**Tables**

**Table 1** The statistical metrics for key differentially expressed genes (DEGs)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Gene Symbol** | **logFC** | **pValue** | **adj.P.Val** | **tvalue** | **Regulation** | **Gene Name** |
| SOCS3 | 1.029557 | 1.21E-08 | 1.21E-08 | 7.082396 | Up | suppressor of cytokine signaling 3 |
| ETS2 | 1.162876 | 5.82E-06 | 5.82E-06 | 5.197414 | Up | ETS proto-oncogene 2, transcription factor |
| ERICD | 1.138842 | 8.01E-06 | 8.01E-06 | 5.099039 | Up | E2F1-regulated inhibitor of cell death |
| SPRY2 | 1.289333 | 4.96E-05 | 4.96E-05 | 4.529091 | Up | sprouty RTK signaling antagonist 2 |
| PLEKHG5 | 1.103153 | 4.14E-05 | 4.14E-05 | 4.58625 | Up | pleckstrin homology and RhoGEF domain containing G5 |
| KLF6 | 1.219624 | 8.62E-05 | 8.62E-05 | 4.353553 | Up | Kruppel like factor 6 |
| RPL39P5 | 1.198859 | 8.25E-05 | 8.25E-05 | 4.367571 | Up | ribosomal protein L39 pseudogene 5 |
| IL1A | 2.500916 | 0.00011 | 0.00011 | 4.274553 | Up | interleukin 1 alpha |
| IL6 | 3.463376 | 0.00013 | 0.00013 | 4.220788 | Up | interleukin 6 |
| EPC1 | 1.17429 | 0.000193 | 0.000193 | 4.092739 | Up | enhancer of polycomb homolog 1 |
| CSF2 | 2.591821 | 6.26E-05 | 6.26E-05 | 4.455695 | Up | colony stimulating factor 2 |
| ADRB2 | 1.050404 | 0.000226 | 0.000226 | 4.040984 | Up | adrenoceptor beta 2 |
| TIPARP | 1.646696 | 0.000261 | 0.000261 | 3.994215 | Up | TCDD inducible poly(ADP-ribose) polymerase |
| COL4A1 | 2.492335 | 7.79E-05 | 7.79E-05 | 4.385885 | Up | collagen type IV alpha 1 chain |
| DUSP1 | 1.950421 | 0.000352 | 0.000352 | 3.895466 | Up | dual specificity phosphatase 1 |
| G0S2 | 1.056752 | 0.000353 | 0.000353 | 3.8946 | Up | G0/G1 switch 2 |
| CD274 | 2.559212 | 0.000383 | 0.000383 | 3.86675 | Up | CD274 molecule |
| GADD45B | 1.037288 | 0.000586 | 0.000586 | 3.724348 | Up | growth arrest and DNA damage inducible beta |
| MB21D2 | 1.524927 | 0.0006 | 0.0006 | 3.716393 | Up | Mab-21 domain containing 2 |
| CD69 | 2.028046 | 0.000315 | 0.000315 | 3.931994 | Up | CD69 molecule |
| CSRNP1 | 1.686588 | 0.000721 | 0.000721 | 3.653985 | Up | cysteine and serine rich nuclear protein 1 |
| AMOTL2 | 1.044122 | 0.000665 | 0.000665 | 3.68167 | Up | angiomotin like 2 |
| SPTBN5 | 1.059205 | 0.000531 | 0.000531 | 3.757737 | Up | spectrin beta, non-erythrocytic 5 |
| FOSB | 1.736709 | 0.000792 | 0.000792 | 3.622197 | Up | FosB proto-oncogene, AP-1 transcription factor subunit |
| OGFR | 1.070808 | 0.000713 | 0.000713 | 3.657808 | Up | opioid growth factor receptor |
| IL11 | 1.198667 | 0.000741 | 0.000741 | 3.644948 | Up | interleukin 11 |
| CXCL3 | 1.515004 | 0.000888 | 0.000888 | 3.583149 | Up | C-X-C motif chemokine ligand 3 |
| TRIM21 | 1.165551 | 0.000906 | 0.000906 | 3.576125 | Up | tripartite motif containing 21 |
| DUSP10 | 0.977857 | 0.000964 | 0.000964 | 3.554731 | Up | dual specificity phosphatase 10 |
| GATA3 | 1.361589 | 0.001006 | 0.001006 | 3.539994 | Up | GATA binding protein 3 |
| MIR6881 | 1.053893 | 0.00036 | 0.00036 | 3.888052 | Up | microRNA 6881 |
| ZNF627 | 1.049596 | 0.001161 | 0.001161 | 3.490391 | Up | zinc finger protein 627 |
| KIF26B | 1.165483 | 0.000853 | 0.000853 | 3.596631 | Up | kinesin family member 26B |
| JUN | 1.811995 | 0.000955 | 0.000955 | 3.557814 | Up | Jun proto-oncogene, AP-1 transcription factor subunit |
| HDX | 1.111154 | 0.001164 | 0.001164 | 3.489549 | Up | highly divergent homeobox |
| IL22RA1 | 1.710662 | 0.000832 | 0.000832 | 3.605157 | Up | interleukin 22 receptor subunit alpha 1 |
| SLC25A28 | 1.117785 | 0.001208 | 0.001208 | 3.476763 | Up | solute carrier family 25 member 28 |
| AHRR | 1.976907 | 0.000703 | 0.000703 | 3.662819 | Up | aryl-hydrocarbon receptor repressor |
| CYP1A1 | 2.582763 | 0.001264 | 0.001264 | 3.460967 | Up | cytochrome P450 family 1 subfamily A member 1 |
| TXNIP | 1.117427 | 0.001073 | 0.001073 | 3.51763 | Up | thioredoxin interacting protein |
| COL8A1 | 0.990515 | 0.000985 | 0.000985 | 3.54749 | Up | collagen type VIII alpha 1 chain |
| EGR3 | 1.828393 | 0.000966 | 0.000966 | 3.554019 | Up | early growth response 3 |
| TCIM | 1.199207 | 0.001273 | 0.001273 | 3.458447 | Up | transcriptional and immune response regulator |
| TICAM1 | 0.991094 | 0.001568 | 0.001568 | 3.385469 | Up | toll like receptor adaptor molecule 1 |
| CXCL9 | 4.005381 | 0.000334 | 0.000334 | 3.91269 | Up | C-X-C motif chemokine ligand 9 |
| TNFAIP3 | 3.039604 | 0.001664 | 0.001664 | 3.364687 | Up | TNF alpha induced protein 3 |
| STX11 | 2.198163 | 0.000686 | 0.000686 | 3.670822 | Up | syntaxin 11 |
| IL12A | 1.796495 | 0.001351 | 0.001351 | 3.437811 | Up | interleukin 12A |
| PLAUR | 1.307972 | 0.001622 | 0.001622 | 3.373573 | Up | plasminogen activator, urokinase receptor |
| EGR2 | 2.487318 | 0.001533 | 0.001533 | 3.393528 | Up | early growth response 2 |
| THEMIS2 | 1.896802 | 0.001812 | 0.001812 | 3.33449 | Up | thymocyte selection associated family member 2 |
| ATF3 | 3.358037 | 0.001895 | 0.001895 | 3.318661 | Up | activating transcription factor 3 |
| ZFP36 | 1.66189 | 0.001798 | 0.001798 | 3.337269 | Up | ZFP36 ring finger protein |
| NFKBIZ | 1.40522 | 0.001728 | 0.001728 | 3.351401 | Up | NFKB inhibitor zeta |
| CHAC1 | 1.209221 | 0.00171 | 0.00171 | 3.354989 | Up | ChaC glutathione specific gamma-glutamylcyclotransferase 1 |
| PGAM1P7 | 0.975288 | 0.001809 | 0.001809 | 3.335094 | Up | phosphoglyceratemutase 1 pseudogene 7 |
| NUAK2 | 2.320463 | 0.002327 | 0.002327 | 3.245474 | Up | NUAK family kinase 2 |
| CXCL2 | 2.091483 | 0.00237 | 0.00237 | 3.238994 | Up | C-X-C motif chemokine ligand 2 |
| SERPINE1 | 1.345573 | 0.001394 | 0.001394 | 3.426875 | Up | serpin family E member 1 |
| USP8P1 | 1.178748 | 0.001238 | 0.001238 | 3.468297 | Up | ubiquitin specific peptidase 8 pseudogene 1 |
| CXCL8 | 0.970987 | 0.001888 | 0.001888 | 3.319985 | Up | C-X-C motif chemokine ligand 8 |
| CPEB2 | 1.287266 | 0.002709 | 0.002709 | 3.190899 | Up | cytoplasmic polyadenylation element binding protein 2 |
| MIR4658 | 1.214578 | 0.000988 | 0.000988 | 3.546126 | Up | microRNA 4658 |
| PCK1 | 2.332999 | 0.000686 | 0.000686 | 3.671182 | Up | phosphoenolpyruvatecarboxykinase 1 |
| PTGS2 | 1.166879 | 0.002825 | 0.002825 | 3.175745 | Up | prostaglandin-endoperoxide synthase 2 |
| PYY2 | 1.951724 | 0.0009 | 0.0009 | 3.578458 | Up | peptide YY 2 (pseudogene) |
| MIR155HG | 2.607755 | 0.003291 | 0.003291 | 3.120187 | Up | MIR155 host gene |
| FST | 1.002466 | 0.003484 | 0.003484 | 3.099328 | Up | follistatin |
| NT5C3AP1 | 1.382344 | 0.003652 | 0.003652 | 3.082118 | Up | 5'-nucleotidase, cytosolic IIIA pseudogene 1 |
| S1PR3 | 1.016866 | 0.003129 | 0.003129 | 3.138595 | Up | sphingosine-1-phosphate receptor 3 |
| SH2D1B | 1.950662 | 0.001057 | 0.001057 | 3.522935 | Up | SH2 domain containing 1B |
| IL15RA | 1.031885 | 0.003663 | 0.003663 | 3.081023 | Up | interleukin 15 receptor subunit alpha |
| MIR6858 | 1.530612 | 0.000995 | 0.000995 | 3.543749 | Up | microRNA 6858 |
| PELI1 | 1.01622 | 0.003845 | 0.003845 | 3.063173 | Up | pellino E3 ubiquitin protein ligase 1 |
| RASGRP3 | 2.152879 | 0.004317 | 0.004317 | 3.020408 | Up | RAS guanyl releasing protein 3 |
| RND1 | 1.676447 | 0.00431 | 0.00431 | 3.021007 | Up | Rho family GTPase 1 |
| RAET1L | 2.341954 | 0.003051 | 0.003051 | 3.147777 | Up | retinoic acid early transcript 1L |
| PMAIP1 | 1.579452 | 0.00395 | 0.00395 | 3.053234 | Up | phorbol-12-myristate-13-acetate-induced protein 1 |
| LINC00702 | 1.692421 | 0.001703 | 0.001703 | 3.356428 | Up | long intergenic non-protein coding RNA 702 |
| ARRDC3 | 2.112019 | 0.003983 | 0.003983 | 3.050118 | Up | arrestin domain containing 3 |
| NFKBIA | 2.468374 | 0.003893 | 0.003893 | 3.058548 | Up | NFKB inhibitor alpha |
| FLRT3 | 1.128602 | 0.004664 | 0.004664 | 2.991615 | Up | fibronectinleucine rich transmembrane protein 3 |
| PTX3 | 2.370746 | 0.004751 | 0.004751 | 2.984718 | Up | pentraxin 3 |
| RASGRP1 | 1.171393 | 0.004796 | 0.004796 | 2.98127 | Up | RAS guanyl releasing protein 1 |
| SNPH | 1.448459 | 0.004712 | 0.004712 | 2.987847 | Up | syntaphilin |
| FAM110B | 1.109894 | 0.004934 | 0.004934 | 2.970648 | Up | family with sequence similarity 110 member B |
| IRF1 | 2.300085 | 0.004348 | 0.004348 | 3.017739 | Up | interferon regulatory factor 1 |
| SSTR2 | 1.261819 | 0.004685 | 0.004685 | 2.989962 | Up | somatostatin receptor 2 |
| INHBA | 1.646008 | 0.004556 | 0.004556 | 3.000373 | Up | inhibin subunit beta A |
| MEG9 | 2.535238 | 0.00317 | 0.00317 | 3.133856 | Up | maternally expressed 9 |
| MT2A | 1.780429 | 0.005458 | 0.005458 | 2.932775 | Up | metallothionein 2A |
| PCF11-AS1 | 0.986792 | 0.00518 | 0.00518 | 2.95242 | Up | PCF11 antisense RNA 1 |
| FILIP1L | 1.100385 | 0.005771 | 0.005771 | 2.911785 | Up | filamin A interacting protein 1 like |
| SNORD99 | 1.243138 | 0.004039 | 0.004039 | 3.045008 | Up | small nucleolar RNA, C/D box 99 |
| PTBP1P | 1.255259 | 0.002482 | 0.002482 | 3.222381 | Up | polypyrimidine tract binding protein 1 pseudogene |
| ZNF433 | 0.986216 | 0.005996 | 0.005996 | 2.897283 | Up | zinc finger protein 433 |
| ISG20 | 1.625812 | 0.005233 | 0.005233 | 2.948589 | Up | interferon stimulated exonuclease gene 20 |
| NPIPB12 | 1.304191 | 0.004596 | 0.004596 | 2.997106 | Up | nuclear pore complex interacting protein family member B12 |
| RNU6-42P | 1.985584 | 0.002162 | 0.002162 | 3.271766 | Up | RNA, U6 small nuclear 42, pseudogene |
| EPHA4 | 1.317026 | 0.006338 | 0.006338 | 2.876247 | Up | EPH receptor A4 |
| PHF11 | 1.023572 | 0.00619 | 0.00619 | 2.885234 | Up | PHD finger protein 11 |
| TMEM140 | 1.901798 | 0.006549 | 0.006549 | 2.863836 | Up | transmembrane protein 140 |
| GJB7 | 2.091619 | 0.002468 | 0.002468 | 3.224359 | Up | gap junction protein beta 7 |
| DRD1 | 1.203743 | 0.004927 | 0.004927 | 2.971207 | Up | dopamine receptor D1 |
| NKX3-1 | 1.66839 | 0.006759 | 0.006759 | 2.85177 | Up | NK3 homeobox 1 |
| HSH2D | 1.388184 | 0.00634 | 0.00634 | 2.876122 | Up | hematopoietic SH2 domain containing |
| CCDC116 | 1.816182 | 0.003193 | 0.003193 | 3.131229 | Up | coiled-coil domain containing 116 |
| LMO2 | 2.357774 | 0.006131 | 0.006131 | 2.888866 | Up | LIM domain only 2 |
| TCAF2P1 | 1.39396 | 0.002514 | 0.002514 | 3.217777 | Up | TRPM8 channel associated factor 2 pseudogene 1 |
| STX19 | 1.228144 | 0.007424 | 0.007424 | 2.815858 | Up | syntaxin 19 |
| NEURL3 | 1.180071 | 0.006801 | 0.006801 | 2.849388 | Up | neuralized E3 ubiquitin protein ligase 3 |
| PIM3 | 0.971536 | 0.006055 | 0.006055 | 2.893626 | Up | Pim-3 proto-oncogene, serine/threonine kinase |
| TRIM5 | 1.060149 | 0.006461 | 0.006461 | 2.868977 | Up | tripartite motif containing 5 |
| PPP1R15A | 2.652991 | 0.005578 | 0.005578 | 2.924601 | Up | protein phosphatase 1 regulatory subunit 15A |
| SUSD3 | 1.860803 | 0.004923 | 0.004923 | 2.971514 | Up | sushi domain containing 3 |
| FBXO6 | 1.003573 | 0.007611 | 0.007611 | 2.806265 | Up | F-box protein 6 |
| VXN | 1.394123 | 0.004571 | 0.004571 | 2.999171 | Up | vexin |
| HIVEP1 | 1.001707 | 0.007557 | 0.007557 | 2.809016 | Up | HIVEP zinc finger 1 |
| IRF7 | 1.729251 | 0.006649 | 0.006649 | 2.858056 | Up | interferon regulatory factor 7 |
| TTLL11-IT1 | 1.253247 | 0.004223 | 0.004223 | 3.028542 | Up | TTLL11 intronic transcript 1 |
| BATF2 | 2.429025 | 0.008237 | 0.008237 | 2.775774 | Up | basic leucine zipper ATF-like transcription factor 2 |
| LSMEM1 | 1.091776 | 0.008071 | 0.008071 | 2.78367 | Up | leucine rich single-pass membrane protein 1 |
| PRKD2 | 1.113189 | 0.006541 | 0.006541 | 2.86427 | Up | protein kinase D2 |
| KLF4 | 1.96856 | 0.007874 | 0.007874 | 2.793199 | Up | Kruppel like factor 4 |
| IL7 | 1.224412 | 0.007628 | 0.007628 | 2.805444 | Up | interleukin 7 |
| SOCS1 | 1.705696 | 0.008894 | 0.008894 | 2.746003 | Up | suppressor of cytokine signaling 1 |
| ZC3H12A | 1.050079 | 0.007753 | 0.007753 | 2.799153 | Up | zinc finger CCCH-type containing 12A |
| CPEB3 | 1.400172 | 0.009168 | 0.009168 | 2.734169 | Up | cytoplasmic polyadenylation element binding protein 3 |
| CCL2 | 1.791533 | 0.0096 | 0.0096 | 2.716167 | Up | C-C motif chemokine ligand 2 |
| RNU6-118P | 1.59562 | 0.004039 | 0.004039 | 3.044986 | Up | RNA, U6 small nuclear 118, pseudogene |
| RTP4 | 2.084552 | 0.009589 | 0.009589 | 2.716614 | Up | receptor transporter protein 4 |
| NPFFR2 | 1.282538 | 0.009832 | 0.009832 | 2.706821 | Up | neuropeptide FF receptor 2 |
| FGF18 | 2.351473 | 0.006955 | 0.006955 | 2.840835 | Up | fibroblast growth factor 18 |
| HLA-F | 1.391048 | 0.008852 | 0.008852 | 2.747861 | Up | major histocompatibility complex, class I, F |
| PTCH2 | 1.044968 | 0.00774 | 0.00774 | 2.799821 | Up | patched 2 |
| FLT3LG | 1.069156 | 0.010147 | 0.010147 | 2.694435 | Up | fms related tyrosine kinase 3 ligand |
| IFIT5 | 1.67296 | 0.00902 | 0.00902 | 2.740526 | Up | interferon induced protein with tetratricopeptide repeats 5 |
| PDE2A | 1.188121 | 0.008243 | 0.008243 | 2.775493 | Up | phosphodiesterase 2A |
| STAT2 | 1.407434 | 0.008501 | 0.008501 | 2.763565 | Up | signal transducer and activator of transcription 2 |
| HM13-IT1 | 1.090514 | 0.008136 | 0.008136 | 2.780538 | Up | HM13 intronic transcript 1 |
| REC8 | 1.021857 | 0.010947 | 0.010947 | 2.664519 | Up | REC8 meiotic recombination protein |
| CAVIN2 | 2.285666 | 0.006243 | 0.006243 | 2.882018 | Up | caveolae associated protein 2 |
| HSPB9 | 1.950222 | 0.005864 | 0.005864 | 2.905719 | Up | heat shock protein family B (small) member 9 |
| SYT1 | 1.240353 | 0.00991 | 0.00991 | 2.70374 | Up | synaptotagmin 1 |
| PPP4R1-AS1 | 1.416349 | 0.00527 | 0.00527 | 2.94595 | Up | PPP4R1 antisense RNA 1 |
| TNF | 4.476993 | 0.010253 | 0.010253 | 2.690364 | Up | tumor necrosis factor |
| NLRP3 | 1.161308 | 0.009898 | 0.009898 | 2.704187 | Up | NLR family pyrin domain containing 3 |
| MT2P1 | 1.653905 | 0.01201 | 0.01201 | 2.627752 | Up | metallothionein 2 pseudogene 1 |
| CCDC65 | 1.167987 | 0.008399 | 0.008399 | 2.768226 | Up | coiled-coil domain containing 65 |
| TDRD7 | 1.057286 | 0.010386 | 0.010386 | 2.685272 | Up | tudor domain containing 7 |
| MAP3K8 | 1.80803 | 0.011453 | 0.011453 | 2.646607 | Up | mitogen-activated protein kinase kinasekinase 8 |
| SNORD45A | 1.256796 | 0.006181 | 0.006181 | 2.885782 | Up | small nucleolar RNA, C/D box 45A |
| EYA1 | 1.132006 | 0.012143 | 0.012143 | 2.623339 | Up | EYA transcriptional coactivator and phosphatase 1 |
| GRM8 | 2.154 | 0.006504 | 0.006504 | 2.866431 | Up | glutamate metabotropic receptor 8 |
| CRTAM | 1.58508 | 0.006252 | 0.006252 | 2.881438 | Up | cytotoxic and regulatory T cell molecule |
| USP18 | 2.34472 | 0.012652 | 0.012652 | 2.606962 | Up | ubiquitin specific peptidase 18 |
| C4A | 1.451882 | 0.012813 | 0.012813 | 2.601887 | Up | complement C4A (Rodgers blood group) |
| EGR1 | 1.66146 | 0.010871 | 0.010871 | 2.66728 | Up | early growth response 1 |
| SEC16B | 1.346299 | 0.013593 | 0.013593 | 2.578155 | Up | SEC16 homolog B, endoplasmic reticulum export factor |
| TLR6 | 1.035853 | 0.011756 | 0.011756 | 2.636266 | Up | toll like receptor 6 |
| RRAD | 1.434268 | 0.013182 | 0.013182 | 2.590506 | Up | RRAD, Ras related glycolysis inhibitor and calcium channel regulator |
| SNORD43 | 1.013019 | 0.006974 | 0.006974 | 2.839796 | Up | small nucleolar RNA, C/D box 43 |
| NT5C3A | 1.362242 | 0.009792 | 0.009792 | 2.708416 | Up | 5'-nucleotidase, cytosolic IIIA |
| PSMB8-AS1 | 1.488965 | 0.013918 | 0.013918 | 2.568645 | Up | PSMB8 antisense RNA 1 (head to head) |
| SNORA75 | 1.356852 | 0.008426 | 0.008426 | 2.766984 | Up | small nucleolar RNA, H/ACA box 75 |
| DDX58 | 1.510966 | 0.010341 | 0.010341 | 2.686996 | Up | DExD/H-box helicase 58 |
| EXOC3L1 | 2.466537 | 0.009826 | 0.009826 | 2.707084 | Up | exocyst complex component 3 like 1 |
| TNFSF10 | 1.557624 | 0.011108 | 0.011108 | 2.658763 | Up | TNF superfamily member 10 |
| KLB | 1.220487 | 0.009959 | 0.009959 | 2.701796 | Up | klotho beta |
| PPM1K | 1.467005 | 0.013458 | 0.013458 | 2.582188 | Up | protein phosphatase, Mg2+/Mn2+ dependent 1K |
| ADAM20P1 | 1.21742 | 0.010682 | 0.010682 | 2.674194 | Up | ADAM metallopeptidase domain 20 pseudogene 1 |
| TRIM69 | 1.112992 | 0.012995 | 0.012995 | 2.596233 | Up | tripartite motif containing 69 |
| ICAM1 | 1.198605 | 0.011427 | 0.011427 | 2.647528 | Up | intercellular adhesion molecule 1 |
| KLF2 | 0.992225 | 0.015396 | 0.015396 | 2.527762 | Up | Kruppel like factor 2 |
| LINC00379 | 1.280167 | 0.007885 | 0.007885 | 2.792652 | Up | long intergenic non-protein coding RNA 379 |
| HLA-V | 2.062224 | 0.014819 | 0.014819 | 2.543277 | Up | major histocompatibility complex, class I, V (pseudogene) |
| MT1E | 1.34699 | 0.015352 | 0.015352 | 2.528933 | Up | metallothionein 1E |
| BDKRB2 | 2.347703 | 0.011723 | 0.011723 | 2.637358 | Up | bradykinin receptor B2 |
| PML | 1.231562 | 0.01112 | 0.01112 | 2.658331 | Up | promyelocyticleukemia |
| TSLP | 1.139512 | 0.013131 | 0.013131 | 2.592064 | Up | thymic stromal lymphopoietin |
| CCL20 | 1.320712 | 0.013951 | 0.013951 | 2.567674 | Up | C-C motif chemokine ligand 20 |
| MXD1 | 1.07566 | 0.01356 | 0.01356 | 2.579134 | Up | MAX dimerization protein 1 |
| MAGI2-AS3 | 1.279478 | 0.012211 | 0.012211 | 2.621132 | Up | MAGI2 antisense RNA 3 |
| MIR6755 | 1.162425 | 0.009661 | 0.009661 | 2.713702 | Up | microRNA 6755 |
| NOCT | 1.603703 | 0.015388 | 0.015388 | 2.527964 | Up | nocturnin |
| UQCRBP1 | 1.075448 | 0.011354 | 0.011354 | 2.650073 | Up | ubiquinol-cytochrome c reductase binding protein pseudogene 1 |
| JAK2 | 1.311816 | 0.015691 | 0.015691 | 2.520035 | Up | Janus kinase 2 |
| CMPK2 | 2.70339 | 0.015326 | 0.015326 | 2.529601 | Up | cytidine/uridine monophosphate kinase 2 |
| CX3CL1 | 1.925664 | 0.015426 | 0.015426 | 2.526979 | Up | C-X3-C motif chemokine ligand 1 |
| SLC5A5 | 2.242138 | 0.010518 | 0.010518 | 2.680321 | Up | solute carrier family 5 member 5 |
| PARP12 | 1.175203 | 0.012789 | 0.012789 | 2.60264 | Up | poly(ADP-ribose) polymerase family member 12 |
| DDR2 | 0.978944 | 0.013894 | 0.013894 | 2.569329 | Up | discoidin domain receptor tyrosine kinase 2 |
| OASL | 2.738979 | 0.014331 | 0.014331 | 2.556821 | Up | 2'-5'-oligoadenylate synthetase like |
| PDE4B | 2.095245 | 0.016787 | 0.016787 | 2.492428 | Up | phosphodiesterase 4B |
| IFI16 | 1.597567 | 0.014307 | 0.014307 | 2.557501 | Up | interferon gamma inducible protein 16 |
| HELZ2 | 1.994702 | 0.011455 | 0.011455 | 2.646565 | Up | helicase with zinc finger 2 |
| TRAF1 | 2.20676 | 0.018458 | 0.018458 | 2.453351 | Up | TNF receptor associated factor 1 |
| ADGRL3 | 1.033359 | 0.01695 | 0.01695 | 2.488459 | Up | adhesion G protein-coupled receptor L3 |
| RPL32P33 | 1.257833 | 0.010268 | 0.010268 | 2.689796 | Up | ribosomal protein L32 pseudogene 33 |
| NPM1P25 | 1.008455 | 0.013652 | 0.013652 | 2.576406 | Up | nucleophosmin 1 pseudogene 25 |
| GPER1 | 1.116291 | 0.015696 | 0.015696 | 2.519906 | Up | G protein-coupled estrogen receptor 1 |
| FOS | 1.706227 | 0.017598 | 0.017598 | 2.473045 | Up | Fos proto-oncogene, AP-1 transcription factor subunit |
| DUSP8 | 1.371125 | 0.016284 | 0.016284 | 2.504892 | Up | dual specificity phosphatase 8 |
| LINC01776 | 1.165105 | 0.011202 | 0.011202 | 2.655405 | Up | long intergenic non-protein coding RNA 1776 |
| ZNF300P1 | 2.24229 | 0.013533 | 0.013533 | 2.579942 | Up | zinc finger protein 300 pseudogene 1 |
| ACHE | 1.544797 | 0.019349 | 0.019349 | 2.433815 | Up | acetylcholinesterase (Cartwright blood group) |
| MIR181B1 | 1.160878 | 0.011121 | 0.011121 | 2.658298 | Up | microRNA 181b-1 |
| CRYZL2P-SEC16B | 1.027383 | 0.019339 | 0.019339 | 2.434045 | Up | CRYZL2P-SEC16B readthrough |
| TTBK1 | 1.503124 | 0.013633 | 0.013633 | 2.576986 | Up | tau tubulin kinase 1 |
| GLCCI1 | 1.148217 | 0.019112 | 0.019112 | 2.438929 | Up | glucocorticoid induced 1 |
| IFNL4 | 4.46189 | 0.01501 | 0.01501 | 2.538078 | Up | interferon lambda 4 (gene/pseudogene) |
| DSCAML1 | 1.460424 | 0.012937 | 0.012937 | 2.598035 | Up | DS cell adhesion molecule like 1 |
| FAP | 2.823863 | 0.018119 | 0.018119 | 2.461027 | Up | fibroblast activation protein alpha |
| SNORA23 | 1.063009 | 0.013827 | 0.013827 | 2.571278 | Up | small nucleolar RNA, H/ACA box 23 |
| RPL23AP67 | 1.335781 | 0.012478 | 0.012478 | 2.612487 | Up | ribosomal protein L23a pseudogene 67 |
| MIR6732 | 1.251011 | 0.017038 | 0.017038 | 2.486355 | Up | microRNA 6732 |
| LINC00944 | 1.508372 | 0.021096 | 0.021096 | 2.397768 | Up | long intergenic non-protein coding RNA 944 |
| MXRA5 | 1.934851 | 0.017135 | 0.017135 | 2.484009 | Up | matrix remodeling associated 5 |
| KRT8P41 | 1.187927 | 0.012931 | 0.012931 | 2.598206 | Up | keratin 8 pseudogene 41 |
| TENT5A | 1.884328 | 0.017779 | 0.017779 | 2.468826 | Up | terminal nucleotidyltransferase 5A |
| PGLYRP2 | 2.929254 | 0.015156 | 0.015156 | 2.534141 | Up | peptidoglycan recognition protein 2 |
| RPS3P2 | 1.464118 | 0.013958 | 0.013958 | 2.567496 | Up | ribosomal protein S3 pseudogene 2 |
| EGR4 | 1.730147 | 0.020773 | 0.020773 | 2.404222 | Up | early growth response 4 |
| DACT1 | 1.295892 | 0.0146 | 0.0146 | 2.54931 | Up | dishevelled binding antagonist of beta catenin 1 |
| CCRL2 | 1.058009 | 0.018202 | 0.018202 | 2.459137 | Up | C-C motif chemokine receptor like 2 |
| PTPN20CP | 1.200421 | 0.013809 | 0.013809 | 2.571804 | Up | protein tyrosine phosphatase non-receptor type 20C, pseudogene |
| UBE2FP1 | 0.976314 | 0.018618 | 0.018618 | 2.449779 | Up | UBE2F pseudogene 1 |
| EPSTI1 | 1.998154 | 0.020865 | 0.020865 | 2.402374 | Up | epithelial stromal interaction 1 |
| C17orf82 | 1.121734 | 0.013795 | 0.013795 | 2.572217 | Up | chromosome 17 open reading frame 82 |
| LINC00921 | 1.081181 | 0.019125 | 0.019125 | 2.438646 | Up | long intergenic non-protein coding RNA 921 |
| RELB | 1.134588 | 0.017791 | 0.017791 | 2.468551 | Up | RELB proto-oncogene, NF-kB subunit |
| OTOG | 1.246961 | 0.014307 | 0.014307 | 2.557504 | Up | otogelin |
| SNED1 | 1.126954 | 0.018021 | 0.018021 | 2.463255 | Up | sushi, nidogen and EGF like domains 1 |
| KRT8P9 | 1.127192 | 0.017976 | 0.017976 | 2.464283 | Up | keratin 8 pseudogene 9 |
| RSAD2 | 2.968518 | 0.017912 | 0.017912 | 2.465764 | Up | radical S-adenosyl methionine domain containing 2 |
| FABP5P7 | 1.183973 | 0.018952 | 0.018952 | 2.442416 | Up | fatty acid binding protein 5 pseudogene 7 |
| RPL3P3 | 1.040919 | 0.01776 | 0.01776 | 2.469267 | Up | ribosomal protein L3 pseudogene 3 |
| HUS1B | 1.176098 | 0.014771 | 0.014771 | 2.544578 | Up | HUS1 checkpoint clamp component B |
| PTGER4 | 1.166411 | 0.017949 | 0.017949 | 2.464901 | Up | prostaglandin E receptor 4 |
| NRIR | 2.534489 | 0.016852 | 0.016852 | 2.490855 | Up | negative regulator of interferon response |
| BAHCC1 | 2.310362 | 0.018059 | 0.018059 | 2.46238 | Up | BAH domain and coiled-coil containing 1 |
| POU5F1P4 | 1.205331 | 0.015216 | 0.015216 | 2.53253 | Up | POU class 5 homeobox 1 pseudogene 4 |
| TRIM38 | 1.011581 | 0.016894 | 0.016894 | 2.489823 | Up | tripartite motif containing 38 |
| HEG1 | 1.405079 | 0.019606 | 0.019606 | 2.428325 | Up | heart development protein with EGF like domains 1 |
| IBA57-DT | 1.270711 | 0.015518 | 0.015518 | 2.524546 | Up | IBA57 divergent transcript |
| GFI1 | 1.038605 | 0.019788 | 0.019788 | 2.424484 | Up | growth factor independent 1 transcriptional repressor |
| IFI44 | 1.333776 | 0.016286 | 0.016286 | 2.504844 | Up | interferon induced protein 44 |
| HCG27 | 1.170291 | 0.023867 | 0.023867 | 2.345765 | Up | HLA complex group 27 |
| SLFN5 | 1.280898 | 0.016339 | 0.016339 | 2.503512 | Up | schlafen family member 5 |
| SNORD51 | 1.151033 | 0.017661 | 0.017661 | 2.471574 | Up | small nucleolar RNA, C/D box 51 |
| HIVEP2 | 1.293468 | 0.018322 | 0.018322 | 2.456407 | Up | HIVEP zinc finger 2 |
| ZNFX1 | 1.627282 | 0.014175 | 0.014175 | 2.561264 | Up | zinc finger NFX1-type containing 1 |
| IFIT1 | 2.561105 | 0.016495 | 0.016495 | 2.499621 | Up | interferon induced protein with tetratricopeptide repeats 1 |
| IFIT3 | 3.218305 | 0.01961 | 0.01961 | 2.428246 | Up | interferon induced protein with tetratricopeptide repeats 3 |
| CLEC4A | 1.189563 | 0.018783 | 0.018783 | 2.446145 | Up | C-type lectin domain family 4 member A |
| GBP1 | 2.03415 | 0.020119 | 0.020119 | 2.417586 | Up | guanylate binding protein 1 |
| NCKAP5 | 0.996077 | 0.023759 | 0.023759 | 2.347681 | Up | NCK associated protein 5 |
| NTNG2 | 1.601333 | 0.017227 | 0.017227 | 2.481819 | Up | netrin G2 |
| NCOA7 | 1.441337 | 0.019458 | 0.019458 | 2.431477 | Up | nuclear receptor coactivator 7 |
| SIX2 | 1.120981 | 0.020052 | 0.020052 | 2.418961 | Up | SIX homeobox 2 |
| SLC30A3 | 2.133137 | 0.018958 | 0.018958 | 2.442283 | Up | solute carrier family 30 member 3 |
| C1QTNF1 | 1.067021 | 0.026362 | 0.026362 | 2.303386 | Up | C1q and TNF related 1 |
| MIR4746 | 1.276655 | 0.017879 | 0.017879 | 2.466522 | Up | microRNA 4746 |
| TRIM40 | 1.454307 | 0.017735 | 0.017735 | 2.469864 | Up | tripartite motif containing 40 |
| RPL7P4 | 1.136645 | 0.017474 | 0.017474 | 2.475968 | Up | ribosomal protein L7 pseudogene 4 |
| PDZD2 | 1.653125 | 0.026708 | 0.026708 | 2.297798 | Up | PDZ domain containing 2 |
| BBC3 | 1.867442 | 0.02492 | 0.02492 | 2.327414 | Up | BCL2 binding component 3 |
| SLC25A2 | 1.698735 | 0.018696 | 0.018696 | 2.448053 | Up | solute carrier family 25 member 2 |
| RBM11 | 1.06029 | 0.027123 | 0.027123 | 2.291171 | Up | RNA binding motif protein 11 |
| TAP1 | 1.637892 | 0.016736 | 0.016736 | 2.493673 | Up | transporter 1, ATP binding cassette subfamily B member |
| GTF2IP5 | 1.205973 | 0.020502 | 0.020502 | 2.409704 | Up | general transcription factor IIipseudogene 5 |
| HSD17B14 | 1.721928 | 0.026856 | 0.026856 | 2.295424 | Up | hydroxysteroid 17-beta dehydrogenase 14 |
| TGIF2P1 | 1.308314 | 0.01858 | 0.01858 | 2.450639 | Up | TGFB induced factor homeobox 2 pseudogene 1 |
| IFIT2 | 3.561866 | 0.019495 | 0.019495 | 2.430687 | Up | interferon induced protein with tetratricopeptide repeats 2 |
| LINC01828 | 0.980615 | 0.023596 | 0.023596 | 2.350603 | Up | long intergenic non-protein coding RNA 1828 |
| CYP21A2 | 1.608816 | 0.020828 | 0.020828 | 2.403107 | Up | cytochrome P450 family 21 subfamily A member 2 |
| ID4 | 1.517486 | 0.023666 | 0.023666 | 2.349345 | Up | inhibitor of DNA binding 4, HLH protein |
| LTB | 1.280863 | 0.027193 | 0.027193 | 2.290071 | Up | lymphotoxin beta |
| BCL3 | 1.233657 | 0.023166 | 0.023166 | 2.358376 | Up | BCL3 transcription coactivator |
| LINC00365 | 1.462171 | 0.019292 | 0.019292 | 2.435048 | Up | long intergenic non-protein coding RNA 365 |
| LINC01842 | 1.02113 | 0.022746 | 0.022746 | 2.366107 | Up | long intergenic non-protein coding RNA 1842 |
| RPS29P5 | 0.981563 | 0.018987 | 0.018987 | 2.441648 | Up | ribosomal protein S29 pseudogene 5 |
| OR52K3P | 3.103385 | 0.024559 | 0.024559 | 2.333614 | Up | olfactory receptor family 52 subfamily K member 3 pseudogene |
| PPP4R4 | 1.863424 | 0.028674 | 0.028674 | 2.267217 | Up | protein phosphatase 4 regulatory subunit 4 |
| UNC93B3 | 1.117507 | 0.022747 | 0.022747 | 2.36608 | Up | unc-93 homolog B3, pseudogene |
| MMP25 | 0.973873 | 0.026311 | 0.026311 | 2.304209 | Up | matrix metallopeptidase 25 |
| LINC01270 | 1.195411 | 0.023609 | 0.023609 | 2.350372 | Up | long intergenic non-protein coding RNA 1270 |
| CPO | 1.34441 | 0.020348 | 0.020348 | 2.412851 | Up | carboxypeptidase O |
| KRT18P23 | 1.092607 | 0.02103 | 0.02103 | 2.399081 | Up | keratin 18 pseudogene 23 |
| HSD17B3 | 0.986893 | 0.021642 | 0.021642 | 2.387047 | Up | hydroxysteroid 17-beta dehydrogenase 3 |
| KRT8P51 | 1.056055 | 0.021823 | 0.021823 | 2.383542 | Up | keratin 8 pseudogene 51 |
| GRIP2 | 2.364844 | 0.022972 | 0.022972 | 2.361941 | Up | glutamate receptor interacting protein 2 |
| NPTX1 | 1.892145 | 0.027887 | 0.027887 | 2.279222 | Up | neuronal pentraxin 1 |
| HIF1A-AS2 | 1.125575 | 0.024679 | 0.024679 | 2.33154 | Up | HIF1A antisense RNA 2 |
| CYLD | 1.094273 | 0.023034 | 0.023034 | 2.360798 | Up | CYLD lysine 63 deubiquitinase |
| MX2 | 2.681049 | 0.024951 | 0.024951 | 2.326879 | Up | MX dynamin like GTPase 2 |
| MIR3149 | 1.183791 | 0.021476 | 0.021476 | 2.390278 | Up | microRNA 3149 |
| ACTBP13 | 1.061712 | 0.027204 | 0.027204 | 2.289892 | Up | ACTB pseudogene 13 |
| GFPT2 | 1.751351 | 0.024276 | 0.024276 | 2.33854 | Up | glutamine-fructose-6-phosphate transaminase 2 |
| IFNL2 | 7.294253 | 0.026645 | 0.026645 | 2.298816 | Up | interferon lambda 2 |
| LINC00592 | 1.216015 | 0.021953 | 0.021953 | 2.381058 | Up | long intergenic non-protein coding RNA 592 |
| SECTM1 | 1.759868 | 0.03083 | 0.03083 | 2.235763 | Up | secreted and transmembrane 1 |
| C11orf96 | 1.785984 | 0.030349 | 0.030349 | 2.242603 | Up | chromosome 11 open reading frame 96 |
| ESRRAP1 | 1.147711 | 0.026589 | 0.026589 | 2.299719 | Up | estrogen-related receptor alpha pseudogene 1 |
| HMGN2P17 | 1.106579 | 0.02261 | 0.02261 | 2.368634 | Up | high mobility group nucleosomal binding domain 2 pseudogene 17 |
| DHX58 | 2.060659 | 0.028206 | 0.028206 | 2.274327 | Up | DExH-box helicase 58 |
| NPR3 | 1.143846 | 0.031319 | 0.031319 | 2.228904 | Up | natriuretic peptide receptor 3 |
| ENO4 | 1.324046 | 0.02347 | 0.02347 | 2.352871 | Up | enolase 4 |
| DNAJB4 | 1.195125 | 0.025158 | 0.025158 | 2.323368 | Up | DnaJ heat shock protein family (Hsp40) member B4 |
| AGAP7P | 1.197694 | 0.024391 | 0.024391 | 2.336542 | Up | ArfGAP with GTPase domain, ankyrin repeat and PH domain 7, pseudogene |
| WIF1 | 1.801026 | 0.027444 | 0.027444 | 2.286126 | Up | WNT inhibitory factor 1 |
| GIMAP2 | 1.450887 | 0.033618 | 0.033618 | 2.197865 | Up | GTPase, IMAP family member 2 |
| SNCA-AS1 | 1.30856 | 0.024784 | 0.024784 | 2.329738 | Up | SNCA antisense RNA 1 |
| IGHEP2 | 1.730187 | 0.025917 | 0.025917 | 2.310664 | Up | immunoglobulin heavy constant epsilon P2 (pseudogene) |
| NKAIN4 | 1.079188 | 0.030231 | 0.030231 | 2.244293 | Up | sodium/potassium transporting ATPase interacting 4 |
| IFNL3 | 6.960425 | 0.030292 | 0.030292 | 2.243419 | Up | interferon lambda 3 |
| APOL6 | 1.972526 | 0.023754 | 0.023754 | 2.347772 | Up | apolipoprotein L6 |
| HLA-K | 1.398083 | 0.031612 | 0.031612 | 2.224833 | Up | major histocompatibility complex, class I, K (pseudogene) |
| APOBEC3G | 1.393513 | 0.034315 | 0.034315 | 2.188823 | Up | apolipoprotein B mRNA editing enzyme catalytic subunit 3G |
| MIR6783 | 1.146925 | 0.026554 | 0.026554 | 2.300273 | Up | microRNA 6783 |
| FAXDC2 | 1.31946 | 0.025905 | 0.025905 | 2.310869 | Up | fatty acid hydroxylase domain containing 2 |
| GRIN3B | 1.025113 | 0.025676 | 0.025676 | 2.314671 | Up | glutamate ionotropic receptor NMDA type subunit 3B |
| NR4A3 | 2.456563 | 0.032207 | 0.032207 | 2.216678 | Up | nuclear receptor subfamily 4 group A member 3 |
| GSN-AS1 | 1.34287 | 0.02662 | 0.02662 | 2.299211 | Up | GSN antisense RNA 1 |
| HSPA8P4 | 1.110122 | 0.028288 | 0.028288 | 2.273064 | Up | heat shock protein family A (Hsp70) member 8 pseudogene 4 |
| RPL5P27 | 1.029437 | 0.028985 | 0.028985 | 2.262557 | Up | ribosomal protein L5 pseudogene 27 |
| HCRTR1 | 1.356253 | 0.026783 | 0.026783 | 2.296597 | Up | hypocretin receptor 1 |
| DTX3L | 1.241553 | 0.022503 | 0.022503 | 2.370634 | Up | deltex E3 ubiquitin ligase 3L |
| PLAC8 | 1.12988 | 0.036412 | 0.036412 | 2.162594 | Up | placenta associated 8 |
| FAM153B | 1.109809 | 0.027683 | 0.027683 | 2.282391 | Up | family with sequence similarity 153 member B |
| KRT18P65 | 1.153395 | 0.027995 | 0.027995 | 2.277555 | Up | keratin 18 pseudogene 65 |
| GMPR | 1.58705 | 0.037047 | 0.037047 | 2.154903 | Up | guanosine monophosphate reductase |
| TAGAP | 1.952626 | 0.031513 | 0.031513 | 2.226205 | Up | T cell activation RhoGTPase activating protein |
| TSACC | 0.983953 | 0.031583 | 0.031583 | 2.22523 | Up | TSSK6 activating cochaperone |
| RNVU1-3 | 1.057849 | 0.028659 | 0.028659 | 2.267445 | Up | RNA, variant U1 small nuclear 3 |
| FAR1-IT1 | 1.242995 | 0.031536 | 0.031536 | 2.22589 | Up | FAR1 intronic transcript 1 |
| LAYN | 1.01366 | 0.034792 | 0.034792 | 2.182737 | Up | layilin |
| PRRX2 | 1.066129 | 0.029118 | 0.029118 | 2.260562 | Up | paired related homeobox 2 |
| OAS1 | 1.597942 | 0.02226 | 0.02226 | 2.375201 | Up | 2'-5'-oligoadenylate synthetase 1 |
| LGALS9DP | 1.229939 | 0.037564 | 0.037564 | 2.148731 | Up | galectin 9D, pseudogene |
| LYL1 | 1.02326 | 0.030923 | 0.030923 | 2.234445 | Up | LYL1 basic helix-loop-helix family member |
| TRPC4 | 2.46787 | 0.033183 | 0.033183 | 2.203595 | Up | transient receptor potential cation channel subfamily C member 4 |
| TRANK1 | 2.363383 | 0.03259 | 0.03259 | 2.211501 | Up | tetratricopeptide repeat and ankyrin repeat containing 1 |
| DNAH17 | 2.326232 | 0.039601 | 0.039601 | 2.125132 | Up | dynein axonemal heavy chain 17 |
| DUSP26 | 1.054625 | 0.03446 | 0.03446 | 2.186973 | Up | dual specificity phosphatase 26 |
| EGOT | 1.086133 | 0.039665 | 0.039665 | 2.124413 | Up | eosinophil granule ontogeny transcript |
| PRDX3P1 | 1.083736 | 0.031075 | 0.031075 | 2.232304 | Up | peroxiredoxin 3 pseudogene 1 |
| SLC6A13 | 1.501002 | 0.036308 | 0.036308 | 2.163859 | Up | solute carrier family 6 member 13 |
| TNFSF13B | 2.065925 | 0.040316 | 0.040316 | 2.117106 | Up | TNF superfamily member 13b |
| ETV7 | 2.824932 | 0.039935 | 0.039935 | 2.121369 | Up | ETS variant transcription factor 7 |
| CXCL11 | 3.746603 | 0.039022 | 0.039022 | 2.131729 | Up | C-X-C motif chemokine ligand 11 |
| IL7R | 1.798366 | 0.039173 | 0.039173 | 2.129999 | Up | interleukin 7 receptor |
| MIR561 | 1.447165 | 0.031861 | 0.031861 | 2.221401 | Up | microRNA 561 |
| RPS15AP36 | 1.015597 | 0.032121 | 0.032121 | 2.217845 | Up | ribosomal protein S15a pseudogene 36 |
| RAB19 | 1.058422 | 0.04094 | 0.04094 | 2.1102 | Up | RAB19, member RAS oncogene family |
| NPM1P8 | 1.170906 | 0.03213 | 0.03213 | 2.217726 | Up | nucleophosmin 1 pseudogene 8 |
| CFAP57 | 1.463252 | 0.041154 | 0.041154 | 2.107843 | Up | cilia and flagella associated protein 57 |
| RNU6-9 | 1.245936 | 0.032744 | 0.032744 | 2.209429 | Up | RNA, U6 small nuclear 9 |
| DNAH3 | 1.414655 | 0.038431 | 0.038431 | 2.13856 | Up | dynein axonemal heavy chain 3 |
| HERC5 | 2.161167 | 0.030697 | 0.030697 | 2.237641 | Up | HECT and RLD domain containing E3 ubiquitin protein ligase 5 |
| GJC3 | 1.038149 | 0.033576 | 0.033576 | 2.198413 | Up | gap junction protein gamma 3 |
| CLPSL1 | 1.039994 | 0.033025 | 0.033025 | 2.205691 | Up | colipase like 1 |
| NANOS3 | 0.973953 | 0.039476 | 0.039476 | 2.126556 | Up | nanos C2HC-type zinc finger 3 |
| HLX | 0.980112 | 0.040761 | 0.040761 | 2.112168 | Up | H2.0 like homeobox |
| PPEF1 | 1.701957 | 0.034682 | 0.034682 | 2.184142 | Up | protein phosphatase with EF-hand domain 1 |
| BNIP3P5 | 1.033777 | 0.034589 | 0.034589 | 2.185322 | Up | BCL2 interacting protein 3 pseudogene 5 |
| RNU6-2 | 1.318645 | 0.034433 | 0.034433 | 2.187314 | Up | RNA, U6 small nuclear 2 |
| FGF19 | 1.848509 | 0.037723 | 0.037723 | 2.14686 | Up | fibroblast growth factor 19 |
| GRIA2 | 1.275124 | 0.034497 | 0.034497 | 2.18649 | Up | glutamate ionotropic receptor AMPA type subunit 2 |
| SAMD9L | 2.208484 | 0.028313 | 0.028313 | 2.272692 | Up | sterile alpha motif domain containing 9 like |
| SOGA3 | 1.273369 | 0.039684 | 0.039684 | 2.124196 | Up | SOGA family member 3 |
| VSTM1 | 1.437544 | 0.036407 | 0.036407 | 2.162649 | Up | V-set and transmembrane domain containing 1 |
| MIR21 | 0.99124 | 0.03483 | 0.03483 | 2.182251 | Up | microRNA 21 |
| SNCAIP | 1.309269 | 0.036092 | 0.036092 | 2.166507 | Up | synuclein alpha interacting protein |
| GLI2 | 1.229791 | 0.042829 | 0.042829 | 2.089831 | Up | GLI family zinc finger 2 |
| ATP5MFP5 | 0.981783 | 0.035159 | 0.035159 | 2.178105 | Up | ATP synthase membrane subunit f pseudogene 5 |
| NLRC5 | 2.313605 | 0.039075 | 0.039075 | 2.131125 | Up | NLR family CARD domain containing 5 |
| MOGAT3 | 1.263134 | 0.035615 | 0.035615 | 2.172396 | Up | monoacylglycerol O-acyltransferase 3 |
| IFNL1 | 6.558198 | 0.042365 | 0.042365 | 2.094759 | Up | interferon lambda 1 |
| RNU6-36P | 1.000687 | 0.035366 | 0.035366 | 2.175511 | Up | RNA, U6 small nuclear 36, pseudogene |
| BARX1 | 1.219153 | 0.035867 | 0.035867 | 2.169275 | Up | BARX homeobox 1 |
| NEURL1 | 1.252787 | 0.036034 | 0.036034 | 2.167215 | Up | neuralized E3 ubiquitin protein ligase 1 |
| UBE2L6 | 1.187087 | 0.028313 | 0.028313 | 2.27269 | Up | ubiquitin conjugating enzyme E2 L6 |
| RPL7P16 | 1.000687 | 0.035979 | 0.035979 | 2.167896 | Up | ribosomal protein L7 pseudogene 16 |
| CAPN9 | 1.164853 | 0.036313 | 0.036313 | 2.1638 | Up | calpain 9 |
| SCARNA21 | 1.112307 | 0.036345 | 0.036345 | 2.163406 | Up | small Cajal body-specific RNA 21 |
| CREB5 | 1.271347 | 0.033318 | 0.033318 | 2.2018 | Up | cAMP responsive element binding protein 5 |
| TTC9B | 1.702168 | 0.042771 | 0.042771 | 2.090449 | Up | tetratricopeptide repeat domain 9B |
| PLA2G4C | 1.765984 | 0.044372 | 0.044372 | 2.073774 | Up | phospholipase A2 group IVC |
| OR52K1 | 1.334067 | 0.037334 | 0.037334 | 2.151468 | Up | olfactory receptor family 52 subfamily K member 1 |
| EEF1B2P1 | 0.984321 | 0.036822 | 0.036822 | 2.15762 | Up | eukaryotic translation elongation factor 1 beta 2 pseudogene 1 |
| RGS16 | 0.995551 | 0.045839 | 0.045839 | 2.058957 | Up | regulator of G protein signaling 16 |
| RPS4XP6 | 0.985811 | 0.038419 | 0.038419 | 2.13869 | Up | ribosomal protein S4X pseudogene 6 |
| C12orf74 | 1.430087 | 0.046128 | 0.046128 | 2.056088 | Up | chromosome 12 open reading frame 74 |
| IL17C | 1.502953 | 0.0387 | 0.0387 | 2.135437 | Up | interleukin 17C |
| ST7-AS2 | 1.093846 | 0.038488 | 0.038488 | 2.137896 | Up | ST7 antisense RNA 2 |
| RPL15P14 | 1.086068 | 0.038276 | 0.038276 | 2.140367 | Up | ribosomal protein L15 pseudogene 14 |
| MKRN4P | 1.066528 | 0.040566 | 0.040566 | 2.114323 | Up | makorin ring finger protein 4, pseudogene |
| RNU6-112P | 1.316138 | 0.039026 | 0.039026 | 2.131687 | Up | RNA, U6 small nuclear 112, pseudogene |
| C4B | 1.325091 | 0.047086 | 0.047086 | 2.046681 | Up | complement C4B (Chido blood group) |
| XRN1 | 1.118066 | 0.0286 | 0.0286 | 2.268334 | Up | 5'-3' exoribonuclease 1 |
| TENT5C | 1.355371 | 0.047524 | 0.047524 | 2.042439 | Up | terminal nucleotidyltransferase 5C |
| CH25H | 4.536363 | 0.044758 | 0.044758 | 2.069841 | Up | cholesterol 25-hydroxylase |
| CXCL10 | 4.060103 | 0.045354 | 0.045354 | 2.06381 | Up | C-X-C motif chemokine ligand 10 |
| ICAM5 | 1.09693 | 0.047503 | 0.047503 | 2.042646 | Up | intercellular adhesion molecule 5 |
| KRT8P21 | 1.050895 | 0.039864 | 0.039864 | 2.122164 | Up | keratin 8 pseudogene 21 |
| DRP2 | 1.00278 | 0.045983 | 0.045983 | 2.057525 | Up | dystrophin related protein 2 |
| IQUB | 0.998389 | 0.044762 | 0.044762 | 2.069799 | Up | IQ motif and ubiquitin domain containing |
| IFNB1 | 7.886233 | 0.046451 | 0.046451 | 2.052901 | Up | interferon beta 1 |
| MIR1260B | 1.000687 | 0.040129 | 0.040129 | 2.119193 | Up | microRNA 1260b |
| ACKR4 | 1.676381 | 0.049108 | 0.049108 | 2.027371 | Up | atypical chemokine receptor 4 |
| LINC00896 | 1.002351 | 0.046506 | 0.046506 | 2.052355 | Up | long intergenic non-protein coding RNA 896 |
| KRT18P32 | 1.040177 | 0.040846 | 0.040846 | 2.111227 | Up | keratin 18 pseudogene 32 |
| RASD1 | 1.869128 | 0.043244 | 0.043244 | 2.085464 | Up | ras related dexamethasone induced 1 |
| RANBP20P | 1.025185 | 0.047951 | 0.047951 | 2.038334 | Up | RAN binding protein 20 pseudogene |
| IFITM2 | 1.503363 | 0.040572 | 0.040572 | 2.114262 | Up | interferon induced transmembrane protein 2 |
| UBA7 | 1.433698 | 0.039971 | 0.039971 | 2.120967 | Up | ubiquitin like modifier activating enzyme 7 |
| RPL21P39 | 1.092851 | 0.042334 | 0.042334 | 2.095097 | Up | ribosomal protein L21 pseudogene 39 |
| LRIT3 | 1.088965 | 0.044742 | 0.044742 | 2.069999 | Up | leucine rich repeat, Ig-like and transmembrane domains 3 |
| RNVU1-6 | 1.013387 | 0.042786 | 0.042786 | 2.090292 | Up | RNA, variant U1 small nuclear 6 |
| RPL7P48 | 1.05168 | 0.042941 | 0.042941 | 2.088652 | Up | ribosomal protein L7 pseudogene 48 |
| GAPDHP14 | 1.025312 | 0.045953 | 0.045953 | 2.057821 | Up | glyceraldehyde-3-phosphate dehydrogenase pseudogene 14 |
| CFAP126 | 1.018579 | 0.043708 | 0.043708 | 2.080627 | Up | cilia and flagella associated protein 126 |
| SLITRK6 | 0.985385 | 0.04893 | 0.04893 | 2.029046 | Up | SLIT and NTRK like family member 6 |
| SLC39A2 | 0.99807 | 0.043863 | 0.043863 | 2.079022 | Up | solute carrier family 39 member 2 |
| BMP2 | 1.088449 | 0.043048 | 0.043048 | 2.087522 | Up | bone morphogenetic protein 2 |
| PROX1 | 2.157738 | 0.046523 | 0.046523 | 2.052189 | Up | prosperohomeobox 1 |
| LINC02208 | 1.163731 | 0.044216 | 0.044216 | 2.075374 | Up | long intergenic non-protein coding RNA 2208 |
| KRT8P13 | 1.061892 | 0.047377 | 0.047377 | 2.043857 | Up | keratin 8 pseudogene 13 |
| FAM71A | 1.384372 | 0.044806 | 0.044806 | 2.069348 | Up | family with sequence similarity 71 member A |
| KRT18P39 | 1.055271 | 0.044327 | 0.044327 | 2.074238 | Up | keratin 18 pseudogene 39 |
| TNFRSF4 | 1.161419 | 0.045014 | 0.045014 | 2.067238 | Up | TNF receptor superfamily member 4 |
| LINC02158 | 1.71431 | 0.04625 | 0.04625 | 2.054877 | Up | long intergenic non-protein coding RNA 2158 |
| SYNPR | 1.148755 | 0.048624 | 0.048624 | 2.031935 | Up | synaptoporin |
| MIR378D2HG | 0.981368 | 0.047575 | 0.047575 | 2.041953 | Up | MIR378D2 host gene |
| MIR616 | 1.253841 | 0.04747 | 0.04747 | 2.042961 | Up | microRNA 616 |
| SPINK9 | 0.983536 | 0.0458 | 0.0458 | 2.059351 | Up | serine peptidase inhibitor, Kazal type 9 |
| ZC3HAV1 | 1.663924 | 0.02955 | 0.02955 | 2.254194 | Up | zinc finger CCCH-type containing, antiviral 1 |
| WASIR1 | 1.008143 | 0.046413 | 0.046413 | 2.053269 | Up | WASH and IL9R antisense RNA 1 |
| NYAP2 | 1.229121 | 0.046708 | 0.046708 | 2.050375 | Up | neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2 |
| FBLN2 | 1.398336 | 0.047561 | 0.047561 | 2.042085 | Up | fibulin 2 |
| IFNA22P | 1.191131 | 0.047354 | 0.047354 | 2.044079 | Up | interferon alpha 22, pseudogene |
| IFIH1 | 2.02643 | 0.031036 | 0.031036 | 2.232862 | Up | interferon induced with helicase C domain 1 |
| DDX60L | 1.599206 | 0.03412 | 0.03412 | 2.191341 | Up | DExD/H-box 60 like |
| ACTA1 | 1.277548 | 0.049708 | 0.049708 | 2.021775 | Up | actin alpha 1, skeletal muscle |
| HCG4B | 1.366816 | 0.048693 | 0.048693 | 2.031275 | Up | HLA complex group 4B |
| RAB44 | 0.976113 | 0.048958 | 0.048958 | 2.02878 | Up | RAB44, member RAS oncogene family |
| FLT3 | 1.052002 | 0.049512 | 0.049512 | 2.023598 | Up | fms related tyrosine kinase 3 |
| MYLPF | 1.062085 | 0.049819 | 0.049819 | 2.020748 | Up | myosin light chain, phosphorylatable, fast skeletal muscle |
| ISG15 | 1.263658 | 0.030733 | 0.030733 | 2.237127 | Up | ISG15 ubiquitin like modifier |
| PARP10 | 1.234323 | 0.030263 | 0.030263 | 2.243842 | Up | poly(ADP-ribose) polymerase family member 10 |
| TRIM22 | 2.76806 | 0.047353 | 0.047353 | 2.044093 | Up | tripartite motif containing 22 |
| IFI35 | 1.186849 | 0.035784 | 0.035784 | 2.17031 | Up | interferon induced protein 35 |
| XAF1 | 2.277595 | 0.048717 | 0.048717 | 2.031053 | Up | XIAP associated factor 1 |
| SP110 | 1.220132 | 0.037857 | 0.037857 | 2.145278 | Up | SP110 nuclear body protein |
| IFITM1 | 1.532486 | 0.046551 | 0.046551 | 2.051918 | Up | interferon induced transmembrane protein 1 |
| SAMD9 | 1.587525 | 0.030596 | 0.030596 | 2.239074 | Up | sterile alpha motif domain containing 9 |
| SAMHD1 | 1.302206 | 0.035925 | 0.035925 | 2.16856 | Up | SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1 |
| OAS2 | 2.244301 | 0.040811 | 0.040811 | 2.111617 | Up | 2'-5'-oligoadenylate synthetase 2 |
| LGALS9 | 1.196441 | 0.048775 | 0.048775 | 2.030501 | Up | galectin 9 |
| PSMB9 | 1.080296 | 0.049952 | 0.049952 | 2.019517 | Up | proteasome 20S subunit beta 9 |
| MAGT1 | -0.46678 | 1.09E-06 | 1.09E-06 | -5.70983 | Down | magnesium transporter 1 |
| CFI | -0.93098 | 1.33E-05 | 1.33E-05 | -4.94224 | Down | complement factor I |
| SGPP1 | -0.42842 | 3.03E-05 | 3.03E-05 | -4.68502 | Down | sphingosine-1-phosphate phosphatase 1 |
| ITM2A | -0.79568 | 3.34E-05 | 3.34E-05 | -4.65404 | Down | integral membrane protein 2A |
| PSAP | -0.50092 | 2.89E-05 | 2.89E-05 | -4.69931 | Down | prosaposin |
| LYZ | -0.58944 | 3.85E-05 | 3.85E-05 | -4.60915 | Down | lysozyme |
| CTSH | -0.59789 | 5.02E-05 | 5.02E-05 | -4.52551 | Down | cathepsin H |
| SLC44A4 | -0.73935 | 6.46E-05 | 6.46E-05 | -4.44558 | Down | solute carrier family 44 member 4 |
| SSPN | -0.72555 | 6.75E-05 | 6.75E-05 | -4.43157 | Down | sarcospan |
| TSPAN8 | -0.68203 | 8.56E-05 | 8.56E-05 | -4.35561 | Down | tetraspanin 8 |
| VWA1 | -0.55974 | 0.00012 | 0.00012 | -4.24652 | Down | von Willebrand factor A domain containing 1 |
| OLFM4 | -0.80311 | 0.000122 | 0.000122 | -4.2421 | Down | olfactomedin 4 |
| TM4SF4 | -0.64526 | 0.000109 | 0.000109 | -4.2794 | Down | transmembrane 4 L six family member 4 |
| PLS1 | -0.43719 | 0.000122 | 0.000122 | -4.24199 | Down | plastin 1 |
| ANXA13 | -1.66049 | 7.64E-05 | 7.64E-05 | -4.39178 | Down | annexin A13 |
| METRN | -0.55327 | 0.000146 | 0.000146 | -4.18407 | Down | meteorin, glial cell differentiation regulator |
| GJB1 | -0.81958 | 0.00016 | 0.00016 | -4.15427 | Down | gap junction protein beta 1 |
| TMBIM6 | -0.51036 | 0.000131 | 0.000131 | -4.21891 | Down | transmembrane BAX inhibitor motif containing 6 |
| CD24 | -0.51865 | 0.000151 | 0.000151 | -4.17251 | Down | CD24 molecule |
| SCGN | -0.99086 | 0.000181 | 0.000181 | -4.11456 | Down | secretagogin, EF-hand calcium binding protein |
| SIAE | -0.52037 | 0.000271 | 0.000271 | -3.98215 | Down | sialic acid acetylesterase |
| UGT1A7 | -0.45953 | 0.000307 | 0.000307 | -3.93991 | Down | UDP glucuronosyltransferase family 1 member A7 |
| UGT1A9 | -0.46823 | 0.000326 | 0.000326 | -3.92013 | Down | UDP glucuronosyltransferase family 1 member A9 |
| UGT1A3 | -0.46877 | 0.000343 | 0.000343 | -3.90325 | Down | UDP glucuronosyltransferase family 1 member A3 |
| UGT1A8 | -0.46698 | 0.00035 | 0.00035 | -3.89726 | Down | UDP glucuronosyltransferase family 1 member A8 |
| HOGA1 | -0.79131 | 0.000329 | 0.000329 | -3.91705 | Down | 4-hydroxy-2-oxoglutarate aldolase 1 |
| SHMT1 | -0.4209 | 0.00036 | 0.00036 | -3.8875 | Down | serine hydroxymethyltransferase 1 |
| UGT1A5 | -0.46515 | 0.000369 | 0.000369 | -3.87933 | Down | UDP glucuronosyltransferase family 1 member A5 |
| SAC3D1 | -0.43211 | 0.000393 | 0.000393 | -3.8582 | Down | SAC3 domain containing 1 |
| GNG12 | -0.41783 | 0.000359 | 0.000359 | -3.88813 | Down | G protein subunit gamma 12 |
| GALM | -0.5502 | 0.00041 | 0.00041 | -3.84468 | Down | galactosemutarotase |
| UGT1A4 | -0.45879 | 0.000415 | 0.000415 | -3.83988 | Down | UDP glucuronosyltransferase family 1 member A4 |
| DNAJC22 | -0.6406 | 0.000451 | 0.000451 | -3.81275 | Down | DnaJ heat shock protein family (Hsp40) member C22 |
| AQP1 | -1.17011 | 0.000306 | 0.000306 | -3.94147 | Down | aquaporin 1 (Colton blood group) |
| TRNP1 | -0.38875 | 0.000407 | 0.000407 | -3.84671 | Down | TMF1 regulated nuclear protein 1 |
| RARRES1 | -0.56345 | 0.00045 | 0.00045 | -3.81304 | Down | retinoic acid receptor responder 1 |
| ADORA1 | -0.9796 | 0.000419 | 0.000419 | -3.83685 | Down | adenosine A1 receptor |
| UGT1A6 | -0.44678 | 0.000557 | 0.000557 | -3.74143 | Down | UDP glucuronosyltransferase family 1 member A6 |
| FDX1 | -0.41547 | 0.000595 | 0.000595 | -3.71951 | Down | ferredoxin 1 |
| PGRMC1 | -0.45097 | 0.000529 | 0.000529 | -3.75906 | Down | progesterone receptor membrane component 1 |
| PROM2 | -0.67421 | 0.000627 | 0.000627 | -3.70129 | Down | prominin 2 |
| PIGN | -0.41433 | 0.000617 | 0.000617 | -3.7068 | Down | phosphatidylinositol glycan anchor biosynthesis class N |
| SLC38A4 | -0.79405 | 0.000539 | 0.000539 | -3.75265 | Down | solute carrier family 38 member 4 |
| PIGK | -0.4078 | 0.00063 | 0.00063 | -3.70002 | Down | phosphatidylinositol glycan anchor biosynthesis class K |
| CEBPZOS | -0.4198 | 0.000649 | 0.000649 | -3.68965 | Down | CEBPZ opposite strand |
| DPYSL2 | -0.49063 | 0.000742 | 0.000742 | -3.6445 | Down | dihydropyrimidinase like 2 |
| OAT | -0.46474 | 0.000772 | 0.000772 | -3.63064 | Down | ornithine aminotransferase |
| ALDH2 | -0.41385 | 0.000807 | 0.000807 | -3.61555 | Down | aldehyde dehydrogenase 2 family member |
| VTCN1 | -0.97713 | 0.000891 | 0.000891 | -3.5817 | Down | V-set domain containing T cell activation inhibitor 1 |
| SPDEF | -0.78179 | 0.000878 | 0.000878 | -3.58696 | Down | SAM pointed domain containing ETS transcription factor |
| ALCAM | -0.44456 | 0.00071 | 0.00071 | -3.65946 | Down | activated leukocyte cell adhesion molecule |
| SCP2 | -0.41269 | 0.000896 | 0.000896 | -3.58005 | Down | sterol carrier protein 2 |
| ALDH6A1 | -0.46343 | 0.001038 | 0.001038 | -3.52913 | Down | aldehyde dehydrogenase 6 family member A1 |
| TRMT2B | -0.37714 | 0.001062 | 0.001062 | -3.5214 | Down | tRNAmethyltransferase 2 homolog B |
| AIF1L | -0.47647 | 0.001086 | 0.001086 | -3.51375 | Down | allograft inflammatory factor 1 like |
| FAHD1 | -0.41952 | 0.001089 | 0.001089 | -3.51274 | Down | fumarylacetoacetate hydrolase domain containing 1 |
| MME | -0.88764 | 0.001092 | 0.001092 | -3.51173 | Down | membrane metalloendopeptidase |
| NR2F2-AS1 | -0.5503 | 0.001173 | 0.001173 | -3.48692 | Down | NR2F2 antisense RNA 1 |
| CRYZ | -0.57692 | 0.001065 | 0.001065 | -3.52039 | Down | crystallin zeta |
| GLYATL2 | -1.13178 | 0.000661 | 0.000661 | -3.68389 | Down | glycine-N-acyltransferase like 2 |
| TMPRSS4 | -0.39083 | 0.001257 | 0.001257 | -3.46293 | Down | transmembrane serine protease 4 |
| TSPAN6 | -0.40619 | 0.00115 | 0.00115 | -3.49376 | Down | tetraspanin 6 |
| RBPMS-AS1 | -0.57454 | 0.001256 | 0.001256 | -3.46318 | Down | RBPMS antisense RNA 1 |
| NOSTRIN | -0.61474 | 0.001355 | 0.001355 | -3.43683 | Down | nitric oxide synthase trafficking |
| SPP1 | -0.60713 | 0.000845 | 0.000845 | -3.59982 | Down | secreted phosphoprotein 1 |
| EPHX1 | -0.48783 | 0.001396 | 0.001396 | -3.42625 | Down | epoxide hydrolase 1 |
| SOSTDC1 | -1.15425 | 0.001117 | 0.001117 | -3.50403 | Down | sclerostin domain containing 1 |
| COX11 | -0.45161 | 0.00153 | 0.00153 | -3.39417 | Down | cytochrome c oxidase copper chaperone COX11 |
| PPT1 | -0.41882 | 0.001477 | 0.001477 | -3.40658 | Down | palmitoyl-protein thioesterase 1 |
| CRP | -1.25615 | 0.0007 | 0.0007 | -3.66439 | Down | C-reactive protein |
| TAGLN2P1 | -0.39463 | 0.001718 | 0.001718 | -3.35342 | Down | transgelin 2 pseudogene 1 |
| HMGB3 | -0.49836 | 0.001534 | 0.001534 | -3.39324 | Down | high mobility group box 3 |
| UGT1A10 | -0.4502 | 0.001601 | 0.001601 | -3.3783 | Down | UDP glucuronosyltransferase family 1 member A10 |
| PRSS33 | -0.87938 | 0.001838 | 0.001838 | -3.32957 | Down | serine protease 33 |
| TCN1 | -0.60793 | 0.001673 | 0.001673 | -3.36276 | Down | transcobalamin 1 |
| REPS2 | -0.50784 | 0.00205 | 0.00205 | -3.29076 | Down | RALBP1 associated Eps domain containing 2 |
| PCSK1N | -0.43131 | 0.002065 | 0.002065 | -3.28814 | Down | proproteinconvertasesubtilisin/kexin type 1 inhibitor |
| C4orf48 | -0.69782 | 0.002204 | 0.002204 | -3.26498 | Down | chromosome 4 open reading frame 48 |
| FAM171A2 | -0.63443 | 0.002233 | 0.002233 | -3.26026 | Down | family with sequence similarity 171 member A2 |
| DSEL | -0.48713 | 0.0021 | 0.0021 | -3.2822 | Down | dermatansulfateepimerase like |
| LINC02532 | -0.65328 | 0.002475 | 0.002475 | -3.22341 | Down | long intergenic non-protein coding RNA 2532 |
| ASAH1 | -0.39025 | 0.002045 | 0.002045 | -3.29169 | Down | N-acylsphingosineamidohydrolase 1 |
| FCGRT | -0.47015 | 0.00225 | 0.00225 | -3.25754 | Down | Fc fragment of IgG receptor and transporter |
| SLC12A2 | -0.58534 | 0.001699 | 0.001699 | -3.35729 | Down | solute carrier family 12 member 2 |
| CLDN16 | -0.6794 | 0.002464 | 0.002464 | -3.22505 | Down | claudin 16 |
| BCKDHB | -0.41787 | 0.002668 | 0.002668 | -3.19641 | Down | branched chain keto acid dehydrogenase E1 subunit beta |
| SEMA3E | -0.49497 | 0.002604 | 0.002604 | -3.20514 | Down | semaphorin 3E |
| EPN3 | -0.418 | 0.002657 | 0.002657 | -3.19777 | Down | epsin 3 |
| SRD5A3 | -0.45001 | 0.002722 | 0.002722 | -3.1891 | Down | steroid 5 alpha-reductase 3 |
| LOX | -0.62134 | 0.002832 | 0.002832 | -3.17481 | Down | lysyl oxidase |
| HSD17B2 | -0.81698 | 0.002767 | 0.002767 | -3.18318 | Down | hydroxysteroid 17-beta dehydrogenase 2 |
| BCAS1 | -0.89748 | 0.002871 | 0.002871 | -3.16989 | Down | breast carcinoma amplified sequence 1 |
| SLC3A1 | -0.71911 | 0.002936 | 0.002936 | -3.16178 | Down | solute carrier family 3 member 1 |
| ACSS1 | -0.5491 | 0.002948 | 0.002948 | -3.1603 | Down | acyl-CoA synthetase short chain family member 1 |
| GATM | -0.52222 | 0.003064 | 0.003064 | -3.14624 | Down | glycine amidinotransferase |
| CENPV | -0.42391 | 0.002958 | 0.002958 | -3.15897 | Down | centromere protein V |
| HACD2 | -0.38233 | 0.002543 | 0.002543 | -3.21358 | Down | 3-hydroxyacyl-CoA dehydratase 2 |
| APOE | -0.61083 | 0.003182 | 0.003182 | -3.13244 | Down | apolipoprotein E |
| CUEDC2 | -0.45942 | 0.003069 | 0.003069 | -3.14562 | Down | CUE domain containing 2 |
| GSTO2 | -0.38908 | 0.003242 | 0.003242 | -3.12564 | Down | glutathione S-transferase omega 2 |
| SERINC5 | -0.46221 | 0.003037 | 0.003037 | -3.14946 | Down | serine incorporator 5 |
| LYPLAL1 | -0.45829 | 0.003363 | 0.003363 | -3.11227 | Down | lysophospholipase like 1 |
| NAALADL2 | -0.42755 | 0.003273 | 0.003273 | -3.12222 | Down | N-acetylated alpha-linked acidic dipeptidase like 2 |
| EFCAB11 | -0.45221 | 0.003521 | 0.003521 | -3.09545 | Down | EF-hand calcium binding domain 11 |
| PSMD10 | -0.47396 | 0.003093 | 0.003093 | -3.14275 | Down | proteasome 26S subunit, non-ATPase 10 |
| GALNT12 | -0.42917 | 0.003351 | 0.003351 | -3.11365 | Down | polypeptide N-acetylgalactosaminyltransferase 12 |
| GSR | -0.37832 | 0.002831 | 0.002831 | -3.17493 | Down | glutathione-disulfidereductase |
| SORBS2 | -0.60397 | 0.003636 | 0.003636 | -3.08374 | Down | sorbin and SH3 domain containing 2 |
| DDC | -0.58323 | 0.003891 | 0.003891 | -3.05882 | Down | dopa decarboxylase |
| ADI1 | -0.44463 | 0.003574 | 0.003574 | -3.09002 | Down | acireductonedioxygenase 1 |
| RIMKLA | -0.88904 | 0.004092 | 0.004092 | -3.04021 | Down | ribosomal modification protein rimK like family member A |
| UGT1A1 | -0.40946 | 0.004137 | 0.004137 | -3.03618 | Down | UDP glucuronosyltransferase family 1 member A1 |
| SORT1 | -0.38343 | 0.003756 | 0.003756 | -3.07174 | Down | sortilin 1 |
| CRLS1 | -0.44641 | 0.004474 | 0.004474 | -3.00715 | Down | cardiolipin synthase 1 |
| PDZK1IP1 | -0.62981 | 0.004227 | 0.004227 | -3.02818 | Down | PDZK1 interacting protein 1 |
| SPR | -0.38089 | 0.003973 | 0.003973 | -3.05107 | Down | sepiapterinreductase |
| SMIM10 | -0.72072 | 0.004574 | 0.004574 | -2.99892 | Down | small integral membrane protein 10 |
| EHMT2-AS1 | -0.88579 | 0.003647 | 0.003647 | -3.08256 | Down | EHMT2 and SLC44A4 antisense RNA 1 |
| FOLR1 | -1.1431 | 0.003475 | 0.003475 | -3.10031 | Down | folate receptor alpha |
| CLGN | -0.69988 | 0.004551 | 0.004551 | -3.00081 | Down | calmegin |
| KPNA2 | -0.39084 | 0.00366 | 0.00366 | -3.08129 | Down | karyopherin subunit alpha 2 |
| FAH | -0.39607 | 0.005027 | 0.005027 | -2.9637 | Down | fumarylacetoacetate hydrolase |
| TMEM59 | -0.45581 | 0.003928 | 0.003928 | -3.0553 | Down | transmembrane protein 59 |
| VEPH1 | -0.45193 | 0.005337 | 0.005337 | -2.94121 | Down | ventricular zone expressed PH domain containing 1 |
| HACD3 | -0.40154 | 0.004028 | 0.004028 | -3.04599 | Down | 3-hydroxyacyl-CoA dehydratase 3 |
| DNLZ | -0.44578 | 0.00577 | 0.00577 | -2.91183 | Down | DNL-type zinc finger |
| ST6GALNAC1 | -0.42569 | 0.005622 | 0.005622 | -2.92163 | Down | ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 1 |
| KLK6 | -0.43792 | 0.004702 | 0.004702 | -2.98858 | Down | kallikrein related peptidase 6 |
| SLC16A10 | -0.76258 | 0.005818 | 0.005818 | -2.9087 | Down | solute carrier family 16 member 10 |
| MAGIX | -0.48625 | 0.005931 | 0.005931 | -2.90146 | Down | MAGI family member, X-linked |
| BCO2 | -0.56805 | 0.005875 | 0.005875 | -2.90499 | Down | beta-carotene oxygenase 2 |
| COLCA2 | -0.94948 | 0.005228 | 0.005228 | -2.94895 | Down | colorectal cancer associated 2 |
| STMN1 | -0.47077 | 0.004392 | 0.004392 | -3.01395 | Down | stathmin 1 |
| HSPE1P4 | -0.44058 | 0.006225 | 0.006225 | -2.88309 | Down | heat shock protein family E (Hsp10) member 1 pseudogene 4 |
| CA12 | -0.70373 | 0.006024 | 0.006024 | -2.89552 | Down | carbonic anhydrase 12 |
| LTC4S | -1.08462 | 0.004673 | 0.004673 | -2.99093 | Down | leukotriene C4 synthase |
| NXNL2 | -1.0576 | 0.004797 | 0.004797 | -2.98117 | Down | nucleoredoxin like 2 |
| RHBDL2 | -0.53298 | 0.006307 | 0.006307 | -2.87813 | Down | rhomboid like 2 |
| AK4 | -0.40547 | 0.005472 | 0.005472 | -2.9318 | Down | adenylate kinase 4 |
| MLEC | -0.47988 | 0.00421 | 0.00421 | -3.02967 | Down | malectin |
| HNMT | -0.46823 | 0.005469 | 0.005469 | -2.93206 | Down | histamine N-methyltransferase |
| MAGEE1 | -0.62146 | 0.006249 | 0.006249 | -2.88166 | Down | MAGE family member E1 |
| PXMP4 | -0.42775 | 0.006079 | 0.006079 | -2.8921 | Down | peroxisomal membrane protein 4 |
| CPM | -0.65192 | 0.006535 | 0.006535 | -2.86463 | Down | carboxypeptidase M |
| NRGN | -0.4896 | 0.006741 | 0.006741 | -2.85278 | Down | neurogranin |
| FAM89B | -0.40528 | 0.006177 | 0.006177 | -2.88603 | Down | family with sequence similarity 89 member B |
| TSPAN10 | -0.41969 | 0.006773 | 0.006773 | -2.85097 | Down | tetraspanin 10 |
| CCDC115 | -0.50597 | 0.005926 | 0.005926 | -2.90175 | Down | coiled-coil domain containing 115 |
| FBP1 | -0.879 | 0.006778 | 0.006778 | -2.85072 | Down | fructose-bisphosphatase 1 |
| PAIP2B | -0.64669 | 0.006785 | 0.006785 | -2.8503 | Down | poly(A) binding protein interacting protein 2B |
| RAD9B | -0.72362 | 0.005904 | 0.005904 | -2.90315 | Down | RAD9 checkpoint clamp component B |
| CDNF | -0.89269 | 0.006191 | 0.006191 | -2.8852 | Down | cerebral dopamine neurotrophic factor |
| RNF128 | -0.46498 | 0.005244 | 0.005244 | -2.94785 | Down | ring finger protein 128 |
| KCNE3 | -0.79151 | 0.00661 | 0.00661 | -2.8603 | Down | potassium voltage-gated channel subfamily E regulatory subunit 3 |
| TMEM238 | -0.68002 | 0.006346 | 0.006346 | -2.87578 | Down | transmembrane protein 238 |
| PCLAF | -0.4371 | 0.005788 | 0.005788 | -2.91068 | Down | PCNA clamp associated factor |
| PDK1 | -0.56719 | 0.00672 | 0.00672 | -2.85398 | Down | pyruvate dehydrogenase kinase 1 |
| CALB1 | -0.92397 | 0.005871 | 0.005871 | -2.90531 | Down | calbindin 1 |
| MDH1 | -0.52824 | 0.005101 | 0.005101 | -2.95815 | Down | malate dehydrogenase 1 |
| PLEKHB1 | -0.50145 | 0.005556 | 0.005556 | -2.92608 | Down | pleckstrin homology domain containing B1 |
| WDR72 | -0.54895 | 0.00751 | 0.00751 | -2.81143 | Down | WD repeat domain 72 |
| ARRB1 | -0.41675 | 0.007438 | 0.007438 | -2.81512 | Down | arrestin beta 1 |
| ENSAP2 | -0.51177 | 0.007766 | 0.007766 | -2.79852 | Down | endosulfine alpha pseudogene 2 |
| NUBPL | -0.38896 | 0.007529 | 0.007529 | -2.81046 | Down | nucleotide binding protein like |
| HAGLR | -0.66013 | 0.007606 | 0.007606 | -2.80653 | Down | HOXD antisense growth-associated long non-coding RNA |
| HADHB | -0.38803 | 0.006429 | 0.006429 | -2.87086 | Down | hydroxyacyl-CoA dehydrogenase trifunctionalmultienzyme complex subunit beta |
| VSIG1 | -0.5897 | 0.008626 | 0.008626 | -2.75789 | Down | V-set and immunoglobulin domain containing 1 |
| ANKS4B | -0.67874 | 0.008683 | 0.008683 | -2.75533 | Down | ankyrin repeat and sterile alpha motif domain containing 4B |
| SLC38A11 | -0.73576 | 0.008043 | 0.008043 | -2.78498 | Down | solute carrier family 38 member 11 |
| CTHRC1 | -0.72027 | 0.006805 | 0.006805 | -2.84917 | Down | collagen triple helix repeat containing 1 |
| FGFR3 | -0.45158 | 0.007536 | 0.007536 | -2.81007 | Down | fibroblast growth factor receptor 3 |
| ANXA10 | -0.3914 | 0.008207 | 0.008207 | -2.77718 | Down | annexin A10 |
| METTL7A | -0.88534 | 0.009349 | 0.009349 | -2.72656 | Down | methyltransferase like 7A |
| DNAH10OS | -0.74962 | 0.008914 | 0.008914 | -2.74511 | Down | dynein axonemal heavy chain 10 opposite strand |
| CYBRD1 | -0.55088 | 0.009524 | 0.009524 | -2.71927 | Down | cytochrome b reductase 1 |
| ACE2 | -0.54396 | 0.009168 | 0.009168 | -2.73419 | Down | angiotensin I converting enzyme 2 |
| AKR1C3 | -0.56373 | 0.007238 | 0.007238 | -2.82556 | Down | aldo-ketoreductase family 1 member C3 |
| GGT1 | -0.56919 | 0.009572 | 0.009572 | -2.71733 | Down | gamma-glutamyltransferase 1 |
| NME5 | -0.68514 | 0.00963 | 0.00963 | -2.71495 | Down | NME/NM23 family member 5 |
| ARL6IP5 | -0.50567 | 0.006894 | 0.006894 | -2.84423 | Down | ADP ribosylation factor like GTPase 6 interacting protein 5 |
| IL20RA | -0.39063 | 0.010033 | 0.010033 | -2.69889 | Down | interleukin 20 receptor subunit alpha |
| MMP7 | -0.61709 | 0.007045 | 0.007045 | -2.83592 | Down | matrix metallopeptidase 7 |
| EFHC2 | -0.85121 | 0.009534 | 0.009534 | -2.7189 | Down | EF-hand domain containing 2 |
| PBXIP1 | -0.54253 | 0.008054 | 0.008054 | -2.78446 | Down | PBX homeobox interacting protein 1 |
| C14orf132 | -0.58628 | 0.010324 | 0.010324 | -2.68764 | Down | chromosome 14 open reading frame 132 |
| SLC25A27 | -0.79693 | 0.010075 | 0.010075 | -2.69724 | Down | solute carrier family 25 member 27 |
| ACE | -0.73381 | 0.010202 | 0.010202 | -2.69231 | Down | angiotensin I converting enzyme |
| AGR2 | -0.48548 | 0.008277 | 0.008277 | -2.77392 | Down | anterior gradient 2, protein disulphide isomerase family member |
| BNIPL | -0.8267 | 0.009771 | 0.009771 | -2.70927 | Down | BCL2 interacting protein like |
| ITIH2 | -0.60334 | 0.0109 | 0.0109 | -2.66621 | Down | inter-alpha-trypsin inhibitor heavy chain 2 |
| ZNF710-AS1 | -0.78809 | 0.010799 | 0.010799 | -2.66991 | Down | ZNF710 antisense RNA 1 |
| PDGFD | -0.64209 | 0.00994 | 0.00994 | -2.70254 | Down | platelet derived growth factor D |
| COA3 | -0.51134 | 0.009145 | 0.009145 | -2.73515 | Down | cytochrome c oxidase assembly factor 3 |
| CFAP73 | -0.69749 | 0.011536 | 0.011536 | -2.64374 | Down | cilia and flagella associated protein 73 |
| CARD9 | -0.3925 | 0.011319 | 0.011319 | -2.65128 | Down | caspase recruitment domain family member 9 |
| SAP30 | -0.4749 | 0.011229 | 0.011229 | -2.65445 | Down | Sin3A associated protein 30 |
| PGP | -0.386 | 0.008842 | 0.008842 | -2.7483 | Down | phosphoglycolate phosphatase |
| ARL6IP1P2 | -0.60694 | 0.011909 | 0.011909 | -2.63111 | Down | ADP ribosylation factor like GTPase 6 interacting protein 1 pseudogene 2 |
| LINC00327 | -0.73999 | 0.010373 | 0.010373 | -2.68579 | Down | long intergenic non-protein coding RNA 327 |
| ATPSCKMT | -0.50355 | 0.011256 | 0.011256 | -2.65352 | Down | ATP synthase c subunit lysine N-methyltransferase |
| SRI | -0.59821 | 0.00904 | 0.00904 | -2.73967 | Down | sorcin |
| TRAPPC6A | -0.75773 | 0.010859 | 0.010859 | -2.66771 | Down | trafficking protein particle complex 6A |
| KLK7 | -0.76267 | 0.01241 | 0.01241 | -2.61468 | Down | kallikrein related peptidase 7 |
| YBX1P10 | -0.51753 | 0.011825 | 0.011825 | -2.63393 | Down | Y-box binding protein 1 pseudogene 10 |
| RTL8B | -0.47752 | 0.012688 | 0.012688 | -2.60582 | Down | retrotransposon Gag like 8B |
| MATN2 | -0.39339 | 0.011846 | 0.011846 | -2.63322 | Down | matrilin 2 |
| WFDC2 | -0.46122 | 0.011833 | 0.011833 | -2.63365 | Down | WAP four-disulfide core domain 2 |
| NBDY | -0.42997 | 0.01082 | 0.01082 | -2.66914 | Down | negative regulator of P-body association |
| SPCS2 | -0.42304 | 0.010306 | 0.010306 | -2.68832 | Down | signal peptidase complex subunit 2 |
| MAD2L1 | -0.38095 | 0.01034 | 0.01034 | -2.68704 | Down | mitotic arrest deficient 2 like 1 |
| SORL1 | -1.11637 | 0.012575 | 0.012575 | -2.60938 | Down | sortilin related receptor 1 |
| PDE1A | -0.95681 | 0.011193 | 0.011193 | -2.65574 | Down | phosphodiesterase 1A |
| SNRPEP4 | -0.4078 | 0.013229 | 0.013229 | -2.58907 | Down | small nuclear ribonucleoprotein polypeptide E pseudogene 4 |
| QPCT | -0.37767 | 0.012069 | 0.012069 | -2.6258 | Down | glutaminyl-peptide cyclotransferase |
| TMEM160 | -0.68435 | 0.01114 | 0.01114 | -2.65761 | Down | transmembrane protein 160 |
| PHGDH | -0.40806 | 0.010445 | 0.010445 | -2.68304 | Down | phosphoglycerate dehydrogenase |
| BCAS3 | -0.41895 | 0.013851 | 0.013851 | -2.57059 | Down | BCAS3 microtubule associated cell migration factor |
| SDHCP3 | -0.79104 | 0.011573 | 0.011573 | -2.64247 | Down | succinate dehydrogenase complex subunit C pseudogene 3 |
| SCNN1A | -0.53791 | 0.013115 | 0.013115 | -2.59256 | Down | sodium channel epithelial 1 alpha subunit |
| IGSF10 | -0.55537 | 0.014548 | 0.014548 | -2.55074 | Down | immunoglobulin superfamily member 10 |
| PLEKHS1 | -0.60046 | 0.014768 | 0.014768 | -2.54466 | Down | pleckstrin homology domain containing S1 |
| ST6GALNAC2 | -0.39995 | 0.014331 | 0.014331 | -2.55684 | Down | ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 2 |
| IGFBP2 | -0.51385 | 0.013486 | 0.013486 | -2.58134 | Down | insulin like growth factor binding protein 2 |
| SPAG16 | -0.53058 | 0.012976 | 0.012976 | -2.59684 | Down | sperm associated antigen 16 |
| HOXA11 | -0.67787 | 0.014618 | 0.014618 | -2.54881 | Down | homeobox A11 |
| CYS1 | -0.80385 | 0.014782 | 0.014782 | -2.54429 | Down | cystin 1 |
| CRYM | -1.04724 | 0.015367 | 0.015367 | -2.52853 | Down | crystallin mu |
| GNG11 | -0.64022 | 0.015309 | 0.015309 | -2.53007 | Down | G protein subunit gamma 11 |
| PCAT7 | -0.59417 | 0.015373 | 0.015373 | -2.52836 | Down | prostate cancer associated transcript 7 |
| MYO3B | -0.51317 | 0.015446 | 0.015446 | -2.52644 | Down | myosin IIIB |
| AP2M1 | -0.41089 | 0.007714 | 0.007714 | -2.80109 | Down | adaptor related protein complex 2 subunit mu 1 |
| NRTN | -0.42622 | 0.015239 | 0.015239 | -2.53193 | Down | neurturin |
| GPSM2 | -0.47617 | 0.013424 | 0.013424 | -2.58321 | Down | G protein signaling modulator 2 |
| ASB9 | -0.41316 | 0.014282 | 0.014282 | -2.55821 | Down | ankyrin repeat and SOCS box containing 9 |
| SUN2 | -0.46432 | 0.011837 | 0.011837 | -2.63351 | Down | Sad1 and UNC84 domain containing 2 |
| TOMM20 | -0.38473 | 0.010534 | 0.010534 | -2.67969 | Down | translocase of outer mitochondrial membrane 20 |
| KCNMB4 | -0.48697 | 0.015023 | 0.015023 | -2.53772 | Down | potassium calcium-activated channel subfamily M regulatory beta subunit 4 |
| ATP5PDP2 | -0.6462 | 0.015744 | 0.015744 | -2.51867 | Down | ATP synthase peripheral stalk subunit d pseudogene 2 |
| CCDC74B | -1.0029 | 0.013756 | 0.013756 | -2.57335 | Down | coiled-coil domain containing 74B |
| ECH1 | -0.44958 | 0.010791 | 0.010791 | -2.67019 | Down | enoyl-CoA hydratase 1 |
| AZGP1 | -0.5984 | 0.016589 | 0.016589 | -2.49729 | Down | alpha-2-glycoprotein 1, zinc-binding |
| KLHDC2 | -0.40843 | 0.0139 | 0.0139 | -2.56916 | Down | kelch domain containing 2 |
| PRIMPOL | -0.39892 | 0.01558 | 0.01558 | -2.52293 | Down | primase and DNA directed polymerase |
| TMEM45B | -0.37827 | 0.014624 | 0.014624 | -2.54865 | Down | transmembrane protein 45B |
| SLAIN1 | -0.38153 | 0.016643 | 0.016643 | -2.49596 | Down | SLAIN motif family member 1 |
| DNAJC9-AS1 | -1.20338 | 0.014086 | 0.014086 | -2.5638 | Down | DNAJC9 antisense RNA 1 |
| ARHGAP19 | -0.43004 | 0.0163 | 0.0163 | -2.5045 | Down | Rho GTPase activating protein 19 |
| SERPINA4 | -0.5724 | 0.015509 | 0.015509 | -2.52478 | Down | serpin family A member 4 |
| LEPR | -0.4178 | 0.01657 | 0.01657 | -2.49777 | Down | leptin receptor |
| PSMG3-AS1 | -0.52351 | 0.016953 | 0.016953 | -2.48839 | Down | PSMG3 antisense RNA 1 (head to head) |
| SYT12 | -0.68091 | 0.015883 | 0.015883 | -2.51507 | Down | synaptotagmin 12 |
| RERG | -0.70304 | 0.016596 | 0.016596 | -2.49712 | Down | RAS like estrogen regulated growth inhibitor |
| BTBD16 | -0.88899 | 0.015431 | 0.015431 | -2.52684 | Down | BTB domain containing 16 |
| ETFB | -0.54425 | 0.012714 | 0.012714 | -2.60498 | Down | electron transfer flavoprotein subunit beta |
| NTRK2 | -0.51677 | 0.018348 | 0.018348 | -2.45582 | Down | neurotrophic receptor tyrosine kinase 2 |
| GNG7 | -0.85502 | 0.018223 | 0.018223 | -2.45867 | Down | G protein subunit gamma 7 |
| ERP27 | -0.7466 | 0.018084 | 0.018084 | -2.46182 | Down | endoplasmic reticulum protein 27 |
| FABP6 | -0.89891 | 0.01736 | 0.01736 | -2.47864 | Down | fatty acid binding protein 6 |
| TRMT9B | -0.87192 | 0.019079 | 0.019079 | -2.43965 | Down | tRNAmethyltransferase 9B (putative) |
| TMEM37 | -0.84092 | 0.018022 | 0.018022 | -2.46324 | Down | transmembrane protein 37 |
| DHRS4L2 | -0.38409 | 0.018843 | 0.018843 | -2.44481 | Down | dehydrogenase/reductase 4 like 2 |
| DBP | -0.55009 | 0.019461 | 0.019461 | -2.43143 | Down | D-box binding PAR bZIP transcription factor |
| PDCD4 | -0.57081 | 0.01663 | 0.01663 | -2.49627 | Down | programmed cell death 4 |
| ABCC4 | -0.37804 | 0.017031 | 0.017031 | -2.48652 | Down | ATP binding cassette subfamily C member 4 |
| RSPH1 | -0.67924 | 0.019742 | 0.019742 | -2.42546 | Down | radial spoke head component 1 |
| RARRES2 | -1.09616 | 0.020292 | 0.020292 | -2.41401 | Down | retinoic acid receptor responder 2 |
| GACAT2 | -0.89674 | 0.01931 | 0.01931 | -2.43465 | Down | gastric cancer associated transcript 2 |
| CD302 | -0.37696 | 0.01816 | 0.01816 | -2.46009 | Down | CD302 molecule |
| MIR193BHG | -0.60372 | 0.020887 | 0.020887 | -2.40193 | Down | MIR193B host gene |
| TTR | -0.87179 | 0.020496 | 0.020496 | -2.40982 | Down | transthyretin |
| PRDX3 | -0.38219 | 0.013342 | 0.013342 | -2.58566 | Down | peroxiredoxin 3 |
| AKR1B10 | -0.6267 | 0.017481 | 0.017481 | -2.47579 | Down | aldo-ketoreductase family 1 member B10 |
| NDUFAF8 | -0.69456 | 0.016805 | 0.016805 | -2.49199 | Down | NADH:ubiquinoneoxidoreductase complex assembly factor 8 |
| ANXA9 | -0.53242 | 0.018233 | 0.018233 | -2.45843 | Down | annexin A9 |
| FGFBP2 | -0.39128 | 0.021826 | 0.021826 | -2.38349 | Down | fibroblast growth factor binding protein 2 |
| TUBA1A | -0.92382 | 0.017846 | 0.017846 | -2.46729 | Down | tubulin alpha 1a |
| HMGB1P1 | -0.4657 | 0.02233 | 0.02233 | -2.37388 | Down | high mobility group box 1 pseudogene 1 |
| ACYP2 | -0.44182 | 0.020861 | 0.020861 | -2.40245 | Down | acylphosphatase 2 |
| CREG2 | -0.88476 | 0.022642 | 0.022642 | -2.36804 | Down | cellular repressor of E1A stimulated genes 2 |
| IQCD | -0.57327 | 0.022704 | 0.022704 | -2.36689 | Down | IQ motif containing D |
| SHH | -0.90573 | 0.021091 | 0.021091 | -2.39787 | Down | sonic hedgehog signaling molecule |
| SEMA5A | -0.80779 | 0.022709 | 0.022709 | -2.3668 | Down | semaphorin 5A |
| CNGA1 | -0.64756 | 0.022769 | 0.022769 | -2.36569 | Down | cyclic nucleotide gated channel subunit alpha 1 |
| PAH | -0.45883 | 0.021426 | 0.021426 | -2.39125 | Down | phenylalanine hydroxylase |
| TGFB2-OT1 | -0.46945 | 0.02296 | 0.02296 | -2.36215 | Down | TGFB2 overlapping transcript 1 |
| OAZ1 | -0.44222 | 0.011684 | 0.011684 | -2.63871 | Down | ornithine decarboxylase antizyme 1 |
| TPBGL | -0.97153 | 0.020877 | 0.020877 | -2.40212 | Down | trophoblast glycoprotein like |
| MMEL1 | -0.77541 | 0.023608 | 0.023608 | -2.35039 | Down | membrane metalloendopeptidase like 1 |
| MIR4700 | -0.43809 | 0.02378 | 0.02378 | -2.34731 | Down | microRNA 4700 |
| FFAR4 | -0.66314 | 0.023876 | 0.023876 | -2.3456 | Down | free fatty acid receptor 4 |
| SYNPR-AS1 | -0.8959 | 0.020945 | 0.020945 | -2.40077 | Down | SYNPR antisense RNA 1 |
| SLC45A1 | -0.70304 | 0.02189 | 0.02189 | -2.38226 | Down | solute carrier family 45 member 1 |
| HMGN1P37 | -0.99803 | 0.020556 | 0.020556 | -2.40862 | Down | high mobility group nucleosome binding domain 1 pseudogene 37 |
| WDR54 | -0.50089 | 0.019586 | 0.019586 | -2.42876 | Down | WD repeat domain 54 |
| GLTPD2 | -0.64725 | 0.024625 | 0.024625 | -2.33247 | Down | glycolipid transfer protein domain containing 2 |
| AGT | -0.6792 | 0.022722 | 0.022722 | -2.36655 | Down | angiotensinogen |
| CFTR | -0.50874 | 0.013227 | 0.013227 | -2.58914 | Down | CF transmembrane conductance regulator |
| ENTPD8 | -0.95426 | 0.024739 | 0.024739 | -2.33051 | Down | ectonucleoside triphosphate diphosphohydrolase 8 |
| CTSV | -0.5691 | 0.018821 | 0.018821 | -2.4453 | Down | cathepsin V |
| PRDX2 | -0.39558 | 0.017233 | 0.017233 | -2.48167 | Down | peroxiredoxin 2 |
| CLDN10 | -0.72557 | 0.020262 | 0.020262 | -2.41462 | Down | claudin 10 |
| RAD51B | -0.4762 | 0.024911 | 0.024911 | -2.32756 | Down | RAD51 paralog B |
| USH1C | -0.56735 | 0.021763 | 0.021763 | -2.38472 | Down | USH1 protein network component harmonin |
| BTD | -0.39756 | 0.023376 | 0.023376 | -2.35456 | Down | biotinidase |
| SRP9 | -0.39062 | 0.015471 | 0.015471 | -2.52577 | Down | signal recognition particle 9 |
| CASR | -0.47076 | 0.022072 | 0.022072 | -2.37877 | Down | calcium sensing receptor |
| KRT14 | -0.49366 | 0.026133 | 0.026133 | -2.30712 | Down | keratin 14 |
| PROM1 | -0.38007 | 0.018214 | 0.018214 | -2.45885 | Down | prominin 1 |
| MCM3AP-AS1 | -0.43448 | 0.024968 | 0.024968 | -2.3266 | Down | MCM3AP antisense RNA 1 |
| SELENOP | -0.76553 | 0.026822 | 0.026822 | -2.29598 | Down | selenoprotein P |
| ARL3 | -0.54734 | 0.021613 | 0.021613 | -2.38761 | Down | ADP ribosylation factor like GTPase 3 |
| VWA2 | -0.58649 | 0.024577 | 0.024577 | -2.33331 | Down | von Willebrand factor A domain containing 2 |
| BDH2 | -0.57138 | 0.025317 | 0.025317 | -2.32068 | Down | 3-hydroxybutyrate dehydrogenase 2 |
| C2orf81 | -0.53116 | 0.02751 | 0.02751 | -2.28509 | Down | chromosome 2 open reading frame 81 |
| UGT2A3 | -0.95168 | 0.027478 | 0.027478 | -2.28559 | Down | UDP glucuronosyltransferase family 2 member A3 |
| HOXA13 | -0.62887 | 0.027794 | 0.027794 | -2.28066 | Down | homeobox A13 |
| NEURL1B | -0.92354 | 0.026681 | 0.026681 | -2.29822 | Down | neuralized E3 ubiquitin protein ligase 1B |
| BPIFB1 | -0.6748 | 0.027931 | 0.027931 | -2.27855 | Down | BPI fold containing family B member 1 |
| IDH1-AS1 | -1.11143 | 0.02736 | 0.02736 | -2.28743 | Down | IDH1 antisense RNA 1 |
| ACBD7 | -0.41044 | 0.025703 | 0.025703 | -2.31422 | Down | acyl-CoA binding domain containing 7 |
| CNTNAP3B | -0.43225 | 0.027004 | 0.027004 | -2.29306 | Down | contactin associated protein like 3B |
| BRI3BP | -0.42394 | 0.017079 | 0.017079 | -2.48536 | Down | BRI3 binding protein |
| LINC02614 | -0.62293 | 0.028476 | 0.028476 | -2.2702 | Down | long intergenic non-protein coding RNA 2614 |
| RAB26 | -0.77343 | 0.028123 | 0.028123 | -2.27559 | Down | RAB26, member RAS oncogene family |
| HHLA2 | -0.78119 | 0.028325 | 0.028325 | -2.27251 | Down | HERV-H LTR-associating 2 |
| HEBP1 | -0.43462 | 0.024886 | 0.024886 | -2.32799 | Down | heme binding protein 1 |
| LRP3 | -0.91184 | 0.026645 | 0.026645 | -2.29881 | Down | LDL receptor related protein 3 |
| SYNGR1 | -0.42523 | 0.023971 | 0.023971 | -2.34392 | Down | synaptogyrin 1 |
| LINC00674 | -0.45812 | 0.029015 | 0.029015 | -2.26211 | Down | long intergenic non-protein coding RNA 674 |
| TSTD1 | -0.68327 | 0.02279 | 0.02279 | -2.36528 | Down | thiosulfate sulfurtransferase like domain containing 1 |
| DHFRP1 | -0.45653 | 0.027573 | 0.027573 | -2.2841 | Down | dihydrofolatereductasepseudogene 1 |
| SYT5 | -0.87394 | 0.029569 | 0.029569 | -2.25391 | Down | synaptotagmin 5 |
| DTYMK | -0.40092 | 0.02003 | 0.02003 | -2.41943 | Down | deoxythymidylate kinase |
| PLA2R1 | -0.46134 | 0.027744 | 0.027744 | -2.28145 | Down | phospholipase A2 receptor 1 |
| TBC1D3B | -1.36297 | 0.027582 | 0.027582 | -2.28397 | Down | TBC1 domain family member 3B |
| SEMA4G | -0.40369 | 0.0259 | 0.0259 | -2.31095 | Down | semaphorin 4G |
| ACSF2 | -0.44736 | 0.021153 | 0.021153 | -2.39664 | Down | acyl-CoA synthetase family member 2 |
| HAGLROS | -0.60327 | 0.031068 | 0.031068 | -2.23241 | Down | HAGLR opposite strand lncRNA |
| HNRNPA1P10 | -0.9639 | 0.026827 | 0.026827 | -2.29589 | Down | heterogeneous nuclear ribonucleoprotein A1 pseudogene 10 |
| STRA6 | -1.1921 | 0.030582 | 0.030582 | -2.23927 | Down | stimulated by retinoic acid 6 |
| SNAP25 | -0.63923 | 0.031465 | 0.031465 | -2.22687 | Down | synaptosome associated protein 25 |
| SRPX | -0.58717 | 0.031004 | 0.031004 | -2.2333 | Down | sushi repeat containing protein X-linked |
| LINC01088 | -0.91401 | 0.026947 | 0.026947 | -2.29397 | Down | long intergenic non-protein coding RNA 1088 |
| LRRC26 | -0.75526 | 0.029946 | 0.029946 | -2.24841 | Down | leucine rich repeat containing 26 |
| LHPP | -0.48928 | 0.029307 | 0.029307 | -2.25776 | Down | phospholysinephosphohistidine inorganic pyrophosphate phosphatase |
| PCDHB12 | -0.39614 | 0.031053 | 0.031053 | -2.23262 | Down | protocadherin beta 12 |
| CRISP3 | -0.826 | 0.032084 | 0.032084 | -2.21835 | Down | cysteine rich secretory protein 3 |
| UBL7-AS1 | -0.37631 | 0.031851 | 0.031851 | -2.22154 | Down | UBL7 antisense RNA 1 (head to head) |
| TMEM121 | -0.82997 | 0.032905 | 0.032905 | -2.20729 | Down | transmembrane protein 121 |
| COX16 | -0.4738 | 0.023986 | 0.023986 | -2.34365 | Down | cytochrome c oxidase assembly factor COX16 |
| CAB39L | -0.38299 | 0.030748 | 0.030748 | -2.23692 | Down | calcium binding protein 39 like |
| SLPI | -0.46993 | 0.024416 | 0.024416 | -2.3361 | Down | secretory leukocyte peptidase inhibitor |
| SAMD13 | -0.67194 | 0.033129 | 0.033129 | -2.2043 | Down | sterile alpha motif domain containing 13 |
| FMO5 | -0.58649 | 0.034026 | 0.034026 | -2.19256 | Down | flavin containing dimethylanilinemonoxygenase 5 |
| ACOT13 | -0.40429 | 0.021379 | 0.021379 | -2.39218 | Down | acyl-CoA thioesterase 13 |
| ATP5IF1 | -0.4335 | 0.02333 | 0.02333 | -2.3554 | Down | ATP synthase inhibitory factor subunit 1 |
| LRRC66 | -0.97614 | 0.030714 | 0.030714 | -2.2374 | Down | leucine rich repeat containing 66 |
| MIR302CHG | -1.06942 | 0.029988 | 0.029988 | -2.2478 | Down | miR-302/367 cluster host gene |
| RPS23P1 | -0.71376 | 0.032422 | 0.032422 | -2.21376 | Down | ribosomal protein S23 pseudogene 1 |
| EML6 | -0.61006 | 0.035838 | 0.035838 | -2.16963 | Down | EMAP like 6 |
| REX1BD | -0.41782 | 0.027441 | 0.027441 | -2.28616 | Down | required for excision 1-B domain containing |
| KCNIP3 | -0.85669 | 0.035692 | 0.035692 | -2.17145 | Down | potassium voltage-gated channel interacting protein 3 |
| CP | -0.80531 | 0.036806 | 0.036806 | -2.15781 | Down | ceruloplasmin |
| SERHL2 | -0.8673 | 0.03571 | 0.03571 | -2.17122 | Down | serine hydrolase like 2 |
| CNIH4 | -0.45142 | 0.023086 | 0.023086 | -2.35984 | Down | cornichon family AMPA receptor auxiliary protein 4 |
| SUMF1 | -0.56581 | 0.0255 | 0.0255 | -2.3176 | Down | sulfatase modifying factor 1 |
| ALG1L | -0.64935 | 0.037374 | 0.037374 | -2.151 | Down | ALG1 chitobiosyldiphosphodolichol beta-mannosyltransferase like |
| TF | -0.92745 | 0.037547 | 0.037547 | -2.14894 | Down | transferrin |
| SLC25A21 | -0.60073 | 0.036986 | 0.036986 | -2.15563 | Down | solute carrier family 25 member 21 |
| SMARCA2 | -0.39335 | 0.026967 | 0.026967 | -2.29366 | Down | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 |
| CD1D | -0.89907 | 0.037042 | 0.037042 | -2.15497 | Down | CD1d molecule |
| ATRAID | -0.43058 | 0.02409 | 0.02409 | -2.34181 | Down | all-trans retinoic acid induced differentiation factor |
| MRPL3P1 | -0.40656 | 0.036626 | 0.036626 | -2.15999 | Down | mitochondrial ribosomal protein L3 pseudogene 1 |
| SERPINA5 | -0.49498 | 0.02753 | 0.02753 | -2.28477 | Down | serpin family A member 5 |
| TUBB4A | -0.51838 | 0.036336 | 0.036336 | -2.16352 | Down | tubulin beta 4A class IVa |
| UBBP4 | -0.85535 | 0.038969 | 0.038969 | -2.13234 | Down | ubiquitin B pseudogene 4 |
| CDC42EP5 | -0.4214 | 0.033788 | 0.033788 | -2.19564 | Down | CDC42 effector protein 5 |
| PCYOX1 | -0.42124 | 0.025382 | 0.025382 | -2.31958 | Down | prenylcysteine oxidase 1 |
| TRAF3IP2-AS1 | -0.47913 | 0.038122 | 0.038122 | -2.14216 | Down | TRAF3IP2 antisense RNA 1 |
| ENDOG | -0.40418 | 0.031482 | 0.031482 | -2.22663 | Down | endonuclease G |
| IL6STP1 | -0.87497 | 0.03963 | 0.03963 | -2.1248 | Down | interleukin 6 signal transducer pseudogene 1 |
| TFRC | -0.42836 | 0.016049 | 0.016049 | -2.51082 | Down | transferrin receptor |
| SATB1-AS1 | -0.58765 | 0.041362 | 0.041362 | -2.10558 | Down | SATB1 antisense RNA 1 |
| LEFTY1 | -0.8092 | 0.039291 | 0.039291 | -2.12865 | Down | left-right determination factor 1 |
| PPA2 | -0.4066 | 0.025658 | 0.025658 | -2.31496 | Down | inorganic pyrophosphatase 2 |
| ROS1 | -0.63081 | 0.036999 | 0.036999 | -2.15548 | Down | ROS proto-oncogene 1, receptor tyrosine kinase |
| CYP4F3 | -0.38185 | 0.036494 | 0.036494 | -2.16159 | Down | cytochrome P450 family 4 subfamily F member 3 |
| HELLPAR | -0.91996 | 0.038353 | 0.038353 | -2.13947 | Down | HELLP associated long non-coding RNA |
| TPGS1 | -0.39445 | 0.034648 | 0.034648 | -2.18456 | Down | tubulin polyglutamylase complex subunit 1 |
| CSPG5 | -0.40082 | 0.036829 | 0.036829 | -2.15753 | Down | chondroitin sulfate proteoglycan 5 |
| NACA2 | -0.46287 | 0.03896 | 0.03896 | -2.13244 | Down | nascent polypeptide associated complex subunit alpha 2 |
| TCTEX1D2 | -0.47264 | 0.036612 | 0.036612 | -2.16015 | Down | Tctex1 domain containing 2 |
| MPC2 | -0.53298 | 0.025348 | 0.025348 | -2.32016 | Down | mitochondrial pyruvate carrier 2 |
| CUTC | -0.45828 | 0.035413 | 0.035413 | -2.17492 | Down | cutC copper transporter |
| ADH6 | -1.01999 | 0.042081 | 0.042081 | -2.0978 | Down | alcohol dehydrogenase 6 (class V) |
| KCNAB1 | -0.66091 | 0.043852 | 0.043852 | -2.07913 | Down | potassium voltage-gated channel subfamily A member regulatory beta subunit 1 |
| LINC00992 | -0.48054 | 0.037478 | 0.037478 | -2.14976 | Down | long intergenic non-protein coding RNA 992 |
| TEX15 | -0.77015 | 0.038871 | 0.038871 | -2.13347 | Down | testis expressed 15, meiosis and synapsis associated |
| SLC39A10 | -0.49705 | 0.025646 | 0.025646 | -2.31517 | Down | solute carrier family 39 member 10 |
| FLYWCH2 | -0.48889 | 0.037002 | 0.037002 | -2.15545 | Down | FLYWCH family member 2 |
| HOXA2 | -0.60382 | 0.044354 | 0.044354 | -2.07396 | Down | homeobox A2 |
| POLR2J2 | -0.78702 | 0.042476 | 0.042476 | -2.09358 | Down | RNA polymerase II subunit J2 |
| LCT | -1.02104 | 0.044215 | 0.044215 | -2.07539 | Down | lactase |
| PRR15L | -0.37843 | 0.033995 | 0.033995 | -2.19296 | Down | proline rich 15 like |
| LINC02280 | -0.77481 | 0.044602 | 0.044602 | -2.07142 | Down | long intergenic non-protein coding RNA 2280 |
| ERFE | -0.55162 | 0.044822 | 0.044822 | -2.06919 | Down | erythroferrone |
| PIN1 | -0.37801 | 0.029635 | 0.029635 | -2.25294 | Down | peptidylprolylcis/trans isomerase, NIMA-interacting 1 |
| UCP2 | -0.52664 | 0.042065 | 0.042065 | -2.09798 | Down | uncoupling protein 2 |
| NR1H4 | -0.54069 | 0.04192 | 0.04192 | -2.09953 | Down | nuclear receptor subfamily 1 group H member 4 |
| SPATA17 | -0.60205 | 0.046598 | 0.046598 | -2.05145 | Down | spermatogenesis associated 17 |
| CYP27A1 | -0.45434 | 0.042177 | 0.042177 | -2.09677 | Down | cytochrome P450 family 27 subfamily A member 1 |
| GSTA4 | -0.75811 | 0.047635 | 0.047635 | -2.04137 | Down | glutathione S-transferase alpha 4 |
| LRRC24 | -0.489 | 0.04585 | 0.04585 | -2.05885 | Down | leucine rich repeat containing 24 |
| C21orf62-AS1 | -0.68584 | 0.046413 | 0.046413 | -2.05328 | Down | C21orf62 antisense RNA 1 |
| COX14 | -0.52304 | 0.036246 | 0.036246 | -2.16461 | Down | cytochrome c oxidase assembly factor COX14 |
| ENTPD3 | -0.49339 | 0.044557 | 0.044557 | -2.07189 | Down | ectonucleoside triphosphate diphosphohydrolase 3 |
| ACO1 | -0.66228 | 0.030729 | 0.030729 | -2.23718 | Down | aconitase 1 |
| CEACAM7 | -1.00983 | 0.046012 | 0.046012 | -2.05724 | Down | CEA cell adhesion molecule 7 |
| TCEA3 | -0.47798 | 0.044834 | 0.044834 | -2.06907 | Down | transcription elongation factor A3 |
| ROM1 | -0.51692 | 0.046146 | 0.046146 | -2.05591 | Down | retinal outer segment membrane protein 1 |
| PNMT | -0.76002 | 0.044521 | 0.044521 | -2.07225 | Down | phenylethanolamine N-methyltransferase |
| ECI2 | -0.48523 | 0.036372 | 0.036372 | -2.16308 | Down | enoyl-CoA delta isomerase 2 |
| NLGN1 | -0.62362 | 0.048973 | 0.048973 | -2.02864 | Down | neuroligin 1 |
| ADGRB3 | -1.04491 | 0.047637 | 0.047637 | -2.04135 | Down | adhesion G protein-coupled receptor B3 |
| KY | -1.21803 | 0.04789 | 0.04789 | -2.03892 | Down | kyphoscoliosis peptidase |
| RAMP1 | -0.70566 | 0.042311 | 0.042311 | -2.09534 | Down | receptor activity modifying protein 1 |
| SNTA1 | -0.39759 | 0.039898 | 0.039898 | -2.12179 | Down | syntrophin alpha 1 |
| LINP1 | -0.4422 | 0.034289 | 0.034289 | -2.18916 | Down | lncRNA in non-homologous end joining pathway 1 |
| TMEM61 | -0.86021 | 0.049938 | 0.049938 | -2.01964 | Down | transmembrane protein 61 |
| LEMD1 | -1.18622 | 0.048602 | 0.048602 | -2.03213 | Down | LEM domain containing 1 |
| NDUFA2 | -0.59611 | 0.029824 | 0.029824 | -2.25019 | Down | NADH:ubiquinoneoxidoreductase subunit A2 |
| ETFDH | -0.39296 | 0.039509 | 0.039509 | -2.12617 | Down | electron transfer flavoprotein dehydrogenase |
| HNRNPA1P55 | -0.71507 | 0.049042 | 0.049042 | -2.02799 | Down | heterogeneous nuclear ribonucleoprotein A1 pseudogene 55 |
| DNAAF4 | -0.52146 | 0.047654 | 0.047654 | -2.04118 | Down | dynein axonemal assembly factor 4 |
| DNPH1 | -0.51715 | 0.032033 | 0.032033 | -2.21905 | Down | 2'-deoxynucleoside 5'-phosphate N-hydrolase 1 |
| METTL7B | -0.45392 | 0.036093 | 0.036093 | -2.16649 | Down | methyltransferase like 7B |
| RPL39L | -0.44192 | 0.038025 | 0.038025 | -2.1433 | Down | ribosomal protein L39 like |
| C2orf74 | -0.42087 | 0.042728 | 0.042728 | -2.09091 | Down | chromosome 2 open reading frame 74 |
| ARHGDIB | -0.50007 | 0.04157 | 0.04157 | -2.10331 | Down | Rho GDP dissociation inhibitor beta |
| ORAI3 | -0.37956 | 0.045819 | 0.045819 | -2.05915 | Down | ORAI calcium release-activated calcium modulator 3 |
| MOGAT1 | -0.51635 | 0.048438 | 0.048438 | -2.0337 | Down | monoacylglycerol O-acyltransferase 1 |
| SYNJ2BP-COX16 | -0.40553 | 0.035524 | 0.035524 | -2.17354 | Down | SYNJ2BP-COX16 readthrough |
| DNAAF3 | -0.50277 | 0.04716 | 0.04716 | -2.04596 | Down | dynein axonemal assembly factor 3 |
| CYP2U1 | -0.40096 | 0.046549 | 0.046549 | -2.05193 | Down | cytochrome P450 family 2 subfamily U member 1 |
| COMMD8 | -0.38216 | 0.039433 | 0.039433 | -2.12704 | Down | COMM domain containing 8 |
| REEP6 | -0.48009 | 0.044376 | 0.044376 | -2.07373 | Down | receptor accessory protein 6 |
| NDUFS7 | -0.41664 | 0.036942 | 0.036942 | -2.15617 | Down | NADH:ubiquinoneoxidoreductase core subunit S7 |
| NEK2 | -0.47265 | 0.039647 | 0.039647 | -2.12461 | Down | NIMA related kinase 2 |
| NTHL1 | -0.37869 | 0.040831 | 0.040831 | -2.1114 | Down | nth like DNA glycosylase 1 |
| AURKA | -0.39942 | 0.03637 | 0.03637 | -2.1631 | Down | aurora kinase A |
| DEPDC1 | -0.37937 | 0.039012 | 0.039012 | -2.13185 | Down | DEP domain containing 1 |
| ACSM3 | -0.4022 | 0.046823 | 0.046823 | -2.04925 | Down | acyl-CoA synthetase medium chain family member 3 |
| CAT | -0.40749 | 0.035942 | 0.035942 | -2.16835 | Down | catalase |
| FKBP3 | -0.38463 | 0.035718 | 0.035718 | -2.17112 | Down | FKBP prolylisomerase 3 |
| MACROD1 | -0.43096 | 0.043535 | 0.043535 | -2.08242 | Down | mono-ADP ribosylhydrolase 1 |
| CARHSP1 | -0.43046 | 0.03964 | 0.03964 | -2.12469 | Down | calcium regulated heat stable protein 1 |
| STC1 | -0.50342 | 0.048514 | 0.048514 | -2.03297 | Down | stanniocalcin 1 |
| BIRC5 | -0.42876 | 0.043263 | 0.043263 | -2.08526 | Down | baculoviral IAP repeat containing 5 |
| HMGN3 | -0.37648 | 0.040553 | 0.040553 | -2.11447 | Down | high mobility group nucleosomal binding domain 3 |
| HSPE1 | -0.42594 | 0.035991 | 0.035991 | -2.16774 | Down | heat shock protein family E (Hsp10) member 1 |
| DPY30 | -0.39353 | 0.045246 | 0.045246 | -2.0649 | Down | dpy-30 histone methyltransferase complex regulatory subunit |
| ODAM | -0.39798 | 0.043536 | 0.043536 | -2.08241 | Down | odontogenic, ameloblast associated |
| UPK1B | -0.543 | 0.049733 | 0.049733 | -2.02155 | Down | uroplakin 1B |
| PGK1 | -0.44301 | 0.02891 | 0.02891 | -2.26367 | Down | phosphoglycerate kinase 1 |
| LSM3 | -0.41046 | 0.04787 | 0.04787 | -2.03911 | Down | LSM3 homolog, U6 small nuclear RNA and mRNA degradation associated |
| TOP2A | -0.45633 | 0.032147 | 0.032147 | -2.21749 | Down | DNA topoisomerase II alpha |
| CYBA | -0.49932 | 0.046118 | 0.046118 | -2.05618 | Down | cytochrome b-245 alpha chain |

**Table 2** The enriched pathway terms of the up regulated differentially expressed genes

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **BIOCYC** | | | | | | | | | |
| **Pathway ID** | **Pathway Name** | | | **P-value** | **FDR B&H** | **FDR B&Y** | **Bonferroni** | **Gene Count** | **Gene** |
| 907943 | superpathway of steroid hormone biosynthesis | | | 2.34E-02 | 1.98E-01 | 7.11E-01 | 4.68E-01 | 2 | HSD17B3,CYP21A2 |
| 782386 | aspirin triggered resolvin E biosynthesis | | | 3.99E-02 | 1.98E-01 | 7.11E-01 | 7.99E-01 | 1 | PTGS2 |
| 142304 | UDP-N-acetyl-D-glucosamine biosynthesis II | | | 9.68E-02 | 2.42E-01 | 8.71E-01 | 1.00E+00 | 1 | GFPT2 |
| 1208955 | protein ubiquitylation | | | 1.15E-01 | 2.56E-01 | 9.22E-01 | 1.00E+00 | 2 | UBE2L6,UBA7 |
| 142279 | adenosine nucleotides degradation | | | 1.50E-01 | 2.73E-01 | 9.84E-01 | 1.00E+00 | 1 | NT5C3A |
| 782393 | CMP phosphorylation | | | 1.84E-01 | 2.84E-01 | 1.00E+00 | 1.00E+00 | 1 | CMPK2 |
| 142242 | triacylglycerol biosynthesis | | | 3.99E-01 | 4.20E-01 | 1.00E+00 | 1.00E+00 | 1 | MOGAT3 |
| 142419 | phospholipases | | | 4.46E-01 | 4.46E-01 | 1.00E+00 | 1.00E+00 | 1 | PLA2G4C |
| 83051 | Cytokine-cytokine receptor interaction | | | 5.49E-17 | 1.12E-14 | 6.61E-14 | 1.12E-14 | 33 | TNFRSF4,CXCL9,CCL2,CCL20,CXCL11,CX3CL1,FLT3,FLT3LG,IFNB1,CSF2,TNFSF13B,IL1A,TSLP,IL6,IL7,IL7R,CXCL8,IL11,IL12A,IL15RA,TNFSF10,INHBA,CXCL10,IL17C,IL22RA1,BMP2,CXCL2,CXCL3,LTB,TNF,IFNL2,IFNL3,IFNL1 |
| 812256 | TNF signaling pathway | | | 3.49E-14 | 3.56E-12 | 2.10E-11 | 7.13E-12 | 20 | TRAF1,CCL2,CCL20,CX3CL1,MAP3K8,FOS,ICAM1,CREB5,CSF2,IL6,CXCL10,BCL3,PTGS2,JUN,NFKBIA,SOCS3,CXCL2,CXCL3,TNF,TNFAIP3 |
| 217173 | Influenza A | | | 7.40E-14 | 5.04E-12 | 2.97E-11 | 1.51E-11 | 24 | DDX58,CCL2,PML,ICAM1,IFNB1,RSAD2,IL1A,IL6,CXCL8,IL12A,TNFSF10,CXCL10,TICAM1,IRF7,STAT2,JAK2,IFIH1,JUN,NFKBIA,SOCS3,OAS1,OAS2,NLRP3,TNF |
| 377873 | Herpes simplex infection | | | 1.97E-11 | 1.01E-09 | 5.93E-09 | 4.02E-09 | 22 | TRAF1,DDX58,HLA-F,CCL2,PML,FOS,IFIT1,IFNB1,IL6,IL12A,TICAM1,IRF7,STAT2,JAK2,IFIH1,JUN,NFKBIA,TAP1,SOCS3,OAS1,OAS2,TNF |
| 1474301 | IL-17 signaling pathway | | | 4.41E-11 | 1.80E-09 | 1.06E-08 | 9.00E-09 | 16 | CCL2,CCL20,FOS,FOSB,CSF2,IL6,CXCL8,CXCL10,IL17C,PTGS2,JUN,NFKBIA,CXCL2,CXCL3,TNF,TNFAIP3 |
| 122191 | NOD-like receptor signaling pathway | | | 1.42E-09 | 4.83E-08 | 2.85E-07 | 2.90E-07 | 19 | CCL2,IFI16,IFNB1,TXNIP,IL6,CXCL8,TICAM1,GBP1,IRF7,STAT2,JUN,NFKBIA,OAS1,OAS2,CXCL2,CXCL3,NLRP3,TNF,TNFAIP3 |
| 83077 | Jak-STAT signaling pathway | | | 1.57E-08 | 3.21E-07 | 1.89E-06 | 3.21E-06 | 17 | IFNB1,CSF2,SOCS1,TSLP,IL6,IL7,IL7R,IL11,IL12A,IL15RA,IL22RA1,STAT2,JAK2,SOCS3,IFNL2,IFNL3,IFNL1 |
| 213306 | Measles | | | 7.85E-08 | 1.23E-06 | 7.27E-06 | 1.60E-05 | 15 | DDX58,IFNB1,IL1A,BBC3,IL6,IL12A,TNFSF10,IRF7,STAT2,JAK2,IFIH1,NFKBIA,OAS1,OAS2,TNFAIP3 |
| 83048 | MAPK signalingpathway | | | 2.07E-04 | 1.84E-03 | 1.08E-02 | 4.23E-02 | 15 | RASGRP3,MAP3K8,FOS,PLA2G4C,IL1A,GADD45B,FGF18,JUN,FGF19,DUSP1,DUSP8,RELB,RASGRP1,TNF,DUSP10 |
| 373901 | HTLV-I infection | | | 2.16E-04 | 1.84E-03 | 1.08E-02 | 4.41E-02 | 15 | HLA-F,ETS2,FOS,ICAM1,ZFP36,CSF2,ATF3,IL6,IL15RA,JUN,NFKBIA,RELB,EGR1,EGR2,TNF |
| 1017634 | cAMPsignaling pathway | | | 6.89E-03 | 3.70E-02 | 2.18E-01 | 1.00E+00 | 10 | PDE4B,ADRB2,FOS,CREB5,SSTR2,JUN,NFKBIA,GRIN3B,DRD1,GRIA2 |
| **Pathway Interaction Database** | | | | | | | | | |
| 137993 | Calcineurin-regulated NFAT-dependent transcription in lymphocytes | | | 2.10E-09 | 2.25E-07 | 1.18E-06 | 2.25E-07 | 11 | FOS,CSF2,CXCL8,GATA3,PTGS2,JUN,EGR1,EGR2,EGR3,EGR4,TNF |
| 138006 | ATF-2 transcription factor network | | | 1.22E-07 | 6.54E-06 | 3.44E-05 | 1.31E-05 | 10 | ACHE,FOS,ATF3,IL6,CXCL8,JUN,DUSP1,DUSP8,SOCS3,DUSP10 |
| 138000 | IL23-mediated signaling events | | | 7.65E-06 | 2.73E-04 | 1.43E-03 | 8.18E-04 | 7 | CXCL9,CCL2,IL6,JAK2,NFKBIA,SOCS3,TNF |
| 137929 | IL27-mediated signaling events | | | 1.04E-05 | 2.78E-04 | 1.46E-03 | 1.11E-03 | 6 | IL6,IL12A,GATA3,STAT2,JAK2,TNF |
| 138014 | Glucocorticoid receptor regulatory network | | | 3.88E-05 | 8.29E-04 | 4.36E-03 | 4.15E-03 | 9 | FOS,ICAM1,CSF2,IL6,CXCL8,GATA3,IRF1,JUN,EGR1 |
| 137932 | IL6-mediated signaling events | | | 2.06E-04 | 3.28E-03 | 1.73E-02 | 2.21E-02 | 6 | FOS,IL6,IRF1,JAK2,JUN,SOCS3 |
| 137922 | IL12-mediated signaling events | | | 2.15E-04 | 3.28E-03 | 1.73E-02 | 2.30E-02 | 7 | HLX,FOS,SOCS1,GADD45B,IL12A,JAK2,RELB |
| 137939 | Direct p53 effectors | | | 3.36E-04 | 4.04E-03 | 2.12E-02 | 3.59E-02 | 10 | CX3CL1,PMAIP1,PML,ATF3,BBC3,BDKRB2,JUN,TAP1,DUSP1,SERPINE1 |
| 137989 | FGF signaling pathway | | | 3.40E-04 | 4.04E-03 | 2.12E-02 | 3.64E-02 | 6 | SPRY2,PLAUR,KLB,FOS,JUN,FGF19 |
| 138018 | Downstream signaling in naive CD8+ T cells | | | 4.78E-04 | 5.12E-03 | 2.69E-02 | 5.12E-02 | 6 | TNFRSF4,FOS,JUN,EGR1,EGR4,TNF |
| **REACTOME** | | | | | | | | | |
| 1269310 | Cytokine Signaling in Immune system | | | 6.11E-35 | 3.85E-32 | 2.70E-31 | 3.85E-32 | 78 | USP18,UBE2L6,DDX58,HLA-F,TRIM22,TNFRSF4,SPTBN5,UBA7,RASGRP3,CCL2,CCL20,TRIM38,PML,KLB,FLT3,FLT3LG,MAP3K8,FOS,ICAM1,IFITM1,SAMHD1,IFITM2,IFI35,IFIT2,IFIT1,IFIT3,TRIM5,IFNB1,MT2A,RSAD2,CSF2,ISG15,TNFSF13B,OASL,SOCS1,XAF1,IL1A,IL6,IL7,IL7R,CXCL8,MX2,IL11,IL12A,IL15RA,CXCL10,IL17C,GATA3,PSMB9,GBP1,IRF1,TRIM21,IRF7,ISG20,IL22RA1,PTGS2,FGF18,STAT2,JAK2,FGF19,DUSP1,DUSP8,SOCS3,PELI1,OAS1,OAS2,RELB,CXCL2,LGALS9,RASGRP1,EGR1,LTB,TNF,DUSP10,HERC5,IFNL2,IFNL3,IFNL1 |
| 1269311 | Interferon Signaling | | | 3.09E-25 | 9.72E-23 | 6.82E-22 | 1.94E-22 | 37 | USP18,UBE2L6,DDX58,HLA-F,TRIM22,UBA7,TRIM38,PML,ICAM1,IFITM1,SAMHD1,IFITM2,IFI35,IFIT2,IFIT1,IFIT3,TRIM5,IFNB1,MT2A,RSAD2,ISG15,OASL,SOCS1,XAF1,MX2,GBP1,IRF1,TRIM21,IRF7,ISG20,STAT2,JAK2,SOCS3,OAS1,OAS2,EGR1,HERC5 |
| 1269312 | Interferon alpha/beta signaling | | | 6.94E-24 | 1.46E-21 | 1.02E-20 | 4.36E-21 | 24 | USP18,HLA-F,IFITM1,SAMHD1,IFITM2,IFI35,IFIT2,IFIT1,IFIT3,IFNB1,RSAD2,ISG15,OASL,SOCS1,XAF1,MX2,IRF1,IRF7,ISG20,STAT2,SOCS3,OAS1,OAS2,EGR1 |
| 1269318 | Signaling by Interleukins | | | 8.36E-14 | 1.32E-11 | 9.23E-11 | 5.26E-11 | 41 | SPTBN5,RASGRP3,CCL2,CCL20,KLB,FLT3,FLT3LG,MAP3K8,FOS,ICAM1,CSF2,SOCS1,IL1A,IL6,IL7,IL7R,CXCL8,IL11,IL12A,IL15RA,CXCL10,IL17C,GATA3,PSMB9,IL22RA1,PTGS2,FGF18,JAK2,FGF19,DUSP1,DUSP8,SOCS3,PELI1,CXCL2,LGALS9,RASGRP1,TNF,DUSP10,IFNL2,IFNL3,IFNL1 |
| 1269314 | Interferon gamma signaling | | | 4.61E-12 | 5.80E-10 | 4.07E-09 | 2.90E-09 | 17 | HLA-F,TRIM22,TRIM38,PML,ICAM1,TRIM5,MT2A,OASL,SOCS1,GBP1,IRF1,TRIM21,IRF7,JAK2,SOCS3,OAS1,OAS2 |
| 1269259 | RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways | | | 1.15E-09 | 1.04E-07 | 7.28E-07 | 7.26E-07 | 14 | UBE2L6,DDX58,UBA7,NLRC5,DHX58,IFNB1,ISG15,CYLD,IRF1,IRF7,IFIH1,NFKBIA,TNFAIP3,HERC5 |
| 1269545 | Class A/1 (Rhodopsin-like receptors) | | | 2.85E-05 | 1.50E-03 | 1.05E-02 | 1.80E-02 | 19 | ADRB2,CXCL9,CCL20,CXCL11,CX3CL1,ACKR4,CXCL8,CXCL10,SSTR2,PTGER4,BDKRB2,NPFFR2,DRD1,GPER1,CCRL2,CXCL2,CXCL3,S1PR3,HCRTR1 |
| 1269203 | Innate Immune System | | | 6.17E-05 | 2.98E-03 | 2.10E-02 | 3.88E-02 | 47 | UBE2L6,DDX58,PGLYRP2,TLR6,PLAC8,SPTBN5,UBA7,RASGRP3,NLRC5,PLAUR,KLB,DHX58,MAP3K8,FOS,IFI16,IFNB1,TXNIP,CSF2,ISG15,SOCS1,CYLD,TICAM1,PSMB9,IRF1,TRIM21,IRF7,FGF18,JAK2,IFIH1,JUN,CLEC4A,PTX3,NFKBIA,C4A,C4B,FGF19,DUSP1,DUSP8,PELI1,RELB,RAB44,NLRP3,MMP25,RASGRP1,DUSP10,TNFAIP3,HERC5 |
| 1269544 | GPCR ligand binding | | | 3.59E-04 | 1.13E-02 | 7.92E-02 | 2.26E-01 | 21 | ADRB2,CXCL9,CCL20,CXCL11,CX3CL1,ACKR4,PTCH2,CXCL8,CXCL10,SSTR2,PTGER4,BDKRB2,NPFFR2,DRD1,GPER1,CCRL2,GRM8,CXCL2,CXCL3,S1PR3,HCRTR1 |
| 1269501 | MAPK family signaling cascades | | | 2.50E-03 | 4.50E-02 | 3.16E-01 | 1.00E+00 | 14 | SPTBN5,RASGRP3,KLB,CSF2,IL6,PSMB9,FGF18,JAK2,JUN,FGF19,DUSP1,DUSP8,RASGRP1,DUSP10 |
| **Gen MAPP** | | | | | | | | | |
| MAP00140 | | C21 Steroid hormone metabolism | | 1.84E-01 | 6.17E-01 | 1.00E+00 | 1.00E+00 | 1 | CYP21A2 |
| MAP00150 | | M Androgen and estrogen metabolism | | 2.93E-01 | 6.17E-01 | 1.00E+00 | 1.00E+00 | 1 | HSD17B3 |
| MAP00020 | | Citrate cycle TCA cycle | | 3.07E-01 | 6.17E-01 | 1.00E+00 | 1.00E+00 | 1 | PCK1 |
| MAP00860 | | Porphyrin and chlorophyll metabolism | | 3.07E-01 | 6.17E-01 | 1.00E+00 | 1.00E+00 | 1 | CPO |
| MAP00590 | | Prostaglandin and leukotriene metabolism | | 3.21E-01 | 6.17E-01 | 1.00E+00 | 1.00E+00 | 1 | PTGS2 |
| MAP00361 | | gamma Hexachlorocyclohexane degradation | | 4.46E-01 | 6.17E-01 | 1.00E+00 | 1.00E+00 | 1 | CYP1A1 |
| MAP00620 | | Pyruvate metabolism | | 4.69E-01 | 6.17E-01 | 1.00E+00 | 1.00E+00 | 1 | PCK1 |
| MAP00230 | | Purine metabolism | | 5.08E-01 | 6.17E-01 | 1.00E+00 | 1.00E+00 | 2 | PDE4B,GMPR |
| MAP00380 | | Tryptophan metabolism | | 6.09E-01 | 6.17E-01 | 1.00E+00 | 1.00E+00 | 1 | CYP1A1 |
| MAP00561 | | Glycerolipid metabolism | | 6.17E-01 | 6.17E-01 | 1.00E+00 | 1.00E+00 | 1 | ACHE |
| **MSigDB C2 BIOCARTA (v6.0)** | | | | | | | | | |
| M5883 | Genes encoding secreted soluble factors | | | 3.08E-10 | 4.78E-08 | 2.69E-07 | 4.78E-08 | 28 | CXCL9,CCL2,CCL20,FST,CXCL11,CX3CL1,FLT3LG,IFNB1,CSF2,TNFSF13B,IL1A,IL6,IL7,CXCL8,IL11,IL12A,TNFSF10,INHBA,CXCL10,IL17C,FGF18,BMP2,FGF19,CXCL2,CXCL3,WIF1,LTB,TNF |
| M6910 | Cytokines and Inflammatory Response | | | 3.36E-09 | 2.60E-07 | 1.46E-06 | 5.21E-07 | 9 | IFNB1,CSF2,IL1A,IL6,IL7,CXCL8,IL11,IL12A,TNF |
| M17406 | Cytokine Network | | | 2.66E-06 | 1.38E-04 | 7.74E-04 | 4.13E-04 | 6 | IFNB1,IL1A,IL6,CXCL8,IL12A,TNF |
| M5298 | Regulation of hematopoiesis by cytokines | | | 8.15E-06 | 2.53E-04 | 1.42E-03 | 1.26E-03 | 5 | CSF2,IL6,IL7,CXCL8,IL11 |
| M3952 | Cells and Molecules involved in local acute inflammatory response | | | 1.62E-05 | 4.20E-04 | 2.36E-03 | 2.52E-03 | 5 | ICAM1,IL1A,IL6,CXCL8,TNF |
| M5885 | Ensemble of genes encoding ECM-associated proteins including ECM-affilaited proteins, ECM regulators and secreted factors | | | 2.03E-05 | 4.50E-04 | 2.53E-03 | 3.15E-03 | 33 | CXCL9,CCL2,C1QTNF1,CCL20,FST,CXCL11,CX3CL1, FLT3LG,IFNB1,CSF2,TNFSF13B,IL1A,IL6,IL7,CXCL8,IL11,IL12A,TNFSF10,INHBA,CXCL10,IL17C,FGF18,BMP2, CLEC4A,FGF19,CXCL2,CXCL3,LGALS9,MMP25,WIF1, SERPINE1,LTB,TNF |
| M5889 | Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins | | | 3.98E-05 | 7.64E-04 | 4.30E-03 | 6.16E-03 | 40 | FBLN2,CXCL9,CCL2,C1QTNF1,CCL20,FST,CXCL11, CX3CL1,COL4A1,COL8A1,FLT3LG,MXRA5,IFNB1,SNED1,CSF2,TNFSF13B,IL1A,IL6,IL7,CXCL8,IL11,IL12A, TNFSF10,INHBA,CXCL10,IL17C,FGF18,BMP2,NTNG2, CLEC4A,FGF19,CXCL2,CXCL3,LGALS9,MMP25,WIF1, SERPINE1,LTB,TNF,OTOG |
| M2579 | Differentiation Pathway in PC12 Cells; this is a specific case of PAC1 Receptor Pathway. | | | 2.67E-04 | 3.18E-03 | 1.79E-02 | 4.13E-02 | 6 | CREB5,JUN,EGR1,EGR2,EGR3,EGR4 |
| M6778 | IL-10 Anti-inflammatory Signaling Pathway | | | 3.12E-04 | 3.46E-03 | 1.94E-02 | 4.84E-02 | 4 | IL1A,IL6,STAT2,TNF |
| M10082 | TNFR2 Signaling Pathway | | | 3.95E-04 | 4.08E-03 | 2.30E-02 | 6.12E-02 | 4 | TRAF1,NFKBIA,DUSP1,TNFAIP3 |
| **Panther DB** | | | | | | | | | |
| P00054 | Toll receptor signaling pathway | | | 6.30E-06 | 3.28E-04 | 1.49E-03 | 3.28E-04 | 8 | TLR6,MAP3K8,IFNB1,TICAM1,PTGS2,JUN,NFKBIA,TNFAIP3 |
| P00036 | Interleukin signaling pathway | | | 9.64E-05 | 2.51E-03 | 1.14E-02 | 5.02E-03 | 9 | FOS,IL1A,IL6,IL7,CXCL8,IL11,IL12A,IL15RA,STAT2 |
| P00006 | Apoptosis signaling pathway | | | 1.05E-03 | 1.82E-02 | 8.24E-02 | 5.44E-02 | 8 | FOS,ATF3,TNFSF10,JUN,NFKBIA,RELB,LTB,TNF |
| P00046 | Oxidative stress response | | | 2.24E-03 | 2.91E-02 | 1.32E-01 | 1.16E-01 | 5 | DUSP26,JUN,DUSP1,DUSP8,DUSP10 |
| P00027 | Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway | | | 7.16E-03 | 7.44E-02 | 3.38E-01 | 3.72E-01 | 7 | RASGRP3,SSTR2,BDKRB2,DRD1,GRM8,RGS16,RASGRP1 |
| P00031 | Inflammation mediated by chemokine and cytokine signaling pathway | | | 1.54E-02 | 1.34E-01 | 6.06E-01 | 8.01E-01 | 9 | ACTA1,CCL2,CCL20,CX3CL1,CXCL8,CXCL10,JAK2,JUN,CCRL2 |
| P00038 | JAK/STAT signaling pathway | | | 4.03E-02 | 2.93E-01 | 1.00E+00 | 1.00E+00 | 2 | SOCS1,JAK2 |
| P00050 | Plasminogen activating cascade | | | 4.51E-02 | 2.93E-01 | 1.00E+00 | 1.00E+00 | 2 | PLAUR,SERPINE1 |
| P00037 | Ionotropic glutamate receptor pathway | | | 6.52E-02 | 3.52E-01 | 1.00E+00 | 1.00E+00 | 3 | STX19,STX11,GRIA2 |
| P02757 | O-antigen biosynthesis | | | 7.83E-02 | 3.52E-01 | 1.00E+00 | 1.00E+00 | 1 | GFPT2 |
| **Pathway Ontology** | | | | | | | | | |
| PW:0000499 | | | Nuclear Factor Kappa B signaling | 1.99E-03 | 7.44E-02 | 3.27E-01 | 8.97E-02 | 3 | NFKBIA,RELB,TNF |
| PW:0000313 | | | c-Jun N-terminal kinases MAPK signaling | 3.31E-03 | 7.44E-02 | 3.27E-01 | 1.49E-01 | 4 | DUSP1,DUSP8,TNF,DUSP10 |
| PW:0000060 | | | long term potentiation | 1.33E-02 | 1.03E-01 | 4.52E-01 | 5.97E-01 | 2 | DRD1,EGR1 |
| PW:0000244 | | | Angiotensin II signaling | 1.64E-02 | 1.03E-01 | 4.52E-01 | 7.37E-01 | 2 | CCL2,JAK2 |
| PW:0000209 | | | JAK-STAT signaling | 2.01E-02 | 1.03E-01 | 4.52E-01 | 9.05E-01 | 3 | STAT2,JAK2,SOCS3 |
| PW:0000356 | | | oxygen homeostasis | 2.06E-02 | 1.03E-01 | 4.52E-01 | 9.26E-01 | 1 | SERPINE1 |
| PW:0000585 | | | orexin/hypocretinsignaling through the orexin/hypocretin receptor 1 | 3.99E-02 | 1.38E-01 | 6.07E-01 | 1.00E+00 | 1 | HCRTR1 |
| PW:0000031 | | | purine metabolic | 5.54E-02 | 1.78E-01 | 7.82E-01 | 1.00E+00 | 3 | PDE2A,PDE4B,GMPR |
| PW:0000104 | | | intrinsic apoptotic | 1.15E-01 | 2.16E-01 | 9.50E-01 | 1.00E+00 | 2 | PMAIP1,BBC3 |
| PW:0000201 | | | canonical Wntsignaling | 6.09E-01 | 6.09E-01 | 1.00E+00 | 1.00E+00 | 1 | WIF1 |
| **SMPDB** | | | | | | | | | |
| SMP00356 | 17-Beta Hydroxysteroid Dehydrogenase III Deficiency | | | 2.06E-02 | 2.61E-01 | 1.00E+00 | 6.79E-01 | 1 | HSD17B3 |
| SMP00373 | Adrenal Hyperplasia Type 3 or Congenital Adrenal Hyperplasia due to 21-hydroxylase Deficiency | | | 2.06E-02 | 2.61E-01 | 1.00E+00 | 6.79E-01 | 1 | CYP21A2 |
| SMP00321 | Intracellular Signalling Through Adenosine Receptor A2b and Adenosine | | | 3.06E-02 | 2.61E-01 | 1.00E+00 | 1.00E+00 | 3 | CXCL8,JUN,NFKBIA |
| SMP00094 | Sulindac Pathway | | | 1.33E-01 | 2.61E-01 | 1.00E+00 | 1.00E+00 | 1 | PTGS2 |
| SMP00320 | Intracellular Signalling Through Adenosine Receptor A2a and Adenosine | | | 1.43E-01 | 2.61E-01 | 1.00E+00 | 1.00E+00 | 2 | JUN,NFKBIA |
| SMP00063 | Tryptophan Metabolism | | | 2.93E-01 | 3.56E-01 | 1.00E+00 | 1.00E+00 | 1 | CYP1A1 |
| SMP00035 | Bile Acid Biosynthesis | | | 2.93E-01 | 3.56E-01 | 1.00E+00 | 1.00E+00 | 1 | CH25H |
| SMP00196 | Leigh Syndrome | | | 3.07E-01 | 3.56E-01 | 1.00E+00 | 1.00E+00 | 1 | PCK1 |
| SMP00025 | Phospholipid Biosynthesis | | | 3.99E-01 | 3.99E-01 | 1.00E+00 | 1.00E+00 | 1 | ACHE |
| SMP00046 | Pyrimidine Metabolism | | | 3.99E-01 | 3.99E-01 | 1.00E+00 | 1.00E+00 | 1 | CMPK2 |

**Table 3** The enriched pathway terms of the down regulated differentially expressed genes

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **BIOCYC** | | | | | | | | |
| **Pathway ID** | **Pathway Name** | | **P-value** | **FDR B&H** | **FDR B&Y** | **Bonferroni** | **Gene Count** | **Gene** |
| 142238 | catecholamine biosynthesis | | 5.58E-04 | 3.89E-02 | 1.97E-01 | 4.85E-02 | 2 | PNMT,DDC |
| 545354 | noradrenaline and adrenaline degradation | | 9.56E-04 | 3.89E-02 | 1.97E-01 | 8.32E-02 | 3 | ADH6,ALDH2,PNMT |
| 142437 | nicotine degradation IV | | 1.34E-03 | 3.89E-02 | 1.97E-01 | 1.17E-01 | 3 | FMO5,UGT1A4,CYP2U1 |
| 545351 | sphingosine and sphingosine-1-phosphate metabolism | | 1.76E-02 | 1.53E-01 | 7.72E-01 | 1.00E+00 | 2 | ASAH1,SGPP1 |
| 142224 | glutathione redox reactions II | | 2.39E-02 | 1.83E-01 | 9.22E-01 | 1.00E+00 | 1 | GSR |
| 782379 | pyrimidine deoxyribonucleotide phosphorylation | | 2.61E-02 | 1.83E-01 | 9.22E-01 | 1.00E+00 | 2 | NME5,DTYMK |
| 142387 | valine degradation | | 3.08E-02 | 1.83E-01 | 9.22E-01 | 1.00E+00 | 2 | ALDH6A1,BCKDHB |
| 545316 | bile acid biosynthesis, neutral pathway | | 3.08E-02 | 1.83E-01 | 9.22E-01 | 1.00E+00 | 2 | SCP2,CYP27A1 |
| 545306 | dolichol and dolichyl phosphate biosynthesis | | 4.62E-02 | 1.83E-01 | 9.22E-01 | 1.00E+00 | 1 | SRD5A3 |
| 142152 | glycine/serine biosynthesis | | 4.62E-02 | 1.83E-01 | 9.22E-01 | 1.00E+00 | 1 | SHMT1 |
| **KEGG** | | | | | | | | |
| 82932 | Ascorbate and aldarate metabolism | | 8.82E-12 | 1.88E-09 | 1.12E-08 | 1.88E-09 | 11 | ALDH2,UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT1A5,UGT1A9,UGT1A4,UGT1A1,UGT1A3,UGT2A3 |
| 82940 | Steroid hormone biosynthesis | | 5.86E-10 | 2.71E-08 | 1.61E-07 | 1.25E-07 | 13 | HSD17B2,UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT1A5,UGT1A9,UGT1A4,UGT1A1,UGT1A3,AKR1C3,SRD5A3,UGT2A3 |
| 83032 | Drug metabolism - cytochrome P450 | | 6.35E-10 | 2.71E-08 | 1.61E-07 | 1.35E-07 | 14 | ADH6,FMO5,UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT1A5,UGT1A9,UGT1A4,UGT1A1,UGT1A3,GSTO2,GSTA4,UGT2A3 |
| 673221 | Chemical carcinogenesis | | 5.62E-09 | 1.50E-07 | 8.89E-07 | 1.20E-06 | 14 | EPHX1,ADH6,UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT1A5,UGT1A9,UGT1A4,UGT1A1,UGT1A3,GSTO2,GSTA4,UGT2A3 |
| 132956 | Metabolic pathways | | 1.27E-08 | 3.00E-07 | 1.78E-06 | 2.70E-06 | 62 | PIGN,RIMKLA,ACO1,MDH1,PGK1,ADH6,FAH,ACSM3,FBP1,HOGA1,SCP2,AK4,ALDH2,PGP,HSD17B2,ALDH6A1,PNMT,UGT1A10,UGT1A8,UGT1A7,DHRS4L2,UGT1A6,UGT1A5,SHMT1,UGT1A9,COX11,UGT1A4,UGT1A1,UGT1A3,CRLS1,PPT1,ASAH1,AKR1C3,ST6GALNAC1,NDUFS7,GALM,SPR,ACSS1,CYP27A1,BDH2,GATM,BCKDHB,NDUFA2,DDC,PHGDH,GGT1,BTD,AKR1B10,PIGK,DTYMK,OAT,GALNT12,LCT,UGT2A3,PAH,POLR2J2,CYP2U1,CYP4F3,ADI1,LTC4S,HADHB,FAHD1 |
| 814926 | Carbon metabolism | | 3.33E-04 | 5.46E-03 | 3.24E-02 | 7.10E-02 | 10 | ACO1,MDH1,PGK1,FBP1,PGP,ALDH6A1,SHMT1,ACSS1,PHGDH,CAT |
| 83075 | Renin-angiotensin system | | 1.82E-03 | 2.59E-02 | 1.54E-01 | 3.88E-01 | 4 | AGT,MME,ACE,ACE2 |
| 82934 | Fatty acid elongation | | 2.51E-03 | 3.34E-02 | 1.99E-01 | 5.35E-01 | 4 | HACD3,PPT1,HACD2,HADHB |
| 552665 | Morphine addiction | | 1.97E-02 | 1.75E-01 | 1.00E+00 | 1.00E+00 | 6 | PDE1A,ADORA1,ARRB1,GNG12,GNG7,GNG11 |
| 99052 | Lysosome | | 2.53E-02 | 1.93E-01 | 1.00E+00 | 1.00E+00 | 7 | SORT1,PPT1,ASAH1,CTSH,CTSV,PSAP,SUMF1 |
| **Pathway Interaction Database** | | | | | | | | |
| 138043 | Signaling mediated by p38-gamma and p38-delta | | 2.61E-02 | 7.67E-01 | 1.00E+00 | 1.00E+00 | 2 | SNTA1,STMN1 |
| 137925 | Aurora A signaling | | 3.51E-02 | 7.67E-01 | 1.00E+00 | 1.00E+00 | 3 | BIRC5,AURKA,OAZ1 |
| 138045 | HIF-1-alpha transcription factor network | | 6.53E-02 | 7.67E-01 | 1.00E+00 | 1.00E+00 | 4 | PGK1,CP,TF,TFRC |
| 137911 | FOXA2 and FOXA3 transcription factor networks | | 8.31E-02 | 7.75E-01 | 1.00E+00 | 1.00E+00 | 3 | TTR,UCP2,TFRC |
| 137912 | Hedgehog signaling events mediated by Gli proteins | | 2.75E-01 | 8.18E-01 | 1.00E+00 | 1.00E+00 | 2 | SHH,SAP30 |
| 137975 | RXR and RAR heterodimerization with other nuclear receptor | | 2.82E-01 | 8.18E-01 | 1.00E+00 | 1.00E+00 | 1 | NR1H4 |
| 138027 | Regulation of Androgen receptor activity | | 3.27E-01 | 8.18E-01 | 1.00E+00 | 1.00E+00 | 2 | SPDEF,SMARCA2 |
| 137927 | Arf1 pathway | | 3.47E-01 | 8.18E-01 | 1.00E+00 | 1.00E+00 | 1 | AP2M1 |
| 138015 | Regulation of cytoplasmic and nuclear SMAD2/3 signaling | | 3.62E-01 | 8.18E-01 | 1.00E+00 | 1.00E+00 | 1 | KPNA2 |
| 138002 | E-cadherin signaling in keratinocytes | | 3.62E-01 | 8.18E-01 | 1.00E+00 | 1.00E+00 | 1 | CASR |
| **REACTOME** | | | | | | | | |
| 1270189 | Biological oxidations | | 1.96E-08 | 7.24E-06 | 5.20E-05 | 1.45E-05 | 22 | EPHX1,ADH6,FDX1,ALDH2,UGT1A8,UGT1A7,UGT1A6,UGT1A5,UGT1A9,UGT1A4,UGT1A1,UGT1A3,ACSS1,CYP27A1,GSTO2,GGT1,NR1H4,GLYATL2,GSTA4,UGT2A3,CYP2U1,CYP4F3 |
| 1270121 | The citric acid (TCA) cycle and respiratory electron transport | | 6.84E-04 | 6.81E-02 | 4.89E-01 | 5.05E-01 | 12 | COX16,PDK1,ETFB,ETFDH,UCP2,SLC25A27,MPC2,COX11,NUBPL,NDUFS7,NDUFA2,COX14 |
| 1268749 | Metabolism of Angiotensinogen to Angiotensins | | 6.91E-04 | 6.81E-02 | 4.89E-01 | 5.10E-01 | 4 | AGT,MME,ACE,ACE2 |
| 1270001 | Metabolism of lipids and lipoproteins | | 7.29E-04 | 6.81E-02 | 4.89E-01 | 5.38E-01 | 34 | FABP6,AP2M1,ACSM3,FDX1,AGT,SCP2,ECI2,HSD17B2,HACD3,UGT1A9,APOE,ACSF2,PLA2R1,CRLS1,PPT1,ASAH1,ACBD7,AKR1C3,PSAP,MOGAT1,ACOT13,CYP27A1,BDH2,GGT1,SGPP1,SUMF1,NR1H4,SRD5A3,HACD2,SLC44A4,CYP2U1,CYP4F3,LTC4S,HADHB |
| 1270127 | Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. | | 7.38E-04 | 6.81E-02 | 4.89E-01 | 5.45E-01 | 10 | COX16,ETFB,ETFDH,UCP2,SLC25A27,COX11,NUBPL,NDUFS7,NDUFA2,COX14 |
| 1270158 | Metabolism of amino acids and derivatives | | 1.02E-03 | 8.40E-02 | 6.03E-01 | 7.56E-01 | 19 | RPL39L,HNMT,FAH,ALDH6A1,PNMT,SHMT1,CRYM,GATM,BCKDHB,PSMD10,DDC,PHGDH,SLC25A21,OAT,OAZ1,GSR,PAH,SERINC5,ADI1 |
| 1270011 | Triglyceride Biosynthesis | | 3.02E-03 | 1.30E-01 | 9.32E-01 | 1.00E+00 | 7 | HACD3,ACSF2,PPT1,ACBD7,MOGAT1,ACOT13,HACD2 |
| 1269624 | Retinoid metabolism and transport | | 3.47E-03 | 1.35E-01 | 9.69E-01 | 1.00E+00 | 5 | TTR,APOE,AKR1C3,AKR1B10,BCO2 |
| 1309221 | Histidine, lysine, phenylalanine, tyrosine, proline and tryptophan catabolism | | 3.83E-03 | 1.41E-01 | 1.00E+00 | 1.00E+00 | 5 | HNMT,FAH,CRYM,SLC25A21,PAH |
| 1268677 | Metabolism of proteins | | 1.72E-01 | 6.24E-01 | 1.00E+00 | 1.00E+00 | 44 | PIGN,CFTR,ETFB,CEACAM7,MAGT1,RPL39L,TTR,TUBB4A,AGT,MME,RAB26,TRAPPC6A,FOLR1,BIRC5,CPM,ST6GALNAC2,ARRB1,IGFBP2,CTSH,SORL1,ST6GALNAC1,MLEC,SPCS2,SRP9,TOMM20,PSMD10,ACE,FFAR4,AURKA,GNG12,TUBA1A,ODAM,SUMF1,RNF128,GNG7,GNG11,CALB1,SRD5A3,PIGK,SEMA5A,GALNT12,ACE2,LYZ,TOP2A |
| **Gen MAPP** | | | | | | | | |
| MAP00120\_ | Bile acid biosynthesis | | 1.82E-03 | 4.54E-02 | 1.97E-01 | 7.84E-02 | 4 | ADH6,ALDH2,CYP27A1,HADHB |
| MAP00280 | Valineleucine and isoleucine degradation | | 2.91E-03 | 4.54E-02 | 1.97E-01 | 1.25E-01 | 4 | ALDH2,ALDH6A1,BCKDHB,HADHB |
| MAP00460 | Cyanoamino acid metabolism | | 3.17E-03 | 4.54E-02 | 1.97E-01 | 1.36E-01 | 2 | SHMT1,GGT1 |
| MAP00350 | Tyrosine metabolism | | 4.96E-03 | 4.86E-02 | 2.11E-01 | 2.13E-01 | 4 | ADH6,FAH,PNMT,DDC |
| MAP00710 | Carbon fixation | | 5.65E-03 | 4.86E-02 | 2.11E-01 | 2.43E-01 | 3 | MDH1,PGK1,FBP1 |
| MAP00590 | Prostaglandin and leukotriene metabolism | | 7.17E-02 | 1.90E-01 | 8.25E-01 | 1.00E+00 | 2 | GGT1,CYP4F3 |
| MAP03020 | RNA polymerase | | 3.31E-01 | 4.19E-01 | 1.00E+00 | 1.00E+00 | 1 | POLR2J2 |
| MAP00220 | Urea cycle and metabolism of amino groups | | 3.31E-01 | 4.19E-01 | 1.00E+00 | 1.00E+00 | 1 | OAT |
| MAP00251 | Glutamate metabolism | | 3.77E-01 | 4.50E-01 | 1.00E+00 | 1.00E+00 | 1 | GSR |
| MAP00910 | Nitrogen metabolism | | 3.92E-01 | 4.55E-01 | 1.00E+00 | 1.00E+00 | 1 | CA12 |
| **MSigDB C2 BIOCARTA (v6.0)** | | | | | | | | |
| M12950 | Angiotensin-converting enzyme 2 regulates heart function | | 3.04E-03 | 1.73E-01 | 8.01E-01 | 1.73E-01 | 3 | AGT,ACE,ACE2 |
| M7239 | Apoptotic DNA fragmentation and tissue homeostasis | | 2.17E-02 | 3.09E-01 | 1.00E+00 | 1.00E+00 | 2 | ENDOG,TOP2A |
| M17370 | Role of Ran in mitotic spindle regulation | | 2.17E-02 | 3.09E-01 | 1.00E+00 | 1.00E+00 | 2 | AURKA,KPNA2 |
| M7772 | fl-arrestins in GPCR Desensitization | | 2.17E-02 | 3.09E-01 | 1.00E+00 | 1.00E+00 | 2 | AP2M1,ARRB1 |
| M3468 | Genes encoding enzymes and their regulators involved in the remodeling of the extracellular matrix | | 5.32E-02 | 5.80E-01 | 1.00E+00 | 1.00E+00 | 10 | SERPINA4,AGT,MMP7,SLPI,CTSH,CTSV,ITIH2,KY,LOX,SERPINA5 |
| M3008 | Genes encoding structural ECM glycoproteins | | 8.93E-02 | 5.80E-01 | 1.00E+00 | 1.00E+00 | 8 | MATN2,CTHRC1,SRPX,VWA1,IGFBP2,SPP1,IGSF10,VWA2 |
| M5880 | Genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins | | 1.06E-01 | 5.80E-01 | 1.00E+00 | 1.00E+00 | 7 | ANXA9,ANXA13,SEMA4G,CSPG5,SEMA3E,SEMA5A,ANXA10 |
| M5889 | Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins | | 1.21E-01 | 5.80E-01 | 1.00E+00 | 1.00E+00 | 30 | MATN2,SERPINA4,AGT,CTHRC1,SRPX,MMP7,ANXA9,ANXA13,SHH,VWA1,SEMA4G,LEFTY1,IGFBP2,CSPG5,PDGFD,SLPI,CTSH,CTSV,SEMA3E,SPP1,ITIH2,IGSF10,VWA2,NRTN,SEMA5A,KY,LOX,FGFBP2,ANXA10,SERPINA5 |
| M5885 | Ensemble of genes encoding ECM-associated proteins including ECM-affilaited proteins, ECM regulators and secreted factors | | 1.65E-01 | 5.80E-01 | 1.00E+00 | 1.00E+00 | 22 | SERPINA4,AGT,MMP7,ANXA9,ANXA13,SHH,SEMA4G,LEFTY1,CSPG5,PDGFD,SLPI,CTSH,CTSV,SEMA3E,ITIH2,NRTN,SEMA5A,KY,LOX,FGFBP2,ANXA10,SERPINA5 |
| M5884 | Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans | | 3.15E-01 | 5.80E-01 | 1.00E+00 | 1.00E+00 | 8 | MATN2,CTHRC1,SRPX,VWA1,IGFBP2,SPP1,IGSF10,VWA2 |
| **Panther DB** | | | | | | | | |
| P05914 | Nicotine degradation | | 3.80E-11 | 2.36E-09 | 1.11E-08 | 2.36E-09 | 9 | UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT1A5,UGT1A9,UGT1A4,UGT1A1,UGT1A3 |
| P02776 | Serine glycine biosynthesis | | 5.20E-03 | 1.61E-01 | 7.59E-01 | 3.22E-01 | 2 | SHMT1,PHGDH |
| P05911 | Angiotensin II-stimulated signaling through G proteins and beta-arrestin | | 8.66E-03 | 1.79E-01 | 8.43E-01 | 5.37E-01 | 4 | AGT,ARRB1,GNG7,GNG11 |
| P04396 | Vitamin D metabolism and pathway | | 1.76E-02 | 1.82E-01 | 8.55E-01 | 1.00E+00 | 2 | FDX1,CYP27A1 |
| P04373 | 5HT1 type receptor mediated signaling pathway | | 1.77E-02 | 1.82E-01 | 8.55E-01 | 1.00E+00 | 4 | SNAP25,GNG12,GNG7,GNG11 |
| P02771 | Pyrimidine Metabolism | | 2.17E-02 | 1.82E-01 | 8.55E-01 | 1.00E+00 | 2 | ALDH6A1,DPYSL2 |
| P02754 | Methylcitrate cycle | | 4.62E-02 | 1.97E-01 | 9.30E-01 | 1.00E+00 | 1 | ACO1 |
| P05734 | Synaptic vesicle trafficking | | 9.99E-02 | 2.66E-01 | 1.00E+00 | 1.00E+00 | 2 | SYT12,SYT5 |
| P00016 | Cytoskeletal regulation by Rho GTPase | | 2.18E-01 | 3.87E-01 | 1.00E+00 | 1.00E+00 | 3 | TUBB4A,MYO3B,STMN1 |
| P00047 | PDGF signaling pathway | | 8.01E-01 | 8.87E-01 | 1.00E+00 | 1.00E+00 | 2 | RERG,SPDEF |
| **Pathway Ontology** | | | | | | | | |
| PW:0000492 | | renin-angiotensin system signaling | 3.26E-04 | 1.35E-02 | 6.76E-02 | 2.70E-02 | 4 | AGT,MME,ACE,ACE2 |
| PW:0000051 | | histidine metabolic | 2.38E-03 | 4.93E-02 | 2.47E-01 | 1.97E-01 | 3 | HNMT,ALDH2,DDC |
| PW:0000047 | | glycine, serine and threonine metabolic | 3.80E-03 | 6.31E-02 | 3.16E-01 | 3.15E-01 | 3 | SHMT1,GATM,PHGDH |
| PW:0000054 | | tryptophan metabolic | 1.58E-02 | 1.48E-01 | 7.38E-01 | 1.00E+00 | 3 | ALDH2,DDC,CAT |
| PW:0000373 | | glutathione conjugation | 1.76E-02 | 1.48E-01 | 7.38E-01 | 1.00E+00 | 2 | GSTO2,GSTA4 |
| PW:0000729 | | statin pharmacokinetics pathway | 3.58E-02 | 1.48E-01 | 7.38E-01 | 1.00E+00 | 2 | UGT1A1,UGT1A3 |
| PW:0000057 | | carbon fixation | 3.58E-02 | 1.48E-01 | 7.38E-01 | 1.00E+00 | 2 | MDH1,FBP1 |
| PW:0000485 | | eicosanoids metabolic | 6.51E-02 | 1.67E-01 | 8.36E-01 | 1.00E+00 | 2 | GGT1,LTC4S |
| PW:0000398 | | homocysteine metabolic | 6.51E-02 | 1.67E-01 | 8.36E-01 | 1.00E+00 | 2 | HNMT,PNMT |
| PW:0000021 | | hypertension | 9.03E-02 | 1.74E-01 | 8.72E-01 | 1.00E+00 | 1 | LOX |
| **SMPDB** | | | | | | | | |
| SMP00054 | | Fatty Acid Elongation In Mitochondria | 4.13E-04 | 5.27E-02 | 2.95E-01 | 6.19E-02 | 3 | PPT1,PRDX3,HADHB |
| SMP00128 | | Gluconeogenesis | 8.59E-04 | 5.27E-02 | 2.95E-01 | 1.29E-01 | 4 | MDH1,PGK1,FBP1,GALM |
| SMP00075 | | Arachidonic Acid Metabolism | 1.05E-03 | 5.27E-02 | 2.95E-01 | 1.58E-01 | 4 | AKR1C3,CYP2U1,CYP4F3,LTC4S |
| SMP00006 | | Tyrosine Metabolism | 2.15E-03 | 7.53E-02 | 4.21E-01 | 3.22E-01 | 4 | FAH,PNMT,CYBA,DDC |
| SMP00004 | | Glycine, Serine and Threonine Metabolism | 2.51E-03 | 7.53E-02 | 4.21E-01 | 3.77E-01 | 4 | ALDH2,SHMT1,GATM,PHGDH |
| SMP00016 | | Propanoate Metabolism | 3.08E-02 | 2.42E-01 | 1.00E+00 | 1.00E+00 | 2 | ALDH6A1,ACSS1 |
| SMP00032 | | Valine, Leucine and Isoleucine Degradation | 3.22E-02 | 2.42E-01 | 1.00E+00 | 1.00E+00 | 3 | ALDH2,ALDH6A1,BCKDHB |
| SMP00020 | | Arginine and Proline Metabolism | 6.51E-02 | 3.32E-01 | 1.00E+00 | 1.00E+00 | 2 | GATM,OAT |
| SMP00066 | | Biotin Metabolism | 6.85E-02 | 3.32E-01 | 1.00E+00 | 1.00E+00 | 1 | BTD |
| SMP00199 | | Maple Syrup Urine Disease | 6.85E-02 | 3.32E-01 | 1.00E+00 | 1.00E+00 | 1 | BCKDHB |

**Table 4** The enriched GO terms of the up regulated differentially expressed genes

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **GO ID** | **CATEGORY** | | **GO Name** | **P Value** | **FDR B&H** | **FDR B&Y** | **Bonferroni** | **Gene Count** | **Gene** |
| GO:0009607 | BP | response to biotic stimulus | | 4.21E-43 | 4.21E-43 | 4.21E-43 | 2.47E-39 | 117 | USP18,PDE2A,PDE4B,DDX58,NT5C3A,IFNL4,HLA-F,APOBEC3G,PGLYRP2,DTX3L,TLR6,TRIM22,PLAC8,CXCL9,NLRC5,CCL2,NOCT,CCL20,CXCL11,CX3CL1,TRIM38,PMAIP1,PML,FLT3,ZC3H12A,DHX58,FOS,TENT5A,ICAM1,IFI44,IFITM1,SAMHD1,IFITM2,IFI16,BATF2,IFI35,IFIT2,IFIT1,IFIT3,ZFP36,TRIM5,IFNB1,TXNIP,MT2A,RSAD2,CSF2,SH2D1B,ISG15,MIR181B1,OASL,CD274,MIR21,SOCS1,RAET1L,XAF1,STX11,TSLP,IL6,CXCL8,MX2,ZC3HAV1,CYLD,CYP1A1,IL12A,TAGAP,CXCL10,TICAM1,GATA3,PSMB9,CMPK2,GBP1,IFIT5,IRF1,TRIM21,IRF7,ISG20,BCL3,PTGER4,IL22RA1,RTP4,PTGS2,GFI1,STAT2,JAK2,IFIH1,BMP2,JUN,CLEC4A,PTX3,GLI2,NFKBIA,C4A,C4B,TAP1,FGF19,GPER1,SOCS3,PELI1,OAS1,OAS2,RELB,CXCL2,CXCL3,NLRP3,LGALS9,RASGRP1,EGR1,CRTAM,SERPINE1,TNF,DUSP10,TNFAIP3,PCK1,HERC5,IFNL2,IFNL3,IFNL1 |
| GO:0006952 | BP | defense response | | 3.55E-39 | 5.21E-36 | 4.82E-35 | 2.08E-35 | 119 | USP18,PDE2A,DDX58,NT5C3A,IFNL4,HLA-F,APOBEC3G,PGLYRP2,DTX3L,TLR6,KLF4,TRIM22,PLAC8,TNFRSF4,ADRB2,CXCL9,NLRC5,CCL2,CCL20,CXCL11,CX3CL1,TRIM38,PMAIP1,PML,THEMIS2,ZC3H12A,DHX58,FOS,ICAM1,IFITM1,SAMHD1,IFITM2,IFI16,BATF2,IFI35,IFIT2,IFIT1,IFIT3,ZFP36,TRIM5,IFNB1,MT2A,RSAD2,PLA2G4C,SH2D1B,ISG15,MIR181B1,OASL,MIR21,SOCS1,RAET1L,XAF1,IL1A,STX11,TSLP,IL6,CXCL8,MX2,ZC3HAV1,CYLD,IL12A,INHBA,TAGAP,CXCL10,TICAM1,IL17C,GATA3,PSMB9,GBP1,IFIT5,IRF1,TRIM21,IRF7,ISG20,BCL3,PTGER4,IL22RA1,RTP4,PTGS2,BDKRB2,GFI1,STAT2,JAK2,IFIH1,BMP2,JUN,TTBK1,CLEC4A,PTX3,NFKBIA,C4A,C4B,TAP1,DRD1,GPER1,SOCS3,PELI1,CCRL2,OAS1,OAS2,NFKBIZ,RELB,CXCL2,CXCL3,S1PR3,NLRP3,LGALS9,MMP25,RASGRP1,EGR1,CRTAM,SERPINE1,TNF,DUSP10,TNFAIP3,HERC5,IFNL2,IFNL3,IFNL1 |
| GO:0034097 | BP | response to cytokine | | 1.86E-38 | 2.18E-35 | 2.02E-34 | 1.09E-34 | 99 | USP18,SPRY2,TRAF1,PDE2A,DDX58,HLA-F,KLF4,TRIM22,KLF2,TNFRSF4,CXCL9,NLRC5,CCL2,CCL20,CXCL11,CX3CL1,TRIM38,PML,FLT3,FLT3LG,ZC3H12A,KLF6,MAP3K8,FOS,ICAM1,IFITM1,SAMHD1,IFITM2,ACKR4,IFI16,IFI35,IFIT2,IFIT1,IFIT3,ZFP36,TRIM5,IFNB1,MT2A,RSAD2,CSF2,ISG15,MIR181B1,TNFSF13B,OASL,CD274,MIR21,SOCS1,XAF1,IL1A,STX11,TSLP,IL6,IL7,IL7R,CXCL8,MX2,CYLD,IL11,IL12A,IL15RA,CXCL10,IL17C,GATA3,PSMB9,GBP1,IRF1,TRIM21,IRF7,ISG20,IL22RA1,PTGS2,GFI1,STAT2,JAK2,IFIH1,JUN,NFKBIA,NKX3-1,GFPT2,GPER1,DUSP1,SOCS3,PELI1,CCRL2,OAS1,OAS2,RELB,CXCL2,CXCL3,LGALS9,EGR1,SERPINE1,LTB,TNF,TNFAIP3,PCK1,IFNL2,IFNL3,IFNL1 |
| GO:0009615 | BP | response to virus | | 7.96E-38 | 7.78E-35 | 7.20E-34 | 4.67E-34 | 56 | DDX58,NT5C3A,IFNL4,APOBEC3G,DTX3L,TRIM22,CXCL9,NLRC5,TRIM38,PMAIP1,PML,FLT3,ZC3H12A,DHX58,IFI44,IFITM1,SAMHD1,IFITM2,IFI16,IFIT2,IFIT1,IFIT3,TRIM5,IFNB1,RSAD2,ISG15,OASL,IL6,MX2,ZC3HAV1,CYP1A1,IL12A,TAGAP,CXCL10,TICAM1,GATA3,GBP1,IFIT5,IRF1,IRF7,ISG20,BCL3,RTP4,STAT2,IFIH1,GLI2,OAS1,OAS2,NLRP3,LGALS9,TNF,TNFAIP3,HERC5,IFNL2,IFNL3,IFNL1 |
| GO:0071345 | BP | cellular response to cytokine stimulus | | 2.30E-37 | 2.30E-37 | 2.30E-37 | 1.35E-33 | 94 | USP18,SPRY2,TRAF1,PDE2A,HLA-F,KLF4,TRIM22,KLF2,TNFRSF4,CXCL9,NLRC5,CCL2,CCL20,CXCL11,CX3CL1,TRIM38,PML,FLT3,FLT3LG,ZC3H12A,KLF6,MAP3K8,FOS,ICAM1,IFITM1,SAMHD1,IFITM2,ACKR4,IFI16,IFI35,IFIT2,IFIT1,IFIT3,ZFP36,TRIM5,IFNB1,MT2A,RSAD2,CSF2,ISG15,MIR181B1,TNFSF13B,OASL,MIR21,SOCS1,XAF1,IL1A,STX11,TSLP,IL6,IL7,IL7R,CXCL8,MX2,CYLD,IL11,IL12A,IL15RA,CXCL10,IL17C,GATA3,PSMB9,GBP1,IRF1,TRIM21,IRF7,ISG20,IL22RA1,PTGS2,GFI1,STAT2,JAK2,NFKBIA,NKX3-1,GFPT2,GPER1,DUSP1,SOCS3,PELI1,CCRL2,OAS1,OAS2,CXCL2,CXCL3,LGALS9,EGR1,SERPINE1,LTB,TNF,TNFAIP3,PCK1,IFNL2,IFNL3,IFNL1 |
| GO:0051607 | BP | defense response to virus | | 3.34E-34 | 1.96E-31 | 1.82E-30 | 1.96E-30 | 47 | DDX58,NT5C3A,IFNL4,APOBEC3G,DTX3L,TRIM22,CXCL9,NLRC5,TRIM38,PMAIP1,PML,ZC3H12A,DHX58,IFITM1,SAMHD1,IFITM2,IFI16,IFIT2,IFIT1,IFIT3,TRIM5,IFNB1,RSAD2,ISG15,OASL,IL6,MX2,ZC3HAV1,TAGAP,CXCL10,TICAM1,GBP1,IFIT5,IRF1,IRF7,ISG20,RTP4,STAT2,IFIH1,OAS1,OAS2,NLRP3,TNFAIP3,HERC5,IFNL2,IFNL3,IFNL1 |
| GO:0045087 | BP | innate immune response | | 9.78E-30 | 5.22E-27 | 4.83E-26 | 5.74E-26 | 79 | USP18,DDX58,IFNL4,HLA-F,APOBEC3G,PGLYRP2,DTX3L,TLR6,TRIM22,NLRC5,CCL2,CCL20,CX3CL1,TRIM38,PML,DHX58,ICAM1,IFITM1,SAMHD1,IFITM2,IFI16,IFI35,IFIT2,IFIT1,IFIT3,TRIM5,IFNB1,MT2A,RSAD2,SH2D1B,ISG15,MIR181B1,OASL,MIR21,SOCS1,RAET1L,XAF1,STX11,MX2,ZC3HAV1,CYLD,IL12A,TICAM1,GATA3,PSMB9,GBP1,IFIT5,IRF1,TRIM21,IRF7,ISG20,GFI1,STAT2,JAK2,IFIH1,CLEC4A,PTX3,NFKBIA,C4A,C4B,TAP1,GPER1,SOCS3,PELI1,OAS1,OAS2,RELB,NLRP3,LGALS9,RASGRP1,EGR1,CRTAM,TNF,DUSP10,TNFAIP3,HERC5,IFNL2,IFNL3,IFNL1 |
| GO:0002682 | BP | regulation of immune system process | | 1.14E-25 | 5.12E-23 | 4.74E-22 | 6.66E-22 | 97 | USP18,PDE4B,DDX58,IFNL4,HLA-F,HLX,APOBEC3G,PGLYRP2,DTX3L,TLR6,TNFRSF4,NLRC5,CCL2,CCL20,CX3CL1,TRIM38,PML,THEMIS2,PRKD2,FLT3,FLT3LG,ZC3H12A,DHX58,MAP3K8,FOS,ICAM1,IFITM1,SAMHD1,IFI16,IFIT1,ZFP36,TRIM5,IFNB1,RSAD2,CSF2,SH2D1B,ISG15,MIR181B1,TNFSF13B,CD274,MIR21,SOCS1,RAET1L,IL1A,TSLP,IL6,IL7,IL7R,CXCL8,ZC3HAV1,CYLD,IL11,IL12A,IL15RA,INHBA,CXCL10,TICAM1,TCIM,GATA3,PSMB9,GBP1,IRF1,IRF7,PTGER4,GFI1,JAK2,IFIH1,JUN,TTBK1,CLEC4A,GLI2,NFKBIA,C4A,C4B,TAP1,GPER1,DUSP1,SOCS3,PELI1,NFKBIZ,NR4A3,RELB,NLRP3,LGALS9,RASGRP1,LMO2,EGR3,ICAM5,CRTAM,SERPINE1,TNF,DUSP10,TNFAIP3,HERC5,IFNL2,IFNL3,IFNL1 |
| GO:0001816 | BP | cytokine production | | 1.15E-24 | 4.82E-22 | 4.46E-21 | 6.75E-21 | 66 | PDE4B,UBE2L6,DDX58,HLA-F,PGLYRP2,TLR6,KLF4,KLF2,TNFRSF4,HEG1,UBA7,NLRC5,CCL2,CCL20,CX3CL1,TRIM38,PML,PRKD2,FLT3,ZC3H12A,DHX58,IFI16,ZFP36,IFNB1,RSAD2,CSF2,ISG15,CD274,MIR21,SOCS1,IL1A,TSLP,IL6,IL7,ZC3HAV1,CYLD,IL12A,INHBA,TICAM1,IL17C,GATA3,GBP1,IRF1,TRIM21,IRF7,BCL3,PTGER4,PTGS2,JAK2,IFIH1,CLEC4A,PELI1,NR4A3,RELB,S1PR3,NLRP3,LGALS9,RASGRP1,EGR1,CRTAM,SERPINE1,LTB,TNF,TNFAIP3,HERC5,IFNL1 |
| GO:0019079 | BP | viral genome replication | | 3.31E-15 | 3.66E-13 | 3.39E-12 | 1.94E-11 | 21 | APOBEC3G,CCL2,TRIM38,ZC3H12A,IFITM1,IFITM2,IFI16,IFIT1,IFNB1,RSAD2,ISG15,OASL,CXCL8,PROX1,ZC3HAV1,IFIT5,ISG20,OAS1,PARP10,TNF,IFNL3 |
| GO:0019058 | BP | viral life cycle | | 1.14E-11 | 6.49E-10 | 6.01E-09 | 6.68E-08 | 28 | APOBEC3G,TNFRSF4,CCL2,TRIM38,PML,ZC3H12A,ICAM1,IFITM1,IFITM2,IFI16,IFIT1,TRIM5,IFNB1,RSAD2,ISG15,OASL,CXCL8,PROX1,ZC3HAV1,IFIT5,TRIM21,ISG20,PTX3,OAS1,LGALS9,PARP10,TNF,IFNL3 |
| GO:0019220 | BP | regulation of phosphate metabolic process | | 1.81E-11 | 9.65E-10 | 8.93E-09 | 1.06E-07 | 76 | SPRY2,PDE2A,PPP1R15A,TLR6,KLF4,TNFRSF4,DACT1,DUSP26,HEG1,ADRB2,NLRC5,CCL2,C1QTNF1,PLAUR,CCL20,TSACC,CX3CL1,PML,KLB,PRKD2,FLT3,FLT3LG,ZC3H12A,MAP3K8,ICAM1,TRIM5,PPP4R4,IFNB1,CSF2,MIR181B1,MIR21,SOCS1,ATF3,IL1A,TSLP,IL6,IL7,PROX1,CYLD,IL11,GADD45B,IL12A,INHBA,CXCL10,TCIM,GBP1,IRF1,PTGER4,PTGS2,BDKRB2,FGF18,STAT2,JAK2,NPFFR2,BMP2,JUN,TTBK1,NKX3-1,FGF19,DRD1,GPER1,DUSP1,DDR2,DUSP8,SOCS3,LGALS9,RASGRP1,EGR1,NEURL1,TNF,DUSP10,TNFAIP3,HCRTR1,HERC5,EPHA4,IFNL1 |
| GO:0016032 | BP | viral process | | 7.54E-11 | 3.48E-09 | 3.22E-08 | 4.42E-07 | 44 | DDX58,APOBEC3G,TRIM22,TNFRSF4,CCL2,TRIM38,PML,FLT3,ZC3H12A,DHX58,ICAM1,IFITM1,IFITM2,IFI16,SP110,IFIT1,ZFP36,TRIM5,IFNB1,RSAD2,ISG15,OASL,RAET1L,CXCL8,PROX1,ZC3HAV1,TICAM1,PSMB9,IFIT5,TRIM21,IRF7,ISG20,GFI1,STAT2,IFIH1,JUN,PTX3,NFKBIA,TAP1,OAS1,LGALS9,PARP10,TNF,IFNL3 |
| GO:0051254 | BP | positive regulation of RNA metabolic process | | 1.16E-10 | 5.19E-09 | 4.80E-08 | 6.83E-07 | 70 | HIVEP1,HIVEP2,DDX58,ETS2,DTX3L,EYA1,PPP1R15A,KLF4,PLAC8,KLF2,CSRNP1,AHRR,ADRB2,NLRC5,CX3CL1,CAVIN2,PRRX2,PML,PRKD2,FLT3LG,ZC3H12A,KLF6,FOS,FOSB,CPEB3,ID4,IFI16,ZFP36,CREB5,IFNB1,EPC1,HELZ2,ATF3,IL1A,SIX2,IL6,PROX1,ZC3HAV1,IL11,INHBA,CXCL10,GATA3,IRF1,IRF7,BCL3,GFI1,STAT2,JAK2,BMP2,JUN,GLI2,NFKBIA,NKX3-1,BARX1,GPER1,NR4A3,RELB,NLRP3,LMO2,EGR1,EGR2,EGR3,EGR4,SERPINE1,NANOS3,NCOA7,TNF,LYL1,PCK1,IFNL1 |
| GO:0009719 | BP | response to endogenous stimulus | | 3.16E-08 | 8.94E-07 | 8.28E-06 | 1.85E-04 | 64 | SPRY2,PDE2A,PDE4B,HIVEP1,ACTA1,TLR6,KLF4,LRIT3,KLF2,ADRB2,XRN1,CCL2,FLRT3,FST,PML,KLB,COL4A1,PRKD2,FLT3,MXRA5,FOS,FOSB,ICAM1,CPEB3,ZFP36,SLC5A5,IFNB1,TXNIP,MIR21,SOCS1,IL6,CXCL8,TNFSF10,INHBA,TICAM1,GATA3,IRF1,SSTR2,PTGER4,PTGS2,FGF18,STAT2,JAK2,NPFFR2,BMP2,JUN,NKX3-1,FGF19,CPEB2,DRD1,GPER1,DUSP1,SOCS3,NR4A3,NLRP3,LMO2,EGR1,EGR2,EGR3,NEURL1,SERPINE1,TNF,PCK1,EPHA4 |
| GO:0009986 | CC | cell surface | | 3.98E-04 | 4.86E-02 | 3.29E-01 | 1.95E-01 | 33 | ACHE,TRPC4,HLA-F,DSCAML1,TNFRSF4,FAP,HEG1,CXCL9,PLAUR,SLITRK6,CX3CL1,FLT3,FLT3LG,ICAM1,ACKR4,CD274,RAET1L,IL1A,IL6,IL7R,IL12A,IL15RA,LAYN,CXCL10,RTP4,BMP2,CCRL2,GRIA2,MMP25,WIF1,CD69,TNF,EPHA4 |
| GO:0045202 | CC | synapse | | 1.18E-02 | 1.92E-01 | 1.00E+00 | 1.00E+00 | 37 | PDE2A,PDE4B,ACHE,PLEKHG5,DSCAML1,SYNPR,DACT1,ADRB2,XRN1,CCL2,FLRT3,CX3CL1,CPEB3,STX19,SNCAIP,STX11,PDZD2,SNPH,SLC30A3,PTGER4,JAK2,NTNG2,SYT1,C4A,C4B,GRIN3B,ADGRL3,CPEB2,DRD1,NPTX1,DRP2,GPER1,GRIA2,GRM8,NEURL1,GRIP2,EPHA4 |
| GO:0031226 | CC | intrinsic component of plasma membrane | | 1.97E-02 | 2.41E-01 | 1.00E+00 | 1.00E+00 | 42 | TRPC4,TLR6,TNFRSF4,ADRB2,RASGRP3,C1QTNF1,PLAUR,FLRT3,SLITRK6,FLT3,FLT3LG,SLC39A2,ICAM1,ACKR4,SLC6A13,IL6,TNFSF10,SSTR2,SLC30A3,BDKRB2,NPFFR2,BMP2,NTNG2,CLEC4A,CPO,GRIN3B,ADGRL3,NPR3,DRD1,GPER1,DDR2,CCRL2,GRIA2,GRM8,S1PR3,ICAM5,CRTAM,CD69,TNF,HCRTR1,EPHA4,IFNL1 |
| GO:0030054 | CC | cell junction | | 2.26E-02 | 2.59E-01 | 1.00E+00 | 1.00E+00 | 33 | DDX58,ACHE,TRPC4,PLEKHG5,DSCAML1,SYNPR,DACT1,FAP,HEG1,PLAUR,FLRT3,AMOTL2,ICAM1,CPEB3,PDZD2,SNPH,LAYN,SLC30A3,JAK2,RND1,SYT1,C4A,C4B,GJB7,GRIN3B,ADGRL3,DRP2,GPER1,DDR2,GRIA2,NEURL1,GJC3,EPHA4 |
| GO:0000790 | CC | nuclear chromatin | | 3.70E-02 | 2.92E-01 | 1.00E+00 | 1.00E+00 | 43 | ZNF627,HIVEP1,HIVEP2,HDX,ETS2,HLX,KLF4,KLF2,CSRNP1,AHRR,ZNF433,PRRX2,KLF6,FOS,FOSB,ETV7,ID4,IFI16,BATF2,SP110,CREB5,ATF3,SIX2,PROX1,GATA3,IRF1,IRF7,GFI1,STAT2,JUN,GLI2,NKX3-1,BARX1,NR4A3,ZNFX1,RELB,LMO2,EGR1,EGR2,EGR3,EGR4,LYL1,MXD1 |
| GO:0043005 | CC | neuron projection | | 5.95E-02 | 3.48E-01 | 1.00E+00 | 1.00E+00 | 36 | PDE2A,PDE4B,ACHE,LRIT3,DSCAML1,SYNPR,SPTBN5,ADRB2,XRN1,CCL2,FLRT3,CX3CL1,FOS,CPEB3,SLC6A13,PDZD2,SNPH,SLC30A3,PTGER4,PTGS2,NTNG2,SYT1,C4A,C4B,GRIN3B,ADGRL3,CPEB2,DRD1,NPTX1,DRP2,GPER1,GRIA2,GRM8,NEURL1,GRIP2,EPHA4 |
| GO:0005789 | CC | endoplasmic reticulum membrane | | 7.98E-02 | 3.61E-01 | 1.00E+00 | 1.00E+00 | 25 | RAB19,HLA-F,PPP1R15A,LRIT3,PLAUR,FLRT3,HSD17B3,PML,ZC3H12A,RSAD2,PLA2G4C,MOGAT3,CYP1A1,IL15RA,CYP21A2,FAXDC2,PTGS2,TAP1,SEC16B,DRD1,GPER1,CH25H,GRIA2,RASGRP1,CRYZL2P-SEC16B |
| GO:0005768 | CC | endosome | | 1.96E-01 | 5.45E-01 | 1.00E+00 | 1.00E+00 | 20 | HLA-F,DTX3L,SAMD9L,ADRB2,ARRDC3,AMOTL2,PML,ACKR4,CD274,ZC3HAV1,IL12A,IL15RA,TICAM1,IRF7,SLC30A3,BDKRB2,JAK2,GPER1,TNF,EPHA4 |
| GO:0098805 | CC | whole membrane | | 2.97E-01 | 6.86E-01 | 1.00E+00 | 1.00E+00 | 33 | PDE2A,TRPC4,HLA-F,DTX3L,PPP1R15A,TLR6,SYNPR,ADRB2,MYLPF,PLAUR,CAVIN2,PMAIP1,PML,ICAM1,RSAD2,CD274,IL7R,TICAM1,IRF7,SLC30A3,PTGS2,JAK2,SYT1,TAP1,SEC16B,DRD1,GRIA2,RAB44,RGS16,MMP25,CRYZL2P-SEC16B,TNF,EPHA4 |
| GO:0005739 | CC | mitochondrion | | 6.47E-01 | 9.41E-01 | 1.00E+00 | 1.00E+00 | 30 | PDE2A,HIVEP1,NT5C3A,PPP1R15A,DUSP26,PMAIP1,FAM110B,G0S2,PPM1K,IFIT3,TXNIP,RSAD2,XAF1,BBC3,MX2,CYP1A1,SNPH,TICAM1,CMPK2,TAP1,NPTX1,GPER1,OAS1,TDRD7,SLC25A2,HSH2D,SLC25A28,PCK1,MXD1,EPHA4 |
| GO:0005125 | MF | cytokine activity | | 7.41E-19 | 6.55E-16 | 4.82E-15 | 6.55E-16 | 31 | IFNL4,CXCL9,CCL2,CCL20,CXCL11,CX3CL1,SECTM1,FLT3LG,IFNB1,CSF2,TNFSF13B,IL1A,TSLP,IL6,IL7,CXCL8,IL11,IL12A,TNFSF10,INHBA,CXCL10,IL17C,BMP2,VSTM1,CXCL2,CXCL3,LTB,TNF,IFNL2,IFNL3,IFNL1 |
| GO:0005102 | MF | signaling receptor binding | | 3.29E-13 | 1.45E-10 | 1.07E-09 | 2.90E-10 | 77 | TRAF1,IFNL4,HLA-F,PYY2,ETS2,TLR6,FAP,ADRB2,CXCL9,CCL2,PLAUR,FLRT3,ARRDC3,CCL20,FST,CXCL11,CX3CL1,CHAC1,KLB,SECTM1,FLT3,FLT3LG,ICAM1,IFNB1,SNED1,CSF2,ISG15,TNFSF13B,OASL,PTCH2,SOCS1,RAET1L,IL1A,TSLP,IL6,IL7,CXCL8,PROX1,IL11,IL12A,TNFSF10,INHBA,CXCL10,IL17C,TCIM,GATA3,RTP4,BDKRB2,FGF18,JAK2,NPFFR2,BMP2,RND1,SYT1,NKX3-1,TAP1,FGF19,VSTM1,DRD1,CCRL2,NR4A3,CXCL2,CXCL3,S1PR3,LGALS9,ICAM5,CRTAM,WIF1,SERPINE1,NCOA7,LTB,TNF,GRIP2,EPHA4,IFNL2,IFNL3,IFNL1 |
| GO:0030545 | MF | receptor regulator activity | | 1.45E-11 | 2.14E-09 | 1.57E-08 | 1.28E-08 | 36 | IFNL4,PYY2,CXCL9,CCL2,FLRT3,CCL20,FST,CXCL11,CX3CL1,SECTM1,FLT3LG,IFNB1,CSF2,TNFSF13B,IL1A,TSLP,IL6,IL7,CXCL8,IL11,IL12A,TNFSF10,INHBA,CXCL10,IL17C,FGF18,BMP2,FGF19,VSTM1,CXCL2,CXCL3,LTB,TNF,IFNL2,IFNL3,IFNL1 |
| GO:0098772 | MF | molecular function regulator | | 8.57E-08 | 1.08E-05 | 7.96E-05 | 7.57E-05 | 66 | SPRY2,IFNL4,PYY2,DTX3L,RRAD,PPP1R15A,TLR6,KLF4,PLEKHG5,ADRB2,RASGRP3,CXCL9,CCL2,FLRT3,CCL20,FST,TSACC,CXCL11,CX3CL1,CLPSL1,SECTM1,FLT3LG,SPINK9,PPP4R4,IFNB1,TXNIP,CSF2,TNFSF13B,SOCS1,IL1A,TSLP,IL6,IL7,CXCL8,IL11,IL12A,TNFSF10,INHBA,TAGAP,CXCL10,IL17C,FGF18,BMP2,JUN,C4A,C4B,NKX3-1,FGF19,VSTM1,CPEB2,SOCS3,DNAJB4,CXCL2,CXCL3,RGS16,LGALS9,MMP25,RASGRP1,SERPINE1,LTB,TNF,AGAP7P,EPHA4,IFNL2,IFNL3,IFNL1 |
| GO:0046914 | MF | transition metal ion binding | | 5.07E-05 | 2.04E-03 | 1.50E-02 | 4.48E-02 | 39 | TRAF1,PDE2A,HIVEP1,DDX58,APOBEC3G,PGLYRP2,KLF4,TRIM22,TRIM38,PML,DHX58,SAMHD1,PPEF1,TRIM5,MT1E,MT2A,XAF1,TRIM40,IL1A,CYLD,CYP1A1,TNFSF10,CYP21A2,GATA3,FAXDC2,TRIM21,IFIH1,GLI2,CPO,DRP2,CH25H,NR4A3,ZNFX1,MMP25,RASGRP1,EGR1,NANOS3,TNFAIP3,PCK1 |
| GO:0000977 | MF | RNA polymerase II regulatory region sequence-specific DNA binding | | 5.93E-05 | 2.04E-03 | 1.50E-02 | 5.24E-02 | 32 | HIVEP1,HIVEP2,ETS2,KLF4,NLRC5,PRRX2,KLF6,FOS,FOSB,ETV7,IFI16,BATF2,ATF3,SIX2,PROX1,GATA3,IRF1,IRF7,STAT2,JUN,GLI2,NKX3-1,BARX1,NR4A3,RELB,LMO2,EGR1,EGR2,EGR3,EGR4,LYL1,MXD1 |
| GO:0016772 | MF | transferase activity, transferring phosphorus-containing groups | | 6.00E-05 | 2.04E-03 | 1.50E-02 | 5.30E-02 | 56 | SPRY2,NT5C3A,APOBEC3G,TLR6,KLF4,TNFRSF4,DUSP26,HEG1,ADRB2,XRN1,NLRC5,CCL2,TSACC,PML,PRKD2,FLT3,MAP3K8,TENT5A,ZFP36,PIM3,OASL,MIR21,SOCS1,IL6,CXCL8,PROX1,GADD45B,CXCL10,TCIM,CMPK2,TENT5C,FGF18,JAK2,ENO4,NPFFR2,BMP2,JUN,TTBK1,DRD1,DUSP1,DDR2,DUSP8,SOCS3,OAS1,OAS2,NUAK2,LGALS9,RASGRP1,EGR1,NEURL1,TNF,DUSP10,TNFAIP3,PCK1,HERC5,EPHA4 |
| GO:0044212 | MF | transcription regulatory region DNA binding | | 8.84E-05 | 2.69E-03 | 1.98E-02 | 7.80E-02 | 36 | HIVEP1,HIVEP2,ETS2,KLF4,NLRC5,PRRX2,KLF6,FOS,FOSB,ETV7,IFI16,BATF2,TIPARP,ATF3,SIX2,PROX1,GATA3,IRF1,IRF7,GFI1,STAT2,JUN,GLI2,NKX3-1,BARX1,NR4A3,RELB,LGALS9,LMO2,EGR1,EGR2,EGR3,EGR4,TNF,LYL1,MXD1 |
| GO:0004672 | MF | protein kinase activity | | 6.23E-04 | 1.28E-02 | 9.42E-02 | 5.51E-01 | 40 | SPRY2,TLR6,TNFRSF4,DUSP26,HEG1,ADRB2,CCL2,TSACC,PRKD2,FLT3,MAP3K8,PIM3,MIR21,SOCS1,IL6,PROX1,GADD45B,CXCL10,TCIM,FGF18,JAK2,NPFFR2,BMP2,JUN,TTBK1,DRD1,DUSP1,DDR2,DUSP8,SOCS3,NUAK2,LGALS9,RASGRP1,EGR1,NEURL1,TNF,DUSP10,TNFAIP3,HERC5,EPHA4 |
| GO:0042802 | MF | identical protein binding | | 7.96E-03 | 7.03E-02 | 5.17E-01 | 1.00E+00 | 50 | TRAF1,PDE2A,DDX58,ACHE,APOBEC3G,TLR6,DSCAML1,FAP,ADRB2,FLRT3,AMOTL2,PML,FLT3,FLT3LG,SAMHD1,IFIT3,TRIM5,SNCAIP,ATF3,ZC3HAV1,TNFSF10,INHBA,GIMAP2,TICAM1,GBP1,TRIM21,PTGS2,STAT2,JAK2,IFIH1,BMP2,JUN,PTX3,NFKBIA,SYT1,TAP1,RBM11,NPR3,GRIA2,NR4A3,RELB,NLRP3,RASGRP1,CRTAM,CD69,TNF,TNFAIP3,GJC3,HSD17B14,EPHA4 |

Biological Process(BP), Cellular Component(CC) and Molecular Functions (MF)

**Table 5** The enriched GO terms of the down regulated differentially expressed genes

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **GO ID** | **CATEGORY** | **GO Name** | **P Value** | **FDR B&H** | **FDR B&Y** | **Bonferroni** | **Gene Count** | **Gene** |
| GO:0043436 | BP | oxoacid metabolic process | 9.03E-16 | 1.67E-12 | 1.53E-11 | 5.00E-12 | 71 | RIMKLA,PDK1,ACO1,ETFB,ETFDH,MDH1,HNMT,PGK1,FABP6,ADH6,FAH,ACSM3,FBP1,HOGA1,AGT,SCP2,ECI2,ALDH6A1,PCYOX1,MPC2,HACD3,FOLR1,UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT1A5,SHMT1,UGT1A9,ACSF2,SLC3A1,UGT1A4,UGT1A1,UGT1A3,CRYM,CSPG5,PPA2,AKR1C3,DHFRP1,SPR,ACSS1,CYP27A1,BDH2,GATM,BCKDHB,PSMD10,GSTO2,DDC,ITIH2,PHGDH,GGT1,ERFE,BTD,NR1H4,SLC25A21,GLYATL2,OAT,OAZ1,HACD2,ECH1,BCO2,BNIPL,UGT2A3,PAH,CYP2U1,CYP4F3,SERINC5,ADI1,LTC4S,HADHB,DSEL |
| GO:0032787 | BP | monocarboxylic acid metabolic process | 2.51E-12 | 1.78E-09 | 1.64E-08 | 1.39E-08 | 46 | PDK1,ETFB,ETFDH,PGK1,FABP6,ADH6,FAH,ACSM3,FBP1,HOGA1,AGT,SCP2,ECI2,MPC2,HACD3,UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT1A5,UGT1A9,ACSF2,UGT1A4,UGT1A1,UGT1A3,CSPG5,AKR1C3,ACSS1,CYP27A1,BDH2,GATM,PHGDH,GGT1,ERFE,BTD,NR1H4,GLYATL2,HACD2,ECH1,BCO2,UGT2A3,CYP2U1,CYP4F3,LTC4S,HADHB,DSEL |
| GO:0010817 | BP | regulation of hormone levels | 1.04E-10 | 4.79E-08 | 4.40E-07 | 5.75E-07 | 40 | CFTR,TTR,HMGN3,ADH6,ADORA1,FDX1,AGT,UCP2,SCP2,MME,HSD17B2,MPC2,UGT1A8,UGT1A7,SHH,UGT1A9,BIRC5,AQP1,UGT1A1,UGT1A3,CRYM,ARRB1,AKR1C3,SNAP25,SLC16A10,KLK6,SPP1,CYP27A1,SRI,ACE,FFAR4,AKR1B10,PCSK1N,NR1H4,SRD5A3,CASR,SLC44A4,LEPR,ACE2,BCO2 |
| GO:0055114 | BP | oxidation-reduction process | 2.33E-09 | 9.92E-07 | 9.12E-06 | 1.29E-05 | 58 | ABCC4,CYBRD1,ACO1,ETFB,ETFDH,MDH1,PGK1,ADH6,TSTD1,FBP1,FDX1,AGT,SCP2,ECI2,ALDH2,HSD17B2,ALDH6A1,PCYOX1,TRMT9B,FMO5,DHRS4L2,COX11,CP,APOE,CRYM,CRYZ,AKR1C3,CYBA,NDUFS7,DHFRP1,SPR,ACSS1,CYP27A1,BDH2,BCKDHB,NDUFA2,GSTO2,PHGDH,SUMF1,PRDX3,AKR1B10,KCNAB1,SRD5A3,CAT,PRDX2,ECH1,LEPR,GSR,BCO2,LOX,PAH,CYP2U1,CYP4F3,ADI1,LTC4S,HADHB,NOSTRIN,FAHD1 |
| GO:0017144 | BP | drug metabolic process | 5.53E-09 | 2.19E-06 | 2.01E-05 | 3.06E-05 | 42 | ATPSCKMT,ACO1,PGK1,ADH6,FAH,AGT,SCP2,AK4,ALDH2,FOLR1,UGT1A7,SHMT1,CRP,UGT1A1,CSPG5,AKR1C3,CTSH,CYBA,NDUFS7,DHFRP1,SPR,ACSS1,CYP27A1,BDH2,GATM,NDUFA2,ACE,DDC,PHGDH,GGT1,BTD,PRDX3,AKR1B10,TCN1,OAT,CAT,PRDX2,SLC44A4,PAH,CYP2U1,ADI1,DSEL |
| GO:0051186 | BP | cofactor metabolic process | 1.14E-08 | 3.95E-06 | 3.64E-05 | 6.33E-05 | 32 | PDK1,ACSM3,SCP2,MPC2,FOLR1,SHMT1,ACSF2,NUBPL,UGT1A4,UGT1A1,PPT1,AKR1C3,CYBA,DHFRP1,SPR,ACOT13,ACSS1,BDH2,GSTO2,GGT1,BTD,HEBP1,PRDX3,AKR1B10,ATP5IF1,TCN1,CAT,HACD2,PRDX2,GSR,GSTA4,PAH |
| GO:0044283 | BP | small molecule biosynthetic process | 1.87E-08 | 6.00E-06 | 5.52E-05 | 1.04E-04 | 41 | EPHX1,PDE1A,RIMKLA,CFTR,MDH1,PGK1,ACSM3,FBP1,HOGA1,AGT,NME5,SCP2,PGP,HACD3,SHMT1,APOE,DNPH1,ASAH1,CSPG5,AKR1C3,DHFRP1,SPR,ACSS1,CYP27A1,BDH2,GATM,PHGDH,GGT1,NR1H4,SRD5A3,DTYMK,NTHL1,OAT,HACD2,LEPR,ENTPD3,PAH,SERINC5,ADI1,LTC4S,DSEL |
| GO:0044255 | BP | cellular lipid metabolic process | 6.57E-08 | 1.73E-05 | 1.59E-04 | 3.64E-04 | 51 | PIGN,PDK1,ETFB,ETFDH,TTR,FABP6,ADH6,ACSM3,AGT,SCP2,FGFR3,ECI2,PGP,HACD3,UGT1A8,UGT1A7,UGT1A9,APOE,ACSF2,UGT1A1,UGT1A3,CRLS1,PPT1,ASAH1,AKR1C3,SORL1,PSAP,MOGAT1,ACSS1,BDH2,GGT1,SGPP1,ERFE,SUMF1,AKR1B10,STRA6,NR1H4,SRD5A3,RARRES2,PIGK,GLYATL2,CAT,HACD2,SLC44A4,ECH1,BCO2,CYP2U1,CYP4F3,SERINC5,LTC4S,HADHB |
| GO:0006629 | BP | lipid metabolic process | 4.88E-07 | 1.01E-04 | 9.29E-04 | 2.70E-03 | 59 | PIGN,PDK1,CFTR,ETFB,ETFDH,TTR,FABP6,ADH6,ADORA1,ACSM3,FDX1,AGT,SCP2,FGFR3,ECI2,PGP,HSD17B2,HACD3,UGT1A8,UGT1A7,SHH,UGT1A9,APOE,ACSF2,UGT1A1,UGT1A3,CRLS1,PPT1,ASAH1,AKR1C3,SORL1,PSAP,MOGAT1,SPP1,ACSS1,CYP27A1,BDH2,GGT1,SGPP1,ERFE,SUMF1,AKR1B10,STRA6,NR1H4,SRD5A3,RARRES2,PIGK,GLYATL2,CAT,HACD2,SLC44A4,ECH1,LEPR,BCO2,CYP2U1,CYP4F3,SERINC5,LTC4S,HADHB |
| GO:0006811 | BP | ion transport | 1.77E-05 | 2.08E-03 | 1.91E-02 | 9.78E-02 | 67 | ATPSCKMT,ABCC4,RAMP1,CFTR,MAGT1,KCNIP3,PGK1,ADORA1,AGT,UCP2,SCNN1A,SCP2,AK4,GLTPD2,CNGA1,PCYOX1,SLC25A27,MPC2,FOLR1,ARL6IP5,CP,NLGN1,APOE,AQP1,SLC3A1,PLA2R1,SLC12A2,CLDN16,TMEM37,SNAP25,SLC45A1,SNTA1,SLC16A10,CYBA,NDUFS7,PSAP,SYT12,SRI,NDUFA2,ACE,STC1,ERFE,LRRC26,KCNAB1,SYT5,KCNMB4,SLC38A11,STRA6,NR1H4,CA12,DPYSL2,SLC25A21,KCNE3,TCN1,SLC38A4,NTRK2,CASR,SLC39A10,SLC44A4,TMBIM6,TF,CLDN10,TFRC,CUTC,ACE2,ORAI3,ROS1 |
| GO:0040007 | BP | growth | 2.16E-05 | 2.48E-03 | 2.29E-02 | 1.19E-01 | 46 | RERG,MATN2,HOXA11,FBP1,PIN1,AGT,FGFR3,ALCAM,PLS1,SELENOP,SORBS2,AGR2,SHH,TMPRSS4,VWA1,APOE,DNPH1,SEMA4G,IGFBP2,SLC12A2,PPT1,CSPG5,SMARCA2,SEMA3E,CYBA,KLK6,PSAP,SPP1,SPR,AZGP1,PSMD10,HAGLR,STC1,IGSF10,AURKA,STRA6,VWA2,RAD51B,DPYSL2,SEMA5A,SLC44A4,LEPR,TFRC,BNIPL,TM4SF4,ROS1 |
| GO:0046903 | BP | secretion | 3.29E-04 | 2.30E-02 | 2.11E-01 | 1.00E+00 | 59 | ABCC4,CFTR,CRISP3,MAGT1,TTR,HMGN3,ADORA1,SERPINA4,AGT,UCP2,QPCT,MME,MMP7,RAB26,METTL7A,SELENOP,MPC2,AGR2,OLFM4,BIRC5,NLGN1,APOE,AQP1,CRP,PLA2R1,ARRB1,PPT1,ASAH1,CSPG5,SLPI,SNAP25,CTSH,SLC16A10,CYBA,PSAP,MLEC,SYT12,SPP1,SRI,ACE,PGRMC1,FFAR4,STC1,SYT5,KCNMB4,NR1H4,DPYSL2,RARRES2,TCN1,NTRK2,VTCN1,CASR,CAT,SLC44A4,TMBIM6,TF,LEPR,SYNGR1,LYZ |
| GO:0005739 | CC | mitochondrion | 1.47E-13 | 8.98E-11 | 6.28E-10 | 8.98E-11 | 86 | ATPSCKMT,COX16,PDK1,ACO1,ETFB,ETFDH,MDH1,ACYP2,TRMT2B,TSTD1,AP2M1,ACSM3,ASB9,HOGA1,PIN1,FDX1,UCP2,SCP2,AK4,ECI2,ALDH2,CEBPZOS,ALDH6A1,PRIMPOL,SERHL2,HSPE1,SLC25A27,MPC2,COA3,HACD3,AGR2,MACROD1,OLFM4,SHMT1,COX11,ACSF2,NUBPL,SLC3A1,CRLS1,CRYM,BRI3BP,DNLZ,PPA2,CYBA,KLK6,NDUFS7,DHFRP1,PSAP,NDUFAF8,SPR,ACOT13,ACSS1,CYP27A1,SRI,BDH2,GATM,TOMM20,BCKDHB,NDUFA2,SGPP1,TMEM160,BTD,HEBP1,PRDX3,AKR1B10,DPYSL2,SLC25A21,ATP5IF1,NRGN,DTYMK,NTHL1,GLYATL2,OAT,CAT,PRDX2,TMBIM6,ECH1,GSR,TFRC,BCO2,ANXA10,SAMD13,HADHB,FAHD1,ENDOG,COX14 |
| GO:0099513 | CC | polymeric cytoskeletal fiber | 4.18E-05 | 2.56E-03 | 1.79E-02 | 2.56E-02 | 48 | CYBRD1,CFTR,TUBB4A,CYS1,PROM2,MYO3B,NME5,SCNN1A,MME,PLS1,FOLR1,BIRC5,NLGN1,APOE,AQP1,SLC3A1,CRP,EFHC2,ARL3,CD24,SNAP25,CTSH,CTSV,CYBA,BCAS3,EML6,AIF1L,ANKS4B,ACE,AURKA,PROM1,NEK2,GNG12,RSPH1,TUBA1A,CD302,SPAG16,TCTEX1D2,DPYSL2,KRT14,CALB1,CFAP73,TPGS1,STMN1,LCT,USH1C,ACE2,PBXIP1 |
| GO:0036477 | CC | somatodendritic compartment | 1.98E-04 | 5.77E-03 | 4.04E-02 | 1.21E-01 | 40 | PDE1A,CFTR,KCNIP3,SORT1,ADORA1,TUBB4A,ALCAM,MME,SLC25A27,SORBS2,PNMT,SHH,NLGN1,APOE,MAGEE1,SCGN,AQP1,ARRB1,PPT1,SNAP25,CTSV,SORL1,CYBA,NDUFS7,SYT12,SRI,PGRMC1,DDC,AURKA,BTD,KCNAB1,SYT5,DPYSL2,KCNE3,CALB1,NRGN,NTRK2,TPGS1,CASR,ENDOG |
| GO:0098805 | CC | whole membrane | 1.14E-03 | 2.20E-02 | 1.54E-01 | 6.97E-01 | 54 | PXMP4,ABCC4,CYBRD1,CFTR,MAGT1,PGK1,SORT1,AP2M1,CYS1,PROM2,ATRAID,SUN2,SCP2,MME,RAB26,FOLR1,TMEM59,SHH,CP,APOE,CCDC115,SCGN,AQP1,SLC3A1,ARRB1,BRI3BP,PPT1,CSPG5,CD24,SNAP25,SORL1,CYBA,PSAP,MLEC,SYT12,SRI,TOMM20,PGRMC1,TUBA1A,REEP6,SYT5,KCNE3,NRGN,NTRK2,CAT,TF,TFRC,ACE2,CD1D,SYNGR1,LTC4S,HADHB,NOSTRIN,SERPINA5 |
| GO:0031226 | CC | intrinsic component of plasma membrane | 1.66E-03 | 2.74E-02 | 1.92E-01 | 1.00E+00 | 54 | RAMP1,CFTR,MAGT1,KCNIP3,ADORA1,PROM2,UPK1B,SCNN1A,FGFR3,ALCAM,MME,CNGA1,RAB26,FOLR1,CP,NLGN1,AQP1,SEMA4G,SLC3A1,UGT1A1,SLC12A2,CSPG5,CD24,SNAP25,SEMA3E,SORL1,SLC16A10,CYBA,ADGRB3,PGRMC1,GGT1,FFAR4,PROM1,LRRC26,KCNAB1,KCNMB4,STRA6,KCNE3,SLC38A4,NTRK2,PCDHB12,CASR,SLC39A10,TMBIM6,LCT,LEPR,TFRC,CD1D,SSPN,TSPAN10,TSPAN8,TSPAN6,ROM1,ROS1 |
| GO:0015629 | CC | actin cytoskeleton | 4.05E-03 | 4.76E-02 | 3.33E-01 | 1.00E+00 | 28 | CYBRD1,CFTR,PROM2,MYO3B,SCNN1A,MME,PLS1,SORBS2,FOLR1,NLGN1,AQP1,SLC3A1,CRP,CD24,SNAP25,CTSV,CYBA,AIF1L,ANKS4B,ACE,SGPP1,PROM1,GNG12,CD302,CALB1,LCT,USH1C,ACE2 |
| GO:0098552 | CC | side of membrane | 4.13E-03 | 4.76E-02 | 3.33E-01 | 1.00E+00 | 24 | FCGRT,SCNN1A,FGFR3,ALCAM,FOLR1,NLGN1,APOE,CD24,SNAP25,CTSV,AZGP1,ACE,GNG12,KCNAB1,GNG7,GNG11,VTCN1,TF,LEPR,GSR,TFRC,HHLA2,CD1D,SERPINA5 |
| GO:0043005 | CC | neuron projection | 4.46E-03 | 4.78E-02 | 3.34E-01 | 1.00E+00 | 48 | CFTR,KCNIP3,HNMT,PLEKHB1,SORT1, ADORA1,TUBB4A,PIN1,MYO3B,ALCAM,MME,CNGA1,SORBS2,PNMT,SHH, NLGN1,APOE,MAGEE1,SCGN,AQP1,CRP,ARL3,ARRB1,PPT1,SNAP25,CTSV,CYBA, NDUFS7,SYT12,SRI,PGRMC1,DDC, AURKA,PROM1,REEP6,KCNAB1,SYT5, DPYSL2,KCNE3,CALB1,NRGN,NRTN, NTRK2,TPGS1,CASR,STMN1,USH1C, ROM1 |
| GO:0030659 | CC | cytoplasmic vesicle membrane | 6.15E-03 | 5.61E-02 | 3.92E-01 | 1.00E+00 | 27 | ABCC4,CFTR,MAGT1,SORT1,AP2M1,MME,RAB26,FOLR1,APOE,SCGN,AQP1,ARRB1,SNAP25,CYBA,PSAP,MLEC,SYT12,SRI,PGRMC1,REEP6,SYT5,NRGN,TF,TFRC,SYNGR1,NOSTRIN,SERPINA5 |
| GO:0015630 | CC | microtubule cytoskeleton | 2.66E-01 | 4.56E-01 | 1.00E+00 | 1.00E+00 | 31 | TUBB4A,CYS1,NME5,SCNN1A,GPSM2, SAC3D1,BIRC5,APOE,EFHC2,ARL3, CENPV,CTSH,PCLAF,BCAS3,ACOT13, EML6,ACE,AURKA,NEK2,RSPH1,TUBA1A,SPAG16,TCTEX1D2,DPYSL2,CFAP73, DNAAF4,TPGS1,STMN1,PBXIP1,TOP2A,MAD2L1 |
| GO:0005794 | CC | Golgi apparatus | 3.14E-01 | 5.04E-01 | 1.00E+00 | 1.00E+00 | 36 | ACO1,KCNIP3,PLEKHB1,SORT1,FGFR3, MME,ITM2A,RAB26,TRAPPC6A,FOLR1, TMEM59,SHH,NLGN1,APOE, ST6GALNAC2,ARL3,ARRB1,MMEL1,PPT1,CSPG5,PDGFD,SNAP25,SORL1,CYBA, ST6GALNAC1,SPP1,SGPP1,DPY30, PCSK1N,CREG2,RNF128,NTRK2, GALNT12,CAT,SERINC5,DSEL |
| GO:0048037 | MF | cofactor binding | 5.36E-10 | 6.15E-07 | 4.69E-06 | 6.15E-07 | 37 | ACO1,ETFDH,MDH1,FDX1,SCP2,ECI2,ALDH2,ALDH6A1,FMO5,SHMT1,BIRC5,NUBPL,CRYM,CRYZ,ACBD7,CYBA,NDUFS7,DHFRP1,SPR,CYP27A1,BDH2,DDC,PHGDH,HEBP1,KCNAB1,CREG2,TCN1,NTHL1,OAT,CAT,TF,GSR,PAH,CYP2U1,CYP4F3,LTC4S,HADHB |
| GO:0016491 | MF | oxidoreductase activity | 9.75E-09 | 2.24E-06 | 1.70E-05 | 1.12E-05 | 50 | ABCC4,CYBRD1,ETFB,ETFDH,MDH1,PGK1,ADH6,FBP1,FDX1,AGT,ALDH2,HSD17B2,ALDH6A1,PCYOX1,TRMT9B,FMO5,DHRS4L2,COX11,CP,APOE,CRYM,CRYZ,AKR1C3,CYBA,NDUFS7,DHFRP1,SPR,CYP27A1,BDH2,BCKDHB,NDUFA2,GSTO2,PHGDH,SUMF1,PRDX3,AKR1B10,KCNAB1,SRD5A3,CAT,PRDX2,GSR,BCO2,LOX,PAH,CYP2U1,CYP4F3,ADI1,LTC4S,HADHB,NOSTRIN |
| GO:0042803 | MF | protein homodimerization activity | 1.44E-05 | 1.57E-03 | 1.19E-02 | 1.65E-02 | 43 | PDK1,KCNIP3,PLEKHB1,HOGA1,SCP2,MME,ANXA9,UGT1A10,UGT1A8,UGT1A7,UGT1A6,AGR2,OLFM4,SHMT1,UGT1A9,BIRC5,BCAS1,APOE,DNPH1,CRP,UGT1A4,UGT1A1,UGT1A3,CRYM,PSAP,GALM,SPR,LHPP,ERFE,GJB1,CARD9,DPY30,SUMF1,ATP5IF1,NTRK2,CASR,CAT,GSR,TFRC,GSTA4,PAH,TOP2A,MAD2L1 |
| GO:0042802 | MF | identical protein binding | 5.34E-04 | 2.33E-02 | 1.78E-01 | 6.13E-01 | 64 | PDK1,ACYP2,KCNIP3,PLEKHB1,TTR,FBP1,HOGA1,SUN2,SCP2,GPSM2,FGFR3,ALCAM,MME,ALDH2,ANXA9,UGT1A10,UGT1A8,UGT1A7,UGT1A6,AGR2,OLFM4,SHMT1,UGT1A9,BIRC5,VWA1,BCAS1,APOE,DNPH1,AQP1,CRP,UGT1A4,UGT1A1,UGT1A3,CRYM,CLDN16,PSAP,GALM,SPR,SRI,LHPP,GSTO2,ERFE,GJB1,CARD9,DPY30,SUMF1,PRDX3,VWA2,DPYSL2,ATP5IF1,NTRK2,CASR,CAT,CLDN10,LEPR,GSR,TFRC,GSTA4,BNIPL,PAH,LTC4S,LYZ,TOP2A,MAD2L1 |
| GO:0008233 | MF | peptidase activity | 1.14E-02 | 1.27E-01 | 9.64E-01 | 1.00E+00 | 40 | CFTR,SERPINA4,WFDC2,AGT,MME,MMP7,HSPE1,ARL6IP5,TMEM59,SHH,TMPRSS4,BIRC5,PRSS33,CPM,CFI,AQP1,ARRB1,MMEL1,SLPI,CTSH,CTSV,SORL1,KLK7,KLK6,SPCS2,TOMM20,PSMD10,ACE,ITIH2,GGT1,RHBDL2,CARD9,PRDX3,PCSK1N,RNF128,RARRES1,PIGK,ACE2,KY,SERPINA5 |
| GO:0098772 | MF | molecular function regulator | 2.54E-02 | 1.43E-01 | 1.00E+00 | 1.00E+00 | 53 | CFTR,KCNIP3,TTR,SERPINA4,METRN,WFDC2,AGT,CDNF,GPSM2,HACD3,UGT1A8,UGT1A7,SHH,BIRC5,DEPDC1,APOE,TBC1D3B,SEMA4G,UGT1A1,LEFTY1,ARHGDIB,ARRB1,CSPG5,PDGFD,SLPI,CD24,CTSH,SNTA1,SEMA3E,PSAP,SPP1,BCAS3,SRI,ADGRB3,ITIH2,STC1,ERFE,PRDX3,LRRC26,KCNAB1,PCSK1N,KCNMB4,ATP5IF1,KCNE3,RARRES1,NRTN,SEMA5A,OAZ1,STMN1,TMBIM6,LTC4S,SERPINA5,ARHGAP19 |
| GO:0005102 | MF | signaling receptor binding | 3.50E-02 | 1.65E-01 | 1.00E+00 | 1.00E+00 | 50 | RERG,TTR,HMGN3,ADORA1,AP2M1,METRN,AGT,CTHRC1,SCP2,CDNF,ALCAM,AGR2,SHH,NLGN1,APOE,AQP1,SEMA4G,CRP,LEFTY1,ARRB1,IGFBP2,CNIH4,ASAH1,CSPG5,PDGFD,CTSH,SEMA3E,PSAP,SPP1,BCAS3,SRI,ACE,STC1,ERFE,PCSK1N,NR1H4,RARRES2,NRTN,DNAAF4,NTRK2,VTCN1,SEMA5A,CASR,CAT,TF,ACE2,HHLA2,CD1D,LOX,TSPAN8 |
| GO:0015318 | MF | inorganic molecular entity transmembrane transporter activity | 4.02E-02 | 1.65E-01 | 1.00E+00 | 1.00E+00 | 32 | ATPSCKMT,ABCC4,CFTR,MAGT1,KCNIP3,SCNN1A,CNGA1,PCYOX1,MPC2,NLGN1,AQP1,SLC3A1,SLC12A2,CLDN16,TMEM37,SNAP25,SLC45A1,SNTA1,SLC16A10,SRI,LRRC26,KCNAB1,KCNMB4,SLC38A11,STRA6,SLC25A21,KCNE3,SLC38A4,SLC39A10,TF,TFRC,ORAI3 |
| GO:0030234 | MF | enzyme regulator activity | 9.38E-02 | 2.43E-01 | 1.00E+00 | 1.00E+00 | 30 | SERPINA4,WFDC2,AGT,GPSM2,HACD3,UGT1A8,UGT1A7,BIRC5,DEPDC1,APOE,TBC1D3B,UGT1A1,ARHGDIB,ARRB1,SLPI,CD24,CTSH,PSAP,BCAS3,ADGRB3,ITIH2,PRDX3,PCSK1N,ATP5IF1,RARRES1,OAZ1,TMBIM6,LTC4S,SERPINA5,ARHGAP19 |
| GO:0016818 | MF | hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides | 1.01E-01 | 2.48E-01 | 1.00E+00 | 1.00E+00 | 39 | ATPSCKMT,RERG,ABCC4,CFTR,ACYP2,TUBB4A,PROM2,PIN1,MYO3B,GPSM2,RAB26,TRAPPC6A,PCYOX1,HACD3,DEPDC1,TBC1D3B,ARHGDIB,ARL3,ARRB1,PPA2,SMARCA2,BCAS3,ADGRB3,LHPP,GNG12,TUBA1A,ODAM,GNG7,GNG11,RAD51B,ATP5IF1,CFAP73,NTRK2,CASR,BNIPL,ENTPD3,TOP2A,ENTPD8,ARHGAP19 |
| GO:0046914 | MF | transition metal ion binding | 1.18E-01 | 2.75E-01 | 1.00E+00 | 1.00E+00 | 30 | ADH6,FDX1,QPCT,MME,MMP7,PRIMPOL,SHH,SHMT1,COX11,CP,BIRC5,CPM,CRYZ,MMEL1,DNLZ,CYP27A1,ACE,SUMF1,NR1H4,CA12,TCEA3,CALB1,TF,CUTC,ACE2,LOX,PAH,CYP2U1,CYP4F3,ADI1 |

Biological Process(BP), Cellular Component(CC) and Molecular Functions (MF)

**Table 6** Topology table for up and down regulated genes

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Regulation** | **Node** | **Degree** | **Betweenness** | **Stress** | **Closeness** | **Clustering Coefficient** |
| Up | JUN | 1463 | 0.391453 | 1.016E+09 | 0.415898 | 2.86E-04 |
| Up | FBXO6 | 621 | 0.12966 | 493715688 | 0.353842 | 5.75E-05 |
| Up | CYLD | 608 | 0.103943 | 382426264 | 0.359075 | 7.80E-04 |
| Up | IFI16 | 432 | 0.074647 | 147288646 | 0.349575 | 0.001063 |
| Up | ADRB2 | 307 | 0.065447 | 120555780 | 0.338941 | 4.13E-04 |
| Up | TRAF1 | 264 | 0.063246 | 72422838 | 0.337611 | 0.001467 |
| Up | TNF | 259 | 0.03929 | 76146724 | 0.344238 | 0.004256 |
| Up | PML | 234 | 0.056839 | 32809074 | 0.374284 | 0.004516 |
| Up | ISG15 | 198 | 0.033378 | 48463634 | 0.341138 | 0.003846 |
| Up | ICAM1 | 172 | 0.020484 | 54377736 | 0.31907 | 8.16E-04 |
| Up | NFKBIA | 171 | 0.026417 | 48434352 | 0.328288 | 0.002352 |
| Up | ZC3HAV1 | 157 | 0.022112 | 12840580 | 0.362234 | 0.011922 |
| Up | LMO2 | 155 | 0.032438 | 32263182 | 0.314392 | 4.36E-04 |
| Up | ACTA1 | 148 | 0.027304 | 30357948 | 0.328193 | 8.50E-04 |
| Up | FOS | 132 | 0.014696 | 19098404 | 0.322621 | 0.007871 |
| Up | PPP1R15A | 130 | 0.015717 | 52057574 | 0.305846 | 0 |
| Up | SPRY2 | 128 | 0.024553 | 23663296 | 0.310628 | 0.002839 |
| Up | STX11 | 110 | 0.022909 | 25856594 | 0.305533 | 0 |
| Up | JAK2 | 109 | 0.018338 | 18613612 | 0.321526 | 0.009346 |
| Up | RELB | 104 | 0.009702 | 17452368 | 0.316176 | 0.006139 |
| Up | TRIM21 | 103 | 0.019363 | 9498044 | 0.339934 | 0.005347 |
| Up | PLAUR | 96 | 0.024508 | 28704600 | 0.297799 | 2.19E-04 |
| Up | MIR21 | 96 | 0.006608 | 34185424 | 0.292104 | 0 |
| Up | TNFAIP3 | 93 | 0.014225 | 10441280 | 0.329735 | 0.018315 |
| Up | UBE2L6 | 91 | 0.01148 | 13366068 | 0.319914 | 0.00293 |
| Up | XRN1 | 91 | 0.017619 | 6441514 | 0.350222 | 0.013675 |
| Up | AMOTL2 | 89 | 0.015533 | 27398694 | 0.29877 | 0 |
| Up | SAMHD1 | 86 | 0.010242 | 19438896 | 0.308118 | 0 |
| Up | SOCS3 | 77 | 0.014788 | 9258178 | 0.322804 | 0.011962 |
| Up | IFIT3 | 76 | 0.005604 | 8632792 | 0.311342 | 0.028508 |
| Up | LGALS9 | 74 | 0.015887 | 21471046 | 0.280482 | 0 |
| Up | PCK1 | 74 | 0.005113 | 16092358 | 0.298315 | 0 |
| Up | CYP1A1 | 70 | 0.011023 | 20286860 | 0.2879 | 0 |
| Up | PSMB9 | 64 | 0.007914 | 24671042 | 0.287682 | 0.001586 |
| Up | ATF3 | 63 | 0.006767 | 2850414 | 0.344176 | 0.029508 |
| Up | DDX58 | 62 | 0.007815 | 3885286 | 0.333177 | 0.015819 |
| Up | SOCS1 | 62 | 0.007568 | 4945796 | 0.310696 | 0.023268 |
| Up | TENT5A | 62 | 0.011895 | 11622694 | 0.29122 | 0 |
| Up | ZFP36 | 62 | 0.009922 | 5629422 | 0.318712 | 0.010048 |
| Up | NLRP3 | 57 | 0.007142 | 11376526 | 0.291789 | 0 |
| Up | CD274 | 56 | 0.011395 | 7918474 | 0.287115 | 0 |
| Up | CREB5 | 56 | 0.009697 | 3368448 | 0.336831 | 0.031447 |
| Up | DNAJB4 | 54 | 0.011227 | 2848256 | 0.34196 | 0.014675 |
| Up | HIVEP1 | 53 | 0.008651 | 7583710 | 0.299921 | 0 |
| Up | ARRDC3 | 52 | 0.009286 | 4496646 | 0.311428 | 0.008296 |
| Up | PRKD2 | 52 | 0.008496 | 8986048 | 0.297285 | 0 |
| Up | EPHA4 | 51 | 0.009698 | 7488664 | 0.298393 | 0 |
| Up | TNFSF13B | 51 | 0.010004 | 14670962 | 0.273765 | 0 |
| Up | FAM110B | 51 | 0.012282 | 5854450 | 0.287391 | 0 |
| Up | GJB7 | 51 | 0.01113 | 6654884 | 0.280247 | 0 |
| Up | IFIT1 | 50 | 0.003257 | 3831088 | 0.307817 | 0.048163 |
| Up | GATA3 | 50 | 0.007535 | 4224572 | 0.309696 | 0.005714 |
| Up | TRIM5 | 49 | 0.004714 | 4647006 | 0.302927 | 0.004625 |
| Up | PPEF1 | 49 | 0.002709 | 10148694 | 0.282518 | 0 |
| Up | SYT1 | 48 | 0.010026 | 11473940 | 0.284712 | 0 |
| Up | STAT2 | 47 | 0.008114 | 3894220 | 0.31474 | 0.006061 |
| Up | TXNIP | 47 | 0.006288 | 7234358 | 0.30968 | 0 |
| Up | IFIT2 | 47 | 0.002695 | 2415382 | 0.316828 | 0.053654 |
| Up | BCL3 | 46 | 0.005598 | 3853674 | 0.350741 | 0.04058 |
| Up | IRF7 | 46 | 0.005525 | 2722200 | 0.308335 | 0.028541 |
| Up | PTGER4 | 46 | 0.008846 | 8712240 | 0.285973 | 0 |
| Up | HERC5 | 46 | 0.00626 | 1999072 | 0.339508 | 0.02029 |
| Up | DUSP1 | 43 | 0.007404 | 9881246 | 0.285729 | 0 |
| Up | IFIH1 | 43 | 0.005107 | 4427676 | 0.295676 | 0.002439 |
| Up | DTX3L | 43 | 0.004014 | 2749452 | 0.307717 | 0.006098 |
| Up | MAP3K8 | 42 | 0.002033 | 5606884 | 0.297316 | 0 |
| Up | EGR1 | 42 | 0.005365 | 10758488 | 0.288984 | 0 |
| Up | DUSP8 | 40 | 0.007103 | 9679710 | 0.275464 | 0 |
| Up | TAP1 | 39 | 0.005951 | 5400094 | 0.284128 | 0.004505 |
| Up | TICAM1 | 38 | 0.00429 | 1735214 | 0.304632 | 0.039683 |
| Up | EPC1 | 37 | 0.005568 | 10528994 | 0.28026 | 0 |
| Up | TRIM69 | 37 | 0.008196 | 1832444 | 0.296555 | 0.001681 |
| Up | NPTX1 | 37 | 0.010108 | 2709042 | 0.306803 | 0 |
| Up | ETS2 | 36 | 0.004578 | 1417696 | 0.336891 | 0.044563 |
| Up | PPM1K | 36 | 0.006375 | 7409146 | 0.28366 | 0 |
| Up | GRIA2 | 35 | 0.008317 | 5355686 | 0.277063 | 0.001681 |
| Up | PTGS2 | 35 | 0.003066 | 5240048 | 0.300524 | 0 |
| Up | MXD1 | 34 | 0.00566 | 6501490 | 0.280219 | 0 |
| Up | BDKRB2 | 33 | 0.006217 | 6153240 | 0.279998 | 0 |
| Up | KLF4 | 32 | 0.002673 | 3840432 | 0.292751 | 0.004032 |
| Up | IRF1 | 32 | 0.001962 | 3474450 | 0.294755 | 0 |
| Up | IFIT5 | 32 | 0.002218 | 1820152 | 0.309208 | 0.032258 |
| Up | FLT3 | 31 | 0.004016 | 1494250 | 0.30156 | 0.027094 |
| Up | ZNFX1 | 31 | 0.004309 | 6508432 | 0.283632 | 0 |
| Up | C4A | 30 | 0.007292 | 3247912 | 0.285614 | 0.002299 |
| Up | TRIM38 | 30 | 0.002344 | 2355780 | 0.292389 | 0.005291 |
| Up | NOCT | 29 | 0.006399 | 2073096 | 0.275504 | 0.002463 |
| Up | SNCAIP | 28 | 0.003401 | 3245970 | 0.286002 | 0 |
| Up | DACT1 | 28 | 0.003146 | 3928826 | 0.291744 | 0 |
| Up | MT2A | 27 | 0.003912 | 4760352 | 0.275544 | 0 |
| Up | USP18 | 27 | 0.003059 | 1225134 | 0.300381 | 0.005698 |
| Up | ZC3H12A | 27 | 0.00213 | 2801102 | 0.289662 | 0 |
| Up | GADD45B | 25 | 0.003888 | 3366314 | 0.272767 | 0 |
| Up | PELI1 | 25 | 0.00249 | 2957160 | 0.277265 | 0 |
| Up | DUSP26 | 25 | 0.004535 | 2941596 | 0.278488 | 0 |
| Up | PROX1 | 24 | 0.004285 | 16107194 | 0.271437 | 0 |
| Up | COL8A1 | 24 | 0.003169 | 2213366 | 0.284015 | 0.032609 |
| Up | CPEB2 | 24 | 0.004295 | 4467186 | 0.274241 | 0 |
| Up | EYA1 | 23 | 0.002153 | 2128522 | 0.275973 | 0 |
| Up | IQUB | 23 | 0.002391 | 1203500 | 0.263202 | 0 |
| Up | BMP2 | 22 | 0.004312 | 18691536 | 0.221641 | 0 |
| Up | DUSP10 | 22 | 0.002204 | 2864262 | 0.280288 | 0 |
| Up | GBP1 | 22 | 0.002595 | 1000546 | 0.297971 | 0.010526 |
| Up | COL4A1 | 22 | 0.002863 | 2607454 | 0.271101 | 0 |
| Up | FAP | 22 | 0.005548 | 3870386 | 0.269698 | 0 |
| Up | OGFR | 22 | 0.002205 | 2655202 | 0.281301 | 0 |
| Up | SUSD3 | 22 | 0.004704 | 4071688 | 0.256165 | 0 |
| Up | SIX2 | 21 | 0.003571 | 8412618 | 0.276712 | 0 |
| Up | SERPINE1 | 21 | 0.002642 | 2835100 | 0.274426 | 0 |
| Up | TNFSF10 | 21 | 0.001951 | 568660 | 0.293325 | 0.035088 |
| Up | SH2D1B | 21 | 0.002804 | 2711936 | 0.275705 | 0 |
| Up | GFI1 | 20 | 0.001671 | 2287272 | 0.280745 | 0 |
| Up | CCL2 | 20 | 0.003651 | 13213044 | 0.254365 | 0 |
| Up | STX19 | 20 | 0.002016 | 4118520 | 0.263629 | 0 |
| Up | GFPT2 | 20 | 0.003471 | 3336484 | 0.262581 | 0 |
| Up | EPSTI1 | 20 | 0.00325 | 3249910 | 0.280981 | 0 |
| Up | ID4 | 19 | 0.002629 | 4326290 | 0.272335 | 0 |
| Up | GLI2 | 19 | 0.001432 | 1621152 | 0.289573 | 0 |
| Up | KIF26B | 19 | 0.002895 | 7592782 | 0.272845 | 0 |
| Up | HSD17B14 | 19 | 0.002848 | 2576328 | 0.267943 | 0 |
| Up | NT5C3A | 19 | 0.003246 | 2228448 | 0.27052 | 0 |
| Up | SP110 | 19 | 0.003311 | 10407810 | 0.270224 | 0 |
| Up | PARP12 | 19 | 0.001835 | 1556266 | 0.289219 | 0 |
| Up | FBLN2 | 17 | 0.002375 | 4342946 | 0.24669 | 0 |
| Up | CXCL8 | 17 | 0.003104 | 5807616 | 0.261602 | 0 |
| Up | BATF2 | 17 | 0.001488 | 673498 | 0.316846 | 0.066176 |
| Up | NUAK2 | 17 | 0.001431 | 1869996 | 0.28655 | 0 |
| Up | DHX58 | 17 | 7.56E-04 | 378214 | 0.283547 | 0.022059 |
| Up | EGR2 | 17 | 0.001365 | 1236754 | 0.273094 | 0 |
| Up | HSH2D | 16 | 0.002763 | 4324164 | 0.251717 | 0 |
| Up | ICAM5 | 16 | 0.003076 | 975228 | 0.287944 | 0.008333 |
| Up | BAHCC1 | 16 | 0.0028 | 2723838 | 0.269009 | 0 |
| Up | HLX | 16 | 0.002307 | 11160974 | 0.260989 | 0 |
| Up | KLF6 | 15 | 0.001547 | 970324 | 0.277414 | 0.019048 |
| Up | PMAIP1 | 15 | 0.001884 | 1642980 | 0.27736 | 0 |
| Up | PTX3 | 15 | 0.002898 | 9388846 | 0.228184 | 0 |
| Up | FST | 15 | 0.004416 | 4435932 | 0.262097 | 0 |
| Up | DDR2 | 15 | 0.001744 | 1518680 | 0.292209 | 0 |
| Up | HELZ2 | 15 | 0.001613 | 443664 | 0.303672 | 0.028571 |
| Up | CAVIN2 | 15 | 0.001682 | 2412720 | 0.268133 | 0 |
| Up | PLEKHG5 | 15 | 0.001572 | 1701170 | 0.276053 | 0 |
| Up | CSF2 | 14 | 0.00116 | 1889870 | 0.269852 | 0 |
| Up | RGS16 | 14 | 0.001861 | 718520 | 0.287667 | 0 |
| Up | TRPC4 | 14 | 0.002828 | 1943444 | 0.264009 | 0 |
| Up | RBM11 | 14 | 0.001878 | 1828290 | 0.272871 | 0 |
| Up | FAM153B | 14 | 0.002653 | 3477710 | 0.257874 | 0 |
| Up | RND1 | 13 | 0.002239 | 1185570 | 0.258885 | 0 |
| Up | TDRD7 | 13 | 0.001582 | 1442486 | 0.260846 | 0 |
| Up | HSPB9 | 13 | 0.00286 | 5829338 | 0.236701 | 0 |
| Up | CCDC116 | 13 | 0.002082 | 461686 | 0.278516 | 0 |
| Up | PDE4B | 13 | 9.28E-04 | 990686 | 0.276739 | 0 |
| Up | MB21D2 | 13 | 0.002789 | 3445016 | 0.299699 | 0.012821 |
| Up | BBC3 | 12 | 0.001158 | 1273498 | 0.274918 | 0 |
| Up | RRAD | 12 | 0.001005 | 1216160 | 0.275558 | 0 |
| Up | XAF1 | 12 | 8.16E-04 | 854676 | 0.271399 | 0 |
| Up | HIVEP2 | 12 | 5.59E-04 | 1066810 | 0.27808 | 0 |
| Up | RASD1 | 12 | 0.001236 | 1637624 | 0.263605 | 0 |
| Up | GRIP2 | 12 | 0.001639 | 459476 | 0.270959 | 0.015152 |
| Up | WIF1 | 12 | 0.001258 | 1533126 | 0.248752 | 0 |
| Up | HSD17B3 | 12 | 0.00121 | 960490 | 0.266448 | 0 |
| Up | CLPSL1 | 12 | 0.002625 | 4984078 | 0.238569 | 0 |
| Up | TRIM22 | 12 | 0.001699 | 3885096 | 0.261988 | 0 |
| Up | CX3CL1 | 11 | 8.21E-04 | 5602570 | 0.221167 | 0 |
| Up | IL7R | 11 | 6.04E-04 | 214668 | 0.279173 | 0.054545 |
| Up | IL15RA | 11 | 8.68E-04 | 439258 | 0.257104 | 0 |
| Up | NCOA7 | 11 | 0.001109 | 1176472 | 0.271528 | 0 |
| Up | TLR6 | 11 | 0.001923 | 546340 | 0.255762 | 0 |
| Up | IL1A | 10 | 7.77E-04 | 3293906 | 0.239706 | 0 |
| Up | PDZD2 | 10 | 9.97E-04 | 1491868 | 0.267514 | 0 |
| Up | DRD1 | 10 | 0.001536 | 1383092 | 0.255371 | 0 |
| Up | ADGRL3 | 10 | 0.001968 | 1838502 | 0.24909 | 0.022222 |
| Up | ISG20 | 10 | 0.001009 | 739652 | 0.238719 | 0 |
| Up | IL12A | 9 | 0.001778 | 5075032 | 0.223481 | 0 |
| Up | INHBA | 9 | 0.001875 | 1683324 | 0.208155 | 0 |
| Up | KLF2 | 9 | 0.00115 | 2979256 | 0.269711 | 0 |
| Up | SLC30A3 | 9 | 0.001761 | 2282282 | 0.252219 | 0 |
| Up | LYL1 | 9 | 7.29E-04 | 325024 | 0.27736 | 0.083333 |
| Up | PARP10 | 9 | 8.53E-04 | 831780 | 0.279777 | 0 |
| Up | RASGRP3 | 9 | 0.001478 | 1136680 | 0.261121 | 0 |
| Up | ETV7 | 9 | 0.001819 | 3573824 | 0.236582 | 0 |
| Up | TENT5C | 9 | 7.10E-04 | 1401768 | 0.266648 | 0 |
| Up | OASL | 9 | 0.001171 | 1046730 | 0.232716 | 0 |
| Up | TRIM40 | 9 | 1.64E-04 | 65598 | 0.273173 | 0.083333 |
| Up | MXRA5 | 9 | 8.23E-04 | 1006366 | 0.262618 | 0 |
| Up | SLC5A5 | 9 | 0.001806 | 2393436 | 0.248155 | 0 |
| Up | FOSB | 8 | 1.57E-04 | 163366 | 0.305813 | 0.285714 |
| Up | IFI35 | 8 | 7.73E-04 | 252820 | 0.275584 | 0.035714 |
| Up | UBA7 | 8 | 0.001825 | 1905274 | 0.260165 | 0 |
| Up | ACHE | 8 | 7.17E-04 | 660488 | 0.260129 | 0 |
| Up | CXCL9 | 8 | 0.001775 | 584820 | 0.193694 | 0 |
| Up | HUS1B | 8 | 0.001773 | 914094 | 0.22299 | 0 |
| Up | NCKAP5 | 8 | 8.91E-05 | 92984 | 0.271243 | 0 |
| Up | TTBK1 | 8 | 3.65E-04 | 856610 | 0.259464 | 0 |
| Up | OAS1 | 8 | 6.22E-04 | 760138 | 0.25976 | 0 |
| Up | CCRL2 | 8 | 0.001801 | 7031454 | 0.228901 | 0 |
| Up | CD69 | 8 | 0.001176 | 2347246 | 0.235689 | 0 |
| Up | C17orf82 | 8 | 9.12E-04 | 1038246 | 0.261638 | 0 |
| Up | GLCCI1 | 8 | 0.001077 | 2135006 | 0.261277 | 0 |
| Up | CCDC65 | 8 | 5.11E-04 | 860378 | 0.253763 | 0 |
| Up | APOL6 | 8 | 8.59E-04 | 1253550 | 0.255061 | 0 |
| Up | SSTR2 | 7 | 0.001449 | 2000906 | 0.262934 | 0 |
| Up | TNFRSF4 | 7 | 4.65E-04 | 227678 | 0.266999 | 0.142857 |
| Up | IL22RA1 | 7 | 0.002111 | 2414238 | 0.247592 | 0 |
| Up | KLB | 7 | 4.75E-04 | 631206 | 0.255394 | 0 |
| Up | RSAD2 | 7 | 0.001763 | 1461322 | 0.248839 | 0 |
| Up | ZNF627 | 7 | 0.002111 | 4319562 | 0.227471 | 0 |
| Up | CSRNP1 | 7 | 3.95E-04 | 377470 | 0.271931 | 0 |
| Up | CXCL2 | 7 | 0.001037 | 1235666 | 0.254913 | 0 |
| Up | C1QTNF1 | 7 | 5.31E-04 | 528034 | 0.261928 | 0 |
| Up | NYAP2 | 7 | 0.001115 | 4594960 | 0.221029 | 0 |
| Up | GIMAP2 | 7 | 0.001056 | 6411806 | 0.216177 | 0 |
| Up | SOGA3 | 7 | 0.001422 | 1398048 | 0.235954 | 0 |
| Up | PHF11 | 7 | 8.65E-04 | 1177296 | 0.246326 | 0 |
| Up | SAMD9 | 7 | 5.62E-04 | 1172518 | 0.244356 | 0 |
| Up | DNAH3 | 7 | 3.73E-04 | 1306158 | 0.26246 | 0 |
| Up | SLFN5 | 7 | 1.09E-04 | 132916 | 0.265254 | 0 |
| Up | HDX | 7 | 4.07E-04 | 93906 | 0.292059 | 0.047619 |
| Up | MYLPF | 7 | 0.001061 | 1102698 | 0.238569 | 0 |
| Up | ZNF433 | 7 | 1.90E-05 | 18816 | 0.239444 | 0 |
| Up | PDE2A | 6 | 4.57E-05 | 44722 | 0.245708 | 0 |
| Up | DRP2 | 6 | 7.14E-04 | 620154 | 0.261843 | 0 |
| Up | CXCL11 | 6 | 8.04E-04 | 968686 | 0.247248 | 0 |
| Up | MX2 | 6 | 1.86E-05 | 16086 | 0.238299 | 0 |
| Up | REC8 | 6 | 7.19E-04 | 1880208 | 0.245284 | 0 |
| Up | FLRT3 | 6 | 6.90E-04 | 524162 | 0.253085 | 0.066667 |
| Up | PLAC8 | 6 | 6.37E-04 | 133872 | 0.290833 | 0 |
| Up | IFITM1 | 6 | 0.001056 | 2302398 | 0.20584 | 0 |
| Up | BARX1 | 6 | 0.001759 | 652470 | 0.196324 | 0 |
| Up | NEURL1 | 6 | 4.14E-04 | 729676 | 0.262824 | 0 |
| Up | TTC9B | 6 | 7.39E-04 | 1226806 | 0.252052 | 0 |
| Up | RPL39P5 | 6 | 9.53E-05 | 127766 | 0.251918 | 0 |
| Up | CCL20 | 5 | 8.10E-04 | 1464858 | 0.25241 | 0 |
| Up | NFKBIZ | 5 | 1.20E-04 | 92196 | 0.259464 | 0 |
| Up | IL6 | 5 | 4.44E-05 | 25698 | 0.236248 | 0 |
| Up | PPP4R4 | 5 | 4.06E-04 | 411532 | 0.26492 | 0 |
| Up | NPR3 | 5 | 8.05E-04 | 1437156 | 0.250485 | 0 |
| Up | HEG1 | 5 | 4.36E-04 | 420686 | 0.258015 | 0 |
| Up | AHRR | 5 | 3.61E-04 | 911582 | 0.245676 | 0 |
| Up | NLRC5 | 5 | 5.05E-05 | 36762 | 0.280787 | 0 |
| Up | CPEB3 | 5 | 7.21E-04 | 1354408 | 0.25798 | 0 |
| Up | DDX60L | 5 | 5.58E-04 | 106390 | 0.285757 | 0 |
| Up | TSLP | 5 | 5.41E-05 | 56036 | 0.269481 | 0 |
| Up | C12orf74 | 5 | 0.001408 | 2101516 | 0.239555 | 0 |
| Up | DSCAML1 | 5 | 7.23E-04 | 404406 | 0.235046 | 0 |
| Up | NR4A3 | 4 | 3.74E-04 | 281622 | 0.258461 | 0 |
| Up | IL11 | 4 | 7.69E-04 | 970820 | 0.247992 | 0 |
| Up | FLT3LG | 4 | 3.52E-04 | 441898 | 0.186687 | 0 |
| Up | PTCH2 | 4 | 3.59E-04 | 239450 | 0.261289 | 0 |
| Up | GRM8 | 4 | 4.88E-05 | 60636 | 0.251016 | 0 |
| Up | SLC25A28 | 4 | 7.17E-04 | 314688 | 0.199173 | 0 |
| Up | IFI44 | 4 | 3.54E-04 | 793396 | 0.238359 | 0 |
| Up | FILIP1L | 4 | 6.95E-06 | 17990 | 0.245836 | 0 |
| Up | OAS2 | 4 | 7.09E-04 | 2206848 | 0.213955 | 0 |
| Up | SAMD9L | 4 | 2.02E-04 | 178878 | 0.252601 | 0 |
| Up | IL7 | 3 | 8.89E-06 | 5468 | 0.244188 | 0 |
| Up | CRTAM | 3 | 0 | 0 | 1 | 0 |
| Up | C4B | 3 | 3.67E-04 | 760652 | 0.233856 | 0 |
| Up | IFNB1 | 3 | 0 | 0 | 0.200508 | 0 |
| Up | IFNL1 | 3 | 7.04E-04 | 286726 | 0.181847 | 0 |
| Up | RASGRP1 | 3 | 3.53E-04 | 1636020 | 0.240132 | 0 |
| Up | GMPR | 3 | 0 | 0 | 0.202034 | 0 |
| Up | GRIN3B | 3 | 7.04E-04 | 419778 | 0.178343 | 0 |
| Up | NTNG2 | 3 | 4.15E-04 | 778996 | 0.234997 | 0 |
| Up | THEMIS2 | 3 | 3.57E-04 | 195936 | 0.225199 | 0 |
| Up | TSACC | 3 | 7.04E-04 | 1012770 | 0.237046 | 0 |
| Up | TRANK1 | 3 | 2.83E-05 | 25900 | 0.234725 | 0 |
| Up | PIM3 | 3 | 2.63E-06 | 7676 | 0.267036 | 0 |
| Up | NANOS3 | 3 | 3.86E-04 | 598848 | 0.235309 | 0 |
| Up | SNPH | 3 | 7.04E-04 | 752350 | 0.181481 | 0 |
| Up | CFAP57 | 3 | 9.67E-06 | 10884 | 0.244545 | 0 |
| Up | TCIM | 3 | 3.56E-04 | 282420 | 0.26812 | 0 |
| Up | IFITM2 | 3 | 6.26E-06 | 2138 | 0.243685 | 0 |
| Up | SNED1 | 3 | 3.61E-04 | 312294 | 0.235484 | 0 |
| Up | SLC39A2 | 3 | 7.04E-04 | 419778 | 0.178343 | 0 |
| Up | DNAH17 | 3 | 2.64E-06 | 7226 | 0.242076 | 0 |
| Up | TMEM140 | 3 | 2.65E-04 | 109188 | 0.252567 | 0 |
| Up | LTB | 2 | 1.38E-06 | 880 | 0.222283 | 0 |
| Up | CXCL10 | 2 | 3.52E-06 | 5504 | 0.181319 | 0 |
| Up | SEC16B | 2 | 9.98E-06 | 1564 | 0.207085 | 0 |
| Up | S1PR3 | 2 | 3.52E-04 | 125910 | 0.193246 | 0 |
| Up | SECTM1 | 2 | 7.60E-07 | 1940 | 0.213184 | 0 |
| Up | SYNPR | 2 | 1 | 2 | 1 | 0 |
| Up | ACKR4 | 2 | 3.52E-04 | 105848 | 0.226086 | 0 |
| Up | CXCL3 | 2 | 2.00E-08 | 2 | 0.176017 | 0 |
| Up | HCRTR1 | 2 | 5.90E-07 | 2934 | 0.240712 | 0 |
| Up | IFNL3 | 2 | 1.47E-05 | 1654 | 0.260022 | 0 |
| Up | TIPARP | 2 | 1.60E-07 | 966 | 0.242107 | 0 |
| Up | AGAP7P | 2 | 1.52E-06 | 1108 | 0.237601 | 0 |
| Up | SLC25A2 | 2 | 1.30E-05 | 15088 | 0.202596 | 0 |
| Up | G0S2 | 2 | 3.52E-04 | 538416 | 0.240101 | 0 |
| Up | CH25H | 2 | 1 | 2 | 1 | 0 |
| Up | CYP21A2 | 2 | 1.40E-07 | 304 | 0.253491 | 0 |
| Up | RAB19 | 2 | 1.30E-05 | 22056 | 0.227946 | 0 |
| Up | SPTBN5 | 2 | 5.75E-06 | 2802 | 0.205156 | 0 |
| Up | LSMEM1 | 2 | 1 | 2 | 1 | 0 |
| Up | RAET1L | 1 | 0 | 0 | 1 | 0 |
| Up | FGF19 | 1 | 0 | 0 | 0.190818 | 0 |
| Up | CHAC1 | 1 | 0 | 0 | 0.183444 | 0 |
| Up | PLA2G4C | 1 | 0 | 0 | 0.203904 | 0 |
| Up | MMP25 | 1 | 0 | 0 | 0.223718 | 0 |
| Up | PRRX2 | 1 | 0 | 0 | 0.187494 | 0 |
| Up | FAXDC2 | 1 | 0 | 0 | 0.251483 | 0 |
| Up | MKRN4P | 1 | 0 | 0 | 0.205691 | 0 |
| Up | FGF18 | 1 | 0 | 0 | 0.232051 | 0 |
| Up | RTP4 | 1 | 0 | 0 | 0.203103 | 0 |
| Up | MT2P1 | 1 | 0 | 0 | 1 | 0 |
| Up | NEURL3 | 1 | 0 | 0 | 0.227362 | 0 |
| Up | CLEC4A | 1 | 0 | 0 | 0.251483 | 0 |
| Up | VSTM1 | 1 | 0 | 0 | 0.251483 | 0 |
| Up | SLC6A13 | 1 | 0 | 0 | 0.207934 | 0 |
| Up | SLITRK6 | 1 | 0 | 0 | 0.194803 | 0 |
| Up | IFNL2 | 1 | 0 | 0 | 0.153871 | 0 |
| Up | MT1E | 1 | 0 | 0 | 0.226068 | 0 |
| Down | PCLAF | 812 | 0.218172 | 359294224 | 0.374432 | 4.31E-04 |
| Down | CFTR | 793 | 0.234611 | 322168046 | 0.383841 | 4.83E-04 |
| Down | TUBA1A | 295 | 0.073386 | 95262602 | 0.34024 | 5.53E-04 |
| Down | AURKA | 288 | 0.066175 | 95293564 | 0.335004 | 4.94E-04 |
| Down | ARRB1 | 278 | 0.063576 | 117688160 | 0.330445 | 7.91E-05 |
| Down | AP2M1 | 240 | 0.051023 | 53956278 | 0.334984 | 0.001395 |
| Down | PIN1 | 233 | 0.05541 | 61425008 | 0.322878 | 8.96E-04 |
| Down | PPT1 | 214 | 0.025145 | 56590318 | 0.326664 | 0.001229 |
| Down | KPNA2 | 210 | 0.048841 | 31690140 | 0.359711 | 0.003298 |
| Down | ECH1 | 171 | 0.037362 | 32902382 | 0.320981 | 0.004128 |
| Down | SORT1 | 140 | 0.033936 | 24033152 | 0.310662 | 6.35E-04 |
| Down | NDUFAF8 | 138 | 0.025397 | 14258978 | 0.304976 | 0.00817 |
| Down | TOP2A | 116 | 0.022369 | 13840310 | 0.337511 | 0.005247 |
| Down | SMARCA2 | 110 | 0.021051 | 15613416 | 0.315526 | 0.004003 |
| Down | PHGDH | 106 | 0.015868 | 17099330 | 0.339224 | 0.002516 |
| Down | PRDX2 | 104 | 0.018527 | 11194300 | 0.352394 | 0.016752 |
| Down | HADHB | 100 | 0.014925 | 23497982 | 0.311752 | 0 |
| Down | PRDX3 | 98 | 0.012844 | 11624744 | 0.335122 | 0.010526 |
| Down | MME | 98 | 0.019032 | 19636640 | 0.306291 | 0 |
| Down | NDUFS7 | 95 | 0.020867 | 10021646 | 0.309713 | 0.007246 |
| Down | TFRC | 92 | 0.015457 | 20619840 | 0.317483 | 7.49E-04 |
| Down | SPP1 | 91 | 0.017414 | 22929672 | 0.295261 | 0 |
| Down | PGK1 | 85 | 0.013136 | 10869004 | 0.351413 | 0.013165 |
| Down | HSPE1 | 84 | 0.016392 | 8167734 | 0.343656 | 0.005737 |
| Down | CARD9 | 83 | 0.017033 | 17706614 | 0.273081 | 0 |
| Down | MAD2L1 | 82 | 0.013467 | 11228100 | 0.302331 | 0.003481 |
| Down | APOE | 82 | 0.015722 | 8495082 | 0.309359 | 0.004747 |
| Down | ECI2 | 81 | 0.017144 | 6745260 | 0.334058 | 0.020772 |
| Down | PSMD10 | 80 | 0.011633 | 18967998 | 0.292947 | 0.006013 |
| Down | HACD3 | 76 | 0.011455 | 8537096 | 0.329334 | 0.00386 |
| Down | DPY30 | 69 | 0.012998 | 3608682 | 0.323761 | 0.007689 |
| Down | KRT14 | 68 | 0.007328 | 6921514 | 0.312215 | 0.004662 |
| Down | PGRMC1 | 67 | 0.011618 | 7275690 | 0.331893 | 0.002261 |
| Down | TTR | 62 | 0.011258 | 3849642 | 0.30946 | 0.00452 |
| Down | PDK1 | 62 | 0.015109 | 5811968 | 0.302862 | 0.001695 |
| Down | TF | 62 | 0.013173 | 4442358 | 0.327097 | 0.013115 |
| Down | LSM3 | 60 | 0.010618 | 3544932 | 0.319411 | 0.007345 |
| Down | SORBS2 | 60 | 0.007529 | 12616146 | 0.290046 | 0 |
| Down | SUN2 | 60 | 0.010092 | 10654138 | 0.297316 | 0 |
| Down | AQP1 | 59 | 0.010857 | 15194568 | 0.266273 | 0 |
| Down | FCGRT | 58 | 0.011796 | 10166374 | 0.274506 | 0 |
| Down | SAP30 | 57 | 0.010382 | 4967848 | 0.286536 | 0.005013 |
| Down | BIRC5 | 57 | 0.010055 | 4138496 | 0.302298 | 0.005387 |
| Down | FGFR3 | 57 | 0.010393 | 14039520 | 0.28944 | 0 |
| Down | VSIG1 | 57 | 0.01306 | 15695216 | 0.270636 | 0 |
| Down | PBXIP1 | 54 | 0.010614 | 10304456 | 0.304632 | 0 |
| Down | SIAE | 54 | 0.013244 | 12796284 | 0.265675 | 0 |
| Down | PDCD4 | 53 | 0.006391 | 5609270 | 0.304453 | 0.002353 |
| Down | COA3 | 53 | 0.008434 | 4984146 | 0.285916 | 0.015239 |
| Down | ARL6IP5 | 52 | 0.009516 | 10225900 | 0.285772 | 0 |
| Down | SORL1 | 52 | 0.013461 | 3187416 | 0.320926 | 0.003017 |
| Down | CRP | 52 | 0.010286 | 12871524 | 0.266473 | 0 |
| Down | LYZ | 52 | 0.009492 | 4965110 | 0.333843 | 0.00905 |
| Down | NEK2 | 51 | 0.007854 | 5234492 | 0.286333 | 0.007979 |
| Down | DPYSL2 | 50 | 0.007286 | 7448216 | 0.298377 | 0 |
| Down | KLHDC2 | 50 | 0.008897 | 5250882 | 0.28447 | 0.001633 |
| Down | OAT | 50 | 0.003591 | 5772930 | 0.300619 | 0 |
| Down | MATN2 | 47 | 0.004801 | 8947738 | 0.275011 | 0 |
| Down | EFHC2 | 46 | 0.00998 | 7644676 | 0.283533 | 0 |
| Down | TOMM20 | 45 | 0.005817 | 6307430 | 0.296045 | 0 |
| Down | ALDH2 | 45 | 0.005548 | 3285442 | 0.300143 | 0.014396 |
| Down | PLS1 | 45 | 0.009691 | 9306744 | 0.293962 | 0 |
| Down | SHMT1 | 45 | 0.007636 | 6740640 | 0.289632 | 0 |
| Down | COMMD8 | 43 | 0.010139 | 10786064 | 0.272244 | 0 |
| Down | CAT | 40 | 0.004514 | 2013782 | 0.317253 | 0.009009 |
| Down | PSAP | 38 | 0.006296 | 1613534 | 0.318212 | 0.011111 |
| Down | SNTA1 | 36 | 0.007213 | 4632886 | 0.271788 | 0 |
| Down | IL20RA | 36 | 0.007017 | 3724834 | 0.261061 | 0 |
| Down | FKBP3 | 36 | 0.003137 | 5467580 | 0.286709 | 0 |
| Down | REEP6 | 36 | 0.006396 | 5434122 | 0.27975 | 0 |
| Down | OLFM4 | 36 | 0.009929 | 9248612 | 0.246518 | 0 |
| Down | FBP1 | 35 | 0.005939 | 7368466 | 0.270006 | 0 |
| Down | ASB9 | 35 | 0.003272 | 2351460 | 0.290446 | 0.001681 |
| Down | MACROD1 | 35 | 0.003592 | 4507598 | 0.287857 | 0 |
| Down | ETFB | 34 | 0.003651 | 3852208 | 0.289543 | 0 |
| Down | NTRK2 | 34 | 0.005945 | 2603946 | 0.291385 | 0.004032 |
| Down | STMN1 | 34 | 0.003516 | 4643746 | 0.294526 | 0 |
| Down | BCAS3 | 34 | 0.006118 | 4646608 | 0.287303 | 0.001783 |
| Down | SPCS2 | 34 | 0.006974 | 5087150 | 0.287682 | 0 |
| Down | SNAP25 | 33 | 0.006639 | 6543728 | 0.268945 | 0 |
| Down | NDUFA2 | 33 | 0.003053 | 2154888 | 0.278598 | 0.022727 |
| Down | OAZ1 | 33 | 0.006126 | 5396496 | 0.283278 | 0 |
| Down | EPN3 | 33 | 0.00504 | 1915204 | 0.29334 | 0.003788 |
| Down | MDH1 | 33 | 0.002594 | 4817858 | 0.297347 | 0 |
| Down | ASAH1 | 33 | 0.00488 | 3587898 | 0.28242 | 0 |
| Down | SRI | 32 | 0.005105 | 1488768 | 0.311138 | 0.009195 |
| Down | LOX | 32 | 0.006177 | 4646592 | 0.2841 | 0 |
| Down | AZGP1 | 32 | 0.005468 | 1872944 | 0.316475 | 0.006897 |
| Down | SERPINA5 | 31 | 0.005857 | 7511304 | 0.251639 | 0 |
| Down | ARL3 | 30 | 0.006232 | 13687072 | 0.262061 | 0 |
| Down | USH1C | 30 | 0.005617 | 5497520 | 0.252063 | 0 |
| Down | CENPV | 30 | 0.003211 | 1920008 | 0.291849 | 0.004598 |
| Down | MAGT1 | 30 | 0.004602 | 2336808 | 0.300143 | 0.006897 |
| Down | PPA2 | 30 | 0.003801 | 2369172 | 0.283222 | 0.002299 |
| Down | LEPR | 29 | 0.005342 | 1235306 | 0.287115 | 0.008547 |
| Down | GSR | 29 | 0.003256 | 4520096 | 0.286276 | 0 |
| Down | TMBIM6 | 28 | 0.006617 | 3930572 | 0.266049 | 0 |
| Down | MAGIX | 28 | 0.003725 | 4110518 | 0.252601 | 0 |
| Down | TCTEX1D2 | 27 | 0.004965 | 3306670 | 0.276712 | 0 |
| Down | SLC12A2 | 27 | 0.003475 | 3319408 | 0.2914 | 0 |
| Down | HMGB3 | 27 | 0.003782 | 4552850 | 0.274599 | 0 |
| Down | SCNN1A | 26 | 0.003296 | 2605722 | 0.275131 | 0 |
| Down | UGT1A10 | 26 | 0.003889 | 2182702 | 0.249857 | 0.076087 |
| Down | SGPP1 | 26 | 0.005535 | 2937084 | 0.260022 | 0 |
| Down | AGR2 | 26 | 0.002769 | 2106576 | 0.273055 | 0 |
| Down | FLYWCH2 | 26 | 0.005095 | 4034146 | 0.282771 | 0 |
| Down | MMP7 | 25 | 0.003941 | 5161756 | 0.24307 | 0 |
| Down | KLK7 | 25 | 0.00322 | 1404854 | 0.274665 | 0 |
| Down | QPCT | 25 | 0.003988 | 1675088 | 0.322859 | 0.003333 |
| Down | KCNIP3 | 24 | 0.002929 | 2031928 | 0.270933 | 0 |
| Down | HACD2 | 24 | 0.00282 | 4108012 | 0.268996 | 0 |
| Down | WDR54 | 24 | 0.004613 | 1636010 | 0.262085 | 0 |
| Down | CCDC74B | 24 | 6.32E-04 | 823160 | 0.25976 | 0.068841 |
| Down | GALNT12 | 24 | 0.003388 | 3320846 | 0.243674 | 0 |
| Down | BRI3BP | 24 | 0.002911 | 3155498 | 0.295537 | 0 |
| Down | REPS2 | 23 | 0.002298 | 943312 | 0.293704 | 0.031621 |
| Down | GNG12 | 23 | 0.002502 | 2644352 | 0.28318 | 0 |
| Down | ATP5IF1 | 23 | 0.001796 | 1882604 | 0.278352 | 0 |
| Down | EPHX1 | 23 | 0.003835 | 3846898 | 0.270365 | 0 |
| Down | CTSV | 23 | 0.003354 | 3298694 | 0.270997 | 0 |
| Down | KLK6 | 23 | 0.003994 | 4351866 | 0.255256 | 0 |
| Down | NR1H4 | 22 | 0.002702 | 2827702 | 0.280814 | 0 |
| Down | SCGN | 22 | 0.004697 | 2842038 | 0.257722 | 0 |
| Down | ENDOG | 22 | 0.002925 | 4844118 | 0.262618 | 0 |
| Down | UCP2 | 22 | 0.003189 | 5093696 | 0.267615 | 0 |
| Down | CYBRD1 | 22 | 0.001991 | 2583536 | 0.267413 | 0 |
| Down | FAM171A2 | 22 | 0.005194 | 6237368 | 0.256524 | 0 |
| Down | SLC39A10 | 22 | 0.003962 | 2959034 | 0.281065 | 0 |
| Down | ACO1 | 22 | 0.002762 | 3211908 | 0.27399 | 0 |
| Down | TRAPPC6A | 21 | 0.00429 | 2846052 | 0.233558 | 0 |
| Down | CLGN | 21 | 0.003204 | 2561754 | 0.274135 | 0.009524 |
| Down | TMEM160 | 21 | 0.003642 | 2914984 | 0.265663 | 0 |
| Down | MLEC | 21 | 0.00103 | 1483940 | 0.293461 | 0 |
| Down | CUTC | 21 | 0.002901 | 2747214 | 0.264784 | 0 |
| Down | ITIH2 | 21 | 0.00462 | 2122054 | 0.311223 | 0.004762 |
| Down | CPM | 21 | 0.001225 | 2025788 | 0.267716 | 0 |
| Down | SCP2 | 20 | 0.00205 | 1341952 | 0.279406 | 0 |
| Down | CARHSP1 | 20 | 0.002367 | 900588 | 0.286941 | 0.031579 |
| Down | TSPAN6 | 20 | 0.003276 | 2297122 | 0.253073 | 0 |
| Down | MPC2 | 20 | 0.002196 | 1540396 | 0.286492 | 0.010526 |
| Down | ALCAM | 19 | 0.002306 | 1806346 | 0.285169 | 0 |
| Down | GPSM2 | 19 | 0.003277 | 2315670 | 0.267817 | 0 |
| Down | CTSH | 19 | 0.001797 | 2514428 | 0.262679 | 0 |
| Down | CUEDC2 | 19 | 0.001548 | 798944 | 0.28263 | 0.011696 |
| Down | DNLZ | 19 | 0.003085 | 3592482 | 0.257255 | 0 |
| Down | NTHL1 | 19 | 0.00223 | 3396078 | 0.265526 | 0 |
| Down | ABCC4 | 19 | 0.001862 | 786850 | 0.313853 | 0.040936 |
| Down | HMGN3 | 19 | 0.002456 | 3109514 | 0.259784 | 0 |
| Down | SLAIN1 | 19 | 0.002817 | 3056466 | 0.269545 | 0 |
| Down | PDGFD | 19 | 0.003428 | 1205058 | 0.264895 | 0.005848 |
| Down | CCDC115 | 18 | 0.002826 | 2285326 | 0.261458 | 0 |
| Down | PCYOX1 | 18 | 0.003583 | 8446758 | 0.23677 | 0 |
| Down | CRYZ | 18 | 0.001913 | 2068000 | 0.273462 | 0 |
| Down | CYBA | 17 | 0.002951 | 3808914 | 0.261229 | 0 |
| Down | CASR | 17 | 0.001909 | 1723524 | 0.264784 | 0 |
| Down | NAALADL2 | 17 | 0.003907 | 2420506 | 0.266986 | 0 |
| Down | BPIFB1 | 17 | 0.003539 | 1290834 | 0.296555 | 0 |
| Down | RAD51B | 16 | 0.002526 | 1468392 | 0.256988 | 0 |
| Down | BNIPL | 16 | 0.002098 | 1205590 | 0.25391 | 0 |
| Down | BCKDHB | 16 | 0.001908 | 899240 | 0.284242 | 0.016667 |
| Down | CA12 | 16 | 0.001737 | 1527784 | 0.266086 | 0 |
| Down | ARHGDIB | 16 | 0.001954 | 1503958 | 0.263997 | 0 |
| Down | SPDEF | 16 | 0.003703 | 2566442 | 0.257092 | 0 |
| Down | ACSF2 | 16 | 0.002256 | 917996 | 0.264193 | 0.008333 |
| Down | ITM2A | 16 | 0.002542 | 3570696 | 0.246829 | 0 |
| Down | SYT12 | 16 | 0.00219 | 2456732 | 0.258885 | 0 |
| Down | AGT | 15 | 0.00203 | 1399880 | 0.271217 | 0 |
| Down | SERPINA4 | 15 | 0.002918 | 2511994 | 0.257933 | 0 |
| Down | MAGEE1 | 15 | 0.002044 | 517062 | 0.264291 | 0.012821 |
| Down | COX11 | 15 | 0.001329 | 551426 | 0.283293 | 0.038095 |
| Down | PIGN | 15 | 0.001677 | 1802516 | 0.258484 | 0 |
| Down | AK4 | 15 | 0.002243 | 1781206 | 0.28655 | 0 |
| Down | GNG7 | 14 | 8.07E-04 | 1203444 | 0.240691 | 0 |
| Down | DNAAF4 | 14 | 0.001692 | 1344800 | 0.265043 | 0 |
| Down | RNF128 | 14 | 0.001893 | 1616230 | 0.261109 | 0 |
| Down | PRIMPOL | 14 | 0.002412 | 743698 | 0.264414 | 0.021978 |
| Down | FAHD1 | 14 | 0.002795 | 644508 | 0.288148 | 0 |
| Down | VWA1 | 14 | 0.002625 | 3346112 | 0.239222 | 0 |
| Down | DEPDC1 | 14 | 0.003306 | 1204126 | 0.251694 | 0 |
| Down | PIGK | 13 | 0.001895 | 1583670 | 0.275906 | 0 |
| Down | ADORA1 | 13 | 0.002795 | 7921574 | 0.247841 | 0 |
| Down | UGT1A9 | 13 | 0.001153 | 582216 | 0.24655 | 0.381818 |
| Down | AKR1B10 | 13 | 9.64E-04 | 612592 | 0.25931 | 0 |
| Down | CP | 13 | 3.16E-04 | 334300 | 0.254319 | 0 |
| Down | CNIH4 | 13 | 9.08E-04 | 657858 | 0.272153 | 0 |
| Down | SUMF1 | 13 | 0.00365 | 5382188 | 0.215244 | 0 |
| Down | BTD | 13 | 0.002291 | 4692120 | 0.244093 | 0 |
| Down | HOGA1 | 13 | 4.42E-04 | 139224 | 0.269378 | 0.109091 |
| Down | SLC16A10 | 13 | 0.002765 | 2327152 | 0.248404 | 0 |
| Down | ACOT13 | 12 | 5.34E-04 | 685904 | 0.266485 | 0 |
| Down | TMEM59 | 12 | 0.00124 | 1195426 | 0.283194 | 0 |
| Down | ALDH6A1 | 12 | 0.002667 | 1929240 | 0.298268 | 0.015152 |
| Down | WFDC2 | 12 | 0.002312 | 3710300 | 0.24253 | 0 |
| Down | UGT1A1 | 12 | 4.90E-04 | 234312 | 0.233146 | 0.488889 |
| Down | ARHGAP19 | 12 | 0.001764 | 1175714 | 0.249791 | 0 |
| Down | SHH | 11 | 0.001553 | 1344250 | 0.229892 | 0 |
| Down | GNG11 | 11 | 6.29E-04 | 446072 | 0.231531 | 0 |
| Down | DBP | 11 | 0.002147 | 1263390 | 0.228248 | 0 |
| Down | AKR1C3 | 11 | 0.001585 | 1883162 | 0.23225 | 0 |
| Down | TRMT2B | 11 | 0.001231 | 364378 | 0.270842 | 0.018182 |
| Down | BDH2 | 11 | 0.001938 | 2940122 | 0.227708 | 0 |
| Down | ACBD7 | 11 | 0.001913 | 2665132 | 0.212745 | 0 |
| Down | KCNAB1 | 10 | 0.001578 | 1441876 | 0.262715 | 0 |
| Down | SLPI | 10 | 6.87E-04 | 730598 | 0.272531 | 0 |
| Down | UGT1A7 | 10 | 1.48E-04 | 147666 | 0.232917 | 0.75 |
| Down | NRGN | 10 | 0.001198 | 804138 | 0.243278 | 0 |
| Down | DTYMK | 10 | 4.07E-04 | 477472 | 0.270816 | 0 |
| Down | UGT1A4 | 10 | 3.52E-04 | 360614 | 0.207236 | 0.75 |
| Down | UGT1A6 | 10 | 2.57E-05 | 29130 | 0.217302 | 0.785714 |
| Down | KCNE3 | 10 | 0.001543 | 1658534 | 0.256015 | 0 |
| Down | NLGN1 | 9 | 0.001779 | 757946 | 0.219036 | 0 |
| Down | CAB39L | 9 | 0.001094 | 1068850 | 0.262885 | 0 |
| Down | HOXA13 | 9 | 0.001512 | 1290038 | 0.226799 | 0 |
| Down | PAIP2B | 9 | 0.001063 | 1289582 | 0.251305 | 0 |
| Down | ADI1 | 9 | 8.03E-04 | 780520 | 0.275411 | 0 |
| Down | SYT5 | 9 | 7.92E-04 | 785402 | 0.239182 | 0 |
| Down | GSTO2 | 9 | 0.002108 | 2906418 | 0.224479 | 0 |
| Down | UGT1A3 | 9 | 0 | 0 | 0.207229 | 1 |
| Down | ADH6 | 9 | 0.001175 | 245930 | 0.276308 | 0 |
| Down | UGT1A8 | 9 | 0 | 0 | 0.207229 | 1 |
| Down | ROS1 | 8 | 6.06E-04 | 472030 | 0.266074 | 0 |
| Down | BCAS1 | 8 | 6.06E-04 | 363330 | 0.268209 | 0 |
| Down | FDX1 | 8 | 0.001103 | 578096 | 0.262254 | 0 |
| Down | RTL8B | 8 | 0.001779 | 672198 | 0.213144 | 0 |
| Down | PLEKHB1 | 8 | 0.001437 | 1463156 | 0.205572 | 0 |
| Down | ACSS1 | 8 | 5.15E-04 | 157658 | 0.275011 | 0.107143 |
| Down | TEX15 | 8 | 4.88E-04 | 386702 | 0.254114 | 0 |
| Down | SEMA4G | 8 | 3.65E-04 | 316380 | 0.239071 | 0 |
| Down | COX16 | 8 | 0.001217 | 335052 | 0.23265 | 0.035714 |
| Down | TPGS1 | 8 | 0.001772 | 1501030 | 0.252972 | 0 |
| Down | AIF1L | 8 | 5.96E-04 | 573374 | 0.269596 | 0 |
| Down | REX1BD | 7 | 4.37E-04 | 306602 | 0.249287 | 0 |
| Down | GSTA4 | 7 | 5.87E-04 | 389590 | 0.23207 | 0 |
| Down | CALB1 | 7 | 0.001079 | 789700 | 0.242831 | 0 |
| Down | PCSK1N | 7 | 0.001089 | 438704 | 0.209043 | 0 |
| Down | ANXA13 | 7 | 0.001413 | 2971764 | 0.231145 | 0 |
| Down | SLC25A21 | 7 | 0.001078 | 835750 | 0.256872 | 0 |
| Down | METTL7A | 7 | 7.06E-04 | 226918 | 0.266136 | 0 |
| Down | SPR | 7 | 1.04E-04 | 183356 | 0.267754 | 0 |
| Down | VWA2 | 7 | 8.79E-04 | 427782 | 0.264033 | 0 |
| Down | HMGB1P1 | 7 | 1.51E-04 | 188006 | 0.261001 | 0 |
| Down | NOSTRIN | 6 | 7.25E-04 | 1004432 | 0.234619 | 0 |
| Down | HOXA2 | 6 | 5.68E-04 | 782382 | 0.239524 | 0 |
| Down | GJB1 | 6 | 4.17E-04 | 275550 | 0.256872 | 0 |
| Down | SRPX | 6 | 3.79E-04 | 352136 | 0.245793 | 0 |
| Down | HOXA11 | 6 | 8.52E-04 | 787204 | 0.243455 | 0 |
| Down | CSPG5 | 6 | 7.25E-04 | 995570 | 0.226501 | 0 |
| Down | DDC | 6 | 3.64E-04 | 211502 | 0.244777 | 0 |
| Down | CRYM | 6 | 7.21E-04 | 929406 | 0.244766 | 0 |
| Down | DNPH1 | 6 | 3.57E-04 | 308250 | 0.232089 | 0 |
| Down | RAB26 | 6 | 0.001431 | 550126 | 0.190658 | 0 |
| Down | GGT1 | 6 | 0.001081 | 2176244 | 0.23106 | 0 |
| Down | TSPAN10 | 6 | 4.57E-04 | 332150 | 0.269162 | 0 |
| Down | ACE2 | 6 | 3.97E-04 | 78710 | 0.242014 | 0 |
| Down | CLDN10 | 6 | 8.18E-04 | 719788 | 0.246572 | 0 |
| Down | DHRS4L2 | 6 | 5.66E-04 | 410300 | 0.233385 | 0 |
| Down | NUBPL | 6 | 8.67E-05 | 104668 | 0.261085 | 0 |
| Down | SYNGR1 | 6 | 6.16E-04 | 562506 | 0.243978 | 0 |
| Down | METTL7B | 6 | 8.00E-04 | 664448 | 0.24189 | 0 |
| Down | SPAG16 | 6 | 0.001417 | 796754 | 0.231691 | 0 |
| Down | PROM1 | 6 | 7.49E-04 | 715970 | 0.244819 | 0 |
| Down | PGP | 6 | 3.25E-04 | 560276 | 0.239737 | 0 |
| Down | FAH | 6 | 8.20E-04 | 1577596 | 0.251305 | 0 |
| Down | ETFDH | 6 | 4.51E-05 | 84272 | 0.258944 | 0 |
| Down | MYO3B | 6 | 9.94E-05 | 140794 | 0.271178 | 0 |
| Down | SERHL2 | 6 | 9.93E-04 | 2370162 | 0.227216 | 0 |
| Down | TMEM37 | 6 | 0.00107 | 444308 | 0.215407 | 0 |
| Down | FOLR1 | 6 | 7.19E-04 | 594236 | 0.247539 | 0 |
| Down | CD1D | 5 | 4.28E-04 | 610068 | 0.239262 | 0 |
| Down | RAMP1 | 5 | 7.04E-04 | 585402 | 0.240183 | 0 |
| Down | PAH | 5 | 3.52E-04 | 1027734 | 0.215627 | 0 |
| Down | ACE | 5 | 9.01E-05 | 31416 | 0.259003 | 0 |
| Down | COX14 | 5 | 2.27E-04 | 74032 | 0.255222 | 0.2 |
| Down | IGFBP2 | 5 | 5.79E-04 | 830356 | 0.247269 | 0 |
| Down | TRMT9B | 5 | 4.62E-04 | 393934 | 0.242158 | 0 |
| Down | NME5 | 5 | 3.76E-04 | 219046 | 0.236386 | 0 |
| Down | ANXA9 | 5 | 8.13E-04 | 1078698 | 0.223807 | 0 |
| Down | UPK1B | 5 | 9.32E-04 | 986068 | 0.23896 | 0 |
| Down | CD302 | 5 | 1.28E-04 | 102000 | 0.236888 | 0 |
| Down | PRSS33 | 5 | 7.92E-04 | 563640 | 0.199859 | 0 |
| Down | ERP27 | 5 | 3.90E-04 | 715786 | 0.231814 | 0 |
| Down | TMPRSS4 | 5 | 9.29E-04 | 1170718 | 0.23875 | 0 |
| Down | HEBP1 | 5 | 5.34E-05 | 32076 | 0.247463 | 0.1 |
| Down | FMO5 | 5 | 0.001061 | 1626188 | 0.205825 | 0 |
| Down | METRN | 5 | 2.65E-04 | 228024 | 0.249156 | 0 |
| Down | SOSTDC1 | 4 | 7.98E-04 | 1232612 | 0.212929 | 0 |
| Down | LTC4S | 4 | 3.52E-04 | 362426 | 0.175176 | 0 |
| Down | PDZK1IP1 | 4 | 5.32E-05 | 29312 | 0.232051 | 0 |
| Down | CD24 | 4 | 7.09E-04 | 1206718 | 0.228938 | 0 |
| Down | ORAI3 | 4 | 0.001056 | 973290 | 0.18522 | 0 |
| Down | NACA2 | 4 | 7.21E-05 | 102110 | 0.256895 | 0 |
| Down | ANKS4B | 4 | 4.70E-04 | 198792 | 0.246443 | 0 |
| Down | ACYP2 | 4 | 1 | 2 | 1 | 0 |
| Down | ATRAID | 4 | 7.25E-04 | 1034828 | 0.232974 | 0 |
| Down | RAD9B | 4 | 7.10E-04 | 847910 | 0.17993 | 0 |
| Down | HNMT | 4 | 7.05E-04 | 602900 | 0.227489 | 0 |
| Down | LCT | 4 | 1.30E-04 | 202466 | 0.265961 | 0 |
| Down | SELENOP | 4 | 3.89E-04 | 783822 | 0.255934 | 0 |
| Down | ODAM | 4 | 7.05E-04 | 1023430 | 0.233885 | 0 |
| Down | GATM | 4 | 3.92E-04 | 330478 | 0.241008 | 0 |
| Down | UGT2A3 | 4 | 7.09E-04 | 285884 | 0.22072 | 0 |
| Down | CFI | 3 | 3.54E-04 | 506448 | 0.230162 | 0 |
| Down | NRTN | 3 | 7.04E-04 | 492878 | 0.191687 | 0 |
| Down | PLEKHS1 | 3 | 3.96E-04 | 274568 | 0.237027 | 0 |
| Down | PNMT | 3 | 2.73E-05 | 47234 | 0.240569 | 0 |
| Down | ANXA10 | 3 | 4.81E-05 | 62170 | 0.246326 | 0 |
| Down | LRP3 | 3 | 7.47E-06 | 2116 | 0.220883 | 0 |
| Down | C4orf48 | 3 | 9.20E-06 | 4274 | 0.194051 | 0 |
| Down | CDNF | 3 | 3.52E-04 | 361602 | 0.199208 | 0 |
| Down | RIMKLA | 3 | 7.04E-04 | 128342 | 0.182871 | 0 |
| Down | GALM | 3 | 1 | 6 | 1 | 0 |
| Down | DNAAF3 | 3 | 1.94E-05 | 5614 | 0.240071 | 0 |
| Down | ROM1 | 3 | 3.55E-04 | 173536 | 0.253355 | 0 |
| Down | PLA2R1 | 3 | 3.61E-04 | 497398 | 0.229873 | 0 |
| Down | TM4SF4 | 3 | 6.82E-05 | 63168 | 0.213032 | 0 |
| Down | LRRC66 | 3 | 4.86E-05 | 34828 | 0.238991 | 0 |
| Down | VEPH1 | 3 | 3.53E-04 | 283260 | 0.211754 | 0 |
| Down | DSEL | 3 | 2.01E-04 | 30300 | 0.263923 | 0 |
| Down | CTHRC1 | 3 | 4.56E-05 | 36850 | 0.228239 | 0 |
| Down | TMEM45B | 3 | 7.04E-04 | 204542 | 0.207706 | 0 |
| Down | SERINC5 | 3 | 6.14E-05 | 120978 | 0.25832 | 0 |
| Down | LEFTY1 | 3 | 3.56E-04 | 256664 | 0.235719 | 0 |
| Down | PDE1A | 3 | 3.56E-04 | 306882 | 0.248328 | 0 |
| Down | ADGRB3 | 3 | 7.04E-04 | 556450 | 0.195567 | 0 |
| Down | IQCD | 3 | 9.81E-06 | 13826 | 0.244083 | 0 |
| Down | UBBP4 | 3 | 3.25E-06 | 3318 | 0.241654 | 0 |
| Down | PCDHB12 | 3 | 4.19E-05 | 32484 | 0.219509 | 0 |
| Down | EML6 | 3 | 3.62E-04 | 1079642 | 0.249879 | 0 |
| Down | EFCAB11 | 3 | 9.02E-05 | 51112 | 0.236661 | 0 |
| Down | PXMP4 | 2 | 6.51E-06 | 3138 | 0.239333 | 0 |
| Down | SAMD13 | 2 | 1.66E-05 | 4492 | 0.242935 | 0 |
| Down | CRISP3 | 2 | 3.52E-04 | 153340 | 0.213473 | 0 |
| Down | HSD17B2 | 2 | 1 | 2 | 1 | 0 |
| Down | ERFE | 2 | 9.90E-07 | 460 | 0.208223 | 0 |
| Down | ACSM3 | 2 | 3.52E-04 | 227006 | 0.237343 | 0 |
| Down | RPL39L | 2 | 3.52E-04 | 552058 | 0.221305 | 0 |
| Down | CRLS1 | 2 | 3.64E-06 | 1822 | 0.206708 | 0 |
| Down | CEACAM7 | 2 | 1 | 2 | 1 | 0 |
| Down | RHBDL2 | 2 | 3.52E-04 | 192488 | 0.229279 | 0 |
| Down | KY | 2 | 3.56E-06 | 7364 | 0.234029 | 0 |
| Down | SLC3A1 | 2 | 3.52E-04 | 690930 | 0.246187 | 0 |
| Down | SLC25A27 | 2 | 6.70E-07 | 408 | 0.210211 | 0 |
| Down | LHPP | 2 | 3.52E-04 | 292702 | 0.240162 | 0 |
| Down | SSPN | 2 | 1.96E-06 | 2908 | 0.229279 | 0 |
| Down | VTCN1 | 2 | 3.52E-04 | 98318 | 0.2071 | 0 |
| Down | ST6GALNAC1 | 2 | 4.10E-07 | 1210 | 0.226573 | 0 |
| Down | SAC3D1 | 2 | 3.20E-05 | 1612 | 0.190633 | 0 |
| Down | TCEA3 | 2 | 1.60E-05 | 6450 | 0.155975 | 0 |
| Down | SLC44A4 | 2 | 7.40E-07 | 1704 | 0.238619 | 0 |
| Down | STRA6 | 2 | 3.03E-06 | 5772 | 0.239565 | 0 |
| Down | ENTPD3 | 2 | 1.13E-04 | 257856 | 0.238689 | 0 |
| Down | LRRC24 | 2 | 3.52E-04 | 410756 | 0.220309 | 0 |
| Down | IGSF10 | 2 | 4.19E-06 | 11938 | 0.248839 | 0 |
| Down | CDC42EP5 | 1 | 0 | 0 | 0.210017 | 0 |
| Down | SEMA3E | 1 | 0 | 0 | 1 | 0 |
| Down | CNGA1 | 1 | 0 | 0 | 1 | 0 |
| Down | SPATA17 | 1 | 0 | 0 | 1 | 0 |
| Down | CLDN16 | 1 | 0 | 0 | 1 | 0 |
| Down | BTBD16 | 1 | 0 | 0 | 0.204168 | 0 |
| Down | CYP27A1 | 1 | 0 | 0 | 0.224071 | 0 |
| Down | GACAT2 | 1 | 0 | 0 | 0.236829 | 0 |
| Down | CYP2U1 | 1 | 0 | 0 | 0.237343 | 0 |
| Down | POLR2J2 | 1 | 0 | 0 | 0.240142 | 0 |
| Down | SLC45A1 | 1 | 0 | 0 | 0.225119 | 0 |
| Down | CYP4F3 | 1 | 0 | 0 | 1 | 0 |
| Down | ATPSCKMT | 1 | 0 | 0 | 0.236829 | 0 |
| Down | RERG | 1 | 0 | 0 | 1 | 0 |
| Down | LYPLAL1 | 1 | 0 | 0 | 0.222214 | 0 |
| Down | PROM2 | 1 | 0 | 0 | 0.240142 | 0 |
| Down | FAM89B | 1 | 0 | 0 | 0.234503 | 0 |
| Down | ST6GALNAC2 | 1 | 0 | 0 | 0.207995 | 0 |
| Down | GLTPD2 | 1 | 0 | 0 | 0.224071 | 0 |
| Down | CREG2 | 1 | 0 | 0 | 0.236829 | 0 |
| Down | CYS1 | 1 | 0 | 0 | 0.246166 | 0 |
| Down | TCN1 | 1 | 0 | 0 | 0.215121 | 0 |
| Down | CFAP73 | 1 | 0 | 0 | 0.231145 | 0 |
| Down | LEMD1 | 1 | 0 | 0 | 0.226663 | 0 |
| Down | LRRC26 | 1 | 0 | 0 | 1 | 0 |
| Down | RSPH1 | 1 | 0 | 0 | 1 | 0 |
| Down | FGFBP2 | 1 | 0 | 0 | 0.214447 | 0 |
| Down | C2orf74 | 1 | 0 | 0 | 0.219934 | 0 |
| Down | MMEL1 | 1 | 0 | 0 | 0.215211 | 0 |

**Table 7** miRNA - target gene interaction table

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Regulation** | **Target Genes** | **Degree** | **MicroRNA** | **Regulation** | **Target Genes** | **Degree** | **MicroRNA** |
| Up | TXNIP | 228 | hsa-mir-4511 | Down | BRI3BP | 123 | hsa-mir-4312 |
| Up | PMAIP1 | 147 | hsa-mir-3924 | Down | FAHD1 | 113 | hsa-mir-4527 |
| Up | APOL6 | 127 | hsa-mir-4478 | Down | CPM | 111 | hsa-mir-4673 |
| Up | CHAC1 | 118 | hsa-mir-3650 | Down | HOXA13 | 111 | hsa-mir-4496 |
| Up | KLF2 | 107 | hsa-mir-4252 | Down | TMBIM6 | 104 | hsa-mir-3153 |
| Up | DNAJB4 | 102 | hsa-mir-4438 | Down | GSR | 104 | hsa-mir-4438 |
| Up | ID4 | 91 | hsa-mir-4265 | Down | SHMT1 | 97 | hsa-mir-3174 |
| Up | TRAF1 | 90 | hsa-mir-6077 | Down | TMEM59 | 88 | hsa-mir-1200 |
| Up | AMOTL2 | 89 | hsa-mir-4284 | Down | MLEC | 88 | hsa-mir-4475 |
| Up | EPHA4 | 74 | hsa-mir-3609 | Down | DSEL | 85 | hsa-mir-8055 |
| Up | BBC3 | 73 | hsa-mir-4770 | Down | PXMP4 | 83 | hsa-mir-4432 |
| Up | PPM1K | 72 | hsa-mir-4459 | Down | KPNA2 | 83 | hsa-mir-5688 |
| Up | TNFAIP3 | 70 | hsa-mir-5700 | Down | TSPAN6 | 81 | hsa-mir-4464 |
| Up | NPTX1 | 69 | hsa-mir-4295 | Down | PDCD4 | 78 | hsa-mir-4748 |
| Up | CYLD | 69 | hsa-mir-3941 | Down | BIRC5 | 78 | hsa-mir-2053 |
| Up | DDR2 | 68 | hsa-mir-2053 | Down | TOMM20 | 77 | hsa-mir-4523 |
| Up | STAT2 | 63 | hsa-mir-3929 | Down | EFCAB11 | 75 | hsa-mir-5702 |
| Up | RRAD | 62 | hsa-mir-4450 | Down | ANKS4B | 74 | hsa-mir-4507 |
| Up | KLF6 | 62 | hsa-mir-4305 | Down | AURKA | 73 | hsa-mir-3611 |
| Up | FGF19 | 62 | hsa-mir-4721 | Down | HACD2 | 69 | hsa-mir-1827 |
| Up | ZNFX1 | 61 | hsa-mir-8067 | Down | FOLR1 | 69 | hsa-mir-4643 |
| Up | FOS | 58 | hsa-mir-8081 | Down | AP2M1 | 69 | hsa-mir-6133 |
| Up | MXD1 | 57 | hsa-mir-5690 | Down | TFRC | 67 | hsa-mir-1299 |
| Up | SSTR2 | 57 | hsa-mir-6131 | Down | SYNGR1 | 64 | hsa-mir-3169 |
| Up | SP110 | 55 | hsa-mir-3674 | Down | PGK1 | 64 | hsa-mir-5683 |
| Up | PLEKHG5 | 54 | hsa-mir-3612 | Down | DNAH10OS | 63 | hsa-mir-3689c |
| Up | CPEB3 | 53 | hsa-mir-5047 | Down | LEFTY1 | 63 | hsa-mir-4251 |
| Up | ZFP36 | 53 | hsa-mir-6126 | Down | STMN1 | 62 | hsa-mir-4459 |
| Up | DTX3L | 51 | hsa-mir-7703 | Down | PCLAF | 62 | hsa-mir-4705 |
| Up | SLC5A5 | 51 | hsa-mir-4257 | Down | SLC16A10 | 61 | hsa-mir-3149 |
| Up | DNAH17 | 51 | hsa-mir-2278 | Down | SEMA3E | 60 | hsa-mir-4294 |
| Up | INHBA | 51 | hsa-mir-5688 | Down | LSM3 | 60 | hsa-mir-5095 |
| Up | CD274 | 47 | hsa-mir-3977 | Down | MOGAT1 | 59 | hsa-mir-4660 |
| Up | SOGA3 | 46 | hsa-mir-1297 | Down | TRMT2B | 57 | hsa-mir-3672 |
| Up | PIM3 | 46 | hsa-mir-4494 | Down | GNG12 | 57 | hsa-mir-4426 |
| Up | CPEB2 | 44 | hsa-mir-4643 | Down | FLYWCH2 | 56 | hsa-mir-4430 |
| Up | PSMB9 | 44 | hsa-mir-3658 | Down | PIN1 | 56 | hsa-mir-4472 |
| Up | GMPR | 43 | hsa-mir-661 | Down | METTL7A | 54 | hsa-mir-4692 |
| Up | SOCS1 | 42 | hsa-mir-4500 | Down | ACBD7 | 54 | hsa-mir-4421 |
| Up | COL4A1 | 42 | hsa-mir-8070 | Down | ALDH6A1 | 54 | hsa-mir-4284 |
| Up | PPP1R15A | 40 | hsa-mir-6165 | Down | DPYSL2 | 54 | hsa-mir-3666 |
| Up | COL8A1 | 39 | hsa-mir-4266 | Down | GJB1 | 53 | hsa-mir-6085 |
| Up | RAB19 | 39 | hsa-mir-4451 | Down | CARHSP1 | 51 | hsa-mir-4255 |
| Up | DUSP10 | 39 | hsa-mir-4791 | Down | GATM | 49 | hsa-mir-4460 |
| Up | JUN | 38 | hsa-mir-4480 | Down | SRP9 | 48 | hsa-mir-3714 |
| Up | IFITM1 | 38 | hsa-mir-644a | Down | DEPDC1 | 48 | hsa-mir-1305 |
| Up | CREB5 | 38 | hsa-mir-3911 | Down | CLDN16 | 47 | hsa-mir-548w |
| Up | GJB7 | 38 | hsa-mir-4272 | Down | AK4 | 45 | hsa-mir-4280 |
| Up | BMP2 | 37 | hsa-mir-4463 | Down | NRGN | 44 | hsa-mir-3141 |
| Up | CXCL8 | 36 | hsa-mir-4662b | Down | DNAAF3 | 43 | hsa-mir-3155a |
| Up | BCL3 | 36 | hsa-mir-3132 | Down | MAGT1 | 43 | hsa-mir-1273f |
| Up | DUSP8 | 36 | hsa-mir-4475 | Down | BTD | 42 | hsa-mir-5100 |
| Up | SAMD9L | 35 | hsa-mir-2110 | Down | NEURL1B | 42 | hsa-mir-2117 |
| Up | TRIM38 | 35 | hsa-mir-4705 | Down | CYBRD1 | 42 | hsa-mir-3199 |
| Up | GLI2 | 35 | hsa-mir-4651 | Down | DNLZ | 41 | hsa-mir-4510 |
| Up | SLFN5 | 35 | hsa-mir-4635 | Down | TUBB4A | 41 | hsa-mir-3974 |
| Up | FAM153B | 35 | hsa-mir-1200 | Down | UBBP4 | 39 | hsa-mir-6132 |
| Up | ICAM1 | 34 | hsa-mir-3975 | Down | CD1D | 39 | hsa-mir-548ac |
| Up | RASGRP3 | 33 | hsa-mir-4264 | Down | PSAP | 39 | hsa-mir-3689d |
| Up | PCK1 | 33 | hsa-mir-548aa | Down | LHPP | 38 | hsa-mir-3929 |
| Up | PROX1 | 33 | hsa-mir-548u | Down | SRD5A3 | 38 | hsa-mir-4481 |
| Up | SOCS3 | 32 | hsa-mir-4473 | Down | LYZ | 38 | hsa-mir-4486 |
| Up | MB21D2 | 32 | hsa-mir-4517 | Down | ARRB1 | 38 | hsa-mir-1470 |
| Up | IRF1 | 32 | hsa-mir-6073 | Down | TPGS1 | 37 | hsa-mir-7703 |
| Up | CXCL10 | 31 | hsa-mir-1231 | Down | PCYOX1 | 37 | hsa-mir-4775 |
| Up | ETS2 | 31 | hsa-mir-3662 | Down | NUBPL | 36 | hsa-mir-6088 |
| Up | NCOA7 | 31 | hsa-mir-5680 | Down | HADHB | 36 | hsa-mir-4493 |
| Up | DUSP1 | 30 | hsa-mir-940 | Down | FFAR4 | 35 | hsa-mir-640 |
| Up | PLAC8 | 30 | hsa-mir-1261 | Down | SEMA4G | 34 | hsa-mir-8085 |
| Up | GLCCI1 | 29 | hsa-mir-4443 | Down | SUN2 | 34 | hsa-mir-4310 |
| Up | NR4A3 | 29 | hsa-mir-6079 | Down | PLEKHS1 | 34 | hsa-mir-3652 |
| Up | PRKD2 | 28 | hsa-mir-378h | Down | AKR1B10 | 34 | hsa-mir-548ax |
| Up | S1PR3 | 28 | hsa-mir-3199 | Down | CCDC115 | 34 | hsa-mir-4471 |
| Up | IFIT3 | 27 | hsa-mir-3926 | Down | TMPRSS4 | 33 | hsa-mir-298 |
| Up | KLF4 | 26 | hsa-mir-663a | Down | GSTO2 | 33 | hsa-mir-8057 |
| Up | SAMHD1 | 26 | hsa-mir-1976 | Down | GPSM2 | 33 | hsa-mir-3135b |
| Up | KLB | 26 | hsa-mir-7641 | Down | KCNIP3 | 32 | hsa-mir-7974 |
| Up | HIVEP2 | 25 | hsa-mir-520e | Down | LRP3 | 32 | hsa-mir-4306 |
| Up | CYP1A1 | 25 | hsa-mir-632 | Down | ETFDH | 31 | hsa-mir-4270 |
| Up | NEURL1 | 25 | hsa-mir-4505 | Down | VWA1 | 30 | hsa-mir-592 |
| Up | ACTA1 | 24 | hsa-mir-1252-3p | Down | PAIP2B | 30 | hsa-mir-1273e |
| Up | ATF3 | 24 | hsa-mir-5000-5p | Down | CRLS1 | 30 | hsa-mir-23c |
| Up | RGS16 | 24 | hsa-mir-548aw | Down | PLS1 | 30 | hsa-mir-577 |
| Up | ARRDC3 | 23 | hsa-mir-5193 | Down | HMGB3 | 30 | hsa-mir-759 |
| Up | SLC25A28 | 23 | hsa-mir-2392 | Down | PGRMC1 | 30 | hsa-mir-3194-5p |
| Up | TLR6 | 23 | hsa-mir-1245a | Down | SSPN | 29 | hsa-mir-4719 |
| Up | GFPT2 | 23 | hsa-mir-5703 | Down | PRDX3 | 29 | hsa-mir-8063 |
| Up | ETV7 | 23 | hsa-mir-6087 | Down | PDK1 | 29 | hsa-mir-138-1-3p |
| Up | FBLN2 | 23 | hsa-mir-548ac | Down | HOXA11 | 28 | hsa-mir-4441 |
| Up | IL6 | 22 | hsa-mir-107 | Down | SEMA5A | 28 | hsa-mir-8077 |
| Up | ZC3HAV1 | 22 | hsa-mir-612 | Down | CREG2 | 27 | hsa-mir-7158-3p |
| Up | NLRC5 | 22 | hsa-mir-4794 | Down | SLC39A10 | 27 | hsa-mir-7106-3p |
| Up | IL7R | 22 | hsa-mir-8052 | Down | SLPI | 26 | hsa-mir-151b |
| Up | SERPINE1 | 22 | hsa-mir-204-5p | Down | GALM | 26 | hsa-mir-4444 |
| Up | NUAK2 | 22 | hsa-mir-4464 | Down | CTSV | 26 | hsa-mir-302f |
| Up | ENO4 | 22 | hsa-mir-6088 | Down | SERPINA4 | 25 | hsa-mir-544a |
| Up | SYT1 | 21 | hsa-mir-711 | Down | QPCT | 25 | hsa-mir-4419a |
| Up | MT1E | 21 | hsa-mir-4302 | Down | SNAP25 | 25 | hsa-mir-641 |
| Up | NYAP2 | 21 | hsa-mir-4780 | Down | VSIG1 | 24 | hsa-mir-4309 |
| Up | EGR3 | 20 | hsa-mir-3978 | Down | RHBDL2 | 24 | hsa-mir-1307-3p |
| Up | PTGS2 | 20 | hsa-mir-558 | Down | LOX | 24 | hsa-mir-5583-3p |
| Up | TNFSF10 | 20 | hsa-mir-5697 | Down | HACD3 | 24 | hsa-mir-3920 |
| Up | SLC30A3 | 20 | hsa-mir-548ap-3p | Down | TCEA3 | 24 | hsa-mir-4433a-3p |
| Up | HLX | 20 | hsa-mir-5572 | Down | CYP2U1 | 24 | hsa-mir-500a-5p |
| Up | OAS2 | 19 | hsa-mir-4531 | Down | CA12 | 24 | hsa-mir-548m |
| Up | MX2 | 19 | hsa-mir-630 | Down | DNAJC22 | 23 | hsa-mir-4772-3p |
| Up | RASGRP1 | 18 | hsa-mir-599 | Down | TTR | 23 | hsa-mir-6890-5p |
| Up | HIVEP1 | 18 | hsa-mir-595 | Down | WDR72 | 23 | hsa-mir-181d-5p |
| Up | TIPARP | 18 | hsa-mir-4799-5p | Down | FDX1 | 23 | hsa-mir-548x-3p |
| Up | MOGAT3 | 18 | hsa-mir-3689d | Down | TMEM37 | 22 | hsa-mir-4709-5p |
| Up | TRIM5 | 16 | hsa-mir-3689e | Down | KY | 22 | hsa-mir-6799-3p |
| Up | RTP4 | 16 | hsa-mir-892c-3p | Down | KCNMB4 | 22 | hsa-mir-190b |
| Up | IFIT1 | 16 | hsa-mir-2054 | Down | CDNF | 21 | hsa-mir-1273g-3p |
| Up | CCRL2 | 16 | hsa-mir-1306-5p | Down | RAD51B | 21 | hsa-mir-6780a-5p |
| Up | SNED1 | 16 | hsa-mir-4666b | Down | ACO1 | 20 | hsa-mir-6858-3p |
| Up | PELI1 | 15 | hsa-mir-4639-3p | Down | ABCC4 | 20 | hsa-let-7f-1-3p |
| Up | CCDC65 | 15 | hsa-mir-4433b-3p | Down | ARL3 | 20 | hsa-mir-4429 |
| Up | RASD1 | 15 | hsa-mir-4488 | Down | UCP2 | 20 | hsa-mir-4739 |
| Up | TSLP | 15 | hsa-mir-4270 | Down | KCNE3 | 19 | hsa-mir-6842-5p |
| Up | XRN1 | 14 | hsa-mir-5011-5p | Down | SHH | 19 | hsa-mir-6882-3p |
| Up | JAK2 | 14 | hsa-mir-5692a | Down | NDUFA2 | 19 | hsa-mir-6755-5p |
| Up | IL1A | 14 | hsa-mir-92a-1-5p | Down | CYP4F3 | 18 | hsa-mir-6849-3p |
| Up | LRIT3 | 14 | hsa-mir-4758-5p | Down | STC1 | 17 | hsa-mir-2276-5p |
| Up | IFNB1 | 13 | hsa-mir-607 | Down | BCAS3 | 17 | hsa-mir-378g |
| Up | BDKRB2 | 13 | hsa-mir-4659a-3p | Down | PHGDH | 17 | hsa-mir-107 |
| Up | NT5C3A | 12 | hsa-mir-582-5p | Down | MAD2L1 | 17 | hsa-mir-376a-3p |
| Up | CLPSL1 | 12 | hsa-mir-2278 | Down | TOP2A | 17 | hsa-mir-7-1-3p |
| Up | EPC1 | 11 | hsa-mir-4742-3p | Down | SIAE | 16 | hsa-mir-6511a-5p |
| Up | HEG1 | 11 | hsa-mir-507 | Down | HHLA2 | 16 | hsa-mir-548n |
| Up | KIF26B | 11 | hsa-mir-6795-3p | Down | SLC38A4 | 16 | hsa-mir-3150b-3p |
| Up | MT2A | 11 | hsa-let-7a-2-3p | Down | RNF128 | 16 | hsa-mir-629-3p |
| Up | IL7 | 11 | hsa-mir-376b-3p | Down | LYPLAL1 | 16 | hsa-mir-7-2-3p |
| Up | FBXO6 | 11 | hsa-mir-7151-3p | Down | HMGN3 | 15 | hsa-mir-5011-5p |
| Up | NFKBIA | 10 | hsa-mir-891a-5p | Down | ITM2A | 15 | hsa-mir-411-5p |
| Up | SPTBN5 | 10 | hsa-mir-4747-5p | Down | SLC12A2 | 15 | hsa-mir-5580-3p |
| Up | MAP3K8 | 10 | hsa-mir-589-5p | Down | SORBS2 | 14 | hsa-mir-6791-3p |
| Up | EGR2 | 10 | hsa-mir-142-3p | Down | EML6 | 14 | hsa-mir-5582-3p |
| Up | PTGER4 | 10 | hsa-mir-519d-3p | Down | SCP2 | 14 | hsa-mir-622 |
| Up | TNF | 10 | hsa-mir-130a-3p | Down | TMEM45B | 13 | hsa-mir-5193 |
| Up | SPRY2 | 10 | hsa-mir-24-2-5p | Down | SPAG16 | 13 | hsa-mir-1260a |
| Up | CCL2 | 10 | hsa-mir-518a-5p | Down | PROM1 | 13 | hsa-mir-514b-5p |
| Up | CX3CL1 | 10 | hsa-mir-5093 | Down | ACSF2 | 13 | hsa-mir-6858-5p |
| Up | HDX | 10 | hsa-mir-6888-5p | Down | OAZ1 | 12 | hsa-mir-6070 |
| Up | PDZD2 | 10 | hsa-mir-8055 | Down | CRYZ | 12 | hsa-mir-6849-5p |
| Up | OTOG | 10 | hsa-mir-3074-5p | Down | REPS2 | 12 | hsa-mir-6817-5p |
| Up | LAYN | 10 | hsa-mir-6501-5p | Down | ARHGAP19 | 12 | hsa-mir-4762-5p |
| Up | PTCH2 | 10 | hsa-mir-6074 | Down | PROM2 | 11 | hsa-mir-6851-5p |
| Up | PPEF1 | 10 | hsa-mir-6809-3p | Down | TRNP1 | 11 | hsa-mir-6720-5p |
| Up | TRIM21 | 10 | hsa-mir-6780b-5p | Down | ST6GALNAC1 | 11 | hsa-mir-4743-3p |
| Up | NCKAP5 | 9 | hsa-mir-6892-5p | Down | SLC25A27 | 11 | hsa-mir-5692c |
| Up | TNFSF13B | 9 | hsa-mir-5681b | Down | PDE1A | 11 | hsa-mir-1264 |
| Up | SECTM1 | 9 | hsa-mir-1281 | Down | SRI | 11 | hsa-let-7f-1-3p |
| Up | BARX1 | 9 | hsa-mir-1268a | Down | SYT5 | 11 | hsa-mir-4691-3p |
| Up | SLC25A2 | 9 | hsa-mir-6771-3p | Down | SAP30 | 11 | hsa-mir-125b-2-3p |
| Up | RAB44 | 8 | hsa-mir-711 | Down | METRN | 11 | hsa-mir-8081 |
| Up | RAET1L | 8 | hsa-mir-448 | Down | CD302 | 11 | hsa-mir-4690-3p |
| Up | CXCL11 | 8 | hsa-mir-548b-3p | Down | SMARCA2 | 11 | hsa-mir-19a-3p |
| Up | EGR1 | 8 | hsa-mir-487a-3p | Down | PPT1 | 11 | hsa-mir-339-5p |
| Up | ZC3H12A | 8 | hsa-mir-3194-5p | Down | ALDH2 | 11 | hsa-mir-8079 |
| Up | GPER1 | 8 | hsa-mir-4750-3p | Down | PIGN | 11 | hsa-mir-3617-5p |
| Up | GATA3 | 7 | hsa-mir-132-3p | Down | SORT1 | 10 | hsa-mir-1185-5p |
| Up | C1QTNF1 | 7 | hsa-mir-6815-5p | Down | NDUFS7 | 10 | hsa-mir-5588-3p |
| Up | DNAH3 | 7 | hsa-mir-519e-5p | Down | FGFR3 | 10 | hsa-mir-8064 |
| Up | SLC39A2 | 7 | hsa-mir-4747-3p | Down | CFAP73 | 9 | hsa-mir-99a-5p |
| Up | SYNPR | 6 | hsa-mir-877-3p | Down | BCAS1 | 9 | hsa-mir-4756-3p |
| Up | PLAUR | 6 | hsa-mir-622 | Down | CCDC74B | 9 | hsa-mir-411-3p |
| Up | OGFR | 6 | hsa-mir-505-3p | Down | RIMKLA | 9 | hsa-mir-6791-5p |
| Up | GRM8 | 6 | sa-mir-7111-3p | Down | CFTR | 9 | hsa-mir-509-3p |
| Up | IFI16 | 6 | hsa-mir-136-5p | Down | PBXIP1 | 9 | hsa-mir-296-3p |
| Up | PDE2A | 6 | hsa-mir-3619-3p | Down | SERINC5 | 9 | hsa-mir-548an |
| Up | IL11 | 6 | hsa-mir-211-5p | Down | TUBA1A | 9 | hsa-mir-10a-5p |
| Up | C17orf82 | 6 | hsa-mir-6802-3p | Down | C21orf62-AS1 | 8 | hsa-mir-548as-3p |
| Up | PDE4B | 5 | hsa-mir-374a-5p | Down | EFHC2 | 8 | hsa-mir-4455 |
| Up | NKX3-1 | 5 | hsa-mir-215-5p | Down | NLGN1 | 8 | hsa-mir-1251-3p |
| Up | CXCL2 | 5 | hsa-mir-223-3p | Down | KCNAB1 | 8 | hsa-mir-513a-3p |
| Up | NFKBIZ | 5 | hsa-mir-193b-3p | Down | CLDN10 | 8 | hsa-mir-6810-3p |
| Up | FST | 5 | hsa-mir-3680-3p | Down | ATRAID | 8 | hsa-mir-548az-5p |
| Up | CXCL3 | 5 | hsa-mir-100-3p | Down | ACOT13 | 8 | hsa-mir-10b-5p |
| Up | IFIT2 | 5 | hsa-mir-645 | Down | ALCAM | 8 | hsa-mir-323a-5p |
| Up | STX11 | 5 | hsa-mir-5188 | Down | ADI1 | 8 | hsa-mir-711 |
| Up | DRP2 | 5 | hsa-mir-7641 | Down | CNIH4 | 8 | hsa-mir-301b-3p |
| Up | IFIT5 | 4 | hsa-mir-146a-5p | Down | SPCS2 | 8 | hsa-mir-4789-5p |
| Up | NPR3 | 4 | hsa-mir-30a-5p | Down | CTHRC1 | 8 | hsa-mir-148b-3p |
| Up | AHRR | 4 | hsa-mir-18a-5p | Down | CRP | 7 | hsa-mir-509-3-5p |
| Up | ICAM5 | 4 | hsa-mir-4707-5p | Down | SLC25A21 | 7 | hsa-mir-4666a-3p |
| Up | TRPC4 | 4 | hsa-mir-33a-5p | Down | SLC44A4 | 7 | hsa-mir-6728-5p |
| Up | USP18 | 4 | hsa-mir-221-3p | Down | VWA2 | 7 | hsa-mir-4749-3p |
| Up | IFIH1 | 4 | hsa-mir-424-5p | Down | SMIM10 | 7 | hsa-mir-431-5p |
| Up | CD69 | 4 | hsa-mir-32-5p | Down | PRR15L | 7 | hsa-mir-4446-5p |
| Up | NTNG2 | 4 | hsa-mir-3613-5p | Down | IGSF10 | 7 | hsa-mir-518a-5p |
| Up | WIF1 | 4 | hsa-mir-374a-5p | Down | PRDX2 | 7 | hsa-mir-339-5p |
| Up | BAHCC1 | 3 | hsa-let-7e-5p | Down | MMP7 | 7 | hsa-mir-543 |
| Up | IL12A | 3 | hsa-mir-10a-5p | Down | NACA2 | 7 | hsa-mir-513c-3p |
| Up | PTX3 | 3 | hsa-mir-9-5p | Down | HOGA1 | 7 | hsa-mir-6771-3p |
| Up | CXCL9 | 3 | hsa-mir-34a-5p | Down | NEK2 | 7 | hsa-mir-4778-5p |
| Up | TRIM22 | 3 | hsa-mir-146a-5p | Down | SGPP1 | 7 | hsa-mir-32-5p |
| Up | IFI44 | 3 | hsa-mir-26b-5p | Down | ECH1 | 7 | hsa-mir-378a-3p |
| Up | NLRP3 | 3 | hsa-mir-223-3p | Down | PSMD10 | 6 | hsa-mir-605-5p |
| Up | GFI1 | 3 | hsa-mir-142-3p | Down | SPP1 | 6 | hsa-mir-299-5p |
| Up | PLA2G4C | 3 | hsa-mir-181a-5p | Down | CAB39L | 6 | hsa-mir-27a-3p |
| Up | FAM110B | 3 | hsa-mir-7109-3p | Down | NTRK2 | 6 | hsa-mir-204-5p |
| Up | OASL | 3 | hsa-mir-1-3p | Down | SLAIN1 | 6 | hsa-mir-302a-3p |
| Up | BATF2 | 3 | hsa-mir-122-5p | Down | MCM3AP-AS1 | 6 | hsa-mir-15b-5p |
| Up | PARP10 | 3 | hsa-mir-421 | Down | PLEKHB1 | 5 | hsa-mir-9-5p |
| Up | PML | 3 | hsa-mir-378a-3p | Down | TRAPPC6A | 5 | hsa-mir-4461 |
| Up | TDRD7 | 2 | hsa-let-7e-5p | Down | CUEDC2 | 4 | hsa-mir-186-5p |
| Up | NOCT | 2 | hsa-mir-296-3p | Down | ERP27 | 4 | hsa-mir-210-3p |
| Up | MMP25 | 2 | hsa-mir-181c-3p | Down | IGFBP2 | 4 | hsa-mir-491-3p |
| Up | CCL20 | 2 | hsa-mir-21-5p | Down | GNG7 | 4 | hsa-mir-4311 |
| Up | TAP1 | 2 | hsa-mir-346 | Down | CAT | 4 | hsa-mir-30b-5p |
| Up | FAXDC2 | 2 | hsa-mir-124-3p | Down | ACSS1 | 4 | hsa-mir-191-5p |
| Up | FILIP1L | 2 | hsa-mir-335-5p | Down | FAH | 4 | hsa-mir-375 |
| Up | LGALS9 | 2 | hsa-mir-22-3p | Down | BDH2 | 4 | hsa-mir-21-5p |
| Up | SNPH | 2 | hsa-mir-375 | Down | KLHDC2 | 4 | hsa-mir-19b-3p |
| Up | TRANK1 | 2 | hsa-mir-26b-5p | Down | NTHL1 | 4 | hsa-mir-93-5p |
| Up | CRTAM | 2 | hsa-mir-335-5p | Down | PRIMPOL | 4 | hsa-mir-16-5p |
| Up | RSAD2 | 2 | hsa-mir-146a-5p | Down | SPDEF | 4 | hsa-mir-510-5p |
| Up | ZNF627 | 2 | hsa-mir-27a-3p | Down | OLFM4 | 4 | hsa-mir-103a-3p |
| Up | HLA-F | 2 | hsa-mir-93-5p | Down | FAM171A2 | 4 | hsa-mir-106b-5p |
| Up | EYA1 | 2 | hsa-mir-562 | Down | PAH | 3 | hsa-mir-590-3p |
| Up | THEMIS2 | 2 | hsa-mir-197-3p | Down | LEPR | 3 | hsa-mir-877-5p |
| Up | RND1 | 2 | hsa-mir-199a-5p | Down | ARL6IP5 | 3 | hsa-mir-31-3p |
| Up | LYL1 | 2 | hsa-mir-10b-5p | Down | SUMF1 | 3 | hsa-mir-148b-3p |
| Up | DDX58 | 2 | hsa-mir-218-5p | Down | DTYMK | 3 | hsa-mir-183-5p |
| Up | HSD17B3 | 2 | hsa-mir-181a-5p | Down | APOE | 3 | hsa-mir-199a-3p |
| Up | GRIA2 | 2 | hsa-mir-181b-5p | Down | OAT | 3 | hsa-mir-1-3p |
| Up | ACHE | 2 | hsa-mir-212-3p | Down | GALNT12 | 3 | hsa-mir-215-5p |
| Up | TICAM1 | 2 | hsa-mir-193b-3p | Down | FKBP3 | 3 | hsa-mir-98-5p |
| Up | FOSB | 2 | hsa-mir-663a | Down | CASR | 3 | hsa-mir-135b-5p |
| Up | ISG20 | 2 | hsa-mir-1-3p | Down | CSPG5 | 3 | hsa-mir-3691-5p |
| Up | ISG15 | 2 | hsa-mir-146a-5p | Down | ROS1 | 3 | hsa-mir-300 |
| Up | HERC5 | 2 | hsa-mir-3529-3p | Down | MDH1 | 3 | hsa-mir-186-5p |
| Up | DACT1 | 2 | hsa-mir-124-3p | Down | CFI | 3 | hsa-mir-181a-5p |
| Up | IRF7 | 2 | hsa-mir-762 | Down | ECI2 | 3 | hsa-mir-877-3p |
| Up | EPSTI1 | 2 | hsa-mir-654-5p | Down | SORL1 | 2 | hsa-mir-127-5p |
| Up | FLT3 | 2 | hsa-mir-150-5p | Down | RAD9B | 2 | hsa-mir-187-5p |
| Up | DUSP26 | 2 | hsa-mir-544a | Down | RAB26 | 2 | hsa-mir-421 |
| Up | DRD1 | 2 | hsa-mir-382-5p | Down | SLC3A1 | 2 | hsa-mir-548e-5p |
| Up | GIMAP2 | 2 | hsa-mir-193b-3p | Down | SYT12 | 2 | hsa-mir-146a-5p |
| Up | HELZ2 | 2 | hsa-mir-6793-3p | Down | AIF1L | 2 | hsa-mir-1229-3p |
| Up | SLC6A13 | 2 | hsa-mir-4709-5p | Down | KRT14 | 2 | hsa-mir-122-5p |
| Up | C11orf96 | 1 | hsa-mir-19b-3p | Down | CYBA | 2 | hsa-mir-320a |
| Up | ADGRL3 | 1 | hsa-mir-20a-5p | Down | MYO3B | 2 | hsa-mir-1-3p |
| Up | RELB | 1 | hsa-mir-26b-5p | Down | SAC3D1 | 2 | hsa-mir-423-3p |
| Up | CH25H | 1 | hsa-mir-26b-5p | Down | PPA2 | 2 | hsa-mir-193b-3p |
| Up | CAPN9 | 1 | hsa-mir-26b-5p | Down | CD24 | 2 | hsa-mir-373-3p |
| Up | HSD17B14 | 1 | hsa-mir-26b-5p | Down | FAM89B | 2 | hsa-mir-7-5p |
| Up | IL22RA1 | 1 | hsa-mir-26b-5p | Down | AGR2 | 2 | hsa-mir-4419a |
| Up | SAMD9 | 1 | hsa-mir-30a-5p | Down | ERFE | 2 | hsa-mir-192-5p |
| Up | PARP12 | 1 | hsa-mir-98-5p | Down | ENTPD3 | 2 | hsa-mir-335-5p |
| Up | CMPK2 | 1 | hsa-mir-192-5p | Down | AKR1C3 | 2 | hsa-mir-98-5p |
| Up | SIX2 | 1 | hsa-mir-181b-5p | Down | TMEM160 | 2 | hsa-mir-185-5p |
| Up | LMO2 | 1 | hsa-mir-223-3p | Down | NR1H4 | 2 | hsa-mir-192-3p |
| Up | CAVIN2 | 1 | hsa-mir-1-3p | Down | ASAH1 | 2 | hsa-mir-92a-3p |
| Up | GBP1 | 1 | hsa-mir-124-3p | Down | NME5 | 2 | hsa-mir-148b-3p |
| Up | PRRX2 | 1 | hsa-mir-124-3p | Down | ROM1 | 2 | hsa-mir-124-3p |
| Up | DSCAML1 | 1 | hsa-mir-124-3p | Down | MME | 2 | hsa-mir-26b-5p |
| Up | SH2D1B | 1 | hsa-mir-124-3p | Down | HSD17B2 | 2 | hsa-mir-124-3p |
| Up | OR52K1 | 1 | hsa-mir-106b-5p | Down | EPHX1 | 2 | hsa-mir-193b-3p |
| Up | TAGAP | 1 | hsa-mir-374a-5p | Down | DHFRP1 | 2 | hsa-mir-24-3p |
| Up | CYP21A2 | 1 | hsa-mir-335-5p | Down | PDGFD | 2 | hsa-mir-21-5p |
| Up | HCRTR1 | 1 | hsa-mir-335-5p | Down | TF | 2 | hsa-mir-19a-3p |
| Up | OAS1 | 1 | hsa-mir-335-5p | Down | ORAI3 | 2 | hsa-mir-18a-5p |
| Up | MYLPF | 1 | hsa-mir-335-5p | Down | TEX15 | 2 | hsa-mir-186-5p |
| Up | XAF1 | 1 | hsa-mir-335-5p | Down | C2orf74 | 2 | hsa-mir-15a-5p |
| Up | TMEM140 | 1 | hsa-mir-335-5p | Down | CENPV | 2 | hsa-mir-28-5p |
| Up | GRIP2 | 1 | hsa-mir-335-5p | Down | COX14 | 2 | hsa-let-7e-5p |
| Up | HSH2D | 1 | hsa-mir-335-5p | Down | SPATA17 | 1 | hsa-mir-6818-3p |
| Up | SEC16B | 1 | hsa-mir-335-5p | Down | CRISP3 | 1 | hsa-mir-1229-3p |
| Up | NEURL3 | 1 | hsa-mir-335-5p | Down | TSTD1 | 1 | hsa-mir-335-5p |
| Up | CPO | 1 | hsa-mir-335-5p | Down | CNTNAP3B | 1 | hsa-mir-335-5p |
| Up | TRIM40 | 1 | hsa-mir-335-5p | Down | C2orf81 | 1 | hsa-mir-335-5p |
| Up | TRIM69 | 1 | hsa-mir-335-5p | Down | GLTPD2 | 1 | hsa-mir-335-5p |
| Up | SUSD3 | 1 | hsa-mir-335-5p | Down | NXNL2 | 1 | hsa-mir-335-5p |
| Up | LSMEM1 | 1 | hsa-mir-335-5p | Down | RERG | 1 | hsa-mir-335-5p |
| Up | STX19 | 1 | hsa-mir-335-5p | Down | VTCN1 | 1 | hsa-mir-335-5p |
| Up | UBA7 | 1 | hsa-mir-455-5p | Down | MMEL1 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | SLC45A1 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | SOSTDC1 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | USH1C | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | RARRES2 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | KLK7 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | LTC4S | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | HOXA2 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | FCGRT | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | FABP6 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | ACE | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | ADGRB3 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | ADH6 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | AQP1 | 1 | hsa-mir-320a |
|  |  |  |  | Down | GSTA4 | 1 | hsa-mir-185-5p |
|  |  |  |  | Down | DDC | 1 | hsa-mir-145-5p |
|  |  |  |  | Down | TCTEX1D2 | 1 | hsa-mir-133a-3p |
|  |  |  |  | Down | AZGP1 | 1 | hsa-mir-128-3p |
|  |  |  |  | Down | SCNN1A | 1 | hsa-mir-125b-5p |
|  |  |  |  | Down | TMEM121 | 1 | hsa-mir-124-3p |
|  |  |  |  | Down | UGT1A10 | 1 | hsa-mir-124-3p |
|  |  |  |  | Down | SNTA1 | 1 | hsa-mir-124-3p |
|  |  |  |  | Down | NRTN | 1 | hsa-mir-124-3p |
|  |  |  |  | Down | CTSH | 1 | hsa-mir-124-3p |
|  |  |  |  | Down | WDR54 | 1 | hsa-mir-23b-3p |
|  |  |  |  | Down | IQCD | 1 | hsa-mir-1-3p |
|  |  |  |  | Down | DPY30 | 1 | hsa-mir-1-3p |
|  |  |  |  | Down | MACROD1 | 1 | hsa-mir-1-3p |
|  |  |  |  | Down | BCKDHB | 1 | hsa-mir-1-3p |
|  |  |  |  | Down | COMMD8 | 1 | hsa-mir-183-5p |
|  |  |  |  | Down | ARHGDIB | 1 | hsa-mir-34a-5p |
|  |  |  |  | Down | SAMD13 | 1 | hsa-mir-192-5p |
|  |  |  |  | Down | RPL39L | 1 | hsa-mir-100-5p |
|  |  |  |  | Down | PGP | 1 | hsa-mir-93-5p |
|  |  |  |  | Down | DNPH1 | 1 | hsa-mir-93-5p |
|  |  |  |  | Down | PCSK1N | 1 | hsa-mir-31-5p |
|  |  |  |  | Down | MAGIX | 1 | hsa-mir-26b-5p |
|  |  |  |  | Down | ACE2 | 1 | hsa-mir-26b-5p |
|  |  |  |  | Down | ODAM | 1 | hsa-mir-26b-5p |
|  |  |  |  | Down | IL20RA | 1 | hsa-mir-26b-5p |
|  |  |  |  | Down | MPC2 | 1 | hsa-mir-26b-5p |
|  |  |  |  | Down | SRPX | 1 | hsa-mir-26b-5p |
|  |  |  |  | Down | TCN1 | 1 | hsa-mir-26b-5p |
|  |  |  |  | Down | PNMT | 1 | hsa-mir-26b-5p |
|  |  |  |  | Down | ENDOG | 1 | hsa-mir-26b-5p |
|  |  |  |  | Down | AGT | 1 | hsa-mir-26b-5p |
|  |  |  |  | Down | KLK6 | 1 | hsa-let-7f-5p |
|  |  |  |  | Down | COX16 | 1 | hsa-let-7e-5p |
|  |  |  |  | Down | SPR | 1 | hsa-let-7b-5p |

Degree – No of miRNA interact with target gene. We taken any one miRNA in table.

**Table 8** TF - target gene interaction table

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Regulation** | **TF** | **Degree** | **Target Gene** | **Regulation** | **TF** | **Degree** | **Target Gene** |
| Up | FOXC1 | 202 | PROX1 | Down | FOXC1 | 261 | SERHL2 |
| Up | GATA2 | 175 | CXCL11 | Down | GATA2 | 183 | CFI |
| Up | YY1 | 122 | C4A | Down | YY1 | 131 | TCN1 |
| Up | FOXL1 | 93 | JAK2 | Down | NFIC | 104 | PGP |
| Up | NFKB1 | 88 | IL15RA | Down | FOXL1 | 102 | PGK1 |
| Up | E2F1 | 82 | FOS | Down | E2F1 | 88 | PDK1 |
| Up | RELA | 77 | FAM110B | Down | SRF | 87 | CSPG5 |
| Up | USF2 | 74 | FLT3LG | Down | USF2 | 87 | UGT1A4 |
| Up | NFIC | 72 | SPTBN5 | Down | STAT3 | 83 | ROS1 |
| Up | CREB1 | 67 | OAS2 | Down | NFKB1 | 81 | CEACAM7 |
| Up | HINFP | 66 | EGR4 | Down | PPARG | 79 | CCDC74B |
| Up | PPARG | 63 | HSD17B14 | Down | MEF2A | 74 | VWA2 |
| Up | TFAP2A | 60 | C1QTNF1 | Down | NFYA | 72 | UGT1A8 |
| Up | TP53 | 59 | DHX58 | Down | CREB1 | 70 | TFRC |
| Up | MEF2A | 57 | SDPR | Down | JUN | 69 | PTPLB |
| Up | POU2F2 | 57 | SLC6A13 | Down | POU2F2 | 69 | KIAA0101 |
| Up | STAT3 | 56 | CD274 | Down | HINFP | 64 | RAD9B |
| Up | SRF | 53 | C4B | Down | TFAP2A | 58 | DNAJC22 |
| Up | HOXA5 | 48 | CYP1A1 | Down | TP53 | 58 | PPT1 |
| Up | SREBF1 | 45 | SYNPR | Down | GATA3 | 57 | BNIPL |
| Up | RUNX2 | 42 | TIPARP | Down | ELK1 | 50 | PRR15L |
| Up | MAX | 41 | HLX | Down | HNF4A | 49 | KIAA1456 |
| Up | HNF4A | 38 | ATF3 | Down | SREBF1 | 49 | KLK7 |
| Up | USF1 | 38 | GRIN3B | Down | PRDM1 | 47 | SLPI |
| Up | TEAD1 | 37 | IL6 | Down | HOXA5 | 45 | NEURL1B |
| Up | NFYA | 37 | PTGER4 | Down | ARID3A | 43 | CRLS1 |
| Up | ELK1 | 35 | SYT1 | Down | RELA | 42 | SEMA5A |
| Up | ZNF354C | 33 | AMOTL2 | Down | ESR1 | 42 | CNGA1 |
| Up | JUND | 33 | FAP | Down | STAT1 | 40 | SHH |
| Up | FOXA1 | 33 | PPEF1 | Down | JUND | 39 | SLAIN1 |
| Up | CEBPB | 32 | DACT1 | Down | ELK4 | 38 | NXNL2 |
| Up | STAT1 | 30 | CCL2 | Down | TFAP2C | 37 | ACE |
| Up | BRCA1 | 30 | CPO | Down | FOXA1 | 37 | PLEKHS1 |
| Up | PRDM1 | 29 | FST | Down | RUNX2 | 36 | SLC44A4 |
| Up | ESR1 | 28 | RND1 | Down | BRCA1 | 35 | TTR |
| Up | E2F6 | 28 | SNCAIP | Down | NR3C1 | 35 | AKR1C3 |
| Up | TP63 | 27 | CPEB3 | Down | MAX | 33 | SEMA4G |
| Up | NR3C1 | 27 | IFIT1 | Down | PRRX2 | 31 | LHPP |
| Up | TFAP2C | 27 | PLEKHG5 | Down | FOS | 31 | ALCAM |
| Up | SREBF2 | 27 | THEMIS2 | Down | TEAD1 | 31 | TF |
| Up | SP1 | 26 | BBC3 | Down | IRF2 | 30 | PTPLAD1 |
| Up | ELK4 | 26 | WIF1 | Down | PAX2 | 30 | SORT1 |
| Up | KLF5 | 25 | VSTM1 | Down | SP1 | 29 | HEBP1 |
| Up | IRF2 | 24 | GRM8 | Down | SREBF2 | 29 | GNG7 |
| Up | ARID3A | 24 | PPM1K | Down | E2F6 | 28 | DPYSL2 |
| Up | FOXF2 | 22 | LRIT3 | Down | CEBPB | 27 | TRMT2B |
| Up | SPIB | 18 | EGR2 | Down | TP63 | 27 | ANXA10 |
| Up | PAX2 | 18 | ID4 | Down | USF1 | 26 | FMO5 |
| Up | NR2F1 | 16 | NCKAP5 | Down | NRF1 | 26 | LYPLAL1 |
| Up | NKX3-2 | 14 | ACTA1 | Down | KLF5 | 25 | REPS2 |
| Up | EN1 | 14 | SOCS1 | Down | NR2F1 | 21 | KCNAB1 |
| Up | PDX1 | 13 | TTC9B | Down | ZNF354C | 20 | HOXA11 |
| Up | SOX5 | 12 | PELI1 | Down | FOXF2 | 19 | TSPAN10 |
| Up | SOX10 | 9 | FBXO6 | Down | NKX3-2 | 17 | RIMKLA |
| Up | NRF1 | 7 | FOSB | Down | EN1 | 17 | BTD |
| Up | NKX2-5 | 7 | SP110 | Down | SOX5 | 14 | MOGAT1 |
| Up | REL | 7 | TAP1 | Down | SOX10 | 14 | NDUFA2 |
| Up | FOXI1 | 6 | EPSTI1 | Down | SRY | 11 | EFHC2 |
| Up | SOX17 | 6 | FGF18 | Down | EGR1 | 11 | CAT |
| Up | FOXD1 | 6 | NANOS3 | Down | ELF5 | 11 | LTC4S |
| Up | NR4A2 | 5 | CSF2 | Down | PDX1 | 10 | ENTPD3 |
| Up | FOXO3 | 5 | CYP21A2 | Down | SOX17 | 10 | ARL6IP5 |
| Up | FEV | 5 | GIMAP2 | Down | SPIB | 8 | IL20RA |
| Up | SRY | 5 | HIVEP1 | Down | NKX2-5 | 6 | COX14 |
| Up | ELF5 | 5 | IRF1 | Down | E2F4 | 6 | CASR |
| Up | MYB | 5 | TLR6 | Down | NFATC2 | 6 | TMPRSS4 |
| Up | NFATC2 | 4 | CCL20 | Down | GATA1 | 6 | RHBDL2 |
| Up | NFIL3 | 4 | EYA1 | Down | HNF1B | 5 | RNF128 |
| Up | ESR2 | 4 | SSTR2 | Down | MYB | 5 | ACE2 |
| Up | HLF | 4 | TNF | Down | FOXI1 | 4 | WDR54 |
| Up | HNF1B | 3 | CD69 | Down | NR2E3 | 4 | ITM2A |
| Up | RREB1 | 3 | CYP21A2 | Down | NFYB | 3 | TOP2A |
| Up | NHLH1 | 3 | CYP21A2 | Down | NKX3-1 | 2 | AKR1B10 |
| Up | PBX1 | 3 | CYP21A2 | Down | REL | 2 | TOMM20 |
| Up | PLAG1 | 3 | TNF | Down | NOBOX | 2 | ECH1 |
| Up | INSM1 | 3 | TNF | Down | ARNT | 2 | PCYOX1 |
| Up | SOX9 | 3 | TNF | Down | ZFX | 2 | SEPP1 |
| Up | REST | 3 | TRIM40 | Down | KLF4 | 2 | TSTD1 |
| Up | PAX6 | 3 | TRIM40 | Down | ESR2 | 1 | CCDC115 |
| Up | CTCF | 3 | TRIM40 | Down | FEV | 1 | HHLA2 |
| Up | NR2E3 | 2 | ISG15 | Down | NR2C2 | 1 | APOE |
| Up | NR2C2 | 2 | MAP3K8 | Down | ESRRB | 1 | SHMT1 |
| Up | NOBOX | 1 | LMO2 | Down | MYCN | 1 | RARRES2 |
| Up | ESRRB | 1 | NLRC5 | Down | MYC | 1 | RARRES2 |
| Up | ARNT | 1 | PDE2A | Down | RUNX1 | 1 | DPY30 |
| Up | E2F4 | 1 | PHF11 |  |  |  |  |
| Up | TFCP2L1 | 1 | CCRN4L |  |  |  |  |
| Up | MYC | 1 | PDE2A |  |  |  |  |
| Up | RUNX1 | 1 | IL22RA1 |  |  |  |  |

Degree – No of TF interact with target gene. We taken any one TF in table