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Transcriptional remodeling in primary hippocampal astrocytes from an Alzheimer's disease mouse model

Ruffinatti F[a#], Tapella L[a#], Gregnanin I[b], Stevano A[a], Chiorino G[b], Canonico PL[a], Distasi C[a], Genazzani AA*[a], Lim D*[a]

Affiliations:

[a]Department of Pharmaceutical Sciences, Università del Piemonte Orientale, Via Bovio 6, 28100, Novara, Italy; [b]Fondazione Edo ed Elvo Tempia, Via Malta, 3, 13900, Biella, Italy

* **Corresponding authors:** Dmitry Lim, Department of Pharmaceutical Sciences, Università del Piemonte Orientale, Via Bovio 6, 28100, Novara, Italy. E-mail: dmitry.lim@uniupo.it; Armando Genazzani, Department of Pharmaceutical Sciences, Università del Piemonte Orientale, Via Bovio 6, 28100, Novara, Italy. E-mail: armando.genazzani@uniupo.it

# **These Authors contributed equally.**

Running title: Transcriptome of cultured astrocytes from 3xTg-AD mice.

Keywords: whole-genome microarray, 3xTg-AD mice, cultured astroglia, cross-platform normalization, early Alzheimer's disease, FAD mutations.

Abstract

Background: It is well known that alterations in astrocytes occur in Alzheimer's Disease and reactive astrogliosis is one of the hallmarks of the disease. Recently, data has emerged that suggests that alterations in astrocytes may also occur early in the pathogenesis of the disease.

Objective: The aim of present work was to characterize the transcriptional alterations occurring in cultured astrocytes from 3xTg-AD mouse pups compared to control non-transgenic mice. Furthermore, we also compared these changes to those reported by others in astrocytes from symptomatic AD mice.

Method: We conducted a whole-genome microarray study on primary cultured astrocytes from the hippocampus of 3xTg-AD and non-transgenic mouse newborn pups. We used cross-platform normalization and an unsupervised hierarchical clustering algorithm to compare our results with other datasets of cultured or freshly isolated astrocytes, including those isolated from plaque-stage APPswe/PS1dE9 AD mice.

Results: We found a set of 993 genes differentially expressed in 3xTg-AD as compared with non-Tg astrocytes. Over-represented gene ontology terms were related to calcium, cell-cell communication, mitochondria, transcription, nucleotide binding and phosphorylation. Of note, no genes related to inflammation were found in cultured 3xTg-AD astrocytes. Comparison with astrocytes isolated from plaque stage APPswe/PS1dE9 showed that 882 out of 993 genes were selectively changed in primary 3xTg-AD astrocytes while 50 genes were co-regulated and 61 were anti-regulated (regulated in the opposite direction in the datasets).

Conclusion: Our data show that in cultured astrocytes from an AD mouse model, transcriptional changes occur and are different from those reported in models mimicking later stages of the disease.

1. INTRODUCTION

Alzheimer's disease (AD) is the most common dementia in the elderly. AD begins with a loss of episodic memory and progresses to cognitive decline and dementia. At the cellular level, AD is characterized by dysfunction of synaptic connectivity and neuronal death [1] and it is established that reactive astrogliosis accompanies the late stages of AD [2].

Astrocytes are a heterogeneous group of cells in the nervous system responsible for housekeeping and homeostatic functions. Implicated in pathogenesis of many neurodegenerative diseases [3], astrocytes may be important determinants of synaptic dysfunction in incipient AD [4; 5]. For example, recent investigations on mice bearing mutations associated with familial forms of AD (FAD) have demonstrated that, during the disease, astrocytes do not merely become activated, but undergo complex biphasic changes. Thus in 3xTg-AD mice, at three months of age astrocytes are found to be atrophic, but, after the burden of amyloid-β (Aβ) deposits, turn to hypertrophic in the areas proximal to amyloid plaques [5; 6].

Transcriptome studies on whole-brain tissues and on fluorescence-activated cell sorting (FACS)-isolated astrocytes from human AD postmortem brains as well as from a symptomatic AD mouse model have shown that at the late AD stages astrocytes exhibit strong inflammatory phenotypes concomitantly with Aβ plaque development [7]. However, much less is known about gene expression alterations and astroglial remodeling in pre-symptomatic AD. Previously, we have shown that, in primary astroglial cultures, Aβ deregulates the expression of genes involved in Ca^{2+} signaling through the activation of Ca^{2+}-dependent gene transcription which determines increased response to a group I glutamate receptor agonist DHPG [8-10]. Deregulation of Ca^{2+} signaling has been found also in astrocytes from the hippocampus of 3xTg-AD mice, in which ATP, but not DHPG-induced Ca^{2+} signals were potentiated in a region-specific manner [11].

In the present study we used primary cultures of purified hippocampal astrocytes from 3xTg-AD mouse pups to explore the effects of FAD-related mutations on gene expression. Using whole-genome microarray and gene ontology (GO) analysis we show that FAD mutations alter expression of a distinct set of genes related to calcium, phosphorylation, mitochondria, gene expression and cell-cell communication.

2. MATERIALS AND METHODS

2.1. Animal handling

The 3xTg-AD mice were obtained from Alexej Verkhratsky (Manchester University, UK; [12], 3xTg-AD mice develop both senile plaques and neurofibrillary tangles [12]). 3xTg-AD and non-transgenic (non-Tg) control mice were housed in the animal facility of the Università del Piemonte Orientale, were kept at three to four per cage, and had unlimited access to water and food. Animals were managed in accordance with European directive 2010/63/UE and with Italian law D.l. 26/2014. The procedures were approved by the local animal-health and ethical committee (Università del Piemonte Orientale) and were authorized by the national authority (Istituto Superiore di Sanità; authorization number N. 22/2013). All efforts were made to reduce the number of animals by following the 3R's rule.

2.2. Astroglial cultures

Primary astroglial cultures were from postnatal day 0-3 (P0-P3) non-Tg and 3xTg-AD mouse pups. Hippocampi were dissected from brains, washed twice in cold HBSS (Sigma, Cat. H6648), minced with a scalpel and incubated in 1x Trypsin (Sigma) for 25 min (5 ml of Trypsin for each 6-8 pups). After neutralization with complete culture medium (DMEM (Sigma, Cat. D5671) supplemented with 2 mM glutamine and 1% penicillin/streptomycin (P/S, both from Sigma)), the tissues were centrifuged (250 xg 3 min) and resuspended in HBSS supplemented with 10 % fetal bovine serum (FBS, Gibco, Cat. 10270), 20 u/ml DNAse and $MgSO_4$. Hippocampal tissues were disaggregated with 30 strokes of 1000 µl automatic pipette. 5 ml of HBSS were added and tissue residues were allowed to sediment. Cellular suspension was transferred in a fresh falcon and, after centrifugation (200 xg, 5 min), pellet was resuspended in complete culture medium and cells were plated in 25 mm^2 flasks (Falcon, Corning, USA). When confluent, astrocytes were detached with trypsin and contaminating microglial cells were eliminated by negative selection using anti-CD11b-conjugated magnetic-activated cell sorting (MACS) beads (Miltenyi Biotech, Cat. 130-093-634). MACS was performed according to manufacturer's instructions. At the end of the separation purified astrocytes were resuspended in complete culture medium and plated for experiments. Immunocytochemical examination using anti-GFAP and anti-Iba1 antibody showed absence of microglial cells present in cultures.

2.3. RNA isolation and whole-genome microarray

Gene expression profiling was evaluated from 5 samples from non-Tg control mice and 5 samples from 3xTg-AD mice. For each sample $0.5x10^6$ of MACS-purified astrocytes were plated in 65 mm Petri dishes in 4 ml of complete culture medium. At 80% confluence the medium was changed to 4 ml DMEM/F12 (Gibco, Cat. 21041-025, supplemented with 2 mM glutamine and 1% P/S). After 24 hours astrocytes were washed with PBS and lysed in 700 µl QIAzole (Qiagen, Milan, Italy). Total RNA was extracted using Absolutely RNA miRNA kit (Agilent) according to manufacturer's instructions. The samples were subject to one-color gene expression profiling with SurePrint G3 mouse GE 8x60K microarrays (Agilent Technologies, Santa

Clara, CA). Slides were scanned with an Agilent C dual-laser microarray scanner and images analyzed with Agilent Feature Extraction software. Raw data were normalized through the quantile between-array normalization algorithm and the empirical Bayes method (LIMMA/Bioconductor package) was used to compute a moderated *t*-statistics for two-class comparison analysis [13]. *P*-values were adjusted for multiple testing by using Benjamini-Hochberg (BH) false discovery rate (FDR) correction [14]. Because of the high degree of correlation between the genewise variance and the average expression ($\rho = 0.9$), no intensity filtering procedure was applied to not alter the variance distribution. On the contrary, LIMMA was applied to the whole unfiltered dataset to preserve full statistical power and then the expression values of the genes called as significantly regulated have been checked *a posteriori* [15]. Functional annotation was performed using the DAVID Bioinformatics Resources v. 6.7 (https://david.ncifcrf.gov/) [16]. False discovery rate (FDR) correction was applied to overrepresented GO terms and cutoff was set to $p < 0.1$ (10%).

2.4. Real-time PCR

Validation of the microarray results by real-time PCR was performed on 4 non-Tg and 4 3xTg-AD astroglial cultures. Total RNA extraction was performed as described above. 0.5-1 µg of total RNA was retrotranscribed using random hexamers and ImProm-II RT system (Promega, Milan, Italy). Real-time PCR was performed using iTaq qPCR master mix according to manufacturer's instructions (Bio-Rad, Segrate, Italy) on a SFX96 Real-time system (Bio-Rad). To normalize raw real-time PCR data, three housekeeping genes were tested: i) β-actin (Actin), ii) S18 ribosomal subunit and iii) polymerase (RNA) II (DNA directed) polypeptide A (RP2a). S18 showed highest stability across the samples and was used for normalization of raw data in all real-time PCR experiments. Sequences of oligonucleotide primers are provided in Supplementary Materials. The real-time PCR data are expressed as delta-C(t) of gene of interest to S18 allowing appreciation of the expression level of a single gene.

2.5. Comparison with the transcriptome database of acutely isolated purified CNS cellular models

To assess the relationship existing among our astrocyte cultures and the samples belonging to the transcriptome framework of acutely isolated purified central nervous system (CNS) cell types as provided by Cahoy et al. [17], GSE9566 series was downloaded from Gene Expression Omnibus (GEO) database (https://www.ncbi.nlm.nih.gov/geo/). It consisted in a transcriptome database made up of 48 independent murine samples measuring the expression levels of more than 20,000 genes. Three main CNS cell types, astrocytes, neurons and oligodendrocytes, are profiled at various postnatal ages, allowing for the identification of those enrichment patterns specifically characterizing each cell type. In particular, for this study, Affymetrix Mouse Genome 430 2.0 Array platform was used, featuring 45,037 oligonucleotide probes (representing 20,832 unique genes) per array. Text matrix file available from GEO database contained $\log_2$ expression values that were already between-array normalized. In order to relate our expression data with those provided by Cahoy and colleagues an "early integration" approach was needed which allowed the data to merge before analysis [18]. To this purpose, the cross-platform normalization (XPN) algorithm was used as described by Shabalin et al. in [19] to produce a single unified dataset. More in detail, Ensembl BioMart on-line application (https://www.ensembl.org) was used to match probes from different platforms (namely Agilent and Affymetrix) and just those 20,932 probes (12,416 unique genes) identified by Cahoy as significantly and consistently expressed in at least one CNS cell type (Supplemental Table S3 in [17]) were used to assembly the common probe-set. This procedure led to a final list of 18,135 cross-platform corresponding probes, representing 11,589 different genes (93.3% of Cahoy's filtering selection). Moreover, only the samples corresponding to one of the groups of interest were retained for XPN procedure and downstream comparison with our dataset, namely acutely isolated P17 astrocytes (n=5), cultured astroglia (n=4) and acutely isolated P16 neurons (n=3). Prior to XPN merging, expression values from each platform were column standardized (zero mean and unitary standard deviation). To reliably evaluate the distance of our samples compared to those from Cahoys's dataset—that includes many different experimental groups—non-Tg $\log_2$ expression values were separately integrated into Cahoy's dataset through XPN algorithm. This precaution allowed indeed to maximally reduce batch effect and helped to rule out possible confounding factors reflecting the inner structure of the two datasets. Specifically, the common experimental conditions adopted for tissue dissociation and cell culturing were likely to put in contact our two cellular models when clustering samples, thus possibly distorting their individual relation to Cahoy's models. Unsupervised hierarchical clustering for sample positioning assessment was performed using Euclidean metric and average linkage criterion. All dendrograms presented in the text reflect this particular choice even if other different metrics would have led to analogous results from a qualitative point of view (not shown). The analysis then proceeded as described in the Results section, searching for those particular genes that were enriched in (or shared by) non-Tg astrocytes cultures compared to the cellular models of interest present in Cahoy's dataset. All these ranked lists of differentially expressed genes were produced through a two-class unpaired rank product (RP) algorithm [20], conducted on $\log_2$ expression values as returned by XPN procedure, controlling FDR at 0.005 level as detailed in Results section. Just for the gene list-associated heatmaps, a further gene/row-wise normalization step (log-mean subtraction) was performed in order to represent the expression values of each gene in terms of $\log_2$ fold-enrichment over their mean value across all samples.

2.6. Comparison with APPswe/PS1dE9 dataset and normally aged mice

To compare our microarray dataset with the AD dataset from the APPswe/PS1dE9 double-transgenic mouse model [7], GSE74615 series was downloaded from Gene Expression Omnibus (GEO) database (https://www.ncbi.nlm.nih.gov/geo/). It consisted in a text matrix file containing $\log_2$ intensity values from 22 samples of cortical microglia and astrocytes isolated from 15- to 18-month-old AD and wild-type (WT) mice. RNA samples were hybridized onto Mouse GE 4x44k v2 microarrays (Agilent). In particular, each array featured 39,429 different probes, the 1% of which (399 probes) being within-array replicates, for a total of 43,020 probes per array. Downloaded data were already normalized through quantile between-array algorithm. Thanks to the presence of an internal control (WT mice), we could address this comparison avoiding the introduction of additional confounding factors by a "late integration" (or meta-analysis) approach [18]. A cross-platform normalization between Orre's and our dataset was indeed not suitable being the two studies representative of two different healthy and AD pathological models. Therefore, unlike what we did for integrating our dataset into the transcriptome framework provided by Cahoy and colleagues, in this case the individual microarray studies were separately processed to obtain two lists of differentially expressed genes (ranked on the basis of their *p*-values) which have been then combined in the final step of the analysis. In particular, for both dataset, differential expression of all genes among groups was tested for significance through an empirical Bayes moderated *t*-test (LIMMA/Bioconductor package). *P*-values were adjusted for multiple comparisons by using BH FDR correction and genes featuring an adj.p.val ≤ 0.05 were marked as significant. APPswe/PS1dE9 whole dataset was employed for the empirical Bayes test, but replicate probes were finally collapsed by mean and microglia data were discarded to retain only the contrast of interest (AD astrocytes vs. WT astrocytes) for downstream comparison with our dataset (4 samples for AD and 4 samples for WT; 2,578 differentially expressed unique genes out of 39.429 different probes). Sharing the same technological platform (i.e. Agilent), the gene-matching procedure between the two datasets was straightforward. All of our 993 significant genes found a correspondence into the APPswe/PS1dE9 dataset: some of them were co- or anti-regulated genes while others genes resulted significantly regulated only in our model. The analysis of the transcriptome intersections between the two datasets then proceeded as described in the *Results,* while its statistical background is detailed in *Appendix: Common significant gene analysis*. To compare the changes in cultured 3xTg-AD astrocytes with those in young-versus-old mice reported by [21], as there is no available original dataset for young mice in GEO database, a list of 926 significantly regulated genes in aged compared to young cortical astrocytes was directly used for comparison (see Supplementary Table 3 in [21]). Official gene symbols were used for gene matching and the whole array (Agilent, Mouse GE 4x44k v2 microarray) has been used as reference for the subsequent analysis. The significance of the transcriptome intersections was assessed through the same approach already mentioned and described in *Appendix*.

2.7. Comparison with human AD dataset

The human AD reference dataset used for comparing our microarray output was made available by Berchtold et al. [22] through the publicly accessible GEO database: series accession number GSE48350. This dataset consisted of 253 samples from 4 brain regions (hippocampus, entorhinal cortex, superior frontal cortex and post-central gyrus), from both normal controls and AD patients. RNA samples were hybridized onto Affymetrix Human HgU133 plus 2.0 microarrays. In particular, each array featured 54,675 different probes and no within-array replicates. Downloaded data were already between-array normalized (GC-Robust Multi-array background adjustment and quantile normalization). Also in this case, thanks to the presence of an internal control (normal non-AD subjects), we could address this comparison between different models through the same "late integration" approach [18] already used for the comparison with APPswe/PS1dE9 double-transgenic mouse dataset. Again, individual microarray studies were separately processed to identify two lists of differentially expressed genes (ranked on the base of their *p*-values) which have been then combined in the final step. In particular, data from Berchtold's dataset were then $\log_2$-transformed and differential expression of all genes among the groups of interest (69- to 99-year-aged control hippocampus, n=24; 74- to 95-year-aged AD hippocampus, n=18) was tested for significance through an empirical Bayes moderated *t*-test (LIMMA/Bioconductor package). *P*-values were adjusted for multiple comparisons by using BH FDR correction and genes with an adj.p.val ≤ 0.05 were marked as significant. This procedure led to the identification of 746 differentially expressed genes. Ensembl BioMart on-line application (https://www.ensembl.org) was then used to find human-mouse orthologous genes and to match probes from different platforms (Agilent and Affymetrix respectively). A virtual set of 21,213 one-to-one orthologous genes was obtained (96.4% of which featuring a "high human orthology confidence"), but just 495 out of the 993 genes that were significant into our murine dataset found an orthologous correspondence within the human dataset provided by Berchtold et al. (329 genes did not featured any human orthology while 169 were not present in Berchtold's dataset). As for the previous comparison with APPswe/PS1dE9 samples, we found co-regulated genes, anti-regulated genes and genes significantly regulated only in our model. The subsequent analysis of the transcriptome intersections between the two datasets is described in the Results section while its statistical background is detailed in the Appendix *Common significant gene analysis.*

2.8. Software used for microarray analysis

Quantile normalizations and empirical Bayes moderated *t*-tests were conducted in R (using LIMMA/Bioconductor package). XPN algorithm was run in MATLAB environment using the code as provided by the author [19]. RP procedures for gene selection and unsupervised hierarchical clustering, such as unsupervised hierarchical clustering and related dendrograms were performed using MeV 4.9.0 (Multi Experiment Viewer, TM4 Software Suite) [23]. The same software was used also to draw dendrograms and heatmaps from expression data. Common significant gene analysis was performed as detailed in *Appendix* through homemade code.

3. RESULTS

3.1. 993 genes are differentially expressed in 3xTg-AD vs non-Tg cultured hippocampal astrocytes

Nine independent cultures were prepared from non-Tg or 3xTg-AD mice. Before plating, astroglial cultures were depleted of microglial cells to avoid contaminations. This resulted in virtually no microglial cells detected by anti-Iba1 immunocytochemical analysis (Fig. 1A). Five non-Tg and five 3xTg-AD cultures were processed for microarray analysis while the remaining cultures were used for validation using real-time PCR. A total of 55,681 Agilent mouse probes were analyzed. Based on our previous experience, we expected overall low changes in gene expression [9; 10]. We therefore did not apply any cut-off for fold change and considered all genes which passed BH FDR correction for multiple comparisons (Adjusted p-value, Adj.p.val) with $p \leq 0.05$. Probes representing long intergenic non-coding RNAs (lincRNA), as well as probes with no gene symbol, no gene name and no description were excluded from the selection. Such an approach yielded 993 differentially expressed genes in 3xTg-AD vs non-Tg samples (Fig. 1B). 536 genes were up-regulated and 457 genes were down-regulated. The full list of differentially expressed genes may be found in Supplementary Table 1, while the top 40 of up- and 40 down regulated genes are listed in Table 1. In total, 33 genes were used for validation by real-time PCR on 4 independent cultures. Of these, 27 genes passed validation and are listed in Supplementary Table 2. Figure 2A demonstrates the high degree of correlation between differential expression obtained in microarray and real-time PCR, while real-time PCR results of a set of 14 genes is shown in Figure 2B, demonstrating the reliability of the microarray results.

3.2. Gene Ontology analysis does not detect inflammation but impairment of cell-cell communication and transcription.

The possible biological significance of the differentially expressed genes was analyzed using DAVID online GO tool v. 6.7 (https://david.ncifcrf.gov/). In the up-regulated genes, the most general over-represented GO terms were *phosphoprotein*, *cytoplasm*, *alternative splicing*, *acetylation*, *transferase* and *nucleotide binding*. More specific GO terms included *mitochondrion*, *ATP binding*, *cell projection*, *Zinc finger*, *C2H2-like* and *Krueppel-associated box, compositionally biased region:Poly-Arg* and *vesicle* (Table 2). The down-regulated genes were specifically enriched in the following general GO terms: *phosphoprotein*, *cytoplasm*, *alternative splicing*, *cytoplasm* and *transport.* More specific over-represented GO terms were *nucleolus*, *cell projection* and *cell junction*, *calcium*, *apoptotic process*, *synapse* and *dendritic spine*, and *extrinsic apoptotic signaling pathway*. The most enriched GO terms among down-regulated genes were *EH domain*, *positive regulation of T cell mediated cytotoxicity*, *triglyceride catabolic process* and *extrinsic apoptotic signaling pathway* (Table 2). Previously, we reported that astroglial Ca^{2+} signaling is deregulated in Aβ-treated astrocytes [8-10] as well as in astrocytes from 3xTg-AD mice [11]. Therefore Ca^{2+}-related genes were of special interest. However, overrepresented Ca^{2+}-related genes in down-regulated hits did not contain genes of the classical "Ca^{2+} signaling toolkit" but almost all coded for Ca^{2+}-regulated proteins involved in cell adhesion, exocytosis but mostly in formation of extracellular matrix (Table 3). Validation of these genes by real-time PCR is shown in Figure 2. Taken together, GO analysis suggests that Ca^{2+}-regulated cell adhesion and cell-cell communication, mitochondria and transcription may be specifically deregulated in 3xTg-AD cultured astrocytes.

3.3. Comparison with cultured and freshly FACS-isolated astrocytes.

To our knowledge, there are no published reports on the transcriptional profile of cultured astrocytes from the hippocampus. Therefore, it was interesting to compare the transcriptional profile of our cultured non-Tg astrocytes with that of cultured cortical astrocytes, freshly FACS-isolated forebrain astrocytes P17 pups, or freshly isolated neurons from P16 pups provided by Cahoy and colleagues [17]. We used the Ensembl BioMart on-line application (https://www.ensembl.org) for matching genes between different platforms, namely Agilent Mouse GE 4x44k v2 and Affymetrix Mouse Genome 430 2.0 Arrays. This procedure led to a set of 18,135 common probes, where only those probes filtered by Cahoy as corresponding to “genes with significant expression in the CNS” (Supplemental Table S3 in [17]) were taken into account. After the two datasets were properly integrated and renormalized through XPN algorithm (see Materials and Methods), they were merged into one single dataset. Since XPN algorithm succeeded in removing the batch effect without altering the original clusterization among samples from Cahoy’s dataset (not shown), we could proceed performing an unsupervised hierarchical clustering (Euclidean distance metric and average linkage criterion) to inspect the positioning of our non-Tg astrocytes compared to the groups profiled by Cahoy et al. Figure 3A shows that our cultured astrocytes resulted more similar to the cultured and freshly isolated astroglia than in respect to any other cell type in Cahoy’s dataset. Secondly, both cultured cellular models were more similar to acutely isolated astrocytes than to neurons. Incidentally, the fact that our samples could penetrate Cahoy’s dataset, clustering with its cultured astroglia, is a good evidence that the batch effect was efficiently removed. Afterwards, we took advantage of the merged dataset to search for the most up- and down-regulated genes in our non-Tg astrocyte cultures compared to acutely isolated astrocytes. We used the rank product method (two class, unpaired) as described in [20] controlling FDR at the strict level of 0.005 to get a basic ranked list of genes representing the most enriched expression patterns in both the groups. Results are shown in Figure 3B,C respectively. In particular, we found 130 up-regulated genes in non-Tg compared to acutely isolated astrocytes (Supplementary Table 3) and 230 down-regulated genes in non-Tg compared to acutely isolated astrocytes (Supplementary Table 4). Notably, even if the statistical test was conducted only by comparing non-Tg against acutely isolated astrocytes, heatmaps clearly showed that Cahoy’s cultured astrocytes closely followed our non-Tg culture expression profiles. This is another evidence of the high degree of similarity between our cultured model and Cahoy’s, restricted in particular to those genes that are the most specific for cultured astrocytes. More in detail, 70.0% of genes enriched in our non-Tg cultures could also be found in Cahoy’s list "Genes statistically enriched in cultured astroglia compared to *in vivo* astrocytes" (Supplemental Table S21 in [17]), while 76.5%of genes down-regulated in non-Tg ould also be found in Cahoy’s list "Genes statistically enriched in *in vivo* astrocytes compared to cultured astroglia" (Supplemental Table S20 in [17]). Taken together, these two percentages give an estimate of the technical reproducibility and the biological variability of *in vitro* astrocyte cell cultures. On the other hand, a complementary list of the most up- and down-regulated genes in our non-Tg cultures compared to Cahoy's cultured astroglia (two class unpaired rank product, FDR=0.005) is provided as supplementary material (Supplementary Tables 5 and 6). As a final qualitative remark, the expression profile of acutely isolated neurons (right side of the heatmaps, Figure 3B,C) also shows how most of the genes that are differentially expressed in non-Tg cultures compared to acutely isolated astrocytes can be indeed ascribable to a neuronal phenotype.

3.4. Comparison with isolated astrocytes from symptomatic AD or normally aged mice

Notably, in cultures from 3xTg-AD, genes involved in immune responses were largely unchanged. This is in sharp contrast with changes occurring in aged plaque stage (15 mo of age) APPswe/PS1dE9 AD mice [7] in which the most prominent change was the up-regulation of a large list of genes related to different aspects of inflammation. We therefore compared our genes with the publicly available dataset by [7] (GEO database accession number: GSE74615). To this purpose, APPswe/PS1dE9 dataset was downloaded and the empirical Bayes method (LIMMA) was used to assess the significance of differential expression of all genes among groups. After *p*-values were adjusted through BH procedure, genes with an adj.p.val ≤ 0.05 were marked as significant. While the original APPswe/PS1dE9 dataset included both cortical astrocyte and microglia samples, only the astrocyte data were retained for use in the following meta-analysis (see *Materials and Methods*).

Each one of the 993 genes we found to be significantly regulated in our model had a direct correspondence within Orre's dataset. In particular the comparison between 3xTg-AD significant genes and APPswe/PS1dE9 dataset allowed to define 6 distinct categories of genes corresponding to 3 relationships between the datasets (see heatmaps and table in Figure 5 for a graphical summary): 1) significantly co-regulated genes (total 50, upward 23, downward 27); 2) significantly changed only in 3xTg-AD astrocytes (total 882; up-regulated 486, down-regulated 396); and 3) genes oppositely regulated in 3xTg-AD and APPswePS1dE9 astrocytes (total 61, up-to-down 27, down-to-up 34). Notably, this kind of analysis could have been alternatively addressed through a K-means algorithm, but in that case the resulting 6 clusters would have been based merely on $\log_2$FC expression values, and all the information related to the *p*-values of the second dataset (APPswe/PS1dE9) would have been ignored. Conversely, to find the common and the specific gene signature of the two pathological models compared, we preferred clustering genes using the more rigorous criterion of the statistical significance compared their own whole dataset. Although a number of methods for the meta-analysis of combined lists of *p*-values from two or more studies exist [18; 24], some of them (e.g. Fisher's, Stouffer's, minP) are too liberal for our purpose—since genes having small *p*-values in just one study are likely to be detected as globally significant—while others (such as maxP) are conservative but too naïve, not addressing the problem of distinguishing concordant and discordant expression fold changes [18], nor the problem of randomly shared genes. In fact, it should be considered that when two datasets are compared in terms of shared significant genes, a certain number of co-/anti-regulated genes is expected to arise just by chance. For this reason, here we propose a novel method for the meta-analysis of *p*-valued lists of genes drawn from two different studies. The procedure makes use of a simple randomized null model based on the binomial distribution to determine which (if any) of the 6 relational categories of genes was significantly enriched (see *Common significant gene analysis* in Appendix). Overall, this method is useful to compare differentially regulated genes between two studies in order to find their "$\log_2$FC-signed" intersections and their statistical significance according to quite conservative criteria.

With reference to the table in Figure 4, the central column contains all genes we found significantly changed only in 3xTg-AD astrocytes (Up-Zero and Down-Zero). All these 882 genes can be considered, as a whole, specific for cultured 3xTg-AD astrocytes, possibly representing early FAD-related alterations. They can also be used for further analysis (such as biological validation through GO analysis, see below) regardless of their categorical *p*-value. However, the smaller the *p*-value, the more likely that the two AD models compared have a substantial overlap, because the number of significant non-shared genes is too low if compared to the null model. In other words, the number of common genes differentially expressed is too high compared to a random expression pattern, such as that resulting from comparing two completely independent disease models. In our case the very low *p*-value assigned to the category of genes significantly downregulated only in 3xTg-AD suggests that at least one of the two other categories of co-regulated and anti-regulated genes (left and right column respectively) were enriched. This allowed us to search for those processes that are in common for both models of early and late AD. In particular, we found 27 common genes significantly down-regulated in both the dataset (Down-Down, expected value=14.9; categorical *p*-value = 0.003) and 34 genes significantly down-regulated in 3xTg-AD and significantly up-regulated in APPswe/PS1dE9 astrocytes (Down-Up, expected value=22.6; categorical *p*-value = 0.013).

To analyze the biological significance of genes specific for primary astrocytes from 3xTgAD mice we first fed to DAVID GO tool a list of 882 genes that that were not changed in APPswe/PS1dE9 astrocytes (Supplementary Table 7) regardless they were up or down-regulated. These genes constitute the major part (89%) of all differentially expressed genes of our dataset, therefore, expectedly, enriched GO terms (Supplementary Table 8) overlapped significantly with those found during the initial analysis (Table 2). This suggests that in the 3xTg-AD cultured astrocytes the altered astroglial functions differ substantially from those altered later on, when deposition of Aβ aggregates is fully expressed. These alterations comprise genes and functions described by GO terms *phosphoproteins*, *cytoplasm*, *alternative splicing*, *nucleotide* and *ATP binding*, *transferase activity*, *mitochondrion*, *cell projection*, *apoptotic process*, *magnesium*, *Kruppel associated box* and *KRAB*.

Next, we analyzed GO significance of two small categories (co-regulated and anti-regulated) in which the number of common genes significantly differed from expected values (Figure 5). In the list of co-down-regulated genes (Down-Down, Figure 5) GO analysis failed to find significantly enriched GO terms. However, in the list of 34 anti-regulated genes (down 3xTg-AD and up in APPswe/PS1dE9 astrocytes, Down-Up) there were 5 GO terms with significantly enriched genes: *membrane*, *nucleolus*, *ribosomal* *protein*, *structural constituent of ribosome*, and *ribonucleoprotein* (Supplementary Table 8), suggesting that ribosomes may be altered in both, pre-plaque and plaque AD stages, but the direction of these alterations is somewhat opposed.

In parallel with APPswe/PS1dE9 dataset it was interesting to explore if cultured 3xTg-AD astrocytes may have common/divergent features with astrocytes from mice subjected to normal ageing from 2.5 to 18 months [21]. The comparison between 3xTg-AD and Orre's dataset of young-versus-old mice led to the detection of 38 common genes, but none of the 6 previously defined relational categories resulted in a significant enrichment compared to random configuration (see Supplementary Table 9). The absence of significant overlap between our AD model and the physiological aging picture provided by Orre and colleagues [21], suggests that the alterations detected in cultures of 3xTg-AD astrocytes may be specific for AD. It is worth noting that, unlike the previous case, for this comparison a list of differentially expressed genes was used as reported by the authors (see *Materials and Methods*). To build the statistical null model we could refer only to the full dimension of the array used by Orre in his study (Agilent, Mouse GE 4x44k v2 microarrays, n_y=39,429 different probes), which has likely led to an overestimation of the size of the dataset, and, as a consequence, to an overestimation of all the enrichment scores (see *Appendix*). Therefore, though no significant overlap have been ultimately detected after correction of p-values for multiple comparisons (as described in *Appendix*), this comparison should be considered merely as an exploratory analysis.

3.5. Comparison with human AD microarray

A this point it was interesting to explore if the changes found in cultured 3xTg-AD astrocytes may have had common/divergent features with the changes observed in postmortem biopsies from symptomatic AD patients. The hypothesis was that this was unlikely to occur, as cultures possibly represent early changes. For this, we downloaded from GEO database the dataset contributed by Berchtold et al. [22] (series accession number: GSE48350). This dataset featured samples from normal controls (young and aged) and AD cases, from 4 brain regions (hippocampus, entorhinal cortex, superior frontal cortex, post-central gyrus). After the assessment of the differential expression (LIMMA/empirical Bayes) and *p*-values adjustment for multiple comparisons (BH procedure), genes with an adj.p.val ≤ 0.05 were marked as significant. Then we restricted our analysis to the groups of interest, retaining just hippocampal samples from both aged control subjects (n=24) and aged AD patients (n=18). During the gene-matching procedure (see *Materials and Methods* for details) we searched for those genes that met the following requirements: i) belonged to the subset of the genes significantly regulated in our mouse dataset; ii) featured at least one human orthologous gene iii) were present (as orthologous gene) within the Berchtold's human dataset. Because of these necessary prerequisites, the pool of significant genes available for comparison with the human dataset decreased from 993 to 495.

Starting from this set of selected genes, the analysis proceeded according to the same methods already described in the previous section and following the same statistical approach. Contrary to what emerged from the comparison with the APPswe/PS1dE9 model, in this case we were not able to find any particular type of enrichment in any of the 6 relational categories previously described. In other words, the empirical configuration of the common significant genes was precisely predicted by the null model, thus suggesting a substantial independence of the two datasets (Supplementary Table 10). While, on the one hand, this negative result can be an indication of the large number of different biological parameters distinguishing the two models compared (mouse vs. human, astrocytes vs. whole-tissue samples, young vs. aged, familial AD vs. sporadic AD), it may also confirm the transcriptional specificity of early astroglial changes compared to the late astroglial changes. Moreover, the near-perfect agreement between empirical and expected values demonstrates the high predictive power of our null model in the case of uncorrelated datasets, and hence the substantial validity of this statistical approach.

4. DISCUSSION

In the present report we have investigated transcriptional alterations in purified cultures of hippocampal astrocytes of 3xTg-AD mice. An obvious limitation of this work is the use of astrocytes in culture, which raises concerns on (i) to which extent the changes in gene expression in cultures reflect the changes occurring in astrocytes *in vivo*, and (ii) to which extent the cultured astrocytes from FAD mice models represent AD. With regard to the first point, while it has been reported that in defined growing conditions gene profiles of cultured astrocytes in different aspects reliably replicate those of freshly isolated astrocytes ([25] and refs therein), our first objective was not to replicate gene expression of astrocytes *in vivo*, but to find the early FAD-related transcriptional signature specific to astrocytes in the hippocampal region as compared with non-Tg astrocytes. With this aim the purity of astrocytes in culture was our first concern because small contaminations of astrocytes with microglial cells would result in the emergence of transcripts related to inflammation. This was successfully achieved by eliminating microglia with anti-CD11b beads. Regarding the second point, we reasoned that astroglial cultures prepared from newborn mouse pups may represent a proxy model for early, pre-plaque, AD because the changes (if any) would have been due to the FAD-related mutations but not due to the burden of Aβ species. Of the three mutations present in 3xTg-AD mice, $PS1_{M146V}$ mutation has been introduced by knock-in of a point mutation of in the PS1 gene and is ubiquitous as it is under the control of the endogenous PS1 promoter [26]. The other mutations, APPswe and Tau_{P301L} have been added later as overexpressing human transgenes under the control of Thy-1.2 promoter, which is considered to be neuronal [12]. Therefore, *in vivo* the effect of the $PS1_{M146V}$ mutation should have direct consequences on astroglial biology, while the effects of APP and Tau mutations should be indirect. In cultured astrocytes, the changes (if any) should be a consequence of PS1 mutation, while the effects of APP and Tau mutations appear to be less probable or indirect, driven by priming before explant.

In contrast to works reporting proinflammatory phenotypes in cultured astrocytes from FAD mouse models [27] as well as in Aβ-exposed astrocytes [28], in our highly purified astroglial cultures from 3xTg-AD hippocampi we found substantially no changes in inflammatory genes with down-regulation of a few genes related to positive regulation of T cell mediated cytotoxicity. Recently, however, we have found that transforming growth factor β (TGF-β) is released by cultured hippocampal astrocytes [29]. Now this observation is corroborated by the finding that TGF-β2 and TGF-β3 are expressed at high levels in hippocampal astrocytes and TGF-β3 is significantly up-regulated in 3xTg-AD with regard to non-Tg astrocytes.

Among highly up-regulated genes in 3xTg-Ad astrocytes the only gene relative to the immune system was C-C motif chemokine ligand 27a (Ccl27a), a member of the β-chemokine family of proinflammatory mediators [30]. However, a closer examination of the 3 probes in the Agilent array for this cytokine, all of which were up-regulated, shows that two probes detected a splice variant of Ccl27a in which the signal peptide was replaced with an alternative stretch of amino acids that allows for nuclear targeting of this isoform. This nucleus-targeted Ccl27a variant, which is called PESKY [30] is the most expressed isoform in primary astrocytes and is able to modulate gene transcription [31]. This finding corroborates the hypothesis that transcriptional reprogramming occurs in 3xTg-AD astrocytes as well as the absence of inflammation. Our results suggest that hippocampal astrocytes from a mouse FAD model are unable to mount a pro-inflammatory phenotype in a cell-autonomous manner. The setup of inflammation likely requires participation of microglial cells which, together with astrocytes, upon exposure to activating stimuli, like Aβ, undergo cascading reactions which result in activation of both microglial and astroglial cells [32]. Such a scenario may be illustrated by a recent report by Balducci et al. [33] in which acute *in vivo* intraventricular delivery of oligomeric Aβ induced rapid and long-lasting inflammatory reactions with astroglial expression of pro-inflammatory cytokines. Such an observation also highlights that the strength of our model, i.e. purified astrocytes, on the other hand limits the possibility to evaluate the relationship between cell types in early AD. In this regard it is interesting to note that in late stages AD pathology patients with APOEε4 allele astrocytes exhibited alterations in genes related to cell adhesion and signaling pathways including calcium signaling and insulin signaling, while changes in expression of inflammatory genes were not reported [34].

Previously, we have suggested that astroglial degeneration, occurring in the very early AD stages, may be linked to deregulated astroglial Ca^{2+} signaling [5; 35]. Reasonably, astroglial degeneration is likely to be associated with the absence or the repression of inflammatory processes, while it would be hardly reconcilable with inflammation. Instead, at later AD stages, in which the inflammatory phenotype is fully expressed [7], astrocytes are found to be reactive and hypertrophic [2].

GO analysis of our dataset suggests that physiological processes and functions which are likely to be altered in 3xTg-AD astrocytes are: phosphorylation, transcription, mitochondrial structure and function, calcium-regulated cell adhesion and cell-cell communication. A survey of the literature suggests that alterations in all these functions occur in symptomatic AD [36; 37]. Considering astroglial cultures from new-born pups a proxy model for the early developing pre-plaque AD, our analysis suggests that phosphorylation, mitochondria, cell adhesion and cell-cell communication are among the first to be altered in astrocytes. In particular, alterations in phosphorylation cascades and in autophagy which are controlled by mammalian target of rapamycin complex 1 (mTORC1) are emerging as possible causes of metabolic dysregulation in neurodegenerative diseases including AD [36; 38; 39]. In this regard, of note is one of the most down-regulated genes in 3xTg-AD astrocytes, Sterile alpha motif domain containing protein 4 (Samd4). Samd4 is a mammalian homolog of Drosophila Smaug gene coding for a protein able to bind RNA and repress translation [40]. While the function of Samd4 in mammalian cells, including astrocytes, is largely unknown, it has recently been reported that mice with missense mutation of Samd4 were exceptionally thin and had severe deficiency in metabolic homeostasis and mTORC1 signaling [41]. Our finding that a protein required for the mTORC1 signaling is strongly downregulated in FAD-expressing astrocytes suggests that such a deregulation may initiate early in AD pathogenesis.

One important feature of late AD, as it has been shown on FACS-isolated astrocytes, is the down-regulation of genes involved in cellular communication and neuronal support [7]. In our dataset, in contrast to genes coding for inflammatory mediators, we found that many gene which code for proteins involved in exocytosis, formation of processes and extracellular matrix, which generally may be involved in communication with surrounding cells and support to neurons, are massively down-regulated in 3xTg-AD astrocytes. This suggests that the impairment of communication between astrocytes and other cells in the brain may begin very early in AD. In line with this observation, Stenovec et al [42] reported impaired vesicle dynamics and reduced evoked secretion of a neuroactive peptide atrial natriuretic peptide in 3xTg-AD cultured astrocytes. These alterations were attributed to mutations in PS1. The impairment of cell-cell communication, in concomitance with compromised housekeeping functions may be at the basis of early astrogliopathy that, in turn, accelerates the impairment in synaptic transmission [43].

Comparison of the dataset presented in this work with the dataset obtained from astrocytes isolated from plaque-stage symptomatic APPswe/PS1dE9 AD mice [7] shows that most altered genes (89%) were specific for cultured astrocytes and were not changed in APPswe/PS1dE9 mice. This suggests that (1) in cultured 3xTg-AD astrocytes as a proxy for early AD, FAD-mutations produce a unique signature of transcriptional remodeling which may be related to changes occurring early in AD; and (2) dynamics of astroglial remodeling are likely to change significantly during AD progression. Alongside the AD-related changes, astrocytes are involved in ageing. Transcriptional changes in AD, however, differ from those related to ageing by exacerbated inflammatory response and increased dysfunction [7; 21]. Our attempt to compare alterations in cultured 3xTg-AD astrocytes with the aged-vs-young changes in mice suggests that FAD-mutations in cultured astrocytes produce changes which are more related to AD pathology than to normal ageing. Considering that in different brain areas the dynamics of AD-related pathology are brain region-specific [5; 11], it is interesting to note that in humans, astrocytic genes, which are mostly expressed during ageing tend to lose their region specificity undergoing global up-regulation [44].

While in AD neuropathological changes are not always followed by cognitive deficit, and cognitively normal subjects may have deposition of amyloid plaques and development of neurofibrillary tangles, it appears important to correlate cognitive damage with astroglial gene expression profile. Such an attempt has been recently made by Barbash and colleagues [45]. In contrast to neuronal and oligodendrocytic genes, which were up-regulated and down-regulated, respectively, in non-demented patients with AD neuropathology, astroglial and microglial genes were up-regulated in both demented and non-demented AD patients as compared with healthy subjects. These results may be interpreted as there is no correlation in astroglial overall transcriptome changes and cognitive damage, but only with neuropathology [45]. However, more detailed examination of functional significance of changed genes is necessary for further understanding of their relation cognitive damage in AD. In this report we analyze the alterations in primary astroglial cultures of FAD-expressing mouse pups, which likely reflect the early stages of AD and may determine or even delay development of both neuropathological and cognitive alterations.

Conclusion

Astrocytes, which are the principal housekeeping and homeostatic cells in the brain, are intimately involved in the pathogenesis of neurodegenerative diseases including AD. The spatio-temporal pattern of astroglial alterations in AD is likely to be complex and in the early, pre-symptomatic disease stages include astrodegeneration and atrophy [5]. In this work we used cultured hippocampal astrocytes from 3xTg-AD mice as a proxy model of early astrocyte involvement in FAD to investigate transcriptional alterations that may characterize early AD using whole-genome microarray technology and subsequent bioinformatics approaches. Our results indicate that, in astrocytes, FAD mutations produce a pattern of alterations which is distinct from that reported in astrocytes at later stages, although a number of genes appear to be common in the two mouse models. Our data reinforce and provide new details to the hypothesis of the early involvement of astrocytes in AD pathogenesis and emphasize the importance of its further investigation.

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Conflict of Interest Statement

The authors declare no conflict of interests.

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Appendix

Common significant gene analysis

Given a statistical criterion for significance assessment and a dataset X featuring x_s significantly regulated genes, one might be interested in comparing it with another dataset Y (containing at least each of the x_s genes) in order to find out how many of those x_s genes are also significantly regulated in Y and how much this overlap is likely to be random, rather than representative of a meaningful common transcriptional pattern.

We say:

- x_{up} and x_{down} the number of genes significantly up- and down-regulated in the dataset X, being $x_s = x_{up} + x_{down}$ the total number of genes that passed the test for significance assessment within dataset X;
- y_{up} and y_{down} the number of genes significantly up- and down-regulated in the dataset Y, being $y_s = y_{up} + y_{down}$ the total number of genes that passed the test for significance assessment within dataset Y;
- n_y the total number of genes present in Y dataset; it will be necessarily $n_y \geq y_s$, even if typically is $n_y >> y_s$; moreover, since Y contains each of the x_s genes by hypothesis, it will also be $n_y \geq x_s$.
- **E**[z] the expectation value of the discrete random variable z.

In this problem we can have basically 6 categories of genes:

UU	*U0*	*UD*
DD	*D0*	*DU*

- *UU* = experimental number of genes that are significantly up-regulated in X and significantly up-regulated in Y (upward co-regulation);
- *DD* = experimental number of genes that are significantly down-regulated in X and significantly down-regulated in Y (downward co-regulation);
- *U0* = experimental number of genes that are significantly up-regulated in X but are not significant in Y ("up-to-zero");
- *D0* = experimental number of genes that are significantly down-regulated in X but are not significant in Y ("down-to-zero");
- *UD* = experimental number of genes that are significantly up-regulated in X and significantly down-regulated in Y ("up-to-down" anti-regulation);
- *DU* = experimental number of genes that are significantly down-regulated in X and significantly up-regulated in Y ("down-to-up" anti-regulation).

Notice that the problem we are addressing is not fully symmetrical in that we are not interested in those genes that are not significant in X (typically X is the dataset to be studied, while Y is an auxiliary dataset used as a reference, comparison or control). Also notice that x_s does not necessarily have to be the full set of significantly regulated genes in X, but just the largest subset suitable for the comparison (i.e.: {significant genes in X} ∩ Y).

If X and Y are independent (e.g. they describe the transcriptome of two completely unrelated pathologies) there should not be any correlation between them, that is to say that significant genes are randomly distributed in the two datasets (at least mutually). Using the previous notations, assuming that X and Y are independent and that both X and Y provide a uniform (even though incomplete) coverage of the transcriptome, starting from the experimental occurrences of the genes called as significant, we can easily predict how many genes we should expect to find by chance in each one of the 6 categories (lower case is used to indicate a discrete random variable):

$\mathbf{E}[uu] = x_{up}\dfrac{y_{up}}{n_y}$	$\mathbf{E}[u0] = x_{up}\left(1-\dfrac{y_s}{n_y}\right)$	$\mathbf{E}[ud] = x_{up}\dfrac{y_{down}}{n_y}$
$\mathbf{E}[dd] = x_{down}\dfrac{y_{down}}{n_y}$	$\mathbf{E}[d0] = x_{down}\left(1-\dfrac{y_s}{n_y}\right)$	$\mathbf{E}[du] = x_{down}\dfrac{y_{up}}{n_y}$

By this way we can define a randomized null model based on the empirical proportions of significant genes in X and Y, the only assumption being the mutually independence of X and Y. In order to compare empirical data {*UU, U0, UD, DD, D0, DU*} to the expected values predicted by the null model, we also need a statistical model describing how the 6 random variables {*uu, u0, ud, dd, d0, du*} distribute around their expected values. Binomial distribution can be used to this purpose: $Pr(k) = \binom{n}{k}p^k(1-p)^{n-k}$, where $\binom{n}{k} = \frac{n!}{k!(n-k)!}$ is the binomial coefficient, represents the probability mass function describing the probability of getting exactly *k* successes in *n* trials, *p* being the probability of a single success in a single trial. In our case a success is intended to be one of the 6 possible gene combinations, *n* is x_{up} or x_{down}, while *p* is equal to y_{up}/n_y rather than y_{down}/n_y, depending on the particular combination of interest. So we have:

$$Pr(uu = k) = \binom{x_{up}}{k}\left(\frac{y_{up}}{n_y}\right)^k\left(1-\frac{y_{up}}{n_y}\right)^{x_{up}-k},$$

$$Pr(u0 = k) = \binom{x_{up}}{k}\left(1-\frac{y_s}{n_y}\right)^k\left(\frac{y_s}{n_y}\right)^{x_{up}-k},$$

$$Pr(ud = k) = \binom{x_{up}}{k}\left(\frac{y_{down}}{n_y}\right)^k\left(1-\frac{y_{down}}{n_y}\right)^{x_{up}-k},$$

$$Pr(dd = k) = \binom{x_{down}}{k}\left(\frac{y_{down}}{n_y}\right)^k\left(1-\frac{y_{down}}{n_y}\right)^{x_{down}-k},$$

$$Pr(d0 = k) = \binom{x_{down}}{k}\left(1-\frac{y_s}{n_y}\right)^k\left(\frac{y_s}{n_y}\right)^{x_{down}-k},$$

$$Pr(du = k) = \binom{x_{down}}{k}\left(\frac{y_{up}}{n_y}\right)^k\left(1-\frac{y_{up}}{n_y}\right)^{x_{down}-k}.$$

Notice that, being **E**[*k*] = *np* the mean of a binomially distributed random variable, these probability mass functions are consistent with the expectation values already showed in table.

Actually, in order to estimate the probability of see a particular experimental configuration {*UU, U0, UD, DD, D0, DU*} under the null hypothesis that X and Y are independent, we are more interested in the cumulative distribution functions, rather than probability mass functions. In particular, for the first combination *UU*, we have:

$$Pr(uu \geq UU) = \sum_{k=UU}^{x_{up}}\binom{x_{up}}{k}\left(\frac{y_{up}}{n_y}\right)^k\left(1-\frac{y_{up}}{n_y}\right)^{x_{up}-k}.$$

Notably, $Pr(uu \geq UU)$ can be regarded as a *p*-value concerning the enrichment of the entire category containing those genes that are significantly up-regulated in both X and Y (upward co-regulation). We call it "categorical *p*-value" (to distinguish it from ordinary *p*-values referred to individual genes) since it answers the question: “How likely is it to have *UU* (or more) genes upwardly co-regulated, under the hypothesis that significant genes are randomly distributed in the two datasets?”

While the same can be said for the other “lateral” categories of genes (*UD*, *DD* and *DU*), the interest in the two “central” categories (those featuring genes that are significantly regulated only in X) concerns their possible “impoverishment” rather than enrichment. In this case, the statistical significance (categorical *p*-value) can be calculated as follow:

$Pr(u0 \leq U0) = \sum_{k=0}^{U0} \binom{x_{up}}{k} \left(1 - \frac{y_s}{n_y}\right)^{k} \left(\frac{y_s}{n_y}\right)^{x_{up}-k}$, and analogously for *D0*.

Notice that, in this kind of problem, the 6 categories of interest are not mutually independent. In particular, because of the 2 constraints $x_{up} = uu + ud + u0$ and $x_{down} = dd + du + d0$ only 4 categories out of 6 are actually independent, and the same applies to the enrichment hypothesis tests. Thus, since each comparative analysis of two datasets implies 4 independent hypothesis tests, we can adjust categorical *p*-values for multiple comparisons according to the usual correction techniques: Adj.p.val = 4 · *p*-value (Bonferroni), Adj.p.val = 1 – (1 – *p*-value)^{4} (Dunn–Šidák), etc.

Incidentally, because of the same two constraints cited above, the expectation values of the central categories could be alternatively computed as:

$$\mathbf{E}[u0] = x_{up} - \mathbf{E}[uu] - \mathbf{E}[ud],$$

$$\mathbf{E}[d0] = x_{down} - \mathbf{E}[dd] - \mathbf{E}[du].$$

Even if the two categories *U0* and *D0* can be further explored and biologically validated regardless of their categorical *p*-values (simply because they are in any case the containers of the specific gene signature, namely those genes specific for the condition studied by X respect to Y), a significant impoverishment of one of them is suggestive of some kind of correlation between X and Y (and hence between the pathologies or treatments they represent). On the contrary, the *p*-values assigned to the lateral categories allow to precisely locate any possible (and statistically significant) overlap of the two dataset (common gene signature), and further investigations should not be justified in the absence of a sufficiently low categorical *p*-value.

Legends

Figure 1. Microarray setup. **A**, Immunofluorescence photographs showing astrocytes marked with GFAP (green) and microglial cells marked with Iba1 (red) antibody. Note the absence of microglia after MACS using anti-CD11b-conjugated beads. Bar, 40 µm. **B**, a scheme of the microarray setup.

Figure 2. Real-time PCR validation of microarray results. A, real-time PCR validation of genes emerged in microarray was performed on four independent astrocyte cultures. X-axis shows microarray $\log_2$ fold change (logFC) of 3xTg-AD vs non-Tg astrocytes, while y-axis shows logFC of real-time PCR, n = 23 genes. B, scatterplots of 14 genes exemplifying the results of real-time PCR validation. Date are expressed as mean ± SD $\Delta C_{(t)}$ of 4 samples each run in triplicate.

Figure 3. Comparison with acutely isolated CNS cellular models. (**A**) Dendrogram showing the positioning of non-Tg astrocyte cultures compared to the other cellular models present the transcriptome database provided by Cahoy et al. (Astros = acutely isolated astrocytes; Neurons = acutely isolated neurons). Dendrograms were obtained through unsupervised hierarchical clustering (Euclidean metric, average linkage). Cahoy's cellular model are labeled in blue. (**B**) Heatmaps of the 130 most upregulated genes in non-Tg compared to acutely isolated astrocytes (Astros). See Supplementary Table 3 for "Genes enriched in non-Tg compared to acutely isolated astrocytes". (**C**) Heatmaps of the 230 most downregulated genes in non-Tg compared to acutely isolated astrocytes (Astros). See Supplementary Table 4 for "Genes enriched in acutely isolated astrocytes compared to non-Tg". Notice the high degree of similarity between our cultured model and Cahoy's cultured astroglia. Both heatmaps (and the corresponding gene lists) were obtained through a RP procedure (FDR ≤ 0.005, two class, unpaired). Expression data were lastly gene-wise normalized (log-mean subtraction) to represent the expression values of each gene in terms of $\log_2$ fold-enrichment over their mean value across all samples.

Figure 4. Comparison with isolated astrocytes from symptomatic APPswe/PS1dE9 AD mice. The results of the statistical comparison between present microarray dataset and the dataset provided by Orre et al. (2014) are reported in table, according to the 6-category template, the conventional notation and the null model introduced in *Materials and Methods* section and detailed in *Appendix* (*Common significant gene analysis*). In particular, in each box of the table are, from top to bottom, the actual (experimental) number of genes belonging to that particular category, the expectation value according to the null model and the related categorical *p*-value. Above and below the table are the $\log_2$FC color-coded heatmaps of the top-20 regulated genes for each category (X = 3xTg-AD vs non-Tg dataset; Y = APPswe/PS1dE9 AD vs WT dataset). A the bottom of the Figure, as an example for the first category (Up-Up = upward co-regulated genes) provided the complete procedure for the calculation of the expectation value and the categorical *p*-value from the null model is shown. Following the arrow: (**1**) the binomial probability mass function representing the null model for the set of upward co-regulated genes (as given in *Appendix: Common significant gene analysis*); (**2**) the numerical values for the constants x_{up}, y_{up} and n_y (see *Materials and Methods*, section *Comparison with*

APPswe/PS1dE9 dataset); (**3**) mean (or expected value), standards deviation and histogram for the null model-binomial distribution; (**4**) the cumulative distribution function (CDF) in its symbolic form (upper) and evaluated (lower) for the particular experimental value UU=23. CDF value corresponds to the red section of the histogram and it is equal to the categorical *p*-value shown in the table.

Table 1. Top 40 of up- and down-regulated genes in 3xTg-AD astrocytes vs non-Tg.

	Probe Name	**Gene Symbol**	**FC**	**Ave Expr**	**adj.P.Val**
	Up-regulated genes				
1	A_52_P267391	Trim12a	40.13	7.97	1.515E-21
2	A_55_P1974432	Gm5067	26.12	7.94	4.182E-23
3	A_55_P2070576	Ccl27a	8.94	8.53	2.516E-15
4	A_55_P2205650	2610507I01Rik	6.80	8.20	1.896E-15
5	A_55_P2064659	Trim12a	6.17	7.01	6.074E-14
6	A_55_P2256646	C130078N14	5.96	6.98	4.552E-12
7	A_55_P2068731	Gm20878	5.80	9.50	5.665E-10
8	A_52_P360330	Map1b	5.77	9.57	2.685E-12
9	A_55_P2068733	Gm20878	5.49	8.49	5.030E-15
10	A_55_P2092750	Car9	4.68	11.43	1.138E-02
11	A_55_P1981756	Vmn2r123	4.67	6.86	6.992E-09
12	A_51_P349888	Ang2	4.66	7.46	1.004E-08
13	A_52_P88793	Zfp933	4.56	8.10	1.763E-14
14	A_52_P238846	Bpnt1	4.53	8.50	7.344E-09
15	A_51_P288549	Jmjd7	4.46	9.04	9.524E-12
16	A_66_P130730	Zfp963	4.42	7.71	2.516E-15
17	A_55_P2112986	Klk1b22	4.41	6.95	1.265E-13
18	A_55_P2134591	BC049715	4.36	7.12	3.811E-16
19	A_55_P2097151	Ptchd2	4.00	7.33	1.714E-13
20	A_51_P277006	Chst8	4.00	9.51	5.274E-04
21	A_55_P2073965	BC049715	3.98	6.93	1.327E-15
22	A_51_P217498	Slc2a4	3.91	8.57	8.451E-09
23	A_55_P2045886	Stk3	3.78	9.20	6.396E-07
24	A_55_P2180869	Ocel1	3.77	11.21	6.741E-11
25	A_55_P2108773	4930427A07Rik	3.74	6.87	5.035E-13
26	A_66_P105689	Trim34a	3.56	8.37	1.752E-08
27	A_66_P134474	Ang3	3.48	7.97	1.877E-06
28	A_55_P1964628	LOC102633627	3.40	13.64	1.627E-08
29	A_51_P293069	Mfsd7b	3.36	9.74	9.791E-06
30	A_55_P2085142	Spp1	3.31	9.07	1.515E-04
31	A_55_P2154387	Bmp4	3.31	12.83	2.007E-03
32	A_51_P413147	Klk1b3	3.25	6.73	1.200E-10
33	A_51_P112627	St6galnac2	3.23	10.19	9.909E-05
34	A_51_P512820	Dera	3.21	8.49	1.344E-05
35	A_55_P2095603	Ccdc65	3.21	10.33	1.100E-06
36	A_51_P477121	Pmaip1	3.16	9.69	1.936E-03
37	A_55_P2130129	Kcnab1	3.14	9.03	2.465E-04
38	A_55_P2373852	2310058N22Rik	3.04	8.18	1.926E-09
39	A_55_P2144597	9030025P20Rik	2.98	10.33	4.017E-06
40	A_51_P180724	Mlh1	2.94	10.33	1.772E-14

Table 1 (Continue).

	ProbeName	**GeneSymbol**	**FC**	**AveExpr**	**adj.P.Val**
	Down-regulated genes				
1	A_55_P1966838	Xaf1	-71.35	9.99	1.65E-09
2	A_52_P516409	Col4a6	-20.09	11.49	1.69E-16
3	A_55_P1966774	Serpina3i	-11.45	8.24	1.11E-03
4	A_66_P130813	Samd4	-10.42	9.71	3.48E-12
5	A_52_P303176	1810037I17Rik	-9.31	12.76	9.75E-16
6	A_55_P2132207	1810037I17Rik	-8.88	11.50	8.74E-16
7	A_55_P2137527	Fam183b	-8.85	10.89	4.38E-06
8	A_52_P111031	Pcdh17	-8.55	9.29	4.62E-09
9	A_55_P2026420	Pou6f1	-8.49	8.57	1.53E-11
10	A_52_P206492	Pop4	-7.95	11.38	1.20E-16
11	A_55_P2105944	Olfr224	-7.23	8.06	2.77E-14
12	A_55_P1952482	Pbp2	-6.54	7.72	5.33E-10
13	A_52_P393314	P2rx7	-5.92	9.92	1.55E-05
14	A_51_P462428	Galnt15	-5.02	10.82	1.10E-05
15	A_55_P2026270	Cfi	-4.87	7.60	8.63E-04
16	A_51_P159453	Serpina3n	-4.78	11.29	2.24E-02
17	A_52_P613498	4833420G17Rik	-4.39	11.73	2.19E-10
18	A_52_P157450	Abhd1	-4.08	9.15	1.95E-13
19	A_51_P297105	Ucp2	-4.02	9.28	3.45E-03
20	A_55_P2074656	Padi2	-3.95	13.12	2.85E-06
21	A_52_P257812	Lpl	-3.91	8.51	3.96E-04
22	A_51_P259296	Lpl	-3.89	10.54	2.14E-03
23	A_52_P597775	Gprc5a	-3.69	10.69	4.87E-05
24	A_55_P2091359	Padi2	-3.54	12.93	9.79E-06
25	A_55_P2045642	Stmn4	-3.40	9.27	1.70E-02
26	A_66_P108247	Ucp3	-3.32	8.74	5.58E-03
27	A_55_P2176792	Sh3gl3	-3.31	9.35	1.20E-10
28	A_66_P105175	Bche	-3.29	10.68	1.00E-08
29	A_51_P128667	Lynx1	-3.29	11.50	8.91E-07
30	A_51_P194249	Stmn4	-3.23	9.25	3.23E-02
31	A_55_P2212603	Apba2	-3.22	9.23	6.98E-05
32	A_55_P1953972	Pdhb	-3.21	12.85	1.48E-09
33	A_55_P1978465	H2-Q5	-3.17	9.54	5.66E-03
34	A_55_P2315012	4930458D05Rik	-3.16	7.04	1.12E-07
35	A_55_P1968276	Tomm22	-3.08	12.76	5.03E-15
36	A_55_P2096867	Gap43	-3.05	10.06	2.29E-03
37	A_55_P2004179	Col2a1	-3.03	10.26	3.04E-02
38	A_55_P2162344	Lrsam1	-3.02	11.18	5.14E-04
39	A_51_P458778	Hpgd	-2.97	7.81	4.38E-03
40	A_55_P2014304	Kank1	-2.95	11.85	8.04E-08

Table 2. Gene ontology analysis.

GO Category	Term	Count	Fold Enrichment	FDR, %
	Up-regulated genes			
UP_KEYWORDS	Phosphoprotein	159	1.2	4.78
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	149	1.2	1.50
UP_KEYWORDS+A2:G25	Alternative splicing	118	1.4	0.04
UP_SEQ_FEATURE	splice variant	110	1.3	7.37
UP_KEYWORDS	Cytoplasm	102	1.3	1.83
UP_KEYWORDS	Acetylation	75	1.4	4.11
UP_KEYWORDS	Transferase	49	1.7	0.43
UP_KEYWORDS	Nucleotide-binding	49	1.6	1.55
GOTERM_CC_DIRECT	GO:0005739~mitochondrion	46	1.5	8.31
GOTERM_MF_DIRECT	GO:0016740~transferase activity	44	1.6	1.99
GOTERM_CC_DIRECT	GO:0005622~intracellular	44	1.5	7.75
UP_KEYWORDS	ATP-binding	38	1.6	6.26
UP_KEYWORDS	Mitochondrion	30	1.6	9.26
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytoplasm	26	2.1	1.21
GOTERM_CC_DIRECT	GO:0042995~cell projection	23	1.8	9.77
INTERPRO	IPR015880:Zinc finger, C2H2-like	22	1.8	9.89
INTERPRO	IPR001909:Krueppel-associated box	15	2.3	7.90
UP_SEQ_FEATURE	compositionally biased region:Poly-Arg	11	3.4	2.40
GOTERM_CC_DIRECT	GO:0031982~vesicle	10	3.4	4.13
	Down-regulated genes			
UP_KEYWORDS	Phosphoprotein	167	1.4	0.001
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	139	1.2	4.123
UP_KEYWORDS	Alternative splicing	105	1.4	0.518
UP_KEYWORDS	Cytoplasm	98	1.4	0.581
UP_KEYWORDS	Transport	46	1.5	7.127
GOTERM_CC_DIRECT	GO:0005730~nucleolus	29	2.0	0.893
GOTERM_CC_DIRECT	GO:0042995~cell projection	24	2.0	3.785
UP_KEYWORDS	Calcium	24	1.8	9.853
UP_KEYWORDS	Cell projection	22	2.0	4.322
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	20	2.0	8.671
UP_KEYWORDS	Cell junction	20	1.9	9.435
GOTERM_CC_DIRECT	GO:0045202~synapse	17	2.0	7.425
UP_KEYWORDS	Polymorphism	10	3.0	8.706
GOTERM_CC_DIRECT	GO:0043197~dendritic spine	9	3.5	5.361
GOTERM_BP_DIRECT	GO:0097191~extrinsic apoptotic signaling pathway	5	7.0	8.711

UP_SEQ_FEATURE	domain:EH	4	37.9	0.161
SMART	SM00027:EH	4	21.5	0.838
INTERPRO	IPR000261:EPS15 homology (EH)	4	22.4	0.950
GOTERM_BP_DIRECT	GO:0001916~positive regulation of T cell mediated cytotoxicity	4	12.0	6.578

Table 3. List of down-regulated genes related to GO term “Calcium”.

ProbeName	GeneSymbol	GeneName	FC	AveExpr	adj.P.Val
A_52_P111031	**Pcdh17**	protocadherin 17	-8.55	9.29	4.6E-09
A_55_P2026270	**Cfi**	complement component factor i	-4.87	7.60	8.6E-04
A_55_P2074656	**Padi2**	peptidyl arginine deiminase, type II	-3.95	13.12	2.9E-06
A_55_P2091359	**Padi2**	peptidyl arginine deiminase, type II	-3.54	12.93	9.8E-06
A_55_P2004179	**Col2a1**	collagen, type II, alpha 1	-3.03	10.26	3.0E-02
A_51_P360918	**Ehd3**	EH-domain containing 3	-2.59	10.17	1.0E-05
A_51_P382970	**Itga9**	integrin alpha 9	-2.55	8.76	9.2E-09
A_55_P2013223	**S100z**	S100 calcium binding protein, zeta	-2.51	6.93	4.5E-03
A_52_P590535	**Fbln2**	fibulin 2	-2.13	12.94	3.5E-02
A_55_P2080880	**Clcnkb**	chloride channel Kb	-2.13	7.37	5.2E-06
A_51_P502437	**Cacna2d3**	calcium channel, voltage-dependent, alpha2/delta subunit 3	-1.95	8.02	2.1E-02
A_51_P135340	**Panx1**	pannexin 1	-1.87	10.51	2.4E-02
A_52_P529195	**Pcdhb4**	protocadherin beta 4	-1.80	7.04	2.1E-05
A_52_P489295	**Adamts1**	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1	-1.77	12.75	2.4E-03
A_55_P2185504	**Masp2**	mannan-binding lectin serine peptidase 2	-1.69	6.99	1.2E-03
A_55_P2021266	**Hpse**	heparanase	-1.68	6.97	7.7E-03
A_55_P2007771	**Catsper2**	cation channel, sperm associated 2	-1.65	8.37	4.4E-02
A_55_P1985410	**Reps2**	RALBP1 associated Eps domain containing protein 2	-1.60	8.04	9.2E-05
A_52_P348031	**Syt9**	synaptotagmin IX	-1.57	8.33	2.9E-03
A_51_P455807	**Ehd4**	EH-domain containing 4	-1.52	11.96	3.3E-02
A_55_P1968858	**Cadps**	Ca2+-dependent secretion activator	-1.51	9.34	1.4E-02
A_66_P104309	**Myl2**	myosin, light polypeptide 2, regulatory, cardiac, slow	-1.45	7.42	1.5E-02
A_55_P2153496	**Ppp2r3d**	protein phosphatase 2 (formerly 2A), regulatory subunit B'', delta	-1.38	7.11	3.8E-03
A_55_P1967500	**Nell1**	NEL-like 1	-1.38	6.77	1.4E-02
A_51_P184223	**Pcdhb7**	protocadherin beta 7	-1.28	7.92	3.9E-02

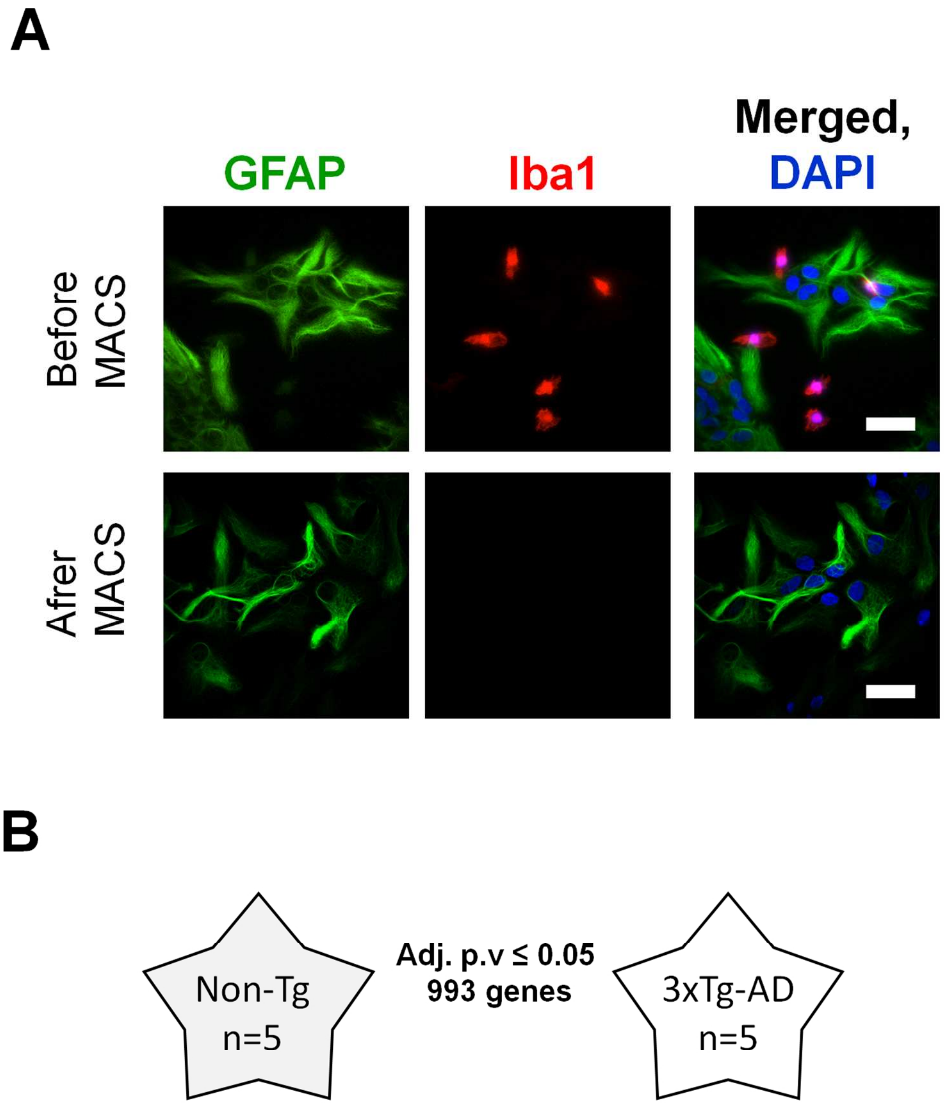

Figure 1. Microarray setup.

122x143mm (300 x 300 DPI)

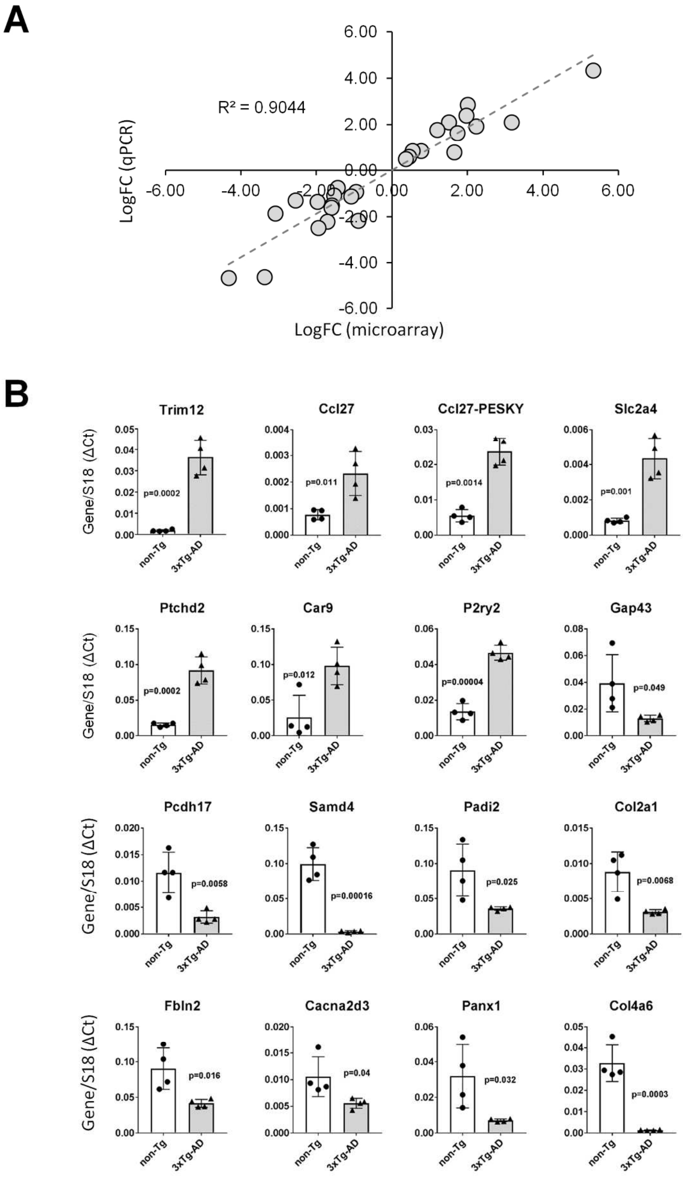

Figure 2. Real-time PCR validation of microarray results.

133x226mm (300 x 300 DPI)

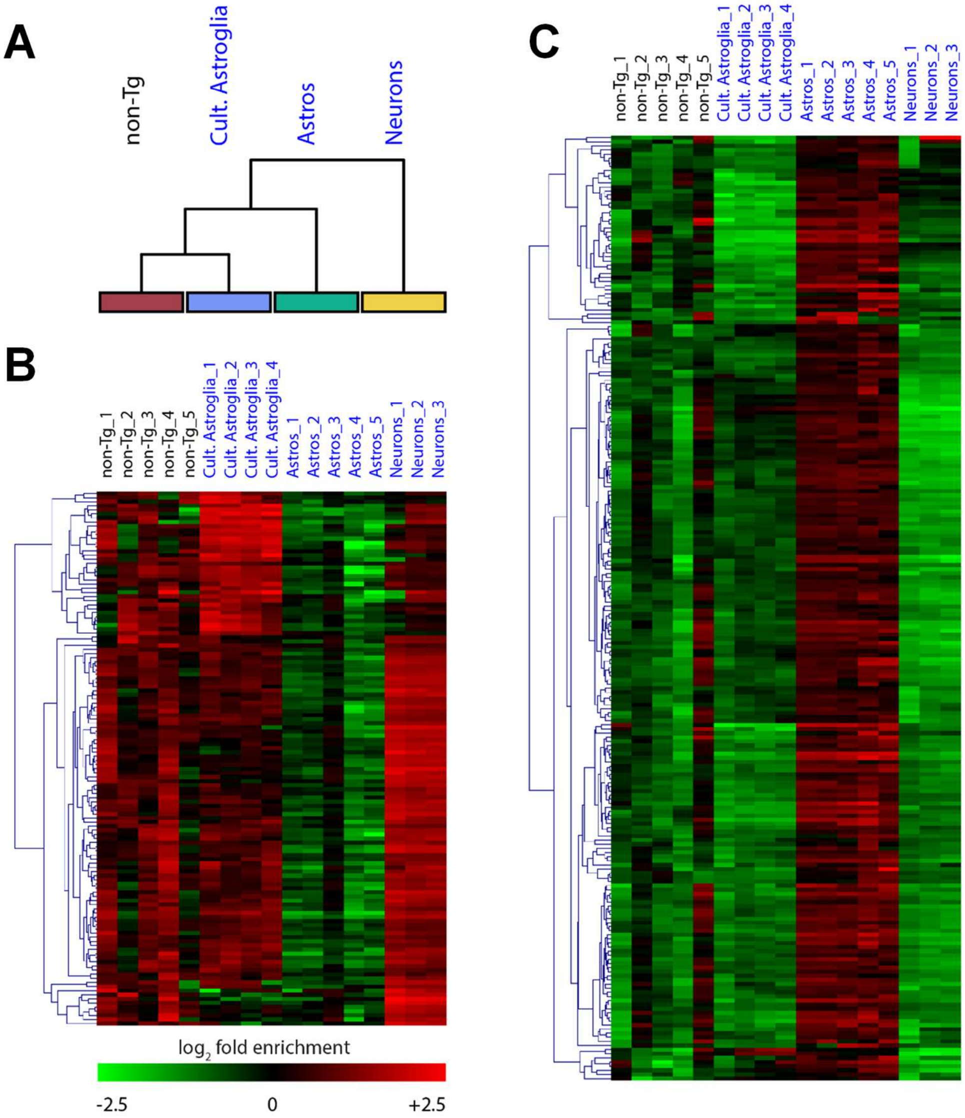

Figure 3. Comparison with acutely isolated CNS cellular models.

150x172mm (300 x 300 DPI)

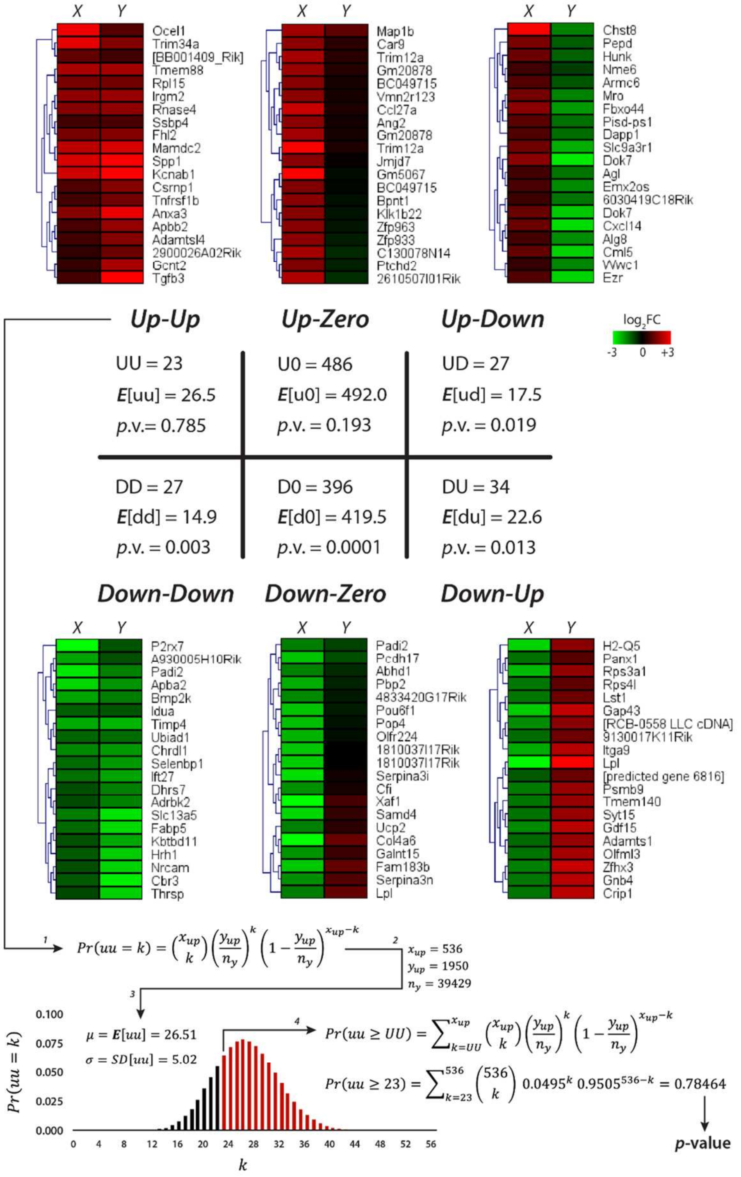

Figure 4. Comparison with isolated astrocytes from symptomatic APPswe/PS1dE9 AD mice.

137x217mm (300 x 300 DPI)

SUPPLEMENTARY MATERIAL

Transcriptional remodeling in primary hippocampal astrocytes from an Alzheimer's disease mouse model.

Ruffinatti FA, Tapella L, Stevano A, Gregnanin I, Chiorino G, Canonico PL, Distasi C, Genazzani AA, Lim D

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Oligonucleotide primers used for quantitative real-time PCR.

Gene	Accession number	Forward Reverse	Sequence 5' to 3'
Trim12a	NM_023835.2	Forward Reverse	TCATTGAAGAGGTGGCCCAG ACCGAACATTCTGCACATCT
Ccl27a	NM_011336.1	Forward Reverse	CCCGCTGTTACTGTTGCTTC CAATCCTCCTCAGCAGCCT
Ccl27a (Pesky)	NM_001048179.1	Forward Reverse	TCTCCAACAAGCCAGAGACT GCTTGGGAGTGGCTGTCTAT
Car9	NM_139305.2	Forward Reverse	GGAGTCCCTTGGGTTAGAGG TGGGGCCAGAGTAGGGTG
Ptchd2	NM_001083342.1	Forward Reverse	CACAGCCTGCAGAACAATGT TTGGAGATGTACACGGTGCT
Slc2a4	NM_009204.2	Forward Reverse	TAAAACAAGATGCCGTCGGG CCAAACTGAAGGGAGCCAAG
Bmp4	NM_007554.3	Forward Reverse	AGTCTGGGGAGGAGGAGG GAGCTCTCACTGGTCCCTG
Kcnab1	NM_010597.4	Forward Reverse	GGGAAGGCTGAGGTGATTCT GTCCCCTTTCTGTCTCAGCT
P2ry2	NM_008773.3	Forward Reverse	ATCCTCACCACCTCAAGAGC GGCAACAGCACGTACTTGAA
Tnrc18	NM_001122730.2	Forward Reverse	TCCATCCTACCTCCACCTGA GGTGCGGGCAGGTAGAAG
Tgfb3	NM_009368.3	Forward Reverse	AGGAGACCTCGGAGTCTGAG CACTGAGGACACATTGAAACGA
Vcp	NM_009503.4	Forward Reverse	CGAGTTCGCCTAGGAGATGT AGAGATTGCCAGTGATGCCT
Ankib1	NM_001289527.1	Forward Reverse	CCTATCAGCACAACACACCG TGTTTCATTGTGCACATTCCG
Panx1	NM_019482.2	Forward Reverse	TCACATGTATTGCCGTGGGT CTCGGGGAGAAGCAGCTTAT
Cacna2d3	NM_009785.1	Forward Reverse	TGCCTGTGAACATCAGTCTGA GCCATATGAGAGACGGATCCC
Fbln2	NM_007992.2	Forward Reverse	GGGCACTCACGATTGTAGCT GCAGGTCTGTCACACACTCA
Grm5	NM_001081414.2	Forward Reverse	GAGGGTTGTACCTTCGGATG AAATCCCTTCCTTCGCTGAC
Chl1	NM_007697.2	Forward Reverse	AGCAGCTGAAATACCACTCTC GGGTTTCCTTTCGCTTCACA
Col2a1	NM_001113515.2	Forward Reverse	GTGAGCCATGATCCGCCTC GGTTCTCCTTTCTGCCCCTT
Gap43	NM_008083.2	Forward	GGAAGAAGGCAGGGGAAGAT

		Reverse	CTGAATTTTGGTCGCAGCCT
Lynx1	NM_011838.4	Forward Reverse	TCATGACCCATCTGCTCACA GTGGTCATACAGTAGGTGGC
Lpl	NM_008509.2	Forward Reverse	GAGATGGAGAGCAAAGCCCT GTCTTCAGGGGTCCTTAGGG
Padi2	NM_008812.2	Forward Reverse	GGGAAAATATGCTGCGGGAAC CACCTTCCGAGTGCTTCAGG
P2rx7	NM_011027.3	Forward Reverse	ACTGCAGACTACACCTTCCC TACAACGCCGGTCAGAAGAG
Pcdh17	NM_001013753.2	Forward Reverse	CTAATTCGAGCGAGACCCCT CTCTCAGGCTGGCTCTTTCT
Samd4	NM_001037221.2	Forward Reverse	TTGTGCCTCAGTATGACGGA AACCCTGAAGATGGCTGACA
Col4a6	NM_053185.2	Forward Reverse	CAAGCATGCACCCTGGATTG AGACTCCATGGCAATCTCGG
S18	NM_213557	Forward Reverse	TGCGAGTACTCAACACCAACA CTGCTTTCCTCAACACCACA
GAPDH	NM_017008	Forward Reverse	CAAGGTCATCCATGACAACTTTG GGGCCATCCACAGTCTTCTG
RP2a	XM_002727723	Forward Reverse	GCACCATCAAGAGAGTGCAG GGATCCATTAGTCCCCCAAG

1.2. Common significant gene analysis

Given a statistical criterion for significance assessment and a dataset X featuring x_s significantly regulated genes, one might be interest in comparing it with another dataset Y (containing at least each of the x_s genes) in order to find out how many of those x_s genes are also significantly regulated in Y and how much this overlap is likely to be random, rather than representative of a meaningful common transcriptional pattern.

We say:

- x_{up} and x_{down} the number of genes significantly up- and down-regulated in the dataset X, being $x_s = x_{up} + x_{down}$ the total number of genes that passed the test for significance assessment within dataset X;
- y_{up} and y_{down} the number of genes significantly up- and down-regulated in the dataset Y, being $y_s = y_{up} + y_{down}$ the total number of genes that passed the test for significance assessment within dataset Y;
- n_y the total number of genes present in Y dataset; it will be necessarily $n_y \geq y_s$, even if typically is $n_y >> y_s$;
- **E**[z] the expectation value of the discrete random variable z.

In this problem we can have basically 6 categories of genes:

UU	*U0*	*UD*
DD	*D0*	*DU*

- *UU* = experimental number of genes that are significantly up-regulated in X and significantly up-regulated in Y (upward co-regulation);
- *DD* = experimental number of genes that are significantly down-regulated in X and significantly down-regulated in Y (downward co-regulation);
- *U0* = experimental number of genes that are significantly up-regulated in X but are not significant in Y (“up-to-zero”);
- *D0* = experimental number of genes that are significantly down-regulated in X but are not significant in Y (“down-to-zero”);
- *UD* = experimental number of genes that are significantly up-regulated in X and significantly down-regulated in Y (“up-to-down” anti-regulation);
- *DU* = experimental number of genes that are significantly down-regulated in X and significantly up-regulated in Y (“down-to-up” anti-regulation).

Notice that the problem we are addressing is not fully symmetrical in that we are not interested in those genes that are not significant in X (typically X is the dataset to be studied, while Y is an auxiliary dataset used as reference/comparison/control).

If X and Y are independent (e.g. they describe the transcriptome of two completely unrelated pathologies) there should not be any correlation between them, that is to say that significant genes are randomly distributed in the two datasets (at least mutually). Using the previous notations, assuming that X and Y are independent and given the experimental occurrences of significant genes present in the two dataset, we can easily predict how many genes we should expect to find by chance in each one of the 6 categories (lower case is used to indicate a discrete random variable):

$\mathbf{E}[uu] = x_{up}\dfrac{y_{up}}{n_y}$	$\mathbf{E}[u0] = x_{up}\left(1 - \dfrac{y_s}{n_y}\right)$	$\mathbf{E}[ud] = x_{up}\dfrac{y_{down}}{n_y}$
$\mathbf{E}[dd] = x_{down}\dfrac{y_{down}}{n_y}$	$\mathbf{E}[d0] = x_{down}\left(1 - \dfrac{y_s}{n_y}\right)$	$\mathbf{E}[du] = x_{down}\dfrac{y_{up}}{n_y}$

By this way we can define a randomized null model based on the empirical proportions of significant genes in X and Y, the only assumption being the mutually independence of X and Y. In order to compare empirical data {*UU, U0, UD, DD, D0, DU*} to the expected values predicted by the null model, we also need a statistical model describing how the 6 random variables {*uu, u0, ud, dd, d0, du*} distribute around their expected values. Binomial distribution can be used to this purpose: $Pr(k) = \binom{n}{k} p^k (1-p)^{n-k}$, where $\binom{n}{k} = \frac{n!}{k!(n-k)!}$ is the binomial coefficient, represents the probability mass function describing the probability of getting exactly *k* successes in *n* trials, *p* being the probability of a single success in a single trial. In our case a success is intended to be one of the 6 possible gene combination, *n* is x_{up} or x_{down}, while *p* is equal to y_{up}/n_y rather than y_{down}/n_y, depending on the particular combination of interest. So we have:

$$Pr(uu = k) = \binom{x_{up}}{k}\left(\frac{y_{up}}{n_y}\right)^k\left(1 - \frac{y_{up}}{n_y}\right)^{x_{up}-k},$$

$$Pr(u0 = k) = \binom{x_{up}}{k}\left(1 - \frac{y_s}{n_y}\right)^k\left(\frac{y_s}{n_y}\right)^{x_{up}-k},$$

$$Pr(ud = k) = \binom{x_{up}}{k}\left(\frac{y_{down}}{n_y}\right)^k\left(1 - \frac{y_{down}}{n_y}\right)^{x_{up}-k},$$

$$Pr(dd = k) = \binom{x_{down}}{k}\left(\frac{y_{down}}{n_y}\right)^k\left(1 - \frac{y_{down}}{n_y}\right)^{x_{down}-k},$$

$$Pr(d0 = k) = \binom{x_{down}}{k}\left(1 - \frac{y_s}{n_y}\right)^k\left(\frac{y_s}{n_y}\right)^{x_{down}-k},$$

$$Pr(du = k) = \binom{x_{down}}{k}\left(\frac{y_{up}}{n_y}\right)^k\left(1 - \frac{y_{up}}{n_y}\right)^{x_{down}-k}.$$

Notice that, being $\mathbf{E}[k] = np$ the mean of a binomially distributed random variable, these probability mass functions are consistent with the expectation values already showed in table.

Actually, in order to estimate the probability of see a particular experimental configuration {*UU, U0, UD, DD, D0, DU*} under the null hypothesis that X and Y are independent, we are more interested in the cumulative distribution functions, rather than probability mass functions. In particular, for the first combination *UU*, we have:

$$Pr(uu \geq UU) = \sum_{k=UU}^{x_{up}}\binom{x_{up}}{k}\left(\frac{y_{up}}{n_y}\right)^k\left(1 - \frac{y_{up}}{n_y}\right)^{x_{up}-k}.$$

Notably, $Pr(uu \geq UU)$ can be regarded as a *p*-value concerning the enrichment of the entire category containing those genes that are significantly up-regulated in both X and Y (upward co-regulation). We call it "categorical *p*-value" (to distinguish it from ordinary *p*-values referred to individual genes) since it answer the question: "How likely is it to have *UU* (or more) genes upwardly co-regulated, under the hypothesis that significant genes are randomly distributed in the two datasets?"

While the same can be said for the other "lateral" categories of genes (*UD*, *DD* and *DU*), the interest in the "central" categories (those featuring genes that are significantly regulated only in X) concerns their possible impoverishment rather than enrichment. In this case, the statistical significance (categorical *p*-value) can be calculated as follow:

$Pr(u0 \leq U0) = \sum_{k=0}^{U0} \binom{x_{up}}{k} \left(1 - \frac{y_s}{n_y}\right)^k \left(\frac{y_s}{n_y}\right)^{x_{up}-k}$, and analogously for *D0*.

Notice that, in this kind of problem, the 6 categories of interest are not mutually independent. In particular, because of the 2 constraints $x_{up} = uu + ud + u0$ and $x_{down} = dd + du + d0$ only 4 categories out of 6 are actually independent, and the same applies to the enrichment hypothesis tests. Since each comparative analysis of two datasets implies 4 independent hypothesis tests, we can adjust categorical *p*-values for multiple comparisons according to the usual correction techniques: Adj.p.val = 4 · *p*-value (Bonferroni), Adj.p.val = 1 – (1 – *p*-value)^{4} (Dunn–Šidák), etc.

Incidentally, because of the same two constraints cited above, the expectation values of the central categories could be alternatively computed as:

$\mathbf{E}[u0] = x_{up} - \mathbf{E}[uu] - \mathbf{E}[ud]$,

$\mathbf{E}[d0] = x_{down} - \mathbf{E}[dd] - \mathbf{E}[du]$.

Even if the two categories *U0* and *D0* can be further explored and biologically validated regardless of their categorical *p*-values (simply because they are in any case the container of all those genes specific for the condition studied by X respect to Y), a significant impoverishment of one of them is suggestive of some kind of correlation between X and Y (and hence between the pathologies or treatments they represent). On the contrary, the *p*-values assigned to the lateral categories allow to precisely locate any possible (and statistically significant) overlapping of the two dataset, and further investigations are not justified in the absence of a sufficiently low categorical *p*-value.

List of differentially expressed genes between non-T

ProbeName	GeneSymb	GeneName
A_52_P267391	Trim12a	tripartite motif-containing 12A
A_55_P1974432	Gm5067	predicted gene 5067
A_55_P2070576	Ccl27a	chemokine (C-C motif) ligand 27A
A_55_P2205650	2610507I01Ri	RIKEN cDNA 2610507I01 gene
A_55_P2064659	Trim12a	tripartite motif-containing 12A
A_55_P2256646	C130078N14	uncharacterized protein C130078N
A_55_P2068731	Gm20878	predicted gene, 20878
A_52_P360330	Map1b	microtubule-associated protein 1B
A_55_P2068733	Gm20878	predicted gene, 20878
A_55_P2092750	Car9	carbonic anhydrase 9
A_55_P1981756	Vmn2r123	vomeronasal 2, receptor 123
A_51_P349888	Ang2	angiogenin, ribonuclease A family
A_52_P88793	Zfp933	zinc finger protein 933
A_52_P238846	Bpnt1	bisphosphate 3'-nucleotidase 1
A_51_P288549	Jmjd7	jumonji domain containing 7
A_66_P130730	Zfp963	zinc finger protein 963
A_55_P2112986	Klk1b22	kallikrein 1-related peptidase b22
A_55_P2134591	BC049715	cDNA sequence BC049715
A_55_P2097151	Ptchd2	patched domain containing 2
A_51_P277006	Chst8	carbohydrate (N-acetylgalactosam
A_55_P2073965	BC049715	cDNA sequence BC049715
A_51_P217498	Slc2a4	solute carrier family 2 (facilitated g
A_55_P2045886	Stk3	serine/threonine kinase 3
A_55_P2180869	Ocel1	occludin/ELL domain containing 1
A_55_P2108773	4930427A07R	RIKEN cDNA 4930427A07 gene
A_66_P105689	Trim34a	tripartite motif-containing 34A
A_66_P134474	Ang3	angiogenin, ribonuclease A family
A_55_P1964628	LOC10263362	tropomyosin alpha-4 chain-like
A_51_P293069	Mfsd7b	major facilitator superfamily doma
A_55_P2085142	Spp1	secreted phosphoprotein 1
A_55_P2154387	Bmp4	bone morphogenetic protein 4
A_51_P413147	Klk1b3	kallikrein 1-related peptidase b3
A_51_P112627	St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2
A_51_P512820	Dera	2-deoxyribose-5-phosphate aldola
A_55_P2095603	Ccdc65	coiled-coil domain containing 65
A_51_P477121	Pmaip1	phorbol-12-myristate-13-acetate-i
A_55_P2130129	Kcnab1	potassium voltage-gated channel,
A_55_P2373852	2310058N22R	RIKEN cDNA 2310058N22 gene
A_55_P2144597	9030025P20R	RIKEN cDNA 9030025P20 gene
A_51_P180724	Mlh1	mutL homolog 1 (E. coli)
A_51_P142896	Cd59a	CD59a antigen
A_55_P2003561	Luzp2	leucine zipper protein 2
A_51_P417321	Zfp236	zinc finger protein 236
A_51_P115953	Ctxn3	cortexin 3
A_55_P2068723	Ccl27a	chemokine (C-C motif) ligand 27A
A_51_P451458	Mamdc2	MAM domain containing 2
A_55_P2068734	Ccl27a	chemokine (C-C motif) ligand 27A
A_55_P2015912	Zfp961	zinc finger protein 961
A_55_P1961395	Pdpn	podoplanin
A_51_P358722	Lancl3	LanC lantibiotic synthetase compo
A_55_P2053551	Mast4	microtubule associated serine/thre
A_55_P2019577	1500011B03R	RIKEN cDNA 1500011B03 gene
A_52_P532687	Ermard	ER membrane associated RNA de
A_52_P209484	Tmem88	transmembrane protein 88
A_52_P490207	Ermard	ER membrane associated RNA de
A_55_P2059357	Myo7a	myosin VIIA

A_51_P507899	Ttc8	tetratricopeptide repeat domain 8
A_55_P2194064	BC023969	cDNA sequence BC023969
A_55_P2067727	Mxra7	matrix-remodelling associated 7
A_55_P2197338	Tnfsf13os	tumor necrosis factor (ligand) sup
A_51_P345316	Cep76	centrosomal protein 76
A_55_P2065726	Snx29	sorting nexin 29
A_55_P2179793	0	0
A_52_P642012	BC006965	cDNA sequence BC006965
A_52_P616332	Atp10d	ATPase, class V, type 10D
A_51_P179504	Ang3	angiogenin, ribonuclease A family
A_55_P2169963	Gm13152	predicted gene 13152
A_52_P559545	Cercam	cerebral endothelial cell adhesion
A_55_P2180196	Ccdc32	coiled-coil domain containing 32
A_52_P135707	Creb3	cAMP responsive element binding
A_52_P598634	1190007I07Ri	RIKEN cDNA 1190007I07 gene
A_52_P587738	P2ry2	purinergic receptor P2Y, G-protei
A_55_P2380428	5430416G10R	RIKEN cDNA 5430416G10 gene
A_66_P122158	Pisd-ps3	phosphatidylserine decarboxylase
A_52_P592909	Dgat2	diacylglycerol O-acyltransferase 2
A_52_P549977	Fam32a	family with sequence similarity 32,
A_51_P125368	Hars	histidyl-tRNA synthetase
A_55_P2019054	Acacb	acetyl-Coenzyme A carboxylase b
A_55_P1987196	Gm3448	predicted gene 3448
A_55_P1960167	Bcat2	branched chain aminotransferase
A_51_P480013	Car11	carbonic anhydrase 11
A_55_P2137611	Irgm2	immunity-related GTPase family
A_55_P2120866	Gm7120	predicted gene 7120
A_51_P418908	Larp1	La ribonucleoprotein domain famil
A_55_P1975874	Bcl2l15	BCLl2-like 15
A_51_P286814	Ncor2	nuclear receptor co-repressor 2
A_55_P2108883	AV356131	expressed sequence AV356131
A_51_P155458	Dok7	docking protein 7
A_55_P2054350	Fbxo44	F-box protein 44
A_55_P2083213	Purb	purine rich element binding protei
A_51_P490747	AI593442	expressed sequence AI593442
A_52_P311853	Ddit4l	DNA-damage-inducible transcript
A_55_P2065059	Wnt2	wingless-related MMTV integratio
A_55_P2056325	Anxa3	annexin A3
A_55_P1998401	Eif2ak4	eukaryotic translation initiation fac
A_55_P2079158	Fam154b	family with sequence similarity 15
A_55_P2153941	Zfp386	zinc finger protein 386 (Kruppel-lik
A_51_P237383	Rnase4	ribonuclease, RNase A family 4
A_55_P1974602	Map2k7	mitogen-activated protein kinase k
A_51_P155174	Zfp672	zinc finger protein 672
A_55_P2097156	Ptchd2	patched domain containing 2
A_52_P295104	Smim5	small integral membrane protein 5
A_55_P2151138	Dynlt1f	dynein light chain Tctex-type 1F
A_55_P2201612	Slc30a7	solute carrier family 30 (zinc trans
A_55_P2109544	Trnt1	tRNA nucleotidyl transferase, CC
A_66_P120770	Ywhaz	tyrosine 3-monooxygenase/tryptop
A_55_P1983268	4930444P10R	RIKEN cDNA 4930444P10 gene
A_51_P191520	Stard10	START domain containing 10
A_66_P130366	Stk38l	serine/threonine kinase 38 like
A_55_P2293414	1700001C19R	RIKEN cDNA 1700001C19 gene
A_55_P2018330	Gm13298	predicted gene 13298
A_55_P2005055	Pepd	peptidase D
A_51_P470989	Paip1	polyadenylate binding protein-inte
A_55_P2127587	Smcr8	Smith-Magenis syndrome chromo
A_55_P1972490	Psg16	pregnancy specific glycoprotein 1

A_55_P1955483	Grb14	growth factor receptor bound prote
A_66_P123055	Gm10845	predicted gene 10845
A_66_P140976	Rpl15	ribosomal protein L15
A_51_P275496	BC026762	cDNA sequence BC026762
A_52_P682745	Dock4	dedicator of cytokinesis 4
A_52_P20639	Rd3	retinal degeneration 3
A_51_P494863	Vmac	vimentin-type intermediate filamer
A_55_P2021094	Tmem181b-ps	transmembrane protein 181B, pse
A_55_P2149382	Gm3448	predicted gene 3448
A_55_P2221647	AI605517	expressed sequence AI605517
A_51_P140237	Fhl2	four and a half LIM domains 2
A_55_P1989524	Fndc1	fibronectin type III domain contain
A_51_P159293	Zbbx	zinc finger, B-box domain containi
A_55_P1995924	Gm13157	predicted gene 13157
A_51_P452820	Rpl31	ribosomal protein L31
A_52_P123738	Rnf41	ring finger protein 41
A_52_P222230	0	0
A_51_P327564	Glb1	galactosidase, beta 1
A_51_P422335	Zfp420	zinc finger protein 420
A_55_P2146749	Rps13	ribosomal protein S13
A_66_P116461	Mro	maestro
A_51_P375558	Myoc	myocilin
A_51_P123604	Ppwd1	peptidylprolyl isomerase domain a
A_55_P1962756	Ttll2	tubulin tyrosine ligase-like family,
A_51_P316801	Wdr60	WD repeat domain 60
A_51_P228193	Ociad1	OCIA domain containing 1
A_55_P1998995	Speg	SPEG complex locus
A_52_P489778	Ablim1	actin-binding LIM protein 1
A_52_P512553	Atg16l2	autophagy related 16-like 2 (S. ce
A_65_P08864	Dph5	DPH5 homolog (S. cerevisiae)
A_55_P1985428	Atg16l2	autophagy related 16-like 2 (S. ce
A_52_P325477	Trim16	tripartite motif-containing 16
A_66_P108434	Ccdc65	coiled-coil domain containing 65
A_51_P502150	Slc9a3r1	solute carrier family 9 (sodium/hyc
A_55_P1970033	Per1	period circadian clock 1
A_51_P409893	Prkar2a	protein kinase, cAMP dependent r
A_55_P2161465	Gm10516	predicted gene 10516
A_55_P2031547	Vmn2r121	vomeronasal 2, receptor 121
A_55_P2062133	Etv3	ets variant gene 3
A_51_P314153	Nr2c2ap	nuclear receptor 2C2-associated p
A_55_P1967539	Hunk	hormonally upregulated Neu-asso
A_51_P140607	Asun	asunder, spermatogenesis regulat
A_55_P2012694	Kcnh5	potassium voltage-gated channel,
A_51_P209183	Cxcl14	chemokine (C-X-C motif) ligand 1
A_52_P253179	Igfbp3	insulin-like growth factor binding p
A_55_P1968977	Stk38l	serine/threonine kinase 38 like
A_55_P1982454	Eps8	epidermal growth factor receptor p
A_55_P2000007	LOC1026393	uncharacterized LOC102639358
A_51_P481821	Spcs3	signal peptidase complex subunit
A_51_P480202	Dlx2	distal-less homeobox 2
A_55_P2127258	Dok7	docking protein 7
A_55_P2062688	Msi1	musashi RNA-binding protein 1
A_55_P2023697	Zfp386	zinc finger protein 386 (Kruppel-lik
A_51_P320022	Atp10a	ATPase, class V, type 10A
A_51_P356579	Mxra7	matrix-remodelling associated 7
A_55_P1967514	Dnah7a	dynein, axonemal, heavy chain 7A
A_52_P217710	Fzd6	frizzled homolog 6 (Drosophila)
A_55_P2036723	Stk36	serine/threonine kinase 36
A_55_P1978226	Park2	Parkinson disease (autosomal rec

A_55_P1999958	0	0
A_66_P112301	C230072F16F	RIKEN cDNA C230072F16 gene
A_51_P244824	Dapp1	dual adaptor for phosphotyrosine
A_55_P1969431	Lyrm5	LYR motif containing 5
A_55_P2145521	Stk38l	serine/threonine kinase 38 like
A_55_P2259125	D7Ertd143e	DNA segment, Chr 7, ERATO Doi
A_55_P2206605	5830444B04R	RIKEN cDNA 5830444B04 gene
A_55_P2151143	Dynlt1c	dynein light chain Tctex-type 1C
A_51_P333965	Cisd2	CDGSH iron sulfur domain 2
A_52_P2710	Cml5	camello-like 5
A_55_P2176248	0	0
A_52_P456561	Abcd1	ATP-binding cassette, sub-family
A_55_P2183735	Pisd	phosphatidylserine decarboxylase
A_52_P565279	Cecr5	cat eye syndrome chromosome re
A_51_P448391	Nkiras1	NFKB inhibitor interacting Ras-like
A_55_P1985693	Fhdc1	FH2 domain containing 1
A_51_P269634	Zfp14	zinc finger protein 14
A_55_P2033480	Gm13298	predicted gene 13298
A_55_P2170509	Yipf4	Yip1 domain family, member 4
A_51_P143468	Klhl26	kelch-like 26
A_52_P436590	Wbscr17	Williams-Beuren syndrome chrom
A_52_P547589	Spag1	sperm associated antigen 1
A_55_P1990134	Cox18	cytochrome c oxidase assembly p
A_55_P2002226	Dzip1	DAZ interacting protein 1
A_66_P101108	Tnrc18	trinucleotide repeat containing 18
A_55_P1987151	Nlrp5	NLR family, pyrin domain containi
A_55_P1988882	Sept9	septin 9
A_55_P2144280	Nnt	nicotinamide nucleotide transhydr
A_55_P2255737	0	0
A_55_P2045114	Tmem242	transmembrane protein 242
A_55_P2186558	Tmem242	transmembrane protein 242
A_55_P2212498	C030005K06F	RIKEN cDNA C030005K06 gene
A_55_P2067652	Boc	biregional cell adhesion molecule-
A_55_P1995992	Gm14432	predicted gene 14432
A_51_P263246	Dusp8	dual specificity phosphatase 8
A_51_P433091	Purb	purine rich element binding protei
A_52_P106620	Tnfrsf11b	tumor necrosis factor receptor sup
A_51_P324934	Mcm3	minichromosome maintenance de
A_55_P2049211	Pisd-ps1	phosphatidylserine decarboxylase
A_51_P193302	Mrps7	mitchondrial ribosomal protein S7
A_51_P342707	Pold2	polymerase (DNA directed), delta
A_55_P2163729	Tvp23a	trans-golgi network vesicle protein
A_55_P2085333	Fbxo44	F-box protein 44
A_55_P1967820	AI661453	expressed sequence AI661453
A_55_P1980292	Purb	purine rich element binding protei
A_55_P1964638	Cxadr	coxsackie virus and adenovirus re
A_55_P1956918	Adamts5	a disintegrin-like and metallopepti
A_55_P2037883	Ino80	INO80 homolog (S. cerevisiae)
A_55_P2173927	Insr	insulin receptor
A_51_P487913	2600006K01R	RIKEN cDNA 2600006K01 gene
A_55_P2028370	0	0
A_55_P1991851	Speg	SPEG complex locus
A_55_P2144285	Nnt	nicotinamide nucleotide transhydr
A_55_P1955568	Extl2	exostoses (multiple)-like 2
A_55_P1976993	Strn	striatin, calmodulin binding protein
A_51_P475228	Armc6	armadillo repeat containing 6
A_55_P2140118	Qpct	glutaminyl-peptide cyclotransferas
A_52_P260696	Arnt2	aryl hydrocarbon receptor nuclear
A_55_P2154943	LOC10263302	uncharacterized LOC102633020

A_52_P627068	Disp2	dispatched homolog 2 (Drosophila
A_55_P2211937	E130101M22	uncharacterized protein E130101M
A_55_P2045658	Nme6	NME/NM23 nucleoside diphospha
A_55_P2322029	3830406C13R	RIKEN cDNA 3830406C13 gene
A_55_P1979929	Prcp	prolylcarboxypeptidase (angiotens
A_52_P646979	D16Ertd472e	DNA segment, Chr 16, ERATO Do
A_55_P2146500	Ccdc107	coiled-coil domain containing 107
A_51_P127915	Rnasek	ribonuclease, RNase K
A_51_P383629	Vps4a	vacuolar protein sorting 4a (yeast)
A_52_P67200	Stt3b	STT3, subunit of the oligosacchary
A_55_P2026818	Slc4a7	solute carrier family 4, sodium bica
A_55_P1955548	Ezr	ezrin
A_55_P1995874	Gm14326	predicted gene 14326
A_55_P2122633	Airn	antisense Igf2r RNA
A_66_P110742	0	0
A_51_P414548	Casp7	caspase 7
A_55_P2035717	Pgap2	post-GPI attachment to proteins 2
A_55_P1974088	Stard6	StAR-related lipid transfer (START
A_55_P2044982	Zfp74	zinc finger protein 74
A_55_P1979330	Dapp1	dual adaptor for phosphotyrosine a
A_55_P1974855	Zfp868	zinc finger protein 868
A_52_P14526	Zyg11b	zyg-II family member B, cell cycle
A_52_P484838	Rfxank	regulatory factor X-associated ank
A_52_P604629	Csrnp1	cysteine-serine-rich nuclear protei
A_55_P2161695	Kdelc1	KDEL (Lys-Asp-Glu-Leu) containin
A_51_P102507	Vps33a	vacuolar protein sorting 33A (yeas
A_55_P2000798	Ccdc144b	coiled-coil domain containing 144B
A_55_P2049095	Atat1	alpha tubulin acetyltransferase 1
A_51_P312748	Oxsm	3-oxoacyl-ACP synthase, mitocho
A_55_P2035667	Gyk	glycerol kinase
A_55_P2048483	D17Zt10e	DNA segment, Chr 17, Zdenek Tra
A_66_P105736	Net1	neuroepithelial cell transforming g
A_52_P244463	D16Ertd472e	DNA segment, Chr 16, ERATO Do
A_51_P487027	Kcnk2	potassium channel, subfamily K, m
A_51_P233027	Rmdn3	regulator of microtubule dynamics
A_51_P310676	Galr2	galanin receptor 2
A_51_P119031	Naa30	N(alpha)-acetyltransferase 30, Na
A_55_P2133220	Arhgef39	Rho guanine nucleotide exchange
A_55_P2028522	Stac	src homology three (SH3) and cys
A_51_P253897	Psca	prostate stem cell antigen
A_51_P261560	Tex33	testis expressed 33
A_51_P186798	0	0
A_55_P2030383	Frmd4a	FERM domain containing 4A
A_55_P2098578	Tubd1	tubulin, delta 1
A_51_P181722	Rbks	ribokinase
A_51_P280532	Supt16	suppressor of Ty 16
A_55_P2118891	Zfp882	zinc finger protein 882
A_55_P1989341	Ntng1	netrin G1
A_52_P644534	Dhrsx	dehydrogenase/reductase (SDR fa
A_66_P138585	4833419G08R	RIKEN cDNA 4833419G08 gene
A_55_P1998947	Trim16	tripartite motif-containing 16
A_55_P1994062	Emx2os	Emx2 opposite strand/antisense tr
A_51_P234544	Azin1	antizyme inhibitor 1
A_52_P1187949	Trim5	tripartite motif-containing 5
A_51_P367780	Adamtsl2	ADAMTS-like 2
A_55_P2146996	Wdr52	WD repeat domain 52
A_51_P149562	Apbb2	amyloid beta (A4) precursor protei
A_55_P2173073	Zfp931	zinc finger protein 931
A_51_P283292	Gm14326	predicted gene 14326

A_52_P376360	Pdgfc	platelet-derived growth factor, C p
A_55_P1954436	Gm7967	predicted gene 7967
A_55_P1988424	Tpi1	triosephosphate isomerase 1
A_65_P02321	Usp36	ubiquitin specific peptidase 36
A_51_P343851	Tgfbrap1	transforming growth factor, beta re
A_55_P1967538	Hunk	hormonally upregulated Neu-asso
A_51_P246727	Mlxip	MLX interacting protein
A_55_P2187043	Tpm1	tropomyosin 1, alpha
A_51_P454103	Manba	mannosidase, beta A, lysosomal
A_52_P494514	Insr	insulin receptor
A_55_P2057994	Mif4gd	MIF4G domain containing
A_55_P2007243	Kcnc1	potassium voltage gated channel,
A_51_P441494	BC100451	cDNA sequence BC100451
A_52_P74576	Ccdc65	coiled-coil domain containing 65
A_55_P1993876	Otud7a	OTU domain containing 7A
A_51_P382928	Cstf3	cleavage stimulation factor, 3' pre-
A_52_P259558	Ogfod1	2-oxoglutarate and iron-dependen
A_55_P2037081	2610305D13F	RIKEN cDNA 2610305D13 gene
A_52_P412529	Fbxo3	F-box protein 3
A_51_P403636	Smad7	SMAD family member 7
A_55_P2062469	Col12a1	collagen, type XII, alpha 1
A_55_P1992715	Igfbp3	insulin-like growth factor binding p
A_55_P2113356	Miip	migration and invasion inhibitory p
A_55_P2060278	Fam45a	family with sequence similarity 45,
A_55_P2039556	Pak6	p21 protein (Cdc42/Rac)-activatec
A_55_P2033445	Tnfrsf1b	tumor necrosis factor receptor sup
A_51_P308029	2010107G23F	RIKEN cDNA 2010107G23 gene
A_55_P2034600	Gm5523	glyceraldehyde-3-phosphate dehy
A_55_P2054300	Alg8	asparagine-linked glycosylation 8
A_52_P563617	Ssbp4	single stranded DNA binding prote
A_55_P2241204	1500015A07R	RIKEN cDNA 1500015A07 gene
A_51_P124748	Tgfb3	transforming growth factor, beta 3
A_66_P113662	Tmem62	transmembrane protein 62
A_55_P1985554	B4galt4	UDP-Gal:betaGlcNAc beta 1,4-ga
A_55_P2148641	Rab4a	RAB4A, member RAS oncogene f
A_55_P1996086	Gm14325	predicted gene 14325
A_55_P1966958	Mef2d	myocyte enhancer factor 2D
A_52_P144794	Tceanc2	transcription elongation factor A (
A_55_P2427685	Agl	amylo-1,6-glucosidase, 4-alpha-gl
A_55_P1969166	Fxr2	fragile X mental retardation, autos
A_55_P1973447	Ybx2	Y box protein 2
A_55_P2052563	Id1	inhibitor of DNA binding 1
A_55_P2078213	1700020I14Ri	RIKEN cDNA 1700020I14 gene
A_52_P110068	Rqcd1	rcd1 (required for cell differentiatic
A_55_P2147791	Fam129c	family with sequence similarity 12
A_55_P2026109	Rpap1	RNA polymerase II associated prc
A_55_P2354336	0	0
A_66_P125212	Mapk1ip1l	mitogen-activated protein kinase 1
A_55_P2076927	Ints10	integrator complex subunit 10
A_52_P558382	Mapk8	mitogen-activated protein kinase
A_55_P2030721	Ankle1	ankyrin repeat and LEM domain c
A_55_P2006525	Adamtsl4	ADAMTS-like 4
A_52_P505143	Jrk	jerky
A_51_P144648	Vps13b	vacuolar protein sorting 13B (yeas
A_55_P2147457	Gm6410	predicted gene 6410
A_55_P2013396	Gm14305	predicted gene 14305
A_55_P2172566	Insr	insulin receptor
A_52_P137691	Trappc5	trafficking protein particle complex
A_55_P2187038	Tpm1	tropomyosin 1, alpha

A_52_P662098	Net1	neuroepithelial cell transforming g
A_51_P315555	Nars	asparaginyl-tRNA synthetase
A_55_P2144075	Pofut2	protein O-fucosyltransferase 2
A_65_P17492	Med29	mediator complex subunit 29
A_51_P213099	Ntng1	netrin G1
A_55_P2212259	4930539J05R	RIKEN cDNA 4930539J05 gene
A_51_P149621	Stt3b	STT3, subunit of the oligosacchary
A_55_P2047962	Gjc2	gap junction protein, gamma 2
A_55_P2158866	Nme6	NME/NM23 nucleoside diphospha
A_55_P1966863	Mad2l2	MAD2 mitotic arrest deficient-like
A_52_P6828	Xk	Kell blood group precursor (McLec
A_55_P2102998	Gm3893	predicted gene 3893
A_55_P2090152	Vmn2r121	vomeronasal 2, receptor 121
A_55_P2041095	Six4	sine oculis-related homeobox 4
A_51_P282179	Mtor	mechanistic target of rapamycin (s
A_51_P397375	Pet112	PET112 homolog (S. cerevisiae)
A_55_P1953226	Gm14484	predicted gene 14484
A_55_P2017140	Vmn2r88	vomeronasal 2, receptor 88
A_55_P2181334	6030419C18R	RIKEN cDNA 6030419C18 gene
A_55_P2121344	Nudcd3	NudC domain containing 3
A_52_P85765	Stard6	StAR-related lipid transfer (START
A_55_P2161958	2410141K09R	RIKEN cDNA 2410141K09 gene
A_55_P2167160	Hdhd2	haloacid dehalogenase-like hydrol
A_55_P2023818	Cysltr1	cysteinyl leukotriene receptor 1
A_55_P2051666	Nfkbib	nuclear factor of kappa light polyp
A_55_P2154049	Myo18a	myosin XVIIIA
A_55_P2121038	Gm10825	predicted gene 10825
A_52_P180826	Ndufaf7	NADH dehydrogenase (ubiquinon
A_55_P2155479	Eps8	epidermal growth factor receptor p
A_55_P2169775	Ano3	anoctamin 3
A_55_P2341950	Crebzf	CREB/ATF bZIP transcription fact
A_55_P2108808	Tubgcp4	tubulin, gamma complex associate
A_55_P2021099	Tmem181a	transmembrane protein 181A
A_52_P329314	0	0
A_55_P2015715	Rab4a	RAB4A, member RAS oncogene f
A_55_P2266880	Kirrel	kin of IRRE like (Drosophila)
A_51_P215190	Efcab11	EF-hand calcium binding domain
A_51_P517381	Cers2	ceramide synthase 2
A_55_P2134645	Fam227a	family with sequence similarity 22
A_55_P2115995	Sms	spermine synthase
A_51_P211341	Eif3j1	eukaryotic translation initiation fac
A_55_P1998194	Snrpn	small nuclear ribonucleoprotein N
A_52_P65494	Iqgap2	IQ motif containing GTPase activa
A_52_P404895	Tmem62	transmembrane protein 62
A_55_P2042146	Fech	ferrochelatase
A_55_P2081398	0	0
A_51_P221132	L2hgdh	L-2-hydroxyglutarate dehydrogena
A_55_P1974442	Sumf2	sulfatase modifying factor 2
A_55_P2105563	1700104L18R	RIKEN cDNA 1700104L18 gene
A_51_P257684	Stau1	staufen (RNA binding protein) hon
A_52_P412452	Cntn6	contactin 6
A_55_P2187171	Sv2c	synaptic vesicle glycoprotein 2c
A_55_P1961645	Vcp	valosin containing protein
A_55_P1955172	Camk2d	calcium/calmodulin-dependent pro
A_55_P2433218	Bloc1s6	biogenesis of lysosomal organelle
A_51_P292368	Tmco6	transmembrane and coiled-coil do
A_55_P2168118	4933406C10R	RIKEN cDNA 4933406C10 gene
A_52_P363216	Gcnt2	glucosaminyl (N-acetyl) transferas
A_55_P2094881	Fgfr2	fibroblast growth factor receptor 2

A_55_P2326337	BC026513	cDNA sequence BC026513
A_66_P111216	4632427E13R	RIKEN cDNA 4632427E13 gene
A_55_P2133165	Wwc1	WW, C2 and coiled-coil domain c
A_55_P2086983	Atxn2	ataxin 2
A_55_P1962174	Rab8a	RAB8A, member RAS oncogene f
A_55_P2018681	G630016G05F	RIKEN cDNA G630016G05 gene
A_52_P417990	Zfp868	zinc finger protein 868
A_51_P125183	Coq5	coenzyme Q5 homolog, methyltra
A_55_P2261772	Lzts1	leucine zipper, putative tumor sup
A_55_P2163363	Clec2f	C-type lectin domain family 2, mer
A_55_P1998392	Eif2ak4	eukaryotic translation initiation fac
A_55_P2098305	Coq5	coenzyme Q5 homolog, methyltra
A_55_P2032478	Sfxn5	sideroflexin 5
A_55_P2092776	Apoo	apolipoprotein O
A_55_P2012241	Ctso	cathepsin O
A_55_P2452384	Mga	MAX gene associated
A_52_P663526	Nmrk1	nicotinamide riboside kinase 1
A_55_P1974063	Gm2545	predicted gene 2545
A_55_P2050592	Gm5785	predicted gene 5785
A_51_P411728	2900026A02F	RIKEN cDNA 2900026A02 gene
A_55_P1970578	Aamdc	adipogenesis associated Mth938
A_52_P299358	Lclat1	lysocardiolipin acyltransferase 1
A_55_P2288285	2310007J06R	RIKEN cDNA 2310007J06 gene
A_55_P2115968	Gm14325	predicted gene 14325
A_51_P336391	Tmem18	transmembrane protein 18
A_52_P67983	Lcmt2	leucine carboxyl methyltransferase
A_51_P114456	Tceanc2	transcription elongation factor A (
A_55_P1962384	Churc1	churchill domain containing 1
A_55_P2053206	Kdm4c	lysine (K)-specific demethylase 4
A_55_P1979246	Cep192	centrosomal protein 192
A_51_P341010	Ercc8	excision repaiross-complementing
A_55_P2388687	1700003G18F	RIKEN cDNA 1700003G18 gene
A_55_P2043430	0	0
A_55_P2078675	0	0
A_55_P2174273	Slco5a1	solute carrier organic anion transp
A_52_P147666	Slc30a7	solute carrier family 30 (zinc trans
A_55_P2085731	Stk38	serine/threonine kinase 38
A_55_P2160737	0	0
A_55_P1965674	Alg2	asparagine-linked glycosylation 2
A_55_P2170911	Gm10366	predicted gene 10366
A_52_P425510	Dnah7a	dynein, axonemal, heavy chain 7
A_55_P2104532	Acacb	acetyl-Coenzyme A carboxylase b
A_55_P2383283	2310001H17F	RIKEN cDNA 2310001H17 gene
A_52_P600946	Ccdc88c	coiled-coil domain containing 88C
A_55_P1999883	Gm14499	predicted gene 14499
A_52_P916539	Zbtb34	zinc finger and BTB domain conta
A_66_P107790	Myl12a	myosin, light chain 12A, regulator
A_55_P2045535	Rsg1	REM2 and RAB-like small GTPas
A_55_P1973896	Vmn2r86	vomeronasal 2, receptor 86
A_55_P2012107	Vmn2r10	vomeronasal 2, receptor 10
A_52_P151905	Gm5132	predicted gene 5132
A_55_P2169909	Ostm1	osteopetrosis associated transme
A_55_P2186460	Emx2os	Emx2 opposite strand/antisense tr
A_51_P381230	Zhx2	zinc fingers and homeoboxes 2
A_55_P2161485	Ptchd2	patched domain containing 2
A_55_P2160910	Faim2	Fas apoptotic inhibitory molecule
A_55_P1986208	Ccnb1ip1	cyclin B1 interacting protein 1
A_52_P622694	Adal	adenosine deaminase-like
A_55_P2293967	Tbc1d5	TBC1 domain family, member 5

A_55_P1953984	Gm11033	predicted gene 11033
A_66_P130911	Proser2	proline and serine rich 2
A_52_P88818	Clybl	citrate lyase beta like
A_55_P2033481	Gm13298	predicted gene 13298
A_66_P122377	Cd84	CD84 antigen
A_51_P320357	Grin2b	glutamate receptor, ionotropic, NM
A_52_P504330	Ankib1	ankyrin repeat and IBR domain co
A_51_P394154	Ddx51	DEAD (Asp-Glu-Ala-Asp) box poly
A_55_P2055642	2810407A14R	RIKEN cDNA 2810407A14 gene
A_52_P219913	Cdan1	congenital dyserythropoietic anem
A_51_P220150	Angptl7	angiopoietin-like 7
A_51_P228865	Zfp72	zinc finger protein 72
A_55_P1993094	Mesdc1	mesoderm development candidate
A_55_P2005853	Nacc2	nucleus accumbens associated 2,
A_51_P473953	Arhgef26	Rho guanine nucleotide exchange
A_55_P2057247	Etohi1	ethanol induced 1
A_51_P226962	Capn15	calpain 15
A_51_P266774	Mfn2	mitofusin 2
A_51_P343429	Slc25a37	solute carrier family 25, member 3
A_55_P2022434	Gpi1	glucose phosphate isomerase 1
A_55_P2025363	Ccnl2	cyclin L2
A_55_P2030433	Gpi1	glucose phosphate isomerase 1
A_55_P2002918	Klc2	kinesin light chain 2
A_55_P1977649	Hoxd8	homeobox D8
A_55_P2031382	Crebzf	CREB/ATF bZIP transcription fact
A_55_P2124016	Nipsnap1	4-nitrophenylphosphatase domain
A_55_P2057268	Magi1	membrane associated guanylate k
A_55_P2139713	Phf13	PHD finger protein 13
A_65_P10433	Rpp14	ribonuclease P 14 subunit
A_55_P2005680	Ipo11	importin 11
A_55_P2134351	Lancl3	LanC lantibiotic synthetase compo
A_66_P122053	Kcnq5	potassium voltage-gated channel,
A_55_P2002220	Dzip1	DAZ interacting protein 1
A_55_P1956687	Rab37	RAB37, member RAS oncogene f
A_52_P221588	Gm5382	predicted gene 5382
A_55_P2062787	Mfap3	microfibrillar-associated protein 3
A_55_P2094484	Gm14137	predicted gene 14137
A_52_P18765	Hsbp1l1	heat shock factor binding protein
A_55_P1983999	Desi1	desumoylating isopeptidase 1
A_51_P495581	Tlr1	toll-like receptor 1
A_55_P2197134	A930018M24R	RIKEN cDNA A930018M24 gene
A_52_P146403	Arhgef38	Rho guanine nucleotide exchange
A_55_P2066219	Gm3455	predicted gene 3455
A_51_P390775	Ube2e1	ubiquitin-conjugating enzyme E2E
A_51_P494006	Scaf8	SR-related CTD-associated factor
A_51_P243134	Adcy6	adenylate cyclase 6
A_55_P1955851	AI593442	expressed sequence AI593442
A_55_P2024555	Ppap2a	phosphatidic acid phosphatase typ
A_55_P2108868	Nufip1	nuclear fragile X mental retardatio
A_51_P375693	Tmem135	transmembrane protein 135
A_55_P1982494	1700012L04R	RIKEN cDNA 1700012L04 gene
A_51_P129100	Sec63	SEC63-like (S. cerevisiae)
A_55_P2003228	Rerg	RAS-like, estrogen-regulated, gro
A_55_P2060722	Uso1	USO1 vesicle docking factor
A_55_P2052210	Gdi2	guanosine diphosphate (GDP) dis
A_55_P1970887	Vmn2r16	vomeronasal 2, receptor 16
A_55_P2061809	Ndufc2	NADH dehydrogenase (ubiquinon
A_65_P10180	Rad23b	RAD23b homolog (S. cerevisiae)
A_55_P2049483	0	0

A_52_P328078	Atp5b	ATP synthase, H+ transporting mi
A_51_P342669	Pgam1	phosphoglycerate mutase 1
A_55_P2217548	4921515G04R	RIKEN cDNA 4921515G04 gene
A_51_P263290	Galnt9	UDP-N-acetyl-alpha-D-galactosam
A_55_P2078815	Xk	Kell blood group precursor (McLeo
A_55_P2107447	Rab37	RAB37, member RAS oncogene f
A_51_P150608	Jagn1	jagunal homolog 1 (Drosophila)
A_52_P580582	Nppa	natriuretic peptide type A
A_51_P107433	Mrpl34	mitochondrial ribosomal protein L3
A_55_P1960621	Gm20764	predicted gene, 20764
A_51_P146303	Mvb12a	multivesicular body subunit 12A
A_51_P242356	Fam114a2	family with sequence similarity 114
A_55_P2041372	Gm3693	predicted gene 3693
A_51_P476711	Skiv2l2	superkiller viralicidic activity 2-like
A_51_P133747	Ppp1r3e	protein phosphatase 1, regulatory
A_51_P288505	Tradd	TNFRSF1A-associated via death
A_55_P1968683	Anks1b	ankyrin repeat and sterile alpha m
A_55_P2177233	Abhd5	abhydrolase domain containing 5
A_55_P2071326	Rpl36	ribosomal protein L36
A_51_P208377	Trappc5	trafficking protein particle complex
A_66_P130612	2810408A11R	RIKEN cDNA 2810408A11 gene
A_52_P133578	Gpr158	G protein-coupled receptor 158
A_51_P289414	Spg11	spastic paraplegia 11
A_55_P2002113	Rpl36	ribosomal protein L36
A_55_P2041893	Gm6404	predicted gene 6404
A_51_P244558	Rab3gap2	RAB3 GTPase activating protein s
A_55_P1999829	Thoc7	THO complex 7 homolog (Drosoph
A_55_P2143499	Pgbd5	piggyBac transposable element de
A_55_P2012096	Bmp8a	bone morphogenetic protein 8a
A_55_P2058953	Rpl13a	ribosomal protein L13A
A_55_P2026054	Usp37	ubiquitin specific peptidase 37
A_55_P2027077	Shc2	SHC (Src homology 2 domain con
A_55_P2067131	Dclre1c	DNA cross-link repair 1C, PSO2 h
A_51_P131025	Ngdn	neuroguidin, EIF4E binding protein
A_55_P1967648	Flcn	folliculin
A_55_P2044967	Zfp74	zinc finger protein 74
A_52_P117576	Casp3	caspase 3
A_51_P184223	Pcdhb7	protocadherin beta 7
A_55_P1956418	Efr3b	EFR3 homolog B (S. cerevisiae)
A_51_P268843	Rasip1	Ras interacting protein 1
A_51_P421140	Tubb6	tubulin, beta 6 class V
A_52_P275678	Gpr135	G protein-coupled receptor 135
A_51_P246677	Rec8	REC8 meiotic recombination prote
A_51_P241943	Sap30l	SAP30-like
A_51_P234627	Nubpl	nucleotide binding protein-like
A_55_P2175915	Ccl28	chemokine (C-C motif) ligand 28
A_52_P47781	Slitrk3	SLIT and NTRK-like family, memb
A_55_P1967983	Use1	unconventional SNARE in the ER
A_51_P167374	Gpatch1	G patch domain containing 1
A_51_P456838	Fbxl21	F-box and leucine-rich repeat prot
A_55_P2056186	Siva1	SIVA1, apoptosis-inducing factor
A_55_P2088711	Sgsm1	small G protein signaling modulato
A_55_P2057941	1700049G17R	RIKEN cDNA 1700049G17 gene
A_52_P561377	Fam160b1	family with sequence similarity 16
A_52_P552589	Map4k1	mitogen-activated protein kinase k
A_55_P2104572	6330416G13R	RIKEN cDNA 6330416G13 gene
A_52_P108321	Ccdc71	coiled-coil domain containing 71
A_55_P2114863	Mgll	monoglyceride lipase
A_55_P2069012	Pidd1	p53 induced death domain protein

A_52_P409457	Ppcdc	phosphopantothenoylcysteine dec
A_51_P517001	D130040H23F	RIKEN cDNA D130040H23 gene
A_52_P595642	Smim7	small integral membrane protein 7
A_52_P179729	Txnl4a	thioredoxin-like 4A
A_55_P2471798	Snap23	synaptosomal-associated protein
A_55_P2167898	Nat9	N-acetyltransferase 9 (GCN5-relat
A_55_P2109585	Plekha7	pleckstrin homology domain conta
A_51_P372156	4930563E22R	RIKEN cDNA 4930563E22 gene
A_55_P1992160	Mbp	myelin basic protein
A_55_P2153797	Prnp	prion protein
A_55_P1974477	Msh3	mutS homolog 3 (E. coli)
A_55_P2183597	Tbc1d2	TBC1 domain family, member 2
A_55_P1981461	5430410E06R	RIKEN cDNA 5430410E06 gene
A_55_P2330545	Zfp81	zinc finger protein 81
A_55_P2027152	Ssh1	slingshot homolog 1 (Drosophila)
A_55_P1970676	Sh3yl1	Sh3 domain YSC-like 1
A_51_P348652	Spast	spastin
A_52_P448870	Rab26	RAB26, member RAS oncogene f
A_55_P2074291	Fbxo6	F-box protein 6
A_51_P122141	Mamstr	MEF2 activating motif and SAP dc
A_55_P2025514	Pnpla3	patatin-like phospholipase domain
A_52_P673499	Shmt1	serine hydroxymethyltransferase
A_52_P73559	Gm7241	predicted pseudogene 7241
A_55_P2079009	Slco2b1	solute carrier organic anion transp
A_55_P2011692	0	0
A_55_P1977454	4930570G19F	RIKEN cDNA 4930570G19 gene
A_55_P2032147	Wnt9a	wingless-type MMTV integration s
A_55_P2003951	Tmem192	transmembrane protein 192
A_52_P734742	Lrrc73	leucine rich repeat containing 73
A_55_P2000027	Spink2	serine peptidase inhibitor, Kazal ty
A_55_P2013203	Oxtr	oxytocin receptor
A_51_P291682	Tmed4	transmembrane emp24 protein tra
A_52_P434841	Coa4	cytochrome c oxidase assembly fa
A_55_P2051313	Gstk1	glutathione S-transferase kappa 1
A_55_P2039061	Trim12c	tripartite motif-containing 12C
A_52_P327402	Cds1	CDP-diacylglycerol synthase 1
A_55_P2115225	Fap	fibroblast activation protein
A_51_P105520	Nomo1	nodal modulator 1
A_55_P2308743	A430106A12F	RIKEN cDNA A430106A12 gene
A_55_P2157360	Tagap1	T cell activation GTPase activating
A_51_P239286	Bcl2l12	BCL2-like 12 (proline rich)
A_55_P2157902	Igsf10	immunoglobulin superfamily, mem
A_51_P216605	Hbp1	high mobility group box transcripti
A_55_P1967500	Nell1	NEL-like 1
A_51_P245546	Synrg	synergin, gamma
A_55_P2153496	Ppp2r3d	protein phosphatase 2 (formerly 2
A_55_P2049448	Phtf1	putative homeodomain transcriptic
A_51_P475628	Paqr6	progestin and adipoQ receptor fan
A_55_P1963687	Tsen54	tRNA splicing endonuclease 54 hc
A_66_P128927	Gm6306	predicted gene 6306
A_66_P133993	Gm5093	predicted gene 5093
A_51_P302942	Rasl10a	RAS-like, family 10, member A
A_51_P341789	Sugp1	SURP and G patch domain contai
A_66_P137383	Ddx55	DEAD (Asp-Glu-Ala-Asp) box poly
A_52_P640386	Usp53	ubiquitin specific peptidase 53
A_55_P2032318	4930522L14R	RIKEN cDNA 4930522L14 gene
A_51_P487547	Ccdc91	coiled-coil domain containing 91
A_55_P1991500	Obfc1	oligonucleotide/oligosaccharide-bi
A_55_P2018847	Crlf2	cytokine receptor-like factor 2

A_55_P2077263	Cenpk	centromere protein K
A_51_P382369	Zfp608	zinc finger protein 608
A_55_P2021892	Ccdc114	coiled-coil domain containing 114
A_55_P2067513	Slc10a3	solute carrier family 10 (sodium/bi
A_55_P2045096	Hjurp	Holliday junction recognition prote
A_55_P1974233	Dtd2	D-tyrosyl-tRNA deacylase 2
A_55_P1971025	Paqr6	progestin and adipoQ receptor fan
A_55_P2037812	Palmd	palmdelphin
A_55_P1968245	Ftl1	ferritin light chain 1
A_55_P2123831	Thap6	THAP domain containing 6
A_55_P1961241	LOC10263459	uncharacterized LOC102634598
A_55_P2063316	Mgll	monoglyceride lipase
A_55_P1975832	1810009N02R	RIKEN cDNA 1810009N02 gene
A_51_P331827	Slc25a41	solute carrier family 25, member 4
A_55_P2007919	Akr1c19	aldo-keto reductase family 1, mem
A_51_P240801	Tmem173	transmembrane protein 173
A_55_P2143075	Ubc	ubiquitin C
A_55_P2145139	0	0
A_51_P469968	H2-M3	histocompatibility 2, M region locu
A_55_P2057127	Nim1k	NIM1 serine/threonine protein kina
A_51_P298802	Bfsp2	beaded filament structural protein
A_51_P468762	Alkbh6	alkB, alkylation repair homolog 6 (
A_55_P2097340	Camkv	CaM kinase-like vesicle-associate
A_55_P2053497	Poli	polymerase (DNA directed), iota
A_51_P437478	Zfp566	zinc finger protein 566
A_52_P343627	Rbp7	retinol binding protein 7, cellular
A_66_P126415	Gm8013	predicted gene 8013
A_55_P2106235	Syngr2	synaptogyrin 2
A_51_P116487	Lsm4	LSM4 homolog, U6 small nuclear
A_52_P472302	Fxyd6	FXYD domain-containing ion trans
A_55_P2008936	Slc2a9	solute carrier family 2 (facilitated g
A_52_P71105	Sertad3	SERTA domain containing 3
A_52_P593037	Acsl5	acyl-CoA synthetase long-chain fa
A_55_P1998872	Slitrk5	SLIT and NTRK-like family, memb
A_66_P122699	Cux2	cut-like homeobox 2
A_66_P128445	Bend7	BEN domain containing 7
A_51_P192139	Zfp74	zinc finger protein 74
A_66_P104309	Myl2	myosin, light polypeptide 2, regula
A_55_P2000304	Terf1	telomeric repeat binding factor 1
A_55_P2137701	Gm13247	predicted gene 13247
A_55_P2007273	Pole	polymerase (DNA directed), epsilo
A_55_P1968200	Hjurp	Holliday junction recognition prote
A_52_P357055	Ccdc91	coiled-coil domain containing 91
A_52_P211418	G2e3	G2/M-phase specific E3 ubiquitin l
A_51_P230439	Ppfibp2	PTPRF interacting protein, binding
A_55_P1961140	Mettl3	methyltransferase like 3
A_55_P2018666	Thrsp	thyroid hormone responsive
A_55_P2223282	B130019D13R	RIKEN cDNA B130019D13 gene
A_55_P2227580	A130072N09R	RIKEN cDNA A130072N09 gene
A_55_P1971174	Cd1d2	CD1d2 antigen
A_55_P2084332	Pigp	phosphatidylinositol glycan anchor
A_51_P151586	Gsg2	germ cell-specific gene 2
A_55_P1968908	Hypk	huntingtin interacting protein K
A_55_P2019113	Apol7b	apolipoprotein L 7b
A_52_P367675	Acin1	apoptotic chromatin condensation
A_51_P465273	Mettl17	methyltransferase like 17
A_51_P421223	Fv1	Friend virus susceptibility 1
A_55_P2131340	Churc1	churchill domain containing 1
A_55_P2061371	Gm15698	transcription elongation factor B (S

A_55_P1970299	Mttp	microsomal triglyceride transfer pr
A_51_P108581	Adrbk2	adrenergic receptor kinase, beta 2
A_52_P67270	4930515G01F	RIKEN cDNA 4930515G01 gene
A_55_P2121846	0	0
A_55_P1968858	Cadps	Ca2+-dependent secretion activat
A_66_P111430	2410006H16F	RIKEN cDNA 2410006H16 gene
A_52_P257686	Rwdd3	RWD domain containing 3
A_55_P2167323	Cort	cortistatin
A_51_P101573	Klc4	kinesin light chain 4
A_55_P2457154	G2e3	G2/M-phase specific E3 ubiquitin l
A_55_P2035951	Haus8	4HAUS augmin-like complex, subu
A_51_P455807	Ehd4	EH-domain containing 4
A_51_P253732	Il17rd	interleukin 17 receptor D
A_55_P2143251	Rims3	regulating synaptic membrane exo
A_51_P414126	Rab19	RAB19, member RAS oncogene fa
A_55_P2137941	Fxyd2	FXYD domain-containing ion trans
A_55_P2072656	Ckmt1	creatine kinase, mitochondrial 1, u
A_51_P312437	Dhrs7	dehydrogenase/reductase (SDR fa
A_52_P664404	Zfp286	zinc finger protein 286
A_55_P2000533	Polk	polymerase (DNA directed), kappa
A_51_P353392	Cript	cysteine-rich PDZ-binding protein
A_55_P2417936	AW125324	expressed sequence AW125324
A_55_P2181009	Gpr180	G protein-coupled receptor 180
A_55_P2028936	5033425G24F	RIKEN cDNA 5033425G24 gene
A_55_P2003541	Nrcam	neuron-glia-CAM-related cell adhe
A_51_P310164	2810459M11F	RIKEN cDNA 2810459M11 gene
A_52_P338956	Aspg	asparaginase homolog (S. cerevis
A_66_P131169	LOC1008622	uncharacterized LOC100862268
A_51_P223569	Ddx4	DEAD (Asp-Glu-Ala-Asp) box poly
A_55_P1974487	Atp8b5	ATPase, class I, type 8B, member
A_55_P2064257	Dnaic2	dynein, axonemal, intermediate ch
A_55_P2075213	Kbtbd11	kelch repeat and BTB (POZ) doma
A_55_P1953103	Nudt7	nudix (nucleoside diphosphate link
A_55_P2014100	Gm7120	predicted gene 7120
A_55_P2108820	Adamts3	a disintegrin-like and metallopeptid
A_52_P1092823	Irx1	Iroquois related homeobox 1 (Dros
A_55_P2045085	Rpl34-ps1	ribosomal protein L34, pseudogen
A_52_P640922	Dcdc2a	doublecortin domain containing 2a
A_51_P327874	Pth1r	parathyroid hormone 1 receptor
A_52_P348031	Syt9	synaptotagmin IX
A_55_P2031692	Gstm6	glutathione S-transferase, mu 6
A_55_P2111148	Gemin5	gem (nuclear organelle) associate
A_55_P2031496	Rufy3	RUN and FYVE domain containing
A_52_P434306	0	0
A_55_P1984690	Ptprr	protein tyrosine phosphatase, rece
A_51_P431870	Map1s	microtubule-associated protein 1S
A_55_P2060991	BC005764	cDNA sequence BC005764
A_51_P218953	Zfp536	zinc finger protein 536
A_55_P1985410	Reps2	RALBP1 associated Eps domain c
A_55_P1956812	Fam83g	family with sequence similarity 83,
A_66_P106611	Gna14	guanine nucleotide binding protein
A_51_P394833	Tshz1	teashirt zinc finger family member
A_51_P477019	Rnaset2a	ribonuclease T2A
A_55_P2169311	4930515G01F	RIKEN cDNA 4930515G01 gene
A_51_P461108	Osbpl10	oxysterol binding protein-like 10
A_55_P2149951	Prx	periaxin
A_51_P116906	Rapgef3	Rap guanine nucleotide exchange
A_55_P2108784	Arhgap22	Rho GTPase activating protein 22
A_51_P413507	2010109A12R	RIKEN cDNA 2010109A12 gene

A_51_P481159	Cbr3	carbonyl reductase 3
A_55_P1954092	0	0
A_66_P112024	0	0
A_55_P1979027	Tmem65	transmembrane protein 65
A_51_P451588	Plekhb1	pleckstrin homology domain conta
A_55_P2045007	Hrh1	histamine receptor H1
A_55_P2096368	LOC1026327	ADP-ribosylation factor 1-like
A_55_P2115127	Mphosph10	M-phase phosphoprotein 10 (U3 s
A_55_P1975120	Gm10777	predicted gene 10777
A_55_P2106150	Cenpk	centromere protein K
A_55_P2036813	0	0
A_55_P2007771	Catsper2	cation channel, sperm associated
A_55_P2157966	Map1a	microtubule-associated protein 1
A_51_P254045	Traip	TRAF-interacting protein
A_55_P1955726	Ptpn5	protein tyrosine phosphatase, non
A_55_P2044602	Siah3	seven in absentia homolog 3 (Dro
A_55_P2021266	Hpse	heparanase
A_55_P2097178	Idua	iduronidase, alpha-L-
A_55_P1999240	Gm2696	predicted gene 2696
A_55_P2185504	Masp2	mannan-binding lectin serine pept
A_55_P1983959	Ftl1	ferritin light chain 1
A_55_P2185950	Bpnt1	bisphosphate 3'-nucleotidase 1
A_55_P2088223	Synpr	synaptoporin
A_55_P2187076	Sncg	synuclein, gamma
A_55_P2121156	LOC1026342	uncharacterized LOC102634215
A_55_P2099540	H2afj	H2A histone family, member J
A_55_P2169227	Ccdc184	coiled-coil domain containing 184
A_55_P2105362	Tmed5	transmembrane emp24 protein tra
A_51_P215374	Slc6a17	solute carrier family 6 (neurotrans
A_55_P2059986	Chst14	carbohydrate (N-acetylgalactosa
A_52_P558609	Clec16a	C-type lectin domain family 16, me
A_55_P2179834	Gatad2a	GATA zinc finger domain containi
A_51_P273609	Itpka	inositol 1,4,5-trisphosphate 3-kina
A_55_P2124026	Synj2	synaptojanin 2
A_51_P348617	2310045N01	RIKEN cDNA 2310045N01 gene
A_51_P408989	L3hypdh	L-3-hydroxyproline dehydratase (t
A_51_P331661	Ubiad1	UbiA prenyltransferase domain co
A_55_P1998299	Itgb4	integrin beta 4
A_55_P2119892	Erbb4	v-erb-a erythroblastic leukemia vir
A_55_P1958597	Slc27a3	solute carrier family 27 (fatty acid
A_55_P2105220	Hscb	HscB iron-sulfur cluster co-chaper
A_55_P2059179	Slc48a1	solute carrier family 48 (heme tran
A_66_P138584	Mnd1	meiotic nuclear divisions 1 homolo
A_52_P116264	Adhfe1	alcohol dehydrogenase, iron conta
A_52_P650325	Slc35e1	solute carrier family 35, member E
A_55_P2095909	Lamtor3	late endosomal/lysosomal adapto
A_52_P489295	Adamts1	a disintegrin-like and metallopepti
A_65_P01247	Hjurp	Holliday junction recognition prote
A_55_P1953387	Fabp5	fatty acid binding protein 5, epider
A_55_P2023707	Camta1	calmodulin binding transcription a
A_51_P497240	E330013P04	RIKEN cDNA E330013P04 gene
A_51_P134812	Chac1	ChaC, cation transport regulator 1
A_55_P1961014	Selenbp1	selenium binding protein 1
A_52_P529195	Pcdhb4	protocadherin beta 4
A_55_P1963508	Slc13a5	solute carrier family 13 (sodium-d
A_55_P2004960	9130017K11	RIKEN cDNA 9130017K11 gene
A_55_P2072391	Acp1	acid phosphatase 1, soluble
A_55_P2183914	Gm7120	predicted gene 7120
A_51_P147034	Ica1l	islet cell autoantigen 1-like

A_55_P2040371	Rnaset2a	ribonuclease T2A
A_51_P116687	1700010I14Ri	RIKEN cDNA 1700010I14 gene
A_55_P2008722	Gm13157	predicted gene 13157
A_51_P474422	Ift27	intraflagellar transport 27
A_55_P1986639	3110070M22F	RIKEN cDNA 3110070M22 gene
A_51_P517430	Cd1d1	CD1d1 antigen
A_55_P2000973	Syt15	synaptotagmin XV
A_51_P135340	Panx1	pannexin 1
A_51_P282268	Snapc1	small nuclear RNA activating com
A_55_P2329298	Gm12758	predicted gene 12758
A_55_P2055087	Prkar2b	protein kinase, cAMP dependent
A_52_P167535	Efcab12	EF-hand calcium binding domain
A_51_P191782	Olfml3	olfactomedin-like 3
A_52_P563375	Lgals2	lectin, galactose-binding, soluble
A_55_P2163774	Crip1	cysteine-rich protein 1 (intestinal)
A_55_P1969497	Lynx1	Ly6/neurotoxin 1
A_52_P463977	Tmem140	transmembrane protein 140
A_51_P477736	4932415M13F	RIKEN cDNA 4932415M13 gene
A_55_P2023864	Mfap1a	microfibrillar-associated protein 1
A_52_P559919	Eif2ak2	eukaryotic translation initiation fac
A_55_P2356736	6720483E21R	RIKEN cDNA 6720483E21 gene
A_55_P2052834	Lst1	leukocyte specific transcript 1
A_55_P1953919	Me3	malic enzyme 3, NADP(+)-depen
A_51_P446796	Camta1	calmodulin binding transcription a
A_51_P464308	Gnb4	guanine nucleotide binding protei
A_55_P2001628	Rps4l	ribosomal protein S4-like
A_52_P38908	Tmem132b	transmembrane protein 132B
A_51_P283968	Adamts18	a disintegrin-like and metallopepti
A_52_P630867	Abcc4	ATP-binding cassette, sub-family
A_55_P1953920	Me3	malic enzyme 3, NADP(+)-depen
A_55_P2105321	Acin1	apoptotic chromatin condensation
A_51_P502437	Cacna2d3	calcium channel, voltage-depende
A_51_P369803	Psmb9	proteasome (prosome, macropain
A_55_P1953087	Mcm3	minichromosome maintenance de
A_55_P2115567	Slc26a1	solute carrier family 26 (sulfate tra
A_55_P2044242	Slc13a5	solute carrier family 13 (sodium-d
A_55_P2079619	Rnf43	ring finger protein 43
A_55_P1959076	Zfp930	zinc finger protein 930
A_55_P2048119	Slc29a4	solute carrier family 29 (nucleosid
A_52_P400509	Atm	ataxia telangiectasia mutated hom
A_51_P506733	P2rx7	purinergic receptor P2X, ligand-ga
A_55_P1973352	0	0
A_55_P2008417	Mnd1	meiotic nuclear divisions 1 homol
A_55_P2106459	Zfhx3	zinc finger homeobox 3
A_55_P2370160	C130009A20F	RIKEN cDNA C130009A20 gene
A_51_P417251	6330403K07R	RIKEN cDNA 6330403K07 gene
A_55_P2067116	Dclre1c	DNA cross-link repair 1C, PSO2 h
A_65_P03606	Rpap2	RNA polymerase II associated pr
A_55_P2062593	Gm4924	predicted gene 4924
A_55_P2155644	2010315B03R	RIKEN cDNA 2010315B03 gene
A_55_P2075313	Zfp619	zinc finger protein 619
A_55_P2048478	Olfml1	olfactomedin-like 1
A_55_P2018181	A730008H23F	RIKEN cDNA A730008H23 gene
A_52_P481279	Drc1	dynein regulatory complex subuni
A_55_P2073642	1600014C10F	RIKEN cDNA 1600014C10 gene
A_55_P2123683	Chrdl1	chordin-like 1
A_55_P2016034	Nlrc5	NLR family, CARD domain contai
A_55_P2035424	Hpgd	hydroxyprostaglandin dehydrogen
A_55_P2059090	Tagap	T cell activation Rho GTPase acti

A_52_P305230	Igsf21	immunoglobulin superfamily, mem
A_55_P1960735	Gdf15	growth differentiation factor 15
A_55_P2090330	Kcnmb4	potassium large conductance calc
A_52_P574653	Bid	BH3 interacting domain death ago
A_55_P2080880	Clcnkb	chloride channel Kb
A_52_P590535	Fbln2	fibulin 2
A_65_P01834	Lima1	LIM domain and actin binding 1
A_55_P2116650	0	0
A_55_P2056557	0	0
A_55_P2079116	0	0
A_55_P2057622	Ocel1	occludin/ELL domain containing 1
A_55_P2041828	Tubb3	tubulin, beta 3 class III
A_52_P124472	Kcnd2	potassium voltage-gated channel,
A_55_P2334927	9.13E+15	uncharacterized 9130022E09
A_52_P573255	Cdc42ep1	CDC42 effector protein (Rho GTP
A_55_P2147280	Myh1	myosin, heavy polypeptide 1, skel
A_55_P1983958	Gm20746	predicted gene, 20746
A_66_P122415	Snhg6	small nucleolar RNA host gene 6
A_52_P48546	Rnf41	ring finger protein 41
A_52_P1042732	Akap5	A kinase (PRKA) anchor protein 5
A_55_P2076303	March8	membrane-associated ring finger
A_55_P2154977	Rpap3	RNA polymerase II associated pro
A_55_P2006035	Galnt15	UDP-N-acetyl-alpha-D-galactosan
A_55_P2133205	Nmt2	N-myristoyltransferase 2
A_55_P1957213	3930401B19R	RIKEN cDNA 3930401B19 gene
A_55_P2115151	Pxylp1	2-phosphoxylose phosphatase 1
A_51_P506937	Mrps12	mitochondrial ribosomal protein S
A_55_P2110290	Tmem254a	transmembrane protein 254a
A_55_P2088720	0	0
A_55_P2209258	B430105A11R	RIKEN cDNA B430105A11 gene
A_52_P250555	Dynll1	dynein light chain LC8-type 1
A_55_P2027852	Ccl25	chemokine (C-C motif) ligand 25
A_52_P8324	Tmem178	transmembrane protein 178
A_52_P441294	Chl1	cell adhesion molecule with homo
A_55_P1967553	Tmem254c	transmembrane protein 254c
A_51_P241210	Lhfpl3	lipoma HMGIC fusion partner-like
A_55_P2029746	0	0
A_55_P1954724	0	0
A_51_P337944	Bmp2k	BMP2 inducible kinase
A_55_P2007673	Lrsam1	leucine rich repeat and sterile alph
A_52_P447196	Col4a6	collagen, type IV, alpha 6
A_52_P650379	Strap	serine/threonine kinase receptor a
A_55_P1976898	Pnp2	purine-nucleoside phosphorylase
A_55_P1994339	Dhrs7c	dehydrogenase/reductase (SDR fa
A_66_P125862	A930005H10R	RIKEN cDNA A930005H10 gene
A_55_P1987499	Pttg1	pituitary tumor-transforming gene
A_55_P2011659	Anapc5	anaphase-promoting complex sub
A_55_P2213214	A030001D20R	RIKEN cDNA A030001D20 gene
A_51_P140690	Stmn3	stathmin-like 3
A_55_P2013223	S100z	S100 calcium binding protein, zeta
A_52_P331762	Lmo1	LIM domain only 1
A_51_P355427	Timp4	tissue inhibitor of metalloproteinas
A_51_P382970	Itga9	integrin alpha 9
A_51_P497985	C2	complement component 2 (within
A_51_P360918	Ehd3	EH-domain containing 3
A_51_P309854	Kcnn2	potassium intermediate/small cond
A_66_P125035	Duxbl2	doubl homeobox B-like 2
A_55_P2063256	Lgals4	lectin, galactose binding, soluble 4
A_51_P497100	Lgals4	lectin, galactose binding, soluble 4

A_51_P129149	Gatad2a	GATA zinc finger domain containi
A_55_P2148534	Nr1d2	nuclear receptor subfamily 1, grou
A_55_P2010936	Fbxo17	F-box protein 17
A_55_P2033425	Grm5	glutamate receptor, metabotropic
A_51_P292357	Rps3a1	ribosomal protein S3A1
A_52_P257625	Esm1	endothelial cell-specific molecule
A_55_P2058791	4833420G17R	RIKEN cDNA 4833420G17 gene
A_55_P2106525	Nmnat3	nicotinamide nucleotide adenylyltr
A_55_P2040600	Exd1	exonuclease 3'-5' domain containi
A_55_P2140212	0	0
A_55_P2093774	Chl1	cell adhesion molecule with homo
A_52_P165773	Prmt8	protein arginine N-methyltransfera
A_55_P2014304	Kank1	KN motif and ankyrin repeat doma
A_51_P458778	Hpgd	hydroxyprostaglandin dehydrogen
A_55_P2162344	Lrsam1	leucine rich repeat and sterile alph
A_55_P2004179	Col2a1	collagen, type II, alpha 1
A_55_P2096867	Gap43	growth associated protein 43
A_55_P1968276	Tomm22	translocase of outer mitochondrial
A_55_P2315012	4930458D05R	RIKEN cDNA 4930458D05 gene
A_55_P1978465	H2-Q5	histocompatibility 2, Q region locu
A_55_P1953972	Pdhb	pyruvate dehydrogenase (lipoami
A_55_P2212603	Apba2	amyloid beta (A4) precursor protei
A_51_P194249	Stmn4	stathmin-like 4
A_51_P128667	Lynx1	Ly6/neurotoxin 1
A_66_P105175	Bche	butyrylcholinesterase
A_55_P2176792	Sh3gl3	SH3-domain GRB2-like 3
A_66_P108247	Ucp3	uncoupling protein 3 (mitochondri
A_55_P2045642	Stmn4	stathmin-like 4
A_55_P2091359	Padi2	peptidyl arginine deiminase, type I
A_52_P597775	Gprc5a	G protein-coupled receptor, family
A_51_P259296	Lpl	lipoprotein lipase
A_52_P257812	Lpl	lipoprotein lipase
A_55_P2074656	Padi2	peptidyl arginine deiminase, type I
A_51_P297105	Ucp2	uncoupling protein 2 (mitochondri
A_52_P157450	Abhd1	abhydrolase domain containing 1
A_52_P613498	4833420G17R	RIKEN cDNA 4833420G17 gene
A_51_P159453	Serpina3n	serine (or cysteine) peptidase inhi
A_55_P2026270	Cfi	complement component factor i
A_51_P462428	Galnt15	UDP-N-acetyl-alpha-D-galactosan
A_52_P393314	P2rx7	purinergic receptor P2X, ligand-ga
A_55_P1952482	Pbp2	phosphatidylethanolamine binding
A_55_P2105944	Olfr224	olfactory receptor 224
A_52_P206492	Pop4	processing of precursor 4, ribonuc
A_55_P2026420	Pou6f1	POU domain, class 6, transcriptio
A_52_P111031	Pcdh17	protocadherin 17
A_55_P2137527	Fam183b	family with sequence similarity 18
A_55_P2132207	1810037I17Ri	RIKEN cDNA 1810037I17 gene
A_52_P303176	1810037I17Ri	RIKEN cDNA 1810037I17 gene
A_66_P130813	Samd4	sterile alpha motif domain containi
A_55_P1966774	Serpina3i	serine (or cysteine) peptidase inhi
A_52_P516409	Col4a6	collagen, type IV, alpha 6
A_55_P1966838	Xaf1	XIAP associated factor 1

g and 3xTg-AD primary hippocampal astrocytes

Description
Mus musculus tripartite motif-containing 12A (Trim12a), mRNA [NM_023835]
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030400B02 pr
Mus musculus chemokine (C-C motif) ligand 27A (Ccl27a), transcript variant 1, mRNA [NM_001048179]
Mus musculus RIKEN cDNA 2610507I01 gene (2610507I01Rik), long non-coding RNA [NR_037964]
Mus musculus tripartite motif-containing 12A (Trim12a), mRNA [NM_023835]
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130078N14 product
Mus musculus predicted gene, 20878 (Gm20878), mRNA [NM_001270431]
Mus musculus microtubule-associated protein 1B (Map1b), mRNA [NM_008634]
Mus musculus predicted gene, 20878 (Gm20878), mRNA [NM_001270431]
Mus musculus carbonic anhydrase 9 (Car9), mRNA [NM_139305]
Mus musculus vomeronasal 2, receptor 123 (Vmn2r123), mRNA [NM_009485]
Mus musculus angiogenin, ribonuclease A family, member 2 (Ang2), mRNA [NM_007449]
Mus musculus zinc finger protein 933 (Zfp933), mRNA [NM_198619]
Mus musculus bisphosphate 3'-nucleotidase 1 (Bpnt1), mRNA [NM_011794]
Mus musculus jumonji domain containing 7 (Jmjd7), mRNA [NM_001114637]
Mus musculus zinc finger protein 963 (Zfp963), mRNA [NM_001200023]
Mus musculus kallikrein 1-related peptidase b22 (Klk1b22), mRNA [NM_010114]
Mus musculus cDNA sequence BC049715 (BC049715), mRNA [NM_178776]
Mus musculus patched domain containing 2 (Ptchd2), mRNA [NM_001083342]
Mus musculus carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8 (Chst8), mRNA [NM_175140]
Mus musculus cDNA sequence BC049715 (BC049715), mRNA [NM_178776]
Mus musculus solute carrier family 2 (facilitated glucose transporter), member 4 (Slc2a4), mRNA [NM_009
Mus musculus serine/threonine kinase 3 (Stk3), mRNA [NM_019635]
Mus musculus occludin/ELL domain containing 1 (Ocel1), mRNA [NM_029865]
Mus musculus RIKEN cDNA 4930427A07 gene (4930427A07Rik), mRNA [NM_134041]
Mus musculus tripartite motif-containing 34A (Trim34a), mRNA [NM_030684]
Mus musculus angiogenin, ribonuclease A family, member 3 (Ang3), mRNA [NM_001123394]
PREDICTED: Mus musculus tropomyosin alpha-4 chain-like (LOC102633627), misc_RNA [XR_385459]
Mus musculus major facilitator superfamily domain containing 7B (Mfsd7b), mRNA [NM_001081259]
Mus musculus secreted phosphoprotein 1 (Spp1), transcript variant 5, mRNA [NM_001204233]
Mus musculus bone morphogenetic protein 4 (Bmp4), mRNA [NM_007554]
Mus musculus kallikrein 1-related peptidase b3 (Klk1b3), mRNA [NM_008693]
Mus musculus ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6
Mus musculus 2-deoxyribose-5-phosphate aldolase homolog (C. elegans) (Dera), mRNA [NM_172733]
Mus musculus coiled-coil domain containing 65 (Ccdc65), mRNA [NM_153518]
Mus musculus phorbol-12-myristate-13-acetate-induced protein 1 (Pmaip1), mRNA [NM_021451]
Mus musculus potassium voltage-gated channel, shaker-related subfamily, beta member 1 (Kcnab1), trans
Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310058N22 product:unc
Mus musculus RIKEN cDNA 9030025P20 gene (9030025P20Rik), mRNA [NM_001123370]
Mus musculus mutL homolog 1 (E. coli) (Mlh1), mRNA [NM_026810]
Mus musculus CD59a antigen (Cd59a), transcript variant 2, mRNA [NM_007652]
Mus musculus leucine zipper protein 2 (Luzp2), mRNA [NM_178705]
Mus musculus zinc finger protein 236 (Zfp236), mRNA [NM_177832]
Mus musculus cortexin 3 (Ctxn3), mRNA [NM_001134697]
Mus musculus chemokine (C-C motif) ligand 27A (Ccl27a), transcript variant 2 (and 1), mRNA [NM_01133
Mus musculus MAM domain containing 2 (Mamdc2), mRNA [NM_174857]
Mus musculus chemokine (C-C motif) ligand 27A (Ccl27a), transcript variant 1, mRNA [NM_001048179]
Mus musculus zinc finger protein 961 (Zfp961), mRNA [NM_001164581]
Mus musculus podoplanin (Pdpn), transcript variant 1, mRNA [NM_010329]
Mus musculus LanC lantibiotic synthetase component C-like 3 (bacterial) (Lancl3), mRNA [NM_173414]
Mus musculus microtubule associated serine/threonine kinase family member 4 (Mast4), mRNA [NM_1751
Mus musculus RIKEN cDNA 1500011B03 gene (1500011B03Rik), transcript variant 2, long non-coding RN
Mus musculus ER membrane associated RNA degradation (Ermard), transcript variant 1, mRNA [NM_001
Mus musculus transmembrane protein 88 (Tmem88), mRNA [NM_025915]
Mus musculus ER membrane associated RNA degradation (Ermard), transcript variant 1, mRNA [NM_001
Mus musculus myosin VIIA (Myo7a), transcript variant 2, mRNA [NM_008663]

Mus musculus tetratricopeptide repeat domain 8 (Ttc8), transcript variant 1, mRNA [NM_029553]
Mus musculus lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730014H17 product:
Mus musculus matrix-remodelling associated 7 (Mxra7), mRNA [NM_026280]
PREDICTED: Mus musculus tumor necrosis factor (ligand) superfamily, member 13, opposite strand (Tnfsf
Mus musculus centrosomal protein 76 (Cep76), mRNA [NM_001081073]
sorting nexin 29 [Source:MGI Symbol;Acc:MGI:1921728] [ENSMUST00000134941]
GAG_IPMAE (P31790) Retrovirus-related Gag polyprotein, partial (43%) [TC1705975]
Mus musculus cDNA sequence BC006965 (BC006965), long non-coding RNA [NR_024085]
Mus musculus ATPase, class V, type 10D (Atp10d), mRNA [NM_153389]
Mus musculus angiogenin, ribonuclease A family, member 3 (Ang3), mRNA [NM_001123394]
Mus musculus predicted gene 13152 (Gm13152), mRNA [NM_001039209]
Mus musculus cerebral endothelial cell adhesion molecule (Cercam), mRNA [NM_207298]
coiled-coil domain containing 32 [Source:MGI Symbol;Acc:MGI:2685477] [ENSMUST00000110834]
Mus musculus cAMP responsive element binding protein 3 (Creb3), mRNA [NM_013497]
Mus musculus RIKEN cDNA 1190007I07 gene (1190007I07Rik), transcript variant 1, mRNA [NM_0011355
Mus musculus purinergic receptor P2Y, G-protein coupled 2 (P2ry2), mRNA [NM_008773]
Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430416G10 product:
Mus musculus phosphatidylserine decarboxylase, pseudogene 3 (Pisd-ps3), non-coding RNA [NR_003518
Mus musculus diacylglycerol O-acyltransferase 2 (Dgat2), mRNA [NM_026384]
Mus musculus family with sequence similarity 32, member A (Fam32a), mRNA [NM_026455]
Mus musculus histidyl-tRNA synthetase (Hars), mRNA [NM_008214]
Mus musculus acetyl-Coenzyme A carboxylase beta (Acacb), mRNA [NM_133904]
Mus musculus predicted gene 3448 (Gm3448), mRNA [NM_001123367]
Mus musculus branched chain aminotransferase 2, mitochondrial (Bcat2), transcript variant 2, mRNA [NM_
Mus musculus carbonic anhydrase 11 (Car11), mRNA [NM_009800]
Mus musculus immunity-related GTPase family M member 2 (Irgm2), mRNA [NM_019440]
Mus musculus predicted gene, EG633640, mRNA (cDNA clone MGC:118117 IMAGE:6309338), complete
Mus musculus La ribonucleoprotein domain family, member 1 (Larp1), mRNA [NM_028451]
Mus musculus BCLl2-like 15 (Bcl2l15), transcript variant 1, mRNA [NM_001142959]
Mus musculus nuclear receptor co-repressor 2 (Ncor2), transcript variant 1, mRNA [NM_011424]
Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330057J19 product
docking protein 7 [Source:MGI Symbol;Acc:MGI:3584043] [ENSMUST00000114270]
Mus musculus F-box protein 44 (Fbxo44), transcript variant 1, mRNA [NM_173401]
Mus musculus purine rich element binding protein B (Purb), mRNA [NM_011221]
Mus musculus expressed sequence AI593442 (AI593442), transcript variant 1, mRNA [NM_001286641]
Mus musculus DNA-damage-inducible transcript 4-like (Ddit4l), mRNA [NM_030143]
Mus musculus wingless-related MMTV integration site 2 (Wnt2), mRNA [NM_023653]
Mus musculus annexin A3 (Anxa3), mRNA [NM_013470]
eukaryotic translation initiation factor 2 alpha kinase 4 [Source:MGI Symbol;Acc:MGI:1353427] [ENSMUST
Mus musculus family with sequence similarity 154, member B (Fam154b), mRNA [NM_177894]
Mus musculus zinc finger protein 386 (Kruppel-like) (Zfp386), transcript variant 1, mRNA [NM_001004066]
Mus musculus ribonuclease, RNase A family 4 (Rnase4), transcript variant 1, mRNA [NM_021472]
Mus musculus mitogen-activated protein kinase kinase 7 (Map2k7), transcript variant 1, mRNA [NM_00104
Mus musculus zinc finger protein 672 (Zfp672), transcript variant 2, non-coding RNA [NR_028331]
Mus musculus patched domain containing 2 (Ptchd2), mRNA [NM_001083342]
Mus musculus small integral membrane protein 5 (Smim5), mRNA [NM_183259]
Mus musculus dynein light chain Tctex-type 1F (Dynlt1f), transcript variant 2, mRNA [NM_001199948]
Mus musculus solute carrier family 30 (zinc transporter), member 7 (Slc30a7), mRNA [NM_023214]
Mus musculus tRNA nucleotidyl transferase, CCA-adding, 1 (Trnt1), transcript variant 1, mRNA [NM_0012
Mus musculus tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptid
Mus musculus RIKEN cDNA 4930444P10 gene (4930444P10Rik), mRNA [NM_001243238]
Mus musculus START domain containing 10 (Stard10), mRNA [NM_019990]
Mus musculus serine/threonine kinase 38 like (Stk38l), mRNA [NM_172734]
Mus musculus RIKEN cDNA 1700001C19 gene (1700001C19Rik), transcript variant 1, mRNA [NM_02929
Mus musculus predicted gene 13298 (Gm13298), mRNA [NM_001085530]
Mus musculus peptidase D (Pepd), mRNA [NM_008820]
Mus musculus polyadenylate binding protein-interacting protein 1 (Paip1), transcript variant 1, mRNA [NM_
Mus musculus Smith-Magenis syndrome chromosome region, candidate 8 homolog (human) (Smcr8), tran
PREDICTED: Mus musculus pregnancy specific glycoprotein 16 (Psg16), transcript variant X2, mRNA [XM_

Mus musculus growth factor receptor bound protein 14 (Grb14), mRNA [NM_016719]
Mus musculus predicted gene 10845 (Gm10845), long non-coding RNA [NR_033535]
Mus musculus ribosomal protein L15 (Rpl15), mRNA [NM_025586]
Mus musculus cDNA clone IMAGE:5065404. [BC029971]
Mus musculus dedicator of cytokinesis 4 (Dock4), mRNA [NM_172803]
Mus musculus retinal degeneration 3 (Rd3), transcript variant 1, mRNA [NM_023727]
Mus musculus vimentin-type intermediate filament associated coiled-coil protein (Vmac), transcript variant
Mus musculus predicted gene, 547127, mRNA (cDNA clone IMAGE:577088), complete cds. [BC096660]
Mus musculus predicted gene 3448 (Gm3448), mRNA [NM_001123367]
Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430517C21 prod
Mus musculus four and a half LIM domains 2 (Fhl2), transcript variant 1, mRNA [NM_010212]
Mus musculus fibronectin type III domain containing 1 (Fndc1), mRNA [NM_001081416]
Mus musculus zinc finger, B-box domain containing (Zbbx), mRNA [NM_172515]
Mus musculus predicted gene 13157 (Gm13157), mRNA [NM_001127189]
Mus musculus ribosomal protein L31 (Rpl31), transcript variant 3, mRNA [NM_053257]
Mus musculus ring finger protein 41 (Rnf41), transcript variant 1, mRNA [NM_001164237]
Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530041D01 proc
Mus musculus galactosidase, beta 1 (Glb1), transcript variant 1, mRNA [NM_009752]
Mus musculus zinc finger protein 420 (Zfp420), mRNA [NM_172740]
Mus musculus ribosomal protein S13 (Rps13), mRNA [NM_026533]
Mus musculus maestro (Mro), mRNA [NM_027741]
Mus musculus myocilin (Myoc), mRNA [NM_010865]
Mus musculus peptidylprolyl isomerase domain and WD repeat containing 1 (Ppwd1), mRNA [NM_172807
Mus musculus tubulin tyrosine ligase-like family, member 2 (Ttll2), mRNA [NM_001098267]
Mus musculus WD repeat domain 60 (Wdr60), mRNA [NM_146039]
Mus musculus OCIA domain containing 1 (Ociad1), transcript variant 1, mRNA [NM_023429]
Mus musculus SPEG complex locus (Speg), transcript variant 3, mRNA [NM_001085371]
Mus musculus actin-binding LIM protein 1 (Ablim1), transcript variant 1, mRNA [NM_178688]
Mus musculus autophagy related 16-like 2 (S. cerevisiae) (Atg16l2), mRNA [NM_001111111]
Mus musculus 4 days neonate thymus cDNA, RIKEN full-length enriched library, clone:B630008G01 produ
Mus musculus autophagy related 16-like 2 (S. cerevisiae) (Atg16l2), mRNA [NM_001111111]
Mus musculus tripartite motif-containing 16 (Trim16), mRNA [NM_053169]
Mus musculus coiled-coil domain containing 65 (Ccdc65), mRNA [NM_153518]
Mus musculus solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1 (Slc9a3r1), mRN
Mus musculus period circadian clock 1 (Per1), transcript variant 1, mRNA [NM_011065]
Mus musculus protein kinase, cAMP dependent regulatory, type II alpha (Prkar2a), mRNA [NM_008924]
Mus musculus predicted gene 10516 (Gm10516), long non-coding RNA [NR_033536]
Mus musculus vomeronasal 2, receptor 121 (Vmn2r121), mRNA [NM_001100616]
Mus musculus ets variant gene 3 (Etv3), transcript variant 1, mRNA [NM_001286844]
Mus musculus nuclear receptor 2C2-associated protein (Nr2c2ap), transcript variant 1, mRNA [NM_00102
Mus musculus hormonally upregulated Neu-associated kinase (Hunk), mRNA [NM_015755]
Mus musculus asunder, spermatogenesis regulator (Asun), mRNA [NM_138757]
Mus musculus potassium voltage-gated channel, subfamily H (eag-related), member 5 (Kcnh5), mRNA [NM
Mus musculus chemokine (C-X-C motif) ligand 14 (Cxcl14), mRNA [NM_019568]
Mus musculus insulin-like growth factor binding protein 3 (Igfbp3), mRNA [NM_008343]
Mus musculus serine/threonine kinase 38 like (Stk38l), mRNA [NM_172734]
Mus musculus epidermal growth factor receptor pathway substrate 8 (Eps8), transcript variant 1, mRNA [N
PREDICTED: Mus musculus uncharacterized LOC102639358 (LOC102639358), transcript variant X1, ncR
Mus musculus signal peptidase complex subunit 3 homolog (S. cerevisiae) (Spcs3), mRNA [NM_029701]
Mus musculus distal-less homeobox 2 (Dlx2), mRNA [NM_010054]
Mus musculus docking protein 7 (Dok7), mRNA [NM_172708]
Mus musculus musashi RNA-binding protein 1 (Msi1), mRNA [NM_008629]
Mus musculus zinc finger protein 386 (Kruppel-like) (Zfp386), transcript variant 1, mRNA [NM_001004066]
Mus musculus ATPase, class V, type 10A (Atp10a), mRNA [NM_009728]
Mus musculus matrix-remodelling associated 7 (Mxra7), mRNA [NM_026280]
Mus musculus dynein, axonemal, heavy chain 7A (Dnah7a), mRNA [NM_001252070]
Mus musculus frizzled homolog 6 (Drosophila) (Fzd6), transcript variant 1, mRNA [NM_008056]
Mus musculus serine/threonine kinase 36 (Stk36), mRNA [NM_175031]
Mus musculus Parkinson disease (autosomal recessive, juvenile) 2, parkin (Park2), mRNA [NM_016694]

Mus musculus 2 cells egg cDNA, RIKEN full-length enriched library, clone:B020040A10 product:unclassifi
PREDICTED: Mus musculus RIKEN cDNA C230072F16 gene (C230072F16Rik), transcript variant X3, nc
Mus musculus dual adaptor for phosphotyrosine and 3-phosphoinositides 1 (Dapp1), mRNA [NM_011932]
Mus musculus LYR motif containing 5 (Lyrm5), transcript variant 1, mRNA [NM_001163628]
Mus musculus serine/threonine kinase 38 like (Stk38l), mRNA [NM_172734]
Mus musculus DNA segment, Chr 7, ERATO Doi 143, expressed (D7Ertd143e), long non-coding RNA [NR
Mus musculus RIKEN cDNA 5830444B04 gene (5830444B04Rik), transcript variant 1, long non-coding RN
Mus musculus dynein light chain Tctex-type 1C (Dynlt1c), mRNA [NM_001166630]
Mus musculus CDGSH iron sulfur domain 2 (Cisd2), mRNA [NM_025902]
Mus musculus camello-like 5 (Cml5), mRNA [NM_023493]
BB001409 RIKEN full-length enriched, 13 days embryo head Mus musculus cDNA clone 3110026C13 3'. [
Mus musculus ATP-binding cassette, sub-family D (ALD), member 1 (Abcd1), mRNA [NM_007435]
Mus musculus phosphatidylserine decarboxylase (Pisd), mRNA [NM_177298]
Mus musculus cat eye syndrome chromosome region, candidate 5 (Cecr5), mRNA [NM_144815]
Mus musculus NFKB inhibitor interacting Ras-like protein 1 (Nkiras1), mRNA [NM_023526]
Mus musculus FH2 domain containing 1 (Fhdc1), transcript variant 1, mRNA [NM_001205355]
Mus musculus zinc finger protein 14 (Zfp14), transcript variant 1, mRNA [NM_011748]
Mus musculus predicted gene 13298 (Gm13298), mRNA [NM_001085530]
Mus musculus Yip1 domain family, member 4 (Yipf4), mRNA [NM_026417]
Mus musculus kelch-like 26 (Klhl26), transcript variant 2, mRNA [NM_178771]
Mus musculus Williams-Beuren syndrome chromosome region 17 homolog (human) (Wbscr17), mRNA [N
Mus musculus sperm associated antigen 1 (Spag1), mRNA [NM_012031]
Mus musculus cytochrome c oxidase assembly protein 18 (Cox18), transcript variant 1, mRNA [NM_00116
Mus musculus DAZ interacting protein 1 (Dzip1), mRNA [NM_025943]
Mus musculus trinucleotide repeat containing 18 (Tnrc18), transcript variant A, mRNA [NM_001122730]
Mus musculus NLR family, pyrin domain containing 5 (Nlrp5), transcript variant 1, mRNA [NM_011860]
Mus musculus septin 9 (Sept9), transcript variant 2, mRNA [NM_001113487]
Mus musculus nicotinamide nucleotide transhydrogenase (Nnt), transcript variant 1, mRNA [NM_008710]
Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130026C10 prod
Mus musculus transmembrane protein 242 (Tmem242), mRNA [NM_027457]
Mus musculus transmembrane protein 242 (Tmem242), mRNA [NM_027457]
Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130009K03 prod
Mus musculus biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) binding prot
Mus musculus predicted gene, OTTMUSG00000016609 (OTTMUSG00000016609), mRNA [NM_0011004
Mus musculus dual specificity phosphatase 8 (Dusp8), mRNA [NM_008748]
Mus musculus purine rich element binding protein B (Purb), mRNA [NM_011221]
Mus musculus tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (Tnfrsf11b), mRN
Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E43000
Mus musculus phosphatidylserine decarboxylase, pseudogene 1 (Pisd-ps1), non-coding RNA [NR_003517
Mus musculus mitchondrial ribosomal protein S7 (Mrps7), mRNA [NM_025305]
Mus musculus polymerase (DNA directed), delta 2, regulatory subunit (Pold2), mRNA [NM_008894]
Mus musculus trans-golgi network vesicle protein 23A (Tvp23a), mRNA [NM_001013778]
Mus musculus F-box protein 44 (Fbxo44), transcript variant 1, mRNA [NM_173401]
Mus musculus expressed sequence AI661453 (AI661453), mRNA [NM_145489]
Mus musculus purine rich element binding protein B (Purb), mRNA [NM_011221]
Mus musculus coxsackie virus and adenovirus receptor (Cxadr), transcript variant 1, mRNA [NM_0010251
Mus musculus a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 5
Mus musculus INO80 homolog (S. cerevisiae) (Ino80), mRNA [NM_026574]
Mus musculus insulin receptor (Insr), mRNA [NM_010568]
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2600006K01 p
BC009829 Sin3A associated protein p30-like {Homo sapiens} (exp=-1; wgp=0; cg=0), complete [TC161034
Mus musculus SPEG complex locus (Speg), transcript variant 2, mRNA [NM_001085370]
Mus musculus nicotinamide nucleotide transhydrogenase (Nnt), transcript variant 1, mRNA [NM_008710]
Mus musculus exostoses (multiple)-like 2 (Extl2), transcript variant 1, mRNA [NM_021388]
Mus musculus striatin, calmodulin binding protein (Strn), mRNA [NM_011500]
Mus musculus armadillo repeat containing 6 (Armc6), mRNA [NM_133972]
Mus musculus glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (Qpct), mRNA [NM_027455]
Mus musculus aryl hydrocarbon receptor nuclear translocator 2 (Arnt2), mRNA [NM_007488]
PREDICTED: Mus musculus uncharacterized LOC102633020 (LOC102633020), ncRNA [XR_382000]

Mus musculus dispatched homolog 2 (Drosophila) (Disp2), mRNA [NM_170593]
Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130101M22 produc
Mus musculus NME/NM23 nucleoside diphosphate kinase 6 (Nme6), mRNA [NM_018757]
PREDICTED: Mus musculus RIKEN cDNA 3830406C13 gene (3830406C13Rik), transcript variant X1, mR
Mus musculus prolylcarboxypeptidase (angiotensinase C) (Prcp), mRNA [NM_028243]
Mus musculus DNA segment, Chr 16, ERATO Doi 472, expressed (D16Ertd472e), transcript variant 2, mR
coiled-coil domain containing 107 [Source:MGI Symbol;Acc:MGI:1913423] [ENSMUST00000107922]
Mus musculus ribonuclease, RNase K (Rnasek), mRNA [NM_173742]
Mus musculus vacuolar protein sorting 4a (yeast) (Vps4a), mRNA [NM_126165]
Mus musculus STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae) (Stt3b),
Mus musculus solute carrier family 4, sodium bicarbonate cotransporter, member 7 (Slc4a7), mRNA [NM_
Mus musculus ezrin (Ezr), mRNA [NM_009510]
Mus musculus predicted gene 14326 (Gm14326), transcript variant 2, mRNA [NM_001282028]
Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length en
predicted gene 9949 [Source:MGI Symbol;Acc:MGI:3647947] [ENSMUST00000067743]
Mus musculus caspase 7 (Casp7), mRNA [NM_007611]
Mus musculus post-GPI attachment to proteins 2 (Pgap2), transcript variant 1, mRNA [NM_001291358]
Mus musculus StAR-related lipid transfer (START) domain containing 6 (Stard6), transcript variant 1, mRN
Mus musculus zinc finger protein 74 (Zfp74), mRNA [NM_178384]
Mus musculus dual adaptor for phosphotyrosine and 3-phosphoinositides 1 (Dapp1), mRNA [NM_011932]
Mus musculus zinc finger protein 868 (Zfp868), transcript variant 1, mRNA [NM_172754]
Mus musculus zyg-ll family member B, cell cycle regulator (Zyg11b), mRNA [NM_001033634]
Mus musculus regulatory factor X-associated ankyrin-containing protein (Rfxank), transcript variant 1, mRN
Mus musculus cysteine-serine-rich nuclear protein 1 (Csrnp1), mRNA [NM_153287]
Mus musculus KDEL (Lys-Asp-Glu-Leu) containing 1 (Kdelc1), mRNA [NM_023645]
Mus musculus vacuolar protein sorting 33A (yeast) (Vps33a), mRNA [NM_029929]
Mus musculus coiled-coil domain containing 144B (Ccdc144b), mRNA [NM_178418]
Mus musculus alpha tubulin acetyltransferase 1 (Atat1), transcript variant 1, mRNA [NM_001142744]
Mus musculus 3-oxoacyl-ACP synthase, mitochondrial (Oxsm), mRNA [NM_027695]
Mus musculus glycerol kinase (Gyk), transcript variant 1, mRNA [NM_008194]
Mus musculus D17Mia10e clone c7 mRNA, partial sequence. [U49252]
Mus musculus neuroepithelial cell transforming gene 1 (Net1), transcript variant 1, mRNA [NM_019671]
Mus musculus DNA segment, Chr 16, ERATO Doi 472, expressed (D16Ertd472e), transcript variant 1, mR
Mus musculus potassium channel, subfamily K, member 2 (Kcnk2), transcript variant 2, mRNA [NM_01060
Mus musculus regulator of microtubule dynamics 3 (Rmdn3), mRNA [NM_001033136]
Mus musculus galanin receptor 2 (Galr2), mRNA [NM_010254]
Mus musculus N(alpha)-acetyltransferase 30, NatC catalytic subunit (Naa30), mRNA [NM_001081430]
Mus musculus Rho guanine nucleotide exchange factor (GEF) 39 (Arhgef39), mRNA [NM_001013377]
Mus musculus src homology three (SH3) and cysteine rich domain (Stac), mRNA [NM_016853]
Mus musculus prostate stem cell antigen (Psca), mRNA [NM_028216]
Mus musculus testis expressed 33 (Tex33), transcript variant 1, mRNA [NM_001163612]
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930439M07 product:uncla
Mus musculus FERM domain containing 4A (Frmd4a), transcript variant 2, mRNA [NM_001177843]
Mus musculus tubulin, delta 1 (Tubd1), transcript variant 1, mRNA [NM_001199045]
Mus musculus ribokinase (Rbks), mRNA [NM_153196]
Mus musculus suppressor of Ty 16 (Supt16), mRNA [NM_033618]
Mus musculus zinc finger protein 882 (Zfp882), mRNA [NM_001166645]
Mus musculus netrin G1 (Ntng1), transcript variant a, mRNA [NM_030699]
Mus musculus dehydrogenase/reductase (SDR family) X chromosome (Dhrsx), mRNA [NM_001033326]
Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833419G08 product:u
Mus musculus tripartite motif-containing 16 (Trim16), mRNA [NM_053169]
Mus musculus Emx2 opposite strand/antisense transcript (non-protein coding) (Emx2os), long non-coding
Mus musculus antizyme inhibitor 1 (Azin1), transcript variant 2, mRNA [NM_018745]
tripartite motif-containing 5 [Source:MGI Symbol;Acc:MGI:3646853] [ENSMUST00000138557]
Mus musculus ADAMTS-like 2 (Adamtsl2), mRNA [NM_029981]
Mus musculus WD repeat domain 52 (Wdr52), mRNA [NM_001033247]
Mus musculus amyloid beta (A4) precursor protein-binding, family B, member 2 (Apbb2), transcript variant
Mus musculus zinc finger protein 931 (Zfp931), mRNA [NM_001162922]
Mus musculus predicted gene 14326 (Gm14326), transcript variant 1, mRNA [NM_001190302]

Mus musculus platelet-derived growth factor, C polypeptide (Pdgfc), mRNA [NM_019971]
PREDICTED: Mus musculus predicted gene 7967 (Gm7967), misc_RNA [XR_387291]
Mus musculus triosephosphate isomerase 1 (Tpi1), mRNA [NM_009415]
Mus musculus ubiquitin specific peptidase 36 (Usp36), mRNA [NM_001033528]
Mus musculus transforming growth factor, beta receptor associated protein 1 (Tgfbrap1), mRNA [NM_0010
Mus musculus hormonally upregulated Neu-associated kinase (Hunk), mRNA [NM_015755]
Mus musculus MLX interacting protein (Mlxip), transcript variant 2, mRNA [NM_133917]
Mus musculus tropomyosin 1, alpha (Tpm1), transcript variant 1, mRNA [NM_001164248]
Mus musculus mannosidase, beta A, lysosomal (Manba), mRNA [NM_027288]
Mus musculus insulin receptor (Insr), mRNA [NM_010568]
Mus musculus MIF4G domain containing (Mif4gd), transcript variant 3, mRNA [NM_001243586]
Mus musculus potassium voltage gated channel, Shaw-related subfamily, member 1 (Kcnc1), transcript var
Mus musculus cDNA sequence BC100451 (BC100451), mRNA [NM_021440]
Mus musculus coiled-coil domain containing 65 (Ccdc65), mRNA [NM_153518]
Mus musculus OTU domain containing 7A (Otud7a), mRNA [NM_130880]
Mus musculus cleavage stimulation factor, 3' pre-RNA, subunit 3 (Cstf3), transcript variant 1, mRNA [NM_1
Mus musculus 2-oxoglutarate and iron-dependent oxygenase domain containing 1 (Ogfod1), transcript vari
Mus musculus RIKEN cDNA 2610305D13 gene (2610305D13Rik), mRNA [NM_145078]
Mus musculus F-box protein 3 (Fbxo3), transcript variant 2, mRNA [NM_020593]
Mus musculus SMAD family member 7 (Smad7), mRNA [NM_001042660]
Mus musculus collagen, type XII, alpha 1 (Col12a1), mRNA [NM_001290308]
insulin-like growth factor binding protein 3 [Source:MGI Symbol;Acc:MGI:96438] [ENSMUST00000135887]
Mus musculus migration and invasion inhibitory protein (Miip), mRNA [NM_001025365]
Mus musculus family with sequence similarity 45, member A (Fam45a), transcript variant 1, mRNA [NM_02
Mus musculus p21 protein (Cdc42/Rac)-activated kinase 6 (Pak6), transcript variant 1, mRNA [NM_00103
Mus musculus tumor necrosis factor receptor superfamily, member 1b (Tnfrsf1b), mRNA [NM_011610]
Mus musculus RIKEN cDNA 2010107G23 gene (2010107G23Rik), mRNA [NM_027251]
Mus musculus predicted pseudogene 5523 (Gm5523), non-coding RNA [NR_004447]
Mus musculus asparagine-linked glycosylation 8 (alpha-1,3-glucosyltransferase) (Alg8), mRNA [NM_19903
Mus musculus single stranded DNA binding protein 4 (Ssbp4), mRNA [NM_133772]
Mus musculus RIKEN cDNA 1500015A07 gene (1500015A07Rik), long non-coding RNA [NR_029432]
Mus musculus transforming growth factor, beta 3 (Tgfb3), mRNA [NM_009368]
Mus musculus transmembrane protein 62 (Tmem62), mRNA [NM_175285]
Mus musculus UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4 (B4galt4), transcript var
Mus musculus RAB4A, member RAS oncogene family (Rab4a), mRNA [NM_009003]
Mus musculus predicted gene 14325 (Gm14325), mRNA [NM_001024849]
Mus musculus myocyte enhancer factor 2D (Mef2d), mRNA [NM_133665]
Mus musculus transcription elongation factor A (SII) N-terminal and central domain containing 2 (Tceanc2),
Mus musculus amylo-1,6-glucosidase, 4-alpha-glucanotransferase (Agl), mRNA [NM_001081326]
Mus musculus fragile X mental retardation, autosomal homolog 2 (Fxr2), mRNA [NM_011814]
Y box protein 2 [Source:MGI Symbol;Acc:MGI:1096372] [ENSMUST00000018698]
Mus musculus inhibitor of DNA binding 1 (Id1), mRNA [NM_010495]
Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, c
Mus musculus rcd1 (required for cell differentiation) homolog 1 (S. pombe) (Rqcd1), mRNA [NM_021383]
Mus musculus family with sequence similarity 129, member C (Fam129c), mRNA [NM_001166213]
Mus musculus RNA polymerase II associated protein 1 (Rpap1), transcript variant 1, mRNA [NM_177294]
Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830223B06 product:hypo
Mus musculus mitogen-activated protein kinase 1 interacting protein 1-like (Mapk1ip1l), mRNA [NM_17868
Mus musculus integrator complex subunit 10 (Ints10), mRNA [NM_027590]
Mus musculus mitogen-activated protein kinase 8 (Mapk8), mRNA [NM_016700]
Mus musculus ankyrin repeat and LEM domain containing 1 (Ankle1), mRNA [NM_172756]
Mus musculus ADAMTS-like 4 (Adamtsl4), mRNA [NM_144899]
Mus musculus jerky (Jrk), mRNA [NM_008415]
Mus musculus vacuolar protein sorting 13B (yeast) (Vps13b), mRNA [NM_177151]
PREDICTED: Mus musculus predicted gene 6410 (Gm6410), misc_RNA [XR_378684]
Mus musculus predicted gene 14305 (Gm14305), mRNA [NM_001099327]
Mus musculus insulin receptor (Insr), mRNA [NM_010568]
Mus musculus trafficking protein particle complex 5 (Trappc5), mRNA [NM_025701]
Mus musculus tropomyosin 1, alpha (Tpm1), transcript variant 1, mRNA [NM_001164248]

Mus musculus neuroepithelial cell transforming gene 1 (Net1), transcript variant 1, mRNA [NM_019671]
Mus musculus asparaginyl-tRNA synthetase (Nars), transcript variant 2, mRNA [NM_027350]
Mus musculus protein O-fucosyltransferase 2 (Pofut2), mRNA [NM_030262]
Mus musculus mediator complex subunit 29 (Med29), mRNA [NM_026042]
Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130203P04 product
Mus musculus RIKEN cDNA 4930539J05 gene (4930539J05Rik), long non-coding RNA [NR_030689]
Mus musculus STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae) (Stt3b),
Mus musculus gap junction protein, gamma 2 (Gjc2), transcript variant 2, mRNA [NM_175452]
Mus musculus NME/NM23 nucleoside diphosphate kinase 6 (Nme6), mRNA [NM_018757]
Mus musculus MAD2 mitotic arrest deficient-like 2 (Mad2l2), mRNA [NM_027985]
Mus musculus Kell blood group precursor (McLeod phenotype) homolog (Xk), mRNA [NM_023500]
Mus musculus predicted gene 3893 (Gm3893), long non-coding RNA [NR_033506]
Mus musculus vomeronasal 2, receptor 121 (Vmn2r121), mRNA [NM_001100616]
Mus musculus sine oculis-related homeobox 4 (Six4), mRNA [NM_011382]
Mus musculus mechanistic target of rapamycin (serine/threonine kinase) (Mtor), mRNA [NM_020009]
Mus musculus PET112 homolog (S. cerevisiae) (Pet112), mRNA [NM_144896]
Mus musculus predicted gene 14484 (Gm14484), mRNA [NM_001025260]
Mus musculus vomeronasal 2, receptor 88 (Vmn2r88), mRNA [NM_011686]
Mus musculus RIKEN cDNA 6030419C18 gene (6030419C18Rik), mRNA [NM_176921]
Mus musculus NudC domain containing 3 (Nudcd3), mRNA [NM_173748]
Mus musculus StAR-related lipid transfer (START) domain containing 6 (Stard6), transcript variant 1, mRN
Mus musculus RIKEN cDNA 2410141K09 gene (2410141K09Rik), transcript variant 1, mRNA [NM_00129
Mus musculus haloacid dehalogenase-like hydrolase domain containing 2 (Hdhd2), transcript variant 3, mR
Mus musculus cysteinyl leukotriene receptor 1 (Cysltr1), transcript variant 1, mRNA [NM_021476]
Mus musculus nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, beta (Nfkbib), m
myosin XVIIIA [Source:MGI Symbol;Acc:MGI:2667185] [ENSMUST00000100795]
Mus musculus predicted gene 10825 (Gm10825), long non-coding RNA [NR_028580]
Mus musculus NADH dehydrogenase (ubiquinone) 1 alpha subcomplex assembly factor 7 (Ndufaf7), mRN
Mus musculus epidermal growth factor receptor pathway substrate 8 (Eps8), transcript variant 1, mRNA [N
PREDICTED: Mus musculus anoctamin 3 (Ano3), transcript variant X3, mRNA [XM_006499262]
Mus musculus CREB/ATF bZIP transcription factor (Crebzf), transcript variant 1, mRNA [NM_145151]
Mus musculus tubulin, gamma complex associated protein 4 (Tubgcp4), transcript variant 1, mRNA [NM_1
Mus musculus transmembrane protein 181A (Tmem181a), mRNA [NM_001033178]
Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830048I15 product:hypot
Mus musculus RAB4A, member RAS oncogene family (Rab4a), mRNA [NM_009003]
Mus musculus kin of IRRE like (Drosophila) (Kirrel), transcript variant 1, mRNA [NM_001170985]
Mus musculus EF-hand calcium binding domain 11 (Efcab11), mRNA [NM_030172]
Mus musculus ceramide synthase 2 (Cers2), mRNA [NM_029789]
family with sequence similarity 227, member A [Source:MGI Symbol;Acc:MGI:1922979] [ENSMUST00000
Mus musculus spermine synthase (Sms), mRNA [NM_009214]
Mus musculus eukaryotic translation initiation factor 3, subunit J1 (Eif3j1), mRNA [NM_144545]
Mus musculus small nuclear ribonucleoprotein N (Snrpn), transcript variant 3, mRNA [NM_001082962]
Mus musculus IQ motif containing GTPase activating protein 2 (Iqgap2), mRNA [NM_027711]
Mus musculus transmembrane protein 62 (Tmem62), mRNA [NM_175285]
Mus musculus ferrochelatase (Fech), mRNA [NM_007998]
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630006J12 produc
Mus musculus L-2-hydroxyglutarate dehydrogenase (L2hgdh), mRNA [NM_145443]
Mus musculus sulfatase modifying factor 2 (Sumf2), mRNA [NM_026445]
Mus musculus RIKEN cDNA 1700104L18 gene (1700104L18Rik), long non-coding RNA [NR_108033]
Mus musculus staufen (RNA binding protein) homolog 1 (Drosophila) (Stau1), transcript variant 3, mRNA [
Mus musculus contactin 6 (Cntn6), mRNA [NM_017383]
Mus musculus synaptic vesicle glycoprotein 2c (Sv2c), mRNA [NM_029210]
Mus musculus valosin containing protein (Vcp), mRNA [NM_009503]
Mus musculus 13 days embryo stomach cDNA, RIKEN full-length enriched library, clone:D530006I24 prod
Mus musculus biogenesis of lysosomal organelles complex-1, subunit 6, pallidin (Bloc1s6), mRNA [NM_01
Mus musculus transmembrane and coiled-coil domains 6 (Tmco6), mRNA [NM_028036]
Mus musculus RIKEN cDNA 4933406C10 gene (4933406C10Rik), long non-coding RNA [NR_044986]
Mus musculus glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (Gcnt2), transcript variant 3, mR
Mus musculus fibroblast growth factor receptor 2 (Fgfr2), transcript variant 1, mRNA [NM_010207]

Mus musculus cDNA sequence BC026513, mRNA (cDNA clone IMAGE:4909841), partial cds. [BC039787]
Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110040I23 product:
Mus musculus WW, C2 and coiled-coil domain containing 1 (Wwc1), mRNA [NM_170779]
Mus musculus ataxin 2 (Atxn2), mRNA [NM_009125]
Mus musculus RAB8A, member RAS oncogene family (Rab8a), mRNA [NM_023126]
PREDICTED: Mus musculus RIKEN cDNA G630016G05 gene (G630016G05Rik), transcript variant X2, mi
Mus musculus zinc finger protein 868 (Zfp868), transcript variant 1, mRNA [NM_172754]
Mus musculus coenzyme Q5 homolog, methyltransferase (yeast) (Coq5), mRNA [NM_026504]
leucine zipper, putative tumor suppressor 1 [Source:MGI Symbol;Acc:MGI:2684762] [ENSMUST0000018
Mus musculus C-type lectin domain family 2, member f (Clec2f), mRNA [NM_001277202]
eukaryotic translation initiation factor 2 alpha kinase 4 [Source:MGI Symbol;Acc:MGI:1353427] [ENSMUST
Mus musculus coenzyme Q5 homolog, methyltransferase (yeast) (Coq5), mRNA [NM_026504]
sideroflexin 5 [Source:MGI Symbol;Acc:MGI:2137681] [ENSMUST00000138489]
Mus musculus apolipoprotein O (Apoo), transcript variant 2, mRNA [NM_001199337]
Mus musculus cathepsin O (Ctso), mRNA [NM_177662]
Mus musculus MAX gene associated (Mga), transcript variant 1, mRNA [NM_013720]
Mus musculus nicotinamide riboside kinase 1 (Nmrk1), mRNA [NM_145497]
Mus musculus 2 days neonate sympathetic ganglion cDNA, RIKEN full-length enriched library, clone:71204
PREDICTED: Mus musculus predicted gene 5785 (Gm5785), mRNA [XM_974939]
Mus musculus RIKEN cDNA 2900026A02 gene (2900026A02Rik), mRNA [NM_172884]
Mus musculus adipogenesis associated Mth938 domain containing (Aamdc), transcript variant 1, mRNA [N
Mus musculus lysocardiolipin acyltransferase 1 (Lclat1), transcript variant 1, mRNA [NM_001081071]
Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310007J06 product:uncl
Mus musculus predicted gene 14325 (Gm14325), mRNA [NM_001024849]
Mus musculus transmembrane protein 18 (Tmem18), mRNA [NM_172049]
Mus musculus leucine carboxyl methyltransferase 2 (Lcmt2), mRNA [NM_177846]
Mus musculus transcription elongation factor A (SII) N-terminal and central domain containing 2 (Tceanc2),
Mus musculus churchill domain containing 1 (Churc1), mRNA [NM_206534]
Mus musculus lysine (K)-specific demethylase 4C (Kdm4c), transcript variant 1, mRNA [NM_144787]
Mus musculus adult inner ear cDNA, RIKEN full-length enriched library, clone:F930115A20 product:hypoth
Mus musculus excision repaiross-complementing rodent repair deficiency, complementation group 8 (Ercc
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610312K03 p
immunoglobulin kappa variable 16-104 [Source:MGI Symbol;Acc:MGI:2685913] [ENSMUST00000103323]
Q8BSH3_MOUSE (Q8BSH3) 12 days embryo male wolffian duct includes surrounding region cDNA, RIKE
Mus musculus solute carrier organic anion transporter family, member 5A1 (Slco5a1), mRNA [NM_172841
Mus musculus solute carrier family 30 (zinc transporter), member 7 (Slc30a7), mRNA [NM_023214]
Mus musculus serine/threonine kinase 38 (Stk38), mRNA [NM_134115]
T cell receptor alpha variable 13N-3 [Source:MGI Symbol;Acc:MGI:3645598] [ENSMUST00000179580]
Mus musculus asparagine-linked glycosylation 2 (alpha-1,3-mannosyltransferase) (Alg2), mRNA [NM_019
Mus musculus RCB-1283 B16 melanoma cDNA, RIKEN full-length enriched library, clone:G430107I07 pro
Mus musculus dynein, axonemal, heavy chain 7A (Dnah7a), mRNA [NM_001252070]
Mus musculus acetyl-Coenzyme A carboxylase beta (Acacb), mRNA [NM_133904]
Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830143P17 product:uncla
Mus musculus coiled-coil domain containing 88C (Ccdc88c), mRNA [NM_026681]
Mus musculus predicted gene 14499 (Gm14499), mRNA [NM_001277184]
Mus musculus zinc finger and BTB domain containing 34 (Zbtb34), transcript variant 1, mRNA [NM_00108
Mus musculus myosin, light chain 12A, regulatory, non-sarcomeric (Myl12a), mRNA [NM_026064]
REM2 and RAB-like small GTPase 1 [Source:MGI Symbol;Acc:MGI:1923416] [ENSMUST00000097813]
Mus musculus vomeronasal 2, receptor 86 (Vmn2r86), mRNA [NM_001103365]
Mus musculus vomeronasal 2, receptor 10 (Vmn2r10), mRNA [NM_009491]
Mus musculus predicted gene 5132 (Gm5132), mRNA [NM_001085517]
osteopetrosis associated transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:2655574] [ENSMUST00
Mus musculus Emx2 opposite strand/antisense transcript (non-protein coding) (Emx2os), long non-coding
Mus musculus zinc fingers and homeoboxes 2 (Zhx2), mRNA [NM_199449]
Mus musculus patched domain containing 2 (Ptchd2), mRNA [NM_001083342]
Mus musculus Fas apoptotic inhibitory molecule 2 (Faim2), transcript variant 1, mRNA [NM_028224]
Mus musculus cyclin B1 interacting protein 1 (Ccnb1ip1), mRNA [NM_001111119]
Mus musculus adenosine deaminase-like (Adal), transcript variant 1, mRNA [NM_029475]
Mus musculus TBC1 domain family, member 5 (Tbc1d5), transcript variant 1, mRNA [NM_001285991]

Mus musculus lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730040L14 product:
Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:4022436C10 product
Mus musculus citrate lyase beta like (Clybl), mRNA [NM_029556]
Mus musculus predicted gene 13298 (Gm13298), mRNA [NM_001085530]
Mus musculus CD84 antigen (Cd84), transcript variant 1, mRNA [NM_013489]
Mus musculus glutamate receptor, ionotropic, NMDA2B (epsilon 2) (Grin2b), mRNA [NM_008171]
Mus musculus ankyrin repeat and IBR domain containing 1 (Ankib1), transcript variant 2, mRNA [NM_0010
Mus musculus DEAD (Asp-Glu-Ala-Asp) box polypeptide 51 (Ddx51), mRNA [NM_027156]
PREDICTED: Mus musculus RIKEN cDNA 2810407A14 gene (2810407A14Rik), transcript variant X1, mis
Mus musculus congenital dyserythropoietic anemia, type I (human) (Cdan1), mRNA [NM_026891]
Mus musculus angiopoietin-like 7 (Angptl7), mRNA [NM_001039554]
Mus musculus zinc finger protein 72 (Zfp72), mRNA [NM_001081680]
Mus musculus mesoderm development candidate 1 (Mesdc1), mRNA [NM_030705]
Mus musculus nucleus accumbens associated 2, BEN and BTB (POZ) domain containing (Nacc2), transcri
Mus musculus Rho guanine nucleotide exchange factor (GEF) 26 (Arhgef26), mRNA [NM_001081295]
Mus musculus ethanol induced 1 (Etohi1), transcript variant 1, mRNA [NM_001177399]
Mus musculus calpain 15 (Capn15), mRNA [NM_015830]
Mus musculus mitofusin 2 (Mfn2), transcript variant 2, mRNA [NM_133201]
Mus musculus solute carrier family 25, member 37 (Slc25a37), mRNA [NM_026331]
Mus musculus glucose phosphate isomerase 1 (Gpi1), mRNA [NM_008155]
Mus musculus cyclin L2 (Ccnl2), mRNA [NM_207678]
Mus musculus glucose phosphate isomerase 1 (Gpi1), mRNA [NM_008155]
Mus musculus kinesin light chain 2 (Klc2), transcript variant 1, mRNA [NM_008451]
Mus musculus homeobox D8 (Hoxd8), transcript variant 1, mRNA [NM_008276]
Mus musculus CREB/ATF bZIP transcription factor (Crebzf), transcript variant 1, mRNA [NM_145151]
Mus musculus 4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. ele
Mus musculus membrane associated guanylate kinase, WW and PDZ domain containing 1 (Magi1), transc
Mus musculus PHD finger protein 13 (Phf13), mRNA [NM_172705]
Mus musculus ribonuclease P 14 subunit (Rpp14), mRNA [NM_025938]
Mus musculus importin 11 (Ipo11), mRNA [NM_029665]
Mus musculus LanC lantibiotic synthetase component C-like 3 (bacterial) (Lancl3), mRNA [NM_173414]
Mus musculus potassium voltage-gated channel, subfamily Q, member 5 (Kcnq5), transcript variant 1, mR
Mus musculus mRNA for mKIAA0996 protein. [AK129256]
Mus musculus RAB37, member RAS oncogene family (Rab37), transcript variant 2, mRNA [NM_00116375
Mus musculus predicted gene 5382 (Gm5382), mRNA [NM_001034100]
Mus musculus microfibrillar-associated protein 3 (Mfap3), transcript variant 1, mRNA [NM_145426]
Mus musculus predicted gene 14137 (Gm14137), mRNA [NM_001039223]
Mus musculus heat shock factor binding protein 1-like 1 (Hsbp1l1), mRNA [NM_001136181]
Mus musculus desumoylating isopeptidase 1 (Desi1), mRNA [NM_134095]
Mus musculus toll-like receptor 1 (Tlr1), transcript variant 1, mRNA [NM_030682]
Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330167E06 produ
Mus musculus Rho guanine nucleotide exchange factor (GEF) 38 (Arhgef38), mRNA [NM_029953]
Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430528A12 prod
Mus musculus ubiquitin-conjugating enzyme E2E 1 (Ube2e1), mRNA [NM_009455]
Mus musculus SR-related CTD-associated factor 8 (Scaf8), mRNA [NM_134123]
Mus musculus adenylate cyclase 6 (Adcy6), mRNA [NM_007405]
Mus musculus expressed sequence AI593442 (AI593442), transcript variant 1, mRNA [NM_001286641]
Mus musculus phosphatidic acid phosphatase type 2A (Ppap2a), transcript variant 1, mRNA [NM_008247]
Mus musculus nuclear fragile X mental retardation protein interacting protein 1 (Nufip1), mRNA [NM_01374
Mus musculus transmembrane protein 135 (Tmem135), mRNA [NM_028343]
Mus musculus RIKEN cDNA 1700012L04 gene (1700012L04Rik), mRNA [NM_029588]
Mus musculus SEC63-like (S. cerevisiae) (Sec63), mRNA [NM_153055]
Mus musculus RAS-like, estrogen-regulated, growth-inhibitor (Rerg), transcript variant 1, mRNA [NM_0011
Mus musculus USO1 vesicle docking factor (Uso1), mRNA [NM_019490]
Mus musculus guanosine diphosphate (GDP) dissociation inhibitor 2 (Gdi2), mRNA [NM_008112]
Mus musculus vomeronasal 2, receptor 16 (Vmn2r16), mRNA [NM_001104627]
Mus musculus NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (Ndufc2), mRNA [NM_024
Mus musculus RAD23b homolog (S. cerevisiae) (Rad23b), mRNA [NM_009011]
UI-M-GI0-cek-h-17-0-UI.r1 NIH_BMAP_GI0 Mus musculus cDNA clone IMAGE: 6840738 5', mRNA seque

Mus musculus ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit (Atp5b), mRNA [NM
Mus musculus phosphoglycerate mutase 1 (Pgam1), mRNA [NM_023418]
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921515G04 product:uncla
Mus musculus UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9 (Ga
Mus musculus Kell blood group precursor (McLeod phenotype) homolog (Xk), mRNA [NM_023500]
Mus musculus RAB37, member RAS oncogene family (Rab37), transcript variant 2, mRNA [NM_00116375
Mus musculus jagunal homolog 1 (Drosophila) (Jagn1), transcript variant 1, mRNA [NM_026365]
Mus musculus natriuretic peptide type A (Nppa), mRNA [NM_008725]
Mus musculus mitochondrial ribosomal protein L34 (Mrpl34), mRNA [NM_053162]
PREDICTED: Mus musculus predicted gene, 20764 (Gm20764), mRNA [XM_003688790]
Mus musculus multivesicular body subunit 12A (Mvb12a), mRNA [NM_028617]
Mus musculus family with sequence similarity 114, member A2 (Fam114a2), transcript variant 2, mRNA [N
PREDICTED: Mus musculus predicted gene 3693 (Gm3693), transcript variant X2, misc_RNA [XR_381755
Mus musculus superkiller viralicidic activity 2-like 2 (S. cerevisiae) (Skiv2l2), mRNA [NM_028151]
Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 3E (Ppp1r3e), mRNA [NM_001167908]
Mus musculus TNFRSF1A-associated via death domain (Tradd), mRNA [NM_001033161]
Mus musculus ankyrin repeat and sterile alpha motif domain containing 1B (Anks1b), transcript variant 4, m
Mus musculus abhydrolase domain containing 5 (Abhd5), mRNA [NM_026179]
Mus musculus ribosomal protein L36 (Rpl36), mRNA [NM_018730]
Mus musculus trafficking protein particle complex 5 (Trappc5), mRNA [NM_025701]
Mus musculus RIKEN cDNA 2810408A11 gene (2810408A11Rik), mRNA [NM_027419]
Mus musculus G protein-coupled receptor 158 (Gpr158), mRNA [NM_001004761]
Mus musculus spastic paraplegia 11 (Spg11), mRNA [NM_145531]
Mus musculus ribosomal protein L36 (Rpl36), mRNA [NM_018730]
PREDICTED: Mus musculus predicted gene 6404 (Gm6404), mRNA [XM_006517804]
Mus musculus RAB3 GTPase activating protein subunit 2 (Rab3gap2), mRNA [NM_001163754]
Mus musculus THO complex 7 homolog (Drosophila) (Thoc7), transcript variant 3, mRNA [NM_001285780
Mus musculus piggyBac transposable element derived 5 (Pgbd5), mRNA [NM_171824]
Mus musculus bone morphogenetic protein 8a (Bmp8a), transcript variant 1, mRNA [NM_001256019]
Mus musculus ribosomal protein L13A (Rpl13a), mRNA [NM_009438]
Mus musculus ubiquitin specific peptidase 37 (Usp37), mRNA [NM_176972]
Mus musculus SHC (Src homology 2 domain containing) transforming protein 2 (Shc2), mRNA [NM_00102
Mus musculus DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae) (Dclre1c), transcript variant 2, mR
Mus musculus neuroguidin, EIF4E binding protein (Ngdn), mRNA [NM_026890]
Mus musculus folliculin (Flcn), transcript variant 2, mRNA [NM_146018]
PREDICTED: Mus musculus zinc finger protein 74 (Zfp74), transcript variant X1, mRNA [XM_006540384]
Mus musculus caspase 3 (Casp3), transcript variant 2, mRNA [NM_009810]
Mus musculus protocadherin beta 7 (Pcdhb7), mRNA [NM_053132]
Mus musculus EFR3 homolog B (S. cerevisiae) (Efr3b), mRNA [NM_001082483]
Mus musculus Ras interacting protein 1 (Rasip1), mRNA [NM_028544]
Mus musculus tubulin, beta 6 class V (Tubb6), mRNA [NM_026473]
Mus musculus G protein-coupled receptor 135 (Gpr135), mRNA [NM_181752]
Mus musculus REC8 meiotic recombination protein (Rec8), mRNA [NM_020002]
Mus musculus SAP30-like (Sap30l), mRNA [NM_001081168]
Mus musculus nucleotide binding protein-like (Nubpl), mRNA [NM_029760]
Mus musculus chemokine (C-C motif) ligand 28 (Ccl28), mRNA [NM_020279]
Mus musculus SLIT and NTRK-like family, member 3 (Slitrk3), mRNA [NM_198864]
Mus musculus unconventional SNARE in the ER 1 homolog (S. cerevisiae) (Use1), transcript variant 3, mR
Mus musculus G patch domain containing 1 (Gpatch1), mRNA [NM_026181]
Mus musculus F-box and leucine-rich repeat protein 21 (Fbxl21), mRNA [NM_178674]
Mus musculus SIVA1, apoptosis-inducing factor (Siva1), transcript variant 1, mRNA [NM_013929]
Mus musculus small G protein signaling modulator 1 (Sgsm1), transcript variant 3, mRNA [NM_001162965
Mus musculus RIKEN cDNA 1700049G17 gene (1700049G17Rik), mRNA [NM_028538]
Mus musculus family with sequence similarity 160, member B1 (Fam160b1), mRNA [NM_145505]
Mus musculus mitogen-activated protein kinase kinase kinase kinase 1 (Map4k1), mRNA [NM_008279]
Mus musculus RIKEN cDNA 6330416G13 gene (6330416G13Rik), mRNA [NM_144905]
Mus musculus coiled-coil domain containing 71 (Ccdc71), mRNA [NM_133744]
Mus musculus monoglyceride lipase (Mgll), transcript variant 1, mRNA [NM_001166251]
leucine-rich and death domain containing [Source:MGI Symbol;Acc:MGI:1889507] [ENSMUST0000013806

Mus musculus phosphopantothenoylcysteine decarboxylase (Ppcdc), mRNA [NM_176831]
Mus musculus RIKEN cDNA D130040H23 gene (D130040H23Rik), mRNA [NM_172491]
Mus musculus small integral membrane protein 7 (Smim7), mRNA [NM_172396]
Mus musculus thioredoxin-like 4A (Txnl4a), transcript variant 1, mRNA [NM_025299]
synaptosomal-associated protein 23 [Source:MGI Symbol;Acc:MGI:109356] [ENSMUST00000110711]
Mus musculus N-acetyltransferase 9 (GCN5-related, putative) (Nat9), mRNA [NM_025400]
Mus musculus pleckstrin homology domain containing, family A member 7 (Plekha7), mRNA [NM_172743]
Mus musculus RIKEN cDNA 4930563E22 gene (4930563E22Rik), mRNA [NM_001163728]
Mus musculus myelin basic protein (Mbp), transcript variant 7, mRNA [NM_010777]
Mus musculus prion protein (Prnp), transcript variant 2, mRNA [NM_001278256]
Mus musculus mutS homolog 3 (E. coli) (Msh3), mRNA [NM_010829]
Mus musculus TBC1 domain family, member 2 (Tbc1d2), mRNA [NM_198664]
Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430410E06 product:
zinc finger protein 81 [Source:MGI Symbol;Acc:MGI:1890752] [ENSMUST00000054072]
Mus musculus slingshot homolog 1 (Drosophila) (Ssh1), mRNA [NM_198109]
Mus musculus Sh3 domain YSC-like 1 (Sh3yl1), transcript variant 1, mRNA [NM_013709]
Mus musculus spastin (Spast), transcript variant 2, mRNA [NM_016962]
Mus musculus RAB26, member RAS oncogene family (Rab26), mRNA [NM_177375]
Mus musculus F-box protein 6 (Fbxo6), transcript variant 1, mRNA [NM_015797]
Mus musculus MEF2 activating motif and SAP domain containing transcriptional regulator (Mamstr), mRNA
Mus musculus patatin-like phospholipase domain containing 3 (Pnpla3), mRNA [NM_054088]
Mus musculus serine hydroxymethyltransferase 1 (soluble) (Shmt1), mRNA [NM_009171]
PREDICTED: Mus musculus predicted pseudogene 7241 (Gm7241), mRNA [XM_006543539]
Mus musculus solute carrier organic anion transporter family, member 2b1 (Slco2b1), transcript variant 1,
Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130094K
Mus musculus RIKEN cDNA 4930570G19 gene (4930570G19Rik), transcript variant 2, long non-coding R
Mus musculus wingless-type MMTV integration site 9A (Wnt9a), mRNA [NM_139298]
Mus musculus transmembrane protein 192 (Tmem192), transcript variant 1, mRNA [NM_028427]
Mus musculus leucine rich repeat containing 73 (Lrrc73), mRNA [NM_001111142]
Mus musculus serine peptidase inhibitor, Kazal type 2 (Spink2), transcript variant 2, mRNA [NM_183284]
Mus musculus oxytocin receptor (Oxtr), mRNA [NM_001081147]
Mus musculus transmembrane emp24 protein transport domain containing 4 (Tmed4), mRNA [NM_13402
Mus musculus cytochrome c oxidase assembly factor 4 (Coa4), mRNA [NM_183270]
Mus musculus glutathione S-transferase kappa 1 (Gstk1), mRNA [NM_029555]
Mus musculus tripartite motif-containing 12C (Trim12c), transcript variant 1, mRNA [NM_001146007]
Mus musculus CDP-diacylglycerol synthase 1 (Cds1), mRNA [NM_173370]
Mus musculus fibroblast activation protein (Fap), mRNA [NM_007986]
Mus musculus nodal modulator 1 (Nomo1), mRNA [NM_153057]
Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530073P05 pro
Mus musculus T cell activation GTPase activating protein 1 (Tagap1), mRNA [NM_147155]
Mus musculus BCL2-like 12 (proline rich) (Bcl2l12), mRNA [NM_029410]
Mus musculus immunoglobulin superfamily, member 10 (Igsf10), mRNA [NM_001162884]
Mus musculus high mobility group box transcription factor 1 (Hbp1), transcript variant 2, mRNA [NM_1779
Mus musculus NEL-like 1 (Nell1), mRNA [NM_001037906]
Mus musculus synergin, gamma (Synrg), mRNA [NM_194341]
Mus musculus protein phosphatase 2 (formerly 2A), regulatory subunit B'', delta (Ppp2r3d), transcript varia
Mus musculus putative homeodomain transcription factor 1 (Phtf1), transcript variant 1, mRNA [NM_01362
Mus musculus progestin and adipoQ receptor family member VI (Paqr6), mRNA [NM_198410]
Mus musculus tRNA splicing endonuclease 54 homolog (S. cerevisiae) (Tsen54), mRNA [NM_029557]
PREDICTED: Mus musculus predicted gene 6306 (Gm6306), mRNA [XM_006500499]
PREDICTED: Mus musculus predicted gene 5093 (Gm5093), mRNA [XM_006543383]
Mus musculus RAS-like, family 10, member A (Rasl10a), mRNA [NM_145216]
Mus musculus SURP and G patch domain containing 1 (Sugp1), mRNA [NM_027481]
Mus musculus DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 (Ddx55), transcript variant 1, mRNA [NM_026
Mus musculus ubiquitin specific peptidase 53 (Usp53), mRNA [NM_133857]
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930522L14 product:simil
Mus musculus coiled-coil domain containing 91 (Ccdc91), mRNA [NM_025911]
Mus musculus oligonucleotide/oligosaccharide-binding fold containing 1 (Obfc1), mRNA [NM_175360]
Mus musculus cytokine receptor-like factor 2 (Crlf2), transcript variant 1, mRNA [NM_001164735]

Mus musculus centromere protein K (Cenpk), transcript variant 1, mRNA [NM_021790]
Mus musculus zinc finger protein 608 (Zfp608), mRNA [NM_175751]
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630055C05 produ
Mus musculus solute carrier family 10 (sodium/bile acid cotransporter family), member 3 (Slc10a3), transcr
Mus musculus Holliday junction recognition protein (Hjurp), mRNA [NM_198652]
Mus musculus D-tyrosyl-tRNA deacylase 2 (Dtd2), mRNA [NM_029545]
Mus musculus progestin and adipoQ receptor family member VI (Paqr6), mRNA [NM_198410]
Mus musculus palmdelphin (Palmd), mRNA [NM_023245]
Mus musculus ferritin light chain 1 (Ftl1), mRNA [NM_010240]
Mus musculus THAP domain containing 6 (Thap6), non-coding RNA [NR_028429]
PREDICTED: Mus musculus uncharacterized LOC102634598 (LOC102634598), misc_RNA [XR_386205]
Mus musculus monoglyceride lipase (Mgll), transcript variant 1, mRNA [NM_001166251]
Mus musculus RIKEN cDNA 1810009N02 gene (1810009N02Rik), mRNA [NM_026939]
Mus musculus solute carrier family 25, member 41 (Slc25a41), mRNA [NM_175333]
Mus musculus aldo-keto reductase family 1, member C19 (Akr1c19), mRNA [NM_001013785]
Mus musculus transmembrane protein 173 (Tmem173), transcript variant 1, mRNA [NM_028261]
Mus musculus ubiquitin C (Ubc), mRNA [NM_019639]
predicted gene 10654 [Source:MGI Symbol;Acc:MGI:3643366] [ENSMUST00000098653]
Mus musculus histocompatibility 2, M region locus 3 (H2-M3), mRNA [NM_013819]
Mus musculus NIM1 serine/threonine protein kinase (Nim1k), mRNA [NM_175538]
Mus musculus beaded filament structural protein 2, phakinin (Bfsp2), mRNA [NM_001002896]
Mus musculus alkB, alkylation repair homolog 6 (E. coli) (Alkbh6), mRNA [NM_198027]
Mus musculus CaM kinase-like vesicle-associated (Camkv), mRNA [NM_145621]
Mus musculus polymerase (DNA directed), iota (Poli), transcript variant 2, mRNA [NM_011972]
Mus musculus zinc finger protein 566 (Zfp566), mRNA [NM_152814]
Mus musculus retinol binding protein 7, cellular (Rbp7), mRNA [NM_022020]
PREDICTED: Mus musculus predicted gene 8013 (Gm8013), transcript variant X4, ncRNA [XR_389350]
Mus musculus synaptogyrin 2 (Syngr2), mRNA [NM_009304]
Mus musculus LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae) (Lsm4), mRNA [NM_0158
Mus musculus FXYD domain-containing ion transport regulator 6 (Fxyd6), mRNA [NM_022004]
Mus musculus solute carrier family 2 (facilitated glucose transporter), member 9 (Slc2a9), transcript variant
Mus musculus SERTA domain containing 3 (Sertad3), mRNA [NM_133210]
Mus musculus acyl-CoA synthetase long-chain family member 5 (Acsl5), mRNA [NM_027976]
Mus musculus SLIT and NTRK-like family, member 5 (Slitrk5), mRNA [NM_198865]
cut-like homeobox 2 [Source:MGI Symbol;Acc:MGI:107321] [ENSMUST00000111752]
BEN domain containing 7 [Source:MGI Symbol;Acc:MGI:2443100] [ENSMUST00000115022]
Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:C330018M05 product:similar to ZF
Mus musculus myosin, light polypeptide 2, regulatory, cardiac, slow (Myl2), mRNA [NM_010861]
Mus musculus telomeric repeat binding factor 1 (Terf1), transcript variant 1, mRNA [NM_009352]
Mus musculus predicted gene 13247 (Gm13247), transcript variant 1, mRNA [NM_001243138]
Mus musculus polymerase (DNA directed), epsilon (Pole), mRNA [NM_011132]
Mus musculus Holliday junction recognition protein (Hjurp), mRNA [NM_198652]
Mus musculus coiled-coil domain containing 91 (Ccdc91), mRNA [NM_025911]
Mus musculus G2/M-phase specific E3 ubiquitin ligase (G2e3), transcript variant 2, mRNA [NM_00116796
Mus musculus PTPRF interacting protein, binding protein 2 (liprin beta 2) (Ppfibp2), transcript variant 1, mR
Mus musculus methyltransferase like 3 (Mettl3), mRNA [NM_019721]
Mus musculus thyroid hormone responsive (Thrsp), mRNA [NM_009381]
Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130019D
Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130072N09 prod
Mus musculus CD1d2 antigen (Cd1d2), transcript variant 1, mRNA [NM_007640]
Mus musculus phosphatidylinositol glycan anchor biosynthesis, class P (Pigp), transcript variant 5, mRNA [
Mus musculus germ cell-specific gene 2 (Gsg2), mRNA [NM_010353]
Mus musculus huntingtin interacting protein K (Hypk), mRNA [NM_026318]
Mus musculus apolipoprotein L 7b (Apol7b), mRNA [NM_001024848]
Mus musculus apoptotic chromatin condensation inducer 1 (Acin1), transcript variant 2, mRNA [NM_02319
Mus musculus methyltransferase like 17 (Mettl17), mRNA [NM_001029990]
Mus musculus Friend virus susceptibility 1 (Fv1), mRNA [NM_010244]
Mus musculus churchill domain containing 1 (Churc1), mRNA [NM_206534]
Mus musculus predicted gene 15698 (Gm15698), non-coding RNA [NR_003564]

Mus musculus microsomal triglyceride transfer protein (Mttp), transcript variant 1, mRNA [NM_001163457]
Mus musculus adrenergic receptor kinase, beta 2 (Adrbk2), transcript variant 1, mRNA [NM_177078]
Mus musculus RIKEN cDNA 4930515G01 gene (4930515G01Rik), long non-coding RNA [NR_027872]
ribosomal protein S3A3 [Source:MGI Symbol;Acc:MGI:3643406] [ENSMUST00000074680]
Mus musculus Ca2+-dependent secretion activator (Cadps), transcript variant 1, mRNA [NM_012061]
Mus musculus RIKEN cDNA 2410006H16 gene (2410006H16Rik), long non-coding RNA [NR_030738]
Mus musculus RWD domain containing 3 (Rwdd3), transcript variant 2, mRNA [NM_028456]
Mus musculus cortistatin (Cort), mRNA [NM_007745]
Mus musculus kinesin light chain 4 (Klc4), mRNA [NM_029091]
Mus musculus G2/M-phase specific E3 ubiquitin ligase (G2e3), transcript variant 3, mRNA [NM_00116796
Mus musculus 4HAUS augmin-like complex, subunit 8 (Haus8), transcript variant 1, mRNA [NM_00116304
Mus musculus EH-domain containing 4 (Ehd4), mRNA [NM_133838]
Mus musculus interleukin 17 receptor D (Il17rd), mRNA [NM_134437]
regulating synaptic membrane exocytosis 3 [Source:MGI Symbol;Acc:MGI:2443331] [ENSMUST000000071
Mus musculus RAB19, member RAS oncogene family (Rab19), mRNA [NM_011226]
Mus musculus FXYD domain-containing ion transport regulator 2 (Fxyd2), transcript variant b, mRNA [NM_
Mus musculus creatine kinase, mitochondrial 1, ubiquitous (Ckmt1), mRNA [NM_009897]
Mus musculus dehydrogenase/reductase (SDR family) member 7 (Dhrs7), mRNA [NM_025522]
Mus musculus zinc finger protein 286 (Zfp286), mRNA [NM_138949]
Mus musculus polymerase (DNA directed), kappa (Polk), mRNA [NM_012048]
Mus musculus cysteine-rich PDZ-binding protein (Cript), mRNA [NM_019936]
mp78f05.y1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:575361 5'. [AI530666]
Mus musculus G protein-coupled receptor 180 (Gpr180), mRNA [NM_021434]
Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, c
Mus musculus neuron-glia-CAM-related cell adhesion molecule (Nrcam), transcript variant 1, mRNA [NM_
Mus musculus RIKEN cDNA 2810459M11 gene (2810459M11Rik), transcript variant 1, mRNA [NM_00114
Mus musculus asparaginase homolog (S. cerevisiae) (Aspg), mRNA [NM_001081169]
Mus musculus uncharacterized LOC100862268 (LOC100862268), transcript variant 1, long non-coding RN
Mus musculus DEAD (Asp-Glu-Ala-Asp) box polypeptide 4 (Ddx4), transcript variant 2, mRNA [NM_01002
Mus musculus ATPase, class I, type 8B, member 5 (Atp8b5), mRNA [NM_177195]
Mus musculus dynein, axonemal, intermediate chain 2 (Dnaic2), mRNA [NM_001034878]
Mus musculus kelch repeat and BTB (POZ) domain containing 11 (Kbtbd11), mRNA [NM_029116]
Mus musculus nudix (nucleoside diphosphate linked moiety X)-type motif 7 (Nudt7), transcript variant 4, m
Mus musculus predicted gene 7120 (Gm7120), transcript variant 2, mRNA [NM_001177666]
Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330442E02
Mus musculus Iroquois related homeobox 1 (Drosophila) (Irx1), mRNA [NM_010573]
Mus musculus ribosomal protein L34, pseudogene 1 (Rpl34-ps1), mRNA [NM_001199350]
Mus musculus doublecortin domain containing 2a (Dcdc2a), transcript variant 1, mRNA [NM_177577]
Mus musculus parathyroid hormone 1 receptor (Pth1r), transcript variant 1, mRNA [NM_011199]
Mus musculus synaptotagmin IX (Syt9), mRNA [NM_021889]
Mus musculus glutathione S-transferase, mu 6 (Gstm6), mRNA [NM_008184]
Mus musculus gem (nuclear organelle) associated protein 5 (Gemin5), transcript variant 1, mRNA [NM_00
Mus musculus RUN and FYVE domain containing 3 (Rufy3), transcript variant 3, mRNA [NM_001289776]
Q8NFW1_HUMAN (Q8NFW1) Alpha 1 type XXII collagen, partial (33%) [TC1681647]
Mus musculus protein tyrosine phosphatase, receptor type, R (Ptprr), transcript variant 1, mRNA [NM_011
Mus musculus microtubule-associated protein 1S (Map1s), mRNA [NM_173013]
Mus musculus cDNA sequence BC005764 (BC005764), transcript variant 1, mRNA [NM_181681]
Mus musculus zinc finger protein 536 (Zfp536), mRNA [NM_172385]
Mus musculus RALBP1 associated Eps domain containing protein 2 (Reps2), transcript variant 1, mRNA [
Mus musculus family with sequence similarity 83, member G (Fam83g), mRNA [NM_178618]
Mus musculus guanine nucleotide binding protein, alpha 14 (Gna14), mRNA [NM_008137]
Mus musculus teashirt zinc finger family member 1 (Tshz1), mRNA [NM_001081300]
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930532K22 product:hypo
Mus musculus RIKEN cDNA 4930515G01 gene (4930515G01Rik), long non-coding RNA [NR_027872]
Mus musculus oxysterol binding protein-like 10 (Osbpl10), mRNA [NM_148958]
Mus musculus periaxin (Prx), transcript variant 2, mRNA [NM_019412]
Mus musculus Rap guanine nucleotide exchange factor (GEF) 3 (Rapgef3), transcript variant 2, mRNA [NM
Mus musculus Rho GTPase activating protein 22 (Arhgap22), mRNA [NM_153800]
Mus musculus RIKEN cDNA 2010109A12 gene (2010109A12Rik), mRNA [NM_029363]

Mus musculus carbonyl reductase 3 (Cbr3), mRNA [NM_173047]
BB713741 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA clone B020049A06 3', mRNA sequ
predicted gene 6816 [Source:MGI Symbol;Acc:MGI:3648347] [ENSMUST00000059737]
Mus musculus transmembrane protein 65 (Tmem65), mRNA [NM_175212]
Mus musculus pleckstrin homology domain containing, family B (evectins) member 1 (Plekhb1), transcript
Mus musculus histamine receptor H1 (Hrh1), transcript variant 1, mRNA [NM_001252643]
PREDICTED: Mus musculus ADP-ribosylation factor 1-like (LOC102632770), misc_RNA [XR_399117]
Mus musculus M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (Mphosph10), mRNA [N
Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830106C12 product:hypo
Mus musculus centromere protein K (Cenpk), transcript variant 1, mRNA [NM_021790]
histone cluster 3, H2ba [Source:MGI Symbol;Acc:MGI:1925553] [ENSMUST00000078267]
Mus musculus cation channel, sperm associated 2 (Catsper2), mRNA [NM_153075]
Mus musculus microtubule-associated protein 1 A (Map1a), transcript variant 1, mRNA [NM_032393]
Mus musculus TRAF-interacting protein (Traip), mRNA [NM_011634]
Mus musculus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), transcript variant 1, mRNA [NM_
Mus musculus seven in absentia homolog 3 (Drosophila) (Siah3), mRNA [NM_001128093]
Mus musculus heparanase (Hpse), mRNA [NM_152803]
Mus musculus iduronidase, alpha-L- (Idua), transcript variant 1, mRNA [NM_008325]
Mus musculus predicted gene 2696 (Gm2696), mRNA [NM_001205009]
Mus musculus mannan-binding lectin serine peptidase 2 (Masp2), transcript variant 2, mRNA [NM_010767
Mus musculus ferritin light chain 1 (Ftl1), mRNA [NM_010240]
Mus musculus bisphosphate 3'-nucleotidase 1 (Bpnt1), mRNA [NM_011794]
Mus musculus synaptoporin (Synpr), transcript variant 2, mRNA [NM_001163032]
Mus musculus synuclein, gamma (Sncg), mRNA [NM_011430]
PREDICTED: Mus musculus uncharacterized LOC102634215 (LOC102634215), ncRNA [XR_386425]
Mus musculus H2A histone family, member J (H2afj), mRNA [NM_177688]
Mus musculus coiled-coil domain containing 184 (Ccdc184), mRNA [NM_177716]
Mus musculus transmembrane emp24 protein transport domain containing 5 (Tmed5), mRNA [NM_02887
Mus musculus solute carrier family 6 (neurotransmitter transporter), member 17 (Slc6a17), mRNA [NM_17
Mus musculus carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14 (Chst14), mRNA [NM_02811
Mus musculus C-type lectin domain family 16, member A (Clec16a), transcript variant 1, mRNA [NM_1775
Mus musculus GATA zinc finger domain containing 2A (Gatad2a), transcript variant 1, mRNA [NM_145596
Mus musculus inositol 1,4,5-trisphosphate 3-kinase A (Itpka), mRNA [NM_146125]
Mus musculus synaptojanin 2 (Synj2), transcript variant 1, mRNA [NM_001113353]
Mus musculus RIKEN cDNA 2310045N01 gene (2310045N01Rik), mRNA [NM_001145552]
Mus musculus L-3-hydroxyproline dehydratase (trans-) (L3hypdh), mRNA [NM_026038]
Mus musculus UbiA prenyltransferase domain containing 1 (Ubiad1), mRNA [NM_027873]
Mus musculus integrin beta 4 (Itgb4), transcript variant 1, mRNA [NM_001005608]
v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) [Source:MGI Symbol;Acc:MGI:104771] [
Mus musculus solute carrier family 27 (fatty acid transporter), member 3 (Slc27a3), mRNA [NM_011988]
Mus musculus HscB iron-sulfur cluster co-chaperone homolog (E. coli) (Hscb), mRNA [NM_153571]
Mus musculus solute carrier family 48 (heme transporter), member 1 (Slc48a1), mRNA [NM_026353]
Mus musculus meiotic nuclear divisions 1 homolog (S. cerevisiae) (Mnd1), mRNA [NM_029797]
Mus musculus alcohol dehydrogenase, iron containing, 1 (Adhfe1), transcript variant 1, mRNA [NM_17523
Mus musculus solute carrier family 35, member E1 (Slc35e1), mRNA [NM_177766]
Mus musculus late endosomal/lysosomal adaptor, MAPK and MTOR activator 3 (Lamtor3), mRNA [NM_01
Mus musculus a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1
Mus musculus Holliday junction recognition protein (Hjurp), mRNA [NM_198652]
Mus musculus fatty acid binding protein 5, epidermal (Fabp5), transcript variant 2, mRNA [NM_001272097]
Mus musculus calmodulin binding transcription activator 1 (Camta1), transcript variant 1, mRNA [NM_0010
Mus musculus RIKEN cDNA E330013P04 gene (E330013P04Rik), long non-coding RNA [NR_026942]
Mus musculus ChaC, cation transport regulator 1 (Chac1), mRNA [NM_026929]
Mus musculus selenium binding protein 1 (Selenbp1), mRNA [NM_009150]
Mus musculus protocadherin beta 4 (Pcdhb4), mRNA [NM_053129]
Mus musculus solute carrier family 13 (sodium-dependent citrate transporter), member 5 (Slc13a5), mRNA
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810451K1
Mus musculus acid phosphatase 1, soluble (Acp1), transcript variant 1, mRNA [NM_001110239]
Mus musculus predicted gene 7120 (Gm7120), transcript variant 2, mRNA [NM_001177666]
Mus musculus islet cell autoantigen 1-like (Ica1l), mRNA [NM_027407]

Mus musculus ribonuclease T2A (Rnaset2a), mRNA [NM_001083938]

Mus musculus RIKEN cDNA 1700010I14 gene (1700010I14Rik), mRNA [NM_025851]

Mus musculus predicted gene 13157 (Gm13157), mRNA [NM_001127189]

Mus musculus intraflagellar transport 27 (Ift27), mRNA [NM_025931]

Mus musculus RIKEN cDNA 3110070M22 gene (3110070M22Rik), long non-coding RNA [NR_027974]

Mus musculus CD1d1 antigen (Cd1d1), mRNA [NM_007639]

Mus musculus synaptotagmin XV (Syt15), transcript variant a, mRNA [NM_181529]

Mus musculus pannexin 1 (Panx1), mRNA [NM_019482]

Mus musculus small nuclear RNA activating complex, polypeptide 1 (Snapc1), mRNA [NM_178392]

Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E33002

Mus musculus protein kinase, cAMP dependent regulatory, type II beta (Prkar2b), mRNA [NM_011158]

Mus musculus EF-hand calcium binding domain 12 (Efcab12), mRNA [NM_001110506]

Mus musculus olfactomedin-like 3 (Olfml3), mRNA [NM_133859]

Mus musculus lectin, galactose-binding, soluble 2 (Lgals2), mRNA [NM_025622]

Mus musculus cysteine-rich protein 1 (intestinal) (Crip1), mRNA [NM_007763]

Mus musculus Ly6/neurotoxin 1 (Lynx1), mRNA [NM_011838]

Mus musculus transmembrane protein 140 (Tmem140), mRNA [NM_197986]

Mus musculus RIKEN cDNA 4932415M13 gene (4932415M13Rik), long non-coding RNA [NR_073205]

Mus musculus microfibrillar-associated protein 1A (Mfap1a), mRNA [NM_026220]

Mus musculus eukaryotic translation initiation factor 2-alpha kinase 2 (Eif2ak2), mRNA [NM_011163]

Mus musculus RIKEN cDNA 6720483E21 gene (6720483E21Rik), long non-coding RNA [NR_040492]

Mus musculus leukocyte specific transcript 1 (Lst1), mRNA [NM_010734]

Mus musculus malic enzyme 3, NADP(+)-dependent, mitochondrial (Me3), mRNA [NM_181407]

Mus musculus calmodulin binding transcription activator 1 (Camta1), transcript variant 1, mRNA [NM_0010

Mus musculus guanine nucleotide binding protein (G protein), beta 4 (Gnb4), mRNA [NM_013531]

Mus musculus ribosomal protein S4-like (Rps4l), non-coding RNA [NR_003634]

Mus musculus transmembrane protein 132B (Tmem132b), mRNA [NM_001190352]

Mus musculus a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1

Mus musculus ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (Abcc4), transcript variant 1, m

Mus musculus malic enzyme 3, NADP(+)-dependent, mitochondrial (Me3), mRNA [NM_181407]

Mus musculus apoptotic chromatin condensation inducer 1 (Acin1), transcript variant 2, mRNA [NM_02319

Mus musculus calcium channel, voltage-dependent, alpha2/delta subunit 3 (Cacna2d3), mRNA [NM_0097

Mus musculus proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) (

Mus musculus minichromosome maintenance deficient 3 (S. cerevisiae) (Mcm3), mRNA [NM_008563]

Mus musculus solute carrier family 26 (sulfate transporter), member 1 (Slc26a1), mRNA [NM_174870]

Mus musculus solute carrier family 13 (sodium-dependent citrate transporter), member 5 (Slc13a5), mRNA

Mus musculus ring finger protein 43 (Rnf43), mRNA [NM_172448]

Mus musculus zinc finger protein 930 (Zfp930), mRNA [NM_001013379]

Mus musculus solute carrier family 29 (nucleoside transporters), member 4 (Slc29a4), mRNA [NM_146257

Mus musculus ataxia telangiectasia mutated homolog (human) (Atm), mRNA [NM_007499]

Mus musculus purinergic receptor P2X, ligand-gated ion channel, 7 (P2rx7), transcript variant 2, mRNA [N

Mus musculus strain ICR clone Li(i)01 endogenous retrovirus U3 region, partial sequence. [FJ654066]

Mus musculus meiotic nuclear divisions 1 homolog (S. cerevisiae) (Mnd1), mRNA [NM_029797]

Mus musculus zinc finger homeobox 3 (Zfhx3), mRNA [NM_007496]

Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930032C08 product

Mus musculus RIKEN cDNA 6330403K07 gene (6330403K07Rik), mRNA [NM_134022]

Mus musculus DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae) (Dclre1c), transcript variant 2, mR

Mus musculus RNA polymerase II associated protein 2 (Rpap2), transcript variant 3, mRNA [NM_0011634

Mus musculus inhibitor of four 1 (Mif1) mRNA, complete cds. [DQ459435]

Mus musculus RIKEN cDNA 2010315B03 gene (2010315B03Rik), transcript variant 1, mRNA [NM_00124

Mus musculus zinc finger protein 619 (Zfp619), mRNA [NM_001004139]

Mus musculus olfactomedin-like 1 (Olfml1), mRNA [NM_172907]

Mus musculus RIKEN cDNA A730008H23 gene (A730008H23Rik), mRNA [NM_172505]

Mus musculus dynein regulatory complex subunit 1 (Drc1), mRNA [NM_001033460]

Mus musculus RIKEN cDNA 1600014C10 gene (1600014C10Rik), transcript variant 1, mRNA [NM_00108

Mus musculus chordin-like 1 (Chrdl1), transcript variant 1, mRNA [NM_001114385]

Mus musculus NLR family, CARD domain containing 5 (Nlrc5), mRNA [NM_001033207]

Mus musculus hydroxyprostaglandin dehydrogenase 15 (NAD) (Hpgd), mRNA [NM_008278]

Mus musculus T cell activation Rho GTPase activating protein (Tagap), mRNA [NM_145968]

Mus musculus immunoglobulin superfamily, member 21 (Igsf21), mRNA [NM_198610]
Mus musculus growth differentiation factor 15 (Gdf15), mRNA [NM_011819]
Mus musculus potassium large conductance calcium-activated channel, subfamily M, beta member 4 (Kcn
Mus musculus BH3 interacting domain death agonist (Bid), mRNA [NM_007544]
Mus musculus chloride channel Kb (Clcnkb), mRNA [NM_019701]
Mus musculus fibulin 2 (Fbln2), transcript variant 1, mRNA [NM_007992]
Mus musculus LIM domain and actin binding 1 (Lima1), transcript variant a, mRNA [NM_001113545]
Mus musculus lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730026I11 product:u
Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length en
Mus musculus cDNA clone IMAGE:40090117. [BC128469]
Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E33003
Mus musculus tubulin, beta 3 class III (Tubb3), mRNA [NM_023279]
Mus musculus potassium voltage-gated channel, Shal-related family, member 2 (Kcnd2), mRNA [NM_019
Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130022E09 product:hyp
Mus musculus CDC42 effector protein (Rho GTPase binding) 1 (Cdc42ep1), mRNA [NM_027219]
Mus musculus myosin, heavy polypeptide 1, skeletal muscle, adult (Myh1), mRNA [NM_030679]
PREDICTED: Mus musculus predicted gene, 20746 (Gm20746), mRNA [XM_006542883]
Mus musculus small nucleolar RNA host gene 6 (Snhg6), long non-coding RNA [NR_024067]
Mus musculus ring finger protein 41 (Rnf41), transcript variant 2, mRNA [NM_026259]
Mus musculus A kinase (PRKA) anchor protein 5 (Akap5), mRNA [NM_001101471]
Mus musculus membrane-associated ring finger (C3HC4) 8 (March8), mRNA [NM_027920]
Mus musculus RNA polymerase II associated protein 3 (Rpap3), mRNA [NM_028003]
Mus musculus UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15 (G
Mus musculus N-myristoyltransferase 2 (Nmt2), transcript variant 1, mRNA [NM_008708]
Mus musculus 13 days embryo whole body cDNA, RIKEN full-length enriched library, clone:3930401B19 p
Mus musculus 2-phosphoxylose phosphatase 1 (Pxylp1), transcript variant 1, mRNA [NM_001289645]
Mus musculus mitochondrial ribosomal protein S12 (Mrps12), mRNA [NM_011885]
Mus musculus transmembrane protein 254a (Tmem254a), transcript variant 1, mRNA [NM_026679]
Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530030H05 pro
Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B430105A11
Mus musculus dynein light chain LC8-type 1 (Dynll1), mRNA [NM_019682]
Mus musculus chemokine (C-C motif) ligand 25 (Ccl25), transcript variant 2, long non-coding RNA [NR_03
Mus musculus transmembrane protein 178 (Tmem178), mRNA [NM_026516]
Mus musculus cell adhesion molecule with homology to L1CAM (Chl1), mRNA [NM_007697]
Mus musculus transmembrane protein 254c (Tmem254c), transcript variant 1, mRNA [NM_001270498]
Mus musculus lipoma HMGIC fusion partner-like 3 (Lhfpl3), transcript variant 2, mRNA [NM_001081231]
Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900019G23 prod
Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900019G23 prod
Mus musculus BMP2 inducible kinase (Bmp2k), mRNA [NM_080708]
Mus musculus leucine rich repeat and sterile alpha motif containing 1 (Lrsam1), mRNA [NM_199302]
Mus musculus collagen, type IV, alpha 6 (Col4a6), mRNA [NM_053185]
Mus musculus serine/threonine kinase receptor associated protein (Strap), mRNA [NM_011499]
Mus musculus purine-nucleoside phosphorylase 2 (Pnp2), mRNA [NM_001123371]
Mus musculus dehydrogenase/reductase (SDR family) member 7C (Dhrs7c), mRNA [NM_001013013]
Mus musculus RIKEN cDNA A930005H10 gene (A930005H10Rik), transcript variant 2, long non-coding R
Mus musculus pituitary tumor-transforming gene 1 (Pttg1), transcript variant 2, mRNA [NM_013917]
Mus musculus anaphase-promoting complex subunit 5 (Anapc5), transcript variant 1, mRNA [NM_021505]
PREDICTED: Mus musculus RIKEN cDNA A030001D20 gene (A030001D20Rik), misc_RNA [XR_105107]
Mus musculus stathmin-like 3 (Stmn3), mRNA [NM_009133]
Mus musculus S100 calcium binding protein, zeta (S100z), mRNA [NM_001081159]
Mus musculus LIM domain only 1 (Lmo1), mRNA [NM_057173]
Mus musculus tissue inhibitor of metalloproteinase 4 (Timp4), mRNA [NM_080639]
Mus musculus integrin alpha 9 (Itga9), transcript variant 1, mRNA [NM_133721]
Mus musculus complement component 2 (within H-2S) (C2), mRNA [NM_013484]
Mus musculus EH-domain containing 3 (Ehd3), mRNA [NM_020578]
Mus musculus potassium intermediate/small conductance calcium-activated channel, subfamily N, membe
Mus musculus doubl homeobox B-like 2 (Duxbl2), mRNA [NM_001177538]
Mus musculus lectin, galactose binding, soluble 4 (Lgals4), mRNA [NM_010706]
Mus musculus lectin, galactose binding, soluble 4 (Lgals4), mRNA [NM_010706]

Mus musculus GATA zinc finger domain containing 2A (Gatad2a), transcript variant 1, mRNA [NM_145596
Mus musculus nuclear receptor subfamily 1, group D, member 2, mRNA (cDNA clone MGC:106146 IMAGE
Mus musculus F-box protein 17 (Fbxo17), mRNA [NM_015796]
Mus musculus glutamate receptor, metabotropic 5 (Grm5), transcript variant b, mRNA [NM_001143834]
Mus musculus ribosomal protein S3A1 (Rps3a1), mRNA [NM_016959]
Mus musculus endothelial cell-specific molecule 1 (Esm1), mRNA [NM_023612]
Mus musculus RIKEN cDNA 4833420G17 gene (4833420G17Rik), transcript variant 1, mRNA [NM_02612
Mus musculus nicotinamide nucleotide adenylyltransferase 3 (Nmnat3), mRNA [NM_144533]
Mus musculus exonuclease 3'-5' domain containing 1 (Exd1), mRNA [NM_172857]
Q3J0L9_RHOS4 (Q3J0L9) Hydrogenase maturation factor F, partial (3%) [TC1616199]
Mus musculus cell adhesion molecule with homology to L1CAM (Chl1), mRNA [NM_007697]
Mus musculus protein arginine N-methyltransferase 8 (Prmt8), mRNA [NM_201371]
Mus musculus KN motif and ankyrin repeat domains 1 (Kank1), mRNA [NM_181404]
Mus musculus hydroxyprostaglandin dehydrogenase 15 (NAD) (Hpgd), mRNA [NM_008278]
Mus musculus leucine rich repeat and sterile alpha motif containing 1 (Lrsam1), mRNA [NM_199302]
Mus musculus collagen, type II, alpha 1 (Col2a1), transcript variant 2, mRNA [NM_001113515]
Mus musculus growth associated protein 43 (Gap43), mRNA [NM_008083]
Mus musculus translocase of outer mitochondrial membrane 22 homolog (yeast) (Tomm22), mRNA [NM_1
Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830138L07 product:uncla
Mus musculus histocompatibility 2, Q region locus 5 (H2-Q5), non-coding RNA [NR_051981]
Mus musculus pyruvate dehydrogenase (lipoamide) beta (Pdhb), mRNA [NM_024221]
Mus musculus amyloid beta (A4) precursor protein-binding, family A, member 2 (Apba2), transcript variant
Mus musculus stathmin-like 4 (Stmn4), mRNA [NM_019675]
Mus musculus Ly6/neurotoxin 1 (Lynx1), mRNA [NM_011838]
Mus musculus butyrylcholinesterase (Bche), mRNA [NM_009738]
Mus musculus SH3-domain GRB2-like 3 (Sh3gl3), transcript variant 1, mRNA [NM_017400]
Mus musculus uncoupling protein 3 (mitochondrial, proton carrier) (Ucp3), mRNA [NM_009464]
Mus musculus stathmin-like 4 (Stmn4), mRNA [NM_019675]
Mus musculus peptidyl arginine deiminase, type II (Padi2), mRNA [NM_008812]
Mus musculus G protein-coupled receptor, family C, group 5, member A (Gprc5a), mRNA [NM_181444]
Mus musculus lipoprotein lipase (Lpl), mRNA [NM_008509]
Mus musculus lipoprotein lipase (Lpl), mRNA [NM_008509]
Mus musculus peptidyl arginine deiminase, type II (Padi2), mRNA [NM_008812]
Mus musculus uncoupling protein 2 (mitochondrial, proton carrier) (Ucp2), mRNA [NM_011671]
Mus musculus abhydrolase domain containing 1 (Abhd1), mRNA [NM_021304]
Mus musculus RIKEN cDNA 4833420G17 gene (4833420G17Rik), transcript variant 1, mRNA [NM_02612
Mus musculus serine (or cysteine) peptidase inhibitor, clade A, member 3N (Serpina3n), mRNA [NM_0092
Mus musculus complement component factor i (Cfi), mRNA [NM_007686]
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15 [Source:MGI Sym
Mus musculus purinergic receptor P2X, ligand-gated ion channel, 7 (P2rx7), transcript variant 1, mRNA [N
Mus musculus phosphatidylethanolamine binding protein 2 (Pbp2), mRNA [NM_029595]
Mus musculus olfactory receptor 224 (Olfr224), mRNA [NM_207695]
Mus musculus processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae) (Pop4), mRNA [NM_
Mus musculus POU domain, class 6, transcription factor 1 (Pou6f1), mRNA [NM_010127]
Mus musculus protocadherin 17 (Pcdh17), mRNA [NM_001013753]
Mus musculus family with sequence similarity 183, member B (Fam183b), transcript variant 1, mRNA [NM_
Mus musculus RIKEN cDNA 1810037I17 gene (1810037I17Rik), mRNA [NM_024461]
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Mus musculus sterile alpha motif domain containing 4 (Samd4), transcript variant 1, mRNA [NM_00103722
Mus musculus serine (or cysteine) peptidase inhibitor, clade A, member 3I (Serpina3i), mRNA [NM_00119
Mus musculus collagen, type IV, alpha 6 (Col4a6), mRNA [NM_053185]
Mus musculus XIAP associated factor 1 (Xaf1), transcript variant 1, mRNA [NM_001037713]

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-1.562962584	11.84753693	8.03792E-08
-1.568266039	7.811720919	0.004381404
-1.595495677	11.18370501	0.000514259
-1.60138222	10.26377656	0.030428182
-1.608736505	10.06212415	0.002286646
-1.623250362	12.76321099	5.03003E-15
-1.6590401	7.042019248	1.12499E-07
-1.663988464	9.535892008	0.005659542
-1.683490724	12.85410198	1.47938E-09
-1.686820938	9.225208525	6.98037E-05
-1.693097435	9.25076796	0.032298961
-1.71821413	11.50331263	8.90582E-07
-1.719959388	10.67728495	1.00373E-08
-1.728042937	9.346406711	1.20027E-10
-1.732205788	8.742824015	0.005579854
-1.765390964	9.267843384	0.016968618
-1.825424764	12.92514476	9.79076E-06
-1.882880186	10.6940361	4.87063E-05
-1.961023445	10.53863681	0.002138263
-1.966798117	8.512458682	0.000396451
-1.981559202	13.12004985	2.85216E-06
-2.008925416	9.278059744	0.003448159
-2.028719361	9.154942083	1.9464E-13
-2.135137596	11.72763205	2.19306E-10
-2.257787149	11.293936	0.022418234
-2.283011075	7.59612213	0.00086345
-2.327912086	10.82348441	1.10279E-05
-2.566482682	9.918835431	1.55236E-05
-2.708851464	7.72208074	5.32555E-10
-2.853577013	8.061203017	2.76734E-14
-2.990439512	11.37800517	1.19839E-16
-3.085193903	8.567395379	1.53107E-11
-3.096400623	9.286752712	4.62079E-09
-3.146347755	10.8863997	4.37739E-06
-3.150307147	11.50210939	8.73791E-16
-3.218676372	12.76378133	9.75281E-16
-3.381084819	9.712777677	3.4835E-12
-3.517707117	8.237049671	0.00111415
-4.328433054	11.49218277	1.68799E-16
-6.156879098	9.98739195	1.65288E-09

Supplimentary Table 2. List of genes validated by real-time PCR.

Gene Symbol	**Gene Name**	**FC uArr**	**Ave Expr**	**Adj.p.value**	**FC pcr**	**p.value**
Trim12a	tripartite motif-containing 12A	40.13	7.97	1.5E-21	20.31	0.0002
Ccl27a	chemokine (C-C motif) ligand 27A	8.94	8.53	2.5E-15	4.30	0.0107
Ccl27a (Pesky)	chemokine (C-C motif) ligand 27A Pesky	2.83	10.15	1.1E-03	4.30	0.0001
Car9	carbonic anhydrase 9	4.68	11.43	1.1E-02	3.83	0.0119
Ptchd2	patched domain containing 2	4.00	7.33	1.7E-13	7.33	0.0000
Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4	3.91	8.57	8.5E-09	5.25	0.0009
Bmp4	bone morphogenetic protein 4	3.31	12.83	2.0E-03	3.11	0.0002
Kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	3.14	9.03	2.5E-04	1.72	0.0223
P2ry2	purinergic receptor P2Y, G-protein coupled 2	2.29	10.79	4.0E-04	3.45	0.0000
Tnrc18	trinucleotide repeat containing 18	1.70	11.77	2.5E-03	1.79	0.0126
TGFb3	transforming growth factor, beta 3	1.46	14.82	4.5E-02	1.80	0.0122
Vcp	valosin containing protein	1.37	15.31	9.0E-04	1.50	0.0012
Ankib1	ankyrin repeat and IBR domain containing 1	1.28	11.36	2.7E-02	1.41	0.0115
Panx1	pannexin 1	-1.8657	10.51056	2.4E-02	-4.48	0.032
Cacna2d3	calcium channel, voltage-dependent, alpha2/delta subunit 3	-1.94831	8.02254	2.1E-02	-1.90	0.040
Fbln2	fibulin 2	-2.13	12.94	3.5E-02	-2.17	0.016
Grm5	glutamate receptor, metabotropic 5	-2.72	7.75	3.0E-02	-4.64	0.023
Chl1	cell adhesion molecule with homology to L1CAM	-2.90	10.44	1.7E-03	-2.13	0.0410
Col2a1	collagen, type II, alpha 1	-3.03	10.26	3.0E-02	-2.83	0.068
Gap43	growth associated protein 43	-3.05	10.06	2.3E-03	-3.03	0.0497
Lynx1	Ly6/neurotoxin 1	-3.29	11.50	8.9E-07	-4.62	0.0050
Lpl	lipoprotein lipase	-3.89	10.54	2.1E-03	-5.57	0.0141
Padi2	peptidyl arginine deiminase, type II	-3.94	13.12	2.9E-06	-2.54	0.025
P2rx7	purinergic receptor P2X, ligand-gated ion channel, 7	-5.92	9.92	1.6E-05	-2.45	0.0004
Pcdh17	protocadherin 17	-8.55	9.29	4.6E-09	-3.64	0.0058
Samd4	sterile alpha motif domain containing 4	-10.42	9.71	3.5E-12	-24.32	0.0000
Col4a6	collagen, type IV, alpha 6	-20.09	11.49	1.7E-16	-24.89	0.0003

Ranked list of genes up-regulated in non-Tg compared to ac

AGILENT SurePrint G3 GE 8x60k prob	AFFY Mouse430 2 probe
A_52_P244193	1437502_x_at
A_55_P2068673	1423281_at
A_52_P244193	1448182_a_at
A_55_P2068673	1423280_at
A_55_P1959748	1433966_x_at
A_55_P2144126	1437185_s_at
A_52_P504268	1418736_at
A_55_P2022569	1435486_at
A_51_P404463	1460049_s_at
A_52_P105537	1426851_a_at
A_52_P244193	1416034_at
A_55_P1995205	1454694_a_at
A_52_P360330	1423274_at
A_55_P2096867	1423537_at
A_55_P1964638	1453282_at
A_51_P126437	1420965_a_at
A_52_P220440	1426712_at
A_52_P93837	1455961_at
A_55_P2092085	1436902_x_at
A_55_P2033362	1427682_a_at
A_55_P2081040	1434848_at
A_52_P229052	1441598_at
A_52_P285024	1454877_at
A_52_P257812	1415904_at
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A_55_P1955457	1425458_a_at
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A_52_P105537	1426852_x_at
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A_55_P2082653	1432750_at

utely isolated astrocytes

AGILENT Gene Symbol	AFFY Gene Symbol	q-value
Cd24a	Cd24a	0
Stmn2	Stmn2	0
Cd24a	Cd24a	0
Stmn2	Stmn2	0
Asns	Asns	0
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B3galnt1	B3galnt1	0
Pak3	Pak3	0
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Nov	Nov	0
Cd24a	Cd24a	0
Top2a	Top2a	0
Map1b	Ints6	0
Gap43	Gap43	2.38E-04
Cxadr	Cxadr	2.38E-04
Enc1	Enc1	2.38E-04
Slc6a15	Slc6a15	2.38E-04
Mme	Mme	2.38E-04
Tmsb10	Tmsb10	2.38E-04
Egr2	Egr2	2.38E-04
Gpr27	0	2.38E-04
Tmeff2	Tmeff2	2.38E-04
Sertad4	Sertad4	2.38E-04
Lpl	Lpl	2.38E-04
Cdk1	Cdk1	2.38E-04
Grb10	Grb10	2.38E-04
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Uchl1	Uchl1	2.38E-04
Spp1	Spp1	2.38E-04
Fscn1	Fscn1	2.38E-04
Nov	Nov	2.38E-04
Anxa3	Anxa3	2.08E-04
Meg3	Meg3	3.03E-04
Bex1	Bex1	3.92E-04
Sphkap	Sphkap	3.92E-04
Lamb1	Lamb1	3.92E-04
Emp1	Emp1	3.92E-04
Cers6	Cers6	6.14E-04
Gas2l3	Gas2l3	7.69E-04
Basp1	Basp1	8.33E-04
Meg3	Meg3	8.94E-04
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Neurod6	Neurod6	8.94E-04
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Egr3	Egr3	9.09E-04
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Ndrg1	Ndrg1	0.001069182
Ephb2	Ephb2	0.00117284
Opcml	Opcml	0.001212121
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Lonrf1	Lonrf1	0.001640212
Scn3b	Scn3b	0.001666667
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Socs2	Socs2	0.001666667
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Erc2	Erc2	0.001621622
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Fstl5	Fstl5	0.002061404
Syt4	Syt4	0.002061404
Gpr85	Gpr85	0.002094017
Tubb3	Tubb3	0.002109705
Thsd7b	Thsd7b	0.002333333
Lmo7	Lmo7	0.002333333
Gpr85	Gpr85	0.002333333
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Bgn	Bgn	0.002329317
Trip13	Trip13	0.002329317
Thbs1	Pald1 | Thbs1	0.00248062
Ptgs2	Ptgs2	0.00248062
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Gpr85	Gpr85	0.002857143

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Grik3	Grik3	0.003432343
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Cxadr	Cxadr	0.003942308
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Hn1	Hn1	0.004049844
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Bmp6	Bmp6	0.00440367
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Tro	Tro	0.004384385
L1cam	L1cam	0.004375
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Grm7	Grm7	0.004473684
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Gng2	Gng2	0.004850949
Cnn2	Cnn2	0.004850949
Etl4	Etl4	0.0048
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Sorcs1	Sorcs1	0.00488189
Ttc9	Ttc9	0.00488189
Meg3	Meg3	0.004909561
Zfp711	Zfp711	0.004948718

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Ranked list of genes down-regulated in non-Tg compared to

AGILENT SurePrint G3 GE 8x60k probe	AFFY Mouse430 2 probe
A_52_P482251	1448397_at
A_51_P208603	1418937_at
A_51_P155873	1428923_at
A_55_P1970090	1449245_at
A_51_P391616	1441430_at
A_51_P406557	1435417_at
A_51_P468260	1419383_at
A_55_P2045299	1457536_at
A_55_P1993503	1434430_s_at
A_52_P67212	1457495_at
A_51_P355427	1423405_at
A_51_P136303	1449316_at
A_51_P452768	1419559_at
A_52_P266686	1417151_a_at
A_51_P430929	1433653_at
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A_51_P268193	1421093_at
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A_55_P2427900	1455304_at
A_51_P127297	1449038_at
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acutely isolated astrocytes

AGILENT Gene Symbol	AFFY Gene Symbol	q-value
Gjb6	Gjb6	0
Dio2	Dio2	0
Ppp1r3g	Ppp1r3g	0
Grin2c	Grin2c	0
Etnppl	0	0
AI464131	AI464131	0
S100b	S100b	0
Gpc5	Gpc5	0
Adora2b	Adora2b	0
2900052N01Rik	2900052N01Rik	0
Timp4	Timp4	0
Cyp4f15	Cyp4f15	0
Cyp4f14	Cyp4f14	0
Ntsr2	Ntsr2	0
Fam20a	Fam20a	0
Etnppl	Etnppl	0
Slc7a10	Slc7a10	0
Slc1a2	Slc1a2	0
Unc13c	Unc13c	0
Hsd11b1	Hsd11b1	0
Bcan	Bcan	0
Ptger4	Ptger4	0
Ttpa	Ttpa	0
S100b	S100b	0
Chrdl1	Chrdl1	0
Fam107a	Fam107a	0
Prss56	Prss56	0
2610034M16Rik	2610034M16Rik	0
Chrdl1	Chrdl1	0
Pygm	Pygm	0
Gpld1	Gpld1	0
Sult1a1	Sult1a1	0
Tph2	Tph2	0
Tril	Tril	0
Hhatl	Hhatl	0
Cdh19	Cdh19	0
Lgi4	Lgi4	5.85E-05
Tril	Tril	5.85E-05
Aifm3	Aifm3	5.85E-05
Prex2	Prex2	5.85E-05
Nrarp	Nrarp	5.85E-05
Gm11627	Gm11627	5.85E-05
Abhd3	Abhd3	5.85E-05
Eva1a	Eva1a	5.85E-05

Fam107a	Fam107a	5.85E-05
S1pr1	S1pr1	5.85E-05
Phkg1	Phkg1	5.85E-05
Hes5	Hes5	5.85E-05
Kcnj16	Kcnj16	5.85E-05
Cep128	Cep128	5.85E-05
Slc39a12	Slc39a12	5.85E-05
Cyp2d22	Cyp2d22	5.85E-05
Myoc	Myoc	5.85E-05
Phkg1	Phkg1	5.85E-05
Gabrg1	Gabrg1	5.85E-05
Eogt	Eogt	5.85E-05
Smim3	Smim3	1.67E-04
Cmtm5	Cmtm5	1.67E-04
Tlcd1	Tlcd1	1.67E-04
Aldoc	Aldoc	1.99E-04
Cep128	Cep128	1.99E-04
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Fam107a	Fam107a	1.99E-04
Tlcd1	Tlcd1	1.99E-04
Tlr3	Tlr3	1.99E-04
Tmem229a	Tmem229a	1.99E-04
Pla2g7	Pla2g7	2.94E-04
Slc13a5	Slc13a5	3.38E-04
Slc39a12	Slc39a12	3.70E-04
Ppp1r3d	Ppp1r3d	3.70E-04
Slc30a10	Slc30a10	3.70E-04
Chrdl1	Chrdl1	3.85E-04
Il18	Il18	3.85E-04
Omg	Omg	3.85E-04
Hepacam	Hepacam	3.85E-04
Gabra2	Gabra2	3.85E-04
Gabrg1	Gabrg1	3.85E-04
Slc25a18	Slc25a18	4.17E-04
Gpr37l1	Gpr37l1	4.17E-04
Slc1a3	Slc1a3	4.37E-04
Ptger4	Ptger4	4.37E-04
Maob	Maob	4.37E-04
Acsbg1	Acsbg1	4.37E-04
Fzd2	Fzd2	4.71E-04
Aldh1a1	Aldh1a1	6.13E-04
Car8	Car8	6.13E-04
Myom3	Myom3	6.44E-04
Slc1a2	Slc1a2	6.74E-04
Tmem229a	Tmem229a	7.41E-04
Slc14a1	Slc14a1	7.69E-04
Aifm3	Aifm3	8.16E-04

Lypd6	Lypd6	8.16E-04
Tmem100	Tmem100	8.16E-04
Ltbp1	Ltbp1	9.03E-04
Cyp2j9	Cyp2j9	9.03E-04
G0s2	G0s2	9.15E-04
Eogt	Eogt	9.15E-04
Fzd2	Fzd2	9.15E-04
Thbs4	Thbs4	9.15E-04
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Akt2	Akt2	9.15E-04
Gm5089	Gm5089	9.94E-04
Slc1a3	Slc1a3	9.94E-04
Unc13c	Unc13c	9.97E-04
Selenbp1	Selenbp1	9.97E-04
Pnpla7	Pnpla7	9.97E-04
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Papss2	Papss2	0.001014493
Il33	Il33	0.001014493
Agmo	Agmo	0.001016949
Egfl6	Egfl6	0.001016949
Apln	Apln	0.001016949
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Phactr3	Phactr3	0.001305556
Atp1a2	Atp1a2	0.001338798
Nat8	Nat8	0.001338798
Slc27a1	Slc27a1	0.001490515
Acot11	Acot11	0.001435897
Aqp4	Aqp4	0.001435897
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Cd38	Cd38	0.001464646
Fgd6	Fgd6	0.001519608
Slc4a4	Slc4a4	0.001519608
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Lypd6	Lypd6	0.001519608
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Hes5	Hes5	0.001873638
Gm6556	Gm6556	0.001873638
Elovl2	Elovl2	0.001991342
Kctd14	Kctd14	0.002086022
Slc9a3r1	Slc9a3r1	0.002067511
Ppara	Ppara	0.002067511
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Tmem51	Tmem51	0.002180293
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Hepacam	Hepacam	0.002409639
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1700019G17Rik	1700019G17Rik	0.002480159
Tfcp2l1	Tfcp2l1	0.002509804
Naaa	Naaa	0.002509804
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Eogt	Eogt	0.00253876
Nkain4	Nkain4	0.002681992
Vcam1	Vcam1	0.002681992
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Hipk2	Hipk2	0.002749529
Oaf	Oaf	0.002752809
Adcy2	Adcy2	0.002811918
Car2	Car2	0.002799264
Gprc5b	Gprc5b	0.002799264
Gramd3	Gramd3	0.002893773
Hlf	Hlf	0.003005465
Dnaic1	Dnaic1	0.003007246
Kcnn2	Kcnn2	0.003028674
Sec14l2	Sec14l2	0.003028674

Rlbp1	Rlbp1	0.003065954
Kctd14	Kctd14	0.003191489
Eya1	Eya1	0.003227513
Naaa	Naaa	0.003245614
Elf5	Elf5	0.003246073
Efhd1	Efhd1	0.00328125
Dab1	Dab1	0.00338488
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Pcdh20	Pcdh20	0.003451179
Timp4	Timp4	0.003500838
Ppap2b	Ppap2b	0.003582089
Gabra2	Gabra2	0.003582089
Dbx2	Dbx2	0.003596059
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Fjx1	Fjx1	0.003788618
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Tmem204	Tmem204	0.004063492
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Cml1	Cml1	0.004166667
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Kcnj10	Kcnj10	0.004592592
Ctso	Ctso	0.004631268
1700019G17Rik	1700019G17Rik	0.004625551
Mfge8	Mfge8	0.004649123
Kcng4	Kcng4	0.004905386
Hopx	Hopx	0.004942029
Qk	Qk	0.004978355

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Ranked list of genes up-regulated in non-Tg astrocytes com

AGILENT SurePrint G3 GE 8x60k prob	**AFFY Mouse430 2 probe**
A_52_P622850	1456010_x_at
A_52_P150950	1452090_a_at
A_55_P2045299	1457536_at
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A_51_P396883	1460408_at
A_55_P2113981	1434819_at
A_55_P2130249	1418791_at
A_51_P274488	1447825_x_at
A_55_P2172470	1423231_at
A_52_P883557	1438751_at
A_55_P1990309	1452894_at
A_52_P150950	1425898_x_at
A_55_P2051849	1416828_at
A_52_P309166	1419420_at
A_55_P1992049	1434141_at
A_55_P2061620	1449147_at
A_51_P127297	1449038_at
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A_51_P509643	1418493_a_at
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A_51_P477458	1421436_at

pared to cultured astroglia from Cahoy's dataset

AGILENT Gene Symbol	AFFY Gene Symbol	q-value
Hes5	Hes5	0
Olfm3	Olfm3	0
Gpc5	Gpc5	0
Pcdh8	Pcdh8	0
Gabrg1	Gabrg1	0
St6gal2	St6gal2	0
Sh3gl2	Sh3gl2	0
Pcdh8	Pcdh8	0
Nrgn	Nrgn	0
Slc30a10	Slc30a10	0
Elavl4	Elavl4	0
Olfm3	Olfm3	0
Snap25	Snap25	0
St6galnac5	St6galnac5	0
Gucy1a3	Gucy1a3	0
Chst1	Chst1	0
Hsd11b1	Hsd11b1	0
Vsnl1	Vsnl1	1.85E-04
Reln	Reln	1.85E-04
Phactr3	Phactr3	1.85E-04
Arpp21	Arpp21	1.85E-04
Fstl5	Fstl5	1.85E-04
Scn8a	Scn8a	1.85E-04
Sept6	Sept6	1.85E-04
Neurod6	Neurod6	1.85E-04
Gabra2	Gabra2	1.85E-04
Lgi1	Lgi1	1.85E-04
Mapt	Mapt	1.85E-04
Elavl4	Elavl4	1.85E-04
Ptn	Ptn	2.22E-04
Snca	Snca	2.22E-04
Arpp21	Arpp21	2.22E-04
Cck	Cck	2.22E-04
Elovl2	Elovl2	2.22E-04
Atp8a1	Atp8a1	2.22E-04
Hba-a1	Hba-a1 | Hba-a2	3.70E-04
Gabrg1	Gabrg1	3.70E-04
Gpr116	Gpr116	4.39E-04
Kcnj3	Kcnj3	5.13E-04
Gucy1b3	Gucy1b3	5.13E-04
Jakmip1	Jakmip1	5.13E-04
Kcnma1	A830039N20Rik	5.56E-04
Ntm	Ntm	6.20E-04
Kcnd2	Kcnd2	6.82E-04

Mapt	Mapt	6.82E-04
Tmem150c	Tmem150c	8.70E-04
Atp2b2	Atp2b2	0.00106383
Syt7	Syt7	0.00106383
Adcyap1r1	Adcyap1r1	0.00106383
Gsg1l	Gsg1l	0.001133333
Prkcb	Prkcb	0.001133333
Rbfox3	Rbfox3	0.001133333
Tenm2	Tenm2	0.001133333
Ntm	Ntm	0.001133333
B3galt2	B3galt2	0.001133333
Pcdh20	Pcdh20	0.001133333
Ngef	Ngef	0.001133333
Atp1a3	Atp1a3	0.001133333
Cnr1	Cnr1	0.001073446
Rasgrp1	Rasgrp1	0.001222222
Fry	Fry	0.001256831
St6galnac5	LOC552874 | St6galnac5	0.001290323
Dclk1	Dclk1	0.001290323
Ldb2	Ldb2	0.001302083
Egfl6	Egfl6	0.001302083
Gabra1	Gabra1	0.001302083
Arhgef7	Arhgef7	0.001302083
Slc7a10	Slc7a10	0.00127451
Lsamp	Lsamp	0.00127451
Grin3a	Grin3a	0.001476191
Lsamp	Lsamp	0.001690141
Myt1l	Myt1l	0.001851852
Pacsin1	Pacsin1	0.001851852
Kcnma1	Kcnma1	0.001936937
Slc30a10	Slc30a10	0.001955556
Omg	Omg	0.002017544
Hba-a1	Hba-a1 | Hba-a2	0.002207792
Pnmal1	4930488B01Rik | Pnmal1	0.002350427
Gabra2	Gabra2	0.002489452
Slco1c1	Slco1c1	0.002541667
Kif21b	Kif21b	0.00255144
Hlf	Hlf	0.00255144
Cldn5	Cldn5	0.002570281
Ntm	Ntm	0.002570281
Unc80	Unc80	0.002570281
Grid2	Grid2	0.00251938
Rgs7bp	Rgs7bp	0.002528736
Gabrg2	Gabrg2	0.002528736
Rab3c	Rab3c	0.00258427
St6galnac5	St6galnac5	0.00258427
Syt16	Syt16	0.002564103

Eps8	Eps8	0.002572464
Kcnip2	Kcnip2	0.002724014
Fut9	Fut9	0.003049645
Cspg5	Cspg5	0.003087719
Cdk5r2	Cdk5r2	0.003090278
Rgs5	Rgs5	0.003090278
Spock2	Spock2	0.003061225
Cadps2	Cadps2	0.003131313
Rbfox1	Rbfox1	0.003166667
Pgbd5	Pgbd5	0.003168317
Cntn4	Cntn4	0.003168317
Myt1l	Myt1l	0.003139159
Rab33a	Rab33a	0.003141026
Unc13c	Unc13c	0.003141026
Tmem178	Tmem178	0.003144654
Hes5	Hes5	0.003302181
Eps8	Eps8	0.003487654
Syt4	Syt4	0.00351682
Sema4a	Sema4a	0.00351682
Hbb-b1	Hbb-b1 | Hbb-b2 | Hbb-bs | Hbb-bt	0.00351682
Snca	Snca	0.003452381
Ptn	Ptn	0.00359882
Ipcef1	Ipcef1	0.00371345
Adcy2	Adcy2	0.00371345
Atp8a1	Atp8a1	0.003706896
Lrrtm3	Lrrtm3	0.003732194
Scn8a	Scn8a	0.0040113
Tac1	Tac1	0.0040113
Atp8a1	Atp8a1	0.004194445
Nr4a2	Nr4a2	0.004269972
Ptbp2	Ptbp2	0.004371585
Kcnq3	B830032F12 | Kcnq3	0.004371585
Tagln3	Tagln3	0.004354839
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Syt7	Syt7	0.004417989
Dclk1	Dclk1	0.004435696
Negr1	Negr1	0.004427083
Rgs7bp	0	0.004418605
Cacna1b	Cacna1b	0.004435897
Lgi1	Lgi1	0.004435897
AI504432	AI504432	0.004671717
Ldb2	Ldb2	0.004786967
Vtn	Vtn	0.004900497
Grid2	Grid2	0.005

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Ranked list of genes down-regulated in non-Tg astrocytes c

AGILENT SurePrint G3 GE 8x60k prob	AFFY Mouse430 2 probe
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A_52_P278336	1416164_at
A_55_P2085142	1449254_at
A_55_P2056325	1460330_at
A_51_P207622	1456084_x_at
A_55_P2017418	1450876_at
A_51_P404463	1460049_s_at
A_55_P2032678	1416121_at
A_55_P1990111	1422629_s_at
A_52_P679105	1431057_a_at
A_55_P2039284	1425964_x_at
A_55_P2087607	1417494_a_at
A_51_P405606	1456174_x_at
A_52_P292792	1455627_at
A_52_P175376	1418091_at
A_51_P450527	1423505_at
A_55_P2017636	1421811_at
A_51_P405606	1423413_at
A_51_P207622	1437718_x_at
A_55_P2111302	1448735_at
A_55_P2017418	1423153_x_at
A_51_P207622	1437685_x_at
A_51_P465281	1419573_a_at
A_55_P2146254	1424254_at
A_55_P2039284	1422943_a_at
A_66_P111562	1417419_at
A_55_P2051681	1424885_at
A_55_P2087607	1417495_x_at
A_55_P2115798	1426260_a_at
A_52_P220879	1455900_x_at
A_51_P427663	1450981_at
A_51_P405606	1420760_s_at
A_51_P341736	1439364_a_at
A_30_P01023502	1421375_a_at
A_52_P185907	1448326_a_at
A_52_P220879	1433428_x_at
A_55_P2055487	1426210_x_at
A_55_P1963154	1450154_at
A_51_P472726	1423946_at
A_52_P220879	1437277_x_at
A_66_P114451	1437409_s_at
A_52_P93837	1455961_at

A_51_P404463	1423261_at
A_55_P2087607	1448734_at
A_55_P2110713	1419091_a_at
A_51_P131408	1418572_x_at
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A_51_P515605	1427883_a_at
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A_51_P222657	1438948_x_at
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A_66_P104815	1448613_at
A_55_P2016647	1448314_at
A_55_P2459897	1434719_at
A_51_P414889	1445897_s_at
A_55_P1952379	1416125_at
A_52_P263095	1452217_at
A_51_P315682	1439764_s_at
A_55_P1980631	1451246_s_at
A_52_P304720	1418476_at
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A_55_P1995205	1454694_a_at
A_55_P2104894	1422437_at
A_52_P413646	1450759_at
A_52_P602847	1424825_a_at
A_52_P372151	1420930_s_at
A_51_P157042	1416953_at
A_52_P223127	1435399_at
A_55_P2086949	1422033_a_at
A_51_P222657	1416695_at
A_52_P52303	1440142_s_at
A_51_P484111	1455978_a_at
A_55_P2002577	1422438_at
A_51_P464387	1417013_at
A_30_P01029470	1460603_at
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A_51_P392687	1456292_a_at
A_55_P2004781	1416239_at

A_52_P679105	1437671_x_at
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A_52_P35048	1416168_at
A_52_P114905	1455239_at
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A_51_P411271	1416543_at
A_51_P168613	1438684_at
A_55_P1978060	1423061_at
A_55_P2028015	1426910_at
A_66_P111562	1417420_at
A_51_P237752	1424130_a_at
A_55_P2105025	1455872_at
A_51_P321341	1427345_a_at
A_52_P426870	1438233_at
A_55_P2087607	1417496_at
A_55_P2007713	1448276_at
A_55_P2013948	1456312_x_at
A_51_P255456	1416613_at
A_55_P2056241	1422861_s_at
A_55_P2213209	1448475_at
A_51_P128876	1423754_at
A_30_P01017425	1434845_at

ompared to cultured astroglia from Cahoy's dataset

AGILENT Gene Symbol	AFFY Gene Symbol	q-value
Akr1c14	Akr1c14	0
Anxa1	Anxa1	0
Ogn	Ogn	0
Fbln5	Fbln5	0
Spp1	Spp1	0
Anxa3	Anxa3	0
Fmod	Fmod	0
Cfh	Cfh	0
1500015O10Rik	1500015O10Rik	0
Lox	Lox	0
Shroom3	Shroom3	0
Prss23	Prss23	0
Hspb1	Hspb1	0
Cp	Cp	0
Ndrg1	Ndrg1	0
Col8a1	Col8a1	1.19E-04
Tfcp2l1	Tfcp2l1	1.19E-04
Tagln	Tagln	1.19E-04
Thbs1	Pald1 | Thbs1	1.19E-04
Ndrg1	Ndrg1	1.19E-04
Fmod	Fmod	1.19E-04
Cp	Cp	1.19E-04
Cfh	Cfh	1.19E-04
Fmod	Fmod	1.19E-04
Lgals1	Lgals1	1.19E-04
Ifitm1	Ifitm1	1.19E-04
Hspb1	Hspb1	1.19E-04
Ccnd1	Ccnd1	2.15E-04
Klhdc8a	Klhdc8a	2.15E-04
Cp	Cp	2.15E-04
0	Ugt1a1 | Ugt1a10 | Ugt1a2 | Ugt1a5	4.17E-04
Tgm2	Tgm2	4.90E-04
Cnn2	Cnn2	4.90E-04
Ndrg1	Ndrg1	4.88E-04
Mmp2	Mmp2	4.88E-04
0	S100a6	4.88E-04
Crabp1	Crabp1	4.88E-04
Tgm2	Tgm2	4.88E-04
Parp3	Parp3	4.88E-04
Folh1	Folh1	4.88E-04
Pdlim2	Pdlim2	6.20E-04
Tgm2	Tgm2	6.20E-04
Gpr126	Gpr126	6.82E-04
Mme	Mme	7.41E-04

1500015O10Rik	1500015O10Rik	8.70E-04
Cp	Cp	0.001020408
Anxa2	Anxa2	0.001020408
Tnfrsf12a	Tnfrsf12a	0.001020408
Lgals1	Lgals1	0.001069182
Col3a1	Col3a1	0.001069182
Ccnd1	Ccnd1	0.001069182
Parp3	Parp3	0.001069182
Akap12	Akap12	0.001358025
Tspo	Tspo	0.001369048
Cd44	Cd44	0.001369048
Ecm1	Ecm1	0.001637427
Cdk1	Cdk1	0.001724138
A2m	A2m	0.001777778
Ifi35	Ifi35	0.001777778
Fkbp5	Fkbp5	0.001912568
Ahnak	Ahnak	0.002239583
Igf2bp2	Igf2bp2	0.002239583
Aurkb	Aurkb	0.002239583
Crlf1	Crlf1	0.002575758
Serping1	Serping1	0.002575758
Ddo	Ddo	0.00254902
Tspo	Tspo	0.00254902
P4ha3	P4ha3	0.002560386
Ndrg1	Ndrg1	0.002571429
Cep55	Cep55	0.002676056
Pla2g4a	Pla2g4a	0.002685185
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Tnfrsf12a	Tnfrsf12a	0.002844445
Pter	Pter	0.002844445
Top2a	Top2a	0.002850877
Col5a2	Col5a2	0.00278481
Bmp6	Bmp6	0.00278481
Glycam1	Glycam1	0.00278481
Ctnnal1	Ctnnal1	0.002705882
Ctgf	Ctgf	0.002705882
Synpo2	Synpo2	0.002705882
Cntf	Cntf | Zfp91 | Zfp91Cntf	0.002705882
Tspo	Tspo	0.002705882
Gfap	Gfap	0.002705882
Matn2	Matn2	0.002720307
Ephx1	Ephx1	0.002720307
Hspb8	Hspb8	0.002954545
0	Samd9l	0.003183521
Tuba1c	Gm6682 | Tuba1c	0.003333333
Vim	Vim	0.003443223
Ass1	Ass1 | Gm5424	0.003514493

Prss23		Prss23	0.003942652
Lgals3		Lgals3	0.00393617
Serpinf1		Serpinf1	0.003964912
Ifitm10		Ifitm10	0.00395189
Vim		Vim	0.00395189
Nfe2l2		Nfe2l2	0.003973064
Nuak1		Nuak1	0.003973064
Arvcf		Arvcf	0.004125413
Pawr		Pawr	0.004125413
Ccnd1		Ccnd1	0.004150327
Ptrf		Ptrf	0.004174757
Fam167a		Fam167a	0.004285714
Sult1a1		Sult1a1	0.004285714
Fam178a		Fam178a	0.004299066
Cp		Cp	0.004299066
Tspan4		Tspan4	0.004567901
Gsn		Gsn	0.004617737
Cyp1b1		Cyp1b1	0.004761905
Pdlim5		Pdlim5	0.004761905
LOC269472		Olfml3	0.004761905
Ifitm3		Ifitm3	0.004778761
	0	Gm20204 | Gm20204	1.1075892

RP-value
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61.248623
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76.01784
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86.75464
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ProbeName	GeneSymbol	GeneName	Description	logFC	AveExpr
A_55_P2180869	Ocel1	occludin/ELL dom	Mus musculus occlu	1.912680866	11.20738139
A_66_P105689	Trim34a	tripartite motif-c	Mus musculus tripa	1.832444376	8.366008201
A_55_P2085142	Spp1	secreted phosph	Mus musculus secre	1.726988441	9.069085973
A_55_P2130129	Kcnab1	potassium voltag	Mus musculus pota	1.64885182	9.034037272
A_51_P451458	Mamdc2	MAM domain cor	Mus musculus MA	1.503395436	9.872073547
A_52_P209484	Tmem88	transmembrane	Mus musculus trans	1.360071196	8.840699972
A_55_P2137611	Irgm2	immunity-related	Mus musculus imm	1.142352135	9.334410797
A_55_P2056325	Anxa3	annexin A3	Mus musculus anne	1.066791	13.70984223
A_51_P237383	Rnase4	ribonuclease, RN	Mus musculus ribor	1.058616352	10.71759463
A_66_P140976	Rpl15	ribosomal protei	Mus musculus ribos	0.958862454	12.01103127
A_51_P140237	Fhl2	four and a half LI	Mus musculus four	0.944947122	12.347438
A_55_P2176248	0	0	BB001409 RIKEN fu	0.789714112	15.19223654
A_52_P604629	Csrnp1	cysteine-serine-ri	Mus musculus cyste	0.636119273	10.39213101
A_51_P149562	Apbb2	amyloid beta (A4)	Mus musculus amyl	0.59661532	12.68664241
A_55_P2033445	Tnfrsf1b	tumor necrosis fa	Mus musculus tum	0.547667986	6.372954616
A_52_P563617	Ssbp4	single stranded D	Mus musculus singl	0.543415824	12.00448531
A_51_P124748	Tgfb3	transforming gro	Mus musculus trans	0.54195087	14.82434995
A_55_P2006525	Adamtsl4	ADAMTS-like 4	Mus musculus ADA	0.52369464	11.96438562
A_52_P363216	Gcnt2	glucosaminyl (N-a	Mus musculus gluc	0.443700852	9.454501915
A_51_P411728	2900026A02Rik	RIKEN cDNA 2900	Mus musculus RIKE	0.412405535	6.947356535
A_55_P2383283	2310001H17Rik	RIKEN cDNA 2310	Mus musculus adul	0.390172821	6.442100669
A_66_P107790	Myl12a	myosin, light chai	Mus musculus myo	0.385361306	16.30849845
A_51_P266774	Mfn2	mitofusin 2	Mus musculus mito	0.341591338	11.2941752

adj.P.Val	Orre-Log_FC	Orre-adj.P.Val
6.74098E-11	0.671147264	0.017244532
1.75238E-08	1.040119507	0.010939297
0.000151451	1.985300298	0.000905207
0.000246485	2.159113265	0.016663479
8.60945E-07	1.706249745	0.023407529
2.13081E-07	1.300105703	0.012253122
0.043028606	1.227755556	0.012427216
8.60945E-07	1.853241477	0.000707922
0.00045366	1.145738027	0.020785778
3.02697E-06	0.916973791	0.007254029
0.002411981	1.050243221	0.044629988
3.57358E-09	0.527909643	0.035359423
0.01141401	1.06350743	0.046781615
0.042282655	1.17925114	0.002867076
0.003725106	0.932289499	0.019878077
0.001311367	0.597294453	0.014909633
0.045134321	2.050401115	0.009907979
0.034730892	1.060613269	0.023818682
0.029590022	1.329891434	0.0203074
0.046775339	0.856409089	0.040114262
0.020221663	1.92503457	0.038211201
0.004062968	1.460600323	0.000771054
0.00320903	0.7318489	0.047061769

ProbeName	GeneSymbol	GeneName	Description	logFC	AveExpr
A_52_P267391	Trim12a	tripartite motif-co	Mus musculus tripa	5.326621277	7.971349421
A_55_P1974432	Gm5067	predicted gene 50	Mus musculus 13 da	4.706882168	7.941454285
A_55_P2070576	Ccl27a	chemokine (C-C m	Mus musculus chem	3.159607921	8.528529626
A_55_P2205650	2610507I01Rik	RIKEN cDNA 2610	Mus musculus RIKE	2.76634258	8.199204967
A_55_P2064659	Trim12a	tripartite motif-co	Mus musculus tripa	2.625034338	7.006201591
A_55_P2256646	C130078N14	uncharacterized p	Mus musculus 16 da	2.57614419	6.975926163
A_55_P2068731	Gm20878	predicted gene, 20	Mus musculus pred	2.535424208	9.5022869
A_52_P360330	Map1b	microtubule-assoc	Mus musculus micr	2.528377361	9.568691036
A_55_P2068733	Gm20878	predicted gene, 20	Mus musculus pred	2.4557783	8.486798968
A_55_P2092750	Car9	carbonic anhydras	Mus musculus carb	2.227984321	11.43046767
A_55_P1981756	Vmn2r123	vomeronasal 2, re	Mus musculus vom	2.222558264	6.863824084
A_51_P349888	Ang2	angiogenin, ribon	Mus musculus angi	2.221223649	7.455657139
A_52_P88793	Zfp933	zinc finger protein	Mus musculus zinc f	2.187870963	8.102504202
A_52_P238846	Bpnt1	bisphosphate 3'-nu	Mus musculus bisph	2.17951172	8.499105459
A_51_P288549	Jmjd7	jumonji domain co	Mus musculus jumo	2.155696224	9.038758021
A_66_P130730	Zfp963	zinc finger protein	Mus musculus zinc f	2.142761169	7.714208648
A_55_P2112986	Klk1b22	kallikrein 1-relatec	Mus musculus kallik	2.141524133	6.950826515
A_55_P2134591	BC049715	cDNA sequence BC	Mus musculus cDNA	2.123548403	7.11520769
A_55_P2097151	Ptchd2	patched domain co	Mus musculus patch	2.000964933	7.331541801
A_55_P2073965	BC049715	cDNA sequence BC	Mus musculus cDNA	1.994500273	6.927881761
A_51_P217498	Slc2a4	solute carrier fami	Mus musculus solut	1.966656603	8.572006753
A_55_P2045886	Stk3	serine/threonine k	Mus musculus serin	1.91680325	9.198570422
A_55_P2108773	4930427A07Rik	RIKEN cDNA 4930	Mus musculus RIKE	1.903303041	6.870745089
A_66_P134474	Ang3	angiogenin, ribon	Mus musculus angi	1.797567531	7.969980889
A_55_P1964628	LOC102633627	tropomyosin alpha	PREDICTED: Mus mu	1.763559756	13.64296854
A_51_P293069	Mfsd7b	major facilitator su	Mus musculus majo	1.750158707	9.743132096
A_55_P2154387	Bmp4	bone morphogene	Mus musculus bone	1.725246422	12.829438
A_51_P413147	Klk1b3	kallikrein 1-relatec	Mus musculus kallik	1.701860019	6.732605311
A_51_P112627	St6galnac2	ST6 (alpha-N-acety	Mus musculus ST6 (	1.692648894	10.18934601
A_51_P512820	Dera	2-deoxyribose-5-p	Mus musculus 2-de	1.680832596	8.494281435
A_55_P2095603	Ccdc65	coiled-coil domain	Mus musculus coile	1.680817626	10.32761111
A_51_P477121	Pmaip1	phorbol-12-myrist	Mus musculus phor	1.661805686	9.694988353
A_55_P2373852	2310058N22Rik	RIKEN cDNA 2310	Mus musculus adult	1.602415256	8.177045633
A_55_P2144597	9030025P20Rik	RIKEN cDNA 9030	Mus musculus RIKE	1.574018429	10.33013058
A_51_P180724	Mlh1	mutL homolog 1 (E	Mus musculus mutL	1.554543727	10.33206306
A_51_P142896	Cd59a	CD59a antigen	Mus musculus CD59	1.5382424	11.07205551
A_55_P2003561	Luzp2	leucine zipper prot	Mus musculus leuci	1.53117695	10.52421298
A_51_P417321	Zfp236	zinc finger protein	Mus musculus zinc f	1.517239691	7.995104458
A_51_P115953	Ctxn3	cortexin 3	Mus musculus corte	1.515844412	7.480665769
A_55_P2068723	Ccl27a	chemokine (C-C m	Mus musculus chem	1.506485285	9.878089363
A_55_P2068734	Ccl27a	chemokine (C-C m	Mus musculus chem	1.501278472	10.14705428
A_55_P2015912	Zfp961	zinc finger protein	Mus musculus zinc f	1.460709523	7.978713091
A_55_P1961395	Pdpn	podoplanin	Mus musculus podo	1.408511896	15.4731878
A_51_P358722	Lancl3	LanC lantibiotic sy	Mus musculus LanC	1.403818102	7.624333535
A_55_P2053551	Mast4	microtubule assoc	Mus musculus micr	1.383573947	9.459809864

A_55_P2019577	1500011B03Rik	RIKEN cDNA 1500(	Mus musculus RIKEI	1.382367568	11.13618528
A_52_P532687	Ermard	ER membrane ass(	Mus musculus ER m	1.374998141	9.208882095
A_52_P490207	Ermard	ER membrane ass(	Mus musculus ER m	1.288727894	8.746606738
A_55_P2059357	Myo7a	myosin VIIA	Mus musculus myos	1.280346209	7.864933543
A_51_P507899	Ttc8	tetratricopeptide r	Mus musculus tetra	1.276939334	10.06822585
A_55_P2194064	BC023969	cDNA sequence BC	Mus musculus lung	1.267825845	7.04159718
A_55_P2067727	Mxra7	matrix-remodelling	Mus musculus matr	1.262225358	11.32684755
A_55_P2197338	Tnfsf13os	tumor necrosis fac	PREDICTED: Mus mu	1.258335257	7.508009275
A_51_P345316	Cep76	centrosomal prote	Mus musculus centr	1.257149573	7.422795425
A_55_P2065726	Snx29	sorting nexin 29	sorting nexin 29 [So	1.257094651	7.59703769
A_55_P2179793	0	0	GAG_IPMAE (P3179	1.25413714	11.05468172
A_52_P642012	BC006965	cDNA sequence BC	Mus musculus cDN/	1.25400917	7.4799979
A_52_P616332	Atp10d	ATPase, class V, ty	Mus musculus ATPa	1.247972291	7.18748402
A_51_P179504	Ang3	angiogenin, ribonu	Mus musculus angic	1.243578938	7.705143143
A_55_P2169963	Gm13152	predicted gene 13	Mus musculus pred	1.236720209	6.482225328
A_52_P559545	Cercam	cerebral endotheli	Mus musculus cerel	1.218979981	8.680124663
A_55_P2180196	Ccdc32	coiled-coil domain	coiled-coil domain c	1.210677001	6.693191129
A_52_P135707	Creb3	cAMP responsive e	Mus musculus cAMI	1.208699556	11.79138848
A_52_P598634	1190007I07Rik	RIKEN cDNA 1190(	Mus musculus RIKEI	1.196215216	10.74842945
A_52_P587738	P2ry2	purinergic recepto	Mus musculus purir	1.195637072	10.79148861
A_55_P2380428	5430416G10Rik	RIKEN cDNA 5430<	Mus musculus 6 day	1.190354222	6.615967993
A_66_P122158	Pisd-ps3	phosphatidylserine	Mus musculus phos	1.175927068	9.074216706
A_52_P592909	Dgat2	diacylglycerol O-ac	Mus musculus diacy	1.173956077	10.39327982
A_52_P549977	Fam32a	family with sequer	Mus musculus famil	1.173692938	11.4060602
A_51_P125368	Hars	histidyl-tRNA synth	Mus musculus histic	1.172348692	11.44773653
A_55_P2019054	Acacb	acetyl-Coenzyme A	Mus musculus acety	1.168117595	8.899943125
A_55_P1987196	Gm3448	predicted gene 34	Mus musculus pred	1.167901495	9.058289041
A_55_P1960167	Bcat2	branched chain an	Mus musculus branc	1.149749383	9.932383882
A_51_P480013	Car11	carbonic anhydras	Mus musculus carbo	1.147119938	10.42364956
A_55_P2120866	Gm7120	predicted gene 71	Mus musculus pred	1.137640533	9.945520617
A_51_P418908	Larp1	La ribonucleoprote	Mus musculus La rik	1.137191779	9.48531631
A_55_P1975874	Bcl2l15	BCLl2-like 15	Mus musculus BCLl2	1.121558908	6.994147168
A_51_P286814	Ncor2	nuclear receptor c	Mus musculus nucle	1.109882524	14.09285663
A_55_P2108883	AV356131	expressed sequenc	Mus musculus adult	1.104483644	10.05893668
A_55_P2083213	Purb	purine rich elemer	Mus musculus purir	1.07740577	10.71629864
A_51_P490747	AI593442	expressed sequenc	Mus musculus expre	1.075390771	7.060184729
A_52_P311853	Ddit4l	DNA-damage-indu	Mus musculus DNA-	1.07360728	11.17332195
A_55_P2065059	Wnt2	wingless-related M	Mus musculus wing	1.071997776	6.654513312
A_55_P1998401	Eif2ak4	eukaryotic translat	eukaryotic translati	1.065720732	7.579710465
A_55_P2079158	Fam154b	family with sequer	Mus musculus famil	1.060527374	7.097166998
A_55_P2153941	Zfp386	zinc finger protein	Mus musculus zinc f	1.059050992	10.08765784
A_55_P1974602	Map2k7	mitogen-activated	Mus musculus mito	1.042915394	7.206717795
A_51_P155174	Zfp672	zinc finger protein	Mus musculus zinc f	1.034852851	9.47375292
A_55_P2097156	Ptchd2	patched domain co	Mus musculus patcl	1.034050443	6.365934281
A_52_P295104	Smim5	small integral mem	Mus musculus smal	1.026324687	7.028001519
A_55_P2151138	Dynlt1f	dynein light chain	Mus musculus dyne	1.011748282	15.31604468
A_55_P2201612	Slc30a7	solute carrier fami	Mus musculus solut	1.003319035	6.695524338

A_55_P2109544	Trnt1	tRNA nucleotidyl t	Mus musculus tRNA	1.001272322	8.431184682
A_66_P120770	Ywhaz	tyrosine 3-monoo	Mus musculus tyros	0.997607559	9.774694003
A_55_P1983268	4930444P10Rik	RIKEN cDNA 4930	Mus musculus RIKE	0.994940226	9.194778744
A_51_P191520	Stard10	START domain con	Mus musculus STAR	0.994448253	10.48259345
A_66_P130366	Stk38l	serine/threonine k	Mus musculus serin	0.993625574	7.328617183
A_55_P2293414	1700001C19Rik	RIKEN cDNA 1700	Mus musculus RIKE	0.990165687	7.960315863
A_55_P2018330	Gm13298	predicted gene 13	Mus musculus pred	0.986638051	6.426310477
A_51_P470989	Paip1	polyadenylate bin	Mus musculus polya	0.972419001	10.13248007
A_55_P2127587	Smcr8	Smith-Magenis syr	Mus musculus Smit	0.96794916	6.547066031
A_55_P1972490	Psg16	pregnancy specific	PREDICTED: Mus mu	0.96746518	12.66758381
A_55_P1955483	Grb14	growth factor rece	Mus musculus grow	0.961537973	10.67699007
A_66_P123055	Gm10845	predicted gene 10	Mus musculus pred	0.961441464	12.63602144
A_51_P275496	BC026762	cDNA sequence BC	Mus musculus cDNA	0.956225426	10.39653181
A_52_P682745	Dock4	dedicator of cytoki	Mus musculus dedi	0.953245847	10.42480206
A_52_P20639	Rd3	retinal degenerati	Mus musculus retin	0.952385121	6.56148348
A_51_P494863	Vmac	vimentin-type inte	Mus musculus vime	0.951203788	9.571912151
A_55_P2021094	Tmem181b-ps	transmembrane pr	Mus musculus pred	0.950888888	7.161708914
A_55_P2149382	Gm3448	predicted gene 34	Mus musculus pred	0.949503743	8.596002824
A_55_P2221647	AI605517	expressed sequen	Mus musculus adult	0.946454699	7.987944032
A_55_P1989524	Fndc1	fibronectin type III	Mus musculus fibro	0.939270273	9.499426291
A_51_P159293	Zbbx	zinc finger, B-box	Mus musculus zinc	0.938960672	7.015945354
A_55_P1995924	Gm13157	predicted gene 13	Mus musculus pred	0.936224377	8.820762873
A_51_P452820	Rpl31	ribosomal protein	Mus musculus ribos	0.935299927	9.628451691
A_52_P123738	Rnf41	ring finger protein	Mus musculus ring	0.934464172	9.579431688
A_52_P222230	0	0	Mus musculus adult	0.932941732	10.09808608
A_51_P327564	Glb1	galactosidase, beta	Mus musculus galac	0.930537406	12.02546985
A_51_P422335	Zfp420	zinc finger protein	Mus musculus zinc	0.926862021	7.796718242
A_55_P2146749	Rps13	ribosomal protein	Mus musculus ribos	0.926468304	15.57163982
A_51_P375558	Myoc	myocilin	Mus musculus myo	0.91987638	7.037334081
A_51_P123604	Ppwd1	peptidylprolyl ison	Mus musculus pept	0.918453225	7.857252107
A_55_P1962756	Ttll2	tubulin tyrosine lig	Mus musculus tubu	0.915979939	6.474892893
A_51_P316801	Wdr60	WD repeat domai	Mus musculus WD	0.91300515	9.671748455
A_51_P228193	Ociad1	OCIA domain cont	Mus musculus OCIA	0.902626422	12.05023919
A_55_P1998995	Speg	SPEG complex locu	Mus musculus SPEG	0.890537687	9.842623979
A_52_P489778	Ablim1	actin-binding LIM	Mus musculus actin	0.888374228	10.72166376
A_52_P512553	Atg16l2	autophagy related	Mus musculus auto	0.884566919	10.25934981
A_65_P08864	Dph5	DPH5 homolog (S.	Mus musculus 4 day	0.882305084	6.622110984
A_55_P1985428	Atg16l2	autophagy related	Mus musculus auto	0.878149304	11.34750968
A_52_P325477	Trim16	tripartite motif-co	Mus musculus tripa	0.875770007	7.500056636
A_66_P108434	Ccdc65	coiled-coil domain	Mus musculus coile	0.8752307	6.761612792
A_55_P1970033	Per1	period circadian cl	Mus musculus perio	0.87102614	11.30179325
A_51_P409893	Prkar2a	protein kinase, cA	Mus musculus prote	0.870456096	8.073370053
A_55_P2161465	Gm10516	predicted gene 10	Mus musculus pred	0.869660084	8.602021347
A_55_P2031547	Vmn2r121	vomeronasal 2, re	Mus musculus vom	0.868193142	6.340248683
A_55_P2062133	Etv3	ets variant gene 3	Mus musculus ets v	0.865016273	8.229462351
A_51_P314153	Nr2c2ap	nuclear receptor 2	Mus musculus nucl	0.857212287	10.25241127
A_51_P140607	Asun	asunder, spermat	Mus musculus asun	0.854600958	11.24260127

A_55_P2012694	Kcnh5	potassium voltage-	Mus musculus pota	0.853264496	8.804906186
A_52_P253179	Igfbp3	insulin-like growth	Mus musculus insul	0.843238604	11.69049314
A_55_P1968977	Stk38l	serine/threonine k	Mus musculus serin	0.839143396	9.521077412
A_55_P1982454	Eps8	epidermal growth	Mus musculus epide	0.83854701	8.848665964
A_55_P2000007	LOC102639358	uncharacterized L	PREDICTED: Mus mu	0.837915964	8.84202077
A_51_P481821	Spcs3	signal peptidase c	Mus musculus signa	0.834205312	11.87147738
A_51_P480202	Dlx2	distal-less homeob	Mus musculus dista	0.831967305	8.505777767
A_55_P2062688	Msi1	musashi RNA-bind	Mus musculus musa	0.824555268	7.664091488
A_55_P2023697	Zfp386	zinc finger protein	Mus musculus zinc	0.824299376	11.04881999
A_51_P320022	Atp10a	ATPase, class V, ty	Mus musculus ATPa	0.823382272	9.570566289
A_51_P356579	Mxra7	matrix-remodelling	Mus musculus matr	0.821065949	7.115904662
A_55_P1967514	Dnah7a	dynein, axonemal,	Mus musculus dyne	0.816310076	7.747422009
A_52_P217710	Fzd6	frizzled homolog 6	Mus musculus frizzl	0.813851943	8.487905687
A_55_P2036723	Stk36	serine/threonine k	Mus musculus serin	0.812564111	6.839913205
A_55_P1978226	Park2	Parkinson disease	Mus musculus Parki	0.809691701	9.930960787
A_55_P1999958	0	0	Mus musculus 2 cel	0.805965228	9.252652714
A_66_P112301	C230072F16Rik	RIKEN cDNA C230	PREDICTED: Mus mu	0.80311273	7.553472865
A_51_P244824	Dapp1	dual adaptor for pl	Mus musculus dual	0.802564631	8.572185508
A_55_P1969431	Lyrm5	LYR motif containi	Mus musculus LYR	0.79913581	11.07024261
A_55_P2145521	Stk38l	serine/threonine k	Mus musculus serin	0.798266378	10.21390203
A_55_P2259125	D7Ertd143e	DNA segment, Chr	Mus musculus DNA	0.796972973	7.136638653
A_55_P2206605	5830444B04Rik	RIKEN cDNA 5830	Mus musculus RIKE	0.79643716	6.400644648
A_55_P2151143	Dynlt1c	dynein light chain	Mus musculus dyne	0.795550998	14.87675664
A_51_P333965	Cisd2	CDGSH iron sulfur	Mus musculus CDG	0.792549929	8.447908953
A_52_P456561	Abcd1	ATP-binding casse	Mus musculus ATP-	0.789316322	8.448857429
A_55_P2183735	Pisd	phosphatidylserin	Mus musculus phos	0.785035418	11.98425589
A_52_P565279	Cecr5	cat eye syndrome	Mus musculus cat e	0.784649746	7.912325413
A_51_P448391	Nkiras1	NFKB inhibitor inte	Mus musculus NFK	0.783418591	9.121554978
A_55_P1985693	Fhdc1	FH2 domain conta	Mus musculus FH2	0.782106906	11.3884465
A_51_P269634	Zfp14	zinc finger protein	Mus musculus zinc	0.776997444	8.491684404
A_55_P2033480	Gm13298	predicted gene 13	Mus musculus pred	0.774332816	6.342741632
A_55_P2170509	Yipf4	Yip1 domain famil	Mus musculus Yip1	0.772816822	11.90136956
A_51_P143468	Klhl26	kelch-like 26	Mus musculus kelch	0.77198704	10.29776949
A_52_P436590	Wbscr17	Williams-Beuren s	Mus musculus Willi	0.769558866	12.28938237
A_52_P547589	Spag1	sperm associated	Mus musculus sper	0.769269498	8.242367136
A_55_P1990134	Cox18	cytochrome c oxid	Mus musculus cyto	0.76750367	10.11076173
A_55_P2002226	Dzip1	DAZ interacting pr	Mus musculus DAZ	0.767356331	6.538813239
A_66_P101108	Tnrc18	trinucleotide repe	Mus musculus trinu	0.76600373	11.76838989
A_55_P1987151	Nlrp5	NLR family, pyrin c	Mus musculus NLR	0.762876701	7.174930312
A_55_P1988882	Sept9	septin 9	Mus musculus septi	0.760689134	13.17396197
A_55_P2144280	Nnt	nicotinamide nucl	Mus musculus nicot	0.755399056	6.408132733
A_55_P2255737	0	0	Mus musculus 16 d	0.751739655	7.646039652
A_55_P2045114	Tmem242	transmembrane p	Mus musculus trans	0.746315876	12.40287643
A_55_P2186558	Tmem242	transmembrane p	Mus musculus trans	0.745602274	11.74115813
A_55_P2212498	C030005K06Rik	RIKEN cDNA C030	Mus musculus 16 d	0.744696963	7.496432326
A_55_P2067652	Boc	biregional cell adh	Mus musculus bireg	0.744606754	10.68001093
A_55_P1995992	Gm14432	predicted gene 14	Mus musculus pred	0.734175842	10.19189597

A_51_P263246	Dusp8	dual specificity ph	Mus musculus dual	0.729339237	8.550859775
A_51_P433091	Purb	purine rich elemer	Mus musculus purir	0.729313164	14.36585406
A_52_P106620	Tnfrsf11b	tumor necrosis fac	Mus musculus tumc	0.724063196	9.178956716
A_51_P324934	Mcm3	minichromosome	Mus musculus 2 day	0.723982874	11.08620242
A_51_P193302	Mrps7	mitchondrial ribos	Mus musculus mitcl	0.719882585	10.07382699
A_51_P342707	Pold2	polymerase (DNA	Mus musculus polyr	0.718347678	10.00505646
A_55_P2163729	Tvp23a	trans-golgi networ	Mus musculus trans	0.714329056	10.78639596
A_55_P2085333	Fbxo44	F-box protein 44	Mus musculus F-bo:	0.711686096	8.802084472
A_55_P1967820	AI661453	expressed sequen	Mus musculus expr	0.707301965	7.567482964
A_55_P1980292	Purb	purine rich elemer	Mus musculus purir	0.70306024	12.08650609
A_55_P1964638	Cxadr	coxsackie virus an	Mus musculus coxsa	0.702794142	10.81708985
A_55_P1956918	Adamts5	a disintegrin-like a	Mus musculus a disi	0.701754973	8.144140925
A_55_P2037883	Ino80	INO80 homolog (S	Mus musculus INO8	0.693705043	7.913768321
A_55_P2173927	Insr	insulin receptor	Mus musculus insul	0.691688622	7.865164283
A_51_P487913	2600006K01Rik	RIKEN cDNA 2600	Mus musculus 10 da	0.69118068	7.997964919
A_55_P2028370	0	0	BC009829 Sin3A ass	0.690461183	6.864620982
A_55_P1991851	Speg	SPEG complex locu	Mus musculus SPEG	0.687259254	9.934616638
A_55_P2144285	Nnt	nicotinamide nucl	Mus musculus nicot	0.68724313	12.56592392
A_55_P1955568	Extl2	exostoses (multipl	Mus musculus exos	0.685268426	11.19675553
A_55_P1976993	Strn	striatin, calmoduli	Mus musculus striat	0.680102547	7.201136783
A_55_P2140118	Qpct	glutaminyl-peptide	Mus musculus gluta	0.678864447	8.702572561
A_52_P260696	Arnt2	aryl hydrocarbon r	Mus musculus aryl h	0.677915652	11.15522419
A_55_P2154943	LOC102633020	uncharacterized L	PREDICTED: Mus mu	0.676814658	6.813185302
A_52_P627068	Disp2	dispatched homol	Mus musculus dispa	0.674397108	7.74997714
A_55_P2211937	E130101M22	uncharacterized p	Mus musculus 0 day	0.671839525	7.244348901
A_55_P2045658	Nme6	NME/NM23 nucle	Mus musculus NME	0.671023993	9.369172174
A_55_P2322029	3830406C13Rik	RIKEN cDNA 3830	PREDICTED: Mus mu	0.66786877	6.852701833
A_55_P1979929	Prcp	prolylcarboxypepti	Mus musculus proly	0.66627182	7.089942414
A_52_P646979	D16Ertd472e	DNA segment, Chr	Mus musculus DNA	0.664518727	8.526185962
A_55_P2146500	Ccdc107	coiled-coil domain	coiled-coil domain c	0.664242439	9.312354149
A_51_P127915	Rnasek	ribonuclease, RNa	Mus musculus ribor	0.660400658	11.60556053
A_51_P383629	Vps4a	vacuolar protein s	Mus musculus vacu	0.659040627	8.892115274
A_52_P67200	Stt3b	STT3, subunit of th	Mus musculus STT3	0.65786142	12.59516264
A_55_P2026818	Slc4a7	solute carrier fami	Mus musculus solut	0.65742112	11.80618119
A_55_P1995874	Gm14326	predicted gene 14	Mus musculus pred	0.655155313	9.473693824
A_55_P2122633	Airn	antisense Igf2r RN	Mus musculus 12 da	0.655073738	9.447841546
A_66_P110742	0	0	predicted gene 994	0.652494644	6.927579723
A_51_P414548	Casp7	caspase 7	Mus musculus caspa	0.652297056	9.262799375
A_55_P2035717	Pgap2	post-GPI attachme	Mus musculus post-	0.649830054	11.01902213
A_55_P1974088	Stard6	StAR-related lipid	Mus musculus StAR	0.644654813	7.252685872
A_55_P2044982	Zfp74	zinc finger protein	Mus musculus zinc	0.643862306	8.623261586
A_55_P1974855	Zfp868	zinc finger protein	Mus musculus zinc	0.642298042	9.44786431
A_52_P14526	Zyg11b	zyg-ll family memb	Mus musculus zyg-ll	0.6399025	8.984744753
A_52_P484838	Rfxank	regulatory factor X	Mus musculus regul	0.638156992	10.24113363
A_55_P2161695	Kdelc1	KDEL (Lys-Asp-Glu-	Mus musculus KDEL	0.633604449	8.732323513
A_51_P102507	Vps33a	vacuolar protein s	Mus musculus vacu	0.632936888	10.47605776
A_55_P2000798	Ccdc144b	coiled-coil domain	Mus musculus coile	0.630687382	8.797090317

A_55_P2049095	Atat1	alpha tubulin acety	Mus musculus alpha	0.630435448	9.141766982
A_51_P312748	Oxsm	3-oxoacyl-ACP syn	Mus musculus 3-oxo	0.629777447	9.01476485
A_55_P2035667	Gyk	glycerol kinase	Mus musculus glyce	0.628787466	8.648364662
A_55_P2048483	D17Zt10e	DNA segment, Chr	Mus musculus D17N	0.628777962	6.992196756
A_66_P105736	Net1	neuroepithelial cel	Mus musculus neur	0.6286504	8.454326837
A_52_P244463	D16Ertd472e	DNA segment, Chr	Mus musculus DNA	0.628406852	9.597217161
A_51_P487027	Kcnk2	potassium channe	Mus musculus pota	0.626168174	9.661418919
A_51_P233027	Rmdn3	regulator of micro	Mus musculus regul	0.625932519	8.988246549
A_51_P310676	Galr2	galanin receptor 2	Mus musculus galar	0.622724432	7.162505651
A_51_P119031	Naa30	N(alpha)-acetyltra	Mus musculus N(alp	0.621554593	9.624039204
A_55_P2133220	Arhgef39	Rho guanine nucle	Mus musculus Rho g	0.616734048	8.642150922
A_55_P2028522	Stac	src homology thre	Mus musculus src h	0.616010766	7.041364257
A_51_P253897	Psca	prostate stem cell	Mus musculus prost	0.615881617	6.42562448
A_51_P261560	Tex33	testis expressed 3	Mus musculus testis	0.615386339	7.329209425
A_51_P186798	0	0	Mus musculus adult	0.61322874	9.016423032
A_55_P2030383	Frmd4a	FERM domain cont	Mus musculus FERM	0.612959998	10.90964601
A_55_P2098578	Tubd1	tubulin, delta 1	Mus musculus tubu	0.612758828	8.954822571
A_51_P181722	Rbks	ribokinase	Mus musculus ribok	0.61159276	9.245800439
A_51_P280532	Supt16	suppressor of Ty 1	Mus musculus supp	0.61157395	8.530965999
A_55_P2118891	Zfp882	zinc finger protein	Mus musculus zinc f	0.610913984	8.294079552
A_55_P1989341	Ntng1	netrin G1	Mus musculus netri	0.60958472	8.476360633
A_52_P644534	Dhrsx	dehydrogenase/re	Mus musculus dehy	0.609560651	9.25671223
A_66_P138585	4833419G08Rik	RIKEN cDNA 4833	Mus musculus 0 day	0.607587363	6.595782617
A_55_P1998947	Trim16	tripartite motif-co	Mus musculus tripa	0.604488449	7.155449916
A_51_P234544	Azin1	antizyme inhibitor	Mus musculus antiz	0.602800226	11.96811488
A_52_P1187949	Trim5	tripartite motif-co	tripartite motif-cont	0.599764892	6.187168827
A_51_P367780	Adamtsl2	ADAMTS-like 2	Mus musculus ADAI	0.599729357	7.341050691
A_55_P2146996	Wdr52	WD repeat domair	Mus musculus WD r	0.597251838	7.020264708
A_55_P2173073	Zfp931	zinc finger protein	Mus musculus zinc f	0.595265308	8.866986993
A_51_P283292	Gm14326	predicted gene 14	Mus musculus pred	0.595082261	9.015347234
A_52_P376360	Pdgfc	platelet-derived gr	Mus musculus plate	0.594601426	10.96578443
A_55_P1954436	Gm7967	predicted gene 79	PREDICTED: Mus mu	0.594041539	9.155739992
A_55_P1988424	Tpi1	triosephosphate is	Mus musculus trios	0.593343466	12.72558299
A_65_P02321	Usp36	ubiquitin specific p	Mus musculus ubiqu	0.591697254	7.853283573
A_51_P343851	Tgfbrap1	transforming grow	Mus musculus trans	0.589821522	7.554407441
A_55_P1967538	Hunk	hormonally upregu	Mus musculus horm	0.588246584	11.69706941
A_51_P246727	Mlxip	MLX interacting pr	Mus musculus MLX	0.588227683	8.368515877
A_55_P2187043	Tpm1	tropomyosin 1, alp	Mus musculus tropo	0.585164286	15.06169489
A_51_P454103	Manba	mannosidase, beta	Mus musculus mann	0.584351312	9.614489926
A_52_P494514	Insr	insulin receptor	Mus musculus insul	0.583352015	8.423305987
A_55_P2057994	Mif4gd	MIF4G domain cor	Mus musculus MIF4	0.5807349	11.5472407
A_55_P2007243	Kcnc1	potassium voltage	Mus musculus pota	0.578759804	9.232521563
A_51_P441494	BC100451	cDNA sequence BC	Mus musculus cDNA	0.576549426	7.490033464
A_52_P74576	Ccdc65	coiled-coil domain	Mus musculus coile	0.575074749	7.18473457
A_55_P1993876	Otud7a	OTU domain conta	Mus musculus OTU	0.56755514	6.807269488
A_51_P382928	Cstf3	cleavage stimulati	Mus musculus cleav	0.567207944	11.55214483
A_52_P259558	Ogfod1	2-oxoglutarate an	Mus musculus 2-oxo	0.564501633	8.350975048

A_55_P2037081	2610305D13Rik	RIKEN cDNA 2610	Mus musculus RIKE	0.564272206	6.91795213
A_52_P412529	Fbxo3	F-box protein 3	Mus musculus F-bo	0.56094732	9.33493547
A_51_P403636	Smad7	SMAD family mem	Mus musculus SMA	0.558336877	8.78753881
A_55_P2062469	Col12a1	collagen, type XII,	Mus musculus colla	0.555681636	11.31206825
A_55_P1992715	Igfbp3	insulin-like growth	insulin-like growth f	0.554260468	7.33220213
A_55_P2113356	Miip	migration and inva	Mus musculus migr	0.552280288	8.129275828
A_55_P2060278	Fam45a	family with seque	Mus musculus famil	0.549155306	10.93484853
A_55_P2039556	Pak6	p21 protein (Cdc4	Mus musculus p21	0.547684608	6.8612788
A_51_P308029	2010107G23Rik	RIKEN cDNA 2010	Mus musculus RIKE	0.54748727	9.996108859
A_55_P2034600	Gm5523	glyceraldehyde-3-	Mus musculus pred	0.546447402	9.212421977
A_55_P2241204	1500015A07Rik	RIKEN cDNA 1500	Mus musculus RIKE	0.54219336	8.26476772
A_66_P113662	Tmem62	transmembrane p	Mus musculus trans	0.538267077	9.893821557
A_55_P1985554	B4galt4	UDP-Gal:betaGlcN	Mus musculus UDP-	0.537628446	10.83785546
A_55_P2148641	Rab4a	RAB4A, member R	Mus musculus RAB	0.537243189	9.172580706
A_55_P1996086	Gm14325	predicted gene 14	Mus musculus pred	0.537186059	9.111250799
A_55_P1966958	Mef2d	myocyte enhancer	Mus musculus myo	0.536620471	7.75838435
A_52_P144794	Tceanc2	transcription elon	Mus musculus trans	0.53455295	7.249346109
A_55_P1969166	Fxr2	fragile X mental re	Mus musculus fragil	0.531489988	12.34194972
A_55_P1973447	Ybx2	Y box protein 2	Y box protein 2 [Sou	0.531057305	7.109701064
A_55_P2052563	Id1	inhibitor of DNA bi	Mus musculus inhib	0.53033599	13.47147372
A_55_P2078213	1700020I14Rik	RIKEN cDNA 1700	Mus musculus 11 da	0.530002687	6.877639522
A_52_P110068	Rqcd1	rcd1 (required for	Mus musculus rcd1	0.529942113	8.065464761
A_55_P2147791	Fam129c	family with seque	Mus musculus famil	0.529236236	7.217970946
A_55_P2026109	Rpap1	RNA polymerase II	Mus musculus RNA	0.527509786	11.77046652
A_55_P2354336	0	0	Mus musculus activ	0.526987573	8.20102921
A_66_P125212	Mapk1ip1l	mitogen-activated	Mus musculus mito	0.526302456	11.42316344
A_55_P2076927	Ints10	integrator comple	Mus musculus integ	0.525810261	10.3795043
A_52_P558382	Mapk8	mitogen-activated	Mus musculus mito	0.525327826	6.850921359
A_55_P2030721	Ankle1	ankyrin repeat an	Mus musculus anky	0.525007257	7.995435084
A_52_P505143	Jrk	jerky	Mus musculus jerky	0.522539156	8.542489357
A_51_P144648	Vps13b	vacuolar protein s	Mus musculus vacu	0.519678366	6.7346537
A_55_P2147457	Gm6410	predicted gene 64	PREDICTED: Mus m	0.519481968	6.166119882
A_55_P2013396	Gm14305	predicted gene 14	Mus musculus pred	0.517683154	7.864612391
A_55_P2172566	Insr	insulin receptor	Mus musculus insul	0.515697068	7.323745759
A_52_P137691	Trappc5	trafficking protein	Mus musculus traffi	0.513420389	9.062810254
A_55_P2187038	Tpm1	tropomyosin 1, al	Mus musculus trop	0.51307192	15.71376893
A_52_P662098	Net1	neuroepithelial ce	Mus musculus neur	0.512228233	6.892396013
A_51_P315555	Nars	asparaginyl-tRNA	Mus musculus aspa	0.509016823	10.21166179
A_55_P2144075	Pofut2	protein O-fucosylt	Mus musculus prot	0.506738417	9.580876216
A_65_P17492	Med29	mediator complex	Mus musculus medi	0.506204122	11.08044267
A_51_P213099	Ntng1	netrin G1	Mus musculus 0 day	0.504996564	9.917510525
A_55_P2212259	4930539J05Rik	RIKEN cDNA 4930	Mus musculus RIKE	0.504221596	6.774963856
A_51_P149621	Stt3b	STT3, subunit of th	Mus musculus STT3	0.50217731	10.53780671
A_55_P2047962	Gjc2	gap junction prote	Mus musculus gap j	0.501911712	8.075503933
A_55_P1966863	Mad2l2	MAD2 mitotic arre	Mus musculus MAD	0.497055694	12.22692429
A_52_P6828	Xk	Kell blood group p	Mus musculus Kell	0.49681471	6.75218636
A_55_P2102998	Gm3893	predicted gene 38	Mus musculus pred	0.496695	6.443091727

A_55_P2090152	Vmn2r121	vomeronasal 2, rec	Mus musculus vome	0.496549998	6.426258453
A_55_P2041095	Six4	sine oculis-related	Mus musculus sine	0.496515097	8.936492814
A_51_P282179	Mtor	mechanistic target	Mus musculus mech	0.49615176	9.600335943
A_51_P397375	Pet112	PET112 homolog (S	Mus musculus PET1	0.491822478	10.63703531
A_55_P1953226	Gm14484	predicted gene 144	Mus musculus pred	0.490968565	6.890348424
A_55_P2017140	Vmn2r88	vomeronasal 2, rec	Mus musculus vome	0.489958584	6.596218494
A_55_P2121344	Nudcd3	NudC domain cont	Mus musculus NudC	0.486613312	14.48644209
A_52_P85765	Stard6	StAR-related lipid t	Mus musculus StAR	0.485532131	7.245921317
A_55_P2161958	2410141K09Rik	RIKEN cDNA 24101	Mus musculus RIKE	0.483897201	8.944749485
A_55_P2167160	Hdhd2	haloacid dehaloge	Mus musculus haloa	0.483636246	8.721553593
A_55_P2023818	Cysltr1	cysteinyl leukotrie	Mus musculus cyste	0.482200122	6.913667873
A_55_P2051666	Nfkbib	nuclear factor of k	Mus musculus nucle	0.481825109	6.924766802
A_55_P2154049	Myo18a	myosin XVIIIA	myosin XVIIIA [Sour	0.481029403	9.351451737
A_55_P2121038	Gm10825	predicted gene 108	Mus musculus pred	0.480494615	6.490948216
A_52_P180826	Ndufaf7	NADH dehydrogen	Mus musculus NADI	0.478197332	12.06995123
A_55_P2155479	Eps8	epidermal growth	Mus musculus epide	0.477778391	6.329612776
A_55_P2169775	Ano3	anoctamin 3	PREDICTED: Mus mu	0.477457485	6.133871034
A_55_P2341950	Crebzf	CREB/ATF bZIP tra	Mus musculus CREE	0.477145148	8.496257562
A_55_P2108808	Tubgcp4	tubulin, gamma co	Mus musculus tubu	0.476459195	9.030731709
A_55_P2021099	Tmem181a	transmembrane pr	Mus musculus trans	0.475629474	11.52617749
A_52_P329314	0	0	Mus musculus activ	0.474168018	8.776230772
A_55_P2015715	Rab4a	RAB4A, member R	Mus musculus RAB4	0.472820882	11.89110055
A_55_P2266880	Kirrel	kin of IRRE like (Dr	Mus musculus kin o	0.469979146	11.97410603
A_51_P215190	Efcab11	EF-hand calcium bi	Mus musculus EF-ha	0.468088991	6.530560013
A_51_P517381	Cers2	ceramide synthase	Mus musculus ceran	0.467385174	11.93577959
A_55_P2134645	Fam227a	family with sequer	family with sequenc	0.466809009	6.952928892
A_55_P2115995	Sms	spermine synthase	Mus musculus sperr	0.46670616	10.36200694
A_51_P211341	Eif3j1	eukaryotic translat	Mus musculus euka	0.465694432	10.78643735
A_55_P1998194	Snrpn	small nuclear ribor	Mus musculus smal	0.465682748	9.972197283
A_52_P65494	Iqgap2	IQ motif containin	Mus musculus IQ m	0.465013328	7.800658437
A_52_P404895	Tmem62	transmembrane pr	Mus musculus trans	0.463251515	7.426336173
A_55_P2042146	Fech	ferrochelatase	Mus musculus ferro	0.458340686	12.87623246
A_55_P2081398	0	0	Mus musculus 3 day	0.457982439	6.874884315
A_51_P221132	L2hgdh	L-2-hydroxyglutara	Mus musculus L-2-h	0.457098176	9.207769539
A_55_P1974442	Sumf2	sulfatase modifyin	Mus musculus sulfa	0.456851178	10.3700016
A_55_P2105563	1700104L18Rik	RIKEN cDNA 17001	Mus musculus RIKE	0.454910321	6.389015679
A_51_P257684	Stau1	staufen (RNA bindi	Mus musculus stauf	0.453790437	10.17502422
A_52_P412452	Cntn6	contactin 6	Mus musculus conta	0.452227075	6.28573148
A_55_P2187171	Sv2c	synaptic vesicle gly	Mus musculus syna	0.451273743	6.044621352
A_55_P1961645	Vcp	valosin containing	Mus musculus valos	0.44903777	15.30971961
A_55_P1955172	Camk2d	calcium/calmoduli	Mus musculus 13 da	0.447763023	7.272524621
A_55_P2433218	Bloc1s6	biogenesis of lysos	Mus musculus bioge	0.44500213	11.46295795
A_51_P292368	Tmco6	transmembrane ar	Mus musculus trans	0.444879683	8.843225584
A_55_P2168118	4933406C10Rik	RIKEN cDNA 49334	Mus musculus RIKE	0.444090327	6.470058176
A_55_P2094881	Fgfr2	fibroblast growth f	Mus musculus fibro	0.440891409	9.97808478
A_55_P2326337	BC026513	cDNA sequence BC	Mus musculus cDNA	0.440689436	6.983094672
A_66_P111216	4632427E13Rik	RIKEN cDNA 46324	Mus musculus 13 da	0.438953046	9.873997921

A_55_P1962174	Rab8a	RAB8A, member R	Mus musculus RAB8	0.424137876	10.59066735
A_55_P2018681	G630016G05Rik	RIKEN cDNA G6300	PREDICTED: Mus mu	0.42271889	6.292352942
A_52_P417990	Zfp868	zinc finger protein	Mus musculus zinc f	0.42043698	6.57986675
A_51_P125183	Coq5	coenzyme Q5 hom	Mus musculus coen	0.419476387	8.945056584
A_55_P2261772	Lzts1	leucine zipper, put	leucine zipper, puta	0.419198928	7.577093736
A_55_P2163363	Clec2f	C-type lectin doma	Mus musculus C-typ	0.41913221	6.343168511
A_55_P1998392	Eif2ak4	eukaryotic translat	eukaryotic translati	0.417164393	7.420248711
A_55_P2098305	Coq5	coenzyme Q5 hom	Mus musculus coen	0.416936983	8.769634807
A_55_P2032478	Sfxn5	sideroflexin 5	sideroflexin 5 [Sour	0.416637414	7.721938883
A_55_P2092776	Apoo	apolipoprotein O	Mus musculus apoli	0.415844374	11.68965048
A_55_P2012241	Ctso	cathepsin O	Mus musculus cathe	0.41559322	7.125120729
A_55_P2452384	Mga	MAX gene associat	Mus musculus MAX	0.415243264	8.932685792
A_52_P663526	Nmrk1	nicotinamide ribos	Mus musculus nicot	0.414414455	8.003857616
A_55_P1974063	Gm2545	predicted gene 25	Mus musculus 2 day	0.413708974	6.218528632
A_55_P2050592	Gm5785	predicted gene 57	PREDICTED: Mus mu	0.413684181	8.461838113
A_55_P1970578	Aamdc	adipogenesis asso	Mus musculus adipo	0.411471092	11.92703754
A_52_P299358	Lclat1	lysocardiolipin acy	Mus musculus lysoc	0.409296709	9.949768884
A_55_P2288285	2310007J06Rik	RIKEN cDNA 2310	Mus musculus adult	0.408617418	6.306220274
A_55_P2115968	Gm14325	predicted gene 14	Mus musculus pred	0.406099667	10.10361514
A_51_P336391	Tmem18	transmembrane pr	Mus musculus trans	0.40553698	12.25146122
A_52_P67983	Lcmt2	leucine carboxyl m	Mus musculus leuci	0.405340924	10.26010917
A_51_P114456	Tceanc2	transcription elong	Mus musculus trans	0.404316557	8.001395018
A_55_P1962384	Churc1	churchill domain c	Mus musculus chur	0.40263635	13.35054757
A_55_P2053206	Kdm4c	lysine (K)-specific	Mus musculus lysin	0.402091708	10.49093052
A_55_P1979246	Cep192	centrosomal prote	Mus musculus adult	0.401581925	6.726663181
A_51_P341010	Ercc8	excision repaiross-	Mus musculus excis	0.398522876	9.191087781
A_55_P2388687	1700003G18Rik	RIKEN cDNA 1700	Mus musculus 10 da	0.397935551	6.495699396
A_55_P2043430	0	0	immunoglobulin kap	0.397025619	6.260679891
A_55_P2078675	0	0	Q8BSH3_MOUSE (C	0.394629866	10.55175122
A_55_P2174273	Slco5a1	solute carrier orga	Mus musculus solut	0.394162375	6.254228174
A_52_P147666	Slc30a7	solute carrier fami	Mus musculus solut	0.392889528	8.867834981
A_55_P2085731	Stk38	serine/threonine k	Mus musculus serin	0.392477146	7.244947197
A_55_P2160737	0	0	T cell receptor alpha	0.392156901	6.228406796
A_55_P2170911	Gm10366	predicted gene 10	Mus musculus RCB-	0.391173241	6.982595294
A_52_P425510	Dnah7a	dynein, axonemal,	Mus musculus dyne	0.39117049	6.474571593
A_55_P2104532	Acacb	acetyl-Coenzyme A	Mus musculus acety	0.390395955	6.37202715
A_52_P600946	Ccdc88c	coiled-coil domain	Mus musculus coile	0.389765394	6.700200388
A_55_P1999883	Gm14499	predicted gene 14	Mus musculus pred	0.387386265	6.58660119
A_52_P916539	Zbtb34	zinc finger and BTB	Mus musculus zinc f	0.38576947	7.042352643
A_55_P2045535	Rsg1	REM2 and RAB-like	REM2 and RAB-like	0.383686004	6.568754731
A_55_P1973896	Vmn2r86	vomeronasal 2, re	Mus musculus vome	0.381511625	6.091046043
A_55_P2012107	Vmn2r10	vomeronasal 2, re	Mus musculus vome	0.379830315	6.27031141
A_52_P151905	Gm5132	predicted gene 51	Mus musculus pred	0.379563561	6.283761675
A_55_P2169909	Ostm1	osteopetrosis asso	osteopetrosis assoc	0.378501009	6.99491057
A_55_P2186460	Emx2os	Emx2 opposite stra	Mus musculus Emx2	0.376192058	6.496326483
A_51_P381230	Zhx2	zinc fingers and hc	Mus musculus zinc f	0.375666934	6.692151172
A_55_P2161485	Ptchd2	patched domain c	Mus musculus patch	0.372827738	6.5520809

A_55_P2160910	Faim2	Fas apoptotic inhi	Mus musculus Fas a	0.371593115	6.831524973
A_55_P1986208	Ccnb1ip1	cyclin B1 interacti	Mus musculus cycli	0.369710291	6.103756239
A_52_P622694	Adal	adenosine deamin	Mus musculus aden	0.365872239	7.522421143
A_55_P2293967	Tbc1d5	TBC1 domain fami	Mus musculus TBC1	0.365251988	9.774149604
A_55_P1953984	Gm11033	predicted gene 11	Mus musculus lung	0.36350122	7.161944693
A_66_P130911	Proser2	proline and serine	Mus musculus 15 d	0.362276281	6.964030088
A_52_P88818	Clybl	citrate lyase beta	Mus musculus citra	0.361906265	9.542409873
A_55_P2033481	Gm13298	predicted gene 13	Mus musculus pred	0.361137232	6.680187468
A_66_P122377	Cd84	CD84 antigen	Mus musculus CD8	0.360506202	6.583811787
A_51_P320357	Grin2b	glutamate recepto	Mus musculus gluta	0.360280168	6.359031467
A_52_P504330	Ankib1	ankyrin repeat an	Mus musculus anky	0.360250064	11.36207192
A_51_P394154	Ddx51	DEAD (Asp-Glu-Al	Mus musculus DEA	0.359877757	10.16927723
A_55_P2055642	2810407A14Rik	RIKEN cDNA 2810	PREDICTED: Mus m	0.358951156	6.040017011
A_52_P219913	Cdan1	congenital dyseryt	Mus musculus cong	0.358850754	8.473046024
A_51_P220150	Angptl7	angiopoietin-like 7	Mus musculus angi	0.357228462	6.165392545
A_51_P228865	Zfp72	zinc finger protein	Mus musculus zinc	0.355300342	7.847411318
A_55_P1993094	Mesdc1	mesoderm develo	Mus musculus mes	0.350713908	6.76590339
A_55_P2005853	Nacc2	nucleus accumben	Mus musculus nucl	0.348924514	15.54803706
A_55_P2057247	Etohi1	ethanol induced 1	Mus musculus etha	0.348267114	7.063109429
A_51_P226962	Capn15	calpain 15	Mus musculus calp	0.344518115	6.57454886
A_51_P343429	Slc25a37	solute carrier fami	Mus musculus solut	0.337178716	10.60161225
A_55_P2025363	Ccnl2	cyclin L2	Mus musculus cycli	0.334404589	9.599327514
A_55_P2002918	Klc2	kinesin light chain	Mus musculus kine	0.328100484	11.33603232
A_55_P1977649	Hoxd8	homeobox D8	Mus musculus hom	0.328027082	6.093584714
A_55_P2031382	Crebzf	CREB/ATF bZIP tra	Mus musculus CRE	0.327529398	10.64772186
A_55_P2124016	Nipsnap1	4-nitrophenylphos	Mus musculus 4-nit	0.327066316	11.36759244
A_55_P2057268	Magi1	membrane associ	Mus musculus mem	0.32681088	12.32067837
A_55_P2139713	Phf13	PHD finger protein	Mus musculus PHD	0.325865291	7.367699171
A_65_P10433	Rpp14	ribonuclease P 14	Mus musculus ribo	0.321284724	9.956294104
A_55_P2005680	Ipo11	importin 11	Mus musculus imp	0.319029262	12.22021613
A_55_P2134351	Lancl3	LanC lantibiotic sy	Mus musculus LanC	0.318940372	6.245579756
A_66_P122053	Kcnq5	potassium voltage	Mus musculus pota	0.312625093	6.374769691
A_55_P2002220	Dzip1	DAZ interacting p	Mus musculus mRN	0.310498076	7.108950154
A_55_P1956687	Rab37	RAB37, member R	Mus musculus RAB	0.308690405	6.946824503
A_52_P221588	Gm5382	predicted gene 53	Mus musculus pred	0.30857958	6.411918635
A_55_P2062787	Mfap3	microfibrillar-asso	Mus musculus micr	0.308502076	11.29521395
A_55_P2094484	Gm14137	predicted gene 14	Mus musculus pred	0.307841674	6.249040867
A_52_P18765	Hsbp1l1	heat shock factor	Mus musculus heat	0.305411046	6.175418302
A_55_P1983999	Desi1	desumoylating iso	Mus musculus desu	0.305050921	9.223225353
A_51_P495581	Tlr1	toll-like receptor 1	Mus musculus toll-l	0.304755981	6.483885608
A_55_P2197134	A930018M24Rik	RIKEN cDNA A930	Mus musculus adul	0.303146333	6.14613498
A_52_P146403	Arhgef38	Rho guanine nucle	Mus musculus Rho	0.297713631	6.022117917
A_55_P2066219	Gm3455	predicted gene 34	Mus musculus adul	0.292306122	6.846252621
A_51_P390775	Ube2e1	ubiquitin-conjugat	Mus musculus ubiq	0.288261272	12.4664347
A_51_P494006	Scaf8	SR-related CTD-as	Mus musculus SR-r	0.287834928	11.40734343
A_51_P243134	Adcy6	adenylate cyclase	Mus musculus aden	0.286563466	10.60793854
A_55_P1955851	AI593442	expressed sequen	Mus musculus expr	0.285949357	6.264288781

A_55_P2024555	Ppap2a	phosphatidic acid	Mus musculus phos	0.28340742	12.70854687
A_55_P2108868	Nufip1	nuclear fragile X m	Mus musculus nucle	0.28340483	8.406819665
A_51_P375693	Tmem135	transmembrane pı	Mus musculus trans	0.282838866	10.08696021
A_55_P1982494	1700012L04Rik	RIKEN cDNA 1700(	Mus musculus RIKEI	0.280394525	6.499018685
A_51_P129100	Sec63	SEC63-like (S. cere	Mus musculus SEC6	0.279371698	9.600818144
A_55_P2003228	Rerg	RAS-like, estrogen-	Mus musculus RAS-	0.278174735	6.186459568
A_55_P2060722	Uso1	USO1 vesicle docki	Mus musculus USO1	0.27386441	11.79810942
A_55_P2052210	Gdi2	guanosine diphosp	Mus musculus guan	0.268127974	15.07008493
A_55_P1970887	Vmn2r16	vomeronasal 2, re	Mus musculus vom	0.267919866	5.980558817
A_65_P10180	Rad23b	RAD23b homolog (	Mus musculus RAD2	0.266502634	11.43165245
A_55_P2049483	0	0	UI-M-GI0-cek-h-17-(	0.265694877	5.93789424
A_52_P328078	Atp5b	ATP synthase, H+ t	Mus musculus ATP s	0.26256479	16.25543189
A_55_P2217548	4921515G04Rik	RIKEN cDNA 49215	Mus musculus adult	0.261423553	6.071820881
A_51_P263290	Galnt9	UDP-N-acetyl-alph	Mus musculus UDP-	0.260345438	6.151726529
A_55_P2078815	Xk	Kell blood group p	Mus musculus Kell b	0.254480206	6.21155289
A_55_P2107447	Rab37	RAB37, member R.	Mus musculus RAB3	0.244140291	7.029616615
A_51_P150608	Jagn1	jagunal homolog 1	Mus musculus jagur	0.2368731	13.19987516
A_52_P580582	Nppa	natriuretic peptide	Mus musculus natri	0.227610422	6.588381243

adj.P.Val	Orre-Log_FC	Orre-adj.P.Val
1.5155E-21	0.494015964	0.101276807
4.18232E-23	-0.208741888	0.86222962
2.51609E-15	0.509514034	0.173245869
1.89631E-15	-0.721426483	0.168073428
6.07388E-14	0.706101378	0.198794714
4.55163E-12	-0.645492101	0.561180497
5.66539E-10	0.382869744	0.300412533
2.68489E-12	1.530274252	0.10751908
5.03003E-15	0.607561951	0.180640491
0.011383754	0.708072732	0.095841743
6.99163E-09	0.417157621	0.732697156
1.00373E-08	0.348358531	0.722818593
1.76297E-14	-0.461955973	0.69554264
7.34401E-09	-0.265301426	0.85895072
9.52423E-12	0.132054376	0.806731065
2.51609E-15	-0.319929586	0.487450339
1.26452E-13	-0.30277199	0.776862477
3.81067E-16	0.423154735	0.751201622
1.71376E-13	-0.511838677	0.522961414
1.32742E-15	-0.104540487	0.937077956
8.45076E-09	1.128015324	0.251670799
6.39585E-07	0.393027073	0.583894548
5.0348E-13	-0.042822396	0.97312979
1.87675E-06	-0.077991108	0.910601338
1.62674E-08	0.700674909	0.157310536
9.79076E-06	-0.346039523	0.750752793
0.002006738	0.363396889	0.739710744
1.20027E-10	-0.321280956	0.739926932
9.90908E-05	1.089900036	0.110643562
1.34408E-05	-0.328214025	0.839521089
1.10036E-06	0.437062716	0.598329105
0.00193586	0.689481662	0.092676384
1.9256E-09	0.861615264	0.251034963
4.0172E-06	-0.363493756	0.486203135
1.77247E-14	-0.184267324	0.609527127
3.00086E-06	1.268073293	0.059985475
0.002874148	-1.61715276	0.065441134
1.94892E-09	-0.181696617	0.81968488
0.000172194	-0.157933401	0.719679153
0.000877619	-0.128163665	0.838921279
0.001129742	-0.086616262	0.918491027
2.92927E-08	-0.489734962	0.595972008
3.00086E-06	-1.135394748	0.284746979
6.62656E-06	1.171930897	0.186324197
6.70599E-07	0.056053329	0.955954662

1.13328E-08	-0.113275734	0.894025902
7.54693E-07	-0.227365388	0.707333422
3.00779E-07	-0.088017319	0.938485136
0.000151278	-0.100899014	0.849011492
3.2388E-06	-0.349722197	0.719898927
6.28876E-05	-0.664151751	0.338510783
0.001641709	0.742797052	0.080935733
4.49879E-06	-0.135059276	0.882935769
1.0619E-08	-0.169947384	0.892526632
1.65847E-12	-0.307697854	0.641328681
3.32214E-07	-0.424691967	0.444760948
0.001489104	-1.157946462	0.330185942
8.45947E-07	0.845414186	0.365791074
0.000101522	0.707672554	0.168664396
3.57358E-09	0.553731131	0.647569617
1.34579E-06	-0.320991989	0.516380365
2.60497E-08	0.213144118	0.725963984
1.9256E-09	-0.204806123	0.573717182
5.21515E-09	-0.481573263	0.072468507
0.000396451	-0.127132138	0.878705558
1.14267E-07	-0.845345713	0.302189147
0.011911037	-0.436640002	0.425322426
6.61822E-08	0.12927286	0.907153397
2.33153E-08	0.28379144	0.580809949
0.002800997	-0.145749407	0.784052969
4.13642E-05	0.226120011	0.69554264
0.000407261	0.086866091	0.887775569
0.001686638	-0.63980779	0.082399826
0.000808174	-0.121826605	0.820857056
8.79673E-09	-0.536393529	0.698553736
0.000189232	-0.175484885	0.809427246
2.63238E-05	-0.013684635	0.992257293
6.28876E-05	0.029962335	0.948802911
1.11737E-05	0.22137264	0.824760267
0.016323043	0.470246434	0.601138648
2.84266E-07	-0.067080822	0.964389247
9.61673E-06	-0.339238132	0.790694488
5.55739E-06	0.059781564	0.975871464
1.9168E-05	-0.013439338	0.990510763
0.000427139	0.447834803	0.738308088
1.43E-09	0.000976591	0.999393864
2.43926E-06	-0.680573205	0.1180523
9.88697E-06	-0.519690316	0.070583758
2.75871E-10	-1.035950628	0.39089491
0.013270961	1.792970376	0.152119333
8.16187E-07	0.536623925	0.067094894
1.0803E-06	-0.402527074	0.714474121

9.10813E-08	-0.0884533	0.944831525
0.017215445	0.214479384	0.728038356
0.000426641	-0.350065867	0.568731758
0.000396451	0.350261399	0.700220974
5.39858E-08	-0.000770162	0.999311806
0.002746233	0.518897284	0.531876039
5.32555E-10	-0.523888849	0.455688565
2.66649E-05	-0.082641617	0.901318559
2.33153E-08	-0.067664713	0.944831525
0.003856341	-0.311484797	0.644089282
0.032023049	0.801679878	0.272374934
9.25444E-05	-0.533474707	0.197890713
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0.03373804	0.269081489	0.636054626
0.037622926	1.104599641	0.167841309
0.029406977	-0.07133184	0.926678896
0.022126019	0.019095725	0.972308321
0.025922503	-0.183055671	0.804321056
0.014394077	-0.042228316	0.957896512
0.045460992	0.38651112	0.77894764
0.04557964	-0.193157067	0.588569274
0.004203953	-0.67525574	0.478371423
0.048646043	0.908993348	0.074897277
0.04557964	0.362902411	0.499762677
0.03366818	-0.031770126	0.969956952
0.04580648	-0.534179197	0.10751908
0.021502423	-0.306600745	0.961860984

ProbeName	GeneSymbol	GeneName	Description	logFC	AveExpr
A_51_P277006	Chst8	carbohydrate (N-a	Mus musculus carb	1.998798403	9.506990359
A_51_P155458	Dok7	docking protein 7	docking protein 7 [S	1.099704047	10.92169511
A_55_P2054350	Fbxo44	F-box protein 44	Mus musculus F-bo	1.094375528	11.4403973
A_55_P2005055	Pepd	peptidase D	Mus musculus pept	0.978903734	14.00742747
A_66_P116461	Mro	maestro	Mus musculus mae	0.919902196	8.853408542
A_51_P502150	Slc9a3r1	solute carrier fami	Mus musculus solut	0.874304136	11.64877569
A_55_P1967539	Hunk	hormonally upreg	Mus musculus horm	0.856801394	12.39458915
A_51_P209183	Cxcl14	chemokine (C-X-C	Mus musculus chem	0.84718745	11.79136499
A_55_P2127258	Dok7	docking protein 7	Mus musculus dock	0.831719821	7.804274362
A_52_P2710	Cml5	camello-like 5	Mus musculus came	0.791982403	6.561499522
A_55_P2049211	Pisd-ps1	phosphatidylserine	Mus musculus phos	0.722973556	12.65183916
A_51_P475228	Armc6	armadillo repeat c	Mus musculus arma	0.679278376	10.62667145
A_55_P1955548	Ezr	ezrin	Mus musculus ezrin	0.656022612	14.14145509
A_55_P1979330	Dapp1	dual adaptor for pl	Mus musculus dual	0.642553318	9.285773136
A_55_P1994062	Emx2os	Emx2 opposite stra	Mus musculus Emx2	0.603575825	6.937128745
A_55_P2054300	Alg8	asparagine-linked	Mus musculus aspa	0.546261365	10.05023853
A_55_P2427685	Agl	amylo-1,6-glucosic	Mus musculus amyl	0.533416528	11.83440315
A_55_P2158866	Nme6	NME/NM23 nucle	Mus musculus NME	0.497635144	11.57278217
A_55_P2181334	6030419C18Rik	RIKEN cDNA 6030	Mus musculus RIKE	0.487781402	7.659255264
A_55_P2133165	Wwc1	WW, C2 and coile	Mus musculus WW,	0.43524986	14.53699509
A_55_P2086983	Atxn2	ataxin 2	Mus musculus ataxi	0.427666332	13.23524556
A_55_P1965674	Alg2	asparagine-linked	Mus musculus aspa	0.3917772	12.77511628
A_51_P473953	Arhgef26	Rho guanine nucle	Mus musculus Rho	0.348289958	12.24174198
A_55_P2022434	Gpi1	glucose phosphate	Mus musculus gluc	0.336512554	16.14117805
A_55_P2030433	Gpi1	glucose phosphate	Mus musculus gluc	0.331171618	15.58858241
A_55_P2061809	Ndufc2	NADH dehydrogen	Mus musculus NAD	0.267545274	14.98538925
A_51_P342669	Pgam1	phosphoglycerate	Mus musculus phos	0.26250287	15.53968412

adj.P.Val	Orre-Log_FC	Orre-adj.P.Val
0.000527398	-1.020809588	0.001347252
0.007527662	-1.84709202	0.009582176
3.56729E-05	-1.227709635	0.015712097
1.69542E-06	-0.729933657	0.028285973
0.001379325	-1.030168616	0.011926881
0.001417212	-1.376082523	0.003271452
5.70527E-07	-0.773139893	0.041430647
0.008896115	-1.724736378	0.001170971
0.017565766	-1.582479166	0.007184006
1.34579E-06	-1.652541234	0.017572167
0.001443363	-0.883124413	0.033965586
0.001789253	-0.676496203	0.045520561
0.001756325	-1.66632014	0.022479083
0.04355309	-0.862129878	0.036372988
0.003464519	-1.089412003	0.004521647
0.001092598	-1.123162944	0.003275647
0.00106005	-0.931225482	0.007552042
0.000808174	-0.481070518	0.049567233
0.031413191	-0.919446508	0.019012689
0.037393167	-1.066002187	0.038947926
0.007459508	-0.812278155	0.035762889
0.023798032	-0.822906418	0.00479841
0.033356178	-1.226972592	0.016222111
0.022431714	-0.53157885	0.025429949
0.03292527	-0.476276205	0.04722026
0.029039158	-0.875073385	0.005907455
0.02976617	-0.761186395	0.006498149

ProbeName	GeneSymbol	GeneName	Description	logFC	AveExpr
A_52_P393314	P2rx7	purinergic receptor	Mus musculus purinerg	-2.566483	9.918835431
A_55_P2091359	Padi2	peptidyl arginine de	Mus musculus peptidy	-1.825425	12.92514476
A_55_P2212603	Apba2	amyloid beta (A4) p	Mus musculus amyloid	-1.686821	9.225208525
A_51_P355427	Timp4	tissue inhibitor of m	Mus musculus tissue ir	-1.339929	9.342884771
A_66_P125862	A930005H10Rik	RIKEN cDNA A9300	Mus musculus RIKEN c	-1.307057	10.74695408
A_51_P337944	Bmp2k	BMP2 inducible kin	Mus musculus BMP2 ir	-1.289259	10.84824895
A_55_P2123683	Chrdl1	chordin-like 1	Mus musculus chordin	-1.06929	9.614315788
A_55_P2044242	Slc13a5	solute carrier famil	Mus musculus solute c	-0.979917	8.652415373
A_51_P474422	Ift27	intraflagellar transp	Mus musculus intraflag	-0.888869	14.3953448
A_55_P1961014	Selenbp1	selenium binding pr	Mus musculus seleniur	-0.846845	10.7388478
A_55_P1953387	Fabp5	fatty acid binding pr	Mus musculus fatty aci	-0.83057	14.93510115
A_51_P331661	Ubiad1	UbiA prenyltransfer	Mus musculus UbiA pr	-0.803178	11.61194832
A_55_P2097178	Idua	iduronidase, alpha-	Mus musculus iduronic	-0.749596	9.374207676
A_55_P2045007	Hrh1	histamine receptor	Mus musculus histamir	-0.709332	7.351788502
A_51_P481159	Cbr3	carbonyl reductase	Mus musculus carbony	-0.692289	12.81832935
A_55_P2075213	Kbtbd11	kelch repeat and BT	Mus musculus kelch re	-0.631394	8.672056845
A_55_P2003541	Nrcam	neuron-glia-CAM-re	Mus musculus neuron-	-0.62582	12.7418749
A_51_P312437	Dhrs7	dehydrogenase/red	Mus musculus dehydro	-0.621441	13.58264256
A_51_P108581	Adrbk2	adrenergic receptor	Mus musculus adrener	-0.593173	9.552982166
A_55_P2018666	Thrsp	thyroid hormone re	Mus musculus thyroid	-0.558281	12.163245
A_55_P1961140	Mettl3	methyltransferase l	Mus musculus methylt	-0.557766	11.63462664
A_66_P104309	Myl2	myosin, light polype	Mus musculus myosin,	-0.539752	7.415807899
A_55_P2063316	Mgll	monoglyceride lipas	Mus musculus monogl	-0.50398	13.43596113
A_55_P1971025	Paqr6	progestin and adipo	Mus musculus progest	-0.501593	9.802427856
A_51_P475628	Paqr6	progestin and adipo	Mus musculus progest	-0.470051	8.884532746
A_55_P2114863	Mgll	monoglyceride lipas	Mus musculus monogl	-0.396421	12.14565961
A_55_P1967648	Flcn	folliculin	Mus musculus folliculir	-0.346075	11.043084

adj.P.Val	Orre-Log_FC	Orre-adj.P.Val
1.55236E-05	-0.660266968	0.010635995
9.79076E-06	-1.027116115	0.028719125
6.98037E-05	-1.163609233	0.013387224
0.032589815	-1.42855087	0.001652405
4.63284E-09	-0.628049827	0.035295834
1.04732E-05	-0.9738674	0.022042658
0.04580648	-1.20652802	0.031366614
0.005110931	-1.80202445	0.000760241
6.05153E-06	-1.29464124	0.000998868
0.003924362	-1.208689375	0.003292044
8.32806E-05	-1.712356135	0.000684927
0.00018418	-0.856881408	0.021458953
0.001598833	-0.674001543	0.04663989
4.04131E-05	-1.616890585	0.033268661
0.00382622	-1.874528145	0.000448772
0.031576242	-1.32556604	0.022634684
0.037915449	-1.670179548	0.046244563
0.022276408	-0.997172138	0.002664326
0.004939663	-1.021467372	0.038072462
0.010457288	-1.643213697	0.000637333
0.014038193	-0.672886374	0.015790447
0.01463281	-0.942381393	0.0008304
0.000509247	-1.306765827	0.00174223
0.021096766	-1.10399589	0.012942182
0.026168571	-0.955519771	0.019897063
0.001056578	-1.517268335	0.002863738
0.022807884	-0.708070717	0.028413072

ProbeName	GeneSymbol	GeneName	Description	logFC	AveExpr
A_55_P1966838	Xaf1	XIAP associated fa	Mus musculus XIAP	-6.156879098	9.98739195
A_52_P516409	Col4a6	collagen, type IV,	Mus musculus colla	-4.328433054	11.49218277
A_55_P1966774	Serpina3i	serine (or cysteine	Mus musculus serir	-3.517707117	8.237049671
A_66_P130813	Samd4	sterile alpha moti	Mus musculus steri	-3.381084819	9.712777677
A_52_P303176	1810037I17Rik	RIKEN cDNA 1810	Mus musculus RIKE	-3.218676372	12.76378133
A_55_P2132207	1810037I17Rik	RIKEN cDNA 1810	Mus musculus RIKE	-3.150307147	11.50210939
A_55_P2137527	Fam183b	family with seque	Mus musculus fami	-3.146347755	10.8863997
A_52_P111031	Pcdh17	protocadherin 17	Mus musculus prot	-3.096400623	9.286752712
A_55_P2026420	Pou6f1	POU domain, clas	Mus musculus POU	-3.085193903	8.567395379
A_52_P206492	Pop4	processing of prec	Mus musculus proc	-2.990439512	11.37800517
A_55_P2105944	Olfr224	olfactory receptor	Mus musculus olfac	-2.853577013	8.061203017
A_55_P1952482	Pbp2	phosphatidyletha	Mus musculus phos	-2.708851464	7.72208074
A_51_P462428	Galnt15	UDP-N-acetyl-alp	UDP-N-acetyl-alpha	-2.327912086	10.82348441
A_55_P2026270	Cfi	complement com	Mus musculus com	-2.283011075	7.59612213
A_51_P159453	Serpina3n	serine (or cysteine	Mus musculus serir	-2.257787149	11.293936
A_52_P613498	4833420G17Rik	RIKEN cDNA 4833	Mus musculus RIKE	-2.135137596	11.72763205
A_52_P157450	Abhd1	abhydrolase doma	Mus musculus abhy	-2.028719361	9.154942083
A_51_P297105	Ucp2	uncoupling protei	Mus musculus unco	-2.008925416	9.278059744
A_55_P2074656	Padi2	peptidyl arginine	Mus musculus pept	-1.981559202	13.12004985
A_52_P257812	Lpl	lipoprotein lipase	Mus musculus lipop	-1.966798117	8.512458682
A_52_P597775	Gprc5a	G protein-couplec	Mus musculus G pr	-1.882880186	10.6940361
A_55_P2045642	Stmn4	stathmin-like 4	Mus musculus stath	-1.765390964	9.267843384
A_66_P108247	Ucp3	uncoupling protei	Mus musculus unco	-1.732205788	8.742824015
A_55_P2176792	Sh3gl3	SH3-domain GRB2	Mus musculus SH3-	-1.728042937	9.346406711
A_66_P105175	Bche	butyrylcholinester	Mus musculus buty	-1.719959388	10.67728495
A_51_P128667	Lynx1	Ly6/neurotoxin 1	Mus musculus Ly6/	-1.71821413	11.50331263
A_51_P194249	Stmn4	stathmin-like 4	Mus musculus stath	-1.693097435	9.25076796
A_55_P1953972	Pdhb	pyruvate dehydro	Mus musculus pyru	-1.683490724	12.85410198
A_55_P2315012	4930458D05Rik	RIKEN cDNA 4930	Mus musculus adul	-1.6590401	7.042019248
A_55_P1968276	Tomm22	translocase of out	Mus musculus trans	-1.623250362	12.76321099
A_55_P2004179	Col2a1	collagen, type II, a	Mus musculus colla	-1.60138222	10.26377656
A_55_P2162344	Lrsam1	leucine rich repea	Mus musculus leuci	-1.595495677	11.18370501
A_51_P458778	Hpgd	hydroxyprostaglar	Mus musculus hydr	-1.568266039	7.811720919
A_55_P2014304	Kank1	KN motif and anky	Mus musculus KN m	-1.562962584	11.84753693
A_52_P165773	Prmt8	protein arginine N	Mus musculus prot	-1.54223841	7.044327945
A_55_P2093774	Chl1	cell adhesion mol	Mus musculus cell a	-1.534507736	10.44255926
A_55_P2140212	0	0	Q3J0L9_RHOS4 (Q3	-1.53256524	11.03368948
A_55_P2040600	Exd1	exonuclease 3'-5'	Mus musculus exon	-1.525678034	8.520248792
A_55_P2106525	Nmnat3	nicotinamide nucl	Mus musculus nico	-1.491097654	8.464035327
A_55_P2058791	4833420G17Rik	RIKEN cDNA 4833	Mus musculus RIKE	-1.485576479	8.419571885
A_52_P257625	Esm1	endothelial cell-sp	Mus musculus endo	-1.476230322	7.936182419
A_55_P2033425	Grm5	glutamate recept	Mus musculus gluta	-1.445020115	7.754319196
A_55_P2010936	Fbxo17	F-box protein 17	Mus musculus F-bo	-1.431784462	9.098136864
A_55_P2148534	Nr1d2	nuclear receptor s	Mus musculus nucl	-1.418944898	9.618498483
A_51_P129149	Gatad2a	GATA zinc finger c	Mus musculus GAT	-1.417803996	10.06687358

A_51_P497100	Lgals4	lectin, galactose b	Mus musculus lect	-1.394429143	9.083050324
A_55_P2063256	Lgals4	lectin, galactose b	Mus musculus lect	-1.384406462	9.160897964
A_66_P125035	Duxbl2	doubl homeobox	Mus musculus dou	-1.384107062	8.150682833
A_51_P309854	Kcnn2	potassium interm	Mus musculus pota	-1.382825841	9.054592244
A_51_P360918	Ehd3	EH-domain contai	Mus musculus EH-d	-1.374346569	10.16522609
A_51_P497985	C2	complement com	Mus musculus com	-1.354036194	9.530156157
A_52_P331762	Lmo1	LIM domain only	Mus musculus LIM	-1.330942564	7.548138306
A_55_P2013223	S100z	S100 calcium bind	Mus musculus S10	-1.326491423	6.933102342
A_51_P140690	Stmn3	stathmin-like 3	Mus musculus stat	-1.321998206	9.494028319
A_55_P2213214	A030001D20Rik	RIKEN cDNA A030	PREDICTED: Mus m	-1.312346267	8.010692055
A_55_P2011659	Anapc5	anaphase-promot	Mus musculus ana	-1.310212874	11.35954614
A_55_P1987499	Pttg1	pituitary tumor-tr	Mus musculus pitu	-1.308267592	13.17460908
A_55_P1994339	Dhrs7c	dehydrogenase/r	Mus musculus deh	-1.305209065	6.754466092
A_55_P1976898	Pnp2	purine-nucleoside	Mus musculus puri	-1.301681346	6.985190238
A_52_P650379	Strap	serine/threonine	Mus musculus seri	-1.299661285	10.59363689
A_52_P447196	Col4a6	collagen, type IV,	Mus musculus colla	-1.292810345	8.244840928
A_55_P2007673	Lrsam1	leucine rich repea	Mus musculus leuc	-1.290806296	11.45712366
A_55_P1954724	0	0	Mus musculus adul	-1.287861539	10.32515557
A_55_P2029746	0	0	Mus musculus adul	-1.285958826	11.11618368
A_51_P241210	Lhfpl3	lipoma HMGIC fus	Mus musculus lipo	-1.284340644	8.019613107
A_55_P1967553	Tmem254c	transmembrane p	Mus musculus tran	-1.277819902	12.04771936
A_52_P441294	Chl1	cell adhesion mol	Mus musculus cell	-1.27532299	11.41555856
A_52_P8324	Tmem178	transmembrane p	Mus musculus tran	-1.273076613	7.695362808
A_55_P2027852	Ccl25	chemokine (C-C	Mus musculus che	-1.259566696	7.416547542
A_52_P250555	Dynll1	dynein light chain	Mus musculus dyn	-1.249217853	8.532070831
A_55_P2209258	B430105A11Rik	RIKEN cDNA B430	Mus musculus 4 da	-1.246870514	9.199220507
A_55_P2088720	0	0	Mus musculus adul	-1.241041739	9.778383825
A_55_P2110290	Tmem254a	transmembrane p	Mus musculus tran	-1.240039813	10.20028868
A_51_P506937	Mrps12	mitochondrial rib	Mus musculus mito	-1.237578376	13.28474287
A_55_P2115151	Pxylp1	2-phosphoxylose	Mus musculus 2-ph	-1.232574717	9.952113468
A_55_P1957213	3930401B19Rik	RIKEN cDNA 3930	Mus musculus 13 d	-1.217322024	10.06362884
A_55_P2133205	Nmt2	N-myristoyltransf	Mus musculus N-m	-1.216097007	8.675213006
A_55_P2006035	Galnt15	UDP-N-acetyl-alp	Mus musculus UDP	-1.210849447	7.273377309
A_55_P2154977	Rpap3	RNA polymerase	Mus musculus RNA	-1.208079308	12.74712555
A_55_P2076303	March8	membrane-associ	Mus musculus mem	-1.204814812	12.02120848
A_52_P1042732	Akap5	A kinase (PRKA) a	Mus musculus A ki	-1.204530816	8.904980631
A_52_P48546	Rnf41	ring finger protei	Mus musculus ring	-1.200195931	8.519484927
A_66_P122415	Snhg6	small nucleolar R	Mus musculus smal	-1.186454912	12.55778235
A_55_P1983958	Gm20746	predicted gene, 2	PREDICTED: Mus m	-1.176907362	14.13568133
A_55_P2147280	Myh1	myosin, heavy pol	Mus musculus myo	-1.176209151	8.320743949
A_52_P573255	Cdc42ep1	CDC42 effector pr	Mus musculus CDC	-1.175193414	13.7926044
A_55_P2334927	9.13002E+15	uncharacterized 9	Mus musculus adul	-1.17230089	10.08795111
A_52_P124472	Kcnd2	potassium voltage	Mus musculus pota	-1.161813793	7.390531663
A_55_P2041828	Tubb3	tubulin, beta 3 cla	Mus musculus tubu	-1.154640221	9.179596699
A_55_P2057622	Ocel1	occludin/ELL dom	Mus musculus 2 da	-1.118246162	6.968431276
A_55_P2079116	0	0	Mus musculus cDN	-1.104652911	9.549861633
A_55_P2056557	0	0	Mus musculus 12 d	-1.104080784	7.188119824

A_65_P01834	Lima1	LIM domain and a	Mus musculus LIM	-1.097432887	9.4342313
A_52_P590535	Fbln2	fibulin 2	Mus musculus fibul	-1.093996254	12.94250986
A_55_P2080880	Clcnkb	chloride channel	Mus musculus chlo	-1.093432417	7.365545407
A_52_P574653	Bid	BH3 interacting d	Mus musculus BH3	-1.093040424	9.627188001
A_55_P2090330	Kcnmb4	potassium large c	Mus musculus pota	-1.089176143	9.227035955
A_52_P305230	Igsf21	immunoglobulin s	Mus musculus imm	-1.084637957	7.380111698
A_55_P2059090	Tagap	T cell activation R	Mus musculus T cel	-1.083238495	8.716056759
A_55_P2035424	Hpgd	hydroxyprostaglar	Mus musculus hydr	-1.074317003	7.136480655
A_55_P2016034	Nlrc5	NLR family, CARD	Mus musculus NLR	-1.072914512	7.882077667
A_55_P2073642	1600014C10Rik	RIKEN cDNA 1600	Mus musculus RIKE	-1.066481948	7.714238037
A_52_P481279	Drc1	dynein regulatory	Mus musculus dyne	-1.055443982	13.18253392
A_55_P2018181	A730008H23Rik	RIKEN cDNA A730	Mus musculus RIKE	-1.054299776	7.487791722
A_55_P2048478	Olfml1	olfactomedin-like	Mus musculus olfac	-1.047088892	10.54004959
A_55_P2075313	Zfp619	zinc finger protein	Mus musculus zinc	-1.046286275	7.246426253
A_55_P2155644	2010315B03Rik	RIKEN cDNA 2010	Mus musculus RIKE	-1.043721456	7.702890424
A_55_P2062593	Gm4924	predicted gene 49	Mus musculus inhit	-1.025819062	9.365154479
A_65_P03606	Rpap2	RNA polymerase I	Mus musculus RNA	-1.015013348	7.598731978
A_55_P2067116	Dclre1c	DNA cross-link rep	Mus musculus DNA	-1.012283165	6.842454651
A_51_P417251	6330403K07Rik	RIKEN cDNA 6330	Mus musculus RIKE	-1.011200848	13.89378848
A_55_P2370160	C130009A20Rik	RIKEN cDNA C130	Mus musculus 15 d	-1.010625441	8.214180271
A_55_P2008417	Mnd1	meiotic nuclear di	Mus musculus meic	-1.001459002	9.396695121
A_55_P1973352	0	0	Mus musculus strai	-1.001231056	6.997009656
A_51_P506733	P2rx7	purinergic recepto	Mus musculus purir	-0.99870721	6.940510888
A_52_P400509	Atm	ataxia telangiecta	Mus musculus atax	-0.997462528	8.427413446
A_55_P2048119	Slc29a4	solute carrier fam	Mus musculus solut	-0.992982222	8.686096717
A_55_P1959076	Zfp930	zinc finger protein	Mus musculus zinc	-0.992804216	7.209102318
A_55_P2079619	Rnf43	ring finger protein	Mus musculus ring	-0.980674207	8.064939843
A_55_P2115567	Slc26a1	solute carrier fam	Mus musculus solut	-0.969683986	7.481536136
A_55_P1953087	Mcm3	minichromosome	Mus musculus mini	-0.968129022	11.14341804
A_51_P502437	Cacna2d3	calcium channel, v	Mus musculus calci	-0.962221758	8.022540062
A_55_P2105321	Acin1	apoptotic chroma	Mus musculus apop	-0.95576469	12.63445814
A_55_P1953920	Me3	malic enzyme 3, N	Mus musculus mali	-0.953796608	12.11485534
A_52_P630867	Abcc4	ATP-binding casse	Mus musculus ATP-	-0.95071448	9.199235192
A_51_P283968	Adamts18	a disintegrin-like a	Mus musculus a dis	-0.94559252	7.148584453
A_52_P38908	Tmem132b	transmembrane p	Mus musculus trans	-0.943684784	12.32166788
A_51_P446796	Camta1	calmodulin bindin	Mus musculus calm	-0.938806673	8.029084983
A_55_P1953919	Me3	malic enzyme 3, N	Mus musculus mali	-0.938219484	12.78076322
A_55_P2356736	6720483E21Rik	RIKEN cDNA 6720	Mus musculus RIKE	-0.934845512	7.048698444
A_52_P559919	Eif2ak2	eukaryotic transla	Mus musculus euka	-0.932749376	10.38326438
A_55_P2023864	Mfap1a	microfibrillar-asso	Mus musculus micr	-0.929622826	10.59280982
A_51_P477736	4932415M13Rik	RIKEN cDNA 4932	Mus musculus RIKE	-0.927067258	6.697441234
A_55_P1969497	Lynx1	Ly6/neurotoxin 1	Mus musculus Ly6/	-0.91552837	6.878404826
A_52_P563375	Lgals2	lectin, galactose-b	Mus musculus lecti	-0.914295845	8.245668406
A_52_P167535	Efcab12	EF-hand calcium b	Mus musculus EF-h	-0.90932356	10.96212449
A_55_P2055087	Prkar2b	protein kinase, cA	Mus musculus prot	-0.908929989	10.02342185
A_55_P2329298	Gm12758	predicted gene 12	Mus musculus 2 day	-0.908030723	7.239072622
A_51_P282268	Snapc1	small nuclear RNA	Mus musculus smal	-0.902064505	9.180275957

A_51_P517430	Cd1d1	CD1d1 antigen	Mus musculus CD1	-0.895878116	10.1105168
A_55_P1986639	3110070M22Rik	RIKEN cDNA 3110	Mus musculus RIKE	-0.89528171	7.824256532
A_55_P2008722	Gm13157	predicted gene 13	Mus musculus pred	-0.883596352	9.60656173
A_51_P116687	1700010I14Rik	RIKEN cDNA 1700	Mus musculus RIKE	-0.87477972	7.97858127
A_55_P2040371	Rnaset2a	ribonuclease T2A	Mus musculus ribo	-0.869114138	13.71026659
A_51_P147034	Ica1l	islet cell autoanti	Mus musculus islet	-0.868364731	8.69777082
A_55_P2183914	Gm7120	predicted gene 71	Mus musculus pred	-0.864147811	7.927760277
A_55_P2072391	Acp1	acid phosphatase	Mus musculus acid	-0.852700759	8.912448535
A_55_P1963508	Slc13a5	solute carrier fam	Mus musculus solu	-0.850735708	8.000988516
A_52_P529195	Pcdhb4	protocadherin be	Mus musculus prot	-0.849945399	7.043555936
A_51_P134812	Chac1	ChaC, cation trans	Mus musculus Cha	-0.844774071	10.36841888
A_51_P497240	E330013P04Rik	RIKEN cDNA E330	Mus musculus RIKE	-0.844765396	8.72807961
A_55_P2023707	Camta1	calmodulin bindin	Mus musculus calm	-0.835058655	8.292413142
A_65_P01247	Hjurp	Holliday junction	Mus musculus Holli	-0.829270832	7.395492019
A_55_P2095909	Lamtor3	late endosomal/ly	Mus musculus late	-0.827157354	8.550491325
A_52_P650325	Slc35e1	solute carrier fam	Mus musculus solu	-0.82154184	8.104474982
A_52_P116264	Adhfe1	alcohol dehydrog	Mus musculus alco	-0.820653163	8.914064684
A_66_P138584	Mnd1	meiotic nuclear di	Mus musculus mei	-0.815750524	8.886104688
A_55_P2059179	Slc48a1	solute carrier fam	Mus musculus solu	-0.81004159	13.10075273
A_55_P2105220	Hscb	HscB iron-sulfur c	Mus musculus Hsc	-0.807694136	12.28189497
A_55_P1958597	Slc27a3	solute carrier fam	Mus musculus solu	-0.806533897	10.39221354
A_55_P2119892	Erbb4	v-erb-a erythrobl	v-erb-a erythroblas	-0.805175492	7.44387188
A_55_P1998299	Itgb4	integrin beta 4	Mus musculus inte	-0.804716433	8.351358579
A_51_P408989	L3hypdh	L-3-hydroxyprolin	Mus musculus L-3-	-0.797873579	9.429268854
A_51_P348617	2310045N01Rik	RIKEN cDNA 2310	Mus musculus RIKE	-0.796333366	13.13596643
A_55_P2124026	Synj2	synaptojanin 2	Mus musculus syna	-0.791329143	9.277978073
A_51_P273609	Itpka	inositol 1,4,5-tris	Mus musculus inosi	-0.788523626	7.336973459
A_55_P2179834	Gatad2a	GATA zinc finger	Mus musculus GAT	-0.782587668	11.70726936
A_52_P558609	Clec16a	C-type lectin dom	Mus musculus C-ty	-0.774440114	9.135758847
A_55_P2059986	Chst14	carbohydrate (N-	Mus musculus carb	-0.773816524	10.15616747
A_51_P215374	Slc6a17	solute carrier fam	Mus musculus solu	-0.773417223	7.374150143
A_55_P2105362	Tmed5	transmembrane e	Mus musculus tran	-0.771893147	9.178735545
A_55_P2169227	Ccdc184	coiled-coil domai	Mus musculus coile	-0.771250879	6.917791641
A_55_P2099540	H2afj	H2A histone famil	Mus musculus H2A	-0.769429041	9.782121086
A_55_P2121156	LOC102634215	uncharacterized L	PREDICTED: Mus m	-0.766437171	6.673007895
A_55_P2187076	Sncg	synuclein, gamma	Mus musculus synu	-0.76410798	7.636786619
A_55_P2088223	Synpr	synaptoporin	Mus musculus syna	-0.760669861	6.512934163
A_55_P2185950	Bpnt1	bisphosphate 3'-n	Mus musculus bisp	-0.756583454	8.664448436
A_55_P1983959	Ftl1	ferritin light chain	Mus musculus ferri	-0.753556952	15.30605533
A_55_P2185504	Masp2	mannan-binding l	Mus musculus man	-0.753143511	6.990580432
A_55_P1999240	Gm2696	predicted gene 26	Mus musculus pred	-0.750089216	10.2949764
A_55_P2021266	Hpse	heparanase	Mus musculus hepa	-0.747821613	6.970430604
A_55_P2044602	Siah3	seven in absentia	Mus musculus seve	-0.733318565	7.304939267
A_55_P1955726	Ptpn5	protein tyrosine p	Mus musculus prot	-0.726347174	6.546976015
A_51_P254045	Traip	TRAF-interacting	Mus musculus TRA	-0.721879342	9.180452669
A_55_P2157966	Map1a	microtubule-asso	Mus musculus micr	-0.721370838	9.367794738
A_55_P2007771	Catsper2	cation channel, sp	Mus musculus cati	-0.71932791	8.371543358

A_55_P2036813	0	0	histone cluster 3, H	-0.714894858	10.43484322
A_55_P2106150	Cenpk	centromere prote	Mus musculus cent	-0.714021248	10.33973892
A_55_P1975120	Gm10777	predicted gene 10	Mus musculus activ	-0.713805022	9.633629823
A_55_P2115127	Mphosph10	M-phase phospho	Mus musculus M-pl	-0.71194352	7.574959028
A_55_P2096368	LOC102632770	ADP-ribosylation f	PREDICTED: Mus m	-0.710643542	12.49347357
A_51_P451588	Plekhb1	pleckstrin homolo	Mus musculus plec	-0.709050858	14.22405549
A_55_P1979027	Tmem65	transmembrane p	Mus musculus trans	-0.701847616	10.42426536
A_55_P1954092	0	0	BB713741 RIKEN fu	-0.698752868	12.30346033
A_51_P413507	2010109A12Rik	RIKEN cDNA 2010	Mus musculus RIKE	-0.688651928	6.812251
A_55_P2108784	Arhgap22	Rho GTPase activa	Mus musculus Rho	-0.688137356	11.21104891
A_51_P116906	Rapgef3	Rap guanine nucle	Mus musculus Rap	-0.685272422	13.75316692
A_55_P2149951	Prx	periaxin	Mus musculus peria	-0.684956015	10.13531086
A_51_P461108	Osbpl10	oxysterol binding	Mus musculus oxys	-0.682059235	7.962313068
A_55_P2169311	4930515G01Rik	RIKEN cDNA 4930	Mus musculus RIKE	-0.681579817	6.703695122
A_51_P477019	Rnaset2a	ribonuclease T2A	Mus musculus adul	-0.680902955	7.43885386
A_51_P394833	Tshz1	teashirt zinc finge	Mus musculus teas	-0.678681382	10.80255508
A_66_P106611	Gna14	guanine nucleotid	Mus musculus guar	-0.677677589	8.386191975
A_55_P1956812	Fam83g	family with seque	Mus musculus fami	-0.675928149	6.64692581
A_55_P1985410	Reps2	RALBP1 associate	Mus musculus RAL	-0.674603957	8.042257813
A_51_P218953	Zfp536	zinc finger protein	Mus musculus zinc	-0.674028528	10.56982114
A_55_P2060991	BC005764	cDNA sequence B	Mus musculus cDN	-0.66926502	7.535671867
A_51_P431870	Map1s	microtubule-asso	Mus musculus micr	-0.667960126	12.34555259
A_55_P1984690	Ptprr	protein tyrosine p	Mus musculus prot	-0.667881529	6.581299389
A_52_P434306	0	0	Q8NFW1_HUMAN	-0.667355779	9.649754062
A_55_P2031496	Rufy3	RUN and FYVE do	Mus musculus RUN	-0.663256388	10.86869213
A_55_P2111148	Gemin5	gem (nuclear orga	Mus musculus gem	-0.65688668	10.40659555
A_55_P2031692	Gstm6	glutathione S-tran	Mus musculus gluta	-0.655180632	9.210465339
A_52_P348031	Syt9	synaptotagmin IX	Mus musculus syna	-0.654460663	8.327190519
A_51_P327874	Pth1r	parathyroid horm	Mus musculus para	-0.650364411	8.882151868
A_52_P640922	Dcdc2a	doublecortin dom	Mus musculus doub	-0.649492628	7.587100373
A_55_P2045085	Rpl34-ps1	ribosomal protein	Mus musculus ribo	-0.648502424	14.32799093
A_52_P1092823	Irx1	Iroquois related h	Mus musculus Iroq	-0.646761588	7.349592041
A_55_P2108820	Adamts3	a disintegrin-like a	Mus musculus adul	-0.638849777	6.65699864
A_55_P2014100	Gm7120	predicted gene 71	Mus musculus pred	-0.638107189	6.806996401
A_55_P1953103	Nudt7	nudix (nucleoside	Mus musculus nudi	-0.637864703	10.25545194
A_55_P2064257	Dnaic2	dynein, axonemal	Mus musculus dyne	-0.630274633	8.390636213
A_55_P1974487	Atp8b5	ATPase, class I, ty	Mus musculus ATPa	-0.629303175	6.822180076
A_51_P223569	Ddx4	DEAD (Asp-Glu-Al	Mus musculus DEA	-0.62905002	6.622449063
A_66_P131169	LOC100862268	uncharacterized L	Mus musculus unch	-0.628680049	6.69161194
A_52_P338956	Aspg	asparaginase hom	Mus musculus aspa	-0.628241548	10.06611532
A_51_P310164	2810459M11Rik	RIKEN cDNA 2810	Mus musculus RIKE	-0.626909774	11.89244788
A_55_P2028936	5033425G24Rik	RIKEN cDNA 5033	Mus musculus 11 d	-0.625547854	6.890613452
A_55_P2181009	Gpr180	G protein-couple	Mus musculus G pr	-0.624550444	6.798522375
A_55_P2417936	AW125324	expressed sequen	mp78f05.y1 Soares	-0.623425317	7.849930106
A_51_P353392	Cript	cysteine-rich PDZ-	Mus musculus cyste	-0.622867594	10.81794644
A_55_P2000533	Polk	polymerase (DNA	Mus musculus poly	-0.622037502	9.398512501
A_52_P664404	Zfp286	zinc finger protein	Mus musculus zinc	-0.622037367	10.36518427

A_55_P2072656	Ckmt1	creatine kinase,	Mus musculus crea	-0.61884061	11.75980585
A_55_P2137941	Fxyd2	FXYD domain-con	Mus musculus FXY	-0.611672447	8.641529844
A_55_P2143251	Rims3	regulating synapti	regulating synaptic	-0.607351966	8.439466739
A_51_P253732	Il17rd	interleukin 17 rec	Mus musculus inter	-0.607331836	8.923142563
A_55_P2457154	G2e3	G2/M-phase spec	Mus musculus G2/	-0.603883427	9.938832239
A_51_P101573	Klc4	kinesin light chain	Mus musculus kine	-0.601913768	11.14096031
A_55_P2167323	Cort	cortistatin	Mus musculus corti	-0.601224344	7.784270421
A_52_P257686	Rwdd3	RWD domain cont	Mus musculus RWD	-0.599845312	8.583303218
A_66_P111430	2410006H16Rik	RIKEN cDNA 2410	Mus musculus RIKE	-0.598883168	12.43387167
A_55_P1968858	Cadps	Ca2+-dependent	Mus musculus Ca2	-0.594774845	9.341019473
A_52_P67270	4930515G01Rik	RIKEN cDNA 4930	Mus musculus RIKE	-0.593215762	6.518906201
A_55_P1970299	Mttp	microsomal trigly	Mus musculus micr	-0.5865943	8.981610299
A_55_P2061371	Gm15698	transcription elon	Mus musculus pred	-0.584142169	7.129086897
A_55_P2131340	Churc1	churchill domain	Mus musculus chur	-0.583044972	11.95122776
A_51_P421223	Fv1	Friend virus susce	Mus musculus Frie	-0.581308579	6.783421774
A_51_P465273	Mettl17	methyltransferase	Mus musculus metl	-0.579305966	8.739388881
A_52_P367675	Acin1	apoptotic chroma	Mus musculus apo	-0.579116752	9.293635462
A_55_P2019113	Apol7b	apolipoprotein L	Mus musculus apol	-0.572998316	8.668444439
A_55_P1968908	Hypk	huntingtin interac	Mus musculus hunt	-0.572592964	11.62842225
A_51_P151586	Gsg2	germ cell-specific	Mus musculus ger	-0.57106147	8.077335091
A_55_P2084332	Pigp	phosphatidylinosi	Mus musculus pho	-0.569703885	8.212483905
A_55_P1971174	Cd1d2	CD1d2 antigen	Mus musculus CD1	-0.567292844	7.798990811
A_55_P2227580	A130072N09Rik	RIKEN cDNA A130	Mus musculus 16 d	-0.559844118	6.673560482
A_55_P2223282	B130019D13Rik	RIKEN cDNA B130	Mus musculus 9.5	-0.558378263	7.195029296
A_51_P230439	Ppfibp2	PTPRF interacting	Mus musculus PTP	-0.55630513	10.34894026
A_52_P211418	G2e3	G2/M-phase spec	Mus musculus G2/	-0.554271362	7.792367244
A_52_P357055	Ccdc91	coiled-coil domai	Mus musculus coile	-0.553942714	7.770909696
A_55_P1968200	Hjurp	Holliday junction	Mus musculus Holli	-0.55155621	7.033226409
A_55_P2007273	Pole	polymerase (DNA	Mus musculus poly	-0.550291814	10.13382839
A_55_P2137701	Gm13247	predicted gene 13	Mus musculus pred	-0.546813814	7.656052718
A_55_P2000304	Terf1	telomeric repeat	Mus musculus telo	-0.546075343	9.872026358
A_51_P192139	Zfp74	zinc finger protei	Mus musculus ES ce	-0.539117791	6.409237197
A_66_P128445	Bend7	BEN domain conta	BEN domain contai	-0.538424509	7.861391583
A_66_P122699	Cux2	cut-like homeobo	cut-like homeobox	-0.53739685	7.345768936
A_55_P1998872	Slitrk5	SLIT and NTRK-lik	Mus musculus SLIT	-0.535909484	8.610305633
A_52_P71105	Sertad3	SERTA domain co	Mus musculus SER	-0.532389964	9.861783381
A_55_P2008936	Slc2a9	solute carrier fam	Mus musculus solu	-0.532021351	7.214637148
A_51_P116487	Lsm4	LSM4 homolog, U	Mus musculus LSM	-0.530560598	13.57404857
A_55_P2106235	Syngr2	synaptogyrin 2	Mus musculus syna	-0.529964886	13.79897881
A_66_P126415	Gm8013	predicted gene 80	PREDICTED: Mus m	-0.528496734	6.685350041
A_52_P343627	Rbp7	retinol binding pr	Mus musculus retin	-0.528055686	6.853990708
A_51_P437478	Zfp566	zinc finger protei	Mus musculus zinc	-0.525914817	9.49558264
A_55_P2053497	Poli	polymerase (DNA	Mus musculus poly	-0.523897824	11.47795665
A_55_P2097340	Camkv	CaM kinase-like v	Mus musculus CaM	-0.523781288	7.664345723
A_51_P468762	Alkbh6	alkB, alkylation re	Mus musculus alkB	-0.523356552	12.08819889
A_51_P298802	Bfsp2	beaded filament s	Mus musculus bea	-0.522173308	7.956404228
A_55_P2057127	Nim1k	NIM1 serine/thre	Mus musculus NIM	-0.521263457	6.49076766

A_55_P2145139	0	0	predicted gene 106	-0.517379933	6.649375349
A_55_P2143075	Ubc	ubiquitin C	Mus musculus ubiq	-0.515250808	16.61461059
A_51_P240801	Tmem173	transmembrane p	Mus musculus tran	-0.513561067	9.911571688
A_55_P2007919	Akr1c19	aldo-keto reducta	Mus musculus aldo	-0.512737911	6.304006357
A_51_P331827	Slc25a41	solute carrier fam	Mus musculus solu	-0.509338122	6.456710962
A_55_P1975832	1810009N02Rik	RIKEN cDNA 1810	Mus musculus RIKE	-0.506346906	10.81241498
A_55_P1961241	LOC102634598	uncharacterized L	PREDICTED: Mus m	-0.503420231	9.192490397
A_55_P2123831	Thap6	THAP domain con	Mus musculus THA	-0.50292242	9.608058208
A_55_P1968245	Ftl1	ferritin light chain	Mus musculus ferri	-0.502896156	17.27428723
A_55_P2037812	Palmd	palmdelphin	Mus musculus palm	-0.502660256	7.526994087
A_55_P1974233	Dtd2	D-tyrosyl-tRNA de	Mus musculus D-ty	-0.498511647	8.995692324
A_55_P2045096	Hjurp	Holliday junction	Mus musculus Holli	-0.496971605	6.68312203
A_55_P2067513	Slc10a3	solute carrier fam	Mus musculus solu	-0.495867287	10.35448148
A_55_P2021892	Ccdc114	coiled-coil domai	Mus musculus 3 da	-0.495838288	8.738892753
A_51_P382369	Zfp608	zinc finger protei	Mus musculus zinc	-0.493057428	10.15897212
A_55_P2077263	Cenpk	centromere prote	Mus musculus cent	-0.491159912	9.796181967
A_55_P2018847	Crlf2	cytokine receptor	Mus musculus cyto	-0.487538832	12.22311955
A_55_P1991500	Obfc1	oligonucleotide/o	Mus musculus olig	-0.48748131	11.17769638
A_51_P487547	Ccdc91	coiled-coil domai	Mus musculus coile	-0.486825904	11.34420614
A_55_P2032318	4930522L14Rik	RIKEN cDNA 4930	Mus musculus adul	-0.486588132	7.441660797
A_52_P640386	Usp53	ubiquitin specific	Mus musculus ubiq	-0.481768787	7.753841713
A_66_P137383	Ddx55	DEAD (Asp-Glu-Al	Mus musculus DEA	-0.481484634	7.7673737
A_51_P341789	Sugp1	SURP and G patch	Mus musculus SUR	-0.480862132	12.83928633
A_51_P302942	Rasl10a	RAS-like, family 1	Mus musculus RAS-	-0.479764409	7.097069326
A_66_P133993	Gm5093	predicted gene 5	PREDICTED: Mus m	-0.478687639	7.624410673
A_66_P128927	Gm6306	predicted gene 63	PREDICTED: Mus m	-0.473064458	7.780634724
A_55_P1963687	Tsen54	tRNA splicing end	Mus musculus tRN	-0.472348364	12.43909794
A_55_P2049448	Phtf1	putative homeod	Mus musculus puta	-0.467956686	11.76027675
A_55_P2153496	Ppp2r3d	protein phosphat	Mus musculus prot	-0.464874953	7.113971128
A_51_P245546	Synrg	synergin, gamma	Mus musculus syne	-0.463458339	10.42186201
A_55_P1967500	Nell1	NEL-like 1	Mus musculus NEL-	-0.461407325	6.769094052
A_51_P216605	Hbp1	high mobility grou	Mus musculus high	-0.460215485	8.599211577
A_55_P2157902	Igsf10	immunoglobulin s	Mus musculus imm	-0.457935852	8.96305814
A_51_P239286	Bcl2l12	BCL2-like 12 (proli	Mus musculus BCL	-0.45634682	9.648729447
A_55_P2157360	Tagap1	T cell activation G	Mus musculus T cel	-0.456021568	8.846243503
A_55_P2308743	A430106A12Rik	RIKEN cDNA A430	Mus musculus adul	-0.455161398	7.933766962
A_55_P2115225	Fap	fibroblast activati	Mus musculus fibr	-0.452820717	6.722753058
A_52_P327402	Cds1	CDP-diacylglycero	Mus musculus CDP-	-0.451307076	6.871725015
A_55_P2039061	Trim12c	tripartite motif-co	Mus musculus tripa	-0.448747311	8.022101966
A_55_P2051313	Gstk1	glutathione S-tran	Mus musculus gluta	-0.447816462	11.34736659
A_52_P434841	Coa4	cytochrome c oxid	Mus musculus cyto	-0.446903622	9.46071069
A_51_P291682	Tmed4	transmembrane e	Mus musculus tran	-0.443998054	10.73423118
A_55_P2013203	Oxtr	oxytocin receptor	Mus musculus oxyt	-0.442780027	8.023385113
A_55_P2000027	Spink2	serine peptidase i	Mus musculus seri	-0.442537681	6.96804014
A_52_P734742	Lrrc73	leucine rich repea	Mus musculus leuci	-0.442136942	8.936830228
A_55_P2003951	Tmem192	transmembrane p	Mus musculus tran	-0.440106598	12.66518165
A_55_P2032147	Wnt9a	wingless-type MM	Mus musculus wing	-0.439482762	10.92706414

A_55_P1977454	4930570G19Rik	RIKEN cDNA 4930	Mus musculus RIKE	-0.435903908	7.161056162
A_55_P2011692	0	0	Mus musculus 12 d	-0.434179405	8.677359589
A_52_P73559	Gm7241	predicted pseudo	PREDICTED: Mus m	-0.430169066	9.586233165
A_52_P673499	Shmt1	serine hydroxyme	Mus musculus seri	-0.430087668	7.142456297
A_55_P2025514	Pnpla3	patatin-like phosp	Mus musculus pata	-0.428814069	6.700148086
A_51_P122141	Mamstr	MEF2 activating	Mus musculus MEF	-0.427829791	6.52676216
A_55_P2074291	Fbxo6	F-box protein 6	Mus musculus F-bo	-0.425180806	13.84031149
A_52_P448870	Rab26	RAB26, member	Mus musculus RAB	-0.424956589	8.087186472
A_51_P348652	Spast	spastin	Mus musculus spas	-0.424725762	12.20201077
A_55_P1970676	Sh3yl1	Sh3 domain YSC-li	Mus musculus Sh3	-0.424228425	9.598710633
A_55_P2027152	Ssh1	slingshot homolo	Mus musculus sling	-0.422795069	6.834679035
A_55_P2330545	Zfp81	zinc finger protei	zinc finger protein	-0.422072903	8.529420477
A_55_P1981461	5430410E06Rik	RIKEN cDNA 5430	Mus musculus 6 da	-0.420509947	6.602185969
A_55_P2183597	Tbc1d2	TBC1 domain fam	Mus musculus TBC	-0.420158886	10.38577948
A_55_P1974477	Msh3	mutS homolog 3 (	Mus musculus mut	-0.420019862	10.7021489
A_55_P2153797	Prnp	prion protein	Mus musculus prio	-0.416155848	10.31468171
A_51_P372156	4930563E22Rik	RIKEN cDNA 4930	Mus musculus RIKE	-0.411011206	7.679272315
A_55_P2109585	Plekha7	pleckstrin homolo	Mus musculus plec	-0.40841751	10.278925
A_55_P2167898	Nat9	N-acetyltransfera	Mus musculus N-ac	-0.407279096	7.689265574
A_55_P2471798	Snap23	synaptosomal-ass	synaptosomal-asso	-0.407062662	10.13514035
A_52_P179729	Txnl4a	thioredoxin-like 4	Mus musculus thio	-0.406120836	12.55293121
A_52_P595642	Smim7	small integral me	Mus musculus smal	-0.406112892	10.50763342
A_51_P517001	D130040H23Rik	RIKEN cDNA D130	Mus musculus RIKE	-0.400511742	6.338211044
A_52_P409457	Ppcdc	phosphopantothe	Mus musculus phos	-0.398509715	6.177407482
A_55_P2069012	Pidd1	p53 induced deat	leucine-rich and de	-0.397772469	9.97175954
A_52_P108321	Ccdc71	coiled-coil domai	Mus musculus coile	-0.396032959	8.637270977
A_55_P2104572	6330416G13Rik	RIKEN cDNA 6330	Mus musculus RIKE	-0.394704756	8.641996503
A_52_P552589	Map4k1	mitogen-activate	Mus musculus mito	-0.3923582	8.471880485
A_52_P561377	Fam160b1	family with seque	Mus musculus fami	-0.38798432	12.37367207
A_55_P2057941	1700049G17Rik	RIKEN cDNA 1700	Mus musculus RIKE	-0.383331981	7.964018539
A_55_P2088711	Sgsm1	small G protein si	Mus musculus smal	-0.3821107	6.60586313
A_51_P456838	Fbxl21	F-box and leucine	Mus musculus F-bo	-0.379835667	6.874468646
A_51_P167374	Gpatch1	G patch domain c	Mus musculus G pa	-0.37911143	9.9860935
A_55_P1967983	Use1	unconventional S	Mus musculus unc	-0.3789746	13.46950848
A_52_P47781	Slitrk3	SLIT and NTRK-lik	Mus musculus SLIT	-0.376113158	6.396932242
A_55_P2175915	Ccl28	chemokine (C-C m	Mus musculus che	-0.374930748	6.151763833
A_51_P234627	Nubpl	nucleotide bindin	Mus musculus nucl	-0.373125451	10.36569262
A_51_P241943	Sap30l	SAP30-like	Mus musculus SAP	-0.373063734	14.28047258
A_51_P246677	Rec8	REC8 meiotic reco	Mus musculus REC	-0.367071601	8.342925093
A_52_P275678	Gpr135	G protein-couple	Mus musculus G pr	-0.36573505	6.810300528
A_51_P421140	Tubb6	tubulin, beta 6 cla	Mus musculus tubu	-0.364131056	14.78805775
A_51_P268843	Rasip1	Ras interacting pr	Mus musculus Ras i	-0.361460853	6.858814738
A_55_P1956418	Efr3b	EFR3 homolog B (	Mus musculus EFR	-0.360229036	9.792465029
A_51_P184223	Pcdhb7	protocadherin be	Mus musculus prot	-0.356613104	7.918822651
A_52_P117576	Casp3	caspase 3	Mus musculus casp	-0.351742878	8.091329134
A_55_P2044967	Zfp74	zinc finger protei	PREDICTED: Mus m	-0.350202078	6.389182029
A_51_P131025	Ngdn	neuroguidin, EIF4	Mus musculus neur	-0.340262798	13.42970696

A_55_P2067131	Dclre1c	DNA cross-link rep	Mus musculus DNA	-0.338402188	6.315412162
A_55_P2027077	Shc2	SHC (Src homolog	Mus musculus SHC	-0.33820507	7.375840756
A_55_P2026054	Usp37	ubiquitin specific	Mus musculus ubiq	-0.333676116	6.919608859
A_55_P2012096	Bmp8a	bone morphogene	Mus musculus bone	-0.330118616	7.33400305
A_55_P2143499	Pgbd5	piggyBac transpos	Mus musculus pigg	-0.32667779	6.992213644
A_55_P1999829	Thoc7	THO complex 7 hc	Mus musculus THO	-0.324738732	13.25310654
A_51_P244558	Rab3gap2	RAB3 GTPase acti	Mus musculus RAB	-0.320028198	11.01221532
A_55_P2002113	Rpl36	ribosomal protein	Mus musculus ribos	-0.308280506	16.65947439
A_51_P289414	Spg11	spastic paraplegia	Mus musculus spas	-0.306241068	11.47302291
A_52_P133578	Gpr158	G protein-couplec	Mus musculus G pr	-0.302885456	6.416264013
A_66_P130612	2810408A11Rik	RIKEN cDNA 2810	Mus musculus RIKE	-0.30270723	7.686468818
A_51_P208377	Trappc5	trafficking protein	Mus musculus traff	-0.297651608	13.16186953
A_55_P2177233	Abhd5	abhydrolase doma	Mus musculus abhy	-0.276226719	9.274185661
A_55_P1968683	Anks1b	ankyrin repeat an	Mus musculus anky	-0.275841965	6.319708996
A_51_P288505	Tradd	TNFRSF1A-associa	Mus musculus TNF	-0.27415141	11.49981129
A_51_P133747	Ppp1r3e	protein phosphata	Mus musculus prot	-0.272996573	6.29524283
A_51_P476711	Skiv2l2	superkiller viralici	Mus musculus supe	-0.270984564	11.41603014
A_55_P2041372	Gm3693	predicted gene 36	PREDICTED: Mus m	-0.2646902	6.199455621
A_51_P242356	Fam114a2	family with seque	Mus musculus fami	-0.262671874	12.80714837
A_51_P146303	Mvb12a	multivesicular boc	Mus musculus mult	-0.260071046	12.17524294
A_55_P1960621	Gm20764	predicted gene, 2	PREDICTED: Mus m	-0.258454404	15.49930838
A_51_P107433	Mrpl34	mitochondrial ribo	Mus musculus mito	-0.248200928	12.30902572

adj.P.Val	Orre-Log_FC	Orre-adj.P.Val
1.65288E-09	1.142724869	0.160126428
1.68799E-16	1.678279674	0.148286687
0.00111415	0.276521938	0.856285005
3.4835E-12	0.849713018	0.247609338
9.75281E-16	0.065397702	0.920220832
8.73791E-16	0.032101359	0.971052049
4.37739E-06	1.601979349	0.136939403
4.62079E-09	-1.246342593	0.095148351
1.53107E-11	-0.4348927	0.346208983
1.19839E-16	-0.29463285	0.553202296
2.76734E-14	-0.227918918	0.76436986
5.32555E-10	-0.565335125	0.64712269
1.10279E-05	0.963523397	0.221847465
0.00086345	0.372087289	0.620916602
0.022418234	1.275249124	0.081367361
2.19306E-10	-0.399166545	0.510246289
1.9464E-13	-0.671109095	0.1423435
0.003448159	0.710352137	0.080953995
2.85216E-06	-1.037247785	0.050508329
0.000396451	1.606931711	0.058847733
4.87063E-05	0.057324928	0.930977484
0.016968618	0.665876263	0.227829936
0.005579854	0.288125691	0.591016158
1.20027E-10	0.852487476	0.203223242
1.00373E-08	0.87696271	0.228263976
8.90582E-07	0.177948445	0.737984738
0.032298961	0.680503994	0.232991983
1.47938E-09	-0.612991048	0.078478102
1.12499E-07	0.619121571	0.164250851
5.03003E-15	0.191531928	0.600619589
0.030428182	-0.154790328	0.854360891
0.000514259	-0.421653429	0.122025146
0.004381404	0.725679062	0.37780821
8.03792E-08	0.147025135	0.90705714
0.003583798	0.9132766	0.171140015
0.001739455	-0.273496341	0.863827852
6.69066E-07	-0.091756023	0.893142157
3.00086E-06	-1.012174185	0.25474915
4.59997E-05	-0.757915491	0.066325331
1.17782E-08	-0.353650207	0.70042947
0.001772617	-0.112859725	0.962512328
0.029882996	0.594754598	0.427097363
8.79673E-09	-0.265966628	0.529308318
1.10279E-05	-0.675059016	0.223691543
1.11591E-09	0.421854979	0.289475858

0.009286241	-0.295782195	0.686189715
0.011447725	-0.305899627	0.691832878
2.57183E-07	-0.613424673	0.283946905
0.000124631	-1.584282679	0.053011793
1.02537E-05	0.628280133	0.408457847
0.030972985	-0.559354504	0.187239299
0.02720596	-1.230463843	0.186703471
0.004452627	0.051163701	0.969437555
0.026361683	0.545463528	0.417027811
3.1151E-07	-0.364747065	0.56625963
4.60298E-08	0.662787674	0.052881943
8.90883E-09	-0.14863164	0.756692535
0.000380425	0.088500281	0.969964566
2.95281E-10	-0.526342386	0.511302615
2.0813E-07	0.044819377	0.953255298
1.23069E-07	-0.071202692	0.882404727
0.004785393	-0.403521443	0.091993005
1.29869E-07	0.04377789	0.9628957
1.87675E-06	-0.11163067	0.888541003
0.038078984	-0.360765364	0.681260954
9.48239E-05	-0.502842706	0.160623939
0.006661276	-0.528933679	0.707697644
1.24605E-05	0.616650301	0.144912553
0.000338177	-0.570124245	0.474083165
8.64891E-08	0.27076903	0.802552215
6.28876E-05	-0.539482757	0.457925459
0.000177844	-0.083079696	0.925518302
6.73139E-05	-0.346003991	0.778235249
8.02961E-12	-0.265245317	0.354709911
1.13328E-08	0.295428837	0.90816598
1.12499E-07	0.03003259	0.973326255
2.22782E-06	-0.093002614	0.949245873
0.000213749	0.909025335	0.386634945
8.8279E-07	-0.026648062	0.964173244
2.82752E-06	0.416415697	0.24076864
3.56596E-07	0.113710815	0.932303384
0.000235777	0.058359829	0.960840137
2.89973E-05	0.21152987	0.456262298
1.18222E-06	0.347243353	0.287095476
0.028177835	0.107025665	0.960938727
2.33153E-08	-0.14847078	0.866071086
8.83882E-05	-0.725308474	0.385110835
0.001479941	-0.957921963	0.121507432
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0.044450672	-0.832723385	0.174878739
5.25828E-07	-0.878381793	0.330185942

0.002522403	0.849196584	0.11410773
0.034978678	1.066752424	0.061811889
5.16704E-06	0.228183729	0.803256511
0.00045366	0.269147757	0.620916602
0.007902317	0.826185911	0.218557489
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8.1122E-08	0.327987134	0.529096273
0.021399671	0.212515961	0.816645104
0.023855751	1.042514284	0.073196754
9.10813E-08	0.462573009	0.435684592
0.000879567	0.556041176	0.24217521
8.45947E-07	-0.36270771	0.67416452
0.000940356	-1.11932272	0.077538087
7.78121E-07	-0.49529212	0.639877775
1.86279E-07	-0.535744497	0.763800599
2.66078E-06	-0.599168408	0.455341412
1.11113E-06	-0.431074839	0.713563846
1.146E-09	-0.412211363	0.623298435
0.000514259	0.007129223	0.994595766
4.25257E-06	-0.906668501	0.187157373
4.0172E-06	0.868287968	0.462835421
6.43246E-09	-0.045700265	0.957349204
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5.91303E-07	-0.107053089	0.955717495
0.012006226	0.956031506	0.075117433
8.8279E-07	-0.146960514	0.937741007
4.04338E-05	0.494367531	0.707273068
0.001494303	-0.86883404	0.111021145
2.49994E-05	0.315838681	0.299230857
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0.000787448	-0.211887665	0.701618101
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0.00422092	0.687410102	0.348274964
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0.000865869	-0.545100208	0.61634742
0.004072369	0.634433589	0.522202668
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0.000920963	0.427011528	0.662385586
2.07012E-07	0.106961267	0.910425311
1.25841E-05	0.003710877	0.997529424
0.000160711	-0.481064873	0.612373412
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2.68225E-07	-0.294849957	0.42823224
8.09056E-05	0.084060238	0.936683764

0.007663307	-0.799612857	0.087898753
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1.40072E-05	0.671385905	0.358784597
7.34401E-09	-0.185177946	0.994687287
1.70362E-05	-0.153604513	0.658218205
0.020608568	0.523662472	0.164475504
5.3738E-05	-0.269786955	0.886173565
1.27463E-06	0.234373467	0.785625151
0.003962279	-1.658537825	0.174152657
2.1228E-05	-0.785319459	0.333027028
0.002858407	0.696637811	0.215594182
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0.049928301	0.728811047	0.434228048
9.70552E-06	-0.267104034	0.803228826
0.00072474	0.119862456	0.952728519
0.000194832	0.292638801	0.661185095
0.00106562	-0.939166723	0.221631516
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0.004781667	-0.366905188	0.117899055
0.003049657	-0.341114529	0.126943494
0.019104179	0.652007915	0.43452554
0.002510213	-0.751272165	0.336696332
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0.000226702	0.156997633	0.726845359
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5.89518E-05	-0.163584726	0.830946743
4.13642E-05	0.675810424	0.052881943
1.36808E-05	-0.298528624	0.766520964
0.000946017	0.176759778	0.80965285
0.000513175	1.550754844	0.12547417
0.00765806	-0.766589405	0.52212154
0.000477922	-0.20109441	0.859532605
0.000274281	0.202085117	0.716982172
0.003787885	-0.320302848	0.796581787
0.000521962	1.360014488	0.10709461
0.004880303	0.862857734	0.373386265
0.000348616	-0.416912256	0.721126308
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0.001177609	-0.623807483	0.375028914
0.00890242	-0.094315912	0.844975737
0.00772897	1.411452151	0.073164284
2.21618E-05	-0.0299814	0.962982937
0.042698802	-0.845915365	0.362927592
0.006862966	-0.592263973	0.335614812
0.000286965	0.135677751	0.845628431
0.04360833	-0.634643815	0.281681955

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0.003868229	-0.790273395	0.061903151
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0.005884175	-0.000641415	0.999188052
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0.003878745	0.773465828	0.136838677
3.67631E-06	-0.250196249	0.730176352
4.67766E-05	-0.193793319	0.823862712
0.010314396	0.325885265	0.685160061
0.002240467	1.152263142	0.146354644
0.000285574	0.378889794	0.699928626
9.19636E-05	0.510347831	0.523508617
0.042062516	0.080698546	0.943489946
0.029423564	0.934807474	0.191076752
0.000787448	-0.255616985	0.366479729
0.000481993	1.355335776	0.10751908
0.026508362	-0.007114081	0.995331835
0.009390759	-0.758024335	0.315758931
0.00191871	-0.146261428	0.677327414
0.001769598	-0.679286967	0.130688021
0.002858407	-1.358564611	0.470354265
0.017812734	0.99453454	0.288434003
0.034713642	0.086919777	0.920220832
0.002850385	0.66253016	0.674404764
0.045840929	-0.402373451	0.781449844
0.033043056	-1.234861806	0.501844606
0.000260743	-0.280319878	0.575827905
0.045599099	-0.851254047	0.063254458
0.002541053	-0.248993552	0.816984648
0.033835141	-0.336948904	0.788558621
0.00011653	-0.418256406	0.392745892
0.012006226	-1.278191806	0.118739514
0.041100571	1.151585772	0.052723907
0.002510213	-0.848286438	0.257895081
0.002730458	-0.346497835	0.60105635
0.00011653	-0.213543303	0.847281021
0.023007997	0.155785852	0.846495297
0.000674134	-0.041710334	0.95306947
0.002881586	0.619262352	0.543422253
0.000140998	-0.901765436	0.145010359

0.002176214	-0.095271676	0.871431046
0.001991538	0.48159877	0.258961956
0.027324146	-0.369490654	0.624907028
0.007527662	0.342720668	0.663728782
0.020217114	-0.270696356	0.730176271
4.5911E-06	0.090277607	0.850567703
0.000661633	-0.375116071	0.376961844
0.028553269	-0.494162913	0.574010703
0.008685806	0.375827546	0.197666255
0.013601838	0.122358191	0.898443164
0.000323863	-0.116362408	0.860738453
0.001301568	-0.312938927	0.787463434
8.22893E-05	0.170140193	0.921782071
0.003210504	0.259876732	0.438452738
0.000514259	-0.277241027	0.621873235
0.000260743	-0.076770896	0.950362378
0.007172418	-0.075961804	0.917867404
0.006429046	0.031392711	0.980311264
0.015764004	0.363949983	0.320973793
0.012348642	0.14592951	0.876257923
0.037707131	-0.650754337	0.494334927
0.007993662	-0.292873763	0.747474484
0.006859216	-0.219000675	0.89778475
0.000797928	-0.242679997	0.757718301
0.021112606	-0.14289943	0.848697356
0.021637715	-0.154867287	0.944533634
0.019045055	0.602354516	0.427097363
0.015607478	-0.140469787	0.905219448
0.013025023	-0.354096889	0.723642875
0.003090152	-0.139223339	0.877278291
0.001913361	0.213873744	0.724262095
0.004785393	-0.219696937	0.841493976
0.04119468	0.1570334	0.848697356
0.000425856	-0.284125666	0.605869922
0.01653793	-1.194971489	0.084520342
0.022158916	-0.240595816	0.742005943
0.000542704	0.467797447	0.570206141
0.005407874	0.393055825	0.12055488
0.000482925	0.532179195	0.080234718
0.000115359	0.801928198	0.380687411
0.027688077	-0.478976559	0.718152474
0.00626386	-0.517260931	0.123316917
0.019650551	-0.286561287	0.491010741
0.04557964	0.377740907	0.746641381
0.030153144	0.13577772	0.686886526
0.041662717	-0.276054081	0.63577198
0.004162645	-1.005040354	0.166109453

0.017101652	-0.020456264	0.980974266
0.001826457	-0.255143155	0.595695059
0.020615605	-0.068581325	0.903742757
0.014657171	-0.373089331	0.572426694
7.18774E-05	-0.749372736	0.270791925
0.017983828	-0.335332834	0.371033405
0.011985314	-1.050870318	0.168238154
0.005449864	-0.412169954	0.687700428
0.001724246	-0.017363805	0.972308321
0.043349698	0.661116342	0.50677422
0.009341844	0.014145369	0.98851048
0.017101652	-0.312552559	0.700453503
0.003987601	0.417026779	0.162591324
0.003787885	-0.272331501	0.735415385
0.010600787	-0.573014145	0.159828032
0.00945011	0.410455624	0.648321778
0.023855751	0.439018315	0.105716718
0.023806401	0.330493939	0.324324776
0.023431976	0.683448852	0.207046344
0.00616295	-0.155556489	0.913752916
0.006924917	0.29181634	0.759460171
0.048012898	-0.453884017	0.563235386
0.001299081	0.023107602	0.95527923
0.010301701	0.240262954	0.800273179
0.007124108	0.087532184	0.930824187
0.004312655	-0.103611753	0.893460837
0.018497258	-0.068005788	0.88829473
0.015496846	0.152089146	0.869910406
0.003849801	0.346927894	0.795848217
0.024841441	0.217045023	0.471401257
0.013999126	0.626241783	0.379023915
0.049458458	-0.646266334	0.247609338
0.016394025	0.46227378	0.611574175
0.038353074	-0.229113621	0.62171436
0.004382502	0.471411262	0.295336754
0.047627976	-0.436165386	0.472872632
0.020805431	1.08588179	0.258168507
0.033356178	0.95926223	0.181086511
0.03327132	0.531505036	0.497571846
0.001997079	-0.452585095	0.26155099
0.014533428	-0.301472041	0.414746594
0.000645478	-0.105064776	0.889718554
0.031479346	-0.504360067	0.575013211
0.033404783	-0.94966159	0.479502812
0.026533243	-0.438472552	0.446475861
0.03239946	-0.0774077	0.846672512
0.03366818	-0.255451735	0.817224457

0.003868229	-0.705241745	0.135046744
0.010074878	-0.498865268	0.64759635
0.007060905	-0.116108895	0.922009705
0.001081614	-0.058486427	0.965738256
0.046707673	-0.164545305	0.817302191
0.011549849	0.583828781	0.133878139
0.02006507	0.166117733	0.581252142
0.04564252	0.278102326	0.792689996
0.021600942	-0.061664499	0.937846213
0.035885563	-0.12149351	0.906045122
0.024269528	0.200648873	0.851391995
0.019991441	0.056133517	0.969713104
0.038760156	0.266715159	0.66770638
0.024043042	-0.54078503	0.683080867
0.024111685	0.362224632	0.597324086
0.015600748	-0.444145898	0.467954352
0.003617399	-0.081265056	0.911524404
0.042331176	-0.887787865	0.116666958
0.032812416	0.1798536	0.820612819
0.035055714	0.124164769	0.83947853
0.003195338	-0.229052491	0.504847906
0.035347485	-0.060938774	0.925344008
0.007536899	-0.958030843	0.325413539
0.000797786	-0.251777072	0.876023417
0.019045055	-0.106859353	0.931131433
0.005406086	0.420496097	0.386286082
0.032589815	-0.634757534	0.084478031
0.004495245	0.267576995	0.842345222
0.019707684	-0.091015065	0.850282216
0.046812846	-0.568231975	0.588960812
0.045460992	-0.031342498	0.97116895
0.045460992	-0.658086795	0.482355396
0.031561579	-0.369802893	0.43031213
0.011921076	0.29336219	0.286725759
0.012170708	0.594873029	0.540951479
0.01297431	-0.485113822	0.482069252
0.022845522	-0.118484724	0.858829701
0.031178225	-0.327333102	0.250189628
0.007124108	0.457608806	0.53705357
0.04749154	-0.032075555	0.973007929
0.025807202	0.476032164	0.361728506
0.012758369	1.016629561	0.084086573
0.03415496	-0.196870488	0.778859269
0.038841625	-0.501864997	0.523701005
0.023768374	-0.375630633	0.611095514
0.002802275	0.224633837	0.721293011
0.019104179	-0.22046459	0.382713303

0.044338313	-0.573988076	0.478984484
0.040192545	0.052799756	0.947334503
0.044323514	0.035927247	0.973756367
0.011374659	-0.376639788	0.686877497
0.010016526	0.037337733	0.975104936
0.019623357	-0.019798497	0.976504324
0.011549849	-0.08962169	0.878705558
0.020703872	0.34278695	0.14119703
0.007637052	-0.11906947	0.822282608
0.017904759	-0.328768607	0.740603358
0.034189408	-0.147430423	0.926867442
0.006053019	-0.43180461	0.06239882
0.025700496	0.107948939	0.893594985
0.014123041	0.172159431	0.915313614
0.04136958	0.468783765	0.068280016
0.049928301	0.687589264	0.464792247
0.024400901	0.269695413	0.588960812
0.013472871	0.988885315	0.446051422
0.046805456	0.293560558	0.28906354
0.032215926	-0.112124245	0.783414487
0.019807083	0.480621118	0.086088543
0.026179106	-0.45390268	0.134324512

ProbeName	**GeneSymbol**	**GeneName**	**Description**	**logFC**	**AveExpr**
A_51_P259296	Lpl	lipoprotein lipase	Mus musculus lipopr	-1.961023445	10.53863681
A_55_P1978465	H2-Q5	histocompatibility 2	Mus musculus histoc	-1.663988464	9.535892008
A_55_P2096867	Gap43	growth associated p	Mus musculus growt	-1.608736505	10.06212415
A_51_P292357	Rps3a1	ribosomal protein S	Mus musculus riboso	-1.46036708	14.50307495
A_51_P382970	Itga9	integrin alpha 9	Mus musculus integri	-1.351976919	8.757361984
A_55_P2116650	0	0	Mus musculus lung R	-1.10377111	8.828398051
A_55_P1960735	Gdf15	growth differentiati	Mus musculus growt	-1.088687615	10.28319672
A_55_P2106459	Zfhx3	zinc finger homeob	Mus musculus zinc fi	-1.010052712	8.340668201
A_51_P369803	Psmb9	proteasome (proso	Mus musculus protea	-0.963065252	10.67436193
A_55_P2001628	Rps4l	ribosomal protein S	Mus musculus riboso	-0.939220016	12.10141308
A_51_P464308	Gnb4	guanine nucleotide	Mus musculus guani	-0.9391572	8.637065817
A_55_P2052834	Lst1	leukocyte specific tr	Mus musculus leuko	-0.935420349	9.52643648
A_52_P463977	Tmem140	transmembrane pr	Mus musculus transm	-0.919020928	9.96346538
A_55_P2163774	Crip1	cysteine-rich protei	Mus musculus cystei	-0.915395828	12.97283366
A_51_P191782	Olfml3	olfactomedin-like 3	Mus musculus olfact	-0.914211713	8.602884528
A_51_P135340	Panx1	pannexin 1	Mus musculus panne	-0.89971548	10.51056148
A_55_P2000973	Syt15	synaptotagmin XV	Mus musculus synapt	-0.899192384	6.884006593
A_55_P2004960	9130017K11Rik	RIKEN cDNA 913001	Mus musculus 10, 11	-0.852685098	7.532819994
A_52_P489295	Adamts1	a disintegrin-like an	Mus musculus a disin	-0.827379384	12.74595804
A_66_P112024	0	0	predicted gene 6816	-0.70174101	11.68203967
A_51_P414126	Rab19	RAB19, member RA	Mus musculus RAB19	-0.609561157	8.039804732
A_51_P455807	Ehd4	EH-domain containi	Mus musculus EH-do	-0.606539442	11.96303719
A_55_P2035951	Haus8	4HAUS augmin-like	Mus musculus 4HAU	-0.604556892	12.67961674
A_55_P2121846	0	0	ribosomal protein S3	-0.593846476	16.01148154
A_52_P593037	Acsl5	acyl-CoA synthetase	Mus musculus acyl-C	-0.535221942	9.966696844
A_52_P472302	Fxyd6	FXYD domain-conta	Mus musculus FXYD	-0.531319508	15.21101819
A_51_P469968	H2-M3	histocompatibility 2	Mus musculus histoc	-0.519228813	8.643048954
A_51_P105520	Nomo1	nodal modulator 1	Mus musculus nodal	-0.452860024	13.6108246
A_55_P2079009	Slco2b1	solute carrier organ	Mus musculus solute	-0.433713878	6.892808091
A_55_P1992160	Mbp	myelin basic protei	Mus musculus myelin	-0.413993257	6.478592337
A_55_P2056186	Siva1	SIVA1, apoptosis-in	Mus musculus SIVA1,	-0.380111236	12.3637751
A_55_P2058953	Rpl13a	ribosomal protein L	Mus musculus riboso	-0.330979256	15.77584397
A_55_P2041893	Gm6404	predicted gene 640	PREDICTED: Mus mus	-0.31280088	15.50642516
A_55_P2071326	Rpl36	ribosomal protein L	Mus musculus riboso	-0.285050556	15.50237923

adj.P.Val	Orre-Log_FC	Orre-adj.P.Val
0.002138263	2.300310172	0.020588553
0.005659542	1.095400427	0.010853939
0.002286646	1.534549449	0.020310107
1.30E-07	1.159248599	0.022479083
9.24E-09	1.432290312	0.030984266
0.002824029	1.103008775	0.035505379
0.00234358	1.475890823	0.029959263
6.68E-05	1.571058738	0.04406641
0.021316806	1.195568717	0.009768585
0.000466592	0.7724143	0.022479083
0.003570734	1.462830423	0.043323509
0.008269886	0.855486614	0.014706557
0.006768385	1.194912543	0.01368295
0.013328699	1.479869423	0.020679583
0.005752664	1.314593295	0.015213125
0.024043042	0.703522655	0.011848366
7.61E-05	1.206623188	0.042870119
0.002774688	0.863387317	0.010153149
0.002352939	1.18883491	0.028313328
0.015404752	0.843857777	0.009585061
0.007993662	0.975357457	0.021980244
0.032697401	1.880255118	0.001780435
0.011775353	0.850035903	0.023924257
0.01463281	1.09546824	0.001887175
0.011511499	1.283903087	0.006122076
0.04119468	1.031697808	0.026852476
0.008188084	0.786736671	0.027384624
0.017975634	0.690060618	0.005963268
0.01463281	1.097696112	0.023980247
0.00429445	1.146770973	0.004021838
0.010471067	0.943997477	0.013463823
0.008188084	0.85748709	0.002800163
0.028012031	0.758588	0.015596586
0.001807237	0.72597553	0.008348755

Category	**Term**	**Count**	**PValue**	**Genes**
UP_KEYWORDS	Phosphoprotein	282	1.62E-06	RAB3GAP2,
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	248	1.61E-04	RAB3GAP2,
UP_KEYWORDS	Alternative splicing	203	7.76E-09	RAB3GAP2,
UP_SEQ_FEATURE	splice variant	189	1.17E-04	RAB3GAP2,
UP_KEYWORDS	Cytoplasm	178	3.13E-06	RAB3GAP2,
GOTERM_MF_DIRECT	GO:0000166~nucleotide bindi	81	0.006219	GNA14, NA
UP_KEYWORDS	Transport	80	0.001058	KCNC1, SLC
UP_KEYWORDS	Nucleotide-binding	78	2.53E-04	GNA14, NA
GOTERM_BP_DIRECT	GO:0006810~transport	78	0.002528	KCNC1, SLC
UP_KEYWORDS	Transferase	74	3.19E-04	NDUFAF7,
GOTERM_MF_DIRECT	GO:0016740~transferase acti	67	0.002022	STK38, DPH
UP_KEYWORDS	ATP-binding	59	0.002958	STK38, NA
UP_KEYWORDS	Mitochondrion	51	6.38E-04	NDUFAF7,
GOTERM_CC_DIRECT	GO:0042995~cell projection	39	7.83E-04	LZTS1, SSH
UP_KEYWORDS	Cell projection	37	4.93E-04	LZTS1, CRI
GOTERM_CC_DIRECT	GO:0048471~perinuclear regi	35	0.005406	SNCG, YWH
GOTERM_BP_DIRECT	GO:0006915~apoptotic proce	30	0.00565	FGFR2, BID
UP_KEYWORDS	Magnesium	27	0.00652	GNA14, ST
INTERPRO	IPR001909:Krueppel-associat	23	0.001542	ZFP14, ZFP
SMART	SM00349:KRAB	22	0.007798	ZFP14, ZFP
GOTERM_CC_DIRECT	GO:0005929~cilium	18	0.00273	RSG1, RAB
UP_KEYWORDS	Polymorphism	17	4.83E-04	POLK, NLR
UP_KEYWORDS	Microtubule	17	0.005302	MAP1A, M
UP_KEYWORDS	Cilium	14	0.004355	RSG1, RAB
GOTERM_CC_DIRECT	GO:0043197~dendritic spine	13	0.002169	ANKS1B, K
GOTERM_BP_DIRECT	GO:0006914~autophagy	12	0.004471	CLEC16A, C
UP_KEYWORDS	Nucleotidyltransferase	8	0.006925	NMNAT3, T
GOTERM_BP_DIRECT	GO:0010918~positive regulati	4	0.001443	BID, TMEM
INTERPRO	IPR026074:Microtubule assoc	3	0.00251	MAP1S, M

Fold Enrichment	**FDR < 10%**
1.258874304	0.002189798
1.209474637	0.22835511
1.444362564	1.05E-05
1.26870976	0.193801331
1.374326461	0.004233428
1.329545455	9.015407645
1.430952067	1.421628831
1.512105977	0.342463426
1.389752615	4.319319894
1.521294975	0.430194122
1.446407005	3.01979113
1.471883281	3.929882471
1.639085939	0.859654985
1.771367719	1.108038993
1.855620862	0.664640029
1.635633747	7.421532919
1.708589247	9.411594779
1.762151554	8.471744169
2.105922577	2.435743388
1.85439727	9.69841229
2.264975425	3.814035677
2.765794136	0.651727069
2.189587025	6.941046186
2.492366382	5.73475535
2.840571657	3.041949506
2.74336865	7.51980065
3.579263	8.974974792
16.23159785	2.487140808
34.15257048	3.9369346

Category	Term	Count	PValue	Genes
UP_KEYWORDS	Membrane	19	0.008025	9130017K1
GOTERM_CC_DIRECT	GO:0005730~nucleolus	6	0.007182	RPL13A, RP
UP_KEYWORDS	Ribosomal protein	4	0.002175	RPL13A, RP
GOTERM_MF_DIRECT	GO:0003735~structural constituent of ribosome	4	0.00485	RPL13A, RP
UP_KEYWORDS	Ribonucleoprotein	4	0.006979	RPL13A, RP

Fold Enrichment	FDR < 10%
1.654266958	8.508138478
4.670308789	7.376940471
14.89655172	2.373863877
11.01388889	5.012444472
9.818181818	7.437309492

Supplementary table 9. Comparison with young-versus-old mouse dataset

Up-Up UU = 12 ***E***[uu] = 7.2 *p*.v. = 0.0592	**Up-Zero** U0 = 516 ***E***[u0] = 523.4 *p*.v. = 0.0308	**Up-Down** UD = 8 ***E***[ud] = 5.4 *p*.v. = 0.1819
Down-Down DD = 8 ***E***[dd] = 4.6 *p*.v. = 0.0972	**Down-Zero** D0 = 439 ***E***[d0] = 446.3 *p*.v. = 0.0248	**Down-Up** DU = 10 ***E***[du] = 6.1 *p*.v. = 0.0893

Supplementary table 10. Comparison with human AD dataset

Up-Up UU = 1 ***E***[uu] = 1.2 *p*.v. = 0.709	**Up-Zero** U0 = 246 ***E***[u0] = 246.6 *p*.v. = 0.447	**Up-Down** UD = 3 ***E***[ud] = 2.2 *p*.v. = 0.375
Down-Down DD = 3 ***E***[dd] = 2.1 *p*.v. = 0.363	**Down-Zero** D0 = 242 ***E***[d0] = 241.6 *p*.v. = 0.653	**Down-Up** DU = 0 ***E***[du] = 1.2 *p*.v. = 1.000