Identification of potential and novel target genes in pituitary prolactinoma by bioinformatics analysis

Vikrant Ghatnatti¹, Basavaraj Vastrad², Swetha Patil³, Chanabasayya Vastrad⁴,* and Iranna Kotturshetti⁵

¹ Department of Endocrinology/Medicine, J N Medical College, Belagavi and KLE Academy of Higher Education & Research 590010, Karnataka, India
² Department of Biochemistry, Basaveshwar College of Pharmacy, Gadag, Karnataka 582103, India
³ Department of Obstetrics and Gynaecology, J N Medical College, Belagavi and KLE Academy of Higher Education & Research 590010, Karnataka, India
⁴ Biostatistics and Bioinformatics, Chanabasava Nilaya, Bharthanagar, Dharwad 580001, Karanataka, India
⁵ Department of Ayurveda, Rajiv Gandhi Education Society’s Ayurvedic Medical College, Ron 562209, Karanataka, India

* Correspondence: Email: channu.vastrad@gmail.com; Tel: 919480073398.

Supplementary

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

| Agilent Id | Gene Symbol | Log FC  | P Value  | FDR  | T value  | Up/Down | Gene Name                      |
|------------|-------------|---------|----------|------|----------|---------|-------------------------------|
| A_23_P328  | SALL1       | 1.833089| 2.06E-12 | 8.77E-8 | 60.26576 | Up      | spalt like transcription factor 1 |
| A_23_P175  | NKX2-2      | 1.814078| 3.68E-11 | 5.54E-7 | 42.7718  | Up      | NK2 homeobox 2                 |
| A_32_P149  | PTCHD1      | 1.891448| 3.91E-11 | 5.54E-7 | 42.46841 | Up      | patched domain containing 1   |
| Gene Symbol | Gene Name                  | Log2 Fold Change | P-Value     | Log10 P-Value | Regulation |
|-------------|----------------------------|-----------------|-------------|--------------|------------|
| BMP7        | bone morphogenetic protein 7 | 1.63854        | 7.17E-11    | 7.63E-07     | Up         |
| TMEM15      | transmembrane protein 154  | 1.53654        | 5.79E-10    | 4.13E-06     | Up         |
| SERTM1      | serine rich and transmembrane domain containing 1 | 1.81721       | 5.83E-10    | 4.13E-06     | Up         |
| SOX9-AS1    | SOX9 antisense RNA 1       | 1.90546        | 9.38E-10    | 4.13E-06     | Up         |
| FAM83F      | family with sequence similarity 83 member F | 1.78891       | 1.62E-09    | 8.1E-06      | Up         |
| SGCD        | sarcoglycan delta          | 2.09438        | 1.81E-09    | 8.1E-06      | Up         |
| C1orf168    | chromosome 1 open reading frame 168 | 1.58821       | 1.93E-09    | 8.1E-06      | Up         |
| GRHL2       | grainyhead like transcription factor 2 | 1.57436       | 2.1E-09     | 9.04E-06     | Up         |
| TDO2        | tryptophan 2,3-dioxygenase  | 1.74504        | 2.66E-09    | 9.04E-06     | Up         |
| SMR3B       | submaxillary gland androgen regulated protein 3B | 1.75937       | 2.76E-09    | 9.04E-06     | Up         |
| SCRGL1      | stimulator of chondrogenesis 1 | 2.12938       | 3.06E-09    | 9.29E-06     | Up         |
| KAZN        | kazrin, periplakin interacting protein | 1.22701       | 3.59E-09    | 1.02E-05     | Up         |
| IL20RA      | interleukin 20 receptor subunit alpha | 1.53544       | 3.86E-09    | 1.03E-05     | Up         |
| CLR1        | clarin 1                   | 1.34046        | 5.2E-09     | 1.27E-05     | Up         |
| FCN2        | ficolin 2                  | 2.07085        | 5.38E-09    | 1.27E-05     | Up         |
| LINC011     | long intergenic non-protein coding RNA 1102 | 1.48053       | 6.97E-09    | 1.56E-05     | Up         |
| DPPA4       | developmental pluripotency associated 4 | 1.23164       | 8.6E-09     | 1.78E-05     | Up         |
| SPTLC3      | serine palmitoyltransferase long chain base subunit 3 | 1.71913       | 8.8E-09     | 1.78E-05     | Up         |
| ATP4A       | ATPase H+/K+ transporting alpha subunit | 1.10887       | 1.14E-08    | 2.2E-05      | Up         |
| IQCJ        | IQ motif containing J      | 1.32675        | 1.73E-08    | 3.2E-05      | Up         |
| MIR503H     | MIR503 host gene           | 1.44726        | 2.34E-08    | 4.14E-05     | Up         |
| GPR12       | G protein-coupled receptor 12 | 1.70145       | 2.66E-08    | 4.53E-05     | Up         |
| SDK2        | sidekick cell adhesion molecule 2 | 1.25476       | 4.19E-08    | 6.6E-05      | Up         |
| SEPT14      | septin 14                  | 1.38970        | 4.95E-08    | 7.45E-05     | Up         |
| Gene Symbol | Description                                      | Fold Change | p-Value 1 | p-Value 2 | p-Value 3 | Regulation                        |
|------------|--------------------------------------------------|-------------|-----------|-----------|-----------|-----------------------------------|
| MIR31H     | MIR31 host gene                                  | 1.48494     | 7.45E-05  | 17.79865  | Up       | MIR31 host gene                   |
| RSPO3      | R-spondin 3                                      | 1.785412    | 7.45E-05  | 17.76502  | Up       | R-spondin 3                       |
| SLC13A5    | solute carrier family 13 member 5               | 1.374669    | 9.03E-05  | 17.25691  | Up       | solute carrier family 13 member 5 |
| TPP2       | tubulin polymerization promoting protein family 2 | 1.134536    | 9.03E-05  | 17.15035  | Up       | tubulin polymerization promoting protein family 2 |
| FGFR2      | fibroblast growth factor receptor 2             | 1.045116    | 9.03E-05  | 17.06439  | Up       | fibroblast growth factor receptor 2 |
| IQCA1      | IQ motif containing with AAA domain 1           | 1.083925    | 9.03E-05  | 17.05136  | Up       | IQ motif containing with AAA domain 1 |
| MGST1      | microsomal glutathione S-transferase 1          | 2.006529    | 9.49E-05  | 16.86567  | Up       | microsomal glutathione S-transferase 1 |
| LOC3877    | collagen alpha-1(X) chain                      | 1.229633    | 9.49E-05  | 16.83959  | Up       | collagen alpha-1(X) chain         |
| FABP7      | fatty acid binding protein 7                    | 1.539766    | 0.000     | 16.54886  | Up       | fatty acid binding protein 7      |
| PON3       | paraoxonase 3                                   | 1.382761    | 0.000     | 16.52506  | Up       | paraoxonase 3                     |
| GAL        | galanin and GMAP prepropeptide                  | 1.402474    | 0.000     | 16.41339  | Up       | galanin and GMAP prepropeptide    |
| PAX6       | paired box 6                                     | 2.074082    | 0.000     | 16.08292  | Up       | paired box 6                      |
| SYPL2      | synaptophysin like 2                            | 1.302737    | 0.000     | 16.06335  | Up       | synaptophysin like 2              |
| DRGX       | dorsal root ganglia homeobox                    | 1.08197     | 0.000     | 15.9954   | Up       | dorsal root ganglia homeobox      |
| LGI1       | leucine rich glioma inactivated 1               | 1.756456    | 0.000     | 15.9945   | Up       | leucine rich glioma inactivated 1 |
| MIR503H    | MIR503 host gene                                | 1.05068     | 0.000     | 15.94943  | Up       | MIR503 host gene                  |
| SLC15A1    | solute carrier family 15 member 1               | 1.538301    | 0.000     | 15.58775  | Up       | solute carrier family 15 member 1 |
| TMPRSS3    | transmembrane protease, serine 3               | 1.596153    | 0.000     | 15.44677  | Up       | transmembrane protease, serine 3  |
| AL59124    |                                         | 1.577183    | 0.000     | 15.43499  | Up       | NA                                |
| ROR2       | receptor tyrosine kinase like orphan receptor 2 | 1.473452    | 0.000     | 15.26237  | Up       | receptor tyrosine kinase like orphan receptor 2 |
| DACT2      | dishevelled binding antagonist of beta catenin 2| 1.389093    | 0.000     | 15.25987  | Up       | dishevelled binding antagonist of beta catenin 2 |
| AL59124    |                                         | 1.506199    | 0.000     | 14.93773  | Up       | NA                                |
| SMTNL2     | smoothelin like 2                               | 1.13931     | 0.000     | 14.72185  | Up       | smoothelin like 2                 |
| KRT40      | keratin 40                                       | 1.57768     | 0.000     | 14.59126  | Up       | keratin 40                         |
| Gene ID | Description | FC | p-value | Adjusted p-value | log2FoldChange | Status |
|---------|-------------|----|---------|------------------|----------------|--------|
| A_23_P214 | FBN2 | 1.687663 | 2.83E-07 | 0.000 | 14.57834 | Up fibrillin 2 |
| A_23_P489 | NTF4 | 1.441871 | 2.84E-07 | 0.000 | 14.57475 | Up neurotrophin 4 |
| A_23_P186 | GBA3 | 0.964336 | 3.42E-07 | 0.000 | 14.24096 | Up glucosylceramidase beta 3 (gene/pseudogene) |
| A_19_P003 | #N/A | 0.933759 | 3.44E-07 | 0.000 | 14.23364 | Up NA |
| A_33_P344 | SRL | 1.279597 | 3.63E-07 | 0.000 | 14.13739 | Up sarcalumenin |
| A_23_P166 | OR7A5 | 1.409749 | 5.03E-07 | 0.000 | 13.58235 | Up olfactory receptor family 7 subfamily A member 5 |
| A_33_P324 | DGKK | 1.719184 | 5.8E-07 | 0.000 | 13.34618 | Up diacylglycerol kinase kappa |
| A_33_P334 | LOC4014 | 1.555765 | 6.8E-07 | 0.000 | 13.08512 | Up uncharacterized LOC401442 |
| A_23_P127 | BBOX1 | 1.969105 | 7.18E-07 | 0.000 | 12.99661 | Up gamma-butyrobetaine hydroxylase 1  |
| A_33_P372 | ART3 | 1.310074 | 7.36E-07 | 0.000 | 12.95714 | Up ADP-ribosyltransferase 3 |
| A_33_P327 | NRK | 1.438252 | 7.49E-07 | 0.000 | 12.93021 | Up Nik related kinase |
| A_33_P332 | LOC6547 | 1.529021 | 8.77E-07 | 0.000 | 12.67915 | Up splicing factor proline/glutamine-rich |
| A_33_P336 | ITIH6 | 0.970677 | 9.01E-07 | 0.000 | 12.63721 | Up inter-alpha-trypsin inhibitor heavy chain family member 6 |
| A_19_P003 | AC00248 | 1.144117 | 1.1E-06 | 0.000 | 12.32129 | Up NA |
| A_33_P322 | ID4 | 1.414675 | 1.11E-06 | 0.000 | 12.31878 | Up inhibitor of DNA binding 4, HLH protein |
| A_33_P328 | #N/A | 1.105066 | 1.11E-06 | 0.000 | 12.31117 | Up NA |
| A_33_P324 | DEFB131 | 1.290266 | 1.31E-06 | 0.000 | 12.05627 | Up defensin beta 131 |
| A_33_P340 | PLIN4 | 1.033075 | 1.33E-06 | 0.000 | 12.03503 | Up perilipin 4 |
| A_33_P350 | LINC012 | 1.129723 | 1.57E-06 | 0.000 | 11.7883 | Up long intergenic non-protein coding RNA 1299 |
| A_32_P324 | LINC002 | 0.971613 | 1.72E-06 | 0.000 | 11.65582 | Up long intergenic non-protein coding RNA 282 |
| A_33_P324 | TRDN | 2.047985 | 1.75E-06 | 0.000 | 11.63034 | Up triadin |
| A_23_P311 | CLIC5 | 1.76 | 1.86E-06 | 0.000 | 11.54202 | Up chloride intracellular channel 5 |
| Gene Name | Log2 Fold Change | p-value | Adjusted p-value | Status | Description |
|-----------|-----------------|---------|-----------------|--------|-------------|
| BTBD17    | 1.379368        | 0.000   | 11.45968        | Up     | BTB domain containing 17 |
| DRC3      | 1.187589        | 0.000   | 11.41367        | Up     | disrupted in renal carcinoma 3 |
| IRX1      | 1.782642        | 0.000   | 11.31183        | Up     | iroquoishomeobox 1 |
| RBFOX3    | 2.121609        | 0.000   | 11.27381        | Up     | RNA binding protein, fox-1 homolog 3 |
| Fcer1a    | 1.675704        | 0.000   | 11.12106        | Up     | Fc fragment of IgE receptor 1a |
| DIRC3     | 1.187589        | 0.000   | 11.03944        | Up     | neuronal guanine nucleotide exchange factor |
| Cckbr     | 1.368159        | 0.000   | 11.03391        | Up     | cholecystokinin B receptor |
| Itln1     | 1.534417        | 0.000   | 11.00679        | Up     | intelectin 1 |
| S100a1    | 1.861029        | 0.000   | 9.94318         | Up     | S100 calcium binding protein A1 |
| Temem13   | 1.402909        | 0.000   | 9.93278         | Up     | transmembrane protein 139 |
| Cbln2     | 1.141876        | 0.000   | 9.92424         | Up     | cerebellin 2 precursor |
| Pmapi1    | 1.187979        | 0.000   | 9.86654         | Up     | phorbol-12-myristate-13-acetate-induced protein 1 |
| Ghrhr     | 1.170394        | 0.000   | 9.83768         | Up     | growth hormone releasing hormone receptor |
| Xdh       | 1.809518        | 0.000   | 9.80343         | Up     | xanthine dehydrogenase |
| Toagar    | 1.604949        | 0.001   | 9.69969         | Up     | TOG array regulator of axonemal microtubules 2 |
| Ccdec17   | 1.42881         | 0.001   | 9.68331         | Up     | coiled-coil domain containing 178 |
| Trim29    | 1.443956        | 0.001   | 9.64492         | Up     | tripartite motif containing 29 |
| Ugta2a2   | 1.479469        | 0.001   | 9.62203         | Up     | UDP glucuronosyltransferase family 2 member A2 |
| Jakmip2   | 1.32862         | 0.001   | 9.59731         | Up     | JAKMIP2 antisense RNA 1 |
| Sox5      | 1.659349        | 0.001   | 9.54464         | Up     | SRY-box 5 |
| S100a1    | 1.494024        | 0.001   | 9.43768         | Up     | S100 calcium binding protein A1 |
| Rprml     | 1.611243        | 0.001   | 9.38091         | Up     | reprimo like |
| Aci12003   | 1.753756        | 0.001   | 9.33104         | Up     | NA |
| Galr1     | 1.619947        | 0.001   | 9.27926         | Up     | galanin receptor 1 |
| Gene Symbol | Gene Name | Fold Change | p-value | q-value | Expression Value | Log2 Fold Change | Description |
|-------------|-----------|--------------|---------|---------|------------------|-----------------|-------------|
| A_23_P831   | 1.058861  | 4.68E-06     | 0.001   | 10.27589 | Up               | growth arrest specific 1 |
| A_33_P330   | 1.085168  | 4.71E-06     | 0.001   | 10.26968 | Up               | protein phosphatase 1 regulatory subunit 17 |
| A_23_P302   | 0.935355  | 4.82E-06     | 0.001   | 10.23827 | Up               | interferon epsilon |
| A_23_P132   | 1.253634  | 4.83E-06     | 0.001   | 10.23304 | Up               | cadherin EGF LAG seven-pass G-type receptor 1 |
| A_23_P299   | 1.051466  | 5.25E-06     | 0.001   | 10.12693 | Up               | chromosome 4 open reading frame 19 |
| A_33_P334   | 1.014551  | 5.73E-06     | 0.001   | 10.01362 | Up               | proopiomelanocortin |
| A_19_P003   | #N/A      | 6.47E-06     | 0.001   | 9.859854 | Up               | NA |
| A_24_P365   | 1.636424  | 6.82E-06     | 0.001   | 9.794187 | Up               | solute carrier family 6 member 14 |
| A_32_P113   | 1.318608  | 6.87E-06     | 0.001   | 9.784901 | Up               | lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase) |
| A_33_P341   | 1.309174  | 7.32E-06     | 0.001   | 9.704786 | Up               | serine palmitoyltransferase long chain base subunit 3 |
| A_23_P101   | 1.847661  | 7.34E-06     | 0.001   | 9.702092 | Up               | kallikrein related peptidase 11 |
| A_32_P416   | 1.535516  | 7.35E-06     | 0.001   | 9.700312 | Up               | coagulation factor V |
| A_33_P336   | 1.605568  | 7.42E-06     | 0.001   | 9.688935 | Up               | contactin associated protein-like 2 |
| A_33_P321   | 1.290311  | 7.68E-06     | 0.001   | 9.645508 | Up               | peptidase inhibitor 16 |
| A_24_P397   | 1.594549  | 8.75E-06     | 0.002   | 9.485334 | Up               | ectonucleotideprophosphatase/phosphodiesterase 6 |
| A_33_P321   | 1.036074  | 9.63E-06     | 0.002   | 9.369347 | Up               | guanylate binding protein family member 6 |
| A_33_P335   | 1.050788  | 9.78E-06     | 0.002   | 9.351444 | Up               | ovo like zinc finger 3 |
| A_23_P112   | 1.350445  | 1E-05        | 0.002   | 9.323343 | Up               | odorant binding protein 2A |
| A_23_P752   | 1.726183  | 1.04E-05     | 0.002   | 9.282412 | Up               | retinol binding protein 4 |
| A_33_P325   | 1.719928  | 1.05E-05     | 0.002   | 9.263686 | Up               | protein phosphatase 1 regulatory subunit 27 |
| A_23_P202   | 1.137137  | 1.1E-05      | 0.002   | 9.21207  | Up               | inter-alpha-trypsin inhibitor heavy chain 2 |
| A_23_P328   | 1.378209  | 1.16E-05     | 0.002   | 9.14984  | Up               | neutralized E3 ubiquitin protein ligase 3 |
| A_23_P416   | 1.122275  | 1.19E-05     | 0.002   | 9.114478 | Up               | chloride intracellular channel 5 |
| A_24_P130   | 1.528046  | 1.2E-05      | 0.002   | 9.110565 | Up               | solute carrier family 16 member 12 |
| Gene Symbol | Description |
|-------------|-------------|
| PPP1R27 | protein phosphatase 1 regulatory subunit 27 |
| RASL11B | RAS like family 11 member B |
| KCNJ12 | potassium voltage-gated channel subfamily J member 12 |
| AQP4 | aquaporin 4 |
| RASL11A | RAS like family 11 member A |
| KCNJ12 | potassium voltage-gated channel subfamily J member 12 |
| AQP4 | aquaporin 4 |
| CD8B | CD8b molecule |
| P2RY2 | purinergic receptor P2Y2 |
| IL22RA1 | interleukin 22 receptor subunit alpha 1 |
| ADAMTS18 | ADAM metallopeptidase with thrombospondin type 1 motif 18 |
| NGFR | nerve growth factor receptor |
| KCNJ16 | potassium voltage-gated channel subfamily J member 16 |
| EFEMP1 | EGF containing fibrilin like extracellular matrix protein 1 |
| CHN2 | chimerin 2 |
| GPHA2 | glycoprotein hormone alpha 2 |
| GHRHR | growth hormone releasing hormone receptor |
| KRT40 | keratin 40 |
| C6orf132 | chromosome 6 open reading frame 132 |
| NRAP | nebulin related anchoring protein |
| IQCJ | IQ motif containing J |
| PHACTR2 | phosphatase and actin regulator 2 |
| EVC2 | EvCiliary complex subunit 2 |
| FOXL2 | forkhead box L2 |
| SLC51A | solute carrier family 51 alpha subunit |
| NR2F1-AS1 | NR2F1 antisense RNA 1 |
| Gene ID  | Gene Symbol | Log2 Fold Change | P-value  | FC   | Regulation                                                                 |
|---------|-------------|------------------|----------|------|-----------------------------------------------------------------------------|
| A_23_P166 | FAM3B      | 1.658734         | 0.004    | 546  | family with sequence similarity 3 member B                               |
| A_24_P236 | DLK1       | 1.084201         | 0.004    | 667  | delta like non-canonical Notch ligand 1                                     |
| A_24_P503 | BLID       | 0.934055         | 0.004    | 764  | BH3-like motif containing, cell death inducer                              |
| A_23_P431 | CALB1      | 1.816152         | 0.004    | 874  | calbindin                                                                   |
| A_33_P334 | UGT2A1     | 1.919609         | 0.004    | 817  | UDP glucuronosyltransferase family 2 member A1 complex locus               |
| A_19_P003 | #N/A       | 0.976388         | 0.004    | 888  | NA                                                                          |
| A_23_P212 | TF         | 1.475208         | 0.005    | 921  | osteoglycin                                                                |
| A_24_P655 | SMAD9      | 1.578849         | 0.005    | 888  | SMAD family member 9                                                        |
| A_19_P008 | LINC005    | 1.475444         | 0.005    | 808  | long intergenic non-protein coding RNA 598                                 |
| A_23_P401 | SOX2       | 1.69957          | 0.005    | 867  | SRY-box 2                                                                  |
| A_23_P500 | KLK12      | 2.06498          | 0.005    | 129  | kallikrein related peptidase 12                                             |
| A_24_P882 | KRT17P1    | 1.106234         | 0.005    | 299  | keratin 17 pseudogene 1                                                     |
| A_23_P110 | SBSBON     | 1.314417         | 0.005    | 496  | somatomedin B and thrombospondin type 1 domain containing                  |
| A_33_P334 | KRT14      | 1.187608         | 0.005    | 55   | keratin 14                                                                 |
| A_32_P930 | DLGAP2     | 1.302276         | 0.005    | 631  | DLG associated protein 2                                                   |
| A_23_P110 | CWH43      | 1.018626         | 0.005    | 709  | cell wall biogenesis 43 C-terminal homolog                                |
| A_33_P334 | AMOT       | 1.359913         | 0.005    | 713  | leucine rich repeat containing 2                                           |
| A_33_P334 | LRRC2      | 0.953096         | 0.005    | 709  | angiomotin                                                                 |
| A_19_P003 | #N/A       | 1.004498         | 0.005    | 857  | NA                                                                          |
| A_33_P334 | LINC005    | 1.256571         | 0.005    | 713  | long intergenic non-protein coding RNA 598                                 |
| A_33_P334 | ZNF385C    | 0.953391         | 0.006    | 119  | zinc finger protein 385C                                                   |
| A_23_P425 | CCK        | 1.622521         | 0.006    | 272  | cholecystokinin                                                            |
| A_23_P632 | HSD11B     | 1.715094         | 0.006    | 272  | hydroxysteroid 11-beta dehydrogenase 1                                   |
| ID     | Gene      | ID       | Description                                                                                                                                 |
|--------|-----------|----------|--------------------------------------------------------------------------------------------------------------------------------------------|
| A_23_P971 | HS3ST4    | 1.269685 | 4.84E-05 0.006 7.581112 Up heparansulfate-glucosamine 3-sulfotransferase 4 |
| A_24_P691 | WFDC21    | 0.992875 | 5.11E-05 0.006 7.524302 Up WAP four-disulfide core domain 21, pseudogene |
| A_19_P008 | #N/A      | 1.104671 | 5.13E-05 0.006 7.520302 Up NA |
| A_33_P326 | SGCD      | 1.257873 | 5.28E-05 0.006 7.492188 Up heparansulfate-glucosamine 3-sulfotransferase 4 |
| A_33_P332 | PRSS8     | 1.069842 | 5.57E-05 0.006 7.439292 Up protease, serine 8 |
| A_33_P324 | OR3A4P    | 1.184305 | 5.63E-05 0.006 7.427986 Up olfactory receptor family 3 subfamily A member 4 pseudogene |
| A_32_P851 | C6orf118  | 1.123262 | 5.67E-05 0.007 7.420158 Up chromosome 6 open reading frame 118 |
| A_19_P008 | MIR503H   | 2.046985 | 6.03E-05 0.007 7.359333 Up MIR503 host gene |
| A_33_P330 | LAD1      | 1.154517 | 6.1E-05 0.007 7.348491 Up ladinin 1 |
| A_33_P336 | MYL10     | 1.181726 | 6.32E-05 0.007 7.31978 Up myosin light chain 10 |
| A_32_P173 | CRISP2    | 1.011029 | 6.4E-05 0.007 7.299777 Up cysteine rich secretory protein 2 |
| A_33_P333 | IHH       | 1.292631 | 6.61E-05 0.007 7.268026 Up indian hedgehog |
| A_24_P395 | CGB3      | 1.492903 | 6.68E-05 0.007 7.257466 Up chorionic gonadotropin beta subunit 3 |
| A_33_P330 | AC12950   | 0.949086 | 7.03E-05 0.007 7.207806 Up NA |
| A_23_P236 | MCOLN2    | 0.940979 | 7.22E-05 0.008 7.182496 Up mucolipin 2 |
| A_32_P206 | LOC1002   | 1.265982 | 7.31E-05 0.008 7.169161 Up uncharacterized LOC100288911 |
| A_32_P232 | TRABD2    | 1.388547 | 7.41E-05 0.008 7.156892 Up TraB domain containing 2B |
| A_23_P241 | SLC39A1   | 1.443756 | 7.43E-05 0.008 7.153512 Up solute carrier family 39 member 12 |
| A_23_P565 | VIT       | 1.322911 | 7.57E-05 0.008 7.135859 Up vitrin |
| A_23_P832 | PRRX2     | 1.098103 | 7.63E-05 0.008 7.128004 Up paired related homeobox 2 |
| A_23_P145 | PPP1R17   | 1.564573 | 7.66E-05 0.008 7.124207 Up protein phosphatase 1 regulatory subunit 17 |
| A_23_P121 | TSHB      | 1.120155 | 7.89E-05 0.008 7.095106 Up thyroid stimulating hormone beta 28 |
| A_23_P537 | RUBCNL    | 1.059222 | 8.04E-05 0.008 7.077398 Up RUN and cysteine rich domain containing beclin 1 interacting protein like |
| A_23_P314 | AGR2      | 1.36206  | 8.09E-05 0.008 7.071021 Up anterior gradient 2, protein disulphide isomerase family member |
| Gene Symbol | Description                                      | Gene Symbol | Description                                      |
|-------------|--------------------------------------------------|-------------|--------------------------------------------------|
| KBTBD1      | kelch repeat and BTB domain containing 12        | GADD45      | growth arrest and DNA damage inducible gamma     |
| LINC021     | long intergenic non-protein coding RNA 2182     | FXYD3       | FXYD domain containing ion transport regulator 3 |
| A_32_P116   | limb and CNS expressed 1                        | A_33_P322   | protease, serine 45                              |
| 7.053992    |                                                 | 7.053472    |                                                 |
| 7.037193    |                                                 | 7.028524    |                                                 |
| 7.022811    |                                                 | 7.019706    |                                                 |
| 7.008653    |                                                 | 6.991076    |                                                 |
| 6.972708    |                                                 | 6.963243    |                                                 |
| 6.951781    |                                                 | 6.94327     |                                                 |
| 6.936563    |                                                 | 6.930503    |                                                 |
| 6.936563    |                                                 | 6.920505    |                                                 |
| 6.917781    |                                                 | 6.90503     |                                                 |
| 6.90503     |                                                 | 6.87276     |                                                 |
| 6.891076    |                                                 | 6.864052    |                                                 |
| 6.860562    |                                                 | 6.820505    |                                                 |
| 6.820505    |                                                 | 6.805414    |                                                 |
| 6.805414    |                                                 | 6.778619    |                                                 |
| 6.788943    |                                                 | 6.733096    |                                                 |
| 6.733096    |                                                 | 6.778619    |                                                 |
| 6.714341    |                                                 | 6.717833    |                                                 |
| 6.717833    |                                                 | 6.706512    |                                                 |
| 6.706512    |                                                 |             |                                                 |
| 6.691076    |                                                 |             |                                                 |
| 6.677861    |                                                 |             |                                                 |
| 6.677861    |                                                 |             |                                                 |
| 6.67067     |                                                 |             |                                                 |
| 6.67067     |                                                 |             |                                                 |
| 6.663512    |                                                 |             |                                                 |
| 6.663512    |                                                 |             |                                                 |

**AIMS Neuroscience**

Volume 8, Issue 2, 254–283.
| Gene      | Accession | FDR   | Fold Change | p-Value | Status | Description                                                                 |
|-----------|-----------|-------|-------------|---------|--------|----------------------------------------------------------------------------|
| CARTPT    | A_23_P167 | 0.00012 | 0.010       | 6.676755 | Up     | CART prepropeptide                                                         |
| CSH1      | A_23_P381 | 0.00012 | 0.010       | 6.676545 | Up     | chorionic somatomammotropin hormone 1                                      |
| GALNT9    | A_23_P252 | 0.00012 | 0.010       | 6.651804 | Up     | polypeptide N-acetylgalactosaminyltransferase 9                            |
| OGN       | A_23_P829 | 0.00012 | 0.010       | 6.628807 | Up     | osteoglycin                                                                |
| FAM153    | A_32_P843 | 0.00013 | 0.010       | 6.618167 | Up     | family with sequence similarity 153 member B                               |
| CSH1      | A_33_P325 | 0.00013 | 0.010       | 6.612967 | Up     | growth arrest and DNA damage inducible gamma                               |
| VSNL1     | A_23_P209 | 0.00013 | 0.011       | 6.59626  | Up     | visinin like 1                                                             |
| KISS1R    | A_33_P323 | 0.00013 | 0.011       | 6.596694 | Up     | KISS1 receptor                                                             |
| FGFR3     | A_23_P212 | 0.00013 | 0.011       | 6.586685 | Up     | fibroblast growth factor receptor 3                                        |
| PROSER2   | A_33_P334 | 0.00013 | 0.011       | 6.57444  | Up     | Wnt family member 5A                                                       |
| FGFR3     | A_23_P357 | 0.00013 | 0.011       | 6.569217 | Up     | CD8b molecule                                                              |
| FXYD3     | A_23_P927 | 0.00016 | 0.012       | 6.426669 | Up     | heat shock protein family B (small) member 3                               |
| PAX6      | A_33_P330 | 0.00016 | 0.012       | 6.416123 | Up     | paired box 6                                                               |
| CYBRD1    | A_24_P345 | 0.00016 | 0.012       | 6.402632 | Up     | cytochrome b reductase 1                                                   |
| FXYD3     | A_33_P322 | 0.00016 | 0.012       | 6.387741 | Up     | FXYD domain containing ion transport regulator 3                            |
| FLJ30901  | A_33_P348 | 0.00017 | 0.012       | 6.371786 | Up     | uncharacterized protein FLJ30901                                           |
| PGR       | A_23_P138 | 0.00017 | 0.012       | 6.35462  | Up     | progesterone receptor                                                      |
| HSD17B    | A_19_P008 | #N/A   | #N/A        | #N/A    | Up     | NA                                                                         |
| OPCML     | A_32_P160 | 0.00018 | 0.013       | 6.316724 | Up     | hydroxysteroid 17-beta dehydrogenase 2                                    |
| FAM217    | A_23_P317 | 0.00018 | 0.013       | 6.268468 | Up     | family with sequence similarity 217 member A                               |
| RXF4      | A_23_P763 | 0.00019 | 0.013       | 6.266747 | Up     | regulatory factor X4                                                       |
| Gene Symbol | Description                  | Log2 Fold Change | P Value     | q Value  | Gene Symbol | Description                  | Log2 Fold Change | P Value     | q Value  |
|-------------|------------------------------|------------------|-------------|----------|-------------|------------------------------|-----------------|-------------|----------|
| AGR3        | Anterior gradient 3, protein disulphide isomerase family member | 1.186616        | 0.00019     | 0.013    | SOX9        | SRY-box 9                    | 1.113591        | 0.00020     | 0.013    |
| SLIT1       | Slit guidance ligand 1       | 1.673787        | 0.00200     | 0.013    | DEUP1       | Deuterosome assembly protein 1 | 1.483472        | 0.00021     | 0.014    |
| SOX9        | Chorionic somatomammotropin hormone like 1 | 1.2167          | 0.00021     | 0.013    | CHST9       | Carbohydrate sulfotransferase 9 | 1.148294        | 0.00022     | 0.014    |
| CSHL1       | Slit guidance ligand 1       | 1.01799         | 0.00222     | 0.015    | SULT1C      | Sulfotransferase family 1C member 2 | 1.072548        | 0.00023     | 0.015    |
| CHST9       | Chorionic somatomammotropin hormone like 1 | 1.182136       | 0.00022     | 0.015    | SULT1C      | Sulfotransferase family 1C member 4 | 1.072548        | 0.00023     | 0.015    |
| NRK         | Nik related kinase          | 1.148294        | 0.00022     | 0.014    | DEUP1       | Deuterosome assembly protein 1 | 1.483472        | 0.00021     | 0.014    |
| SULT1C      | Sulfotransferase family 1C member 2 | 1.072548        | 0.00023     | 0.015    | SULT1C      | Sulfotransferase family 1C member 4 | 1.072548        | 0.00023     | 0.015    |
| DYDC2       | Dpy-30 domain containing 2   | 1.072548        | 0.00023     | 0.015    | SULT1C      | Sulfotransferase family 1C member 4 | 1.072548        | 0.00023     | 0.015    |
| CFAP74      | Cilia and flagella associated protein 74 | 1.034589       | 0.00023     | 0.015    | SULT1C      | Sulfotransferase family 1C member 4 | 1.072548        | 0.00023     | 0.015    |
| SNTG2       | Syntrophin gamma 2           | 1.884616        | 0.00023     | 0.015    | SULT1C      | Sulfotransferase family 1C member 4 | 1.072548        | 0.00023     | 0.015    |
| ZNF750      | Zinc finger protein 750      | 1.064614        | 0.00023     | 0.015    | ZNF750      | Zinc finger protein 750       | 1.064614        | 0.00023     | 0.015    |
| TAC4        | Tachykinin 4 (hemokinin)     | 1.141906        | 0.00024     | 0.015    | TAC4        | Tachykinin 4 (hemokinin)      | 1.141906        | 0.00024     | 0.015    |
| AGMO        | Alkylglycerolmonoxygenase     | 1.074353        | 0.00024     | 0.015    | AGMO        | Alkylglycerolmonoxygenase     | 1.074353        | 0.00024     | 0.015    |
| PTER        | Phosphotriesterase related   | 1.057567        | 0.00024     | 0.015    | PTER        | Phosphotriesterase related    | 1.057567        | 0.00024     | 0.015    |
| CTRB1       | Chymotrypsinogen B1          | 1.081155        | 0.00024     | 0.015    | CTRB1       | Chymotrypsinogen B1          | 1.081155        | 0.00024     | 0.015    |
| DLEC1       | Deleted in lung and esophageal cancer 1 | 1.106803       | 0.00025     | 0.015    | DLEC1       | Deleted in lung and esophageal cancer 1 | 1.106803       | 0.00025     | 0.015    |
| COL21A      | Collagen type XXI alpha 1 chain | 1.493919       | 0.00025     | 0.015    | COL21A      | Collagen type XXI alpha 1 chain | 1.493919       | 0.00025     | 0.015    |
| LINC018     | Long intergenic non-protein coding RNA 1852 | 0.977693       | 0.00025     | 0.015    | LINC018     | Long intergenic non-protein coding RNA 1852 | 0.977693       | 0.00025     | 0.015    |
| ATF7IP2     | Activating transcription factor 7 interacting protein 2 | 1.079212       | 0.00025     | 0.015    | ATF7IP2     | Activating transcription factor 7 interacting protein 2 | 1.079212       | 0.00025     | 0.015    |
| NEFM        | Neurofilament medium         | 1.748709        | 0.00026     | 0.015    | NEFM        | Neurofilament medium         | 1.748709        | 0.00026     | 0.015    |
| AC00248     | S100 calcium binding protein A14 | 1.245626       | 0.00027     | 0.016    | AC00248     | S100 calcium binding protein A14 | 1.245626       | 0.00027     | 0.016    |
| Gene Symbol | Description                  | log2 Fold Change | p Value | adjusted p Value | Classification |
|-------------|------------------------------|-----------------|---------|-----------------|----------------|
| AOX1        | Aldehyde oxidase 1           | 1.160692        | 0.00028 | 0.016           | Up             |
| KLRF1       | Killer cell lectin like receptor F1 | 0.936194    | 0.00028 | 0.016           | Up             |
| KCNIP4-IT1  | KCNIP4 intronic transcript 1 | 1.113185        | 0.00028 | 0.016           | Up             |
| ENTPD8      | Ectonucleoside triphosphate diphosphohydrolase 8 | 0.994821     | 0.00029 | 0.016           | Up             |
| CCDC68      | Coiled-coil domain containing 68 | 1.63892       | 0.00029 | 0.016           | Up             |
| IRX2        | Iroquoishomeobox 2           | 0.941375        | 0.00030 | 0.016           | Up             |
| CNKSR3      | CNKSR family member 3        | 1.102873        | 0.00030 | 0.016           | Up             |
| CRYM        | Crystallin mu                | 0.956236        | 0.00030 | 0.017           | Up             |
| FFA3        | Free fatty acid receptor 3   | 1.175134        | 0.00031 | 0.017           | Up             |
| MYZAP       | Myocardial zonulaadherens protein | 1.382209    | 0.00031 | 0.017           | Up             |
| PDE6A       | Phosphodiesterase 6A         | 1.325565        | 0.00031 | 0.017           | Up             |
| ABCA8       | ATP binding cassette subfamily A member 8 | 1.154317    | 0.00033 | 0.017           | Up             |
| PHACTR      | Phosphatase and actin regulator 3 | 1.093945     | 0.00037 | 0.018           | Up             |
| Gene Symbol | Description                                      | Value 1 | Value 2 | Value 3 | Value 4 | Value 5 |
|-------------|--------------------------------------------------|---------|---------|---------|---------|---------|
| IL20RA      | interleukin 20 receptor subunit alpha            | 1.2574  | 0.00038 | 0.019   | 5.6753  | Up      |
| LEFTY2      | left-right determination factor 2                | 1.2629  | 0.00038 | 0.019   | 5.6674  | Up      |
| ITGBL1      | integrin subunit beta like 1                     | 1.3250  | 0.00039 | 0.019   | 5.6545  | Up      |
| RHBDL3      | rhomboid like 3                                 | 1.1385  | 0.00040 | 0.019   | 5.6286  | Up      |
| GH1         | growth hormone 1                                 | 1.1844  | 0.00041 | 0.019   | 5.6181  | Up      |
| CPEDI       | cadherin like and PC-esterase domain containing 1| 1.0749  | 0.00041 | 0.019   | 5.6120  | Up      |
| STRA6       | stimulated by retinoic acid 6                    | 1.0857  | 0.00041 | 0.020   | 5.6083  | Up      |
| FOXL2N      | FOXL2 neighbor                                   | 1.8145  | 0.00041 | 0.020   | 5.6081  | Up      |
| CT45A1      | cancer/testis antigen family 45 member A1        | 1.2062  | 0.00042 | 0.020   | 5.5865  | Up      |
| C2orf40     | chromosome 2 open reading frame 40               | 1.0245  | 0.00043 | 0.020   | 5.5795  | Up      |
| FGFR3       | fibroblast growth factor receptor 3              | 1.0247  | 0.00043 | 0.020   | 5.5786  | Up      |
| EYA4        | EYA transcriptional coactivator and phosphatase 4| 1.4613  | 0.00044 | 0.020   | 5.5673  | Up      |
| TNFRSF14    | TNFRSF14 antisense RNA 1                         | 1.0337  | 0.00044 | 0.020   | 5.5601  | Up      |
| AMZ1        | archaelysin family metallopeptidase 1            | 1.2913  | 0.00044 | 0.020   | 5.5585  | Up      |
| AL03338     | NA                                                | 1.0466  | 0.00044 | 0.020   | 5.5560  | Up      |
| CACNA1A     | calcium voltage-gated channel subunit alpha 1 A  | 1.1991  | 0.00046 | 0.020   | 5.5240  | Up      |
| FAM196      | family with sequence similarity 196 member A     | 1.1047  | 0.00046 | 0.020   | 5.5216  | Up      |
| CA12        | carbonic anhydrase 12                            | 1.1399  | 0.00046 | 0.020   | 5.5151  | Up      |
| GAS7        | growth arrest specific 7                         | 1.0856  | 0.00047 | 0.020   | 5.5135  | Up      |
| HPGD        | hydroxyprostaglandin dehydrogenase 15- (NAD)     | 1.3967  | 0.00047 | 0.020   | 5.5090  | Up      |
| AL16041     | NA                                                | 1.1924  | 0.00048 | 0.021   | 5.4800  | Up      |
| FMO5        | flavin containing monooxygenase 5                | 1.1603  | 0.00048 | 0.021   | 5.4800  | Up      |
| Gene Symbol | Description | Fold Change | p-value | q-value | Regulation Status |
|-------------|-------------|-------------|---------|---------|-------------------|
| SCGB1D | secretoglobin family 1D member 2 | 1.294842 | 0.00049 | 0.021 | Up |
| PLIN5 | perilipin 5 | 1.34129 | 0.00049 | 0.021 | Up |
| KCNA1 | potassium voltage-gated channel subfamily A member 1 | 1.463762 | 0.00049 | 0.021 | Up |
| MSX2P1 | mshhomeobox 2 pseudogene 1 | 1.197032 | 0.00051 | 0.021 | Up |
| ALDOB | aldolase, fructose-bisphosphate B | 1.370957 | 0.00051 | 0.021 | Up |
| RHOD | ras homolog family member D | 1.601066 | 0.00051 | 0.021 | Up |
| GJB7 | gap junction protein beta 7 | 1.405572 | 0.00052 | 0.021 | Up |
| PRR15L | proline rich 15 like | 0.938926 | 0.00052 | 0.021 | Up |
| IRX2 | iroquoishomeobox 2 | 1.76183 | 0.00053 | 0.022 | Up |
| ALDH1A | aldehyde dehydrogenase 1 family member A3 | 1.435514 | 0.00054 | 0.022 | Up |
| EYA2 | EYA transcriptional coactivator and phosphatase 2 | 1.179968 | 0.00054 | 0.022 | Up |
| KRT19 | keratin 19 | 0.946868 | 0.00055 | 0.022 | Up |
| LINC025 | long intergenic non-protein coding RNA 2562 | 1.027445 | 0.00055 | 0.022 | Up |
| LY6H | lymphocyte antigen 6 family member H | 1.829315 | 0.00055 | 0.022 | Up |
| MYBPH | myosin binding protein H like | 1.079067 | 0.00055 | 0.022 | Up |
| RASGRP | RAS guanyl releasing protein 1 | 0.942131 | 0.00056 | 0.022 | Up |
| GH2 | growth hormone 2 | 2.09163 | 0.00057 | 0.022 | Up |
| FAM19A | family with sequence similarity 19 member A5, C-C motif chemokine like | 1.339382 | 0.00057 | 0.022 | Up |
| RPRML | re pri mo like | 0.963599 | 0.00059 | 0.023 | Up |
| ASXL3 | additional sex combs like 3, transcriptional regulator | 1.030682 | 0.00060 | 0.023 | Up |
| LINC025 | long intergenic non-protein coding RNA 2562 | 1.317451 | 0.00060 | 0.023 | Up |
| TEPP | testis, prostate and placenta expressed | 1.140263 | 0.00061 | 0.023 | Up |
| PDZRN3 | PDZ domain containing ring finger 3 | 1.396019 | 0.00061 | 0.023 | Up |
| Accession | Gene Symbol | Log2FoldChange | p-value | Adjusted p-value | Regulation | Gene Description |
|-----------|-------------|----------------|---------|-----------------|-----------|------------------|
| A_33_P334 | AC09657     | 0.958785       | 0.00062 | 0.023           | Up        | NA               |
| A_24_P469 | KCNS2       | 1.033156       | 0.00063 | 0.024           | Up        | potassium voltage-gated channel modifier subfamily S member 2 |
| A_24_P561 | ALKAL2      | 1.48007        | 0.00063 | 0.024           | Up        | ALK and LTK ligand 2 |
| A_33_P328 | VANGL2      | 1.487347       | 0.00064 | 0.024           | Up        | VANGL planar cell polarity protein 2 |
| A_33_P327 | WASIR1      | 0.992418       | 0.00064 | 0.024           | Up        | WASH and IL9R antisense RNA 1 |
| A_33_P335 | GRIK1-AS1   | 0.971052       | 0.00065 | 0.024           | Up        | GRIK1 antisense RNA 1 |
| A_32_P225 | PRDM16      | 1.315384       | 0.00065 | 0.024           | Up        | PR/SET domain 16 |
| A_23_P148 | PLAC1       | 0.962204       | 0.00065 | 0.024           | Up        | placenta specific 1 |
| A_33_P327 | SH3BP4      | 1.281724       | 0.00066 | 0.024           | Up        | SH3 domain binding protein 4 |
| A_23_P217 | COL4A6      | 1.479885       | 0.00066 | 0.024           | Up        | collagen type IV alpha 6 chain |
| A_33_P328 | NEUROD1     | 1.700584       | 0.00066 | 0.024           | Up        | neuronal differentiation 1 |
| A_33_P328 | IL6R        | 1.168827       | 0.00066 | 0.024           | Up        | interleukin 6 receptor |
| A_23_P312 | TEX26       | 1.26024        | 0.00066 | 0.024           | Up        | testis expressed 26 |
| A_33_P329 | FSHB        | 2.112742       | 0.00066 | 0.024           | Up        | follicle stimulating hormone beta subunit |
| A_23_P207 | CSH2        | 1.34608        | 0.00066 | 0.024           | Up        | chorionic somatomamotropin hormone 2 |
| A_33_P332 | CNTNAP      | 1.057166       | 0.00067 | 0.024           | Up        | contactin associated protein like 3B |
| A_23_P159 | CHRDL1      | 1.077118       | 0.00067 | 0.024           | Up        | chordin like 1 |
| A_33_P351 | NWD1        | 1.146885       | 0.00068 | 0.025           | Up        | NACHT and WD repeat domain containing 1 |
| A_33_P333 | CPXM2       | 1.235098       | 0.00069 | 0.025           | Up        | carboxypeptidase X, M14 family member 2 |
| A_33_P328 | WWC2        | 0.99086        | 0.00071 | 0.025           | Up        | WW and C2 domain containing 2 |
| A_24_P254 | PAGE4       | 1.146619       | 0.00071 | 0.025           | Up        | PAGE family member 4 |
| A_23_P136 | APOD        | 1.229853       | 0.00071 | 0.025           | Up        | apolipoprotein D |
| A_23_P309 | GJB7        | 1.662038       | 0.00073 | 0.026           | Up        | gap junction protein beta 7 |
| A_33_P327 | TRBV20      | 0.942031       | 0.00075 | 0.026           | Up        | T-cell receptor beta variable 20/OR9-2 (non-functional) |
| Gene ID   | Gene Name  | FDR   | Log2 Fold Change | p-value | Status            | Description                                                                 |
|-----------|------------|-------|-----------------|---------|-------------------|-----------------------------------------------------------------------------|
| A_23_P232 | RXRG       | 0.00076 | 0.026           | 5.125969 | Up               | retinoid X receptor gamma                                                  |
| A_23_P340 | RNF175     | 0.00077 | 0.026           | 5.117906 | Up               | ring finger protein 175                                                    |
| A_23_P398 | IGSF11      | 0.00077 | 0.026           | 5.113508 | Up               | immunoglobulin superfamily member 11                                       |
| A_32_P187 | SCN2B      | 0.00078 | 0.026           | 5.103165 | Up               | sodium voltage-gated channel beta subunit 2                               |
| A_23_P125 | TMEM25A    | 0.00079 | 0.026           | 5.098126 | Up               | transmembrane protein 255A                                                |
| A_23_P143 | OVOL2      | 0.00079 | 0.026           | 5.097858 | Up               | ovo like zinc finger 2                                                     |
| A_32_P607 | CCDC15     | 0.00079 | 0.026           | 5.096324 | Up               | coiled-coil domain containing 158                                          |
| A_32_P141 | ARMC4      | 0.0008  | 0.027           | 5.090047 | Up               | armadillo repeat containing 4                                              |
| A_33_P323 | C9orf152   | 0.00083 | 0.027           | 5.060268 | Up               | chromosome 9 open reading frame 152                                       |
| A_23_P381 | ASXL3      | 0.00086 | 0.028           | 5.033829 | Up               | additional sex combs like 3, transcriptional regulator                    |
| A_23_P114 | CYP4B1     | 0.00087 | 0.028           | 5.018238 | Up               | cytochrome P450 family 4 subfamily B member 1                              |
| A_23_P392 | DLGAP2     | 0.00087 | 0.028           | 5.016681 | Up               | DLG associated protein 2                                                   |
| A_33_P332 | ALKAL2     | 0.00088 | 0.028           | 5.008349 | Up               | ALK and LTK ligand 2                                                       |
| A_23_P110 | PCDHB1     | 0.00091 | 0.029           | 4.987739 | Up               | protocadherin beta 1                                                       |
| A_23_P150 | TPH1       | 0.00092 | 0.029           | 4.978952 | Up               | tryptophan hydroxylase 1                                                  |
| A_23_P154 | AOX1       | 0.00094 | 0.029           | 4.96208 | Up               | aldehyde oxidase 1                                                         |
| A_23_P864 | CH25H      | 0.00096 | 0.030           | 4.944873 | Up               | cholesterol 25-hydroxylase                                                 |
| A_33_P328 | SLC39A8    | 0.00098 | 0.030           | 4.93375 | Up               | solute carrier family 39 member 8                                          |
| A_23_P143 | S100B      | 0.00099 | 0.030           | 4.91915 | Up               | S100 calcium binding protein B                                             |
| A_33_P329 | MALRD1     | 0.00100 | 0.030           | 4.915254 | Up               | MAM and LDL receptor class A domain containing 1                           |
| A_32_P348 | B3GALT      | 0.00101 | 0.030           | 4.908374 | Up               | B3GALT5 antisense RNA 1                                                    |
| A_33_P331 | CLEC9A     | 0.00101 | 0.030           | 4.907676 | Up               | C-type lectin domain containing 9A                                       |
| A_24_P190 | SLPI        | 0.00102 | 0.031           | 4.900711 | Up               | secretory leukocyte peptidase inhibitor                                    |
| A_32_P491 | PGR         | 0.00105 | 0.031           | 4.880628 | Up               | progesterone receptor                                                      |
| Gene Symbol | Description | Fold Change | P-value | FDR | Expression | Regulation |
|-------------|-------------|-------------|---------|-----|------------|------------|
| SSTR2       | Somatostatin receptor 2 | 1.022938 | 0.00105 | 0.031 | 4.880106 | Up |
| AP00047     | Fibroblast growth factor 1 | 1.1851   | 0.00106 | 0.031 | 4.87134   | Up |
| FLRT2       | Fibronectinleucine rich transmembrane protein 2 | 0.96055 | 0.00110 | 0.032 | 4.844468 | Up |
| C2orf71     | Chromosome 2 open reading frame 71 | 0.973752 | 0.00111 | 0.032 | 4.835307 | Up |
| COL13A      | Collagen type XIII alpha 1 chain | 1.167848 | 0.00113 | 0.032 | 4.819329 | Up |
| CACNA2D3    | Calcium voltage-gated channel auxiliary subunit alpha2delta 3 | 1.461394 | 0.00115 | 0.032 | 4.811744 | Up |
| NR0B1       | Nuclear receptor subfamily 0 group B member 1 | 1.455678 | 0.00117 | 0.033 | 4.796121 | Up |
| CALB2       | Calbindin 2 | 1.452992 | 0.00117 | 0.033 | 4.796121 | Up |
| STMN2       | Stathmin 2 | 1.55252  | 0.00119 | 0.033 | 4.785019 | Up |
| SCGB1D      | Secretoglobin family 1D member 1 | 1.242168 | 0.00119 | 0.033 | 4.784787 | Up |
| FGFL1       | Fibroblast growth factor 1 | 0.986971 | 0.00120 | 0.033 | 4.777304 | Up |
| KCNA1       | Potassium voltage-gated channel subfamily A member 1 | 1.237757 | 0.00121 | 0.033 | 4.769327 | Up |
| FOXL2       | Forkhead box L2 | 1.411075 | 0.00126 | 0.034 | 4.740819 | Up |
| MAP3K1      | Mitogen-activated protein kinase 15 | 1.119098 | 0.00127 | 0.034 | 4.734086 | Up |
| AC10087     | Proprotein convertase subtilisin/kexin type 2 | 1.53053 | 0.00129 | 0.034 | 4.722827 | Up |
| TXLNB       | Taxilin beta | 1.116641 | 0.00134 | 0.035 | 4.694487 | Up |
| LOC1486      | T brachyury transcription factor | 0.957229 | 0.00135 | 0.035 | 4.690142 | Up |
| LOC1486      | Uncharacterized LOC148638 | 1.189409 | 0.00135 | 0.035 | 4.689917 | Up |
| ERBB4       | Erb-b2 receptor tyrosine kinase 4 | 1.80022 | 0.00140 | 0.036 | 4.66067 | Up |
| PCSK2       | Proproteinconvertasesubtilisin/kexin type 2 | 1.403328 | 0.00143 | 0.036 | 4.645726 | Up |
| Gene Symbol | Description | Fold Change | p-value | FC Fold | Function |
|-------------|-------------|-------------|---------|---------|----------|
| FNDC11      | fibronectin type III domain containing 11 | 1.20722 | 0.00144 | 0.036   | Up      |
| DMKN        | dermokine | 0.95874 | 0.00147 | 0.037   | Up      |
| TGFBR3      | transforming growth factor beta receptor 3 | 1.016642 | 0.00148 | 0.037   | Up      |
| MN1         | MN1 proto-oncogene, transcriptional regulator | 0.940638 | 0.00149 | 0.037   | Up      |
| SLIT1       | slit guidance ligand 1 | 1.425281 | 0.00150 | 0.037   | Up      |
| DMKN        | dermokine | 0.95874 | 0.00147 | 0.037   | Up      |
| TGFBR3      | transforming growth factor beta receptor 3 | 1.016642 | 0.00148 | 0.037   | Up      |
| MN1         | MN1 proto-oncogene, transcriptional regulator | 0.940638 | 0.00149 | 0.037   | Up      |
| SLIT1       | slit guidance ligand 1 | 1.425281 | 0.00150 | 0.037   | Up      |
| DMKN        | dermokine | 0.95874 | 0.00147 | 0.037   | Up      |
| TGFBR3      | transforming growth factor beta receptor 3 | 1.016642 | 0.00148 | 0.037   | Up      |
| MN1         | MN1 proto-oncogene, transcriptional regulator | 0.940638 | 0.00149 | 0.037   | Up      |
| SLIT1       | slit guidance ligand 1 | 1.425281 | 0.00150 | 0.037   | Up      |
| Gene ID  | Description | FDR  | P-value | log2 Fold Change | State | Description |
|---------|-------------|------|---------|------------------|-------|-------------|
| A_33_P339 | ESPNL 1.098479 | 0.00193 | 0.042 | 4.4272 | Up | espin-like |
| A_23_P691 | FAM198 1.114636 | 0.00193 | 0.042 | 4.426766 | Up | family with sequence similarity 198 member A |
| A_33_P321 | EFCAB1 1.067562 | 0.00196 | 0.042 | 4.419076 | Up | EF-hand calcium binding domain 1 |
| A_23_P344 | FAM124 1.051178 | 0.00204 | 0.042 | 4.389351 | Up | family with sequence similarity 124 member A |
| A_23_P117 | CPLX3 1.042413 | 0.00211 | 0.044 | 4.365519 | Up | complexin 3 |
| A_33_P377 | ADARB2 1.299361 | 0.00212 | 0.044 | 4.362717 | Up | adenosine deaminase, RNA specific B2 (inactive) |
| A_33_P324 | DMKN 1.021837 | 0.00212 | 0.044 | 4.361736 | Up | dermokine |
| A_33_P328 | #N/A 0.990478 | 0.00212 | 0.044 | 4.361056 | Up | NA |
| A_19_P008 | #N/A 1.16815 | 0.00213 | 0.044 | 4.358693 | Up | NA |
| A_23_P102 | BANK1 1.035706 | 0.00215 | 0.045 | 4.342172 | Up | B-cell scaffold protein with ankyrin repeats 1 |
| A_23_P338 | HIF3A 1.003302 | 0.00220 | 0.045 | 4.335127 | Up | hypoxia inducible factor 3 alpha subunit |
| A_23_P146 | EFCAB1 1.496561 | 0.00224 | 0.045 | 4.323259 | Up | EF-hand calcium binding domain 1 |
| A_24_P929 | FLJ42393 1.329889 | 0.00225 | 0.046 | 4.319918 | Up | uncharacterized LOC401105 |
| A_24_P418 | CNTNAP 1.053068 | 0.00225 | 0.046 | 4.319016 | Up | contactin associated protein-like 3 |
| A_23_P768 | CCNJL 1.325275 | 0.00225 | 0.046 | 4.319918 | Up | cyclin J like |
| A_33_P341 | ADAM32 0.990478 | 0.00228 | 0.046 | 4.310264 | Up | ADAM metallopeptidase domain 32 |
| A_23_P307 | PHYHD1 1.331487 | 0.00231 | 0.046 | 4.298482 | Up | phytanoyl-CoA dioxygenase domain containing 1 |
| A_33_P322 | ARMC3 1.169263 | 0.00234 | 0.047 | 4.289263 | Up | armadillo repeat containing 3 |
| A_32_P313 | LAMA1 1.220699 | 0.00236 | 0.047 | 4.284963 | Up | laminin subunit alpha 1 |
| A_33_P326 | TMIE 0.93458 | 0.00236 | 0.047 | 4.284906 | Up | transmembrane inner ear |
| A_33_P325 | SPINK8 0.974261 | 0.00238 | 0.047 | 4.287059 | Up | serine peptidase inhibitor, Kazal type 8 (putative) |
| A_33_P328 | DNA12 1.079141 | 0.00238 | 0.047 | 4.277946 | Up | dynein axonemal intermediate chain 2 |
| A_33_P321 | RPS3AP1 1.011099 | 0.00242 | 0.047 | 4.265334 | Up | ribosomal protein S3a pseudogene 14 |
| A_23_P641 | KIAA154 1.381953 | 0.00253 | 0.048 | 4.236572 | Up | KIAA1549 like |
| Gene Symbol | Gene | Fold Change | p-value | q-value | Function Description |
|-------------|------|-------------|---------|---------|----------------------|
| SEZ6L       | 1.445032 | 0.00253     | 0.048   | 4.235657 | Up seizure related 6 homolog like |
| LINC002     | 1.002045 | 0.00259     | 0.049   | 4.219266 | Up long intergenic non-protein coding RNA 242 |
| KRTAP5-AS1  | -1.18091 | 7.62E-08    | 9.03E-05| -17.1132 | Down KRTAP5-1/KRTAP5-2 antisense RNA 1 |
| TRIM24      | -0.41581 | 1.15E-06    | 0.000   | -12.2547 | Down tripartite motif containing 24 |
| LINC002     | 1.002045 | 0.00259     | 0.049   | -11.7307 | Down NA |
| OR4A15      | -0.42416 | 2.37E-06    | 0.000   | -11.2005 | Down olfactory receptor family 4 subfamily A member 15 |
| KLHL13      | -0.37716 | 4.64E-06    | 0.000   | -10.5164 | Down kelch like family member 13 |
| KRT87P      | -0.94844 | 4.21E-06    | 0.000   | -10.4139 | Down keratin 87 pseudogene |
| ZRANB2-AS1  | -0.56876 | 4.36E-06    | 0.000   | -10.3675 | Down ZRANB2 antisense RNA 1 |
| #N/A        | -0.41168 | 4.64E-06    | 0.000   | -10.2869 | Down NA |
| SIN3-HDAC complex associated factor |
| SIRNCA F   | -0.52736 | 4.72E-06    | 0.000   | -10.2635 | Down SIN3-HDAC complex associated factor |
| MAGEB2      | -0.36511 | 5.16E-06    | 0.000   | -10.1497 | Down MAGE family member B2 |
| #N/A        | -0.74048 | 5.89E-06    | 0.000   | -9.97785 | Down NA |
| LINC003     | -0.31923 | 6.44E-06    | 0.000   | -9.87313 | Down long intergenic non-protein coding RNA 398 |
| #N/A        | -0.49672 | 6.45E-06    | 0.000   | -9.86335 | Down NA |
| C3orf80     | -1.01528 | 9.53E-06    | 0.000   | -9.38237 | Down chromosome 3 open reading frame 80 |
| #N/A        | -0.56281 | 1.14E-06    | 0.000   | -9.16497 | Down NA |
| PPBP         | -1.54696 | 1.17E-05    | 0.000   | -9.13962 | Down pro-platelet basic protein |
| TTK          | -1.24521 | 1.18E-05    | 0.000   | -9.12483 | Down TTK protein kinase |
| FAM71D      | -0.93751 | 1.24E-05    | 0.000   | -9.06826 | Down family with sequence similarity 71 member D |
| #N/A        | -0.74662 | 1.25E-05    | 0.000   | -9.06195 | Down NA |
| NOXRE D1    | -0.73831 | 1.46E-05    | 0.000   | -8.92458 | Down NADP dependent oxidoreductase domain containing 1 |
| TRIM77      | -0.40971 | 1.46E-05    | 0.000   | -8.88124 | Down tripartite motif containing 77 |
| TOP2A       | -1.2832  | 1.69E-05    | 0.000   | -8.71249 | Down topoisomerase (DNA) II alpha |
| Gene Symbol | LogFC | p Value | Adj. p Value | % DE | Description |
|-------------|-------|---------|--------------|------|-------------|
| KIF18A      | -1.15029 | 1.7E-05 | 0.003 | 236 | Down kinesin family member 18A |
| TPX2        | -0.6427 | 1.98E-05 | 0.003 | 585 | Down TPX2, microtubule nucleation factor |
| #N/A        | -0.90037 | 2.08E-05 | 0.003 | 738 | Down NA |
| #N/A        | -1.06535 | 2.11E-05 | 0.003 | 766 | Down NA |
| #N/A        | -0.54282 | 2.66E-05 | 0.004 | 416 | Down NA |
| POC1A       | -0.3445 | 2.71E-05 | 0.004 | 457 | Down POC1 centriolar protein A |
| #N/A        | -0.38569 | 2.75E-05 | 0.004 | 497 | Down NA |
| ARHGAP29    | -0.93195 | 2.78E-05 | 0.004 | 538 | Down Rho GTPase activating protein 29 |
| NRG1        | -0.34435 | 2.93E-05 | 0.004 | 679 | Down neuregulin 1 |
| PLC4        | -0.74316 | 3.14E-05 | 0.004 | 861 | Down phospholipase C delta 4 |
| CADPS2      | -0.29264 | 3.19E-05 | 0.004 | 888 | Down calcium dependent secretion activator 2 |
| ACER2       | -0.29305 | 3.24E-05 | 0.004 | 921 | Down alkaline ceramidase 2 |
| CCNF        | -0.96239 | 3.27E-05 | 0.004 | 954 | Down cyclin F |
| NIFK-AS1    | -0.43661 | 3.3E-05 | 0.004 | 986 | Down NIFK antisense RNA 1 |
| #N/A        | -0.54203 | 3.63E-05 | 0.005 | 271 | Down NA |
| #N/A        | -0.31475 | 3.87E-05 | 0.005 | 513 | Down NA |
| GTSE1       | -0.80101 | 4.28E-05 | 0.005 | 822 | Down G2 and S-phase expressed 1 |
| TRHDE       | -0.85404 | 4.36E-05 | 0.005 | 857 | Down thyrotropin releasing hormone degrading enzyme |
| ARHGEF3-AS1 | -0.50887 | 4.6E-05 | 0.006 | 857 | Down ARHGEF3 antisense RNA 1 |
| SOX4        | -0.48583 | 4.82E-05 | 0.006 | 272 | Down SRY-box 4 |
| #N/A        | -0.29663 | 5.04E-05 | 0.006 | 496 | Down NA |
| #N/A        | 0.00000 | 5.06E-05 | 0.006 | 496 | Down deleted in lymphocytic leukemia 1 (non-protein coding) |
| #N/A        | -0.6208 | 5.14E-05 | 0.006 | 53 | Down NA |
| #N/A        | -0.9916 | 5.6E-05 | 0.006 | 971 | Down NA |
| ID    | Gene Symbol | p-Value | Fold Change | Downregulation | Description |
|-------|-------------|---------|-------------|----------------|-------------|
| A_23_P118 | PLK1 | -0.46167 | 5.73E-05 | 0.007 | Down | polo like kinase 1 |
| A_33_P327 | HAUS6 | -0.4113 | 5.81E-05 | 0.007 | Down | HAUS augmin like complex subunit 6 |
| A_19_P003 | GPALPP | -0.33064 | 6.19E-05 | 0.007 | Down | GPALPP motifs containing 1 |
| A_23_P124 | BUB1 | -1.18787 | 6.27E-05 | 0.007 | Down | BUB1 mitotic checkpoint serine/threonine kinase |
| A_24_P145 | SERINC2 | -0.77141 | 6.37E-05 | 0.007 | Down | serine incorporator 2 |
| A_33_P323 | KIF14 | -1.33322 | 6.4E-05 | 0.007 | Down | kinesin family member 14 |
| A_33_P359 | HSP90A | -0.61836 | 6.54E-05 | 0.007 | Down | heat shock protein 90 alpha family class B member 6, pseudogene |
| A_24_P122 | VWA1 | -0.91594 | 6.68E-05 | 0.007 | Down | von Willebrand factor A domain containing 1 |
| A_33_P342 | FRMPD3 | -0.97088 | 6.84E-05 | 0.007 | Down | FERM and PDZ domain containing 3 |
| A_23_P185 | PTTG2 | -0.3236 | 7.36E-05 | 0.008 | Down | pituitary tumor-transforming 2 |
| A_19_P003 | RANP3 | -0.44835 | 7.63E-05 | 0.008 | Down | RAN, member RAS oncogene family pseudogene 3 |
| A_33_P337 | HOXA4 | -0.54254 | 8.02E-05 | 0.008 | Down | homeobox A4 |
| A_33_P331 | #N/A | -0.32148 | 8.12E-05 | 0.008 | Down | NA |
| A_24_P219 | SEL1L | -0.34542 | 8.34E-05 | 0.008 | Down | SEL1L ERAD E3 ligase adaptor subunit |
| A_33_P335 | NUSAP1 | -0.45817 | 8.45E-05 | 0.008 | Down | nucleolar and spindle associated protein 1 |
| A_33_P334 | CELA3A | -0.49673 | 8.54E-05 | 0.008 | Down | chymotrypsin like elastase family member 3A |
| A_19_P003 | #N/A | -0.4191 | 8.65E-05 | 0.008 | Down | NA |
| A_32_P160 | DOK6 | -0.68558 | 9.11E-05 | 0.008 | Down | docking protein 6 |
| A_33_P341 | AC02229 | -0.35285 | 9.32E-05 | 0.009 | Down | NA |
| A_19_P003 | #N/A | -0.48869 | 9.37E-05 | 0.009 | Down | NA |
| A_19_P003 | #N/A | -0.61999 | 0.00010 | 0.009 | Down | NA |
| A_33_P326 | TMEM26 | -0.63529 | 0.00010 | 0.009 | Down | transmembrane protein 262 |
| A_33_P328 | NRG1 | -0.32711 | 0.00010 | 0.009 | Down | neuregulin 1 |
| A_23_P819 | PSORS1 | -0.36148 | 0.00010 | 0.009 | Down | psoriasis susceptibility 1 candidate 2 |
| ID     | Gene Name       | Fold Change | p Value | Adjusted p Value | Downregulated  | Description                                                                 |
|--------|-----------------|-------------|---------|-----------------|-----------------|-----------------------------------------------------------------------------|
| A_19_P003 | DHX15          | -1.24559    | 8       | 6              | Down            | DEAH-box helicase 15                                                       |
| A_23_P352 | NEK2           | -1.05848    | 8       | 9              | Down            | NIMA related kinase 2                                                       |
| A_33_P326 | CICP24         | -0.35944    | 7       | 0              | Down            | capicua transcriptional repressor pseudogene 24                           |
| A_33_P340 | LRRC69         | -0.4054     | 5       | 0              | Down            | leucine rich repeat containing 69                                          |
| A_23_P366 | TAS2R7         | -0.56665    | 4       | 0              | Down            | taste 2 receptor member 7                                                   |
| A_24_P314 | SPC24          | -1.03137    | 4       | 0              | Down            | SPC24, NDC80 kinetochore complex component                                  |
| A_19_P008 | #/N/A           | -0.86237    | 8       | 8              | Down            | NA                                                                         |
| A_19_P008 | #/N/A           | -0.30162    | 8       | 8              | Down            | NA                                                                         |
| A_33_P321 | #/N/A           | -0.6112     | 1       | 1              | Down            | NA                                                                         |
| A_33_P335 | AC09282        | -0.31328    | 4       | 4              | Down            | NA                                                                         |
| A_19_P008 | #/N/A           | -0.48588    | 5       | 5              | Down            | NA                                                                         |
| A_23_P700 | HMMR           | -0.49422    | 8       | 8              | Down            | hyaluronan mediated motility receptor                                       |
| A_33_P377 | LINC009        | -0.84694    | 29      | 29             | Down            | long intergenic non-protein coding RNA 929                                |
| A_19_P003 | PTP4A1         | -0.3095     | 5       | 5              | Down            | protein tyrosine phosphatase type IVA, member 1                             |
| A_19_P003 | #/N/A           | -0.29491    | 5       | 5              | Down            | NA                                                                         |
| A_23_P193 | CARMIL         | -0.377      | 3       | 3              | Down            | capping protein regulator and myosin 1 linker                              |
| A_33_P332 | DAZAP2         | -0.33412    | 5       | 5              | Down            | DAZ associated protein 2                                                   |
| A_33_P333 | #/N/A           | -0.62324    | 6       | 6              | Down            | NA                                                                         |
| A_23_P104 | CDC5           | -0.36513    | 6       | 6              | Down            | cell division cycle associated 5                                           |
| A_19_P003 | #/N/A           | -0.32397    | 8       | 8              | Down            | NA                                                                         |
| A_19_P003 | #/N/A           | -0.87023    | 2       | 2              | Down            | NA                                                                         |
| A_19_P003 | #/N/A           | -0.48391    | 3       | 3              | Down            | NA                                                                         |
| A_19_P008 | #/N/A           | -0.51725    | 5       | 5              | Down            | NA                                                                         |
| A_19_P008 | #/N/A           | -0.46945    | 6       | 6              | Down            | NA                                                                         |
| Probe Set ID       | Entrez Gene ID | Gene Symbol | log2 Fold Change | p-value   | Adjusted p-value | Function and Description                                      |
|-------------------|----------------|-------------|------------------|-----------|------------------|---------------------------------------------------------------|
| A_33_P320         | 9703           | #N/A        | -0.38403         | 0.0015    | 0.012            | Down NA                                                      |
| A_19_P008         | 01014          | ANTXR2      | -0.33022         | 0.0016    | 0.012            | Down anthrax toxin receptor 2                                 |
| A_19_P003         | 27255          | #N/A        | -0.33261         | 0.0016    | 0.012            | Down NA                                                      |
| A_19_P003         | 21594          | FBXL5       | -0.89313         | 0.0017    | 0.012            | Down F-box and leucine rich repeat protein 5                 |
| A_33_P342         | 0704           | #N/A        | -0.3589          | 0.0017    | 0.012            | Down NA                                                      |
| A_33_P331         | 6903           | RBPMS-AS1   | -0.40474         | 0.0017    | 0.012            | Down RBPMS antisense RNA 1                                   |
| A_23_P300         | 100            | PLA2G2      | -0.52315         | 0.0017    | 0.012            | Down phospholipase A2 group IID                              |
| A_33_P329         | 5077           | AC09216     | -0.32979         | 0.0018    | 0.013            | Down NA                                                      |
| A_33_P337         | 5334           | DAB1        | -1.09252         | 0.0018    | 0.013            | Down DAB1, reelin adaptor protein                             |
| A_23_P113         | 97             | TTTY13      | -0.69508         | 0.0018    | 0.013            | Down testis-specific transcript, Y-linked 13 (non-protein coding) |
| A_23_P346         | 884            | RBPLJ       | -0.32051         | 0.0019    | 0.013            | Down recombination signal binding protein for immunoglobulin kappa J region like |
| A_19_P008         | 04053          | #N/A        | -0.35416         | 0.0019    | 0.013            | Down NA                                                      |
| A_19_P003         | 22074          | #N/A        | -0.36755         | 0.0002    | 0.013            | Down NA                                                      |
| A_19_P003         | 27072          | #N/A        | -0.34689         | 0.0020    | 0.013            | Down NA                                                      |
| A_33_P338         | 6344           | FANCA       | -0.32132         | 0.0020    | 0.013            | Down Fanconianemia complementation group A                   |
| A_33_P334         | 0468           | CENPI       | -0.73725         | 0.0020    | 0.014            | Down centromere protein 1                                    |
| A_19_P003         | 30152          | #N/A        | -0.44423         | 0.0020    | 0.014            | Down NA                                                      |
| A_19_P008         | 06633          | #N/A        | -0.48611         | 0.0020    | 0.014            | Down NA                                                      |
| A_19_P003         | 31152          | #N/A        | -0.61926         | 0.0021    | 0.014            | Down NA                                                      |
| A_19_P008         | 11393          | #N/A        | -0.30534         | 0.0021    | 0.014            | Down NA                                                      |
| A_33_P330         | 4268           | LOC6433     | -0.67616         | 0.0021    | 0.014            | Down uncharacterized LOC643327                              |
| A_33_P321         | 4690           | NLGN1       | -0.39399         | 0.0021    | 0.014            | Down neurophin 1                                             |
| A_33_P329         | 495            | POU3F2      | -1.77448         | 0.0021    | 0.014            | Down POU class 3 homeobox 2                                  |
| A_23_P425         | 332            | PPP4R4      | -0.37974         | 0.0021    | 0.014            | Down protein phosphatase 4 regulatory subunit 4              |
| Gene symbol | Gene name | Fold change | p-value | q-value | Status | Description |
|-------------|-----------|-------------|---------|---------|--------|-------------|
| GPR6        | G protein-coupled receptor 6 | -0.42562 | 0.00022 | 0.014  | Down   | G protein-coupled receptor 6 |
| PAX4        | paired box 4 | -0.32483 | 0.00022 | 0.014  | Down   | paired box 4 |
| AC09275     | NA        | -0.39132  | 0.00022 | 0.014  | Down   | NA |
| ASXL2       | additional sex combs like 2, transcriptional regulator | -0.31774 | 0.00022 | 0.014  | Down   | additional sex combs like 2, transcriptional regulator |
| IGFL3       | IGF like family member 3 | -1.0725  | 0.00023 | 0.015  | Down   | IGF like family member 3 |
| SAT1P1      | phosphoserine aminotransferase 1 pseudogene 1 | -0.62563 | 0.00023 | 0.015  | Down   | phosphoserine aminotransferase 1 pseudogene 1 |
| GRK2        | glutamate ionotropic receptor kainate type subunit 2 | -0.39339 | 0.00023 | 0.015  | Down   | glutamate ionotropic receptor kainate type subunit 2 |
| PTG3P       | pituitary tumor-transforming 3, pseudogene | -0.61312  | 0.00024 | 0.015  | Down   | pituitary tumor-transforming 3, pseudogene |
| NCAPG       | non-SMC condensin I complex subunit G | -0.80641  | 0.00024 | 0.015  | Down   | non-SMC condensin I complex subunit G |
| SLC19A1     | solute carrier family 19 member 1 | -0.38232  | 0.00024 | 0.015  | Down   | solute carrier family 19 member 1 |
| LINC021     | long intergenic non-protein coding RNA 2156 | -0.97878  | 0.00025 | 0.015  | Down   | long intergenic non-protein coding RNA 2156 |
| INHBE       | inhibin beta E subunit | -0.87769  | 0.00025 | 0.015  | Down   | inhibin beta E subunit |
| XIST_EX     | X-chromosome inactivation gene exon 1 | -0.52726  | 0.00025 | 0.015  | Down   | X-chromosome inactivation gene exon 1 |
| FIBCD1      | fibrinogen C domain containing 1 | -0.32728  | 0.00025 | 0.015  | Down   | fibrinogen C domain containing 1 |
| RGS5        | regulator of G protein signaling 5 | -0.31195  | 0.00026 | 0.015  | Down   | regulator of G protein signaling 5 |
| INHBE       | inhibin beta E subunit | -0.47038  | 0.00026 | 0.015  | Down   | inhibin beta E subunit |
| FLJ44715    | uncharacterized LOC386671 | -0.66365  | 0.00026 | 0.015  | Down   | uncharacterized LOC386671 |
| GUCA2B      | guanylatecyclase activator 2B | -0.45895  | 0.00026 | 0.016  | Down   | guanylatecyclase activator 2B |
| CCNB2       | cyclin B2 | -0.68899  | 0.00027 | 0.016  | Down   | cyclin B2 |
| KMT2B       | lysine methyltransferase 2B | -0.33926  | 0.00027 | 0.016  | Down   | lysine methyltransferase 2B |
| Gene Name | Description | Fold Change | p-value | q-value | Significance | RNA Category |
|-----------|-------------|-------------|---------|---------|--------------|--------------|
| ADAMT     | ADAMTS like 1 | -0.30204   | 0.00027 | 0.016   | Down         | NA           |
| SL1       |             | 4           | 143     |         |              |              |
| #N/A      |             | 0.00027     | 0.016   | -5.96357| Down         | ADAMTS like 1|
| 5         |             | 0.00028     | 0.016   | -5.95971| Down         | NA           |
| #N/A      |             | 0.00028     | 0.016   | -5.94611| Down         | NA           |
| 335       |             | 0.00028     | 0.016   | -5.94164| Down         | NA           |
| #N/A      |             | 0.00028     | 0.016   | -5.90168| Down         | NA           |
| N/A       |             | 0.00028     | 0.016   | -5.89393| Down         | NA           |
| LINC011   | long intergenic non-protein coding RNA 1122 | -0.33078 | 0.00029 | 0.016   | Down         | NA           |
| 851       |             |             |         |         |              |              |
| #N/A      |             | -0.67432    | 0.00029 | 0.016   | Down         | long intergenic non-protein coding RNA 691 |
| 9         |             | 851         |         |         |              |              |
| LINC006   | long intergenic non-protein coding RNA 91 | -0.52782 | 0.00030 | 0.017   | Down         | NA           |
| 851       |             |             |         |         |              |              |
| ANKRD2    | ankyrin repeat domain 20 family member A2 | -0.35467 | 0.00030 | 0.017   | Down         | NA           |
| 851       |             |             |         |         |              |              |
| 0A2       |             |             |         |         |              |              |
| LRFN1     | leucine rich repeat and fibronectin type III domain containing 1 | -0.35467 | 0.00030 | 0.017   | Down         | NA           |
| 851       |             |             |         |         |              |              |
| PKLR      | pyruvate kinase, liver and RBC | -0.29705 | 0.00031 | 0.017   | Down         | NA           |
| 267       |             |             |         |         |              |              |
| SLC25A1   | solute carrier family 25 member 15 | -0.30272 | 0.00031 | 0.017   | Down         | NA           |
| 267       |             |             |         |         |              |              |
| #N/A      |             | -0.38846    | 0.00031 | 0.017   | Down         | NA           |
| 267       |             |             |         |         |              |              |
| GABRQ     | gamma-aminobutyric acid type A receptor theta subunit | -0.68191 | 0.00031 | 0.017   | Down         | NA           |
| 276       |             |             |         |         |              |              |
| #N/A      |             | -0.32077    | 0.00032 | 0.017   | Down         | NA           |
| 276       |             |             |         |         |              |              |
| PRC1      | protein regulator of cytokinesis 1 | -0.3017  | 0.00032 | 0.017   | Down         | NA           |
| 42        |             |             |         |         |              |              |
| AMIGO2    | adhesion molecule with Ig like domain 2 | -0.44866 | 0.00032 | 0.017   | Down         | NA           |
| 507       |             |             |         |         |              |              |
| AC02527   | gamma-aminobutyric acid type A receptor theta subunit | -0.61913 | 0.00032 | 0.017   | Down         | NA           |
| 606       |             |             |         |         |              |              |
| Gene Name       | Log2 Fold Change | P-value     | q-value  | Expression   | Downstream Annotation                                                                 |
|-----------------|-----------------|-------------|----------|--------------|---------------------------------------------------------------------------------------|
| SUMO2P          | -0.31129        | 0.00033     | 0.017    | Down SUMO2 pseudogene 8                                                                 |
| CDC45P          | -0.42634        | 0.00033     | 0.017    | Down cell division cycle 45                                                           |
| CENPUP          | -0.53283        | 0.00034     | 0.017    | Down centromere protein U                                                              |
| PRDM11P         | -0.38799        | 0.00034     | 0.017    | Down PR/SET domain 11                                                                  |
| LOC100133920    | -0.29115        | 0.00034     | 0.017    | Down methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like pseudogene     |
| KIF11P          | -0.32887        | 0.00037     | 0.018    | Down kinesin family member 1                                                           |
| CYP27B1P        | -0.41362        | 0.00037     | 0.018    | Down cytochrome P450 family 27 subfamily B member 1                                    |
| LINC013555      | -0.32230        | 0.00038     | 0.019    | Down long intergenic non-protein coding RNA 1355                                      |
| RPL36P2         | -0.39151        | 0.00038     | 0.019    | Down ribosomal protein L36 pseudogene 20                                              |
| LOC100132197    | -0.31421        | 0.00038     | 0.019    | Down uncharacterized LOC648691                                                        |
| OR6T1P          | -0.39762        | 0.00040     | 0.019    | Down olfactory receptor family 6 subfamily T member 1                                 |
| POLQP           | -0.61577        | 0.00040     | 0.019    | Down DNA polymerase theta                                                              |
| Gene Symbol | Gene Name | Log2 Fold Change | P-Value | Adjusted P-Value | Adjusted Fold Change | Regulation Status |
|-------------|-----------|------------------|---------|------------------|---------------------|-------------------|
| COL5A1-AS1  | COL5A1 antisense RNA 1 | -0.30006 | 0.00041 | 0.019 | -5.62161 | Down |
| GRIK2       | glutamate ionotropic receptor kainate type subunit 2 | -0.50891 | 0.00041 | 0.019 | -5.61973 | Down |
| RASSF3      | Ras association domain family member 3 | -0.78014 | 0.00041 | 0.020 | -5.60582 | Down |
| GRIK2       | glutamate ionotropic receptor kainate type subunit 2 | -0.50891 | 0.00041 | 0.019 | -5.61973 | Down |
| COL5A1-AS1  | COL5A1 antisense RNA 1 | -0.30006 | 0.00041 | 0.019 | -5.62161 | Down |
| RASSF3      | Ras association domain family member 3 | -0.78014 | 0.00041 | 0.020 | -5.60582 | Down |
| PBK         | PDZ binding kinase | -1.44872 | 0.00041 | 0.020 | -5.58052 | Down |
| SLC12A5-AS1 | SLC12A5 and MMP9 antisense RNA 1 | -0.71833 | 0.00041 | 0.020 | -5.57988 | Down |
| CENPA       | centromere protein A | -1.04472 | 0.00041 | 0.020 | -5.57587 | Down |
| GSK1        | GS homeobox 1 | -0.37056 | 0.00044 | 0.020 | -5.56016 | Down |
| PBK         | PDZ binding kinase | -1.44872 | 0.00041 | 0.020 | -5.58052 | Down |
| SLC12A5-AS1 | SLC12A5 and MMP9 antisense RNA 1 | -0.71833 | 0.00041 | 0.020 | -5.57988 | Down |
| CENPA       | centromere protein A | -1.04472 | 0.00041 | 0.020 | -5.57587 | Down |
| PBK         | PDZ binding kinase | -1.44872 | 0.00041 | 0.020 | -5.58052 | Down |
| CENPA       | centromere protein A | -1.04472 | 0.00041 | 0.020 | -5.57587 | Down |
| PBK         | PDZ binding kinase | -1.44872 | 0.00041 | 0.020 | -5.58052 | Down |
| CENPA       | centromere protein A | -1.04472 | 0.00041 | 0.020 | -5.57587 | Down |
| PBK         | PDZ binding kinase | -1.44872 | 0.00041 | 0.020 | -5.58052 | Down |
| CENPA       | centromere protein A | -1.04472 | 0.00041 | 0.020 | -5.57587 | Down |
| PBK         | PDZ binding kinase | -1.44872 | 0.00041 | 0.020 | -5.58052 | Down |
| CENPA       | centromere protein A | -1.04472 | 0.00041 | 0.020 | -5.57587 | Down |
| PBK         | PDZ binding kinase | -1.44872 | 0.00041 | 0.020 | -5.58052 | Down |
| CENPA       | centromere protein A | -1.04472 | 0.00041 | 0.020 | -5.57587 | Down |
| PBK         | PDZ binding kinase | -1.44872 | 0.00041 | 0.020 | -5.58052 | Down |
| CENPA       | centromere protein A | -1.04472 | 0.00041 | 0.020 | -5.57587 | Down |
| Gene Symbol | #/A   | gene expression | p-value | fold change | status  | description                                                      |
|-------------|-------|-----------------|---------|-------------|---------|----------------------------------------------------------------|
| A_19_P003   | #/A   | -0.53921        | 0.00049 | 0.021       | Down    | NA                                                             |
| A_19_P003   | #/A   | -0.4143         | 0.00050 | 0.021       | Down    | NA                                                             |
| A_19_P003   | AL1387 | -0.49995        | 0.00050 | 0.021       | Down    | NA                                                             |
| A_19_P003   | #/A   | -1.04798        | 0.00050 | 0.021       | Down    | NA                                                             |
| A_19_P003   | #/A   | -0.67146        | 0.00051 | 0.021       | Down    | NA                                                             |
| A_19_P003   | #/A   | -0.31011        | 0.00052 | 0.021       | Down    | NA                                                             |
| A_19_P008   | #/A   | -0.31009        | 0.00052 | 0.021       | Down    | NA                                                             |
| A_19_P008   | RNU6-485P | -0.54041        | 0.00052 | 0.021       | Down    | RNA, U6 small nuclear 485, pseudogene                        |
| A_19_P008   | #/A   | -0.41158        | 0.00053 | 0.021       | Down    | NA                                                             |
| A_19_P003   | #/A   | -0.53067        | 0.00053 | 0.022       | Down    | NA                                                             |
| A_23_P256   | KIF20A | -0.95047        | 0.00053 | 0.022       | Down    | kinesin family member 20A                                     |
| A_19_P003   | #/A   | -0.32421        | 0.00054 | 0.022       | Down    | NA                                                             |
| A_33_P321   | LINC014 | -0.53677        | 0.00054 | 0.022       | Down    | long intergenic non-protein coding RNA 1415                  |
| A_23_P153   | CNKSR2 | -0.3422         | 0.00055 | 0.022       | Down    | connector enhancer of kinase suppressor of Ras 2              |
| A_24_P918   | LOC6535 | -0.5441         | 0.00055 | 0.022       | Down    | uncharacterized LOC653581                                     |
| A_33_P325   | GOLGA6 | -0.6024         | 0.00055 | 0.022       | Down    | golgin A6 family member A                                     |
| A_19_P003   | #/A   | -0.52403        | 0.00056 | 0.022       | Down    | NA                                                             |
| A_24_P228   | B4GALT | -0.29383        | 0.00057 | 0.022       | Down    | beta-1,4-galactosyltransferase 6                             |
| A_33_P329   | ARHGAP | -0.53734        | 0.00057 | 0.022       | Down    | Rho GTPase activating protein 42                             |
| A_32_P816   | LINC005 | -0.78125        | 0.00057 | 0.022       | Down    | long intergenic non-protein coding RNA 599                   |
| A_19_P003   | #/A   | -0.74238        | 0.00058 | 0.023       | Down    | NA                                                             |
| A_32_P489   | KRT28  | -0.76908        | 0.00059 | 0.023       | Down    | keratin 28                                                     |
| A_19_P003   | #/A   | -0.58573        | 0.00059 | 0.023       | Down    | NA                                                             |
| A_24_P498   | GDPD4  | -0.51369        | 0.0006  | 0.023       | Down    | glycerophosphodiesterphosphodiesterase domain containing 4   |
| Gene Symbol | Description | Fold Change | p-value | q-value | Status | Expression | Downstream Effect |
|-------------|-------------|-------------|---------|---------|--------|------------|------------------|
| CALML3-AS1  | CALML3 antisense RNA 1 | -0.33578 | 0.00060 | 0.023  |
| CDKN3       | cyclin dependent kinase inhibitor 3 | -0.66678 | 0.00061 | 0.023  |
| CALML3      | CALML3 antisense RNA 1 | -0.33578 | 0.00060 | 0.023  |
| CDKN3       | cyclin dependent kinase inhibitor 3 | -0.66678 | 0.00061 | 0.023  |
| MTFR2       | mitochondrial fission regulator 2 | -0.604  | 0.00062 | 0.023  |
| LOC1002     | uncharacterized LOC100268168 | -0.58393 | 0.00062 | 0.023  |
| DCAF4L      | DDB1 and CUL4 associated factor 4 like 2 | -0.56011 | 0.00062 | 0.023  |
| TEX22       | testis expressed 22 | -0.42187 | 0.00064 | 0.024  |
| TXN4        | uncharacterized LOC339874 | -0.3826  | 0.00067 | 0.024  |
| AC08749     | chromosome 20 open reading frame 203 | -1.00413 | 0.00068 | 0.025  |
| C2orf20     | chromosome 20 open reading frame 203 | -0.77482 | 0.00069 | 0.025  |
| LINC020     | long intergenic non-protein coding RNA 2099 | -0.33593 | 0.00070 | 0.025  |
| YTHDF1      | YTH N6-methyladenosine RNA binding protein 1 | -0.33159 | 0.00072 | 0.025  |
| Gene               | Description                                                                 |
|--------------------|------------------------------------------------------------------------------|
| RBMY1B             | RNA binding motif protein, Y-linked, family 1, member B                      |
| FOXM1              | forkhead box M1                                                              |
| GLYATL             | glycine-N-acetyltransferase like 3                                           |
| BIRC5              | baculoviral IAP repeat containing 5                                         |
| PVT1               | Pvt1 oncogene (non-protein coding)                                          |
| Glycine-N-acyltransferase like 3 |                                                               |
| L1CAM              | L1 cell adhesion molecule                                                   |
| SV2C               | synaptic vesicle glycoprotein 2C                                             |
| KIF15              | kinesin family member 15                                                    |
| Gene Symbol | Description | Log2 Fold Change | p-value | Adjusted p-value |
|-------------|-------------|-----------------|---------|-----------------|
| FANCD2      | Fanconi anemia complementation group D2 | -0.60919 | 0.00085 | 0.028 | -5.03582 | Down |
| LINC009     | long intergenic non-protein coding RNA 963 | -0.30593 | 0.00086 | 0.028 | -5.03397 | Down |
| RACGAP      | RacGTPase activating protein 1 | -0.42374 | 0.00086 | 0.028 | -5.02725 | Down |
| FAM20C      | FAM20C, golgi associated secretory pathway kinase | -0.51837 | 0.00086 | 0.028 | -5.02725 | Down |
| NUF2        | NUF2, NDC80 kinetochore complex component | -0.61002 | 0.00087 | 0.028 | -5.0222 | Down |
| AL39075     | long intergenic non-protein coding RNA 963 | -0.8147 | 0.00087 | 0.028 | -5.01818 | Down |
| QSOX1       | quiescin sulfhydryl oxidase 1 | -0.35457 | 0.00091 | 0.028 | -4.99053 | Down |
| TSIX        | TSIX transcript, XIST antisense RNA | -0.70329 | 0.00091 | 0.028 | -4.9834 | Down |
| SLITRK6     | SLIT and NTRK like family member 6 | -0.43506 | 0.00092 | 0.028 | -4.98064 | Down |
| H19_conserved_region_1 | H19 conserved region 1 | -0.3534 | 0.00092 | 0.028 | -4.97455 | Down |
| TSIX        | TSIX transcript, XIST antisense RNA | -0.70329 | 0.00091 | 0.028 | -4.9834 | Down |
| SLITRK6     | SLIT and NTRK like family member 6 | -0.43506 | 0.00092 | 0.028 | -4.98064 | Down |
| H19_conserved_region_1 | H19 conserved region 1 | -0.3534 | 0.00092 | 0.028 | -4.97455 | Down |
| family_with_sequence_similarity_91_member_1 | family with sequence similarity 91 member 1 | -0.29173 | 0.00092 | 0.028 | -4.97835 | Down |
| AC13125     | AC13125 | -0.52376 | 0.00094 | 0.028 | -4.95867 | Down |
| LINC015     | long intergenic non-protein coding RNA 1539 | -0.87469 | 0.00095 | 0.028 | -4.95741 | Down |
| AC13125     | AC13125 | -0.52376 | 0.00094 | 0.028 | -4.95867 | Down |
| LINC015     | long intergenic non-protein coding RNA 1539 | -0.87469 | 0.00095 | 0.028 | -4.95741 | Down |
| SCEL        | sciellin | -0.88136 | 0.00096 | 0.028 | -4.94922 | Down |
| CXCR3       | C-X-C motif chemokine receptor 3 | -0.34048 | 0.00096 | 0.028 | -4.9487 | Down |
| RFT1        | RFT1 homolog | -0.30228 | 0.00096 | 0.028 | -4.94632 | Down |
| AL35511     | pregnancy specific beta-1-glycoprotein 5 | -0.72741 | 0.00097 | 0.030 | -4.93841 | Down |
| ID      | Symbol   | Description                   | log2FoldChange | pValue   | Adjusted pValue | Annotation                  |
|---------|----------|-------------------------------|----------------|----------|-----------------|-----------------------------|
| A_19_P003 | AC09118  | Down NA                       | -0.29208       | 0.00098  | 0.030           |                             |
| 20343   |          |                               |                |          |                 |                             |
| A_23_P887 | RAD51    | Down RAD51 recombinase         | -0.39275       | 0.00099  | 0.030           |                             |
| 31      |          |                               |                |          |                 |                             |
| A_33_P330 | ADAMT    | Down ADAMTS like 1            | -0.46865       | 0.00099  | 0.030           |                             |
| 2025    | SL1      |                               |                |          |                 |                             |
| A_23_P116 | HMGB4    | Down high mobility group 4    | -0.58702       | 0.00100  | 0.030           |                             |
| 97      |          |                               |                |          |                 |                             |
| A_33_P323 | AC23372  | Down NA                       | -0.31016       | 0.00102  | 0.031           |                             |
| 6218    |          |                               |                |          |                 |                             |
| A_23_P150 | TROAP    | Down trophinin associated protein | -0.33946     | 0.00102  | 0.031           |                             |
| 935     |          |                               |                |          |                 |                             |
| A_19_P008 | #N/A     | Down NA                       | -0.4439        | 0.00102  | 0.031           |                             |
| 00553   |          |                               |                |          |                 |                             |
| A_33_P323 | SBK3     | Down SH3 domain binding kinase family member 3 | -0.30291     | 0.00102  | 0.031           |                             |
| 7744    |          |                               |                |          |                 |                             |
| A_33_P339 | RASSF10  | Down Ras association domain family member 10 | -0.42863     | 0.00102  | 0.031           |                             |
| 9634    |          |                               |                |          |                 |                             |
| A_33_P329 | SYPL1P2 | Down synaptophysin like 1 pseudogene 2 | -0.34807     | 0.00102  | 0.031           |                             |
| 3138    |          |                               |                |          |                 |                             |
| A_33_P336 | PROX2    | Down prosperhomeobox 2         | -0.52367       | 0.00104  | 0.031           |                             |
| 2178    |          |                               |                |          |                 |                             |
| A_33_P321 | SLC5A10  | Down solute carrier family 5 member 10 | -0.36279     | 0.00104  | 0.031           |                             |
| 0418    |          |                               |                |          |                 |                             |
| A_19_P003 | LINC002  | Down long intergenic non-protein coding RNA 211 | -0.39501     | 0.00104  | 0.031           |                             |
| 17612   |          |                               |                |          |                 |                             |
| A_19_P008 | #N/A     | Down NA                       | -0.66576       | 0.00105  | 0.031           |                             |
| 01257   |          |                               |                |          |                 |                             |
| A_23_P571 | SLC52A3  | Down solute carrier family 52 member 3 | -0.69684     | 0.00105  | 0.031           |                             |
| 10      |          |                               |                |          |                 |                             |
| A_19_P003 | #N/A     | Down NA                       | -0.31138       | 0.00108  | 0.032           |                             |
| 29700   |          |                               |                |          |                 |                             |
| A_19_P008 | #N/A     | Down NA                       | -0.45195       | 0.00110  | 0.032           |                             |
| 02359   |          |                               |                |          |                 |                             |
| A_33_P341 | ZC3H12   | Down zinc finger CCCH-type containing 12D | -0.50596     | 0.00110  | 0.032           |                             |
| 9399    | D        |                               |                |          |                 |                             |
| A_33_P342 | LOC1001  | Down uncharacterized LOC100129275 | -0.30291     | 0.00110  | 0.032           |                             |
| 3590    | 29275    |                               |                |          |                 |                             |
| A_19_P008 | #N/A     | Down NA                       | -0.6284        | 0.00111  | 0.032           |                             |
| 13611   |          |                               |                |          |                 |                             |
| A_33_P380 | HJURP    | Down Holliday junction recognition protein | -0.92005     | 0.00112  | 0.032           |                             |
| 7062    |          |                               |                |          |                 |                             |
| A_19_P008 | #N/A     | Down NA                       | -0.30787       | 0.00112  | 0.032           |                             |
| 03592   |          |                               |                |          |                 |                             |
| ERCC−001| #N/A     | Down NA                       | -0.36448       | 0.00112  | 0.032           |                             |
| 20_69   |          |                               |                |          |                 |                             |
| A_19_P003 | #N/A     | Down NA                       | -0.41537       | 0.00113  | 0.032           |                             |
| 26471   |          |                               |                |          |                 |                             |

**Note:** The table represents gene expression data with the following columns: gene ID, symbol, description, log2FoldChange, pValue, adjusted pValue, and annotation. The data indicates down-regulated genes with negative log2FoldChange values.
| Gene Symbol | Description | Log2 Fold Change | p-value | Adj. p-value | Status | Associated Gene(s) |
|-------------|-------------|-----------------|---------|-------------|--------|-------------------|
| LINC018     | Long intergenic non-protein coding RNA 1814 | -0.31826 | 0.033   | 0.00115     | Down   | chromosome 1 open reading frame 189 |
| VN1R33      | Vomeronasal 1 receptor 33 pseudogene | -0.69788 | 0.033   | 0.00115     | Down   | proline-serine-threonine phosphatase interacting protein 2 |
| LINC018     | Long intergenic non-protein coding RNA 1814 | -0.31826 | 0.033   | 0.00115     | Down   | long intergenic non-protein coding RNA 1814 |
| PSTIP2      | Proline-serine-threonine phosphatase interacting protein 2 | -0.38392 | 0.033   | 0.00117     | Down   | proline-serine-threonine phosphatase interacting protein 2 |
| XKR6        | XK related 6 | -0.45688 | 0.033   | 0.00118     | Down   | XK related 6 |
| GALNTL      | Polypeptide N-acetylgalactosaminyltransferase-like 6 | -0.3736  | 0.033   | 0.00118     | Down   | polypeptide N-acetylgalactosaminyltransferase-like 6 |
| EXD1        | Exonuclease 3'-5' domain containing 1 | -0.69087 | 0.033   | 0.00119     | Down   | exonuclease 3'-5' domain containing 1 |
| SPATA4      | Spermatogenesis associated 42 (non-protein coding) | -1.07945 | 0.033   | 0.00120     | Down   | spermatogenesis associated 42 (non-protein coding) |
| SLC2A13     | Solute carrier family 2 member 13 | -0.83023 | 0.033   | 0.00121     | Down   | solute carrier family 2 member 13 |
| EXD1        | Exonuclease 3'-5' domain containing 1 | -0.69087 | 0.033   | 0.00119     | Down   | exonuclease 3'-5' domain containing 1 |
| GRIP1       | Glutamate receptor interacting protein 1 | -0.30525 | 0.034   | 0.00123     | Down   | glutamate receptor interacting protein 1 |
| POU3F3      | POU class 3 homeobox 3 | -1.22314 | 0.034   | 0.00124     | Down   | POU class 3 homeobox 3 |
| C3orf80     | Chromosome 3 open reading frame 80 | -0.92969 | 0.034   | 0.00124     | Down   | chromosome 3 open reading frame 80 |
| CPN1        | Carboxypeptidase N subunit 1 | -0.39421 | 0.034   | 0.00125     | Down   | carboxypeptidase N subunit 1 |
| SPC25       | SPC25, NDC80 kinetochore complex component | -0.89359 | 0.034   | 0.00126     | Down   | SPC25, NDC80 kinetochore complex component |
| C12orf6     | Chromosome 12 open reading frame 66 | -0.75124 | 0.034   | 0.00127     | Down   | chromosome 12 open reading frame 66 |
| MELK        | Maternal embryonic leucine zipper kinase | -1.00289 | 0.034   | 0.00128     | Down   | maternal embryonic leucine zipper kinase |

*Note: The table above lists genes with significant fold changes and associated p-values, indicating potential differences in expression levels.*
| ProbeID       | Gene Symbol | Fold Change | FDR  | z-value | Function                                                                 |
|---------------|-------------|-------------|------|---------|---------------------------------------------------------------------------|
| A_23_P944     | TLE4        | -0.40005    | 0.00129 | 0.034   | -4.7262 Down transducin like enhancer of split 4                          |
| A_23_P133     | MND1        | -0.49815    | 0.00129 | 0.034   | -4.72607 Down meiotic nuclear divisions 1                                  |
| A_23_P113     | ZMAT3       | -0.30962    | 0.00130 | 0.035   | -4.71552 Down zinc finger matrin-type 3                                    |
| A_19_P003     | #/N/A       | -0.66499    | 0.00131 | 0.035   | -4.71182 Down NA                                                           |
| A_24_P202     | ATP2A3      | -0.53341    | 0.00131 | 0.035   | -4.71075 Down ATPase sarcoplastic/endoplasmic reticulum Ca2+ transporting 3 |
| A_19_P008     | #/N/A       | -0.58374    | 0.00131 | 0.035   | -4.70957 Down NA                                                           |
| A_23_P113     | GRIP1       | -0.48946    | 0.00133 | 0.035   | -4.70303 Down glutamate receptor interacting protein 1                     |
| A_33_P338     | CENPM       | -0.34165    | 0.00133 | 0.035   | -4.70031 Down centromere protein M                                          |
| A_19_P008     | #/N/A       | -0.46632    | 0.00133 | 0.035   | -4.69913 Down NA                                                           |
| A_33_P330     | GRIK2       | -0.39228    | 0.00134 | 0.035   | -4.6979 Down glutamate ionotropic receptor kainate type subunit 2          |
| A_33_P326     | AC00245     | -0.41286    | 0.00134 | 0.035   | -4.697 Down NA                                                             |
| A_33_P323     | AL04977     | -0.76663    | 0.00134 | 0.035   | -4.69629 Down NA                                                           |
| A_33_P322     | ZSCAN2      | -0.34477    | 0.00134 | 0.035   | -4.69368 Down zinc finger and SCAN domain containing 2                     |
| A_23_P305     | GPR26       | -0.92643    | 0.00135 | 0.035   | -4.68974 Down G protein-coupled receptor 26                                |
| A_33_P336     | NXPH4       | -0.59888    | 0.00135 | 0.035   | -4.68905 Down neurexophilin 4                                              |
| A_33_P337     | UNCSD       | -0.48731    | 0.00136 | 0.035   | -4.68463 Down unc-5 netrin receptor D                                      |
| A_19_P003     | #/N/A       | -0.50683    | 0.00136 | 0.035   | -4.68448 Down NA                                                           |
| A_33_P330     | FOXB2       | -0.65239    | 0.00136 | 0.035   | -4.68318 Down forkhead box B2                                             |
| A_33_P327     | BX64963     | -0.29717    | 0.00137 | 0.035   | -4.67918 Down NA                                                           |
| A_33_P335     | RNF215      | -0.40503    | 0.00137 | 0.035   | -4.67845 Down ring finger protein 215                                      |
| A_19_P003     | STMN1       | -0.29389    | 0.00137 | 0.035   | -4.67818 Down stathmin 1                                                  |
| A_23_P202     | ACRV1       | -0.7613     | 0.00138 | 0.035   | -4.67571 Down acrosomal vesicle protein 1                                  |
| A_33_P321     | #/N/A       | -0.3866     | 0.00138 | 0.035   | -4.67563 Down NA                                                           |
| Gene         | Symbol | Log2 Fold Change | p-value | FDR | Expression | Regulation |
|--------------|--------|-----------------|---------|-----|------------|------------|
| AC00722      | 1.1    | -0.88118        | 0.00139 | 0.036 | 0.000000004 | Down | NA        |
| CCNB2P       |        | -0.39557        | 0.00144 | 0.036 | 0.000000004 | Down | cyclin B2 pseudogene 1 |
| RCC1         |        | -0.30159        | 0.00153 | 0.038 | 0.000000004 | Down | regulator of chromosome condensation 1 |
| NPVF         |        | -0.82435        | 0.00154 | 0.038 | 0.000000004 | Down | neuropeptide VF precursor |
| ADAMT        | S7     | -0.32513        | 0.00154 | 0.038 | 0.000000004 | Down | ADAM metallopeptidase with thrombospondin type 1 motif 7 |
| PRR11        |        | -0.3487         | 0.00154 | 0.038 | 0.000000004 | Down | proline rich 11 |
| LCE1B        |        | -0.72876        | 0.00157 | 0.038 | 0.000000004 | Down | late cornified envelope 1B |
| CRNDE        |        | -0.54523        | 0.00157 | 0.038 | 0.000000004 | Down | colorectal neoplasia differentially expressed |
| TRAV8-2      |        | -0.29523        | 0.00157 | 0.038 | 0.000000004 | Down | T-cell receptor alpha variable 8–2 |
| NHLRC4       |        | -0.31401        | 0.00158 | 0.038 | 0.000000004 | Down | NHL repeat containing 4 |
| Gene          | Description                          | FDR   | Fold Change | Log2FoldChange | Annotation                                |
|--------------|--------------------------------------|-------|-------------|----------------|-------------------------------------------|
| CCNA1        | Down cyclin A1                       | 0.00160 | 0.038       | -4.56561       |                                           |
| TLE4         | Down transducin like enhancer of split 4 | 0.00162 | 0.039       | -4.55641       |                                           |
| LINC003      | Down long intergenic non-protein coding RNA 309 | 0.00163 | 0.039       | -4.54961       |                                           |
| AC06395      | Down NA                              | 0.00166 | 0.039       | -4.54185       |                                           |
| PARPB        | Down PARP1 binding protein           | 0.00166 | 0.039       | -4.53606       |                                           |
| HIGD1B       | Down HIG1 hypoxia inducible domain family member 1B | 0.00167 | 0.039       | -4.53395       |                                           |
| TLE4         | Down transducin like enhancer of split 4 | 0.00169 | 0.039       | -4.51922       |                                           |
| DEFA3        | Down defensin alpha 3                | 0.00169 | 0.039       | -4.51368       |                                           |
| DISC1        | Down disrupted in schizophrenia 1    | 0.00170 | 0.039       | -4.5060        |                                           |
| SLC35G5      | Down solute carrier family 35 member G5 | 0.00171 | 0.040       | -4.51438       |                                           |
| COLEC10      | Down collectin subfamily member 10   | 0.00171 | 0.040       | -4.48197       |                                           |
| LOC7296      | Down uncharacterized LOC729652       | 0.00172 | 0.040       | -4.48326       |                                           |
| PNPLA7       | Down patatin like phospholipase domain containing 7 | 0.00173 | 0.040       | -4.48005       |                                           |
| LINC005      | Down long intergenic non-protein coding RNA 588 | 0.00174 | 0.041       | -4.47935       |                                           |
| RAD51D       | Down RAD51 paralog D                 | 0.00182 | 0.041       | -4.47282       |                                           |
| Gene Symbol | Name | Log2 Fold Change | Fold Change | p-value | Differentially Expressed |
|-------------|------|-----------------|-------------|----------|-------------------------|
| TLE4       | Transducin like enhancer of split 4 | -0.46781 | 0.00184 | 0.041 | Down |
| MYO1D      | Myosin ID | -0.33354 | 0.00185 | 0.041 | Down |
| CXCR2      | C-X-C motif chemokine receptor 2 | -0.69558 | 0.00185 | 0.041 | Down |
| POU3F4     | POU class 3 homeobox 4 | -0.39357 | 0.00185 | 0.041 | Down |
| SATL1      | Spermidine/spermine N1-acetyl transferase-like 1 | -1.01787 | 0.00185 | 0.041 | Down |
| RNF29      | Homeobox A6 | -0.30358 | 0.00193 | 0.042 | Down |
| CCNB2P     | Cyclin B2 pseudogene 1 | -0.32921 | 0.00191 | 0.042 | Down |
| ZSCAN1     | Zinc finger and SCAN domain containing 1 | -0.32731 | 0.00192 | 0.042 | Down |
| OMP        | Olfactory marker protein | -0.39895 | 0.00192 | 0.042 | Down |
| SPINK5     | Serine peptidase inhibitor, Kazal type 5 | -0.73247 | 0.00193 | 0.042 | Down |
| HOMA6      | Homeobox A6 | -0.30358 | 0.00193 | 0.042 | Down |
| CCNB2P     | Cyclin B2 pseudogene 1 | -0.32921 | 0.00191 | 0.042 | Down |
| ZSCAN1     | Zinc finger and SCAN domain containing 1 | -0.32731 | 0.00192 | 0.042 | Down |
| OMP        | Olfactory marker protein | -0.39895 | 0.00192 | 0.042 | Down |
| SPINK5     | Serine peptidase inhibitor, Kazal type 5 | -0.73247 | 0.00193 | 0.042 | Down |
| HOMA6      | Homeobox A6 | -0.30358 | 0.00193 | 0.042 | Down |
| Gene ID       | Gene Name     | Log2 Fold Change | Log10 P-Value | Adjusted P-Value | Expression Direction | Description                                               |
|--------------|---------------|------------------|---------------|------------------|----------------------|----------------------------------------------------------|
| A_19_P003    | PVT1          | -0.46956         | 0.00199       | 0.043            | Down                 | Pvt1 oncogene (non-protein coding)                       |
|              | LINC011       | -0.35717         | 0.00200       | 0.043            | Down                 | long intergenic non-protein coding RNA 1133             |
| A_33_P325    | FAM95B        | -0.73977         | 0.00201       | 0.043            | Down                 | family with sequence similarity 95 member B1            |
| 6287         |               |                  |               |                  |                      |                                                         |
| A_33_P334    | FAM231        | -0.29791         | 0.00202       | 0.043            | Down                 | family with sequence similarity 231 member A            |
| 8794         | A             |                  |               |                  |                      |                                                         |
| A_33_P323    | #/N/A         | -0.46784         | 0.00205       | 0.043            | Down                 | NA                                                       |
| 3886         |               |                  |               |                  |                      |                                                         |
| A_19_P008    | #/N/A         | -0.3931          | 0.00206       | 0.044            | Down                 | NA                                                       |
| 40574        |               |                  |               |                  |                      |                                                         |
| A_19_P003    | #/N/A         | -0.31167         | 0.00207       | 0.044            | Down                 | NA                                                       |
| 24503        |               |                  |               |                  |                      |                                                         |
| A_33_P331    | KIAA195       | -0.42171         | 0.00210       | 0.044            | Down                 | KIAA1958                                                |
| 4341         | 8             |                  |               |                  |                      |                                                         |
| A_33_P338    | #/N/A         | -0.32689         | 0.00211       | 0.044            | Down                 | NA                                                       |
| 1613         |               |                  |               |                  |                      |                                                         |
| A_33_P339    | TMEM40        | -0.29537         | 0.00211       | 0.044            | Down                 | transmembrane protein 40                                |
| 1418         | 7             |                  |               |                  |                      |                                                         |
| A_23_P148    | CTAG1A        | -1.15888         | 0.00212       | 0.044            | Down                 | cancer/testis antigen 1A                                |
| 541          |               |                  |               |                  |                      |                                                         |
| A_19_P003    | AC01874       | -0.70496         | 0.00213       | 0.044            | Down                 | NA                                                       |
| 21443        | 2.1           |                  |               |                  |                      |                                                         |
| A_19_P008    | #/N/A         | -0.7287          | 0.00213       | 0.044            | Down                 | NA                                                       |
| 12873        |               |                  |               |                  |                      |                                                         |
| A_33_P371    | CHRNA7        | -0.31719         | 0.00213       | 0.044            | Down                 | cholinergic receptor nicotinic alpha 7 subunit          |
| 9083         | 9             |                  |               |                  |                      |                                                         |
| A_24_P740    | PARD6G        | -0.31074         | 0.00214       | 0.044            | Down                 | Par-6 family cell polarity regulator gamma              |
| 70           |               |                  |               |                  |                      |                                                         |
| A_19_P003    | AC10446       | -0.89737         | 0.00215       | 0.045            | Down                 | NA                                                       |
| 17759        | 1.1           |                  |               |                  |                      |                                                         |
| A_33_P334    | PRSS56        | -0.35326         | 0.00215       | 0.045            | Down                 | protease, serine 56                                     |
| 5309         | 8             |                  |               |                  |                      |                                                         |
| A_19_P008    | TSSC2         | -0.58666         | 0.00216       | 0.045            | Down                 | tumor suppressing subtransferable candidate 2 pseudogene|
| 04601        | 3             |                  |               |                  |                      |                                                         |
| A_19_P003    | #/N/A         | -0.59541         | 0.00216       | 0.045            | Down                 | NA                                                       |
| 29437        |               |                  |               |                  |                      |                                                         |
| A_23_P429    | DDIAS         | -0.4245          | 0.00219       | 0.045            | Down                 | DNA damage induced apoptosis suppressor                 |
| 491          | 1             |                  |               |                  |                      |                                                         |
| A_32_P196    | ZSCAN2        | -0.29268         | 0.00219       | 0.045            | Down                 | zinc finger and SCAN domain containing 25              |
| 115          | 6             |                  |               |                  |                      |                                                         |
| A_23_P208    | ZNF160        | -0.37222         | 0.00221       | 0.045            | Down                 | zinc finger protein 160                                 |
| 240          | 5             |                  |               |                  |                      |                                                         |
| A_19_P003    | AL12165       | -0.3691          | 0.00222       | 0.045            | Down                 | NA                                                       |
| 26743        | 5.1           |                  |               |                  |                      |                                                         |
| A_33_P340    | AC13356       | -0.65338         | 0.00222       | 0.045            | Down                 | NA                                                       |
| 7631         | 5.1           |                  |               |                  |                      |                                                         |
| Gene ID     | Gene Name | Log2 Fold Change | P-Value | q-Value | Expression Value | Function Description |
|-------------|-----------|------------------|---------|---------|------------------|----------------------|
| A_33_P329   | CCL3L3    | -0.572           | 0.00222 | 0.045   | 834              | Down C-C motif chemokine ligand 3 like 3 |
| A_19_P008   | #N/A      | -0.41452         | 0.00222 | 0.045   | 845              | Down NA              |
| A_19_P003   | #N/A      | -0.29106         | 0.00222 | 0.045   | 897              | Down NA              |
| A_32_P620   | CCDC18    | -0.31268         | 0.00222 | 0.045   | 061              | Down coiled-coil domain containing 182 |
| A_33_P326   | TCEANC    | -0.33479         | 0.00222 | 0.045   | 08               | Down transcription elongation factor A N-terminal and central domain containing 2 |
| A_23_P717   | CKS2      | -0.30604         | 0.00222 | 0.045   | 08               | Down CDC28 protein kinase regulatory subunit 2 |
| A_32_P120   | LOC7279   | -0.38371         | 0.00222 | 0.045   | 11               | Down uncharacterized LOC727916 |
| A_23_P515   | HSD3B2    | -0.56617         | 0.00222 | 0.045   | 11               | Down hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 |
| A_33_P341   | RAD21L    | -0.49999         | 0.00222 | 0.045   | 219              | Down RAD21 cohesin complex component like 1 |
| A_23_P118   | HS3ST2    | -0.78188         | 0.00222 | 0.045   | 327              | Down heparansulfate-glucosamine 3-sulfotransferase 2 |
| A_24_P838   | GRM5      | -0.6979          | 0.00222 | 0.045   | 451              | Down glutamate metabotropic receptor 5 |
| A_33_P334   | OR5M1     | -1.13651         | 0.00229 | 0.045   | 535              | Down olfactory receptor family 5 subfamily M member 1 |
| A_23_P252   | SPEF2     | -0.34362         | 0.00232 | 0.045   | 876              | Down sperm flagellar 2 |
| A_33_P325   | KRTAP1-5  | -0.53907         | 0.00233 | 0.045   | 96               | Down keratin associated protein 1-5 |
| A_33_P334   | KIR3DX    | -0.35799         | 0.00235 | 0.047   | 403              | Down killer cell immunoglobulin like receptor, three Ig domains X1 |
| A_33_P330   | SSU72P2   | -0.8223          | 0.00235 | 0.047   | 403              | Down SSU72 pseudogene 2 |
| A_33_P328   | #N/A      | -0.30238         | 0.00235 | 0.047   | 883              | Down NA              |
| A_24_P944   | EYS       | -0.99854         | 0.00236 | 0.047   | 861              | Down eyes shut homolog (Drosophila) |
| A_33_P327   | #N/A      | -0.3572          | 0.00238 | 0.047   | 187              | Down NA              |
| A_33_P331   | OR4Q3     | -0.71413         | 0.00240 | 0.047   | 533              | Down olfactory receptor family 4 subfamily Q member 3 |
| A_19_P003   | AC09118   | -0.34391         | 0.00241 | 0.047   | 55               | Down NA              |
| A_33_P331   | LINC007   | -0.70239         | 0.00243 | 0.047   | 883              | Down long intergenic non-protein coding RNA 703 |
| A_33_P336   | LINC011   | -0.7252          | 0.00243 | 0.047   | 883              | Down long intergenic non-protein coding RNA 1182 |
| Gene Reference | Gene Name | Fold Change | p-value | q-value | Status | Description |
|---------------|-----------|-------------|---------|---------|--------|-------------|
| A_33_P321     | OR13J1    | -0.85672    | 0.00244 | 0.047   | Down   | olfactory receptor family 13 subfamily J member 1 |
| A_23_P401     | LINC003   | -0.35474    | 0.00244 | 0.047   | Down   | long intergenic non-protein coding RNA 304 |
| A_24_P297     | MAMST     | -0.40407    | 0.00245 | 0.047   | Down   | MEF2 activating motif and SAP domain containing transcriptional regulator |
| A_23_P110     | CENPH     | -0.52312    | 0.00245 | 0.047   | Down   | centromere protein H |
| A_23_P580     | C3orf52   | -0.46294    | 0.00246 | 0.047   | Down   | chromosome 3 open reading frame 52 |
| A_24_P472     | UNC13A    | -0.32027    | 0.00247 | 0.047   | Down   | unc-13 homolog A |
| A_24_P221     | PSAT1P3   | -0.97228    | 0.00248 | 0.047   | Down   | phosphoserine aminotransferase 1 pseudogene |
| A_33_P329     | RUFY4     | -0.33366    | 0.00248 | 0.047   | Down   | RUN and FYVE domain containing 4 |
| A_33_P336     | FLJ13224  | -0.47084    | 0.00249 | 0.047   | Down   | uncharacterized LOC79857 |
| A_33_P325     | MALT1     | -0.71248    | 0.00251 | 0.047   | Down   | MYT1L antisense RNA 1 |
| A_33_P323     | GPR17     | -0.61794    | 0.00252 | 0.047   | Down   | G protein-coupled receptor 17 |
| A_33_P337     | #N/A      | -0.48123    | 0.00252 | 0.047   | Down   | oxidation resistance 1 |
| A_33_P332     | LINC005   | -0.29513    | 0.00252 | 0.047   | Down   | long intergenic non-protein coding RNA 596 |
| A_33_P341     | CR38165   | -1.16255    | 0.00255 | 0.048   | Down   | RAD21 cohesin complex component like 1 |
| A_23_P477     | RAD21L    | -0.45966    | 0.00255 | 0.048   | Down   | RAD21 cohesin complex component like 1 |
| A_19_P003     | AC00611   | -0.29745    | 0.00252 | 0.047   | Down   | oxidation resistance 1 |
| A_19_P008     | CR38165   | -1.16255    | 0.00255 | 0.048   | Down   | oxidation resistance 1 |
| A_33_P341     | OR11H7    | -0.35919    | 0.00259 | 0.049   | Down   | olfactory receptor family 11 subfamily H member 7 (gene/pseudogene) |
| A_33_P324     | CASK      | -0.39817    | 0.00261 | 0.049   | Down   | calcium/calmodulin dependent serine protein kinase |
| A_33_P341     | AC12359   | -0.86069    | 0.00261 | 0.049   | Down   | oxidation resistance 1 |

AIMS Neuroscience  
Volume 8, Issue 2, 254–283.
Table 2. The enriched pathway terms of the up-regulated differentially expressed genes.

| Pathway ID | Pathway Name | P-value | FDR B&H | FDR B&Y | Bonferroni | Gene Count | Gene |
|------------|--------------|---------|---------|---------|------------|-------------|----------------|
| 54529 | retinoate biosynthesis II | 1.62E-03 | 4.52E-02 | 1.78E-01 | 4.52E-02 | 02 | XDH,RBP4 |
| 6 | retinoate biosynthesis I | 7.21E-03 | 1.01E-01 | 3.97E-01 | 2.02E-01 | 02 | ALDH1A3,RBP4 |
| 5 | nicotine degradation IV | 1.13E-02 | 1.06E-01 | 4.16E-01 | 3.18E-01 | 02 | FMO5,AOX1 |
| 7 | the visual cycle I (vertebrates) | 2.51E-02 | 1.54E-01 | 6.05E-01 | 7.02E-01 | 02 | LRAT,RBP4 |
| 4 | retinol biosynthesis | 3.18E-02 | 1.54E-01 | 6.05E-01 | 8.89E-01 | 02 | LRAT,RBP4 |
| 3 | catecholamine biosynthesis | 3.30E-02 | 1.54E-01 | 6.05E-01 | 9.24E-01 | 01 | PNMT |
| 8 | L-carnitine biosynthesis | 4.91E-02 | 1.72E-01 | 6.74E-01 | 1.00E+00 | 01 | BBOX1 |
| 8 | guanosine nucleotides degradation | 4.91E-02 | 1.72E-01 | 6.74E-01 | 1.00E+00 | 01 | XDH |

| Pathway ID | Pathway Name | P-value | FDR B&H | FDR B&Y | Bonferroni | Gene Count | Gene |
|------------|--------------|---------|---------|---------|------------|-------------|----------------|
| 102613 | Signaling pathways regulating pluripotency of stem cells | 5.18E-04 | 5.12E-02 | 2.94E-01 | 8.97E-02 | 09 | FGFR3,FGFR2,WNT5A,ID4,SOX2,INHBA,LEFTY2,PAX6,SMAD9 |
| 6 | Neuroactive ligand-receptor interaction | 7.68E-04 | 5.12E-02 | 2.94E-01 | 1.33E-01 | 13 | TSHB,CSH1,CSH2,FSHB,GALR1,STR2,GH1,GH2,GHR,KISS1R,GNRHR,CCKBR,P2RY2 |
| 83032 | Drug metabolism - cytochrome P450 | 1.06E-03 | 5.12E-02 | 2.94E-01 | 1.84E-01 | 06 | UGT2A2,MGST1,ALDH1A3,FMO5,AOX1,UGT2A1 |
| 83077 | Jak-STAT signaling pathway | 1.18E-03 | 5.12E-02 | 2.94E-01 | 2.05E-01 | 09 | AOX1,CSH1,CSH2,IFNE,IL6R,IL20RA,IL22RA1,GH1,GH2 |
| 83031 | Metabolism of xenobiotics by cytochrome P450 | 7.71E-03 | 2.56E-01 | 1.00E+00 | 1.00E+00 | 05 | UGT2A2,MGST1,HSD11B1,ALDH1A3,UGT2A1 |
| 83096 | Maturity onset diabetes of the young | 8.89E-03 | 2.56E-01 | 1.00E+00 | 1.00E+00 | 03 | NEUROD1,NKX2-2,PAX6 |
| 673221 | Chemical carcinogenesis | 1.18E-02 | 2.80E-01 | 1.00E+00 | 1.00E+00 | 05 | UGT2A2,MGST1,HSD11B1,ALDH1A3,UGT2A1 |
| Pathway Interaction Database | REACTOME | GenMAPP |
|----------------------------|----------|---------|
| 137983 ALK2 signaling events | 126875 Peptide hormone biosynthesis | 127034 POU5F1 (OCT4), SOX2, NANOG activate genes related to proliferation |
| 137948 BMP receptor signaling | 126875 Glycoprotein hormones | 126954 GPCR ligand binding |
| | 126955 Hormone ligand-binding receptors | | 126954 Regulation of gene expression in endocrine-committed (NEUROG3+) progenitor cells |
| | 126932 Prolactin receptor signaling | | |
| ID    | Pathway                                                                 | Signatures | MAPK | p-value | MAF | Log2FoldChange | adjLog2FoldChange | Genes                                                                 |
|-------|-------------------------------------------------------------------------|------------|------|---------|-----|----------------|------------------|-----------------------------------------------------------------------|
| MAP0015 | Androgen and estrogen metabolism                                       | 3.18E-02   | 2.47E-01 | 8.99E-01 | 6.67E-01 | 02             | HSD11B1, HSD17B2 | S100A14, VIT, S100A1, S100B, FBN2, EFEMP1, FN2, SBSPO1, SPON1, FGF1, ITHI6, COL4A6, COL8A2, FRAS1, SFRP2, COL13A1, ITLN1, WNT5A, ADAM32, CSH1, CSH2, CSHH1, SLIT1, SLPI, IFN1, IHH, MEGF11, INHBA, LAMA1, ITHI2, GH1, GH2, BMP7, COL21A1, ADAMTS18, CHRD1, CLEC9A, NTF4, OGN, LEFTY2, RSPO3, MEGF6, CBLN2 |
| MAP0038 | Tryptophan metabolism                                                  | 4.08E-02   | 2.47E-01 | 8.99E-01 | 8.56E-01 | 03             | AOX1, CYP4B1, TDO2 | S100A14, S100A1, S100B, FGF1, SFRP2, WNT5A, CSH1, CSH2, CSHL1, IFNE, IHH, MEGF11, INHBA, LA MA1, ITHI2, GH1, GH2, BMP7, COL21A1, ADAMTS18, CHRD1, CLEC9A, NTF4, LEFTY2, MEGF6, CB LN2, LGI1 |
| MAP0091 | Nitrogen metabolism                                                   | 4.70E-02   | 2.47E-01 | 8.99E-01 | 9.68E-01 | 02             | CA8, CA12        | S100A14, S100A1, S100B, FBN2, EFEMP1, FN2, SBSPO1, SPON1, FGF1, ITHI6, COL4A6, COL8A2, FRAS1, SFRP2, COL13A1, ITLN1, WNT5A, ADAM32, CSH1, SCSH2, CSHH1, SLIT1, SLPI, IFN1, IHH, MEGF11, INHBA, LAMA1, ITHI2, GH1, GH2, BMP7, CHRD1, CLEC9A, NTF4, LEFTY2, RSPO3, MEGF6, CB LN2, LGI1 |

**MSigDB C2 BIOMARKERS (v6.0)**

| ID    | Description                                                                 | Signatures | MAPK | p-value | MAF | Log2FoldChange | adjLog2FoldChange | Genes                                                                 |
|-------|-----------------------------------------------------------------------------|------------|------|---------|-----|----------------|------------------|-----------------------------------------------------------------------|
| M5889 | Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins | 1.18E-09   | 5.44E-08 | 2.40E-07 | 5.44E-08 | 45             | S100A14, VIT, S100A1, S100B, FBN2, EFEMP1, FN2, SBSPO1, SPON1, FGF1, ITHI6, COL4A6, COL8A2, FRAS1, SFRP2, COL13A1, ITLN1, WNT5A, ADAM32, CSH1, CSH2, CSHH1, SLIT1, SLPI, IFN1, IHH, MEGF11, INHBA, LAMA1, ITHI2, GH1, GH2, BMP7, CHRD1, CLEC9A, NTF4, OGN, LEFTY2, RSPO3, MEGF6, CB LN2, LGI1 |
| M5883 | Genes encoding secreted soluble factors                                     | 2.79E-07   | 6.41E-06 | 2.83E-05 | 1.28E-05 | 21             | S100A14, S100A1, S100B, FGF1, SFRP2, WNT5A, CSH1, CSH2, CSHL1, IFNE, IHH, MEGF11, INHBA, GH1, GH2, BMP7, CHRD1, NTF4, LEFTY2, MEGF6, CB LN2 |
| M5884 | Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans | 1.42E-05   | 2.18E-04 | 9.63E-04 | 6.54E-04 | 16             | S100A14, S100A1, S100B, FGF1, SFRP2, WNT5A, CSH1, CSH2, CSHL1, IFNE, IHH, MEGF11, INHBA, GH1, GH2, BMP7, CHRD1, NTF4, LEFTY2, MEGF6, CB LN2, LGI1 |
| M5885 | Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors | 1.94E-05   | 2.23E-04 | 9.84E-04 | 8.91E-04 | 29             | S100A14, S100A1, S100B, FCN2, FGF1, ITHI6, SFRP2, ITLN1, WNT5A, ADAM32, CSH1, CSH2, CSHL1, SLPI, IFNE, IHH, MEGF11, INHBA, ITIH2, GH1, GH2, BMP7, ADAMTS18, CHRD1, CLEC9A, NTF4, LEFTY2, MEGF6, CB LN2 |
| M3008 | Genes encoding structural ECM glycoproteins                               | 4.35E-04   | 4.00E-03 | 1.77E-02 | 2.00E-02 | 11             | S100A14, S100A1, S100B, FGF1, SFRP2, WNT5A, ADAM32, CSH1, CSH2, CSHL1, SLPI, IFNE, IHH, MEGF11, INHBA, ITIH2, GH1, GH2, BMP7, ADAMTS18, CHRD1, CLEC9A, NTF4, LEFTY2, MEGF6, CB LN2 |

*AIMS Neuroscience* Volume 8, Issue 2, 254–283.
| ID     | Pathway                                                                 | P-value | E-value | p-value  | q-value | Symbol(s)          |
|--------|--------------------------------------------------------------------------|---------|---------|----------|---------|--------------------|
| M4557  | Biosynthesis of neurotransmitters                                        | 3.95E-03| 3.03E-02| 1.34E-01 | 1.82E-01| PNMT,TPH1          |
| M3005  | Genes encoding collagen proteins                                         | 5.99E-03| 3.94E-02| 1.74E-01 | 2.76E-01| COL4A6,COL8A2,COL13A1, COL21A1 |
| M16518 | Wnt/Ca2+/cyclic GMP signaling.                                            | 4.30E-02| 2.47E-01| 1.00E+00 | 1.00E+00| PDE6A,TF           |

**PantherDB**

| ID     | Pathway                                                                 | P-value | E-value | p-value  | q-value | Symbol(s)          |
|--------|--------------------------------------------------------------------------|---------|---------|----------|---------|--------------------|
| P02723 | Adenine and hypoxanthine salvage pathway                                 | 5.47E-03| 2.19E-01| 9.36E-01 | 2.19E-01| AOX1,XDH           |
| P04371 | 5-Hydroxytryptamine biosynthesis                                         | 4.91E-02| 6.50E-01| 1.00E+00 | 1.00E+00| TPH1               |

**Pathway Ontology**

| ID     | Pathway                                                                 | P-value | E-value | p-value  | q-value | Symbol(s)          |
|--------|--------------------------------------------------------------------------|---------|---------|----------|---------|--------------------|
| PW-000036 | melanocortin system                                                     | 1.13E-02| 1.52E-01| 6.35E-01 | 4.08E-01| PCSK2,POMC         |
| PW-00004 | androgen and estrogen metabolic                                          | 1.37E-02| 1.52E-01| 6.35E-01 | 4.94E-01| HSD11B1,UGT2A1     |
| PW-00037 | calcium homeostasis                                                      | 1.69E-02| 1.52E-01| 6.35E-01 | 6.09E-01| S100A1             |
| PW-00013 | Vitamin B6 metabolic                                                    | 1.69E-02| 1.52E-01| 6.35E-01 | 6.09E-01| AOX1               |
| PW-00020 | the planar cell polarity Wntsignaling                                   | 2.51E-02| 1.80E-01| 7.53E-01 | 9.02E-01| CELSR1,VANGL2      |

**SMPDB**

| ID     | Pathway                                                                 | P-value | E-value | p-value  | q-value | Symbol(s)          |
|--------|--------------------------------------------------------------------------|---------|---------|----------|---------|--------------------|
| SMP0063 | Tryptophan Metabolism                                                   | 2.59E-03| 1.16E-01| 5.13E-01 | 1.19E-01| AOX1,TDO2,TPH1     |
| SMP0220 | Xanthine Dehydrogenase Deficiency (Xanthinuria)                          | 1.69E-02| 1.16E-01| 5.13E-01 | 7.78E-01| XDH                |
| SMP0203 | Molybdenium Cofactor Deficiency                                         | 1.69E-02| 1.16E-01| 5.13E-01 | 7.78E-01| XDH                |
| SMP0246 | Pirenzepine Pathway                                                     | 3.18E-02| 1.16E-01| 5.13E-01 | 1.00E+00| ATP4A,CCKBR        |
| SMP0232 | Cimetidine Pathway                                                      | 3.18E-02| 1.16E-01| 5.13E-01 | 1.00E+00| ATP4A,CCKBR        |
| SMP0028 | Caffeine Metabolism                                                     | 3.30E-02| 1.16E-01| 5.13E-01 | 1.00E+00| XDH                |
| SMP0233 | Nizatidine Pathway                                                      | 3.53E-02| 1.16E-01| 5.13E-01 | 1.00E+00| ATP4A,CCKBR        |
| SMP0226 | Omeprazole Pathway                                                      | 3.53E-02| 1.16E-01| 5.13E-01 | 1.00E+00| ATP4A,CCKBR        |
Table 3 The enriched pathway terms of the down-regulated differentially expressed genes

| Pathway ID | Pathway Name                                      | P-value | FDR B&H | FDR B&Y | Bonferroni B&Y | Gene Count | Gene          |
|------------|---------------------------------------------------|---------|---------|---------|----------------|------------|---------------|
| 545291     | vitamin D3 biosynthesis                           | 2.55E-02| 2.81E-01| 8.48E-01| 2.81E-01       | 01         | CYP27B1       |
| 83054      | Cell cycle                                        | 1.09E-03| 1.56E-01| 8.62E-01| 1.56E-01       | 07         | TTK,CDC45,PLK1,PTT,G2,BUB1,CCNA1,CCNB2 |
| 169306     | Pancreatic secretion                              | 7.88E-03| 5.44E-01| 1.00E+00| 1.00E+00       | 05         | RYR2,ATP2A3,ATP2B2,PLA2G2D,CELA3A |
| 83055      | p53 signaling pathway                             | 1.19E-02| 5.44E-01| 1.00E+00| 1.00E+00       | 04         | GTSE1,CCNG2,ZMAT3,CCNB2 |
| 413367     | Lactosylceramide biosynthesis                     | 2.55E-02| 5.44E-01| 1.00E+00| 1.00E+00       | 01         | B4GALT6       |
| 413391     | Cholecalciferol biosynthesis                      | 2.55E-02| 5.44E-01| 1.00E+00| 1.00E+00       | 01         | CYP27B1       |
| 83050      | Calcium signaling pathway                         | 3.01E-02| 5.44E-01| 1.00E+00| 1.00E+00       | 06         | CHRNA7,RYR2,ATP2A3,ATP2B2,PLA2G2D,CELA3A,GRM5 |
| 377262     | Fanconianemia pathway                             | 3.36E-02| 5.44E-01| 1.00E+00| 1.00E+00       | 03         | FANCA,FANCD2,RAD5,1 |
| 119304     | Progesterone-mediated oocyte maturation           | 3.51E-02| 5.44E-01| 1.00E+00| 1.00E+00       | 04         | PLK1,BUB1,CCNA1,CCNB2 |
| 199556     | Vitamin digestion and absorption                  | 3.77E-02| 5.44E-01| 1.00E+00| 1.00E+00       | 02         | SLC19A1,SLC52A3 |
| 413396     | Steroid hormone biosynthesis, cholesterol =>progenolone => progesterone | 3.81E-02| 5.44E-01| 1.00E+00| 1.00E+00       | 01         | HSD3B2       |
| 83096      | Maturity onset diabetes of the young              | 4.36E-02| 5.67E-01| 1.00E+00| 1.00E+00       | 02         | PKLR,PAX4     |

Pathway Interaction Database

| Pathway ID | Pathway Name                  | P-value | FDR B&H | FDR B&Y | Bonferroni B&Y | Gene Count | Gene          |
|------------|-------------------------------|---------|---------|---------|----------------|------------|---------------|
| 138080     | Aurora B signaling network     | 1.16E-09| 4.30E-08| 1.81E-07| 4.30E-08       | 09         | CENPA,KLHL13,KIF23,BIRC5,RACGAP1,NCAPG,BUB1,STMN1,KIF20A |
| 137935     | FOXM1 transcription factor     | 6.86E-06| 1.27E-04| 5.33E-04| 2.54E-04       | 06         | CENPA,PLK1,FOXM1,BIRC5,NEK2,CCNB2 |
| ID    | Reactome Name                                      | P-value1 | P-value2 | P-value3 | P-value4 | Signaling Events | Genes                                                                 |
|-------|---------------------------------------------------|----------|----------|----------|----------|------------------|----------------------------------------------------------------------|
| 138007| PLK1 signaling events                             | 1.93E-05 | 2.38E-04 | 1.00E-03 | 7.15E-04 | 06               | PLK1, SPC24, TPX2, BUB1, CENPU, KIF20A                                 |
| 137925| Aurora A signaling                                | 6.31E-04 | 5.83E-03 | 2.45E-02 | 2.33E-02 | 04               | CENPA, BIRC5, TPX2, DL GAP5                                           |
| 137959| BARD1 signaling events                            | 5.96E-03 | 4.41E-02 | 1.85E-01 | 2.20E-01 | 03               | FANCA, FANCD2, RAD5                                                  |
|       | REACTOME                                           |          |          |          |          |                  |                                                                      |
| 1269820| Mitotic Prometaphase                              | 1.04E-11 | 5.07E-09 | 3.43E-08 | 5.07E-09 | 15               | KIF18A, CENPA, SPC25, CENPM, PLK1, BIRC5, SPC24, CENPH, CENPI, CDCA5, NUF2, NCAPG, BUB1, CENPU, CCNB2 |
| 1269821| Resolution of Sister Chromatid Cohesion           | 4.85E-11 | 1.18E-08 | 7.97E-08 | 2.36E-08 | 14               | KIF18A, CENPA, SPC25, CENPM, PLK1, BIRC5, SPC24, CENPH, CENPI, CDCA5, NUF2, BUB1, CENPU, CCNB2 |
| 1269741| Cell Cycle                                        | 2.94E-10 | 4.76E-08 | 3.22E-07 | 1.43E-07 | 30               | KIF18A, CENPA, HJURP, SPC25, MND1, HMMR, CDC45, CENPM, PLK1, FOXM1, KIF23, GTSE1, BIRC5, SPC24, CENPH, CENPI, TPX2, CDC5A5, HAUS6, NUF2, NEK2, NCAPG, BUB1, CCNA1, RAD51, CENPU, RFC3, KIF20A, CCNB2, TOP2A |
| 1269763| Cell Cycle, Mitotic                                | 4.25E-10 | 5.16E-08 | 3.49E-07 | 2.07E-07 | 27               | KIF18A, CENPA, SPC25, HMMR, CDC45, CENPM, PLK1, FOXM1, KIF23, GTSE1, BIRC5, SPC24, CENPH, CENPI, TPX2, CDC5A5, HAUS6, NUF2, NEK2, NCAPG, BUB1, CCNA1, CENPU, RFC3, KIF20A, CCNB2, TOP2A |
| 1269519| RHO GTPases Activate Formins                      | 3.21E-08 | 3.12E-06 | 2.11E-05 | 1.56E-05 | 12               | KIF18A, CENPA, SPC25, CENPM, PLK1, BIRC5, SPC24, CENPH, CENPI, NUF2, BUB1, CENPU |
| 1269378| Kinesins                                          | 6.18E-08 | 5.01E-06 | 3.39E-05 | 3.00E-05 | 08               | KIF18A, KIF23, RACGAP1, KIF21B, KIF26A, KIF15, KIF11, KIF20A         |
| 1269826| Separation of Sister Chromatids                   | 2.79E-07 | 1.94E-05 | 1.31E-04 | 1.36E-04 | 13               | KIF18A, CENPA, SPC25, CENPM, PLK1, BIRC5, SPC24, CENPH, CENPI, CD |

*AIMS Neuroscience*
| ID     | Pathology                                | Scores | Genes                                                                 |
|--------|------------------------------------------|--------|----------------------------------------------------------------------|
| 1269810| M Phase                                  | 5.07E-07| CA5,NUF2,BUB1,CENPU KIF18A,CENPA,SPC25, CENPM,PLK1,KIF23,BIRC5,SPC24,CENPH,CE NP1,CDC25,A NUF2,NCA PG,BUB1,CENPU,KIF20 A,CCNB2 |
| 1269825| Mitotic Anaphase                         | 5.75E-07| KIF18A,CENPA,SPC25, CENPM,PLK1,BIRC5,SPC24,CENPH,CE NP1,CDC25,NUF2,NCA PG,BUB1,CENPU,KIF20 A,CCNB2 |
| 1269823| Mitotic Metaphase and Anaphase           | 6.12E-07| KIF18A,CENPA,SPC25, CENPM,PLK1,BIRC5,SPC24,CENPH,CE NP1,CDC25,NUF2,BUB1,CENPU KIF18A,CENPA,SPC25, CENPM,PLK1,BIRC5,SPC24,CENPH,CE NP1,CDC25,NUF2,BUB1,CENPU |
| 1269799| G2/M Transition                          | 6.15E-04| HMMR,PLK1,FOXM1,G TSE1,TPX2,HAUS6,NE K2,CCNA1,CCNB2                 |

**MSigDB C2 BIOCARTA (v6.0)**

| ID     | Pathway                                                                 | Scores | Genes                                                                 |
|--------|-------------------------------------------------------------------------|--------|----------------------------------------------------------------------|
| M17370 | Role of Ran in mitotic spindle regulation                               | 2.34E-04| RCC1,TPX2,KIF15                                                      |
| M16334 | Eph Kinases and ephrins support platelet aggregation                    | 6.90E-03| LICAM,EPHB1                                                          |
| M9703  | Role of BRCA1, BRCA2 and ATR in Cancer Susceptibility                   | 2.94E-02| FANCD2,RAD51                                                         |

**PantherDB**

| ID     | Pathway                                                                 | Scores | Genes                                                                 |
|--------|-------------------------------------------------------------------------|--------|----------------------------------------------------------------------|
| P00031 | Inflammation mediated by chemokine and cytokine signaling pathway       | 1.17E-02| PF4,VWF,CCL3L3,CAS K,CXCR2,CXCR3,PLCD 4                             |

**Pathway Ontology**

| ID     | Pathway                                                                 | Scores | Genes                                                                 |
|--------|-------------------------------------------------------------------------|--------|----------------------------------------------------------------------|
| PW:0000194 | O-Glycans biosynthetic                                                     | 1.30E-02| 5.02E-02 1.95E-01 3.52E-01 01 B4GALT6                               |
| PW:0000164 | ganglioside biosynthetic                                                   | 1.30E-02| 5.02E-02 1.95E-01 3.52E-01 01 B4GALT6                               |
| PW:0000196 | globoside metabolic                                                       | 1.30E-02| 5.02E-02 1.95E-01 3.52E-01 01 B4GALT6                               |
| PW:0000197 | glycosphingolipid metabolic                                               | 1.30E-02| 5.02E-02 1.95E-01 3.52E-01 01 B4GALT6                               |
| PW:0000161 | glycosylphosphatidylinositol anchor biosynthetic                           | 1.30E-02| 5.02E-02 1.95E-01 3.52E-01 01 B4GALT6                               |
| PW:0000162 | glycosphingolipid biosynthetic-lactoserries                               | 1.30E-02| 5.02E-02 1.95E-01 3.52E-01 01 B4GALT6                               |
### Table 4. The enriched GO terms of the up-regulated differentially expressed genes.

| GO ID | CATEGO | GO Name | P Value | FDR B&H | FDR B&Y | Bonferroni | Gene Count | Gene                  |
|-------|--------|---------|---------|---------|---------|------------|------------|----------------------|
| GO:0  | BP     | sensory organ morphogenesis | 1.00E-12 | 4.43E-09 | 3.97E-08 | 4.43E-09  | 28         | EYA4,FBN2,EFEMP1,SALL1,CLIC5,TMIE,FGFR3,FGFR2,ALDH1A3,CLRN1,PRRX2,COL8A2,SDK2,WNT5A,CELSR1,IHH,MEGF11,SOX2,SOX9,GAS1,BMP7,FOXL2,STRA6,CALB1,ROR2,RBP4,VANGL2,PAX6 |

**PW:0000163** glycosphingolipid biosynthetic-neolactoserides

**PW:0000192** N-Glycans biosynthetic

**PW:0000017** Huntington disease

---

**PDB**

**SMP00266** Eptifibatide Pathway

**SMP00261** Ticlopidine Pathway

**SMP00265** Abciximab Pathway

**SMP00264** Dipyridamole Pathway

**SMP00263** Cilostazol Pathway

**SMP00267** Tirofiban Pathway

**SMP00336** Vitamin A Deficiency

**SMP00260** Clopidogrel Pathway

**SMP00367** Carvedilol Pathway

**SMP00368** Labetalol Pathway

---

**Aims Neuroscience**

Volume 8, Issue 2, 254–283.
| GO: 0  | BP     | Description                  | FDR  | q-value  | p-value  | Genes                        |
|--------|--------|------------------------------|------|----------|----------|------------------------------|
| GO:04856 | 2      | embryonic organ morphogenesis | 1.04E-11 | 2.29E-08 | 2.06E-07 | EYA4, GRHL2, OVOL2, FBN2, EFEMP1, SALL1, CLIC5, TMIE, FGFR2, ALDH1A3, CLRN1, PRRX2, WNT5A, CELSR1, IHH, RNF207, SOX2, SOX9, GAS1, BMP7, NEUROD1, FOXL2, TBXT, STA6, ROR2, RBP4, VANGL2, PAX6 |
| GO:04856 | 8      | embryonic organ development   | 5.52E-11 | 7.17E-08 | 6.43E-07 | EYA4, GRHL2, OVOL2, FBN2, EFEMP1, SALL1, CLIC5, TMIE, FGFR2, ALDH1A3, CLRN1, PRRX2, WNT5A, CELSR1, IHH, RNF207, SOX2, SOX9, PLAC1, GAS1, BMP7, NEUROD1, FOXL2, NRK, TBXT, STA6, KRT19, ROR2, RBP4, RUNX1, VANGL2, RSP03, PAX6 |
| GO:00742 | 3      | sensory organ development     | 6.48E-11 | 7.17E-08 | 6.43E-07 | EYA4, PDE6A, GRHL2, FBN2, EFEMP1, SALL1, CLIC5, TMIE, FGFR3, FGFR2, ALDH1A3, CLRN1, PRRX2, COL8A2, SDK2, WNT5A, CELSR1, IHH, PRDM16, MEGF11, SOX2, SOX9, INHBA, GAS1, LAMA1, BMP7, NEUROD1, FOXL2, ADAMT18, CHRD1L1, STA6, CALB1, NTF4, ROR2, RBP4, VANGL2, PAX6 |
| GO:04859 | 8      | embryonic morphogenesis       | 7.43E-10 | 6.57E-07 | 5.89E-06 | EYA4, EYA2, GRHL2, OVOL2, FBN2, EFEMP1, SALL1, CLIC5, TMIE, AMOT, FGFR2, ALDH1A3, CLRN1, PRRX2, FRAS1, SFPI2, WNT5A, TRIM71, IRX1, CELSR1, IHH, RNF207, SOX2, SOX9, INHBA, GAS1, BMP7, NEUROD1, FOXL2, ADAMT18, CHRD1L1, STA6, CALB1, NTF4, ROR2, RBP4, VANGL2, RSP03, PAX6, IRX2 |
| GO:00988 | 7      | animal organ morphogenesis    | 3.37E-09 | 2.28E-06 | 2.05E-05 | EYA4, GRHL2, PGR, OVOL2, FBN2, EFEMP1, SALL1, CLIC5, TMIE, FGFR1, FGFR3, FGFR2, LRT2, ALDH1A3, CLRN1, PRRX2, COL8A2, FRAS1, SDK2, |

*AIMS Neuroscience*
| GO:004859 | BP | eye morphogenesis | 3.61E-09 | 2.28E-06 | 2.05E-05 | 1.60E-05 | 18 |
| --- | --- | --- | --- | --- | --- | --- | --- |
| GO:000979 | BP | embryo development | 5.07E-09 | 2.80E-06 | 2.51E-05 | 2.24E-05 | 50 |
| GO:006042 | BP | epithelium development | 7.84E-09 | 3.85E-06 | 3.45E-05 | 3.47E-05 | 54 |
| GO:007208 | BP | stem cell proliferation | 1.16E-08 | 5.13E-06 | 4.60E-05 | 5.13E-05 | 17 |

| Gene Symbols | GO:004859 | GO:000979 | GO:006042 | GO:007208 |
|--------------|-----------|-----------|-----------|-----------|
| SFRP2, COL13A1, WNT5A, ID4, IRX1, CELSR1, SLIT1, IHH, RNF207, MEGF11, SOX2, SOX9, INHBA, GAS1, LAMA1, BM P7, NEUROD1, FOXL2, NGFR, TBXT, STRA6, CALB1, NTF4, ROR2, RBP4, VANGL2, RSPO3, TGFBR3, PAX6, NYR1 | 3.61E-09 | 2.05E-05 | 1.60E-05 | 18 |
| FBN2, EFEMP1, FGF3, ALD H1A3, COL8A2, SDK2, WNT5 A, IHH, MEGF11, SOX2, SOX9, GAS1, BMP7, FOXL2, STRA6, CALB1, RBP4, PAX6 | 5.07E-09 | 2.51E-05 | 2.24E-05 | 50 |
| LRAT, ERBB4, EYA4, EYA2, G RH2, OVOL2, FBN2, EFEMP1, SALL1, CIC5, TMIE, AMOT, FGF2, ALDH1A3, HSD17B, CLRN1, PRRX2, FRAS1, SFR P2, WNT5A, TRIM71, IRX1, CELSR1, IHH, RNF207, SOX2, SOX5, SOX9, PLAC1, INHBA, GAS1, LAMA1, DLK1, BMP7, NEUROD1, FOXL2, NRK, TBXT, STRA6, KRT19, ROR2, RBP4, RUNX1, CUBN, VANGL2, RSPO3, TGFBR3, P2RY2, PAX6, IRX2 | 7.84E-09 | 3.45E-05 | 3.47E-05 | 54 |
| ERBB4, DACT2, PTER, GRHL2, PGR, OVOL2, SALL1, CIC5, NROB1, FGF1, FGF3, FGF2, ALDH1A3, CLRN1, DEU1, FRAS1, SFRP2, WNT5A, AGR2, ID4, XDH, TRIM71, IRX1, CELSR1, IHH, RNF207, SOX2, SOX9, PRSS8, INHBA, GAS1, LAMA1, BMP7, NEUROD1, FOXL2, NGFR, TBXT, NNX2-2, KAZN, STRA6, KRT14, CALB1, NTF4, ROR2, OCA2, RUNX1, VANGL2, RSPO3, TGFBR3, ZNF750, GAL, PAX6, IRX2, S MAD9 | 1.16E-08 | 4.60E-05 | 5.13E-05 | 17 |
| GO:0 03101 | CC extracellular matrix | 1.21E-08 | 4.58E-06 | 2.98E-05 | 4.58E-06 | 28 |
|---|---|---|---|---|---|---|
| GO:0 00561 | CC extracellular space | 1.37E-07 | 2.60E-05 | 1.69E-04 | 5.19E-05 | 55 |
| GO:0 04442 | CC extracellular matrix component | 2.57E-04 | 3.26E-02 | 2.13E-01 | 9.78E-02 | 10 |
| GO:0 00560 | CC basement membrane | 8.42E-04 | 8.00E-02 | 5.21E-01 | 3.20E-01 | 08 |
| GO:0 04320 | CC perikaryon | 1.16E-03 | 8.84E-02 | 5.76E-01 | 4.42E-01 | 09 |
| GO:0 00578 | CC endoplasmic reticulum lumen | 1.46E-03 | 9.27E-02 | 6.04E-01 | 5.56E-01 | 11 |
| GO:0 03470 | CC cation channel complex | 4.96E-03 | 2.47E-01 | 1.00E+00 | 1.00E+00 | 09 |
| GO:0 00578 | CC endoplasmic reticulum | 7.05E-03 | 2.47E-01 | 1.00E+00 | 1.00E+00 | 45 |

PAX6

VIT, MFAP4, FBN2, EFEMP1, SBSPON, SPON1, FGF1, FGF2, FLRT2, COL4A6, COL8A2, FAS1, SFRP2, WNT5A, SLIT1, SLPI, IHH, LAMA1, BMP7, COL21A1, ADAMTS18, CPXM2, LAD1, RUNX1, OGN, TF, LEF TY2, TGFBR3

PCS2, CRISP2, SCRG1, TAC4, F5, S100B, EFEMP1, FCN2, SLPON1, FGF1, FLRT2, SPINK8, SFRP2, PI16, WNT5A, AGR2, POMC, PON3, XDH, AP0D, CARPT, SCGB1D2, SCGB1D1, CSL, ASIP, SLIT1, SLPI, C2orf40, IFNE, IHH, CTRB1, ATP4A1, IL6R, PRSS8, INHBA, LAMA1, DLK1, ITIH2, SMR3B, GH1, BMP7, KLK11, CPXM2, RBP4, KLK12, FAM3B, OGN, TF, CCK, LEFTY2, TGFBR3, GAL, D作业N, CBLN2, LGI1

MFAP4, FBN2, EFEMP1, COL4A6, COL8A2, FRAS1, LAMA1, LAD1, RUNX1, TF

EFEMP1, COL4A6, COL8A2, FRAS1, LAMA1, LAD1, RUNX1, TF

PCS2, PGR, RBFOX3, PNMT, CNTNAP2, KCNA1, NGFR, CACNA1A, CCK

TRDN, F5, SPON1, SRL, COL4A6, COL8A2, COL13A1, WNT5A, ERP27, COL21A1, NTF4

TRDN, SCN2B, CNTNAP2, CACNA2D3, KCNA1, KCNQ1, KCNJ16, KCNS2, CACNA1A

SPTLC3, LRAT, CPED1, TRDN, F5, PGR, S100A1, MGST1, SLPON1, TMRPRSS3, SRL, PLA2G4A, FGF3, FLRT2, HSDB1B1, HSD17B2, SLC51A, FXRD2, ALOD, COL4A6, COL8A2, COL13A1, FMO5, WNT5A, AGR2
| GO:009066 | CC | glycoprotein complex | 7.07E-03 | 2.47E-01 | 1.00E+00 | 1.00E+00 | 03 | SGCD, KRT19, SNTG2 |
| GO:003122 | CC | intrinsic component of plasma membrane | 0.02817 | 3.24E-01 | 1.00E+00 | 1.00E+00 | 42 | KLRF1, FCER1A, SCN2B, FGF R3, FGFR2, FLRT2, FXYD3, C OL13A1, SGCD, AQP4, CELS R1, ART3, SLC15A1, CNTNAP 2, SLC13A5, ATP4A1, IL6R, TR ABD2B, PRSS8, GALR1, GAS 1, SSTR2, SLC16A12, SLC39A 8, KCNA1, KISS1R, KCNG1, K CNJ12, KCNJ16, NGFR, KCNS 2, GNRHR, GPR12, FFAR3, RO R2, CCKBR, TGFB3, SLC39 A12, CD8B, P2RY2, TSPAN8, S LC6A14 |
| GO:000517 | MF | hormone activity | 4.87E-08 | 3.94E-05 | 2.87E-04 | 3.94E-05 | 14 | CGB3, TSHB, POMC, CARTPT, CSH1, CSH2, CSHL1, FSHB, I NHBA, GPHA2, GH1, GH2, CC K, GAL |
| GO:000510 | MF | signaling receptor binding | 4.24E-06 | 1.71E-03 | 1.25E-02 | 3.43E-03 | 54 | ERBB4, CGB3, S100A14, TSH B, TAC4, TRDN, PGR, S100B, E FEMP1, PPP1R1B, NR0B1, NG EF, FGFl, FLRT2, SFRP2, WNT 5A, AGR2, POMC, AKAL2, C ARTPT, CSH1, CSH2, CSHL1, ASIP, FSHB, SLIT1, RASL11B, IFNE, IHH, IL6R, INHBA, LAM A1, GPHA2, GH1, GH2, BMP7, FOXL2, NGFR, NTF4, ROR2, F AM3B, OGN, TF, CCK, CCKBR, LEFTY2, RSPO3, TGFB3, G AL, CD8B, P2RY2, TSPAN8, S NGT2, LG1 |
| GO:000485 | MF | xanthine dehydrogenase activity | 3.25E-04 | 6.58E-02 | 4.79E-01 | 2.63E-01 | 2 | AOX1, XDH |
| GO:0001672 | MF | oxidoreductase activity, acting on | 3.25E-04 | 6.58E-02 | 4.79E-01 | 2.63E-01 | 2 | AOX1, XDH |
Table 5. The enriched GO terms of the down-regulated differentially expressed genes.

| GO ID   | CATEGOR | GO Name                  | P Value | FDR B&H | FDR B&Y | Bonferroni B&H | Gene Count | Gene |
|---------|----------|--------------------------|---------|---------|---------|----------------|------------|------|
| GO:000280 BP nuclear division | 2.87E-18 | 6.44E-15 | 5.58E-01 | 9.45E-15 | 41 | NUSAP1,KIF18A,SPC25,RCC1,TTK,FANCA,FANCD2,CKS2,KLHL13,CLTC,PLK1,KIF23,BIRC5,SPC24,CENPH,TPX2,RACGA,P1,MTBP,CDCA5,PTTG2,HAUS6,DLGAP5,PKB,RAD21L1,NUF2,NEK2,PTTG3P,NCAPG,KIF15,BUB1,CCNA1,KIF14,KIF11,RA D51,RAD51D,PRC1,EDN1,CCN F,CCNG2,CCNB2,TOP2A |

Note: Biological Process (BP), Cellular Component (CC) and Molecular Functions (MF).
| GO:0048285 BP | organelle fission | 3.91E-18 | 6.44E-15 | 5.58E-14 | 1.29E-14 | 42 | NUSAP1, KIF18A, SPC25, RCC1, TTK, FANCA, FANCD2, CKS2, K LHL13, CLTC, PLK1, KIF23, BIRC5, SPC24, CENPH, TPX2, RACG AP1, MTBP, MTFR2, CDCA5, PTTG2, HAUS6, DLGAP5, PBK, RAD21, L1, NUF2, NEK2, PTTG3P, NCAF, KIF15, BUB1, CCNA1, KIF14, K IF11, RAD51, RAD51D, PRC1, EDN1, CCNF, CCNG2, CCNB2, TOP2A |
|-------------|------------------|---------|---------|---------|---------|---|------------------|
| GO:0007059 BP | chromosome segregation | 1.04E-17 | 1.14E-14 | 9.91E-14 | 3.43E-14 | 31 | NUSAP1, KIF18A, CENPA, HJU1, P, SPC25, RCC1, TTK, FANCD2, C ENPM, PLK1, KIF23, BIRC5, SPC24, CENPH, CENPI, RACGAP1, M TBP, CDCA5, PTTG2, DLGAP5, RAD21L1, NUF2, NEK2, PTTG3P, NC APG, BUB1, KIF14, KIF11, CENPU, PRC1, TOP2A |
| GO:0098813 BP | nuclear chromosome segregation | 8.97E-17 | 7.37E-14 | 6.40E-13 | 2.95E-12 | 28 | NUSAP1, KIF18A, CENPA, SPC25, TTK, FANCD2, CENPM, PLK1, K IF23, BIRC5, SPC24, CENPH, CENPI, RACGAP1, MTBP, CDCA5, P TPG2, DLGAP5, RAD21L1, NUF2, NEK2, PTTG3P, NCA PG, BUB1, K IF14, CENPU, PRC1, TOP2A |
| GO:0022402 BP | cell cycle process | 1.35E-15 | 8.90E-13 | 7.72E-12 | 4.45E-12 | 58 | NUSAP1, CDK3, KIF18A, CENPA, SPC25, RCC1, HMMR, TTK, CD C45, FANCA, FANCD2, CKS2, CENPM, KHL13, ZC3H12D, CLTC, PLK1, FOXM1, KIF23, GTSE1, B1RC5, SPC24, CENPH, CENPI, TPX2, RACGAP1, MTBP, CDCA5, PTTG2, SOX4, HAUS6, CYP27B1, DLGAP5, PBK, RAD21L1, NUF2, ME LK, NEK2, PTTG3P, NCA PG, KIF15, BUB1, CCNA1, KIF14, SLC39 A5, KIF11, RAD51, RAD51D, CENPU, STM1, PRC1, EDN1, KIF20A, CCNF, CCNG2, DDIAS, CCNB2, TOP2A |
| GO:0000819 BP | sister chromatid segregation | 2.90E-15 | 1.59E-12 | 1.38E-11 | 9.53E-12 | 24 | NUSAP1, KIF18A, CENPA, SPC25, TTK, CENPM, PLK1, KIF23, BIR C5, SPC24, CENPH, CENPI, RACGAP1, MTBP, CDCA5, DLGAP5, N UF2, NEK2, NCA PG, BUB1, KIF14 |
| GO:1903047 BP | mitotic cell cycle process | 2.55E-14 | 1.20E-11 | 1.04E-10 | 8.38E-11 | 45 |
| GO:0007049 BP | cell cycle | 3.07E-14 | 1.26E-11 | 1.09E-10 | 1.01E-10 | 64 |
| GO:0000278 BP | mitotic cell cycle | 5.56E-13 | 2.03E-10 | 1.76E-09 | 1.83E-09 | 45 |
| GO:0051301 BP | cell division | 2.86E-12 | 9.41E-10 | 8.16E-09 | 9.41E-09 | 35 |

- **GO:1903047 BP**: mitotic cell cycle process
  - NUSAP1, CDKN3, KIF18A, CENP A, SPC25, RCC1, HMMR, TTK, CD C45, CKS2, KLHL13, ZC3H12D, CLTC, PLK1, FOXM1, KIF23, GTSE 1, BIRC5, SPC24, CENPH, TPX2, RACGAP1, MTBP, CDC45, SOX4, HAUS6, DLGAP5, PBK, NUF2, MLK, NEK2, NACAP, KIF15, BUB 1, CCNA1, KIF14, KIF11, STMN1, PRC1, EDN1, KIF20A, CCNF, CC NG2, CCNB2, TOP2A

- **GO:0007049 BP**: cell cycle
  - NUSAP1, CDKN3, KIF18A, CENP A, EXD1, HJURP, SPC25, RCC1, M ND1, HMMR, TTK, CDC45, FANC A, FANCD2, CKS2, CENPM, KLHL13, ZC3H12D, CLTC, PLK1, FOX M1, KIF23, GTSE1, BIRC5, SPC24, CENPH, CENPI, TPX2, RACGAP1, MTBP, PRR11, CDC45, PTTG2, SOX4, HAUS6, CYP2B1, DLGAP5, PBK, RAD21L1, PARD6G, NUF2, MELK, PTP4A1, NEK2, PTTG3P, NCAPG, KIF15, BUB1, CCNA1, KI F14, SLC39A5, KIF11, RAD51, RA D51D, CENPU, STMN1, PRC1, ED N1, KIF20A, CCNF, CCNG2, DDI AS, CCNB2, TOP2A

- **GO:0000278 BP**: mitotic cell cycle
  - NUSAP1, CDKN3, KIF18A, CENP A, SPC25, RCC1, HMMR, TTK, CD C45, CKS2, KLHL13, ZC3H12D, CLTC, PLK1, FOXM1, KIF23, GTSE 1, BIRC5, SPC24, CENPH, TPX2, RACGAP1, MTBP, CDC45, SOX4, HAUS6, DLGAP5, PBK, NUF2, MLK, NEK2, NACAP, KIF15, BUB 1, CCNA1, KIF14, KIF11, STMN1, PRC1, EDN1, KIF20A, CCNF, CC NG2, CCNB2, TOP2A

- **GO:0051301 BP**: cell division
  - NUSAP1, SPC25, RCC1, TTK, CK S2, KLHL13, PLK1, KIF23, BIRC5, POU3F2, POU3F3, PPBP, SPC24, TPX2, RACGAP1, MTBP, CDC45, HAUS6, DLGAP5, PARD6G, NUF 2, NEK2, NACAP, BUB1, CCNA1, KIF14, KIF11, STMN1, PRC1, ED
| GO:0000793  | CC  | condensed chromosome | 5.65E-11 | 2.22E-08 | 1.46E-07 | 2.22E-08 | 19 | N1,KIF20A,CCNF,CCNG2,CCN B2,TOPO2A, CENPA,HJURP,SPC25,RCC1,FA NCD2,CENPM,PLK1,BIRC5,SPC24,CENPH,CDCA5,RAD21L1,NUF2,NEK2,NCAPG,BUB1,RAD51,CENPU,TOPO2A |
|-------------|-----|----------------------|----------|----------|----------|----------|----|---------------------------------------------------------------|
| GO:0000776  | CC  | kinetochore          | 1.20E-10 | 2.36E-08 | 1.55E-07 | 4.72E-08 | 15 | KIF18A,CENPA,HJURP,SPC25,CENPM,PLK1,BIRC5,SPC24,CENPH, CENPI,MTBP,NUF2,NEK2,BUB1,CENPU |
| GO:0000775  | CC  | chromosome, centromeric region | 4.29E-09 | 5.33E-07 | 3.49E-06 | 1.69E-06 | 16 | KIF18A,CENPA,HJURP,SPC25,CENPM,PLK1,BIRC5,SPC24,CENPH, CENPI,MTBP,CDCA5,NUF2,NEK2,BUB1,CENPU |
| GO:0000777  | CC  | condensed chromosome, kinetochore | 5.42E-09 | 5.33E-07 | 3.49E-06 | 2.13E-06 | 12 | CENPA,HJURP,SPC25,CENPM,PLK1,BIRC5,SPC24,CENPH,NUF2,NEK2,BUB1,CENPU |
| GO:0005819  | CC  | spindle              | 7.20E-09 | 5.66E-07 | 3.71E-06 | 2.83E-06 | 20 | NUSAP1,KIF18A,TTK,CLTC,PLK1,KIF23,POC1A,BIRC5,TPX2, RACGAP1,HAUS6,DLGAP5,PTP4A1,NEK2,KIF15,KIF14,KIF11, RASSF10,PRC1,KIF20A |
| GO:0000779  | CC  | condensed chromosome, centromeric region | 1.72E-08 | 1.13E-06 | 7.38E-06 | 6.76E-06 | 12 | CENPA,HJURP,SPC25,CENPM,PLK1,BIRC5,SPC24,CENPH,NUF2,NEK2,BUB1,CENPU |
| GO:0005871  | CC  | kinesin complex      | 4.58E-08 | 2.57E-06 | 1.69E-05 | 1.80E-05 | 09 | KIF18A,KIF23,KIF21B,KIF26A,DISC1,KIF15,KIF14,KIF11,KIF20A |
| GO:0015630  | CC  | microtubule cytoskeleton | 1.43E-07 | 7.01E-06 | 4.59E-05 | 5.61E-05 | 38 | NUSAP1,KIF18A,SPEF2,TTK,CDCA5,CLTC,C12orf66,PLK1,KIF23,POC1A,GTSE1,BIRC5,TPX2, RACGAP1,KIF21B,HAUS6,KIF26A,DISC1,DLGAP5,DAIB1,PTP4A1,NEK2,NCAPG,KIF15,CCNA1,KIF14,RASSF3,KIF11,RAD51, RAD51D,CENPU,RASSF10,STMN1,PRC1,KIF20A,CCNF,CCNB1, TOP2A |
| GO:0005694  | CC  | chromosome           | 4.51E-07 | 1.97E-05 | 1.29E-04 | 1.77E-04 | 33 | NUSAP1,KIF18A,CENPA,HJURP,SPC25,RCC1,CDCA5,FANCD2, S NHHCAF,CENPM,CLTC,PLK1, |

*AIMS Neuroscience*
| GO:0044430  | CC | cytoskeletal part | 9.84E-07 | 3.65E-05 | 2.39E-04 | 3.87E-04 | 44 | BIRC5, SPC24, CENPH, CENPI, MCBP, POLQ, CDC45, HMGB4, RA21L1, NUF2, TRIM24, NEK2, NCAPG, BUB1, PARBP, RAD51, RA D51D, CENPU, RFC3, ASXL2, TOP2A |
|-------------|----|------------------|----------|----------|----------|----------|----|------------------|
| GO:0008017  | MF | microtubule binding | 6.06E-06 | 2.40E-03 | 1.73E-02 | 4.63E-03 | 13 | NUSAP1, KIF18A, SPEF2, TTK, ADD2, CDC45, CLTC, PLK1, KIF23, POC1A, CARMIL1, GTSE1, BIRC5, KRT87P, TPX2, RACGAP1, MYBPC1, KIF21B, HAUS6, MYO1D, KIF26A, DISC1, DLGAP5, DAB1, PTP4A1, NEK2, NCAPG, KIF15, KIF14, RASSF3, KRTAP5-7, KIF11, RAD51, RAD51D, KRT28, CENPU, RASSF10, STMN1, PRC1, KIF20A, CCNF, CCNB2, KRTAP1-5, TOP2A |
| GO:0003777  | MF | microtubule motor activity | 8.30E-06 | 2.40E-03 | 1.73E-02 | 6.34E-03 | 08 | KIF18A, KIF23, KIF21B, KIF26A, KIF15, KIF14, KIF11, PRC1, KIF20A |
| GO:0015631  | MF | tubulin binding | 9.41E-06 | 2.40E-03 | 1.73E-02 | 7.19E-03 | 15 | NUSAP1, KIF18A, PLK1, KIF23, BIRC5, RACGAP1, KIF21B, KIF26A, KIF15, KIF14, KIF11, PRC1, KIF20A |
| GO:0008574  | MF | ATP-dependent microtubule motor activity, plus-end-directed | 6.32E-05 | 1.05E-02 | 7.57E-02 | 4.83E-02 | 04 | KIF18A, KIF26A, KIF14, KIF11 |
| GO:0003774  | MF | motor activity | 6.86E-05 | 1.05E-02 | 7.57E-02 | 5.24E-02 | 09 | KIF18A, KIF23, KIF21B, MYO1D, KIF26A, KIF15, KIF14, KIF11, KIF20A |
| GO:1990939  | MF | ATP-dependent microtubule motor activity | 1.01E-04 | 1.14E-02 | 8.19E-02 | 7.71E-02 | 04 | KIF18A, KIF26A, KIF14, KIF11 |
| GO:0016887  | MF | ATPase activity | 1.04E-04 | 1.14E-02 | 8.19E-02 | 7.95E-02 | 17 | KIF18A, KIF23, POLQ, ATP2A3, A TP2B2, KIF21B, MYO1D, KIF26A |

_AIMS Neuroscience_
Table 6. Topology table for up and down regulated genes.

| Category | Node    | Degree | Betweenness | Stress     | Closeness | Clustering Coefficient |
|----------|---------|--------|-------------|------------|-----------|------------------------|
| Up       | SALL1   | 20     | 6.73E-03    | 599040     | 0.270852  | 0.026316               |
| Up       | BMP7    | 42     | 1.85E-02    | 2547692    | 0.241805  | 0                      |
| Up       | FAM83F  | 2      | 5.08E-04    | 43304      | 0.20099   | 0                      |
| Up       | SGCD    | 8      | 3.55E-03    | 808402     | 0.171417  | 0                      |
| Up       | C1orf168| 1      | 0.00E+00    | 0          | 0.171291  | 0                      |
| Up       | GRHL2   | 7      | 1.70E-03    | 324668     | 0.243088  | 0                      |
| Up       | TDO2    | 18     | 3.51E-03    | 741118     | 0.221367  | 0                      |
| Up       | SMR3B   | 11     | 2.91E-03    | 241848     | 0.209856  | 0                      |
| Up       | SCRG1   | 1      | 0.00E+00    | 0          | 0.171291  | 0                      |
| Up       | IL20RA  | 36     | 1.30E-02    | 3240444    | 0.233049  | 0                      |
| Up       | FCN2    | 7      | 2.56E-03    | 197754     | 0.189402  | 0                      |
| Up       | DPPA4   | 105    | 5.28E-02    | 8404518    | 0.278355  | 1.90E-04               |
| Up       | ATP4A   | 91     | 4.54E-02    | 4727962    | 0.263514  | 0                      |
| Up       | GPR12   | 2      | 5.02E-04    | 50910      | 0.215258  | 0                      |
| Up       | SDK2    | 11     | 1.32E-03    | 347148     | 0.206891  | 0                      |
| Up       | SEPT14  | 9      | 3.56E-03    | 546322     | 0.189457  | 0                      |
| Up       | RSPO3   | 5      | 2.03E-03    | 178044     | 0.172718  | 0                      |
| Up       | SLC13A5 | 2      | 1.07E-04    | 16672      | 0.203829  | 0                      |
| Up       | FGFR2   | 93     | 5.79E-02    | 6781948    | 0.291174  | 0.003175               |
| Up       | MGST1   | 7      | 1.66E-03    | 259370     | 0.209421  | 0                      |
| Gene   | Exp Change | p-value  | PMID     | FDR      |
|--------|------------|----------|----------|----------|
| FABP7  | 3.53E-03   | 0.198368 | 348144   | 0.05     |
| PON3   | 1.00E+00   | 0.198368 | 2        | 0        |
| GAL    | 2.89E-03   | 0.219065 | 341670   | 0.05     |
| PAX6   | 2.00E-02   | 0.266617 | 1487900  | 0.002775 |
| SYPL2  | 3.97E-03   | 0.216559 | 648624   | 0.05     |
| LGI1   | 5.08E-04   | 0.185225 | 71602    | 0.05     |
| SLC15A1| 2.63E-02   | 0.251196 | 646218   | 0.05     |
| TMPRSS3| 1.58E-02   | 0.24797  | 3314720  | 0.05     |
| ROR2   | 1.54E-02   | 0.257031 | 2469916  | 0.05     |
| DACT2  | 1.06E-03   | 0.177576 | 191246   | 0.05     |
| SYMTNL2| 4.38E-03   | 0.241701 | 927394   | 0.05     |
| KRT40  | 1.59E-01   | 0.304829 | 22565808 | 0.05     |
| FBN2   | 6.88E-03   | 0.220957 | 1381044  | 0.05     |
| NTF4   | 2.03E-03   | 0.13475  | 147964   | 0.05     |
| GBA3   | 5.08E-04   | 0.148844 | 52696    | 0.05     |
| SLIT1  | 5.08E-04   | 0.176676 | 49644    | 0.05     |
| OR7A5  | 0.00E+00   | 0.214321 | 0        | 0        |
| BBXO1  | 6.49E-03   | 0.226003 | 440000   | 0.05     |
| ART3   | 8.13E-03   | 0.239993 | 976682   | 0.05     |
| ID4    | 3.35E-03   | 0.231447 | 782844   | 0.05     |
| PLIN4  | 7.56E-05   | 0.213461 | 37378    | 0.05     |
| TRDN   | 1.31E-02   | 0.247674 | 2095642  | 0.05     |
| CLIC5  | 2.39E-03   | 0.208391 | 360044   | 0.05     |
| RXR1   | 0.00E+00   | 0.200969 | 0        | 0        |
| FCER1A | 3.26E-05   | 0.185557 | 5636     | 0.05     |
| NGEF   | 7.48E-03   | 0.208005 | 1282594  | 0.05     |
| CCKBR  | 6.42E-03   | 0.225189 | 1313620  | 0.05     |
| ITLN1  | 3.22E-03   | 0.223274 | 584478   | 0.05     |
| S100A1 | 5.90E-03   | 0.251533 | 824942   | 0.05     |
| TMEM139| 3.55E-03   | 0.184289 | 258886   | 0.05     |
| PMAIP1 | 4.74E-03   | 0.230621 | 615246   | 0.05     |
| GHRHR  | 0.00E+00   | 0        | 1        | 0        |
| XDH    | 5.08E-04   | 0.200601 | 44858    | 0.05     |
| TRIM29 | 6.13E-02   | 0.297553 | 9041322  | 0.05     |
| UGT2A2 | 0.00E+00   | 0        | 1        | 0        |
| SOX5   | 1.43E-02   | 0.275378 | 1508376  | 0.05     |
| S100A1 | 5.90E-03   | 0.251533 | 824942   | 0.05     |
| GALR1  | 0.00E+00   | 0        | 0        | 0        |
| GAS1   | 1.01E-03   | 0.226575 | 43314    | 0.05     |
| PPP1R17| 0.00E+00   | 0        | 1        | 0        |
| IFNE   | 2.80E-03   | 0.217901 | 416368   | 0.05     |
| CELSR1 | 4.71E-03   | 0.223388 | 588542   | 0.05     |
| C4orf19| 5.94E-04   | 0.20404  | 75814    | 0.05     |
| POMC   | 5.46E-03   | 0.221941 | 738136   | 0.05     |
| LRAT   | 0.00E+00   | 0        | 1        | 0        |
| KLK11  | 1.36E-02   | 0.236335 | 2408872  | 0.05     |
|   | Gene   | Log2 Fold Change | Expression Value | p-Value | Corrected p-Value |
|---|---------|------------------|------------------|---------|------------------|
| Up | F5      | 4.61E-03         | 881738           | 0.220265| 0                |
| Up | CNTNAP2 | 2.06E-03         | 345082           | 0.217348| 0                |
| Up | ENPP6   | 1.39E-02         | 3610524          | 0.233408| 0                |
| Up | GBP6    | 1.02E-03         | 53086            | 0.167077| 0                |
| Up | OBP2A   | 3.04E-03         | 662994           | 0.170129| 0                |
| Up | RBP4    | 4.72E-03         | 550068           | 0.226992| 0                |
| Up | PPP1R27 | 0.00E+00         | 0                | 0.166294| 0                |
| Up | ITIH2   | 5.09E-03         | 851246           | 0.219884| 0                |
| Up | NEURL3  | 0.00E+00         | 0                | 0.166294| 0                |
| Up | Cлиц5   | 2.39E-03         | 360044           | 0.208391| 0                |
| Up | PPP1R27 | 0.00E+00         | 0                | 0.166294| 0                |
| Up | RASL11B | 1.08E-03         | 251748           | 0.233312| 0                |
| Up | KCNJ12  | 4.14E-03         | 1228964          | 0.207786| 0                |
| Up | AQP4    | 5.64E-04         | 54624            | 0.198508| 0                |
| Up | CDBB    | 5.08E-04         | 43304            | 0.20099 | 0                |
| Up | P2RY2   | 9.10E-04         | 137648           | 0.233077| 0                |
| Up | IL22RA1 | 2.15E-03         | 456438           | 0.199181| 0                |
| Up | RNF207  | 6.33E-04         | 99124            | 0.213496| 0                |
| Up | ADAMTS18| 7.80E-04         | 175548           | 0.216858| 0                |
| Up | NGFR    | 1.93E-02         | 2626710          | 0.258024| 0                |
| Up | KCNJ16  | 0.00E+00         | 0                | 1       | 0                |
| Up | EFEMP1  | 3.53E-02         | 3383126          | 0.271749| 0                |
| Up | CHN2    | 3.42E-03         | 578204           | 0.234506| 0                |
| Up | GPHA2   | 6.38E-03         | 1083752          | 0.214718| 0                |
| Up | GHRHR   | 0.00E+00         | 0                | 1       | 0                |
| Up | KRT40   | 1.59E-01         | 22565808         | 0.304829| 0                |
| Up | C6orf132| 0.00E+00         | 0                | 0.195135| 0                |
| Up | NRAP    | 2.54E-03         | 723962           | 0.182437| 0                |
| Up | PHACTR2 | 5.85E-03         | 1042524          | 0.242609| 0                |
| Up | EVC2    | 4.01E-02         | 3002590          | 0.269961| 0                |
| Up | FOXL2   | 2.86E-02         | 8356260          | 0.257889| 0                |
| Up | FAM3B   | 5.47E-03         | 400338           | 0.24077 | 0                |
| Up | DLK1    | 3.09E-02         | 5339202          | 0.257485| 0                |
| Up | BLID    | 2.22E-03         | 427182           | 0.219345| 0                |
| Up | CALB1   | 1.87E-03         | 281870           | 0.227635| 0                |
| Up | OGN     | 3.36E-03         | 588086           | 0.221218| 0                |
| Up | TF      | 3.30E-02         | 5546776          | 0.282609| 0                |
| Up | SMAD9   | 7.87E-02         | 8103704          | 0.303093| 0                |
| Up | SOX2    | 2.07E-01         | 37524600         | 0.318174| 0                |
| Up | KRT14   | 2.76E-02         | 6537242          | 0.277277| 0                |
| Up | DLGAP2  | 8.62E-03         | 607018           | 0.259128| 0                |
| Up | LRRC2   | 1.61E-05         | 2042             | 0.164853| 0                |
| Up | AMOT    | 6.81E-02         | 13889668         | 0.286702| 0                |
| Up | ZNF385C | 2.12E-03         | 396460           | 0.198308| 0                |
| Up | CCK     | 5.08E-04         | 109288           | 0.183825| 0                |
| Up | HSD11B1 | 5.27E-03         | 800492           | 0.218251| 0                |
| Gene    | Log2FDR | p-value | log2FC | Expression | FoldChange |
|---------|---------|---------|--------|------------|------------|
| SGCD    | 3.55E-03| 0.171417| 808402 |            | 1          |
| PRSS8   | 0.00E+00| 0       | 0      | 1          | 0          |
| C6orf118| 1.11E-03| 0.220228| 182260 |            | 1          |
| LAD1    | 2.00E-03| 0.222492| 282468 |            | 1          |
| MYL10   | 3.70E-04| 0.215777| 73004  |            | 0          |
| CRISP2  | 2.02E-03| 0.218082| 232114 |            | 1          |
| IHH     | 5.08E-04| 0.159532| 70496  |            | 0          |
| MCOLN2  | 0.00E+00| 0       | 0      | 1          | 0          |
| SLC39A12| 3.22E-02| 0.249178| 4986186|            | 1          |
| TSHB    | 6.40E-03| 0.237848| 1264174|            | 0          |
| GADD45G | 2.74E-02| 0.271843| 5419566|            | 0          |
| COL51A1 | 1.80E-03| 0.20662  | 219094 |            | 0          |
| LIX1    | 1.00E+00| 0.21205  | 653142 |            | 0          |
| PRSS45  | 1.00E+00| 0       | 6      | 1          | 0          |
| MAFAP4  | 1.38E-03| 0.216631| 246964 |            | 0          |
| SPON1   | 1.02E-03| 0.214367| 109098 |            | 0          |
| NFIX    | 5.02E-03| 0.232403| 1428620|            | 0          |
| COL8A2  | 6.18E-03| 0.221205| 653142 |            | 0          |
| GNHR    | 0.00E+00| 0       | 0      | 1          | 0          |
| SULT1C2 | 4.91E-03| 0.215375| 344354 |            | 0          |
| CA8     | 1.30E-02| 0.262215| 1324240|            | 0          |
| CHRDL1  | 7.97E-04| 0.198089| 108788 |            | 0          |
| MEGF6   | 1.43E-03| 0.228083| 100130 |            | 0          |
| RPRM    | 3.81E-03| 0.211331| 39669  |            | 0          |
| OCA2    | 8.78E-05| 0.168788| 7862   |            | 0          |
| MPPED1  | 8.03E-03| 0.222492| 1622472|            | 0          |
| CARTPT  | 1.00E+00| 0       | 6      | 1          | 0          |
| CSH1    | 5.61E-03| 0.257014| 475316 |            | 0          |
| GALNT9  | 0.00E+00| 0       | 0      | 1          | 0          |
| OGN     | 3.36E-03| 0.219969| 588086 |            | 0          |
| FAM153B | 5.40E-03| 0.2049  | 935250 |            | 0          |
| GADD45G | 2.74E-02| 0.271843| 5419566|            | 0          |
| VSNL1   | 1.31E-03| 0.199151| 162184 |            | 0          |
| KISS1R  | 1.02E-03| 0.182319| 144830 |            | 0          |
| FGFR3   | 2.12E-02| 0.268434| 2766462|            | 0          |
| WNT5A   | 7.80E-03| 0.206349| 881282 |            | 0          |
| CDB8    | 5.08E-04| 0.20099 | 43304  |            | 0          |
| SFRP2   | 3.65E-03| 0.223769| 988952 |            | 0          |
| HSPB3   | 9.14E-03| 0.24811  | 1066592|            | 0          |
| PAX6    | 2.00E-02| 0.266617| 1487900|            | 0.002775   |
| CYBDR1  | 7.61E-03| 0.221255| 1486198|            | 0          |
| FXYD3   | 1.80E-03| 0.20662  | 219094 |            | 0          |
| PGR     | 3.40E-02| 0.28689 | 5124700|            | 0          |
| HSD17B2 | 5.08E-04| 0.152911| 61020  |            | 0          |
| Gene | Rank | Fold Change | Expression | FDR | P-value |
|------|------|-------------|------------|-----|---------|
| OPCML | 11   | 9.23E-03    | 415810     | 0.253949 | 0       |
| RFX4  | 4    | 5.08E-04    | 68768      | 0.194519 | 0       |
| AGR3  | 14   | 3.65E-03    | 622642     | 0.231135 | 0       |
| SLIT1 | 2    | 5.08E-04    | 49644      | 0.176676 | 0       |
| SOX9  | 19   | 4.66E-03    | 1135172    | 0.228918 | 0       |
| CSHL1 | 3    | 1.02E-03    | 142558     | 0.195484 | 0       |
| CHST9 | 4    | 4.30E-04    | 57912      | 0.2136   | 0       |
| SULT1C2 | 10  | 4.91E-03   | 344354     | 0.215375 | 0       |
| DYDC2 | 1    | 0.00E+00    | 0          | 1       | 0       |
| SLIT1 | 4    | 1.52E-03    | 98748      | 0.177265 | 0       |
| SNTG2 | 14   | 4.17E-03    | 686616     | 0.201051 | 0       |
| ZNF750| 1    | 0.00E+00    | 0          | 0.196381| 0       |
| TAC4  | 3    | 1.00E+00    | 6          | 1       | 0       |
| PTER  | 14   | 4.59E-03    | 989784     | 0.223477 | 0       |
| CTRB1 | 2    | 1.00E+00    | 2          | 1       | 0       |
| COL21A1| 2   | 0.00E+00    | 0          | 0       | 0       |
| ATF7IP2| 4   | 7.03E-04    | 79612      | 0.215258 | 0       |
| NEFM  | 50   | 2.12E-02    | 4143078    | 0.272012 | 0       |
| S100A14| 21  | 8.84E-03    | 986808     | 0.265288 | 0       |
| AOX1  | 6    | 1.58E-03    | 130420     | 0.202895 | 0       |
| KLRF1 | 5    | 6.70E-04    | 77804      | 0.192503 | 0       |
| CCDC68| 13   | 5.14E-03    | 436104     | 0.208269 | 0       |
| CNKSR3| 9    | 2.74E-03    | 263976     | 0.196244 | 0       |
| CRYM  | 4    | 5.65E-04    | 44096      | 0.209666 | 0       |
| MYZAP | 1    | 0.00E+00    | 0          | 0.213484| 0       |
| PDE6A | 4    | 1.43E-04    | 8434       | 0.238597 | 0       |
| INHBA | 8    | 2.57E-03    | 734598     | 0.176407 | 0       |
| CNTNAP3| 33  | 1.34E-02    | 1433542    | 0.259393 | 0       |
| FAM153C| 2   | 5.08E-04    | 85808      | 0.170078 | 0       |
| C6orf141| 74  | 3.72E-02    | 9207512    | 0.260292 | 0       |
| RUNX1 | 79   | 3.50E-02    | 4622022    | 0.286015 | 0       |
| TRIM71| 17   | 6.52E-03    | 713150     | 0.220623 | 0       |
| PNMT  | 3    | 5.88E-04    | 55878      | 0.215493 | 0       |
| PRSS50| 25   | 9.88E-03    | 1981826    | 0.256663 | 0       |
| SLC47A1| 27  | 1.28E-02    | 762514     | 0.222832 | 0       |
| PHACTR3| 29  | 1.17E-02    | 1887264    | 0.234506 | 0       |
| IL20RA| 36   | 1.30E-02    | 3240444    | 0.233049 | 0       |
| LEFTY2| 3    | 1.02E-03    | 95398      | 0.147528 | 0       |
| RHBDL3| 4    | 1.52E-03    | 323400     | 0.165874 | 0       |
| GH1   | 85   | 3.79E-02    | 5815610    | 0.26716  | 0       |
| STRA6 | 2    | 5.08E-04    | 57684      | 0.184652 | 0       |
| FRAS1 | 33   | 1.76E-02    | 1896950    | 0.244978 | 0       |
| CT45A1| 3    | 1.00E+00    | 6          | 1       | 0       |
| FGFR3 | 49   | 2.12E-02    | 2766462    | 0.268434 | 0       |
| EYA4  | 26   | 6.49E-03    | 1286994    | 0.239075 | 0       |
| AMZ1  | 12   | 3.35E-03    | 644006     | 0.193934 | 0       |
| gene      | fold change | p-value | FPKM value | log2FC | Fold change | p-value | FPKM value |
|-----------|-------------|---------|------------|--------|-------------|---------|------------|
| CACNA1A   | 5.07E-02    | 0.00E+00 | 4392082    | 0      | 0.272841    | 0       | 0          |
| CA12      | 3.67E-03    | 0.00E+00 | 625692     | 0      | 0.218106    | 0       | 0          |
| GAS7      | 9.64E-03    | 0.00E+00 | 1499288    | 0      | 0.218894    | 0       | 0          |
| HPGD      | 0.00E+00    | 0       | 0          | 0      | 0.214321    | 0       | 0          |
| FMOS      | 9.24E-04    | 0.00E+00 | 141874     | 0      | 0.217516    | 0       | 0          |
| SCGB1D2   | 2.67E-03    | 0.00E+00 | 252442     | 0      | 0.209376    | 0       | 0          |
| PLIN5     | 2.54E-03    | 0.00E+00 | 488350     | 0      | 0.178558    | 0       | 0          |
| KCNA1     | 2.68E-03    | 0.00E+00 | 237802     | 0      | 0.195435    | 0       | 0          |
| ALDOB     | 1.11E-02    | 0.00E+00 | 1644614    | 0      | 0.253084    | 0       | 0          |
| RHOD      | 7.80E-03    | 0.00E+00 | 1084918    | 0      | 0.189786    | 0       | 0          |
| GJB7      | 2.16E-02    | 0.00E+00 | 2788870    | 0      | 0.243992    | 0       | 0          |
| ALDH1A3   | 2.42E-03    | 0.00E+00 | 378026     | 0      | 0.220327    | 0       | 0          |
| EYA2      | 4.15E-02    | 0.00E+00 | 6323538    | 0      | 0.281237    | 0       | 0          |
| KRT19     | 2.60E-02    | 0.00E+00 | 7305954    | 0      | 0.276926    | 0       | 0          |
| LY6H      | 5.57E-04    | 0.00E+00 | 60178      | 0      | 0.176092    | 0       | 0          |
| MYBPHL    | 2.32E-03    | 0.00E+00 | 246776     | 0      | 0.198308    | 0       | 0          |
| RASGRP1   | 3.51E-04    | 0.00E+00 | 53352      | 0      | 0.195019    | 0       | 0          |
| GH2       | 8.82E-06    | 0.00E+00 | 644        | 0      | 0.197325    | 0       | 0          |
| FERMT1    | 4.58E-03    | 0.00E+00 | 653358     | 0      | 0.227097    | 0       | 0          |
| ASXL3     | 5.08E-04    | 0.00E+00 | 44514      | 0      | 0.172627    | 0       | 0          |
| TEPP      | 0.00E+00    | 0       | 0          | 0      | 0.209354    | 0       | 0          |
| PDZRN3    | 4.13E-03    | 0.00E+00 | 858088     | 0      | 0.195387    | 0       | 0          |
| KCNS2     | 0.00E+00    | 0       | 0          | 0      | 0.148569    | 0       | 0          |
| VANGL2    | 1.46E-02    | 0.00E+00 | 1934604    | 0      | 0.232321    | 0       | 0          |
| PRDM16    | 1.44E-03    | 0.00E+00 | 306010     | 0      | 0.223972    | 0       | 0          |
| PLAC1     | 6.67E-03    | 0.00E+00 | 1205836    | 0      | 0.224957    | 0       | 0          |
| SH3BP4    | 1.67E-02    | 0.00E+00 | 2668100    | 0      | 0.262618    | 0       | 0          |
| COL4A6    | 4.29E-03    | 0.00E+00 | 288964     | 0      | 0.222241    | 0       | 0          |
| NEUROD1   | 3.84E-03    | 0.00E+00 | 758734     | 0      | 0.219016    | 0       | 0          |
| IL6R      | 6.73E-03    | 0.00E+00 | 876290     | 0      | 0.223845    | 0       | 0          |
| FSHB      | 1.00E+00    | 0       | 2          | 0      | 1           | 0       | 0          |
| CSH2      | 5.61E-03    | 0.00E+00 | 475316     | 0      | 0.257014    | 0       | 0          |
| CNTNAP3B  | 7.15E-03    | 0.00E+00 | 582922     | 0      | 0.190741    | 0       | 0          |
| CHRDL1    | 7.97E-04    | 0.00E+00 | 108788     | 0      | 0.198089    | 0       | 0          |
| NWI1      | 0.00E+00    | 0       | 0          | 0      | 0.175339    | 0       | 0          |
| WWC2      | 3.48E-03    | 0.00E+00 | 975000     | 0      | 0.230041    | 0       | 0          |
| APOD      | 3.56E-02    | 0.00E+00 | 2147634    | 0      | 0.271412    | 0       | 0          |
| GJB7      | 2.16E-02    | 0.00E+00 | 2788870    | 0      | 0.243992    | 0       | 0          |
| RXRG      | 1.14E-02    | 0.00E+00 | 2426724    | 0      | 0.228268    | 0       | 0          |
| RNF175    | 2.24E-05    | 0.00E+00 | 1134       | 0      | 0.179355    | 0       | 0          |
| IG5F11    | 0.00E+00    | 0       | 0          | 0      | 0           | 0       | 0          |
| SCN2B     | 3.56E-02    | 0.00E+00 | 7895890    | 0      | 0.255896    | 0       | 0          |
| OVOL2     | 0.00E+00    | 0       | 0          | 0      | 0.216108    | 0       | 0          |
| CCDC158   | 2.91E-03    | 0.00E+00 | 441576     | 0      | 0.225705    | 0       | 0          |
| ASXL3     | 5.08E-04    | 0.00E+00 | 44514      | 0      | 0.172627    | 0       | 0          |
| CYP4B1    | 1.00E+00    | 0       | 2          | 0      | 1           | 0       | 0          |
| Up  | Gene   | log2FoldChange | LogFold  | adjPValue | log10Fold  |
|-----|--------|----------------|----------|-----------|-----------|
| Up  | DLGAP2 | 14             | 8.62E-03 | 0.259128  | 0         |
| Up  | TPH1   | 7              | 1.87E-03 | 0.227635  | 0         |
| Up  | AOX1   | 6              | 1.58E-03 | 0.202895  | 0         |
| Up  | SLC39A8| 26             | 1.05E-02 | 0.220179  | 0         |
| Up  | S100B  | 33             | 1.07E-02 | 0.252922  | 0         |
| Up  | SLPI   | 7              | 4.10E-03 | 0.209143  | 0         |
| Up  | PGR    | 68             | 3.40E-02 | 0.28689   | 0         |
| Up  | SSTR2  | 7              | 2.14E-03 | 0.229425  | 0         |
| Up  | FLRT2  | 3              | 0.00E+00 | 0         | 1         |
| Up  | C2orf71| 5              | 2.03E-03 | 0.182386  | 0         |
| Up  | COL13A1| 2              | 0.00E+00 | 0         | 0         |
| Up  | CACNA2D3| 1              | 0.00E+00 | 0         | 1         |
|   |   |   |   |   |   |
|---|---|---|---|---|---|
| Up | HIF3A | 3 | 6.24E-04 | 67108 | 0.19472 | 0 |
| Up | CNTNAP3 | 33 | 1.34E-02 | 1433542 | 0.23593 | 0 |
| Up | CCNJL | 39 | 1.50E-02 | 3448762 | 0.26053 | 0 |
| Up | ADAM32 | 21 | 6.74E-03 | 1279704 | 0.22318 | 0 |
| Up | PHYHD1 | 3 | 7.04E-04 | 88272 | 0.21490 | 0 |
| Up | LAMA1 | 31 | 1.32E-02 | 3129918 | 0.24829 | 0 |
| Up | DNAI2 | 12 | 3.01E-03 | 467486 | 0.2 | 0 |
| Down | TRIM24 | 66 | 2.39E-02 | 7566812 | 0.29262 | 0 |
| Down | KHL13 | 30 | 8.55E-03 | 2607752 | 0.27949 | 0 |
| Down | MAGEB2 | 46 | 1.08E-02 | 4326748 | 0.26857 | 0 |
| Down | PPBP | 22 | 7.30E-03 | 2718118 | 0.22063 | 0 |
| Down | TTK | 77 | 3.23E-02 | 12267556 | 0.31332 | 0.721E-04 |
| Down | FAM71D | 3 | 6.39E-05 | 15292 | 0.19756 | 0 |
| Down | TOP2A | 102 | 4.15E-02 | 13126864 | 0.32332 | 0.00291 |
| Down | KIF18A | 27 | 9.22E-03 | 1047074 | 0.27294 | 0.00284 |
| Down | TPX2 | 45 | 1.33E-02 | 5212220 | 0.28332 | 0.00303 |
| Down | POC1A | 3 | 2.10E-04 | 38988 | 0.26371 | 0 |
| Down | ARHGAP29 | 14 | 2.99E-03 | 1435976 | 0.25409 | 0 |
| Down | NRG1 | 66 | 2.98E-02 | 8652224 | 0.27787 | 0 |
| Down | PLCD4 | 3 | 1.07E-03 | 235394 | 0.22488 | 0 |
| Down | CADPS2 | 15 | 4.01E-03 | 1430040 | 0.22412 | 0 |
| Down | CCNF | 13 | 2.36E-03 | 321772 | 0.26673 | 0 |
| Down | GTSE1 | 141 | 5.29E-02 | 7085030 | 0.33762 | 0.00871 |
| Down | TRHDE | 15 | 4.61E-03 | 1973410 | 0.23257 | 0 |
| Down | SOX4 | 27 | 1.24E-02 | 7096428 | 0.25821 | 0 |
| Down | DLEU1 | 21 | 6.78E-03 | 2289500 | 0.25346 | 0 |
| Down | PLK1 | 276 | 1.64E-01 | 39488508 | 0.35244 | 0.00101 |
| Down | HAUS6 | 53 | 1.32E-02 | 7866150 | 0.28825 | 0 |
| Down | BUB1 | 95 | 4.02E-02 | 4659062 | 0.31816 | 0.00864 |
| Down | SERINC2 | 8 | 2.18E-03 | 1257316 | 0.20618 | 0 |
| Down | KIF14 | 62 | 1.75E-02 | 10376292 | 0.28468 | 0 |
| Down | VWA1 | 14 | 4.26E-03 | 366250 | 0.21001 | 0 |
| Down | PTTG2 | 1 | 0.00E+00 | 0 | 0.22482 | 0 |
| Down | SEL1L | 58 | 2.60E-02 | 9557720 | 0.27056 | 0 |
| Down | NUSAP1 | 35 | 1.32E-02 | 2253376 | 0.30036 | 0.00891 |
| Down | CELA3A | 12 | 3.00E-03 | 434718 | 0.23481 | 0 |
| Down | DOK6 | 6 | 7.47E-04 | 300368 | 0.23466 | 0 |
| Down | NRG1 | 66 | 2.98E-02 | 8652224 | 0.27787 | 0 |
| Down | DHX15 | 208 | 9.39E-02 | 39966314 | 0.32084 | 0 |
| Down | NEK2 | 52 | 1.53E-02 | 5682386 | 0.27739 | 0 |
| Down | TAS2R7 | 14 | 5.78E-03 | 635150 | 0.24792 | 0.01098 |
| Down | SPCC24 | 41 | 1.22E-02 | 1425412 | 0.29152 | 0.03902 |
| Down | HMMR | 44 | 1.23E-02 | 3764124 | 0.28300 | 0.00317 |
| Down | PTP4A1 | 53 | 2.21E-02 | 5500792 | 0.25643 | 0 |
| Down | DAZAP2 | 99 | 4.35E-02 | 9779248 | 0.28839 | 0.00365 |
| Down | CDC5 | 55 | 1.97E-02 | 1719302 | 0.3 | 0.002903 |
| Gene     | Down | Fold Change | Expression | p-value | Adj. p-value |
|----------|------|-------------|------------|---------|--------------|
| ANTXR2   | 12   | 3.36E-03    | 876552     | 0.218842|              |
| FBXL5    | 41   | 1.34E-02    | 1287978    | 0.299253| 0.006748     |
| PLA2G2D  | 1    | 0.00E+00    | 0          | 0.206084| 0            |
| DAB1     | 67   | 2.85E-02    | 5666990    | 0.279457| 0.007689     |
| RBPJL    | 2    | 5.37E-04    | 117698     | 0.224851|              |
| FANCA    | 86   | 2.87E-02    | 13664846   | 0.284167|              |
| NLGN1    | 11   | 3.82E-03    | 881670     | 0.215525|              |
| POU3F2   | 10   | 2.82E-03    | 567692     | 0.225258|              |
| PPP4R4   | 3    | 5.68E-04    | 157816     | 0.205041|              |
| GPR6     | 2    | 5.37E-04    | 60688      | 0.210938|              |
| PAX4     | 3    | 1.07E-03    | 234714     | 0.21372 |              |
| ASXL2    | 18   | 6.05E-03    | 1686090    | 0.242263|              |
| IGFL3    | 1    | 0.00E+00    | 0          | 1       | 0            |
| GRK12    | 13   | 4.44E-03    | 430606     | 0.243976| 0.025641     |
| NCAPG    | 52   | 1.62E-02    | 5737472    | 0.285517|              |
| SLC19A1  | 3    | 5.43E-04    | 132382     | 0.188974|              |
| EPHB1    | 14   | 3.21E-03    | 1135208    | 0.242942|              |
| INHBE    | 15   | 7.30E-03    | 1600282    | 0.257445|              |
| FIBCD1   | 1    | 0.00E+00    | 0          | 1       | 0            |
| RG5      | 7    | 2.09E-03    | 462166     | 0.237446|              |
| CCNB2    | 36   | 8.70E-03    | 3365996    | 0.275673| 0.009524     |
| ADAMTS1L | 7    | 2.82E-03    | 352088     | 0.208506|              |
| FAM83A   | 7    | 1.40E-03    | 115518     | 0.279038| 0.047619     |
| LRFN1    | 20   | 9.73E-03    | 1618782    | 0.237416|              |
| PKLR     | 19   | 4.89E-03    | 591642     | 0.267308| 0.005848     |
| SLC25A15 | 15   | 5.26E-03    | 1022014    | 0.258069|              |
| PRC1     | 29   | 6.84E-03    | 1142838    | 0.294452| 0.031339     |
| AMIGO2   | 6    | 1.08E-03    | 410596     | 0.178235|              |
| KIF11    | 134  | 5.97E-02    | 17181634   | 0.31282 |              |
| G2E3     | 6    | 1.27E-03    | 455226     | 0.215806|              |
| OR6T1    | 1    | 0.00E+00    | 0          | 0.225613|              |
| POLQ     | 1    | 0.00E+00    | 0          | 1       | 0            |
| GRK2     | 13   | 4.44E-03    | 430606     | 0.243976| 0.025641     |
| RASSF3   | 28   | 7.78E-03    | 3540288    | 0.258176|              |
| PBK      | 107  | 4.20E-02    | 12464178   | 0.300775|              |
| CENPA    | 88   | 3.07E-02    | 4765456    | 0.300799| 0.006293     |
| LYNX1    | 1    | 0.00E+00    | 0          | 0.189426|              |
| ASPDH    | 10   | 3.69E-03    | 974500     | 0.235242|              |
| DLGAP5   | 23   | 7.53E-03    | 2047406    | 0.302705| 0.019763     |
| KIF20A   | 38   | 9.99E-03    | 3761204    | 0.277108|              |
| CNKSR2   | 10   | 2.74E-03    | 698616     | 0.245083|              |
| GOLGA6A  | 1    | 0.00E+00    | 0          | 0.194204|              |
| B4GALT6  | 4    | 1.00E+00    | 12         | 1        | 0            |
| KRT28    | 1    | 0.00E+00    | 0          | 1        | 0            |
| CDKN3    | 29   | 1.03E-02    | 1383840    | 0.274414| 0.002849     |
| DCAF4L2  | 7    | 1.14E-03    | 263466     | 0.229603|              |
| Down | Gene          | N  | Adj. p-value | Fold Change | p-value | q-value |
|------|---------------|----|--------------|-------------|---------|---------|
| Down | CALHM1        | 2  | 0.00E+00     | 0           | 0       | 0       |
| Down | ADD2          | 17 | 5.29E-03     | 1384972     | 0.251723| 0       |
| Down | CDKN3         | 29 | 1.03E-02     | 1383840     | 0.274414| 0.002849|
| Down | RYR2          | 28 | 8.08E-03     | 2614302     | 0.258642| 0       |
| Down | C20orf203     | 2  | 1.00E+00     | 2           | 1       | 0       |
| Down | YTHDF1        | 61 | 2.13E-02     | 7937228     | 0.298366| 0       |
| Down | FOXM1         | 80 | 2.74E-02     | 8443400     | 0.298749| 0.002331|
| Down | GJA4          | 3  | 1.07E-03     | 514922      | 0.181296| 0       |
| Down | PF4           | 11 | 5.89E-03     | 2016954     | 0.188248| 0.027778|
| Down | ANKfy1        | 41 | 1.24E-02     | 5747558     | 0.26362 | 0       |
| Down | AKAP3         | 10 | 3.76E-03     | 892188      | 0.240046| 0       |
| Down | DCAF12L2      | 11 | 3.30E-03     | 771012      | 0.231472| 0       |
| Down | BDNF          | 11 | 4.67E-03     | 1264752     | 0.242373| 0       |
| Down | BIRC5         | 61 | 2.10E-02     | 6990168     | 0.290549| 0       |
| Down | SLC39A5       | 45 | 1.94E-02     | 2952184     | 0.228407| 0       |
| Down | GLYATL3       | 1  | 0.00E+00     | 0           | 0.190715| 0       |
| Down | LiCAM         | 24 | 6.90E-03     | 2825930     | 0.267884| 0       |
| Down | SV2C          | 7  | 2.26E-03     | 545018      | 0.20922 | 0       |
| Down | KIF15         | 27 | 7.88E-03     | 1833408     | 0.267865| 0       |
| Down | FANCD2        | 74 | 3.14E-02     | 6501308     | 0.312978| 0.004813|
| Down | RACGAP1       | 89 | 3.18E-02     | 7802394     | 0.304263| 0.005107|
| Down | FAM20C        | 12 | 4.87E-03     | 828322      | 0.200852| 0       |
| Down | NUF2          | 44 | 1.42E-02     | 2296298     | 0.301725| 3.38E-02|
| Down | QSOX1         | 15 | 4.90E-03     | 1223750     | 0.241087| 0       |
| Down | SLITRK6       | 1  | 0.00E+00     | 0           | 0.206759| 0       |
| Down | FAM91A1       | 23 | 7.07E-03     | 2542312     | 0.2639  | 0       |
| Down | GPR161        | 16 | 8.15E-03     | 864880      | 0.246363| 0.008333|
| Down | SCEL          | 14 | 5.37E-03     | 1611186     | 0.249883| 0       |
| Down | CXCR3         | 6  | 2.15E-03     | 733476      | 0.158492| 0.066667|
| Down | RFT1          | 21 | 6.86E-03     | 2273166     | 0.225517| 0       |
| Down | PSG5          | 4  | 1.24E-03     | 315510      | 0.199775| 0       |
| Down | RAD51         | 120| 4.54E-02     | 8161594     | 0.307324| 0.001883|
| Down | ADAMTSL1      | 7  | 2.82E-03     | 352088      | 0.208506| 0       |
| Down | HMGB4         | 3  | 6.06E-04     | 146328      | 0.226988| 0       |
| Down | TROAP         | 33 | 1.24E-02     | 1251972     | 0.293872| 0.006452|
| Down | RASSF10       | 38 | 1.21E-02     | 3884098     | 0.259851| 0       |
| Down | ZC3H12D       | 1  | 0.00E+00     | 0           | 1       | 0       |
| Down | HJURP         | 21 | 4.31E-03     | 873270      | 0.271041| 0.035088|
| Down | XKR6          | 1  | 0.00E+00     | 0           | 0.225613| 0       |
| Down | Unc5D         | 1  | 0.00E+00     | 0           | 0.201809| 0       |
| Down | C1orf189      | 2  | 1.00E+00     | 2           | 1       | 0       |
| Down | PSTPIP2       | 8  | 1.87E-03     | 472358      | 0.247427| 0       |
| Down | XKR6          | 1  | 0.00E+00     | 0           | 0.225613| 0       |
| Down | EXD1          | 1  | 0.00E+00     | 0           | 1       | 0       |
| Down | KIF21B        | 30 | 9.70E-03     | 2431650     | 0.256842| 0       |
| Down | GRIP1         | 53 | 1.84E-02     | 6233398     | 0.270372| 0.001569|
| Gene      | DE    | Log2FoldChange | FDR   | Adjusted_FDR |
|-----------|-------|----------------|-------|--------------|
| POU3F3    | 3     | 5.62E-04       | 0.208387 | 0            |
| CPN1      | 6     | 1.71E-03       | 0.22172 | 0            |
| SPC25     | 35    | 6.24E-03       | 0.27207 | 0.052101     |
| C12ORF66  | 4     | 1.61E-03       | 0.201711 | 0            |
| MELK      | 23    | 6.63E-03       | 0.250673 | 0            |
| TLE4      | 28    | 9.56E-03       | 0.252507 | 0            |
| MND1      | 7     | 2.70E-03       | 0.224986 | 0            |
| ZMAT3     | 24    | 7.69E-03       | 0.271931 | 0            |
| ATP2A3    | 53    | 2.39E-02       | 0.256171 | 0            |
| GRIP1     | 53    | 1.84E-02       | 0.270372 | 0.001569     |
| CENPM     | 15    | 2.31E-03       | 0.25524 | 0.114286     |
| GRIK2     | 13    | 4.44E-03       | 0.243976 | 0.025641     |
| ZSCAN2    | 1     | 0.00E+00       | 0      | 0            |
| GRP26     | 1     | 0.00E+00       | 0      | 0            |
| NXPH4     | 4     | 1.61E-03       | 0.17246 | 0            |
| UNC5D     | 1     | 0.00E+00       | 0.201809 | 0            |
| RNF215    | 1     | 0.00E+00       | 0      | 0            |
| STMN1     | 65    | 2.51E-02       | 0.286065 | 4.81E-04     |
| ARHGAP20  | 2     | 1.00E-05       | 0.219564 | 0            |
| FAM72D    | 1     | 0.00E+00       | 0.225613 | 0            |
| HTR3D     | 4     | 7.06E-04       | 0.180646 | 0            |
| ATP2B2    | 118   | 5.57E-02       | 0.275124 | 2.90E-04     |
| CCNG2     | 11    | 3.40E-03       | 0.210806 | 0            |
| RCC1      | 102   | 3.87E-02       | 0.314165 | 0.001941     |
| NPVF      | 3     | 3.46E-05       | 0.217653 | 0            |
| KIF23     | 62    | 2.33E-02       | 0.306515 | 0.015819     |
| PSG11     | 4     | 1.12E-03       | 0.188324 | 0            |
| PRR11     | 95    | 3.70E-02       | 0.259923 | 0            |
| LCE1B     | 22    | 1.04E-02       | 0.209408 | 0            |
| CCNA1     | 83    | 2.81E-02       | 0.2972  | 2.47E-03     |
| TLE4      | 28    | 9.56E-03       | 0.252507 | 0            |
| HIGD1B    | 3     | 1.00E+00       | 0      | 0            |
| OXR1      | 10    | 1.57E-03       | 0.225914 | 0            |
| DEFA3     | 1     | 0.00E+00       | 0.184876 | 0            |
| DISC1     | 138   | 5.45E-02       | 0.288949 | 0            |
| CLTC      | 333   | 1.73E-01       | 0.345833 | 0.001483     |
| MTBP      | 7     | 9.00E-04       | 0.25191 | 0            |
| COLEC10   | 14    | 5.78E-03       | 0.230569 | 0            |
| PPLA7     | 1     | 0.00E+00       | 0      | 0            |
| TLE4      | 28    | 9.56E-03       | 0.252507 | 0            |
| MYO1D     | 58    | 2.01E-02       | 0.297723 | 0            |
| CXCR2     | 9     | 2.70E-03       | 0.206862 | 0            |
| POU3F4    | 3     | 3.10E-04       | 0.214335 | 0            |
| KIF26A    | 3     | 5.58E-04       | 0.213757 | 0            |
| VWF       | 20    | 6.90E-03       | 0.226877 | 0            |
| ZSCAN12   | 40    | 1.72E-02       | 0.249014 | 0            |
| Regulation | target Genes | Degree | Top MicroRNA | Regulation | target Genes | Degree | Top MicroRNA |
|------------|--------------|--------|--------------|------------|--------------|--------|--------------|
| Up         | SALL1        | 53     | hsa-mir-548b-3p | Down       | TRIM24       | 21     | hsa-mir-4477a |
| Up         | NKX2-2       | 20     | hsa-mir-6829-3p | Down       | KLHL13       | 1      | hsa-mir-218-5p |
| Up         | PTCHD1       | 60     | hsa-mir-548a-3p | Down       | MAGEB2       | 2      | hsa-mir-98-5p |
| Up         | BMP7         | 22     | hsa-mir-6890-3p | Down       | C3orf52      | 10     | hsa-mir-3153 |
| Up         | TMEI5M14     | 49     | hsa-mir-3187-3p | Down       | PPBP         | 1      | hsa-mir-335-5p |
| Up         | SERTM1       | 13     | hsa-mir-3924 | Down       | TTK          | 7      | hsa-mir-376a-3p |
| Up         | FAM83F       | 94     | hsa-mir-612 | Down       | TOP2A        | 17     | hsa-mir-708-5p |
| Up         | SGCD         | 41     | hsa-mir-4761-5p | Down       | KIF18A       | 2      | hsa-mir-192-5p |
| Up         | C1orf168     | 2      | hsa-mir-148b-3p | Down       | TPX2         | 1      | hsa-mir-193b-3p |
| Up         | GRHL2        | 1      | hsa-mir-26b-5p | Down       | POC1A        | 69     | hsa-mir-3605-5p |
| Up         | SMR3B        | 1      | hsa-mir-495-3p | Down       | ARHGAP29     | 25     | hsa-mir-6814-5p |
| Up         | SCRG1        | 33     | hsa-mir-1304-3p | Down       | NRG1         | 1      | hsa-mir-124-3p |
| Up         | IL20RA       | 1      | hsa-mir-26b-5p | Down       | CADPS2       | 4      | hsa-mir-30c-5p |
| Up         | FCN2         | 8      | hsa-mir-8064 | Down       | ACER2        | 46     | hsa-let-7d-5p |
| Up         | DPPA4        | 1      | hsa-mir-26b-5p | Down       | CCNF         | 102    | hsa-mir-324-3p |

**Table 7.** miRNA-target gene interaction table.
| Up    | hsa-mir-206  | Down  | GTSE1  | 2 hsa-mir-484 |
|-------|--------------|-------|--------|--------------|
| Up    | hsa-mir-1289 | Down  | SOX4   | 160 hsa-mir-519a-3p |
| Up    | hsa-mir-644a | Down  | DLEU1  | 31 hsa-mir-616-5p |
| Up    | hsa-mir-335-5p | Down  | PLK1   | 17 hsa-mir-3120-3p |
| Up    | hsa-mir-19b-1-5p | Down  | HAUS6  | 14 hsa-mir-5582-3p |
| Up    | hsa-mir-193b-3p | Down  | BUB1   | 67 hsa-mir-497-3p |
| Up    | hsa-mir-652-3p | Down  | SERINC2 | 1 hsa-mir-335-5p |
| Up    | hsa-mir-6823-3p | Down  | KIF14  | 14 hsa-mir-3133 |
| Up    | hsa-mir-335-5p | Down  | VWA1   | 30 hsa-mir-592 |
| Up    | hsa-mir-4671-5p | Down  | FRMPD3 | 18 hsa-mir-6511a-3p |
| Up    | hsa-mir-599  | Down  | SEL1L  | 12 hsa-mir-548as-3p |
| Up    | hsa-mir-615-3p | Down  | NUSAP1 | 1 hsa-let-7b-5p |
| Up    | hsa-mir-7977 | Down  | DOK6   | 23 hsa-mir-3679-3p |
| Up    | hsa-mir-204-5p | Down  | NRG1   | 1 hsa-mir-124-3p |
| Up    | hsa-mir-451a | Down  | DHX15  | 7 hsa-mir-221-3p |
| Up    | hsa-mir-128-3p | Down  | NEK2   | 2 hsa-mir-92a-3p |
| Up    | hsa-mir-3652 | Down  | TAS2R7 | 1 hsa-mir-142-3p |
| Up    | hsa-mir-23c  | Down  | SP2C4  | 26 hsa-mir-3664-5p |
| Up    | hsa-mir-124-3p | Down  | HMRR   | 5 hsa-mir-106b-5p |
| Up    | hsa-mir-18a-3p | Down  | PTP4A1 | 132 hsa-mir-186-5p |
| Up    | hsa-mir-5787 | Down  | DAZAP2 | 109 hsa-mir-511-5p |
| Up    | hsa-mir-4477a | Down  | CDCA5  | 4 hsa-mir-331-3p |
| Up    | hsa-mir-122-5p | Down  | ANTXR2 | 60 hsa-mir-3065-5p |
| Up    | hsa-mir-335-5p | Down  | FBXL5  | 31 hsa-mir-4731-3p |
| Up    | hsa-mir-4311 | Down  | PLA2G2D | 20 hsa-mir-548au-3p |
| Up    | hsa-mir-335-5p | Down  | RBP1L   | 25 hsa-mir-6731-5p |
| Up    | hsa-mir-501-3p | Down  | CENPI   | 2 hsa-mir-192-5p |
| Up    | hsa-mir-4480 | Down  | NLGN1  | 8 hsa-mir-670-3p |
| Up    | hsa-mir-335-5p | Down  | POU3F2  | 19 hsa-mir-6781-5p |
| Up    | hsa-mir-148a-3p | Down  | PAX4   | 8 hsa-mir-4783-5p |
| Up    | hsa-mir-138-5p | Down  | ASXL2  | 48 hsa-mir-5002-5p |
| Up    | hsa-mir-6819-3p | Down  | GRIK2  | 1 hsa-mir-26b-5p |
| Up    | hsa-mir-411-3p | Down  | NCAPG  | 20 hsa-mir-664b-3p |
| Up    | hsa-mir-26b-5p | Down  | SLC19A1 | 9 hsa-mir-4422 |
| Up    | hsa-mir-1268a | Down  | EPHB1  | 18 hsa-mir-548aw |
| Up    | hsa-mir-548u  | Down  | INHBE  | 2 hsa-mir-98-5p |
| Up    | hsa-mir-555  | Down  | FIBCD1 | 12 hsa-mir-6717-5p |
| Up    | hsa-mir-132-3p | Down  | RGS5   | 42 hsa-mir-4255 |
| Up    | hsa-mir-130b-5p | Down  | GUCA2B  | 1 hsa-mir-335-5p |
| Up    | hsa-mir-449b-5p | Down  | CCNB2  | 6 hsa-let-7f-5p |
| Up    | hsa-mir-335-5p | Down  | ADAMTS1 | 2 hsa-mir-25-3p |
| Up    | hsa-mir-4786-5p | Down  | FAM53A  | 5 hsa-mir-5090 |
| Up    | hsa-mir-92a-3p | Down  | LRFRN1 | 18 hsa-mir-6687-3p |
| Up    | hsa-mir-1273f | Down  | SLC25A15 | 20 hsa-mir-6720-3p |
| Up    | hsa-mir-488-3p | Down  | GABRQ  | 1 hsa-mir-335-5p |
| Up    | hsa-mir-26b-5p | Down  | PRC1   | 17 hsa-mir-3977 |
| Up  | Gene   | Fold Change | Down  | Gene   | Fold Change |
|-----|--------|-------------|-------|--------|-------------|
| LRAT | hsa-mir-4770 | 47          | AMIGO2 | hsa-mir-155-5p | 2          |
| SPTLC3 | hsa-mir-6514-5p | 32          | CDC45  | hsa-mir-575   | 2          |
| KKL11 | hsa-mir-335-5p | 1           | PRDM11 | hsa-mir-335-5p | 1          |
| F5   | hsa-mir-634   | 4           | CYP27B1 | hsa-mir-1178-5p | 12         |
| CNTNAP2 | hsa-mir-571   | 14          | KIF11  | hsa-mir-4495  | 15         |
| PI16 | hsa-mir-1-1   | 2           | G2E3   | hsa-mir-520g-3p | 54         |
| ENPP6 | hsa-mir-6077  | 24          | POLQ   | hsa-mir-664a-5p | 86         |
| GBP6  | hsa-mir-548j-3p | 24          | GRIK2  | hsa-mir-26b-5p | 1          |
| NEURL3 | hsa-mir-335-5p | 1           | RASSF3 | hsa-mir-20a-3p | 3          |
| CLIC5 | hsa-mir-4301  | 54          | PBK    | hsa-mir-4699-3p | 4          |
| RASL11B | hsa-mir-3137 | 7           | CENPA  | hsa-mir-4719  | 23         |
| KCNJ12 | hsa-mir-770-5p | 24          | LYNX1  | hsa-mir-744-5p | 1          |
| AQP4  | hsa-mir-320a  | 1           | EVX2   | hsa-mir-33b-3p | 9          |
| P2RY2 | hsa-mir-4433b-3p | 16          | KRT5P-7 | hsa-mir-26b-5p | 1          |
| IL22RA1 | hsa-mir-26b-5p | 1           | DLGAP5 | hsa-mir-520e   | 21         |
| RNF207 | hsa-mir-3190-5p | 10          | EDN1   | hsa-mir-379-5p | 57         |
| ADAMTS18 | hsa-mir-588   | 16          | KIF20A | hsa-mir-23a-3p | 5          |
| NGFR  | hsa-mir-6732-5p | 23          | CNKSR2 | hsa-mir-6808-3p | 10         |
| KCNJ16 | hsa-mir-148b-3p | 1           | GOLGA6A | hsa-mir-450b-5p | 4          |
| GPHA2 | hsa-mir-1180-5p | 24          | B4GALT6 | hsa-mir-1248  | 19         |
| C6orf132 | hsa-mir-4638-5p | 48          | ARHGP42 | hsa-mir-6131   | 22         |
| PHACTR2 | hsa-mir-590-3p | 47          | KRT28  | hsa-mir-1229-3p | 1          |
| EVC2  | hsa-mir-6873-3p | 18          | CDKN3  | hsa-mir-4695-3p | 18         |
| FOXL2 | hsa-mir-1253   | 10          | DCAF4L2 | hsa-mir-494-3p | 2          |
| FAM3B | hsa-mir-335-5p | 1           |        |        |             |
| DLK1  | hsa-mir-15a-5p | 1           |        |        |             |
| BLID  | hsa-mir-335-5p | 1           |        |        |             |
| UGT2A1 | hsa-mir-4762-5p | 10          |        |        |             |
| OGN   | hsa-mir-526b-5p | 1           |        |        |             |
| TF    | hsa-mir-19a-3p | 2           |        |        |             |
| SMAD9 | hsa-mir-4419b  | 45          |        |        |             |
| LINC00598 | hsa-mir-890 | 209         |        |        |             |
| SOX2  | hsa-mir-126-3p | 15          |        |        |             |
| KLK12 | hsa-mir-1-3p   | 2           |        |        |             |
| KRT14 | hsa-mir-124-3p | 2           |        |        |             |
| DLGAP2 | hsa-mir-20a-3p | 8           |        |        |             |
| LRRC2 | hsa-mir-3914   | 46          |        |        |             |
| AMOT  | hsa-mir-500a-5p | 23          |        |        |             |
| LINC00598 | hsa-mir-518a-5p | 209        |        |        |             |
| HSD11B1 | hsa-mir-26b-5p | 2           |        |        |             |
| SGCD  | hsa-mir-4698   | 41          |        |        |             |
| PRSS8 | hsa-mir-335-5p | 1           |        |        |             |
| C6orf118 | hsa-mir-1-1    | 2           |        |        |             |
| CRISP2 | hsa-mir-27a-3p | 2           |        |        |             |
| IHH   | hsa-mir-6839-5p | 22          |        |        |             |
| MCOLN2 | hsa-mir-6731-3p | 18          |        |        |             |
| Up  | Gene   | Count | miRNA             |
|-----|--------|-------|-------------------|
| Up  | SLC39A12 | 1     | hsa-mir-335-5p    |
| Up  | VIT     | 1     | hsa-mir-124-3p    |
| Up  | PRRX2   | 1     | hsa-mir-124-3p    |
| Up  | PPP1R17 | 1     | hsa-mir-335-5p    |
| Up  | TSHB    | 1     | hsa-mir-26b-5p    |
| Up  | AGR2    | 2     | hsa-mir-197-3p    |
| Up  | KBTBD12 | 39    | hsa-mir-4675      |
| Up  | GADD45G | 1     | hsa-mir-181a-5p   |
| Up  | LIX1    | 3     | hsa-mir-4668-5p   |
| Up  | PRSS45  | 8     | hsa-mir-765       |
| Up  | MFAP4   | 1     | hsa-mir-124-3p    |
| Up  | ESPNL   | 1     | hsa-mir-375       |
| Up  | NFIX    | 67    | hsa-mir-4488      |
| Up  | EVC2    | 18    | hsa-mir-1236-3p   |
| Up  | COL8A2  | 2     | hsa-mir-124-3p    |
| Up  | GNRHR   | 4     | hsa-mir-1-3p      |
| Up  | SULT1C2 | 2     | hsa-mir-7-5p      |
| Up  | CA8     | 54    | hsa-mir-646       |
| Up  | CHRD1L1 | 54    | hsa-mir-583       |
| Up  | RPRM    | 32    | hsa-mir-939-5p    |
| Up  | OCA2    | 12    | hsa-mir-1299      |
| Up  | MPPED1  | 15    | hsa-mir-516a-3p   |
| Up  | OGN     | 1     | hsa-mir-526b-5p   |
| Up  | GADD45G | 1     | hsa-mir-181a-5p   |
| Up  | VSNL1   | 25    | hsa-mir-6873-5p   |
| Up  | FGFR3   | 9     | hsa-mir-425-5p    |
| Up  | WNT5A   | 29    | hsa-mir-4680-3p   |
| Up  | SFRP2   | 2     | hsa-mir-218-5p    |
| Up  | HSPB3   | 1     | hsa-mir-335-5p    |
| Up  | PAX6    | 23    | hsa-mir-223-3p    |
| Up  | CYBRD1  | 42    | hsa-mir-4517      |
| Up  | PGR     | 2     | hsa-mir-181a-5p   |
| Up  | HSD17B2 | 2     | hsa-mir-124-3p    |
| Up  | OPCML   | 9     | hsa-mir-3149      |
| Up  | AGR3    | 1     | hsa-mir-335-5p    |
| Up  | SLIT1   | 33    | hsa-mir-4726-5p   |
| Up  | SOX9    | 30    | hsa-mir-1323      |
| Up  | CSHL1   | 1     | hsa-mir-16-5p     |
| Up  | CHST9   | 2     | hsa-mir-92a-3p    |
| Up  | NRK     | 1     | hsa-mir-335-5p    |
| Up  | SULT1C2 | 2     | hsa-mir-7-5p      |
| Up  | SULT1C4 | 10    | hsa-mir-6833-3p   |
| Up  | SNTG2   | 1     | hsa-mir-146a-5p   |
| Up  | TAC4    | 1     | hsa-mir-335-5p    |
| Up  | AGMO    | 23    | hsa-mir-1976      |
| Up  | PTER    | 2     | hsa-mir-130b-3p   |
| mRNA | Hsa-mir ID |
|------|-----------|
| CTRB1 | hsa-mir-335-5p |
| COL21A1 | hsa-mir-29c-3p |
| ATF7IP2 | hsa-mir-548c-3p |
| NEFM | hsa-let-7a-5p |
| S100A14 | hsa-mir-16-5p |
| AOX1 | hsa-mir-26b-5p |
| KLRF1 | hsa-mir-335-5p |
| CCDC68 | hsa-mir-6808-5p |
| IRX2 | hsa-mir-607 |
| CNKSR3 | hsa-mir-2276-3p |
| MYZAP | hsa-mir-7153-3p |
| PDE6A | hsa-mir-4757-5p |
| ABCA8 | hsa-mir-192-5p |
| INHBA | hsa-mir-548i |
| LDLRAD2 | hsa-mir-3974 |
| CNTNAP3 | hsa-mir-1226-3p |
| C6orf141 | hsa-mir-1827 |
| RUNX1 | hsa-mir-1179 |
| TRIM71 | hsa-mir-3607-3p |
| PNMT | hsa-mir-26b-5p |
| PRSS50 | hsa-mir-124-3p |
| SLC47A1 | hsa-mir-637 |
| IL20RA | hsa-mir-26b-5p |
| LEFTY2 | hsa-mir-4267 |
| ITGBL1 | hsa-mir-579-3p |
| RHBDL3 | hsa-mir-8485 |
| GH1 | hsa-mir-7-5p |
| FRAS1 | hsa-mir-124-3p |
| CT45A1 | hsa-mir-335-5p |
| FGFR3 | hsa-mir-4764-5p |
| EYA4 | hsa-mir-203a-3p |
| AMZ1 | hsa-mir-1470 |
| CACNA1A | hsa-mir-4734 |
| FAM196A | hsa-mir-335-5p |
| CA12 | hsa-mir-2355-3p |
| GAS7 | hsa-mir-384 |
| HPGD | hsa-mir-664a-3p |
| SCGB1D2 | hsa-mir-26b-5p |
| PLIN5 | hsa-mir-1184 |
| ALDOB | hsa-mir-378a-3p |
| GJB7 | hsa-mir-653-5p |
| PRR15L | hsa-mir-3679-3p |
| IRX2 | hsa-mir-6808-3p |
| ALDH1A3 | hsa-mir-1304-5p |
| EYA2 | hsa-mir-30a-5p |
| KRT19 | hsa-mir-193b-3p |
| Up  | Gene     | Change | miRNA     |
|-----|----------|--------|-----------|
| Up  | LY6H     | 17     | hsa-mir-3188 |
| Up  | MYBPHL   | 19     | hsa-mir-4304 |
| Up  | RASGRP1  | 13     | hsa-mir-3161 |
| Up  | FERMT1   | 4      | hsa-mir-9-5p  |
| Up  | ASXL3    | 28     | hsa-mir-1297 |
| Up  | PDZRN3   | 1      | hsa-mir-197-3p |
| Up  | KCNS2    | 19     | hsa-mir-888-3p |
| Up  | VANGL2   | 34     | hsa-mir-4733-5p |
| Up  | PRDM16   | 6      | hsa-mir-133a-3p |
| Up  | SH3BP4   | 42     | hsa-mir-663b |
| Up  | COL4A6   | 2      | hsa-mir-197-3p |
| Up  | NEUROD1  | 17     | hsa-mir-6738-3p |
| Up  | IL6R     | 55     | hsa-mir-509-5p |
| Up  | FSHB     | 7      | hsa-mir-3121-5p |
| Up  | CHRDL1   | 54     | hsa-mir-4510 |
| Up  | NWD1     | 75     | hsa-mir-548ap-3p |
| Up  | CPXM2    | 14     | hsa-mir-4539 |
| Up  | WWC2     | 39     | hsa-mir-596 |
| Up  | GJB7     | 38     | hsa-mir-642a-5p |
| Up  | IGSF11   | 4      | hsa-mir-3163 |
| Up  | SCN2B    | 46     | hsa-mir-4708-5p |
| Up  | CCDC158  | 15     | hsa-mir-1261 |
| Up  | ASXL3    | 28     | hsa-mir-708-3p |
| Up  | DLGAP2   | 8      | hsa-mir-4635 |
| Up  | AOX1     | 1      | hsa-mir-26b-5p |
| Up  | CH25H    | 1      | hsa-mir-26b-5p |
| Up  | SLC39A8  | 6      | hsa-mir-331-3p |
| Up  | S100B    | 2      | hsa-mir-29a-3p |
| Up  | SLPI     | 26     | hsa-mir-298 |
| Up  | PGR      | 2      | hsa-mir-126-3p |
| Up  | SSTR2    | 35     | hsa-mir-6787-3p |
| Up  | C2orf71  | 12     | hsa-mir-3065-3p |
| Up  | COL13A1  | 28     | hsa-mir-940 |
| Up  | CACNA2D3 | 15     | hsa-mir-6503-3p |
| Up  | NR0B1    | 1      | hsa-mir-561-3p |
| Up  | CALB2    | 1      | hsa-mir-335-5p |
| Up  | SCGB1D1  | 2      | hsa-mir-26b-5p |
| Up  | FGF1     | 24     | hsa-mir-589-3p |
| Up  | FOXL2    | 10     | hsa-mir-520a-5p |
| Up  | MKX      | 31     | hsa-mir-548p |
| Up  | TXLNB    | 27     | hsa-mir-642a-5p |
| Up  | ERBB4    | 7      | hsa-mir-302b-3p |
| Up  | PCSK2    | 25     | hsa-mir-660-5p |
| Up  | DMKN     | 18     | hsa-mir-6720-5p |
| Up  | TGFBR3   | 67     | hsa-mir-548aq-3p |
| Up  | MN1      | 17     | hsa-mir-188-3p |
Table 8. TF-target gene interaction table.

| Regulation | TF   | Degree | Gene  | Regulation | TF   | Degree | Gene  |
|------------|------|--------|-------|------------|------|--------|-------|
| Up         | EZH2 | 73     | IRX1  | Up         | CREM | 10     | ACER2 |
| Up         | WT1  | 12     | ADAMTS18 | Down     | TRIM28 | 14     | ARHGAP29 |
| Up         | ZNF76| 22     | ADARB2 | Down      | GATAD1 | 11     | FLJ13224 |
| Up         | SUZ12| 30     | CACNA2D3 | Down    | SIN3A | 28     | ANTXR2 |
| Up         | EBF1 | 14     | CSHL1  | Down      | PHF8  | 31     | AKAP3 |
| Up         | FOSL2| 10     | AGR2   | Down      | MXD4  | 20     | BIRC5 |
| Up         | ZNF217| 9      | AMZ1   | Down      | SAP30 | 31     | HOXA4 |
| Up         | NFIA | 11     | ALDOB  | Down      | STAT1 | 7      | CDCA5 |
| Up         | ZNF644| 17     | ATF7IP2 | Down     | GLI4  | 8      | ASPDH |
| Up         | GATA4| 14     | CHN2   | Down      | KDM5B | 31     | ATP2A3 |
| Up         | NR2F2| 6      | AOX1   | Down      | KDM5A | 35     | CCNF |
| Up         | CREB1| 14     | CNKSR3 | Down      | ZEB1  | 26     | C3orf52 |
| Up         | ZBTB33| 25     | APOD   | Down      | AT1  | 23     | CKS2 |
| Up         | TFE3 | 14     | CNKSR3 | Down      | NR2C2 | 19     | C1orf189 |
| Up         | MBD4 | 10     | DPPA4  | Down      | TFDP1 | 26     | CADPS2 |

Note: Degree: No of miRNA interact with target gene. We taken any one miRNA in table.
| Up  | Down  | Gene   | Fold Change |
|-----|-------|--------|-------------|
| Up  | MYBL2 | HSD17B2 | 10          |
| Up  | ZFP64 | C6orf1132 | 15          |
| Up  | ATF1  | CCDC68 | 18          |
| Up  | GATAD2A | CRYM | 18          |
| Up  | RCOR2 | FGFR3 | 13          |
| Up  | BCL6  | KISS1R | 11          |
| Up  | FOXA3 | DMKN | 15          |
| Up  | YY1   | FABP7 | 9           |
| Up  | HMG20B | IL6R | 16          |
| Up  | ZNF7  | PNMT | 2           |
| Up  | NFIC  | FMO5 | 4           |
| Up  | HNF4G | PRR15L | 10          |
| Up  | MBD1  | DACT2 | 27          |
| Up  | THAP1 | FCN2 | 6           |
| Up  | RARA  | DMKN | 6           |
| Up  | ETV4  | ITIH2 | 10          |
| Up  | L3MBTL2 | AMOT | 19          |
| Up  | CTBP1 | ASXL3 | 2           |
| Up  | NONO  | GRHL2 | 3           |
| Up  | PPARG | CSH1 | 19          |
| Up  | MAZ   | BMP7 | 28          |
| Up  | CBFB  | FFAR3 | 7           |
| Up  | SMAD4 | CCIC3 | 14          |
| Up  | RNF2  | CCNJL | 12          |
| Up  | ATF4  | FRAS1 | 4           |
| Up  | HBP1  | LOC100288911 | 16   |
| Up  | ATF3  | C6orf141 | 12    |
| Up  | KLF11 | LINC00242 | 14  |
| Up  | ZNF580 | ARMC4 | 19          |
| Up  | GATA1 | PHYHD1 | 15         |
| Up  | CTCF  | ATP4A | 22          |
| Up  | ZBTB26 | FAM3B | 16          |
| Up  | ZNF589 | CA12 | 11          |
| Up  | PKNOX1 | CSH2 | 11          |
| Up  | ZEB1  | AQP4 | 11          |
| Up  | ZNF263 | CLIC3 | 15          |
| Up  | KLF1  | C9orf152 | 17    |
| Up  | ZNF558 | ARMC3 | 7           |
| Up  | TBX21 | DMKN | 5           |
| Up  | ZNF324 | WNT5A | 13          |
| Up  | ZNF547 | NGFR | 2           |
| Up  | ZNF202 | ARMC4 | 2           |
| Up  | ZNF175 | ART3 | 8           |
| Up  | ZNF239 | ASXL3 | 4           |
| Up  | ZNF121 | CELSR1 | 11    |
| Up  | TARDBP | MKX | 7           |

*AIMS Neuroscience* Volume 8, Issue 2, 254–283.
| Up     | Down        | Gene         | Up     | Down        | Gene         |
|--------|-------------|--------------|--------|-------------|--------------|
| SP3    |            | FAM196A      | PRDM2  |            | CPLX3        |
|        |             |              | BCOR   |            | KISS1R       |
|        |             |              | POLR2H |            | GJB7         |
|        |             |              | CEBPA  |            | SLC6A14      |
|        |             |              | TRIM24 |            | LDLRAD2      |
|        |             |              | NR2F1  |            | IL22RA1      |
|        |             |              | NCO1   |            | KAZN         |
|        |             |              | NR4A1  |            | FOXL2        |
|        |             |              | GMEB2  |            | PRSS8        |
|        |             |              | THRB   |            | CTRIB1       |
|        |             |              | TGIF2  |            | NFIX         |
|        |             |              | NFYC   |            | FMO5         |
|        |             |              | ZNF512 |            | CT45A1       |
|        |             |              | GABPA  |            | EVC2         |
|        |             |              | ARID4B |            | PPP1R27      |
|        |             |              | KDM1A  |            | PLIN4        |
|        |             |              | DMAP1  |            | C1orf168     |
|        |             |              | KLF7   |            | ENTPD8       |
|        |             |              | GLIS2  |            | KCNJ12       |
|        |             |              | ZNF146 |            | OVOL3        |
|        |             |              | SP1    |            | NTF4         |
|        |             |              | ZNF488 |            | FXYD3        |
|        |             |              | BCL11A |            | KRT19        |
|        |             |              | ZNF341 |            | COL13A1      |
|        |             |              | BCL11B |            | EYA4         |
|        |             |              | ZBTB7A |            | SALL1        |
|        |             |              | HIC1   |            | FGFR2        |
|        |             |              | ZNF501 |            | FAM198A      |
|        |             |              | SOX13  |            | MGST1        |
|        |             |              | ESRRA  |            | ESRRA        |
|        |             |              | INSM2  |            | PMAIP1       |
|        |             |              | ZNF2   |            | GAS1         |
|        |             |              | ZNF610 |            | ROR2         |
|        |             |              | ETV6   |            | BMP7         |
|        |             |              | ZNF394 |            | CACNA2D3     |
|        |             |              | ZNF18  |            | RNF207       |
|        |             |              | ZNF24  |            | DNAI2        |
|        |             |              | KLF8   |            | NXX2-2       |
|        |             |              | ELF3   |            | BTBD17       |
|        |             |              | DIDO1  |            | LEFTY2       |
|        |             |              | RERE   |            | SOX9         |
|        |             |              | ZNF197 |            | WWC2         |
|        |             |              | MLX    |            | FLJ42393     |
|        |             |              | FOSL1  |            | FMO5         |

**AIMS Neuroscience**

Volume 8, Issue 2, 254–283.
|     | Up |     | Down |     |     |   |
|-----|----|-----|------|-----|-----|---|
| ESR1 | 3  | LGH1 |      | ZBTB17 | 8  | POU3F3 |
| ZFP2 | 12 | STRA6 |      | EMTT2 | 1  | BDNF |
| POLR2A | 7  | LDLRAD2 |      | MYNN | 21 | C20orf203 |
| NFIL3 | 11 | NEURL3 |      | KLF13 | 11 | INHBE |
| KLF16 | 21 | GH2 |      | FOSL1 | 18 | PTP4A1 |
| KLF4 | 16 | GADD45G |      | CTCF | 12 | PKLR |
| REST | 13 | RHBDL3 |      | ZNF644 | 17 | MAMSTR |
| RAD21 | 17 | RBP4 |      | SSRP1 | 9  | TRIM24 |
| MXD3 | 14 | S100A1 |      | RERE | 18 | PTTG2 |
| SCRT1 | 7  | GPR37L1 |      | CEBPG | 7  | MTBP |
| ZNF335 | 10 | RPRML |      | ZHX2 | 11 | LOC339874 |
| ELF1 | 11 | DLEC1 |      | ETS1 | 18 | CNIH2 |
| GATA2 | 7  | CA8 |      | SCRT2 | 6  | SLC52A3 |
| KLF9 | 26 | CCKBR |      | GMEB2 | 15 | ZSCAN12 |
| RXRB | 11 | TMEM139 |      | MYC | 5  | FANCA |
| DPF2 | 6  | GRHL2 |      | SCRT1 | 3  | STMN1 |
| NR2F6 | 15 | PTER |      | THR | 12 | SLC25A15 |
| ZNF71 | 10 | EFEMP1 |      | ZNF197 | 18 | RASSF10 |
| ZNF101 | 7  | RNF207 |      | ZBTB7A | 28 | QSOX1 |
| ZNF502 | 5  | HIF3A |      | ZNF394 | 24 | ZNF160 |
| ZNF140 | 1  | C6orf141 |      | ZBTB40 | 7  | G2E3 |
| ZNF292 | 9  | C6orf141 |      | ZNF140 | 1  | C6orf141 |
| ZNF264 | 2  | OVO3 |      | ZNF2 | 9  | PNPLA7 |
| CUX1 | 9  | SYT12 |      | ZNF407 | 8  | CCNB2 |
| GH11B | 6  | TGFRB3 |      | ZBTB11 | 21 | RAD51 |
| ZNF382 | 9  | KCNG1 |      | MAFG | 3  | CLTC |
| PRDM12 | 1  | C6orf141 |      | ZNF264 | 2  | OVO3 |
| FOS | 3  | IL6R |      | RCOR2 | 10 | CDKN3 |
| PRDM10 | 14 | STRA6 |      | NR4A1 | 12 | C20orf203 |
| TEAD3 | 14 | TF |      | TFP4 | 16 | RFT1 |
| IRF1 | 10 | TEPP |      | ZNF101 | 11 | CADPS2 |
| SIRT6 | 5  | CA8 |      | ZNF341 | 11 | NXXPH4 |
| MIXL1 | 3  | MYBPHL |      | MEF2D | 12 | RCC1 |
| ZBTB11 | 9  | SLC39A8 |      | YY1 | 10 | KIF18A |
| CREB3L1 | 9  | RASL11B |      | EBF1 | 8  | KIR3DX1 |
| TFD1 | 29 | VSNL1 |      | TSHZ1 | 11 | PKLR |
| HMBOX1 | 5  | TMEM154 |      | PKNOX1 | 4  | LYNX1 |
| BHLHE40 | 7  | PPP1R27 |      | WT1 | 15 | RAD21L1 |
| BACH1 | 3  | PNMT |      | FOXA3 | 14 | FOXM1 |
| FOXJ2 | 7  | S100B |      | PRDM1 | 10 | PRDM1 |
| SMARCA4 | 5  | FAM83F |      | ZNF610 | 16 | SLC19A1 |
| SIN3A | 17 | PAX6 |      | ZNF18 | 17 | DISC1 |
| ZBTB40 | 6  | HPGD |      | KLF7 | 20 | NHLRC4 |
| ID3 | 13 | SRL |      | ZBTB33 | 15 | HOXA6 |
| TRIM28 | 4  | FBN2 |      | GLIS2 | 19 | ZBTB33 |
| Up/Down | Gene 1 | Fold Change 1 | Up/Down | Gene 2 | Fold Change 2 |
|---------|--------|--------------|---------|--------|--------------|
| Up      | HDAC1  | 13           | Down    | KLF4   | 8            |
| Up      | SMARCE1| 8            | Down    | SUPT5H | 7            |
| Up      | GLI4   | 4            | Down    | ARNT   | 6            |
| Up      | SCRT2  | 3            | Down    | EGR2   | 13           |
| Up      | GLIS1  | 15           | Down    | ZNF382 | 6            |
| Up      | EGR2   | 15           | Down    | RFX1   | 7            |
| Up      | ATF2   | 4            | Down    | ELK1   | 23           |
| Up      | HHEX   | 5            | Down    | ZNF71  | 17           |
| Up      | STAT3  | 5            | Down    | DDX20  | 16           |
| Up      | CEBPG  | 14           | Down    | SP1    | 25           |
| Up      | HCFC1  | 4            | Down    | TEAD2  | 1            |
| Up      | TFA4   | 14           | Down    | SMARCA5| 13           |
| Up      | NR2C2  | 10           | Down    | ZNF83  | 9            |
| Up      | HMGN3  | 8            | Down    | ZNF24  | 22           |
| Up      | FOXM1  | 7            | Down    | DMT1   | 5            |
| Up      | EGR1   | 7            | Down    | GTF2A2 | 7            |
| Up      | IRF4   | 7            | Down    | E2F5   | 13           |
| Up      | DRAP1  | 14           | Down    | IRF2   | 7            |
| Up      | SP7    | 10           | Down    | HMBOX1 | 5            |
| Up      | NCOA1  | 3            | Down    | CREB3  | 4            |
| Up      | CREM   | 8            | Down    | ZNF623 | 9            |
| Up      | HMG20A | 12           | Down    | JUND   | 8            |
| Up      | LEF1   | 3            | Down    | MBD2   | 9            |
| Up      | DNMT1  | 1            | Down    | ATF3   | 12           |
| Up      | ZNF423 | 18           | Down    | MIXL1  | 6            |
| Up      | TEAD1  | 9            | Down    | ZNF512 | 7            |
| Up      | ADNP   | 8            | Down    | ATF2   | 6            |
| Up      | HES1   | 5            | Down    | ZFP2   | 23           |
| Up      | ARNT   | 2            | Down    | MAFK   | 5            |
| Up      | ZFP37  | 13           | Down    | KLF1   | 21           |
| Up      | ZBTB17 | 4            | Down    | HADA   | 1            |
| Up      | MYNN   | 10           | Down    | ETS2   | 2            |
| Up      | ARID1B | 7            | Down    | RELA   | 3            |
| Up      | PRKXANK| 8            | Down    | NR2F6  | 22           |
| Up      | ZNF143 | 4            | Down    | HES1   | 2            |
| Up      | SP2    | 17           | Down    | ZHX1   | 2            |
| Up      | CDC5L  | 5            | Down    | TSC22D| 1            |
| Up      | ZNF16  | 4            | Down    | BACH1  | 6            |
| Up      | PRDM1  | 4            | Down    | DIO2   | 4            |
| Up      | TRIM22 | 6            | Down    | CUX1   | 7            |
| Up      | GTF2F1 | 11           | Down    | ETV6   | 3            |
| Up      | TSHZ1  | 5            | Down    | ARID1B | 12           |
| Up      | RFX1   | 5            | Down    | ZNF207 | 15           |
| Up      | PTTG1  | 1            | Down    | IRF1   | 24           |
| Up      | MEF2D  | 8            | Down    | GATA4  | 6            |
| Up      | SSRP1  | 15           | Down    | NFIA   | 9            |

**AIMS Neuroscience** Volume 8, Issue 2, 254–283.
| Up  | Down |
|-----|------|
| NRF1 | SALL1 |
| KDM5A | CRYM |
| RCOR1 | GRHL2 |
| HDAC2 | ESPNL |
| HDAC6 | SSTR2 |
| SMARCA5 | GH2 |
| E2F5 | CSH2 |
| HDGF | CSHL1 |
| ETV1 | DLEC1 |
| PYGO2 | CYBRD1 |
| ELK1 | FOXL2 |
| KDM5B | WWC2 |
| NFRKB | LEFTY2 |
| MITF | RASGRP1 |
| PHF8 | ID4 |
| ZNF639 | MYBPHL |
| SAP30 | LOC100288911 |
| CREB3 | SRL |
| KLF6 | VANGL2 |
| ZKSCAN1 | DLK1 |
| CBX9 | SOX2 |
| ZNF138 | DMKN |
| ZNF366 | WNT5A |
| SUPTH5 | S100B |
| USF2 | SYPL2 |
| POU5F1 | DPPA4 |
| EHMT2 | DRGX |
| CTBP2 | LRT1 |
| CEBPB | PMAIP1 |
| SREBF2 | MN1 |
| MTA1 | GPR37L1 |
| CCNT2 | FGFR3 |
| JUND | KRT19 |
| KLF13 | KISS1R |
| MBD2 | LG1 |
| ZFX | PAX6 |
| WRNIP1 | ERP27 |
| MLLT1 | LY6H |
| ZNF584 | EVC2 |
| HLF | FAM217A |
| IKZF1 | PHYHD1 |
| TEAD4 | ITIH2 |
| CEBPD | SLC39A8 |
| FOXA2 | FAM83F |
| GATA1 | OR7A5 |
| ZNF8 | FXYD3 |

**Up:** Transcription factors that are upregulated.

**Down:** Transcription factors that are downregulated.
| Gene  | Up/Down | Gene  | Up/Down |
|-------|---------|-------|---------|
| MAFK  | Up      | TDO2  | Down    |
| STAT1 | Up      | FFAR3 | Down    |
| MXD4  | Up      | SH3BP4| Down    |
| SMC3  | Up      | FLRT2 | Down    |
| GTF2A2| Up      | FOXL2 | Down    |
| MNT   | Up      | FRAS1 | Down    |
| ZNF641| Up      | FXYD3 | Down    |
| ZNF535C| Up    | FXYD3 | Down    |
| CHD1  | Up      | IRX2  | Down    |
| ZNF592| Up      | GRHL2 | Down    |
| ZNF207| Up      | GRHL2 | Down    |
| NFATC1| Up      | S100A14| Down   |
| FOXK2 | Up      | LY6H  | Down    |
| GATAD2B| Up    | RHOD  | Down    |
| MYC   | Up      | SYT12 | Down    |
| SIX4  | Up      | GRHL2 | Down    |
| MTA3  | Up      | S100A14| Down   |
| GTF2E2| Up      | HSD11B1| Down  |
| TBX3  | Up      | PNMT  | Down    |
| EED   | Up      | NEURL3| Down    |
| JUNB  | Up      | KAZN  | Down    |
| YBX1  | Up      | KCNJ12| Down    |
| MAFF  | Up      | KCNJ16| Down    |
| GTF3C2| Up      | KISS1R| Down    |
| ZBTB1 | Up      | TGFB3 | Down    |
| IRF2  | Up      | KISS1R| Down    |
| ZHX2  | Up      | NFIX  | Down    |
| CHD4  | Up      | KISS1R| Down    |
| SMA5  | Up      | RNF207| Down    |
| MCM3  | Up      | KLK11 | Down    |
| TAL1  | Up      | TEPP  | Down    |
| RELA  | Up      | PNMT  | Down    |
| PTRF  | Up      | LEFTY2| Down    |
| ARID3A| Up      | LY6H  | Down    |
| NFE2  | Up      | TMEM139| Down   |
| ETS1  | Up      | ZNF385C| Down  |
| AEBP2 | Up      | OVL3  | Down    |
| NFE2L2| Up      | RHOD  | Down    |
| DDX20 | Up      | PDE6A | Down    |
| EP300 | Up      | PI16  | Down    |
| MTA2  | Up      | RHBDL3| Down    |
| KAT2A | Up      | PMAIP1| Down    |
| POU2F2| Up      | PMAIP1| Down    |
| TCF7  | Up      | PMAIP1| Down    |
| PML   | Up      | S100A1| Down    |
| NR3C1 | Up      | PNMT  | Down    |

**AIMS Neuroscience**

Volume 8, Issue 2, 254–283.
| Up  | MAX  | 2 | RNF207 | Down | MAFF | 2 | KIF18A |
| --- | --- | --- | ------ | ---- | ---- | --- | ------ |
| Up  | ZNF707 | 1 | PPP1R27 | Down | GATA3 | 5 | SPEF2 |
| Up  | MXII | 2 | PRSS8 | Down | HLF | 2 | RAD21L1 |
| Up  | NFB | 1 | PRR15L | Down | THRAP3 | 3 | RCC1 |
| Up  | GATA3 | 1 | PRR15L | Down | ZNF8 | 1 | LRFN1 |
| Up  | DEK | 2 | RHOD | Down | ZNF239 | 2 | ZNF160 |
| Up  | E2F6 | 1 | RNF207 | Down | SIX5 | 1 | MAMSTR |
| Up  | TAF7 | 2 | S100A1 | Down | RBBP5 | 2 | MTBP |
| Up  | HDAC8 | 1 | RUNX1 | Down | DPF2 | 5 | PRC1 |
| Up  | ZNF83 | 1 | RUNX1 | Down | MITF | 2 | ZBTB33 |
| Up  | RUNX3 | 1 | RUNX1 | Down | SREBF2 | 5 | PNPLA7 |
| Up  | SPI1 | 1 | RUNX1 | Down | ZNF585B | 1 | OXR1 |
| Up  | SREBF1 | 1 | RUNX1 | Down | NFE2 | 5 | PF4 |
| Up  | GTF2B | 1 | S100A1 | Down | MCM7 | 1 | PKLR |
| Up  | PBX2 | 1 | SALL1 | Down | FOXK2 | 1 | PRR11 |
| Up  | ZNF407 | 1 | SYPL2 | Down | ZNF592 | 1 | PVT1 |
| Up  | HNF4A | 1 | TF | Down | ZNF140 | 1 | SLC5A10 |
| Up  | RXRA | 2 | TPPP2 | Down | ZNF146 | 2 | TROAP |
| Up  | TEAD2 | 1 | WWC2 | Down | TBX3 | 2 | ZC3H12D |
|     |       |    |       | Down | HHEX | 1 | TPX2 |
|     |       |    |       | Down | CEBPZ | 1 | TSSC2 |
|     |       |    |       | Down | SP4 | 1 | ZSCAN12 |

Note: Degree: No of target gene interact with TF. We taken any one target gene in table. TF transcription factors.