptidyltransferase activity                                           | 0.25076 | 0.45457 | 0 | 0 | 2  | 52   |
| GO:0016879 ligase activity, carbon-nitrogen bonds                           | 2  | 0.25076 | 0.585  | 0.038 | Molecular  | GO:0016879 ligase activity, carbon-nitrogen bonds                                 | 0.25076 | 0.45457 | 0 | 0 | 2  | 52   |
| GO:0034703 cation channel complex                                           | 6  | 0.25077 | 1.728  | 0.023 | Cellular   | GO:0034703 cation channel complex                                                 | 0.25077 | 0.466   | 0 | 0 | 6  | 235  |
| GO:0015075 ion transmembrane transporter activity                           | 19 | 0.2516  | 5.556  | 0.022 | Molecular  | GO:0015075 ion transmembrane transporter activity                                 | 0.2516  | 0.45457 | 0 | 0 | 19 | 883  |
| GO:0010543 regulation of platelet activation                                | 2  | 0.25165 | 0.619  | 0.038 | Biological | GO:0010543 regulation of platelet activation                                      | 0.25165 | 0.44724 | 0 | 0 | 2  | 53   |
| GO:0060071 Wnt signaling pathway, planar cell polarity pathway              | 2  | 0.25165 | 0.619  | 0.038 | Biological | GO:0060071 Wnt signaling pathway, planar cell polarity pathway                    | 0.25165 | 0.44724 | 0 | 0 | 2  | 53   |
| GO:0061462 protein translocation to lysosome                                | 2  | 0.25165 | 0.619  | 0.038 | Biological | GO:0061462 protein translocation to lysosome                                      | 0.25165 | 0.44724 | 0 | 0 | 2  | 53   |
| GO:0030133 transport vesicle                                                | 10 | 0.25202 | 2.967  | 0.023 | Cellular   | GO:0030133 transport vesicle                                                      | 0.25202 | 0.466   | 0 | 0 | 10 | 431  |
| GO:0046887 positive regulation of hormone secretion                         | 4  | 0.25234 | 1.238  | 0.029 | Biological | GO:0046887 positive regulation of hormone secretion                               | 0.25234 | 0.44724 | 0 | 0 | 4  | 140  |
| GO:0009266 response to temperature stimulus                                 | 5  | 0.25244 | 1.548  | 0.027 | Biological | GO:0009266 response to temperature stimulus                                       | 0.25244 | 0.44724 | 0 | 0 | 5  | 186  |
| GO:0010721 negative regulation of cell development                          | 5  | 0.25244 | 1.548  | 0.027 | Biological | GO:0010721 negative regulation of cell development                                | 0.25244 | 0.44724 | 0 | 0 | 5  | 186  |
| GO:0057444 TIM23 mitochondrial import inner membrane translocase c          | 1  | 0.25267 | 0.292  | 0.067 | Cellular   | GO:0057444 TIM23 mitochondrial import inner membrane translocase complex          | 0.25267 | 0.466   | 0 | 0 | 1  | 16   |
| GO:0032156 septin cytoskeleton                                              | 1  | 0.25267 | 0.292  | 0.067 | Cellular   | GO:0032156 septin cytoskeleton                                                    | 0.25267 | 0.466   | 0 | 0 | 1  | 16   |
| GO:0098554 cytoplasmic side of endoplasmic reticulum membrane               | 1  | 0.25267 | 0.292  | 0.067 | Cellular   | GO:0098554 cytoplasmic side of endoplasmic reticulum membrane                     | 0.25267 | 0.466   | 0 | 0 | 1  | 16   |
| GO:0006952 defense response                                                 | 36 | 0.25387 | 11.146 | 0.02  | Biological | GO:0006952 defense response                                                       | 0.25387 | 0.44724 | 0 | 0 | 36 | 1758 |
| GO:0000397 sulfur amino acid biosynthetic process                           | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0000397 sulfur amino acid biosynthetic process                                 | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0002371 dendritic cytokine production                                    | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0002371 dendritic cytokine production                                          | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0002073 regulation of dendritic cell cytokine production                 | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0002073 regulation of dendritic cell cytokine production                       | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0003188 heart valve formation                                            | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0003188 heart valve formation                                                  | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0003413 chondrocyte differentiation involved in endochondral bone        | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0003413 chondrocyte differentiation involved in endochondral bone morphogen    | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0006266 DNA ligation                                                     | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0006266 DNA ligation                                                           | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0006771 glycine-terminated metabolic process                             | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0006771 glycine-terminated metabolic process                                   | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0006825 copper ion transport                                             | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0006825 copper ion transport                                                   | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0007028 cytoplasm organization                                           | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0007028 cytoplasm organization                                                 | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0009074 aromatic amino acid family catabolic process                     | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0009074 aromatic amino acid family catabolic process                           | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0010763 positive regulation of fibroblast migration                      | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0010763 positive regulation of fibroblast migration                            | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0010819 regulation of cell chemotaxis                                    | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0010819 regulation of cell chemotaxis                                          | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0014819 regulation of skeletal muscle contraction                        | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0014819 regulation of skeletal muscle contraction                              | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0019511 peptidyl-proline hydroxylation                                   | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0019511 peptidyl-proline hydroxylation                                         | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0021783 preangionotic parasympathetic fiber development                  | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0021783 preangionotic parasympathetic fiber development                        | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0030852 regulation of granulocyte differentiation                        | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0030852 regulation of granulocyte differentiation                              | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0034374 low-density lipoprotein particle remodeling                      | 1  | 0.25509 | 0.31   | 0.062 | Biological | GO:0034374 low-density lipoprotein particle remodeling                            | 0.25509 | 0.44724 | 0 | 0 | 1  | 16   |
| GO:0034375 high-density lipoprotein particle remodeling                     | 1  | 0.25509 | 0.31   |       |            |                                                                                   |         |         |   |   |    |      |

|                                                                                            |    |         |       |       |            |                                                                                            |         |         |   |   |    |     |
|--------------------------------------------------------------------------------------------|----|---------|-------|-------|------------|--------------------------------------------------------------------------------------------|---------|---------|---|---|----|-----|
| GO:1904680 peptide transmembrane transporter activity                                      | 1  | 0.25878 | 0.292 | 0.062 | Molecular  | GO:1904680 peptide transmembrane transporter activity                                      | 0.25878 | 0.45457 | 0 | 0 | 1  | 16  |
| GO:0030414 peptidase inhibitor activity                                                    | 5  | 0.25963 | 1.462 | 0.027 | Molecular  | GO:0030414 peptidase inhibitor activity                                                    | 0.25963 | 0.45514 | 0 | 0 | 5  | 185 |
| GO:0001750 photoreceptor outer segment                                                     | 3  | 0.25986 | 0.88  | 0.031 | Cellular   | GO:0001750 photoreceptor outer segment                                                     | 0.25986 | 0.47738 | 0 | 0 | 3  | 98  |
| GO:000041 transition metal ion transport                                                   | 3  | 0.26014 | 0.929 | 0.031 | Biological | GO:000041 transition metal ion transport                                                   | 0.26014 | 0.45299 | 0 | 0 | 3  | 97  |
| GO:0009798 axis specification                                                              | 3  | 0.26014 | 0.929 | 0.031 | Biological | GO:0009798 axis specification                                                              | 0.26014 | 0.45299 | 0 | 0 | 3  | 97  |
| GO:0030516 regulation of axon extension                                                    | 3  | 0.26014 | 0.929 | 0.031 | Biological | GO:0030516 regulation of axon extension                                                    | 0.26014 | 0.45299 | 0 | 0 | 3  | 97  |
| GO:1901019 regulation of calcium ion transmembrane transporter activity                    | 3  | 0.26014 | 0.929 | 0.031 | Biological | GO:1901019 regulation of calcium ion transmembrane transporter activity                    | 0.26014 | 0.45299 | 0 | 0 | 3  | 97  |
| GO:0045444 fat cell differentiation                                                        | 6  | 0.26183 | 1.858 | 0.031 | Biological | GO:0045444 fat cell differentiation                                                        | 0.26183 | 0.45572 | 0 | 0 | 6  | 268 |
| GO:0051962 positive regulation of nervous system development                               | 7  | 0.26199 | 2.167 | 0.025 | Biological | GO:0051962 positive regulation of nervous system development                               | 0.26199 | 0.45572 | 0 | 0 | 7  | 294 |
| GO:1903829 positive regulation of cellular protein localization                            | 7  | 0.26199 | 2.167 | 0.025 | Biological | GO:1903829 positive regulation of cellular protein localization                            | 0.26199 | 0.45572 | 0 | 0 | 7  | 284 |
| GO:0030324 lung development                                                                | 5  | 0.26275 | 1.548 | 0.026 | Biological | GO:0030324 lung development                                                                | 0.26275 | 0.45689 | 0 | 0 | 5  | 189 |
| GO:0051213 dryogenerative activity                                                         | 3  | 0.26312 | 0.877 | 0.031 | Molecular  | GO:0051213 dryogenerative activity                                                         | 0.26312 | 0.46032 | 0 | 0 | 3  | 96  |
| GO:0050576 transition metal ion homeostasis                                                | 4  | 0.26393 | 1.238 | 0.059 | Biological | GO:0050576 transition metal ion homeostasis                                                | 0.26393 | 0.45937 | 0 | 0 | 4  | 143 |
| GO:0050538 recycling endosome membrane                                                     | 3  | 0.26453 | 0.88  | 0.03  | Cellular   | GO:0050538 recycling endosome membrane                                                     | 0.26453 | 0.48256 | 0 | 0 | 3  | 99  |
| GO:0045185 maintenance of protein location                                                 | 3  | 0.26507 | 0.929 | 0.031 | Biological | GO:0045185 maintenance of protein location                                                 | 0.26507 | 0.45937 | 0 | 0 | 3  | 98  |
| GO:0062014 negative regulation of small molecule metabolic process                         | 3  | 0.26507 | 0.929 | 0.031 | Biological | GO:0062014 negative regulation of small molecule metabolic process                         | 0.26507 | 0.45937 | 0 | 0 | 3  | 98  |
| GO:0003229 ventricular cardiac muscle tissue development                                   | 2  | 0.26521 | 0.819 | 0.038 | Biological | GO:0003229 ventricular cardiac muscle tissue development                                   | 0.26521 | 0.45937 | 0 | 0 | 2  | 55  |
| GO:0033444 cholesterol efflux                                                              | 2  | 0.26521 | 0.819 | 0.038 | Biological | GO:0033444 cholesterol efflux                                                              | 0.26521 | 0.45937 | 0 | 0 | 2  | 55  |
| GO:0051055 negative regulation of lipid biosynthetic process                               | 2  | 0.26521 | 0.819 | 0.038 | Biological | GO:0051055 negative regulation of lipid biosynthetic process                               | 0.26521 | 0.45937 | 0 | 0 | 2  | 55  |
| GO:0052372 modulation by symbiont of entry into host                                       | 2  | 0.26521 | 0.819 | 0.038 | Biological | GO:0052372 modulation by symbiont of entry into host                                       | 0.26521 | 0.45937 | 0 | 0 | 2  | 55  |
| GO:0030666 endocytic vesicle membrane                                                      | 5  | 0.26571 | 1.484 | 0.026 | Cellular   | GO:0030666 endocytic vesicle membrane                                                      | 0.26571 | 0.48256 | 0 | 0 | 5  | 192 |
| GO:0001650 fibrillar center                                                                | 4  | 0.26585 | 1.187 | 0.028 | Cellular   | GO:0001650 fibrillar center                                                                | 0.26585 | 0.48256 | 0 | 0 | 4  | 145 |
| GO:0090901 postsynaptic specialization, intracellular component                            | 1  | 0.26608 | 0.297 | 0.059 | Cellular   | GO:0090901 postsynaptic specialization, intracellular component                            | 0.26608 | 0.48256 | 0 | 0 | 1  | 17  |
| GO:0010876 lipid localization                                                              | 11 | 0.26791 | 3.406 | 0.023 | Biological | GO:0010876 lipid localization                                                              | 0.26791 | 0.45937 | 0 | 0 | 11 | 483 |
| GO:0001991 regulation of systemic arterial blood pressure by circulation                   | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0001991 regulation of systemic arterial blood pressure by circulation                   | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0003198 epithelial to mesenchymal transition involved in endocardia                     | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0003198 epithelial to mesenchymal transition involved in endocardia                     | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0000474 N-terminal protein amino acid acetylation                                       | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0000474 N-terminal protein amino acid acetylation                                       | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0008695 Gsk3 inhibition                                                                 | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0008695 Gsk3 inhibition                                                                 | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0006957 complement activation, alternative pathway                                      | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0006957 complement activation, alternative pathway                                      | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0009068 aspartate family amino acid catabolic process                                   | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0009068 aspartate family amino acid catabolic process                                   | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0009071 serine family amino acid catabolic process                                      | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0009071 serine family amino acid catabolic process                                      | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0009886 post-embryonic animal morphogenesis                                             | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0009886 post-embryonic animal morphogenesis                                             | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0010865 regulation of cholesterol storage                                               | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0010865 regulation of cholesterol storage                                               | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0016045 detection of bacterium                                                          | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0016045 detection of bacterium                                                          | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0019184 nonribosomal peptide biosynthetic process                                       | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0019184 nonribosomal peptide biosynthetic process                                       | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0021513 spinal cord dorsal/ventral patterning                                           | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0021513 spinal cord dorsal/ventral patterning                                           | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0031649 heat generation                                                                 | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0031649 heat generation                                                                 | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0032774 prolactin secretion                                                             | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0032774 prolactin secretion                                                             | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0033599 regulation of mammary gland epithelial cell proliferation                       | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0033599 regulation of mammary gland epithelial cell proliferation                       | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0033623 regulation of integrin activation                                               | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0033623 regulation of integrin activation                                               | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0034134 toll-like receptor 2 signaling pathway                                          | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0034134 toll-like receptor 2 signaling pathway                                          | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0035689 protein C-linked mannosylation                                                  | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0035689 protein C-linked mannosylation                                                  | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0036005 response to mycobacterium colony-stimulating factor                             | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0036005 response to mycobacterium colony-stimulating factor                             | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0036159 inner dynein arm assembly                                                       | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0036159 inner dynein arm assembly                                                       | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0036507 protein demannosylation                                                         | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0036507 protein demannosylation                                                         | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0036508 protein alpha-1,2-demannosylation                                               | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0036508 protein alpha-1,2-demannosylation                                               | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0043129 surfactant homeostasis                                                          | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0043129 surfactant homeostasis                                                          | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0043249 erythrocyte maturation                                                          | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0043249 erythrocyte maturation                                                          | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0044764 multi-organism cellular process                                                 | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0044764 multi-organism cellular process                                                 | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0045722 positive regulation of gluconeogenesis                                          | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0045722 positive regulation of gluconeogenesis                                          | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0048532 anatomical structure arrangement                                                | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0048532 anatomical structure arrangement                                                | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0048875 chemical homeostasis within a tissue                                            | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0048875 chemical homeostasis within a tissue                                            | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0051890 cellular response to prolactin/E stimulus                                       | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0051890 cellular response to prolactin/E stimulus                                       | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0072224 melanophagocytosis development                                                  | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0072224 melanophagocytosis development                                                  | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0098712 L-glutamate import across plasma membrane                                       | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0098712 L-glutamate import across plasma membrane                                       | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0098877 neurotransmitter receptor transport to plasma membrane                          | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0098877 neurotransmitter receptor transport to plasma membrane                          | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:009149 regulation of postsynaptic neurotransmitter receptor internalization             | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:009149 regulation of postsynaptic neurotransmitter receptor internalization             | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:0098509 regulation of postsynaptic calcium ion concentration                            | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:0098509 regulation of postsynaptic calcium ion concentration                            | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:1900334 regulation of cellular response to heat                                         | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:1900334 regulation of cellular response to heat                                         | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:1900117 regulation of execution phase of apoptosis                                      | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:1900117 regulation of execution phase of apoptosis                                      | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:1902336 regulation of leukocyte tethering or rolling                                    | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:1902336 regulation of leukocyte tethering or rolling                                    | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:1903587 regulation of blood vessel endothelial cell proliferation involved in sprouting | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:1903587 regulation of blood vessel endothelial cell proliferation involved in sprouting | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:1903830 macrophage transmembrane transport                                              | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:1903830 macrophage transmembrane transport                                              | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:1904003 embryonic brain development                                                     | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:1904003 embryonic brain development                                                     | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:2000696 regulation of epithelial cell differentiation involved in kidney development    | 1  | 0.26869 | 0.31  | 0.059 | Biological | GO:2000696 regulation of epithelial cell differentiation involved in kidney development    | 0.26869 | 0.45937 | 0 | 0 | 1  | 17  |
| GO:020037 heme binding                                                                     | 4  | 0.26986 | 1.17  | 0.028 | Molecular  | GO:020037 heme binding                                                                     | 0.26986 | 0.46643 | 0 | 0 | 4  | 142 |
| GO:0051851 modulation by host of symbiont process                                          | 3  | 0.27    | 0.928 | 0.03  | Biological | GO:0051851 modulation by host of symbiont process                                          | 0.27    | 0.46131 | 0 | 0 | 3  | 99  |
| GO:1901222 regulation of NIK/NF-kappaB signaling                                           | 3  | 0.27    | 0.928 | 0.03  | Biological | GO:1901222 regulation of NIK/NF-kappaB signaling                                           | 0.27    | 0.46131 | 0 | 0 | 3  | 99  |
| GO:0096362 cell-cell adhesion mediator activity                                            | 2  | 0.27143 | 0.585 | 0.038 | Molecular  | GO:0096362 cell-cell adhesion mediator activity                                            | 0.27143 | 0.46643 | 0 | 0 | 2  | 55  |
| GO:0006383 transcription by RNA polymerase III                                             | 2  | 0.27198 | 0.619 | 0.036 | Biological | GO:0006383 transcription by RNA polymerase III                                             | 0.27198 | 0.46406 | 0 | 0 | 2  | 56  |
| GO:0010332 response to gamma radiation                                                     | 2  | 0.27198 | 0.619 | 0.036 | Biological | GO:0010332 response to gamma radiation                                                     | 0.27198 | 0.46406 | 0 | 0 | 2  | 56  |
| GO:0042987 amyloid precursor protein catabolic process                                     | 2  | 0.27198 | 0.619 | 0.036 | Biological | GO:0042987 amyloid precursor protein catabolic process                                     | 0.27198 | 0.46406 | 0 | 0 | 2  | 56  |
| GO:0046164 alcohol catabolic process                                                       | 4  | 0.27198 | 0.619 | 0.036 | Biological | GO:0046164 alcohol catabolic process                                                       | 0.27198 | 0.46406 | 0 | 0 | 4  | 145 |
| GO:0014065 phosphatidylinositol 3-kinase signaling                                         | 4  | 0.27239 | 1.238 | 0.028 | Biological | GO:0014065 phosphatidylinositol 3-kinase signaling                                         | 0.27239 | 0.46459 | 0 | 0 | 4  | 145 |
| GO:0005001 transmembrane receptor protein tyrosine phosphatase activity                    | 1  | 0.27253 | 0.292 | 0.059 | Molecular  | GO:0005001 transmembrane receptor protein tyrosine phosphatase activity                    | 0.27253 | 0.46643 | 0 | 0 | 1  | 17  |
| GO:0005521 lamin binding                                                                   | 1  | 0.27253 | 0.292 | 0.059 | Molecular  | GO:0005521 lamin binding                                                                   | 0.27253 | 0.46643 | 0 | 0 | 1  | 17  |
| GO:0008574 plus-end-directed microtubule motor activity                                    | 1  | 0.27253 | 0.292 | 0.059 | Molecular  | GO:0008574 plus-end-directed microtubule motor activity                                    | 0.27253 | 0.46643 | 0 | 0 | 1  | 17  |
| GO:0015095 magnesium ion transmembrane transporter activity                                | 1  | 0.27253 | 0.292 | 0.059 | Molecular  | GO:0015095 magnesium ion transmembrane transporter activity                                | 0.27253 | 0.46643 | 0 | 0 | 1  | 17  |
| GO:0015923 mannose activity                                                                | 1  | 0.27253 | 0.292 | 0.059 | Molecular  | GO:0015923 mannose activity                                                                | 0.27253 | 0.46643 | 0 | 0 | 1  | 17  |
| GO:0019198 transmembrane receptor protein phosphatase activity                             | 1  | 0.27253 | 0.292 | 0.059 | Molecular  | GO:0019198 transmembrane receptor protein phosphatase activity                             | 0.27253 | 0.46643 | 0 | 0 | 1  | 17  |
| GO:0035497 cAMP response element binding                                                   | 1  | 0.27253 | 0.292 | 0.059 | Molecular  | GO:0035497 cAMP response element binding                                                   | 0.27253 | 0.46643 | 0 | 0 | 1  | 17  |
| GO:0095907 ligand-gated ion channel activity involved in regulation of presynaptic release | 1  | 0.27253 | 0.292 | 0.059 | Molecular  | GO:0095907 ligand-gated ion channel activity involved in regulation of presynaptic release | 0.27253 | 0.46643 | 0 | 0 | 1  | 17  |
| GO:0740327 lipase activity                                                                 | 1  | 0.27253 | 0.292 | 0.059 | Molecular  | GO:0740327 lipase activity                                                                 | 0.27253 | 0.46643 | 0 | 0 | 1  | 17  |
| GO:0072659 protein localization to plasma membrane                                         | 7  | 0.27321 | 2.167 | 0.024 | Biological | GO:0072659 protein localization to plasma membrane                                         | 0.27321 | 0.46583 | 0 | 0 | 7  | 288 |
| GO:0032587 ruffle membrane                                                                 | 3  | 0.27429 | 0.89  | 0.03  | Cellular   | GO:0032587 ruffle membrane                                                                 | 0.27429 | 0.49577 | 0 | 0 | 3  | 101 |
| GO:0001657 ureteric bud development                                                        | 3  | 0.27495 | 0.929 | 0.03  | Biological | GO:0001657 ureteric bud development                                                        | 0.27495 | 0.49831 | 0 | 0 | 3  | 100 |
| GO:0006721 terpenoid metabolic process                                                     | 3  | 0.27495 | 0.929 | 0.03  | Biological | GO:0006721 terpenoid metabolic process                                                     | 0.27495 | 0.49831 | 0 | 0 | 3  | 100 |
| GO:0070252 actin-mediated cell contraction                                                 | 3  | 0.27495 | 0.929 | 0.03  | Biological | GO:0070252 actin-mediated cell contraction                                                 | 0.27495 | 0.49831 | 0 | 0 | 3  | 100 |
| GO:0051346 negative regulation of hydrolase activity                                       | 8  |         |       |       |            |                                                                                            |         |         |   |   |    |     |

|                                                                                       |    |         |       |       |            |                                                                                       |         |         |   |   |    |      |
|---------------------------------------------------------------------------------------|----|---------|-------|-------|------------|---------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0004896 cytokine receptor activity                                                 | 3  | 0.28323 | 0.877 | 0.03  | Molecular  | GO:0004896 cytokine receptor activity                                                 | 0.28323 | 0.47612 | 0 | 0 | 3  | 100  |
| GO:0007163 establishment or maintenance of cell polarity                              | 6  | 0.28355 | 1.858 | 0.029 | Biological | GO:0007163 establishment or maintenance of cell polarity                              | 0.28355 | 0.47343 | 0 | 0 | 6  | 243  |
| GO:0032946 positive regulation of mononuclear cell proliferation                      | 4  | 0.28455 | 1.238 | 0.027 | Biological | GO:0032946 positive regulation of mononuclear cell proliferation                      | 0.28455 | 0.47448 | 0 | 0 | 4  | 148  |
| GO:0050768 negative regulation of neurogenesis                                        | 4  | 0.28455 | 1.238 | 0.027 | Biological | GO:0050768 negative regulation of neurogenesis                                        | 0.28455 | 0.47448 | 0 | 0 | 4  | 148  |
| GO:0006641 triglyceride metabolic process                                             | 3  | 0.28487 | 0.929 | 0.029 | Biological | GO:0006641 triglyceride metabolic process                                             | 0.28487 | 0.47484 | 0 | 0 | 3  | 102  |
| GO:0014013 regulation of oogenesis                                                    | 3  | 0.28487 | 0.929 | 0.029 | Biological | GO:0014013 regulation of oogenesis                                                    | 0.28487 | 0.47484 | 0 | 0 | 3  | 102  |
| GO:0041568 lipopeptide biosynthetic process                                           | 3  | 0.28487 | 0.929 | 0.029 | Biological | GO:0041568 lipopeptide biosynthetic process                                           | 0.28487 | 0.47484 | 0 | 0 | 3  | 102  |
| GO:0016655 oocyte maturation, acting on NAD(P)H, quinone or similar compound          | 2  | 0.28521 | 0.585 | 0.034 | Biological | GO:0016655 oocyte maturation, acting on NAD(P)H, quinone or similar compound          | 0.28521 | 0.47612 | 0 | 0 | 2  | 57   |
| GO:0001541 ovarian follicle development                                               | 2  | 0.28553 | 0.619 | 0.034 | Biological | GO:0001541 ovarian follicle development                                               | 0.28553 | 0.47516 | 0 | 0 | 2  | 58   |
| GO:0006767 water-soluble vitamin metabolic process                                    | 2  | 0.28553 | 0.619 | 0.034 | Biological | GO:0006767 water-soluble vitamin metabolic process                                    | 0.28553 | 0.47516 | 0 | 0 | 2  | 58   |
| GO:0043407 negative regulation of MAP kinase activity                                 | 2  | 0.28553 | 0.619 | 0.034 | Biological | GO:0043407 negative regulation of MAP kinase activity                                 | 0.28553 | 0.47516 | 0 | 0 | 2  | 58   |
| GO:0050879 multicellular organismal movement                                          | 2  | 0.28553 | 0.619 | 0.034 | Biological | GO:0050879 multicellular organismal movement                                          | 0.28553 | 0.47516 | 0 | 0 | 2  | 58   |
| GO:0051243 establishment of spindle localization                                      | 2  | 0.28553 | 0.619 | 0.034 | Biological | GO:0051243 establishment of spindle localization                                      | 0.28553 | 0.47516 | 0 | 0 | 2  | 58   |
| GO:0034399 nuclear periphery                                                          | 4  | 0.28586 | 1.187 | 0.027 | Cellular   | GO:0034399 nuclear periphery                                                          | 0.28586 | 0.5094  | 0 | 0 | 4  | 150  |
| GO:0004115 3',5'-cyclic-AMP phosphodiesterase activity                                | 1  | 0.28603 | 0.292 | 0.056 | Molecular  | GO:0004115 3',5'-cyclic-AMP phosphodiesterase activity                                | 0.28603 | 0.47612 | 0 | 0 | 1  | 18   |
| GO:0008070 phospholipase A1 activity                                                  | 1  | 0.28603 | 0.292 | 0.056 | Molecular  | GO:0008070 phospholipase A1 activity                                                  | 0.28603 | 0.47612 | 0 | 0 | 1  | 18   |
| GO:0015172 acidic amino acid transmembrane transporter activity                       | 1  | 0.28603 | 0.292 | 0.056 | Molecular  | GO:0015172 acidic amino acid transmembrane transporter activity                       | 0.28603 | 0.47612 | 0 | 0 | 1  | 18   |
| GO:0015556 C4-dicarboxylate transmembrane transporter activity                        | 1  | 0.28603 | 0.292 | 0.056 | Molecular  | GO:0015556 C4-dicarboxylate transmembrane transporter activity                        | 0.28603 | 0.47612 | 0 | 0 | 1  | 18   |
| GO:0016854 racemase and epimerase activity                                            | 1  | 0.28603 | 0.292 | 0.056 | Molecular  | GO:0016854 racemase and epimerase activity                                            | 0.28603 | 0.47612 | 0 | 0 | 1  | 18   |
| GO:0034185 apolipoprotein binding                                                     | 1  | 0.28603 | 0.292 | 0.056 | Molecular  | GO:0034185 apolipoprotein binding                                                     | 0.28603 | 0.47612 | 0 | 0 | 1  | 18   |
| GO:0043395 heparan sulfate proteoglycan binding                                       | 1  | 0.28603 | 0.292 | 0.056 | Molecular  | GO:0043395 heparan sulfate proteoglycan binding                                       | 0.28603 | 0.47612 | 0 | 0 | 1  | 18   |
| GO:0050811 GABA receptor binding                                                      | 1  | 0.28603 | 0.292 | 0.056 | Molecular  | GO:0050811 GABA receptor binding                                                      | 0.28603 | 0.47612 | 0 | 0 | 1  | 18   |
| GO:009186 structural constituent of postsynapse                                       | 1  | 0.28603 | 0.292 | 0.056 | Molecular  | GO:009186 structural constituent of postsynapse                                       | 0.28603 | 0.47612 | 0 | 0 | 1  | 18   |
| GO:0015276 ligand-gated ion channel activity                                          | 4  | 0.28635 | 1.17  | 0.027 | Molecular  | GO:0015276 ligand-gated ion channel activity                                          | 0.28635 | 0.47612 | 0 | 0 | 4  | 146  |
| GO:0022834 ligand-gated channel activity                                              | 4  | 0.28635 | 1.17  | 0.027 | Molecular  | GO:0022834 ligand-gated channel activity                                              | 0.28635 | 0.47612 | 0 | 0 | 4  | 146  |
| GO:0015631 tubulin binding                                                            | 9  | 0.28644 | 2.632 | 0.023 | Molecular  | GO:0015631 tubulin binding                                                            | 0.28644 | 0.47612 | 0 | 0 | 9  | 385  |
| GO:0043481 protein kinase B signaling                                                 | 5  | 0.28719 | 1.548 | 0.026 | Biological | GO:0043481 protein kinase B signaling                                                 | 0.28719 | 0.47775 | 0 | 0 | 5  | 196  |
| GO:0001775 cell activation                                                            | 24 | 0.28742 | 1.43  | 0.027 | Biological | GO:0001775 cell activation                                                            | 0.28742 | 0.47781 | 0 | 0 | 24 | 1159 |
| GO:1903532 positive regulation of secretion by cell                                   | 2  | 0.28742 | 1.167 | 0.024 | Biological | GO:1903532 positive regulation of secretion by cell                                   | 0.28742 | 0.47781 | 0 | 0 | 2  | 73   |
| GO:0030660 Golgi-associated vesicle membrane                                          | 2  | 0.28781 | 0.593 | 0.034 | Cellular   | GO:0030660 Golgi-associated vesicle membrane                                          | 0.28781 | 0.50818 | 0 | 0 | 2  | 59   |
| GO:0061135 endopeptidase regulator activity                                           | 5  | 0.28799 | 1.462 | 0.026 | Molecular  | GO:0061135 endopeptidase regulator activity                                           | 0.28799 | 0.47777 | 0 | 0 | 5  | 193  |
| GO:0015908 fatty acid transport                                                       | 3  | 0.28984 | 0.929 | 0.029 | Biological | GO:0015908 fatty acid transport                                                       | 0.28984 | 0.48152 | 0 | 0 | 3  | 103  |
| GO:0003499 bone mineralization                                                        | 3  | 0.28984 | 0.929 | 0.029 | Biological | GO:0003499 bone mineralization                                                        | 0.28984 | 0.48152 | 0 | 0 | 3  | 103  |
| GO:0005261 cation channel activity                                                    | 8  | 0.29119 | 2.339 | 0.024 | Molecular  | GO:0005261 cation channel activity                                                    | 0.29119 | 0.48216 | 0 | 0 | 8  | 338  |
| GO:1901682 sulfur compound transmembrane transporter activity                         | 2  | 0.29209 | 0.585 | 0.034 | Molecular  | GO:1901682 sulfur compound transmembrane transporter activity                         | 0.29209 | 0.48273 | 0 | 0 | 2  | 58   |
| GO:0046686 response to cadmium ion                                                    | 2  | 0.2923  | 0.619 | 0.034 | Biological | GO:0046686 response to cadmium ion                                                    | 0.2923  | 0.48309 | 0 | 0 | 2  | 59   |
| GO:0051353 positive regulation of oxidoreductase activity                             | 2  | 0.2923  | 0.619 | 0.034 | Biological | GO:0051353 positive regulation of oxidoreductase activity                             | 0.2923  | 0.48309 | 0 | 0 | 2  | 59   |
| GO:0095223 cytokine receptor region                                                   | 1  | 0.29233 | 0.292 | 0.056 | Molecular  | GO:0095223 cytokine receptor region                                                   | 0.29233 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0051607 defense response to virus                                                  | 7  | 0.29315 | 2.167 | 0.024 | Biological | GO:0051607 defense response to virus                                                  | 0.29315 | 0.48309 | 0 | 0 | 7  | 295  |
| GO:0140546 defense response to symbiont                                               | 7  | 0.29315 | 2.167 | 0.024 | Biological | GO:0140546 defense response to symbiont                                               | 0.29315 | 0.48309 | 0 | 0 | 7  | 295  |
| GO:0042102 positive regulation of T cell proliferation                                | 3  | 0.29481 | 0.929 | 0.029 | Biological | GO:0042102 positive regulation of T cell proliferation                                | 0.29481 | 0.48309 | 0 | 0 | 3  | 104  |
| GO:0008286 negative regulation of cellular response to growth factor stimulus         | 3  | 0.29481 | 0.929 | 0.029 | Biological | GO:0008286 negative regulation of cellular response to growth factor stimulus         | 0.29481 | 0.48309 | 0 | 0 | 3  | 104  |
| GO:0031410 cytokine receptor activity                                                 | 4  | 0.29513 | 1.43  | 0.027 | Biological | GO:0031410 cytokine receptor activity                                                 | 0.29513 | 0.48309 | 0 | 0 | 4  | 159  |
| GO:0001845 phagocytosis assembly                                                      | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0001845 phagocytosis assembly                                                      | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0002283 neutrophil activation involved in immune response                          | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0002283 neutrophil activation involved in immune response                          | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0002483 antigen processing and presentation of endogenous peptide antigen          | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0002483 antigen processing and presentation of endogenous peptide antigen          | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0003215 cardiac right ventricle morphogenesis                                      | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0003215 cardiac right ventricle morphogenesis                                      | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0006044 N-acetylglucosamine metabolic process                                      | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0006044 N-acetylglucosamine metabolic process                                      | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0006309 apoptotic DNA fragmentation                                                | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0006309 apoptotic DNA fragmentation                                                | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0007617 mating behavior                                                            | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0007617 mating behavior                                                            | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0009070 serine family amino acid biosynthetic process                              | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0009070 serine family amino acid biosynthetic process                              | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0010544 negative regulation of platelet activation                                 | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0010544 negative regulation of platelet activation                                 | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0031259 positive regulation of macrophage chemotaxis                               | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0031259 positive regulation of macrophage chemotaxis                               | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0010878 cholesterol storage                                                        | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0010878 cholesterol storage                                                        | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0014048 regulation of glutamate secretion                                          | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0014048 regulation of glutamate secretion                                          | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0016553 base conversion or substitution editing                                    | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0016553 base conversion or substitution editing                                    | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0021511 spiral cord patterning                                                     | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0021511 spiral cord patterning                                                     | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0030302 negative regulation of bone mineralization                                 | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0030302 negative regulation of bone mineralization                                 | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0031645 negative regulation of nervous system process                              | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0031645 negative regulation of nervous system process                              | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0032328 alanine transport                                                          | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0032328 alanine transport                                                          | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0032793 positive regulation of CREB transcription factor activity                  | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0032793 positive regulation of CREB transcription factor activity                  | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0036003 positive regulation of transcription from RNA polymerase II promoter       | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0036003 positive regulation of transcription from RNA polymerase II promoter       | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0043116 negative regulation of membrane permeability                               | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0043116 negative regulation of membrane permeability                               | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0043517 positive regulation of DNA damage response, signal transduction by protein | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0043517 positive regulation of DNA damage response, signal transduction by protein | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0045540 regulation of cholesterol biosynthetic process                             | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0045540 regulation of cholesterol biosynthetic process                             | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0045655 regulation of monocyte differentiation                                     | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0045655 regulation of monocyte differentiation                                     | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0045945 positive regulation of transcription by RNA polymerase III                 | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0045945 positive regulation of transcription by RNA polymerase III                 | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0048245 positive regulation of cytokinesis                                         | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0048245 positive regulation of cytokinesis                                         | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0050965 detection of temperature stimulus involved in sensory perception of pain   | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0050965 detection of temperature stimulus involved in sensory perception of pain   | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0051938 L-glutamate import                                                         | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0051938 L-glutamate import                                                         | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0051988 regulation of attachment of spindle microtubules to kinetochore            | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0051988 regulation of attachment of spindle microtubules to kinetochore            | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0071360 cellular response to exogenous dsRNA                                       | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0071360 cellular response to exogenous dsRNA                                       | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0071786 endoplasmic reticulum tubular network organization                         | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0071786 endoplasmic reticulum tubular network organization                         | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0071800 podosome assembly                                                          | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0071800 podosome assembly                                                          | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0097094 craniofacial suture morphogenesis                                          | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0097094 craniofacial suture morphogenesis                                          | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0097202 activation of cysteine-type endopeptidase activity                         | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0097202 activation of cysteine-type endopeptidase activity                         | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:0106118 regulation of steroid biosynthetic process                                 | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:0106118 regulation of steroid biosynthetic process                                 | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:1901659 glycosylated protein biosynthetic process                                  | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:1901659 glycosylated protein biosynthetic process                                  | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:1904862 inhibitory synapse assembly                                                | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:1904862 inhibitory synapse assembly                                                | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:1905146 lysosomal protein catabolic process                                        | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:1905146 lysosomal protein catabolic process                                        | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:2001135 regulation of endocytic recycling                                          | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:2001135 regulation of endocytic recycling                                          | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:2001185 regulation of CDB-positive, alpha-beta T cell activation                   | 1  | 0.29513 | 0.31  | 0.053 | Biological | GO:2001185 regulation of CDB-positive, alpha-beta T cell activation                   | 0.29513 | 0.48309 | 0 | 0 | 1  | 19   |
| GO:2004584 positive regulation of lipid metabolic process                             | 1  | 0.29684 | 2.339 | 0.024 | Biological | GO:2004584 positive regulation of lipid metabolic process                             | 0.29684 | 0.48372 | 0 | 0 | 1  | 151  |
| GO:0002682 regulation of immune system process                                        | 31 | 0.29694 | 9.598 | 0.02  | Biological | GO:0002682 regulation of immune system process                                        | 0.29694 | 0.48572 | 0 | 0 | 31 | 1532 |
| GO:0045787 positive regulation of cell cycle                                          | 8  | 0.2974  | 2.477 | 0.023 | Biological | GO:0045787 positive regulation of cell cycle                                          | 0.2974  | 0.48611 | 0 | 0 | 8  | 346  |
| GO:0097708 intracellular vesicle                                                      | 49 | 0.29809 | 14.54 | 0.019 | Cellular   | GO:0097708 intracellular vesicle                                                      | 0.29809 | 0.52117 | 0 | 0 | 49 | 2513 |
| GO:0016279 protein-lysine N-methyltransferase activity                                | 2  | 0.29809 | 0.585 | 0.034 | Molecular  | GO:0016279 protein-lysine N-methyltransferase activity                                | 0.29809 | 0.48808 | 0 | 0 | 2  | 59   |
| GO:0002886 leukocyte mediated immunity                                                | 2  | 0.29809 | 0.585 | 0.034 | Molecular  | GO:0002886 leukocyte mediated immunity                                                | 0.29809 | 0.48823 | 0 | 0 |    |      |

|                                                                                     |    |         |        |       |            |                                                                                     |         |         |   |   |    |      |
|-------------------------------------------------------------------------------------|----|---------|--------|-------|------------|-------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0051546 keratinocyte migration                                                   | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:0051546 keratinocyte migration                                                   | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:0051797 regulation of hair follicle development                                  | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:0051797 regulation of hair follicle development                                  | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:006004 relax                                                                     | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:006004 relax                                                                     | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:0060231 mesenchymal to epithelial transition                                     | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:0060231 mesenchymal to epithelial transition                                     | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:0060340 positive regulation of type I interferon-mediated signaling p            | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:0060340 positive regulation of type I interferon-mediated signaling pathway      | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:0071371 cellular response to gonadotropin stimulus                               | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:0071371 cellular response to gonadotropin stimulus                               | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:0071605 monocyte chemotactic protein-1 production                                | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:0071605 monocyte chemotactic protein-1 production                                | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:0071837 regulation of monocyte chemotactic protein-1 production                  | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:0071837 regulation of monocyte chemotactic protein-1 production                  | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:0073202 plasma membrane tubulation                                               | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:0073202 plasma membrane tubulation                                               | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:0098543 detection of other organism                                              | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:0098543 detection of other organism                                              | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:1900227 positive regulation of NLRP3 inflammasome complex asse                   | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:1900227 positive regulation of NLRP3 inflammasome complex assembly               | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:2000010 positive regulation of protein localization to cell surface              | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:2000010 positive regulation of protein localization to cell surface              | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:2000434 regulation of protein maturation                                         | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:2000434 regulation of protein maturation                                         | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:2000810 regulation of bicellular tight junction assembly                         | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:2000810 regulation of bicellular tight junction assembly                         | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:2001014 regulation of skeletal muscle cell differentiation                       | 1  | 0.308   | 0.31   | 0.05  | Biological | GO:2001014 regulation of skeletal muscle cell differentiation                       | 0.308   | 0.49315 | 0 | 0 | 1  | 20   |
| GO:0071248 cellular response to metal ion                                           | 5  | 0.30845 | 1.548  | 0.028 | Biological | GO:0071248 cellular response to metal ion                                           | 0.30845 | 0.49372 | 0 | 0 | 5  | 202  |
| GO:0004487 monooxygenase activity                                                   | 3  | 0.30854 | 0.877  | 0.029 | Molecular  | GO:0004487 monooxygenase activity                                                   | 0.30854 | 0.49758 | 0 | 0 | 3  | 105  |
| GO:0009411 response to UV                                                           | 4  | 0.3091  | 1.238  | 0.028 | Biological | GO:0009411 response to UV                                                           | 0.3091  | 0.49493 | 0 | 0 | 4  | 154  |
| GO:0051961 negative regulation of nervous system development                        | 4  | 0.3091  | 1.238  | 0.028 | Biological | GO:0051961 negative regulation of nervous system development                        | 0.3091  | 0.49493 | 0 | 0 | 4  | 154  |
| GO:0009617 response to bacterium                                                    | 16 | 0.30911 | 4.954  | 0.021 | Biological | GO:0009617 response to bacterium                                                    | 0.30911 | 0.49493 | 0 | 0 | 16 | 758  |
| GO:0021549 cerebellum development                                                   | 3  | 0.30977 | 0.929  | 0.028 | Biological | GO:0021549 cerebellum development                                                   | 0.30977 | 0.49504 | 0 | 0 | 3  | 107  |
| GO:1901890 positive regulation of cell junction assembly                            | 3  | 0.30977 | 0.929  | 0.028 | Biological | GO:1901890 positive regulation of cell junction assembly                            | 0.30977 | 0.49504 | 0 | 0 | 3  | 107  |
| GO:0022836 gated channel activity                                                   | 8  | 0.31017 | 2.338  | 0.023 | Molecular  | GO:0022836 gated channel activity                                                   | 0.31017 | 0.49774 | 0 | 0 | 8  | 345  |
| GO:0046906 tetrapyrole binding                                                      | 4  | 0.31133 | 1.17   | 0.028 | Molecular  | GO:0046906 tetrapyrole binding                                                      | 0.31133 | 0.49774 | 0 | 0 | 4  | 152  |
| GO:0016773 phosphotransferase activity, alcohol group as acceptor                   | 15 | 0.31143 | 4.386  | 0.022 | Molecular  | GO:0016773 phosphotransferase activity, alcohol group as acceptor                   | 0.31143 | 0.49774 | 0 | 0 | 15 | 696  |
| GO:0032870 cellular response to hormone stimulus                                    | 13 | 0.31159 | 4.025  | 0.021 | Biological | GO:0032870 cellular response to hormone stimulus                                    | 0.31159 | 0.49778 | 0 | 0 | 13 | 605  |
| GO:0016755 aminocyclotransferase activity                                           | 1  | 0.31227 | 0.292  | 0.05  | Molecular  | GO:0016755 aminocyclotransferase activity                                           | 0.31227 | 0.49774 | 0 | 0 | 1  | 20   |
| GO:0010300 phospholipid binding                                                     | 1  | 0.31227 | 0.292  | 0.05  | Molecular  | GO:0010300 phospholipid binding                                                     | 0.31227 | 0.49774 | 0 | 0 | 1  | 20   |
| GO:001658 branching involved in ureteric bud morphogenesis                          | 2  | 0.31254 | 0.619  | 0.032 | Biological | GO:001658 branching involved in ureteric bud morphogenesis                          | 0.31254 | 0.49866 | 0 | 0 | 2  | 62   |
| GO:0050922 negative regulation of chemotaxis                                        | 2  | 0.31254 | 0.619  | 0.032 | Biological | GO:0050922 negative regulation of chemotaxis                                        | 0.31254 | 0.49866 | 0 | 0 | 2  | 62   |
| GO:0060393 regulation of pathway-restricted SMAD protein phosphoryl                 | 2  | 0.31254 | 0.619  | 0.032 | Biological | GO:0060393 regulation of pathway-restricted SMAD protein phosphorylation            | 0.31254 | 0.49866 | 0 | 0 | 2  | 62   |
| GO:0072348 sulfur compound transport                                                | 2  | 0.31254 | 0.619  | 0.032 | Biological | GO:0072348 sulfur compound transport                                                | 0.31254 | 0.49866 | 0 | 0 | 2  | 62   |
| GO:0010098 basal RNA polymerase II transcription machinery binding                  | 1  | 0.31267 | 0.585  | 0.033 | Molecular  | GO:0010098 basal RNA polymerase II transcription machinery binding                  | 0.31267 | 0.49774 | 0 | 0 | 1  | 20   |
| GO:0001099 basal RNA polymerase II transcription machinery binding                  | 1  | 0.31267 | 0.585  | 0.033 | Molecular  | GO:0001099 basal RNA polymerase II transcription machinery binding                  | 0.31267 | 0.49774 | 0 | 0 | 1  | 20   |
| GO:0007159 leukocyte cell-cell adhesion                                             | 9  | 0.31269 | 2.786  | 0.022 | Biological | GO:0007159 leukocyte cell-cell adhesion                                             | 0.31269 | 0.49875 | 0 | 0 | 9  | 402  |
| GO:0031331 positive regulation of cellular catabolic process                        | 10 | 0.31373 | 3.096  | 0.022 | Biological | GO:0031331 positive regulation of cellular catabolic process                        | 0.31373 | 0.50024 | 0 | 0 | 10 | 453  |
| GO:0032147 activation of protein kinase activity                                    | 3  | 0.31476 | 0.929  | 0.028 | Biological | GO:0032147 activation of protein kinase activity                                    | 0.31476 | 0.50173 | 0 | 0 | 3  | 108  |
| GO:005244 voltage-gated channel activity                                            | 1  | 0.31683 | 1.462  | 0.028 | Molecular  | GO:005244 voltage-gated channel activity                                            | 0.31683 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0090316 positive regulation of intracellular protein transport                   | 4  | 0.31734 | 1.238  | 0.028 | Biological | GO:0090316 positive regulation of intracellular protein transport                   | 0.31734 | 0.50226 | 0 | 0 | 4  | 156  |
| GO:0060077 inhibitory synapse                                                       | 1  | 0.31763 | 0.297  | 0.048 | Cellular   | GO:0060077 inhibitory synapse                                                       | 0.31763 | 0.54641 | 0 | 0 | 1  | 21   |
| GO:0003655 regulation of transcription, DNA-templated                               | 67 | 0.31842 | 20.743 | 0.019 | Biological | GO:0003655 regulation of transcription, DNA-templated                               | 0.31842 | 0.50226 | 0 | 0 | 67 | 3469 |
| GO:0005075 RNA polymerase II transcription regulator complex                        | 6  | 0.3188  | 1.78   | 0.023 | Cellular   | GO:0005075 RNA polymerase II transcription regulator complex                        | 0.3188  | 0.54666 | 0 | 0 | 6  | 257  |
| GO:0007078 synovial synovial by plasma membrane fusion                              | 2  | 0.31926 | 0.619  | 0.032 | Biological | GO:0007078 synovial synovial by plasma membrane fusion                              | 0.31926 | 0.50226 | 0 | 0 | 2  | 63   |
| GO:0002712 regulation of B cell mediated immunity                                   | 2  | 0.31926 | 0.619  | 0.032 | Biological | GO:0002712 regulation of B cell mediated immunity                                   | 0.31926 | 0.50226 | 0 | 0 | 2  | 63   |
| GO:0002889 regulation of immunoglobulin mediated immune response                    | 2  | 0.31926 | 0.619  | 0.032 | Biological | GO:0002889 regulation of immunoglobulin mediated immune response                    | 0.31926 | 0.50226 | 0 | 0 | 2  | 63   |
| GO:0022029 telencephalon cell migration                                             | 2  | 0.31926 | 0.619  | 0.032 | Biological | GO:0022029 telencephalon cell migration                                             | 0.31926 | 0.50226 | 0 | 0 | 2  | 63   |
| GO:0030865 cortical cytoskeleton organization                                       | 2  | 0.31926 | 0.619  | 0.032 | Biological | GO:0030865 cortical cytoskeleton organization                                       | 0.31926 | 0.50226 | 0 | 0 | 2  | 63   |
| GO:0031683 lipopolysaccharide-mediated signaling pathway                            | 2  | 0.31926 | 0.619  | 0.032 | Biological | GO:0031683 lipopolysaccharide-mediated signaling pathway                            | 0.31926 | 0.50226 | 0 | 0 | 2  | 63   |
| GO:0034605 cellular response to heat                                                | 2  | 0.31926 | 0.619  | 0.032 | Biological | GO:0034605 cellular response to heat                                                | 0.31926 | 0.50226 | 0 | 0 | 2  | 63   |
| GO:0035306 positive regulation of dephosphorylation                                 | 2  | 0.31926 | 0.619  | 0.032 | Biological | GO:0035306 positive regulation of dephosphorylation                                 | 0.31926 | 0.50226 | 0 | 0 | 2  | 63   |
| GO:0048247 lymphocyte chemotaxis                                                    | 2  | 0.31926 | 0.619  | 0.032 | Biological | GO:0048247 lymphocyte chemotaxis                                                    | 0.31926 | 0.50226 | 0 | 0 | 2  | 63   |
| GO:0051653 spindle localization                                                     | 2  | 0.31926 | 0.619  | 0.032 | Biological | GO:0051653 spindle localization                                                     | 0.31926 | 0.50226 | 0 | 0 | 2  | 63   |
| GO:004053 cell-cell fusion                                                          | 3  | 0.31976 | 0.929  | 0.028 | Biological | GO:004053 cell-cell fusion                                                          | 0.31976 | 0.50226 | 0 | 0 | 3  | 109  |
| GO:0030301 cholesterol transport                                                    | 3  | 0.31976 | 0.929  | 0.028 | Biological | GO:0030301 cholesterol transport                                                    | 0.31976 | 0.50226 | 0 | 0 | 3  | 109  |
| GO:0033138 positive regulation of peptidyl-serine phosphorylation                   | 3  | 0.31976 | 0.929  | 0.028 | Biological | GO:0033138 positive regulation of peptidyl-serine phosphorylation                   | 0.31976 | 0.50226 | 0 | 0 | 3  | 109  |
| GO:0090277 positive regulation of peptide hormone secretion                         | 3  | 0.31976 | 0.929  | 0.028 | Biological | GO:0090277 positive regulation of peptide hormone secretion                         | 0.31976 | 0.50226 | 0 | 0 | 3  | 109  |
| GO:1903506 regulation of nucleic acid-templated transcription                       | 67 | 0.32028 | 20.743 | 0.019 | Biological | GO:1903506 regulation of nucleic acid-templated transcription                       | 0.32028 | 0.50226 | 0 | 0 | 67 | 3471 |
| GO:0001502 cardiac crescent                                                         | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0001502 cardiac crescent                                                         | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0006700 C21-steroid hormone biosynthetic process                                 | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0006700 C21-steroid hormone biosynthetic process                                 | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0006896 Golgi to vacuole transport                                               | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0006896 Golgi to vacuole transport                                               | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0007194 negative regulation of adenylate cyclase activity                        | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0007194 negative regulation of adenylate cyclase activity                        | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0007625 grooming behavior                                                        | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0007625 grooming behavior                                                        | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0003040 determine of adult lifespan                                              | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0003040 determine of adult lifespan                                              | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0009067 aspartate family amino acid biosynthetic process                         | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0009067 aspartate family amino acid biosynthetic process                         | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0009713 catechol-containing compound biosynthetic process                        | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0009713 catechol-containing compound biosynthetic process                        | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0010881 regulation of cardiac muscle contraction by regulation of the release    | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0010881 regulation of cardiac muscle contraction by regulation of the release    | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0021756 striatum development                                                     | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0021756 striatum development                                                     | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0024210 circadian sleep/wake cycle process                                       | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0024210 circadian sleep/wake cycle process                                       | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0030277 maintenance of gastrointestinal epithelium                               | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0030277 maintenance of gastrointestinal epithelium                               | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0030449 regulation of complement activation                                      | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0030449 regulation of complement activation                                      | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0030728 ovulation                                                                | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0030728 ovulation                                                                | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0030963 notochord development                                                    | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0030963 notochord development                                                    | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0032332 positive regulation of chondrocyte differentiation                       | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0032332 positive regulation of chondrocyte differentiation                       | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0032928 regulation of superoxide anion generation                                | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0032928 regulation of superoxide anion generation                                | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0033762 response to glucagon                                                     | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0033762 response to glucagon                                                     | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0035313 wound healing, spreading of epidermal cells                              | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0035313 wound healing, spreading of epidermal cells                              | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0035809 regulation of urine volume                                               | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0035809 regulation of urine volume                                               | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0042423 catecholamine biosynthetic process                                       | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0042423 catecholamine biosynthetic process                                       | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0043373 CD4-positive, alpha-beta T cell lineage commitment                       | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0043373 CD4-positive, alpha-beta T cell lineage commitment                       | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0043651 linoleic acid metabolic process                                          | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0043651 linoleic acid metabolic process                                          | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0044794 positive regulation by host of viral process                             | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0044794 positive regulation by host of viral process                             | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0045624 positive regulation of T-helper cell differentiation                     | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0045624 positive regulation of T-helper cell differentiation                     | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0048670 regulation of collateral sprouting                                       | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0048670 regulation of collateral sprouting                                       | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0051315 attachment of mitotic spindle microtubules to kinetochore                | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0051315 attachment of mitotic spindle microtubules to kinetochore                | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0051767 nitric-oxide synthase biosynthetic process                               | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0051767 nitric-oxide synthase biosynthetic process                               | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0051769 regulation of nitric-oxide synthase biosynthetic process                 | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0051769 regulation of nitric-oxide synthase biosynthetic process                 | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0060550 positive regulation of cell migration involved in sprouting angiogenesis | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0060550 positive regulation of cell migration involved in sprouting angiogenesis | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0067049 motor neuron apoptotic process                                           | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0067049 motor neuron apoptotic process                                           | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |
| GO:0097503 sialylation                                                              | 1  | 0.32063 | 0.31   | 0.048 | Biological | GO:0097503 sialylation                                                              | 0.32063 | 0.50226 | 0 | 0 | 1  | 21   |

|                                                                                          |    |         |       |         |             |                                                                                          |         |         |   |   |    |      |
|------------------------------------------------------------------------------------------|----|---------|-------|---------|-------------|------------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0071222 cellular response to lipopolysaccharide                                       | 5  | 0.33352 | 1.548 | 0.024   | Biochemical | GO:0071222 cellular response to lipopolysaccharide                                       | 0.33352 | 0.51551 | 0 | 0 | 5  | 209  |
| GO:1904064 positive regulation of cation transmembrane transport                         | 4  | 0.33385 | 1.238 | 0.025   | Biological  | GO:1904064 positive regulation of cation transmembrane transport                         | 0.33385 | 0.51577 | 0 | 0 | 4  | 160  |
| GO:0051056 regulation of small GTPase mediated signal transduction                       | 7  | 0.33391 | 2.167 | 0.023   | Biological  | GO:0051056 regulation of small GTPase mediated signal transduction                       | 0.33391 | 0.51577 | 0 | 0 | 7  | 309  |
| GO:0005711 multivesicular body                                                           | 2  | 0.33436 | 0.593 | 0.03    | Cellular    | GO:0005711 multivesicular body                                                           | 0.33436 | 0.56431 | 0 | 0 | 2  | 66   |
| GO:0031093 platelet alpha granule lumen                                                  | 2  | 0.33436 | 0.593 | 0.03    | Cellular    | GO:0031093 platelet alpha granule lumen                                                  | 0.33436 | 0.56431 | 0 | 0 | 2  | 66   |
| GO:0032612 interleukin-1 production                                                      | 3  | 0.33474 | 0.929 | 0.027   | Biological  | GO:0032612 interleukin-1 production                                                      | 0.33474 | 0.5166  | 0 | 0 | 3  | 112  |
| GO:0032652 regulation of interleukin-1 production                                        | 3  | 0.33474 | 0.929 | 0.027   | Biological  | GO:0032652 regulation of interleukin-1 production                                        | 0.33474 | 0.5166  | 0 | 0 | 3  | 112  |
| GO:0120034 positive regulation of plasma membrane bounded cell projection assembly       | 3  | 0.33474 | 0.929 | 0.027   | Biological  | GO:0120034 positive regulation of plasma membrane bounded cell projection assembly       | 0.33474 | 0.5166  | 0 | 0 | 3  | 112  |
| GO:0072330 monocarboxylic acid biosynthetic process                                      | 2  | 0.33712 | 1.548 | 0.024   | Biological  | GO:0072330 monocarboxylic acid biosynthetic process                                      | 0.33712 | 0.52011 | 0 | 0 | 5  | 210  |
| GO:0001614 purinergic nucleotide receptor activity                                       | 1  | 0.33756 | 0.292 | 0.045   | Molecular   | GO:0001614 purinergic nucleotide receptor activity                                       | 0.33756 | 0.52132 | 0 | 0 | 1  | 22   |
| GO:0016502 nucleotide receptor activity                                                  | 1  | 0.33756 | 0.292 | 0.045   | Molecular   | GO:0016502 nucleotide receptor activity                                                  | 0.33756 | 0.52132 | 0 | 0 | 1  | 22   |
| GO:0031683 G-protein beta/gamma-subunit complex binding                                  | 1  | 0.33756 | 0.292 | 0.045   | Molecular   | GO:0031683 G-protein beta/gamma-subunit complex binding                                  | 0.33756 | 0.52132 | 0 | 0 | 1  | 22   |
| GO:0030674 protein-macromolecule adaptor activity                                        | 3  | 0.33772 | 2.338 | 0.023   | Molecular   | GO:0030674 protein-macromolecule adaptor activity                                        | 0.33772 | 0.52132 | 0 | 0 | 1  | 359  |
| GO:0043679 exon terminus                                                                 | 3  | 0.33833 | 0.89  | 0.028   | Cellular    | GO:0043679 exon terminus                                                                 | 0.33833 | 0.56794 | 0 | 0 | 3  | 114  |
| GO:0008333 endosome to lysosome transport                                                | 2  | 0.33932 | 0.619 | 0.03    | Biological  | GO:0008333 endosome to lysosome transport                                                | 0.33932 | 0.52269 | 0 | 0 | 2  | 66   |
| GO:0014015 positive regulation of gliogenesis                                            | 2  | 0.33932 | 0.619 | 0.03    | Biological  | GO:0014015 positive regulation of gliogenesis                                            | 0.33932 | 0.52269 | 0 | 0 | 2  | 66   |
| GO:0015800 acidic amino acid transport                                                   | 2  | 0.33932 | 0.619 | 0.03    | Biological  | GO:0015800 acidic amino acid transport                                                   | 0.33932 | 0.52269 | 0 | 0 | 2  | 66   |
| GO:0021855 forebrain cell migration                                                      | 2  | 0.33932 | 0.619 | 0.03    | Biological  | GO:0021855 forebrain cell migration                                                      | 0.33932 | 0.52269 | 0 | 0 | 2  | 66   |
| GO:1901224 positive regulation of NIK/NF-kappaB signaling                                | 2  | 0.33932 | 0.619 | 0.03    | Biological  | GO:1901224 positive regulation of NIK/NF-kappaB signaling                                | 0.33932 | 0.52269 | 0 | 0 | 2  | 66   |
| GO:0009063 cellular amino acid catabolic process                                         | 3  | 0.33974 | 0.929 | 0.027   | Biological  | GO:0009063 cellular amino acid catabolic process                                         | 0.33974 | 0.52285 | 0 | 0 | 3  | 113  |
| GO:0010522 regulation of calcium ion transport into cytosol                              | 3  | 0.33974 | 0.929 | 0.027   | Biological  | GO:0010522 regulation of calcium ion transport into cytosol                              | 0.33974 | 0.52285 | 0 | 0 | 3  | 113  |
| GO:0046634 regulation of alpha-beta T cell activation                                    | 3  | 0.33974 | 0.929 | 0.027   | Biological  | GO:0046634 regulation of alpha-beta T cell activation                                    | 0.33974 | 0.52285 | 0 | 0 | 3  | 113  |
| GO:0051701 biological process involved in interaction with host                          | 2  | 0.34073 | 1.548 | 0.024   | Biological  | GO:0051701 biological process involved in interaction with host                          | 0.34073 | 0.52421 | 0 | 0 | 5  | 211  |
| GO:0060076 excitatory synapse                                                            | 2  | 0.34095 | 0.593 | 0.03    | Cellular    | GO:0060076 excitatory synapse                                                            | 0.34095 | 0.56794 | 0 | 0 | 2  | 67   |
| GO:0005868 cytoplasmic dynein complex                                                    | 1  | 0.34204 | 0.297 | 0.043   | Cellular    | GO:0005868 cytoplasmic dynein complex                                                    | 0.34204 | 0.56794 | 0 | 0 | 1  | 23   |
| GO:0071682 endocytic vesicle lumen                                                       | 1  | 0.34204 | 0.297 | 0.043   | Cellular    | GO:0071682 endocytic vesicle lumen                                                       | 0.34204 | 0.56794 | 0 | 0 | 1  | 23   |
| GO:0009685 glycoprotein complex                                                          | 1  | 0.34204 | 0.297 | 0.043   | Cellular    | GO:0009685 glycoprotein complex                                                          | 0.34204 | 0.56794 | 0 | 0 | 1  | 23   |
| GO:0005741 mitochondrial outer membrane                                                  | 5  | 0.34288 | 1.484 | 0.023   | Cellular    | GO:0005741 mitochondrial outer membrane                                                  | 0.34288 | 0.56794 | 0 | 0 | 5  | 214  |
| GO:0051020 GTPase binding                                                                | 7  | 0.34314 | 2.047 | 0.023   | Molecular   | GO:0051020 GTPase binding                                                                | 0.34314 | 0.52876 | 0 | 0 | 7  | 307  |
| GO:0031668 cellular response to extracellular stimulus                                   | 6  | 0.34416 | 1.858 | 0.023   | Biological  | GO:0031668 cellular response to extracellular stimulus                                   | 0.34416 | 0.52609 | 0 | 0 | 6  | 262  |
| GO:0031396 regulation of protein ubiquitination                                          | 5  | 0.34433 | 1.548 | 0.024   | Biological  | GO:0031396 regulation of protein ubiquitination                                          | 0.34433 | 0.52609 | 0 | 0 | 5  | 212  |
| GO:0002363 alpha-beta T cell lineage commitment                                          | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0002363 alpha-beta T cell lineage commitment                                          | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0003035 negative regulation of systemic arterial blood pressure                       | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0003035 negative regulation of systemic arterial blood pressure                       | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0003283 atrial septum development                                                     | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0003283 atrial septum development                                                     | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0007039 protein catabolic process in the vacuole                                      | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0007039 protein catabolic process in the vacuole                                      | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0016338 calcium-independent cell-cell adhesion via plasma membrane cell-cell junction | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0016338 calcium-independent cell-cell adhesion via plasma membrane cell-cell junction | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0023019 signal transduction involved in regulation of gene expression                 | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0023019 signal transduction involved in regulation of gene expression                 | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0031280 negative regulation of cyclase activity                                       | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0031280 negative regulation of cyclase activity                                       | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0032288 myelin assembly                                                               | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0032288 myelin assembly                                                               | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0032891 negative regulation of organic acid transport                                 | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0032891 negative regulation of organic acid transport                                 | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0036158 outer dynein arm assembly                                                     | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0036158 outer dynein arm assembly                                                     | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0042745 circadian sleep/wake cycle                                                    | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0042745 circadian sleep/wake cycle                                                    | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0045822 negative regulation of heart contraction                                      | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0045822 negative regulation of heart contraction                                      | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0046599 regulation of centriole replication                                           | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0046599 regulation of centriole replication                                           | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0046794 transport of virus                                                            | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0046794 transport of virus                                                            | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0050961 detection of temperature stimulus involved in sensory perception              | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0050961 detection of temperature stimulus involved in sensory perception              | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0051904 pigment granule transport                                                     | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0051904 pigment granule transport                                                     | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0060045 positive regulation of cardiac muscle cell proliferation                      | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0060045 positive regulation of cardiac muscle cell proliferation                      | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0072677 eosinophil migration                                                          | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0072677 eosinophil migration                                                          | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0097164 ammonium ion metabolic process                                                | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0097164 ammonium ion metabolic process                                                | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0098856 intestinal lipid absorption                                                   | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0098856 intestinal lipid absorption                                                   | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:1900746 regulation of vascular endothelial growth factor signaling pathway            | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:1900746 regulation of vascular endothelial growth factor signaling pathway            | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0093939 regulation of protein localization to synapse                                 | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:0093939 regulation of protein localization to synapse                                 | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:1904996 positive regulation of leukocyte adhesion to vascular endothelium             | 1  | 0.3452  | 0.31  | 0.043   | Biological  | GO:1904996 positive regulation of leukocyte adhesion to vascular endothelium             | 0.3452  | 0.52609 | 0 | 0 | 1  | 23   |
| GO:0006801 superoxide metabolic process                                                  | 2  | 0.34597 | 0.619 | 0.03    | Biological  | GO:0006801 superoxide metabolic process                                                  | 0.34597 | 0.52609 | 0 | 0 | 2  | 67   |
| GO:0006949 syncytium formation                                                           | 2  | 0.34597 | 0.619 | 0.03    | Biological  | GO:0006949 syncytium formation                                                           | 0.34597 | 0.52609 | 0 | 0 | 2  | 67   |
| GO:0014910 regulation of smooth muscle cell migration                                    | 2  | 0.34597 | 0.619 | 0.03    | Biological  | GO:0014910 regulation of smooth muscle cell migration                                    | 0.34597 | 0.52609 | 0 | 0 | 2  | 67   |
| GO:0016825 protein synthesis                                                             | 2  | 0.34597 | 0.619 | 0.03    | Biological  | GO:0016825 protein synthesis                                                             | 0.34597 | 0.52609 | 0 | 0 | 2  | 67   |
| GO:0040014 regulation of multicellular organism growth                                   | 2  | 0.34597 | 0.619 | 0.03    | Biological  | GO:0040014 regulation of multicellular organism growth                                   | 0.34597 | 0.52609 | 0 | 0 | 2  | 67   |
| GO:0045453 bone resorption                                                               | 2  | 0.34597 | 0.619 | 0.03    | Biological  | GO:0045453 bone resorption                                                               | 0.34597 | 0.52609 | 0 | 0 | 2  | 67   |
| GO:0045600 positive regulation of fat cell differentiation                               | 2  | 0.34597 | 0.619 | 0.03    | Biological  | GO:0045600 positive regulation of fat cell differentiation                               | 0.34597 | 0.52609 | 0 | 0 | 2  | 67   |
| GO:0050771 negative regulation of anagenesis                                             | 2  | 0.34597 | 0.619 | 0.03    | Biological  | GO:0050771 negative regulation of anagenesis                                             | 0.34597 | 0.52609 | 0 | 0 | 2  | 67   |
| GO:0060389 positive regulation of protein localization to synapse                        | 2  | 0.34597 | 0.619 | 0.03    | Biological  | GO:0060389 positive regulation of protein localization to synapse                        | 0.34597 | 0.52609 | 0 | 0 | 2  | 67   |
| GO:0070830 bicellular tight junction assembly                                            | 2  | 0.34597 | 0.619 | 0.03    | Biological  | GO:0070830 bicellular tight junction assembly                                            | 0.34597 | 0.52609 | 0 | 0 | 2  | 67   |
| GO:2000379 positive regulation of reactive oxygen species metabolic process              | 2  | 0.34597 | 0.619 | 0.03    | Biological  | GO:2000379 positive regulation of reactive oxygen species metabolic process              | 0.34597 | 0.52609 | 0 | 0 | 2  | 67   |
| GO:1903037 regulation of leukocyte cell-cell adhesion                                    | 8  | 0.34609 | 2.477 | 0.022   | Biological  | GO:1903037 regulation of leukocyte cell-cell adhesion                                    | 0.34609 | 0.52609 | 0 | 0 | 8  | 364  |
| GO:0032640 tumor necrosis factor production                                              | 4  | 0.34627 | 1.238 | 0.025   | Biological  | GO:0032640 tumor necrosis factor production                                              | 0.34627 | 0.52609 | 0 | 0 | 4  | 163  |
| GO:0032690 regulation of cytokine stimulus factor production                             | 4  | 0.34627 | 1.238 | 0.025   | Biological  | GO:0032690 regulation of cytokine stimulus factor production                             | 0.34627 | 0.52609 | 0 | 0 | 4  | 163  |
| GO:0060759 regulation of response to cytokine stimulus                                   | 4  | 0.34627 | 1.238 | 0.025   | Biological  | GO:0060759 regulation of response to cytokine stimulus                                   | 0.34627 | 0.52609 | 0 | 0 | 4  | 163  |
| GO:0071453 cellular response to oxygen levels                                            | 4  | 0.34627 | 1.238 | 0.025   | Biological  | GO:0071453 cellular response to oxygen levels                                            | 0.34627 | 0.52609 | 0 | 0 | 4  | 163  |
| GO:0042054 histone methyltransferase activity                                            | 2  | 0.34665 | 0.585 | 0.03    | Molecular   | GO:0042054 histone methyltransferase activity                                            | 0.34665 | 0.52967 | 0 | 0 | 2  | 66   |
| GO:0098631 cell adhesion mediator activity                                               | 2  | 0.34665 | 0.585 | 0.03    | Molecular   | GO:0098631 cell adhesion mediator activity                                               | 0.34665 | 0.52967 | 0 | 0 | 2  | 66   |
| GO:0042504 response to stimulus                                                          | 5  | 0.34704 | 1.548 | 0.023   | Biological  | GO:0042504 response to stimulus                                                          | 0.34704 | 0.52947 | 0 | 0 | 5  | 213  |
| GO:0042833 small molecule biosynthetic process                                           | 12 | 0.34876 | 3.715 | 0.021   | Biological  | GO:0042833 small molecule biosynthetic process                                           | 0.34876 | 0.52949 | 0 | 0 | 12 | 571  |
| GO:0071900 regulation of protein serine/threonine kinase activity                        | 8  | 0.34883 | 2.477 | 0.022   | Biological  | GO:0071900 regulation of protein serine/threonine kinase activity                        | 0.34883 | 0.52949 | 0 | 0 | 8  | 365  |
| GO:0051046 regulation of secretion                                                       | 13 | 0.34893 | 4.025 | 0.021   | Biological  | GO:0051046 regulation of secretion                                                       | 0.34893 | 0.52949 | 0 | 0 | 13 | 623  |
| GO:0022860 inorganic cation transmembrane transporter activity                           | 13 | 0.34895 | 3.801 | 0.021   | Molecular   | GO:0022860 inorganic cation transmembrane transporter activity                           | 0.34895 | 0.52967 | 0 | 0 | 13 | 613  |
| GO:0051983 regulation of synapse assembly                                                | 3  | 0.34951 | 0.929 | 0.027   | Biological  | GO:0051983 regulation of synapse assembly                                                | 0.34951 | 0.52967 | 0 | 0 | 3  | 115  |
| GO:0016881 acid-amino acid ligase activity                                               | 1  | 0.34985 | 0.292 | 0.043   | Molecular   | GO:0016881 acid-amino acid ligase activity                                               | 0.34985 | 0.52967 | 0 | 0 | 1  | 23   |
| GO:0030215 semaphorin receptor binding                                                   | 1  | 0.34985 | 0.292 | 0.043   | Molecular   | GO:0030215 semaphorin receptor binding                                                   | 0.34985 | 0.52967 | 0 | 0 | 1  | 23   |
| GO:0033558 protein deacetylase activity                                                  | 1  | 0.34985 | 0.292 | 0.043   | Molecular   | GO:0033558 protein deacetylase activity                                                  | 0.34985 | 0.52967 | 0 | 0 | 1  | 23   |
| GO:0042171 lysophosphatidic acid acyltransferase activity                                | 1  | 0.34985 | 0.292 | 0.043   | Molecular   | GO:0042171 lysophosphatidic acid acyltransferase activity                                | 0.34985 | 0.52967 | 0 | 0 | 1  | 23   |
| GO:0071617 lysophosphatidic acid acyltransferase activity                                | 1  | 0.34985 | 0.292 | 0.043   | Molecular   | GO:0071617 lysophosphatidic acid acyltransferase activity                                | 0.34985 | 0.52967 | 0 | 0 | 1  | 23   |
| GO:0098918 structural constituent of synapse                                             | 1  | 0.34985 | 0.292 | 0.043   | Molecular   | GO:0098918 structural constituent of synapse                                             | 0.34985 | 0.52967 | 0 | 0 | 1  | 23   |
| GO:0120020 cholesterol transfer activity                                                 | 1  | 0.34985 | 0.292 | 0.043   | Molecular   | GO:0120020 cholesterol transfer activity                                                 | 0.34985 | 0.52967 | 0 | 0 | 1  | 23   |
| GO:0006811 ion transport                                                                 | 32 | 0.35007 | 9.907 | 0.02    | Biological  | GO:0006811 ion transport                                                                 | 0.35007 | 0.53186 | 0 | 0 | 32 | 1626 |
| GO:0098862 cluster of actin-based cell projections                                       | 4  | 0.35007 | 1.67  | 0.024   | Cellular    | GO:0098862 cluster of actin-based cell projections                                       | 0.35007 | 0.53186 | 0 | 0 | 4  | 166  |
| GO:0031100 organ regeneration                                                            | 2  | 0.35259 | 0.619 | 0.029   | Biological  | GO:0031100 organ regeneration                                                            | 0.35259 | 0.53407 | 0 | 0 | 2  | 68   |
| GO:0035567 non-canonical Wnt signaling pathway                                           | 2  | 0.35259 | 0.619 | 0.029</ |             |                                                                                          |         |         |   |   |    |      |

|                                                                                                   |    |         |        |       |            |                                                                                                 |         |         |   |   |    |      |
|---------------------------------------------------------------------------------------------------|----|---------|--------|-------|------------|-------------------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0005884 actin filament                                                                         | 3  | 0.36297 | 0.89   | 0.025 | Cellular C | GO:00005 actin filament                                                                         | 0.36297 | 0.58667 | 0 | 0 | 3  | 119  |
| GO:0030254 multicellular organism reproduction                                                    | 19 | 0.36313 | 5.882  | 0.02  | Biological | GO:00032 multicellular organism reproduction                                                    | 0.36313 | 0.54198 | 0 | 0 | 19 | 945  |
| GO:0051348 negative regulation of transferase activity                                            | 6  | 0.36361 | 1.358  | 0.022 | Biological | GO:00061 negative regulation of transferase activity                                            | 0.36361 | 0.54254 | 0 | 0 | 6  | 288  |
| GO:0010906 regulation of glucose metabolic process                                                | 3  | 0.36465 | 0.929  | 0.020 | Biological | GO:00010 regulation of glucose metabolic process                                                | 0.36465 | 0.54279 | 0 | 0 | 3  | 118  |
| GO:0090100 positive regulation of transmembrane receptor protein serine/threonine kinase activity | 3  | 0.36465 | 0.929  | 0.025 | Biological | GO:00090 positive regulation of transmembrane receptor protein serine/threonine kinase activity | 0.36465 | 0.54279 | 0 | 0 | 3  | 118  |
| GO:0044419 biological process involved in interspecies interaction between organisms              | 33 | 0.36488 | 10.217 | 0.02  | Biological | GO:00044 biological process involved in interspecies interaction between organisms              | 0.36488 | 0.54279 | 0 | 0 | 33 | 1690 |
| GO:0030328 cardiac ventricle morphogenesis                                                        | 2  | 0.36577 | 0.619  | 0.029 | Biological | GO:00032 cardiac ventricle morphogenesis                                                        | 0.36577 | 0.54279 | 0 | 0 | 2  | 70   |
| GO:0006081 cellular aldehyde metabolic process                                                    | 2  | 0.36577 | 0.619  | 0.029 | Biological | GO:00060 cellular aldehyde metabolic process                                                    | 0.36577 | 0.54279 | 0 | 0 | 2  | 70   |
| GO:0030193 regulation of blood coagulation                                                        | 2  | 0.36577 | 0.619  | 0.029 | Biological | GO:00030 regulation of blood coagulation                                                        | 0.36577 | 0.54279 | 0 | 0 | 2  | 70   |
| GO:0034394 protein localization to cell surface                                                   | 2  | 0.36577 | 0.619  | 0.029 | Biological | GO:00034 protein localization to cell surface                                                   | 0.36577 | 0.54279 | 0 | 0 | 2  | 70   |
| GO:0095618 vesicle cytoskeletal trafficking                                                       | 2  | 0.36577 | 0.619  | 0.029 | Biological | GO:00095 vesicle cytoskeletal trafficking                                                       | 0.36577 | 0.54279 | 0 | 0 | 2  | 70   |
| GO:0071219 cellular response to molecule of bacterial origin                                      | 5  | 0.366   | 1.548  | 0.023 | Biological | GO:00071 cellular response to molecule of bacterial origin                                      | 0.366   | 0.54279 | 0 | 0 | 5  | 218  |
| GO:000475 internal cytoskeleton assembly                                                          | 4  | 0.36697 | 1.238  | 0.024 | Biological | GO:00047 internal cytoskeleton assembly                                                         | 0.36697 | 0.54279 | 0 | 0 | 4  | 168  |
| GO:0006937 regulation of muscle contraction                                                       | 4  | 0.36697 | 1.238  | 0.024 | Biological | GO:00069 regulation of muscle contraction                                                       | 0.36697 | 0.54279 | 0 | 0 | 4  | 168  |
| GO:0050657 monovalent inorganic cation homeostasis                                                | 4  | 0.36697 | 1.238  | 0.024 | Biological | GO:00050 monovalent inorganic cation homeostasis                                                | 0.36697 | 0.54279 | 0 | 0 | 4  | 168  |
| GO:0071706 tumor necrosis factor superfamily cytokine production                                  | 4  | 0.36697 | 1.238  | 0.024 | Biological | GO:00071 tumor necrosis factor superfamily cytokine production                                  | 0.36697 | 0.54279 | 0 | 0 | 4  | 168  |
| GO:1903555 tumor necrosis factor superfamily cytokine production                                  | 4  | 0.36697 | 1.238  | 0.024 | Biological | GO:19035 regulation of tumor necrosis factor superfamily cytokine production                    | 0.36697 | 0.54279 | 0 | 0 | 4  | 168  |
| GO:0019117 photoreceptor inner segment                                                            | 2  | 0.36708 | 0.593  | 0.028 | Cellular C | GO:00011 photoreceptor inner segment                                                            | 0.36708 | 0.59153 | 0 | 0 | 2  | 71   |
| GO:0044389 ubiquitin-like protein ligase binding                                                  | 7  | 0.36725 | 2.047  | 0.022 | Molecular  | GO:00044 ubiquitin-like protein ligase binding                                                  | 0.36725 | 0.54835 | 0 | 0 | 7  | 315  |
| GO:0003081 regulation of systemic arterial blood pressure by renin-angiotensin system             | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00030 regulation of systemic arterial blood pressure by renin-angiotensin system             | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0003148 outflow tract septum morphogenesis                                                     | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00031 outflow tract septum morphogenesis                                                     | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0003181 atrioventricular valve morphogenesis                                                   | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00031 atrioventricular valve morphogenesis                                                   | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0006517 protein dephosphorylation                                                              | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00065 protein dephosphorylation                                                              | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0006658 phosphatidylinositol metabolic process                                                 | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00066 phosphatidylinositol metabolic process                                                 | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0006706 steroid catabolic process                                                              | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00066 steroid catabolic process                                                              | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0010155 regulation of proton transport                                                         | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00010 regulation of proton transport                                                         | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0014047 glutamate secretion                                                                    | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00014 glutamate secretion                                                                    | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0018904 ethanol metabolic process                                                              | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00018 ethanol metabolic process                                                              | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0021884 forebrain neuron development                                                           | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00021 forebrain neuron development                                                           | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0032331 negative regulation of chondrocyte differentiation                                     | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00032 negative regulation of chondrocyte differentiation                                     | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0035235 ionotropic glutamate receptor signaling pathway                                        | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00035 ionotropic glutamate receptor signaling pathway                                        | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0035458 cellular response to interferon-beta                                                   | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00035 cellular response to interferon-beta                                                   | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0043576 regulation of respiratory gaseous exchange                                             | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00043 regulation of respiratory gaseous exchange                                             | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0046697 decarboxylation                                                                        | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00046 decarboxylation                                                                        | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0046716 muscle cell cellular homeostasis                                                       | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00046 muscle cell cellular homeostasis                                                       | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0048011 neurotrophin TRK receptor signaling pathway                                            | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00048 neurotrophin TRK receptor signaling pathway                                            | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0051350 negative regulation of lysate activity                                                 | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00051 negative regulation of lysate activity                                                 | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0051450 myoblast proliferation                                                                 | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00051 myoblast proliferation                                                                 | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0060571 morphogenesis of an epithelial fold                                                    | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00060 morphogenesis of an epithelial fold                                                    | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0060575 intestinal epithelial cell differentiation                                             | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00060 intestinal epithelial cell differentiation                                             | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0070841 inclusion body assembly                                                                | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00070 inclusion body assembly                                                                | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0070861 regulation of protein exit from endoplasmic reticulum                                  | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00070 regulation of protein exit from endoplasmic reticulum                                  | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0072202 cell differentiation involved in metanephros development                               | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00072 cell differentiation involved in metanephros development                               | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0072576 liver morphogenesis                                                                    | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00072 liver morphogenesis                                                                    | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0090023 positive regulation of neutrophil chemotaxis                                           | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00090 positive regulation of neutrophil chemotaxis                                           | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0098581 detection of external biotic stimulus                                                  | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00098 detection of external biotic stimulus                                                  | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0098743 cell aggregation                                                                       | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:00098 cell aggregation                                                                       | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:1902455 negative regulation of stem cell population maintenance                                | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:19024 negative regulation of stem cell population maintenance                                | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:1902547 regulation of cellular response to vascular endothelial growth factor stimulus         | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:19025 regulation of cellular response to vascular endothelial growth factor stimulus         | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:1903792 negative regulation of anion transport                                                 | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:19037 negative regulation of anion transport                                                 | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:1903859 regulation of dendrite extension                                                       | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:19038 regulation of dendrite extension                                                       | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:1903902 positive regulation of viral life cycle                                                | 1  | 0.36889 | 0.31   | 0.04  | Biological | GO:19039 positive regulation of viral life cycle                                                | 0.36889 | 0.54279 | 0 | 0 | 1  | 25   |
| GO:0019058 viral life cycle                                                                       | 7  | 0.36944 | 2.167  | 0.027 | Biological | GO:00019 viral life cycle                                                                       | 0.36944 | 0.54339 | 0 | 0 | 7  | 361  |
| GO:0002062 chondrocyte differentiation                                                            | 3  | 0.36961 | 0.929  | 0.025 | Biological | GO:00020 chondrocyte differentiation                                                            | 0.36961 | 0.54339 | 0 | 0 | 3  | 119  |
| GO:0002440 production of molecular mediator of immune response                                    | 5  | 0.36962 | 1.548  | 0.023 | Biological | GO:00020 production of molecular mediator of immune response                                    | 0.36962 | 0.54339 | 0 | 0 | 5  | 219  |
| GO:0043903 regulation of biological process involved in symbiotic interaction                     | 2  | 0.37232 | 0.619  | 0.028 | Biological | GO:00043 regulation of biological process involved in symbiotic interaction                     | 0.37232 | 0.54704 | 0 | 0 | 2  | 71   |
| GO:0057036 regulation of plasma lipoprotein particle levels                                       | 2  | 0.37232 | 0.619  | 0.028 | Biological | GO:00057 regulation of plasma lipoprotein particle levels                                       | 0.37232 | 0.54704 | 0 | 0 | 2  | 71   |
| GO:0009178 RNA polymerase II cis-regulatory region sequence-specific DNA binding                  | 24 | 0.37376 | 7.018  | 0.02  | Molecular  | GO:00091 RNA polymerase II cis-regulatory region sequence-specific DNA binding                  | 0.37376 | 0.55141 | 0 | 0 | 24 | 1195 |
| GO:0005112 Notch binding                                                                          | 1  | 0.37376 | 0.292  | 0.04  | Molecular  | GO:00051 Notch binding                                                                          | 0.37376 | 0.55141 | 0 | 0 | 1  | 25   |
| GO:0005385 zinc ion transmembrane transporter activity                                            | 1  | 0.37376 | 0.292  | 0.04  | Molecular  | GO:00053 zinc ion transmembrane transporter activity                                            | 0.37376 | 0.55141 | 0 | 0 | 1  | 25   |
| GO:0008266 poly(U) RNA binding                                                                    | 1  | 0.37376 | 0.292  | 0.04  | Molecular  | GO:00082 poly(U) RNA binding                                                                    | 0.37376 | 0.55141 | 0 | 0 | 1  | 25   |
| GO:0043225 ATPase-coupled inorganic anion transmembrane transporter activity                      | 1  | 0.37376 | 0.292  | 0.04  | Molecular  | GO:00043 ATPase-coupled inorganic anion transmembrane transporter activity                      | 0.37376 | 0.55141 | 0 | 0 | 1  | 25   |
| GO:0070006 metal ion transmembrane transporter activity                                           | 1  | 0.37376 | 0.292  | 0.04  | Molecular  | GO:00070 metal ion transmembrane transporter activity                                           | 0.37376 | 0.55141 | 0 | 0 | 1  | 25   |
| GO:0104016 transcription regulator inhibitor activity                                             | 1  | 0.37376 | 0.292  | 0.04  | Molecular  | GO:00140 transcription regulator inhibitor activity                                             | 0.37376 | 0.55141 | 0 | 0 | 1  | 25   |
| GO:0016032 viral process                                                                          | 9  | 0.37408 | 2.786  | 0.021 | Biological | GO:00016 viral process                                                                          | 0.37408 | 0.54943 | 0 | 0 | 9  | 426  |
| GO:0045184 establishment of protein localization                                                  | 33 | 0.37417 | 10.217 | 0.019 | Biological | GO:00045 establishment of protein localization                                                  | 0.37417 | 0.54943 | 0 | 0 | 33 | 1697 |
| GO:0030278 regulation of ossification                                                             | 3  | 0.37457 | 0.928  | 0.025 | Biological | GO:00030 regulation of ossification                                                             | 0.37457 | 0.5497  | 0 | 0 | 3  | 120  |
| GO:0058050 defense response to Gram-positive bacterium                                            | 3  | 0.37457 | 0.928  | 0.025 | Biological | GO:00058 defense response to Gram-positive bacterium                                            | 0.37457 | 0.55052 | 0 | 0 | 3  | 120  |
| GO:1903169 regulation of calcium ion transmembrane transporter activity                           | 4  | 0.37525 | 1.238  | 0.024 | Biological | GO:19031 regulation of calcium ion transmembrane transporter activity                           | 0.37525 | 0.55052 | 0 | 0 | 4  | 170  |
| GO:0031347 regulation of defense response                                                         | 13 | 0.37641 | 4.025  | 0.02  | Biological | GO:00031 regulation of defense response                                                         | 0.37641 | 0.55206 | 0 | 0 | 13 | 636  |
| GO:0032281 AMPA glutamate receptor complex                                                        | 1  | 0.37703 | 0.297  | 0.038 | Cellular C | GO:00032 AMPA glutamate receptor complex                                                        | 0.37703 | 0.60032 | 0 | 0 | 1  | 26   |
| GO:0042958 axonal growth cone                                                                     | 1  | 0.37703 | 0.297  | 0.038 | Cellular C | GO:00044 axonal growth cone                                                                     | 0.37703 | 0.60032 | 0 | 0 | 1  | 26   |
| GO:0046930 poro complex                                                                           | 1  | 0.37703 | 0.297  | 0.038 | Cellular C | GO:00046 poro complex                                                                           | 0.37703 | 0.60032 | 0 | 0 | 1  | 26   |
| GO:0097381 photoreceptor disc membrane                                                            | 1  | 0.37703 | 0.297  | 0.038 | Cellular C | GO:00097 photoreceptor disc membrane                                                            | 0.37703 | 0.60032 | 0 | 0 | 1  | 26   |
| GO:0046637 regulation of alpha-beta T cell differentiation                                        | 2  | 0.37885 | 0.619  | 0.028 | Biological | GO:00046 regulation of alpha-beta T cell differentiation                                        | 0.37885 | 0.55226 | 0 | 0 | 2  | 72   |
| GO:0086003 cardiac muscle cell contraction                                                        | 2  | 0.37885 | 0.619  | 0.028 | Biological | GO:00086 cardiac muscle cell contraction                                                        | 0.37885 | 0.55226 | 0 | 0 | 2  | 72   |
| GO:0021092 light junction assembly                                                                | 2  | 0.37885 | 0.619  | 0.028 | Biological | GO:00120 light junction assembly                                                                | 0.37885 | 0.55226 | 0 | 0 | 2  | 72   |
| GO:1900046 regulation of hemostasis                                                               | 2  | 0.37885 | 0.619  | 0.028 | Biological | GO:19004 regulation of hemostasis                                                               | 0.37885 | 0.55226 | 0 | 0 | 2  | 72   |
| GO:1902475 L-alpha-amino acid transmembrane transporter activity                                  | 2  | 0.37885 | 0.619  | 0.028 | Biological | GO:19024 L-alpha-amino acid transmembrane transporter activity                                  | 0.37885 | 0.55226 | 0 | 0 | 2  | 72   |
| GO:0027676 lymphocyte migration                                                                   | 3  | 0.37953 | 0.929  | 0.025 | Biological | GO:00072 lymphocyte migration                                                                   | 0.37953 | 0.55226 | 0 | 0 | 3  | 121  |
| GO:0006760 folate-containing compound metabolic process                                           | 1  | 0.38041 | 0.31   | 0.038 | Biological | GO:00060 folate-containing compound metabolic process                                           | 0.38041 | 0.55226 | 0 | 0 | 1  | 26   |
| GO:0010460 positive regulation of heart rate                                                      | 1  | 0.38041 | 0.31   | 0.038 | Biological | GO:00010 positive regulation of heart rate                                                      | 0.38041 | 0.55226 | 0 | 0 | 1  | 26   |
| GO:0010615 positive regulation of cardiac muscle hypertrophy                                      | 1  | 0.38041 | 0.31   | 0.038 | Biological | GO:00010 positive regulation of cardiac muscle hypertrophy                                      | 0.38041 | 0.55226 | 0 | 0 | 1  | 26   |
| GO:0010623 programmed cell death involved in cell development                                     | 1  | 0.38041 | 0.31   | 0.038 | Biological | GO:00010 programmed cell death involved in cell development                                     | 0.38041 | 0.55226 | 0 | 0 | 1  | 26   |
| GO:0010882 regulation of cardiac muscle contraction by calcium ion signaling                      | 1  | 0.38041 | 0.31   | 0.038 | Biological | GO:00010 regulation of cardiac muscle contraction by calcium ion signaling                      | 0.38041 | 0.55226 | 0 | 0 | 1  | 26   |
| GO:0019883 antigen processing and presentation of endogenous antigen                              | 1  | 0.38041 | 0.31   | 0.038 | Biological | GO:00019 antigen processing and presentation of endogenous antigen                              | 0.38041 | 0.55226 | 0 | 0 | 1  | 26   |
| GO:0033233 regulation of protein catabolism                                                       | 1  | 0.38041 | 0.31   | 0.038 | Biological | GO:00033 regulation of protein catabolism                                                       | 0.38041 | 0.55226 | 0 | 0 | 1  | 26   |
| GO:0034377 plasma lipoprotein particle assembly                                                   | 1  | 0.38041 | 0.31   | 0.038 | Biological | GO:00034 plasma lipoprotein particle assembly                                                   | 0.38041 | 0.55226 | 0 | 0 | 1  | 26   |
| GO:0034695 response to prostaglandin E                                                            | 1  | 0.38041 | 0.31   | 0.038 | Biological | GO:00034 response to prostaglandin E                                                            | 0.38041 | 0.55226 | 0 | 0 | 1  | 26   |
| GO:0035988 chondrocyte proliferation                                                              | 1  | 0.38041 | 0.31   | 0.038 | Biological |                                                                                                 |         |         |   |   |    |      |

|                                                                                    |    |         |        |       |            |                                                                                    |         |         |   |   |    |      |
|------------------------------------------------------------------------------------|----|---------|--------|-------|------------|------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0042402 cellular bioenergetic amino acid catabolic process                      | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:0042402 cellular bioenergetic amino acid catabolic process                      | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:0044304 thyroid hormone metabolic process                                       | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:0044304 thyroid hormone metabolic process                                       | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:0045636 positive regulation of epidermal cell differentiation                   | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:0045636 positive regulation of epidermal cell differentiation                   | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:0045939 negative regulation of steroid metabolic process                        | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:0045939 negative regulation of steroid metabolic process                        | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:0046639 negative regulation of alpha-beta T cell differentiation                | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:0046639 negative regulation of alpha-beta T cell differentiation                | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:0050926 regulation of positive chemotaxis                                       | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:0050926 regulation of positive chemotaxis                                       | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:0051953 negative regulation of amine transport                                  | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:0051953 negative regulation of amine transport                                  | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:0070498 interferon-gamma-mediated signaling pathway                             | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:0070498 interferon-gamma-mediated signaling pathway                             | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:0090200 positive regulation of release of cytochrome c from mitochondria        | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:0090200 positive regulation of release of cytochrome c from mitochondria        | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:1903055 positive regulation of extracellular matrix organization                | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:1903055 positive regulation of extracellular matrix organization                | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:1903077 negative regulation of protein localization to plasma membrane          | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:1903077 negative regulation of protein localization to plasma membrane          | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:1905023 positive regulation of macrophage migration                             | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:1905023 positive regulation of macrophage migration                             | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:2000737 negative regulation of stem cell differentiation                        | 1  | 0.39172 | 0.31   | 0.037 | Biological | GO:2000737 negative regulation of stem cell differentiation                        | 0.39172 | 0.56066 | 0 | 0 | 1  | 27   |
| GO:0031214 biomineral tissue development                                           | 4  | 0.39177 | 1.238  | 0.023 | Biological | GO:0031214 biomineral tissue development                                           | 0.39177 | 0.56066 | 0 | 0 | 4  | 174  |
| GO:0110148 biomineralization                                                       | 4  | 0.39177 | 1.238  | 0.023 | Biological | GO:0110148 biomineralization                                                       | 0.39177 | 0.56066 | 0 | 0 | 4  | 174  |
| GO:0005977 glycogen metabolic process                                              | 2  | 0.39181 | 0.619  | 0.027 | Biological | GO:0005977 glycogen metabolic process                                              | 0.39181 | 0.56066 | 0 | 0 | 2  | 74   |
| GO:0006467 protein N-linked glycosylation                                          | 2  | 0.39181 | 0.619  | 0.027 | Biological | GO:0006467 protein N-linked glycosylation                                          | 0.39181 | 0.56066 | 0 | 0 | 2  | 74   |
| GO:014909 smooth muscle cell migration                                             | 2  | 0.39181 | 0.619  | 0.027 | Biological | GO:014909 smooth muscle cell migration                                             | 0.39181 | 0.56066 | 0 | 0 | 2  | 74   |
| GO:0042246 tissue regeneration                                                     | 2  | 0.39181 | 0.619  | 0.027 | Biological | GO:0042246 tissue regeneration                                                     | 0.39181 | 0.56066 | 0 | 0 | 2  | 74   |
| GO:0086001 cardiac muscle cell action potential                                    | 2  | 0.39181 | 0.619  | 0.027 | Biological | GO:0086001 cardiac muscle cell action potential                                    | 0.39181 | 0.56066 | 0 | 0 | 2  | 74   |
| GO:010008 endosome membrane                                                        | 11 | 0.39204 | 3.264  | 0.02  | Cellular   | GO:010008 endosome membrane                                                        | 0.39204 | 0.61328 | 0 | 0 | 11 | 544  |
| GO:000079 excitatory postsynaptic potential                                        | 3  | 0.39433 | 0.929  | 0.024 | Biological | GO:000079 excitatory postsynaptic potential                                        | 0.39433 | 0.5841  | 0 | 0 | 3  | 124  |
| GO:001227 DNA-binding transcription repressor activity, RNA polymerase II-specific | 7  | 0.39451 | 2.047  | 0.022 | Molecular  | GO:001227 DNA-binding transcription repressor activity, RNA polymerase II-specific | 0.39451 | 0.57175 | 0 | 0 | 7  | 324  |
| GO:0004101 response to xenobiotic stimulus                                         | 9  | 0.39484 | 2.786  | 0.021 | Biological | GO:0004101 response to xenobiotic stimulus                                         | 0.39484 | 0.56447 | 0 | 0 | 9  | 438  |
| GO:0034764 positive regulation of transmembrane transport                          | 5  | 0.39493 | 1.548  | 0.022 | Biological | GO:0034764 positive regulation of transmembrane transport                          | 0.39493 | 0.56447 | 0 | 0 | 5  | 226  |
| GO:0099003 vesicle-mediated transport in synapse                                   | 5  | 0.39493 | 1.548  | 0.022 | Biological | GO:0099003 vesicle-mediated transport in synapse                                   | 0.39493 | 0.56447 | 0 | 0 | 5  | 226  |
| GO:0006075 cellular modified amino acid metabolic process                          | 4  | 0.39589 | 1.238  | 0.023 | Biological | GO:0006075 cellular modified amino acid metabolic process                          | 0.39589 | 0.56568 | 0 | 0 | 4  | 175  |
| GO:0032496 response to lipopolysaccharide                                          | 1  | 0.39679 | 0.292  | 0.037 | Molecular  | GO:0032496 response to lipopolysaccharide                                          | 0.39679 | 0.57175 | 0 | 0 | 1  | 27   |
| GO:0004683 calmodulin-dependent protein kinase activity                            | 1  | 0.39679 | 0.292  | 0.037 | Molecular  | GO:0004683 calmodulin-dependent protein kinase activity                            | 0.39679 | 0.57175 | 0 | 0 | 1  | 27   |
| GO:0004709 MAP kinase kinase kinase activity                                       | 1  | 0.39679 | 0.292  | 0.037 | Molecular  | GO:0004709 MAP kinase kinase kinase activity                                       | 0.39679 | 0.57175 | 0 | 0 | 1  | 27   |
| GO:0008066 glutamate receptor activity                                             | 1  | 0.39679 | 0.292  | 0.037 | Molecular  | GO:0008066 glutamate receptor activity                                             | 0.39679 | 0.57175 | 0 | 0 | 1  | 27   |
| GO:0035250 UDP-galactose 4-epimerase activity                                      | 1  | 0.39679 | 0.292  | 0.037 | Molecular  | GO:0035250 UDP-galactose 4-epimerase activity                                      | 0.39679 | 0.57175 | 0 | 0 | 1  | 27   |
| GO:0140326 ATPase-dependent intramembrane lipid transporter activity               | 9  | 0.39744 | 2.786  | 0.021 | Biological | GO:0140326 ATPase-dependent intramembrane lipid transporter activity               | 0.39744 | 0.56727 | 0 | 0 | 9  | 435  |
| GO:0006869 lipid transport                                                         | 9  | 0.39744 | 2.786  | 0.021 | Biological | GO:0006869 lipid transport                                                         | 0.39744 | 0.56727 | 0 | 0 | 9  | 435  |
| GO:0002067 glandular epithelial cell differentiation                               | 2  | 0.39824 | 0.619  | 0.027 | Biological | GO:0002067 glandular epithelial cell differentiation                               | 0.39824 | 0.56727 | 0 | 0 | 2  | 75   |
| GO:0006073 cellular glucan metabolic process                                       | 2  | 0.39824 | 0.619  | 0.027 | Biological | GO:0006073 cellular glucan metabolic process                                       | 0.39824 | 0.56727 | 0 | 0 | 2  | 75   |
| GO:0034103 regulation of tissue remodeling                                         | 2  | 0.39824 | 0.619  | 0.027 | Biological | GO:0034103 regulation of tissue remodeling                                         | 0.39824 | 0.56727 | 0 | 0 | 2  | 75   |
| GO:0043297 apical junction assembly                                                | 2  | 0.39824 | 0.619  | 0.027 | Biological | GO:0043297 apical junction assembly                                                | 0.39824 | 0.56727 | 0 | 0 | 2  | 75   |
| GO:0044042 glucan metabolic process                                                | 2  | 0.39824 | 0.619  | 0.027 | Biological | GO:0044042 glucan metabolic process                                                | 0.39824 | 0.56727 | 0 | 0 | 2  | 75   |
| GO:0050795 regulation of behavior                                                  | 2  | 0.39824 | 0.619  | 0.027 | Biological | GO:0050795 regulation of behavior                                                  | 0.39824 | 0.56727 | 0 | 0 | 2  | 75   |
| GO:0050818 regulation of coagulation                                               | 2  | 0.39824 | 0.619  | 0.027 | Biological | GO:0050818 regulation of coagulation                                               | 0.39824 | 0.56727 | 0 | 0 | 2  | 75   |
| GO:0050517 cardiac muscle tissue growth                                            | 2  | 0.39824 | 0.619  | 0.027 | Biological | GO:0050517 cardiac muscle tissue growth                                            | 0.39824 | 0.56727 | 0 | 0 | 2  | 75   |
| GO:0071479 cellular response to ionizing radiation                                 | 11 | 0.39903 | 3.216  | 0.021 | Molecular  | GO:0071479 cellular response to ionizing radiation                                 | 0.39903 | 0.57317 | 0 | 0 | 11 | 532  |
| GO:0003712 transcriptional coregulator activity                                    | 11 | 0.39903 | 3.216  | 0.021 | Molecular  | GO:0003712 transcriptional coregulator activity                                    | 0.39903 | 0.57317 | 0 | 0 | 11 | 532  |
| GO:0001891 phagocytic cup                                                          | 1  | 0.39931 | 0.297  | 0.036 | Cellular   | GO:0001891 phagocytic cup                                                          | 0.39931 | 0.61923 | 0 | 0 | 1  | 28   |
| GO:0032809 neuronal cell body membrane                                             | 1  | 0.39931 | 0.297  | 0.036 | Cellular   | GO:0032809 neuronal cell body membrane                                             | 0.39931 | 0.61923 | 0 | 0 | 1  | 28   |
| GO:0071782 endoplasmic reticulum tubular network                                   | 1  | 0.39931 | 0.297  | 0.036 | Cellular   | GO:0071782 endoplasmic reticulum tubular network                                   | 0.39931 | 0.61923 | 0 | 0 | 1  | 28   |
| GO:1900782 protein tyrosine kinase binding                                         | 3  | 0.39977 | 0.585  | 0.027 | Molecular  | GO:1900782 protein tyrosine kinase binding                                         | 0.39977 | 0.57317 | 0 | 0 | 3  | 127  |
| GO:0017022 myosin binding                                                          | 2  | 0.39977 | 0.585  | 0.027 | Molecular  | GO:0017022 myosin binding                                                          | 0.39977 | 0.57317 | 0 | 0 | 2  | 74   |
| GO:0034767 positive regulation of ion transmembrane transport                      | 4  | 0.4     | 1.238  | 0.023 | Biological | GO:0034767 positive regulation of ion transmembrane transport                      | 0.4     | 0.56764 | 0 | 0 | 4  | 176  |
| GO:0048015 phosphatidylinositol-mediated signaling                                 | 4  | 0.4     | 1.238  | 0.023 | Biological | GO:0048015 phosphatidylinositol-mediated signaling                                 | 0.4     | 0.56764 | 0 | 0 | 4  | 176  |
| GO:0051252 regulation of RNA metabolic process                                     | 71 | 0.40127 | 21.381 | 0.019 | Biological | GO:0051252 regulation of RNA metabolic process                                     | 0.40127 | 0.56764 | 0 | 0 | 71 | 3772 |
| GO:0031863 nuclear nucleosome assembly                                             | 3  | 0.40283 | 0.31   | 0.036 | Biological | GO:0031863 nuclear nucleosome assembly                                             | 0.40283 | 0.56764 | 0 | 0 | 3  | 128  |
| GO:0044281 small molecule metabolic process                                        | 35 | 0.40279 | 10.836 | 0.019 | Biological | GO:0044281 small molecule metabolic process                                        | 0.40279 | 0.56764 | 0 | 0 | 35 | 1826 |
| GO:0003171 atrioventricular valve development                                      | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0003171 atrioventricular valve development                                      | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0003272 endocardial cushion formation                                           | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0003272 endocardial cushion formation                                           | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0005979 regulation of glycogen biosynthetic process                             | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0005979 regulation of glycogen biosynthetic process                             | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0002853 nitric oxide-mediated signal transduction                               | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0002853 nitric oxide-mediated signal transduction                               | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0007342 fusion of sperm to egg plasma membrane involved in single fertilization | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0007342 fusion of sperm to egg plasma membrane involved in single fertilization | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0009310 amine catabolic process                                                 | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0009310 amine catabolic process                                                 | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0010575 positive regulation of vascular endothelial growth factor production    | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0010575 positive regulation of vascular endothelial growth factor production    | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0010800 positive regulation of peptidyl-threonine phosphorylation               | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0010800 positive regulation of peptidyl-threonine phosphorylation               | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0010982 regulation of glycogen biosynthetic process                             | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0010982 regulation of glycogen biosynthetic process                             | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0018126 protein hydrolysis                                                      | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0018126 protein hydrolysis                                                      | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0021801 cerebral cortex radial glia-guided migration                            | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0021801 cerebral cortex radial glia-guided migration                            | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0022030 telencephalon glial cell migration                                      | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0022030 telencephalon glial cell migration                                      | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0030194 positive regulation of blood coagulation                                | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0030194 positive regulation of blood coagulation                                | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0031684 regulation of lipopolysaccharide-mediated signaling pathway             | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0031684 regulation of lipopolysaccharide-mediated signaling pathway             | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0032469 endoplasmic reticulum calcium ion homeostasis                           | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0032469 endoplasmic reticulum calcium ion homeostasis                           | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0033598 mammary gland epithelial cell proliferation                             | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0033598 mammary gland epithelial cell proliferation                             | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0034063 stress granule assembly                                                 | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0034063 stress granule assembly                                                 | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0036037 CD8-positive, alpha-beta T cell activation                              | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0036037 CD8-positive, alpha-beta T cell activation                              | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0036292 RIG-I signaling pathway                                                 | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0036292 RIG-I signaling pathway                                                 | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0042537 benzene-containing compound metabolic process                           | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0042537 benzene-containing compound metabolic process                           | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0045116 protein neddylation                                                     | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0045116 protein neddylation                                                     | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0048668 collateral sprouting                                                    | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0048668 collateral sprouting                                                    | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0048843 negative regulation of axon extension involved in axon guidance         | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0048843 negative regulation of axon extension involved in axon guidance         | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0050996 positive regulation of lipid catabolic process                          | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0050996 positive regulation of lipid catabolic process                          | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0051984 positive regulation of chromosome segregation                           | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0051984 positive regulation of chromosome segregation                           | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0055023 positive regulation of cardiac muscle tissue growth                     | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0055023 positive regulation of cardiac muscle tissue growth                     | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0060333 interferon-gamma-mediated signaling pathway                             | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0060333 interferon-gamma-mediated signaling pathway                             | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0062149 detection of stimulus involved in sensory perception of pain            | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0062149 detection of stimulus involved in sensory perception of pain            | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0071088 negative regulation of biomimetic tissue development                    | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0071088 negative regulation of biomimetic tissue development                    | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0071624 positive regulation of granulocyte chemotaxis                           | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0071624 positive regulation of granulocyte chemotaxis                           | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0110150 negative regulation of biomineralization                                | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:0110150 negative regulation of biomineralization                                | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:1900448 positive regulation of homeostasis                                      | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:1900448 positive regulation of homeostasis                                      | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:1901223 positive regulation of NIK/NF-kappaB signaling                          | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:1901223 positive regulation of NIK/NF-kappaB signaling                          | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:1903579 negative regulation of ATP metabolic process                            | 1  | 0.40283 | 0.31   | 0.036 | Biological | GO:1903579 negative regulation of ATP metabolic process                            | 0.40283 | 0.56764 | 0 | 0 | 1  | 28   |
| GO:0003231 cardiac ventricle development                                           | 3  | 0.40415 | 0.929  | 0.024 | Biological | GO:0003231                                                                         |         |         |   |   |    |      |

|                                                                                        |    |         |        |       |            |                                                                                     |         |         |   |   |    |      |
|----------------------------------------------------------------------------------------|----|---------|--------|-------|------------|-------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0008157 protein phosphatase 1 binding                                               | 1  | 0.41898 | 0.292  | 0.034 | Molecular  | GO:0008 protein phosphatase 1 binding                                               | 0.41898 | 0.59217 | 0 | 0 | 1  | 29   |
| GO:0070325 lipoprotein particle receptor binding                                       | 1  | 0.41898 | 0.292  | 0.034 | Molecular  | GO:0070 lipoprotein particle receptor binding                                       | 0.41898 | 0.59217 | 0 | 0 | 1  | 29   |
| GO:0015370 sulfate/sulfonate symporter activity                                        | 2  | 0.41917 | 0.585  | 0.028 | Molecular  | GO:0015 sulfate/sulfonate symporter activity                                        | 0.41917 | 0.59217 | 0 | 0 | 2  | 77   |
| GO:0071241 cellular response to inorganic substance                                    | 5  | 0.42015 | 1.548  | 0.021 | Biological | GO:0071 cellular response to inorganic substance                                    | 0.42015 | 0.59282 | 0 | 0 | 5  | 233  |
| GO:0009963 magnesium-dependent protein serine/threonine phosphatase                    | 1  | 0.42081 | 0.297  | 0.033 | Cellular   | GO:0009 magnesium-dependent protein serine/threonine phosphatase                    | 0.42081 | 0.63366 | 0 | 0 | 1  | 30   |
| GO:0031528 microvillus membrane                                                        | 1  | 0.42081 | 0.297  | 0.033 | Cellular   | GO:0031 microvillus membrane                                                        | 0.42081 | 0.63366 | 0 | 0 | 1  | 30   |
| GO:0032839 dendrite cytoplasm                                                          | 1  | 0.42081 | 0.297  | 0.033 | Cellular   | GO:0032 dendrite cytoplasm                                                          | 0.42081 | 0.63366 | 0 | 0 | 1  | 30   |
| GO:0043207 response to external biotic stimulus                                        | 29 | 0.42108 | 8.978  | 0.010 | Biological | GO:0043 response to external biotic stimulus                                        | 0.42108 | 0.59282 | 0 | 0 | 29 | 1578 |
| GO:0015087 channel activity                                                            | 10 | 0.42109 | 2.924  | 0.02  | Molecular  | GO:0015 channel activity                                                            | 0.42109 | 0.59392 | 0 | 0 | 10 | 489  |
| GO:0061134 peptidase regulator activity                                                | 5  | 0.42316 | 1.462  | 0.022 | Molecular  | GO:0061 peptidase regulator activity                                                | 0.42316 | 0.59955 | 0 | 0 | 5  | 230  |
| GO:0044282 small molecule catabolic process                                            | 8  | 0.42346 | 2.477  | 0.02  | Biological | GO:0044 small molecule catabolic process                                            | 0.42346 | 0.5828  | 0 | 0 | 8  | 392  |
| GO:0022803 passive transmembrane transporter activity                                  | 10 | 0.42359 | 2.924  | 0.02  | Molecular  | GO:0022 passive transmembrane transporter activity                                  | 0.42359 | 0.59955 | 0 | 0 | 10 | 400  |
| GO:0006639 acylglycerol metabolic process                                              | 1  | 0.42364 | 0.929  | 0.023 | Biological | GO:0006 acylglycerol metabolic process                                              | 0.42364 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0010595 regulation of cellular ketone metabolic process                             | 3  | 0.42364 | 0.929  | 0.023 | Biological | GO:0010 regulation of cellular ketone metabolic process                             | 0.42364 | 0.5828  | 0 | 0 | 3  | 130  |
| GO:0061041 regulation of wound healing                                                 | 3  | 0.42364 | 0.929  | 0.023 | Biological | GO:0061 regulation of wound healing                                                 | 0.42364 | 0.5828  | 0 | 0 | 3  | 130  |
| GO:0008652 cellular amino acid biosynthetic process                                    | 2  | 0.42366 | 0.619  | 0.025 | Biological | GO:0008 cellular amino acid biosynthetic process                                    | 0.42366 | 0.5828  | 0 | 0 | 2  | 79   |
| GO:0030500 regulation of bone mineralization                                           | 2  | 0.42366 | 0.619  | 0.025 | Biological | GO:0030 regulation of bone mineralization                                           | 0.42366 | 0.5828  | 0 | 0 | 2  | 79   |
| GO:0051966 regulation of synaptic transmission, glutamatergic                          | 2  | 0.42366 | 0.619  | 0.025 | Biological | GO:0051 regulation of synaptic transmission, glutamatergic                          | 0.42366 | 0.5828  | 0 | 0 | 2  | 79   |
| GO:0009636 response to toxic substance                                                 | 5  | 0.42374 | 1.548  | 0.021 | Biological | GO:0009 response to toxic substance                                                 | 0.42374 | 0.5828  | 0 | 0 | 5  | 234  |
| GO:0031300 intrinsic component of organelle membrane                                   | 2  | 0.42427 | 0.593  | 0.025 | Cellular   | GO:0031 intrinsic component of organelle membrane                                   | 0.42427 | 0.63366 | 0 | 0 | 2  | 80   |
| GO:0031301 integral component of organelle membrane                                    | 2  | 0.42427 | 0.593  | 0.025 | Cellular   | GO:0031 integral component of organelle membrane                                    | 0.42427 | 0.63366 | 0 | 0 | 2  | 80   |
| GO:0002360 T cell lineage commitment                                                   | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0002 T cell lineage commitment                                                   | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0002825 regulation of T-helper 1 type immune response                               | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0002 regulation of T-helper 1 type immune response                               | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0006622 protein targeting to lysosome                                               | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0006 protein targeting to lysosome                                               | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0006656 phosphatidylcholine biosynthetic process                                    | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0006 phosphatidylcholine biosynthetic process                                    | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0007202 activation of phospholipase C activity                                      | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0007 activation of phospholipase C activity                                      | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0014741 negative regulation of muscle hypertrophy                                   | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0014 negative regulation of muscle hypertrophy                                   | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0015740 C4-deposition in blood                                                      | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0015 C4-deposition in blood                                                      | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0015813 L-glutamate transmembrane transport                                         | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0015 L-glutamate transmembrane transport                                         | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0018200 peptidyl-glutamic acid modification                                         | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0018 peptidyl-glutamic acid modification                                         | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0030947 regulation of vascular endothelial growth factor receptor signaling pathway | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0030 regulation of vascular endothelial growth factor receptor signaling pathway | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0031365 N-terminal protein amino acid modification                                  | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0031 N-terminal protein amino acid modification                                  | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0034087 protein localization to Golgi apparatus                                     | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0034 protein localization to Golgi apparatus                                     | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0034368 protein-lipid complex remodeling                                            | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0034 protein-lipid complex remodeling                                            | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0034369 plasma lipoprotein particle remodeling                                      | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0034 plasma lipoprotein particle remodeling                                      | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0034698 response to gonadotropin                                                    | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0034 response to gonadotropin                                                    | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0035521 monoubiquitinated histone deubiquitination                                  | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0035 monoubiquitinated histone deubiquitination                                  | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0035522 monoubiquitinated histone H2A deubiquitination                              | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0035 monoubiquitinated histone H2A deubiquitination                              | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0035774 positive regulation of insulin secretion involved in cellular response to   | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0035 positive regulation of insulin secretion involved in cellular response to   | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0043094 cellular metabolic compound salvage                                         | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0043 cellular metabolic compound salvage                                         | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0043171 peptide catabolic process                                                   | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0043 peptide catabolic process                                                   | 0.42444 | 0.5828  | 0 | 0 | 1  | 29   |
| GO:0044342 type B pancreatic cell proliferation                                        | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0044 type B pancreatic cell proliferation                                        | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0050820 positive regulation of coagulation                                          | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0050 positive regulation of coagulation                                          | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0060674 placenta blood vessel development                                           | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0060 placenta blood vessel development                                           | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0072539 T-helper 17 cell differentiation                                            | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0072 T-helper 17 cell differentiation                                            | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0090140 regulation of mitochondrial fission                                         | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0090 regulation of mitochondrial fission                                         | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0090382 phagosome maturation                                                        | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0090 phagosome maturation                                                        | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0097096 response to thyroid hormone                                                 | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0097 response to thyroid hormone                                                 | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0098901 regulation of cardiac muscle cell action potential                          | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0098 regulation of cardiac muscle cell action potential                          | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0099505 regulation of presynaptic membrane potential                                | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0099 regulation of presynaptic membrane potential                                | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0099558 maintenance of synapse structure                                            | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:0099 maintenance of synapse structure                                            | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:1949494 regulation of leukocyte adhesion to vascular endothelial cell               | 1  | 0.42444 | 0.31   | 0.033 | Biological | GO:1949 regulation of leukocyte adhesion to vascular endothelial cell               | 0.42444 | 0.5828  | 0 | 0 | 1  | 30   |
| GO:0042396 cellular adhesion                                                           | 7  | 0.42536 | 1.858  | 0.021 | Biological | GO:0042 cellular adhesion                                                           | 0.42536 | 0.5839  | 0 | 0 | 7  | 347  |
| GO:0043270 positive regulation of ion transport                                        | 6  | 0.42536 | 1.858  | 0.021 | Biological | GO:0043 positive regulation of ion transport                                        | 0.42536 | 0.5839  | 0 | 0 | 6  | 287  |
| GO:0009615 response to virus                                                           | 8  | 0.42623 | 2.477  | 0.02  | Biological | GO:0009 response to virus                                                           | 0.42623 | 0.58494 | 0 | 0 | 8  | 393  |
| GO:0072686 mitotic spindle                                                             | 4  | 0.42833 | 1.187  | 0.022 | Cellular   | GO:0072 mitotic spindle                                                             | 0.42833 | 0.63366 | 0 | 0 | 4  | 185  |
| GO:0032940 secretion by cell                                                           | 16 | 0.42834 | 4.954  | 0.019 | Biological | GO:0032 secretion by cell                                                           | 0.42834 | 0.58755 | 0 | 0 | 16 | 821  |
| GO:0006838 neutral synaptic transmission, postsynaptic                                 | 3  | 0.42848 | 0.929  | 0.023 | Biological | GO:0006 neutral synaptic transmission, postsynaptic                                 | 0.42848 | 0.58755 | 0 | 0 | 3  | 131  |
| GO:0009555 chemical synaptic transmission, postsynaptic                                | 3  | 0.42848 | 0.929  | 0.023 | Biological | GO:0009 chemical synaptic transmission, postsynaptic                                | 0.42848 | 0.58755 | 0 | 0 | 3  | 131  |
| GO:0098797 plasma membrane protein complex                                             | 12 | 0.42895 | 3.561  | 0.02  | Cellular   | GO:0098 plasma membrane protein complex                                             | 0.42895 | 0.63366 | 0 | 0 | 12 | 614  |
| GO:0005540 hyaluronic acid binding                                                     | 1  | 0.42976 | 0.292  | 0.033 | Molecular  | GO:0005 hyaluronic acid binding                                                     | 0.42976 | 0.59835 | 0 | 0 | 1  | 30   |
| GO:0008378 galactosyltransferase activity                                              | 1  | 0.42976 | 0.292  | 0.033 | Molecular  | GO:0008 galactosyltransferase activity                                              | 0.42976 | 0.59835 | 0 | 0 | 1  | 30   |
| GO:0016417 S-acyltransferase activity                                                  | 1  | 0.42976 | 0.292  | 0.033 | Molecular  | GO:0016 S-acyltransferase activity                                                  | 0.42976 | 0.59835 | 0 | 0 | 1  | 30   |
| GO:0048875 ephrin receptor binding                                                     | 1  | 0.42976 | 0.292  | 0.033 | Molecular  | GO:0048 ephrin receptor binding                                                     | 0.42976 | 0.59835 | 0 | 0 | 1  | 30   |
| GO:0070717 poly-purine tract binding                                                   | 1  | 0.42976 | 0.292  | 0.033 | Molecular  | GO:0070 poly-purine tract binding                                                   | 0.42976 | 0.59835 | 0 | 0 | 1  | 30   |
| GO:0007260 tyrosine phosphorylation of STAT protein                                    | 2  | 0.42993 | 0.619  | 0.025 | Biological | GO:0007 tyrosine phosphorylation of STAT protein                                    | 0.42993 | 0.58888 | 0 | 0 | 2  | 80   |
| GO:0050772 positive regulation of axonogenesis                                         | 2  | 0.42993 | 0.619  | 0.025 | Biological | GO:0050 positive regulation of axonogenesis                                         | 0.42993 | 0.58888 | 0 | 0 | 2  | 80   |
| GO:0072091 regulation of stem cell proliferation                                       | 2  | 0.42993 | 0.619  | 0.025 | Biological | GO:0072 regulation of stem cell proliferation                                       | 0.42993 | 0.58888 | 0 | 0 | 2  | 80   |
| GO:1901616 organic hydroxy compound catabolic process                                  | 2  | 0.42993 | 0.619  | 0.025 | Biological | GO:1901 organic hydroxy compound catabolic process                                  | 0.42993 | 0.58888 | 0 | 0 | 2  | 80   |
| GO:0002102 podosome                                                                    | 1  | 0.43126 | 0.297  | 0.032 | Cellular   | GO:0002 podosome                                                                    | 0.43126 | 0.63366 | 0 | 0 | 1  | 31   |
| GO:0008305 integrin complex                                                            | 1  | 0.43126 | 0.297  | 0.032 | Cellular   | GO:0008 integrin complex                                                            | 0.43126 | 0.63366 | 0 | 0 | 1  | 31   |
| GO:0031941 filamentous actin                                                           | 1  | 0.43126 | 0.297  | 0.032 | Cellular   | GO:0031 filamentous actin                                                           | 0.43126 | 0.63366 | 0 | 0 | 1  | 31   |
| GO:0042498 cell body membrane                                                          | 1  | 0.43126 | 0.297  | 0.032 | Cellular   | GO:0042 cell body membrane                                                          | 0.43126 | 0.63366 | 0 | 0 | 1  | 31   |
| GO:0070791 endoplasmic reticulum exit site                                             | 1  | 0.43126 | 0.297  | 0.032 | Cellular   | GO:0070 endoplasmic reticulum exit site                                             | 0.43126 | 0.63366 | 0 | 0 | 1  | 31   |
| GO:0048545 response to steroid hormone                                                 | 7  | 0.43202 | 2.167  | 0.02  | Biological | GO:0048 response to steroid hormone                                                 | 0.43202 | 0.59158 | 0 | 0 | 7  | 342  |
| GO:0007219 Notch signaling pathway                                                     | 4  | 0.43273 | 1.238  | 0.022 | Biological | GO:0007 Notch signaling pathway                                                     | 0.43273 | 0.5917  | 0 | 0 | 4  | 184  |
| GO:0007202 positive regulation of production of molecular mediator of immune response  | 3  | 0.43331 | 0.929  | 0.023 | Biological | GO:0007 positive regulation of production of molecular mediator of immune response  | 0.43331 | 0.5917  | 0 | 0 | 3  | 132  |
| GO:0035303 regulation of transcription                                                 | 3  | 0.43331 | 0.929  | 0.023 | Biological | GO:0035 regulation of transcription                                                 | 0.43331 | 0.5917  | 0 | 0 | 3  | 132  |
| GO:0006351 transcription, DNA-templated                                                | 67 | 0.43431 | 20.743 | 0.019 | Biological | GO:0006 transcription, DNA-templated                                                | 0.43431 | 0.5917  | 0 | 0 | 67 | 3588 |
| GO:0051403 stress-activated MAPK cascade                                               | 5  | 0.43449 | 1.548  | 0.021 | Biological | GO:0051 stress-activated MAPK cascade                                               | 0.43449 | 0.5917  | 0 | 0 | 5  | 237  |
| GO:0001958 endochondral ossification                                                   | 1  | 0.43495 | 0.31   | 0.032 | Biological | GO:0001 endochondral ossification                                                   | 0.43495 | 0.5917  | 0 | 0 | 1  | 31   |
| GO:0006821 cellular component disassembly involved in execution phase of apoptosis     | 1  | 0.43495 | 0.31   | 0.032 | Biological | GO:0006 cellular component disassembly involved in execution phase of apoptosis     | 0.43495 | 0.5917  | 0 | 0 | 1  | 31   |
| GO:0008156 negative regulation of DNA replication                                      | 1  | 0.43495 | 0.31   | 0.032 | Biological | GO:0008 negative regulation of DNA replication                                      | 0.43495 | 0.5917  | 0 | 0 | 1  | 31   |
| GO:0010039 response to iron                                                            | 1  | 0.43495 | 0.31   | 0.032 | Biological | GO:0010 response to iron                                                            | 0.43495 | 0.5917  | 0 | 0 | 1  | 31   |
| GO:0010669 epithelial structure maintenance                                            | 1  | 0.43495 | 0.31   | 0.032 | Biological | GO:0010 epithelial structure maintenance                                            | 0.43495 | 0.5917  | 0 | 0 | 1  | 31   |
| GO:0021522 spinal cord motor neuron differentiation                                    | 1  | 0.43495 | 0.31   | 0.032 | Biological | GO:0021 spinal cord motor neuron differentiation                                    | 0.43495 | 0.5917  | 0 | 0 | 1  | 31   |
| GO:0036075 replacement ossification                                                    | 1  | 0.43495 | 0.31   | 0.032 | Biological | GO:0036 replacement ossification                                                    | 0.43495 | 0.5917  | 0 | 0 | 1  | 31   |
| GO:0045648 positive regulation of erythrocyte differentiation                          | 1  | 0.43495 | 0.31   | 0.032 | Biological | GO:0045 positive regulation of erythrocyte differentiation                          | 0.43495 | 0.5917  | 0 | 0 | 1  | 31   |
| GO:0045907 positive regulation of vasorestriction                                      | 1  | 0.43495 | 0.31   | 0.032 | Biological | GO:0045 positive regulation of vasorestriction                                      | 0.43495 | 0.5917  | 0 | 0 | 1  | 31   |
| GO:0050951 sensory perception of temperature stimulus                                  | 1  | 0.43495 | 0.31   | 0.032 | Biological | GO:0050 sensory perception of temperature stimulus                                  | 0.43495 | 0.5917  | 0 | 0 | 1  | 31   |
| GO:0051883 killing of cells in other organism involved in symbiotic interaction        | 1  | 0.43495 | 0.31   | 0.032 | Biological | GO:0051 killing of cells in other organism                                          |         |         |   |   |    |      |

|                                                                                      |    |         |       |       |              |                                                                                   |         |         |   |   |    |      |
|--------------------------------------------------------------------------------------|----|---------|-------|-------|--------------|-----------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0042383 sarcolemma                                                                | 3  | 0.45456 | 0.89  | 0.022 | Cellular C   | GO:0042 sarcolemma                                                                | 0.45456 | 0.65594 | 0 | 0 | 3  | 138  |
| GO:0015630 microtubule cytoskeleton                                                  | 26 | 0.45458 | 7.715 | 0.019 | Cellular C   | GO:0015 microtubule cytoskeleton                                                  | 0.45458 | 0.65594 | 0 | 0 | 26 | 1382 |
| GO:0010710 positive regulation of cell morphogenesis involved in differentiation     | 2  | 0.45483 | 0.619 | 0.024 | Biological P | GO:0010 positive regulation of cell morphogenesis involved in differentiation     | 0.45483 | 0.60858 | 0 | 0 | 2  | 849  |
| GO:000118 histone desacetylation complex                                             | 2  | 0.45487 | 0.593 | 0.024 | Cellular C   | GO:0000 histone desacetylation complex                                            | 0.45487 | 0.65594 | 0 | 0 | 2  | 85   |
| GO:0002063 chondrocyte development                                                   | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0002 chondrocyte development                                                   | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0002719 negative regulation of cytokine production involved in immune response    | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0002 negative regulation of cytokine production involved in immune response    | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0006026 aminoglycan catabolic process                                             | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0006 aminoglycan catabolic process                                             | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:000308 DNA catabolic process                                                      | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0003 DNA catabolic process                                                     | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:000616 glycoprotein catabolic process                                             | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0006 glycoprotein catabolic process                                            | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0014808 release of sequestered calcium ion into cytosol by sarcoplasmic reticulum | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0014 release of sequestered calcium ion into cytosol by sarcoplasmic reticulum | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0018345 protein palmitoylation                                                    | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0018 protein palmitoylation                                                    | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0030204 chondroitin sulfate metabolic process                                     | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0030 chondroitin sulfate metabolic process                                     | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0031198 response to hypoxia                                                       | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0031 response to hypoxia                                                       | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0034260 negative regulation of GTPase activity                                    | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0034 negative regulation of GTPase activity                                    | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0034389 lipid droplet organization                                                | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0034 lipid droplet organization                                                | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0040018 positive regulation of multicellular organism growth                      | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0040 positive regulation of multicellular organism growth                      | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0040020 regulation of meiotic nuclear division                                    | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0040 regulation of meiotic nuclear division                                    | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0042558 telomere-containing compound metabolic process                            | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0042 telomere-containing compound metabolic process                            | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0044372 positive regulation of CD4-positive, alpha-beta T cell differentiation    | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0044 positive regulation of CD4-positive, alpha-beta T cell differentiation    | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0043552 positive regulation of phosphatidylinositol 3-kinase activity             | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0043 positive regulation of phosphatidylinositol 3-kinase activity             | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0045761 regulation of adenylyate cyclase activity                                 | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0045 regulation of adenylyate cyclase activity                                 | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0050901 leukocyte tethering or rolling                                            | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0050 leukocyte tethering or rolling                                            | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0051642 centrosome localization                                                   | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0051 centrosome localization                                                   | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0060317 cardiac epithelial to mesenchymal transition                              | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0060 cardiac epithelial to mesenchymal transition                              | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0061036 positive regulation of cartilage development                              | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0061 positive regulation of cartilage development                              | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0061842 microtubule organizing center localization                                | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0061 microtubule organizing center localization                                | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0071425 hematopoietic stem cell proliferation                                     | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0071 hematopoietic stem cell proliferation                                     | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:008005 ventricular cardiac muscle cell action potential                           | 1  | 0.4554  | 0.31  | 0.03  | Biological   | GO:0080 ventricular cardiac muscle cell action potential                          | 0.4554  | 0.60858 | 0 | 0 | 1  | 33   |
| GO:0019897 protein kinase regulator activity                                         | 5  | 0.4558  | 1.462 | 0.021 | Molecular    | GO:0019 protein kinase regulator activity                                         | 0.4558  | 0.62555 | 0 | 0 | 5  | 239  |
| GO:0051302 regulation of cell division                                               | 4  | 0.45697 | 1.238 | 0.021 | Biological   | GO:0051 regulation of cell division                                               | 0.45697 | 0.61034 | 0 | 0 | 4  | 190  |
| GO:0007586 digestion                                                                 | 3  | 0.45721 | 0.929 | 0.022 | Biological   | GO:0007 digestion                                                                 | 0.45721 | 0.61034 | 0 | 0 | 3  | 137  |
| GO:0051147 regulation of muscle cell differentiation                                 | 3  | 0.45721 | 0.929 | 0.022 | Biological   | GO:0051 regulation of muscle cell differentiation                                 | 0.45721 | 0.61034 | 0 | 0 | 3  | 137  |
| GO:1904019 epithelial cell apoptotic process                                         | 3  | 0.45721 | 0.929 | 0.022 | Biological   | GO:1904 epithelial cell apoptotic process                                         | 0.45721 | 0.61034 | 0 | 0 | 3  | 137  |
| GO:0044092 negative regulation of molecular function                                 | 19 | 0.45827 | 5.882 | 0.019 | Biological   | GO:0044 negative regulation of molecular function                                 | 0.45827 | 0.61159 | 0 | 0 | 19 | 999  |
| GO:0019318 hexose metabolic process                                                  | 5  | 0.45938 | 1.548 | 0.02  | Biological   | GO:0019 hexose metabolic process                                                  | 0.45938 | 0.61292 | 0 | 0 | 5  | 244  |
| GO:0014896 muscle hypertrophy                                                        | 2  | 0.46071 | 0.619 | 0.024 | Biological   | GO:0014 muscle hypertrophy                                                        | 0.46071 | 0.61429 | 0 | 0 | 2  | 85   |
| GO:0045069 regulation of viral genome replication                                    | 2  | 0.46071 | 0.619 | 0.024 | Biological   | GO:0045 regulation of viral genome replication                                    | 0.46071 | 0.61429 | 0 | 0 | 2  | 85   |
| GO:0002365 leukocyte chemotaxis involved in immune response                          | 6  | 0.46078 | 1.858 | 0.023 | Molecular    | GO:0002 leukocyte chemotaxis involved in immune response                          | 0.46078 | 0.61429 | 0 | 0 | 6  | 298  |
| GO:0005251 delayed rectifier potassium channel activity                              | 1  | 0.46094 | 0.292 | 0.03  | Molecular    | GO:0005 delayed rectifier potassium channel activity                              | 0.46094 | 0.62664 | 0 | 0 | 1  | 33   |
| GO:0017080 sodium channel regulator activity                                         | 1  | 0.46094 | 0.292 | 0.03  | Molecular    | GO:0017 sodium channel regulator activity                                         | 0.46094 | 0.62664 | 0 | 0 | 1  | 33   |
| GO:0019239 deaminase activity                                                        | 1  | 0.46094 | 0.292 | 0.03  | Molecular    | GO:0019 deaminase activity                                                        | 0.46094 | 0.62664 | 0 | 0 | 1  | 33   |
| GO:0030332 cyclin binding                                                            | 1  | 0.46094 | 0.292 | 0.03  | Molecular    | GO:0030 cyclin binding                                                            | 0.46094 | 0.62664 | 0 | 0 | 1  | 33   |
| GO:0042287 MYHC protein binding                                                      | 1  | 0.46094 | 0.292 | 0.03  | Molecular    | GO:0042 MYHC protein binding                                                      | 0.46094 | 0.62664 | 0 | 0 | 1  | 33   |
| GO:0140662 ATP-dependent protein folding chaperone                                   | 1  | 0.46094 | 0.292 | 0.03  | Molecular    | GO:0140 ATP-dependent protein folding chaperone                                   | 0.46094 | 0.62664 | 0 | 0 | 1  | 33   |
| GO:0032872 regulation of stress-activated MAPK cascade                               | 4  | 0.46097 | 1.238 | 0.021 | Biological   | GO:0032 regulation of stress-activated MAPK cascade                               | 0.46097 | 0.61438 | 0 | 0 | 4  | 191  |
| GO:0090543 Flemming body                                                             | 1  | 0.46152 | 0.297 | 0.029 | Cellular C   | GO:0090 Flemming body                                                             | 0.46152 | 0.66374 | 0 | 0 | 1  | 34   |
| GO:0006986 response to unfolded protein                                              | 3  | 0.46193 | 0.928 | 0.022 | Biological   | GO:0006 response to unfolded protein                                              | 0.46193 | 0.61534 | 0 | 0 | 3  | 138  |
| GO:0034101 erythrocyte homeostasis                                                   | 3  | 0.46193 | 0.928 | 0.022 | Biological   | GO:0034 erythrocyte homeostasis                                                   | 0.46193 | 0.61534 | 0 | 0 | 3  | 138  |
| GO:0006914 autophagy                                                                 | 11 | 0.46233 | 3.406 | 0.019 | Biological   | GO:0006 autophagy                                                                 | 0.46233 | 0.61553 | 0 | 0 | 11 | 568  |
| GO:0061919 process utilizing autophagic mechanism                                    | 11 | 0.46233 | 3.406 | 0.019 | Biological   | GO:0061 process utilizing autophagic mechanism                                    | 0.46233 | 0.61553 | 0 | 0 | 11 | 568  |
| GO:0031098 stress-activated protein kinase signaling cascade                         | 5  | 0.46292 | 1.548 | 0.02  | Biological   | GO:0031 stress-activated protein kinase signaling cascade                         | 0.46292 | 0.61593 | 0 | 0 | 5  | 245  |
| GO:0071216 cellular response to biotic stimulus                                      | 5  | 0.46292 | 1.548 | 0.02  | Biological   | GO:0071 cellular response to biotic stimulus                                      | 0.46292 | 0.61593 | 0 | 0 | 5  | 245  |
| GO:0030320 cellular signal transduction metabolic process                            | 6  | 0.46308 | 1.858 | 0.023 | Molecular    | GO:0030 cellular signal transduction metabolic process                            | 0.46308 | 0.61593 | 0 | 0 | 6  | 298  |
| GO:0030652 coated vesicle membrane                                                   | 4  | 0.46422 | 1.187 | 0.021 | Cellular C   | GO:0030 coated vesicle membrane                                                   | 0.46422 | 0.66583 | 0 | 0 | 4  | 194  |
| GO:0010959 regulation of metal ion transport                                         | 8  | 0.46482 | 2.477 | 0.02  | Biological   | GO:0010 regulation of metal ion transport                                         | 0.46482 | 0.61593 | 0 | 0 | 8  | 407  |
| GO:0007369 gastrulation                                                              | 4  | 0.46497 | 1.238 | 0.021 | Biological   | GO:0007 gastrulation                                                              | 0.46497 | 0.61593 | 0 | 0 | 4  | 192  |
| GO:0002021 response to dietary excess                                                | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0002 response to dietary excess                                                | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0003382 epithelial cell morphogenesis                                             | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0003 epithelial cell morphogenesis                                             | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0009012 nucleobase metabolic process                                              | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0009 nucleobase metabolic process                                              | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0030212 hyaluronan metabolic process                                              | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0030 hyaluronan metabolic process                                              | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0033561 regulation of water loss via skin                                         | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0033 regulation of water loss via skin                                         | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0035025 positive regulation of Rho protein signal transduction                    | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0035 positive regulation of Rho protein signal transduction                    | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0035308 negative regulation of protein dephosphorylation                          | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0035 negative regulation of protein dephosphorylation                          | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0036475 neuron death in response to oxidative stress                              | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0036 neuron death in response to oxidative stress                              | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0039528 cytoplasmic pattern recognition receptor signaling pathway                | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0039 cytoplasmic pattern recognition receptor signaling pathway in response    | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0044546 NLRP3 inflammasome complex assembly                                       | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0044 NLRP3 inflammasome complex assembly                                       | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0046255 response to pain                                                          | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0046 response to pain                                                          | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0048841 regulation of axon extension involved in axon guidance                    | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0048 regulation of axon extension involved in axon guidance                    | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0060074 synapse maturation                                                        | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0060 synapse maturation                                                        | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0071354 cellular response to interleukin-6                                        | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0071 cellular response to interleukin-6                                        | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0080111 DNA demethylation                                                         | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:0080 DNA demethylation                                                         | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:1903514 release of sequestered calcium ion into cytosol by endoplasmic reticulum  | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:1903 release of sequestered calcium ion into cytosol by endoplasmic reticulum  | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:2004046 positive regulation of T cell migration                                   | 1  | 0.46534 | 0.31  | 0.029 | Biological   | GO:2004 positive regulation of T cell migration                                   | 0.46534 | 0.61593 | 0 | 0 | 1  | 34   |
| GO:0021954 central nervous system neuron development                                 | 2  | 0.46675 | 0.619 | 0.023 | Biological   | GO:0021 central nervous system neuron development                                 | 0.46675 | 0.6173  | 0 | 0 | 2  | 86   |
| GO:0035050 embryonic heart tube development                                          | 2  | 0.46675 | 0.619 | 0.023 | Biological   | GO:0035 embryonic heart tube development                                          | 0.46675 | 0.6173  | 0 | 0 | 2  | 86   |
| GO:0048041 focal adhesion assembly                                                   | 2  | 0.46675 | 0.619 | 0.023 | Biological   | GO:0048 focal adhesion assembly                                                   | 0.46675 | 0.6173  | 0 | 0 | 2  | 86   |
| GO:0045334 clathrin-coated endocytic vesicle                                         | 2  | 0.46685 | 0.593 | 0.023 | Cellular C   | GO:0045 clathrin-coated endocytic vesicle                                         | 0.46685 | 0.66782 | 0 | 0 | 2  | 87   |
| GO:0051640 organelle localization                                                    | 11 | 0.46698 | 3.406 | 0.019 | Biological   | GO:0051 organelle localization                                                    | 0.46698 | 0.61744 | 0 | 0 | 11 | 568  |
| GO:0001701 in utero embryonic development                                            | 8  | 0.46756 | 2.477 | 0.02  | Biological   | GO:0001 in utero embryonic development                                            | 0.46756 | 0.61804 | 0 | 0 | 8  | 408  |
| GO:0006366 transcription by RNA polymerase II                                        | 50 | 0.46772 | 15.48 | 0.019 | Biological   | GO:0006 transcription by RNA polymerase II                                        | 0.46772 | 0.6181  | 0 | 0 | 50 | 2693 |
| GO:0016810 hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds     | 3  | 0.46799 | 0.877 | 0.022 | Molecular    | GO:0016 hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds     | 0.46799 | 0.63524 | 0 | 0 | 3  | 137  |
| GO:0007185 neuropeptide receptor binding                                             | 2  | 0.47095 | 0.292 | 0.029 | Molecular    | GO:0007 neuropeptide receptor binding                                             | 0.47095 | 0.63625 | 0 | 0 | 2  | 86   |
| GO:0071889 14-3-3 protein binding                                                    | 2  | 0.47095 | 0.292 | 0.029 | Molecular    | GO:0071 14-3-3 protein binding                                                    | 0.47095 | 0.63625 | 0 | 0 | 2  | 86   |
| GO:0090482 vitamin transmembrane transporter activity                                | 1  | 0.47095 | 0.292 | 0.029 | Molecular    | GO:0090 vitamin transmembrane transporter activity                                | 0.47095 | 0.63625 | 0 | 0 | 1  | 34   |
| GO:1990752 microtubule end                                                           | 3  | 0.47124 | 0.297 | 0.029 | Cellular C   | GO:1990 microtubule end                                                           | 0.47124 | 0.6723  | 0 | 0 | 3  | 140  |
| GO:0007269 neurotransmitter secretion                                                | 3  | 0.47134 | 0.929 | 0.021 | Biological   | GO:0007 neurotransmitter secretion                                                | 0.47134 | 0.62255 | 0 | 0 | 3  | 140  |
| GO:0096943 signal release from synapse                                               | 3  | 0.47134 | 0.929 | 0.021 | Biological   | GO:0096 signal release from synapse                                               | 0.47134 | 0.62255 | 0 | 0 | 3  | 140  |
| GO:0032370 positive regulation of lipid transport                                    | 2  | 0.47275 | 0.619 | 0.023 | Biological   | GO:0032 positive regulation of lipid transport                                    | 0.47275 | 0.62392 | 0 | 0 | 2  | 87   |
| GO:0042632 cholesterol homeostasis                                                   | 2  | 0.47275 | 0.619 | 0.023 | Biological   | GO:0042 cholesterol homeostasis                                                   | 0.47275 | 0.62392 | 0 | 0 | 2  | 87   |
| GO:0070301 cellular response to hydrogen peroxide                                    | 2  | 0.47275 | 0.619 | 0.023 | Biological   | GO:0070 cellular response to hydrogen peroxide                                    | 0.47275 | 0.62392 | 0 | 0 | 2  | 87   |
| GO:0016798 hydrolase activity, acting on glycosyl bonds                              | 3  | 0.47276 | 0.877 | 0.    |              |                                                                                   |         |         |   |   |    |      |

|                                                                            |    |         |       |      |            |                                                                                |         |         |   |   |    |      |
|----------------------------------------------------------------------------|----|---------|-------|------|------------|--------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0045111 intermediate filament cytoskeleton                              | 5  | 0.48787 | 1.484 | 0.02 | Cellular C | GO:00445 intermediate filament cytoskeleton                                    | 0.48787 | 0.68217 | 0 | 0 | 5  | 255  |
| GO:0032388 positive regulation of intracellular transport                  | 4  | 0.48871 | 1.238 | 0.02 | Biological | GO:00322 positive regulation of intracellular transport                        | 0.48871 | 0.63657 | 0 | 0 | 4  | 188  |
| GO:0001508 action potential                                                | 3  | 0.48892 | 0.928 | 0.02 | Biological | GO:00011 action potential                                                      | 0.48892 | 0.63781 | 0 | 0 | 3  | 144  |
| GO:0071322 cellular response to carbohydrate stimulus                      | 3  | 0.48992 | 0.929 | 0.02 | Biological | GO:00711 cellular response to carbohydrate stimulus                            | 0.48992 | 0.63781 | 0 | 0 | 3  | 144  |
| GO:0048787 presynaptic active zone membrane                                | 1  | 0.49017 | 0.297 | 0.02 | Cellular C | GO:00408 presynaptic active zone membrane                                      | 0.49017 | 0.68217 | 0 | 0 | 1  | 37   |
| GO:0030134 COPII-coated ER to Golgi transport vesicle                      | 2  | 0.49033 | 0.593 | 0.02 | Cellular C | GO:00300 COPII-coated ER to Golgi transport vesicle                            | 0.49033 | 0.68217 | 0 | 0 | 2  | 91   |
| GO:0016814 hydrolase activity, acting on carbon-nitrogen (but not peptide) | 1  | 0.49041 | 0.292 | 0.02 | Molecular  | GO:00166 hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds | 0.49041 | 0.65238 | 0 | 0 | 1  | 36   |
| GO:0030291 protein serine/threonine kinase inhibitor activity              | 1  | 0.49041 | 0.292 | 0.02 | Biological | GO:00301 protein serine/threonine kinase inhibitor activity                    | 0.49041 | 0.65238 | 0 | 0 | 1  | 36   |
| GO:0043394 proteoglycan binding                                            | 1  | 0.49041 | 0.292 | 0.02 | Biological | GO:00433 proteoglycan binding                                                  | 0.49041 | 0.65238 | 0 | 0 | 1  | 36   |
| GO:0033273 response to vitamin                                             | 2  | 0.4905  | 0.619 | 0.02 | Biological | GO:00333 response to vitamin                                                   | 0.4905  | 0.63791 | 0 | 0 | 2  | 90   |
| GO:0050886 endocrine process                                               | 2  | 0.4905  | 0.619 | 0.02 | Biological | GO:00500 endocrine process                                                     | 0.4905  | 0.63791 | 0 | 0 | 2  | 90   |
| GO:0071277 cellular response to calcium ion                                | 2  | 0.4905  | 0.619 | 0.02 | Biological | GO:00711 cellular response to calcium ion                                      | 0.4905  | 0.63791 | 0 | 0 | 2  | 90   |
| GO:2000117 negative regulation of cysteine-type endopeptidase activity     | 2  | 0.4905  | 0.619 | 0.02 | Biological | GO:20001 negative regulation of cysteine-type endopeptidase activity           | 0.4905  | 0.63791 | 0 | 0 | 2  | 90   |
| GO:0034702 ion channel complex                                             | 6  | 0.49091 | 1.78  | 0.01 | Cellular C | GO:00304 ion channel complex                                                   | 0.49091 | 0.68217 | 0 | 0 | 6  | 311  |
| GO:0070925 organelle assembly                                              | 18 | 0.49124 | 5.573 | 0.01 | Biological | GO:00700 organelle assembly                                                    | 0.49124 | 0.6387  | 0 | 0 | 18 | 963  |
| GO:0003341 cilium movement                                                 | 4  | 0.49263 | 1.238 | 0.02 | Biological | GO:00030 cilium movement                                                       | 0.49263 | 0.63963 | 0 | 0 | 4  | 199  |
| GO:0071757 regulation of exocytosis                                        | 4  | 0.49263 | 1.238 | 0.02 | Biological | GO:00710 regulation of exocytosis                                              | 0.49263 | 0.63963 | 0 | 0 | 4  | 199  |
| GO:0003714 transcription repressor activity                                | 4  | 0.49368 | 1.17  | 0.02 | Biological | GO:00036 transcription repressor activity                                      | 0.49368 | 0.65406 | 0 | 0 | 4  | 196  |
| GO:0008514 organic anion transmembrane transporter activity                | 4  | 0.49368 | 1.17  | 0.02 | Molecular  | GO:00080 organic anion transmembrane transporter activity                      | 0.49368 | 0.65406 | 0 | 0 | 4  | 196  |
| GO:0030135 coated vesicle                                                  | 6  | 0.49402 | 1.78  | 0.01 | Cellular C | GO:00300 coated vesicle                                                        | 0.49402 | 0.68471 | 0 | 0 | 6  | 312  |
| GO:0003230 cardiac atrium development                                      | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00030 cardiac atrium development                                            | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0009595 detection of biotic stimulus                                    | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00090 detection of biotic stimulus                                          | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0016486 peptide hormone processing                                      | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00160 peptide hormone processing                                            | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0019068 viron assembly                                                  | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00190 viron assembly                                                        | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0021696 cerebellar cortex morphogenesis                                 | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00210 cerebellar cortex morphogenesis                                       | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0032965 regulation of collagen biosynthetic process                     | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00320 regulation of collagen biosynthetic process                           | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0032800 response to vitamin D                                           | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00323 response to vitamin D                                                 | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0045191 regulation of isotype switching                                 | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00450 regulation of isotype switching                                       | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0045652 regulation of megakaryocyte differentiation                     | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00455 regulation of megakaryocyte differentiation                           | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0046320 regulation of fatty acid oxidation                              | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00460 regulation of fatty acid oxidation                                    | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0060122 inner ear receptor cell stereocilium organization               | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00600 inner ear receptor cell stereocilium organization                     | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0070741 response to interleukin-6                                       | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00700 response to interleukin-6                                             | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0090504 epiboly                                                         | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:00900 epiboly                                                               | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:1900777 negative regulation of cellular response to insulin stimulus    | 1  | 0.49411 | 0.31  | 0.02 | Biological | GO:19000 negative regulation of cellular response to insulin stimulus          | 0.49411 | 0.63963 | 0 | 0 | 1  | 37   |
| GO:0043543 protein acylation                                               | 5  | 0.49438 | 1.548 | 0.02 | Biological | GO:00430 protein acylation                                                     | 0.49438 | 0.63963 | 0 | 0 | 5  | 254  |
| GO:0010324 membrane invagination                                           | 3  | 0.49451 | 0.929 | 0.02 | Biological | GO:00100 membrane invagination                                                 | 0.49451 | 0.63963 | 0 | 0 | 3  | 145  |
| GO:0034341 response to interferon-gamma                                    | 3  | 0.49451 | 0.929 | 0.02 | Biological | GO:00340 response to interferon-gamma                                          | 0.49451 | 0.63963 | 0 | 0 | 3  | 145  |
| GO:0050571 positive regulation of lymphocyte proliferation                 | 3  | 0.49451 | 0.929 | 0.02 | Biological | GO:00500 positive regulation of lymphocyte proliferation                       | 0.49451 | 0.63963 | 0 | 0 | 3  | 145  |
| GO:0019955 cytokine binding                                                | 3  | 0.49628 | 0.877 | 0.02 | Molecular  | GO:00190 cytokine binding                                                      | 0.49628 | 0.65406 | 0 | 0 | 3  | 143  |
| GO:0140375 immune receptor activity                                        | 3  | 0.49628 | 0.877 | 0.02 | Molecular  | GO:01400 immune receptor activity                                              | 0.49628 | 0.65406 | 0 | 0 | 3  | 143  |
| GO:0046883 regulation of hormone secretion                                 | 5  | 0.49783 | 1.548 | 0.02 | Biological | GO:00460 regulation of hormone secretion                                       | 0.49783 | 0.64375 | 0 | 0 | 5  | 255  |
| GO:0001889 liver development                                               | 3  | 0.49909 | 0.929 | 0.02 | Biological | GO:00010 liver development                                                     | 0.49909 | 0.64521 | 0 | 0 | 3  | 146  |
| GO:0000217 DNA secondary structure binding                                 | 1  | 0.49987 | 0.292 | 0.02 | Biological | GO:00002 DNA secondary structure binding                                       | 0.49987 | 0.65406 | 0 | 0 | 1  | 37   |
| GO:0008200 ion channel inhibitor activity                                  | 1  | 0.49987 | 0.292 | 0.02 | Biological | GO:00080 ion channel inhibitor activity                                        | 0.49987 | 0.65406 | 0 | 0 | 1  | 37   |
| GO:0015248 sterol transporter activity                                     | 1  | 0.49987 | 0.292 | 0.02 | Molecular  | GO:00150 sterol transporter activity                                           | 0.49987 | 0.65406 | 0 | 0 | 1  | 37   |
| GO:0016409 palmitoyltransferase activity                                   | 1  | 0.49987 | 0.292 | 0.02 | Molecular  | GO:00160 palmitoyltransferase activity                                         | 0.49987 | 0.65406 | 0 | 0 | 1  | 37   |
| GO:0045505 dynein intermediate chain binding                               | 1  | 0.49987 | 0.292 | 0.02 | Molecular  | GO:00450 dynein intermediate chain binding                                     | 0.49987 | 0.65406 | 0 | 0 | 1  | 37   |
| GO:0038023 protein receptor activity                                       | 28 | 0.49999 | 8.187 | 0.01 | Molecular  | GO:00380 protein receptor activity                                             | 0.49999 | 0.65406 | 0 | 0 | 28 | 1419 |
| GO:0008089 molecular transducer activity                                   | 28 | 0.49999 | 8.187 | 0.01 | Molecular  | GO:00080 molecular transducer activity                                         | 0.49999 | 0.65406 | 0 | 0 | 28 | 1419 |
| GO:0035304 regulation of protein dephosphorylation                         | 2  | 0.50213 | 0.619 | 0.02 | Biological | GO:00350 regulation of protein dephosphorylation                               | 0.50213 | 0.64758 | 0 | 0 | 2  | 92   |
| GO:0045666 positive regulation of neuron differentiation                   | 2  | 0.50213 | 0.619 | 0.02 | Biological | GO:00450 positive regulation of neuron differentiation                         | 0.50213 | 0.64758 | 0 | 0 | 2  | 92   |
| GO:0060270 DNA replication initiation                                      | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00600 DNA replication initiation                                            | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0010623 negative regulation of phosphatase activity                     | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00100 negative regulation of phosphatase activity                           | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0019432 triglyceride biosynthetic process                               | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00190 triglyceride biosynthetic process                                     | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0030279 negative regulation of ossification                             | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00300 negative regulation of ossification                                   | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0035883 enteroendocrine cell differentiation                            | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00350 enteroendocrine cell differentiation                                  | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0042401 cellular biogenic amine biosynthetic process                    | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00420 cellular biogenic amine biosynthetic process                          | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0043388 positive cell selection                                         | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00430 positive cell selection                                               | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0044743 protein transmembrane import into intracellular organelle       | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00440 protein transmembrane import into intracellular organelle             | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0045616 regulation of keratinocyte differentiation                      | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00450 regulation of keratinocyte differentiation                            | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0045746 negative regulation of Notch signaling pathway                  | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00450 negative regulation of Notch signaling pathway                        | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0045773 positive regulation of axon extension                           | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00450 positive regulation of axon extension                                 | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:004846 axon extension involved in axon guidance                         | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00480 axon extension involved in axon guidance                              | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0050654 chondroitin sulfate proteoglycan metabolic process              | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00500 chondroitin sulfate proteoglycan metabolic process                    | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0060043 regulation of cardiac muscle cell proliferation                 | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00600 regulation of cardiac muscle cell proliferation                       | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0070306 lens fiber cell differentiation                                 | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:00700 lens fiber cell differentiation                                       | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:1902284 neuron projection extension involved in neuron projection       | 1  | 0.50335 | 0.31  | 0.02 | Biological | GO:19020 neuron projection extension involved in neuron projection guidance    | 0.50335 | 0.64758 | 0 | 0 | 1  | 38   |
| GO:0060718 regulation of embryonic development                             | 3  | 0.50364 | 0.929 | 0.02 | Biological | GO:00600 regulation of embryonic development                                   | 0.50364 | 0.64758 | 0 | 0 | 3  | 147  |
| GO:0012016 regulation of cold-induced thermogenesis                        | 3  | 0.50364 | 0.929 | 0.02 | Biological | GO:00120 regulation of cold-induced thermogenesis                              | 0.50364 | 0.64758 | 0 | 0 | 3  | 147  |
| GO:1903900 regulation of viral life cycle                                  | 3  | 0.50364 | 0.929 | 0.02 | Biological | GO:19030 regulation of viral life cycle                                        | 0.50364 | 0.64758 | 0 | 0 | 3  | 147  |
| GO:0071396 cellular response to lipid                                      | 11 | 0.5039  | 3.406 | 0.01 | Biological | GO:00710 cellular response to lipid                                            | 0.5039  | 0.64774 | 0 | 0 | 11 | 586  |
| GO:0043393 regulation of protein binding                                   | 4  | 0.5043  | 1.238 | 0.02 | Biological | GO:00430 regulation of protein binding                                         | 0.5043  | 0.64809 | 0 | 0 | 4  | 202  |
| GO:051704 multi-organism process                                           | 21 | 0.5046  | 6.502 | 0.01 | Biological | GO:05170 multi-organism process                                                | 0.5046  | 0.64883 | 0 | 0 | 21 | 1135 |
| GO:0048511 rhythmic process                                                | 6  | 0.50503 | 1.858 | 0.01 | Biological | GO:00480 rhythmic process                                                      | 0.50503 | 0.6487  | 0 | 0 | 6  | 312  |
| GO:0008276 protein methyltransferase activity                              | 2  | 0.50512 | 0.585 | 0.02 | Molecular  | GO:00080 protein methyltransferase activity                                    | 0.50512 | 0.65001 | 0 | 0 | 2  | 91   |
| GO:0140657 ATP-dependent activity                                          | 11 | 0.50529 | 3.216 | 0.01 | Molecular  | GO:01400 ATP-dependent activity                                                | 0.50529 | 0.65001 | 0 | 0 | 11 | 577  |
| GO:0030659 cytoplasmic vesicle membrane                                    | 22 | 0.50551 | 6.528 | 0.01 | Cellular C | GO:00300 cytoplasmic vesicle membrane                                          | 0.50551 | 0.65983 | 0 | 0 | 22 | 1204 |
| GO:0045995 regulation of embryonic development                             | 2  | 0.50787 | 0.619 | 0.02 | Biological | GO:00450 regulation of embryonic development                                   | 0.50787 | 0.65156 | 0 | 0 | 2  | 92   |
| GO:0050829 defense response to Gram-negative bacterium                     | 2  | 0.50787 | 0.619 | 0.02 | Biological | GO:00500 defense response to Gram-negative bacterium                           | 0.50787 | 0.65156 | 0 | 0 | 2  | 93   |
| GO:0051781 positive regulation of cell division                            | 2  | 0.50787 | 0.619 | 0.02 | Biological | GO:00510 positive regulation of cell division                                  | 0.50787 | 0.65156 | 0 | 0 | 2  | 93   |
| GO:0002791 regulation of peptide secretion                                 | 4  | 0.50817 | 1.238 | 0.02 | Biological | GO:00020 regulation of peptide secretion                                       | 0.50817 | 0.65156 | 0 | 0 | 4  | 203  |
| GO:0095054 synaptic vesicle cycle                                          | 4  | 0.50817 | 1.238 | 0.02 | Biological | GO:00950 synaptic vesicle cycle                                                | 0.50817 | 0.65156 | 0 | 0 | 4  | 203  |
| GO:0006977 nucleus organization                                            | 3  | 0.50818 | 0.929 | 0.02 | Biological | GO:00060 nucleus organization                                                  | 0.50818 | 0.65156 | 0 | 0 | 3  | 148  |
| GO:006106 cold-induced thermogenesis                                       | 3  | 0.50818 | 0.929 | 0.02 | Biological | GO:00610 cold-induced thermogenesis                                            | 0.50818 | 0.65156 | 0 | 0 | 3  | 148  |
| GO:0070461 SAGA-type complex                                               | 1  | 0.50842 | 0.297 | 0.02 | Cellular C | GO:00700 SAGA-type complex                                                     | 0.50842 | 0.70104 | 0 | 0 | 1  | 39   |
| GO:0004623 phospholipase A2 activity                                       | 1  | 0.50916 | 0.292 | 0.02 | Molecular  | GO:00040 phospholipase A2 activity                                             | 0.50916 | 0.66033 | 0 | 0 | 1  | 38   |
| GO:0016248 channel inhibitor activity                                      | 1  | 0.50916 | 0.292 | 0.02 | Molecular  | GO:00160 channel inhibitor activity                                            | 0.50916 | 0.66033 | 0 | 0 | 1  | 38   |
| GO:0042887 amide transmembrane transporter activity                        | 1  | 0.50916 | 0.292 | 0.02 | Molecular  | GO:00420 amide transmembrane transporter activity                              | 0.50916 | 0.66033 | 0 | 0 | 1  | 38   |
| GO:0016301 kinase activity                                                 | 15 | 0.50935 | 4.366 | 0.01 | Molecular  | GO:00160 kinase activity                                                       | 0.50935 | 0.66033 | 0 | 0 | 15 | 795  |
| GO:0005768 endosome                                                        | 19 | 0.50982 | 5.638 | 0.01 | Cellular C | GO:00050 endosome                                                              | 0.50982 | 0.70117 | 0 | 0 | 19 | 1040 |
| GO:0005253 anion channel activity                                          | 2  | 0.51094 | 0.585 | 0.02 | Molecular  | GO:00050 anion channel activity                                                | 0.51094 | 0.66041 | 0 | 0 | 2  | 92   |
| GO:0072341 modified amino                                                  |    |         |       |      |            |                                                                                |         |         |   |   |    |      |

|                                                                              |     |         |        |       |            |                                                                                  |         |         |   |   |     |      |
|------------------------------------------------------------------------------|-----|---------|--------|-------|------------|----------------------------------------------------------------------------------|---------|---------|---|---|-----|------|
| GO:007296 sarcolemmal reticulum calcium ion transport                        | 1   | 0.52133 | 0.31   | 0.025 | Biological | GO:007070 sarcolemmal reticulum calcium ion transport                            | 0.52133 | 0.65996 | 0 | 0 | 1   | 40   |
| GO:0071392 cellular response to estradiol stimulus                           | 1   | 0.52133 | 0.31   | 0.025 | Biological | GO:007071 cellular response to estradiol stimulus                                | 0.52133 | 0.65996 | 0 | 0 | 1   | 40   |
| GO:014048 signaling receptor ligand precursor processing                     | 1   | 0.52133 | 0.31   | 0.025 | Biological | GO:014049 signaling receptor ligand precursor processing                         | 0.52133 | 0.65996 | 0 | 0 | 1   | 40   |
| GO:1901532 regulation of hematopoietic progenitor cell differentiation       | 1   | 0.52133 | 0.31   | 0.025 | Biological | GO:1901533 regulation of hematopoietic progenitor cell differentiation           | 0.52133 | 0.65996 | 0 | 0 | 1   | 40   |
| GO:2000279 negative regulation of DNA biosynthetic process                   | 1   | 0.52133 | 0.31   | 0.025 | Biological | GO:2000280 negative regulation of DNA biosynthetic process                       | 0.52133 | 0.65996 | 0 | 0 | 1   | 40   |
| GO:0015318 inorganic molecular entity transmembrane transporter activity     | 14  | 0.52177 | 0.094  | 0.019 | Molecular  | GO:0015319 inorganic molecular entity transmembrane transporter activity         | 0.52177 | 0.66449 | 0 | 0 | 14  | 747  |
| GO:0032956 regulation of actin cytoskeleton organization                     | 7   | 0.52247 | 2.167  | 0.019 | Biological | GO:0032957 regulation of actin cytoskeleton organization                         | 0.52247 | 0.66122 | 0 | 0 | 7   | 373  |
| GO:1906023 response to cytokine inhibitory factor                            | 1   | 0.52486 | 1.518  | 0.019 | Biological | GO:1906024 response to cytokine inhibitory factor                                | 0.52486 | 0.66408 | 0 | 0 | 1   | 98   |
| GO:0035986 monosaccharide metabolic process                                  | 5   | 0.52514 | 1.548  | 0.019 | Biological | GO:0035987 monosaccharide metabolic process                                      | 0.52514 | 0.66427 | 0 | 0 | 5   | 263  |
| GO:0032391 photoreceptor connecting cilium                                   | 1   | 0.52602 | 0.297  | 0.024 | Cellular   | GO:0032392 photoreceptor connecting cilium                                       | 0.52602 | 0.70886 | 0 | 0 | 1   | 41   |
| GO:0032590 dendrite membrane                                                 | 1   | 0.52602 | 0.297  | 0.024 | Cellular   | GO:0032591 dendrite membrane                                                     | 0.52602 | 0.70886 | 0 | 0 | 1   | 41   |
| GO:0019599 regulation of cytokine-mediated signaling pathway                 | 3   | 0.52609 | 0.929  | 0.02  | Biological | GO:0019600 regulation of cytokine-mediated signaling pathway                     | 0.52609 | 0.66514 | 0 | 0 | 3   | 152  |
| GO:0010675 positive regulation of cytoskeletal metabolic process             | 3   | 0.52609 | 0.929  | 0.02  | Biological | GO:0010676 positive regulation of cytoskeletal metabolic process                 | 0.52609 | 0.66514 | 0 | 0 | 3   | 152  |
| GO:0005547 phosphatidylinositol-3,4,5-trisphosphate binding                  | 1   | 0.52723 | 0.292  | 0.025 | Molecular  | GO:0005548 phosphatidylinositol-3,4,5-trisphosphate binding                      | 0.52723 | 0.66849 | 0 | 0 | 1   | 40   |
| GO:0016620 oxidoreductase activity, acting on the aldehyde or oxo group      | 1   | 0.52723 | 0.292  | 0.025 | Molecular  | GO:0016621 oxidoreductase activity, acting on the aldehyde or oxo group of donor | 0.52723 | 0.66849 | 0 | 0 | 1   | 40   |
| GO:0019213 deacetylase activity                                              | 1   | 0.52723 | 0.292  | 0.025 | Molecular  | GO:0019214 deacetylase activity                                                  | 0.52723 | 0.66849 | 0 | 0 | 1   | 40   |
| GO:0060205 cytoplasmic vesicle lumen                                         | 6   | 0.52775 | 1.78   | 0.019 | Cellular   | GO:0060206 cytoplasmic vesicle lumen                                             | 0.52775 | 0.70942 | 0 | 0 | 6   | 323  |
| GO:0042391 regulation of membrane potential                                  | 8   | 0.52983 | 2.477  | 0.019 | Biological | GO:0042392 regulation of membrane potential                                      | 0.52983 | 0.66725 | 0 | 0 | 8   | 431  |
| GO:0034705 potassium channel complex                                         | 2   | 0.52982 | 0.593  | 0.02  | Cellular   | GO:0034706 potassium channel complex                                             | 0.52982 | 0.71041 | 0 | 0 | 2   | 98   |
| GO:0002714 positive regulation of B cell mediated immunity                   | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0002715 positive regulation of B cell mediated immunity                       | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0002891 positive regulation of immunoglobulin mediated immune response    | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0002892 positive regulation of immunoglobulin mediated immune response        | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0030866 cortical actin cytoskeleton organization                          | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0030867 cortical actin cytoskeleton organization                              | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0031053 regulation of histone deacetylation                               | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0031054 regulation of histone deacetylation                                   | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0032509 endosome transport via multivesicular body sorting pathway        | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0032510 endosome transport via multivesicular body sorting pathway            | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0032733 positive regulation of interleukin-10 production                  | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0032734 positive regulation of interleukin-10 production                      | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0042554 superoxide anion generation                                       | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0042555 superoxide anion generation                                           | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0043403 skeletal muscle tissue regeneration                               | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0043404 skeletal muscle tissue regeneration                                   | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0045479 positive regulation of cytoskeletal metabolic process             | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0045480 positive regulation of cytoskeletal metabolic process                 | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0045622 regulation of T-helper cell differentiation                       | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0045623 regulation of T-helper cell differentiation                           | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0060338 regulation of type I interferon-mediated signaling pathway        | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0060339 regulation of type I interferon-mediated signaling pathway            | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0060412 ventricular septum morphogenesis                                  | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0060413 ventricular septum morphogenesis                                      | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0086031 regulation of heart rate by cardiac conduction                    | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0086032 regulation of heart rate by cardiac conduction                        | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0140487 integrated regulation of cell cycle signaling                     | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:0140488 integrated regulation of cell cycle signaling                         | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:1904037 positive regulation of epithelial cell apoptotic process          | 1   | 0.53008 | 0.31   | 0.024 | Biological | GO:1904038 positive regulation of epithelial cell apoptotic process              | 0.53008 | 0.66725 | 0 | 0 | 1   | 41   |
| GO:0060497 protein lipidation                                                | 2   | 0.53043 | 0.619  | 0.021 | Biological | GO:0060498 protein lipidation                                                    | 0.53043 | 0.66725 | 0 | 0 | 2   | 97   |
| GO:0016079 synaptic vesicle exocytosis                                       | 2   | 0.53043 | 0.619  | 0.021 | Biological | GO:0016080 synaptic vesicle exocytosis                                           | 0.53043 | 0.66725 | 0 | 0 | 2   | 97   |
| GO:0016575 histone deacetylation                                             | 2   | 0.53043 | 0.619  | 0.021 | Biological | GO:0016576 histone deacetylation                                                 | 0.53043 | 0.66725 | 0 | 0 | 2   | 97   |
| GO:0043255 positive regulation of carbohydrate biosynthetic process          | 7   | 0.53043 | 0.619  | 0.021 | Biological | GO:0043256 positive regulation of carbohydrate biosynthetic process              | 0.53043 | 0.66725 | 0 | 0 | 7   | 319  |
| GO:0015711 organic anion transport                                           | 2   | 0.53096 | 2.167  | 0.019 | Biological | GO:0015712 organic anion transport                                               | 0.53096 | 0.66775 | 0 | 0 | 7   | 376  |
| GO:0032412 regulation of ion transmembrane transporter activity              | 5   | 0.53187 | 1.548  | 0.019 | Biological | GO:0032413 regulation of ion transmembrane transporter activity                  | 0.53187 | 0.66872 | 0 | 0 | 5   | 265  |
| GO:0008202 steroid metabolic process                                         | 6   | 0.53279 | 1.858  | 0.019 | Biological | GO:0008203 steroid metabolic process                                             | 0.53279 | 0.66971 | 0 | 0 | 6   | 321  |
| GO:0016653 peptide receptor activity                                         | 3   | 0.5328  | 0.877  | 0.02  | Molecular  | GO:0016654 peptide receptor activity                                             | 0.5328  | 0.67456 | 0 | 0 | 3   | 151  |
| GO:0031983 vesicle lumen                                                     | 1   | 0.53379 | 1.78   | 0.019 | Cellular   | GO:0031984 vesicle lumen                                                         | 0.53379 | 0.71296 | 0 | 0 | 1   | 325  |
| GO:0089866 hippocampal mossy fiber to CA3 synapse                            | 1   | 0.53458 | 0.297  | 0.024 | Cellular   | GO:0089867 hippocampal mossy fiber to CA3 synapse                                | 0.53458 | 0.71296 | 0 | 0 | 1   | 42   |
| GO:0032869 cellular response to insulin stimulus                             | 4   | 0.53483 | 1.238  | 0.019 | Biological | GO:0032870 cellular response to insulin stimulus                                 | 0.53483 | 0.67187 | 0 | 0 | 4   | 210  |
| GO:0051216 cartilage development                                             | 4   | 0.53483 | 1.238  | 0.019 | Biological | GO:0051217 cartilage development                                                 | 0.53483 | 0.67187 | 0 | 0 | 4   | 210  |
| GO:2001236 regulation of extrinsic apoptotic signaling pathway               | 3   | 0.53491 | 0.929  | 0.019 | Biological | GO:2001237 regulation of extrinsic apoptotic signaling pathway                   | 0.53491 | 0.67187 | 0 | 0 | 3   | 154  |
| GO:0051924 regulation of calcium ion transport                               | 5   | 0.53522 | 1.548  | 0.019 | Biological | GO:0051925 regulation of calcium ion transport                                   | 0.53522 | 0.672   | 0 | 0 | 5   | 266  |
| GO:0143522 export from cell                                                  | 16  | 0.53542 | 4.954  | 0.018 | Biological | GO:0143523 export from cell                                                      | 0.53542 | 0.672   | 0 | 0 | 16  | 877  |
| GO:0012506 vesicle membrane                                                  | 22  | 0.53594 | 6.528  | 0.018 | Cellular   | GO:0012507 vesicle membrane                                                      | 0.53594 | 0.71296 | 0 | 0 | 22  | 1223 |
| GO:0043279 response to alkaloid                                              | 2   | 0.53596 | 0.619  | 0.02  | Biological | GO:0043280 response to alkaloid                                                  | 0.53596 | 0.672   | 0 | 0 | 2   | 98   |
| GO:0044284 cellular polysaccharide metabolic process                         | 2   | 0.53596 | 0.619  | 0.02  | Biological | GO:0044285 cellular polysaccharide metabolic process                             | 0.53596 | 0.672   | 0 | 0 | 2   | 98   |
| GO:0045087 positive regulation of cell cycle signaling                       | 1   | 0.53596 | 0.619  | 0.02  | Biological | GO:0045088 positive regulation of cell cycle signaling                           | 0.53596 | 0.672   | 0 | 0 | 1   | 42   |
| GO:0012062 positive regulation of cold-induced thermogenesis                 | 2   | 0.53596 | 0.619  | 0.02  | Biological | GO:0012063 positive regulation of cold-induced thermogenesis                     | 0.53596 | 0.672   | 0 | 0 | 2   | 98   |
| GO:2001237 negative regulation of extrinsic apoptotic signaling pathway      | 2   | 0.53596 | 0.619  | 0.02  | Biological | GO:2001238 negative regulation of extrinsic apoptotic signaling pathway          | 0.53596 | 0.672   | 0 | 0 | 2   | 98   |
| GO:0046915 transition metal ion transmembrane transporter activity           | 1   | 0.53601 | 0.292  | 0.024 | Molecular  | GO:0046916 transition metal ion transmembrane transporter activity               | 0.53601 | 0.67665 | 0 | 0 | 1   | 41   |
| GO:0048487 beta-tubulin binding                                              | 1   | 0.53601 | 0.292  | 0.024 | Molecular  | GO:0048488 beta-tubulin binding                                                  | 0.53601 | 0.67665 | 0 | 0 | 1   | 41   |
| GO:0008021 synaptic vesicle                                                  | 4   | 0.53687 | 1.187  | 0.019 | Cellular   | GO:0008022 synaptic vesicle                                                      | 0.53687 | 0.6732  | 0 | 0 | 4   | 213  |
| GO:0006040 amino sugar metabolic process                                     | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:0006041 amino sugar metabolic process                                         | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:0007099 centriole replication                                             | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:0007099 centriole replication                                                 | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:0010712 regulation of collagen metabolic process                          | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:0010713 regulation of collagen metabolic process                              | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:0010830 regulation of myofibril differentiation                           | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:0010831 regulation of myofibril differentiation                               | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:0140144 negative regulation of gliogenesis                                | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:0140145 negative regulation of gliogenesis                                    | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:0042119 neutrophil activation                                             | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:0042120 neutrophil activation                                                 | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:0050892 intestinal absorption                                             | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:0050893 intestinal absorption                                                 | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:0050913 sensory perception of bitter taste                                | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:0050914 sensory perception of bitter taste                                    | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:0012078 steroid hormone biosynthetic process                              | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:0012079 steroid hormone biosynthetic process                                  | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:1902714 regulation of phospholipase C activity                            | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:1902715 regulation of phospholipase C activity                                | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:1902991 regulation of amyloid precursor protein catabolic process         | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:1902992 regulation of amyloid precursor protein catabolic process             | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:2000008 regulation of protein localization to cell surface                | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:2000009 regulation of protein localization to cell surface                    | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:0005016 positive regulation of CD4-positive, alpha-beta T cell activation | 1   | 0.53687 | 0.31   | 0.024 | Biological | GO:0005017 positive regulation of CD4-positive, alpha-beta T cell activation     | 0.53687 | 0.6732  | 0 | 0 | 1   | 42   |
| GO:0009914 hormone transport                                                 | 6   | 0.53688 | 1.858  | 0.019 | Biological | GO:0009915 hormone transport                                                     | 0.53688 | 0.67329 | 0 | 0 | 6   | 323  |
| GO:0008170 N-methyltransferase activity                                      | 2   | 0.53637 | 0.586  | 0.021 | Molecular  | GO:0008171 N-methyltransferase activity                                          | 0.53637 | 0.67989 | 0 | 0 | 2   | 97   |
| GO:0043269 regulation of ion transport                                       | 13  | 0.53993 | 4.025  | 0.018 | Biological | GO:0043270 regulation of ion transport                                           | 0.53993 | 0.67444 | 0 | 0 | 13  | 713  |
| GO:0071702 organic substance transport                                       | 45  | 0.54074 | 13.932 | 0.018 | Biological | GO:0071703 organic substance transport                                           | 0.54074 | 0.67528 | 0 | 0 | 45  | 2482 |
| GO:0051341 regulation of oxidoreductase activity                             | 2   | 0.54144 | 0.619  | 0.02  | Biological | GO:0051342 regulation of oxidoreductase activity                                 | 0.54144 | 0.67599 | 0 | 0 | 2   | 99   |
| GO:0069556 amino transmembrane transporter                                   | 5   | 0.54188 | 1.548  | 0.019 | Biological | GO:0069557 amino transmembrane transporter                                       | 0.54188 | 0.67637 | 0 | 0 | 5   | 268  |
| GO:0004743 protein acetylation                                               | 4   | 0.54232 | 1.238  | 0.019 | Biological | GO:0004744 protein acetylation                                                   | 0.54232 | 0.67641 | 0 | 0 | 4   | 212  |
| GO:0016051 carbohydrate biosynthetic process                                 | 4   | 0.54232 | 1.238  | 0.019 | Biological | GO:0016052 carbohydrate biosynthetic process                                     | 0.54232 | 0.67641 | 0 | 0 | 4   | 212  |
| GO:0050821 protein stabilization                                             | 4   | 0.54232 | 1.238  | 0.019 | Biological | GO:0050822 protein stabilization                                                 | 0.54232 | 0.67641 | 0 | 0 | 4   | 212  |
| GO:0003824 catalytic activity                                                | 106 | 0.54323 | 30.994 | 0.018 | Molecular  | GO:0003825 catalytic activity                                                    | 0.54323 | 0.68291 | 0 | 0 | 106 | 5745 |
| GO:0016877 nitrogen activity, forming carbon-sulfur bonds                    | 1   | 0.54463 | 0.292  | 0.024 | Molecular  | GO:0016878 nitrogen activity, forming carbon-sulfur bonds                        | 0.54463 | 0.68391 | 0 | 0 | 1   | 42   |
| GO:0030331 estrogen receptor binding                                         | 1   | 0.54478 | 1.145  | 0.019 | Biological | GO:0030332 estrogen receptor binding                                             | 0.54478 | 0.67847 | 0 | 0 | 1   | 42   |
| GO:0071705 nitrogen compound transport                                       | 37  | 0.54478 | 11.455 | 0.018 | Biological | GO:0071706 nitrogen compound transport                                           | 0.54478 | 0.67847 | 0 | 0 | 37  | 2044 |
| GO:0004553 hydrolase activity, hydrolyzing O-glycosyl compounds              | 2   | 0.54491 | 0.585  | 0.02  | Molecular  | GO:0004554 hydrolase activity, hydrolyzing O-glycosyl compounds                  | 0.54491 | 0.68291 | 0 | 0 | 2   | 98   |
| GO:0018205 peptidyl-lysine modification                                      | 7   | 0.545   | 2.167  | 0.018 | Biological | GO:0018206 peptidyl-lysine modification                                          | 0.545   | 0.67847 | 0 | 0 | 7   | 381  |
| GO:0031330 negative regulation of cellular catabolic process                 | 5   | 0.54519 | 1.548  | 0.019 | Biological | GO:0031331 negative regulation of cellular catabolic process                     | 0.54519 | 0.67847 | 0 | 0 | 5   | 269  |
| GO:0005887 integral component of plasma membrane                             | 8   | 0.54529 | 2.374  | 0.019 | Cellular   | GO:0005888 integral component of plasma membrane                                 | 0.54529 | 0.67847 | 0 | 0 | 8   | 442  |
| GO:00                                                                        |     |         |        |       |            |                                                                                  |         |         |   |   |     |      |

|                                                                          |    |         |        |       |            |                                                                                   |         |         |   |   |    |      |
|--------------------------------------------------------------------------|----|---------|--------|-------|------------|-----------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:1902476 chloride transmembrane transport                              | 2  | 0.56292 | 0.619  | 0.019 | Biological | GO:1902 chloride transmembrane transport                                          | 0.56292 | 0.69126 | 0 | 0 | 2  | 103  |
| GO:008552 side of membrane                                               | 12 | 0.56306 | 3.561  | 0.018 | Cellular   | GO:008552 side of membrane                                                        | 0.56306 | 0.73849 | 0 | 0 | 12 | 676  |
| GO:0031226 intrinsic component of plasma membrane                        | 8  | 0.56318 | 2.374  | 0.018 | Cellular   | GO:0031226 intrinsic component of plasma membrane                                 | 0.56318 | 0.73849 | 0 | 0 | 8  | 449  |
| GO:0005598 iron ion binding                                              | 3  | 0.56349 | 0.877  | 0.019 | Molecular  | GO:0005598 iron ion binding                                                       | 0.56349 | 0.69813 | 0 | 0 | 3  | 58   |
| GO:0002701 negative regulation of production of molecular mediator of    | 1  | 0.56355 | 0.31   | 0.022 | Biological | GO:0002701 negative regulation of production of molecular mediator of immune re   | 0.56355 | 0.69126 | 0 | 0 | 1  | 45   |
| GO:0031279 regulation of cyclase activity                                | 1  | 0.56355 | 0.31   | 0.022 | Biological | GO:0031279 regulation of cyclase activity                                         | 0.56355 | 0.69126 | 0 | 0 | 1  | 45   |
| GO:0043551 regulation of phosphatidylinositol 3-kinase activity          | 1  | 0.56355 | 0.31   | 0.022 | Biological | GO:0043551 regulation of phosphatidylinositol 3-kinase activity                   | 0.56355 | 0.69126 | 0 | 0 | 1  | 45   |
| GO:0045646 regulation of embryonic differentiation                       | 1  | 0.56355 | 0.31   | 0.022 | Biological | GO:0045646 regulation of embryonic differentiation                                | 0.56355 | 0.69126 | 0 | 0 | 1  | 45   |
| GO:0045663 positive regulation of myoblast differentiation               | 1  | 0.56355 | 0.31   | 0.022 | Biological | GO:0045663 positive regulation of myoblast differentiation                        | 0.56355 | 0.69126 | 0 | 0 | 1  | 45   |
| GO:0045840 positive regulation of mitotic nuclear division               | 1  | 0.56355 | 0.31   | 0.022 | Biological | GO:0045840 positive regulation of mitotic nuclear division                        | 0.56355 | 0.69126 | 0 | 0 | 1  | 45   |
| GO:0048701 embryonic cranial skeleton morphogenesis                      | 1  | 0.56355 | 0.31   | 0.022 | Biological | GO:0048701 embryonic cranial skeleton morphogenesis                               | 0.56355 | 0.69126 | 0 | 0 | 1  | 45   |
| GO:0071827 plasma lipoprotein particle organization                      | 1  | 0.56355 | 0.31   | 0.022 | Biological | GO:0071827 plasma lipoprotein particle organization                               | 0.56355 | 0.69126 | 0 | 0 | 1  | 45   |
| GO:0070799 energy                                                        | 1  | 0.56355 | 0.31   | 0.022 | Biological | GO:0070799 energy                                                                 | 0.56355 | 0.69126 | 0 | 0 | 1  | 45   |
| GO:2000378 negative regulation of reactive oxygen species metabolic p    | 1  | 0.56355 | 0.31   | 0.022 | Biological | GO:2000378 negative regulation of reactive oxygen species metabolic process       | 0.56355 | 0.69126 | 0 | 0 | 1  | 45   |
| GO:0022898 regulation of transmembrane transporter activity              | 5  | 0.56484 | 1.548  | 0.018 | Biological | GO:0022898 regulation of transmembrane transporter activity                       | 0.56484 | 0.69246 | 0 | 0 | 5  | 275  |
| GO:0030902 hindbrain development                                         | 3  | 0.56504 | 0.929  | 0.019 | Biological | GO:0030902 hindbrain development                                                  | 0.56504 | 0.69246 | 0 | 0 | 3  | 161  |
| GO:1903034 regulation of response to wounding                            | 3  | 0.56504 | 0.929  | 0.019 | Biological | GO:1903034 regulation of response to wounding                                     | 0.56504 | 0.69246 | 0 | 0 | 3  | 161  |
| GO:1900445 adaptive thermogenesis                                        | 3  | 0.56504 | 0.929  | 0.019 | Biological | GO:1900445 adaptive thermogenesis                                                 | 0.56504 | 0.69246 | 0 | 0 | 3  | 161  |
| GO:0034785 regulation of ion transmembrane transport                     | 9  | 0.56522 | 2.786  | 0.018 | Biological | GO:0034785 regulation of ion transmembrane transport                              | 0.56522 | 0.69252 | 0 | 0 | 9  | 501  |
| GO:0019233 sensory perception of pain                                    | 2  | 0.56818 | 0.619  | 0.019 | Biological | GO:0019233 sensory perception of pain                                             | 0.56818 | 0.69598 | 0 | 0 | 2  | 104  |
| GO:0004715 non-membrane spanning protein tyrosine kinase activity        | 1  | 0.56954 | 0.292  | 0.022 | Molecular  | GO:0004715 non-membrane spanning protein tyrosine kinase activity                 | 0.56954 | 0.70159 | 0 | 0 | 1  | 45   |
| GO:0051879 Hsp90 protein binding                                         | 1  | 0.56954 | 0.292  | 0.022 | Molecular  | GO:0051879 Hsp90 protein binding                                                  | 0.56954 | 0.70159 | 0 | 0 | 1  | 45   |
| GO:0000292 regulation of humoral immune response                         | 1  | 0.57148 | 0.31   | 0.022 | Biological | GO:0000292 regulation of humoral immune response                                  | 0.57148 | 0.6983  | 0 | 0 | 1  | 46   |
| GO:0014888 striated muscle adaptation                                    | 1  | 0.57148 | 0.31   | 0.022 | Biological | GO:0014888 striated muscle adaptation                                             | 0.57148 | 0.6983  | 0 | 0 | 1  | 46   |
| GO:0016578 histone deubiquitination                                      | 1  | 0.57148 | 0.31   | 0.022 | Biological | GO:0016578 histone deubiquitination                                               | 0.57148 | 0.6983  | 0 | 0 | 1  | 46   |
| GO:0043029 T cell homeostasis                                            | 1  | 0.57148 | 0.31   | 0.022 | Biological | GO:0043029 T cell homeostasis                                                     | 0.57148 | 0.6983  | 0 | 0 | 1  | 46   |
| GO:0045747 positive regulation of Notch signaling pathway                | 1  | 0.57148 | 0.31   | 0.022 | Biological | GO:0045747 positive regulation of Notch signaling pathway                         | 0.57148 | 0.6983  | 0 | 0 | 1  | 46   |
| GO:0046460 neutral lipid biosynthetic process                            | 1  | 0.57148 | 0.31   | 0.022 | Biological | GO:0046460 neutral lipid biosynthetic process                                     | 0.57148 | 0.6983  | 0 | 0 | 1  | 46   |
| GO:0046463 acylglycerol biosynthetic process                             | 1  | 0.57148 | 0.31   | 0.022 | Biological | GO:0046463 acylglycerol biosynthetic process                                      | 0.57148 | 0.6983  | 0 | 0 | 1  | 46   |
| GO:0046636 negative regulation of alpha-beta T cell activation           | 1  | 0.57148 | 0.31   | 0.022 | Biological | GO:0046636 negative regulation of alpha-beta T cell activation                    | 0.57148 | 0.6983  | 0 | 0 | 1  | 46   |
| GO:0097300 programmed necrotic cell death                                | 1  | 0.57148 | 0.31   | 0.022 | Biological | GO:0097300 programmed necrotic cell death                                         | 0.57148 | 0.6983  | 0 | 0 | 1  | 46   |
| GO:1901021 positive regulation of calcium ion transmembrane transport    | 1  | 0.57148 | 0.31   | 0.022 | Biological | GO:1901021 positive regulation of calcium ion transmembrane transporter activity  | 0.57148 | 0.6983  | 0 | 0 | 1  | 46   |
| GO:0004567 protein folding                                               | 4  | 0.57163 | 1.238  | 0.019 | Biological | GO:0004567 protein folding                                                        | 0.57163 | 0.69832 | 0 | 0 | 4  | 238  |
| GO:0015914 phospholipid transport                                        | 2  | 0.57339 | 0.619  | 0.019 | Biological | GO:0015914 phospholipid transport                                                 | 0.57339 | 0.69965 | 0 | 0 | 2  | 105  |
| GO:0022600 digestive system process                                      | 2  | 0.57339 | 0.619  | 0.019 | Biological | GO:0022600 digestive system process                                               | 0.57339 | 0.69965 | 0 | 0 | 2  | 105  |
| GO:0035249 synaptic transmission, glutamatergic                          | 2  | 0.57339 | 0.619  | 0.019 | Biological | GO:0035249 synaptic transmission, glutamatergic                                   | 0.57339 | 0.69965 | 0 | 0 | 2  | 105  |
| GO:1905477 positive regulation of protein localization to membrane       | 2  | 0.57339 | 0.619  | 0.019 | Biological | GO:1905477 positive regulation of protein localization to membrane                | 0.57339 | 0.69965 | 0 | 0 | 2  | 105  |
| GO:0040029 regulation of gene expression, epigenetic                     | 3  | 0.57342 | 0.829  | 0.019 | Biological | GO:0040029 regulation of gene expression, epigenetic                              | 0.57342 | 0.69965 | 0 | 0 | 3  | 163  |
| GO:0000776 kinetochore                                                   | 3  | 0.57397 | 0.89   | 0.018 | Cellular   | GO:0000776 kinetochore                                                            | 0.57397 | 0.75048 | 0 | 0 | 3  | 165  |
| GO:0043195 terminal bouton                                               | 1  | 0.57513 | 0.297  | 0.021 | Cellular   | GO:0043195 terminal bouton                                                        | 0.57513 | 0.75048 | 0 | 0 | 1  | 47   |
| GO:0029093 regulation of supramolecular fiber organization               | 7  | 0.57523 | 2.167  | 0.018 | Biological | GO:0029093 regulation of supramolecular fiber organization                        | 0.57523 | 0.70169 | 0 | 0 | 7  | 392  |
| GO:0001764 phosphotyrosine residue binding                               | 1  | 0.57754 | 0.292  | 0.022 | Molecular  | GO:0001764 phosphotyrosine residue binding                                        | 0.57754 | 0.70843 | 0 | 0 | 1  | 46   |
| GO:0032265 phosphotyrosine 3-phosphate binding                           | 1  | 0.57754 | 0.292  | 0.022 | Molecular  | GO:0032265 phosphotyrosine 3-phosphate binding                                    | 0.57754 | 0.70843 | 0 | 0 | 1  | 46   |
| GO:0006644 phospholipid metabolic process                                | 7  | 0.57793 | 2.167  | 0.018 | Biological | GO:0006644 phospholipid metabolic process                                         | 0.57793 | 0.70339 | 0 | 0 | 7  | 393  |
| GO:0051726 regulation of cell cycle                                      | 20 | 0.57813 | 6.192  | 0.018 | Biological | GO:0051726 regulation of cell cycle                                               | 0.57813 | 0.70339 | 0 | 0 | 20 | 1124 |
| GO:0042116 macrophage activation                                         | 2  | 0.57856 | 0.619  | 0.019 | Biological | GO:0042116 macrophage activation                                                  | 0.57856 | 0.70339 | 0 | 0 | 2  | 106  |
| GO:0006775 fat-soluble vitamin metabolic process                         | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0006775 fat-soluble vitamin metabolic process                                  | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0010824 regulation of centrosome duplication                          | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0010824 regulation of centrosome duplication                                   | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0021575 hindbrain morphogenesis                                       | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0021575 hindbrain morphogenesis                                                | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0030517 negative regulation of axon extension                         | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0030517 negative regulation of axon extension                                  | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0030521 androgen receptor signaling pathway                           | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0030521 androgen receptor signaling pathway                                    | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0032527 protein exit from endoplasmic reticulum                       | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0032527 protein exit from endoplasmic reticulum                                | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0032654 collagen biosynthetic process                                 | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0032654 collagen biosynthetic process                                          | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0035384 thioester biosynthetic process                                | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0035384 thioester biosynthetic process                                         | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0042220 response to cocaine                                           | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0042220 response to cocaine                                                    | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0046189 phenol-containing compound biosynthetic process               | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0046189 phenol-containing compound biosynthetic process                        | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0048634 regulation of muscle organ development                        | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0048634 regulation of muscle organ development                                 | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0071616 acyl-CoA biosynthetic process                                 | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0071616 acyl-CoA biosynthetic process                                          | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0072583 clathrin-dependent endocytosis                                | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0072583 clathrin-dependent endocytosis                                         | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0090199 regulation of release of cytochrome c from mitochondria       | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0090199 regulation of release of cytochrome c from mitochondria                | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0120163 negative regulation of cold-induced thermogenesis             | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:0120163 negative regulation of cold-induced thermogenesis                      | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:1902459 positive regulation of stem cell population maintenance       | 1  | 0.57931 | 0.31   | 0.021 | Biological | GO:1902459 positive regulation of stem cell population maintenance                | 0.57931 | 0.70339 | 0 | 0 | 1  | 47   |
| GO:0008905 negative regulation of catabolic process                      | 6  | 0.58045 | 1.858  | 0.018 | Biological | GO:0008905 negative regulation of catabolic process                               | 0.58045 | 0.71283 | 0 | 0 | 6  | 338  |
| GO:0016787 hydrolase activity                                            | 45 | 0.58113 | 13.158 | 0.018 | Molecular  | GO:0016787 hydrolase activity                                                     | 0.58113 | 0.71283 | 0 | 0 | 45 | 2476 |
| GO:0031267 small GTPase binding                                          | 5  | 0.58276 | 1.462  | 0.018 | Molecular  | GO:0031267 small GTPase binding                                                   | 0.58276 | 0.71372 | 0 | 0 | 5  | 276  |
| GO:0097542 ciliary tip                                                   | 1  | 0.58281 | 0.297  | 0.021 | Cellular   | GO:0097542 ciliary tip                                                            | 0.58281 | 0.75865 | 0 | 0 | 1  | 48   |
| GO:0016042 lipid catabolic process                                       | 6  | 0.58335 | 1.858  | 0.018 | Biological | GO:0016042 lipid catabolic process                                                | 0.58335 | 0.70795 | 0 | 0 | 6  | 338  |
| GO:0033279 cardiac septum development                                    | 2  | 0.58368 | 0.619  | 0.018 | Biological | GO:0033279 cardiac septum development                                             | 0.58368 | 0.71064 | 0 | 0 | 2  | 107  |
| GO:0002683 negative regulation of immune system process                  | 8  | 0.5837  | 2.477  | 0.018 | Biological | GO:0002683 negative regulation of immune system process                           | 0.5837  | 0.70804 | 0 | 0 | 8  | 452  |
| GO:0019894 kinesin binding                                               | 1  | 0.58539 | 0.292  | 0.021 | Molecular  | GO:0019894 kinesin binding                                                        | 0.58539 | 0.71372 | 0 | 0 | 1  | 47   |
| GO:0061733 peptide-lysine-N-acetyltransferase activity                   | 1  | 0.58539 | 0.292  | 0.021 | Molecular  | GO:0061733 peptide-lysine-N-acetyltransferase activity                            | 0.58539 | 0.71372 | 0 | 0 | 1  | 47   |
| GO:0005524 ATP binding                                                   | 27 | 0.58558 | 7.895  | 0.018 | Molecular  | GO:0005524 ATP binding                                                            | 0.58558 | 0.71372 | 0 | 0 | 27 | 1495 |
| GO:0018393 internal peptide-lysine acylation                             | 3  | 0.58581 | 0.929  | 0.018 | Biological | GO:0018393 internal peptide-lysine acylation                                      | 0.58581 | 0.70963 | 0 | 0 | 3  | 166  |
| GO:0051494 negative regulation of cytoskeleton organization              | 3  | 0.58581 | 0.929  | 0.018 | Biological | GO:0051494 negative regulation of cytoskeleton organization                       | 0.58581 | 0.70963 | 0 | 0 | 3  | 165  |
| GO:0010466 negative regulation of peptidase activity                     | 4  | 0.58589 | 1.238  | 0.018 | Biological | GO:0010466 negative regulation of peptidase activity                              | 0.58589 | 0.70963 | 0 | 0 | 4  | 224  |
| GO:0035091 phosphatidylinositol binding                                  | 5  | 0.58597 | 1.462  | 0.018 | Molecular  | GO:0035091 phosphatidylinositol binding                                           | 0.58597 | 0.71372 | 0 | 0 | 5  | 277  |
| GO:0019884 antigen processing and presentation of exogenous antigen      | 1  | 0.587   | 0.31   | 0.021 | Biological | GO:0019884 antigen processing and presentation of exogenous antigen               | 0.587   | 0.70963 | 0 | 0 | 1  | 48   |
| GO:0031641 regulation of myelination                                     | 1  | 0.587   | 0.31   | 0.021 | Biological | GO:0031641 regulation of myelination                                              | 0.587   | 0.70963 | 0 | 0 | 1  | 48   |
| GO:0035987 endodermal cell differentiation                               | 1  | 0.587   | 0.31   | 0.021 | Biological | GO:0035987 endodermal cell differentiation                                        | 0.587   | 0.70963 | 0 | 0 | 1  | 48   |
| GO:0036230 granulocyte activation                                        | 1  | 0.587   | 0.31   | 0.021 | Biological | GO:0036230 granulocyte activation                                                 | 0.587   | 0.70963 | 0 | 0 | 1  | 48   |
| GO:0043124 negative regulation of I-kappaB kinase/NF-kappaB signaling    | 1  | 0.587   | 0.31   | 0.021 | Biological | GO:0043124 negative regulation of I-kappaB kinase/NF-kappaB signaling             | 0.587   | 0.70963 | 0 | 0 | 1  | 48   |
| GO:0051359 regulation of lysate activity                                 | 1  | 0.587   | 0.31   | 0.021 | Biological | GO:0051359 regulation of lysate activity                                          | 0.587   | 0.70963 | 0 | 0 | 1  | 48   |
| GO:0069716 coronary vasculature development                              | 1  | 0.587   | 0.31   | 0.021 | Biological | GO:0069716 coronary vasculature development                                       | 0.587   | 0.70963 | 0 | 0 | 1  | 48   |
| GO:0071825 protein-lipid complex subunit organization                    | 1  | 0.587   | 0.31   | 0.021 | Biological | GO:0071825 protein-lipid complex subunit organization                             | 0.587   | 0.70963 | 0 | 0 | 1  | 48   |
| GO:1902041 regulation of extrinsic apoptotic signaling pathway via death | 1  | 0.587   | 0.31   | 0.021 | Biological | GO:1902041 regulation of extrinsic apoptotic signaling pathway via death domain r | 0.587   | 0.70963 | 0 | 0 | 1  | 48   |
| GO:1902930 regulation of alcohol biosynthetic process                    | 1  | 0.587   | 0.31   | 0.021 | Biological | GO:1902930 regulation of alcohol biosynthetic process                             | 0.587   | 0.70963 | 0 | 0 | 1  | 48   |
| GO:2004044 regulation of T cell migration                                | 1  | 0.587   | 0.31   | 0.021 | Biological | GO:2004044 regulation of T cell migration                                         | 0.587   | 0.70963 | 0 | 0 | 1  | 48   |
| GO:0046494 lymphocyte activation                                         | 15 | 0.58728 | 4.34   | 0.018 | Biological | GO:0046494 lymphocyte activation                                                  | 0.58728 | 0.70927 | 0 | 0 | 15 | 849  |
| GO:0005903 brush border                                                  | 2  | 0.58756 | 0.593  | 0.018 | Cellular   | GO:0005903 brush border                                                           | 0.58756 |         |   |   |    |      |

|                                                                                            |     |         |        |       |            |                                                                                            |         |         |   |   |     |       |
|--------------------------------------------------------------------------------------------|-----|---------|--------|-------|------------|--------------------------------------------------------------------------------------------|---------|---------|---|---|-----|-------|
| GO:0043277 apoptotic cell clearance                                                        | 1   | 0.60924 | 0.31   | 0.02  | Biological | GO:0043277 apoptotic cell clearance                                                        | 0.60924 | 0.72701 | 0 | 0 | 1   | 51    |
| GO:0045058 T cell selection                                                                | 1   | 0.60924 | 0.31   | 0.02  | Biological | GO:0045058 T cell selection                                                                | 0.60924 | 0.72701 | 0 | 0 | 1   | 51    |
| GO:0045776 negative regulation of blood pressure                                           | 1   | 0.60924 | 0.31   | 0.02  | Biological | GO:0045776 negative regulation of blood pressure                                           | 0.60924 | 0.72701 | 0 | 0 | 1   | 51    |
| GO:0050119 inner ear receptor cell development                                             | 1   | 0.60924 | 0.31   | 0.02  | Biological | GO:0050119 inner ear receptor cell development                                             | 0.60924 | 0.72701 | 0 | 0 | 1   | 51    |
| GO:1900047 negative regulation of hemostasis                                               | 1   | 0.60924 | 0.31   | 0.02  | Biological | GO:1900047 negative regulation of hemostasis                                               | 0.60924 | 0.72701 | 0 | 0 | 1   | 51    |
| GO:0000287 magnesium ion binding                                                           | 4   | 0.60942 | 1.17   | 0.018 | Molecular  | GO:0000287 magnesium ion binding                                                           | 0.60942 | 0.73198 | 0 | 0 | 4   | 227   |
| GO:0014704 intercalated disc                                                               | 1   | 0.61216 | 0.297  | 0.019 | Cellular   | GO:0014704 intercalated disc                                                               | 0.61216 | 0.78164 | 0 | 0 | 1   | 52    |
| GO:0032526 response to retinoic acid                                                       | 1   | 0.61343 | 0.519  | 0.019 | Biological | GO:0032526 response to retinoic acid                                                       | 0.61343 | 0.73184 | 0 | 0 | 2   | 119   |
| GO:0057698 receptor signaling pathway via STAT                                             | 3   | 0.61382 | 0.929  | 0.017 | Biological | GO:0057698 receptor signaling pathway via STAT                                             | 0.61382 | 0.73213 | 0 | 0 | 3   | 173   |
| GO:0032535 regulation of cellular component size                                           | 7   | 0.61487 | 2.167  | 0.017 | Biological | GO:0032535 regulation of cellular component size                                           | 0.61487 | 0.73321 | 0 | 0 | 7   | 407   |
| GO:0010043 response to zinc ion                                                            | 1   | 0.61638 | 0.31   | 0.019 | Biological | GO:0010043 response to zinc ion                                                            | 0.61638 | 0.73395 | 0 | 0 | 1   | 52    |
| GO:0045778 positive regulation of ossification                                             | 1   | 0.61638 | 0.31   | 0.019 | Biological | GO:0045778 positive regulation of ossification                                             | 0.61638 | 0.73395 | 0 | 0 | 1   | 52    |
| GO:0046580 negative regulation of Ras protein signal transduction                          | 1   | 0.61638 | 0.31   | 0.019 | Biological | GO:0046580 negative regulation of Ras protein signal transduction                          | 0.61638 | 0.73395 | 0 | 0 | 1   | 52    |
| GO:0048013 ephrin receptor signaling pathway                                               | 1   | 0.61638 | 0.31   | 0.019 | Biological | GO:0048013 ephrin receptor signaling pathway                                               | 0.61638 | 0.73395 | 0 | 0 | 1   | 52    |
| GO:0060425 lung morphogenesis                                                              | 1   | 0.61638 | 0.31   | 0.019 | Biological | GO:0060425 lung morphogenesis                                                              | 0.61638 | 0.73395 | 0 | 0 | 1   | 52    |
| GO:0120009 intermembrane lipid transfer                                                    | 1   | 0.61638 | 0.31   | 0.019 | Biological | GO:0120009 intermembrane lipid transfer                                                    | 0.61638 | 0.73395 | 0 | 0 | 1   | 52    |
| GO:0006694 steroid biosynthetic process                                                    | 3   | 0.61771 | 0.929  | 0.017 | Biological | GO:0006694 steroid biosynthetic process                                                    | 0.61771 | 0.73519 | 0 | 0 | 3   | 174   |
| GO:0007254 JNK cascade                                                                     | 3   | 0.61771 | 0.929  | 0.017 | Biological | GO:0007254 JNK cascade                                                                     | 0.61771 | 0.73519 | 0 | 0 | 3   | 174   |
| GO:0000779 condensed chromosome, centromeric region                                        | 3   | 0.61773 | 0.88   | 0.017 | Cellular   | GO:0000779 condensed chromosome, centromeric region                                        | 0.61773 | 0.78887 | 0 | 0 | 3   | 176   |
| GO:0002821 positive regulation of adaptive immune response                                 | 2   | 0.61823 | 0.619  | 0.018 | Biological | GO:0002821 positive regulation of adaptive immune response                                 | 0.61823 | 0.73548 | 0 | 0 | 2   | 114   |
| GO:1904029 regulation of cyclin-dependent protein kinase activity                          | 2   | 0.61823 | 0.619  | 0.018 | Biological | GO:1904029 regulation of cyclin-dependent protein kinase activity                          | 0.61823 | 0.73548 | 0 | 0 | 2   | 114   |
| GO:0071704 organic substance metabolic process                                             | 197 | 0.61986 | 60.991 | 0.018 | Biological | GO:0071704 organic substance metabolic process                                             | 0.61986 | 0.73722 | 0 | 0 | 197 | 10922 |
| GO:0051495 positive regulation of cytokelstein organization                                | 4   | 0.62031 | 1.238  | 0.017 | Biological | GO:0051495 positive regulation of cytokelstein organization                                | 0.62031 | 0.73758 | 0 | 0 | 4   | 234   |
| GO:0034451 centriolar satellite                                                            | 2   | 0.62148 | 0.593  | 0.017 | Cellular   | GO:0034451 centriolar satellite                                                            | 0.62148 | 0.78977 | 0 | 0 | 2   | 116   |
| GO:0034212 peptide N-acetyltransferase activity                                            | 1   | 0.62251 | 0.292  | 0.019 | Molecular  | GO:0034212 peptide N-acetyltransferase activity                                            | 0.62251 | 0.7446  | 0 | 0 | 1   | 52    |
| GO:0051018 protein kinase A binding                                                        | 1   | 0.62251 | 0.292  | 0.019 | Molecular  | GO:0051018 protein kinase A binding                                                        | 0.62251 | 0.7446  | 0 | 0 | 1   | 52    |
| GO:0120013 lipid transfer activity                                                         | 1   | 0.62251 | 0.292  | 0.019 | Molecular  | GO:0120013 lipid transfer activity                                                         | 0.62251 | 0.7446  | 0 | 0 | 1   | 52    |
| GO:0031532 actin cytoskeleton reorganization                                               | 2   | 0.62298 | 0.619  | 0.017 | Biological | GO:0031532 actin cytoskeleton reorganization                                               | 0.62298 | 0.73826 | 0 | 0 | 2   | 115   |
| GO:0046916 cellular transition metal ion homeostasis                                       | 2   | 0.62298 | 0.619  | 0.017 | Biological | GO:0046916 cellular transition metal ion homeostasis                                       | 0.62298 | 0.73826 | 0 | 0 | 2   | 115   |
| GO:0002204 somatic recombination of immunoglobulin genes involved in                       | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0002204 somatic recombination of immunoglobulin genes involved in                       | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0002208 somatic diversification of immunoglobulins involved in immune respon            | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0002208 somatic diversification of immunoglobulins involved in immune respon            | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0006749 glutathione metabolic process                                                   | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0006749 glutathione metabolic process                                                   | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0006890 retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum           | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0006890 retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum           | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0010823 negative regulation of mitochondrion organization                               | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0010823 negative regulation of mitochondrion organization                               | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0019083 viral transcription                                                             | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0019083 viral transcription                                                             | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0045190 isotype switching                                                               | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0045190 isotype switching                                                               | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0045197 establishment or maintenance of epithelial cell apical/basal polarity           | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0045197 establishment or maintenance of epithelial cell apical/basal polarity           | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0045332 phospholipid transfer                                                           | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0045332 phospholipid transfer                                                           | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0045599 negative regulation of fat cell differentiation                                 | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0045599 negative regulation of fat cell differentiation                                 | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0048146 positive regulation of fibroblast proliferation                                 | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0048146 positive regulation of fibroblast proliferation                                 | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0050732 negative regulation of peptidyl-tyrosine phosphorylation                        | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0050732 negative regulation of peptidyl-tyrosine phosphorylation                        | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0060896 endocrine hormone secretion                                                     | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0060896 endocrine hormone secretion                                                     | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0070169 positive regulation of biomineral tissue development                            | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0070169 positive regulation of biomineral tissue development                            | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0110151 positive regulation of biomineralization                                        | 1   | 0.62339 | 0.31   | 0.019 | Biological | GO:0110151 positive regulation of biomineralization                                        | 0.62339 | 0.73826 | 0 | 0 | 1   | 53    |
| GO:0031348 negative regulation of defense response                                         | 4   | 0.62365 | 1.238  | 0.017 | Biological | GO:0031348 negative regulation of defense response                                         | 0.62365 | 0.73838 | 0 | 0 | 4   | 235   |
| GO:0031349 positive regulation of defense response                                         | 5   | 0.62405 | 1.548  | 0.017 | Biological | GO:0031349 positive regulation of defense response                                         | 0.62405 | 0.73869 | 0 | 0 | 5   | 294   |
| GO:0005775 vacuolar lumen                                                                  | 3   | 0.62535 | 0.86   | 0.017 | Cellular   | GO:0005775 vacuolar lumen                                                                  | 0.62535 | 0.78995 | 0 | 0 | 3   | 178   |
| GO:0002872 positive regulation of protein catabolic process based on somatic recombination | 9   | 0.62543 | 2.786  | 0.017 | Biological | GO:0002872 positive regulation of protein catabolic process based on somatic recombination | 0.62543 | 0.74029 | 0 | 0 | 9   | 527   |
| GO:0010498 proteasomal protein catabolic process                                           | 9   | 0.626   | 2.786  | 0.017 | Biological | GO:0010498 proteasomal protein catabolic process                                           | 0.626   | 0.74064 | 0 | 0 | 9   | 527   |
| GO:0030286 dynein complex                                                                  | 1   | 0.62606 | 0.297  | 0.019 | Cellular   | GO:0030286 dynein complex                                                                  | 0.62606 | 0.78995 | 0 | 0 | 1   | 54    |
| GO:0030315 T-tubule                                                                        | 1   | 0.62606 | 0.297  | 0.019 | Cellular   | GO:0030315 T-tubule                                                                        | 0.62606 | 0.78995 | 0 | 0 | 1   | 54    |
| GO:0021761 limbic system development                                                       | 2   | 0.62769 | 0.818  | 0.017 | Biological | GO:0021761 limbic system development                                                       | 0.62769 | 0.74225 | 0 | 0 | 2   | 116   |
| GO:0045892 positive regulation of T cell differentiation                                   | 2   | 0.62769 | 0.818  | 0.017 | Biological | GO:0045892 positive regulation of T cell differentiation                                   | 0.62769 | 0.74225 | 0 | 0 | 2   | 116   |
| GO:0018394 peptidyl-lysine acetylation                                                     | 3   | 0.62924 | 0.929  | 0.017 | Biological | GO:0018394 peptidyl-lysine acetylation                                                     | 0.62924 | 0.74306 | 0 | 0 | 3   | 177   |
| GO:0004889 cysteine-type endopeptidase inhibitor activity                                  | 1   | 0.62952 | 0.292  | 0.019 | Molecular  | GO:0004889 cysteine-type endopeptidase inhibitor activity                                  | 0.62952 | 0.75092 | 0 | 0 | 1   | 53    |
| GO:0005444 calcium-dependent phospholipid binding                                          | 1   | 0.62952 | 0.292  | 0.019 | Molecular  | GO:0005444 calcium-dependent phospholipid binding                                          | 0.62952 | 0.75092 | 0 | 0 | 1   | 53    |
| GO:0006695 cholesterol biosynthetic process                                                | 1   | 0.63028 | 0.31   | 0.019 | Biological | GO:0006695 cholesterol biosynthetic process                                                | 0.63028 | 0.74306 | 0 | 0 | 1   | 54    |
| GO:0009409 response to cold                                                                | 1   | 0.63028 | 0.31   | 0.019 | Biological | GO:0009409 response to cold                                                                | 0.63028 | 0.74306 | 0 | 0 | 1   | 54    |
| GO:0010611 regulation of cardiac muscle hypertrophy                                        | 1   | 0.63028 | 0.31   | 0.019 | Biological | GO:0010611 regulation of cardiac muscle hypertrophy                                        | 0.63028 | 0.74306 | 0 | 0 | 1   | 54    |
| GO:0021695 cerebellar cortex development                                                   | 1   | 0.63028 | 0.31   | 0.019 | Biological | GO:0021695 cerebellar cortex development                                                   | 0.63028 | 0.74306 | 0 | 0 | 1   | 54    |
| GO:0042149 cellular response to glucose starvation                                         | 1   | 0.63028 | 0.31   | 0.019 | Biological | GO:0042149 cellular response to glucose starvation                                         | 0.63028 | 0.74306 | 0 | 0 | 1   | 54    |
| GO:0043525 positive regulation of neuron apoptotic process                                 | 1   | 0.63028 | 0.31   | 0.019 | Biological | GO:0043525 positive regulation of neuron apoptotic process                                 | 0.63028 | 0.74306 | 0 | 0 | 1   | 54    |
| GO:0046915 regulation of centrosome cycle                                                  | 1   | 0.63028 | 0.31   | 0.019 | Biological | GO:0046915 regulation of centrosome cycle                                                  | 0.63028 | 0.74306 | 0 | 0 | 1   | 54    |
| GO:0048260 positive regulation of receptor-mediated endocytosis                            | 1   | 0.63028 | 0.31   | 0.019 | Biological | GO:0048260 positive regulation of receptor-mediated endocytosis                            | 0.63028 | 0.74306 | 0 | 0 | 1   | 54    |
| GO:0050819 negative regulation of coagulation                                              | 1   | 0.63028 | 0.31   | 0.019 | Biological | GO:0050819 negative regulation of coagulation                                              | 0.63028 | 0.74306 | 0 | 0 | 1   | 54    |
| GO:0055021 regulation of cardiac muscle tissue growth                                      | 1   | 0.63028 | 0.31   | 0.019 | Biological | GO:0055021 regulation of cardiac muscle tissue growth                                      | 0.63028 | 0.74306 | 0 | 0 | 1   | 54    |
| GO:0061178 regulation of insulin secretion involved in cellular response to glucose        | 1   | 0.63028 | 0.31   | 0.019 | Biological | GO:0061178 regulation of insulin secretion involved in cellular response to glucose        | 0.63028 | 0.74306 | 0 | 0 | 1   | 54    |
| GO:1902653 secretory granule biosynthetic process                                          | 1   | 0.63028 | 0.31   | 0.019 | Biological | GO:1902653 secretory granule biosynthetic process                                          | 0.63028 | 0.74306 | 0 | 0 | 1   | 54    |
| GO:0005769 early endosome                                                                  | 7   | 0.6308  | 2.077  | 0.017 | Cellular   | GO:0005769 early endosome                                                                  | 0.6308  | 0.79061 | 0 | 0 | 7   | 418   |
| GO:0031967 organelle envelope                                                              | 22  | 0.63101 | 6.528  | 0.017 | Cellular   | GO:0031967 organelle envelope                                                              | 0.63101 | 0.79061 | 0 | 0 | 22  | 1285  |
| GO:0031975 envelope                                                                        | 22  | 0.63101 | 6.528  | 0.017 | Cellular   | GO:0031975 envelope                                                                        | 0.63101 | 0.79061 | 0 | 0 | 22  | 1285  |
| GO:0097367 carbohydrate derivative binding                                                 | 41  | 0.63203 | 11.988 | 0.018 | Molecular  | GO:0097367 carbohydrate derivative binding                                                 | 0.63203 | 0.75287 | 0 | 0 | 41  | 2301  |
| GO:1904724 tertiary granule lumen                                                          | 1   | 0.63282 | 0.519  | 0.019 | Cellular   | GO:1904724 tertiary granule lumen                                                          | 0.63282 | 0.74014 | 0 | 0 | 1   | 55    |
| GO:0035725 sodium ion transmembrane transport                                              | 3   | 0.63303 | 0.929  | 0.017 | Biological | GO:0035725 sodium ion transmembrane transport                                              | 0.63303 | 0.74595 | 0 | 0 | 3   | 178   |
| GO:0051650 establishment of vesicle localization                                           | 3   | 0.63303 | 0.929  | 0.017 | Biological | GO:0051650 establishment of vesicle localization                                           | 0.63303 | 0.74595 | 0 | 0 | 3   | 178   |
| GO:0042593 glucose homeostasis                                                             | 4   | 0.63356 | 1.238  | 0.017 | Biological | GO:0042593 glucose homeostasis                                                             | 0.63356 | 0.74641 | 0 | 0 | 4   | 238   |
| GO:0008374 O-acetyltransferase activity                                                    | 1   | 0.63641 | 0.292  | 0.019 | Molecular  | GO:0008374 O-acetyltransferase activity                                                    | 0.63641 | 0.75632 | 0 | 0 | 1   | 54    |
| GO:0042628 ATP-coupled transmembrane transporter activity                                  | 2   | 0.63641 | 0.292  | 0.019 | Molecular  | GO:0042628 ATP-coupled transmembrane transporter activity                                  | 0.63641 | 0.75632 | 0 | 0 | 2   | 119   |
| GO:0035500 carbohydrate homeostasis                                                        | 4   | 0.63683 | 1.238  | 0.017 | Biological | GO:0035500 carbohydrate homeostasis                                                        | 0.63683 | 0.74733 | 0 | 0 | 4   | 239   |
| GO:0032649 regulation of interferon-gamma production                                       | 2   | 0.63697 | 0.619  | 0.017 | Biological | GO:0032649 regulation of interferon-gamma production                                       | 0.63697 | 0.74733 | 0 | 0 | 2   | 118   |
| GO:0009395 phospholipid catabolic process                                                  | 1   | 0.63704 | 0.31   | 0.018 | Biological | GO:0009395 phospholipid catabolic process                                                  | 0.63704 | 0.74733 | 0 | 0 | 1   | 55    |
| GO:0010518 positive regulation of phospholipase activity                                   | 1   | 0.63704 | 0.31   | 0.018 | Biological | GO:0010518 positive regulation of phospholipase activity                                   | 0.63704 | 0.74733 | 0 | 0 | 1   | 55    |
| GO:0030520 intracellular estrogen receptor signaling pathway                               | 1   | 0.63704 | 0.31   | 0.018 | Biological | GO:0030520 intracellular estrogen receptor signaling pathway                               | 0.63704 | 0.74733 | 0 | 0 | 1   | 55    |
| GO:0031113 regulation of microtubule polymerization                                        | 1   | 0.63704 | 0.31   | 0.018 | Biological | GO:0031113 regulation of microtubule polymerization                                        | 0.63704 | 0.74733 | 0 | 0 | 1   | 55    |
| GO:0033047 regulation of mitotic sister chromatid segregation                              | 1   | 0.63704 | 0.31   | 0.018 | Biological | GO:0033047 regulation of mitotic sister chromatid segregation                              | 0.63704 | 0.74733 | 0 | 0 | 1   | 55    |
| GO:0035036 sperm-egg recognition                                                           | 1   | 0.63704 | 0.31   | 0.018 | Biological | GO:0035036 sperm-egg recognition                                                           | 0.63704 | 0.74733 | 0 | 0 | 1   | 55    |
| GO:0042572 retinol metabolic process                                                       | 1   | 0.63704 | 0.31   | 0.018 | Biological | GO:0042572 retinol metabolic process                                                       | 0.63704 | 0.74733 | 0 | 0 | 1   | 55    |
| GO:0045071 negative regulation of viral genome replication                                 | 1   | 0.63704 | 0.31   | 0.018 | Biological | GO:0045071 negative regulation of viral genome replication                                 | 0.63704 | 0.74733 | 0 | 0 | 1   | 55    |
| GO:0048010 vascular endothelial growth factor receptor signaling pathway                   | 1   | 0.63704 | 0.     |       |            |                                                                                            |         |         |   |   |     |       |

|                                                                                       |    |         |        |       |            |                                                                                       |         |         |   |   |    |      |
|---------------------------------------------------------------------------------------|----|---------|--------|-------|------------|---------------------------------------------------------------------------------------|---------|---------|---|---|----|------|
| GO:0051932 synaptic transmission, GABAergic                                           | 1  | 0.65659 | 0.31   | 0.017 | Biological | GO:0051932 synaptic transmission, GABAergic                                           | 0.65659 | 0.76203 | 0 | 0 | 1  | 58   |
| GO:0061245 establishment or maintenance of bipolar cell polarity                      | 1  | 0.65659 | 0.31   | 0.017 | Biological | GO:0061245 establishment or maintenance of bipolar cell polarity                      | 0.65659 | 0.76203 | 0 | 0 | 1  | 58   |
| GO:0070534 protein K63-linked ubiquitination                                          | 1  | 0.65659 | 0.31   | 0.017 | Biological | GO:0070534 protein K63-linked ubiquitination                                          | 0.65659 | 0.76203 | 0 | 0 | 1  | 58   |
| GO:1904813 ficoidin-1-rich granule lumen                                              | 2  | 0.65757 | 0.593  | 0.016 | Cellular   | GO:1904813 ficoidin-1-rich granule lumen                                              | 0.65757 | 0.80771 | 0 | 0 | 2  | 124  |
| GO:0001533 cornified envelope                                                         | 1  | 0.65866 | 0.297  | 0.017 | Cellular   | GO:0001533 cornified envelope                                                         | 0.65866 | 0.80771 | 0 | 0 | 1  | 59   |
| GO:1903293 phosphatase complex                                                        | 1  | 0.65866 | 0.297  | 0.017 | Cellular   | GO:1903293 phosphatase complex                                                        | 0.65866 | 0.80771 | 0 | 0 | 1  | 59   |
| GO:0002833 positive regulation of response to biotic stimulus                         | 3  | 0.6588  | 0.929  | 0.016 | Biological | GO:0002833 positive regulation of response to biotic stimulus                         | 0.6588  | 0.76441 | 0 | 0 | 3  | 185  |
| GO:0015389 primary active transmembrane transporter activity                          | 1  | 0.65881 | 0.877  | 0.016 | Molecular  | GO:0015389 primary active transmembrane transporter activity                          | 0.65881 | 0.77214 | 0 | 0 | 1  | 187  |
| GO:1901981 phosphatidylinositol phosphate binding                                     | 3  | 0.65881 | 0.877  | 0.016 | Molecular  | GO:1901981 phosphatidylinositol phosphate binding                                     | 0.65881 | 0.77214 | 0 | 0 | 3  | 182  |
| GO:0071346 cellular response to interferon-gamma                                      | 2  | 0.65937 | 0.619  | 0.016 | Biological | GO:0071346 cellular response to interferon-gamma                                      | 0.65937 | 0.76489 | 0 | 0 | 2  | 123  |
| GO:2000112 regulation of cellular macromolecule biosynthetic process                  | 70 | 0.66121 | 21.672 | 0.016 | Biological | GO:2000112 regulation of cellular macromolecule biosynthetic process                  | 0.66121 | 0.76685 | 0 | 0 | 70 | 3966 |
| GO:0030672 synaptic vesicle membrane                                                  | 2  | 0.66189 | 0.593  | 0.016 | Cellular   | GO:0030672 synaptic vesicle membrane                                                  | 0.66189 | 0.80771 | 0 | 0 | 2  | 125  |
| GO:0096011 exocytic vesicle transport                                                 | 2  | 0.66189 | 0.593  | 0.016 | Cellular   | GO:0096011 exocytic vesicle transport                                                 | 0.66189 | 0.80771 | 0 | 0 | 2  | 125  |
| GO:0034612 response to tumor necrosis factor                                          | 4  | 0.66228 | 1.238  | 0.016 | Biological | GO:0034612 response to tumor necrosis factor                                          | 0.66228 | 0.767   | 0 | 0 | 4  | 247  |
| GO:0046395 carboxylic acid catabolic process                                          | 4  | 0.66228 | 1.238  | 0.016 | Biological | GO:0046395 carboxylic acid catabolic process                                          | 0.66228 | 0.767   | 0 | 0 | 4  | 247  |
| GO:0002221 pattern recognition receptor signaling pathway                             | 3  | 0.66237 | 0.929  | 0.016 | Biological | GO:0002221 pattern recognition receptor signaling pathway                             | 0.66237 | 0.767   | 0 | 0 | 3  | 186  |
| GO:0045309 protein phosphorylated amino acid binding                                  | 1  | 0.6627  | 0.292  | 0.017 | Molecular  | GO:0045309 protein phosphorylated amino acid binding                                  | 0.6627  | 0.77554 | 0 | 0 | 1  | 58   |
| GO:0031514 molle cilium                                                               | 4  | 0.66278 | 1.187  | 0.016 | Cellular   | GO:0031514 molle cilium                                                               | 0.66278 | 0.80771 | 0 | 0 | 4  | 250  |
| GO:0002011 morphogenesis of an epithelial sheet                                       | 1  | 0.66287 | 0.31   | 0.017 | Biological | GO:0002011 morphogenesis of an epithelial sheet                                       | 0.66287 | 0.767   | 0 | 0 | 1  | 59   |
| GO:0033287 negative regulation of intracellular transport                             | 1  | 0.66287 | 0.31   | 0.017 | Biological | GO:0033287 negative regulation of intracellular transport                             | 0.66287 | 0.767   | 0 | 0 | 1  | 59   |
| GO:0034204 lipid translocation                                                        | 1  | 0.66287 | 0.31   | 0.017 | Biological | GO:0034204 lipid translocation                                                        | 0.66287 | 0.767   | 0 | 0 | 1  | 59   |
| GO:0045604 regulation of epidermal cell differentiation                               | 1  | 0.66287 | 0.31   | 0.017 | Biological | GO:0045604 regulation of epidermal cell differentiation                               | 0.66287 | 0.767   | 0 | 0 | 1  | 59   |
| GO:0045620 negative regulation of lymphocyte differentiation                          | 1  | 0.66287 | 0.31   | 0.017 | Biological | GO:0045620 negative regulation of lymphocyte differentiation                          | 0.66287 | 0.767   | 0 | 0 | 1  | 59   |
| GO:0051058 negative regulation of small GTPase mediated signal transduction           | 1  | 0.66287 | 0.31   | 0.017 | Biological | GO:0051058 negative regulation of small GTPase mediated signal transduction           | 0.66287 | 0.767   | 0 | 0 | 1  | 59   |
| GO:1902808 positive regulation of cell cycle G1/S phase transition                    | 1  | 0.66287 | 0.31   | 0.017 | Biological | GO:1902808 positive regulation of cell cycle G1/S phase transition                    | 0.66287 | 0.767   | 0 | 0 | 1  | 59   |
| GO:0034763 negative regulation of transmembrane transport                             | 2  | 0.66371 | 0.619  | 0.016 | Biological | GO:0034763 negative regulation of transmembrane transport                             | 0.66371 | 0.76762 | 0 | 0 | 2  | 124  |
| GO:0072655 establishment of protein localization to mitochondrion                     | 2  | 0.66371 | 0.619  | 0.016 | Biological | GO:0072655 establishment of protein localization to mitochondrion                     | 0.66371 | 0.76762 | 0 | 0 | 2  | 124  |
| GO:0008749 response to glucose                                                        | 3  | 0.66582 | 0.929  | 0.016 | Biological | GO:0008749 response to glucose                                                        | 0.66582 | 0.76981 | 0 | 0 | 3  | 187  |
| GO:0043112 receptor metabolic process                                                 | 3  | 0.66582 | 0.929  | 0.016 | Biological | GO:0043112 receptor metabolic process                                                 | 0.66582 | 0.76981 | 0 | 0 | 3  | 187  |
| GO:0071375 cellular response to peptide hormone stimulus                              | 5  | 0.66725 | 1.548  | 0.016 | Biological | GO:0071375 cellular response to peptide hormone stimulus                              | 0.66725 | 0.77117 | 0 | 0 | 5  | 309  |
| GO:0019208 phosphatase regulator activity                                             | 2  | 0.66823 | 0.585  | 0.016 | Molecular  | GO:0019208 phosphatase regulator activity                                             | 0.66823 | 0.77972 | 0 | 0 | 2  | 123  |
| GO:0004536 deoxyribonuclease activity                                                 | 1  | 0.66897 | 0.292  | 0.017 | Molecular  | GO:0004536 deoxyribonuclease activity                                                 | 0.66897 | 0.77972 | 0 | 0 | 1  | 59   |
| GO:0016765 transferase activity, transferring alkyl or aryl (other than methyl) group | 1  | 0.66897 | 0.292  | 0.017 | Molecular  | GO:0016765 transferase activity, transferring alkyl or aryl (other than methyl) group | 0.66897 | 0.77972 | 0 | 0 | 1  | 59   |
| GO:0009948 anterior/posterior axis specification                                      | 1  | 0.66904 | 0.31   | 0.017 | Biological | GO:0009948 anterior/posterior axis specification                                      | 0.66904 | 0.77164 | 0 | 0 | 1  | 60   |
| GO:0032613 interleukin-10 production                                                  | 1  | 0.66904 | 0.31   | 0.017 | Biological | GO:0032613 interleukin-10 production                                                  | 0.66904 | 0.77164 | 0 | 0 | 1  | 60   |
| GO:0032653 regulation of interleukin-10 production                                    | 1  | 0.66904 | 0.31   | 0.017 | Biological | GO:0032653 regulation of interleukin-10 production                                    | 0.66904 | 0.77164 | 0 | 0 | 1  | 60   |
| GO:0036202 TORC1 signaling                                                            | 1  | 0.66904 | 0.31   | 0.017 | Biological | GO:0036202 TORC1 signaling                                                            | 0.66904 | 0.77164 | 0 | 0 | 1  | 60   |
| GO:0081164 regulation of protein import into nucleus                                  | 1  | 0.66904 | 0.31   | 0.017 | Biological | GO:0081164 regulation of protein import into nucleus                                  | 0.66904 | 0.77164 | 0 | 0 | 1  | 60   |
| GO:0086065 cell communication involved in cardiac conduction                          | 1  | 0.66904 | 0.31   | 0.017 | Biological | GO:0086065 cell communication involved in cardiac conduction                          | 0.66904 | 0.77164 | 0 | 0 | 1  | 60   |
| GO:0090303 positive regulation of wound healing                                       | 1  | 0.66904 | 0.31   | 0.017 | Biological | GO:0090303 positive regulation of wound healing                                       | 0.66904 | 0.77164 | 0 | 0 | 1  | 60   |
| GO:0097352 autophagosome maturation                                                   | 1  | 0.66904 | 0.31   | 0.017 | Biological | GO:0097352 autophagosome maturation                                                   | 0.66904 | 0.77164 | 0 | 0 | 1  | 60   |
| GO:2001244 positive regulation of intrinsic apoptotic signaling pathway               | 1  | 0.66904 | 0.31   | 0.017 | Biological | GO:2001244 positive regulation of intrinsic apoptotic signaling pathway               | 0.66904 | 0.77164 | 0 | 0 | 1  | 60   |
| GO:0006650 glycolysis/gluconeogenesis                                                 | 5  | 0.67001 | 1.548  | 0.016 | Biological | GO:0006650 glycolysis/gluconeogenesis                                                 | 0.67001 | 0.77257 | 0 | 0 | 5  | 310  |
| GO:0002790 peptide secretion                                                          | 4  | 0.67151 | 1.238  | 0.016 | Biological | GO:0002790 peptide secretion                                                          | 0.67151 | 0.77413 | 0 | 0 | 4  | 250  |
| GO:0032559 adenylyl ribonucleotide binding                                            | 27 | 0.67211 | 7.895  | 0.017 | Molecular  | GO:0032559 adenylyl ribonucleotide binding                                            | 0.67211 | 0.78224 | 0 | 0 | 27 | 1558 |
| GO:0019079 viral genome replication                                                   | 2  | 0.67227 | 0.619  | 0.016 | Biological | GO:0019079 viral genome replication                                                   | 0.67227 | 0.77482 | 0 | 0 | 2  | 126  |
| GO:0046982 protein heterodimerization activity                                        | 6  | 0.67294 | 1.754  | 0.016 | Molecular  | GO:0046982 protein heterodimerization activity                                        | 0.67294 | 0.78224 | 0 | 0 | 6  | 365  |
| GO:1900351 transport complex                                                          | 7  | 0.67455 | 2.017  | 0.016 | Cellular   | GO:1900351 transport complex                                                          | 0.67455 | 0.77611 | 0 | 0 | 7  | 436  |
| GO:0001654 organic acid catabolic process                                             | 4  | 0.67455 | 1.238  | 0.016 | Biological | GO:0001654 organic acid catabolic process                                             | 0.67455 | 0.77611 | 0 | 0 | 4  | 251  |
| GO:0045017 glycerolipid biosynthetic process                                          | 4  | 0.67455 | 1.238  | 0.016 | Biological | GO:0045017 glycerolipid biosynthetic process                                          | 0.67455 | 0.77611 | 0 | 0 | 4  | 251  |
| GO:0016126 sterol biosynthetic process                                                | 1  | 0.67509 | 0.31   | 0.016 | Biological | GO:0016126 sterol biosynthetic process                                                | 0.67509 | 0.77611 | 0 | 0 | 1  | 61   |
| GO:0016447 somatic recombination of immunoglobulin gene segments                      | 1  | 0.67509 | 0.31   | 0.016 | Biological | GO:0016447 somatic recombination of immunoglobulin gene segments                      | 0.67509 | 0.77611 | 0 | 0 | 1  | 61   |
| GO:0042306 regulation of protein import into nucleus                                  | 1  | 0.67509 | 0.31   | 0.016 | Biological | GO:0042306 regulation of protein import into nucleus                                  | 0.67509 | 0.77611 | 0 | 0 | 1  | 61   |
| GO:0042733 embryonic digit morphogenesis                                              | 1  | 0.67509 | 0.31   | 0.016 | Biological | GO:0042733 embryonic digit morphogenesis                                              | 0.67509 | 0.77611 | 0 | 0 | 1  | 61   |
| GO:0044788 modulation by host of viral process                                        | 1  | 0.67509 | 0.31   | 0.016 | Biological | GO:0044788 modulation by host of viral process                                        | 0.67509 | 0.77611 | 0 | 0 | 1  | 61   |
| GO:0046824 positive regulation of nucleocytoplasmic transport                         | 1  | 0.67509 | 0.31   | 0.016 | Biological | GO:0046824 positive regulation of nucleocytoplasmic transport                         | 0.67509 | 0.77611 | 0 | 0 | 1  | 61   |
| GO:0051785 positive regulation of nuclear division                                    | 1  | 0.67509 | 0.31   | 0.016 | Biological | GO:0051785 positive regulation of nuclear division                                    | 0.67509 | 0.77611 | 0 | 0 | 1  | 61   |
| GO:0094020 regulation of heart growth                                                 | 1  | 0.67509 | 0.31   | 0.016 | Biological | GO:0094020 regulation of heart growth                                                 | 0.67509 | 0.77611 | 0 | 0 | 1  | 61   |
| GO:0070255 necrotic cell death                                                        | 1  | 0.67509 | 0.31   | 0.016 | Biological | GO:0070255 necrotic cell death                                                        | 0.67509 | 0.77611 | 0 | 0 | 1  | 61   |
| GO:0046879 hormone secretion                                                          | 5  | 0.67549 | 1.548  | 0.016 | Biological | GO:0046879 hormone secretion                                                          | 0.67549 | 0.77638 | 0 | 0 | 5  | 312  |
| GO:0016570 histone modification                                                       | 8  | 0.6757  | 2.477  | 0.016 | Biological | GO:0016570 histone modification                                                       | 0.6757  | 0.77645 | 0 | 0 | 8  | 491  |
| GO:0058661 inorganic anion transmembrane transport                                    | 2  | 0.67648 | 0.518  | 0.016 | Biological | GO:0058661 inorganic anion transmembrane transport                                    | 0.67648 | 0.77698 | 0 | 0 | 2  | 127  |
| GO:1904950 negative regulation of establishment of protein localization               | 2  | 0.67648 | 0.518  | 0.016 | Biological | GO:1904950 negative regulation of establishment of protein localization               | 0.67648 | 0.77698 | 0 | 0 | 2  | 127  |
| GO:0005267 potassium channel activity                                                 | 2  | 0.67683 | 0.585  | 0.016 | Molecular  | GO:0005267 potassium channel activity                                                 | 0.67683 | 0.78571 | 0 | 0 | 2  | 125  |
| GO:0002697 regulation of immune effector process                                      | 6  | 0.67781 | 1.858  | 0.016 | Biological | GO:0002697 regulation of immune effector process                                      | 0.67781 | 0.77803 | 0 | 0 | 6  | 373  |
| GO:0050727 regulation of inflammatory response                                        | 6  | 0.67781 | 1.858  | 0.016 | Biological | GO:0050727 regulation of inflammatory response                                        | 0.67781 | 0.77803 | 0 | 0 | 6  | 373  |
| GO:0031326 regulation of cellular biosynthetic process                                | 73 | 0.67786 | 22.601 | 0.017 | Biological | GO:0031326 regulation of cellular biosynthetic process                                | 0.67786 | 0.77803 | 0 | 0 | 73 | 4172 |
| GO:0034504 protein localization                                                       | 5  | 0.67882 | 1.548  | 0.016 | Biological | GO:0034504 protein localization                                                       | 0.67882 | 0.77925 | 0 | 0 | 5  | 313  |
| GO:0022408 negative regulation of cell-cell adhesion                                  | 3  | 0.67983 | 0.929  | 0.016 | Biological | GO:0022408 negative regulation of cell-cell adhesion                                  | 0.67983 | 0.77953 | 0 | 0 | 3  | 191  |
| GO:0007041 lysosomal transport                                                        | 2  | 0.68065 | 0.619  | 0.016 | Biological | GO:0007041 lysosomal transport                                                        | 0.68065 | 0.77953 | 0 | 0 | 2  | 128  |
| GO:0071333 cellular response to glucose stimulus                                      | 2  | 0.68065 | 0.619  | 0.016 | Biological | GO:0071333 cellular response to glucose stimulus                                      | 0.68065 | 0.77953 | 0 | 0 | 2  | 128  |
| GO:0032943 mononuclear cell proliferation                                             | 5  | 0.6809  | 1.548  | 0.016 | Biological | GO:0032943 mononuclear cell proliferation                                             | 0.6809  | 0.77953 | 0 | 0 | 5  | 314  |
| GO:0019229 regulation of cellular maturation                                          | 1  | 0.68104 | 0.31   | 0.016 | Biological | GO:0019229 regulation of cellular maturation                                          | 0.68104 | 0.77953 | 0 | 0 | 1  | 62   |
| GO:0031122 cytoplasmic microtubule organization                                       | 1  | 0.68104 | 0.31   | 0.016 | Biological | GO:0031122 cytoplasmic microtubule organization                                       | 0.68104 | 0.77953 | 0 | 0 | 1  | 62   |
| GO:0032615 interleukin-12 production                                                  | 1  | 0.68104 | 0.31   | 0.016 | Biological | GO:0032615 interleukin-12 production                                                  | 0.68104 | 0.77953 | 0 | 0 | 1  | 62   |
| GO:0032655 regulation of interleukin-12 production                                    | 1  | 0.68104 | 0.31   | 0.016 | Biological | GO:0032655 regulation of interleukin-12 production                                    | 0.68104 | 0.77953 | 0 | 0 | 1  | 62   |
| GO:0048255 mRNA stabilization                                                         | 1  | 0.68104 | 0.31   | 0.016 | Biological | GO:0048255 mRNA stabilization                                                         | 0.68104 | 0.77953 | 0 | 0 | 1  | 62   |
| GO:0056994 regulation of lipid catabolic process                                      | 1  | 0.68104 | 0.31   | 0.016 | Biological | GO:0056994 regulation of lipid catabolic process                                      | 0.68104 | 0.77953 | 0 | 0 | 1  | 62   |
| GO:0072666 establishment of protein localization to vacuole                           | 1  | 0.68104 | 0.31   | 0.016 | Biological | GO:0072666 establishment of protein localization to vacuole                           | 0.68104 | 0.77953 | 0 | 0 | 1  | 62   |
| GO:0001786 phosphatidylserine binding                                                 | 1  | 0.68117 | 0.292  | 0.016 | Molecular  | GO:0001786 phosphatidylserine binding                                                 | 0.68117 | 0.78863 | 0 | 0 | 1  | 61   |
| GO:0005507 copper ion binding                                                         | 1  | 0.68117 | 0.292  | 0.016 | Molecular  | GO:0005507 copper ion binding                                                         | 0.68117 | 0.78863 | 0 | 0 | 1  | 61   |
| GO:0043436 oxoacid metabolic process                                                  | 16 | 0.68202 | 4.354  | 0.017 | Biological | GO:0043436 oxoacid metabolic process                                                  | 0.68202 | 0.78848 | 0 | 0 | 16 | 961  |
| GO:0002819 regulation of adaptive immune response                                     | 3  | 0.68324 | 0.929  | 0.016 | Biological | GO:0002819 regulation of adaptive immune response                                     | 0.68324 | 0.78135 | 0 | 0 | 3  | 192  |
| GO:0009746 response to hexose                                                         | 3  | 0.68324 | 0.929  | 0.016 | Biological | GO:0009746 response to hexose                                                         | 0.68324 | 0.78135 | 0 | 0 | 3  | 192  |
| GO:0009889 regulation of biosynthetic process                                         | 74 | 0.68325 | 22.91  | 0.017 | Biological | GO:0009889 regulation of biosynthetic process                                         | 0.68325 | 0.78135 | 0 | 0 | 74 | 4234 |
| GO:0002699 positive regulation of immune effector process                             | 4  | 0.68354 | 1.238  | 0.016 | Biological | GO:0002699 positive regulation of immune effector process                             | 0.68354 | 0.78138 | 0 | 0 | 4  | 254  |
| GO:0006989 phagocytosis                                                               | 5  | 0.68359 | 1.548  | 0.016 | Biological | GO:0006989 phagocytosis                                                               | 0.68359 | 0.78138 | 0 | 0 | 5  | 316  |
| GO:0006911 phagocytosis, engulfment                                                   | 2  | 0.68477 | 0.619  | 0.016 | Biological | GO:0006911 phagocytosis, engulfment                                                   | 0.68477 | 0.78237 | 0 | 0 | 2  | 129  |
| GO:0031109 microtubule polymerization or depolymerization                             |    |         |        |       |            |                                                                                       |         |         |   |   |    |      |

|                                                                                   |     |         |        |       |            |          |                                                                        |         |         |   |   |     |       |
|-----------------------------------------------------------------------------------|-----|---------|--------|-------|------------|----------|------------------------------------------------------------------------|---------|---------|---|---|-----|-------|
| GO:002696 positive regulation of leukocyte activation                             | 7   | 0.70784 | 2.167  | 0.016 | Biological | GO:00020 | positive regulation of leukocyte activation                            | 0.70784 | 0.79994 | 0 | 0 | 7   | 446   |
| GO:003168 platelet activation                                                     | 2   | 0.7086  | 0.619  | 0.015 | Biological | GO:0030  | platelet activation                                                    | 0.7086  | 0.80018 | 0 | 0 | 2   | 135   |
| GO:001645 somatic diversification of immunoglobulins                              | 1   | 0.70917 | 0.31   | 0.015 | Biological | GO:0016  | somatic diversification of immunoglobulins                             | 0.70917 | 0.80018 | 0 | 0 | 1   | 87    |
| GO:003257 maintenance of protein location in cell                                 | 1   | 0.70917 | 0.31   | 0.015 | Biological | GO:0032  | maintenance of protein location in cell                                | 0.70917 | 0.80018 | 0 | 0 | 1   | 67    |
| GO:003519 somatic stem cell population maintenance                                | 1   | 0.70917 | 0.31   | 0.015 | Biological | GO:0035  | somatic stem cell population maintenance                               | 0.70917 | 0.80018 | 0 | 0 | 1   | 67    |
| GO:005081 multicellular organismal water homeostasis                              | 1   | 0.70917 | 0.31   | 0.015 | Biological | GO:0050  | multicellular organismal water homeostasis                             | 0.70917 | 0.80018 | 0 | 0 | 1   | 67    |
| GO:006193 positive regulation of lipase activity                                  | 1   | 0.70917 | 0.31   | 0.015 | Biological | GO:0060  | positive regulation of lipase activity                                 | 0.70917 | 0.80018 | 0 | 0 | 1   | 67    |
| GO:007013 regulation of protein processing                                        | 1   | 0.70917 | 0.31   | 0.015 | Biological | GO:0070  | regulation of protein processing                                       | 0.70917 | 0.80018 | 0 | 0 | 1   | 67    |
| GO:004284 response to monosaccharide                                              | 3   | 0.70955 | 0.929  | 0.015 | Biological | GO:0042  | response to monosaccharide                                             | 0.70955 | 0.80025 | 0 | 0 | 3   | 200   |
| GO:009076 regulation of peptide hormone secretion                                 | 3   | 0.70955 | 0.929  | 0.015 | Biological | GO:0090  | regulation of peptide hormone secretion                                | 0.70955 | 0.80025 | 0 | 0 | 3   | 200   |
| GO:000548 phospholipid transporter activity                                       | 1   | 0.70974 | 0.292  | 0.015 | Molecular  | GO:0005  | phospholipid transporter activity                                      | 0.70974 | 0.80449 | 0 | 0 | 1   | 66    |
| GO:0015453 oxidoreductase-driven active transmembrane transporter activity        | 1   | 0.70974 | 0.292  | 0.015 | Molecular  | GO:0015  | oxidoreductase-driven active transmembrane transporter activity        | 0.70974 | 0.80449 | 0 | 0 | 1   | 66    |
| GO:009710 scaffold protein binding                                                | 1   | 0.71037 | 0.297  | 0.015 | Cellular   | GO:0097  | scaffold protein binding                                               | 0.71037 | 0.80454 | 0 | 0 | 1   | 68    |
| GO:000578 peroxisomal membrane                                                    | 1   | 0.71037 | 0.297  | 0.015 | Cellular   | GO:0005  | peroxisomal membrane                                                   | 0.71037 | 0.80454 | 0 | 0 | 1   | 68    |
| GO:0031903 microbody membrane                                                     | 1   | 0.71037 | 0.297  | 0.015 | Cellular   | GO:0031  | microbody membrane                                                     | 0.71037 | 0.80454 | 0 | 0 | 1   | 68    |
| GO:0006082 organic acid metabolic process                                         | 16  | 0.71135 | 4.954  | 0.016 | Biological | GO:0006  | organic acid metabolic process                                         | 0.71135 | 0.80207 | 0 | 0 | 16  | 980   |
| GO:004586 negative regulation of cell cycle                                       | 6   | 0.71149 | 1.858  | 0.016 | Biological | GO:0045  | negative regulation of cell cycle                                      | 0.71149 | 0.80207 | 0 | 0 | 6   | 387   |
| GO:0005622 intracellular anatomical structure                                     | 287 | 0.71223 | 79.228 | 0.018 | Cellular   | GO:0005  | intracellular anatomical structure                                     | 0.71223 | 0.80435 | 0 | 0 | 287 | 15008 |
| GO:0006470 protein dephosphorylation                                              | 4   | 0.71226 | 1.238  | 0.015 | Biological | GO:0006  | protein dephosphorylation                                              | 0.71226 | 0.80204 | 0 | 0 | 4   | 254   |
| GO:0002705 positive regulation of leukocyte mediated immunity                     | 2   | 0.71243 | 0.619  | 0.015 | Biological | GO:0002  | positive regulation of leukocyte mediated immunity                     | 0.71243 | 0.80204 | 0 | 0 | 2   | 136   |
| GO:0007052 mitotic spindle organization                                           | 2   | 0.71243 | 0.619  | 0.015 | Biological | GO:0007  | mitotic spindle organization                                           | 0.71243 | 0.80204 | 0 | 0 | 2   | 136   |
| GO:0007368 determination of left/right symmetry                                   | 2   | 0.71243 | 0.619  | 0.015 | Biological | GO:0007  | determination of left/right symmetry                                   | 0.71243 | 0.80204 | 0 | 0 | 2   | 136   |
| GO:003025 protein kinase activator activity                                       | 2   | 0.71331 | 0.585  | 0.015 | Molecular  | GO:0030  | protein kinase activator activity                                      | 0.71331 | 0.80749 | 0 | 0 | 2   | 134   |
| GO:0015909 long-chain fatty acid transport                                        | 1   | 0.71449 | 0.31   | 0.015 | Biological | GO:0015  | long-chain fatty acid transport                                        | 0.71449 | 0.80346 | 0 | 0 | 1   | 68    |
| GO:0030837 negative regulation of actin filament polymerization                   | 1   | 0.71449 | 0.31   | 0.015 | Biological | GO:0030  | negative regulation of actin filament polymerization                   | 0.71449 | 0.80346 | 0 | 0 | 1   | 68    |
| GO:0046513 ceramide biosynthetic process                                          | 1   | 0.71449 | 0.31   | 0.015 | Biological | GO:0046  | ceramide biosynthetic process                                          | 0.71449 | 0.80346 | 0 | 0 | 1   | 68    |
| GO:0046826 regulation of insulin receptor signaling pathway                       | 1   | 0.71449 | 0.31   | 0.015 | Biological | GO:0046  | regulation of insulin receptor signaling pathway                       | 0.71449 | 0.80346 | 0 | 0 | 1   | 68    |
| GO:0046888 negative regulation of hormone secretion                               | 1   | 0.71449 | 0.31   | 0.015 | Biological | GO:0046  | negative regulation of hormone secretion                               | 0.71449 | 0.80346 | 0 | 0 | 1   | 68    |
| GO:000776 regulation of cellular response to insulin stimulus                     | 1   | 0.71449 | 0.31   | 0.015 | Biological | GO:0007  | regulation of cellular response to insulin stimulus                    | 0.71449 | 0.80346 | 0 | 0 | 1   | 68    |
| GO:2000144 positive regulation of DNA-templated transcription, initiation         | 1   | 0.71449 | 0.31   | 0.015 | Biological | GO:2000  | positive regulation of DNA-templated transcription, initiation         | 0.71449 | 0.80346 | 0 | 0 | 1   | 68    |
| GO:0008080 N-acetyltransferase activity                                           | 1   | 0.71513 | 0.292  | 0.015 | Molecular  | GO:0008  | N-acetyltransferase activity                                           | 0.71513 | 0.80849 | 0 | 0 | 1   | 67    |
| GO:0051249 regulation of lymphocyte activation                                    | 9   | 0.71578 | 2.786  | 0.016 | Biological | GO:0051  | regulation of lymphocyte activation                                    | 0.71578 | 0.80446 | 0 | 0 | 9   | 570   |
| GO:000605 glucose metabolic process                                               | 3   | 0.71586 | 0.929  | 0.015 | Biological | GO:0006  | glucose metabolic process                                              | 0.71586 | 0.80446 | 0 | 0 | 3   | 202   |
| GO:0030073 insulin secretion                                                      | 3   | 0.71586 | 0.929  | 0.015 | Biological | GO:0030  | insulin secretion                                                      | 0.71586 | 0.80446 | 0 | 0 | 3   | 202   |
| GO:0032368 regulation of lipid transport                                          | 2   | 0.71621 | 0.619  | 0.015 | Biological | GO:0032  | regulation of lipid transport                                          | 0.71621 | 0.80448 | 0 | 0 | 2   | 137   |
| GO:0050853 B cell receptor signaling pathway                                      | 2   | 0.71621 | 0.619  | 0.015 | Biological | GO:0050  | B cell receptor signaling pathway                                      | 0.71621 | 0.80448 | 0 | 0 | 2   | 137   |
| GO:0002548 monocyte chemotaxis                                                    | 1   | 0.71971 | 0.31   | 0.014 | Biological | GO:0002  | monocyte chemotaxis                                                    | 0.71971 | 0.80687 | 0 | 0 | 1   | 69    |
| GO:0038034 signal transduction in absence of ligand                               | 1   | 0.71971 | 0.31   | 0.014 | Biological | GO:0038  | signal transduction in absence of ligand                               | 0.71971 | 0.80687 | 0 | 0 | 1   | 69    |
| GO:0050959 sensory perception of taste                                            | 1   | 0.71971 | 0.31   | 0.014 | Biological | GO:0050  | sensory perception of taste                                            | 0.71971 | 0.80687 | 0 | 0 | 1   | 69    |
| GO:0097192 extrinsic apoptotic signaling pathway in absence of ligand             | 1   | 0.71971 | 0.31   | 0.014 | Biological | GO:0097  | extrinsic apoptotic signaling pathway in absence of ligand             | 0.71971 | 0.80687 | 0 | 0 | 1   | 69    |
| GO:0150116 regulation of cell-substrate junction organization                     | 1   | 0.71971 | 0.31   | 0.014 | Biological | GO:0150  | regulation of cell-substrate junction organization                     | 0.71971 | 0.80687 | 0 | 0 | 1   | 69    |
| GO:0008020 anion transport                                                        | 8   | 0.71975 | 2.477  | 0.016 | Biological | GO:0008  | anion transport                                                        | 0.71975 | 0.80687 | 0 | 0 | 8   | 512   |
| GO:0006023 cholesterol metabolic process                                          | 2   | 0.71995 | 0.619  | 0.014 | Biological | GO:0006  | cholesterol metabolic process                                          | 0.71995 | 0.80687 | 0 | 0 | 2   | 138   |
| GO:0030317 flagellated sperm motility                                             | 2   | 0.71995 | 0.619  | 0.014 | Biological | GO:0030  | flagellated sperm motility                                             | 0.71995 | 0.80687 | 0 | 0 | 2   | 138   |
| GO:0097222 sperm motility                                                         | 2   | 0.71995 | 0.619  | 0.014 | Biological | GO:0097  | sperm motility                                                         | 0.71995 | 0.80687 | 0 | 0 | 2   | 138   |
| GO:0090924 plasma membrane invagination                                           | 2   | 0.71995 | 0.619  | 0.014 | Biological | GO:0090  | plasma membrane invagination                                           | 0.71995 | 0.80687 | 0 | 0 | 2   | 138   |
| GO:0070663 regulation of leukocyte proliferation                                  | 4   | 0.7205  | 1.238  | 0.015 | Biological | GO:0070  | regulation of leukocyte proliferation                                  | 0.7205  | 0.8073  | 0 | 0 | 4   | 267   |
| GO:0005059 anion transporter activity                                             | 5   | 0.72051 | 1.462  | 0.015 | Molecular  | GO:0005  | anion transporter activity                                             | 0.72051 | 0.81361 | 0 | 0 | 5   | 324   |
| GO:0040587 innate immune response                                                 | 15  | 0.72109 | 4.644  | 0.016 | Biological | GO:0040  | innate immune response                                                 | 0.72109 | 0.80779 | 0 | 0 | 15  | 928   |
| GO:0001669 acrosomal vesicle                                                      | 2   | 0.72145 | 0.93   | 0.014 | Cellular   | GO:0001  | acrosomal vesicle                                                      | 0.72145 | 0.86348 | 0 | 0 | 2   | 140   |
| GO:0002244 hematopoietic progenitor cell differentiation                          | 2   | 0.72364 | 0.619  | 0.014 | Biological | GO:0002  | hematopoietic progenitor cell differentiation                          | 0.72364 | 0.81047 | 0 | 0 | 2   | 139   |
| GO:0006305 DNA alkylation                                                         | 1   | 0.72484 | 0.31   | 0.014 | Biological | GO:0006  | DNA alkylation                                                         | 0.72484 | 0.81054 | 0 | 0 | 1   | 70    |
| GO:0006306 DNA methylation                                                        | 1   | 0.72484 | 0.31   | 0.014 | Biological | GO:0006  | DNA methylation                                                        | 0.72484 | 0.81054 | 0 | 0 | 1   | 70    |
| GO:0045109 intermediate filament organization                                     | 1   | 0.72484 | 0.31   | 0.014 | Biological | GO:0045  | intermediate filament organization                                     | 0.72484 | 0.81054 | 0 | 0 | 1   | 70    |
| GO:0051881 regulation of mitochondrial membrane potential                         | 1   | 0.72484 | 0.31   | 0.014 | Biological | GO:0051  | regulation of mitochondrial membrane potential                         | 0.72484 | 0.81054 | 0 | 0 | 1   | 70    |
| GO:0060411 cardiac septum morphogenesis                                           | 1   | 0.72484 | 0.31   | 0.014 | Biological | GO:0060  | cardiac septum morphogenesis                                           | 0.72484 | 0.81054 | 0 | 0 | 1   | 70    |
| GO:0061512 protein localization to cilium                                         | 1   | 0.72484 | 0.31   | 0.014 | Biological | GO:0061  | protein localization to cilium                                         | 0.72484 | 0.81054 | 0 | 0 | 1   | 70    |
| GO:190317 regulation of protein maturation                                        | 1   | 0.72484 | 0.31   | 0.014 | Biological | GO:1903  | regulation of protein maturation                                       | 0.72484 | 0.81054 | 0 | 0 | 1   | 70    |
| GO:0018010 regulation of protein localization to nucleus                          | 2   | 0.7273  | 0.619  | 0.014 | Biological | GO:0018  | regulation of protein localization to nucleus                          | 0.7273  | 0.81303 | 0 | 0 | 2   | 140   |
| GO:0032102 negative regulation of response to external stimulus                   | 6   | 0.7274  | 1.858  | 0.015 | Biological | GO:0032  | negative regulation of response to external stimulus                   | 0.7274  | 0.81303 | 0 | 0 | 6   | 394   |
| GO:0043335 phagocytotic vesicle                                                   | 2   | 0.72869 | 0.593  | 0.014 | Cellular   | GO:0043  | phagocytotic vesicle                                                   | 0.72869 | 0.8688  | 0 | 0 | 2   | 142   |
| GO:000271 polysaccharide biosynthetic process                                     | 1   | 0.72988 | 0.31   | 0.014 | Biological | GO:0002  | polysaccharide biosynthetic process                                    | 0.72988 | 0.81435 | 0 | 0 | 1   | 71    |
| GO:0002562 somatic diversification of immune receptors via germline recombination | 1   | 0.72988 | 0.31   | 0.014 | Biological | GO:0002  | somatic diversification of immune receptors via germline recombination | 0.72988 | 0.81435 | 0 | 0 | 1   | 71    |
| GO:0016444 somatic cell DNA recombination                                         | 1   | 0.72988 | 0.31   | 0.014 | Biological | GO:0016  | somatic cell DNA recombination                                         | 0.72988 | 0.81435 | 0 | 0 | 1   | 71    |
| GO:0032922 circadian regulation of gene expression                                | 1   | 0.72988 | 0.31   | 0.014 | Biological | GO:0032  | circadian regulation of gene expression                                | 0.72988 | 0.81435 | 0 | 0 | 1   | 71    |
| GO:0043489 RNA stabilization                                                      | 1   | 0.72988 | 0.31   | 0.014 | Biological | GO:0043  | RNA stabilization                                                      | 0.72988 | 0.81435 | 0 | 0 | 1   | 71    |
| GO:0072678 T cell migration                                                       | 1   | 0.72988 | 0.31   | 0.014 | Biological | GO:0072  | T cell migration                                                       | 0.72988 | 0.81435 | 0 | 0 | 1   | 71    |
| GO:1903036 positive regulation of response to wounding                            | 2   | 0.72988 | 0.619  | 0.014 | Biological | GO:1903  | positive regulation of response to wounding                            | 0.72988 | 0.81435 | 0 | 0 | 2   | 141   |
| GO:2000036 regulation of stem cell population maintenance                         | 1   | 0.72988 | 0.31   | 0.014 | Biological | GO:2000  | regulation of stem cell population maintenance                         | 0.72988 | 0.81435 | 0 | 0 | 1   | 71    |
| GO:0019005 syntaxin binding                                                       | 1   | 0.73074 | 0.292  | 0.014 | Molecular  | GO:0019  | syntaxin binding                                                       | 0.73074 | 0.82398 | 0 | 0 | 1   | 70    |
| GO:0035869 ciliary transition zone                                                | 1   | 0.73077 | 0.297  | 0.014 | Cellular   | GO:0035  | ciliary transition zone                                                | 0.73077 | 0.8688  | 0 | 0 | 1   | 72    |
| GO:0070821 tertiary granule membrane                                              | 1   | 0.73077 | 0.297  | 0.014 | Cellular   | GO:0070  | tertiary granule membrane                                              | 0.73077 | 0.8688  | 0 | 0 | 1   | 72    |
| GO:0032628 lipid metabolism                                                       | 3   | 0.73118 | 0.929  | 0.014 | Biological | GO:0032  | lipid metabolism                                                       | 0.73118 | 0.81361 | 0 | 0 | 3   | 207   |
| GO:0006955 immune response                                                        | 33  | 0.73381 | 10.217 | 0.017 | Biological | GO:0006  | immune response                                                        | 0.73381 | 0.81785 | 0 | 0 | 33  | 1979  |
| GO:0007049 cell cycle                                                             | 30  | 0.73381 | 9.288  | 0.017 | Biological | GO:0007  | cell cycle                                                             | 0.73381 | 0.81785 | 0 | 0 | 30  | 1807  |
| GO:0050884 regulation of mRNA processing                                          | 2   | 0.73449 | 0.619  | 0.014 | Biological | GO:0050  | regulation of mRNA processing                                          | 0.73449 | 0.81785 | 0 | 0 | 2   | 142   |
| GO:0003143 embryonic heart tube morphogenesis                                     | 1   | 0.73482 | 0.31   | 0.014 | Biological | GO:0003  | embryonic heart tube morphogenesis                                     | 0.73482 | 0.81785 | 0 | 0 | 1   | 72    |
| GO:0006024 glycosaminoglycan biosynthetic process                                 | 1   | 0.73482 | 0.31   | 0.014 | Biological | GO:0006  | glycosaminoglycan biosynthetic process                                 | 0.73482 | 0.81785 | 0 | 0 | 1   | 72    |
| GO:0006089 nitric oxide biosynthetic process                                      | 1   | 0.73482 | 0.31   | 0.014 | Biological | GO:0006  | nitric oxide biosynthetic process                                      | 0.73482 | 0.81785 | 0 | 0 | 1   | 72    |
| GO:0043627 response to estrogen                                                   | 1   | 0.73482 | 0.31   | 0.014 | Biological | GO:0043  | response to estrogen                                                   | 0.73482 | 0.81785 | 0 | 0 | 1   | 72    |
| GO:0050766 positive regulation of phagocytosis                                    | 1   | 0.73482 | 0.31   | 0.014 | Biological | GO:0050  | positive regulation of phagocytosis                                    | 0.73482 | 0.81785 | 0 | 0 | 1   | 72    |
| GO:0061371 determination of heart left/right asymmetry                            | 1   | 0.73482 | 0.31   | 0.014 | Biological | GO:0061  | determination of heart left/right asymmetry                            | 0.73482 | 0.81785 | 0 | 0 | 1   | 72    |
| GO:1902733 negative regulation of mRNA catabolic process                          | 1   | 0.73482 | 0.31   | 0.014 | Biological | GO:1902  | negative regulation of mRNA catabolic process                          | 0.73482 | 0.81785 | 0 | 0 | 1   | 72    |
| GO:0008234 cysteine-type peptidase activity                                       | 3   | 0.73537 | 0.877  | 0.015 | Molecular  | GO:0008  | cysteine-type peptidase activity                                       | 0.73537 | 0.82533 | 0 | 0 | 3   | 205   |
| GO:0032153 cell division site                                                     | 1   | 0.73564 | 0.297  | 0.014 | Cellular   | GO:0032  | cell division site                                                     | 0.73564 | 0.82765 | 0 | 0 | 1   | 73    |
| GO:0019209 kinase activator activity                                              | 2   | 0.73567 | 0.585  | 0.014 | Molecular  | GO:0019  | kinase activator activity                                              | 0.73567 | 0.82533 | 0 | 0 | 2   | 140   |
| GO:0002039 p53 binding                                                            | 1   | 0.73575 | 0.292  | 0.014 | Molecular  | GO:0002  | p53 binding                                                            | 0.73575 | 0.82533 | 0 | 0 | 1   | 73    |
| GO:0043621 protein self-association                                               | 1   | 0.73575 | 0.292  | 0.014 | Molecular  | GO:0043  | protein self-association                                               | 0.73575 | 0.82533 |   |   |     |       |

|                                                                        |     |         |        |       |            |                                                                          |         |         |   |   |     |       |
|------------------------------------------------------------------------|-----|---------|--------|-------|------------|--------------------------------------------------------------------------|---------|---------|---|---|-----|-------|
| GO:0010821 regulation of mitochondrion organization                    | 2   | 0.7584  | 0.619  | 0.013 | Biological | GO:0010101 regulation of mitochondrion organization                      | 0.7584  | 0.83616 | 0 | 0 | 2   | 149   |
| GO:0036126 sperm flagellum                                             | 2   | 0.75931 | 0.593  | 0.013 | Cellular   | GO:00036 sperm flagellum                                                 | 0.75931 | 0.88697 | 0 | 0 | 2   | 151   |
| GO:0003724 RNA release activity                                        | 1   | 0.75944 | 0.292  | 0.013 | Molecular  | GO:00037 RNA release activity                                            | 0.75944 | 0.8378  | 0 | 0 | 1   | 76    |
| GO:0003725 double-stranded RNA binding                                 | 1   | 0.75944 | 0.292  | 0.013 | Molecular  | GO:00037 double-stranded RNA binding                                     | 0.75944 | 0.8378  | 0 | 0 | 1   | 76    |
| GO:0007224 smoothed signaling pathway                                  | 2   | 0.76166 | 0.619  | 0.013 | Biological | GO:00072 smoothed signaling pathway                                      | 0.76166 | 0.83799 | 0 | 0 | 2   | 150   |
| GO:0031023 microtubule organizing center organization                  | 2   | 0.76166 | 0.619  | 0.013 | Biological | GO:00310 microtubule organizing center organization                      | 0.76166 | 0.83799 | 0 | 0 | 2   | 150   |
| GO:0050728 negative regulation of inflammatory response                | 2   | 0.76166 | 0.619  | 0.013 | Biological | GO:00507 negative regulation of inflammatory response                    | 0.76166 | 0.83799 | 0 | 0 | 2   | 150   |
| GO:0006254 cilium movement involved in cell motility                   | 2   | 0.76166 | 0.619  | 0.013 | Biological | GO:00062 cilium movement involved in cell motility                       | 0.76166 | 0.83799 | 0 | 0 | 2   | 150   |
| GO:0002200 somatic diversification of immune receptors                 | 1   | 0.76265 | 0.31   | 0.013 | Biological | GO:00022 somatic diversification of immune receptors                     | 0.76265 | 0.83799 | 0 | 0 | 1   | 78    |
| GO:0019226 transmission of nerve impulse                               | 1   | 0.76265 | 0.31   | 0.013 | Biological | GO:00192 transmission of nerve impulse                                   | 0.76265 | 0.83799 | 0 | 0 | 1   | 78    |
| GO:0045814 negative regulation of gene expression, epigenetic          | 1   | 0.76265 | 0.31   | 0.013 | Biological | GO:00458 negative regulation of gene expression, epigenetic              | 0.76265 | 0.83799 | 0 | 0 | 1   | 78    |
| GO:0046209 nitric oxide metabolic process                              | 1   | 0.76265 | 0.31   | 0.013 | Biological | GO:00462 nitric oxide metabolic process                                  | 0.76265 | 0.83799 | 0 | 0 | 1   | 78    |
| GO:0070628 heterotrimeric G-protein organization                       | 1   | 0.76265 | 0.31   | 0.013 | Biological | GO:00706 heterotrimeric G-protein organization                           | 0.76265 | 0.83799 | 0 | 0 | 1   | 78    |
| GO:1903533 regulation of protein targeting                             | 1   | 0.76265 | 0.31   | 0.013 | Biological | GO:19035 regulation of protein targeting                                 | 0.76265 | 0.83799 | 0 | 0 | 1   | 78    |
| GO:0070661 leukocyte proliferation                                     | 5   | 0.76367 | 1.548  | 0.014 | Biological | GO:00706 leukocyte proliferation                                         | 0.76367 | 0.83892 | 0 | 0 | 5   | 348   |
| GO:0015748 organophosphate ester transport                             | 2   | 0.76488 | 0.619  | 0.013 | Biological | GO:00157 organophosphate ester transport                                 | 0.76488 | 0.83989 | 0 | 0 | 2   | 151   |
| GO:0051592 response to calcium ion                                     | 2   | 0.76488 | 0.619  | 0.013 | Biological | GO:00515 response to calcium ion                                         | 0.76488 | 0.83989 | 0 | 0 | 2   | 151   |
| GO:0001057 reactive nitrogen species metabolic process                 | 1   | 0.76787 | 0.31   | 0.013 | Biological | GO:00010 reactive nitrogen species metabolic process                     | 0.76787 | 0.84203 | 0 | 0 | 1   | 79    |
| GO:0008186 ATP-dependent activity, acting on RNA                       | 1   | 0.76831 | 0.292  | 0.013 | Molecular  | GO:00081 ATP-dependent activity, acting on RNA                           | 0.76831 | 0.84543 | 0 | 0 | 1   | 78    |
| GO:0035064 methylated histone binding                                  | 1   | 0.76831 | 0.292  | 0.013 | Molecular  | GO:00350 methylated histone binding                                      | 0.76831 | 0.84543 | 0 | 0 | 1   | 78    |
| GO:0007005 mitochondrion organization                                  | 8   | 0.76854 | 2.477  | 0.015 | Biological | GO:00070 mitochondrion organization                                      | 0.76854 | 0.84533 | 0 | 0 | 8   | 538   |
| GO:0008976 vesicle-mediated transport to the plasma membrane           | 2   | 0.77121 | 0.619  | 0.013 | Biological | GO:00089 vesicle-mediated transport to the plasma membrane               | 0.77121 | 0.8456  | 0 | 0 | 2   | 153   |
| GO:0001895 retina homeostasis                                          | 1   | 0.77126 | 0.31   | 0.013 | Biological | GO:00018 retina homeostasis                                              | 0.77126 | 0.8456  | 0 | 0 | 1   | 80    |
| GO:0003300 cardiac muscle hypertrophy                                  | 1   | 0.77126 | 0.31   | 0.013 | Biological | GO:00033 cardiac muscle hypertrophy                                      | 0.77126 | 0.8456  | 0 | 0 | 1   | 80    |
| GO:0006900 vesicle budding from membrane                               | 1   | 0.77126 | 0.31   | 0.013 | Biological | GO:00069 vesicle budding from membrane                                   | 0.77126 | 0.8456  | 0 | 0 | 1   | 80    |
| GO:2000142 regulation of DNA-templated transcription, initiation       | 1   | 0.77126 | 0.31   | 0.013 | Biological | GO:20001 regulation of DNA-templated transcription, initiation           | 0.77126 | 0.8456  | 0 | 0 | 1   | 80    |
| GO:0005254 chloride channel activity                                   | 1   | 0.77262 | 0.292  | 0.013 | Molecular  | GO:00052 chloride channel activity                                       | 0.77262 | 0.84802 | 0 | 0 | 1   | 79    |
| GO:0030971 receptor tyrosine kinase binding                            | 1   | 0.77262 | 0.292  | 0.013 | Molecular  | GO:00309 receptor tyrosine kinase binding                                | 0.77262 | 0.84802 | 0 | 0 | 1   | 79    |
| GO:0016607 nuclear speck                                               | 6   | 0.77573 | 1.78   | 0.014 | Cellular   | GO:00166 nuclear speck                                                   | 0.77573 | 0.90184 | 0 | 0 | 6   | 421   |
| GO:0016125 steroid metabolic process                                   | 2   | 0.77432 | 0.619  | 0.013 | Biological | GO:00161 steroid metabolic process                                       | 0.77432 | 0.84876 | 0 | 0 | 2   | 154   |
| GO:0002532 production of molecular mediator involved in inflammatory   | 1   | 0.77545 | 0.31   | 0.012 | Biological | GO:00025 production of molecular mediator involved in inflammatory       | 0.77545 | 0.84907 | 0 | 0 | 1   | 81    |
| GO:0006543 fibroblast growth factor receptor signaling pathway         | 1   | 0.77545 | 0.31   | 0.012 | Biological | GO:00065 fibroblast growth factor receptor signaling pathway             | 0.77545 | 0.84907 | 0 | 0 | 1   | 81    |
| GO:0009054 glutamate family amino acid metabolic process               | 1   | 0.77545 | 0.31   | 0.012 | Biological | GO:00090 glutamate family amino acid metabolic process                   | 0.77545 | 0.84907 | 0 | 0 | 1   | 81    |
| GO:1901264 carbohydrate derivative transport                           | 1   | 0.77545 | 0.31   | 0.012 | Biological | GO:19012 carbohydrate derivative transport                               | 0.77545 | 0.84907 | 0 | 0 | 1   | 81    |
| GO:0021177 positive regulation of organelle assembly                   | 1   | 0.77545 | 0.31   | 0.012 | Biological | GO:00211 positive regulation of organelle assembly                       | 0.77545 | 0.84907 | 0 | 0 | 1   | 81    |
| GO:0140034 methylation-dependent protein binding                       | 1   | 0.77685 | 0.292  | 0.013 | Molecular  | GO:01400 methylation-dependent protein binding                           | 0.77685 | 0.85159 | 0 | 0 | 1   | 80    |
| GO:0043229 intracellular organelle                                     | 235 | 0.77742 | 69.733 | 0.018 | Cellular   | GO:00432 intracellular organelle                                         | 0.77742 | 0.90298 | 0 | 0 | 235 | 13366 |
| GO:0034645 cellular macromolecule biosynthetic process                 | 83  | 0.77817 | 3.264  | 0.015 | Cellular   | GO:00346 cellular macromolecule biosynthetic process                     | 0.77817 | 0.85111 | 0 | 0 | 83  | 4890  |
| GO:0005929 cilium                                                      | 11  | 0.77817 | 3.264  | 0.015 | Cellular   | GO:00059 cilium                                                          | 0.77817 | 0.90298 | 0 | 0 | 11  | 736   |
| GO:0005901 caveola                                                     | 1   | 0.77977 | 0.297  | 0.012 | Cellular   | GO:00059 caveola                                                         | 0.77977 | 0.90298 | 0 | 0 | 1   | 83    |
| GO:0044242 cellular lipid catabolic process                            | 3   | 0.78097 | 0.929  | 0.013 | Biological | GO:00442 cellular lipid catabolic process                                | 0.78097 | 0.85455 | 0 | 0 | 3   | 225   |
| GO:0007136 cellular response to tumor necrosis factor                  | 3   | 0.78097 | 0.929  | 0.013 | Biological | GO:00071 cellular response to tumor necrosis factor                      | 0.78097 | 0.85455 | 0 | 0 | 3   | 225   |
| GO:0008897 exocytosis                                                  | 5   | 0.78252 | 1.548  | 0.014 | Cellular   | GO:00088 exocytosis                                                      | 0.78252 | 0.85612 | 0 | 0 | 5   | 357   |
| GO:1900542 mitochondrial transmembrane transport                       | 2   | 0.78343 | 0.619  | 0.013 | Biological | GO:19005 mitochondrial transmembrane transport                           | 0.78343 | 0.85612 | 0 | 0 | 2   | 157   |
| GO:0032272 negative regulation of protein polymerization               | 1   | 0.7836  | 0.31   | 0.012 | Biological | GO:00322 negative regulation of protein polymerization                   | 0.7836  | 0.85612 | 0 | 0 | 1   | 83    |
| GO:0032410 negative regulation of transporter activity                 | 1   | 0.7836  | 0.31   | 0.012 | Biological | GO:00324 negative regulation of transporter activity                     | 0.7836  | 0.85612 | 0 | 0 | 1   | 83    |
| GO:0072527 pyrimidine-containing compound metabolic process            | 1   | 0.7836  | 0.31   | 0.012 | Biological | GO:00725 pyrimidine-containing compound metabolic process                | 0.7836  | 0.85612 | 0 | 0 | 1   | 83    |
| GO:1905412 positive regulation of calcium ion transmembrane transport  | 1   | 0.7836  | 0.31   | 0.012 | Biological | GO:19054 positive regulation of calcium ion transmembrane transport      | 0.7836  | 0.85612 | 0 | 0 | 1   | 83    |
| GO:1904427 positive regulation of calcium ion transmembrane transport  | 1   | 0.7836  | 0.31   | 0.012 | Biological | GO:19044 positive regulation of calcium ion transmembrane transport      | 0.7836  | 0.85612 | 0 | 0 | 1   | 83    |
| GO:0015103 inorganic anion transmembrane transporter activity          | 2   | 0.78515 | 0.585  | 0.013 | Molecular  | GO:00151 inorganic anion transmembrane transporter activity              | 0.78515 | 0.8596  | 0 | 0 | 2   | 155   |
| GO:0007600 sensory perception                                          | 15  | 0.78522 | 4.844  | 0.015 | Biological | GO:00076 sensory perception                                              | 0.78522 | 0.8577  | 0 | 0 | 15  | 974   |
| GO:0006094 gluconeogenesis                                             | 1   | 0.78756 | 0.31   | 0.012 | Biological | GO:00060 gluconeogenesis                                                 | 0.78756 | 0.85913 | 0 | 0 | 1   | 84    |
| GO:0034356 endocytic recycling                                         | 1   | 0.78756 | 0.31   | 0.012 | Biological | GO:00343 endocytic recycling                                             | 0.78756 | 0.85913 | 0 | 0 | 1   | 84    |
| GO:0036465 synaptic vesicle recycling                                  | 1   | 0.78756 | 0.31   | 0.012 | Biological | GO:00364 synaptic vesicle recycling                                      | 0.78756 | 0.85913 | 0 | 0 | 1   | 84    |
| GO:0043299 leukocyte degranulation                                     | 1   | 0.78756 | 0.31   | 0.012 | Biological | GO:00432 leukocyte degranulation                                         | 0.78756 | 0.85913 | 0 | 0 | 1   | 84    |
| GO:0045921 positive regulation of exocytosis                           | 1   | 0.78756 | 0.31   | 0.012 | Biological | GO:00459 positive regulation of exocytosis                               | 0.78756 | 0.85913 | 0 | 0 | 1   | 84    |
| GO:1902369 negative regulation of RNA catabolic process                | 1   | 0.78756 | 0.31   | 0.012 | Biological | GO:19023 negative regulation of RNA catabolic process                    | 0.78756 | 0.85913 | 0 | 0 | 1   | 84    |
| GO:0006791 rough endoplasmic reticulum                                 | 1   | 0.78768 | 0.297  | 0.012 | Cellular   | GO:00067 rough endoplasmic reticulum                                     | 0.78768 | 0.86172 | 0 | 0 | 1   | 85    |
| GO:0004527 exonuclease activity                                        | 1   | 0.78908 | 0.292  | 0.012 | Molecular  | GO:00045 exonuclease activity                                            | 0.78908 | 0.86172 | 0 | 0 | 1   | 83    |
| GO:0016209 antioxidant activity                                        | 1   | 0.78908 | 0.292  | 0.012 | Molecular  | GO:00162 antioxidant activity                                            | 0.78908 | 0.86172 | 0 | 0 | 1   | 83    |
| GO:0007596 blood coagulation                                           | 3   | 0.79095 | 0.929  | 0.013 | Biological | GO:00075 blood coagulation                                               | 0.79095 | 0.86225 | 0 | 0 | 3   | 229   |
| GO:0015081 sodium ion transmembrane transporter activity               | 2   | 0.7911  | 0.585  | 0.013 | Molecular  | GO:00150 sodium ion transmembrane transporter activity                   | 0.7911  | 0.86279 | 0 | 0 | 2   | 157   |
| GO:0006140 regulation of nucleoside metabolic process                  | 1   | 0.79146 | 0.31   | 0.012 | Biological | GO:00061 regulation of nucleoside metabolic process                      | 0.79146 | 0.86225 | 0 | 0 | 1   | 85    |
| GO:0007492 endoderm development                                        | 1   | 0.79146 | 0.31   | 0.012 | Biological | GO:00074 endoderm development                                            | 0.79146 | 0.86225 | 0 | 0 | 1   | 85    |
| GO:0010921 regulation of phosphatase activity                          | 1   | 0.79146 | 0.31   | 0.012 | Biological | GO:00109 regulation of phosphatase activity                              | 0.79146 | 0.86225 | 0 | 0 | 1   | 85    |
| GO:0048889 positive regulation of lipid biosynthetic process           | 1   | 0.79146 | 0.31   | 0.012 | Biological | GO:00488 positive regulation of lipid biosynthetic process               | 0.79146 | 0.86225 | 0 | 0 | 1   | 85    |
| GO:1903351 cellular response to dopamine                               | 1   | 0.79146 | 0.31   | 0.012 | Biological | GO:19033 cellular response to dopamine                                   | 0.79146 | 0.86225 | 0 | 0 | 1   | 85    |
| GO:0016052 carbohydrate catabolic process                              | 2   | 0.79217 | 0.619  | 0.013 | Biological | GO:00160 carbohydrate catabolic process                                  | 0.79217 | 0.86288 | 0 | 0 | 2   | 160   |
| GO:0043235 receptor complex                                            | 6   | 0.79237 | 1.78   | 0.014 | Cellular   | GO:00432 receptor complex                                                | 0.79237 | 0.91362 | 0 | 0 | 6   | 431   |
| GO:0016772 transferase activity, transferring phosphorus-containing gr | 15  | 0.79253 | 4.386  | 0.016 | Molecular  | GO:00167 transferase activity, transferring phosphorus-containing groups | 0.79253 | 0.86279 | 0 | 0 | 15  | 964   |
| GO:0016791 phosphatase activity                                        | 4   | 0.79305 | 1.17   | 0.014 | Molecular  | GO:00167 phosphatase activity                                            | 0.79305 | 0.86279 | 0 | 0 | 4   | 292   |
| GO:0030163 protein catabolic process                                   | 16  | 0.79398 | 4.854  | 0.015 | Biological | GO:00301 protein catabolic process                                       | 0.79398 | 0.86462 | 0 | 0 | 16  | 1041  |
| GO:0051100 negative regulation of binding                              | 2   | 0.79528 | 0.619  | 0.013 | Biological | GO:00511 negative regulation of binding                                  | 0.79528 | 0.86565 | 0 | 0 | 2   | 161   |
| GO:1903350 response to dopamine                                        | 1   | 0.79528 | 0.619  | 0.013 | Biological | GO:19033 response to dopamine                                            | 0.79528 | 0.86565 | 0 | 0 | 1   | 86    |
| GO:0070820 tertiary granule                                            | 2   | 0.79546 | 0.593  | 0.012 | Cellular   | GO:00708 tertiary granule                                                | 0.79546 | 0.91521 | 0 | 0 | 2   | 163   |
| GO:0060348 bone development                                            | 3   | 0.7958  | 0.929  | 0.013 | Biological | GO:00603 bone development                                                | 0.7958  | 0.86594 | 0 | 0 | 3   | 231   |
| GO:0030098 lymphocyte differentiation                                  | 6   | 0.79588 | 0.585  | 0.014 | Molecular  | GO:00300 lymphocyte differentiation                                      | 0.79588 | 0.86594 | 0 | 0 | 6   | 428   |
| GO:1901586 organonitrogen compound biosynthetic process                | 28  | 0.79616 | 8.669  | 0.016 | Biological | GO:19015 organonitrogen compound biosynthetic process                    | 0.79616 | 0.86594 | 0 | 0 | 28  | 1752  |
| GO:0005546 phosphatidylinositol-4,5-bisphosphate binding               | 1   | 0.79687 | 0.292  | 0.012 | Molecular  | GO:00055 phosphatidylinositol-4,5-bisphosphate binding                   | 0.79687 | 0.86585 | 0 | 0 | 1   | 85    |
| GO:0005819 spindle                                                     | 6   | 0.79773 | 1.78   | 0.014 | Cellular   | GO:00058 spindle                                                         | 0.79773 | 0.91585 | 0 | 0 | 6   | 434   |
| GO:0032787 monocarboxylic acid metabolic process                       | 9   | 0.79802 | 2.786  | 0.015 | Biological | GO:00327 monocarboxylic acid metabolic process                           | 0.79802 | 0.86765 | 0 | 0 | 9   | 618   |
| GO:0008306 associative learning                                        | 1   | 0.79903 | 0.31   | 0.011 | Biological | GO:00083 associative learning                                            | 0.79903 | 0.86765 | 0 | 0 | 1   | 87    |
| GO:0008344 adult locomotory behavior                                   | 1   | 0.79903 | 0.31   | 0.011 | Biological | GO:00083 adult locomotory behavior                                       | 0.79903 | 0.86765 | 0 | 0 | 1   | 87    |
| GO:0010507 negative regulation of autophagy                            | 1   | 0.79903 | 0.31   | 0.011 | Biological | GO:00105 negative regulation of autophagy                                | 0.79903 | 0.86765 | 0 | 0 | 1   | 87    |
| GO:0019319 hexose biosynthetic process                                 | 1   | 0.79903 | 0.31   | 0.011 | Biological | GO:00193 hexose biosynthetic process                                     | 0.79903 | 0.86765 | 0 | 0 | 1   | 87    |
| GO:0021766 hippocampus development                                     | 1   | 0.79903 | 0.31   | 0.011 | Biological | GO:00217 hippocampus development                                         | 0.79903 | 0.86765 | 0 | 0 | 1   | 87    |
| GO:0030453 ubiquitin-dependent ERAD pathway                            | 1   | 0.79903 | 0.31   | 0.011 | Biological | GO:00304 ubiquitin-dependent ERAD pathway                                | 0.79903 | 0.86765 | 0 | 0 | 1   | 87    |
| GO:0030771 T cell differentiation in thymus                            | 2   | 0.79974 | 0.585  | 0.013 | Molecular  | GO:00307 T cell differentiation in thymus                                | 0.79974 | 0.86769 | 0 | 0 | 2   | 160   |
| GO:0003823 antigen binding                                             | 2   | 0.79974 | 0.585  | 0.013 | Molecular  | GO:00038 antigen binding                                                 | 0.79974 | 0.86769 | 0 | 0 | 2   | 160   |
| GO:0045055 regulated exocytosis                                        | 3   | 0.80055 | 0.929  | 0.013 | Biological | GO:00450 regulated exocytosis                                            | 0.80055 | 0.86889 | 0 | 0 | 3   | 233   |
| GO:0001539 cilium or flagellum-dependent cell motility                 | 2   | 0.80068 | 0.619  | 0.012 | Biological | GO:00015 cil                                                             |         |         |   |   |     |       |

|                                                                                |     |         |        |       |            |          |                                                                     |         |         |   |   |     |       |
|--------------------------------------------------------------------------------|-----|---------|--------|-------|------------|----------|---------------------------------------------------------------------|---------|---------|---|---|-----|-------|
| GO:0046651 lymphocyte proliferation                                            | 4   | 0.81989 | 1.238  | 0.013 | Biological | GO:00466 | lymphocyte proliferation                                            | 0.81989 | 0.88024 | 0 | 0 | 4   | 310   |
| GO:0030641 regulation of cellular pH                                           | 1   | 0.82013 | 0.31   | 0.011 | Biological | GO:00306 | regulation of cellular pH                                           | 0.82013 | 0.88024 | 0 | 0 | 1   | 93    |
| GO:000696 dendritic spine development                                          | 1   | 0.82013 | 0.31   | 0.011 | Biological | GO:00069 | dendritic spine development                                         | 0.82013 | 0.88024 | 0 | 0 | 1   | 33    |
| GO:200106 regulation of leukocyte apoptotic process                            | 1   | 0.82013 | 0.31   | 0.011 | Biological | GO:20010 | regulation of leukocyte apoptotic process                           | 0.82013 | 0.88024 | 0 | 0 | 1   | 93    |
| GO:003196 mitochondrial membrane                                               | 11  | 0.82042 | 3.264  | 0.014 | Cellular   | GO:00319 | mitochondrial membrane                                              | 0.82042 | 0.92781 | 0 | 0 | 11  | 767   |
| GO:0044249 cellular biosynthetic process                                       | 100 | 0.82083 | 30.96  | 0.017 | Biological | GO:00442 | cellular biosynthetic process                                       | 0.82083 | 0.8808  | 0 | 0 | 100 | 5881  |
| GO:0030411 secretory granule                                                   | 13  | 0.82202 | 3.858  | 0.015 | Cellular   | GO:00304 | secretory granule                                                   | 0.82202 | 0.92781 | 0 | 0 | 13  | 893   |
| GO:0016358 dendrite development                                                | 3   | 0.82243 | 0.31   | 0.011 | Biological | GO:00163 | dendrite development                                                | 0.82243 | 0.88264 | 0 | 0 | 3   | 243   |
| GO:000422 autophagy of mitochondrion                                           | 1   | 0.82343 | 0.31   | 0.011 | Biological | GO:00042 | autophagy of mitochondrion                                          | 0.82343 | 0.88264 | 0 | 0 | 1   | 94    |
| GO:0043648 dicarboxylic acid metabolic process                                 | 1   | 0.82343 | 0.31   | 0.011 | Biological | GO:00436 | dicarboxylic acid metabolic process                                 | 0.82343 | 0.88264 | 0 | 0 | 1   | 94    |
| GO:0061726 mitochondrion disassembly                                           | 1   | 0.82343 | 0.31   | 0.011 | Biological | GO:00617 | mitochondrion disassembly                                           | 0.82343 | 0.88264 | 0 | 0 | 1   | 94    |
| GO:009869 protein oxidant detoxification                                       | 1   | 0.82343 | 0.31   | 0.011 | Biological | GO:00986 | protein oxidant detoxification                                      | 0.82343 | 0.88264 | 0 | 0 | 1   | 94    |
| GO:0051170 import into nucleus                                                 | 2   | 0.82428 | 0.619  | 0.012 | Biological | GO:00511 | import into nucleus                                                 | 0.82428 | 0.88517 | 0 | 0 | 2   | 172   |
| GO:1901136 carbohydrate derivative catabolic process                           | 2   | 0.82428 | 0.619  | 0.012 | Biological | GO:19011 | carbohydrate derivative catabolic process                           | 0.82428 | 0.88517 | 0 | 0 | 2   | 172   |
| GO:0017076 purine nucleotide binding                                           | 31  | 0.82508 | 9.064  | 0.016 | Molecular  | GO:00170 | purine nucleotide binding                                           | 0.82508 | 0.88553 | 0 | 0 | 31  | 1929  |
| GO:0051219 phosphoprotein binding                                              | 1   | 0.82523 | 0.292  | 0.011 | Molecular  | GO:00512 | phosphoprotein binding                                              | 0.82523 | 0.88553 | 0 | 0 | 1   | 93    |
| GO:0016853 isomerase activity                                                  | 2   | 0.82632 | 0.585  | 0.012 | Molecular  | GO:00168 | isomerase activity                                                  | 0.82632 | 0.88553 | 0 | 0 | 2   | 170   |
| GO:0035082 axoneme assembly                                                    | 1   | 0.82667 | 0.31   | 0.011 | Biological | GO:00350 | axoneme assembly                                                    | 0.82667 | 0.88502 | 0 | 0 | 1   | 95    |
| GO:0044070 regulation of anion transport                                       | 1   | 0.82667 | 0.31   | 0.011 | Biological | GO:00440 | regulation of anion transport                                       | 0.82667 | 0.88502 | 0 | 0 | 1   | 95    |
| GO:0050776 regulation of immune response                                       | 14  | 0.8267  | 4.334  | 0.015 | Biological | GO:00507 | regulation of immune response                                       | 0.8267  | 0.88502 | 0 | 0 | 14  | 948   |
| GO:0002706 regulation of lymphocyte mediated immunity                          | 2   | 0.82674 | 0.619  | 0.012 | Biological | GO:00027 | regulation of lymphocyte mediated immunity                          | 0.82674 | 0.88502 | 0 | 0 | 2   | 173   |
| GO:0006031 generation of precursor metabolites and energy                      | 7   | 0.82689 | 2.167  | 0.014 | Biological | GO:00060 | generation of precursor metabolites and energy                      | 0.82689 | 0.88502 | 0 | 0 | 7   | 511   |
| GO:0030072 peptide hormone secretion                                           | 2   | 0.82748 | 0.89   | 0.012 | Cellular   | GO:00300 | peptide hormone secretion                                           | 0.82748 | 0.93039 | 0 | 0 | 2   | 172   |
| GO:0032838 plasma membrane bounded cell projection cytoplasm                   | 3   | 0.82748 | 0.89   | 0.012 | Cellular   | GO:00328 | plasma membrane bounded cell projection cytoplasm                   | 0.82748 | 0.93039 | 0 | 0 | 3   | 248   |
| GO:0016887 ATP hydrolysis activity                                             | 5   | 0.82781 | 1.462  | 0.013 | Molecular  | GO:00168 | ATP hydrolysis activity                                             | 0.82781 | 0.88553 | 0 | 0 | 5   | 375   |
| GO:0032553 ribonucleotide binding                                              | 31  | 0.82921 | 9.064  | 0.016 | Molecular  | GO:00325 | ribonucleotide binding                                              | 0.82921 | 0.88553 | 0 | 0 | 31  | 1934  |
| GO:1905369 endopeptidase complex                                               | 1   | 0.82949 | 0.297  | 0.01  | Cellular   | GO:19053 | endopeptidase complex                                               | 0.82949 | 0.93039 | 0 | 0 | 1   | 97    |
| GO:0036454 cytoskeletal protein granule                                        | 3   | 0.82953 | 0.98   | 0.013 | Cellular   | GO:00364 | cytoskeletal protein granule                                        | 0.82953 | 0.93039 | 0 | 0 | 3   | 249   |
| GO:0022412 cellular process involved in reproduction in multicellular organism | 6   | 0.82955 | 1.858  | 0.013 | Biological | GO:00224 | cellular process involved in reproduction in multicellular organism | 0.82955 | 0.88742 | 0 | 0 | 6   | 448   |
| GO:0061337 cardiac conduction                                                  | 1   | 0.82984 | 0.31   | 0.01  | Biological | GO:00613 | cardiac conduction                                                  | 0.82984 | 0.88742 | 0 | 0 | 1   | 96    |
| GO:1903312 negative regulation of mRNA metabolic process                       | 1   | 0.82984 | 0.31   | 0.01  | Biological | GO:19033 | negative regulation of mRNA metabolic process                       | 0.82984 | 0.88742 | 0 | 0 | 1   | 96    |
| GO:0030695 GTPase regulator activity                                           | 7   | 0.83031 | 2.047  | 0.014 | Molecular  | GO:00306 | GTPase regulator activity                                           | 0.83031 | 0.88553 | 0 | 0 | 7   | 505   |
| GO:0005699 nucleoside triphosphate regulator activity                          | 7   | 0.83031 | 2.047  | 0.014 | Molecular  | GO:00056 | nucleoside triphosphate regulator activity                          | 0.83031 | 0.88553 | 0 | 0 | 7   | 505   |
| GO:0016197 endosomal transport                                                 | 3   | 0.83127 | 0.929  | 0.012 | Biological | GO:00161 | endosomal transport                                                 | 0.83127 | 0.88876 | 0 | 0 | 3   | 247   |
| GO:0016407 acetyltransferase activity                                          | 1   | 0.83168 | 0.292  | 0.011 | Molecular  | GO:00164 | acetyltransferase activity                                          | 0.83168 | 0.8859  | 0 | 0 | 1   | 95    |
| GO:0022900 electron transport chain                                            | 2   | 0.83394 | 0.619  | 0.011 | Molecular  | GO:00229 | electron transport chain                                            | 0.83394 | 0.89142 | 0 | 0 | 2   | 176   |
| GO:0010467 gene expression                                                     | 101 | 0.83466 | 31.269 | 0.017 | Biological | GO:00104 | gene expression                                                     | 0.83466 | 0.892   | 0 | 0 | 101 | 5962  |
| GO:0098657 import into cell                                                    | 3   | 0.83531 | 0.929  | 0.012 | Biological | GO:00986 | import into cell                                                    | 0.83531 | 0.8859  | 0 | 0 | 3   | 249   |
| GO:0031248 protein acetyltransferase complex                                   | 1   | 0.83562 | 0.297  | 0.01  | Cellular   | GO:00312 | protein acetyltransferase complex                                   | 0.83562 | 0.93469 | 0 | 0 | 1   | 99    |
| GO:0006029 proteoglycan metabolic process                                      | 1   | 0.83602 | 0.31   | 0.01  | Biological | GO:00060 | proteoglycan metabolic process                                      | 0.83602 | 0.89269 | 0 | 0 | 1   | 98    |
| GO:0044728 DNA methylation or demethylation                                    | 1   | 0.83602 | 0.31   | 0.01  | Biological | GO:00447 | DNA methylation or demethylation                                    | 0.83602 | 0.89269 | 0 | 0 | 1   | 98    |
| GO:0051952 regulation of amine transport                                       | 1   | 0.83602 | 0.31   | 0.01  | Biological | GO:00519 | regulation of amine transport                                       | 0.83602 | 0.89269 | 0 | 0 | 1   | 98    |
| GO:0019827 stem cell population maintenance                                    | 2   | 0.83628 | 0.619  | 0.011 | Biological | GO:00198 | stem cell population maintenance                                    | 0.83628 | 0.89274 | 0 | 0 | 2   | 179   |
| GO:0044238 primary metabolic process                                           | 179 | 0.83643 | 55.418 | 0.017 | Biological | GO:00442 | primary metabolic process                                           | 0.83643 | 0.89274 | 0 | 0 | 179 | 10264 |
| GO:0042742 defense response to bacterium                                       | 5   | 0.83745 | 1.548  | 0.013 | Biological | GO:00427 | defense response to bacterium                                       | 0.83745 | 0.89363 | 0 | 0 | 5   | 387   |
| GO:0043202 lysosomal lumen                                                     | 1   | 0.8386  | 0.297  | 0.01  | Cellular   | GO:00432 | lysosomal lumen                                                     | 0.8386  | 0.93469 | 0 | 0 | 1   | 100   |
| GO:1902493 acetyltransferase complex                                           | 1   | 0.8386  | 0.297  | 0.01  | Cellular   | GO:19024 | acetyltransferase complex                                           | 0.8386  | 0.93469 | 0 | 0 | 1   | 100   |
| GO:0034820 cellular response to unfolded protein                               | 1   | 0.83903 | 0.31   | 0.01  | Biological | GO:00348 | cellular response to unfolded protein                               | 0.83903 | 0.89504 | 0 | 0 | 1   | 99    |
| GO:0009056 catabolic process                                                   | 42  | 0.83912 | 13.003 | 0.016 | Biological | GO:00090 | catabolic process                                                   | 0.83912 | 0.89504 | 0 | 0 | 42  | 2620  |
| GO:0140030 modification-dependent protein binding                              | 2   | 0.8407  | 0.585  | 0.011 | Molecular  | GO:01400 | modification-dependent protein binding                              | 0.8407  | 0.89441 | 0 | 0 | 2   | 176   |
| GO:0030833 regulation of actin filament polymerization                         | 2   | 0.84087 | 0.619  | 0.011 | Biological | GO:00308 | regulation of actin filament polymerization                         | 0.84087 | 0.89556 | 0 | 0 | 2   | 179   |
| GO:0009314 response to radiation                                               | 6   | 0.84172 | 1.858  | 0.013 | Biological | GO:00093 | response to radiation                                               | 0.84172 | 0.89556 | 0 | 0 | 6   | 456   |
| GO:0031647 protein stability                                                   | 4   | 0.84181 | 1.238  | 0.013 | Biological | GO:00316 | protein stability                                                   | 0.84181 | 0.89556 | 0 | 0 | 4   | 322   |
| GO:0042773 ATP synthesis coupled electron transport                            | 1   | 0.84198 | 0.31   | 0.01  | Biological | GO:00427 | ATP synthesis coupled electron transport                            | 0.84198 | 0.89556 | 0 | 0 | 1   | 100   |
| GO:0042775 mitochondrial ATP synthesis coupled electron transport              | 1   | 0.84198 | 0.31   | 0.01  | Biological | GO:00427 | mitochondrial ATP synthesis coupled electron transport              | 0.84198 | 0.89556 | 0 | 0 | 1   | 100   |
| GO:0071868 cellular response to monamine stimulus                              | 1   | 0.84198 | 0.31   | 0.01  | Biological | GO:00718 | cellular response to monamine stimulus                              | 0.84198 | 0.89556 | 0 | 0 | 1   | 100   |
| GO:0071870 cellular response to catecholamine stimulus                         | 1   | 0.84198 | 0.31   | 0.01  | Biological | GO:00718 | cellular response to catecholamine stimulus                         | 0.84198 | 0.89556 | 0 | 0 | 1   | 100   |
| GO:0010020 regulation of cytoskeleton structure organization                   | 1   | 0.84198 | 0.31   | 0.01  | Biological | GO:00100 | regulation of cytoskeleton structure organization                   | 0.84198 | 0.89556 | 0 | 0 | 1   | 101   |
| GO:0043487 regulation of RNA stability                                         | 2   | 0.84312 | 0.619  | 0.011 | Biological | GO:00434 | regulation of RNA stability                                         | 0.84312 | 0.89723 | 0 | 0 | 2   | 180   |
| GO:0045580 regulation of T cell differentiation                                | 2   | 0.84312 | 0.619  | 0.011 | Biological | GO:00455 | regulation of T cell differentiation                                | 0.84312 | 0.89723 | 0 | 0 | 2   | 180   |
| GO:0050851 antigen receptor-mediated signaling pathway                         | 3   | 0.84315 | 0.929  | 0.012 | Biological | GO:00508 | antigen receptor-mediated signaling pathway                         | 0.84315 | 0.89723 | 0 | 0 | 3   | 253   |
| GO:0000775 chromosome, centromeric region                                      | 3   | 0.84328 | 0.89   | 0.012 | Cellular   | GO:00007 | chromosome, centromeric region                                      | 0.84328 | 0.93795 | 0 | 0 | 3   | 256   |
| GO:0008135 transmembrane factor activity, RNA binding                          | 1   | 0.84488 | 0.31   | 0.01  | Molecular  | GO:00081 | transmembrane factor activity, RNA binding                          | 0.84488 | 0.89842 | 0 | 0 | 1   | 99    |
| GO:0002275 myeloid cell activation involved in immune response                 | 1   | 0.84488 | 0.31   | 0.01  | Biological | GO:00022 | myeloid cell activation involved in immune response                 | 0.84488 | 0.89842 | 0 | 0 | 1   | 101   |
| GO:0019080 viral gene expression                                               | 1   | 0.84488 | 0.31   | 0.01  | Biological | GO:00190 | viral gene expression                                               | 0.84488 | 0.89842 | 0 | 0 | 1   | 101   |
| GO:0050764 regulation of phagocytosis                                          | 1   | 0.84488 | 0.31   | 0.01  | Biological | GO:00507 | regulation of phagocytosis                                          | 0.84488 | 0.89842 | 0 | 0 | 1   | 101   |
| GO:0006068 positive regulation of cell cycle process                           | 3   | 0.84506 | 0.929  | 0.012 | Biological | GO:00060 | positive regulation of cell cycle process                           | 0.84506 | 0.89842 | 0 | 0 | 3   | 254   |
| GO:1901565 organic cyclic compound biosynthetic process                        | 2   | 0.84535 | 0.619  | 0.011 | Biological | GO:19015 | organic cyclic compound biosynthetic process                        | 0.84535 | 0.90592 | 0 | 0 | 2   | 137   |
| GO:0008727 maintenance of cell number                                          | 2   | 0.84535 | 0.619  | 0.011 | Biological | GO:00087 | maintenance of cell number                                          | 0.84535 | 0.89842 | 0 | 0 | 2   | 181   |
| GO:0000226 microtubule cytoskeleton organization                               | 9   | 0.84593 | 2.786  | 0.014 | Biological | GO:00002 | microtubule cytoskeleton organization                               | 0.84593 | 0.89885 | 0 | 0 | 9   | 653   |
| GO:0004725 protein tyrosine phosphatase activity                               | 1   | 0.84679 | 0.292  | 0.01  | Molecular  | GO:00047 | protein tyrosine phosphatase activity                               | 0.84679 | 0.89867 | 0 | 0 | 1   | 100   |
| GO:0005796 Golgi lumen                                                         | 1   | 0.84721 | 0.297  | 0.01  | Cellular   | GO:00057 | Golgi lumen                                                         | 0.84721 | 0.93853 | 0 | 0 | 1   | 103   |
| GO:0101002 lumen, l-rich granule                                               | 1   | 0.84731 | 0.593  | 0.011 | Cellular   | GO:01010 | lumen, l-rich granule                                               | 0.84731 | 0.93853 | 0 | 0 | 1   | 104   |
| GO:0004867 serine-type endopeptidase inhibitor activity                        | 1   | 0.84964 | 0.292  | 0.01  | Molecular  | GO:00048 | serine-type endopeptidase inhibitor activity                        | 0.84964 | 0.8995  | 0 | 0 | 1   | 101   |
| GO:0019888 protein phosphatase regulator activity                              | 1   | 0.84964 | 0.292  | 0.01  | Molecular  | GO:00198 | protein phosphatase regulator activity                              | 0.84964 | 0.8995  | 0 | 0 | 1   | 101   |
| GO:0009416 response to light stimulus                                          | 4   | 0.85026 | 1.238  | 0.012 | Biological | GO:00094 | response to light stimulus                                          | 0.85026 | 0.90276 | 0 | 0 | 4   | 327   |
| GO:0007040 lysosome organization                                               | 1   | 0.85051 | 0.31   | 0.01  | Biological | GO:00070 | lysosome organization                                               | 0.85051 | 0.90276 | 0 | 0 | 1   | 103   |
| GO:0071887 response to monamine                                                | 1   | 0.85051 | 0.31   | 0.01  | Biological | GO:00718 | response to monamine                                                | 0.85051 | 0.90276 | 0 | 0 | 1   | 103   |
| GO:0071869 response to catecholamine                                           | 1   | 0.85051 | 0.31   | 0.01  | Biological | GO:00718 | response to catecholamine                                           | 0.85051 | 0.90276 | 0 | 0 | 1   | 103   |
| GO:0080171 lytic vacuole organization                                          | 1   | 0.85051 | 0.31   | 0.01  | Biological | GO:00801 | lytic vacuole organization                                          | 0.85051 | 0.90276 | 0 | 0 | 1   | 103   |
| GO:0080134 regulation of response to stress                                    | 21  | 0.85133 | 6.502  | 0.015 | Biological | GO:00801 | regulation of response to stress                                    | 0.85133 | 0.90343 | 0 | 0 | 21  | 1398  |
| GO:0061013 regulation of mRNA catabolic process                                | 2   | 0.85164 | 0.619  | 0.011 | Biological | GO:00610 | regulation of mRNA catabolic process                                | 0.85164 | 0.90378 | 0 | 0 | 2   | 184   |
| GO:0035496 altered binding                                                     | 1   | 0.85245 | 0.292  | 0.01  | Molecular  | GO:00354 | altered binding                                                     | 0.85245 | 0.90136 | 0 | 0 | 1   | 102   |
| GO:0034708 methylesterase complex                                              | 1   | 0.8527  | 0.297  | 0.01  | Cellular   | GO:00347 | methylesterase complex                                              | 0.8527  | 0.94255 | 0 | 0 | 1   | 105   |
| GO:0032231 regulation of actin filament bundle assembly                        | 1   | 0.85325 | 0.31   | 0.01  | Biological | GO:00322 | regulation of actin filament bundle assembly                        | 0.85325 | 0.9049  | 0 | 0 | 1   | 104   |
| GO:0033209 tumor necrosis factor-mediated signaling pathway                    | 1   | 0.85325 | 0.31   | 0.01  | Biological | GO:00332 | tumor necrosis factor-mediated signaling pathway                    | 0.85325 | 0.9049  | 0 | 0 | 1   | 104   |
| GO:005525 GTP binding                                                          | 5   | 0.85367 | 1.462  | 0.013 | Molecular  | GO:00552 | GTP binding                                                         | 0.85367 | 0.90156 | 0 | 0 | 5   | 369   |
| GO:0070946 protein modification by small protein removal                       | 1   |         |        |       |            |          |                                                                     |         |         |   |   |     |       |

|                                                                           |     |         |        |       |            |                                                                           |         |         |   |   |     |       |
|---------------------------------------------------------------------------|-----|---------|--------|-------|------------|---------------------------------------------------------------------------|---------|---------|---|---|-----|-------|
| GO:0030004 cellular monovalent inorganic cation homeostasis               | 1   | 0.88464 | 0.31   | 0.009 | Biological | GO:0030004 cellular monovalent inorganic cation homeostasis               | 0.88464 | 0.92872 | 0 | 0 | 1   | 117   |
| GO:0030518 intracellular steroid hormone receptor signaling pathway       | 1   | 0.88464 | 0.31   | 0.009 | Biological | GO:0030518 intracellular steroid hormone receptor signaling pathway       | 0.88464 | 0.92872 | 0 | 0 | 1   | 117   |
| GO:1905037 autophagosome organization                                     | 1   | 0.88464 | 0.31   | 0.009 | Biological | GO:1905037 autophagosome organization                                     | 0.88464 | 0.92872 | 0 | 0 | 1   | 117   |
| GO:001824 blastocyst development                                          | 1   | 0.88676 | 0.31   | 0.008 | Biological | GO:001824 blastocyst development                                          | 0.88676 | 0.93035 | 0 | 0 | 1   | 118   |
| GO:0007088 regulation of mitotic nuclear division                         | 1   | 0.88676 | 0.31   | 0.008 | Biological | GO:0007088 regulation of mitotic nuclear division                         | 0.88676 | 0.93035 | 0 | 0 | 1   | 118   |
| GO:0034440 lipid oxidation                                                | 1   | 0.88676 | 0.31   | 0.008 | Biological | GO:0034440 lipid oxidation                                                | 0.88676 | 0.93035 | 0 | 0 | 1   | 118   |
| GO:0016064 immunoglobulin mediated immune response                        | 2   | 0.88753 | 0.619  | 0.01  | Biological | GO:0016064 immunoglobulin mediated immune response                        | 0.88753 | 0.93096 | 0 | 0 | 2   | 203   |
| GO:0015850 organic hydroxy compound transport                             | 3   | 0.88805 | 0.326  | 0.009 | Biological | GO:0015850 organic hydroxy compound transport                             | 0.88805 | 0.93131 | 0 | 0 | 3   | 280   |
| GO:0005829 cytosol                                                        | 89  | 0.88839 | 26.409 | 0.016 | Cellular   | GO:0005829 cytosol                                                        | 0.88839 | 0.968   | 0 | 0 | 89  | 5467  |
| GO:0009055 electron transfer activity                                     | 1   | 0.88874 | 0.292  | 0.009 | Molecular  | GO:0009055 electron transfer activity                                     | 0.88874 | 0.92173 | 0 | 0 | 1   | 117   |
| GO:0035967 cellular response to topologically incorrect protein           | 1   | 0.88884 | 0.31   | 0.008 | Biological | GO:0035967 cellular response to topologically incorrect protein           | 0.88884 | 0.93175 | 0 | 0 | 1   | 119   |
| GO:0061640 cytoskeleton-dependent cytokinesis                             | 1   | 0.88884 | 0.31   | 0.008 | Biological | GO:0061640 cytoskeleton-dependent cytokinesis                             | 0.88884 | 0.93175 | 0 | 0 | 1   | 119   |
| GO:0004843 thiol-dependent leukotriene                                    | 1   | 0.89041 | 0.297  | 0.008 | Biological | GO:0004843 thiol-dependent leukotriene                                    | 0.89041 | 0.93278 | 0 | 0 | 1   | 118   |
| GO:0026988 negative regulation of immune effector process                 | 1   | 0.89088 | 0.31   | 0.008 | Biological | GO:0026988 negative regulation of immune effector process                 | 0.89088 | 0.93358 | 0 | 0 | 1   | 120   |
| GO:0042752 regulation of circadian rhythm                                 | 1   | 0.89088 | 0.31   | 0.008 | Biological | GO:0042752 regulation of circadian rhythm                                 | 0.89088 | 0.93358 | 0 | 0 | 1   | 120   |
| GO:0095668 cytoplasmic region                                             | 3   | 0.89185 | 0.89   | 0.01  | Cellular   | GO:0095668 cytoplasmic region                                             | 0.89185 | 0.96877 | 0 | 0 | 3   | 286   |
| GO:0006511 ubiquitin-dependent protein catabolic process                  | 9   | 0.89206 | 2.786  | 0.013 | Biological | GO:0006511 ubiquitin-dependent protein catabolic process                  | 0.89206 | 0.93454 | 0 | 0 | 9   | 696   |
| GO:0019724 B cell mediated immunity                                       | 2   | 0.89237 | 0.619  | 0.01  | Biological | GO:0019724 B cell mediated immunity                                       | 0.89237 | 0.93467 | 0 | 0 | 2   | 208   |
| GO:0006304 DNA modification                                               | 1   | 0.89288 | 0.31   | 0.008 | Biological | GO:0006304 DNA modification                                               | 0.89288 | 0.93482 | 0 | 0 | 1   | 121   |
| GO:0044237 cellular metabolic process                                     | 180 | 0.89289 | 55.728 | 0.017 | Biological | GO:0044237 cellular metabolic process                                     | 0.89289 | 0.93482 | 0 | 0 | 180 | 10444 |
| GO:0016604 nuclear body                                                   | 11  | 0.89329 | 3.264  | 0.013 | Cellular   | GO:0016604 nuclear body                                                   | 0.89329 | 0.96877 | 0 | 0 | 11  | 837   |
| GO:0048515 spermatid differentiation                                      | 2   | 0.89395 | 0.619  | 0.01  | Biological | GO:0048515 spermatid differentiation                                      | 0.89395 | 0.93554 | 0 | 0 | 2   | 207   |
| GO:0050717 negative regulation of immune response                         | 2   | 0.89395 | 0.619  | 0.01  | Biological | GO:0050717 negative regulation of immune response                         | 0.89395 | 0.93554 | 0 | 0 | 2   | 207   |
| GO:0043227 membrane-bounded organelle                                     | 230 | 0.89453 | 68.249 | 0.017 | Cellular   | GO:0043227 membrane-bounded organelle                                     | 0.89453 | 0.96877 | 0 | 0 | 230 | 13306 |
| GO:0002224 toll-like receptor signaling pathway                           | 1   | 0.89485 | 0.31   | 0.008 | Biological | GO:0002224 toll-like receptor signaling pathway                           | 0.89485 | 0.93563 | 0 | 0 | 1   | 122   |
| GO:0022904 respiratory electron transport chain                           | 1   | 0.89485 | 0.31   | 0.008 | Biological | GO:0022904 respiratory electron transport chain                           | 0.89485 | 0.93563 | 0 | 0 | 1   | 122   |
| GO:0071887 leukocyte apoptotic process                                    | 1   | 0.89485 | 0.31   | 0.008 | Biological | GO:0071887 leukocyte apoptotic process                                    | 0.89485 | 0.93563 | 0 | 0 | 1   | 122   |
| GO:0043471 positive regulation of GTPase activity                         | 1   | 0.89488 | 0.31   | 0.008 | Biological | GO:0043471 positive regulation of GTPase activity                         | 0.89488 | 0.93563 | 0 | 0 | 1   | 122   |
| GO:0110053 regulation of actin filament organization                      | 3   | 0.89498 | 0.929  | 0.011 | Biological | GO:0110053 regulation of actin filament organization                      | 0.89498 | 0.93563 | 0 | 0 | 3   | 285   |
| GO:0051053 negative regulation of DNA metabolic process                   | 1   | 0.89678 | 0.31   | 0.008 | Biological | GO:0051053 negative regulation of DNA metabolic process                   | 0.89678 | 0.93712 | 0 | 0 | 1   | 123   |
| GO:0051224 negative regulation of protein transport                       | 1   | 0.89678 | 0.31   | 0.008 | Biological | GO:0051224 negative regulation of protein transport                       | 0.89678 | 0.93712 | 0 | 0 | 1   | 123   |
| GO:0022853 active on transmembrane transporter activity                   | 3   | 0.89719 | 0.877  | 0.011 | Molecular  | GO:0022853 active on transmembrane transporter activity                   | 0.89719 | 0.92828 | 0 | 0 | 3   | 282   |
| GO:0007162 negative regulation of GTPase activity                         | 2   | 0.89747 | 0.619  | 0.01  | Biological | GO:0007162 negative regulation of GTPase activity                         | 0.89747 | 0.93763 | 0 | 0 | 2   | 124   |
| GO:0002455 humoral immune response mediated by circulating immunoglobulin | 1   | 0.89867 | 0.31   | 0.008 | Biological | GO:0002455 humoral immune response mediated by circulating immunoglobulin | 0.89867 | 0.93852 | 0 | 0 | 1   | 124   |
| GO:018022 peptidyl-lysine methylation                                     | 1   | 0.89867 | 0.31   | 0.008 | Biological | GO:018022 peptidyl-lysine methylation                                     | 0.89867 | 0.93852 | 0 | 0 | 1   | 124   |
| GO:0051321 meiotic cell cycle                                             | 3   | 0.89895 | 0.929  | 0.011 | Biological | GO:0051321 meiotic cell cycle                                             | 0.89895 | 0.93861 | 0 | 0 | 3   | 288   |
| GO:0006813 centrosome                                                     | 8   | 0.89904 | 2.374  | 0.012 | Cellular   | GO:0006813 centrosome                                                     | 0.89904 | 0.97169 | 0 | 0 | 8   | 645   |
| GO:0009057 macromolecule catabolic process                                | 20  | 0.89916 | 6.192  | 0.014 | Biological | GO:0009057 macromolecule catabolic process                                | 0.89916 | 0.93863 | 0 | 0 | 20  | 1401  |
| GO:0044257 cellular protein catabolic process                             | 11  | 0.89966 | 3.406  | 0.013 | Biological | GO:0044257 cellular protein catabolic process                             | 0.89966 | 0.93896 | 0 | 0 | 11  | 835   |
| GO:0001704 formation of primary germ layer                                | 1   | 0.90053 | 0.31   | 0.008 | Biological | GO:0001704 formation of primary germ layer                                | 0.90053 | 0.93948 | 0 | 0 | 1   | 125   |
| GO:0002078 regulation of DNA biosynthetic process                         | 1   | 0.90053 | 0.31   | 0.008 | Biological | GO:0002078 regulation of DNA biosynthetic process                         | 0.90053 | 0.93948 | 0 | 0 | 1   | 125   |
| GO:0009079 translation regulator activity, nucleic acid binding           | 1   | 0.90053 | 0.292  | 0.008 | Molecular  | GO:0009079 translation regulator activity, nucleic acid binding           | 0.90053 | 0.92961 | 0 | 0 | 1   | 123   |
| GO:0110053 regulation of actin filament organization                      | 1   | 0.90053 | 0.292  | 0.008 | Molecular  | GO:0110053 regulation of actin filament organization                      | 0.90053 | 0.92961 | 0 | 0 | 1   | 123   |
| GO:0019941 modification-dependent protein catabolic process               | 9   | 0.90098 | 2.786  | 0.013 | Biological | GO:0019941 modification-dependent protein catabolic process               | 0.90098 | 0.93974 | 0 | 0 | 9   | 706   |
| GO:0045619 regulation of lymphocyte differentiation                       | 2   | 0.9015  | 0.619  | 0.009 | Biological | GO:0045619 regulation of lymphocyte differentiation                       | 0.9015  | 0.93989 | 0 | 0 | 2   | 212   |
| GO:1902600 proton transmembrane transport                                 | 2   | 0.9015  | 0.619  | 0.009 | Biological | GO:1902600 proton transmembrane transport                                 | 0.9015  | 0.93989 | 0 | 0 | 2   | 212   |
| GO:0001578 microtubule bundle formation                                   | 1   | 0.90236 | 0.31   | 0.008 | Biological | GO:0001578 microtubule bundle formation                                   | 0.90236 | 0.9402  | 0 | 0 | 1   | 126   |
| GO:0002626 insulin receptor signaling pathway                             | 1   | 0.90236 | 0.31   | 0.008 | Biological | GO:0002626 insulin receptor signaling pathway                             | 0.90236 | 0.9402  | 0 | 0 | 1   | 126   |
| GO:0031623 receptor internalization                                       | 1   | 0.90236 | 0.31   | 0.008 | Biological | GO:0031623 receptor internalization                                       | 0.90236 | 0.9402  | 0 | 0 | 1   | 126   |
| GO:0008047 enzyme activator activity                                      | 1   | 0.90248 | 0.292  | 0.008 | Molecular  | GO:0008047 enzyme activator activity                                      | 0.90248 | 0.93041 | 0 | 0 | 1   | 124   |
| GO:0071383 cellular response to steroid hormone stimulus                  | 2   | 0.90294 | 0.619  | 0.009 | Biological | GO:0071383 cellular response to steroid hormone stimulus                  | 0.90294 | 0.94061 | 0 | 0 | 2   | 213   |
| GO:0140534 endoplasmic reticulum protein-containing complex               | 1   | 0.90331 | 0.297  | 0.008 | Cellular   | GO:0140534 endoplasmic reticulum protein-containing complex               | 0.90331 | 0.97434 | 0 | 0 | 1   | 128   |
| GO:0050868 negative regulation of cell activation                         | 1   | 0.90415 | 0.31   | 0.008 | Biological | GO:0050868 negative regulation of cell activation                         | 0.90415 | 0.94168 | 0 | 0 | 1   | 127   |
| GO:0003697 single-stranded DNA binding                                    | 1   | 0.9043  | 0.292  | 0.008 | Molecular  | GO:0003697 single-stranded DNA binding                                    | 0.9043  | 0.93118 | 0 | 0 | 1   | 125   |
| GO:0007623 circadian rhythm                                               | 2   | 0.90437 | 0.619  | 0.009 | Biological | GO:0007623 circadian rhythm                                               | 0.90437 | 0.94171 | 0 | 0 | 2   | 214   |
| GO:0010639 negative regulation of organelle organization                  | 4   | 0.90505 | 1.238  | 0.011 | Biological | GO:0010639 negative regulation of organelle organization                  | 0.90505 | 0.94222 | 0 | 0 | 4   | 367   |
| GO:0005815 microtubule organizing center                                  | 11  | 0.90525 | 3.264  | 0.013 | Cellular   | GO:0005815 microtubule organizing center                                  | 0.90525 | 0.97447 | 0 | 0 | 11  | 852   |
| GO:0051051 negative regulation of cell activation                         | 5   | 0.90545 | 1.548  | 0.009 | Biological | GO:0051051 negative regulation of cell activation                         | 0.90545 | 0.94238 | 0 | 0 | 5   | 438   |
| GO:0050866 negative regulation of cell activation                         | 2   | 0.90578 | 0.619  | 0.009 | Biological | GO:0050866 negative regulation of cell activation                         | 0.90578 | 0.94239 | 0 | 0 | 2   | 215   |
| GO:0071805 potassium ion transmembrane transport                          | 2   | 0.90578 | 0.619  | 0.009 | Biological | GO:0071805 potassium ion transmembrane transport                          | 0.90578 | 0.94239 | 0 | 0 | 2   | 215   |
| GO:0044262 cellular carbohydrate metabolic process                        | 3   | 0.90649 | 0.929  | 0.011 | Biological | GO:0044262 cellular carbohydrate metabolic process                        | 0.90649 | 0.94293 | 0 | 0 | 3   | 284   |
| GO:0051028 mRNA transport                                                 | 1   | 0.90764 | 0.31   | 0.008 | Biological | GO:0051028 mRNA transport                                                 | 0.90764 | 0.94393 | 0 | 0 | 1   | 129   |
| GO:1903046 meiotic cell cycle process                                     | 1   | 0.90854 | 0.619  | 0.009 | Biological | GO:1903046 meiotic cell cycle process                                     | 0.90854 | 0.94467 | 0 | 0 | 1   | 129   |
| GO:0005003 protein-containing complex assembly                            | 24  | 0.90891 | 7.43   | 0.014 | Biological | GO:0005003 protein-containing complex assembly                            | 0.90891 | 0.94471 | 0 | 0 | 24  | 1663  |
| GO:0006334 nucleosome assembly                                            | 1   | 0.90934 | 0.31   | 0.008 | Biological | GO:0006334 nucleosome assembly                                            | 0.90934 | 0.94471 | 0 | 0 | 1   | 130   |
| GO:0051983 regulation of chromosome segregation                           | 1   | 0.90934 | 0.31   | 0.008 | Biological | GO:0051983 regulation of chromosome segregation                           | 0.90934 | 0.94471 | 0 | 0 | 1   | 130   |
| GO:0072329 monocarboxylic acid catabolic process                          | 1   | 0.90934 | 0.31   | 0.008 | Biological | GO:0072329 monocarboxylic acid catabolic process                          | 0.90934 | 0.94471 | 0 | 0 | 1   | 130   |
| GO:0004197 cysteine-type endopeptidase activity                           | 1   | 0.90968 | 0.292  | 0.008 | Molecular  | GO:0004197 cysteine-type endopeptidase activity                           | 0.90968 | 0.94522 | 0 | 0 | 1   | 128   |
| GO:0007276 gamete generation                                              | 10  | 0.91002 | 3.096  | 0.013 | Biological | GO:0007276 gamete generation                                              | 0.91002 | 0.94522 | 0 | 0 | 10  | 783   |
| GO:1902024 oxidoreductase complex                                         | 1   | 0.91015 | 0.297  | 0.008 | Cellular   | GO:1902024 oxidoreductase complex                                         | 0.91015 | 0.97777 | 0 | 0 | 1   | 132   |
| GO:0043632 modification-dependent macromolecule catabolic process         | 9   | 0.91086 | 2.786  | 0.013 | Biological | GO:0043632 modification-dependent macromolecule catabolic process         | 0.91086 | 0.94565 | 0 | 0 | 9   | 718   |
| GO:0000018 regulation of DNA recombination                                | 1   | 0.9111  | 0.31   | 0.008 | Biological | GO:0000018 regulation of DNA recombination                                | 0.9111  | 0.94565 | 0 | 0 | 1   | 131   |
| GO:0051928 positive regulation of calcium ion transport                   | 1   | 0.9111  | 0.31   | 0.008 | Biological | GO:0051928 positive regulation of calcium ion transport                   | 0.9111  | 0.94565 | 0 | 0 | 1   | 131   |
| GO:0017111 nucleoside-triphosphatase activity                             | 9   | 0.91207 | 2.632  | 0.013 | Molecular  | GO:0017111 nucleoside-triphosphatase activity                             | 0.91207 | 0.93695 | 0 | 0 | 9   | 708   |
| GO:0007033 vacuole organization                                           | 2   | 0.91254 | 0.619  | 0.009 | Biological | GO:0007033 vacuole organization                                           | 0.91254 | 0.94705 | 0 | 0 | 2   | 220   |
| GO:0004519 endonuclease activity                                          | 1   | 0.91453 | 0.292  | 0.008 | Molecular  | GO:0004519 endonuclease activity                                          | 0.91453 | 0.93837 | 0 | 0 | 1   | 131   |
| GO:0057193 intrinsic apoptotic signaling pathway                          | 3   | 0.91465 | 0.929  | 0.011 | Biological | GO:0057193 intrinsic apoptotic signaling pathway                          | 0.91465 | 0.94804 | 0 | 0 | 3   | 301   |
| GO:0072594 establishment of protein localization to organelle             | 5   | 0.91524 | 1.548  | 0.011 | Biological | GO:0072594 establishment of protein localization to organelle             | 0.91524 | 0.94846 | 0 | 0 | 5   | 439   |
| GO:0006956 complement activation                                          | 1   | 0.91582 | 0.31   | 0.007 | Biological | GO:0006956 complement activation                                          | 0.91582 | 0.94898 | 0 | 0 | 1   | 134   |
| GO:0006275 regulation of DNA replication                                  | 1   | 0.91736 | 0.31   | 0.007 | Biological | GO:0006275 regulation of DNA replication                                  | 0.91736 | 0.95107 | 0 | 0 | 1   | 135   |
| GO:0007498 mesoderm development                                           | 1   | 0.91736 | 0.31   | 0.007 | Biological | GO:0007498 mesoderm development                                           | 0.91736 | 0.95107 | 0 | 0 | 1   | 135   |
| GO:0006168 methyltransferase activity                                     | 2   | 0.91843 | 0.585  | 0.009 | Molecular  | GO:0006168 methyltransferase activity                                     | 0.91843 | 0.94725 | 0 | 0 | 2   | 136   |
| GO:0051301 cell division                                                  | 8   | 0.91885 | 2.477  | 0.012 | Biological | GO:0051301 cell division                                                  | 0.91885 | 0.95199 | 0 | 0 | 8   | 681   |
| GO:0050852 T cell receptor signaling pathway                              | 1   | 0.91888 | 0.31   | 0.007 | Biological | GO:0050852 T cell receptor signaling pathway                              | 0.91888 | 0.95199 | 0 | 0 | 1   | 136   |
| GO:0098754 detoxification                                                 | 1   | 0.91888 | 0.31   | 0.007 | Biological | GO:0098754 detoxification                                                 | 0.91888 | 0.95199 | 0 | 0 | 1   | 136   |
| GO:1903311 regulation of mRNA metabolic process                           | 3   | 0.91901 | 0.929  | 0.011 | Biological | GO:1903311 regulation of mRNA metabolic process                           | 0.91901 | 0.95199 | 0 | 0 | 3   | 305   |
| GO:0002911 protein kinase complex                                         | 1   | 0.91905 | 0.297  | 0.007 | Cellular   | GO:0002911 protein kinase complex                                         | 0.91905 | 0.98549 | 0 | 0 | 1   | 137   |
| GO:0015831 nucleoside-containing compound transport                       | 2   | 0.92015 | 0.619  | 0.009 | Biological | GO:0015831 nucleoside-containing compound transport                       | 0.92015 | 0.95299 | 0 | 0 | 2   | 226   |
| GO:0007098 centrosome cycle                                               | 1   | 0.92037 | 0.31   | 0.007 | Biological | GO:0007098 centrosome cycle                                               | 0.92037 | 0.953   | 0 | 0 | 1   | 137   |
| GO:0002443 leukocyte mediated immunity                                    | 5   | 0.92067 | 1.548  | 0.011 | Biological | GO:0                                                                      |         |         |   |   |     |       |

|                                                                             |    |         |        |      |            |                                                                            |         |         |   |   |    |       |
|-----------------------------------------------------------------------------|----|---------|--------|------|------------|----------------------------------------------------------------------------|---------|---------|---|---|----|-------|
| GO:0019666 organelle inner membrane                                         | 6  | 0.95066 | 1.78   | 0.01 | Cellular C | GO:001919 organelle inner membrane                                         | 0.95066 | 0.99856 | 0 | 0 | 6  | 577   |
| GO:0046434 organophosphate catabolic process                                | 1  | 0.95085 | 0.31   | 0.08 | Biological | GO:00406 organophosphate catabolic process                                 | 0.95085 | 0.97508 | 0 | 0 | 1  | 163   |
| GO:0051250 negative regulation of lymphocyte activation                     | 1  | 0.95085 | 0.31   | 0.08 | Biological | GO:005051 negative regulation of lymphocyte activation                     | 0.95085 | 0.97508 | 0 | 0 | 1  | 163   |
| GO:0032896 regulation of microtubule-based process                          | 2  | 0.95087 | 0.619  | 0.08 | Biological | GO:003032 regulation of microtubule-based process                          | 0.95087 | 0.97508 | 0 | 0 | 2  | 258   |
| GO:0002764 immune response-regulating signaling pathway                     | 5  | 0.95196 | 1.548  | 0.01 | Biological | GO:000002 immune response-regulating signaling pathway                     | 0.95196 | 0.97599 | 0 | 0 | 5  | 499   |
| GO:0051236 establishment of RNA localization                                | 1  | 0.95264 | 0.31   | 0.06 | Biological | GO:005051 establishment of RNA localization                                | 0.95264 | 0.97629 | 0 | 0 | 1  | 165   |
| GO:0000445 regulation of G1/S transition of mitotic cell cycle              | 1  | 0.95264 | 0.31   | 0.08 | Biological | GO:000004 regulation of G1/S transition of mitotic cell cycle              | 0.95264 | 0.97629 | 0 | 0 | 1  | 165   |
| GO:0019897 extrinsic component of plasma membrane                           | 1  | 0.95271 | 0.297  | 0.01 | Cellular C | GO:001919 extrinsic component of plasma membrane                           | 0.95271 | 0.99856 | 0 | 0 | 1  | 167   |
| GO:005802 trans-Golgi network                                               | 2  | 0.95376 | 0.593  | 0.08 | Cellular C | GO:000002 trans-Golgi network                                              | 0.95376 | 0.99856 | 0 | 0 | 2  | 265   |
| GO:0051168 nuclear export                                                   | 1  | 0.95437 | 0.31   | 0.06 | Biological | GO:000051 nuclear export                                                   | 0.95437 | 0.97786 | 0 | 0 | 1  | 167   |
| GO:0006261 DNA-dependent DNA replication                                    | 1  | 0.95521 | 0.31   | 0.06 | Biological | GO:000006 DNA-dependent DNA replication                                    | 0.95521 | 0.97827 | 0 | 0 | 1  | 168   |
| GO:0034250 positive regulation of cellular amide metabolic process          | 1  | 0.95521 | 0.31   | 0.08 | Biological | GO:000034 positive regulation of cellular amide metabolic process          | 0.95521 | 0.97827 | 0 | 0 | 1  | 168   |
| GO:004271 cellular nitrogen compound biosynthetic process                   | 75 | 0.95539 | 23.22  | 0.09 | Biological | GO:000042 cellular nitrogen compound biosynthetic process                  | 0.95539 | 0.97827 | 0 | 0 | 75 | 4812  |
| GO:0033043 regulation of organelle organization                             | 15 | 0.95602 | 4.644  | 0.13 | Biological | GO:000033 regulation of organelle organization                             | 0.95602 | 0.97876 | 0 | 0 | 15 | 1198  |
| GO:0016482 cytosolic transport                                              | 1  | 0.95684 | 0.31   | 0.06 | Biological | GO:000016 cytosolic transport                                              | 0.95684 | 0.97939 | 0 | 0 | 1  | 170   |
| GO:0090305 nucleic acid phosphodiester bond hydrolysis                      | 2  | 0.95725 | 0.619  | 0.07 | Biological | GO:000090 nucleic acid phosphodiester bond hydrolysis                      | 0.95725 | 0.97961 | 0 | 0 | 2  | 267   |
| GO:0042113 B cell activation                                                | 3  | 0.95822 | 0.929  | 0.08 | Biological | GO:000042 B cell activation                                                | 0.95822 | 0.9802  | 0 | 0 | 3  | 354   |
| GO:0019361 organic cyclic compound catabolic process                        | 5  | 0.95828 | 1.548  | 0.01 | Biological | GO:000019 organic cyclic compound catabolic process                        | 0.95828 | 0.9802  | 0 | 0 | 5  | 511   |
| GO:0021022 positive regulation of response to DNA damage stimulus           | 1  | 0.95841 | 0.31   | 0.08 | Biological | GO:000021 positive regulation of response to DNA damage stimulus           | 0.95841 | 0.9802  | 0 | 0 | 1  | 172   |
| GO:0043933 protein-containing complex subunit organization                  | 25 | 0.95927 | 7.74   | 0.14 | Biological | GO:000043 protein-containing complex subunit organization                  | 0.95927 | 0.98088 | 0 | 0 | 25 | 1849  |
| GO:0043433 negative regulation of DNA-binding transcription factor activity | 1  | 0.96139 | 0.31   | 0.06 | Biological | GO:000043 negative regulation of DNA-binding transcription factor activity | 0.96139 | 0.98285 | 0 | 0 | 1  | 176   |
| GO:0051054 positive regulation of DNA metabolic process                     | 2  | 0.96225 | 0.619  | 0.07 | Biological | GO:000051 positive regulation of DNA metabolic process                     | 0.96225 | 0.98348 | 0 | 0 | 2  | 275   |
| GO:0004951 RNA modification                                                 | 1  | 0.9628  | 0.31   | 0.06 | Biological | GO:000009 RNA modification                                                 | 0.9628  | 0.98348 | 0 | 0 | 1  | 178   |
| GO:0017148 negative regulation of translation                               | 1  | 0.9628  | 0.31   | 0.06 | Biological | GO:000017 negative regulation of translation                               | 0.9628  | 0.98348 | 0 | 0 | 1  | 178   |
| GO:0072331 signal transduction by p53 class mediator                        | 1  | 0.9628  | 0.31   | 0.06 | Biological | GO:000072 signal transduction by p53 class mediator                        | 0.9628  | 0.98348 | 0 | 0 | 1  | 178   |
| GO:0006163 purine nucleotide metabolic process                              | 4  | 0.96411 | 1.238  | 0.09 | Biological | GO:000006 purine nucleotide metabolic process                              | 0.96411 | 0.98461 | 0 | 0 | 4  | 446   |
| GO:0042655 cellular macromolecule catabolic process                         | 14 | 0.96444 | 4.334  | 0.12 | Biological | GO:000044 cellular macromolecule catabolic process                         | 0.96444 | 0.98671 | 0 | 0 | 14 | 1164  |
| GO:0006325 chromatin organization                                           | 6  | 0.96632 | 1.858  | 0.01 | Biological | GO:000006 chromatin organization                                           | 0.96632 | 0.98671 | 0 | 0 | 6  | 658   |
| GO:0031461 cullin-RING ubiquitin ligase complex                             | 1  | 0.96664 | 0.297  | 0.05 | Cellular C | GO:000031 cullin-RING ubiquitin ligase complex                             | 0.96664 | 1       | 0 | 0 | 1  | 186   |
| GO:0007283 spermatogenesis                                                  | 6  | 0.96731 | 1.858  | 0.01 | Biological | GO:000007 spermatogenesis                                                  | 0.96731 | 0.98728 | 0 | 0 | 6  | 607   |
| GO:0006479 protein methylation                                              | 1  | 0.96794 | 0.31   | 0.05 | Biological | GO:000006 protein methylation                                              | 0.96794 | 0.98743 | 0 | 0 | 1  | 186   |
| GO:0008213 protein alkylation                                               | 1  | 0.96794 | 0.31   | 0.05 | Biological | GO:000008 protein alkylation                                               | 0.96794 | 0.98743 | 0 | 0 | 1  | 186   |
| GO:0090407 organophosphate biosynthetic process                             | 6  | 0.96886 | 1.858  | 0.01 | Biological | GO:000090 organophosphate biosynthetic process                             | 0.96886 | 0.98743 | 0 | 0 | 6  | 658   |
| GO:0032259 methylation                                                      | 3  | 0.97055 | 0.929  | 0.08 | Biological | GO:000032 methylation                                                      | 0.97055 | 0.98949 | 0 | 0 | 3  | 379   |
| GO:0071466 cellular response to xenobiotic stimulus                         | 1  | 0.97079 | 0.31   | 0.05 | Biological | GO:000071 cellular response to xenobiotic stimulus                         | 0.97079 | 0.98949 | 0 | 0 | 1  | 191   |
| GO:0031974 membrane-enclosed lumen                                          | 87 | 0.97081 | 25.816 | 0.15 | Cellular C | GO:000031 membrane-enclosed lumen                                          | 0.97081 | 1       | 0 | 0 | 87 | 5667  |
| GO:0043233 organelle lumen                                                  | 87 | 0.97081 | 25.816 | 0.15 | Cellular C | GO:000043 organelle lumen                                                  | 0.97081 | 1       | 0 | 0 | 87 | 5667  |
| GO:0070013 intracellular organelle lumen                                    | 87 | 0.97081 | 25.816 | 0.15 | Cellular C | GO:000070 intracellular organelle lumen                                    | 0.97081 | 1       | 0 | 0 | 87 | 5667  |
| GO:0006401 RNA catabolic process                                            | 2  | 0.97108 | 0.619  | 0.07 | Biological | GO:000006 RNA catabolic process                                            | 0.97108 | 0.98949 | 0 | 0 | 2  | 292   |
| GO:0046700 heterocyclic catabolic process                                   | 4  | 0.9712  | 1.238  | 0.09 | Biological | GO:000046 heterocyclic catabolic process                                   | 0.9712  | 0.98949 | 0 | 0 | 4  | 463   |
| GO:0000910 cytokinesis                                                      | 1  | 0.97133 | 0.31   | 0.05 | Biological | GO:000009 cytokinesis                                                      | 0.97133 | 0.98949 | 0 | 0 | 1  | 192   |
| GO:0042770 signal transduction in response to DNA damage                    | 1  | 0.97133 | 0.31   | 0.05 | Biological | GO:000042 signal transduction in response to DNA damage                    | 0.97133 | 0.98949 | 0 | 0 | 1  | 192   |
| GO:0002695 negative regulation of leukocyte activation                      | 1  | 0.97186 | 0.31   | 0.05 | Biological | GO:000026 negative regulation of leukocyte activation                      | 0.97186 | 0.98949 | 0 | 0 | 1  | 193   |
| GO:0006323 DNA packaging                                                    | 1  | 0.97186 | 0.31   | 0.05 | Biological | GO:000006 DNA packaging                                                    | 0.97186 | 0.98949 | 0 | 0 | 1  | 193   |
| GO:1902806 regulation of cell cycle G1/S phase transition                   | 1  | 0.97186 | 0.31   | 0.05 | Biological | GO:000019 regulation of cell cycle G1/S phase transition                   | 0.97186 | 0.98949 | 0 | 0 | 1  | 193   |
| GO:0044270 cellular nitrogen compound catabolic process                     | 4  | 0.97337 | 1.238  | 0.09 | Biological | GO:000044 cellular nitrogen compound catabolic process                     | 0.97337 | 0.99064 | 0 | 0 | 4  | 469   |
| GO:0009600 aerobic respiration                                              | 1  | 0.97338 | 0.31   | 0.05 | Biological | GO:000009 aerobic respiration                                              | 0.97338 | 0.99064 | 0 | 0 | 1  | 196   |
| GO:0048232 male gamete germination                                          | 6  | 0.97374 | 1.858  | 0.01 | Biological | GO:000074 male gamete germination                                          | 0.97374 | 0.99103 | 0 | 0 | 6  | 628   |
| GO:0071897 DNA biosynthetic process                                         | 1  | 0.97436 | 0.31   | 0.05 | Biological | GO:000071 DNA biosynthetic process                                         | 0.97436 | 0.99103 | 0 | 0 | 1  | 198   |
| GO:0140013 meiotic nuclear division                                         | 1  | 0.97436 | 0.31   | 0.05 | Biological | GO:000040 meiotic nuclear division                                         | 0.97436 | 0.99103 | 0 | 0 | 1  | 198   |
| GO:0004930 G protein-coupled receptor activity                              | 9  | 0.97446 | 2.632  | 0.01 | Molecular  | GO:000004 G protein-coupled receptor activity                              | 0.97446 | 0.98584 | 0 | 0 | 9  | 835   |
| GO:0098687 chromosomal region                                               | 3  | 0.97495 | 0.89   | 0.08 | Cellular C | GO:000098 chromosomal region                                               | 0.97495 | 1       | 0 | 0 | 3  | 395   |
| GO:0006296 spermatogenesis                                                  | 1  | 0.97529 | 0.31   | 0.05 | Biological | GO:000006 spermatogenesis                                                  | 0.97529 | 0.99169 | 0 | 0 | 1  | 201   |
| GO:0019047 mitotic cell cycle process                                       | 8  | 0.97541 | 2.477  | 0.01 | Biological | GO:000019 mitotic cell cycle process                                       | 0.97541 | 0.99169 | 0 | 0 | 8  | 780   |
| GO:0006403 RNA localization                                                 | 1  | 0.97575 | 0.31   | 0.05 | Biological | GO:000006 RNA localization                                                 | 0.97575 | 0.99184 | 0 | 0 | 1  | 201   |
| GO:0019637 organophosphate metabolic process                                | 11 | 0.97672 | 3.406  | 0.01 | Biological | GO:000019 organophosphate metabolic process                                | 0.97672 | 0.99262 | 0 | 0 | 11 | 999   |
| GO:0030496 midbody                                                          | 1  | 0.97732 | 0.297  | 0.05 | Cellular C | GO:000030 midbody                                                          | 0.97732 | 1       | 0 | 0 | 1  | 207   |
| GO:0000377 RNA splicing, via transference reactions with bulged             | 2  | 0.97755 | 0.619  | 0.07 | Biological | GO:000003 RNA splicing, via transference reactions with bulged adenosine   | 0.97755 | 0.99303 | 0 | 0 | 2  | 319   |
| GO:0000398 mRNA splicing, via spliceosome                                   | 2  | 0.97755 | 0.619  | 0.07 | Biological | GO:000000 mRNA splicing, via spliceosome                                   | 0.97755 | 0.99303 | 0 | 0 | 2  | 308   |
| GO:0050864 regulation of B cell activation                                  | 1  | 0.9779  | 0.31   | 0.05 | Biological | GO:000050 regulation of B cell activation                                  | 0.9779  | 0.99303 | 0 | 0 | 1  | 206   |
| GO:0019439 aromatic compound catabolic process                              | 4  | 0.97815 | 1.238  | 0.08 | Biological | GO:000019 aromatic compound catabolic process                              | 0.97815 | 0.99303 | 0 | 0 | 4  | 484   |
| GO:0048193 Golgi vesicle transport                                          | 2  | 0.97826 | 0.619  | 0.06 | Biological | GO:000048 Golgi vesicle transport                                          | 0.97826 | 0.99303 | 0 | 0 | 2  | 310   |
| GO:0000701 mitotic chromosome segregation                                   | 1  | 0.97831 | 0.31   | 0.05 | Biological | GO:000007 mitotic chromosome segregation                                   | 0.97831 | 0.99303 | 0 | 0 | 1  | 207   |
| GO:0000375 RNA splicing, via transference reactions                         | 2  | 0.97894 | 0.619  | 0.06 | Biological | GO:000000 RNA splicing, via transference reactions                         | 0.97894 | 0.99346 | 0 | 0 | 2  | 312   |
| GO:0032991 protein-containing complex                                       | 88 | 0.97986 | 26.113 | 0.15 | Cellular C | GO:000032 protein-containing complex                                       | 0.97986 | 1       | 0 | 0 | 88 | 5800  |
| GO:0006282 regulation of DNA repair                                         | 1  | 0.98096 | 0.31   | 0.05 | Biological | GO:000006 regulation of DNA repair                                         | 0.98096 | 0.99531 | 0 | 0 | 1  | 214   |
| GO:0006959 humoral immune response                                          | 2  | 0.98234 | 0.619  | 0.06 | Biological | GO:000006 humoral immune response                                          | 0.98234 | 0.99622 | 0 | 0 | 2  | 323   |
| GO:0016236 macrophage activation                                            | 2  | 0.98262 | 0.619  | 0.06 | Biological | GO:000016 macrophage activation                                            | 0.98262 | 0.99622 | 0 | 0 | 2  | 324   |
| GO:0043414 macromolecule methylation                                        | 1  | 0.98265 | 0.31   | 0.05 | Biological | GO:000043 macromolecule methylation                                        | 0.98265 | 0.99622 | 0 | 0 | 1  | 219   |
| GO:0009152 purine ribonucleotide biosynthetic process                       | 1  | 0.98265 | 0.31   | 0.05 | Biological | GO:000009 purine ribonucleotide biosynthetic process                       | 0.98265 | 0.99622 | 0 | 0 | 1  | 219   |
| GO:0031981 nuclear lumen                                                    | 66 | 0.98275 | 19.585 | 0.15 | Cellular C | GO:000031 nuclear lumen                                                    | 0.98275 | 1       | 0 | 0 | 66 | 4531  |
| GO:0004518 nuclease activity                                                | 1  | 0.98316 | 0.292  | 0.05 | Molecular  | GO:000004 nuclease activity                                                | 0.98316 | 0.99348 | 0 | 0 | 1  | 217   |
| GO:0061135 regulation of cellular response to stress                        | 7  | 0.98392 | 2.167  | 0.01 | Biological | GO:000061 regulation of cellular response to stress                        | 0.98392 | 0.99717 | 0 | 0 | 7  | 744   |
| GO:0006518 peptide metabolic process                                        | 9  | 0.98399 | 2.786  | 0.01 | Biological | GO:000006 peptide metabolic process                                        | 0.98399 | 0.99717 | 0 | 0 | 9  | 893   |
| GO:0034655 nucleobase-containing compound catabolic process                 | 3  | 0.98435 | 0.929  | 0.07 | Biological | GO:000034 nucleobase-containing compound catabolic process                 | 0.98435 | 0.99733 | 0 | 0 | 3  | 423   |
| GO:0006364 rRNA processing                                                  | 1  | 0.98506 | 0.31   | 0.04 | Cellular C | GO:000006 rRNA processing                                                  | 0.98506 | 0.99784 | 0 | 0 | 1  | 227   |
| GO:0000382 G1/S transition of mitotic cell cycle                            | 1  | 0.98587 | 0.31   | 0.04 | Biological | GO:000000 G1/S transition of mitotic cell cycle                            | 0.98587 | 0.99847 | 0 | 0 | 1  | 230   |
| GO:0045930 negative regulation of mitotic cell cycle                        | 1  | 0.98613 | 0.31   | 0.04 | Biological | GO:000045 negative regulation of mitotic cell cycle                        | 0.98613 | 0.99853 | 0 | 0 | 1  | 231   |
| GO:0000918 sister chromatid segregation                                     | 1  | 0.98639 | 0.31   | 0.04 | Biological | GO:000000 sister chromatid segregation                                     | 0.98639 | 0.99858 | 0 | 0 | 1  | 232   |
| GO:0009260 ribonucleotide biosynthetic process                              | 1  | 0.98664 | 0.31   | 0.04 | Biological | GO:000009 ribonucleotide biosynthetic process                              | 0.98664 | 0.99864 | 0 | 0 | 1  | 233   |
| GO:0032993 protein-DNA complex                                              | 1  | 0.98695 | 0.297  | 0.04 | Cellular C | GO:000032 protein-DNA complex                                              | 0.98695 | 1       | 0 | 0 | 1  | 237   |
| GO:0005840 ribosome                                                         | 1  | 0.98765 | 0.297  | 0.04 | Cellular C | GO:000005 ribosome                                                         | 0.98765 | 1       | 0 | 0 | 1  | 240   |
| GO:0005654 nucleosome                                                       | 59 | 0.98791 | 17.507 | 0.14 | Cellular C | GO:000005 nucleosome                                                       | 0.98791 | 1       | 0 | 0 | 59 | 4171  |
| GO:0006164 purine nucleotide biosynthetic process                           | 1  | 0.98805 | 0.31   | 0.04 | Biological | GO:000006 purine nucleotide biosynthetic process                           | 0.98805 | 0.99987 | 0 | 0 | 1  | 239   |
| GO:0046390 ribose phosphate biosynthetic process                            | 1  | 0.98827 | 0.31   | 0.04 | Biological | GO:000046 ribose phosphate biosynthetic process                            | 0.98827 | 0.99989 | 0 | 0 | 1  | 240   |
| GO:0140097 catalytic activity, acting on DNA                                | 1  | 0.98911 | 0.292  | 0.04 | Molecular  | GO:000040 catalytic activity, acting on DNA                                | 0.98911 | 0.99833 | 0 | 0 | 1  | 240   |
| GO:0002449 lymphocyte mediated immunity                                     | 2  | 0.98928 | 0.619  | 0.06 | Biological | GO:000024 lymphocyte mediated immunity                                     | 0.98928 | 1       | 0 | 0 | 2  | 36912 |
| GO:0055998 nucleic acid-containing small molecule metabolic process         | 5  | 0.98913 | 1.548  | 0.09 | Biological | GO:000055 nucleic acid-containing small molecule metabolic process         | 0.98913 | 1       | 0 | 0 | 5  | 419   |
| GO:0010608 posttranscriptional regulation of gene expression                | 4  | 0.9892  | 1.238  | 0.07 | Biological | GO:000010 posttranscriptional regulation of gene expression                | 0.9892  | 1       | 0 | 0 | 4  | 536   |
| GO:0008380 RNA splicing                                                     | 3  | 0.98933 | 0.929  | 0.07 | Biological | GO:000008 RNA splicing                                                     | 0.98933 | 1       | 0 | 0 | 3  | 449   |
| GO:0009117 nucleotide metabolic process                                     | 4  |         |        |      |            |                                                                            |         |         |   |   |    |       |

|                                                                 |     |         |       |       |            |                                                                 |         |   |   |   |     |       |
|-----------------------------------------------------------------|-----|---------|-------|-------|------------|-----------------------------------------------------------------|---------|---|---|---|-----|-------|
| GO:0006412 translation                                          | 3   | 0.99981 | 0.929 | 0.004 | Biological | GO:0006412 translation                                          | 0.99981 | 1 | 0 | 0 | 3   | 706   |
| GO:0022613 ribonucleoprotein complex biogenesis                 | 1   | 0.99982 | 0.31  | 0.002 | Biological | GO:0022613 ribonucleoprotein complex biogenesis                 | 0.99982 | 1 | 0 | 0 | 1   | 462   |
| GO:0140640 catalytic activity, acting on a nucleic acid         | 2   | 0.99987 | 0.585 | 0.003 | Molecular  | GO:0140640 catalytic activity, acting on a nucleic acid         | 0.99987 | 1 | 0 | 0 | 2   | 605   |
| GO:0009593 detection of chemical stimulus                       | 1   | 0.99987 | 0.31  | 0.002 | Biological | GO:0009593 detection of chemical stimulus                       | 0.99987 | 1 | 0 | 0 | 1   | 481   |
| GO:0034622 cellular protein-containing complex assembly         | 7   | 0.99991 | 2.167 | 0.006 | Biological | GO:0034622 cellular protein-containing complex assembly         | 0.99991 | 1 | 0 | 0 | 7   | 1137  |
| GO:0007606 sensory perception of chemical stimulus              | 1   | 0.99991 | 0.31  | 0.002 | Biological | GO:0007606 sensory perception of chemical stimulus              | 0.99991 | 1 | 0 | 0 | 1   | 501   |
| GO:0050906 detection of stimulus involved in sensory perception | 1   | 0.99993 | 0.31  | 0.002 | Biological | GO:0050906 detection of stimulus involved in sensory perception | 0.99993 | 1 | 0 | 0 | 1   | 514   |
| GO:0006396 RNA processing                                       | 4   | 0.99998 | 1.238 | 0.004 | Biological | GO:0006396 RNA processing                                       | 0.99998 | 1 | 0 | 0 | 4   | 957   |
| GO:0003723 RNA binding                                          | 12  | 0.99999 | 3.509 | 0.007 | Molecular  | GO:0003723 RNA binding                                          | 0.99999 | 1 | 0 | 0 | 12  | 1722  |
| GO:1990904 ribonucleoprotein complex                            | 1   | 1       | 0.297 | 0.001 | Cellular   | GO:1990904 ribonucleoprotein complex                            | 1       | 1 | 0 | 0 | 1   | 729   |
| GO:0003674 molecular function                                   | 342 | 1       | 100   | 0.019 | Molecular  | GO:0003674 molecular function                                   | 1       | 1 | 0 | 0 | 342 | 18452 |
| GO:0005575 cellular component                                   | 337 | 1       | 100   | 0.018 | Cellular   | GO:0005575 cellular component                                   | 1       | 1 | 0 | 0 | 337 | 18696 |
| GO:0008150 biological process                                   | 323 | 1       | 100   | 0.018 | Biological | GO:0008150 biological process                                   | 1       | 1 | 0 | 0 | 323 | 17718 |

Supplementary Table 6: The result of KEGG analysis

| id                                                         | num | pvalue  | per    | ratio | class      | ID      | Descriptio    | Pvalue  | Qvalue  | Up | Down | fg num | bg num |
|------------------------------------------------------------|-----|---------|--------|-------|------------|---------|---------------|---------|---------|----|------|--------|--------|
| Pathways in cancer                                         | 22  | 0.00016 | 15.172 | 0.04  | Human D    | ko05200 | Pathways      | 0.00016 | 0.03992 | 0  | 0    | 22     | 546    |
| AGE-RAGE signaling pathway in diabetic complications       | 8   | 0.00042 | 5.517  | 0.077 | Human D    | ko04933 | AGE-RAGE      | 0.00042 | 0.05164 | 0  | 0    | 8      | 104    |
| Vascular smooth muscle contraction                         | 9   | 0.00066 | 6.207  | 0.065 | Organism   | ko04270 | Vascular      | 0.00066 | 0.05399 | 0  | 0    | 9      | 139    |
| Glycosphingolipid biosynthesis - lacto and neolacto series | 4   | 0.00128 | 2.759  | 0.143 | Metabolis  | ko00601 | Glycosph      | 0.00128 | 0.07803 | 0  | 0    | 4      | 28     |
| Protein digestion and absorption                           | 7   | 0.00224 | 4.828  | 0.067 | Organism   | ko04974 | Protein di    | 0.00224 | 0.08419 | 0  | 0    | 7      | 105    |
| Choline metabolism in cancer                               | 7   | 0.00236 | 4.828  | 0.066 | Human D    | ko05231 | Choline m     | 0.00236 | 0.08419 | 0  | 0    | 7      | 106    |
| Glycosphingolipid biosynthesis - globo and isoglobo series | 3   | 0.00242 | 2.069  | 0.188 | Metabolis  | ko00603 | Glycosph      | 0.00242 | 0.08419 | 0  | 0    | 3      | 16     |
| GnRH signaling pathway                                     | 6   | 0.00598 | 4.138  | 0.063 | Organism   | ko04912 | GnRH sig      | 0.00598 | 0.16892 | 0  | 0    | 6      | 95     |
| MAPK signaling pathway                                     | 12  | 0.00623 | 8.276  | 0.04  | Environm   | ko04010 | MAPK sig      | 0.00623 | 0.16892 | 0  | 0    | 12     | 303    |
| Inflammatory mediator regulation of TRP channels           | 6   | 0.0084  | 4.138  | 0.059 | Organism   | ko04750 | Inflammat     | 0.0084  | 0.17091 | 0  | 0    | 6      | 102    |
| Renin secretion                                            | 5   | 0.0085  | 3.448  | 0.068 | Organism   | ko04924 | Renin sec     | 0.0085  | 0.17091 | 0  | 0    | 5      | 73     |
| Renal cell carcinoma                                       | 5   | 0.00951 | 3.448  | 0.067 | Human D    | ko05211 | Renal cel     | 0.00951 | 0.17091 | 0  | 0    | 5      | 75     |
| Focal adhesion                                             | 9   | 0.01061 | 6.207  | 0.043 | Cellular P | ko04510 | Focal adf     | 0.01061 | 0.17091 | 0  | 0    | 9      | 210    |
| Gastric acid secretion                                     | 5   | 0.01116 | 3.448  | 0.064 | Organism   | ko04971 | Gastric ac    | 0.01116 | 0.17091 | 0  | 0    | 5      | 78     |
| Ether lipid metabolism                                     | 4   | 0.01149 | 2.759  | 0.078 | Metabolis  | ko00565 | Ether lipid   | 0.01149 | 0.17091 | 0  | 0    | 4      | 51     |
| Apelin signaling pathway                                   | 7   | 0.01154 | 4.828  | 0.049 | Environm   | ko04371 | Apelin sig    | 0.01154 | 0.17091 | 0  | 0    | 7      | 142    |
| Proteoglycans in cancer                                    | 9   | 0.01191 | 6.207  | 0.042 | Human D    | ko05205 | Proteogly     | 0.01191 | 0.17091 | 0  | 0    | 9      | 214    |
| Glutamatergic synapse                                      | 6   | 0.01582 | 4.138  | 0.051 | Organism   | ko04724 | Glutamatergic | 0.01582 | 0.20608 | 0  | 0    | 6      | 117    |
| Phototransduction - fly                                    | 3   | 0.01605 | 2.069  | 0.097 | Organism   | ko04745 | Phototran     | 0.01605 | 0.20608 | 0  | 0    | 3      | 31     |
| ErbB signaling pathway                                     | 5   | 0.01807 | 3.448  | 0.057 | Environm   | ko04012 | ErbB sig      | 0.01807 | 0.22043 | 0  | 0    | 5      | 88     |
| Oxytocin signaling pathway                                 | 7   | 0.02034 | 4.828  | 0.044 | Organism   | ko04921 | Oxytocin      | 0.02034 | 0.22836 | 0  | 0    | 7      | 159    |
| ECM-receptor interaction                                   | 5   | 0.02059 | 3.448  | 0.055 | Environm   | ko04512 | ECM-rece      | 0.02059 | 0.22836 | 0  | 0    | 5      | 91     |
| Mucin type O-glycan biosynthesis                           | 3   | 0.02395 | 2.069  | 0.083 | Metabolis  | ko00512 | Mucin typ     | 0.02395 | 0.25403 | 0  | 0    | 3      | 36     |
| Hepatitis B                                                | 7   | 0.02506 | 4.828  | 0.042 | Human D    | ko05161 | Hepatitis     | 0.02506 | 0.25478 | 0  | 0    | 7      | 166    |
| Relaxin signaling pathway                                  | 6   | 0.02777 | 4.138  | 0.045 | Organism   | ko04926 | Relaxin s     | 0.02777 | 0.25835 | 0  | 0    | 6      | 133    |
| Long-term potentiation                                     | 4   | 0.02993 | 2.759  | 0.059 | Organism   | ko04720 | Long-term     | 0.02993 | 0.25835 | 0  | 0    | 4      | 68     |
| Glycerophospholipid metabolism                             | 5   | 0.03062 | 3.448  | 0.05  | Metabolis  | ko00564 | Glyceroph     | 0.03062 | 0.25835 | 0  | 0    | 5      | 101    |
| Melanogenesis                                              | 5   | 0.03062 | 3.448  | 0.05  | Organism   | ko04916 | Melanoge      | 0.03062 | 0.25835 | 0  | 0    | 5      | 101    |
| Ras signaling pathway                                      | 9   | 0.03076 | 6.207  | 0.036 | Environm   | ko04014 | Ras signa     | 0.03076 | 0.25835 | 0  | 0    | 9      | 252    |
| cGMP-PKG signaling pathway                                 | 7   | 0.03216 | 4.828  | 0.04  | Environm   | ko04022 | cGMP-PK       | 0.03216 | 0.25835 | 0  | 0    | 7      | 175    |
| Amphetamine addiction                                      | 4   | 0.03282 | 2.759  | 0.057 | Human D    | ko05031 | Ampheta       | 0.03282 | 0.25835 | 0  | 0    | 4      | 70     |
| Nitrogen metabolism                                        | 2   | 0.03418 | 1.379  | 0.118 | Metabolis  | ko00910 | Nitrogen      | 0.03418 | 0.26061 | 0  | 0    | 2      | 17     |
| Non-small cell lung cancer                                 | 4   | 0.04076 | 2.759  | 0.053 | Human D    | ko05223 | Non-smal      | 0.04076 | 0.30065 | 0  | 0    | 4      | 75     |
| Parathyroid hormone synthesis, secretion and action        | 5   | 0.04189 | 3.448  | 0.045 | Organism   | ko04928 | Parathyro     | 0.04189 | 0.30065 | 0  | 0    | 5      | 110    |
| Leishmaniasis                                              | 6   | 0.04336 | 4.138  | 0.041 | Human D    | ko05140 | Leishman      | 0.04336 | 0.30225 | 0  | 0    | 6      | 148    |
| cAMP signaling pathway                                     | 8   | 0.04619 | 5.517  | 0.035 | Environm   | ko04024 | cAMP sig      | 0.04619 | 0.30709 | 0  | 0    | 8      | 230    |
| NOD-like receptor signaling pathway                        | 7   | 0.04679 | 4.828  | 0.037 | Organism   | ko04621 | NOD-like      | 0.04679 | 0.30709 | 0  | 0    | 7      | 190    |
| Arrhythmogenic right ventricular cardiomyopathy            | 4   | 0.04782 | 2.759  | 0.051 | Human D    | ko05412 | Arrhythm      | 0.04782 | 0.30709 | 0  | 0    | 4      | 79     |
| Cell adhesion molecules                                    | 6   | 0.04957 | 4.138  | 0.039 | Environm   | ko04514 | Cell adhe     | 0.04957 | 0.31011 | 0  | 0    | 6      | 153    |
| Calcium signaling pathway                                  | 10  | 0.05176 | 6.897  | 0.031 | Environm   | ko04020 | Calcium s     | 0.05176 | 0.31571 | 0  | 0    | 10     | 321    |
| Pancreatic cancer                                          | 4   | 0.05354 | 2.759  | 0.049 | Human D    | ko05212 | Pancreati     | 0.05354 | 0.31864 | 0  | 0    | 4      | 82     |
| HIF-1 signaling pathway                                    | 5   | 0.05702 | 3.448  | 0.042 | Environm   | ko04066 | HIF-1 sig     | 0.05702 | 0.32913 | 0  | 0    | 5      | 120    |
| Sphingolipid metabolism                                    | 3   | 0.058   | 2.069  | 0.059 | Metabolis  | ko00600 | Sphingoli     | 0.058   | 0.32913 | 0  | 0    | 3      | 51     |
| EGFR tyrosine kinase inhibitor resistance                  | 4   | 0.05962 | 2.759  | 0.047 | Human D    | ko05121 | EGFR tyr      | 0.05962 | 0.3306  | 0  | 0    | 4      | 85     |
| Cysteine and methionine metabolism                         | 3   | 0.06366 | 2.069  | 0.057 | Metabolis  | ko00270 | Cysteine      | 0.06366 | 0.34519 | 0  | 0    | 3      | 53     |
| Hypertrophic cardiomyopathy                                | 4   | 0.06826 | 2.759  | 0.045 | Human D    | ko05410 | Hypertrop     | 0.06826 | 0.36208 | 0  | 0    | 4      | 89     |
| Thyroid hormone signaling pathway                          | 5   | 0.07301 | 3.448  | 0.039 | Organism   | ko04919 | Thyroid h     | 0.07301 | 0.37307 | 0  | 0    | 5      | 129    |
| alpha-Linolenic acid metabolism                            | 2   | 0.07388 | 1.379  | 0.077 | Metabolis  | ko00592 | alpha-Lin     | 0.07388 | 0.37307 | 0  | 0    | 2      | 26     |
| Platelet activation                                        | 5   | 0.07492 | 3.448  | 0.038 | Organism   | ko04611 | Platelet a    | 0.07492 | 0.37307 | 0  | 0    | 5      | 130    |
| Cytokine-cytokine receptor interaction                     | 9   | 0.07988 | 6.207  | 0.03  | Environm   | ko04060 | Cytokine-     | 0.07988 | 0.38196 | 0  | 0    | 9      | 303    |
| Morphine addiction                                         | 4   | 0.07993 | 2.759  | 0.043 | Human D    | ko05032 | Morphine      | 0.07993 | 0.38196 | 0  | 0    | 4      | 94     |
| MicroRNAs in cancer                                        | 6   | 0.0814  | 4.138  | 0.034 | Human D    | ko05206 | MicroRNA      | 0.0814  | 0.38196 | 0  | 0    | 6      | 174    |
| TGF-beta signaling pathway                                 | 4   | 0.08737 | 2.759  | 0.041 | Environm   | ko04350 | TGF-beta      | 0.08737 | 0.39514 | 0  | 0    | 4      | 97     |
| Long-term depression                                       | 3   | 0.08869 | 2.069  | 0.049 | Organism   | ko04730 | Long-term     | 0.08869 | 0.39514 | 0  | 0    | 3      | 61     |
| Dopaminergic synapse                                       | 5   | 0.08907 | 3.448  | 0.036 | Organism   | ko04728 | Dopamine      | 0.08907 | 0.39514 | 0  | 0    | 5      | 137    |
| Glycerolipid metabolism                                    | 3   | 0.09899 | 2.069  | 0.047 | Metabolis  | ko00561 | Glyceroli     | 0.09899 | 0.43133 | 0  | 0    | 3      | 64     |
| Circadian entrainment                                      | 4   | 0.10323 | 2.759  | 0.039 | Organism   | ko04713 | Circadian     | 0.10323 | 0.43887 | 0  | 0    | 4      | 103    |
| Arachidonic acid metabolism                                | 3   | 0.10612 | 2.069  | 0.045 | Metabolis  | ko00590 | Arachidonic   | 0.10612 | 0.43887 | 0  | 0    | 3      | 66     |
| GnRH secretion                                             | 3   | 0.10612 | 2.069  | 0.045 | Organism   | ko04929 | GnRH se       | 0.10612 | 0.43887 | 0  | 0    | 3      | 66     |
| Spinocerebellar ataxia                                     | 5   | 0.11151 | 3.448  | 0.034 | Human D    | ko05017 | Spinocere     | 0.11151 | 0.45347 | 0  | 0    | 5      | 147    |
| Inflammatory bowel disease                                 | 3   | 0.12477 | 2.069  | 0.042 | Human D    | ko05321 | Inflammat     | 0.12477 | 0.49908 | 0  | 0    | 3      | 71     |
| Th17 cell differentiation                                  | 4   | 0.13541 | 2.759  | 0.035 | Organism   | ko04659 | Th17 cell     | 0.13541 | 0.52444 | 0  | 0    | 4      | 114    |
| Toxoplasmosis                                              | 4   | 0.13541 | 2.759  | 0.035 | Human D    | ko05145 | Toxoplas      | 0.13541 | 0.52444 | 0  | 0    | 4      | 114    |
| TNF signaling pathway                                      | 4   | 0.13852 | 2.759  | 0.035 | Environm   | ko04668 | TNF signa     | 0.13852 | 0.52734 | 0  | 0    | 4      | 115    |
| Thyroid hormone synthesis                                  | 3   | 0.14048 | 2.069  | 0.04  | Organism   | ko04918 | Thyroid h     | 0.14048 | 0.52734 | 0  | 0    | 3      | 75     |
| Glioma                                                     | 3   | 0.15682 | 2.069  | 0.038 | Human D    | ko05214 | Glioma        | 0.15682 | 0.57168 | 0  | 0    | 3      | 79     |
| Bladder cancer                                             | 2   | 0.15816 | 1.379  | 0.049 | Human D    | ko05219 | Bladder c     | 0.15816 | 0.57168 | 0  | 0    | 2      | 41     |
| Aldosterone-regulated sodium reabsorption                  | 2   | 0.16428 | 1.379  | 0.048 | Organism   | ko04960 | Aldostero     | 0.16428 | 0.57168 | 0  | 0    | 2      | 42     |
| Growth hormone synthesis, secretion and action             | 4   | 0.16439 | 2.759  | 0.033 | Organism   | ko04935 | Growth h      | 0.16439 | 0.57168 | 0  | 0    | 4      | 123    |
| Hepatocellular carcinoma                                   | 5   | 0.16924 | 3.448  | 0.03  | Human D    | ko05225 | Hepatocel     | 0.16924 | 0.57168 | 0  | 0    | 5      | 169    |
| Ferroptosis                                                | 2   | 0.17044 | 1.379  | 0.047 | Cellular P | ko04216 | Ferroptos     | 0.17044 | 0.57168 | 0  | 0    | 2      | 43     |
| Fat digestion and absorption                               | 2   | 0.17044 | 1.379  | 0.047 | Organism   | ko04975 | Fat diges     | 0.17044 | 0.57168 | 0  | 0    | 2      | 43     |
| Sphingolipid signaling pathway                             | 4   | 0.17112 | 2.759  | 0.032 | Environm   | ko04071 | Sphingoli     | 0.17112 | 0.57168 | 0  | 0    | 4      | 125    |
| Coronavirus disease - COVID-19                             | 8   | 0.17338 | 5.517  | 0.026 | Human D    | ko05171 | Coronavir     | 0.17338 | 0.57168 | 0  | 0    | 8      | 312    |
| Neurotrophin signaling pathway                             | 4   | 0.18139 | 2.759  | 0.031 | Organism   | ko04722 | Neurotrop     | 0.18139 | 0.58232 | 0  | 0    | 4      | 128    |
| Wnt signaling pathway                                      | 5   | 0.18377 | 3.448  | 0.029 | Environm   | ko04310 | Wnt signa     | 0.18377 | 0.58232 | 0  | 0    | 5      | 174    |
| Fc gamma R-mediated phagocytosis                           | 5   | 0.18377 | 3.448  | 0.029 | Organism   | ko04666 | Fc gamm       | 0.18377 | 0.58232 | 0  | 0    | 5      | 174    |
| Osteoclast differentiation                                 | 4   | 0.18834 | 2.759  | 0.031 | Organism   | ko04380 | Osteoclas     | 0.18834 | 0.58918 | 0  | 0    | 4      | 130    |
| Amoebiasis                                                 | 5   | 0.1927  | 3.448  | 0.028 | Human D    | ko05146 | Amoebias      | 0.1927  | 0.59516 | 0  | 0    | 5      | 177    |
| Other types of O-glycan biosynthesis                       | 2   | 0.19545 | 1.379  | 0.043 | Metabolis  | ko00514 | Other typ     | 0.19545 | 0.59612 | 0  | 0    | 2      | 47     |
| Purine metabolism                                          | 4   | 0.20251 | 2.759  | 0.03  | Metabolis  | ko00230 | Purine me     | 0.20251 | 0.61004 | 0  | 0    | 4      | 134    |
| Phospholipase D signaling pathway                          | 6   | 0.20591 | 4.138  | 0.026 | Environm   | ko04072 | Phosphol      | 0.20591 | 0.61182 | 0  | 0    | 6      | 229    |
| Cocaine addiction                                          | 2   | 0.20812 | 1.379  | 0.041 | Human D    | ko05030 | Cocaine a     | 0.20812 | 0.61182 | 0  | 0    | 2      | 49     |
| Gap junction                                               | 3   | 0.21793 | 2.069  | 0.032 | Cellular P | ko04540 | Gap junct     | 0.21793 | 0.62321 | 0  | 0    | 3      | 93     |
| Colorectal cancer                                          | 3   | 0.21793 | 2.069  | 0.032 | Human D    | ko05210 | Colorecta     | 0.21793 | 0.62321 | 0  | 0    | 3      | 93     |
| Human cytomegalovirus infection                            | 6   | 0.21965 | 4.138  | 0.026 | Human D    | ko05163 | Human cy      | 0.21965 | 0.62321 | 0  | 0    | 6      | 234    |
| Apoptosis                                                  | 4   | 0.22433 | 2.759  | 0.029 | Cellular P | ko04210 | Apoptosis     | 0.22433 | 0.62916 | 0  | 0    | 4      | 140    |
| Cholesterol metabolism                                     | 2   | 0.22728 | 1.379  | 0.038 | Organism   | ko04979 | Cholester     | 0.22728 | 0.63016 | 0  | 0    | 2      | 52     |
| Axon guidance                                              | 5   | 0.22985 | 3.448  | 0.026 | Organism   | ko04360 | Axon guid     | 0.22985 | 0.63016 | 0  | 0    | 5      | 189    |
| N-Glycan biosynthesis                                      | 2   | 0.2337  | 1.379  | 0.038 | Metabolis  | ko00510 | N-Glycan      | 0.2337  | 0.63193 | 0  | 0    | 2      | 53     |
| PI3K-Akt signaling pathway                                 | 10  | 0.23787 | 6.897  | 0.023 | Environm   | ko04151 | PI3K-Akt      | 0.23787 | 0.63193 | 0  | 0    | 10     | 443    |
| Endocrine and other factor-regulated calcium reabsorption  | 2   | 0.24012 | 1.379  | 0.037 | Organism   | ko04961 | Endocrine     | 0.24012 | 0.63193 | 0  | 0    | 2      | 54     |
| Th1 and Th2 cell differentiation                           | 3   | 0.24086 | 2.069  | 0.031 | Organism   | ko04658 | Th1 and       | 0.24086 | 0.63193 | 0  | 0    | 3      | 98     |
| Salivary secretion                                         | 3   | 0.24549 | 2.069  | 0.03  | Organism   | ko04970 | Salivary s    | 0.24549 | 0.63372 | 0  | 0    | 3      | 99     |
| Signaling pathways regulating pluripotency of stem cells   | 4   | 0.24673 | 2.759  | 0.027 | Cellular P | ko04550 | Signaling     | 0.24673 | 0.63372 |    |      |        |        |

|                                                            |    |         |       |       |            |         |             |         |         |   |   |    |      |
|------------------------------------------------------------|----|---------|-------|-------|------------|---------|-------------|---------|---------|---|---|----|------|
| Salmonella infection                                       | 6  | 0.31368 | 4.138 | 0.023 | Human D    | ko05132 | Salmonell   | 0.31368 | 0.66542 | 0 | 0 | 6  | 266  |
| mTOR signaling pathway                                     | 4  | 0.31635 | 2.759 | 0.024 | Environm   | ko04150 | mTOR sig    | 0.31635 | 0.66542 | 0 | 0 | 4  | 164  |
| Dilated cardiomyopathy                                     | 4  | 0.31635 | 2.759 | 0.024 | Human D    | ko05414 | Dilated ca  | 0.31635 | 0.66542 | 0 | 0 | 4  | 164  |
| Serotonergic synapse                                       | 3  | 0.32101 | 2.069 | 0.026 | Organism   | ko04726 | Serotoner   | 0.32101 | 0.66946 | 0 | 0 | 3  | 115  |
| Rheumatoid arthritis                                       | 4  | 0.32816 | 2.759 | 0.024 | Human D    | ko05323 | Rheumat     | 0.32816 | 0.67358 | 0 | 0 | 4  | 167  |
| Cholinergic synapse                                        | 3  | 0.33054 | 2.069 | 0.026 | Organism   | ko04725 | Choliner    | 0.33054 | 0.67358 | 0 | 0 | 3  | 117  |
| Mannose type O-glycan biosynthesis                         | 1  | 0.33127 | 0.69  | 0.043 | Metabolis  | ko00515 | Mannose     | 0.33127 | 0.67358 | 0 | 0 | 1  | 23   |
| Human immunodeficiency virus 1 infection                   | 5  | 0.34361 | 3.448 | 0.022 | Human D    | ko05170 | Human im    | 0.34361 | 0.68915 | 0 | 0 | 5  | 223  |
| RIG-I-like receptor signaling pathway                      | 2  | 0.34912 | 1.379 | 0.028 | Organism   | ko04622 | RIG-I-like  | 0.34912 | 0.68915 | 0 | 0 | 2  | 71   |
| Leukocyte transendothelial migration                       | 3  | 0.34957 | 2.069 | 0.025 | Organism   | ko04670 | Leukocyte   | 0.34957 | 0.68915 | 0 | 0 | 3  | 121  |
| Hematopoietic cell lineage                                 | 4  | 0.35187 | 2.759 | 0.023 | Organism   | ko04640 | Hematopo    | 0.35187 | 0.68915 | 0 | 0 | 4  | 173  |
| Vitamin digestion and absorption                           | 1  | 0.3543  | 0.69  | 0.04  | Organism   | ko04977 | Vitamin d   | 0.3543  | 0.68915 | 0 | 0 | 1  | 25   |
| Epstein-Barr virus infection                               | 6  | 0.35689 | 4.138 | 0.021 | Human D    | ko05169 | Epstein-B   | 0.35689 | 0.68915 | 0 | 0 | 6  | 280  |
| Mitophagy - animal                                         | 2  | 0.3617  | 1.379 | 0.027 | Cellular P | ko04137 | Mitophag    | 0.3617  | 0.68915 | 0 | 0 | 2  | 73   |
| Pathways of neurodegeneration - multiple diseases          | 10 | 0.3636  | 6.897 | 0.02  | Human D    | ko05022 | Pathways    | 0.3636  | 0.68915 | 0 | 0 | 10 | 499  |
| Rap1 signaling pathway                                     | 5  | 0.36434 | 3.448 | 0.022 | Environm   | ko04015 | Rap1 sig    | 0.36434 | 0.68915 | 0 | 0 | 5  | 229  |
| Influenza A                                                | 4  | 0.36769 | 2.759 | 0.023 | Human D    | ko05164 | Influenza   | 0.36769 | 0.69012 | 0 | 0 | 4  | 177  |
| NF-kappa B signaling pathway                               | 4  | 0.37164 | 2.759 | 0.022 | Environm   | ko04064 | NF-kappa    | 0.37164 | 0.69222 | 0 | 0 | 4  | 178  |
| Biosynthesis of unsaturated fatty acids                    | 1  | 0.37654 | 0.69  | 0.037 | Metabolis  | ko01040 | Biosynthe   | 0.37654 | 0.69602 | 0 | 0 | 1  | 27   |
| Biosynthesis of amino acids                                | 2  | 0.38658 | 1.379 | 0.026 | Metabolis  | ko01230 | Biosynthe   | 0.38658 | 0.70014 | 0 | 0 | 2  | 77   |
| Folate biosynthesis                                        | 1  | 0.38737 | 0.69  | 0.036 | Metabolis  | ko00790 | Folate bio  | 0.38737 | 0.70014 | 0 | 0 | 1  | 28   |
| Maturity onset diabetes of the young                       | 1  | 0.38737 | 0.69  | 0.036 | Human D    | ko04950 | Maturity d  | 0.38737 | 0.70014 | 0 | 0 | 1  | 28   |
| PPAR signaling pathway                                     | 2  | 0.39273 | 1.379 | 0.026 | Organism   | ko03320 | PPAR sig    | 0.39273 | 0.70461 | 0 | 0 | 2  | 78   |
| Hippo signaling pathway - multiple species                 | 1  | 0.39802 | 0.69  | 0.034 | Environm   | ko04392 | Hippo sig   | 0.39802 | 0.7082  | 0 | 0 | 1  | 29   |
| Linoleic acid metabolism                                   | 1  | 0.40848 | 0.69  | 0.033 | Metabolis  | ko00591 | Linoleic a  | 0.40848 | 0.7082  | 0 | 0 | 1  | 30   |
| Antifolate resistance                                      | 1  | 0.40848 | 0.69  | 0.033 | Human D    | ko01523 | Antifolate  | 0.40848 | 0.7082  | 0 | 0 | 1  | 30   |
| Phototransduction                                          | 1  | 0.40848 | 0.69  | 0.033 | Organism   | ko04744 | Phototran   | 0.40848 | 0.7082  | 0 | 0 | 1  | 30   |
| Pertussis                                                  | 2  | 0.41103 | 1.379 | 0.025 | Human D    | ko05133 | Pertussis   | 0.41103 | 0.7082  | 0 | 0 | 2  | 81   |
| Metabolic pathways                                         | 29 | 0.41215 | 20    | 0.018 | Metabolis  | ko01100 | Metabolic   | 0.41215 | 0.7082  | 0 | 0 | 29 | 1591 |
| Glyoxylate and dicarboxylate metabolism                    | 1  | 0.42887 | 0.69  | 0.031 | Metabolis  | ko00630 | Glyoxylat   | 0.42887 | 0.72669 | 0 | 0 | 1  | 32   |
| Apoptosis - multiple species                               | 1  | 0.42887 | 0.69  | 0.031 | Cellular P | ko04215 | Apoptosis   | 0.42887 | 0.72669 | 0 | 0 | 1  | 32   |
| Estrogen signaling pathway                                 | 3  | 0.44319 | 2.069 | 0.021 | Organism   | ko04915 | Estrogen    | 0.44319 | 0.74578 | 0 | 0 | 3  | 141  |
| Propanoate metabolism                                      | 1  | 0.44855 | 0.69  | 0.029 | Metabolis  | ko00640 | Propanoa    | 0.44855 | 0.74964 | 0 | 0 | 1  | 34   |
| Insulin secretion                                          | 2  | 0.46422 | 1.379 | 0.022 | Organism   | ko04911 | Insulin se  | 0.46422 | 0.75861 | 0 | 0 | 2  | 90   |
| Tuberculosis                                               | 5  | 0.46741 | 3.448 | 0.019 | Human D    | ko05152 | Tuberculo   | 0.46741 | 0.75861 | 0 | 0 | 5  | 259  |
| GABAergic synapse                                          | 2  | 0.46995 | 1.379 | 0.022 | Organism   | ko04727 | GABAerg     | 0.46995 | 0.75861 | 0 | 0 | 2  | 91   |
| Chemical carcinogenesis - receptor activation              | 4  | 0.47289 | 2.759 | 0.02  | Human D    | ko05207 | Chemical    | 0.47289 | 0.75861 | 0 | 0 | 4  | 204  |
| Measles                                                    | 3  | 0.47926 | 2.069 | 0.02  | Human D    | ko05162 | Measles     | 0.47926 | 0.75861 | 0 | 0 | 3  | 149  |
| Small cell lung cancer                                     | 2  | 0.48695 | 1.379 | 0.021 | Human D    | ko05222 | Small cell  | 0.48695 | 0.75861 | 0 | 0 | 2  | 94   |
| Gastric cancer                                             | 3  | 0.49251 | 2.069 | 0.02  | Human D    | ko05226 | Gastric ca  | 0.49251 | 0.75861 | 0 | 0 | 3  | 152  |
| Complement and coagulation cascades                        | 2  | 0.49254 | 1.379 | 0.021 | Organism   | ko04610 | Complem     | 0.49254 | 0.75861 | 0 | 0 | 2  | 95   |
| Viral carcinogenesis                                       | 4  | 0.4955  | 2.759 | 0.019 | Human D    | ko05203 | Viral carc  | 0.4955  | 0.75861 | 0 | 0 | 4  | 210  |
| Autophagy - animal                                         | 3  | 0.49689 | 2.069 | 0.02  | Cellular P | ko04140 | Autophag    | 0.49689 | 0.75861 | 0 | 0 | 3  | 153  |
| B cell receptor signaling pathway                          | 3  | 0.49689 | 2.069 | 0.02  | Organism   | ko04662 | B cell rec  | 0.49689 | 0.75861 | 0 | 0 | 3  | 153  |
| IL-17 signaling pathway                                    | 2  | 0.49809 | 1.379 | 0.021 | Organism   | ko04657 | IL-17 sig   | 0.49809 | 0.75861 | 0 | 0 | 2  | 96   |
| Retrograde endocannabinoid signaling                       | 3  | 0.50126 | 2.069 | 0.019 | Organism   | ko04723 | Retrograd   | 0.50126 | 0.75861 | 0 | 0 | 3  | 154  |
| PD-L1 expression and PD-1 checkpoint pathway in cancer     | 2  | 0.5036  | 1.379 | 0.021 | Human D    | ko05235 | PD-L1 ex    | 0.5036  | 0.75861 | 0 | 0 | 2  | 97   |
| Alanine, aspartate and glutamate metabolism                | 1  | 0.50366 | 0.69  | 0.025 | Metabolis  | ko00250 | Alanine, a  | 0.50366 | 0.75861 | 0 | 0 | 1  | 40   |
| Toll and lmd signaling pathway                             | 1  | 0.50366 | 0.69  | 0.025 | Organism   | ko04624 | Toll and l  | 0.50366 | 0.75861 | 0 | 0 | 1  | 40   |
| Nicotine addiction                                         | 1  | 0.5123  | 0.69  | 0.024 | Human D    | ko05033 | Nicotine a  | 0.5123  | 0.76688 | 0 | 0 | 1  | 41   |
| Various types of N-glycan biosynthesis                     | 1  | 0.52079 | 0.69  | 0.024 | Metabolis  | ko00513 | Various ty  | 0.52079 | 0.77308 | 0 | 0 | 1  | 42   |
| Hippo signaling pathway                                    | 3  | 0.52278 | 2.069 | 0.019 | Environm   | ko04390 | Hippo sig   | 0.52278 | 0.77308 | 0 | 0 | 3  | 159  |
| Prostate cancer                                            | 2  | 0.53058 | 1.379 | 0.02  | Human D    | ko05215 | Prostate c  | 0.53058 | 0.77365 | 0 | 0 | 2  | 102  |
| Diabetic cardiomyopathy                                    | 4  | 0.53225 | 2.759 | 0.018 | Human D    | ko05415 | Diabetic c  | 0.53225 | 0.77365 | 0 | 0 | 4  | 220  |
| Hepatitis C                                                | 3  | 0.53545 | 2.069 | 0.019 | Human D    | ko05160 | Hepatitis   | 0.53545 | 0.77365 | 0 | 0 | 3  | 162  |
| Lipid and atherosclerosis                                  | 4  | 0.53585 | 2.759 | 0.018 | Human D    | ko05417 | Lipid and   | 0.53585 | 0.77365 | 0 | 0 | 4  | 221  |
| Tryptophan metabolism                                      | 1  | 0.54538 | 0.69  | 0.022 | Metabolis  | ko00380 | Tryptoph    | 0.54538 | 0.78038 | 0 | 0 | 1  | 45   |
| Human papillomavirus infection                             | 6  | 0.54924 | 4.138 | 0.017 | Human D    | ko05165 | Human pa    | 0.54924 | 0.78038 | 0 | 0 | 6  | 343  |
| Toll-like receptor signaling pathway                       | 2  | 0.55143 | 1.379 | 0.019 | Organism   | ko04620 | Toll-like r | 0.55143 | 0.78038 | 0 | 0 | 2  | 106  |
| ABC transporters                                           | 1  | 0.5533  | 0.69  | 0.022 | Environm   | ko02010 | ABC trans   | 0.5533  | 0.78038 | 0 | 0 | 1  | 46   |
| Apoptosis - fly                                            | 1  | 0.56873 | 0.69  | 0.021 | Cellular P | ko04214 | Apoptosis   | 0.56873 | 0.7899  | 0 | 0 | 1  | 48   |
| Protein processing in endoplasmic reticulum                | 3  | 0.5723  | 2.069 | 0.018 | Genetic li | ko04141 | Protein pr  | 0.5723  | 0.7899  | 0 | 0 | 3  | 171  |
| Alzheimer disease                                          | 7  | 0.57331 | 4.828 | 0.017 | Human D    | ko05010 | Alzheim     | 0.57331 | 0.7899  | 0 | 0 | 7  | 411  |
| Human T-cell leukemia virus 1 infection                    | 4  | 0.57456 | 2.759 | 0.017 | Human D    | ko05166 | Human T-    | 0.57456 | 0.7899  | 0 | 0 | 4  | 232  |
| Pyruvate metabolism                                        | 1  | 0.57624 | 0.69  | 0.02  | Metabolis  | ko00620 | Pyruvate    | 0.57624 | 0.7899  | 0 | 0 | 1  | 49   |
| Carbohydrate digestion and absorption                      | 1  | 0.58362 | 0.69  | 0.02  | Organism   | ko04973 | Carbohyd    | 0.58362 | 0.79555 | 0 | 0 | 1  | 50   |
| Chemical carcinogenesis - reactive oxygen species          | 4  | 0.58819 | 2.759 | 0.017 | Human D    | ko05208 | Chemical    | 0.58819 | 0.79654 | 0 | 0 | 4  | 236  |
| Vibrio cholerae infection                                  | 1  | 0.59088 | 0.69  | 0.02  | Human D    | ko05110 | Vibrio cho  | 0.59088 | 0.79654 | 0 | 0 | 1  | 51   |
| Tight junction                                             | 3  | 0.60352 | 2.069 | 0.017 | Cellular P | ko04530 | Tight junc  | 0.60352 | 0.80912 | 0 | 0 | 3  | 179  |
| Ovarian steroidogenesis                                    | 1  | 0.61866 | 0.69  | 0.018 | Organism   | ko04913 | Ovarian s   | 0.61866 | 0.8204  | 0 | 0 | 1  | 55   |
| Malaria                                                    | 1  | 0.61866 | 0.69  | 0.018 | Human D    | ko05144 | Malaria     | 0.61866 | 0.8204  | 0 | 0 | 1  | 55   |
| Hedgehog signaling pathway                                 | 1  | 0.63184 | 0.69  | 0.018 | Environm   | ko04340 | Hedgehog    | 0.63184 | 0.83335 | 0 | 0 | 1  | 57   |
| Fatty acid metabolism                                      | 1  | 0.64457 | 0.69  | 0.017 | Metabolis  | ko01212 | Fatty acid  | 0.64457 | 0.84557 | 0 | 0 | 1  | 59   |
| Endocytosis                                                | 4  | 0.67326 | 2.759 | 0.015 | Cellular P | ko04144 | Endocyto    | 0.67326 | 0.8708  | 0 | 0 | 4  | 263  |
| Hippo signaling pathway - fly                              | 1  | 0.67451 | 0.69  | 0.016 | Environm   | ko04391 | Hippo sig   | 0.67451 | 0.8708  | 0 | 0 | 1  | 64   |
| Cytosolic DNA-sensing pathway                              | 1  | 0.67451 | 0.69  | 0.016 | Organism   | ko04623 | Cytosolic   | 0.67451 | 0.8708  | 0 | 0 | 1  | 64   |
| Cortisol synthesis and secretion                           | 1  | 0.68578 | 0.69  | 0.015 | Organism   | ko04927 | Cortisol s  | 0.68578 | 0.87448 | 0 | 0 | 1  | 66   |
| Lysine degradation                                         | 1  | 0.69126 | 0.69  | 0.015 | Metabolis  | ko00310 | Lysine de   | 0.69126 | 0.87448 | 0 | 0 | 1  | 67   |
| FoxO signaling pathway                                     | 2  | 0.69457 | 1.379 | 0.014 | Environm   | ko04068 | FoxO sig    | 0.69457 | 0.87448 | 0 | 0 | 2  | 138  |
| Longevity regulating pathway - multiple species            | 1  | 0.69665 | 0.69  | 0.015 | Organism   | ko04213 | Longevity   | 0.69665 | 0.87448 | 0 | 0 | 1  | 68   |
| Neutrophil extracellular trap formation                    | 4  | 0.70154 | 2.759 | 0.015 | Organism   | ko04613 | Neutroph    | 0.70154 | 0.87448 | 0 | 0 | 4  | 273  |
| Chemical carcinogenesis - DNA adducts                      | 1  | 0.70195 | 0.69  | 0.014 | Human D    | ko05204 | Chemical    | 0.70195 | 0.87448 | 0 | 0 | 1  | 69   |
| Glycolysis / Gluconeogenesis                               | 1  | 0.70715 | 0.69  | 0.014 | Metabolis  | ko00010 | Glycolysis  | 0.70715 | 0.87448 | 0 | 0 | 1  | 70   |
| Acute myeloid leukemia                                     | 1  | 0.70715 | 0.69  | 0.014 | Human D    | ko05221 | Acute my    | 0.70715 | 0.87448 | 0 | 0 | 1  | 70   |
| Epithelial cell signaling in Helicobacter pylori infection | 1  | 0.71227 | 0.69  | 0.014 | Human D    | ko05120 | Epithelial  | 0.71227 | 0.87448 | 0 | 0 | 1  | 71   |
| Fluid shear stress and atherosclerosis                     | 2  | 0.71323 | 1.379 | 0.014 | Human D    | ko05418 | Fluid she   | 0.71323 | 0.87448 | 0 | 0 | 2  | 143  |
| Oocyte meiosis                                             | 2  | 0.71681 | 1.379 | 0.014 | Cellular P | ko04114 | Oocyte m    | 0.71681 | 0.87451 | 0 | 0 | 2  | 144  |
| p53 signaling pathway                                      | 1  | 0.72223 | 0.69  | 0.014 | Cellular P | ko04115 | p53 signa   | 0.72223 | 0.87604 | 0 | 0 | 1  | 73   |
| Adherens junction                                          | 1  | 0.72709 | 0.69  | 0.014 | Cellular P | ko04520 | Adherens    | 0.72709 | 0.87604 | 0 | 0 | 1  | 74   |
| Adrenergic signaling in cardiomyocytes                     | 2  | 0.73088 | 1.379 | 0.014 | Organism   | ko04261 | Adrenerg    | 0.73088 | 0.87604 | 0 | 0 | 2  | 148  |
| Antigen processing and presentation                        | 1  | 0.74115 | 0.69  | 0.013 | Organism   | ko04612 | Antigen p   | 0.74115 | 0.87604 | 0 | 0 | 1  | 77   |
| Prolactin signaling pathway                                | 1  | 0.74115 | 0.69  | 0.013 | Organism   | ko04917 | Prolactin   | 0.74115 | 0.87604 | 0 | 0 | 1  | 77   |
| Synaptic vesicle cycle                                     | 1  | 0.74567 | 0.69  | 0.013 | Organism   | ko04721 | Synaptic    | 0.74567 | 0.87604 | 0 | 0 | 1  | 78   |
| Chronic myeloid leukemia                                   | 1  | 0.74567 | 0.69  | 0.013 | Human D    | ko05220 | Chronic m   | 0.74567 | 0.87604 | 0 | 0 | 1  | 78   |
| Breast cancer                                              | 2  | 0.74763 | 1.379 | 0.013 | Human D    | ko05224 | Breast ca   | 0.74763 | 0.87604 | 0 | 0 | 2  | 153  |
| Prion disease                                              | 4  | 0.75038 | 2.759 | 0.014 | Human D    | ko05020 | Prion dise  | 0.75038 | 0.87604 | 0 | 0 | 4  | 292  |
| Phagosome                                                  | 3  | 0.76608 | 2.069 | 0.013 | Cellular P | ko04145 | Phag        |         |         |   |   |    |      |

|                                         |   |         |       |       |            |         |            |         |         |   |   |   |     |
|-----------------------------------------|---|---------|-------|-------|------------|---------|------------|---------|---------|---|---|---|-----|
| Carbon metabolism                       | 1 | 0.87897 | 0.69  | 0.008 | Metabolis  | ko01200 | Carbon m   | 0.87897 | 0.93655 | 0 | 0 | 1 | 120 |
| Primary immunodeficiency                | 1 | 0.88924 | 0.69  | 0.008 | Human D    | ko05340 | Primary ir | 0.88924 | 0.94337 | 0 | 0 | 1 | 125 |
| Systemic lupus erythematosus            | 2 | 0.89573 | 1.379 | 0.009 | Human D    | ko05322 | Systemic   | 0.89573 | 0.94524 | 0 | 0 | 2 | 218 |
| Cell cycle                              | 1 | 0.90043 | 0.69  | 0.008 | Cellular P | ko04110 | Cell cycle | 0.90043 | 0.94524 | 0 | 0 | 1 | 131 |
| Viral myocarditis                       | 1 | 0.9039  | 0.69  | 0.008 | Human D    | ko05416 | Viral myo  | 0.9039  | 0.94524 | 0 | 0 | 1 | 133 |
| Amyotrophic lateral sclerosis           | 4 | 0.9065  | 2.759 | 0.01  | Human D    | ko05014 | Amyotrop   | 0.9065  | 0.94524 | 0 | 0 | 4 | 385 |
| Fc epsilon RI signaling pathway         | 1 | 0.91514 | 0.69  | 0.007 | Organism   | ko04664 | Fc epsilon | 0.91514 | 0.94737 | 0 | 0 | 1 | 140 |
| Lysosome                                | 1 | 0.9181  | 0.69  | 0.007 | Cellular P | ko04142 | Lysosome   | 0.9181  | 0.94737 | 0 | 0 | 1 | 142 |
| Alcoholic liver disease                 | 1 | 0.92372 | 0.69  | 0.007 | Human D    | ko04936 | Alcoholic  | 0.92372 | 0.94737 | 0 | 0 | 1 | 146 |
| Huntington disease                      | 3 | 0.92408 | 2.069 | 0.009 | Human D    | ko05016 | Huntingto  | 0.92408 | 0.94737 | 0 | 0 | 3 | 324 |
| Ubiquitin mediated proteolysis          | 1 | 0.93021 | 0.69  | 0.007 | Genetic H  | ko04120 | Ubiquitin  | 0.93021 | 0.94967 | 0 | 0 | 1 | 151 |
| Staphylococcus aureus infection         | 1 | 0.95368 | 0.69  | 0.006 | Human D    | ko05150 | Staphyloc  | 0.95368 | 0.9664  | 0 | 0 | 1 | 174 |
| Transcriptional misregulation in cancer | 2 | 0.95657 | 1.379 | 0.007 | Human D    | ko05202 | Transcrip  | 0.95657 | 0.9664  | 0 | 0 | 2 | 278 |
| Pathogenic Escherichia coli infection   | 2 | 0.95848 | 1.379 | 0.007 | Human D    | ko05130 | Pathogen   | 0.95848 | 0.9664  | 0 | 0 | 2 | 281 |
| Yersinia infection                      | 1 | 0.97854 | 0.69  | 0.005 | Human D    | ko05135 | Yersinia i | 0.97854 | 0.98257 | 0 | 0 | 1 | 217 |
| Thermogenesis                           | 1 | 0.98726 | 0.69  | 0.004 | Organism   | ko04714 | Thermoge   | 0.98726 | 0.98726 | 0 | 0 | 1 | 246 |

**Supplementary Table 7: Overlap genes in DEGREE, EPC, MCC and MNC**

| <b>DEGREE</b> | <b>EPC</b> | <b>MCC</b> | <b>MNC</b> | <b>Overlap gene</b> |
|---------------|------------|------------|------------|---------------------|
| JUN           | JUN        | TIMP1      | JUN        | JUN                 |
| STAT1         | STAT1      | JUN        | SOX9       | STAT1               |
| SOX9          | TIMP1      | TGFB2      | STAT1      | SOX9                |
| COL1A2        | SOX9       | MMP1       | COL1A2     | COL1A2              |
| APOE          | COL1A2     | COL1A2     | APOE       | APOE                |
| TIMP1         | TIMP3      | TIMP3      | TIMP1      | TIMP1               |
| TIMP3         | APOE       | CSF1       | TIMP3      | TIMP3               |
| AR            | CSF1       | TGFA       | CSF1       | PRKCA               |
| PRKCA         | TGFB2      | STAT1      | PRKCA      | CSF1                |
| CSF1          | MMP1       | SOX9       | TGFB2      | ACTA2               |
| ACTA2         | EGR1       | APOE       | MMP1       | TGFB2               |
| TGFB2         | ACTA2      | ACTA2      | GRIN2B     | TAGLN               |
| TAGLN         | PRKCA      | GRIN2B     | TAGLN      | MMP1                |
| MMP1          | TGFA       | TAGLN      | DDX58      | FBLN2               |
| FLNC          | FBLN2      | MMP10      | ACTA2      | TGFA                |
| GRIN2B        | AR         | FBLN2      | FBLN2      | EGR1                |
| ERBB4         | KITLG      | COL14A1    | COL12A1    |                     |
| FBLN2         | TAGLN      | COL12A1    | EGR1       |                     |
| DDX58         | ERBB4      | PRKCA      | TGFA       |                     |
| KITLG         | EPAS1      | EGR1       | KITLG      |                     |
| TGFA          |            |            |            |                     |
| EGR1          |            |            |            |                     |
| MAPT          |            |            |            |                     |

\*multiple nodes may be included within the same ranking

**Supplementary Table 8: Demographic characteristics of platinum resistant cases in TCGA OC cohort**

| <b>Characteristics</b> |                | <b>Number</b> | <b>Proportion (%)</b> |
|------------------------|----------------|---------------|-----------------------|
| All cases              | /              | 90            | 100                   |
| Age                    | < 60 years old | 43            | 47.78                 |
|                        | ≥ 60 years old | 47            | 52.22                 |
| Stage                  | IIC            | 1             | 1.11                  |
|                        | IIIB           | 1             | 1.11                  |
|                        | IIIC           | 75            | 83.33                 |
|                        | IV             | 13            | 14.44                 |
| Grade                  | G2             | 8             | 8.89                  |
|                        | G3             | 81            | 90.00                 |
|                        | NA             | 1             | 1.11                  |
| Race                   | White          | 82            | 91.11                 |
|                        | non-White      | 8             | 8.89                  |

Supplementary Table 9

| ID           | Age  | Race      | TUMOR | GRADE |
|--------------|------|-----------|-------|-------|
| TCGA.04.1338 | < 60 | White     | IIIC  | G3    |
| TCGA.04.1349 | < 60 | White     | IV    | G3    |
| TCGA.04.1362 | ≥ 60 | White     | IIC   | G3    |
| TCGA.04.1364 | < 60 | White     | IIIC  | G3    |
| TCGA.04.1525 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.04.1638 | ≥ 60 | Non-white | IV    | G3    |
| TCGA.09.0366 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.09.0369 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.10.0926 | < 60 | White     | IIIC  | G3    |
| TCGA.10.0931 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.10.0934 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.10.0937 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.10.0938 | < 60 | White     | IIIC  | G3    |
| TCGA.13.0717 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.13.0720 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.13.0723 | < 60 | White     | IIIC  | G3    |
| TCGA.13.0724 | < 60 | White     | IV    | G3    |
| TCGA.13.0725 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.13.0727 | < 60 | White     | IIIC  | G3    |
| TCGA.13.0755 | < 60 | White     | IV    | G3    |
| TCGA.13.0757 | < 60 | White     | IIIC  | G3    |
| TCGA.13.0764 | < 60 | White     | IV    | G3    |
| TCGA.13.0791 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.13.0795 | < 60 | White     | IIIC  | G3    |
| TCGA.13.0803 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.13.0804 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.13.0805 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.13.0893 | ≥ 60 | Non-white | IIIC  | G3    |
| TCGA.13.0904 | < 60 | White     | IIIC  | G3    |
| TCGA.13.0911 | ≥ 60 | White     | IV    | G3    |
| TCGA.13.0920 | < 60 | White     | IIIC  | G3    |
| TCGA.13.1477 | ≥ 60 | White     | IV    | G2    |
| TCGA.13.1483 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.13.1485 | ≥ 60 | White     | IV    | G2    |
| TCGA.13.1500 | < 60 | White     | IIIC  | G3    |
| TCGA.23.1027 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.23.1028 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.23.1117 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.23.2079 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.24.0970 | < 60 | White     | IIIC  | G3    |
| TCGA.24.0980 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.24.0982 | < 60 | White     | IIIC  | G3    |
| TCGA.24.1431 | < 60 | White     | IIIC  | G3    |
| TCGA.24.1434 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.24.1464 | < 60 | White     | IIIC  | G3    |
| TCGA.24.1548 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.24.1552 | < 60 | White     | IIIC  | G3    |
| TCGA.24.1557 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.24.1558 | < 60 | White     | IIIC  | G3    |
| TCGA.24.1560 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.24.1562 | < 60 | White     | IIIC  | G3    |
| TCGA.24.1564 | < 60 | White     | IIIC  | G3    |
| TCGA.24.1565 | < 60 | White     | IIIC  | G3    |
| TCGA.24.1567 | ≥ 60 | White     | IIIB  | G3    |
| TCGA.24.1923 | ≥ 60 | White     | IIIC  | G3    |
| TCGA.24.1924 | < 60 | White     | IIIC  | G3    |

|              |      |           |      |    |
|--------------|------|-----------|------|----|
| TCGA.24.1928 | < 60 | White     | IIIC | G3 |
| TCGA.24.2033 | < 60 | White     | IIIC | G3 |
| TCGA.25.1315 | ≥ 60 | White     | IIIC | G3 |
| TCGA.25.1316 | ≥ 60 | White     | IIIC | G3 |
| TCGA.25.1318 | ≥ 60 | White     | IIIC | G3 |
| TCGA.25.1328 | ≥ 60 | White     | IIIC | G3 |
| TCGA.25.1626 | < 60 | White     | IIIC | G3 |
| TCGA.25.1628 | < 60 | White     | IIIC | G3 |
| TCGA.25.1634 | < 60 | White     | IIIC | G3 |
| TCGA.25.2393 | < 60 | White     | IIIC | G3 |
| TCGA.25.2399 | < 60 | White     | IIIC | G3 |
| TCGA.25.2409 | < 60 | White     | IV   | G3 |
| TCGA.29.1696 | ≥ 60 | White     | IIIC | G2 |
| TCGA.29.1698 | ≥ 60 | Non-white | IIIC | G3 |
| TCGA.29.1701 | ≥ 60 | White     | IIIC | G3 |
| TCGA.29.1702 | < 60 | White     | IIIC | G3 |
| TCGA.29.1703 | ≥ 60 | Non-white | IIIC | G2 |
| TCGA.29.1705 | ≥ 60 | White     | IIIC | G2 |
| TCGA.29.1775 | ≥ 60 | White     | IIIC | G2 |
| TCGA.30.1714 | < 60 | White     | IV   | G3 |
| TCGA.30.1856 | ≥ 60 | White     | IIIC | G3 |
| TCGA.30.1866 | < 60 | White     | IV   | G2 |
| TCGA.30.1891 | < 60 | White     | IIIC | G2 |
| TCGA.30.1892 | ≥ 60 | White     | IIIC | G3 |
| TCGA.31.1953 | ≥ 60 | Non-white | IIIC | G3 |
| TCGA.36.1578 | < 60 | Non-white | IV   | G3 |
| TCGA.36.1580 | < 60 | Non-white | IIIC | G3 |
| TCGA.57.1586 | < 60 | White     | IIIC | G3 |
| TCGA.61.1733 | < 60 | White     | IIIC | G3 |
| TCGA.61.1738 | ≥ 60 | Non-white | IIIC | G3 |
| TCGA.61.1901 | < 60 | White     | IV   | G3 |
| TCGA.61.1906 | ≥ 60 | White     | IIIC | G3 |
| TCGA.61.2000 | < 60 | White     | IIIC | G3 |
| TCGA.61.2110 | ≥ 60 | White     | IIIC | NA |

Supplementary Table 10: Related Compounds

| Compound ID | Pref Name         | CAS            | Pubchem ID    | ChEMBL ID    | Formula | Smiles                                                                                 | Target ID | Protein Name             | Symbol | Uniprot |
|-------------|-------------------|----------------|---------------|--------------|---------|----------------------------------------------------------------------------------------|-----------|--------------------------|--------|---------|
| C0004       | Delphinidin       | NA             | CID:128853    | CHEMBL276780 | C15H10O | Oc1cc(O)c2c(c1)[o+](c(c2)O)c1cc(O)c(c1)O                                               | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0038       | Eckol             | CAS:88798-74-7 | CID:145937    | CHEMBL471187 | C18H12O | C1=C(C=C(C=C1O))OC2=C(C=C(C3=C2OC4=C(C=C3)OC2=CC(=O)C=C4)OC2=CC(=O)C=C4)OC2=CC(=O)C=C4 | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0041       | Emodin            | CAS:518-82-1   | CID:3220      | CHEMBL289277 | C15H10O | CC1=CC2=C(C(=C1)O)C(=O)C3=C(C2=O)C=C(C=C3)OC2=CC(=O)C=C4                               | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0053       | Esculetin         | CAS:305-01-1   | CID:5281416   | CHEMBL244743 | C9H6O4  | C1=CC(=O)OC2=C(C(=C(C21)O)O                                                            | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0164       | Kaempferol        | CAS:520-18-3   | CID:5280863   | CHEMBL150    | C15H10O | C1=CC(=CC=C(C2=C(C(=O)C3=C(C=C(C3O2)O                                                  | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0199       | Luteolin          | CAS:491-70-3   | CID:5280445   | CHEMBL151    | C15H10O | C1=CC(=C(C=C(C1C2=CC(=O)C3=C(C=C(C3O2)O                                                | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0305       | Phorbol Myristate | CAS:16561-29-8 | CID:27924     | CHEMBL279115 | C36H56O | CCCCCCCCCCCCC(C(=O)OC)C@H1[C@@H](O)C                                                   | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0352       | Quercetin         | CAS:117-39-5   | CID:5280343   | CHEMBL50     | C15H10O | C1=CC(=C(C=C(C1C2=C(C(=O)C3=C(C=C(C3O2)O                                               | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0476       | Ursolic Acid      | CAS:77-52-1    | CID:64945     | CHEMBL169    | C30H48O | CC1CCC2(CCC3(C(=CC4C3)CC5C4(CCC(C5(C                                                   | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0485       | Wogonin           | CAS:632-85-9   | CID:5281703   | CHEMBL16171  | C16H12O | COC1=C(C=C(C2=C1OC(=CC2=O)C3=CC=CC=C3                                                  | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0639       | (+/-)Nicotine     | NA             | CID:942       | CHEMBL440464 | C10H14N | CN1CCCC1C2=CN=CC=C2                                                                    | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0739       | (1E,6E)-1,7-Bis(4 | NA             | CID:969516    | CHEMBL140    | C21H20O | COC1=C(C=C(C(=C1)C=CC(=O)CC(=O)C=CC2=CC(=                                              | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0805       | Bornyl Acetate    | CAS:76-49-3    | CID:6950274   | NA           | C12H20O | CC(=O)OC(C@H)1C[C@@H]2C([C@@H]1(C)CC2)(C)C                                             | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0914       | Apigenin          | CAS:520-36-5   | CID:5280443   | CHEMBL28     | C15H10O | C1=CC(=CC=C(C1C2=CC(=O)C3=C(C=C(C3O2)O)C                                               | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0930       | Astragaloside Iv  | CAS:84687-43-4 | CID:124761776 | NA           | C41H68O | OC[C@H]1O[C@@H](O[C@@H]2[C@@H]3[C@@H]4[C@@H]3                                          | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C0989       | hypericin         | CAS:548-04-9   | CID:5281051   | NA           | C30H16O | CC1=CC(=C2C3=C4C5=C(C(=CC(=C5C2=O)O)O)C6                                               | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C1110       | lutein            | CAS:127-40-2   | CID:6433159   | NA           | C40H56O | CC1=C(C(C(C(C1)O)C)C=C(C=C(C=C(C=C(C=C(C=C                                             | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C1171       | Berberine         | CAS:2086-83-1  | CID:2353      | CHEMBL295124 | C20H18N | COc1c(O)c(Cc2c1c[n+](CCc3c(c1c2)cc1c(c3)OC                                             | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C1177       | Beta Carotene     | NA             | CID:5280489   | CHEMBL1293   | C40H56  | CC1=C(C(C(C(C1)C)C=C(C=C(C=C(C=C(C=C(C=C(C                                             | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C1214       | Capsaicin         | CAS:404-86-4   | CID:1548943   | CHEMBL294199 | C18H27N | CC(C(C=CCCCC(=O)NCC1=CC(=C(C=C1)O)OC                                                   | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C1222       | Celastrol         | NA             | CID:122724    | CHEMBL301982 | C29H38O | CC1=C(C(=O)C=C2C1=CC=C3C2CCC4(C3)CC5(C                                                 | T80QJF    | Interstitial collagenase | MMP1   | P03956  |
| C1250       | Colchicine        | CAS:64-86-8    | CID:6167      | CHEMBL107    | C22H25N | CC(=O)NC1CCC2=CC=C(C1C=C2C3=CC=C(C(=O)C                                                | T80QJF    | Interstitial collagenase | MMP1   | P03956  |

**Table 11: IC50 of A2780DDP and Ovc4r to cisplatin and Quercetin**

| Cell     | Compound  | IC50 (µM) | Resistance Indices |
|----------|-----------|-----------|--------------------|
| A2780    | cisplatin | 1.69      | 3.46               |
| A2780DDP | cisplatin | 5.85      |                    |
| Ovc4r    | cisplatin | 2.29      | 3.03               |
| Ovc4rDDP | cisplatin | 6.94      |                    |
| A2780    | Quercetin | 16.82     | /                  |
| A2780DDP | Quercetin | 44.09     |                    |
| Ovc4r    | Quercetin | 20.24     | /                  |
| Ovc4rDDP | Quercetin | 45.45     |                    |