**F:\学习工作\投稿资料\未投稿记录\Journal of Neurophysiology\F S1.tif**

**Figure S1. Length distribution of small RNA library for Intruder, Observer and Control groups.** The distribution of nucleotide lengths of clean small RNA reads varied from 10 to 44 nucleotides in each library and the most abundant length was 22 nucleotides.

F:\学习工作\投稿资料\未投稿记录\Journal of Neurophysiology\F S2.tif

**Figure S2. Small RNA categories annotation for Intruder, Observer and Control groups.** All of the high-quality clean reads larger than 18 nucleotides were mapped to the mouse genome and these genome-matched reads were divided into different categories of small RNAs according to their biogenesis and annotation. The most abundant RNA category from each library was miRNA.

**Table S1. qRT-PCR prime information.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene ID** | **Symbol** | **Accession** | **Prime sequence** | **Lengths** | **Tm(℃)** |
| 110862 | Kcnq3 | NM\_152923 | Forward 5’- GGTCTCTTGGATCGGGTTCG-3’  Reverse 5’-CCAGCATCTTCAGAACTCTGCC-3 | 20 | 60.18 |
| 22 | 61.26 |
| 16438 | Itpr1 | NM\_010585 | Forward 5’-CAAGCAACTGCTGGAGGAGA-3’  Reverse 5’- TTCAAGCTCCTGCTCTGTGG-3’ | 20 | 59.96 |
| 20 | 59.96 |
| 66066 | Gng11 | NM\_025331 | Forward 5’- AGTTGCAGAGACAACAGGTATC-3’  Reverse 5’- TGAAATGACACAGCTGCCCT-3’ | 22 | 58.07 |
| 20 | 59.89 |
| 15558 | Htr2a | NM\_172812 | Forward 5’- TCTCACCATTGCGGGAAACA-3’  Reverse 5’- GCCACCGGTACCCATACAG-3’ | 20 | 59.89 |
| 19 | 59.85 |
| 12555 | Cdh15 | NM\_007662 | Forward 5’- CAGCCAGATTAACGTGAGCC-3’  Reverse 5’- GACGTTCAGCGTTTGCTCTC-3’ | 20 | 58.99 |
| 20 | 59.84 |
| 12504 | Cd4 | NM\_013488 | Forward 5’- CTCCTTCGGCTTTCTGGGTT-3’  Reverse 5’- TGCCTGGCGCTGTTGG-3’ | 20 | 59.96 |
| 16 | 60.32 |
| 54598 | Calcrl | NM\_018782 | Forward 5’- TGGATGGTCTAACACTCAGGTCAT-3’  Reverse 5’- AGCAACCTGTGACCTTGGATT-3’ | 24 | 61.06 |
| 21 | 59.85 |
| 13636 | Efna1 | NM\_010107 | Forward 5’- CCGCGCTATGGAGTTCCTTT-3’  Reverse 5’- CCTCACGGAACTTGGGATTTG-3’ | 20 | 60.46 |
| 21 | 59.19 |
| 19395 | Rasgrp2 | NM\_011242 | Forward 5’- TAAAGGACTTGGGGGTCCGA-3’  Reverse 5’- TGTGGATCTCGCACCTTTCC-3’ | 20 | 60.18 |
| 20 | 60.04 |
| 207565 | Camkk2 | NM\_145358 | Forward 5’- CCTGAAATCAAGCTGCACCC-3’  Reverse 5’- CAGTGTGCAGTTCTCGTCCT-3’ | 20 | 59.47 |
| 20 | 59.97 |
| 72293 | Nkd2 | NM\_028186 | Forward 5’- AGAGAGAGTCCCGAAGGGG-3’  Reverse 5’- GCAGCACAACTTCTAGGGAAC-3’ | 19 | 59.69 |
| 21 | 59.19 |
| 13492 | Drd5 | NM\_013503 | Forward 5’- TTGGGAGCTAGACGGGAGAA-3’  Reverse 5’- CTGTGCAATGCGGTAGATGC-3’ | 20 | 59.96 |
| 20 | 59.97 |
| 15565 | Htr6 | NM\_021358 | Forward 5’- GCATAGCTCAGGCCGTATGT-3’  Reverse 5’- TCCCGCATGAAGAGGGGATA-3’ | 20 | 59.97 |
| 20 | 60.11 |
| 26427 | Creb3l1 | NM\_011957 | Forward 5’- ACGCCGTCTTGGAACCTTTC-3’  Reverse 5’- GGAAGTGCGCATTGTTGAGG-3’ | 20 | 60.88 |
| 20 | 60.11 |
| 14709 | Gng8 | NM\_010320 | Forward 5’- GGAGACTGTTCCCATGTCCA-3’  Reverse 5’- CATCCTTAGCGTGCGTTTCG-3’ | 20 | 59.02 |
| 20 | 59.97 |
| 18034 | Nfkb2 | NM\_019408 | Forward 5’- GTTGAGAAGCCTGGTGGACA-3’  Reverse 5’- TCTTTCACCTCTGTGCTGGG-3’ | 20 | 59.89 |
| 20 | 59.6 |
| 18439 | P2rx7 | NM\_011027 | Forward 5’- GCCTGGGAAGTAGGTCTAGC-3’  Reverse 5’- CGCTCACCAAAGCAAAGCTAAT-3’ | 20 | 59.25 |
| 22 | 60.1 |
| 237362 | Npffr1 | NM\_001177511 | Forward 5’- CAGTATGGAGGCGGAACCCT-3’  Reverse 5’- CGGAGAGGAGTGCTGGTAGT-3’ | 20 | 61.34 |
| 20 | 60.68 |
| 12865 | Cox7a1 | NM\_009944 | Forward 5’- TCTTCCAGGCCGACAATGAC-3’  Reverse 5’- GCCCAGCCCAAGCAGTATAA-3’ | 20 | 60.04 |
| 20 | 60.11 |
| 21817 | Tgm2 | NM\_009373 | Forward 5’- TTCTACTGGCTACCAGGGCT-3’  Reverse 5’- TCCTCGAACTGCCCAAAGTT-3’ | 20 | 59.96 |
| 20 | 59.53 |
| 193740 | Hspa1a | NM\_010479 | Forward 5’- ACGTGGGCTTTATCTTCCCTG-3’  Reverse 5’- AACAAATCACATCAGCGGGG-3’ | 21 | 60.07 |
| 20 | 58.82 |
| 2828187 | GAPDH | XM\_011241214.1 | Forward 5’-AGAACATCATCCCTGCATCCA-3’  Reverse 5’-CCGTTCAGCTCTGGGATGAC-3’ | 110 | 60 |
| 110 | 60 |

**Table S2. Filtering transcriptome raw data and Alignment.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **Total Raw Reads(Mb)** | **Total Clean Reads(Mb)** | **Total Clean Bases(Gb)** | **Clean Reads Q20(%)** | **Clean Reads Q30(%)** | **Clean Reads Ratio (%)** | **Total Mapping Ratio** | **Uniquely Mapping Ratio** |
| Control\_1 | 57.16 | 44.44 | 6.67 | 97.64 | 92.98 | 77.74 | 90.34% | 71.15% |
| Control\_2 | 55.53 | 44.21 | 6.63 | 97.7 | 93.12 | 79.61 | 90.84% | 71.75% |
| Control\_3 | 56.82 | 44.9 | 6.74 | 97.81 | 93.24 | 79.03 | 91.28% | 75.76% |
| Intruder\_1 | 55.53 | 44.61 | 6.69 | 97.97 | 93.69 | 80.33 | 91.58% | 72.66% |
| Intruder\_2 | 58.61 | 44.78 | 6.72 | 97.78 | 93.33 | 76.4 | 88.87% | 73.45% |
| Intruder\_3 | 55.53 | 44.31 | 6.65 | 97.69 | 92.99 | 79.79 | 89.45% | 73.58% |
| Observer\_1 | 55.53 | 44.36 | 6.65 | 97.68 | 93.03 | 79.88 | 88.67% | 70.48% |
| Observer\_2 | 55.53 | 45.25 | 6.79 | 97.75 | 93.16 | 81.5 | 88.23% | 70.38% |
| Observer\_3 | 58.8 | 45.13 | 6.77 | 97.69 | 92.97 | 76.77 | 88.62% | 73.27% |

**Table S3. Filtering small RNA library raw data and quality control.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample name** | **Sequence type** | **Raw tag count** | **Clean tag count** | **Percentage(%)** | **Total tag** | **Mapped tag** | **Percentage(%)** |
| Control\_1 | SE50 | 30544739 | 29009949 | 94.98 | 29009949 | 27180505 | 93.69 |
| Control\_2 | SE50 | 29796981 | 28276001 | 94.9 | 28276001 | 26607359 | 94.1 |
| Control\_3 | SE50 | 29730977 | 27622595 | 92.91 | 27622595 | 26234861 | 94.98 |
| Intruder\_1 | SE50 | 30701253 | 27556705 | 89.76 | 27556705 | 26094426 | 94.69 |
| Intruder\_2 | SE50 | 30663799 | 28258280 | 92.16 | 28258280 | 26647790 | 94.3 |
| Intruder\_3 | SE50 | 30916892 | 28390517 | 91.83 | 28390517 | 26845665 | 94.56 |
| Observer\_1 | SE50 | 31336586 | 29339909 | 93.63 | 29339909 | 28011252 | 95.47 |
| Observer\_2 | SE50 | 30712556 | 28766486 | 93.66 | 28766486 | 27607893 | 95.97 |
| Observer\_3 | SE50 | 30404788 | 28141305 | 92.56 | 28141305 | 26254349 | 93.29 |

**Table S4. mRNAs with differential expression over 1.5 folds and their characteristics in Intruder mice versus Control mice.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Symbol** | **Gene ID** | **Means (Intruder)** | **Means (Control)** | **Log2(Intruder/Control)** | **Up/Down Regulation** | **Gene Name** |
| *Aspa* | 11484 | 5.827 | 13.890 | -1.253 | DOWN | aspartoacylase |
| *Adssl1* | 11565 | 8.940 | 19.357 | -1.114 | DOWN | adenylosuccinate synthetase like 1 |
| *Aebp1* | 11568 | 0.930 | 3.657 | -1.975 | DOWN | AE binding protein 1 |
| *Amy1* | 11722 | 5.097 | 8.663 | -0.765 | DOWN | amylase 1, salivary |
| *Anxa5* | 11747 | 15.087 | 29.623 | -0.973 | DOWN | annexin A5 |
| *Apoc3* | 11814 | 1.830 | 0.887 | 1.045 | UP | apolipoprotein C-III |
| *Apod* | 11815 | 30.187 | 59.297 | -0.974 | DOWN | apolipoprotein D |
| *Nr2f2* | 11819 | 19.000 | 30.323 | -0.674 | DOWN | nuclear receptor subfamily 2, group F, member 2 |
| *Arc* | 11838 | 38.257 | 25.003 | 0.614 | UP | activity regulated cytoskeletal-associated protein |
| *Arpc1b* | 11867 | 12.103 | 19.630 | -0.698 | DOWN | actin related protein 2/3 complex, subunit 1B |
| *Fxyd2* | 11936 | 5.187 | 7.847 | -0.597 | DOWN | FXYD domain-containing ion transport regulator 2 |
| *Brca2* | 12190 | 1.653 | 2.513 | -0.604 | DOWN | breast cancer 2, early onset |
| *Btg2* | 12227 | 6.403 | 4.150 | 0.626 | UP | B cell translocation gene 2, anti-proliferative |
| *Tspo* | 12257 | 3.343 | 6.647 | -0.991 | DOWN | translocator protein |
| *C4b* | 12268 | 3.707 | 8.697 | -1.230 | DOWN | complement component 4B |
| *Ddr1* | 12305 | 23.623 | 44.223 | -0.905 | DOWN | discoidin domain receptor family, member 1 |
| *Calb2* | 12308 | 14.000 | 26.240 | -0.906 | DOWN | calbindin 2 |
| *Capza1* | 12340 | 10.390 | 15.830 | -0.607 | DOWN | capping protein muscle Z-line, alpha 1 |
| *Car2* | 12349 | 80.497 | 136.740 | -0.764 | DOWN | carbonic anhydrase 2 |
| *Runx2* | 12393 | 2.247 | 1.453 | 0.628 | UP | runt related transcription factor 2 |
| *Ccs* | 12460 | 12.417 | 19.897 | -0.680 | DOWN | copper chaperone for superoxide dismutase |
| *Cd24a* | 12484 | 2.513 | 4.580 | -0.866 | DOWN | CD24a antigen |
| *Cd4* | 12504 | 10.507 | 5.353 | 0.973 | UP | CD4 antigen |
| *Cd63* | 12512 | 62.997 | 100.693 | -0.677 | DOWN | CD63 antigen |
| *Cd9* | 12527 | 21.730 | 44.077 | -1.020 | DOWN | CD9 antigen |
| *Cdh15* | 12555 | 2.077 | 4.827 | -1.217 | DOWN | cadherin 15 |
| *Cdr2* | 12585 | 5.737 | 9.513 | -0.730 | DOWN | cerebellar degeneration-related 2 |
| *Chrm3* | 12671 | 11.580 | 6.667 | 0.797 | UP | cholinergic receptor, muscarinic 3, cardiac |
| *Cnp* | 12799 | 130.320 | 276.420 | -1.085 | DOWN | 2',3'-cyclic nucleotide 3' phosphodiesterase |
| *Cobl* | 12808 | 23.697 | 15.250 | 0.636 | UP | cordon-bleu WH2 repeat |
| *Col9a3* | 12841 | 6.337 | 19.430 | -1.616 | DOWN | collagen, type IX, alpha 3 |
| *Cox6a2* | 12862 | 5.930 | 8.940 | -0.592 | DOWN | cytochrome c oxidase subunit VIa polypeptide 2 |
| *Cox7a1* | 12865 | 2.013 | 4.657 | -1.210 | DOWN | cytochrome c oxidase subunit VIIa 1 |
| *Cp* | 12870 | 1.853 | 2.843 | -0.617 | DOWN | ceruloplasmin |
| *Crip1* | 12925 | 4.637 | 8.280 | -0.837 | DOWN | cysteine-rich protein 1 |
| *Pcdha4* | 12936 | 2.797 | 1.563 | 0.839 | UP | protocadherin alpha 4 |
| *Csrp1* | 13007 | 110.390 | 177.480 | -0.685 | DOWN | cysteine and glycine-rich protein 1 |
| *Ctbp2* | 13017 | 4.620 | 7.067 | -0.613 | DOWN | C-terminal binding protein 2 |
| *Cyp2j6* | 13110 | 4.587 | 7.220 | -0.655 | DOWN | cytochrome P450, family 2, subfamily j, polypeptide 6 |
| *Dbi* | 13167 | 87.083 | 139.637 | -0.681 | DOWN | diazepam binding inhibitor |
| *Dcn* | 13179 | 2.410 | 8.777 | -1.865 | DOWN | decorin |
| *Ddx6* | 13209 | 36.587 | 55.347 | -0.597 | DOWN | DEAD box polypeptide 6 |
| *Dio2* | 13371 | 9.163 | 5.837 | 0.651 | UP | deiodinase, iodothyronine, type II |
| *Dll3* | 13389 | 1.153 | 1.987 | -0.785 | DOWN | delta-like 3 |
| *Drd2* | 13489 | 62.173 | 38.890 | 0.677 | UP | dopamine receptor D2 |
| *Efna1* | 13636 | 1.900 | 4.150 | -1.127 | DOWN | ephrin A1 |
| *Efs* | 13644 | 3.707 | 6.743 | -0.863 | DOWN | embryonal Fyn-associated substrate |
| *Egr1* | 13653 | 95.503 | 56.043 | 0.769 | UP | early growth response 1 |
| *Egr2* | 13654 | 2.690 | 1.587 | 0.762 | UP | early growth response 2 |
| *Egr3* | 13655 | 35.543 | 23.227 | 0.614 | UP | early growth response 3 |
| *Stom* | 13830 | 2.043 | 3.127 | -0.614 | DOWN | stomatin |
| *Erbb3* | 13867 | 2.337 | 5.343 | -1.193 | DOWN | erb-b2 receptor tyrosine kinase 3 |
| *Evi2a* | 14017 | 15.640 | 30.627 | -0.970 | DOWN | ecotropic viral integration site 2a |
| *Fadd* | 14082 | 0.853 | 1.410 | -0.725 | DOWN | Fas -associated via death domain |
| *Fah* | 14085 | 8.007 | 14.130 | -0.819 | DOWN | fumarylacetoacetate hydrolase |
| *Fbn1* | 14118 | 0.867 | 1.783 | -1.041 | DOWN | fibrillin 1 |
| *Fcgr1* | 14129 | 1.780 | 1.137 | 0.647 | UP | Fc receptor, IgG, high affinity I |
| *Fgfr2* | 14183 | 7.007 | 11.503 | -0.715 | DOWN | fibroblast growth factor receptor 2 |
| *Fnbp1* | 14269 | 25.543 | 38.517 | -0.593 | DOWN | formin binding protein 1 |
| *Gab1* | 14388 | 7.843 | 14.310 | -0.867 | DOWN | growth factor receptor bound protein 2-associated protein 1 |
| *Gfap* | 14580 | 21.990 | 76.810 | -1.804 | DOWN | glial fibrillary acidic protein |
| *Ggh* | 14590 | 5.133 | 8.967 | -0.805 | DOWN | gamma-glutamyl hydrolase |
| *Gjb1* | 14618 | 5.600 | 17.753 | -1.665 | DOWN | gap junction protein, beta 1 |
| *Gngt2* | 14710 | 1.807 | 2.797 | -0.630 | DOWN | guanine nucleotide binding protein , gamma transducing activity polypeptide 2 |
| *Pdpn* | 14726 | 2.460 | 3.747 | -0.607 | DOWN | podoplanin |
| *Gpc3* | 14734 | 3.493 | 5.590 | -0.678 | DOWN | glypican 3 |
| *Lpar1* | 14745 | 6.193 | 14.613 | -1.238 | DOWN | lysophosphatidic acid receptor 1 |
| *Gpr37* | 14763 | 19.953 | 46.330 | -1.215 | DOWN | G protein-coupled receptor 37 |
| *Gstp1* | 14870 | 246.790 | 389.747 | -0.659 | DOWN | glutathione S-transferase, pi 1 |
| *Gstt1* | 14871 | 4.437 | 7.487 | -0.755 | DOWN | glutathione S-transferase, theta 1 |
| *H2-T24* | 15042 | 2.953 | 1.850 | 0.675 | UP | histocompatibility 2, T region locus 24 |
| *Heph* | 15203 | 1.260 | 2.010 | -0.674 | DOWN | hephaestin |
| *Hsd11b1* | 15483 | 4.813 | 7.577 | -0.655 | DOWN | hydroxysteroid 11-beta dehydrogenase 1 |
| *Htr1a* | 15550 | 3.803 | 5.800 | -0.609 | DOWN | 5-hydroxytryptamine receptor 1A |
| *Htr1b* | 15551 | 13.980 | 9.007 | 0.634 | UP | 5-hydroxytryptamine receptor 1B |
| *Htr1d* | 15552 | 6.187 | 3.223 | 0.941 | UP | 5-hydroxytryptamine receptor 1D |
| *Htr2a* | 15558 | 7.010 | 2.937 | 1.255 | UP | 5-hydroxytryptamine receptor 2A |
| *Igf2* | 16002 | 7.253 | 24.697 | -1.768 | DOWN | insulin-like growth factor 2 |
| *Cd74* | 16149 | 1.340 | 3.037 | -1.180 | DOWN | CD74 antigen |
| *Isl1* | 16392 | 2.137 | 4.047 | -0.921 | DOWN | ISL1 transcription factor, LIM/homeodomain |
| *Itga5* | 16402 | 3.127 | 1.687 | 0.890 | UP | integrin alpha 5 |
| *Itih3* | 16426 | 6.297 | 14.737 | -1.227 | DOWN | inter-alpha trypsin inhibitor, heavy chain 3 |
| *Itpr1* | 16438 | 65.353 | 38.480 | 0.764 | UP | inositol 1,4,5-trisphosphate receptor 1 |
| *Kcnab3* | 16499 | 9.283 | 14.990 | -0.691 | DOWN | potassium voltage-gated channel, shaker-related subfamily, beta member 3 |
| *Kcnb1* | 16500 | 23.873 | 15.550 | 0.618 | UP | potassium voltage gated channel, Shab-related subfamily, member 1 |
| *Kif13b* | 16554 | 5.797 | 9.790 | -0.756 | DOWN | kinesin family member 13B |
| *Lama5* | 16776 | 1.293 | 2.193 | -0.762 | DOWN | laminin, alpha 5 |
| *Rpsa* | 16785 | 168.050 | 254.633 | -0.600 | DOWN | ribosomal protein SA |
| *Lcn2* | 16819 | 2.223 | 0.810 | 1.457 | UP | lipocalin 2 |
| *Lig1* | 16881 | 2.583 | 4.340 | -0.748 | DOWN | ligase I, DNA, ATP-dependent |
| *Lipg* | 16891 | 1.923 | 0.867 | 1.150 | UP | lipase, endothelial |
| *Llgl1* | 16897 | 14.403 | 22.247 | -0.627 | DOWN | lethal giant larvae homolog 1 |
| *Lpl* | 16956 | 10.677 | 5.297 | 1.011 | UP | lipoprotein lipase |
| *Ltc4s* | 17001 | 4.413 | 9.153 | -1.052 | DOWN | leukotriene C4 synthase |
| *Tm4sf1* | 17112 | 4.380 | 7.053 | -0.687 | DOWN | transmembrane 4 superfamily member 1 |
| *Mafk* | 17135 | 4.160 | 6.473 | -0.638 | DOWN | v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K |
| *Mmp2* | 17390 | 0.770 | 2.443 | -1.666 | DOWN | matrix metallopeptidase 2 |
| *Ndst2* | 17423 | 1.653 | 2.737 | -0.727 | DOWN | N-deacetylase/N-sulfotransferase 2 |
| *Mobp* | 17433 | 138.743 | 297.100 | -1.099 | DOWN | myelin-associated oligodendrocytic basic protein |
| *Mog* | 17441 | 32.690 | 79.867 | -1.289 | DOWN | myelin oligodendrocyte glycoprotein |
| *Mt1* | 17748 | 202.007 | 323.483 | -0.679 | DOWN | metallothionein 1 |
| *Mt2* | 17750 | 87.023 | 143.570 | -0.722 | DOWN | metallothionein 2 |
| *Myh6* | 17888 | 0.950 | 2.000 | -1.074 | DOWN | myosin, heavy polypeptide 6, cardiac muscle, alpha |
| *Ngfr* | 18053 | 3.310 | 10.827 | -1.710 | DOWN | nerve growth factor receptor |
| *Nkx2-2* | 18088 | 2.387 | 4.200 | -0.815 | DOWN | NK2 homeobox 2 |
| *Cldn11* | 18417 | 79.517 | 205.120 | -1.367 | DOWN | claudin 11 |
| *Pcsk6* | 18553 | 5.747 | 8.840 | -0.621 | DOWN | proprotein convertase subtilisin/kexin type 6 |
| *Padi2* | 18600 | 5.503 | 11.927 | -1.116 | DOWN | peptidyl arginine deiminase, type II |
| *Enpp2* | 18606 | 38.660 | 247.310 | -2.677 | DOWN | ectonucleotide pyrophosphatase/phosphodiesterase 2 |
| *Piga* | 18700 | 2.227 | 3.367 | -0.596 | DOWN | phosphatidylinositol glycan anchor biosynthesis, class A |
| *Plp1* | 18823 | 411.547 | 923.057 | -1.165 | DOWN | proteolipid protein 1 |
| *Pltp* | 18830 | 33.077 | 53.807 | -0.702 | DOWN | phospholipid transfer protein |
| *Pmp22* | 18858 | 6.847 | 13.160 | -0.943 | DOWN | peripheral myelin protein 22 |
| *Sept4* | 18952 | 86.487 | 178.570 | -1.046 | DOWN | septin 4 |
| *Ppfibp2* | 19024 | 2.070 | 4.603 | -1.153 | DOWN | PTPRF interacting protein, binding protein 2 |
| *Sypl* | 19027 | 6.640 | 10.273 | -0.630 | DOWN | synaptophysin-like protein |
| *Prox1* | 19130 | 1.530 | 3.080 | -1.009 | DOWN | prospero homeobox 1 |
| *Klk6* | 19144 | 1.633 | 11.497 | -2.815 | DOWN | kallikrein related-peptidase 6 |
| *Ptrf* | 19285 | 4.357 | 7.097 | -0.704 | DOWN | polymerase I and transcript release factor |
| *Pvalb* | 19293 | 25.733 | 79.790 | -1.633 | DOWN | parvalbumin |
| *Rasgrp2* | 19395 | 51.917 | 32.667 | 0.668 | UP | RAS, guanyl releasing protein 2 |
| *Rasgrp1* | 19419 | 117.427 | 76.907 | 0.611 | UP | RAS guanyl releasing protein 1 |
| *Rbp4* | 19662 | 11.253 | 6.157 | 0.870 | UP | retinol binding protein 4, plasma |
| *Rdh5* | 19682 | 1.070 | 10.583 | -3.306 | DOWN | retinol dehydrogenase 5 |
| *Reln* | 19699 | 7.667 | 4.357 | 0.815 | UP | reelin |
| *Rom1* | 19881 | 2.573 | 4.147 | -0.688 | DOWN | rod outer segment membrane protein 1 |
| *Rpl10a* | 19896 | 4.260 | 8.887 | -1.061 | DOWN | ribosomal protein L10A |
| *Rps29* | 20090 | 21.917 | 34.580 | -0.658 | DOWN | ribosomal protein S29 |
| *Scx* | 20289 | 1.440 | 2.340 | -0.700 | DOWN | scleraxis |
| *Ccl17* | 20295 | 0.480 | 2.037 | -2.085 | DOWN | chemokine ligand 17 |
| *Selenbp1* | 20341 | 3.583 | 5.520 | -0.623 | DOWN | selenium binding protein 1 |
| *Sema4d* | 20354 | 14.873 | 23.467 | -0.658 | DOWN | sema domain, immunoglobulin domain , transmembrane domain and short cytoplasmic domain, 4D |
| *Sorbs3* | 20410 | 7.837 | 16.570 | -1.080 | DOWN | sorbin and SH3 domain containing 3 |
| *Shd* | 20420 | 8.317 | 13.170 | -0.663 | DOWN | src homology 2 domain-containing transforming protein D |
| *Shmt1* | 20425 | 1.137 | 2.883 | -1.343 | DOWN | serine hydroxymethyltransferase 1 |
| *Slc12a2* | 20496 | 10.320 | 19.073 | -0.886 | DOWN | solute carrier family 12, member 2 |
| *Slc16a1* | 20501 | 5.503 | 8.383 | -0.607 | DOWN | solute carrier family 16, member 1 |
| *Slc4a2* | 20535 | 8.697 | 21.937 | -1.335 | DOWN | solute carrier family 4, member 2 |
| *Slfn2* | 20556 | 1.430 | 0.813 | 0.814 | UP | schlafen 2 |
| *Sncg* | 20618 | 3.107 | 8.920 | -1.522 | DOWN | synuclein, gamma |
| *Sox10* | 20665 | 19.040 | 41.563 | -1.126 | DOWN | SRY-box 10 |
| *Sox13* | 20668 | 2.510 | 4.177 | -0.735 | DOWN | SRY-box 13 |
| *Sox9* | 20682 | 4.963 | 7.890 | -0.669 | DOWN | SRY-box 9 |
| *Sp100* | 20684 | 1.590 | 0.977 | 0.703 | UP | nuclear antigen Sp100 |
| *Spint2* | 20733 | 26.313 | 48.413 | -0.880 | DOWN | serine protease inhibitor, Kunitz type 2 |
| *Tcf15* | 21407 | 1.063 | 1.603 | -0.592 | DOWN | transcription factor 15 |
| *Tcn2* | 21452 | 7.580 | 12.680 | -0.742 | DOWN | transcobalamin 2 |
| *Tnfaip6* | 21930 | 2.813 | 6.810 | -1.275 | DOWN | tumor necrosis factor alpha induced protein 6 |
| *Tnnt1* | 21955 | 0.723 | 3.540 | -2.291 | DOWN | troponin T1, skeletal, slow |
| *Trex1* | 22040 | 3.290 | 5.063 | -0.622 | DOWN | three prime repair exonuclease 1 |
| *Trf* | 22041 | 100.177 | 222.150 | -1.149 | DOWN | transferrin |
| *Trip6* | 22051 | 1.543 | 2.410 | -0.643 | DOWN | thyroid hormone receptor interactor 6 |
| *Rsph1* | 22092 | 2.777 | 13.957 | -2.330 | DOWN | radial spoke head 1 homolog |
| *Tuba1c* | 22146 | 0.720 | 34.923 | -5.600 | DOWN | tubulin, alpha 1C |
| *Uba52* | 22186 | 77.577 | 164.887 | -1.088 | DOWN | ubiquitin A-52 residue ribosomal protein fusion product 1 |
| *Ugt8a* | 22239 | 11.000 | 23.700 | -1.107 | DOWN | UDP galactosyltransferase 8A |
| *Vamp8* | 22320 | 4.957 | 9.757 | -0.977 | DOWN | vesicle-associated membrane protein 8 |
| *Vim* | 22352 | 12.053 | 18.663 | -0.631 | DOWN | vimentin |
| *Wnt10a* | 22409 | 1.243 | 0.730 | 0.768 | UP | wingless-type MMTV integration site family, member 10A |
| *Zbtb7b* | 22724 | 3.917 | 6.797 | -0.795 | DOWN | zinc finger and BTB domain containing 7B |
| *Zfp85* | 22746 | 0.877 | 1.377 | -0.651 | DOWN | zinc finger protein 85 |
| *Aloxe3* | 23801 | 2.643 | 4.000 | -0.598 | DOWN | arachidonate lipoxygenase 3 |
| *Car14* | 23831 | 3.163 | 11.980 | -1.921 | DOWN | carbonic anhydrase 14 |
| *Tiam2* | 24001 | 28.113 | 18.697 | 0.588 | UP | T cell lymphoma invasion and metastasis 2 |
| *Ldb3* | 24131 | 2.567 | 4.030 | -0.651 | DOWN | LIM domain binding 3 |
| *Esrrg* | 26381 | 3.940 | 6.463 | -0.714 | DOWN | estrogen-related receptor gamma |
| *Homer1* | 26556 | 31.277 | 18.440 | 0.762 | UP | homer scaffolding protein 1 |
| *Micall1* | 27008 | 9.747 | 16.510 | -0.760 | DOWN | microtubule associated monooxygenase, calponin and LIM domain containing -like 1 |
| *Sgsh* | 27029 | 1.657 | 2.530 | -0.611 | DOWN | N-sulfoglucosamine sulfohydrolase |
| *Sh3d19* | 27059 | 3.427 | 5.743 | -0.745 | DOWN | SH3 domain protein D19 |
| *Dok3* | 27261 | 2.320 | 1.373 | 0.756 | UP | docking protein 3 |
| *Pdk4* | 27273 | 2.233 | 5.803 | -1.378 | DOWN | pyruvate dehydrogenase kinase, isoenzyme 4 |
| *Plekhb1* | 27276 | 129.350 | 277.710 | -1.102 | DOWN | pleckstrin homology domain containing, family B member 1 |
| *Npas3* | 27386 | 1.653 | 2.567 | -0.635 | DOWN | neuronal PAS domain protein 3 |
| *1700088E04Rik* | 27660 | 2.227 | 5.290 | -1.248 | DOWN | RIKEN cDNA 1700088E04 gene |
| *Trim36* | 28105 | 1.360 | 2.687 | -0.982 | DOWN | tripartite motif-containing 36 |
| *Slc22a4* | 30805 | 2.587 | 4.123 | -0.673 | DOWN | solute carrier family 22, member 4 |
| *Olig2* | 50913 | 16.660 | 26.963 | -0.695 | DOWN | oligodendrocyte transcription factor 2 |
| *Rcn3* | 52377 | 2.677 | 4.407 | -0.719 | DOWN | reticulocalbin 3, EF-hand calcium binding domain |
| *Rps28* | 54127 | 165.950 | 254.180 | -0.615 | DOWN | ribosomal protein S28 |
| *Rpl36* | 54217 | 245.713 | 382.010 | -0.637 | DOWN | ribosomal protein L36 |
| *Elovl1* | 54325 | 8.977 | 18.397 | -1.035 | DOWN | elongation of very long chain fatty acids -like 1 |
| *Ctnnal1* | 54366 | 2.753 | 5.050 | -0.875 | DOWN | catenin , alpha-like 1 |
| *Cpq* | 54381 | 3.763 | 6.370 | -0.759 | DOWN | carboxypeptidase Q |
| *Calcrl* | 54598 | 1.173 | 2.033 | -0.793 | DOWN | calcitonin receptor-like |
| *Foxo4* | 54601 | 5.803 | 8.773 | -0.596 | DOWN | forkhead box O4 |
| *Tbc1d8* | 54610 | 12.990 | 8.293 | 0.647 | UP | TBC1 domain family, member 8 |
| *Hes6* | 55927 | 8.543 | 13.203 | -0.628 | DOWN | hairy and enhancer of split 6 |
| *Gbp3* | 55932 | 2.460 | 1.363 | 0.852 | UP | guanylate binding protein 3 |
| *Heyl* | 56198 | 1.103 | 1.890 | -0.777 | DOWN | hairy/enhancer-of-split related with YRPW motif-like |
| *Rhog* | 56212 | 20.040 | 40.800 | -1.026 | DOWN | ras homolog family member G |
| *Gkap1* | 56278 | 9.893 | 14.870 | -0.588 | DOWN | G kinase anchoring protein 1 |
| *Mycbp* | 56309 | 2.550 | 3.870 | -0.602 | DOWN | MYC binding protein |
| *Amotl2* | 56332 | 5.913 | 9.190 | -0.636 | DOWN | angiomotin-like 2 |
| *Kcnip3* | 56461 | 37.977 | 24.203 | 0.650 | UP | Kv channel interacting protein 3, calsenilin |
| *Rbms2* | 56516 | 2.187 | 3.327 | -0.605 | DOWN | RNA binding motif, single stranded interacting protein 2 |
| *Litaf* | 56722 | 7.440 | 15.960 | -1.101 | DOWN | LPS-induced TN factor |
| *Hacl1* | 56794 | 1.330 | 2.333 | -0.811 | DOWN | 2-hydroxyacyl-CoA lyase 1 |
| *Rps27* | 57294 | 353.790 | 530.720 | -0.585 | DOWN | ribosomal protein S27 |
| *Dnajc4* | 57431 | 2.093 | 4.287 | -1.034 | DOWN | DnaJ heat shock protein family member C4 |
| *Sall1* | 58198 | 4.233 | 9.463 | -1.161 | DOWN | sal-like 1 |
| *Dusp10* | 63953 | 1.407 | 3.197 | -1.184 | DOWN | dual specificity phosphatase 10 |
| *Sirt2* | 64383 | 82.680 | 124.570 | -0.591 | DOWN | sirtuin 2 |
| *Sostdc1* | 66042 | 1.363 | 8.700 | -2.674 | DOWN | sclerostin domain containing 1 |
| *Gng11* | 66066 | 9.420 | 18.523 | -0.976 | DOWN | guanine nucleotide binding protein , gamma 11 |
| *Josd2* | 66124 | 25.887 | 43.400 | -0.745 | DOWN | Josephin domain containing 2 |
| *Fbxo36* | 66153 | 2.533 | 4.880 | -0.946 | DOWN | F-box protein 36 |
| *Nudt14* | 66174 | 4.673 | 7.167 | -0.617 | DOWN | nudix -type motif 14 |
| *Serpinb1a* | 66222 | 3.353 | 7.613 | -1.183 | DOWN | serine peptidase inhibitor, clade B, member 1a |
| *Adamtsl5* | 66548 | 1.547 | 1.023 | 0.596 | UP | ADAMTS-like 5 |
| *Trim13* | 66597 | 3.953 | 6.160 | -0.640 | DOWN | tripartite motif-containing 13 |
| *Mcm8* | 66634 | 2.193 | 1.020 | 1.105 | UP | minichromosome maintenance 8 homologous recombination repair factor |
| *Ormdl2* | 66844 | 1.870 | 2.837 | -0.601 | DOWN | ORM1-like 2 |
| *1700010I14Rik* | 66931 | 1.063 | 1.667 | -0.648 | DOWN | RIKEN cDNA 1700010I14 gene |
| *Trim59* | 66949 | 3.720 | 6.713 | -0.852 | DOWN | tripartite motif-containing 59 |
| *Gatm* | 67092 | 26.170 | 49.733 | -0.926 | DOWN | glycine amidinotransferase |
| *D16Ertd472e* | 67102 | 1.193 | 2.290 | -0.940 | DOWN | DNA segment, Chr 16, ERATO Doi 472, expressed |
| *Nkain1* | 67149 | 22.570 | 35.030 | -0.634 | DOWN | Na+/K+ transporting ATPase interacting 1 |
| *Rpl37* | 67281 | 130.147 | 196.837 | -0.597 | DOWN | ribosomal protein L37 |
| *1700047M11Rik* | 67330 | 5.217 | 10.067 | -0.948 | DOWN | RIKEN cDNA 1700047M11 gene |
| *4930404I05Rik* | 67394 | 1.500 | 0.920 | 0.705 | UP | RIKEN cDNA 4930404I05 gene |
| *Ankrd33b* | 67434 | 11.320 | 6.303 | 0.845 | UP | ankyrin repeat domain 33B |
| *Frmd8* | 67457 | 6.947 | 13.257 | -0.932 | DOWN | FERM domain containing 8 |
| *Nudt7* | 67528 | 2.277 | 4.150 | -0.866 | DOWN | nudix -type motif 7 |
| *Dusp6* | 67603 | 18.087 | 11.917 | 0.602 | UP | dual specificity phosphatase 6 |
| *Rpl38* | 67671 | 252.573 | 388.797 | -0.622 | DOWN | ribosomal protein L38 |
| *Pllp* | 67801 | 19.440 | 43.470 | -1.161 | DOWN | plasma membrane proteolipid |
| *Nmb* | 68039 | 1.703 | 4.393 | -1.367 | DOWN | neuromedin B |
| *Wls* | 68151 | 9.623 | 14.530 | -0.594 | DOWN | wntless homolog |
| *Cgnl1* | 68178 | 2.950 | 4.877 | -0.725 | DOWN | cingulin-like 1 |
| *Gstm7* | 68312 | 9.573 | 20.640 | -1.108 | DOWN | glutathione S-transferase, mu 7 |
| *Dpm3* | 68563 | 20.860 | 33.493 | -0.683 | DOWN | dolichyl-phosphate mannosyltransferase polypeptide 3 |
| *Anln* | 68743 | 5.110 | 12.380 | -1.277 | DOWN | anillin, actin binding protein |
| *Rreb1* | 68750 | 7.353 | 11.830 | -0.686 | DOWN | ras responsive element binding protein 1 |
| *1110038B12Rik* | 68763 | 1.857 | 3.483 | -0.908 | DOWN | RIKEN cDNA 1110038B12 gene |
| *Dock5* | 68813 | 0.890 | 1.957 | -1.137 | DOWN | dedicator of cytokinesis 5 |
| *Lppos* | 68841 | 0.943 | 1.707 | -0.855 | DOWN | LIM domain containing preferred translocation partner in lipoma, opposite strand |
| *Smim1* | 68859 | 1.743 | 4.230 | -1.279 | DOWN | small integral membrane protein 1 |
| *Rnf122* | 68867 | 1.153 | 1.963 | -0.767 | DOWN | ring finger protein 122 |
| *Gkn3* | 68888 | 4.860 | 2.517 | 0.949 | UP | gastrokine 3 |
| *Dnaic1* | 68922 | 1.057 | 1.980 | -0.906 | DOWN | dynein, axonemal, intermediate chain 1 |
| *1810010H24Rik* | 69066 | 1.277 | 2.230 | -0.805 | DOWN | RIKEN cDNA 1810010H24 gene |
| *Sat2* | 69215 | 2.987 | 5.503 | -0.882 | DOWN | spermidine/spermine N1-acetyl transferase 2 |
| *Rfc3* | 69263 | 3.473 | 5.850 | -0.752 | DOWN | replication factor C 3 |
| *Dnajc17* | 69408 | 9.113 | 13.770 | -0.595 | DOWN | DnaJ heat shock protein family member C17 |
| *2310015A10Rik* | 69548 | 1.123 | 2.323 | -1.048 | DOWN | RIKEN cDNA 2310015A10 gene |
| *2310022B05Rik* | 69551 | 25.493 | 45.557 | -0.838 | DOWN | RIKEN cDNA 2310022B05 gene |
| *Gpx8* | 69590 | 1.460 | 5.253 | -1.847 | DOWN | glutathione peroxidase 8 |
| *Cd164l2* | 69655 | 2.637 | 1.657 | 0.670 | UP | CD164 sialomucin-like 2 |
| *Mif4gd* | 69674 | 6.863 | 13.027 | -0.924 | DOWN | MIF4G domain containing |
| *Thap3* | 69876 | 11.107 | 17.423 | -0.650 | DOWN | THAP domain containing, apoptosis associated protein 3 |
| *Apitd1* | 69928 | 2.980 | 5.393 | -0.856 | DOWN | apoptosis-inducing, TAF9-like domain 1 |
| *Nt5dc2* | 70021 | 2.020 | 3.140 | -0.636 | DOWN | 5'-nucleotidase domain containing 2 |
| *Cmtm8* | 70031 | 0.957 | 1.937 | -1.017 | DOWN | CKLF-like MARVEL transmembrane domain containing 8 |
| *Cyp4f16* | 70101 | 0.923 | 2.103 | -1.188 | DOWN | cytochrome P450, family 4, subfamily f, polypeptide 16 |
| *Megf10* | 70417 | 2.640 | 4.637 | -0.813 | DOWN | multiple EGF-like-domains 10 |
| *Tspan15* | 70423 | 6.023 | 10.347 | -0.781 | DOWN | tetraspanin 15 |
| *Eef2kmt* | 70511 | 1.297 | 2.193 | -0.758 | DOWN | eukaryotic elongation factor 2 lysine methyltransferase |
| *Tmem144* | 70652 | 2.787 | 4.447 | -0.674 | DOWN | transmembrane protein 144 |
| *6330409D20Rik* | 70730 | 0.947 | 1.767 | -0.900 | DOWN | RIKEN cDNA 6330409D20 gene |
| *Tspan2* | 70747 | 27.143 | 53.890 | -0.989 | DOWN | tetraspanin 2 |
| *Ggnbp1* | 70772 | 1.467 | 2.637 | -0.846 | DOWN | gametogenetin binding protein 1 |
| *D7Ertd443e* | 71007 | 1.400 | 2.197 | -0.650 | DOWN | DNA segment, Chr 7, ERATO Doi 443, expressed |
| *Foxn3* | 71375 | 3.757 | 5.837 | -0.636 | DOWN | forkhead box N3 |
| *Snx20* | 71607 | 0.857 | 1.460 | -0.769 | DOWN | sorting nexin 20 |
| *Rarres2* | 71660 | 3.820 | 7.063 | -0.887 | DOWN | retinoic acid receptor responder 2 |
| *Etnppl* | 71760 | 4.203 | 6.427 | -0.613 | DOWN | ethanolamine phosphate phospholyase |
| *Haus5* | 71909 | 1.633 | 2.590 | -0.665 | DOWN | HAUS augmin-like complex, subunit 5 |
| *Rnf135* | 71956 | 1.373 | 2.857 | -1.057 | DOWN | ring finger protein 135 |
| *Myh14* | 71960 | 11.300 | 18.250 | -0.692 | DOWN | myosin, heavy polypeptide 14 |
| *Nkd2* | 72293 | 0.830 | 1.293 | -0.640 | DOWN | naked cuticle 2 homolog |
| *Ccdc74a* | 72315 | 2.037 | 3.287 | -0.690 | DOWN | coiled-coil domain containing 74A |
| *Pdia5* | 72599 | 3.270 | 2.150 | 0.605 | UP | protein disulfide isomerase associated 5 |
| *Rspo3* | 72780 | 3.147 | 1.683 | 0.903 | UP | R-spondin 3 |
| *Zbtb8a* | 73680 | 2.520 | 1.603 | 0.652 | UP | zinc finger and BTB domain containing 8a |
| *1110017D15Rik* | 73721 | 1.833 | 7.277 | -1.989 | DOWN | RIKEN cDNA 1110017D15 gene |
| *Fam161a* | 73873 | 1.183 | 2.300 | -0.959 | DOWN | family with sequence similarity 161, member A |
| *Hapln2* | 73940 | 8.720 | 25.540 | -1.550 | DOWN | hyaluronan and proteoglycan link protein 2 |
| *Palm3* | 74337 | 1.540 | 2.347 | -0.608 | DOWN | paralemmin 3 |
| *Elovl7* | 74559 | 2.373 | 5.550 | -1.226 | DOWN | ELOVL family member 7, elongation of long chain fatty acids |
| *Hhatl* | 74770 | 2.463 | 4.683 | -0.927 | DOWN | hedgehog acyltransferase-like |
| *Efcab10* | 75040 | 1.643 | 0.923 | 0.832 | UP | EF-hand calcium binding domain 10 |
| *Rasd2* | 75141 | 145.327 | 86.377 | 0.751 | UP | RASD family, member 2 |
| *4930538K18Rik* | 75180 | 0.787 | 1.407 | -0.838 | DOWN | RIKEN cDNA 4930538K18 gene |
| *Prkd3* | 75292 | 2.557 | 4.243 | -0.731 | DOWN | protein kinase D3 |
| *Cklf* | 75458 | 0.620 | 1.897 | -1.613 | DOWN | chemokine-like factor |
| *Dcaf17* | 75763 | 2.443 | 1.380 | 0.824 | UP | DDB1 and CUL4 associated factor 17 |
| *Cers2* | 76893 | 23.537 | 45.740 | -0.959 | DOWN | ceramide synthase 2 |
| *Bcas1* | 76960 | 41.000 | 89.380 | -1.124 | DOWN | breast carcinoma amplified sequence 1 |
| *Zfp955a* | 77652 | 1.847 | 2.883 | -0.643 | DOWN | zinc finger protein 955A |
| *Ermn* | 77767 | 12.360 | 23.213 | -0.909 | DOWN | ermin, ERM-like protein |
| *Fam53b* | 77938 | 5.477 | 8.420 | -0.621 | DOWN | family with sequence similarity 53, member B |
| *Rdh12* | 77974 | 0.773 | 1.350 | -0.804 | DOWN | retinol dehydrogenase 12 |
| *Spink8* | 78709 | 2.793 | 4.840 | -0.793 | DOWN | serine peptidase inhibitor, Kazal type 8 |
| *Mctp1* | 78771 | 19.037 | 12.597 | 0.596 | UP | multiple C2 domains, transmembrane 1 |
| *Tsc22d4* | 78829 | 18.707 | 30.017 | -0.682 | DOWN | TSC22 domain family, member 4 |
| *Egfl8* | 81701 | 1.043 | 1.620 | -0.635 | DOWN | EGF-like domain 8 |
| *Tfap4* | 83383 | 0.830 | 1.807 | -1.122 | DOWN | transcription factor AP4 |
| *Nedd4l* | 83814 | 33.030 | 21.983 | 0.587 | UP | neural precursor cell expressed, developmentally down-regulated gene 4-like |
| *Jam3* | 83964 | 17.827 | 28.940 | -0.699 | DOWN | junction adhesion molecule 3 |
| *Nat8f3* | 93674 | 3.343 | 1.767 | 0.920 | UP | N-acetyltransferase 8 family member 3 |
| *Nkd1* | 93960 | 3.407 | 5.487 | -0.688 | DOWN | naked cuticle 1 homolog |
| *B3gnt9* | 97440 | 1.380 | 3.823 | -1.470 | DOWN | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 |
| *Eps8l2* | 98845 | 1.207 | 2.910 | -1.270 | DOWN | EPS8-like 2 |
| *Cercam* | 99151 | 3.670 | 7.903 | -1.107 | DOWN | cerebral endothelial cell adhesion molecule |
| *Ldlrap1* | 100017 | 1.343 | 2.673 | -0.993 | DOWN | low density lipoprotein receptor adaptor protein 1 |
| *Pcsk9* | 100102 | 1.633 | 0.810 | 1.012 | UP | proprotein convertase subtilisin/kexin type 9 |
| *Phactr4* | 100169 | 2.037 | 4.020 | -0.981 | DOWN | phosphatase and actin regulator 4 |
| *Plekho2* | 102595 | 2.163 | 3.403 | -0.654 | DOWN | pleckstrin homology domain containing, family O member 2 |
| *Phldb1* | 102693 | 24.007 | 46.840 | -0.964 | DOWN | pleckstrin homology like domain, family B, member 1 |
| *Sept10* | 103080 | 0.953 | 1.767 | -0.890 | DOWN | septin 10 |
| *Itga9* | 104099 | 3.863 | 2.267 | 0.769 | UP | integrin alpha 9 |
| *Meig1* | 104362 | 0.953 | 1.777 | -0.898 | DOWN | meiosis expressed gene 1 |
| *Cdc42ep1* | 104445 | 6.203 | 13.117 | -1.080 | DOWN | CDC42 effector protein 1 |
| *Sptssa* | 104725 | 13.283 | 20.200 | -0.605 | DOWN | serine palmitoyltransferase, small subunit A |
| *Slain1* | 105439 | 22.607 | 40.167 | -0.829 | DOWN | SLAIN motif family, member 1 |
| *Amigo2* | 105827 | 5.523 | 8.567 | -0.633 | DOWN | adhesion molecule with Ig like domain 2 |
| *Macrod1* | 107227 | 9.817 | 17.817 | -0.860 | DOWN | MACRO domain containing 1 |
| *Carns1* | 107239 | 3.217 | 7.443 | -1.210 | DOWN | carnosine synthase 1 |
| *Dio3* | 107585 | 2.043 | 3.427 | -0.746 | DOWN | deiodinase, iodothyronine type III |
| *4930447M23Rik* | 108871 | 3.280 | 1.357 | 1.274 | UP | RIKEN cDNA 4930447M23 gene |
| *Aif1l* | 108897 | 1.737 | 3.157 | -0.862 | DOWN | allograft inflammatory factor 1-like |
| *Fam212b* | 109050 | 23.257 | 14.290 | 0.703 | UP | family with sequence similarity 212, member B |
| *Rarres1* | 109222 | 0.593 | 1.717 | -1.533 | DOWN | retinoic acid receptor responder 1 |
| *Triobp* | 110253 | 3.340 | 5.317 | -0.671 | DOWN | TRIO and F-actin binding protein |
| *Qdpr* | 110391 | 127.657 | 223.400 | -0.807 | DOWN | quinoid dihydropteridine reductase |
| *Kcnq3* | 110862 | 10.503 | 6.197 | 0.761 | UP | potassium voltage-gated channel, subfamily Q, member 3 |
| *Fam57a* | 116972 | 4.830 | 7.830 | -0.697 | DOWN | family with sequence similarity 57, member A |
| *Ttyh2* | 117160 | 10.553 | 26.217 | -1.313 | DOWN | tweety family member 2 |
| *Gjc3* | 118446 | 11.253 | 24.537 | -1.125 | DOWN | gap junction protein, gamma 3 |
| *Gjc2* | 118454 | 11.047 | 25.760 | -1.222 | DOWN | gap junction protein, gamma 2 |
| *Cdhr1* | 170677 | 4.327 | 1.653 | 1.388 | UP | cadherin-related family member 1 |
| *Cyp4f13* | 170716 | 3.690 | 6.247 | -0.759 | DOWN | cytochrome P450, family 4, subfamily f, polypeptide 13 |
| *Trhr2* | 170732 | 3.620 | 2.043 | 0.825 | UP | thyrotropin releasing hormone receptor 2 |
| *Rac3* | 170758 | 5.050 | 8.620 | -0.771 | DOWN | RAS-related C3 botulinum substrate 3 |
| *Hps1* | 192236 | 4.300 | 6.620 | -0.622 | DOWN | Hermansky-Pudlak syndrome 1 |
| *Pld6* | 194908 | 1.633 | 1.060 | 0.624 | UP | phospholipase D family, member 6 |
| *Camkk2* | 207565 | 54.667 | 35.480 | 0.624 | UP | calcium/calmodulin-dependent protein kinase kinase 2, beta |
| *Galnt6* | 207839 | 2.530 | 6.590 | -1.381 | DOWN | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 |
| *Tmem63a* | 208795 | 10.210 | 25.287 | -1.308 | DOWN | transmembrane protein 63a |
| *Dhtkd1* | 209692 | 1.840 | 2.963 | -0.688 | DOWN | dehydrogenase E1 and transketolase domain containing 1 |
| *Slc38a5* | 209837 | 2.260 | 1.420 | 0.670 | UP | solute carrier family 38, member 5 |
| *March11* | 211147 | 3.883 | 2.560 | 0.601 | UP | membrane-associated ring finger 11 |
| *Plekhh1* | 211945 | 5.377 | 12.487 | -1.216 | DOWN | pleckstrin homology domain containing, family H member 1 |
| *Paox* | 212503 | 2.483 | 3.750 | -0.595 | DOWN | polyamine oxidase |
| *Cfap44* | 212517 | 1.067 | 2.047 | -0.940 | DOWN | cilia and flagella associated protein 44 |
| *Pdlim2* | 213019 | 5.913 | 14.550 | -1.299 | DOWN | PDZ and LIM domain 2 |
| *Lgi3* | 213469 | 31.707 | 51.587 | -0.702 | DOWN | leucine-rich repeat LGI family, member 3 |
| *Plekhg1* | 213783 | 1.717 | 3.403 | -0.987 | DOWN | pleckstrin homology domain containing, family G member 1 |
| *Nipal4* | 214112 | 1.327 | 2.600 | -0.971 | DOWN | NIPA-like domain containing 4 |
| *Cnksr3* | 215748 | 1.647 | 2.620 | -0.670 | DOWN | Cnksr family member 3 |
| *Ilvbl* | 216136 | 8.080 | 12.933 | -0.679 | DOWN | ilvB -like |
| *Mfap3* | 216760 | 7.333 | 4.677 | 0.649 | UP | microfibrillar-associated protein 3 |
| *Pacs2* | 217893 | 28.563 | 44.920 | -0.653 | DOWN | phosphofurin acidic cluster sorting protein 2 |
| *Chdh* | 218865 | 0.890 | 2.157 | -1.277 | DOWN | choline dehydrogenase |
| *Nrbp2* | 223649 | 38.707 | 61.377 | -0.665 | DOWN | nuclear receptor binding protein 2 |
| *Pla2g16* | 225845 | 8.770 | 15.827 | -0.852 | DOWN | phospholipase A2, group XVI |
| *Myrf* | 225908 | 10.130 | 25.163 | -1.313 | DOWN | myelin regulatory factor |
| *Opalin* | 226115 | 14.440 | 34.070 | -1.238 | DOWN | oligodendrocytic myelin paranodal and inner loop protein |
| *BC026585* | 226527 | 3.723 | 6.003 | -0.689 | DOWN | cDNA sequence BC026585 |
| *Cdh19* | 227485 | 1.240 | 2.443 | -0.979 | DOWN | cadherin 19, type 2 |
| *Ddx31* | 227674 | 1.420 | 2.147 | -0.596 | DOWN | DEAD/H box polypeptide 31 |
| *Gsn* | 227753 | 25.280 | 65.540 | -1.374 | DOWN | gelsolin |
| *Mavs* | 228607 | 2.377 | 4.117 | -0.793 | DOWN | mitochondrial antiviral signaling protein |
| *Nudt6* | 229228 | 3.623 | 2.287 | 0.664 | UP | nudix -type motif 6 |
| *Spg20* | 229285 | 12.160 | 18.617 | -0.614 | DOWN | spastic paraplegia 20, spartin homolog |
| *Galnt12* | 230145 | 1.507 | 0.910 | 0.727 | UP | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 |
| *Tesk2* | 230661 | 1.417 | 3.110 | -1.134 | DOWN | testis-specific kinase 2 |
| *Tmem125* | 230678 | 4.503 | 10.360 | -1.202 | DOWN | transmembrane protein 125 |
| *Thnsl2* | 232078 | 0.727 | 1.540 | -1.084 | DOWN | threonine synthase-like 2 |
| *Dera* | 232449 | 0.783 | 2.397 | -1.613 | DOWN | deoxyribose-phosphate aldolase |
| *Insc* | 233752 | 1.830 | 3.927 | -1.101 | DOWN | inscuteable homolog |
| *Arhgef10* | 234094 | 8.710 | 15.337 | -0.816 | DOWN | Rho guanine nucleotide exchange factor 10 |
| *C1qtnf5* | 235312 | 9.237 | 19.327 | -1.065 | DOWN | C1q and tumor necrosis factor related protein 5 |
| *Plscr4* | 235527 | 0.800 | 1.280 | -0.678 | DOWN | phospholipid scramblase 4 |
| *Glyctk* | 235582 | 1.983 | 1.250 | 0.666 | UP | glycerate kinase |
| *6430571L13Rik* | 235599 | 1.407 | 2.127 | -0.596 | DOWN | RIKEN cDNA 6430571L13 gene |
| *Stard8* | 236920 | 2.960 | 1.883 | 0.652 | UP | START domain containing 8 |
| *Kcnh5* | 238271 | 1.170 | 0.773 | 0.597 | UP | potassium voltage-gated channel, subfamily H, member 5 |
| *Aard* | 239435 | 0.963 | 1.587 | -0.720 | DOWN | alanine and arginine rich domain containing protein |
| *St18* | 240690 | 0.807 | 1.763 | -1.128 | DOWN | suppression of tumorigenicity 18 |
| *Pnpla7* | 241274 | 3.533 | 6.893 | -0.964 | DOWN | patatin-like phospholipase domain containing 7 |
| *Sspo* | 243369 | 1.070 | 1.937 | -0.856 | DOWN | SCO-spondin |
| *Olfml1* | 244198 | 4.040 | 8.770 | -1.118 | DOWN | olfactomedin-like 1 |
| *Dlgap2* | 244310 | 17.203 | 11.290 | 0.608 | UP | discs, large homolog-associated protein 2 |
| *Vasn* | 246154 | 2.043 | 3.340 | -0.709 | DOWN | vasorin |
| *Dusp15* | 252864 | 8.587 | 14.600 | -0.766 | DOWN | dual specificity phosphatase-like 15 |
| *Plekhg3* | 263406 | 3.030 | 6.730 | -1.151 | DOWN | pleckstrin homology domain containing, family G member 3 |
| *Slc26a11* | 268512 | 1.853 | 3.130 | -0.756 | DOWN | solute carrier family 26, member 11 |
| *Gsg1l* | 269994 | 33.580 | 18.473 | 0.862 | UP | GSG1-like |
| *Magee2* | 272790 | 3.743 | 5.777 | -0.626 | DOWN | melanoma antigen, family E, 2 |
| *Lrrc10b* | 278795 | 79.180 | 40.653 | 0.962 | UP | leucine rich repeat containing 10B |
| *Kif19a* | 286942 | 1.297 | 2.447 | -0.916 | DOWN | kinesin family member 19A |
| *Hist1h4k* | 319160 | 3.647 | 1.727 | 1.079 | UP | histone cluster 1, H4k |
| *Hist2h2aa2* | 319192 | 2.977 | 11.633 | -1.966 | DOWN | histone cluster 2, H2aa2 |
| *Prr18* | 320111 | 8.447 | 24.750 | -1.551 | DOWN | proline rich 18 |
| *Sox2ot* | 320478 | 9.503 | 17.590 | -0.888 | DOWN | SOX2 overlapping transcript |
| *Bhlha9* | 320522 | 0.887 | 1.737 | -0.970 | DOWN | basic helix-loop-helix family, member a9 |
| *Tmem88b* | 320587 | 14.823 | 36.283 | -1.291 | DOWN | transmembrane protein 88B |
| *Enpp6* | 320981 | 2.343 | 5.763 | -1.298 | DOWN | ectonucleotide pyrophosphatase/phosphodiesterase 6 |
| *Slfn5* | 327978 | 1.443 | 0.817 | 0.822 | UP | schlafen 5 |
| *Nostrin* | 329416 | 2.573 | 1.663 | 0.630 | UP | nitric oxide synthase trafficker |
| *Adamts3* | 330119 | 8.303 | 5.383 | 0.625 | UP | a disintegrin-like and metallopeptidase with thrombospondin type 1 motif, 3 |
| *Saxo2* | 330577 | 2.087 | 3.643 | -0.804 | DOWN | stablizer of axonemal microtubules 2 |
| *Mapk15* | 332110 | 0.960 | 2.230 | -1.216 | DOWN | mitogen-activated protein kinase 15 |
| *Nefh* | 380684 | 17.820 | 27.853 | -0.644 | DOWN | neurofilament, heavy polypeptide |
| *Zfp395* | 380912 | 2.503 | 4.143 | -0.727 | DOWN | zinc finger protein 395 |
| *Prob1* | 381148 | 2.070 | 4.133 | -0.998 | DOWN | proline rich basic protein 1 |
| *Xkr8* | 381560 | 1.057 | 1.687 | -0.675 | DOWN | X-linked Kx blood group related 8 |
| *Plpp4* | 381925 | 8.730 | 5.523 | 0.660 | UP | phospholipid phosphatase 4 |
| *Znrf2* | 387524 | 4.867 | 8.383 | -0.785 | DOWN | zinc and ring finger 2 |
| *BC051226* | 407803 | 3.767 | 2.430 | 0.632 | UP | cDNA sequence BC051226 |
| *4930404N11Rik* | 432479 | 1.763 | 3.040 | -0.786 | DOWN | RIKEN cDNA 4930404N11 gene |
| *Npcd* | 504193 | 1.100 | 3.000 | -1.447 | DOWN | neuronal pentraxin chromo domain |
| *Scrt2* | 545474 | 14.303 | 9.400 | 0.606 | UP | scratch family zinc finger 2 |
| *Ccpg1os* | 546143 | 2.417 | 4.460 | -0.884 | DOWN | cell cycle progression 1, opposite strand |
| *Gpr52* | 620246 | 20.913 | 11.847 | 0.820 | UP | G protein-coupled receptor 52 |
| *Dok6* | 623279 | 2.927 | 1.307 | 1.163 | UP | docking protein 6 |
| *Syndig1l* | 627191 | 81.310 | 48.047 | 0.759 | UP | synapse differentiation inducing 1 like |
| *Smco3* | 654818 | 2.523 | 4.033 | -0.677 | DOWN | single-pass membrane protein with coiled-coil domains 3 |
| *Sec14l5* | 665119 | 4.837 | 11.280 | -1.222 | DOWN | SEC14-like lipid binding 5 |
| *Gm12657* | 667250 | 2.197 | 0.983 | 1.160 | UP | predicted gene 12657 |
| *Kif26a* | 668303 | 1.320 | 2.120 | -0.684 | DOWN | kinesin family member 26A |
| *Rnaset2a* | 100037283 | 20.850 | 38.577 | -0.888 | DOWN | ribonuclease T2A |
| *Gm11744* | 100038570 | 3.250 | 5.537 | -0.769 | DOWN | predicted gene 11744 |
| *Gm13629* | 100038743 | 1.710 | 3.250 | -0.926 | DOWN | predicted gene 13629 |
| *Fancf* | 100040608 | 1.873 | 3.073 | -0.714 | DOWN | Fanconi anemia, complementation group F |
| *9030025P20Rik* | 100041574 | 2.403 | 4.257 | -0.825 | DOWN | RIKEN cDNA 9030025P20 gene |
| *2810410L24Rik* | 100042332 | 3.593 | 5.863 | -0.706 | DOWN | RIKEN cDNA 2810410L24 gene |
| *Gm10584* | 100043682 | 1.297 | 0.620 | 1.064 | UP | predicted gene 10584 |
| *Gm13293* | 100503147 | 1.750 | 4.447 | -1.345 | DOWN | predicted gene 13293 |
| *Fam181a* | 100504156 | 0.730 | 2.337 | -1.678 | DOWN | family with sequence similarity 181, member A |
| *Gm12709* | 100504717 | 1.447 | 2.577 | -0.833 | DOWN | predicted gene 12709 |
| *C230037L18Rik* | 100532730 | 1.050 | 2.640 | -1.330 | DOWN | RIKEN cDNA C230037L18 gene |
| *Ttc39aos1* | 102635290 | 0.817 | 1.313 | -0.685 | DOWN | Ttc39a opposite strand RNA 1 |
| *Gm35612* | 102639259 | 0.563 | 1.090 | -0.952 | DOWN | predicted gene, 35612 |
| *Emc8-1190005i06rik* | 105734727 | 2.417 | 4.010 | -0.731 | DOWN | Emc8-1190005I06Rik readthrough |
| *Cmc4* | 105886298 | 2.977 | 4.613 | -0.632 | DOWN | C-x-C motif containing 4 |

**Table S5. Signaling pathways identified by KEGG function analysis based on DEGs data in Intruder mice versus Control mice.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **KEGG Entry** | **Term** | **Count** | **%(involved genes/total genes)** | **P Value** | **Genes** |
| mmu04978 | Mineral absorption | 5 | 1.142 | 0.012 | *Fxyd2, Mt2, Mt1, Heph, Trf* |
| mmu05205 | Proteoglycans in cancer | 11 | 2.511 | 0.013 | *Wnt10A, Gpc3, Tfap4, Itga5, Erbb3, Gab1, Igf2, Dcn, Cd63, Mmp2, Itpr1* |
| mmu03010 | Ribosome | 9 | 2.055 | 0.014 | *Rpsa, Rps27, Rps28, Rps29, Rpl36, Rpl37, Rpl10A, Rpl38, Uba52* |
| mmu04726 | Serotonergic synapse | 8 | 1.826 | 0.025 | *Htr1B, Gngt2, Htr1A, Cyp2J6, Gng11, Htr1D, Itpr1, Htr2A* |
| mmu04014 | Ras signaling pathway | 11 | 2.511 | 0.028 | *Fgfr2, Pla2G16, Gngt2, Rac3, Efna1, Rasgrp1, Rasgrp2, Gab1, Gng11, Ngfr, Foxo4* |
| mmu04972 | Pancreatic secretion | 6 | 1.370 | 0.067 | *Fxyd2, Chrm3, Slc12A2, Slc4A2, Car2, Itpr1* |
| mmu00565 | Ether lipid metabolism | 4 | 0.913 | 0.070 | *Enpp6, Pla2G16, Ugt8A, Enpp2* |
| mmu04970 | Salivary secretion | 5 | 1.142 | 0.086 | *Fxyd2, Chrm3, Slc12A2, Slc4A2, Itpr1* |
| mmu04640 | Hematopoietic cell lineage | 5 | 1.142 | 0.110 | *Cd9, Itga5, Cd4, Fcgr1, Cd24A* |
| mmu00480 | Glutathione metabolism | 4 | 0.913 | 0.117 | *Gstt1, Gpx8, Gstp1, Gstm7* |
| mmu04540 | Gap junction | 5 | 1.142 | 0.117 | *Drd2, Lpar1, Tuba1C, Itpr1, Htr2A* |
| mmu00590 | Arachidonic acid metabolism | 5 | 1.142 | 0.128 | *Pla2G16, Cyp2J6, Cyp4F13, Gpx8, Ltc4S* |
| mmu05200 | Pathways in cancer | 13 | 2.968 | 0.156 | *Fgfr2, Wnt10A, Ctbp2, Brca2, Fadd, Gng11, Lpar1, Mmp2, Gngt2, Lama5, Rac3, Rasgrp1, Rasgrp2* |
| mmu00980 | Metabolism of xenobiotics by cytochrome P450 | 4 | 0.913 | 0.162 | *Hsd11B1, Gstt1, Gstp1, Gstm7* |
| mmu04080 | Neuroactive ligand-receptor interaction | 10 | 2.283 | 0.168 | *Htr1B, Tspo, Htr1A, Chrm3, Trhr2, Drd2, Calcrl, Lpar1, Htr1D, Htr2A* |
| mmu04015 | Rap1 signaling pathway | 8 | 1.826 | 0.185 | *Fgfr2, Rac3, Efna1, Drd2, Rasgrp2, Ngfr, Lpar1, Prkd3* |
| mmu04971 | Gastric acid secretion | 4 | 0.913 | 0.206 | *Chrm3, Slc4A2, Car2, Itpr1* |
| mmu00260 | Glycine, serine and threonine metabolism | 3 | 0.685 | 0.216 | *Shmt1, Chdh, Gatm* |
| mmu04725 | Cholinergic synapse | 5 | 1.142 | 0.232 | *Gngt2, Kcnq3, Chrm3, Gng11, Itpr1* |
| mmu04260 | Cardiac muscle contraction | 4 | 0.913 | 0.235 | *Fxyd2, Cox7A1, Cox6A2, Myh6* |
| mmu05100 | Bacterial invasion of epithelial cells | 4 | 0.913 | 0.241 | *Arpc1B, Itga5, Gab1, Rhog* |
| mmu00790 | Folate biosynthesis | 2 | 0.457 | 0.249 | *Ggh, Qdpr* |
| mmu03320 | PPAR signaling pathway | 4 | 0.913 | 0.252 | *Lpl, Apoc3, Dbi, Pltp* |
| mmu04024 | cAMP signaling pathway | 7 | 1.598 | 0.258 | *Fxyd2, Htr1B, Htr1A, Rac3, Drd2, Htr1D, Sox9* |
| mmu05034 | Alcoholism | 7 | 1.598 | 0.277 | *Hist2H2Aa2, Gngt2, Hist1H4K, Gm12657, Drd2, Gng11, Camkk2* |
| mmu04514 | Cell adhesion molecules (CAMs) | 6 | 1.370 | 0.277 | *Itga9, Cdh15, Cd4, H2-T24, Cldn11, Jam3* |
| mmu00330 | Arginine and proline metabolism | 3 | 0.685 | 0.289 | *Gatm, Sat2, Carns1* |
| mmu04512 | ECM-receptor interaction | 4 | 0.913 | 0.300 | *Itga9, Itga5, Lama5, Reln* |
| mmu03460 | Fanconi anemia pathway | 3 | 0.685 | 0.305 | *Apitd1, Brca2, Fancf* |
| mmu00910 | Nitrogen metabolism | 2 | 0.457 | 0.312 | *Car14, Car2* |
| mmu04810 | Regulation of actin cytoskeleton | 7 | 1.598 | 0.323 | *Fgfr2, Itga9, Arpc1B, Chrm3, Rac3, Itga5, Gsn* |
| mmu05204 | Chemical carcinogenesis | 4 | 0.913 | 0.324 | *Hsd11B1, Gstt1, Gstp1, Gstm7* |
| mmu04151 | PI3K-Akt signaling pathway | 10 | 2.283 | 0.355 | *Fgfr2, Itga9, Gngt2, Efna1, Itga5, Lama5, Gng11, Reln, Ngfr, Lpar1* |
| mmu04530 | Tight junction | 5 | 1.142 | 0.358 | *Myh14, Cldn11, Myh6, Jam3, Llgl1* |
| mmu04310 | Wnt signaling pathway | 5 | 1.142 | 0.368 | *Wnt10A, Nkd1, Nkd2, Ctbp2, Rac3* |
| mmu04964 | Proximal tubule bicarbonate reclamation | 2 | 0.457 | 0.384 | *Fxyd2, Car2* |
| mmu03430 | Mismatch repair | 2 | 0.457 | 0.384 | *Rfc3, Lig1* |
| mmu05322 | Systemic lupus erythematosus | 5 | 1.142 | 0.398 | *Hist2H2Aa2, Hist1H4K, Gm12657, C4B, Fcgr1* |
| mmu04144 | Endocytosis | 8 | 1.826 | 0.402 | *Fgfr2, Arpc1B, Erbb3, Capza1, Spg20, Nedd4L, H2-T24, Ldlrap1* |
| mmu00340 | Histidine metabolism | 2 | 0.457 | 0.411 | *Aspa, Carns1* |
| mmu00982 | Drug metabolism - cytochrome P450 | 3 | 0.685 | 0.423 | *Gstt1, Gstp1, Gstm7* |
| mmu00062 | Fatty acid elongation | 2 | 0.457 | 0.436 | *Elovl1, Elovl7* |
| mmu04918 | Thyroid hormone synthesis | 3 | 0.685 | 0.453 | *Fxyd2, Gpx8, Itpr1* |
| mmu04724 | Glutamatergic synapse | 4 | 0.913 | 0.459 | *Gngt2, Gng11, Homer1, Itpr1* |
| mmu04976 | Bile secretion | 3 | 0.685 | 0.460 | *Fxyd2, Slc4A2, Car2* |
| mmu00512 | Mucin type O-Glycan biosynthesis | 2 | 0.457 | 0.461 | *Galnt6, Galnt12* |
| mmu05416 | Viral myocarditis | 3 | 0.685 | 0.516 | *Rac3, H2-T24, Myh6* |
| mmu04612 | Antigen processing and presentation | 3 | 0.685 | 0.536 | *Cd4, H2-T24, Cd74* |
| mmu03030 | DNA replication | 2 | 0.457 | 0.538 | *Rfc3, Lig1* |
| mmu05010 | Alzheimer's disease | 5 | 1.142 | 0.542 | *Lpl, Cox7A1, Cox6A2, Fadd, Itpr1* |
| mmu04146 | Peroxisome | 3 | 0.685 | 0.543 | *Hacl1, Paox, Nudt7* |
| mmu04611 | Platelet activation | 4 | 0.913 | 0.546 | *Vamp8, Rasgrp1, Rasgrp2, Itpr1* |
| mmu04666 | Fc gamma R-mediated phagocytosis | 3 | 0.685 | 0.549 | *Arpc1B, Gsn, Fcgr1* |
| mmu00250 | Alanine, aspartate and glutamate metabolism | 2 | 0.457 | 0.558 | *Aspa, Adssl1* |
| mmu04728 | Dopaminergic synapse | 4 | 0.913 | 0.562 | *Gngt2, Drd2, Gng11, Itpr1* |
| mmu04020 | Calcium signaling pathway | 5 | 1.142 | 0.562 | *Chrm3, Trhr2, Erbb3, Itpr1, Htr2A* |
| mmu04727 | GABAergic synapse | 3 | 0.685 | 0.569 | *Slc38A5, Gngt2, Gng11* |
| mmu05203 | Viral carcinogenesis | 6 | 1.370 | 0.569 | *Egr3, Egr2, Hist1H4K, Sp100, Gsn, H2-T24* |
| mmu04960 | Aldosterone-regulated sodium reabsorption | 2 | 0.457 | 0.586 | *Fxyd2, Nedd4L* |
| mmu00860 | Porphyrin and chlorophyll metabolism | 2 | 0.457 | 0.595 | *Heph, Cp* |
| mmu04973 | Carbohydrate digestion and absorption | 2 | 0.457 | 0.604 | *Amy1, Fxyd2* |
| mmu00564 | Glycerophospholipid metabolism | 3 | 0.685 | 0.611 | *Pnpla7, Etnppl, Pla2G16* |
| mmu05161 | Hepatitis B | 4 | 0.913 | 0.620 | *Mavs, Egr3, Egr2, Fadd* |
| mmu03420 | Nucleotide excision repair | 2 | 0.457 | 0.621 | *Rfc3, Lig1* |
| mmu04713 | Circadian entrainment | 3 | 0.685 | 0.634 | *Gngt2, Gng11, Itpr1* |
| mmu05012 | Parkinson's disease | 4 | 0.913 | 0.634 | *Cox7A1, Gpr37, Drd2, Cox6A2* |
| mmu04010 | MAPK signaling pathway | 6 | 1.370 | 0.650 | *Fgfr2, Rac3, Rasgrp1, Rasgrp2, Dusp10, Dusp6* |
| mmu00600 | Sphingolipid metabolism | 2 | 0.457 | 0.653 | *Ugt8A, Cers2* |
| mmu04723 | Retrograde endocannabinoid signaling | 3 | 0.685 | 0.661 | *Gngt2, Gng11, Itpr1* |
| mmu04330 | Notch signaling pathway | 2 | 0.457 | 0.661 | *Ctbp2, Dll3* |
| mmu04510 | Focal adhesion | 5 | 1.142 | 0.665 | *Itga9, Rac3, Itga5, Lama5, Reln* |
| mmu00591 | Linoleic acid metabolism | 2 | 0.457 | 0.668 | *Pla2G16, Cyp2J6* |
| mmu05150 | Staphylococcus aureus infection | 2 | 0.457 | 0.668 | *C4B, Fcgr1* |
| mmu05168 | Herpes simplex infection | 5 | 1.142 | 0.668 | *Mavs, Sp100, Fadd, H2-T24, Cd74* |
| mmu05014 | Amyotrophic lateral sclerosis (ALS) | 2 | 0.457 | 0.676 | *Nefh, Ccs* |
| mmu05202 | Transcriptional misregulation in cancer | 4 | 0.913 | 0.706 | *Gm12657, Ngfr, Fcgr1, Runx2* |
| mmu04919 | Thyroid hormone signaling pathway | 3 | 0.685 | 0.710 | *Fxyd2, Dio2, Dio3* |
| mmu00561 | Glycerolipid metabolism | 2 | 0.457 | 0.722 | *Lpl, Lipg* |
| mmu04145 | Phagosome | 4 | 0.913 | 0.735 | *Itga5, H2-T24, Fcgr1, Tuba1C* |
| mmu04670 | Leukocyte transendothelial migration | 3 | 0.685 | 0.745 | *Cldn11, Jam3, Mmp2* |
| mmu04142 | Lysosome | 3 | 0.685 | 0.749 | *Sgsh, Litaf, Cd63* |
| mmu01100 | Metabolic pathways | 26 | 5.936 | 0.753 | *Etnppl, Sgsh, Galnt6, Ndst2, Cyp2J6, Sat2, Ltc4S, Fah, Aspa, Cers2, Galnt12, Piga, Chdh, Shmt1, Amy1, Adssl1, Pla2G16, Gatm, Ugt8A, Qdpr, Cyp4F13, Rdh12, Cox6A2, Hsd11B1, Lipg, Dpm3* |
| mmu04623 | Cytosolic DNA-sensing pathway | 2 | 0.457 | 0.757 | *Mavs, Trex1* |
| mmu05212 | Pancreatic cancer | 2 | 0.457 | 0.762 | *Rac3, Brca2* |
| mmu04750 | Inflammatory mediator regulation of TRP channels | 3 | 0.685 | 0.765 | *Cyp2J6, Itpr1, Htr2A* |
| mmu04360 | Axon guidance | 3 | 0.685 | 0.776 | *Rac3, Efna1, Sema4D* |
| mmu04622 | RIG-I-like receptor signaling pathway | 2 | 0.457 | 0.777 | *Mavs, Fadd* |
| mmu05412 | Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 2 | 0.457 | 0.792 | *Itga9, Itga5* |
| mmu04062 | Chemokine signaling pathway | 4 | 0.913 | 0.805 | *Gngt2, Rasgrp2, Gng11, Ccl17* |
| mmu05133 | Pertussis | 2 | 0.457 | 0.805 | *C4B, Itga5* |
| mmu04550 | Signaling pathways regulating pluripotency of stem cells | 3 | 0.685 | 0.807 | *Fgfr2, Wnt10A, Isl1* |
| mmu05016 | Huntington's disease | 4 | 0.913 | 0.811 | *Cox7A1, Cox6A2, Dnaic1, Itpr1* |
| mmu05132 | Salmonella infection | 2 | 0.457 | 0.822 | *Arpc1B, Rhog* |
| mmu05410 | Hypertrophic cardiomyopathy (HCM) | 2 | 0.457 | 0.826 | *Itga9, Itga5* |
| mmu03018 | RNA degradation | 2 | 0.457 | 0.837 | *Btg2, Ddx6* |
| mmu05414 | Dilated cardiomyopathy | 2 | 0.457 | 0.841 | *Itga9, Itga5* |
| mmu04925 | Aldosterone synthesis and secretion | 2 | 0.457 | 0.851 | *Prkd3, Itpr1* |
| mmu04911 | Insulin secretion | 2 | 0.457 | 0.851 | *Fxyd2, Chrm3* |
| mmu04012 | ErbB signaling pathway | 2 | 0.457 | 0.854 | *Erbb3, Gab1* |
| mmu04912 | GnRH signaling pathway | 2 | 0.457 | 0.857 | *Mmp2, Itpr1* |
| mmu04974 | Protein digestion and absorption | 2 | 0.457 | 0.857 | *Fxyd2, Col9A3* |
| mmu00830 | Retinol metabolism | 2 | 0.457 | 0.860 | *Rdh12, Rdh5* |
| mmu05166 | HTLV-I infection | 5 | 1.142 | 0.861 | *Egr1, Wnt10A, Tspo, Egr2, H2-T24* |
| mmu05032 | Morphine addiction | 2 | 0.457 | 0.872 | *Gngt2, Gng11* |
| mmu04915 | Estrogen signaling pathway | 2 | 0.457 | 0.886 | *Mmp2, Itpr1* |
| mmu05231 | Choline metabolism in cancer | 2 | 0.457 | 0.893 | *Rac3, Slc22A4* |
| mmu04660 | T cell receptor signaling pathway | 2 | 0.457 | 0.900 | *Rasgrp1, Cd4* |
| mmu05152 | Tuberculosis | 3 | 0.685 | 0.900 | *Fadd, Fcgr1, Cd74* |
| mmu05146 | Amoebiasis | 2 | 0.457 | 0.925 | *Lama5, Serpinb1A* |
| mmu04722 | Neurotrophin signaling pathway | 2 | 0.457 | 0.933 | *Gab1, Ngfr* |
| mmu04071 | Sphingolipid signaling pathway | 2 | 0.457 | 0.936 | *Rac3, Cers2* |
| mmu04270 | Vascular smooth muscle contraction | 2 | 0.457 | 0.940 | *Calcrl, Itpr1* |
| mmu04068 | FoxO signaling pathway | 2 | 0.457 | 0.949 | *Homer1, Foxo4* |
| mmu05160 | Hepatitis C | 2 | 0.457 | 0.951 | *Mavs, Cldn11* |
| mmu00190 | Oxidative phosphorylation | 2 | 0.457 | 0.954 | *Cox7A1, Cox6A2* |
| mmu04261 | Adrenergic signaling in cardiomyocytes | 2 | 0.457 | 0.964 | *Fxyd2, Myh6* |
| mmu04390 | Hippo signaling pathway | 2 | 0.457 | 0.965 | *Wnt10A, Llgl1* |
| mmu04932 | Non-alcoholic fatty liver disease (NAFLD) | 2 | 0.457 | 0.970 | *Cox7A1, Cox6A2* |
| mmu04921 | Oxytocin signaling pathway | 2 | 0.457 | 0.970 | *Itpr1, Camkk2* |
| mmu04022 | cGMP-PKG signaling pathway | 2 | 0.457 | 0.978 | *Fxyd2, Itpr1* |
| mmu05206 | MicroRNAs in cancer | 3 | 0.685 | 0.985 | *Itga5, Erbb3, Vim* |
| mmu05169 | Epstein-Barr virus infection | 2 | 0.457 | 0.992 | *Vim, H2-T24* |
| mmu04923 | Regulation of lipolysis in adipocytes | 1 | 0.228 | 1.000 | *Pla2G16* |
| mmu04610 | Complement and coagulation cascades | 1 | 0.228 | 1.000 | *C4B* |
| mmu00630 | Glyoxylate and dicarboxylate metabolism | 1 | 0.228 | 1.000 | *Shmt1* |
| mmu01200 | Carbon metabolism | 1 | 0.228 | 1.000 | *Shmt1* |
| mmu05230 | Central carbon metabolism in cancer | 1 | 0.228 | 1.000 | *Fgfr2* |
| mmu04924 | Renin secretion | 1 | 0.228 | 1.000 | *Itpr1* |
| mmu00534 | Glycosaminoglycan biosynthesis - heparan sulfate / heparin | 1 | 0.228 | 1.000 | *Ndst2* |
| mmu00030 | Pentose phosphate pathway | 1 | 0.228 | 1.000 | *Dera* |
| mmu00563 | Glycosylphosphatidylinositol(GPI)-anchor biosynthesis | 1 | 0.228 | 1.000 | *Piga* |
| mmu04913 | Ovarian steroidogenesis | 1 | 0.228 | 1.000 | *Cyp2J6* |
| mmu05030 | Cocaine addiction | 1 | 0.228 | 1.000 | *Drd2* |
| mmu01130 | Biosynthesis of antibiotics | 1 | 0.228 | 1.000 | *Shmt1* |
| mmu04668 | TNF signaling pathway | 1 | 0.228 | 1.000 | *Fadd* |
| mmu03410 | Base excision repair | 1 | 0.228 | 1.000 | *Lig1* |
| mmu05210 | Colorectal cancer | 1 | 0.228 | 1.000 | *Rac3* |
| mmu05340 | Primary immunodeficiency | 1 | 0.228 | 1.000 | *Cd4* |
| mmu01230 | Biosynthesis of amino acids | 1 | 0.228 | 1.000 | *Shmt1* |
| mmu05219 | Bladder cancer | 1 | 0.228 | 1.000 | *Mmp2* |
| mmu00531 | Glycosaminoglycan degradation | 1 | 0.228 | 1.000 | *Sgsh* |
| mmu04961 | Endocrine and other factor-regulated calcium reabsorption | 1 | 0.228 | 1.000 | *Fxyd2* |
| mmu05020 | Prion diseases | 1 | 0.228 | 1.000 | *Egr1* |
| mmu05211 | Renal cell carcinoma | 1 | 0.228 | 1.000 | *Gab1* |
| mmu00670 | One carbon pool by folate | 1 | 0.228 | 1.000 | *Shmt1* |
| mmu05320 | Autoimmune thyroid disease | 1 | 0.228 | 1.000 | *H2-T24* |
| mmu00500 | Starch and sucrose metabolism | 1 | 0.228 | 1.000 | *Amy1* |
| mmu04130 | SNARE interactions in vesicular transport | 1 | 0.228 | 1.000 | *Vamp8* |
| mmu04066 | HIF-1 signaling pathway | 1 | 0.228 | 1.000 | *Trf* |
| mmu00510 | N-Glycan biosynthesis | 1 | 0.228 | 1.000 | *Dpm3* |
| mmu03440 | Homologous recombination | 1 | 0.228 | 1.000 | *Brca2* |
| mmu00460 | Cyanoamino acid metabolism | 1 | 0.228 | 1.000 | *Shmt1* |
| mmu00230 | Purine metabolism | 1 | 0.228 | 1.000 | *Adssl1* |
| mmu04070 | Phosphatidylinositol signaling system | 1 | 0.228 | 1.000 | *Itpr1* |
| mmu04977 | Vitamin digestion and absorption | 1 | 0.228 | 1.000 | *Tcn2* |
| mmu05145 | Toxoplasmosis | 1 | 0.228 | 1.000 | *Lama5* |
| mmu05162 | Measles | 1 | 0.228 | 1.000 | *Mavs* |
| mmu04950 | Maturity onset diabetes of the young | 1 | 0.228 | 1.000 | *Nkx2-2* |
| mmu04966 | Collecting duct acid secretion | 1 | 0.228 | 1.000 | *Car2* |
| mmu05142 | Chagas disease (American trypanosomiasis) | 1 | 0.228 | 1.000 | *Fadd* |
| mmu04210 | Apoptosi | 1 | 0.228 | 1.000 | *Fadd* |
| mmu04114 | Oocyte meiosis | 1 | 0.228 | 1.000 | *Itpr1* |
| mmu00140 | Steroid hormone biosynthesis | 1 | 0.228 | 1.000 | *Hsd11B1* |
| mmu00350 | Tyrosine metabolism | 1 | 0.228 | 1.000 | *Fah* |
| mmu04730 | Long-term depression | 1 | 0.228 | 1.000 | *Itpr1* |
| mmu04152 | AMPK signaling pathway | 1 | 0.228 | 1.000 | *Camkk2* |
| mmu05222 | Small cell lung cancer | 1 | 0.228 | 1.000 | *Lama5* |
| mmu04060 | Cytokine-cytokine receptor interaction | 1 | 0.228 | 1.000 | *Ngfr* |
| mmu00410 | beta-Alanine metabolism | 1 | 0.228 | 1.000 | *Carns1* |
| mmu04120 | Ubiquitin mediated proteolysis | 1 | 0.228 | 1.000 | *Nedd4L* |
| mmu05330 | Allograft rejection | 1 | 0.228 | 1.000 | *H2-T24* |
| mmu04650 | Natural killer cell mediated cytotoxicity | 1 | 0.228 | 1.000 | *Rac3* |
| mmu05217 | Basal cell carcinoma | 1 | 0.228 | 1.000 | *Wnt10A* |
| mmu04662 | B cell receptor signaling pathway | 1 | 0.228 | 1.000 | *Rac3* |
| mmu05215 | Prostate cancer | 1 | 0.228 | 1.000 | *Fgfr2* |
| mmu04520 | Adherens junction | 1 | 0.228 | 1.000 | *Rac3* |
| mmu04370 | VEGF signaling pathway | 1 | 0.228 | 1.000 | *Rac3* |
| mmu04350 | TGF-beta signaling pathway | 1 | 0.228 | 1.000 | *Dcn* |
| mmu04920 | Adipocytokine signaling pathway | 1 | 0.228 | 1.000 | *Camkk2* |
| mmu04922 | Glucagon signaling pathway | 1 | 0.228 | 1.000 | *Itpr1* |
| mmu05220 | Chronic myeloid leukemia | 1 | 0.228 | 1.000 | *Ctbp2* |
| mmu04620 | Toll-like receptor signaling pathway | 1 | 0.228 | 1.000 | *Fadd* |
| mmu05332 | Graft-versus-host disease | 1 | 0.228 | 1.000 | *H2-T24* |
| mmu04940 | Type I diabetes mellitus | 1 | 0.228 | 1.000 | *H2-T24* |
| mmu05031 | Amphetamine addiction | 1 | 0.228 | 1.000 | *Arc* |
| mmu04621 | NOD-like receptor signaling pathway | 1 | 0.228 | 1.000 | *Trip6* |
| mmu04720 | Long-term potentiation | 1 | 0.228 | 1.000 | *Itpr1* |
| mmu04380 | Osteoclast differentiation | 1 | 0.228 | 1.000 | *Fcgr1* |
| mmu05140 | Leishmaniasis | 1 | 0.228 | 1.000 | *Fcgr1* |
| mmu00592 | alpha-Linolenic acid metabolism | 1 | 0.228 | 1.000 | *Pla2G16* |
| mmu05164 | Influenza A | 1 | 0.228 | 1.000 | *Mavs* |
| mmu04916 | Melanogenesis | 1 | 0.228 | 1.000 | *Wnt10A* |
| mmu04664 | Fc epsilon RI signaling pathway | 1 | 0.228 | 1.000 | *Rac3* |

**Table S6. mRNAs with differential expression over 1.5 folds and their characteristics in Intruder mice versus Observer mice.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Symbol** | **Gene ID** | **Means (Intruder)** | **Means (Observer)** | **log2(Intruder/Observer)** | **Up/Down Regulation** | **Gene Name** |
| *Adm* | 11535 | 0.897 | 3.225 | -1.847 | DOWN | adrenomedullin |
| *Aebp1* | 11568 | 0.930 | 1.565 | -0.751 | DOWN | AE binding protein 1 |
| *Amy1* | 11722 | 5.097 | 8.445 | -0.729 | DOWN | amylase 1, salivary |
| *Birc5* | 11799 | 0.337 | 1.110 | -1.721 | DOWN | baculoviral IAP repeat-containing 5 |
| *Apoc3* | 11814 | 1.830 | 0.975 | 0.908 | UP | apolipoprotein C-III |
| *Bcl2a1b* | 12045 | 0.393 | 1.115 | -1.503 | DOWN | B cell leukemia/lymphoma 2 related protein A1b |
| *Casp6* | 12368 | 1.787 | 0.915 | 0.965 | UP | caspase 6 |
| *Cldn5* | 12741 | 32.910 | 52.240 | -0.667 | DOWN | claudin 5 |
| *Cox7a1* | 12865 | 2.013 | 3.050 | -0.599 | DOWN | cytochrome c oxidase subunit VIIa 1 |
| *Crip1* | 12925 | 4.637 | 7.565 | -0.706 | DOWN | cysteine-rich protein 1 |
| *Drd5* | 13492 | 0.867 | 1.500 | -0.791 | DOWN | dopamine receptor D5 |
| *Foxf2* | 14238 | 1.760 | 2.705 | -0.620 | DOWN | forkhead box F2 |
| *Fli1* | 14247 | 0.627 | 1.530 | -1.288 | DOWN | Friend leukemia integration 1 |
| *Slc6a13* | 14412 | 1.233 | 1.875 | -0.604 | DOWN | solute carrier family 6, member 13 |
| *Gng8* | 14709 | 1.490 | 0.920 | 0.696 | UP | guanine nucleotide binding protein , gamma 8 |
| *Gpx3* | 14778 | 8.067 | 12.460 | -0.627 | DOWN | glutathione peroxidase 3 |
| *Gstm2* | 14863 | 0.977 | 1.535 | -0.652 | DOWN | glutathione S-transferase, mu 2 |
| *Gstm4* | 14865 | 7.697 | 4.665 | 0.722 | UP | glutathione S-transferase, mu 4 |
| *H2-Q4* | 15015 | 4.180 | 2.025 | 1.046 | UP | histocompatibility 2, Q region locus 4 |
| *H2-Q7* | 15018 | 1.740 | 0.590 | 1.560 | UP | histocompatibility 2, Q region locus 7 |
| *H2-T9* | 15051 | 4.927 | 3.185 | 0.629 | UP | histocompatibility 2, T region locus 9 |
| *Hic1* | 15248 | 1.200 | 1.835 | -0.613 | DOWN | hypermethylated in cancer 1 |
| *Hmox1* | 15368 | 2.100 | 3.705 | -0.819 | DOWN | heme oxygenase 1 |
| *Htr6* | 15565 | 4.477 | 2.820 | 0.667 | UP | 5-hydroxytryptamine receptor 6 |
| *Kdr* | 16542 | 3.053 | 6.085 | -0.995 | DOWN | kinase insert domain protein receptor |
| *Sspn* | 16651 | 1.847 | 2.950 | -0.676 | DOWN | sarcospan |
| *Lcn2* | 16819 | 2.223 | 0.275 | 3.015 | UP | lipocalin 2 |
| *Lef1* | 16842 | 0.983 | 1.960 | -0.995 | DOWN | lymphoid enhancer binding factor 1 |
| *Psmb9* | 16912 | 1.743 | 0.680 | 1.358 | UP | proteasome subunit, beta type 9 |
| *Lst1* | 16988 | 3.217 | 0.515 | 2.643 | UP | leukocyte specific transcript 1 |
| *Mab21l1* | 17116 | 0.927 | 1.560 | -0.751 | DOWN | mab-21-like 1 |
| *Smad6* | 17130 | 1.010 | 2.035 | -1.011 | DOWN | SMAD family member 6 |
| *Mdk* | 17242 | 5.420 | 8.610 | -0.668 | DOWN | midkine |
| *Mid1* | 17318 | 1.773 | 4.475 | -1.335 | DOWN | midline 1 |
| *Mmp2* | 17390 | 0.770 | 1.430 | -0.893 | DOWN | matrix metallopeptidase 2 |
| *Mtcp1* | 17763 | 1.417 | 2.255 | -0.671 | DOWN | mature T cell proliferation 1 |
| *Nudt1* | 17766 | 4.977 | 2.725 | 0.869 | UP | nudix -type motif 1 |
| *Nfkb2* | 18034 | 1.457 | 0.910 | 0.679 | UP | nuclear factor of kappa light polypeptide gene enhancer in B cells 2, p49/p100 |
| *Ogg1* | 18294 | 2.890 | 4.865 | -0.751 | DOWN | 8-oxoguanine DNA-glycosylase 1 |
| *Otx1* | 18423 | 0.920 | 1.515 | -0.720 | DOWN | orthodenticle homeobox 1 |
| *P2rx7* | 18439 | 1.913 | 1.145 | 0.741 | UP | purinergic receptor P2X, ligand-gated ion channel, 7 |
| *Pou3f2* | 18992 | 1.397 | 2.230 | -0.675 | DOWN | POU domain, class 3, transcription factor 2 |
| *Ptgds* | 19215 | 159.040 | 350.905 | -1.142 | DOWN | prostaglandin D2 synthase |
| *Ptprcap* | 19265 | 0.387 | 1.050 | -1.441 | DOWN | protein tyrosine phosphatase, receptor type, C polypeptide-associated protein |
| *S100a11* | 20195 | 7.217 | 11.940 | -0.726 | DOWN | S100 calcium binding protein A11 |
| *St6galnac2* | 20446 | 1.720 | 1.145 | 0.587 | UP | ST6 -N-acetylgalactosaminide alpha-2,6-sialyltransferase 2 |
| *Slfn2* | 20556 | 1.430 | 0.625 | 1.194 | UP | schlafen 2 |
| *Sp100* | 20684 | 1.590 | 0.835 | 0.929 | UP | nuclear antigen Sp100 |
| *Tbx1* | 21380 | 1.013 | 1.700 | -0.746 | DOWN | T-box 1 |
| *Tcf15* | 21407 | 1.063 | 1.795 | -0.755 | DOWN | transcription factor 15 |
| *Tead2* | 21677 | 1.297 | 0.700 | 0.889 | UP | TEA domain family member 2 |
| *Tekt1* | 21689 | 1.360 | 0.640 | 1.087 | UP | tektin 1 |
| *Tfpi* | 21788 | 1.073 | 1.625 | -0.598 | DOWN | tissue factor pathway inhibitor |
| *Tgfbr3* | 21814 | 1.337 | 2.020 | -0.596 | DOWN | transforming growth factor, beta receptor III |
| *Tgm2* | 21817 | 4.317 | 2.875 | 0.586 | UP | transglutaminase 2, C polypeptide |
| *Tnfaip6* | 21930 | 2.813 | 4.520 | -0.684 | DOWN | tumor necrosis factor alpha induced protein 6 |
| *Uxt* | 22294 | 2.990 | 1.065 | 1.489 | UP | ubiquitously expressed transcript |
| *Zap70* | 22637 | 0.577 | 1.085 | -0.912 | DOWN | zeta-chain associated protein kinase |
| *Tekt2* | 24084 | 0.650 | 1.350 | -1.054 | DOWN | tektin 2 |
| *Creb3l1* | 26427 | 2.443 | 1.535 | 0.671 | UP | cAMP responsive element binding protein 3-like 1 |
| *Deb1* | 26901 | 21.703 | 13.865 | 0.646 | UP | differentially expressed in B16F101 |
| *Eif2s3y* | 26908 | 14.907 | 8.320 | 0.841 | UP | eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked |
| *Islr* | 26968 | 1.193 | 1.865 | -0.644 | DOWN | immunoglobulin superfamily containing leucine-rich repeat |
| *Cartpt* | 27220 | 4.857 | 7.415 | -0.610 | DOWN | CART prepropeptide |
| *Dok3* | 27261 | 2.320 | 4.215 | -0.861 | DOWN | docking protein 3 |
| *Ifi27* | 52668 | 34.023 | 20.165 | 0.755 | UP | interferon, alpha-inducible protein 27 |
| *Hif3a* | 53417 | 2.090 | 1.375 | 0.604 | UP | hypoxia inducible factor 3, alpha subunit |
| *Ybx2* | 53422 | 3.380 | 2.060 | 0.714 | UP | Y box protein 2 |
| *Hpgds* | 54486 | 1.517 | 1.000 | 0.601 | UP | hematopoietic prostaglandin D synthase |
| *Apbb1ip* | 54519 | 1.230 | 1.885 | -0.616 | DOWN | amyloid beta precursor protein-binding, family B, member 1 interacting protein |
| *Gbp3* | 55932 | 2.460 | 1.395 | 0.818 | UP | guanylate binding protein 3 |
| *Isg20* | 57444 | 0.833 | 1.760 | -1.079 | DOWN | interferon-stimulated protein |
| *Riiad1* | 66353 | 2.667 | 0.410 | 2.701 | UP | regulatory subunit of type II PKA R-subunit domain containing 1 |
| *Nudt8* | 66387 | 7.300 | 4.405 | 0.729 | UP | nudix -type motif 8 |
| *Arrdc4* | 66412 | 2.803 | 4.860 | -0.794 | DOWN | arrestin domain containing 4 |
| *Adamtsl5* | 66548 | 1.547 | 0.875 | 0.822 | UP | ADAMTS-like 5 |
| *4933404O12Rik* | 66752 | 3.770 | 2.215 | 0.767 | UP | RIKEN cDNA 4933404O12 gene |
| *0610009L18Rik* | 66838 | 3.723 | 1.975 | 0.915 | UP | RIKEN cDNA 0610009L18 gene |
| *Trim59* | 66949 | 3.720 | 5.675 | -0.609 | DOWN | tripartite motif-containing 59 |
| *2700046G09Rik* | 67188 | 1.453 | 0.565 | 1.363 | UP | RIKEN cDNA 2700046G09 gene |
| *Zfp329* | 67230 | 1.383 | 2.355 | -0.768 | DOWN | zinc finger protein 329 |
| *Ccdc53* | 67282 | 12.497 | 8.170 | 0.613 | UP | coiled-coil domain containing 53 |
| *5730559C18Rik* | 67313 | 1.683 | 1.095 | 0.620 | UP | RIKEN cDNA 5730559C18 gene |
| *Nudt7* | 67528 | 2.277 | 4.085 | -0.843 | DOWN | nudix -type motif 7 |
| *Eqtn* | 67753 | 2.227 | 1.360 | 0.711 | UP | equatorin, sperm acrosome associated |
| *Rtp4* | 67775 | 2.223 | 1.115 | 0.996 | UP | receptor transporter protein 4 |
| *Fam212a* | 68176 | 1.940 | 1.220 | 0.669 | UP | family with sequence similarity 212, member A |
| *Dusp23* | 68440 | 2.487 | 1.205 | 1.045 | UP | dual specificity phosphatase 23 |
| *Ifitm1* | 68713 | 2.077 | 3.255 | -0.648 | DOWN | interferon induced transmembrane protein 1 |
| *Nat8f5* | 69049 | 1.457 | 0.720 | 1.017 | UP | N-acetyltransferase 8 family member 5 |
| *1810010H24Rik* | 69066 | 1.277 | 2.000 | -0.648 | DOWN | RIKEN cDNA 1810010H24 gene |
| *Plekha4* | 69217 | 1.170 | 1.860 | -0.669 | DOWN | pleckstrin homology domain containing, family A member 4 |
| *Bst2* | 69550 | 6.517 | 2.585 | 1.334 | UP | bone marrow stromal cell antigen 2 |
| *Med30* | 69790 | 12.260 | 18.940 | -0.627 | DOWN | mediator complex subunit 30 |
| *Apitd1* | 69928 | 2.980 | 4.550 | -0.611 | DOWN | apoptosis-inducing, TAF9-like domain 1 |
| *Nt5dc2* | 70021 | 2.020 | 3.515 | -0.799 | DOWN | 5'-nucleotidase domain containing 2 |
| *Ifi35* | 70110 | 2.610 | 1.335 | 0.967 | UP | interferon-induced protein 35 |
| *6330409D20Rik* | 70730 | 0.947 | 1.725 | -0.866 | DOWN | RIKEN cDNA 6330409D20 gene |
| *Arrdc2* | 70807 | 5.060 | 3.315 | 0.610 | UP | arrestin domain containing 2 |
| *Atoh8* | 71093 | 0.857 | 1.375 | -0.683 | DOWN | atonal bHLH transcription factor 8 |
| *Rnf135* | 71956 | 1.373 | 2.370 | -0.787 | DOWN | ring finger protein 135 |
| *Tdrp* | 72148 | 6.847 | 10.960 | -0.679 | DOWN | testis development related protein |
| *Ccdc74a* | 72315 | 2.037 | 1.315 | 0.631 | UP | coiled-coil domain containing 74A |
| *Lypd1* | 72585 | 42.303 | 26.850 | 0.656 | UP | Ly6/Plaur domain containing 1 |
| *3110009E18Rik* | 73103 | 3.120 | 2.030 | 0.620 | UP | RIKEN cDNA 3110009E18 gene |
| *Glipr1* | 73690 | 3.527 | 1.550 | 1.186 | UP | GLI pathogenesis-related 1 |
| *Pi16* | 74116 | 1.913 | 0.695 | 1.461 | UP | peptidase inhibitor 16 |
| *Tmem114* | 74720 | 1.380 | 0.895 | 0.625 | UP | transmembrane protein 114 |
| *4930538K18Rik* | 75180 | 0.787 | 1.520 | -0.950 | DOWN | RIKEN cDNA 4930538K18 gene |
| *Nat8f4* | 75541 | 4.667 | 2.605 | 0.841 | UP | N-acetyltransferase 8 family member 4 |
| *Fggy* | 75578 | 5.237 | 2.155 | 1.281 | UP | FGGY carbohydrate kinase domain containing |
| *2010001A14Rik* | 76516 | 2.967 | 1.780 | 0.737 | UP | RIKEN cDNA 2010001A14 gene |
| *1700109H08Rik* | 77036 | 1.423 | 0.880 | 0.694 | UP | RIKEN cDNA 1700109H08 gene |
| *Notum* | 77583 | 0.963 | 1.710 | -0.828 | DOWN | notum pectinacetylesterase homolog |
| *Rhoj* | 80837 | 1.433 | 0.845 | 0.762 | UP | ras homolog family member J |
| *Nat8f3* | 93674 | 3.343 | 2.145 | 0.640 | UP | N-acetyltransferase 8 family member 3 |
| *Ldlrap1* | 100017 | 1.343 | 2.460 | -0.873 | DOWN | low density lipoprotein receptor adaptor protein 1 |
| *Cyp4v3* | 102294 | 1.650 | 3.020 | -0.872 | DOWN | cytochrome P450, family 4, subfamily v, polypeptide 3 |
| *Itga9* | 104099 | 3.863 | 2.510 | 0.622 | UP | integrin alpha 9 |
| *4930447M23Rik* | 108871 | 3.280 | 1.705 | 0.944 | UP | RIKEN cDNA 4930447M23 gene |
| *Upk1a* | 109637 | 0.953 | 1.440 | -0.595 | DOWN | uroplakin 1A |
| *Cela1* | 109901 | 1.147 | 2.025 | -0.820 | DOWN | chymotrypsin-like elastase family, member 1 |
| *Sugct* | 192136 | 1.620 | 2.450 | -0.597 | DOWN | succinyl-CoA glutarate-CoA transferase |
| *Zbtb12* | 193736 | 3.057 | 1.970 | 0.634 | UP | zinc finger and BTB domain containing 12 |
| *Hspa1a* | 193740 | 6.033 | 10.355 | -0.779 | DOWN | heat shock protein 1A |
| *Pld6* | 194908 | 1.633 | 0.995 | 0.715 | UP | phospholipase D family, member 6 |
| *Mterf1b* | 208595 | 2.227 | 1.420 | 0.649 | UP | mitochondrial transcription termination factor 1b |
| *Gpr139* | 209776 | 1.020 | 2.300 | -1.173 | DOWN | G protein-coupled receptor 139 |
| *Slc38a5* | 209837 | 2.260 | 1.375 | 0.717 | UP | solute carrier family 38, member 5 |
| *Metrnl* | 210029 | 3.590 | 2.115 | 0.763 | UP | meteorin, glial cell differentiation regulator-like |
| *P3h2* | 210530 | 0.443 | 1.225 | -1.466 | DOWN | prolyl 3-hydroxylase 2 |
| *Ccdc114* | 211535 | 1.170 | 1.925 | -0.718 | DOWN | coiled-coil domain containing 114 |
| *Zfp729a* | 212281 | 0.950 | 2.135 | -1.168 | DOWN | zinc finger protein 729a |
| *A430105I19Rik* | 214239 | 1.663 | 1.095 | 0.603 | UP | RIKEN cDNA A430105I19 gene |
| *Syde2* | 214804 | 0.670 | 1.200 | -0.841 | DOWN | synapse defective 1, Rho GTPase, homolog 2 |
| *Stox1* | 216021 | 1.477 | 0.970 | 0.606 | UP | storkhead box 1 |
| *AU041133* | 216177 | 1.173 | 0.635 | 0.886 | UP | expressed sequence AU041133 |
| *Efemp1* | 216616 | 1.343 | 2.265 | -0.754 | DOWN | epidermal growth factor-containing fibulin-like extracellular matrix protein 1 |
| *Chdh* | 218865 | 0.890 | 1.685 | -0.921 | DOWN | choline dehydrogenase |
| *Tfb1m* | 224481 | 3.383 | 2.070 | 0.709 | UP | transcription factor B1, mitochondrial |
| *Lyplal1* | 226791 | 4.430 | 2.905 | 0.609 | UP | lysophospholipase-like 1 |
| *6820408C15Rik* | 228778 | 1.677 | 0.925 | 0.858 | UP | RIKEN cDNA 6820408C15 gene |
| *Nudt6* | 229228 | 3.623 | 2.395 | 0.597 | UP | nudix -type motif 6 |
| *Tmem69* | 230657 | 3.080 | 1.970 | 0.645 | UP | transmembrane protein 69 |
| *Thnsl2* | 232078 | 0.727 | 1.205 | -0.730 | DOWN | threonine synthase-like 2 |
| *Npffr1* | 237362 | 0.927 | 1.610 | -0.797 | DOWN | neuropeptide FF receptor 1 |
| *Zfp366* | 238803 | 1.720 | 3.195 | -0.893 | DOWN | zinc finger protein 366 |
| *Zfp760* | 240034 | 2.770 | 1.530 | 0.856 | UP | zinc finger protein 760 |
| *Bbs12* | 241950 | 1.780 | 1.030 | 0.789 | UP | Bardet-Biedl syndrome 12 |
| *Nfkbid* | 243910 | 1.007 | 1.615 | -0.682 | DOWN | nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, delta |
| *Ccdc113* | 244608 | 2.047 | 1.235 | 0.729 | UP | coiled-coil domain containing 113 |
| *Olfr1344* | 257882 | 0.507 | 1.575 | -1.636 | DOWN | olfactory receptor 1344 |
| *Klk8* | 259277 | 1.463 | 0.920 | 0.670 | UP | kallikrein related-peptidase 8 |
| *Hist1h4n* | 319161 | 0.227 | 1.230 | -2.440 | DOWN | histone cluster 1, H4n |
| *9630013A20Rik* | 319903 | 0.493 | 1.045 | -1.083 | DOWN | RIKEN cDNA 9630013A20 gene |
| *Vwc2* | 319922 | 3.290 | 2.150 | 0.614 | UP | von Willebrand factor C domain containing 2 |
| *Spink10* | 328971 | 1.170 | 0.350 | 1.741 | UP | serine peptidase inhibitor, Kazal type 10 |
| *Mblac1* | 330216 | 3.500 | 2.260 | 0.631 | UP | metallo-beta-lactamase domain containing 1 |
| *Obscn* | 380698 | 1.953 | 0.990 | 0.980 | UP | obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF |
| *Mks1* | 380718 | 2.093 | 1.380 | 0.601 | UP | Meckel syndrome, type 1 |
| *A230065H16Rik* | 380787 | 2.447 | 3.780 | -0.628 | DOWN | RIKEN cDNA A230065H16 gene |
| *Siah3* | 380918 | 1.860 | 1.185 | 0.650 | UP | seven in absentia homolog 3 |
| *Tmsb15l* | 399591 | 3.543 | 2.290 | 0.630 | UP | thymosin beta 15b like |
| *BC051226* | 407803 | 3.767 | 2.025 | 0.895 | UP | cDNA sequence BC051226 |
| *4930404N11Rik* | 432479 | 1.763 | 2.900 | -0.718 | DOWN | RIKEN cDNA 4930404N11 gene |
| *B830017H08Rik* | 433004 | 1.673 | 1.010 | 0.728 | UP | RIKEN cDNA B830017H08 gene |
| *Zkscan4* | 544922 | 2.063 | 1.295 | 0.672 | UP | zinc finger with KRAB and SCAN domains 4 |
| *Bvht* | 545261 | 0.913 | 1.560 | -0.772 | DOWN | braveheart long non-coding RNA |
| *C530005A16Rik* | 654318 | 2.233 | 1.370 | 0.705 | UP | RIKEN cDNA C530005A16 gene |
| *Gm14326* | 665211 | 4.290 | 2.480 | 0.791 | UP | predicted gene 14326 |
| *Gm12657* | 667250 | 2.197 | 1.255 | 0.808 | UP | predicted gene 12657 |
| *Gm2694* | 100040294 | 2.357 | 4.080 | -0.792 | DOWN | predicted gene 2694 |
| *Gm15319* | 100040599 | 2.893 | 1.525 | 0.924 | UP | predicted gene 15319 |
| *Gm9833* | 100041480 | 1.593 | 0.900 | 0.824 | UP | myelin basic protein expression factor 2, repressor pseudogene |
| *Gm3383* | 100041515 | 0.810 | 1.645 | -1.022 | DOWN | predicted gene 3383 |
| *1300002E11Rik* | 100043489 | 2.017 | 1.230 | 0.713 | UP | RIKEN cDNA 1300002E11 gene |
| *Gm44504* | 100169864 | 4.017 | 6.125 | -0.609 | DOWN | predicted readthrough transcript , 44504 |
| *Gm10509* | 100310809 | 0.753 | 1.325 | -0.815 | DOWN | zinc finger protein 51 pseudogene |
| *Zfp729b* | 100416706 | 1.557 | 0.650 | 1.260 | UP | zinc finger protein 729b |
| *Gm12709* | 100504717 | 1.447 | 3.220 | -1.154 | DOWN | predicted gene 12709 |
| *C230037L18Rik* | 100532730 | 1.050 | 2.625 | -1.322 | DOWN | RIKEN cDNA C230037L18 gene |

**Table S7. Signaling pathways identified by KEGG function analysis based on DEGs data in Intruder mice versus Observer mice.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **KEGG Entry** | **Term** | **Count** | **%(involved genes/total genes)** | **P Value** | **Genes** |
| mmu05203 | Viral carcinogenesis | 6 | 3.315 | 0.016 | *Hist1h4n, Sp100, H2-T9, Creb3L1, Nfkb2, H2-Q7* |
| mmu04144 | Endocytosis | 6 | 3.315 | 0.033 | *H2-T9, Ccdc53, Hspa1A, Ldlrap1, H2-Q7, Kdr* |
| mmu00480 | Glutathione metabolism | 3 | 1.657 | 0.049 | *Gstm2, Gstm4, Gpx3* |
| mmu04514 | Cell adhesion molecules (CAMs) | 4 | 2.210 | 0.087 | *Itga9, H2-T9, Cldn5, H2-Q7* |
| mmu04612 | Antigen processing and presentation | 3 | 1.657 | 0.098 | *H2-T9, Hspa1A, H2-Q7* |
| mmu00590 | Arachidonic acid metabolism | 3 | 1.657 | 0.113 | *Ptgds, Gpx3, Hpgds* |
| mmu04064 | NF-kappa B signaling pathway | 3 | 1.657 | 0.130 | *Bcl2A1B, Zap70, Nfkb2* |
| mmu04915 | Estrogen signaling pathway | 3 | 1.657 | 0.132 | *Creb3L1, Hspa1A, Mmp2* |
| mmu05034 | Alcoholism | 4 | 2.210 | 0.142 | *Hist1H4N, Gng8, Gm12657, Creb3L1* |
| mmu05169 | Epstein-Barr virus infection | 4 | 2.210 | 0.162 | *H2-T9, Hspa1A, Nfkb2, H2-Q7* |
| mmu04151 | PI3K-Akt signaling pathway | 5 | 2.762 | 0.191 | *Gng8, Itga9, Creb3L1, Mtcp1, Kdr* |
| mmu04728 | Dopaminergic synapse | 3 | 1.657 | 0.215 | *Gng8, Drd5, Creb3L1* |
| mmu05200 | Pathways in cancer | 5 | 2.762 | 0.255 | *Gng8, Lef1, Birc5, Nfkb2, Mmp2* |
| mmu04390 | Hippo signaling pathway | 3 | 1.657 | 0.256 | *Lef1, Tead2, Birc5* |
| mmu04080 | Neuroactive ligand-receptor interaction | 4 | 2.210 | 0.281 | *P2Rx7, Drd5, Htr6, Npffr1* |
| mmu05332 | Graft-versus-host disease | 2 | 1.105 | 0.288 | *H2-T9, H2-Q7* |
| mmu05202 | Transcriptional misregulation in cancer | 3 | 1.657 | 0.292 | *Fli1, Bcl2A1B, Gm12657* |
| mmu05330 | Allograft rejection | 2 | 1.105 | 0.306 | *H2-T9, H2-Q7* |
| mmu05134 | Legionellosis | 2 | 1.105 | 0.310 | *Hspa1A, Nfkb2* |
| mmu04020 | Calcium signaling pathway | 3 | 1.657 | 0.326 | *P2Rx7, Drd5, Htr6* |
| mmu04940 | Type I diabetes mellitus | 2 | 1.105 | 0.333 | *H2-T9, H2-Q7* |
| mmu00980 | Metabolism of xenobiotics by cytochrome P450 | 2 | 1.105 | 0.341 | *Gstm2, Gstm4* |
| mmu05210 | Colorectal cancer | 2 | 1.105 | 0.341 | *Lef1, Birc5* |
| mmu00982 | Drug metabolism - cytochrome P450 | 2 | 1.105 | 0.350 | *Gstm2, Gstm4* |
| mmu04024 | cAMP signaling pathway | 3 | 1.657 | 0.366 | *Drd5, Htr6, Creb3L1* |
| mmu04918 | Thyroid hormone synthesis | 2 | 1.105 | 0.367 | *Gpx3, Creb3L1* |
| mmu05016 | Huntington's disease | 3 | 1.657 | 0.369 | *Cox7A1, Tgm2, Creb3L1* |
| mmu05412 | Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 2 | 1.105 | 0.371 | *Itga9, Lef1* |
| mmu05320 | Autoimmune thyroid disease | 2 | 1.105 | 0.371 | *H2-T9, H2-Q7* |
| mmu05168 | Herpes simplex infection | 3 | 1.657 | 0.392 | *Sp100, H2-T9, H2-Q7* |
| mmu05416 | Viral myocarditis | 2 | 1.105 | 0.403 | *H2-T9, H2-Q7* |
| mmu04727 | GABAergic synapse | 2 | 1.105 | 0.434 | *Gng8, Slc38A5* |
| mmu05215 | Prostate cancer | 2 | 1.105 | 0.437 | *Lef1, Creb3L1* |
| mmu04014 | Ras signaling pathway | 3 | 1.657 | 0.439 | *Gng8, Zap70, Kdr* |
| mmu05204 | Chemical carcinogenesis | 2 | 1.105 | 0.452 | *Gstm2, Gstm4* |
| mmu04916 | Melanogenesis | 2 | 1.105 | 0.477 | *Lef1, Creb3L1* |
| mmu04725 | Cholinergic synapse | 2 | 1.105 | 0.523 | *Gng8, Creb3L1* |
| mmu05166 | HTLV-I infection | 3 | 1.657 | 0.542 | *H2-T9, Nfkb2, H2-Q7* |
| mmu04670 | Leukocyte transendothelial migration | 2 | 1.105 | 0.547 | *Cldn5, Mmp2* |
| mmu04726 | Serotonergic synapse | 2 | 1.105 | 0.579 | *Gng8, Htr6* |
| mmu05161 | Hepatitis B | 2 | 1.105 | 0.616 | *Creb3L1, Birc5* |
| mmu05322 | Systemic lupus erythematosus | 2 | 1.105 | 0.619 | *Hist1H4N, Gm12657* |
| mmu04145 | Phagosome | 2 | 1.105 | 0.681 | *H2-T9, H2-Q7* |
| mmu05205 | Proteoglycans in cancer | 2 | 1.105 | 0.737 | *Mmp2, Kdr* |
| mmu04510 | Focal adhesion | 2 | 1.105 | 0.744 | *Itga9, Kdr* |
| mmu04015 | Rap1 signaling pathway | 2 | 1.105 | 0.756 | *Apbb1Ip, Kdr* |
| mmu04010 | MAPK signaling pathway | 2 | 1.105 | 0.812 | *Hspa1A, Nfkb2* |
| mmu01100 | Metabolic pathways | 4 | 2.210 | 0.993 | *Amy1, Chdh, Ptgds, Hpgds* |
| mmu05216 | Thyroid cancer | 1 | 0.552 | 1.000 | *Lef1* |
| mmu04660 | T cell receptor signaling pathway | 1 | 0.552 | 1.000 | *Zap70* |
| mmu04724 | Glutamatergic synapse | 1 | 0.552 | 1.000 | *Gng8* |
| mmu05219 | Bladder cancer | 1 | 0.552 | 1.000 | *Mmp2* |
| mmu00260 | Glycine, serine and threonine metabolism | 1 | 0.552 | 1.000 | *Chdh* |
| mmu04520 | Adherens junction | 1 | 0.552 | 1.000 | *Lef1* |
| mmu04152 | AMPK signaling pathway | 1 | 0.552 | 1.000 | *Creb3L1* |
| mmu05032 | Morphine addiction | 1 | 0.552 | 1.000 | *Gng8* |
| mmu04973 | Carbohydrate digestion and absorption | 1 | 0.552 | 1.000 | *Amy1* |
| mmu04022 | cGMP-PKG signaling pathway | 1 | 0.552 | 1.000 | *Creb3L1* |
| mmu04713 | Circadian entrainment | 1 | 0.552 | 1.000 | *Gng8* |
| mmu04668 | TNF signaling pathway | 1 | 0.552 | 1.000 | *Creb3L1* |
| mmu04611 | Platelet activation | 1 | 0.552 | 1.000 | *Apbb1Ip* |
| mmu04380 | Osteoclast differentiation | 1 | 0.552 | 1.000 | *Nfkb2* |
| mmu04931 | Insulin resistance | 1 | 0.552 | 1.000 | *Creb3L1* |
| mmu00860 | Porphyrin and chlorophyll metabolism | 1 | 0.552 | 1.000 | *Hmox1* |
| mmu00190 | Oxidative phosphorylation | 1 | 0.552 | 1.000 | *Cox7A1* |
| mmu04610 | Complement and coagulation cascades | 1 | 0.552 | 1.000 | *Tfpi* |
| mmu04310 | Wnt signaling pathway | 1 | 0.552 | 1.000 | *Lef1* |
| mmu05012 | Parkinson's disease | 1 | 0.552 | 1.000 | *Cox7A1* |
| mmu04723 | Retrograde endocannabinoid signaling | 1 | 0.552 | 1.000 | *Gng8* |
| mmu04550 | Signaling pathways regulating pluripotency of stem cells | 1 | 0.552 | 1.000 | *Otx1* |
| mmu04530 | Tight junction | 1 | 0.552 | 1.000 | *Cldn5* |
| mmu03460 | Fanconi anemia pathway | 1 | 0.552 | 1.000 | *Apitd1* |
| mmu04740 | Olfactory transduction | 1 | 0.552 | 1.000 | *Olfr1344* |
| mmu04120 | Ubiquitin mediated proteolysis | 1 | 0.552 | 1.000 | *Mid1* |
| mmu04146 | Peroxisome | 1 | 0.552 | 1.000 | *Nudt7* |
| mmu05340 | Primary immunodeficiency | 1 | 0.552 | 1.000 | *Zap70* |
| mmu04911 | Insulin secretion | 1 | 0.552 | 1.000 | *Creb3L1* |
| mmu05164 | Influenza A | 1 | 0.552 | 1.000 | *Hspa1A* |
| mmu04260 | Cardiac muscle contraction | 1 | 0.552 | 1.000 | *Cox7A1* |
| mmu03320 | PPAR signaling pathway | 1 | 0.552 | 1.000 | *Apoc3* |
| mmu05410 | Hypertrophic cardiomyopathy (HCM) | 1 | 0.552 | 1.000 | *Itga9* |
| mmu04141 | Protein processing in endoplasmic reticulum | 1 | 0.552 | 1.000 | *Hspa1A* |
| mmu04810 | Regulation of actin cytoskeleton | 1 | 0.552 | 1.000 | *Itga9* |
| mmu05160 | Hepatitis C | 1 | 0.552 | 1.000 | *Cldn5* |
| mmu04060 | Cytokine-cytokine receptor interaction | 1 | 0.552 | 1.000 | *Kdr* |
| mmu04210 | Apoptosis | 1 | 0.552 | 1.000 | *Casp6* |
| mmu04062 | Chemokine signaling pathway | 1 | 0.552 | 1.000 | *Gng8* |
| mmu04912 | GnRH signaling pathway | 1 | 0.552 | 1.000 | *Mmp2* |
| mmu04932 | Non-alcoholic fatty liver disease (NAFLD) | 1 | 0.552 | 1.000 | *Cox7A1* |
| mmu04978 | Mineral absorption | 1 | 0.552 | 1.000 | *Hmox1* |
| mmu03050 | Proteasome | 1 | 0.552 | 1.000 | *Psmb9* |
| mmu05010 | Alzheimer's disease | 1 | 0.552 | 1.000 | *Cox7A1* |
| mmu05213 | Endometrial cancer | 1 | 0.552 | 1.000 | *Lef1* |
| mmu04370 | VEGF signaling pathway | 1 | 0.552 | 1.000 | *Kdr* |
| mmu05031 | Amphetamine addiction | 1 | 0.552 | 1.000 | *Creb3L1* |
| mmu04350 | TGF-beta signaling pathway | 1 | 0.552 | 1.000 | *Smad6* |
| mmu04962 | Vasopressin-regulated water reabsorption | 1 | 0.552 | 1.000 | *Creb3L1* |
| mmu04650 | Natural killer cell mediated cytotoxicity | 1 | 0.552 | 1.000 | *Zap70* |
| mmu05162 | Measles | 1 | 0.552 | 1.000 | *Hspa1A* |
| mmu04261 | Adrenergic signaling in cardiomyocytes | 1 | 0.552 | 1.000 | *Creb3L1* |
| mmu04919 | Thyroid hormone signaling pathway | 1 | 0.552 | 1.000 | *Med30* |
| mmu05221 | Acute myeloid leukemia | 1 | 0.552 | 1.000 | *Lef1* |
| mmu04925 | Aldosterone synthesis and secretion | 1 | 0.552 | 1.000 | *Creb3L1* |
| mmu05217 | Basal cell carcinoma | 1 | 0.552 | 1.000 | *Lef1* |
| mmu05414 | Dilated cardiomyopathy | 1 | 0.552 | 1.000 | *Itga9* |
| mmu03410 | Base excision repair | 1 | 0.552 | 1.000 | *Ogg1* |
| mmu03040 | Spliceosome | 1 | 0.552 | 1.000 | *Hspa1A* |
| mmu05030 | Cocaine addiction | 1 | 0.552 | 1.000 | *Creb3L1* |
| mmu05145 | Toxoplasmosis | 1 | 0.552 | 1.000 | *Hspa1A* |
| mmu04922 | Glucagon signaling pathway | 1 | 0.552 | 1.000 | *Creb3L1* |
| mmu03013 | RNA transport | 1 | 0.552 | 1.000 | *Eif2S3Y* |
| mmu00500 | Starch and sucrose metabolism | 1 | 0.552 | 1.000 | *Amy1* |
| mmu04512 | ECM-receptor interaction | 1 | 0.552 | 1.000 | *Itga9* |

**Table S8. miRNAs with quantitative change over 1.5 folds and their characteristics in Intruder mice versus Control mice.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **miRNA id** | **Expression (Intruder)** | **Expression (Control)** | **log2Ratio (Intruder /Control)** | **Up/down regulation** | **P value** |
| miR-451a | 301.273 | 14.357 | 4.383 | UP | 0 |
| miR-1247-5p | 38.637 | 100.750 | -1.363 | DOWN | 0 |
| miR-1249-3p | 163.670 | 335.900 | -1.021 | DOWN | 0 |
| miR-1298-5p | 97.003 | 1669.903 | -4.087 | DOWN | 0 |
| miR-151-3p | 90.803 | 208.313 | -1.179 | DOWN | 0 |
| miR-204-3p | 21.893 | 69.590 | -1.653 | DOWN | 0 |
| miR-204-5p | 5094.923 | 17266.200 | -1.740 | DOWN | 0 |
| miR-219a-2-3p | 1733.000 | 3953.507 | -1.184 | DOWN | 0 |
| miR-219a-5p | 805.650 | 2917.613 | -1.847 | DOWN | 0 |
| miR-219b-5p | 22.927 | 342.660 | -3.891 | DOWN | 0 |
| miR-338-3p | 432.220 | 871.247 | -1.004 | DOWN | 0 |
| miR-34a-5p | 2310.910 | 4925.833 | -1.092 | DOWN | 0 |
| miR-34b-3p | 23.357 | 198.707 | -3.067 | DOWN | 0 |
| miR-34c-3p | 17.700 | 129.287 | -2.853 | DOWN | 0 |
| miR-34c-5p | 8.273 | 91.140 | -3.440 | DOWN | 0 |
| miR-3547-3p | 43.270 | 93.470 | -1.094 | DOWN | 0 |
| miR-375-3p | 49.230 | 130.633 | -1.380 | DOWN | 0 |
| miR-532-5p | 429.583 | 1001.087 | -1.191 | DOWN | 0 |
| miR-671-5p | 36.247 | 82.417 | -1.160 | DOWN | 0 |
| miR-448-3p | 7.487 | 32.630 | -2.101 | DOWN | 2.26E-296 |
| miR-133a-3p | 23.863 | 57.183 | -1.255 | DOWN | 1.83E-249 |
| miR-3473b | 0.500 | 11.980 | -4.585 | DOWN | 1.22E-219 |
| miR-532-3p | 25.193 | 54.550 | -1.105 | DOWN | 5.1E-193 |
| miR-34b-5p | 4.367 | 20.010 | -2.175 | DOWN | 1.5E-190 |
| miR-669f-5p | 10.837 | 27.117 | -1.322 | DOWN | 1.24E-129 |
| miR-378d | 31.480 | 13.333 | 1.208 | UP | 1.3E-129 |
| let-7b-3p | 7.930 | 22.193 | -1.469 | DOWN | 3.4E-124 |
| miR-296-3p | 10.547 | 24.323 | -1.182 | DOWN | 2.213E-97 |
| miR-466b-5p | 0.957 | 4.293 | -2.141 | DOWN | 1.403E-41 |
| miR-676-5p | 5.970 | 12.393 | -1.031 | DOWN | 5.666E-41 |
| miR-467h | 0.220 | 2.477 | -3.462 | DOWN | 9.468E-40 |
| miR-7019-3p | 3.483 | 0.707 | 2.350 | UP | 1.356E-38 |
| miR-3095-3p | 2.187 | 6.103 | -1.479 | DOWN | 4.602E-36 |
| miR-1306-5p | 1.277 | 4.457 | -1.802 | DOWN | 1.442E-34 |
| miR-539-3p | 1.833 | 5.130 | -1.465 | DOWN | 6.087E-30 |
| miR-6395 | 1.893 | 0.230 | 3.043 | UP | 6.628E-28 |
| miR-339-5p | 2.623 | 6.223 | -1.214 | DOWN | 3.228E-27 |
| miR-98-3p | 2.653 | 6.163 | -1.195 | DOWN | 1.742E-26 |
| miR-466o-5p | 4.237 | 1.510 | 1.509 | UP | 1.951E-26 |
| miR-216a-5p | 1.083 | 3.547 | -1.697 | DOWN | 6.086E-26 |
| miR-15b-3p | 3.030 | 6.343 | -1.055 | DOWN | 1.193E-22 |
| miR-144-3p | 1.190 | 0.110 | 3.433 | UP | 9.119E-20 |
| miR-183-5p | 4.503 | 2.197 | 1.057 | UP | 1.044E-16 |
| miR-34a-3p | 1.400 | 3.307 | -1.234 | DOWN | 1.149E-15 |
| miR-182-5p | 4.293 | 2.137 | 1.029 | UP | 2.219E-15 |
| miR-879-5p | 1.230 | 3.063 | -1.286 | DOWN | 3.228E-15 |
| miR-3105-5p | 0.233 | 1.183 | -2.319 | DOWN | 9.54E-14 |
| miR-7092-3p | 1.037 | 0.251 | 2.121 | UP | 2.489E-11 |
| miR-466p-3p | 0.997 | 2.283 | -1.182 | DOWN | 1.244E-10 |
| miR-466d-5p | 1.227 | 0.377 | 1.723 | UP | 2.964E-10 |
| miR-344e-5p | 0.087 | 0.657 | -2.914 | DOWN | 3.001E-10 |
| miR-3076-3p | 0.943 | 2.140 | -1.160 | DOWN | 8.665E-10 |
| miR-466c-3p | 1.440 | 0.547 | 1.399 | UP | 5.561E-09 |
| miR-3962 | 1.903 | 0.887 | 1.119 | UP | 1.525E-08 |
| miR-224-5p | 0.727 | 1.680 | -1.193 | DOWN | 2.799E-08 |
| miR-483-5p | 0.827 | 1.817 | -1.120 | DOWN | 4.082E-08 |
| miR-205-5p | 1.660 | 0.733 | 1.181 | UP | 4.417E-08 |
| miR-483-3p | 0.110 | 0.597 | -2.412 | DOWN | 6.061E-08 |
| miR-5100 | 0.123 | 0.623 | -2.317 | DOWN | 6.745E-08 |
| miR-709 | 0.410 | 0.047 | 3.077 | UP | 3.173E-07 |
| miR-669m-5p | 0.540 | 1.243 | -1.180 | DOWN | 2.206E-06 |
| miR-6959-3p | 0.453 | 1.060 | -1.200 | DOWN | 9.344E-06 |
| miR-214-3p | 0.557 | 1.207 | -1.104 | DOWN | 9.755E-06 |
| miR-1912-3p | 0.040 | 0.303 | -3.026 | DOWN | 1.274E-05 |
| miR-670-5p | 0.233 | 0.700 | -1.552 | DOWN | 1.28E-05 |
| miR-3058-5p | 0.397 | 0.933 | -1.234 | DOWN | 2.041E-05 |
| miR-7025-3p | 0.074 | 0.353 | -2.240 | DOWN | 6.678E-05 |
| miR-466e-3p | 0.223 | 0.620 | -1.469 | DOWN | 7.357E-05 |
| miR-7213-5p | 0.644 | 0.261 | 1.369 | UP | 0.0001067 |
| miR-8106 | 0.243 | 0.037 | 2.770 | UP | 0.0001576 |
| miR-3103-3p | 0.110 | 0.400 | -1.841 | DOWN | 0.0001791 |
| miR-1193-5p | 0.513 | 0.184 | 1.519 | UP | 0.0001923 |
| miR-6481 | 0.040 | 0.240 | -2.704 | DOWN | 0.0002256 |
| miR-18a-3p | 0.173 | 0.487 | -1.481 | DOWN | 0.0004118 |
| miR-186-3p | 0.493 | 0.183 | 1.448 | UP | 0.0004432 |
| miR-6952-3p | 0.237 | 0.583 | -1.304 | DOWN | 0.0004443 |

**Table S9. The changed miRNAs predict target mRNAs in Intruder mice versus Control mice.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **miRNA id** | **Up/Down Regulation** | **Target id** | **Gene Name** | **Up/Down Regulation** |
| mmu-miR-6395 | UP | NM\_018730 | Rpl36 | DOWN |
| mmu-miR-6395 | UP | NM\_001039365 | Mobp | DOWN |
| mmu-miR-7213-5p | UP | NM\_001039365 | Mobp | DOWN |
| mmu-miR-7092-3p | UP | NM\_001163183 | Plekhb1 | DOWN |
| mmu-miR-7092-3p | UP | NM\_013746 | Plekhb1 | DOWN |
| mmu-miR-7019-3p | UP | NM\_001146318 | Cnp | DOWN |
| mmu-miR-7213-5p | UP | NM\_001146318 | Cnp | DOWN |
| mmu-miR-7019-3p | UP | NM\_009923 | Cnp | DOWN |
| mmu-miR-451a | UP | NM\_008770 | Cldn11 | DOWN |
| mmu-miR-205-5p | UP | NM\_008770 | Cldn11 | DOWN |
| mmu-miR-1193-5p | UP | NM\_008770 | Cldn11 | DOWN |
| mmu-miR-186-3p | UP | NM\_026069 | Rpl37 | DOWN |
| mmu-miR-3962 | UP | NM\_007830 | Dbi | DOWN |
| mmu-miR-182-5p | UP | NM\_001122765 | Sirt2 | DOWN |
| mmu-miR-466o-5p | UP | NM\_001164369 | Bcas1 | DOWN |
| mmu-miR-7092-3p | UP | NM\_001282966 | Cd63 | DOWN |
| mmu-miR-3962 | UP | NM\_001136077 | Enpp2 | DOWN |
| mmu-miR-1193-5p | UP | NM\_001301354 | Apod | DOWN |
| mmu-miR-6395 | UP | NM\_153537 | Phldb1 | DOWN |
| mmu-miR-34a-5p | DOWN | NM\_029182 | Rasd2 | UP |
| mmu-miR-34c-5p | DOWN | NM\_029182 | Rasd2 | UP |
| mmu-miR-671-5p | DOWN | NM\_029182 | Rasd2 | UP |
| mmu-miR-3095-3p | DOWN | NM\_029182 | Rasd2 | UP |
| mmu-miR-1306-5p | DOWN | NM\_029182 | Rasd2 | UP |
| mmu-miR-378d | UP | NM\_011437 | Sox10 | DOWN |
| mmu-miR-144-3p | UP | NM\_011437 | Sox10 | DOWN |
| mmu-miR-6395 | UP | NM\_029789 | Cers2 | DOWN |
| mmu-miR-7019-3p | UP | NM\_001081170 | Pacs2 | DOWN |
| mmu-miR-8106 | UP | NM\_001291445 | Pacs2 | DOWN |
| mmu-miR-1193-5p | UP | NM\_001291445 | Pacs2 | DOWN |
| mmu-miR-709 | UP | NM\_001033394 | Tmem88b | DOWN |
| mmu-miR-709 | UP | NM\_001198831 | Ddr1 | DOWN |
| mmu-miR-451a | UP | NM\_172962 | Ddr1 | DOWN |
| mmu-miR-183-5p | UP | NM\_172962 | Ddr1 | DOWN |
| mmu-miR-1193-5p | UP | NM\_172962 | Ddr1 | DOWN |
| mmu-miR-186-3p | UP | NM\_172962 | Ddr1 | DOWN |
| mmu-miR-466c-3p | UP | NM\_001038700 | Fnbp1 | DOWN |
| mmu-miR-7019-3p | UP | NM\_001177649 | Fnbp1 | DOWN |
| mmu-miR-6395 | UP | NM\_019406 | Fnbp1 | DOWN |
| mmu-miR-8106 | UP | NM\_001110826 | Ddx6 | DOWN |
| mmu-miR-186-3p | UP | NM\_007841 | Ddx6 | DOWN |
| mmu-miR-466c-3p | UP | NM\_001033711 | Evi2a | DOWN |
| mmu-miR-709 | UP | NM\_001033711 | Evi2a | DOWN |
| mmu-miR-7019-3p | UP | NM\_009448 | Tuba1c | DOWN |
| mmu-miR-1912-3p | DOWN | NM\_011246 | Rasgrp1 | UP |
| mmu-miR-6395 | UP | NM\_175452 | Gjc2 | DOWN |
| mmu-miR-375-3p | DOWN | NM\_007913 | Egr1 | UP |
| mmu-miR-483-3p | DOWN | NM\_007913 | Egr1 | UP |
| mmu-miR-1193-5p | UP | NM\_023277 | Jam3 | DOWN |
| mmu-miR-3962 | UP | NM\_178774 | Prr18 | DOWN |
| mmu-miR-7213-5p | UP | NM\_178774 | Prr18 | DOWN |
| mmu-miR-7019-3p | UP | NM\_009673 | Anxa5 | DOWN |
| mmu-miR-7092-3p | UP | NM\_001033481 | Myrf | DOWN |
| mmu-miR-3962 | UP | NM\_001033481 | Myrf | DOWN |
| mmu-miR-1193-5p | UP | NM\_029972 | Ermn | DOWN |
| mmu-miR-466d-5p | UP | NM\_011674 | Ugt8a | DOWN |
| mmu-miR-7092-3p | UP | NM\_011464 | Spint2 | DOWN |
| mmu-miR-1306-5p | DOWN | NM\_010077 | Drd2 | UP |
| mmu-miR-34a-3p | DOWN | NM\_010077 | Drd2 | UP |
| mmu-miR-709 | UP | NM\_026672 | Gstm7 | DOWN |
| mmu-miR-378d | UP | NM\_001302498 | Gjb1 | DOWN |
| mmu-miR-709 | UP | NM\_025331 | Gng11 | DOWN |
| mmu-miR-186-3p | UP | NM\_025331 | Gng11 | DOWN |
| mmu-miR-378d | UP | NM\_013660 | Sema4d | DOWN |
| mmu-miR-3473b | DOWN | NM\_001276684 | Arc | UP |
| mmu-miR-3095-3p | DOWN | NM\_001276684 | Arc | UP |
| mmu-miR-15b-3p | DOWN | NM\_001276684 | Arc | UP |
| mmu-miR-18a-3p | DOWN | NM\_001276684 | Arc | UP |
| mmu-miR-448-3p | DOWN | NM\_018790 | Arc | UP |
| mmu-miR-879-5p | DOWN | NM\_018790 | Arc | UP |
| mmu-miR-467h | DOWN | NM\_010585 | Itpr1 | UP |
| mmu-miR-466o-5p | UP | NM\_144895 | Spg20 | DOWN |
| mmu-miR-709 | UP | NM\_144895 | Spg20 | DOWN |
| mmu-miR-3076-3p | DOWN | NM\_011242 | Rasgrp2 | UP |
| mmu-miR-182-5p | UP | NM\_019980 | Litaf | DOWN |
| mmu-miR-205-5p | UP | NM\_008407 | Itih3 | DOWN |
| mmu-miR-709 | UP | NM\_010599 | Kcnab3 | DOWN |
| mmu-miR-144-3p | UP | NM\_183261 | Nr2f2 | DOWN |
| mmu-miR-466c-3p | UP | NM\_019422 | Elovl1 | DOWN |
| mmu-miR-205-5p | UP | NM\_019422 | Elovl1 | DOWN |
| mmu-miR-709 | UP | NM\_019422 | Elovl1 | DOWN |
| mmu-miR-219a-2-3p | DOWN | NM\_001199676 | Camkk2 | UP |
| mmu-miR-671-5p | DOWN | NM\_001199676 | Camkk2 | UP |
| mmu-miR-676-5p | DOWN | NM\_001199676 | Camkk2 | UP |
| mmu-miR-339-5p | DOWN | NM\_001199676 | Camkk2 | UP |
| mmu-miR-15b-3p | DOWN | NM\_001199676 | Camkk2 | UP |
| mmu-miR-375-3p | DOWN | NM\_145358 | Camkk2 | UP |
| mmu-miR-18a-3p | DOWN | NM\_145358 | Camkk2 | UP |
| mmu-miR-7092-3p | UP | NM\_001271538 | Myh14 | DOWN |
| mmu-miR-205-5p | UP | NM\_028021 | Myh14 | DOWN |
| mmu-miR-3962 | UP | NM\_023142 | Arpc1b | DOWN |
| mmu-miR-466d-5p | UP | NM\_134054 | Sptssa | DOWN |
| mmu-miR-669f-5p | DOWN | NM\_001111140 | Lrrc10b | UP |
| mmu-miR-467h | DOWN | NM\_001111140 | Lrrc10b | UP |
| mmu-miR-7092-3p | UP | NM\_010336 | Lpar1 | DOWN |
| mmu-miR-466c-3p | UP | NM\_172989 | Lpar1 | DOWN |
| mmu-miR-451a | UP | NM\_177461 | Micall1 | DOWN |
| mmu-miR-205-5p | UP | NM\_177461 | Micall1 | DOWN |
| mmu-miR-378d | UP | NM\_011177 | Klk6 | DOWN |
| mmu-miR-451a | UP | NM\_009797 | Capza1 | DOWN |
| mmu-miR-466d-5p | UP | NM\_009797 | Capza1 | DOWN |
| mmu-miR-7092-3p | UP | NM\_028390 | Anln | DOWN |
| mmu-miR-182-5p | UP | NM\_027219 | Cdc42ep1 | DOWN |
| mmu-miR-451a | UP | NM\_008885 | Pmp22 | DOWN |
| mmu-miR-466o-5p | UP | NM\_008885 | Pmp22 | DOWN |
| mmu-miR-144-3p | UP | NM\_016892 | Ccs | DOWN |
| mmu-miR-709 | UP | NM\_139269 | Pla2g16 | DOWN |
| mmu-miR-7019-3p | UP | NM\_181073 | Plekhh1 | DOWN |
| mmu-miR-466c-3p | UP | NM\_181073 | Plekhh1 | DOWN |
| mmu-miR-709 | UP | NM\_181073 | Plekhh1 | DOWN |
| mmu-miR-7019-3p | UP | NM\_026169 | Frmd8 | DOWN |
| mmu-miR-205-5p | UP | NM\_026169 | Frmd8 | DOWN |
| mmu-miR-451a | UP | NM\_001253892 | Slc4a2 | DOWN |
| mmu-miR-451a | UP | NM\_009207 | Slc4a2 | DOWN |
| mmu-miR-3962 | UP | NM\_033217 | Ngfr | DOWN |
| mmu-miR-3547-3p | DOWN | NM\_001114386 | Nedd4l | UP |
| mmu-miR-133a-3p | DOWN | NM\_001114386 | Nedd4l | UP |
| mmu-miR-539-3p | DOWN | NM\_001114386 | Nedd4l | UP |
| mmu-miR-98-3p | DOWN | NM\_001114386 | Nedd4l | UP |
| mmu-miR-3105-5p | DOWN | NM\_001114386 | Nedd4l | UP |
| mmu-miR-669m-5p | DOWN | NM\_001114386 | Nedd4l | UP |
| mmu-miR-1912-3p | DOWN | NM\_001114386 | Nedd4l | UP |
| mmu-miR-7025-3p | DOWN | NM\_001114386 | Nedd4l | UP |
| mmu-miR-6395 | UP | NM\_001271407 | Sorbs3 | DOWN |
| mmu-miR-3962 | UP | NM\_001271407 | Sorbs3 | DOWN |
| mmu-miR-7213-5p | UP | NM\_001271408 | Sorbs3 | DOWN |
| mmu-miR-7019-3p | UP | NM\_011366 | Sorbs3 | DOWN |
| mmu-miR-466o-5p | UP | NM\_011366 | Sorbs3 | DOWN |
| mmu-miR-466d-5p | UP | NM\_011366 | Sorbs3 | DOWN |
| mmu-miR-186-3p | UP | NM\_001253736 | Pdlim2 | DOWN |
| mmu-miR-182-5p | UP | NM\_145978 | Pdlim2 | DOWN |
| mmu-miR-183-5p | UP | NM\_010176 | Fah | DOWN |
| mmu-miR-3962 | UP | NM\_010176 | Fah | DOWN |
| mmu-miR-296-3p | DOWN | NM\_001111331 | Kcnip3 | UP |
| mmu-miR-151-3p | DOWN | NM\_001291005 | Kcnip3 | UP |
| mmu-miR-1249-3p | DOWN | NM\_019789 | Kcnip3 | UP |
| mmu-miR-532-3p | DOWN | NM\_019789 | Kcnip3 | UP |
| mmu-miR-676-5p | DOWN | NM\_019789 | Kcnip3 | UP |
| mmu-miR-339-5p | DOWN | NM\_019789 | Kcnip3 | UP |
| mmu-miR-3076-3p | DOWN | NM\_019789 | Kcnip3 | UP |
| mmu-miR-3058-5p | DOWN | NM\_019789 | Kcnip3 | UP |
| mmu-miR-3962 | UP | NM\_172751 | Arhgef10 | DOWN |
| mmu-miR-8106 | UP | NM\_139139 | Dnajc17 | DOWN |
| mmu-miR-7092-3p | UP | NM\_010207 | Fgfr2 | DOWN |
| mmu-miR-466d-5p | UP | NM\_201601 | Fgfr2 | DOWN |
| mmu-miR-466d-5p | UP | NM\_173751 | Ilvbl | DOWN |
| mmu-miR-709 | UP | NM\_001243584 | Mif4gd | DOWN |
| mmu-miR-1193-5p | UP | NM\_027162 | Mif4gd | DOWN |
| mmu-miR-3962 | UP | NM\_172383 | Tmem125 | DOWN |
| mmu-miR-186-3p | UP | NM\_172383 | Tmem125 | DOWN |
| mmu-miR-1247-5p | DOWN | NM\_001101488 | Gsg1l | UP |
| mmu-miR-3473b | DOWN | NM\_001101488 | Gsg1l | UP |
| mmu-miR-339-5p | DOWN | NM\_001101488 | Gsg1l | UP |
| mmu-miR-183-5p | UP | NM\_021390 | Sall1 | DOWN |
| mmu-miR-34b-5p | DOWN | NM\_001122998 | Tiam2 | UP |
| mmu-miR-15b-3p | DOWN | NM\_001286758 | Tiam2 | UP |
| mmu-miR-879-5p | DOWN | NM\_001286758 | Tiam2 | UP |
| mmu-miR-483-3p | DOWN | NM\_001286758 | Tiam2 | UP |
| mmu-miR-133a-3p | DOWN | NM\_011878 | Tiam2 | UP |
| mmu-miR-669f-5p | DOWN | NM\_011878 | Tiam2 | UP |
| mmu-miR-676-5p | DOWN | NM\_011878 | Tiam2 | UP |
| mmu-miR-879-5p | DOWN | NM\_011878 | Tiam2 | UP |
| mmu-miR-1193-5p | UP | NM\_172907 | Olfml1 | DOWN |
| mmu-miR-466e-3p | DOWN | NM\_001289925 | Egr3 | UP |
| mmu-miR-18a-3p | DOWN | NM\_001289925 | Egr3 | UP |
| mmu-miR-467h | DOWN | NM\_001289927 | Egr3 | UP |
| mmu-miR-466p-3p | DOWN | NM\_001289927 | Egr3 | UP |
| mmu-miR-219a-5p | DOWN | NM\_018781 | Egr3 | UP |
| mmu-miR-1249-3p | DOWN | NM\_018781 | Egr3 | UP |
| mmu-miR-670-5p | DOWN | NM\_018781 | Egr3 | UP |
| mmu-miR-6395 | UP | NM\_019764 | Amotl2 | DOWN |
| mmu-miR-186-3p | UP | NM\_019764 | Amotl2 | DOWN |
| mmu-miR-378d | UP | NM\_001190319 | C1qtnf5 | DOWN |
| mmu-miR-183-5p | UP | NM\_145613 | C1qtnf5 | DOWN |
| mmu-miR-182-5p | UP | NM\_013635 | Sypl | DOWN |
| mmu-miR-7019-3p | UP | NM\_198710 | Sypl | DOWN |
| mmu-miR-466o-5p | UP | NM\_198710 | Sypl | DOWN |
| mmu-miR-7092-3p | UP | NM\_198710 | Sypl | DOWN |
| mmu-miR-466d-5p | UP | NM\_198710 | Sypl | DOWN |
| mmu-miR-219a-5p | DOWN | NM\_001284189 | Homer1 | UP |
| mmu-miR-3095-3p | DOWN | NM\_001284189 | Homer1 | UP |
| mmu-miR-216a-5p | DOWN | NM\_001284189 | Homer1 | UP |
| mmu-miR-219a-5p | DOWN | NM\_147176 | Homer1 | UP |
| mmu-miR-1249-3p | DOWN | NM\_147176 | Homer1 | UP |
| mmu-miR-6952-3p | DOWN | NM\_147176 | Homer1 | UP |
| mmu-miR-375-3p | DOWN | NM\_152134 | Homer1 | UP |
| mmu-miR-466d-5p | UP | NM\_009196 | Slc16a1 | DOWN |
| mmu-miR-466c-3p | UP | NM\_009196 | Slc16a1 | DOWN |
| mmu-miR-98-3p | DOWN | NM\_001282993 | Cobl | UP |
| mmu-miR-338-3p | DOWN | NM\_001282994 | Cobl | UP |
| mmu-miR-151-3p | DOWN | NM\_001282994 | Cobl | UP |
| mmu-miR-669m-5p | DOWN | NM\_001282994 | Cobl | UP |
| mmu-miR-34c-3p | DOWN | NM\_172496 | Cobl | UP |
| mmu-miR-204-3p | DOWN | NM\_172496 | Cobl | UP |
| mmu-miR-532-3p | DOWN | NM\_172496 | Cobl | UP |
| mmu-miR-483-5p | DOWN | NM\_172496 | Cobl | UP |
| mmu-miR-466e-3p | DOWN | NM\_172496 | Cobl | UP |
| mmu-miR-186-3p | UP | NM\_001177868 | Rreb1 | DOWN |
| mmu-miR-7092-3p | UP | NM\_001177869 | Rreb1 | DOWN |
| mmu-miR-183-5p | UP | NM\_026830 | Rreb1 | DOWN |
| mmu-miR-182-5p | UP | NM\_026830 | Rreb1 | DOWN |
| mmu-miR-466d-5p | UP | NM\_026830 | Rreb1 | DOWN |
| mmu-miR-709 | UP | NM\_207298 | Cercam | DOWN |
| mmu-miR-466c-3p | UP | NM\_009398 | Tnfaip6 | DOWN |
| mmu-miR-709 | UP | NM\_001130458 | Tcn2 | DOWN |
| mmu-miR-8106 | UP | NM\_001130458 | Tcn2 | DOWN |
| mmu-miR-8106 | UP | NM\_015749 | Tcn2 | DOWN |
| mmu-miR-296-3p | DOWN | NM\_030174 | Mctp1 | UP |
| mmu-miR-709 | UP | NM\_007672 | Cdr2 | DOWN |
| mmu-miR-378d | UP | NM\_001161768 | Galnt6 | DOWN |
| mmu-miR-7213-5p | UP | NM\_025863 | Trim59 | DOWN |
| mmu-miR-8106 | UP | NM\_025863 | Trim59 | DOWN |
| mmu-miR-466o-5p | UP | NM\_019479 | Hes6 | DOWN |
| mmu-miR-709 | UP | NM\_009936 | Col9a3 | DOWN |
| mmu-miR-1249-3p | DOWN | NM\_026268 | Dusp6 | UP |
| mmu-miR-6959-3p | DOWN | NM\_026268 | Dusp6 | UP |
| mmu-miR-466e-3p | DOWN | NM\_026268 | Dusp6 | UP |
| mmu-miR-6481 | DOWN | NM\_026268 | Dusp6 | UP |
| mmu-miR-6395 | UP | NM\_153804 | Plekhg3 | DOWN |
| mmu-miR-144-3p | UP | NM\_153804 | Plekhg3 | DOWN |
| mmu-miR-7213-5p | UP | NM\_153804 | Plekhg3 | DOWN |
| mmu-miR-709 | UP | NM\_199143 | Znrf2 | DOWN |
| mmu-miR-1249-3p | DOWN | NM\_001160410 | Scrt2 | UP |
| mmu-miR-3473b | DOWN | NM\_001160410 | Scrt2 | UP |
| mmu-miR-6395 | UP | NM\_212473 | Fam53b | DOWN |
| mmu-miR-709 | UP | NM\_212473 | Fam53b | DOWN |
| mmu-miR-466d-5p | UP | NM\_177304 | Enpp6 | DOWN |
| mmu-miR-3962 | UP | NM\_177304 | Enpp6 | DOWN |
| mmu-miR-205-5p | UP | NM\_177304 | Enpp6 | DOWN |
| mmu-miR-7213-5p | UP | NM\_177304 | Enpp6 | DOWN |
| mmu-miR-709 | UP | NM\_130882 | Cyp4f13 | DOWN |
| mmu-miR-6395 | UP | NM\_009565 | Zbtb7b | DOWN |
| mmu-miR-205-5p | UP | NM\_007446 | Amy1 | DOWN |
| mmu-miR-186-3p | UP | NM\_001277903 | Tnnt1 | DOWN |
| mmu-miR-219a-5p | DOWN | NM\_001146330 | Gpr52 | UP |
| mmu-miR-451a | UP | NM\_010153 | Erbb3 | DOWN |
| mmu-miR-7092-3p | UP | NM\_001164220 | Trim13 | DOWN |
| mmu-miR-205-5p | UP | NM\_001164220 | Trim13 | DOWN |
| mmu-miR-186-3p | UP | NM\_023233 | Trim13 | DOWN |
| mmu-miR-205-5p | UP | NM\_183186 | Foxn3 | DOWN |
| mmu-miR-451a | UP | NM\_001164602 | Amigo2 | DOWN |
| mmu-miR-7213-5p | UP | NM\_001164602 | Amigo2 | DOWN |
| mmu-miR-466c-3p | UP | NM\_011448 | Sox9 | DOWN |
| mmu-miR-186-3p | UP | NM\_011448 | Sox9 | DOWN |
| mmu-miR-466d-5p | UP | NM\_009980 | Ctbp2 | DOWN |
| mmu-miR-466o-5p | UP | NM\_029001 | Elovl7 | DOWN |
| mmu-miR-709 | UP | NM\_029001 | Elovl7 | DOWN |
| mmu-miR-34b-3p | DOWN | NM\_001145965 | Dlgap2 | UP |
| mmu-miR-676-5p | DOWN | NM\_001145965 | Dlgap2 | UP |
| mmu-miR-539-3p | DOWN | NM\_001145965 | Dlgap2 | UP |
| mmu-miR-483-3p | DOWN | NM\_172910 | Dlgap2 | UP |
| mmu-miR-709 | UP | NM\_001122736 | Igf2 | DOWN |
| mmu-miR-7092-3p | UP | NM\_010514 | Igf2 | DOWN |
| mmu-miR-1193-5p | UP | NM\_010514 | Igf2 | DOWN |
| mmu-miR-466e-3p | DOWN | NM\_001163356 | Fam212b | UP |
| mmu-miR-34b-3p | DOWN | NM\_175398 | Fam212b | UP |
| mmu-miR-3547-3p | DOWN | NM\_175398 | Fam212b | UP |
| mmu-miR-3473b | DOWN | NM\_175398 | Fam212b | UP |
| mmu-miR-339-5p | DOWN | NM\_175398 | Fam212b | UP |
| mmu-miR-216a-5p | DOWN | NM\_175398 | Fam212b | UP |
| mmu-miR-669m-5p | DOWN | NM\_175398 | Fam212b | UP |
| mmu-miR-214-3p | DOWN | NM\_175398 | Fam212b | UP |
| mmu-miR-18a-3p | DOWN | NM\_175398 | Fam212b | UP |
| mmu-miR-378d | UP | NM\_027263 | Apitd1 | DOWN |
| mmu-miR-709 | UP | NM\_027263 | Apitd1 | DOWN |
| mmu-miR-7092-3p | UP | NM\_001316724 | Nudt14 | DOWN |
| mmu-miR-6395 | UP | NM\_001039156 | Triobp | DOWN |
| mmu-miR-466d-5p | UP | NM\_001039156 | Triobp | DOWN |
| mmu-miR-466d-5p | UP | NM\_138579 | Triobp | DOWN |
| mmu-miR-7019-3p | UP | NM\_008986 | Ptrf | DOWN |
| mmu-miR-6395 | UP | NM\_008986 | Ptrf | DOWN |
| mmu-miR-183-5p | UP | NM\_173767 | Insc | DOWN |
| mmu-miR-466c-3p | UP | NM\_173767 | Insc | DOWN |
| mmu-miR-205-5p | UP | NM\_173767 | Insc | DOWN |
| mmu-miR-183-5p | UP | NM\_008536 | Tm4sf1 | DOWN |
| mmu-miR-3962 | UP | NM\_001123370 | 9030025P20Rik | DOWN |
| mmu-miR-205-5p | UP | NM\_001001979 | Megf10 | DOWN |
| mmu-miR-375-3p | DOWN | NM\_018775 | Tbc1d8 | UP |
| mmu-miR-7213-5p | UP | NM\_008905 | Ppfibp2 | DOWN |
| mmu-miR-186-3p | UP | NM\_008905 | Ppfibp2 | DOWN |
| mmu-miR-182-5p | UP | NM\_009150 | Selenbp1 | DOWN |
| mmu-miR-7213-5p | UP | NM\_009150 | Selenbp1 | DOWN |
| mmu-miR-709 | UP | NM\_027280 | Nkd1 | DOWN |
| mmu-miR-7213-5p | UP | NM\_027280 | Nkd1 | DOWN |
| mmu-miR-451a | UP | NM\_010919 | Nkx2-2 | DOWN |
| mmu-miR-34c-5p | DOWN | NM\_001080963 | Plpp4 | UP |
| mmu-miR-3105-5p | DOWN | NM\_001080963 | Plpp4 | UP |
| mmu-miR-483-3p | DOWN | NM\_001080963 | Plpp4 | UP |
| mmu-miR-448-3p | DOWN | NM\_152923 | Kcnq3 | UP |
| mmu-miR-709 | UP | NM\_016697 | Gpc3 | DOWN |
| mmu-miR-378d | UP | NM\_001270646 | Prob1 | DOWN |
| mmu-miR-6395 | UP | NM\_001270646 | Prob1 | DOWN |
| mmu-miR-7213-5p | UP | NM\_027852 | Rarres2 | DOWN |
| mmu-miR-1249-3p | DOWN | NM\_033269 | Chrm3 | UP |
| mmu-miR-375-3p | DOWN | NM\_033269 | Chrm3 | UP |
| mmu-miR-1912-3p | DOWN | NM\_033269 | Chrm3 | UP |
| mmu-miR-205-5p | UP | NM\_029239 | Prkd3 | DOWN |
| mmu-miR-466o-5p | UP | NM\_001033253 | Plekhg1 | DOWN |
| mmu-miR-144-3p | UP | NM\_001159942 | Plekhg1 | DOWN |
| mmu-miR-1193-5p | UP | NM\_001048005 | 1110017D15Rik | DOWN |
| mmu-miR-7213-5p | UP | NM\_001253788 | 1110017D15Rik | DOWN |
| mmu-miR-3962 | UP | NM\_001163722 | Smim1 | DOWN |
| mmu-miR-183-5p | UP | NM\_001039071 | Ldb3 | DOWN |
| mmu-miR-3962 | UP | NM\_001039072 | Ldb3 | DOWN |
| mmu-miR-1193-5p | UP | NM\_001039072 | Ldb3 | DOWN |
| mmu-miR-466c-3p | UP | NM\_001039073 | Ldb3 | DOWN |
| mmu-miR-6395 | UP | NM\_001039074 | Ldb3 | DOWN |
| mmu-miR-466c-3p | UP | NM\_001039074 | Ldb3 | DOWN |
| mmu-miR-3962 | UP | NM\_001039074 | Ldb3 | DOWN |
| mmu-miR-7092-3p | UP | NM\_001039075 | Ldb3 | DOWN |
| mmu-miR-451a | UP | NM\_001039076 | Ldb3 | DOWN |
| mmu-miR-378d | UP | NM\_133223 | Rac3 | DOWN |
| mmu-miR-205-5p | UP | NM\_133223 | Rac3 | DOWN |
| mmu-miR-709 | UP | NM\_133223 | Rac3 | DOWN |
| mmu-miR-6481 | DOWN | NM\_011255 | Rbp4 | UP |
| mmu-miR-709 | UP | NM\_001206382 | Mavs | DOWN |
| mmu-miR-466c-3p | UP | NM\_001206383 | Mavs | DOWN |
| mmu-miR-451a | UP | NM\_001206385 | Mavs | DOWN |
| mmu-miR-466c-3p | UP | NM\_144888 | Mavs | DOWN |
| mmu-miR-219a-2-3p | DOWN | NM\_001081401 | Adamts3 | UP |
| mmu-miR-532-5p | DOWN | NM\_001081401 | Adamts3 | UP |
| mmu-miR-669f-5p | DOWN | NM\_001081401 | Adamts3 | UP |
| mmu-miR-224-5p | DOWN | NM\_001081401 | Adamts3 | UP |
| mmu-miR-15b-3p | DOWN | NM\_177872 | Adamts3 | UP |
| mmu-miR-879-5p | DOWN | NM\_177872 | Adamts3 | UP |
| mmu-miR-466o-5p | UP | NM\_199029 | Zfp395 | DOWN |
| mmu-miR-7019-3p | UP | NM\_146251 | Pnpla7 | DOWN |
| mmu-miR-183-5p | UP | NM\_009073 | Rom1 | DOWN |
| mmu-miR-466o-5p | UP | NM\_027009 | Rfc3 | DOWN |
| mmu-miR-7092-3p | UP | NM\_001271915 | B3gnt9 | DOWN |
| mmu-miR-7092-3p | UP | NM\_178879 | B3gnt9 | DOWN |
| mmu-miR-466c-3p | UP | NM\_178879 | B3gnt9 | DOWN |
| mmu-miR-3962 | UP | NM\_001161797 | Phactr4 | DOWN |
| mmu-miR-205-5p | UP | NM\_026991 | Sat2 | DOWN |
| mmu-miR-6395 | UP | NM\_001083188 | Lig1 | DOWN |
| mmu-miR-6395 | UP | NM\_020566 | Dnajc4 | DOWN |
| mmu-miR-451a | UP | NM\_145144 | Aif1l | DOWN |
| mmu-miR-466c-3p | UP | NM\_145144 | Aif1l | DOWN |
| mmu-miR-205-5p | UP | NM\_001038664 | Gngt2 | DOWN |
| mmu-miR-7213-5p | UP | NM\_001038664 | Gngt2 | DOWN |
| mmu-miR-219a-5p | DOWN | NM\_145426 | Mfap3 | UP |
| mmu-miR-34c-5p | UP | NM\_145426 | Mfap3 | UP |
| mmu-miR-671-5p | UP | NM\_145426 | Mfap3 | UP |
| mmu-let-7b-3p | DOWN | NM\_145426 | Mfap3 | UP |
| mmu-miR-1306-5p | DOWN | NM\_145426 | Mfap3 | UP |
| mmu-miR-539-3p | DOWN | NM\_145426 | Mfap3 | UP |
| mmu-miR-466p-3p | DOWN | NM\_145426 | Mfap3 | UP |
| mmu-miR-6481 | DOWN | NM\_145426 | Mfap3 | UP |
| mmu-miR-34c-5p | DOWN | NM\_180599 | Mfap3 | UP |
| mmu-miR-133a-3p | DOWN | NM\_180599 | Mfap3 | UP |
| mmu-miR-34b-5p | DOWN | NM\_180599 | Mfap3 | UP |
| mmu-miR-15b-3p | DOWN | NM\_180599 | Mfap3 | UP |
| mmu-miR-186-3p | UP | NM\_019687 | Slc22a4 | DOWN |
| mmu-miR-451a | UP | NM\_018761 | Ctnnal1 | DOWN |
| mmu-miR-451a | UP | NM\_025386 | Fbxo36 | DOWN |
| mmu-miR-186-3p | UP | NM\_025386 | Fbxo36 | DOWN |
| mmu-miR-34b-3p | DOWN | NM\_008509 | Lpl | UP |
| mmu-miR-34c-3p | DOWN | NM\_008509 | Lpl | UP |
| mmu-miR-466o-5p | UP | NM\_001290181 | Nudt7 | DOWN |
| mmu-miR-466d-5p | UP | NM\_001290181 | Nudt7 | DOWN |
| mmu-miR-183-5p | UP | NM\_001290182 | Nudt7 | DOWN |
| mmu-miR-1193-5p | UP | NM\_146151 | Tesk2 | DOWN |
| mmu-miR-34b-3p | DOWN | NM\_013488 | Cd4 | UP |
| mmu-miR-34c-3p | DOWN | NM\_013488 | Cd4 | UP |
| mmu-miR-204-3p | DOWN | NM\_013488 | Cd4 | UP |
| mmu-miR-339-5p | DOWN | NM\_013488 | Cd4 | UP |
| mmu-miR-669m-5p | DOWN | NM\_013488 | Cd4 | UP |
| mmu-miR-1298-5p | DOWN | NM\_001310464 | Reln | UP |
| mmu-miR-5100 | DOWN | NM\_011261 | Reln | UP |
| mmu-miR-7019-3p | UP | NM\_001304362 | Cgnl1 | DOWN |
| mmu-miR-451a | UP | NM\_026599 | Cgnl1 | DOWN |
| mmu-miR-7019-3p | UP | NM\_026599 | Cgnl1 | DOWN |
| mmu-miR-133a-3p | DOWN | NM\_010050 | Dio2 | UP |
| mmu-miR-676-5p | DOWN | NM\_010050 | Dio2 | UP |
| mmu-miR-467h | DOWN | NM\_010050 | Dio2 | UP |
| mmu-miR-3105-5p | DOWN | NM\_010050 | Dio2 | UP |
| mmu-miR-3076-3p | DOWN | NM\_010050 | Dio2 | UP |
| mmu-miR-451a | UP | NM\_001081386 | Cdh19 | DOWN |
| mmu-miR-378d | UP | NM\_001081386 | Cdh19 | DOWN |
| mmu-miR-144-3p | UP | NM\_001081131 | Dhtkd1 | DOWN |
| mmu-miR-204-3p | DOWN | NM\_007570 | Btg2 | UP |
| mmu-miR-133a-3p | DOWN | NM\_007570 | Btg2 | UP |
| mmu-miR-7019-3p | UP | NM\_009775 | Tspo | DOWN |
| mmu-miR-183-5p | UP | NM\_183136 | Spink8 | DOWN |
| mmu-miR-7092-3p | UP | NM\_183136 | Spink8 | DOWN |
| mmu-miR-378d | UP | NM\_013515 | Stom | DOWN |
| mmu-miR-7213-5p | UP | NM\_001081001 | Brca2 | DOWN |
| mmu-miR-8106 | UP | NM\_001039080 | Rbms2 | DOWN |
| mmu-miR-709 | UP | NM\_019711 | Rbms2 | DOWN |
| mmu-miR-6395 | UP | NM\_001136240 | Chdh | DOWN |
| mmu-miR-3962 | UP | NM\_001136240 | Chdh | DOWN |
| mmu-miR-6395 | UP | NM\_175343 | Chdh | DOWN |
| mmu-miR-466o-5p | UP | NM\_013780 | Npas3 | DOWN |
| mmu-miR-466c-3p | UP | NM\_013780 | Npas3 | DOWN |
| mmu-miR-466c-3p | UP | NM\_172546 | Cnksr3 | DOWN |
| mmu-miR-378d | UP | NM\_177780 | Dock5 | DOWN |
| mmu-miR-133a-3p | DOWN | NM\_001310774 | 11-Mar | UP |
| mmu-miR-1249-3p | DOWN | NM\_177597 | 11-Mar | UP |
| mmu-miR-466b-5p | DOWN | NM\_177597 | 11-Mar | UP |
| mmu-miR-219b-5p | DOWN | NM\_133202 | Trhr2 | UP |
| mmu-miR-448-3p | DOWN | NM\_133202 | Trhr2 | UP |
| mmu-miR-34b-5p | DOWN | NM\_133202 | Trhr2 | UP |
| mmu-miR-451a | UP | NM\_001293560 | Ccbl2 | DOWN |
| mmu-miR-205-5p | UP | NM\_001293560 | Ccbl2 | DOWN |
| mmu-miR-6395 | UP | NM\_013905 | Heyl | DOWN |
| mmu-miR-8106 | UP | NM\_001276248 | Cp | DOWN |
| mmu-miR-219a-5p | DOWN | NM\_001164441 | Ankrd33b | UP |
| mmu-miR-34a-5p | DOWN | NM\_001164441 | Ankrd33b | UP |
| mmu-miR-204-3p | DOWN | NM\_001164441 | Ankrd33b | UP |
| mmu-miR-671-5p | DOWN | NM\_001164441 | Ankrd33b | UP |
| mmu-miR-539-3p | DOWN | NM\_001164441 | Ankrd33b | UP |
| mmu-miR-214-3p | DOWN | NM\_001164441 | Ankrd33b | UP |
| mmu-miR-7025-3p | DOWN | NM\_001164441 | Ankrd33b | UP |
| mmu-miR-18a-3p | DOWN | NM\_001164441 | Ankrd33b | UP |
| mmu-miR-5100 | DOWN | NM\_026153 | Ankrd33b | UP |
| mmu-miR-1247-5p | DOWN | NM\_027496 | Ankrd33b | UP |
| mmu-miR-224-5p | DOWN | NM\_027496 | Ankrd33b | UP |
| mmu-miR-466o-5p | UP | NM\_001252438 | D16Ertd472e | DOWN |
| mmu-miR-186-3p | UP | NM\_001252438 | D16Ertd472e | DOWN |
| mmu-miR-186-3p | UP | NM\_001252439 | D16Ertd472e | DOWN |
| mmu-miR-466o-5p | UP | NM\_001252440 | D16Ertd472e | DOWN |
| mmu-miR-466o-5p | UP | NM\_019975 | Hacl1 | DOWN |
| mmu-miR-378d | UP | NM\_133191 | Eps8l2 | DOWN |
| mmu-miR-8106 | UP | NM\_010329 | Pdpn | DOWN |
| mmu-miR-466d-5p | UP | NM\_001244693 | St18 | DOWN |
| mmu-miR-709 | UP | NM\_027999 | Haus5 | DOWN |
| mmu-miR-34a-3p | DOWN | NM\_008309 | Htr1d | UP |
| mmu-miR-709 | UP | NM\_011639 | Trip6 | DOWN |
| mmu-miR-205-5p | UP | NM\_024180 | Ormdl2 | DOWN |
| mmu-miR-7019-3p | UP | NM\_010856 | Myh6 | DOWN |
| mmu-miR-182-5p | UP | NM\_001024910 | 43353 | DOWN |
| mmu-miR-183-5p | UP | NM\_001024911 | 43353 | DOWN |
| mmu-miR-182-5p | UP | NM\_001024911 | 43353 | DOWN |
| mmu-miR-466d-5p | UP | NM\_175486 | 6430571L13Rik | DOWN |
| mmu-miR-378d | UP | NM\_201368 | Xkr8 | DOWN |
| mmu-miR-466o-5p | UP | NM\_201368 | Xkr8 | DOWN |
| mmu-miR-182-5p | UP | NM\_201368 | Xkr8 | DOWN |
| mmu-miR-34c-3p | DOWN | NM\_172812 | Htr2a | UP |
| mmu-miR-34b-5p | DOWN | NM\_172812 | Htr2a | UP |
| mmu-miR-183-5p | UP | NM\_018782 | Calcrl | DOWN |
| mmu-miR-205-5p | UP | NM\_018782 | Calcrl | DOWN |
| mmu-miR-182-5p | UP | NM\_029295 | Cklf | DOWN |
| mmu-miR-451a | UP | NM\_025312 | Sostdc1 | DOWN |
| mmu-miR-709 | UP | NM\_025312 | Sostdc1 | DOWN |
| mmu-miR-7019-3p | UP | NM\_027127 | Gpx8 | DOWN |
| mmu-miR-466c-3p | UP | NM\_027127 | Gpx8 | DOWN |
| mmu-miR-1912-3p | DOWN | NM\_001037842 | Nat8f3 | UP |
| mmu-miR-3095-3p | DOWN | NM\_008207 | H2-T24 | UP |
| mmu-miR-3076-3p | DOWN | NM\_008207 | H2-T24 | UP |
| mmu-miR-709 | UP | NM\_027840 | Snx20 | DOWN |
| mmu-miR-1306-5p | DOWN | NM\_013739 | Dok3 | UP |
| mmu-miR-7025-3p | DOWN | NM\_013739 | Dok3 | UP |
| mmu-miR-7213-5p | UP | NM\_028877 | Palm3 | DOWN |
| mmu-miR-144-3p | UP | NM\_001159627 | Heph | DOWN |
| mmu-miR-3962 | UP | NM\_001159627 | Heph | DOWN |
| mmu-miR-466o-5p | UP | NM\_001159628 | Heph | DOWN |
| mmu-miR-466d-5p | UP | NM\_177922 | Mapk15 | DOWN |
| mmu-miR-709 | UP | NM\_177922 | Mapk15 | DOWN |
| mmu-miR-3076-3p | DOWN | NM\_181547 | Nostrin | UP |
| mmu-miR-448-3p | DOWN | NM\_001256493 | 2210404O09Rik | UP |
| mmu-miR-34b-5p | DOWN | NM\_153561 | Nudt6 | UP |
| mmu-miR-709 | UP | NM\_001042605 | Cd74 | DOWN |
| mmu-miR-34c-3p | DOWN | NM\_001113514 | Itga9 | UP |
| mmu-miR-219a-5p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-3547-3p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-3473b | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-532-3p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-466b-5p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-1306-5p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-539-3p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-879-5p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-6481 | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-18a-3p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-378d | UP | NM\_173428 | Sspo | DOWN |
| mmu-miR-466o-5p | UP | NM\_173428 | Sspo | DOWN |
| mmu-miR-709 | UP | NM\_173428 | Sspo | DOWN |
| mmu-miR-466o-5p | UP | NM\_001291857 | Aebp1 | DOWN |
| mmu-miR-709 | UP | NM\_001291857 | Aebp1 | DOWN |
| mmu-miR-6395 | UP | NM\_028186 | Nkd2 | DOWN |
| mmu-miR-466d-5p | UP | NM\_028186 | Nkd2 | DOWN |
| mmu-miR-375-3p | DOWN | NM\_001289492 | Gbp3 | UP |
| mmu-miR-676-5p | DOWN | NM\_001289493 | Gbp3 | UP |
| mmu-let-7b-3p | DOWN | NM\_018734 | Gbp3 | UP |
| mmu-miR-34a-3p | DOWN | NM\_018734 | Gbp3 | UP |
| mmu-miR-3103-3p | DOWN | NM\_018734 | Gbp3 | UP |
| mmu-miR-466b-5p | DOWN | NM\_010186 | Fcgr1 | UP |
| mmu-miR-6952-3p | DOWN | NM\_010186 | Fcgr1 | UP |
| mmu-miR-3473b | DOWN | NM\_027152 | Cd164l2 | UP |
| mmu-miR-1247-5p | DOWN | NM\_172479 | Slc38a5 | UP |
| mmu-miR-532-3p | DOWN | NM\_172479 | Slc38a5 | UP |
| mmu-miR-98-3p | DOWN | NM\_172479 | Slc38a5 | UP |
| mmu-miR-1298-5p | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-1249-3p | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-3547-3p | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-3473b | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-296-3p | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-467h | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-879-5p | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-669m-5p | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-6959-3p | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-3058-5p | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-3103-3p | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-18a-3p | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-6952-3p | DOWN | NM\_199018 | Stard8 | UP |
| mmu-miR-7213-5p | UP | NM\_175138 | Dnaic1 | DOWN |
| mmu-miR-151-3p | DOWN | NM\_001165980 | Dcaf17 | UP |
| mmu-miR-467h | DOWN | NM\_001165980 | Dcaf17 | UP |
| mmu-miR-224-5p | DOWN | NM\_001165980 | Dcaf17 | UP |
| mmu-miR-879-5p | DOWN | NM\_001165981 | Dcaf17 | UP |
| mmu-miR-6952-3p | DOWN | NM\_001165981 | Dcaf17 | UP |
| mmu-miR-6959-3p | DOWN | NM\_001165982 | Dcaf17 | UP |
| mmu-miR-532-5p | DOWN | NM\_001145920 | Runx2 | UP |
| mmu-miR-671-5p | DOWN | NM\_001145920 | Runx2 | UP |
| mmu-miR-532-3p | DOWN | NM\_001145920 | Runx2 | UP |
| mmu-let-7b-3p | DOWN | NM\_001145920 | Runx2 | UP |
| mmu-miR-98-3p | DOWN | NM\_001145920 | Runx2 | UP |
| mmu-miR-7025-3p | DOWN | NM\_001145920 | Runx2 | UP |
| mmu-miR-151-3p | DOWN | NM\_001146038 | Runx2 | UP |
| mmu-miR-466e-3p | DOWN | NM\_001146038 | Runx2 | UP |
| mmu-miR-483-5p | DOWN | NM\_001271627 | Runx2 | UP |
| mmu-miR-18a-3p | DOWN | NM\_001271627 | Runx2 | UP |
| mmu-miR-204-5p | DOWN | NM\_001271630 | Runx2 | UP |
| mmu-miR-219a-2-3p | DOWN | NM\_001271630 | Runx2 | UP |
| mmu-miR-669f-5p | DOWN | NM\_001271630 | Runx2 | UP |
| mmu-miR-466p-3p | DOWN | NM\_001271630 | Runx2 | UP |
| mmu-miR-670-5p | DOWN | NM\_001271630 | Runx2 | UP |
| mmu-miR-3547-3p | DOWN | NM\_001271631 | Runx2 | UP |
| mmu-miR-669f-5p | DOWN | NM\_001271631 | Runx2 | UP |
| mmu-miR-3095-3p | DOWN | NM\_001271631 | Runx2 | UP |
| mmu-miR-1249-3p | DOWN | NM\_009820 | Runx2 | UP |
| mmu-miR-1306-5p | DOWN | NM\_009820 | Runx2 | UP |
| mmu-miR-344e-5p | DOWN | NM\_009820 | Runx2 | UP |
| mmu-miR-7092-3p | UP | NM\_001033247 | Cfap44 | DOWN |
| mmu-miR-466d-5p | UP | NM\_001033247 | Cfap44 | DOWN |
| mmu-miR-219a-5p | DOWN | NM\_001039586 | Glyctk | UP |
| mmu-miR-204-3p | DOWN | NM\_001039586 | Glyctk | UP |
| mmu-miR-3058-5p | DOWN | NM\_001039586 | Glyctk | UP |
| mmu-miR-18a-3p | DOWN | NM\_001039586 | Glyctk | UP |
| mmu-miR-6952-3p | DOWN | NM\_001039586 | Glyctk | UP |
| mmu-miR-15b-3p | DOWN | NM\_174846 | Glyctk | UP |
| mmu-miR-144-3p | UP | NM\_001013360 | Npcd | DOWN |
| mmu-miR-183-5p | UP | NM\_001013360 | Npcd | DOWN |
| mmu-miR-709 | UP | NM\_029198 | 4930538K18Rik | DOWN |
| mmu-miR-133a-3p | DOWN | NM\_001314041 | Itga5 | UP |
| mmu-miR-133a-3p | DOWN | NM\_010577 | Itga5 | UP |
| mmu-miR-296-3p | DOWN | NM\_010577 | Itga5 | UP |
| mmu-miR-532-5p | DOWN | NM\_172693 | Galnt12 | UP |
| mmu-miR-466b-5p | DOWN | NM\_172693 | Galnt12 | UP |
| mmu-miR-1193-5p | UP | NM\_008610 | Mmp2 | DOWN |
| mmu-miR-133a-3p | DOWN | NM\_011408 | Slfn2 | UP |
| mmu-miR-5100 | DOWN | NM\_011408 | Slfn2 | UP |
| mmu-miR-219a-5p | DOWN | NM\_028603 | Zbtb8a | UP |
| mmu-miR-375-3p | DOWN | NM\_028603 | Zbtb8a | UP |
| mmu-miR-1247-5p | DOWN | NM\_028603 | Zbtb8a | UP |
| mmu-miR-224-5p | DOWN | NM\_028603 | Zbtb8a | UP |
| mmu-miR-466p-3p | DOWN | NM\_028351 | Rspo3 | UP |
| mmu-miR-1249-3p | DOWN | NM\_029152 | Efcab10 | UP |
| mmu-miR-670-5p | DOWN | NM\_029152 | Efcab10 | UP |
| mmu-miR-3058-5p | DOWN | NM\_029152 | Efcab10 | UP |
| mmu-miR-3103-3p | DOWN | NM\_029152 | Efcab10 | UP |
| mmu-miR-34c-5p | DOWN | NM\_001285435 | Adamtsl5 | UP |
| mmu-miR-224-5p | DOWN | NM\_001285435 | Adamtsl5 | UP |
| mmu-miR-204-5p | DOWN | NM\_001313713 | Sp100 | UP |
| mmu-miR-879-5p | DOWN | NM\_013673 | Sp100 | UP |
| mmu-miR-3547-3p | DOWN | NM\_025653 | 3110001I22Rik | UP |
| mmu-miR-34a-5p | DOWN | NM\_007766 | Pcdha4 | UP |
| mmu-miR-3547-3p | DOWN | NM\_172805 | Kcnh5 | UP |
| mmu-miR-1306-5p | DOWN | NM\_172805 | Kcnh5 | UP |
| mmu-miR-224-5p | DOWN | NM\_172805 | Kcnh5 | UP |
| mmu-miR-6481 | DOWN | NM\_172805 | Kcnh5 | UP |
| mmu-miR-204-5p | DOWN | NM\_010720 | Lipg | UP |
| mmu-miR-532-3p | DOWN | NM\_010720 | Lipg | UP |
| mmu-let-7b-3p | DOWN | NM\_010720 | Lipg | UP |
| mmu-miR-98-3p | DOWN | NM\_010720 | Lipg | UP |
| mmu-miR-879-5p | DOWN | NM\_001290283 | Pld6 | UP |
| mmu-miR-3105-5p | DOWN | NM\_001290283 | Pld6 | UP |
| mmu-miR-1249-3p | DOWN | NM\_183139 | Pld6 | UP |
| mmu-miR-6959-3p | DOWN | NM\_009518 | Wnt10a | UP |
| mmu-miR-448-3p | DOWN | NM\_130878 | Cdhr1 | UP |
| mmu-let-7b-3p | DOWN | NM\_130878 | Cdhr1 | UP |
| mmu-miR-1912-3p | DOWN | NM\_130878 | Cdhr1 | UP |
| mmu-miR-296-3p | DOWN | NM\_001289755 | Apoc3 | UP |
| mmu-miR-219a-5p | DOWN | NM\_001289833 | Apoc3 | UP |
| mmu-miR-339-5p | DOWN | NM\_001291054 | Mcm8 | UP |
| mmu-miR-3095-3p | DOWN | NM\_025676 | Mcm8 | UP |
| mmu-miR-18a-3p | DOWN | NM\_025676 | Mcm8 | UP |
| mmu-miR-216a-5p | DOWN | NM\_183201 | Slfn5 | UP |
| mmu-miR-3076-3p | DOWN | NM\_183201 | Slfn5 | UP |
| mmu-miR-670-5p | DOWN | NM\_183201 | Slfn5 | UP |
| mmu-miR-466e-3p | DOWN | NM\_183201 | Slfn5 | UP |
| mmu-miR-1298-5p | DOWN | NM\_153565 | Pcsk9 | UP |
| mmu-miR-532-5p | DOWN | NM\_153565 | Pcsk9 | UP |
| mmu-miR-34c-3p | DOWN | NM\_153565 | Pcsk9 | UP |
| mmu-miR-34c-5p | DOWN | NM\_153565 | Pcsk9 | UP |
| mmu-miR-671-5p | DOWN | NM\_153565 | Pcsk9 | UP |
| mmu-miR-466p-3p | DOWN | NM\_153565 | Pcsk9 | UP |
| mmu-miR-483-3p | DOWN | NM\_001081019 | Gm12657 | UP |
| mmu-miR-34a-5p | DOWN | NM\_008491 | Lcn2 | UP |
| mmu-miR-133a-3p | DOWN | NM\_008491 | Lcn2 | UP |
| mmu-miR-34b-5p | DOWN | NM\_008491 | Lcn2 | UP |
| mmu-miR-344e-5p | DOWN | NM\_008491 | Lcn2 | UP |
| mmu-miR-3058-5p | DOWN | NM\_008491 | Lcn2 | UP |

**Table S10. miRNAs with quantitative change over 1.5 folds and their characteristics in Intruder mice versus Observer mice.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **miRNA id** | **Expression (Intruder)** | **Expression (Observer)** | **Log2 Ratio (Intruder/Observer)** | **Up/down regulation** | **P value** |
| let-7a-1-3p | 107.680 | 6.573 | 4.064 | UP | 0 |
| miR-1298-5p | 97.003 | 2205.523 | -4.490 | DOWN | 0 |
| miR-204-3p | 21.893 | 102.543 | -2.214 | DOWN | 0 |
| miR-204-5p | 5094.923 | 28817.597 | -2.478 | DOWN | 0 |
| miR-211-5p | 34.400 | 117.660 | -1.749 | DOWN | 0 |
| miR-212-5p | 150.853 | 74.283 | 1.058 | UP | 0 |
| miR-219a-5p | 805.650 | 2019.947 | -1.301 | DOWN | 0 |
| miR-219b-5p | 22.927 | 368.247 | -3.992 | DOWN | 0 |
| miR-3065-5p | 41.607 | 8.617 | 2.294 | UP | 0 |
| miR-3074-5p | 1280.743 | 486.627 | 1.407 | UP | 0 |
| miR-34b-3p | 23.357 | 688.237 | -4.861 | DOWN | 0 |
| miR-34b-5p | 4.367 | 70.113 | -3.985 | DOWN | 0 |
| miR-34c-3p | 17.700 | 253.417 | -3.825 | DOWN | 0 |
| miR-34c-5p | 8.273 | 90.067 | -3.423 | DOWN | 0 |
| miR-375-3p | 49.230 | 253.680 | -2.336 | DOWN | 0 |
| miR-448-3p | 7.487 | 57.753 | -2.926 | DOWN | 0 |
| miR-449a-5p | 65.053 | 135.800 | -1.043 | DOWN | 0 |
| miR-451a | 301.273 | 820.137 | -1.455 | DOWN | 0 |
| miR-669c-5p | 22.243 | 3.123 | 2.870 | UP | 3.44E-299 |
| miR-199a-3p | 27.993 | 67.693 | -1.247 | DOWN | 1.26E-292 |
| miR-551b-3p | 70.720 | 32.767 | 1.163 | UP | 4.86E-282 |
| miR-673-5p | 52.860 | 25.470 | 1.137 | UP | 1.41E-204 |
| miR-10b-5p | 4.407 | 13.000 | -1.556 | DOWN | 1.68E-80 |
| miR-202-5p | 1.603 | 5.770 | -1.829 | DOWN | 7.60E-46 |
| miR-540-5p | 9.900 | 4.283 | 1.224 | UP | 6.89E-44 |
| miR-3105-5p | 0.233 | 2.253 | -3.248 | DOWN | 5.33E-35 |
| miR-467h | 0.220 | 2.280 | -3.288 | DOWN | 1.83E-34 |
| miR-483-5p | 0.827 | 3.520 | -2.075 | DOWN | 1.37E-33 |
| miR-466c-3p | 1.440 | 0.097 | 3.932 | UP | 1.99E-26 |
| miR-344e-5p | 0.087 | 1.357 | -3.952 | DOWN | 7.32E-25 |
| miR-205-5p | 1.660 | 4.350 | -1.375 | DOWN | 1.68E-23 |
| miR-466b-5p | 0.957 | 2.987 | -1.624 | DOWN | 3.90E-21 |
| miR-7019-3p | 3.483 | 1.357 | 1.442 | UP | 5.56E-21 |
| miR-3095-3p | 2.187 | 4.933 | -1.163 | DOWN | 5.77E-21 |
| miR-879-5p | 1.230 | 3.297 | -1.431 | DOWN | 1.28E-19 |
| miR-7070-3p | 3.457 | 1.477 | 1.294 | UP | 6.48E-18 |
| miR-1306-5p | 1.277 | 3.110 | -1.304 | DOWN | 2.51E-16 |
| miR-1912-3p | 0.040 | 0.590 | -3.985 | DOWN | 8.09E-12 |
| miR-214-3p | 0.557 | 1.643 | -1.533 | DOWN | 2.80E-11 |
| miR-669p-5p | 1.197 | 0.347 | 1.830 | UP | 5.70E-11 |
| miR-483-3p | 0.110 | 0.703 | -2.639 | DOWN | 5.29E-10 |
| miR-144-3p | 1.190 | 2.420 | -1.036 | DOWN | 1.98E-09 |
| miR-3080-5p | 1.627 | 0.680 | 1.311 | UP | 2.56E-09 |
| miR-7092-3p | 1.037 | 0.334 | 1.728 | UP | 4.53E-09 |
| miR-196b-5p | 0.297 | 0.930 | -1.627 | DOWN | 1.56E-07 |
| miR-224-5p | 0.727 | 1.600 | -1.121 | DOWN | 2.11E-07 |
| miR-344h-5p | 0.537 | 0.104 | 2.363 | UP | 2.37E-07 |
| miR-669m-5p | 0.540 | 0.110 | 2.363 | UP | 2.37E-07 |
| miR-709 | 0.410 | 0.060 | 2.796 | UP | 8.99E-07 |
| miR-214-5p | 0.233 | 0.737 | -1.633 | DOWN | 2.75E-06 |
| miR-421-5p | 0.563 | 0.190 | 1.597 | UP | 4.54E-05 |
| miR-1895 | 0.717 | 0.283 | 1.347 | UP | 5.52E-05 |
| miR-199b-5p | 0.210 | 0.603 | -1.511 | DOWN | 5.82E-05 |
| miR-3070-3p | 0.090 | 0.377 | -2.119 | DOWN | 5.86E-05 |

**Table S11. The changed miRNAs predict target mRNAs in Intruder mice versus Observer mice.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **miRNA id** | **Up/Down Regulation** | **Target id** | **Gene Name** | **Up/Down Regulation** |
| mmu-miR-199a-3p | DOWN | NM\_194066 | Ifi27 | UP |
| mmu-miR-199a-3p | DOWN | NM\_145100 | Lypd1 | UP |
| mmu-miR-3105-5p | DOWN | NM\_145100 | Lypd1 | UP |
| mmu-miR-483-5p | DOWN | NM\_145100 | Lypd1 | UP |
| mmu-miR-34b-3p | DOWN | NM\_012011 | Eif2s3y | UP |
| mmu-miR-3074-5p | UP | NM\_027212 | Med30 | DOWN |
| mmu-miR-448-3p | DOWN | NM\_027487 | Ccdc53 | UP |
| mmu-miR-7092-3p | UP | NM\_013732 | Cartpt | DOWN |
| mmu-miR-3074-5p | UP | NM\_001012336 | Mdk | DOWN |
| mmu-miR-540-5p | UP | NM\_001012336 | Mdk | DOWN |
| mmu-miR-344h-5p | UP | NM\_001012336 | Mdk | DOWN |
| mmu-miR-344h-5p | UP | NM\_001291481 | Mdk | DOWN |
| mmu-miR-344h-5p | UP | NM\_001291483 | Mdk | DOWN |
| mmu-miR-466c-3p | UP | NM\_009398 | Tnfaip6 | DOWN |
| mmu-let-7a-1-3p | UP | NM\_025863 | Trim59 | DOWN |
| mmu-miR-421-5p | UP | NM\_025863 | Trim59 | DOWN |
| mmu-miR-449a-5p | DOWN | NM\_025529 | Nudt8 | UP |
| mmu-miR-214-5p | DOWN | NM\_027560 | Arrdc2 | UP |
| mmu-miR-449a-5p | DOWN | NM\_001113412 | Fggy | UP |
| mmu-miR-205-5p | DOWN | NM\_029347 | Fggy | UP |
| mmu-miR-709 | UP | NM\_027263 | Apitd1 | DOWN |
| mmu-miR-1912-3p | DOWN | NM\_001160411 | Gstm4 | UP |
| mmu-miR-540-5p | UP | NM\_007763 | Crip1 | DOWN |
| mmu-miR-540-5p | UP | NM\_001101503 | A230065H16Rik | DOWN |
| mmu-miR-214-5p | DOWN | NM\_001198561 | H2-Q7 | UP |
| mmu-miR-3095-3p | DOWN | NM\_010394 | H2-Q7 | UP |
| mmu-miR-709 | UP | NM\_173744 | Tdrp | DOWN |
| mmu-miR-483-5p | DOWN | NM\_146106 | Lyplal1 | UP |
| mmu-miR-1298-5p | DOWN | NM\_008637 | Nudt1 | UP |
| mmu-miR-448-3p | DOWN | NM\_008637 | Nudt1 | UP |
| mmu-miR-199b-5p | DOWN | NM\_029331 | Nat8f4 | UP |
| mmu-miR-451a | DOWN | NM\_009373 | Tgm2 | UP |
| mmu-miR-214-5p | DOWN | NM\_009373 | Tgm2 | UP |
| mmu-miR-7019-3p | UP | NM\_001290506 | Mid1 | DOWN |
| mmu-miR-709 | UP | NM\_010797 | Mid1 | DOWN |
| mmu-miR-1912-3p | DOWN | NM\_010320 | Gng8 | UP |
| mmu-miR-449a-5p | DOWN | NM\_010399 | H2-T9 | UP |
| mmu-miR-214-3p | DOWN | NM\_010399 | H2-T9 | UP |
| mmu-miR-669p-5p | UP | NM\_025549 | Arrdc4 | DOWN |
| mmu-miR-10b-5p | DOWN | NM\_177033 | Vwc2 | UP |
| mmu-miR-7070-3p | UP | NM\_172264 | Chdh | DOWN |
| mmu-miR-669c-5p | UP | NM\_175343 | Chdh | DOWN |
| mmu-miR-344h-5p | UP | NM\_175343 | Chdh | DOWN |
| mmu-miR-10b-5p | DOWN | NM\_144797 | Metrnl | UP |
| mmu-miR-3105-5p | DOWN | NM\_144797 | Metrnl | UP |
| mmu-miR-214-5p | DOWN | NM\_144797 | Metrnl | UP |
| mmu-miR-1306-5p | DOWN | NM\_016875 | Ybx2 | UP |
| mmu-miR-214-5p | DOWN | NM\_016875 | Ybx2 | UP |
| mmu-miR-7070-3p | UP | NM\_028019 | Rnf135 | DOWN |
| mmu-miR-540-5p | UP | NM\_001163473 | 1810010H24Rik | DOWN |
| mmu-miR-344h-5p | UP | NM\_001163473 | 1810010H24Rik | DOWN |
| mmu-miR-1298-5p | DOWN | NM\_027320 | Ifi35 | UP |
| mmu-miR-199b-5p | DOWN | NM\_027320 | Ifi35 | UP |
| mmu-miR-669c-5p | UP | NM\_145554 | Ldlrap1 | DOWN |
| mmu-let-7a-1-3p | UP | NM\_010225 | Foxf2 | DOWN |
| mmu-miR-7092-3p | UP | NM\_010225 | Foxf2 | DOWN |
| mmu-miR-214-5p | DOWN | NM\_026597 | Fam212a | UP |
| mmu-miR-3105-5p | DOWN | NM\_198886 | Zbtb12 | UP |
| mmu-miR-467h | DOWN | NM\_198886 | Zbtb12 | UP |
| mmu-miR-1912-3p | DOWN | NM\_198886 | Zbtb12 | UP |
| mmu-miR-1895 | UP | NM\_001014836 | 4930404N11Rik | DOWN |
| mmu-miR-1306-5p | DOWN | NM\_001038887 | P2rx7 | UP |
| mmu-miR-196b-5p | DOWN | NM\_011027 | P2rx7 | UP |
| mmu-miR-224-5p | DOWN | NM\_011027 | P2rx7 | UP |
| mmu-miR-344e-5p | DOWN | NM\_001166164 | Ccdc74a | UP |
| mmu-miR-344e-5p | DOWN | NM\_013585 | Psmb9 | UP |
| mmu-miR-421-5p | UP | NM\_008899 | Pou3f2 | DOWN |
| mmu-miR-3095-3p | DOWN | NM\_010734 | Lst1 | UP |
| mmu-miR-204-5p | DOWN | NM\_026725 | Dusp23 | UP |
| mmu-miR-551b-3p | UP | NM\_026046 | Zfp329 | DOWN |
| mmu-miR-421-5p | UP | NM\_026046 | Zfp329 | DOWN |
| mmu-miR-709 | UP | NM\_001310837 | Sspn | DOWN |
| mmu-miR-421-5p | UP | NM\_010656 | Sspn | DOWN |
| mmu-miR-7070-3p | UP | NM\_175263 | Notum | DOWN |
| mmu-miR-669m-5p | UP | NM\_175263 | Notum | DOWN |
| mmu-miR-709 | UP | NM\_175263 | Notum | DOWN |
| mmu-miR-7092-3p | UP | NM\_010703 | Lef1 | DOWN |
| mmu-miR-144-3p | DOWN | NM\_001008501 | Zfp760 | UP |
| mmu-miR-1298-5p | DOWN | NM\_011957 | Creb3l1 | UP |
| mmu-miR-466b-5p | DOWN | NM\_011957 | Creb3l1 | UP |
| mmu-let-7a-1-3p | UP | NM\_010430 | Hic1 | DOWN |
| mmu-miR-551b-3p | UP | NM\_010430 | Hic1 | DOWN |
| mmu-miR-709 | UP | NM\_010430 | Hic1 | DOWN |
| mmu-miR-449a-5p | DOWN | NM\_008940 | Klk8 | UP |
| mmu-miR-1912-3p | DOWN | NM\_001037842 | Nat8f3 | UP |
| mmu-miR-214-5p | DOWN | NM\_001037842 | Nat8f3 | UP |
| mmu-miR-7070-3p | UP | NM\_008183 | Gstm2 | DOWN |
| mmu-miR-709 | UP | NM\_008183 | Gstm2 | DOWN |
| mmu-miR-421-5p | UP | NM\_019456 | Apbb1ip | DOWN |
| mmu-miR-7019-3p | UP | NM\_008542 | Smad6 | DOWN |
| mmu-miR-34b-3p | DOWN | NM\_001039115 | Zkscan4 | UP |
| mmu-miR-1306-5p | DOWN | NM\_001039115 | Zkscan4 | UP |
| mmu-miR-144-3p | DOWN | NM\_001039115 | Zkscan4 | UP |
| mmu-miR-214-5p | DOWN | NM\_001039115 | Zkscan4 | UP |
| mmu-miR-199a-3p | DOWN | NM\_025506 | Riiad1 | UP |
| mmu-miR-669p-5p | UP | NM\_011532 | Tbx1 | DOWN |
| mmu-miR-1912-3p | DOWN | NM\_028608 | Glipr1 | UP |
| mmu-miR-144-3p | DOWN | NM\_028608 | Glipr1 | UP |
| mmu-miR-199b-5p | DOWN | NM\_028608 | Glipr1 | UP |
| mmu-miR-199a-3p | DOWN | NM\_001291044 | Nudt6 | UP |
| mmu-miR-34b-5p | DOWN | NM\_153561 | Nudt6 | UP |
| mmu-miR-196b-5p | DOWN | NM\_153561 | Nudt6 | UP |
| mmu-miR-204-3p | DOWN | NM\_023275 | Rhoj | UP |
| mmu-miR-205-5p | DOWN | NM\_023275 | Rhoj | UP |
| mmu-miR-3105-5p | DOWN | NM\_001128093 | Siah3 | UP |
| mmu-miR-1306-5p | DOWN | NM\_001128093 | Siah3 | UP |
| mmu-miR-1912-3p | DOWN | NM\_001128093 | Siah3 | UP |
| mmu-miR-214-3p | DOWN | NM\_001128093 | Siah3 | UP |
| mmu-miR-7019-3p | UP | NM\_172142 | Nfkbid | DOWN |
| mmu-miR-3070-3p | DOWN | NM\_001042670 | Mterf1b | UP |
| mmu-miR-34c-3p | DOWN | NM\_001113514 | Itga9 | UP |
| mmu-miR-219a-5p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-10b-5p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-466b-5p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-879-5p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-1306-5p | DOWN | NM\_133721 | Itga9 | UP |
| mmu-miR-669m-5p | UP | NM\_146015 | Efemp1 | DOWN |
| mmu-miR-709 | UP | NM\_146015 | Efemp1 | DOWN |
| mmu-miR-3080-5p | UP | NM\_013503 | Drd5 | DOWN |
| mmu-miR-709 | UP | NM\_001291857 | Aebp1 | DOWN |
| mmu-miR-1895 | UP | NM\_009636 | Aebp1 | DOWN |
| mmu-miR-196b-5p | DOWN | NM\_009180 | St6galnac2 | UP |
| mmu-miR-1298-5p | DOWN | NM\_172914 | Ccdc113 | UP |
| mmu-miR-451a | DOWN | NM\_172914 | Ccdc113 | UP |
| mmu-miR-1912-3p | DOWN | NM\_172914 | Ccdc113 | UP |
| mmu-miR-144-3p | DOWN | NM\_172914 | Ccdc113 | UP |
| mmu-let-7a-1-3p | UP | NM\_001039373 | Mtcp1 | DOWN |
| mmu-miR-375-3p | DOWN | NM\_001289492 | Gbp3 | UP |
| mmu-miR-7070-3p | UP | NM\_183146 | Zfp729a | DOWN |
| mmu-miR-202-5p | DOWN | NM\_023386 | Rtp4 | UP |
| mmu-miR-3074-5p | UP | NM\_001291094 | Gm3383 | DOWN |
| mmu-miR-199b-5p | DOWN | NM\_177829 | Spink10 | UP |
| mmu-miR-1298-5p | DOWN | NM\_019455 | Hpgds | UP |
| mmu-miR-466b-5p | DOWN | NM\_019455 | Hpgds | UP |
| mmu-miR-34b-3p | DOWN | NM\_016868 | Hif3a | UP |
| mmu-miR-669p-5p | UP | NM\_001195431 | Islr | DOWN |
| mmu-miR-709 | UP | NM\_029198 | 4930538K18Rik | DOWN |
| mmu-miR-669m-5p | UP | NM\_001177319 | Tfpi | DOWN |
| mmu-miR-3080-5p | UP | NM\_011576 | Tfpi | DOWN |
| mmu-let-7a-1-3p | UP | NM\_001033929 | Thnsl2 | DOWN |
| mmu-miR-7019-3p | UP | NM\_011023 | Otx1 | DOWN |
| mmu-miR-7092-3p | UP | NM\_011023 | Otx1 | DOWN |
| mmu-miR-212-5p | UP | NM\_001289766 | Zap70 | DOWN |
| mmu-miR-669p-5p | UP | NM\_001289766 | Zap70 | DOWN |
| mmu-miR-199a-3p | DOWN | NM\_001177369 | Nfkb2 | UP |
| mmu-miR-34c-5p | DOWN | NM\_019408 | Nfkb2 | UP |
| mmu-miR-344e-5p | DOWN | NM\_019408 | Nfkb2 | UP |
| mmu-miR-204-3p | DOWN | NM\_001008502 | Bbs12 | UP |
| mmu-miR-483-5p | DOWN | NM\_001008502 | Bbs12 | UP |
| mmu-miR-449a-5p | DOWN | NM\_001255992 | Bbs12 | UP |
| mmu-miR-202-5p | DOWN | NM\_001255992 | Bbs12 | UP |
| mmu-miR-879-5p | DOWN | NM\_001255992 | Bbs12 | UP |
| mmu-miR-1298-5p | DOWN | NM\_001171512 | Obscn | UP |
| mmu-miR-449a-5p | DOWN | NM\_001171512 | Obscn | UP |
| mmu-miR-1306-5p | DOWN | NM\_001171512 | Obscn | UP |
| mmu-miR-214-3p | DOWN | NM\_001171512 | Obscn | UP |
| mmu-miR-144-3p | DOWN | NM\_001171512 | Obscn | UP |
| mmu-miR-219b-5p | DOWN | NM\_199152 | Obscn | UP |
| mmu-miR-34c-5p | DOWN | NM\_199152 | Obscn | UP |
| mmu-miR-34b-5p | DOWN | NM\_199152 | Obscn | UP |
| mmu-miR-449a-5p | DOWN | NM\_199152 | Obscn | UP |
| mmu-miR-1306-5p | DOWN | NM\_199152 | Obscn | UP |
| mmu-miR-214-3p | DOWN | NM\_199152 | Obscn | UP |
| mmu-miR-199b-5p | DOWN | NM\_199152 | Obscn | UP |
| mmu-miR-551b-3p | DOWN | NM\_001166064 | Syde2 | DOWN |
| mmu-miR-466b-5p | DOWN | NM\_009811 | Casp6 | UP |
| mmu-miR-205-5p | DOWN | NM\_001163064 | AU041133 | UP |
| mmu-miR-709 | UP | NM\_026815 | Upk1a | DOWN |
| mmu-miR-34c-5p | DOWN | NM\_001285435 | Adamtsl5 | UP |
| mmu-miR-224-5p | DOWN | NM\_001285435 | Adamtsl5 | UP |
| mmu-miR-204-5p | DOWN | NM\_001313713 | Sp100 | UP |
| mmu-miR-199a-3p | DOWN | NM\_001313714 | Sp100 | UP |
| mmu-miR-879-5p | DOWN | NM\_013673 | Sp100 | UP |
| mmu-miR-1895 | UP | NM\_007534 | Bcl2a1b | DOWN |
| mmu-miR-669p-5p | UP | NM\_001033243 | Ccdc114 | DOWN |
| mmu-miR-205-5p | DOWN | NM\_001285498 | Tead2 | UP |
| mmu-miR-483-3p | DOWN | NM\_011565 | Tead2 | UP |
| mmu-miR-34c-5p | DOWN | NM\_001282006 | Tekt1 | UP |
| mmu-miR-211-5p | DOWN | NM\_001282006 | Tekt1 | UP |
| mmu-miR-3070-3p | DOWN | NM\_001282006 | Tekt1 | UP |
| mmu-let-7a-1-3p | UP | NM\_008026 | Fli1 | DOWN |
| mmu-miR-1895 | UP | NM\_008026 | Fli1 | DOWN |
| mmu-miR-3105-5p | DOWN | NM\_001290283 | Pld6 | UP |
| mmu-miR-879-5p | DOWN | NM\_001290283 | Pld6 | UP |
| mmu-miR-1298-5p | DOWN | NM\_001033260 | Stox1 | UP |
| mmu-miR-219a-5p | DOWN | NM\_001289833 | Apoc3 | UP |
| mmu-miR-669m-5p | UP | NM\_001012273 | Birc5 | DOWN |
| mmu-miR-483-3p | DOWN | NM\_001081019 | Gm12657 | UP |
| mmu-miR-1895 | UP | NM\_016933 | Ptprcap | DOWN |
| mmu-miR-669c-5p | UP | NM\_001024138 | Gpr139 | DOWN |
| mmu-miR-7092-3p | UP | NM\_011902 | Tekt2 | DOWN |
| mmu-miR-1895 | UP | NM\_001291220 | Isg20 | DOWN |
| mmu-miR-34b-5p | DOWN | NM\_008491 | Lcn2 | UP |
| mmu-miR-344e-5p | DOWN | NM\_008491 | Lcn2 | UP |