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**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.

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**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.

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**Figure S3. Dissection of amygdala tissue was based on The Mouse Brain in Stereotaxic Coordinates.**

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**Figure S4.** The anxiety level tested by elevated-plus maze for control (blue bars), observer (green bars) and intruder groups (pink bars) before (day0) and after social stress (day6). The indicator used to measure the anxiety in the mice was the percentage of time that mice spent in the open arms. Values in controls are 10.54±2.31 and 8.90±1.73 at Day0 and Day6 (p=0.61, paired t-test, n=12), respectively. Values in observers are 10.56±2.44 and 4.80±1.36 before and after psychological stress (p<0.05, paired-t test, n=11) .Values in intruders are 10.44±2.18 and 2.60±0.65 (p<0.01, paired t-test, n=13) before and after physical/psychological stresses.

**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 |