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

This is a pre print version of the following article:

Original Citation:

Availability:

This version is available <http://hdl.handle.net/2318/1784701> since 2021-04-10T00:34:50Z

Published version:

DOI:10.2174/1567205015666180613113924

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3 **Transcriptional remodeling in primary hippocampal astrocytes from an Alzheimer's disease mouse**
4 **model**
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30 **Running title:** Transcriptome of cultured astrocytes from 3xTg-AD mice.
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32 **Keywords:** whole-genome microarray, 3xTg-AD mice, cultured astroglia, cross-platform normalization,
33 early Alzheimer's disease, FAD mutations.
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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 APP^{swe}/PS1^{dE9} 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 APP^{swe}/PS1^{dE9} 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 ($A\beta$) 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 $A\beta$ 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, $A\beta$ 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 Verkhursky (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 MgSO₄. 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 mm² 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 Biotec, 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 0.5x10⁶ 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 QIAzol (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

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3 Clara, CA). Slides were scanned with an Agilent C dual-laser microarray scanner and images analyzed with
4 Agilent Feature Extraction software. Raw data were normalized through the quantile between-array
5 normalization algorithm and the empirical Bayes method (LIMMA/Bioconductor package) was used to
6 compute a moderated *t*-statistics for two-class comparison analysis [13]. *P*-values were adjusted for multiple
7 testing by using Benjamini-Hochberg (BH) false discovery rate (FDR) correction [14]. Because of the high
8 degree of correlation between the genewise variance and the average expression ($\rho = 0.9$), no intensity
9 filtering procedure was applied to not alter the variance distribution. On the contrary, LIMMA was applied to
10 the whole unfiltered dataset to preserve full statistical power and then the expression values of the genes
11 called as significantly regulated have been checked *a posteriori* [15]. Functional annotation was performed
12 using the DAVID Bioinformatics Resources v. 6.7 (<https://david.ncifcrf.gov/>) [16]. False discovery rate
13 (FDR) correction was applied to overrepresented GO terms and cutoff was set to $p < 0.1$ (10%).
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19 20 **2.4. Real-time PCR**

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22 Validation of the microarray results by real-time PCR was performed on 4 non-Tg and 4 3xTg-AD astroglial
23 cultures. Total RNA extraction was performed as described above. 0.5-1 μ g of total RNA was
24 retrotranscribed using random hexamers and ImProm-II RT system (Promega, Milan, Italy). Real-time PCR
25 was performed using iTaq qPCR master mix according to manufacturer's instructions (Bio-Rad, Segrate,
26 Italy) on a SFX96 Real-time system (Bio-Rad). To normalize raw real-time PCR data, three housekeeping
27 genes were tested: i) β -actin (Actin), ii) S18 ribosomal subunit and iii) polymerase (RNA) II (DNA directed)
28 polypeptide A (RP2a). S18 showed highest stability across the samples and was used for normalization of
29 raw data in all real-time PCR experiments. Sequences of oligonucleotide primers are provided in
30 Supplementary Materials. The real-time PCR data are expressed as delta-C(t) of gene of interest to S18
31 allowing appreciation of the expression level of a single gene.
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38 **2.5. Comparison with the transcriptome database of acutely isolated purified CNS cellular models**

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40 To assess the relationship existing among our astrocyte cultures and the samples belonging to the
41 transcriptome framework of acutely isolated purified central nervous system (CNS) cell types as provided by
42 Cahoy et al. [17], GSE9566 series was downloaded from Gene Expression Omnibus (GEO) database
43 (<https://www.ncbi.nlm.nih.gov/geo/>). It consisted in a transcriptome database made up of 48 independent
44 murine samples measuring the expression levels of more than 20,000 genes. Three main CNS cell types,
45 astrocytes, neurons and oligodendrocytes, are profiled at various postnatal ages, allowing for the
46 identification of those enrichment patterns specifically characterizing each cell type. In particular, for this
47 study, Affymetrix Mouse Genome 430 2.0 Array platform was used, featuring 45,037 oligonucleotide probes
48 (representing 20,832 unique genes) per array. Text matrix file available from GEO database contained \log_2
49 expression values that were already between-array normalized. In order to relate our expression data with
50 those provided by Cahoy and colleagues an "early integration" approach was needed which allowed the data
51 to merge before analysis [18]. To this purpose, the cross-platform normalization (XPN) algorithm was used
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3 as described by Shabalín et al. in [19] to produce a single unified dataset. More in detail, Ensembl BioMart
4 on-line application (<https://www.ensembl.org>) was used to match probes from different platforms (namely
5 Agilent and Affymetrix) and just those 20,932 probes (12,416 unique genes) identified by Cahoy as
6 significantly and consistently expressed in at least one CNS cell type (Supplemental Table S3 in [17]) were
7 used to assemble the common probe-set. This procedure led to a final list of 18,135 cross-platform
8 corresponding probes, representing 11,589 different genes (93.3% of Cahoy's filtering selection). Moreover,
9 only the samples corresponding to one of the groups of interest were retained for XPN procedure and
10 downstream comparison with our dataset, namely acutely isolated P17 astrocytes (n=5), cultured astroglia
11 (n=4) and acutely isolated P16 neurons (n=3). Prior to XPN merging, expression values from each platform
12 were column standardized (zero mean and unitary standard deviation). To reliably evaluate the distance of
13 our samples compared to those from Cahoy's dataset—that includes many different experimental groups—
14 non-Tg \log_2 expression values were separately integrated into Cahoy's dataset through XPN algorithm. This
15 precaution allowed indeed to maximally reduce batch effect and helped to rule out possible confounding
16 factors reflecting the inner structure of the two datasets. Specifically, the common experimental conditions
17 adopted for tissue dissociation and cell culturing were likely to put in contact our two cellular models when
18 clustering samples, thus possibly distorting their individual relation to Cahoy's models. Unsupervised
19 hierarchical clustering for sample positioning assessment was performed using Euclidean metric and average
20 linkage criterion. All dendrograms presented in the text reflect this particular choice even if other different
21 metrics would have led to analogous results from a qualitative point of view (not shown). The analysis then
22 proceeded as described in the Results section, searching for those particular genes that were enriched in (or
23 shared by) non-Tg astrocytes cultures compared to the cellular models of interest present in Cahoy's dataset.
24 All these ranked lists of differentially expressed genes were produced through a two-class unpaired rank
25 product (RP) algorithm [20], conducted on \log_2 expression values as returned by XPN procedure, controlling
26 FDR at 0.005 level as detailed in Results section. Just for the gene list-associated heatmaps, a further
27 gene/row-wise normalization step (log-mean subtraction) was performed in order to represent the expression
28 values of each gene in terms of \log_2 fold-enrichment over their mean value across all samples.
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42 **2.6. Comparison with APPswe/PS1dE9 dataset and normally aged mice**

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44 To compare our microarray dataset with the AD dataset from the APPswe/PS1dE9 double-transgenic mouse
45 model [7], GSE74615 series was downloaded from Gene Expression Omnibus (GEO) database
46 (<https://www.ncbi.nlm.nih.gov/geo/>). It consisted in a text matrix file containing \log_2 intensity values from
47 22 samples of cortical microglia and astrocytes isolated from 15- to 18-month-old AD and wild-type (WT)
48 mice. RNA samples were hybridized onto Mouse GE 4x44k v2 microarrays (Agilent). In particular, each
49 array featured 39,429 different probes, the 1% of which (399 probes) being within-array replicates, for a total
50 of 43,020 probes per array. Downloaded data were already normalized through quantile between-array
51 algorithm. Thanks to the presence of an internal control (WT mice), we could address this comparison
52 avoiding the introduction of additional confounding factors by a “late integration” (or meta-analysis)
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3 approach [18]. A cross-platform normalization between Orre's and our dataset was indeed not suitable being
4 the two studies representative of two different healthy and AD pathological models. Therefore, unlike what
5 we did for integrating our dataset into the transcriptome framework provided by Cahoy and colleagues, in
6 this case the individual microarray studies were separately processed to obtain two lists of differentially
7 expressed genes (ranked on the basis of their p -values) which have been then combined in the final step of
8 the analysis. In particular, for both dataset, differential expression of all genes among groups was tested for
9 significance through an empirical Bayes moderated t -test (LIMMA/Bioconductor package). P -values were
10 adjusted for multiple comparisons by using BH FDR correction and genes featuring an $\text{adj.p.val} \leq 0.05$ were
11 marked as significant. APPswe/PS1dE9 whole dataset was employed for the empirical Bayes test, but
12 replicate probes were finally collapsed by mean and microglia data were discarded to retain only the contrast
13 of interest (AD astrocytes vs. WT astrocytes) for downstream comparison with our dataset (4 samples for
14 AD and 4 samples for WT; 2,578 differentially expressed unique genes out of 39,429 different probes).
15 Sharing the same technological platform (i.e. Agilent), the gene-matching procedure between the two
16 datasets was straightforward. All of our 993 significant genes found a correspondence into the
17 APPswe/PS1dE9 dataset: some of them were co- or anti-regulated genes while others genes resulted
18 significantly regulated only in our model. The analysis of the transcriptome intersections between the two
19 datasets then proceeded as described in the *Results*, while its statistical background is detailed in *Appendix*:
20 *Common significant gene analysis*. To compare the changes in cultured 3xTg-AD astrocytes with those in
21 young-versus-old mice reported by [21], as there is no available original dataset for young mice in GEO
22 database, a list of 926 significantly regulated genes in aged compared to young cortical astrocytes was
23 directly used for comparison (see Supplementary Table 3 in [21]). Official gene symbols were used for gene
24 matching and the whole array (Agilent, Mouse GE 4x44k v2 microarray) has been used as reference for the
25 subsequent analysis. The significance of the transcriptome intersections was assessed through the same
26 approach already mentioned and described in *Appendix*.

2.7. Comparison with human AD dataset

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41 The human AD reference dataset used for comparing our microarray output was made available by Berchtold
42 et al. [22] through the publicly accessible GEO database: series accession number GSE48350. This dataset
43 consisted of 253 samples from 4 brain regions (hippocampus, entorhinal cortex, superior frontal cortex and
44 post-central gyrus), from both normal controls and AD patients. RNA samples were hybridized onto
45 Affymetrix Human HgU133 plus 2.0 microarrays. In particular, each array featured 54,675 different probes
46 and no within-array replicates. Downloaded data were already between-array normalized (GC-Robust Multi-
47 array background adjustment and quantile normalization). Also in this case, thanks to the presence of an
48 internal control (normal non-AD subjects), we could address this comparison between different models
49 through the same "late integration" approach [18] already used for the comparison with APPswe/PS1dE9
50 double-transgenic mouse dataset. Again, individual microarray studies were separately processed to identify
51 two lists of differentially expressed genes (ranked on the base of their p -values) which have been then
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3 combined in the final step. In particular, data from Berchtold's dataset were then \log_2 -transformed and
4 differential expression of all genes among the groups of interest (69- to 99-year-aged control hippocampus,
5 $n=24$; 74- to 95-year-aged AD hippocampus, $n=18$) was tested for significance through an empirical Bayes
6 moderated t -test (LIMMA/Bioconductor package). P -values were adjusted for multiple comparisons by
7 using BH FDR correction and genes with an $\text{adj.p.val} \leq 0.05$ were marked as significant. This procedure led
8 to the identification of 746 differentially expressed genes. Ensembl BioMart on-line application
9 (<https://www.ensembl.org>) was then used to find human-mouse orthologous genes and to match probes from
10 different platforms (Agilent and Affymetrix respectively). A virtual set of 21,213 one-to-one orthologous
11 genes was obtained (96.4% of which featuring a "high human orthology confidence"), but just 495 out of the
12 993 genes that were significant into our murine dataset found an orthologous correspondence within the
13 human dataset provided by Berchtold et al. (329 genes did not featured any human orthology while 169 were
14 not present in Berchtold's dataset). As for the previous comparison with APPswe/PS1dE9 samples, we found
15 co-regulated genes, anti-regulated genes and genes significantly regulated only in our model. The subsequent
16 analysis of the transcriptome intersections between the two datasets is described in the Results section while
17 its statistical background is detailed in the Appendix *Common significant gene analysis*.
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25 26 **2.8. Software used for microarray analysis**

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

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3 shown in Figure 2. Taken together, GO analysis suggests that Ca^{2+} -regulated cell adhesion and cell-cell
4 communication, mitochondria and transcription may be specifically deregulated in 3xTg-AD cultured
5 astrocytes.
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8 **3.3. Comparison with cultured and freshly FACS-isolated astrocytes.**

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10 To our knowledge, there are no published reports on the transcriptional profile of cultured astrocytes from
11 the hippocampus. Therefore, it was interesting to compare the transcriptional profile of our cultured non-Tg
12 astrocytes with that of cultured cortical astrocytes, freshly FACS-isolated forebrain astrocytes P17 pups, or
13 freshly isolated neurons from P16 pups provided by Cahoy and colleagues [17]. We used the Ensembl
14 BioMart on-line application (<https://www.ensembl.org>) for matching genes between different platforms,
15 namely Agilent Mouse GE 4x44k v2 and Affymetrix Mouse Genome 430 2.0 Arrays. This procedure led to a
16 set of 18,135 common probes, where only those probes filtered by Cahoy as corresponding to “genes with
17 significant expression in the CNS” (Supplemental Table S3 in [17]) were taken into account. After the two
18 datasets were properly integrated and renormalized through XPN algorithm (see Materials and Methods),
19 they were merged into one single dataset. Since XPN algorithm succeeded in removing the batch effect
20 without altering the original clusterization among samples from Cahoy’s dataset (not shown), we could
21 proceed performing an unsupervised hierarchical clustering (Euclidean distance metric and average linkage
22 criterion) to inspect the positioning of our non-Tg astrocytes compared to the groups profiled by Cahoy et al.
23 Figure 3A shows that our cultured astrocytes resulted more similar to the cultured and freshly isolated
24 astroglia than in respect to any other cell type in Cahoy’s dataset. Secondly, both cultured cellular models
25 were more similar to acutely isolated astrocytes than to neurons. Incidentally, the fact that our samples could
26 penetrate Cahoy’s dataset, clustering with its cultured astroglia, is a good evidence that the batch effect was
27 efficiently removed. Afterwards, we took advantage of the merged dataset to search for the most up- and
28 down-regulated genes in our non-Tg astrocyte cultures compared to acutely isolated astrocytes. We used the
29 rank product method (two class, unpaired) as described in [20] controlling FDR at the strict level of 0.005 to
30 get a basic ranked list of genes representing the most enriched expression patterns in both the groups. Results
31 are shown in Figure 3B,C respectively. In particular, we found 130 up-regulated genes in non-Tg compared
32 to acutely isolated astrocytes (Supplementary Table 3) and 230 down-regulated genes in non-Tg compared to
33 acutely isolated astrocytes (Supplementary Table 4). Notably, even if the statistical test was conducted only
34 by comparing non-Tg against acutely isolated astrocytes, heatmaps clearly showed that Cahoy’s cultured
35 astrocytes closely followed our non-Tg culture expression profiles. This is another evidence of the high
36 degree of similarity between our cultured model and Cahoy’s, restricted in particular to those genes that are
37 the most specific for cultured astrocytes. More in detail, 70.0% of genes enriched in our non-Tg cultures
38 could also be found in Cahoy’s list “Genes statistically enriched in cultured astroglia compared to *in vivo*
39 astrocytes” (Supplemental Table S21 in [17]), while 76.5% of genes down-regulated in non-Tg could also be
40 found in Cahoy’s list “Genes statistically enriched in *in vivo* astrocytes compared to cultured astroglia”
41 (Supplemental Table S20 in [17]). Taken together, these two percentages give an estimate of the technical
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3 reproducibility and the biological variability of *in vitro* astrocyte cell cultures. On the other hand, a
4 complementary list of the most up- and down-regulated genes in our non-Tg cultures compared to Cahoy's
5 cultured astroglia (two class unpaired rank product, FDR=0.005) is provided as supplementary material
6 (Supplementary Tables 5 and 6). As a final qualitative remark, the expression profile of acutely isolated
7 neurons (right side of the heatmaps, Figure 3B,C) also shows how most of the genes that are differentially
8 expressed in non-Tg cultures compared to acutely isolated astrocytes can be indeed ascribable to a neuronal
9 phenotype.
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13 14 **3.4. Comparison with isolated astrocytes from symptomatic AD or normally aged mice**

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16 Notably, in cultures from 3xTg-AD, genes involved in immune responses were largely unchanged. This is in
17 sharp contrast with changes occurring in aged plaque stage (15 mo of age) APPswe/PS1dE9 AD mice [7] in
18 which the most prominent change was the up-regulation of a large list of genes related to different aspects of
19 inflammation. We therefore compared our genes with the publicly available dataset by [7] (GEO database
20 accession number: GSE74615). To this purpose, APPswe/PS1dE9 dataset was downloaded and the empirical
21 Bayes method (LIMMA) was used to assess the significance of differential expression of all genes among
22 groups. After *p*-values were adjusted through BH procedure, genes with an $\text{adj.p.val} \leq 0.05$ were marked as
23 significant. While the original APPswe/PS1dE9 dataset included both cortical astrocyte and microglia
24 samples, only the astrocyte data were retained for use in the following meta-analysis (see *Materials and*
25 *Methods*).
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31 Each one of the 993 genes we found to be significantly regulated in our model had a direct correspondence
32 within Orre's dataset. In particular the comparison between 3xTg-AD significant genes and APPswe/PS1dE9
33 dataset allowed to define 6 distinct categories of genes corresponding to 3 relationships between the datasets
34 (see heatmaps and table in Figure 5 for a graphical summary): 1) significantly co-regulated genes (total 50,
35 upward 23, downward 27); 2) significantly changed only in 3xTg-AD astrocytes (total 882; up-regulated
36 486, down-regulated 396); and 3) genes oppositely regulated in 3xTg-AD and APPswePS1dE9 astrocytes
37 (total 61, up-to-down 27, down-to-up 34). Notably, this kind of analysis could have been alternatively
38 addressed through a K-means algorithm, but in that case the resulting 6 clusters would have been based
39 merely on $\log_2\text{FC}$ expression values, and all the information related to the *p*-values of the second dataset
40 (APPswe/PS1dE9) would have been ignored. Conversely, to find the common and the specific gene
41 signature of the two pathological models compared, we preferred clustering genes using the more rigorous
42 criterion of the statistical significance compared their own whole dataset. Although a number of methods for
43 the meta-analysis of combined lists of *p*-values from two or more studies exist [18; 24], some of them (e.g.
44 Fisher's, Stouffer's, minP) are too liberal for our purpose—since genes having small *p*-values in just one
45 study are likely to be detected as globally significant—while others (such as maxP) are conservative but too
46 naïve, not addressing the problem of distinguishing concordant and discordant expression fold changes [18],
47 nor the problem of randomly shared genes. In fact, it should be considered that when two datasets are
48 compared in terms of shared significant genes, a certain number of co-/anti-regulated genes is expected to
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3 arise just by chance. For this reason, here we propose a novel method for the meta-analysis of p -valued lists
4 of genes drawn from two different studies. The procedure makes use of a simple randomized null model
5 based on the binomial distribution to determine which (if any) of the 6 relational categories of genes was
6 significantly enriched (see *Common significant gene analysis* in Appendix). Overall, this method is useful to
7 compare differentially regulated genes between two studies in order to find their “log₂FC-signed”
8 intersections and their statistical significance according to quite conservative criteria.
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12 With reference to the table in Figure 4, the central column contains all genes we found significantly changed
13 only in 3xTg-AD astrocytes (Up-Zero and Down-Zero). All these 882 genes can be considered, as a whole,
14 specific for cultured 3xTg-AD astrocytes, possibly representing early FAD-related alterations. They can also
15 be used for further analysis (such as biological validation through GO analysis, see below) regardless of their
16 categorical p -value. However, the smaller the p -value, the more likely that the two AD models compared
17 have a substantial overlap, because the number of significant non-shared genes is too low if compared to the
18 null model. In other words, the number of common genes differentially expressed is too high compared to a
19 random expression pattern, such as that resulting from comparing two completely independent disease
20 models. In our case the very low p -value assigned to the category of genes significantly downregulated only
21 in 3xTg-AD suggests that at least one of the two other categories of co-regulated and anti-regulated genes
22 (left and right column respectively) were enriched. This allowed us to search for those processes that are in
23 common for both models of early and late AD. In particular, we found 27 common genes significantly down-
24 regulated in both the dataset (Down-Down, expected value=14.9; categorical p -value = 0.003) and 34 genes
25 significantly down-regulated in 3xTg-AD and significantly up-regulated in APPswe/PS1dE9 astrocytes
26 (Down-Up, expected value=22.6; categorical p -value = 0.013).
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35 To analyze the biological significance of genes specific for primary astrocytes from 3xTgAD mice we first
36 fed to DAVID GO tool a list of 882 genes that that were not changed in APPswe/PS1dE9 astrocytes
37 (Supplementary Table 7) regardless they were up or down-regulated. These genes constitute the major part
38 (89%) of all differentially expressed genes of our dataset, therefore, expectedly, enriched GO terms
39 (Supplementary Table 8) overlapped significantly with those found during the initial analysis (Table 2). This
40 suggests that in the 3xTg-AD cultured astrocytes the altered astroglial functions differ substantially from
41 those altered later on, when deposition of A β aggregates is fully expressed. These alterations comprise genes
42 and functions described by GO terms *phosphoproteins*, *cytoplasm*, *alternative splicing*, *nucleotide* and *ATP*
43 *binding*, *transferase activity*, *mitochondrion*, *cell projection*, *apoptotic process*, *magnesium*, *Kruppel*
44 *associated box* and *KRAB*.
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51 Next, we analyzed GO significance of two small categories (co-regulated and anti-regulated) in which the
52 number of common genes significantly differed from expected values (Figure 5). In the list of co-down-
53 regulated genes (Down-Down, Figure 5) GO analysis failed to find significantly enriched GO terms.
54 However, in the list of 34 anti-regulated genes (down 3xTg-AD and up in APPswe/PS1dE9 astrocytes,
55 Down-Up) there were 5 GO terms with significantly enriched genes: *membrane*, *nucleolus*, *ribosomal*
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3 *protein, structural constituent of ribosome, and ribonucleoprotein* (Supplementary Table 8), suggesting that
4 ribosomes may be altered in both, pre-plaque and plaque AD stages, but the direction of these alterations is
5 somewhat opposed.
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8 In parallel with APP^{swe}/PS1^{dE9} dataset it was interesting to explore if cultured 3xTg-AD astrocytes may
9 have common/divergent features with astrocytes from mice subjected to normal ageing from 2.5 to 18
10 months [21]. The comparison between 3xTg-AD and Orre's dataset of young-versus-old mice led to the
11 detection of 38 common genes, but none of the 6 previously defined relational categories resulted in a
12 significant enrichment compared to random configuration (see Supplementary Table 9). The absence of
13 significant overlap between our AD model and the physiological aging picture provided by Orre and
14 colleagues [21], suggests that the alterations detected in cultures of 3xTg-AD astrocytes may be specific for
15 AD. It is worth noting that, unlike the previous case, for this comparison a list of differentially expressed
16 genes was used as reported by the authors (see *Materials and Methods*). To build the statistical null model
17 we could refer only to the full dimension of the array used by Orre in his study (Agilent, Mouse GE 4x44k
18 v2 microarrays, $n_y=39,429$ different probes), which has likely led to an overestimation of the size of the
19 dataset, and, as a consequence, to an overestimation of all the enrichment scores (see *Appendix*). Therefore,
20 though no significant overlap have been ultimately detected after correction of p-values for multiple
21 comparisons (as described in *Appendix*), this comparison should be considered merely as an exploratory
22 analysis.
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33 3.5. Comparison with human AD microarray

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35 A this point it was interesting to explore if the changes found in cultured 3xTg-AD astrocytes may have had
36 common/divergent features with the changes observed in postmortem biopsies from symptomatic AD
37 patients. The hypothesis was that this was unlikely to occur, as cultures possibly represent early changes. For
38 this, we downloaded from GEO database the dataset contributed by Berchtold et al. [22] (series accession
39 number: GSE48350). This dataset featured samples from normal controls (young and aged) and AD cases,
40 from 4 brain regions (hippocampus, entorhinal cortex, superior frontal cortex, post-central gyrus). After the
41 assessment of the differential expression (LIMMA/empirical Bayes) and *p*-values adjustment for multiple
42 comparisons (BH procedure), genes with an $\text{adj.p.val} \leq 0.05$ were marked as significant. Then we restricted
43 our analysis to the groups of interest, retaining just hippocampal samples from both aged control subjects
44 ($n=24$) and aged AD patients ($n=18$). During the gene-matching procedure (see *Materials and Methods* for
45 details) we searched for those genes that met the following requirements: i) belonged to the subset of the
46 genes significantly regulated in our mouse dataset; ii) featured at least one human orthologous gene iii) were
47 present (as orthologous gene) within the Berchtold's human dataset. Because of these necessary
48 prerequisites, the pool of significant genes available for comparison with the human dataset decreased from
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3 Starting from this set of selected genes, the analysis proceeded according to the same methods already
4 described in the previous section and following the same statistical approach. Contrary to what emerged
5 from the comparison with the APP^{swe}/PS1^{dE9} model, in this case we were not able to find any particular
6 type of enrichment in any of the 6 relational categories previously described. In other words, the empirical
7 configuration of the common significant genes was precisely predicted by the null model, thus suggesting a
8 substantial independence of the two datasets (Supplementary Table 10). While, on the one hand, this
9 negative result can be an indication of the large number of different biological parameters distinguishing the
10 two models compared (mouse vs. human, astrocytes vs. whole-tissue samples, young vs. aged, familial AD
11 vs. sporadic AD), it may also confirm the transcriptional specificity of early astroglial changes compared to
12 the late astroglial changes. Moreover, the near-perfect agreement between empirical and expected values
13 demonstrates the high predictive power of our null model in the case of uncorrelated datasets, and hence the
14 substantial validity of this statistical approach.
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24 4. DISCUSSION

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26 In the present report we have investigated transcriptional alterations in purified cultures of hippocampal
27 astrocytes of 3xTg-AD mice. An obvious limitation of this work is the use of astrocytes in culture, which
28 raises concerns on (i) to which extent the changes in gene expression in cultures reflect the changes
29 occurring in astrocytes *in vivo*, and (ii) to which extent the cultured astrocytes from FAD mice models
30 represent AD. With regard to the first point, while it has been reported that in defined growing conditions
31 gene profiles of cultured astrocytes in different aspects reliably replicate those of freshly isolated astrocytes
32 ([25] and refs therein), our first objective was not to replicate gene expression of astrocytes *in vivo*, but to
33 find the early FAD-related transcriptional signature specific to astrocytes in the hippocampal region as
34 compared with non-Tg astrocytes. With this aim the purity of astrocytes in culture was our first concern
35 because small contaminations of astrocytes with microglial cells would result in the emergence of transcripts
36 related to inflammation. This was successfully achieved by eliminating microglia with anti-CD11b beads.
37 Regarding the second point, we reasoned that astroglial cultures prepared from newborn mouse pups may
38 represent a proxy model for early, pre-plaque, AD because the changes (if any) would have been due to the
39 FAD-related mutations but not due to the burden of A β species. Of the three mutations present in 3xTg-AD
40 mice, PS1_{M146V} mutation has been introduced by knock-in of a point mutation of in the PS1 gene and is
41 ubiquitous as it is under the control of the endogenous PS1 promoter [26]. The other mutations, APP^{swe} and
42 Tau_{P301L} have been added later as overexpressing human transgenes under the control of Thy-1.2 promoter,
43 which is considered to be neuronal [12]. Therefore, *in vivo* the effect of the PS1_{M146V} mutation should have
44 direct consequences on astroglial biology, while the effects of APP and Tau mutations should be indirect. In
45 cultured astrocytes, the changes (if any) should be a consequence of PS1 mutation, while the effects of APP
46 and Tau mutations appear to be less probable or indirect, driven by priming before explant.
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3 In contrast to works reporting proinflammatory phenotypes in cultured astrocytes from FAD mouse models
4 [27] as well as in A β -exposed astrocytes [28], in our highly purified astroglial cultures from 3xTg-AD
5 hippocampi we found substantially no changes in inflammatory genes with down-regulation of a few genes
6 related to positive regulation of T cell mediated cytotoxicity. Recently, however, we have found that
7 transforming growth factor β (TGF- β) is released by cultured hippocampal astrocytes [29]. Now this
8 observation is corroborated by the finding that TGF- β 2 and TGF- β 3 are expressed at high levels in
9 hippocampal astrocytes and TGF- β 3 is significantly up-regulated in 3xTg-AD with regard to non-Tg
10 astrocytes.
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15 Among highly up-regulated genes in 3xTg-Ad astrocytes the only gene relative to the immune system was
16 C-C motif chemokine ligand 27a (Ccl27a), a member of the β -chemokine family of proinflammatory
17 mediators [30]. However, a closer examination of the 3 probes in the Agilent array for this cytokine, all of
18 which were up-regulated, shows that two probes detected a splice variant of Ccl27a in which the signal
19 peptide was replaced with an alternative stretch of amino acids that allows for nuclear targeting of this
20 isoform. This nucleus-targeted Ccl27a variant, which is called PESKY [30] is the most expressed isoform in
21 primary astrocytes and is able to modulate gene transcription [31]. This finding corroborates the hypothesis
22 that transcriptional reprogramming occurs in 3xTg-AD astrocytes as well as the absence of inflammation.
23 Our results suggest that hippocampal astrocytes from a mouse FAD model are unable to mount a pro-
24 inflammatory phenotype in a cell-autonomous manner. The setup of inflammation likely requires
25 participation of microglial cells which, together with astrocytes, upon exposure to activating stimuli, like A β ,
26 undergo cascading reactions which result in activation of both microglial and astroglial cells [32]. Such a
27 scenario may be illustrated by a recent report by Balducci et al. [33] in which acute *in vivo* intraventricular
28 delivery of oligomeric A β induced rapid and long-lasting inflammatory reactions with astroglial expression
29 of pro-inflammatory cytokines. Such an observation also highlights that the strength of our model, i.e.
30 purified astrocytes, on the other hand limits the possibility to evaluate the relationship between cell types in
31 early AD. In this regard it is interesting to note that in late stages AD pathology patients with APOE ϵ 4 allele
32 astrocytes exhibited alterations in genes related to cell adhesion and signaling pathways including calcium
33 signaling and insulin signaling, while changes in expression of inflammatory genes were not reported [34].
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44 Previously, we have suggested that astroglial degeneration, occurring in the very early AD stages, may be
45 linked to deregulated astroglial Ca²⁺ signaling [5; 35]. Reasonably, astroglial degeneration is likely to be
46 associated with the absence or the repression of inflammatory processes, while it would be hardly
47 reconcilable with inflammation. Instead, at later AD stages, in which the inflammatory phenotype is fully
48 expressed [7], astrocytes are found to be reactive and hypertrophic [2].
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52 GO analysis of our dataset suggests that physiological processes and functions which are likely to be altered
53 in 3xTg-AD astrocytes are: phosphorylation, transcription, mitochondrial structure and function, calcium-
54 regulated cell adhesion and cell-cell communication. A survey of the literature suggests that alterations in all
55 these functions occur in symptomatic AD [36; 37]. Considering astroglial cultures from new-born pups a
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3 proxy model for the early developing pre-plaque AD, our analysis suggests that phosphorylation,
4 mitochondria, cell adhesion and cell-cell communication are among the first to be altered in astrocytes. In
5 particular, alterations in phosphorylation cascades and in autophagy which are controlled by mammalian
6 target of rapamycin complex 1 (mTORC1) are emerging as possible causes of metabolic dysregulation in
7 neurodegenerative diseases including AD [36; 38; 39]. In this regard, of note is one of the most down-
8 regulated genes in 3xTg-AD astrocytes, Sterile alpha motif domain containing protein 4 (Samd4). Samd4 is a
9 mammalian homolog of *Drosophila* Smaug gene coding for a protein able to bind RNA and repress
10 translation [40]. While the function of Samd4 in mammalian cells, including astrocytes, is largely unknown,
11 it has recently been reported that mice with missense mutation of Samd4 were exceptionally thin and had
12 severe deficiency in metabolic homeostasis and mTORC1 signaling [41]. Our finding that a protein required
13 for the mTORC1 signaling is strongly downregulated in FAD-expressing astrocytes suggests that such a
14 deregulation may initiate early in AD pathogenesis.
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21 One important feature of late AD, as it has been shown on FACS-isolated astrocytes, is the down-regulation
22 of genes involved in cellular communication and neuronal support [7]. In our dataset, in contrast to genes
23 coding for inflammatory mediators, we found that many gene which code for proteins involved in
24 exocytosis, formation of processes and extracellular matrix, which generally may be involved in
25 communication with surrounding cells and support to neurons, are massively down-regulated in 3xTg-AD
26 astrocytes. This suggests that the impairment of communication between astrocytes and other cells in the
27 brain may begin very early in AD. In line with this observation, Stenovc et al [42] reported impaired vesicle
28 dynamics and reduced evoked secretion of a neuroactive peptide atrial natriuretic peptide in 3xTg-AD
29 cultured astrocytes. These alterations were attributed to mutations in PS1. The impairment of cell-cell
30 communication, in concomitance with compromised housekeeping functions may be at the basis of early
31 astroglial pathology that, in turn, accelerates the impairment in synaptic transmission [43].
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39 Comparison of the dataset presented in this work with the dataset obtained from astrocytes isolated from
40 plaque-stage symptomatic APP^{swe}/PS1^{dE9} AD mice [7] shows that most altered genes (89%) were specific
41 for cultured astrocytes and were not changed in APP^{swe}/PS1^{dE9} mice. This suggests that (1) in cultured
42 3xTg-AD astrocytes as a proxy for early AD, FAD-mutations produce a unique signature of transcriptional
43 remodeling which may be related to changes occurring early in AD; and (2) dynamics of astroglial
44 remodeling are likely to change significantly during AD progression. **Alongside the AD-related changes,**
45 **astrocytes are involved in ageing. Transcriptional changes in AD, however, differ from those related to**
46 **ageing by exacerbated inflammatory response and increased dysfunction [7; 21]. Our attempt to compare**
47 **alterations in cultured 3xTg-AD astrocytes with the aged-vs-young changes in mice suggests that FAD-**
48 **mutations in cultured astrocytes produce changes which are more related to AD pathology than to normal**
49 **ageing. Considering that in different brain areas the dynamics of AD-related pathology are brain region-**
50 **specific [5; 11], it is interesting to note that in humans, astrocytic genes, which are mostly expressed during**
51 **ageing tend to lose their region specificity undergoing global up-regulation [44].**
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3 While in AD neuropathological changes are not always followed by cognitive deficit, and cognitively normal
4 subjects may have deposition of amyloid plaques and development of neurofibrillary tangles, it appears
5 important to correlate cognitive damage with astroglial gene expression profile. Such an attempt has been
6 recently made by Barbash and colleagues [45]. In contrast to neuronal and oligodendrocytic genes, which
7 were up-regulated and down-regulated, respectively, in non-demented patients with AD neuropathology,
8 astroglial and microglial genes were up-regulated in both demented and non-demented AD patients as
9 compared with healthy subjects. These results may be interpreted as there is no correlation in astroglial
10 overall transcriptome changes and cognitive damage, but only with neuropathology [45]. However, more
11 detailed examination of functional significance of changed genes is necessary for further understanding of
12 their relation cognitive damage in AD. In this report we analyze the alterations in primary astroglial cultures
13 of FAD-expressing mouse pups, which likely reflect the early stages of AD and may determine or even delay
14 development of both neuropathological and cognitive alterations.
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26 Conclusion

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

This work had the following financial supports: grants 2013-0795 to AAG and 2014-1094 to DL from the Fondazione Cariplo; grant 2015 to CD and 2016 to DL from The Università del Piemonte Orientale; and grant PRIN-2015N4FKJ4 to PLC from the Italian Ministry of Education.

Conflict of Interest Statement

The authors declare no conflict of interests.

For Review Only

References

- [1] Spiers-Jones TL, Hyman BT. The intersection of amyloid beta and tau at synapses in Alzheimer's disease. *Neuron* 82: 756-71.(2014).
- [2] Ben Haim L, Carrillo-de Sauvage M-A, Ceyzériat K, Escartin C. Elusive roles for reactive astrocytes in neurodegenerative diseases. *Frontiers in Cellular Neuroscience* 9: 278.(2015).
- [3] Ferrer I. Diversity of astroglial responses across human neurodegenerative disorders and brain aging. *Brain Pathology (Zurich, Switzerland)* 27: 645-74.(2017).
- [4] Verkhatsky A, Zorec R, Rodríguez JJ, Parpura V. Astroglia dynamics in ageing and Alzheimer's disease. *Current Opinion in Pharmacology* 26: 74-79.(2016).
- [5] Lim D, Rodríguez-Arellano JJ, Parpura V, Zorec R, Zeidán-Chuliá F, Genazzani AA, *et al.* Calcium signalling toolkits in astrocytes and spatio-temporal progression of Alzheimer's disease. *Current Alzheimer Research* 13: 359-69.(2016).
- [6] Yeh C-Y, Vadhvana B, Verkhatsky A, Rodríguez JJ. Early astrocytic atrophy in the entorhinal cortex of a triple transgenic animal model of Alzheimer's disease. *ASN neuro* 3: 271-79.(2011).
- [7] Orre M, Kamphuis W, Osborn LM, Jansen AHP, Kooijman L, Bossers K, *et al.* Isolation of glia from Alzheimer's mice reveals inflammation and dysfunction. *Neurobiology of Aging* 35: 2746-60.(2014).
- [8] Grolla AA, Fakhfour G, Balzaretto G, Marcello E, Gardoni F, Canonico PL, *et al.* A β leads to Ca²⁺ signaling alterations and transcriptional changes in glial cells. *Neurobiology of Aging* 34: 511-22.(2013).
- [9] Lim D, Iyer A, Ronco V, Grolla AA, Canonico PL, Aronica E, *et al.* Amyloid beta deregulates astroglial mGluR5-mediated calcium signaling via calcineurin and Nf-kB. *Glia* 61: 1134-45.(2013).
- [10] Ronco V, Grolla AA, Glasnov TN, Canonico PL, Verkhatsky A, Genazzani AA, *et al.* Differential deregulation of astrocytic calcium signalling by amyloid- β , TNF α , IL-1 β and LPS. *Cell Calcium* 55: 219-29.(2014).
- [11] Grolla AA, Sim JA, Lim D, Rodriguez JJ, Genazzani AA, Verkhatsky A. Amyloid- β and Alzheimer's disease type pathology differentially affects the calcium signalling toolkit in astrocytes from different brain regions. *Cell Death & Disease* 4: e623.(2013).
- [12] Oddo S, Caccamo A, Shepherd JD, Murphy MP, Golde TE, Kaye R, *et al.* Triple-transgenic model of Alzheimer's disease with plaques and tangles: intracellular A β and synaptic dysfunction. *Neuron* 39: 409-21.(2003).
- [13] Smyth GK. Linear models and empirical bayes methods for assessing differential expression in microarray experiments. *Statistical Applications in Genetics and Molecular Biology* 3: Article3.(2004).

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2
3 [14] Benjamini Y, Hochberg Y. Controlling the False Discovery Rate: A Practical and Powerful
4 Approach to Multiple Testing. *Journal of the Royal Statistical Society Series B (Methodological)*
5 57: 289-300.(1995).
6
7 [15] Bourgon R, Gentleman R, Huber W. Independent filtering increases detection power for high-
8 throughput experiments. *Proceedings of the National Academy of Sciences of the United States of*
9 *America* 107: 9546-51.(2010).
10
11 [16] Huang DW, Sherman BT, Lempicki RA. Systematic and integrative analysis of large gene lists
12 using DAVID bioinformatics resources. *Nature Protocols* 4: 44-57.(2009).
13
14 [17] Cahoy JD, Emery B, Kaushal A, Foo LC, Zamanian JL, Christopherson KS, *et al.* A
15 transcriptome database for astrocytes, neurons, and oligodendrocytes: a new resource for
16 understanding brain development and function. *The Journal of Neuroscience* 28: 264-78.(2008).
17
18 [18] Walsh CJ, Hu P, Batt J, Santos CCD. Microarray Meta-Analysis and Cross-Platform
19 Normalization: Integrative Genomics for Robust Biomarker Discovery. *Microarrays (Basel,*
20 *Switzerland)* 4: 389-406.(2015).
21
22 [19] Shabalina AA, Tjelmeland H, Fan C, Perou CM, Nobel AB. Merging two gene-expression
23 studies via cross-platform normalization. *Bioinformatics* 24: 1154-60.(2008).
24
25 [20] Breitling R, Armengaud P, Amtmann A, Herzyk P. Rank products: a simple, yet powerful, new
26 method to detect differentially regulated genes in replicated microarray experiments. *FEBS letters*
27 573: 83-92.(2004).
28
29 [21] Orre M, Kamphuis W, Osborn LM, Melief J, Kooijman L, Huitinga I, *et al.* Acute isolation
30 and transcriptome characterization of cortical astrocytes and microglia from young and aged mice.
31 *Neurobiology of Aging* 35: 1-14.(2014).
32
33 [22] Berchtold NC, Sabbagh MN, Beach TG, Kim RC, Cribbs DH, Cotman CW. Brain gene
34 expression patterns differentiate mild cognitive impairment from normal aged and Alzheimer's
35 disease. *Neurobiology of Aging* 35: 1961-72.(2014).
36
37 [23] Saeed AI, Sharov V, White J, Li J, Liang W, Bhagabati N, *et al.* TM4: a free, open-source
38 system for microarray data management and analysis. *BioTechniques* 34: 374-78.(2003).
39
40 [24] Chang L-C, Lin H-M, Sibille E, Tseng GC. Meta-analysis methods for combining multiple
41 expression profiles: comparisons, statistical characterization and an application guideline. *BMC*
42 *bioinformatics* 14: 368.(2013).
43
44 [25] Hertz L, Chen Y, Song D. Astrocyte Cultures Mimicking Brain Astrocytes in Gene
45 Expression, Signaling, Metabolism and K⁺ Uptake and Showing Astrocytic Gene Expression
46 Overlooked by Immunohistochemistry and In Situ Hybridization. *Neurochemical Research* 42: 254-
47 71.(2017).
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3 [26] Guo Q, Fu W, Sopher BL, Miller MW, Ware CB, Martin GM, *et al.* Increased vulnerability of
4 hippocampal neurons to excitotoxic necrosis in presenilin-1 mutant knock-in mice. *Nature Medicine*
5 5: 101-06.(1999).
- 6
7 [27] van Gijssel-Bonnello M, Baranger K, Benech P, Rivera S, Khrestchatisky M, de Reggi M, *et al.*
8 Metabolic changes and inflammation in cultured astrocytes from the 5xFAD mouse model of
9 Alzheimer's disease: Alleviation by pantethine. *PloS One* 12: e0175369.(2017).
- 10
11 [28] Wang H-M, Zhang T, Huang J-K, Sun X-J. 3-N-butylphthalide (NBP) attenuates the amyloid-
12 β -induced inflammatory responses in cultured astrocytes via the nuclear factor- κ B signaling
13 pathway. *Cellular Physiology and Biochemistry* 32: 235-42.(2013).
- 14
15 [29] Tapella L, Cerruti M, Biocotino I, Stevano A, Rocchio F, Canonico PL, *et al.* TGF- β 2 and
16 TGF- β 3 from cultured β -amyloid-treated or 3xTg-AD-derived astrocytes may mediate astrocyte-
17 neuron communication. *The European Journal of Neuroscience* 47: 211-21.(2018).
- 18
19 [30] Baird JW, Nibbs RJ, Komai-Koma M, Connolly JA, Ottersbach K, Clark-Lewis I, *et al.*
20 ESkine, a novel beta-chemokine, is differentially spliced to produce secretable and nuclear targeted
21 isoforms. *The Journal of Biological Chemistry* 274: 33496-503.(1999).
- 22
23 [31] Nibbs RJB, Graham GJ. CCL27/PESKY: a novel paradigm for chemokine function. *Expert*
24 *Opinion on Biological Therapy* 3: 15-22.(2003).
- 25
26 [32] Schubert P, Morino T, Miyazaki H, Ogata T, Nakamura Y, Marchini C, *et al.* Cascading glia
27 reactions: a common pathomechanism and its differentiated control by cyclic nucleotide signaling.
28 *Annals of the New York Academy of Sciences* 903: 24-33.(2000).
- 29
30 [33] Balducci C, Frasca A, Zotti M, La Vitola P, Mhillaj E, Grigoli E, *et al.* Toll-like receptor 4-
31 dependent glial cell activation mediates the impairment in memory establishment induced by β -
32 amyloid oligomers in an acute mouse model of Alzheimer's disease. *Brain, Behavior, and Immunity*
33 60: 188-97.(2017).
- 34
35 [34] Simpson JE, Ince PG, Shaw PJ, Heath PR, Raman R, Garwood CJ, *et al.* Microarray analysis
36 of the astrocyte transcriptome in the aging brain: relationship to Alzheimer's pathology and APOE
37 genotype. *Neurobiology of Aging* 32: 1795-807.(2011).
- 38
39 [35] Lim D, Ronco V, Grolla AA, Verkhratsky A, Genazzani AA. Glial calcium signalling in
40 Alzheimer's disease. *Reviews of Physiology, Biochemistry and Pharmacology* 167: 45-65.(2014).
- 41
42 [36] Perluigi M, Di Domenico F, Butterfield DA. mTOR signaling in aging and neurodegeneration:
43 At the crossroad between metabolism dysfunction and impairment of autophagy. *Neurobiology of*
44 *Disease* 84: 39-49.(2015).
- 45
46 [37] Grimm A, Friedland K, Eckert A. Mitochondrial dysfunction: the missing link between aging
47 and sporadic Alzheimer's disease. *Biogerontology* 17: 281-96.(2016).
- 48
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2
3 [38] Maiese K. Taking aim at Alzheimer's disease through the mammalian target of rapamycin.
4 Annals of Medicine 46: 587-96.(2014).
5
6 [39] Kiriyama Y, Nochi H. The Function of Autophagy in Neurodegenerative Diseases.
7 International Journal of Molecular Sciences 16: 26797-812.(2015).
8
9 [40] Chen L, Dumelie JG, Li X, Cheng MH, Yang Z, Laver JD, *et al.* Global regulation of mRNA
10 translation and stability in the early Drosophila embryo by the Smaug RNA-binding protein.
11 Genome Biology 15: R4.(2014).
12
13 [41] Chen Z, Holland W, Shelton JM, Ali A, Zhan X, Won S, *et al.* Mutation of mouse Samd4
14 causes leanness, myopathy, uncoupled mitochondrial respiration, and dysregulated mTORC1
15 signaling. Proceedings of the National Academy of Sciences of the United States of America 111:
16 7367-72.(2014).
17
18 [42] Stenovec M, Trkov S, Lasič E, Terzieva S, Kreft M, Rodríguez Arellano JJ, *et al.* Expression
19 of familial Alzheimer disease presenilin 1 gene attenuates vesicle traffic and reduces peptide
20 secretion in cultured astrocytes devoid of pathologic tissue environment. Glia 64: 317-29.(2016).
21
22 [43] Verkhatsky A, Sofroniew MV, Messing A, deLanerolle NC, Rempe D, Rodríguez JJ, *et al.*
23 Neurological diseases as primary gliopathies: a reassessment of neurocentrism. ASN neuro 42012).
24
25 [44] Soreq L, Consortium UBE, Consortium NABE, Rose J, Soreq E, Hardy J, *et al.* Major Shifts in
26 Glial Regional Identity Are a Transcriptional Hallmark of Human Brain Aging. Cell Reports 18:
27 557-70.(2017).
28
29 [45] Barbash S, Garfinkel BP, Maoz R, Simchovitz A, Nadorp B, Guffanti A, *et al.* Alzheimer's
30 brains show inter-related changes in RNA and lipid metabolism. Neurobiology of Disease 106: 1-
31 13.(2017).
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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 $n_y \gg y_s$; 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 } \cap 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):

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

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 $\mathbf{E}[k] = np$ 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 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:

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

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: $\text{Adj.p.val} = 4 \cdot p\text{-value}$ (Bonferroni), $\text{Adj.p.val} = 1 - (1 - p\text{-value})^4$ (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 ($\log\text{FC}$) of 3xTg-AD vs non-Tg astrocytes, while y-axis shows $\log\text{FC}$ of real-time PCR, $n = 23$ genes. **B**, scatterplots of 14 genes exemplifying the results of real-time PCR validation. Data are expressed as mean \pm 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 ($\text{FDR} \leq 0.005$, 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 APP^{swe}/PS1^{dE9} 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 $\log_2\text{FC}$ color-coded heatmaps of the top-20 regulated genes for each category ($X = 3\text{xTg-AD vs non-Tg dataset}$; $Y = \text{APP}^{\text{swe}}/\text{PS1}^{\text{dE9}} \text{ AD vs WT dataset}$). At 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*

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APP_{swe}/PS1_{dE9} 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.

For Review Only

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	2610507101Rik	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	Ocell1	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

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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

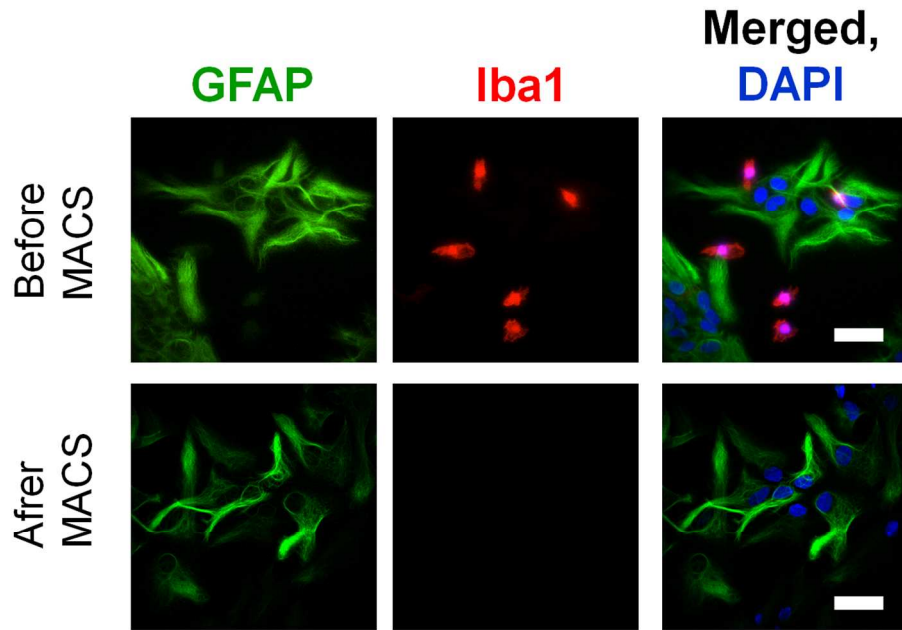
For Review Only

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 metalloproteinase (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	Ca ²⁺ -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

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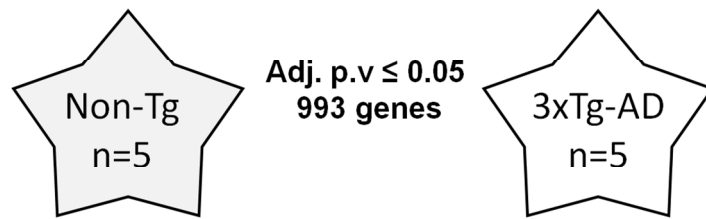


Figure 1. Microarray setup.

122x143mm (300 x 300 DPI)

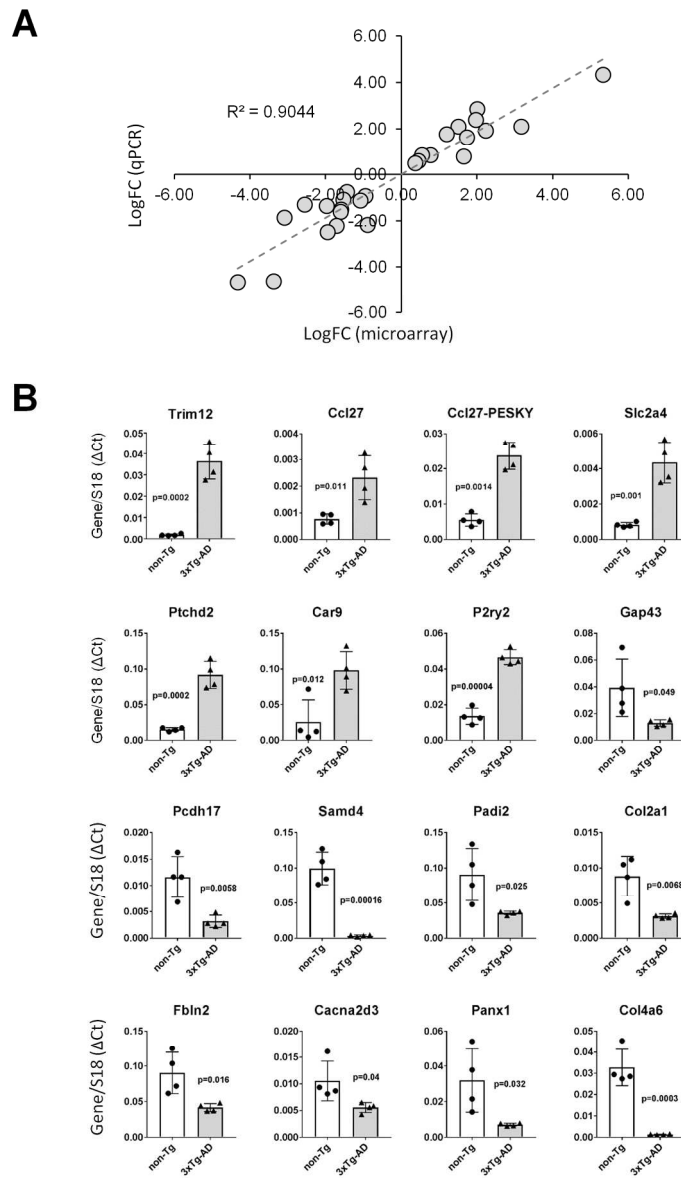


Figure 2. Real-time PCR validation of microarray results.

133x226mm (300 x 300 DPI)

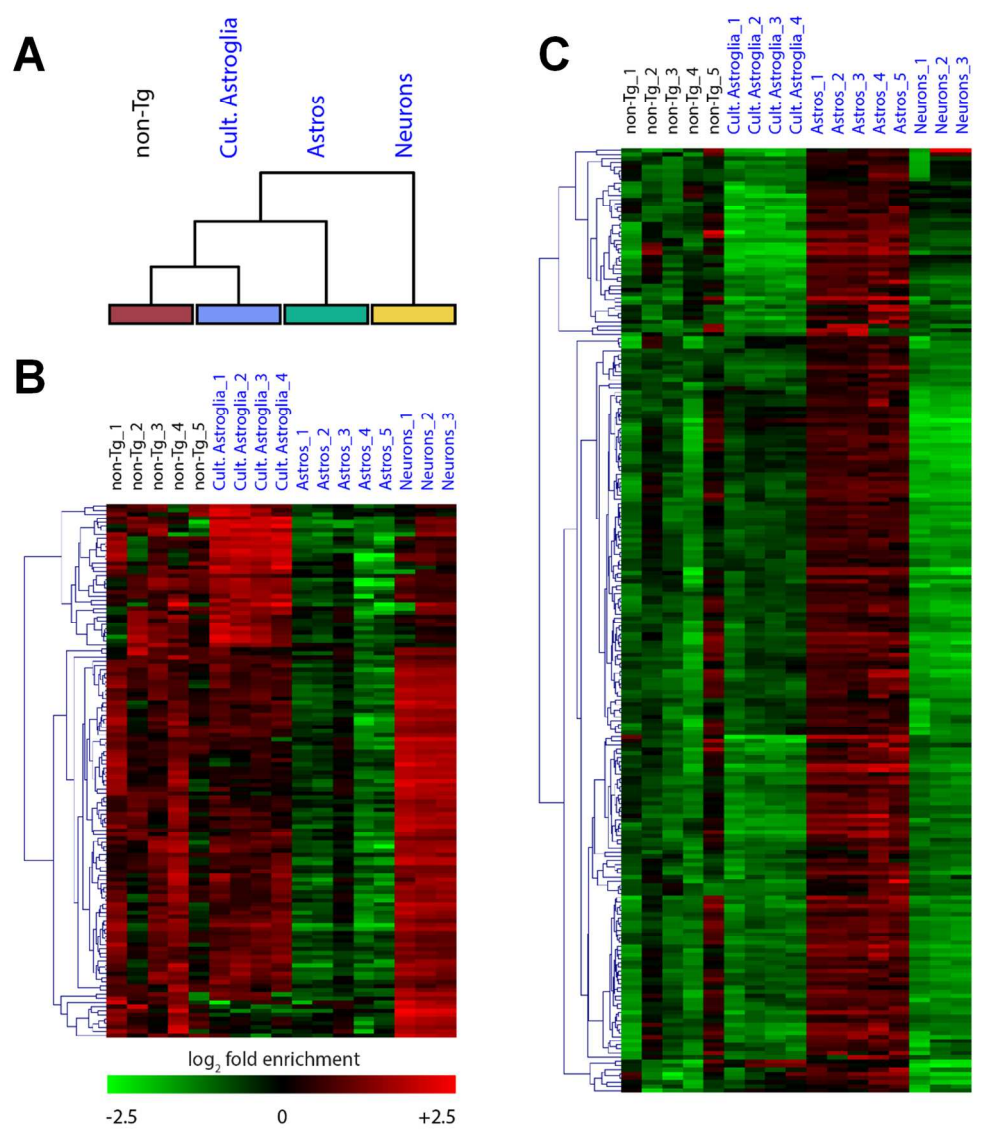


Figure 3. Comparison with acutely isolated CNS cellular models.

150x172mm (300 x 300 DPI)

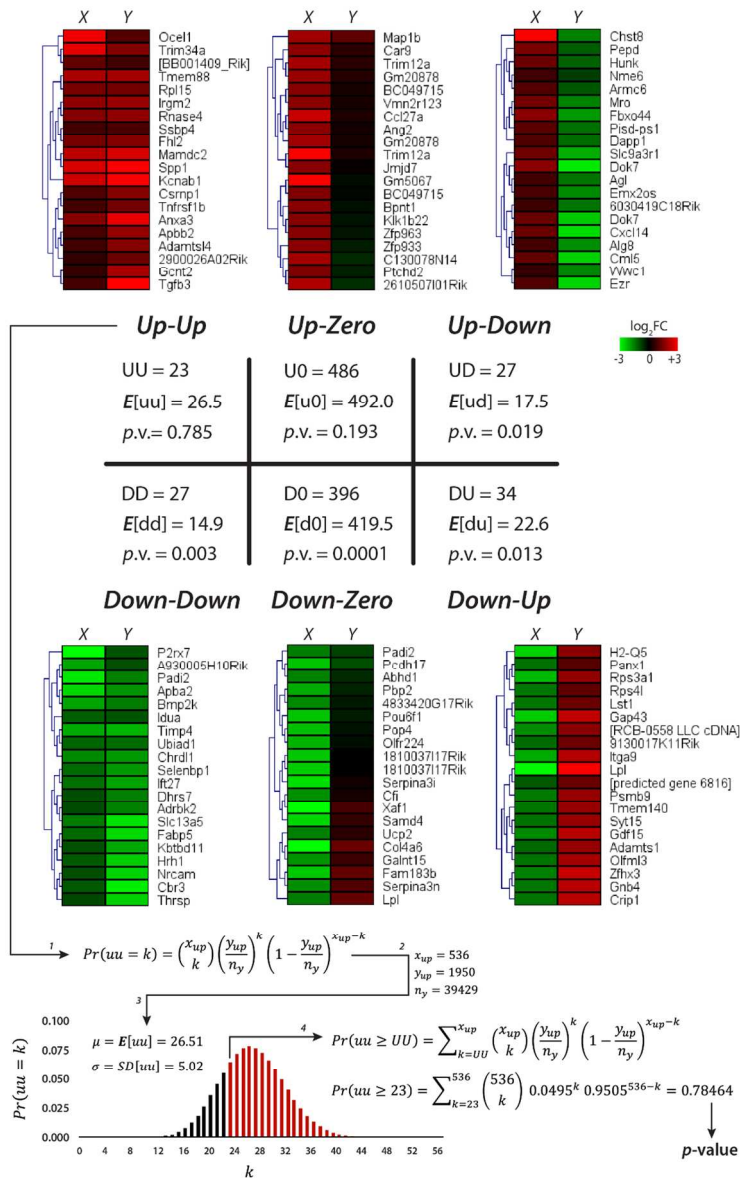


Figure 4. Comparison with isolated astrocytes from symptomatic APPsw/PS1dE9 AD mice.

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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Supplementary Table 2	List of genes validated by real-time PCR	Supplementary Table 2
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Supplementary Table 5	List of genes up-regulated in non-Tg astrocytes compared to cultured astroglia from Cahoy's (2014) dataset	Supplementary Tables 5-6
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Supplementary Table 7	Lists of co- and anti-regulated genes as compared with Orre et al (2014)	Supplementary Table 7
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Supplementary Table 9	Comparison with human AD dataset	Supplementary Table 9

Oligonucleotide primers used for quantitative real-time PCR.

Gene	Accession number	Forward Reverse	Sequence 5' to 3'
Trim12a	NM_023835.2	Forward Reverse	TCATTGAAGAGGTGGCCAG ACCGAACATTCTGCACATCT
Ccl27a	NM_011336.1	Forward Reverse	CCCGCTGTTACTGTTGCTTC CAATCCTCCTCAGCAGCCT
Ccl27a (Pesky)	NM_001048179.1	Forward Reverse	TCTCCAACAAGCCAGAGACT GCTTGGGAGTGGCTGTCTAT
Car9	NM_139305.2	Forward Reverse	GGAGTCCCTTGGGTAGAGG TGGGGCCAGAGTAGGGTG
Ptchd2	NM_001083342.1	Forward Reverse	CACAGCCTGCAGAACAATGT TTGGAGATGTACACGGTGCT
Slc2a4	NM_009204.2	Forward Reverse	TAAAACAAGATGCCGTCGGG CCAAACTGAAGGGAGCCAAG
Bmp4	NM_007554.3	Forward Reverse	AGTCTGGGGAGGAGGAGG GAGCTCTACTGGTCCCTG
Kcnab1	NM_010597.4	Forward Reverse	GGGAAGGCTGAGGTGATTCT GTCCCCTTTCTGTCTCAGCT
P2ry2	NM_008773.3	Forward Reverse	ATCCTCACACCTCAAGAGC GGCAACAGCACGTACTIONGAA
Tnrc18	NM_001122730.2	Forward Reverse	TCCATCCTACCTCCACCTGA GGTGCGGGCAGGTAGAAAG
Tgfb3	NM_009368.3	Forward Reverse	AGGAGACCTCGGAGTCTGAG CACTGAGGACACATTGAAACGA
Vcp	NM_009503.4	Forward Reverse	CGAGTTCGCCTAGGAGATGT AGAGATTGCCAGTGATGCCT
Ankib1	NM_001289527.1	Forward Reverse	CCTATCAGCACAAACACACCG 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 GGGTTTCCTTCGCTTCACA
Col2a1	NM_001113515.2	Forward Reverse	GTGAGCCATGATCCGCCTC GGTTCTCCTTTCTGCCCTT
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 CACCTTCGAGTGCTTCAGG
P2rx7	NM_011027.3	Forward Reverse	ACTGCAGACTACACCTTCCC TACAACGCCGGTCAGAAGAG
Pcdh17	NM_001013753.2	Forward Reverse	CTAATTCGAGCGAGACCCCT CTCTCAGGCTGGCTCTTTCT
Samd4	NM_001037221.2	Forward Reverse	TTGTGCCTCAGTATGACGGA AACCCCTGAAGATGGCTGACA
Col4a6	NM_053185.2	Forward Reverse	CAAGCATGCACCCTGGATTG AGACTCCATGGCAATCTCGG
S18	NM_213557	Forward Reverse	TGCGAGTACTCAACACCAACA CTGCTTTCTCAACACCACA
GAPDH	NM_017008	Forward Reverse	CAAGGTCATCCATGACAACTTTG GGGCCATCCACAGTCTTCTG
RP2a	XM_002727723	Forward Reverse	GCACCATCAAGAGAGTGCAG GGATCCATTAGTCCCCAAG

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 $n_y \gg y_s$;
- $E[z]$ 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):

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

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?”

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3 While the same can be said for the other “lateral” categories of genes (UD , DD and DU), the interest in the
4 “central” categories (those featuring genes that are significantly regulated only in X) concerns their possible
5 impoverishment rather than enrichment. In this case, the statistical significance (categorical p -value) can be
6 calculated as follow:
7

$$8 \quad Pr(u0 \leq U0) = \sum_{k=0}^{U0} \binom{x_{up}}{k} \left(1 - \frac{y_s}{n_y}\right)^k \left(\frac{y_s}{n_y}\right)^{x_{up}-k}, \text{ and analogously for } D0.$$

10
11 Notice that, in this kind of problem, the 6 categories of interest are not mutually independent. In particular,
12 because of the 2 constraints $x_{up} = uu + ud + u0$ and $x_{down} = dd + du + d0$ only 4 categories out of 6 are
13 actually independent, and the same applies to the enrichment hypothesis tests. Since each comparative
14 analysis of two datasets implies 4 independent hypothesis tests, we can adjust categorical p -values for
15 multiple comparisons according to the usual correction techniques: Adj.p.val = $4 \cdot p$ -value (Bonferroni),
16 Adj.p.val = $1 - (1 - p\text{-value})^4$ (Dunn–Šidák), etc.
17

18
19 Incidentally, because of the same two constraints cited above, the expectation values of the central categories
20 could be alternatively computed as:
21

$$22 \quad \mathbf{E}[u0] = x_{up} - \mathbf{E}[uu] - \mathbf{E}[ud],$$

$$23 \quad \mathbf{E}[d0] = x_{down} - \mathbf{E}[dd] - \mathbf{E}[du].$$

24
25 Even if the two categories $U0$ and $D0$ can be further explored and biologically validated regardless of their
26 categorical p -values (simply because they are in any case the container of all those genes specific for the
27 condition studied by X respect to Y), a significant impoverishment of one of them is suggestive of some kind
28 of correlation between X and Y (and hence between the pathologies or treatments they represent). On the
29 contrary, the p -values assigned to the lateral categories allow to precisely locate any possible (and
30 statistically significant) overlapping of the two dataset, and further investigations are not justified in the
31 absence of a sufficiently low categorical p -value.
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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 C130078I
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	vomeroneural 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-acetylgalactosaminyl) transferase 8
A_55_P2073965	BC049715	cDNA sequence BC049715
A_51_P217498	Slc2a4	solute carrier family 2 (facilitated glucose transporter) member 4
A_55_P2045886	Stk3	serine/threonine kinase 3
A_55_P2180869	Ocln1	occludin/ELL domain containing 1
A_55_P2108773	4930427A07Ri	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 domain containing 7B
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-acetylneuraminyl-2-acetylaminosaccharide 6S alpha-D-glucosyltransferase 2)
A_51_P512820	Dera	2-deoxyribose-5-phosphate aldolase
A_55_P2095603	Ccdc65	coiled-coil domain containing 65
A_51_P477121	Pmaip1	phorbol-12-myristate-13-acetate-inducible protein 1
A_55_P2130129	Kcnab1	potassium voltage-gated channel, non-voltage-activated subfamily B member 1
A_55_P2373852	2310058N22Ri	RIKEN cDNA 2310058N22 gene
A_55_P2144597	9030025P20Ri	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	Ctnn3	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	Pdprn	podoplanin
A_51_P358722	Lancl3	LanC lantibiotic synthetase component 3
A_55_P2053551	Mast4	microtubule associated serine/threonine kinase 4
A_55_P2019577	1500011B03Ri	RIKEN cDNA 1500011B03 gene
A_52_P532687	Ermard	ER membrane associated RNA deacetylase
A_52_P209484	Tmem88	transmembrane protein 88
A_52_P490207	Ermard	ER membrane associated RNA deacetylase
A_55_P2059357	Myo7a	myosin VIIA

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2	A_51_P507899	Ttc8	tetratricopeptide repeat domain 8
3	A_55_P2194064	BC023969	cDNA sequence BC023969
4	A_55_P2067727	Mxra7	matrix-remodelling associated 7
5	A_55_P2197338	Tnfsf13os	tumor necrosis factor (ligand) superfamily 13
6	A_51_P345316	Cep76	centrosomal protein 76
7	A_55_P2065726	Snx29	sorting nexin 29
8	A_55_P2179793		0 0
9	A_52_P642012	BC006965	cDNA sequence BC006965
10	A_52_P616332	Atp10d	ATPase, class V, type 10D
11	A_51_P179504	Ang3	angiogenin, ribonuclease A family
12	A_55_P2169963	Gm13152	predicted gene 13152
13	A_52_P559545	Cercam	cerebral endothelial cell adhesion molecule
14	A_55_P2180196	Ccdc32	coiled-coil domain containing 32
15	A_52_P135707	Creb3	cAMP responsive element binding protein 3
16	A_52_P598634	1190007I07Ri	RIKEN cDNA 1190007I07 gene
17	A_52_P587738	P2ry2	purinergic receptor P2Y, G-protein coupled receptor 2
18	A_55_P2380428	5430416G10F	RIKEN cDNA 5430416G10 gene
19	A_66_P122158	Pisd-ps3	phosphatidylserine decarboxylase
20	A_52_P592909	Dgat2	diacylglycerol O-acyltransferase 2
21	A_52_P549977	Fam32a	family with sequence similarity 32, member A
22	A_51_P125368	Hars	histidyl-tRNA synthetase
23	A_55_P2019054	Acacb	acetyl-Coenzyme A carboxylase b
24	A_55_P1987196	Gm3448	predicted gene 3448
25	A_55_P1960167	Bcat2	branched chain aminotransferase
26	A_51_P480013	Car11	carbonic anhydrase 11
27	A_55_P2137611	Irgm2	immunity-related GTPase family N
28	A_55_P2120866	Gm7120	predicted gene 7120
29	A_51_P418908	Larp1	La ribonucleoprotein domain family 1
30	A_55_P1975874	Bcl2l15	BCL2-like 15
31	A_51_P286814	Ncor2	nuclear receptor co-repressor 2
32	A_55_P2108883	AV356131	expressed sequence AV356131
33	A_51_P155458	Dok7	docking protein 7
34	A_55_P2054350	Fbxo44	F-box protein 44
35	A_55_P2083213	Purb	purine rich element binding protein
36	A_51_P490747	AI593442	expressed sequence AI593442
37	A_52_P311853	Ddit4l	DNA-damage-inducible transcript 4-like
38	A_55_P2065059	Wnt2	wingless-related MMTV integrator 2
39	A_55_P2056325	Anxa3	annexin A3
40	A_55_P1998401	Eif2ak4	eukaryotic translation initiation factor 2A kinase 4
41	A_55_P2079158	Fam154b	family with sequence similarity 154, member B
42	A_55_P2153941	Zfp386	zinc finger protein 386 (Kruppel-like zinc finger protein 386)
43	A_51_P237383	Rnase4	ribonuclease, RNase A family 4
44	A_55_P1974602	Map2k7	mitogen-activated protein kinase 7
45	A_51_P155174	Zfp672	zinc finger protein 672
46	A_55_P2097156	Ptchd2	patched domain containing 2
47	A_52_P295104	Smim5	small integral membrane protein 5
48	A_55_P2151138	Dynlt1f	dynein light chain Tctex-type 1F
49	A_55_P2201612	Slc30a7	solute carrier family 30 (zinc transporters) member 7
50	A_55_P2109544	Trnt1	tRNA nucleotidyl transferase, CCA-terminating
51	A_66_P120770	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-hydroxylase
52	A_55_P1983268	4930444P10R	RIKEN cDNA 4930444P10 gene
53	A_51_P191520	Stard10	START domain containing 10
54	A_66_P130366	Stk38l	serine/threonine kinase 38 like
55	A_55_P2293414	1700001C19F	RIKEN cDNA 1700001C19 gene
56	A_55_P2018330	Gm13298	predicted gene 13298
57	A_55_P2005055	Pepd	peptidase D
58	A_51_P470989	Paip1	polyadenylate binding protein-interacting protein 1
59	A_55_P2127587	Smcr8	Smith-Magenis syndrome chromosome 17 breakpoint region protein
60	A_55_P1972490	Psg16	pregnancy specific glycoprotein 16

1				
2	A_55_P1955483	Grb14	growth factor receptor bound prote	
3	A_66_P123055	Gm10845	predicted gene 10845	
4	A_66_P140976	Rpl15	ribosomal protein L15	
5	A_51_P275496	BC026762	cDNA sequence BC026762	
6	A_52_P682745	Dock4	dedicator of cytokinesis 4	
7	A_52_P20639	Rd3	retinal degeneration 3	
8	A_51_P494863	Vmac	vimentin-type intermediate filamer	
9	A_55_P2021094	Tmem181b-ps	transmembrane protein 181B, pse	
10	A_55_P2149382	Gm3448	predicted gene 3448	
11	A_55_P2221647	Al605517	expressed sequence Al605517	
12	A_51_P140237	Fhl2	four and a half LIM domains 2	
13	A_55_P1989524	Fndc1	fibronectin type III domain containi	
14	A_51_P159293	Zbbx	zinc finger, B-box domain containi	
15	A_55_P1995924	Gm13157	predicted gene 13157	
16	A_51_P452820	Rpl31	ribosomal protein L31	
17	A_52_P123738	Rnf41	ring finger protein 41	
18	A_52_P222230		0	0
19	A_51_P327564	Glb1	galactosidase, beta 1	
20	A_51_P422335	Zfp420	zinc finger protein 420	
21	A_55_P2146749	Rps13	ribosomal protein S13	
22	A_66_P116461	Mro	maestro	
23	A_51_P375558	Myoc	myocilin	
24	A_51_P123604	Ppwd1	peptidylprolyl isomerase domain a	
25	A_55_P1962756	Tlll2	tubulin tyrosine ligase-like family, i	
26	A_51_P316801	Wdr60	WD repeat domain 60	
27	A_51_P228193	Ociad1	O CIA domain containing 1	
28	A_55_P1998995	Speg	SPEG complex locus	
29	A_52_P489778	Ablim1	actin-binding LIM protein 1	
30	A_52_P512553	Atg16l2	autophagy related 16-like 2 (S. ce	
31	A_65_P08864	Dph5	DPH5 homolog (S. cerevisiae)	
32	A_55_P1985428	Atg16l2	autophagy related 16-like 2 (S. ce	
33	A_52_P325477	Trim16	tripartite motif-containing 16	
34	A_66_P108434	Ccdc65	coiled-coil domain containing 65	
35	A_51_P502150	Slc9a3r1	solute carrier family 9 (sodium/hyc	
36	A_55_P1970033	Per1	period circadian clock 1	
37	A_51_P409893	Prkar2a	protein kinase, cAMP dependent r	
38	A_55_P2161465	Gm10516	predicted gene 10516	
39	A_55_P2031547	Vmn2r121	vomer nasal 2, receptor 121	
40	A_55_P2062133	Etv3	ets variant gene 3	
41	A_51_P314153	Nr2c2ap	nuclear receptor 2C2-associated p	
42	A_55_P1967539	Hunk	hormonally upregulated Neu-asso	
43	A_51_P140607	Asun	asunder, spermatogenesis regulat	
44	A_55_P2012694	Kcnh5	potassium voltage-gated channel,	
45	A_51_P209183	Cxcl14	chemokine (C-X-C motif) ligand 14	
46	A_52_P253179	Igfbp3	insulin-like growth factor binding p	
47	A_55_P1968977	Stk38l	serine/threonine kinase 38 like	
48	A_55_P1982454	Eps8	epidermal growth factor receptor p	
49	A_55_P2000007	LOC10263935	uncharacterized LOC102639358	
50	A_51_P481821	Spes3	signal peptidase complex subunit	
51	A_51_P480202	Dlx2	distal-less homeobox 2	
52	A_55_P2127258	Dok7	docking protein 7	
53	A_55_P2062688	Msi1	musashi RNA-binding protein 1	
54	A_55_P2023697	Zfp386	zinc finger protein 386 (Kruppel-lik	
55	A_51_P320022	Atp10a	ATPase, class V, type 10A	
56	A_51_P356579	Mxra7	matrix-remodelling associated 7	
57	A_55_P1967514	Dnah7a	dynein, axonemal, heavy chain 7A	
58	A_52_P217710	Fzd6	frizzled homolog 6 (Drosophila)	
59	A_55_P2036723	Stk36	serine/threonine kinase 36	
60	A_55_P1978226	Park2	Parkinson disease (autosomal rec	

1				
2	A_55_P1999958	0		0
3	A_66_P112301	C230072F16F	RIKEN cDNA C230072F16 gene	
4	A_51_P244824	Dapp1	dual adaptor for phosphotyrosine :	
5	A_55_P1969431	Lym5	LYR motif containing 5	
6	A_55_P2145521	Stk38l	serine/threonine kinase 38 like	
7	A_55_P2259125	D7Erttd143e	DNA segment, Chr 7, ERATO Doi	
8	A_55_P2206605	5830444B04R	RIKEN cDNA 5830444B04 gene	
9	A_55_P2151143	Dynlt1c	dynein light chain Tctex-type 1C	
10	A_51_P333965	Cisd2	CDGSH iron sulfur domain 2	
11	A_52_P2710	Cml5	camello-like 5	
12	A_55_P2176248	0		0
13	A_52_P456561	Abcd1	ATP-binding cassette, sub-family I	
14	A_55_P2183735	Pisd	phosphatidylserine decarboxylase	
15	A_52_P565279	Cecr5	cat eye syndrome chromosome re	
16	A_51_P448391	Nkiras1	NFKB inhibitor interacting Ras-like	
17	A_55_P1985693	Fhdc1	FH2 domain containing 1	
18	A_51_P269634	Zfp14	zinc finger protein 14	
19	A_55_P2033480	Gm13298	predicted gene 13298	
20	A_55_P2170509	Yipf4	Yip1 domain family, member 4	
21	A_51_P143468	Klhl26	kelch-like 26	
22	A_52_P436590	Wbscr17	Williams-Beuren syndrome chrom	
23	A_52_P547589	Spag1	sperm associated antigen 1	
24	A_55_P1990134	Cox18	cytochrome c oxidase assembly p	
25	A_55_P2002226	Dzip1	DAZ interacting protein 1	
26	A_66_P101108	Tnrc18	trinucleotide repeat containing 18	
27	A_55_P1987151	Nlrp5	NLR family, pyrin domain containi	
28	A_55_P1988882	Sept9	septin 9	
29	A_55_P2144280	Nnt	nicotinamide nucleotide transhydr	
30	A_55_P2255737	0		0
31	A_55_P2045114	Tmem242	transmembrane protein 242	
32	A_55_P2186558	Tmem242	transmembrane protein 242	
33	A_55_P2212498	C030005K06F	RIKEN cDNA C030005K06 gene	
34	A_55_P2067652	Boc	biregional cell adhesion molecule-	
35	A_55_P1995992	Gm14432	predicted gene 14432	
36	A_51_P263246	Dusp8	dual specificity phosphatase 8	
37	A_51_P433091	Purb	purine rich element binding proteir	
38	A_52_P106620	Tnfrsf11b	tumor necrosis factor receptor sup	
39	A_51_P324934	Mcm3	minichromosome maintenance de	
40	A_55_P2049211	Pisd-ps1	phosphatidylserine decarboxylase	
41	A_51_P193302	Mrps7	mitochondrial ribosomal protein S7	
42	A_51_P342707	Pold2	polymerase (DNA directed), delta	
43	A_55_P2163729	Tvp23a	trans-golgi network vesicle protein	
44	A_55_P2085333	Fbxo44	F-box protein 44	
45	A_55_P1967820	Al661453	expressed sequence Al661453	
46	A_55_P1980292	Purb	purine rich element binding proteir	
47	A_55_P1964638	Cxadr	coxsackie virus and adenovirus re	
48	A_55_P1956918	Adamts5	a disintegrin-like and metalloptic	
49	A_55_P2037883	Ino80	INO80 homolog (S. cerevisiae)	
50	A_55_P2173927	Insr	insulin receptor	
51	A_51_P487913	2600006K01R	RIKEN cDNA 2600006K01 gene	
52	A_55_P2028370	0		0
53	A_55_P1991851	Speg	SPEG complex locus	
54	A_55_P2144285	Nnt	nicotinamide nucleotide transhydr	
55	A_55_P1955568	Extl2	exostoses (multiple)-like 2	
56	A_55_P1976993	Strn	striatin, calmodulin binding protein	
57	A_51_P475228	Armc6	armadillo repeat containing 6	
58	A_55_P2140118	Qpct	glutaminy-peptide cyclotransferas	
59	A_52_P260696	Arnt2	aryl hydrocarbon receptor nuclear	
60	A_55_P2154943	LOC10263302	uncharacterized LOC102633020	

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2	A_52_P627068	Disp2	dispatched homolog 2 (Drosophila	
3	A_55_P2211937	E130101M22	uncharacterized protein E130101M	
4	A_55_P2045658	Nme6	NME/NM23 nucleoside diphospha	
5	A_55_P2322029	3830406C13F	RIKEN cDNA 3830406C13 gene	
6	A_55_P1979929	Prcp	prolylcarboxypeptidase (angiotens	
7	A_52_P646979	D16Ert472e	DNA segment, Chr 16, ERATO Dc	
8	A_55_P2146500	Ccdc107	coiled-coil domain containing 107	
9	A_51_P127915	Rnasek	ribonuclease, RNase K	
10	A_51_P383629	Vps4a	vacuolar protein sorting 4a (yeast)	
11	A_52_P67200	Stt3b	STT3, subunit of the oligosacchar	
12	A_55_P2026818	Slc4a7	solute carrier family 4, sodium bica	
13	A_55_P1955548	Ezr	ezrin	
14	A_55_P1995874	Gm14326	predicted gene 14326	
15	A_55_P2122633	Airn	antisense Igf2r RNA	
16	A_66_P110742		0	0
17	A_51_P414548	Casp7	caspase 7	
18	A_55_P2035717	Pgap2	post-GPI attachment to proteins 2	
19	A_55_P1974088	Stard6	StAR-related lipid transfer (STAR)	
20	A_55_P2044982	Zfp74	zinc finger protein 74	
21	A_55_P1979330	Dapp1	dual adaptor for phosphotyrosine	
22	A_55_P1974855	Zfp868	zinc finger protein 868	
23	A_52_P14526	Zyg11b	zyg-II family member B, cell cycle	
24	A_52_P484838	Rfxank	regulatory factor X-associated ank	
25	A_52_P604629	Csrnp1	cysteine-serine-rich nuclear protei	
26	A_55_P2161695	Kdelc1	KDEL (Lys-Asp-Glu-Leu) containir	
27	A_51_P102507	Vps33a	vacuolar protein sorting 33A (yeas	
28	A_55_P2000798	Ccdc144b	coiled-coil domain containing 144b	
29	A_55_P2049095	Atat1	alpha tubulin acetyltransferase 1	
30	A_51_P312748	Oxsm	3-oxoacyl-ACP synthase, mitocho	
31	A_55_P2035667	Gyk	glycerol kinase	
32	A_55_P2048483	D17Zt10e	DNA segment, Chr 17, Zdenek Tr	
33	A_66_P105736	Net1	neuroepithelial cell transforming g	
34	A_52_P244463	D16Ert472e	DNA segment, Chr 16, ERATO Dc	
35	A_51_P487027	Kcnk2	potassium channel, subfamily K, n	
36	A_51_P233027	Rmdn3	regulator of microtubule dynamics	
37	A_51_P310676	Galr2	galanin receptor 2	
38	A_51_P119031	Naa30	N(alpha)-acetyltransferase 30, Na	
39	A_55_P2133220	Arhgef39	Rho guanine nucleotide exchange	
40	A_55_P2028522	Stac	src homology three (SH3) and cys	
41	A_51_P253897	Psca	prostate stem cell antigen	
42	A_51_P261560	Tex33	testis expressed 33	
43	A_51_P186798		0	0
44	A_55_P2030383	Frm4a	FERM domain containing 4A	
45	A_55_P2098578	Tubd1	tubulin, delta 1	
46	A_51_P181722	Rbks	ribokinase	
47	A_51_P280532	Supt16	suppressor of Ty 16	
48	A_55_P2118891	Zfp882	zinc finger protein 882	
49	A_55_P1989341	Ntng1	netrin G1	
50	A_52_P644534	Dhrsx	dehydrogenase/reductase (SDR fr	
51	A_66_P138585	4833419G08F	RIKEN cDNA 4833419G08 gene	
52	A_55_P1998947	Trim16	tripartite motif-containing 16	
53	A_55_P1994062	Emx2os	Emx2 opposite strand/antisense tr	
54	A_51_P234544	Azin1	antizyme inhibitor 1	
55	A_52_P1187949	Trim5	tripartite motif-containing 5	
56	A_51_P367780	Adamtsl2	ADAMTS-like 2	
57	A_55_P2146996	Wdr52	WD repeat domain 52	
58	A_51_P149562	Apbb2	amyloid beta (A4) precursor protei	
59	A_55_P2173073	Zfp931	zinc finger protein 931	
60	A_51_P283292	Gm14326	predicted gene 14326	

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2	A_52_P376360	Pdgfc	platelet-derived growth factor, C p
3	A_55_P1954436	Gm7967	predicted gene 7967
4	A_55_P1988424	Tpi1	triosephosphate isomerase 1
5	A_65_P02321	Usp36	ubiquitin specific peptidase 36
6	A_51_P343851	Tgfbra1	transforming growth factor, beta re
7	A_55_P1967538	Hunk	hormonally upregulated Neu-asso
8	A_51_P246727	MLXip	MLX interacting protein
9	A_55_P2187043	Tpm1	tropomyosin 1, alpha
10	A_51_P454103	Manba	mannosidase, beta A, lysosomal
11	A_52_P494514	Insr	insulin receptor
12	A_55_P2057994	Mif4gd	MIF4G domain containing
13	A_55_P2007243	Kcnc1	potassium voltage gated channel,
14	A_51_P441494	BC100451	cDNA sequence BC100451
15	A_52_P74576	Ccdc65	coiled-coil domain containing 65
16	A_55_P1993876	Otud7a	OTU domain containing 7A
17	A_51_P382928	Cstf3	cleavage stimulation factor, 3' pre-
18	A_52_P259558	Ogfod1	2-oxoglutarate and iron-dependen
19	A_55_P2037081	2610305D13F	RIKEN cDNA 2610305D13 gene
20	A_52_P412529	Fbxo3	F-box protein 3
21	A_51_P403636	Smad7	SMAD family member 7
22	A_55_P2062469	Col12a1	collagen, type XII, alpha 1
23	A_55_P1992715	Igfbp3	insulin-like growth factor binding p
24	A_55_P2113356	Miip	migration and invasion inhibitory p
25	A_55_P2060278	Fam45a	family with sequence similarity 45,
26	A_55_P2039556	Pak6	p21 protein (Cdc42/Rac)-activatec
27	A_55_P2033445	Tnfrsf1b	tumor necrosis factor receptor sup
28	A_51_P308029	2010107G23F	RIKEN cDNA 2010107G23 gene
29	A_55_P2034600	Gm5523	glyceraldehyde-3-phosphate dehy
30	A_55_P2054300	Alg8	asparagine-linked glycosylation 8
31	A_52_P563617	Ssbp4	single stranded DNA binding prote
32	A_55_P2241204	1500015A07R	RIKEN cDNA 1500015A07 gene
33	A_51_P124748	Tgfb3	transforming growth factor, beta 3
34	A_66_P113662	Tmem62	transmembrane protein 62
35	A_55_P1985554	B4galt4	UDP-Gal:betaGlcNAc beta 1,4-gal
36	A_55_P2148641	Rab4a	RAB4A, member RAS oncogene f
37	A_55_P1996086	Gm14325	predicted gene 14325
38	A_55_P1966958	Mef2d	myocyte enhancer factor 2D
39	A_52_P144794	Tceanc2	transcription elongation factor A (ε
40	A_55_P2427685	Agl	amylo-1,6-glucosidase, 4-alpha-gl
41	A_55_P1969166	Fxr2	fragile X mental retardation, autos
42	A_55_P1973447	Ybx2	Y box protein 2
43	A_55_P2052563	Id1	inhibitor of DNA binding 1
44	A_55_P2078213	1700020I14Ri	RIKEN cDNA 1700020I14 gene
45	A_52_P110068	Rqcd1	rcd1 (required for cell differentiat
46	A_55_P2147791	Fam129c	family with sequence similarity 129
47	A_55_P2026109	Rpap1	RNA polymerase II associated pro
48	A_55_P2354336		0 0
49	A_66_P125212	Mapk1ip11	mitogen-activated protein kinase 1
50	A_55_P2076927	Ints10	integrator complex subunit 10
51	A_52_P558382	Mapk8	mitogen-activated protein kinase ε
52	A_55_P2030721	Ankle1	ankyrin repeat and LEM domain c
53	A_55_P2006525	Adamtsl4	ADAMTS-like 4
54	A_52_P505143	Jrk	jerky
55	A_51_P144648	Vps13b	vacuolar protein sorting 13B (yeas
56	A_55_P2147457	Gm6410	predicted gene 6410
57	A_55_P2013396	Gm14305	predicted gene 14305
58	A_55_P2172566	Insr	insulin receptor
59	A_52_P137691	Trappc5	trafficking protein particle complex
60	A_55_P2187038	Tpm1	tropomyosin 1, alpha

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2	A_52_P662098	Net1	neuroepithelial cell transforming g
3	A_51_P315555	Nars	asparaginyl-tRNA synthetase
4	A_55_P2144075	Pofut2	protein O-fucosyltransferase 2
5	A_65_P17492	Med29	mediator complex subunit 29
6	A_51_P213099	Ntng1	netrin G1
7	A_55_P2212259	4930539J05R	RIKEN cDNA 4930539J05 gene
8	A_51_P149621	Stt3b	STT3, subunit of the oligosacchar
9	A_55_P2047962	Gjc2	gap junction protein, gamma 2
10	A_55_P2158866	Nme6	NME/NM23 nucleoside diphospha
11	A_55_P1966863	Mad2l2	MAD2 mitotic arrest deficient-like ;
12	A_52_P6828	Xk	Kell blood group precursor (McLec
13	A_55_P2102998	Gm3893	predicted gene 3893
14	A_55_P2090152	Vmn2r121	vomeronasal 2, receptor 121
15	A_55_P2041095	Six4	sine oculis-related homeobox 4
16	A_51_P282179	Mtor	mechanistic target of rapamycin (s
17	A_51_P397375	Pet112	PET112 homolog (S. cerevisiae)
18	A_55_P1953226	Gm14484	predicted gene 14484
19	A_55_P2017140	Vmn2r88	vomeronasal 2, receptor 88
20	A_55_P2181334	6030419C18F	RIKEN cDNA 6030419C18 gene
21	A_55_P2121344	Nudcd3	NudC domain containing 3
22	A_52_P85765	Stard6	StAR-related lipid transfer (STAR)
23	A_55_P2161958	2410141K09R	RIKEN cDNA 2410141K09 gene
24	A_55_P2167160	Hdhd2	haloacid dehalogenase-like hydrol
25	A_55_P2023818	Cysltr1	cysteinyl leukotriene receptor 1
26	A_55_P2051666	Nfkbib	nuclear factor of kappa light polyp
27	A_55_P2154049	Myo18a	myosin XVIIIa
28	A_55_P2121038	Gm10825	predicted gene 10825
29	A_52_P180826	Ndufaf7	NADH dehydrogenase (ubiquinon
30	A_55_P2155479	Eps8	epidermal growth factor receptor p
31	A_55_P2169775	Ano3	anoctamin 3
32	A_55_P2341950	Crebzf	CREB/ATF bZIP transcription fact
33	A_55_P2108808	Tubgcp4	tubulin, gamma complex associate
34	A_55_P2021099	Tmem181a	transmembrane protein 181A
35	A_52_P329314		0 0
36	A_55_P2015715	Rab4a	RAB4A, member RAS oncogene f
37	A_55_P2266880	Kirrel	kin of IRRE like (Drosophila)
38	A_51_P215190	Efcab11	EF-hand calcium binding domain
39	A_51_P517381	Cers2	ceramide synthase 2
40	A_55_P2134645	Fam227a	family with sequence similarity 22;
41	A_55_P2115995	Sms	spermine synthase
42	A_51_P211341	Eif3j1	eukaryotic translation initiation fac
43	A_55_P1998194	Snrpn	small nuclear ribonucleoprotein N
44	A_52_P65494	Iqgap2	IQ motif containing GTPase activa
45	A_52_P404895	Tmem62	transmembrane protein 62
46	A_55_P2042146	Fech	ferrochelataase
47	A_55_P2081398		0 0
48	A_51_P221132	L2hgdh	L-2-hydroxyglutarate dehydrogen
49	A_55_P1974442	Sumf2	sulfatase modifying factor 2
50	A_55_P2105563	1700104L18R	RIKEN cDNA 1700104L18 gene
51	A_51_P257684	Stau1	stau1 (RNA binding protein) hon
52	A_52_P412452	Cntn6	contactin 6
53	A_55_P2187171	Sv2c	synaptic vesicle glycoprotein 2c
54	A_55_P1961645	Vcp	valosin containing protein
55	A_55_P1955172	Camk2d	calcium/calmodulin-dependent prc
56	A_55_P2433218	Bloc1s6	biogenesis of lysosomal organelle
57	A_51_P292368	Tmco6	transmembrane and coiled-coil do
58	A_55_P2168118	4933406C10F	RIKEN cDNA 4933406C10 gene
59	A_52_P363216	Gcnt2	glucosaminyl (N-acetyl) transferas
60	A_55_P2094881	Fgfr2	fibroblast growth factor receptor 2

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2	A_55_P2326337	BC026513	cDNA sequence BC026513
3	A_66_P111216	4632427E13R	RIKEN cDNA 4632427E13 gene
4	A_55_P2133165	Wwc1	WW, C2 and coiled-coil domain cc
5	A_55_P2086983	Atxn2	ataxin 2
6	A_55_P1962174	Rab8a	RAB8A, member RAS oncogene f
7	A_55_P2018681	G630016G05F	RIKEN cDNA G630016G05 gene
8	A_52_P417990	Zfp868	zinc finger protein 868
9	A_51_P125183	Coq5	coenzyme Q5 homolog, methyltra
10	A_55_P2261772	Lzts1	leucine zipper, putative tumor sup
11	A_55_P2163363	Clec2f	C-type lectin domain family 2, mer
12	A_55_P1998392	Eif2ak4	eukaryotic translation initiation fac
13	A_55_P2098305	Coq5	coenzyme Q5 homolog, methyltra
14	A_55_P2032478	Sfxn5	sideroflexin 5
15	A_55_P2092776	Apoo	apolipoprotein O
16	A_55_P2012241	Ctso	cathepsin O
17	A_55_P2452384	Mga	MAX gene associated
18	A_52_P663526	Nmrk1	nicotinamide riboside kinase 1
19	A_55_P1974063	Gm2545	predicted gene 2545
20	A_55_P2050592	Gm5785	predicted gene 5785
21	A_51_P411728	2900026A02R	RIKEN cDNA 2900026A02 gene
22	A_55_P1970578	Aamdc	adipogenesis associated Mth938 c
23	A_52_P299358	Lclat1	lysocardiolipin acyltransferase 1
24	A_55_P2288285	2310007J06R	RIKEN cDNA 2310007J06 gene
25	A_55_P2115968	Gm14325	predicted gene 14325
26	A_51_P336391	Tmem18	transmembrane protein 18
27	A_52_P67983	Lcmt2	leucine carboxyl methyltransferas
28	A_51_P114456	Tceanc2	transcription elongation factor A (ε
29	A_55_P1962384	Churc1	churchill domain containing 1
30	A_55_P2053206	Kdm4c	lysine (K)-specific demethylase 4C
31	A_55_P1979246	Cep192	centrosomal protein 192
32	A_51_P341010	Erc8	excision repaircross-complementing
33	A_55_P2388687	1700003G18F	RIKEN cDNA 1700003G18 gene
34	A_55_P2043430	0	0
35	A_55_P2078675	0	0
36	A_55_P2174273	Slco5a1	solute carrier organic anion transp
37	A_52_P147666	Slc30a7	solute carrier family 30 (zinc transp
38	A_55_P2085731	Stk38	serine/threonine kinase 38
39	A_55_P2160737	0	0
40	A_55_P1965674	Alg2	asparagine-linked glycosylation 2
41	A_55_P2170911	Gm10366	predicted gene 10366
42	A_52_P425510	Dnah7a	dynein, axonemal, heavy chain 7A
43	A_55_P2104532	Acacb	acetyl-Coenzyme A carboxylase b
44	A_55_P2383283	2310001H17F	RIKEN cDNA 2310001H17 gene
45	A_52_P600946	Ccdc88c	coiled-coil domain containing 88C
46	A_55_P1999883	Gm14499	predicted gene 14499
47	A_52_P916539	Zbtb34	zinc finger and BTB domain conta
48	A_66_P107790	Myl12a	myosin, light chain 12A, regulatory
49	A_55_P2045535	Rsg1	REM2 and RAB-like small GTPasi
50	A_55_P1973896	Vmn2r86	vomer nasal 2, receptor 86
51	A_55_P2012107	Vmn2r10	vomer nasal 2, receptor 10
52	A_52_P151905	Gm5132	predicted gene 5132
53	A_55_P2169909	Ostm1	osteopetrosis associated transmei
54	A_55_P2186460	Emx2os	Emx2 opposite strand/antisense tr
55	A_51_P381230	Zhx2	zinc fingers and homeoboxes 2
56	A_55_P2161485	Ptchd2	patched domain containing 2
57	A_55_P2160910	Faim2	Fas apoptotic inhibitory molecule ;
58	A_55_P1986208	Ccnb1ip1	cyclin B1 interacting protein 1
59	A_52_P622694	Adal	adenosine deaminase-like
60	A_55_P2293967	Tbc1d5	TBC1 domain family, member 5

1			
2	A_55_P1953984	Gm11033	predicted gene 11033
3	A_66_P130911	Proser2	proline and serine rich 2
4	A_52_P88818	Clybl	citrate lyase beta like
5	A_55_P2033481	Gm13298	predicted gene 13298
6	A_66_P122377	Cd84	CD84 antigen
7	A_51_P320357	Grin2b	glutamate receptor, ionotropic, NV
8	A_52_P504330	Ankib1	ankyrin repeat and IBR domain co
9	A_51_P394154	Ddx51	DEAD (Asp-Glu-Ala-Asp) box poly
10	A_55_P2055642	2810407A14R	RIKEN cDNA 2810407A14 gene
11	A_52_P219913	Cdan1	congenital dyserythropoietic anem
12	A_51_P220150	Angptl7	angiopoietin-like 7
13	A_51_P228865	Zfp72	zinc finger protein 72
14	A_55_P1993094	Mesdc1	mesoderm development candidate
15	A_55_P2005853	Nacc2	nucleus accumbens associated 2,
16	A_51_P473953	Arhgef26	Rho guanine nucleotide exchange
17	A_55_P2057247	Etohi1	ethanol induced 1
18	A_51_P226962	Capn15	calpain 15
19	A_51_P266774	Mfn2	mitofusin 2
20	A_51_P343429	Slc25a37	solute carrier family 25, member 3
21	A_55_P2022434	Gpi1	glucose phosphate isomerase 1
22	A_55_P2025363	Ccnl2	cyclin L2
23	A_55_P2030433	Gpi1	glucose phosphate isomerase 1
24	A_55_P2002918	Klc2	kinesin light chain 2
25	A_55_P1977649	Hoxd8	homeobox D8
26	A_55_P2031382	Crebzf	CREB/ATF bZIP transcription fact
27	A_55_P2124016	Nipsnap1	4-nitrophenylphosphatase domain
28	A_55_P2057268	Magi1	membrane associated guanylate k
29	A_55_P2139713	Phf13	PHD finger protein 13
30	A_65_P10433	Rpp14	ribonuclease P 14 subunit
31	A_55_P2005680	Ipo11	importin 11
32	A_55_P2134351	Lancl3	LanC lantibiotic synthetase compc
33	A_66_P122053	Kcnq5	potassium voltage-gated channel,
34	A_55_P2002220	Dzip1	DAZ interacting protein 1
35	A_55_P1956687	Rab37	RAB37, member RAS oncogene f
36	A_52_P221588	Gm5382	predicted gene 5382
37	A_55_P2062787	Mfap3	microfibrillar-associated protein 3
38	A_55_P2094484	Gm14137	predicted gene 14137
39	A_52_P18765	Hsbp111	heat shock factor binding protein 1
40	A_55_P1983999	Desi1	desumoylating isopeptidase 1
41	A_51_P495581	Tlr1	toll-like receptor 1
42	A_55_P2197134	A930018M24F	RIKEN cDNA A930018M24 gene
43	A_52_P146403	Arhgef38	Rho guanine nucleotide exchange
44	A_55_P2066219	Gm3455	predicted gene 3455
45	A_51_P390775	Ube2e1	ubiquitin-conjugating enzyme E2E
46	A_51_P494006	Scaf8	SR-related CTD-associated factor
47	A_51_P243134	Adcy6	adenylate cyclase 6
48	A_55_P1955851	AI593442	expressed sequence AI593442
49	A_55_P2024555	Ppap2a	phosphatidic acid phosphatase ty
50	A_55_P2108868	Nufip1	nuclear fragile X mental retardatio
51	A_51_P375693	Tmem135	transmembrane protein 135
52	A_55_P1982494	1700012L04R	RIKEN cDNA 1700012L04 gene
53	A_51_P129100	Sec63	SEC63-like (<i>S. cerevisiae</i>)
54	A_55_P2003228	Rerg	RAS-like, estrogen-regulated, gro
55	A_55_P2060722	Uso1	USO1 vesicle docking factor
56	A_55_P2052210	Gdi2	guanosine diphosphate (GDP) dis
57	A_55_P1970887	Vmn2r16	vomer nasal 2, receptor 16
58	A_55_P2061809	Ndufc2	NADH dehydrogenase (ubiquinon
59	A_65_P10180	Rad23b	RAD23b homolog (<i>S. cerevisiae</i>)
60	A_55_P2049483	0	0

1			
2	A_52_P328078	Atp5b	ATP synthase, H ⁺ transporting mi
3	A_51_P342669	Pgam1	phosphoglycerate mutase 1
4	A_55_P2217548	4921515G04F	RIKEN cDNA 4921515G04 gene
5	A_51_P263290	Galnt9	UDP-N-acetyl-alpha-D-galactosan
6	A_55_P2078815	Xk	Kell blood group precursor (McLec
7	A_55_P2107447	Rab37	RAB37, member RAS oncogene f
8	A_51_P150608	Jagn1	jagunal homolog 1 (Drosophila)
9	A_52_P580582	Nppa	natriuretic peptide type A
10	A_51_P107433	Mrpl34	mitochondrial ribosomal protein L3
11	A_55_P1960621	Gm20764	predicted gene, 20764
12	A_51_P146303	Mvb12a	multivesicular body subunit 12A
13	A_51_P242356	Fam114a2	family with sequence similarity 114
14	A_55_P2041372	Gm3693	predicted gene 3693
15	A_51_P476711	Skiv2l2	superkiller viralicidic activity 2-like
16	A_51_P133747	Ppp1r3e	protein phosphatase 1, regulatory
17	A_51_P288505	Tradd	TNFRSF1A-associated via death r
18	A_55_P1968683	Anks1b	ankyrin repeat and sterile alpha m
19	A_55_P2177233	Abhd5	abhydrolase domain containing 5
20	A_55_P2071326	Rpl36	ribosomal protein L36
21	A_51_P208377	Trappc5	trafficking protein particle complex
22	A_66_P130612	2810408A11R	RIKEN cDNA 2810408A11 gene
23	A_52_P133578	Gpr158	G protein-coupled receptor 158
24	A_51_P289414	Spg11	spastic paraplegia 11
25	A_55_P2002113	Rpl36	ribosomal protein L36
26	A_55_P2041893	Gm6404	predicted gene 6404
27	A_51_P244558	Rab3gap2	RAB3 GTPase activating protein s
28	A_55_P1999829	Thoc7	THO complex 7 homolog (Drosopl
29	A_55_P2143499	Pgbd5	piggyBac transposable element de
30	A_55_P2012096	Bmp8a	bone morphogenetic protein 8a
31	A_55_P2058953	Rpl13a	ribosomal protein L13A
32	A_55_P2026054	Usp37	ubiquitin specific peptidase 37
33	A_55_P2027077	Shc2	SHC (Src homology 2 domain con
34	A_55_P2067131	Dclre1c	DNA cross-link repair 1C, PSO2 h
35	A_51_P131025	Ngdn	neuroguidin, EIF4E binding protei
36	A_55_P1967648	Fln	folliculin
37	A_55_P2044967	Zfp74	zinc finger protein 74
38	A_52_P117576	Casp3	caspase 3
39	A_51_P184223	Pcdhb7	protocadherin beta 7
40	A_55_P1956418	Efr3b	EFR3 homolog B (S. cerevisiae)
41	A_51_P268843	Rasip1	Ras interacting protein 1
42	A_51_P421140	Tubb6	tubulin, beta 6 class V
43	A_52_P275678	Gpr135	G protein-coupled receptor 135
44	A_51_P246677	Rec8	REC8 meiotic recombination prote
45	A_51_P241943	Sap30l	SAP30-like
46	A_51_P234627	Nubpl	nucleotide binding protein-like
47	A_55_P2175915	Ccl28	chemokine (C-C motif) ligand 28
48	A_52_P47781	Slitrk3	SLIT and NTRK-like family, memb
49	A_55_P1967983	Use1	unconventional SNARE in the ER
50	A_51_P167374	Gpatch1	G patch domain containing 1
51	A_51_P456838	Fbxl21	F-box and leucine-rich repeat prot
52	A_55_P2056186	Siva1	SIVA1, apoptosis-inducing factor
53	A_55_P2088711	Sgsm1	small G protein signaling modulato
54	A_55_P2057941	1700049G17F	RIKEN cDNA 1700049G17 gene
55	A_52_P561377	Fam160b1	family with sequence similarity 160
56	A_52_P552589	Map4k1	mitogen-activated protein kinase k
57	A_55_P2104572	6330416G13F	RIKEN cDNA 6330416G13 gene
58	A_52_P108321	Ccdc71	coiled-coil domain containing 71
59	A_55_P2114863	Mgll	monoglyceride lipase
60	A_55_P2069012	Pidd1	p53 induced death domain protein

1			
2	A_52_P409457	Ppcdc	phosphopantothenoylcysteine dec
3	A_51_P517001	D130040H23F	RIKEN cDNA D130040H23 gene
4	A_52_P595642	Smim7	small integral membrane protein 7
5	A_52_P179729	Txn14a	thioredoxin-like 4A
6	A_55_P2471798	Snap23	synaptosomal-associated protein :
7	A_55_P2167898	Nat9	N-acetyltransferase 9 (GCN5-relat
8	A_55_P2109585	Plekha7	pleckstrin homology domain conta
9	A_51_P372156	4930563E22R	RIKEN cDNA 4930563E22 gene
10	A_55_P1992160	Mbp	myelin basic protein
11	A_55_P2153797	Prnp	prion protein
12	A_55_P1974477	Msh3	mutS homolog 3 (E. coli)
13	A_55_P2183597	Tbc1d2	TBC1 domain family, member 2
14	A_55_P1981461	5430410E06R	RIKEN cDNA 5430410E06 gene
15	A_55_P2330545	Zfp81	zinc finger protein 81
16	A_55_P2027152	Ssh1	slingshot homolog 1 (Drosophila)
17	A_55_P1970676	Sh3yl1	Sh3 domain YSC-like 1
18	A_51_P348652	Spast	spastin
19	A_52_P448870	Rab26	RAB26, member RAS oncogene f
20	A_55_P2074291	Fbxo6	F-box protein 6
21	A_51_P122141	Mamstr	MEF2 activating motif and SAP dc
22	A_55_P2025514	Pnpla3	patatin-like phospholipase domain
23	A_52_P673499	Shmt1	serine hydroxymethyltransferase 1
24	A_52_P73559	Gm7241	predicted pseudogene 7241
25	A_55_P2079009	Slco2b1	solute carrier organic anion transp
26	A_55_P2011692		0 0
27	A_55_P1977454	4930570G19F	RIKEN cDNA 4930570G19 gene
28	A_55_P2032147	Wnt9a	wingless-type MMTV integration s
29	A_55_P2003951	Tmem192	transmembrane protein 192
30	A_52_P734742	Lrrc73	leucine rich repeat containing 73
31	A_55_P2000027	Spink2	serine peptidase inhibitor, Kazal ty
32	A_55_P2013203	Oxtr	oxytocin receptor
33	A_51_P291682	Tmed4	transmembrane emp24 protein tra
34	A_52_P434841	Coa4	cytochrome c oxidase assembly fa
35	A_55_P2051313	Gstk1	glutathione S-transferase kappa 1
36	A_55_P2039061	Trim12c	tripartite motif-containing 12C
37	A_52_P327402	Cds1	CDP-diacylglycerol synthase 1
38	A_55_P2115225	Fap	fibroblast activation protein
39	A_51_P105520	Nomo1	nodal modulator 1
40	A_55_P2308743	A430106A12F	RIKEN cDNA A430106A12 gene
41	A_55_P2157360	Tagap1	T cell activation GTPase activating
42	A_51_P239286	Bcl2l12	BCL2-like 12 (proline rich)
43	A_55_P2157902	Igsf10	immunoglobulin superfamily, mem
44	A_51_P216605	Hbp1	high mobility group box transcripti
45	A_55_P1967500	Nell1	NEL-like 1
46	A_51_P245546	Synrg	synergin, gamma
47	A_55_P2153496	Ppp2r3d	protein phosphatase 2 (formerly 2.
48	A_55_P2049448	Phtf1	putative homeodomain transcriptic
49	A_51_P475628	Paqr6	progesterone and adipoQ receptor fan
50	A_55_P1963687	Tsen54	tRNA splicing endonuclease 54 hc
51	A_66_P128927	Gm6306	predicted gene 6306
52	A_66_P133993	Gm5093	predicted gene 5093
53	A_51_P302942	Rasl10a	RAS-like, family 10, member A
54	A_51_P341789	Sugp1	SURP and G patch domain contai
55	A_66_P137383	Ddx55	DEAD (Asp-Glu-Ala-Asp) box poly
56	A_52_P640386	Usp53	ubiquitin specific peptidase 53
57	A_55_P2032318	4930522L14R	RIKEN cDNA 4930522L14 gene
58	A_51_P487547	Ccdc91	coiled-coil domain containing 91
59	A_55_P1991500	Obfc1	oligonucleotide/oligosaccharide-bi
60	A_55_P2018847	Crlf2	cytokine receptor-like factor 2

1			
2	A_55_P2077263	Cenpk	centromere protein K
3	A_51_P382369	Zfp608	zinc finger protein 608
4	A_55_P2021892	Ccdc114	coiled-coil domain containing 114
5	A_55_P2067513	Slc10a3	solute carrier family 10 (sodium/bil
6	A_55_P2045096	Hjrp	Holliday junction recognition prote
7	A_55_P1974233	Dtd2	D-tyrosyl-tRNA deacylase 2
8	A_55_P1971025	Paqr6	progesterin and adipoQ receptor fan
9	A_55_P2037812	Palmd	palmdelphin
10	A_55_P1968245	Ftl1	ferritin light chain 1
11	A_55_P2123831	Thap6	THAP domain containing 6
12	A_55_P1961241	LOC10263459	uncharacterized LOC102634598
13	A_55_P2063316	Mgll	monoglyceride lipase
14	A_55_P1975832	1810009N02F	RIKEN cDNA 1810009N02 gene
15	A_51_P331827	Slc25a41	solute carrier family 25, member 4
16	A_55_P2007919	Akr1c19	aldo-keto reductase family 1, mem
17	A_51_P240801	Tmem173	transmembrane protein 173
18	A_55_P2143075	Ubc	ubiquitin C
19	A_55_P2145139		0 0
20	A_51_P469968	H2-M3	histocompatibility 2, M region locu
21	A_55_P2057127	Nim1k	NIM1 serine/threonine protein kin
22	A_51_P298802	Bfsp2	beaded filament structural protein
23	A_51_P468762	Alkbh6	alkB, alkylation repair homolog 6 (
24	A_55_P2097340	Camkv	CaM kinase-like vesicle-associate
25	A_55_P2053497	Poli	polymerase (DNA directed), iota
26	A_51_P437478	Zfp566	zinc finger protein 566
27	A_52_P343627	Rbp7	retinol binding protein 7, cellular
28	A_66_P126415	Gm8013	predicted gene 8013
29	A_55_P2106235	Syngn2	synaptogyrin 2
30	A_51_P116487	Lsm4	LSM4 homolog, U6 small nuclear
31	A_52_P472302	Fxyd6	FXD domain-containing ion trans
32	A_55_P2008936	Slc2a9	solute carrier family 2 (facilitated g
33	A_52_P71105	Sertad3	SERTA domain containing 3
34	A_52_P593037	Acs15	acyl-CoA synthetase long-chain fa
35	A_55_P1998872	Slitrk5	SLIT and NTRK-like family, memb
36	A_66_P122699	Cux2	cut-like homeobox 2
37	A_66_P128445	Bend7	BEN domain containing 7
38	A_51_P192139	Zfp74	zinc finger protein 74
39	A_66_P104309	Myl2	myosin, light polypeptide 2, regula
40	A_55_P2000304	Terf1	telomeric repeat binding factor 1
41	A_55_P2137701	Gm13247	predicted gene 13247
42	A_55_P2007273	Pole	polymerase (DNA directed), epsil
43	A_55_P1968200	Hjrp	Holliday junction recognition prote
44	A_52_P357055	Ccdc91	coiled-coil domain containing 91
45	A_52_P211418	G2e3	G2/M-phase specific E3 ubiquitin l
46	A_51_P230439	Ppfbp2	PTPRF interacting protein, binding
47	A_55_P1961140	Mettl3	methyltransferase like 3
48	A_55_P2018666	Thrsp	thyroid hormone responsive
49	A_55_P2223282	B130019D13F	RIKEN cDNA B130019D13 gene
50	A_55_P2227580	A130072N09F	RIKEN cDNA A130072N09 gene
51	A_55_P1971174	Cd1d2	CD1d2 antigen
52	A_55_P2084332	Pigp	phosphatidylinositol glycan anchor
53	A_51_P151586	Gsg2	germ cell-specific gene 2
54	A_55_P1968908	Hypk	huntingtin interacting protein K
55	A_55_P2019113	Apol7b	apolipoprotein L 7b
56	A_52_P367675	Acin1	apoptotic chromatin condensation
57	A_51_P465273	Mettl17	methyltransferase like 17
58	A_51_P421223	Fv1	Friend virus susceptibility 1
59	A_55_P2131340	Churc1	churchill domain containing 1
60	A_55_P2061371	Gm15698	transcription elongation factor B (ε

1			
2	A_55_P1970299	Mttp	microsomal triglyceride transfer pr
3	A_51_P108581	Adrbk2	adrenergic receptor kinase, beta 2
4	A_52_P67270	4930515G01F	RIKEN cDNA 4930515G01 gene
5	A_55_P2121846		0 0
6	A_55_P1968858	Cadps	Ca2+-dependent secretion activat
7	A_66_P111430	2410006H16F	RIKEN cDNA 2410006H16 gene
8	A_52_P257686	Rwdd3	RWD domain containing 3
9	A_55_P2167323	Cort	cortistatin
10	A_51_P101573	Klc4	kinesin light chain 4
11	A_55_P2457154	G2e3	G2/M-phase specific E3 ubiquitin l
12	A_55_P2035951	Haus8	4HAUS augmin-like complex, sub
13	A_51_P455807	Ehd4	EH-domain containing 4
14	A_51_P253732	Il17rd	interleukin 17 receptor D
15	A_55_P2143251	Rims3	regulating synaptic membrane exc
16	A_51_P414126	Rab19	RAB19, member RAS oncogene f
17	A_55_P2137941	Fxyd2	FXYP domain-containing ion trans
18	A_55_P2072656	Ckmt1	creatine kinase, mitochondrial 1, u
19	A_51_P312437	Dhrs7	dehydrogenase/reductase (SDR f
20	A_52_P664404	Zfp286	zinc finger protein 286
21	A_55_P2000533	Polk	polymerase (DNA directed), kapp
22	A_51_P353392	Cript	cysteine-rich PDZ-binding protein
23	A_55_P2417936	AW125324	expressed sequence AW125324
24	A_55_P2181009	Gpr180	G protein-coupled receptor 180
25	A_55_P2028936	5033425G24F	RIKEN cDNA 5033425G24 gene
26	A_55_P2003541	Nrcam	neuron-glia-CAM-related cell adhe
27	A_51_P310164	2810459M11F	RIKEN cDNA 2810459M11 gene
28	A_52_P338956	Aspg	asparaginase homolog (S. cerevis
29	A_66_P131169	LOC10086226	uncharacterized LOC100862268
30	A_51_P223569	Ddx4	DEAD (Asp-Glu-Ala-Asp) box poly
31	A_55_P1974487	Atp8b5	ATPase, class I, type 8B, member
32	A_55_P2064257	Dnaic2	dynein, axonemal, intermediate ct
33	A_55_P2075213	Kbtbd11	kelch repeat and BTB (POZ) dom
34	A_55_P1953103	Nudt7	nudix (nucleoside diphosphate lin
35	A_55_P2014100	Gm7120	predicted gene 7120
36	A_55_P2108820	Adamts3	a disintegrin-like and metalloptic
37	A_52_P1092823	Irx1	Iroquois related homeobox 1 (Dro
38	A_55_P2045085	Rpl34-ps1	ribosomal protein L34, pseudogen
39	A_52_P640922	Dcdc2a	doublecortin domain containing 2
40	A_51_P327874	Pth1r	parathyroid hormone 1 receptor
41	A_52_P348031	Syt9	synaptotagmin IX
42	A_55_P2031692	Gstm6	glutathione S-transferase, mu 6
43	A_55_P2111148	Gemin5	gem (nuclear organelle) associate
44	A_55_P2031496	Rufy3	RUN and FYVE domain containin
45	A_52_P434306		0 0
46	A_55_P1984690	Ptprr	protein tyrosine phosphatase, rec
47	A_51_P431870	Map1s	microtubule-associated protein 1S
48	A_55_P2060991	BC005764	cDNA sequence BC005764
49	A_51_P218953	Zfp536	zinc finger protein 536
50	A_55_P1985410	Reps2	RALBP1 associated Eps domain c
51	A_55_P1956812	Fam83g	family with sequence similarity 83,
52	A_66_P106611	Gna14	guanine nucleotide binding proteir
53	A_51_P394833	Tshz1	teashirt zinc finger family member
54	A_51_P477019	Rnaset2a	ribonuclease T2A
55	A_55_P2169311	4930515G01F	RIKEN cDNA 4930515G01 gene
56	A_51_P461108	Osbpl10	oxysterol binding protein-like 10
57	A_55_P2149951	Prx	periaxin
58	A_51_P116906	Rapgef3	Rap guanine nucleotide exchange
59	A_55_P2108784	Arhgap22	Rho GTPase activating protein 22
60	A_51_P413507	2010109A12R	RIKEN cDNA 2010109A12 gene

1				
2	A_51_P481159	Cbr3	carbonyl reductase 3	
3	A_55_P1954092		0	0
4	A_66_P112024		0	0
5	A_55_P1979027	Tmem65	transmembrane protein 65	
6	A_51_P451588	Plekhb1	pleckstrin homology domain conta	
7	A_55_P2045007	Hrh1	histamine receptor H1	
8	A_55_P2096368	LOC10263277	ADP-ribosylation factor 1-like	
9	A_55_P2115127	Mphosph10	M-phase phosphoprotein 10 (U3 s	
10	A_55_P1975120	Gm10777	predicted gene 10777	
11	A_55_P2106150	Cenpk	centromere protein K	
12	A_55_P2036813		0	0
13	A_55_P2007771	Catsper2	cation channel, sperm associated	
14	A_55_P2157966	Map1a	microtubule-associated protein 1 /	
15	A_51_P254045	Traip	TRAF-interacting protein	
16	A_55_P1955726	Ptpn5	protein tyrosine phosphatase, non	
17	A_55_P2044602	Siah3	seven in absentia homolog 3 (Dro:	
18	A_55_P2021266	Hpse	heparanase	
19	A_55_P2097178	Idua	iduronidase, alpha-L-	
20	A_55_P1999240	Gm2696	predicted gene 2696	
21	A_55_P2185504	Masp2	mannan-binding lectin serine pept	
22	A_55_P1983959	Ftl1	ferritin light chain 1	
23	A_55_P2185950	Bpnt1	bisphosphate 3'-nucleotidase 1	
24	A_55_P2088223	Synpr	synaptoporin	
25	A_55_P2187076	Sncg	synuclein, gamma	
26	A_55_P2121156	LOC10263421	uncharacterized LOC102634215	
27	A_55_P2099540	H2afj	H2A histone family, member J	
28	A_55_P2169227	Ccdc184	coiled-coil domain containing 184	
29	A_55_P2105362	Tmed5	transmembrane emp24 protein tra	
30	A_51_P215374	Slc6a17	solute carrier family 6 (neurotrans	
31	A_55_P2059986	Chst14	carbohydrate (N-acetyl)galactosyl	
32	A_52_P558609	Clec16a	C-type lectin domain family 16, me	
33	A_55_P2179834	Gatad2a	GATA zinc finger domain containir	
34	A_51_P273609	Itpka	inositol 1,4,5-trisphosphate 3-kina	
35	A_55_P2124026	Synj2	synaptojanin 2	
36	A_51_P348617	2310045N01F	RIKEN cDNA 2310045N01 gene	
37	A_51_P408989	L3hypdh	L-3-hydroxyproline dehydratase (ti	
38	A_51_P331661	Ubiad1	UbiA prenyltransferase domain co	
39	A_55_P1998299	Itgba4	integrin beta 4	
40	A_55_P2119892	ErbB4	v-erb-a erythroblastic leukemia vir	
41	A_55_P1958597	Slc27a3	solute carrier family 27 (fatty acid t	
42	A_55_P2105220	Hscb	HscB iron-sulfur cluster co-chaper	
43	A_55_P2059179	Slc48a1	solute carrier family 48 (heme tran	
44	A_66_P138584	Mnd1	meiotic nuclear divisions 1 homolc	
45	A_52_P116264	Adhfe1	alcohol dehydrogenase, iron conte	
46	A_52_P650325	Slc35e1	solute carrier family 35, member E	
47	A_55_P2095909	Lamtor3	late endosomal/lysosomal adaptor	
48	A_52_P489295	Adamts1	a disintegrin-like and metallopeptic	
49	A_65_P01247	Hjrp	Holliday junction recognition prote	
50	A_55_P1953387	Fabp5	fatty acid binding protein 5, epider	
51	A_55_P2023707	Camta1	calmodulin binding transcription ac	
52	A_51_P497240	E330013P04F	RIKEN cDNA E330013P04 gene	
53	A_51_P134812	Chac1	ChaC, cation transport regulator 1	
54	A_55_P1961014	Selenbp1	selenium binding protein 1	
55	A_52_P529195	Pcdhb4	protocadherin beta 4	
56	A_55_P1963508	Slc13a5	solute carrier family 13 (sodium-de	
57	A_55_P2004960	9130017K11R	RIKEN cDNA 9130017K11 gene	
58	A_55_P2072391	Acp1	acid phosphatase 1, soluble	
59	A_55_P2183914	Gm7120	predicted gene 7120	
60	A_51_P147034	Ica1l	islet cell autoantigen 1-like	

1			
2	A_55_P2040371	Rnaset2a	ribonuclease T2A
3	A_51_P116687	1700010I14Ri	RIKEN cDNA 1700010I14 gene
4	A_55_P2008722	Gm13157	predicted gene 13157
5	A_51_P474422	Ift27	intraflagellar transport 27
6	A_55_P1986639	3110070M22F	RIKEN cDNA 3110070M22 gene
7	A_51_P517430	Cd1d1	CD1d1 antigen
8	A_55_P2000973	Syt15	synaptotagmin XV
9	A_51_P135340	Panx1	pannexin 1
10	A_51_P282268	Snopc1	small nuclear RNA activating com
11	A_55_P2329298	Gm12758	predicted gene 12758
12	A_55_P2055087	Prkar2b	protein kinase, cAMP dependent r
13	A_52_P167535	Efcab12	EF-hand calcium binding domain
14	A_51_P191782	Olfml3	olfactomedin-like 3
15	A_52_P563375	Lgals2	lectin, galactose-binding, soluble 2
16	A_55_P2163774	Crip1	cysteine-rich protein 1 (intestinal)
17	A_55_P1969497	Lynx1	Ly6/neurotoxin 1
18	A_52_P463977	Tmem140	transmembrane protein 140
19	A_51_P477736	4932415M13F	RIKEN cDNA 4932415M13 gene
20	A_55_P2023864	Mfap1a	microfibrillar-associated protein 1A
21	A_52_P559919	Eif2ak2	eukaryotic translation initiation fac
22	A_55_P2356736	6720483E21R	RIKEN cDNA 6720483E21 gene
23	A_55_P2052834	Lst1	leukocyte specific transcript 1
24	A_55_P1953919	Me3	malic enzyme 3, NADP(+)-depend
25	A_51_P446796	Camta1	calmodulin binding transcription ac
26	A_51_P464308	Gnb4	guanine nucleotide binding proteir
27	A_55_P2001628	Rps4l	ribosomal protein S4-like
28	A_52_P38908	Tmem132b	transmembrane protein 132B
29	A_51_P283968	Adamts18	a disintegrin-like and metallopeptic
30	A_52_P630867	Abcc4	ATP-binding cassette, sub-family 4
31	A_55_P1953920	Me3	malic enzyme 3, NADP(+)-depend
32	A_55_P2105321	Acin1	apoptotic chromatin condensation
33	A_51_P502437	Cacna2d3	calcium channel, voltage-depende
34	A_51_P369803	Psmb9	proteasome (prosome, macropain
35	A_55_P1953087	Mcm3	minichromosome maintenance de
36	A_55_P2115567	Slc26a1	solute carrier family 26 (sulfate tra
37	A_55_P2044242	Slc13a5	solute carrier family 13 (sodium-de
38	A_55_P2079619	Rnf43	ring finger protein 43
39	A_55_P1959076	Zfp930	zinc finger protein 930
40	A_55_P2048119	Slc29a4	solute carrier family 29 (nucleosid
41	A_52_P400509	Atm	ataxia telangiectasia mutated hom
42	A_51_P506733	P2rx7	purinergic receptor P2X, ligand-ga
43	A_55_P1973352		0 0
44	A_55_P2008417	Mnd1	meiotic nuclear divisions 1 homolc
45	A_55_P2106459	Zfhx3	zinc finger homeobox 3
46	A_55_P2370160	C130009A20F	RIKEN cDNA C130009A20 gene
47	A_51_P417251	6330403K07R	RIKEN cDNA 6330403K07 gene
48	A_55_P2067116	Dclre1c	DNA cross-link repair 1C, PSO2 h
49	A_65_P03606	Rpap2	RNA polymerase II associated pro
50	A_55_P2062593	Gm4924	predicted gene 4924
51	A_55_P2155644	2010315B03R	RIKEN cDNA 2010315B03 gene
52	A_55_P2075313	Zfp619	zinc finger protein 619
53	A_55_P2048478	Olfml1	olfactomedin-like 1
54	A_55_P2018181	A730008H23F	RIKEN cDNA A730008H23 gene
55	A_52_P481279	Drc1	dynein regulatory complex subunil
56	A_55_P2073642	1600014C10F	RIKEN cDNA 1600014C10 gene
57	A_55_P2123683	Chrdl1	chordin-like 1
58	A_55_P2016034	Nlrc5	NLR family, CARD domain contain
59	A_55_P2035424	Hpgd	hydroxyprostaglandin dehydrogen
60	A_55_P2059090	Tagap	T cell activation Rho GTPase activ

1			
2	A_52_P305230	Igsf21	immunoglobulin superfamily, mem
3	A_55_P1960735	Gdf15	growth differentiation factor 15
4	A_55_P2090330	Kcnmb4	potassium large conductance calc
5	A_52_P574653	Bid	BH3 interacting domain death ago
6	A_55_P2080880	Clcnkb	chloride channel Kb
7	A_52_P590535	Fbln2	fibulin 2
8	A_65_P01834	Lima1	LIM domain and actin binding 1
9	A_55_P2116650		0 0
10	A_55_P2056557		0 0
11	A_55_P2079116		0 0
12	A_55_P2057622	Ocel1	occludin/ELL domain containing 1
13	A_55_P2041828	Tubb3	tubulin, beta 3 class III
14	A_52_P124472	Kcnd2	potassium voltage-gated channel,
15	A_55_P2334927	9.13E+15	uncharacterized 9130022E09
16	A_52_P573255	Cdc42ep1	CDC42 effector protein (Rho GTP
17	A_55_P2147280	Myh1	myosin, heavy polypeptide 1, skel
18	A_55_P1983958	Gm20746	predicted gene, 20746
19	A_66_P122415	Snhg6	small nucleolar RNA host gene 6
20	A_52_P48546	Rnf41	ring finger protein 41
21	A_52_P1042732	Akap5	A kinase (PRKA) anchor protein 5
22	A_55_P2076303	March8	membrane-associated ring finger (
23	A_55_P2154977	Rpap3	RNA polymerase II associated pro
24	A_55_P2006035	Galnt15	UDP-N-acetyl-alpha-D-galactosan
25	A_55_P2133205	Nmt2	N-myristoyltransferase 2
26	A_55_P1957213	3930401B19R	RIKEN cDNA 3930401B19 gene
27	A_55_P2115151	Pxylp1	2-phosphoxylose phosphatase 1
28	A_51_P506937	Mrps12	mitochondrial ribosomal protein S'
29	A_55_P2110290	Tmem254a	transmembrane protein 254a
30	A_55_P2088720		0 0
31	A_55_P2209258	B430105A11F	RIKEN cDNA B430105A11 gene
32	A_52_P250555	Dynll1	dynein light chain LC8-type 1
33	A_55_P2027852	Ccl25	chemokine (C-C motif) ligand 25
34	A_52_P8324	Tmem178	transmembrane protein 178
35	A_52_P441294	Chl1	cell adhesion molecule with homol
36	A_55_P1967553	Tmem254c	transmembrane protein 254c
37	A_51_P241210	Lhfp13	lipoma HMGIC fusion partner-like
38	A_55_P2029746		0 0
39	A_55_P1954724		0 0
40	A_51_P337944	Bmp2k	BMP2 inducible kinase
41	A_55_P2007673	Lrsam1	leucine rich repeat and sterile alp
42	A_52_P447196	Col4a6	collagen, type IV, alpha 6
43	A_52_P650379	Strap	serine/threonine kinase receptor a
44	A_55_P1976898	Pnp2	purine-nucleoside phosphorylase :
45	A_55_P1994339	Dhrs7c	dehydrogenase/reductase (SDR fr
46	A_66_P125862	A930005H10F	RIKEN cDNA A930005H10 gene
47	A_55_P1987499	Pttg1	pituitary tumor-transforming gene
48	A_55_P2011659	Anapc5	anaphase-promoting complex sub
49	A_55_P2213214	A030001D20F	RIKEN cDNA A030001D20 gene
50	A_51_P140690	Stmn3	stathmin-like 3
51	A_55_P2013223	S100z	S100 calcium binding protein, zeta
52	A_52_P331762	Lmo1	LIM domain only 1
53	A_51_P355427	Timp4	tissue inhibitor of metalloproteinas
54	A_51_P382970	Itga9	integrin alpha 9
55	A_51_P497985	C2	complement component 2 (within
56	A_51_P360918	Ehd3	EH-domain containing 3
57	A_51_P309854	Kcnn2	potassium intermediate/small conc
58	A_66_P125035	Duxbl2	doubl homeobox B-like 2
59	A_55_P2063256	Lgals4	lectin, galactose binding, soluble 4
60	A_51_P497100	Lgals4	lectin, galactose binding, soluble 4

1			
2	A_51_P129149	Gatad2a	GATA zinc finger domain containi
3	A_55_P2148534	Nr1d2	nuclear receptor subfamily 1, grou
4	A_55_P2010936	Fbxo17	F-box protein 17
5	A_55_P2033425	Grm5	glutamate receptor, metabotropic :
6	A_51_P292357	Rps3a1	ribosomal protein S3A1
7	A_52_P257625	Esm1	endothelial cell-specific molecule
8	A_55_P2058791	4833420G17F	RIKEN cDNA 4833420G17 gene
9	A_55_P2106525	Nmnat3	nicotinamide nucleotide adenyltr
10	A_55_P2040600	Exd1	exonuclease 3'-5' domain containi
11	A_55_P2140212		0 0
12	A_55_P2093774	Chl1	cell adhesion molecule with homol
13	A_52_P165773	Prmt8	protein arginine N-methyltransfera
14	A_55_P2014304	Kank1	KN motif and ankyrin repeat doma
15	A_51_P458778	Hpgd	hydroxyprostaglandin dehydrogen
16	A_55_P2162344	Lrsam1	leucine rich repeat and sterile alpr
17	A_55_P2004179	Col2a1	collagen, type II, alpha 1
18	A_55_P2096867	Gap43	growth associated protein 43
19	A_55_P1968276	Tomm22	translocase of outer mitochondrial
20	A_55_P2315012	4930458D05F	RIKEN cDNA 4930458D05 gene
21	A_55_P1978465	H2-Q5	histocompatibility 2, Q region locu:
22	A_55_P1953972	Pdhb	pyruvate dehydrogenase (lipoamic
23	A_55_P2212603	Apba2	amyloid beta (A4) precursor protei
24	A_51_P194249	Stmn4	stathmin-like 4
25	A_51_P128667	Lynx1	Ly6/neurotoxin 1
26	A_66_P105175	Bche	butyrylcholinesterase
27	A_55_P2176792	Sh3gl3	SH3-domain GRB2-like 3
28	A_66_P108247	Ucp3	uncoupling protein 3 (mitochondria
29	A_55_P2045642	Stmn4	stathmin-like 4
30	A_55_P2091359	Padi2	peptidyl arginine deiminase, type I
31	A_52_P597775	Gprc5a	G protein-coupled receptor, family
32	A_51_P259296	Lpl	lipoprotein lipase
33	A_52_P257812	Lpl	lipoprotein lipase
34	A_55_P2074656	Padi2	peptidyl arginine deiminase, type I
35	A_51_P297105	Ucp2	uncoupling protein 2 (mitochondria
36	A_52_P157450	Abhd1	abhydrolase domain containing 1
37	A_52_P613498	4833420G17F	RIKEN cDNA 4833420G17 gene
38	A_51_P159453	Serpina3n	serine (or cysteine) peptidase inhil
39	A_55_P2026270	Cfi	complement component factor i
40	A_51_P462428	Galnt15	UDP-N-acetyl-alpha-D-galactosan
41	A_52_P393314	P2rx7	purinergic receptor P2X, ligand-ga
42	A_55_P1952482	Pbp2	phosphatidylethanolamine binding
43	A_55_P2105944	Olf2r224	olfactory receptor 224
44	A_52_P206492	Pop4	processing of precursor 4, ribonuc
45	A_55_P2026420	Pou6f1	POU domain, class 6, transcription
46	A_52_P111031	Pcdh17	protocadherin 17
47	A_55_P2137527	Fam183b	family with sequence similarity 18:
48	A_55_P2132207	1810037I17Ri	RIKEN cDNA 1810037I17 gene
49	A_52_P303176	1810037I17Ri	RIKEN cDNA 1810037I17 gene
50	A_66_P130813	Samd4	sterile alpha motif domain containi
51	A_55_P1966774	Serpina3i	serine (or cysteine) peptidase inhil
52	A_52_P516409	Col4a6	collagen, type IV, alpha 6
53	A_55_P1966838	Xaf1	XIAP associated factor 1
54			
55			
56			
57			
58			
59			
60			

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 (Ocl1), 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-neuraminy1-2,3-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_011336]
 Mus musculus MAM domain containing 2 (Mamd2), 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]

1 Mus musculus tetratricopeptide repeat domain 8 (Ttc8), transcript variant 1, mRNA [NM_029553]
2 Mus musculus lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730014H17 product:
3 Mus musculus matrix-remodelling associated 7 (Mxra7), mRNA [NM_026280]
4 PREDICTED: Mus musculus tumor necrosis factor (ligand) superfamily, member 13, opposite strand (Tnfsf
5 Mus musculus centrosomal protein 76 (Cep76), mRNA [NM_001081073]
6 sorting nexin 29 [Source:MGI Symbol;Acc:MGI:1921728] [ENSMUST00000134941]
7 GAG_IPMAE (P31790) Retrovirus-related Gag polyprotein, partial (43%) [TC1705975]
8 Mus musculus cDNA sequence BC006965 (BC006965), long non-coding RNA [NR_024085]
9 Mus musculus ATPase, class V, type 10D (Atp10d), mRNA [NM_153389]
10 Mus musculus angiogenin, ribonuclease A family, member 3 (Ang3), mRNA [NM_001123394]
11 Mus musculus predicted gene 13152 (Gm13152), mRNA [NM_001039209]
12 Mus musculus cerebral endothelial cell adhesion molecule (Cercam), mRNA [NM_207298]
13 coiled-coil domain containing 32 [Source:MGI Symbol;Acc:MGI:2685477] [ENSMUST00000110834]
14 Mus musculus cAMP responsive element binding protein 3 (Creb3), mRNA [NM_013497]
15 Mus musculus RIKEN cDNA 1190007I07 gene (1190007I07Rik), transcript variant 1, mRNA [NM_0011355]
16 Mus musculus purinergic receptor P2Y, G-protein coupled 2 (P2ry2), mRNA [NM_008773]
17 Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430416G10 product:
18 Mus musculus phosphatidylserine decarboxylase, pseudogene 3 (Pisd-ps3), non-coding RNA [NR_003518]
19 Mus musculus diacylglycerol O-acyltransferase 2 (Dgat2), mRNA [NM_026384]
20 Mus musculus family with sequence similarity 32, member A (Fam32a), mRNA [NM_026455]
21 Mus musculus histidyl-tRNA synthetase (Hars), mRNA [NM_008214]
22 Mus musculus acetyl-Coenzyme A carboxylase beta (Acacb), mRNA [NM_133904]
23 Mus musculus predicted gene 3448 (Gm3448), mRNA [NM_001123367]
24 Mus musculus branched chain aminotransferase 2, mitochondrial (Bcat2), transcript variant 2, mRNA [NM_
25 Mus musculus carbonic anhydrase 11 (Car11), mRNA [NM_009800]
26 Mus musculus immunity-related GTPase family M member 2 (Irgm2), mRNA [NM_019440]
27 Mus musculus predicted gene, EG633640, mRNA (cDNA clone MGC:118117 IMAGE:6309338), complete
28 Mus musculus La ribonucleoprotein domain family, member 1 (Larp1), mRNA [NM_028451]
29 Mus musculus BCL2-like 15 (Bcl2l15), transcript variant 1, mRNA [NM_001142959]
30 Mus musculus nuclear receptor co-repressor 2 (Ncor2), transcript variant 1, mRNA [NM_011424]
31 Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330057J19 product:
32 docking protein 7 [Source:MGI Symbol;Acc:MGI:3584043] [ENSMUST00000114270]
33 Mus musculus F-box protein 44 (Fbxo44), transcript variant 1, mRNA [NM_173401]
34 Mus musculus purine rich element binding protein B (Purb), mRNA [NM_011221]
35 Mus musculus expressed sequence AI593442 (AI593442), transcript variant 1, mRNA [NM_001286641]
36 Mus musculus DNA-damage-inducible transcript 4-like (Ddit4l), mRNA [NM_030143]
37 Mus musculus wingless-related MMTV integration site 2 (Wnt2), mRNA [NM_023653]
38 Mus musculus annexin A3 (Anxa3), mRNA [NM_013470]
39 eukaryotic translation initiation factor 2 alpha kinase 4 [Source:MGI Symbol;Acc:MGI:1353427] [ENSMUST
40 Mus musculus family with sequence similarity 154, member B (Fam154b), mRNA [NM_177894]
41 Mus musculus zinc finger protein 386 (Kruppel-like) (Zfp386), transcript variant 1, mRNA [NM_001004066]
42 Mus musculus ribonuclease, RNase A family 4 (Rnase4), transcript variant 1, mRNA [NM_021472]
43 Mus musculus mitogen-activated protein kinase kinase 7 (Map2k7), transcript variant 1, mRNA [NM_00104
44 Mus musculus zinc finger protein 672 (Zfp672), transcript variant 2, non-coding RNA [NR_028331]
45 Mus musculus patched domain containing 2 (Ptchd2), mRNA [NM_001083342]
46 Mus musculus small integral membrane protein 5 (Smim5), mRNA [NM_183259]
47 Mus musculus dynein light chain Tctex-type 1F (Dyntl1f), transcript variant 2, mRNA [NM_001199948]
48 Mus musculus solute carrier family 30 (zinc transporter), member 7 (Slc30a7), mRNA [NM_023214]
49 Mus musculus tRNA nucleotidyl transferase, CCA-adding, 1 (Trnt1), transcript variant 1, mRNA [NM_0012
50 Mus musculus tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptid
51 Mus musculus RIKEN cDNA 4930444P10 gene (4930444P10Rik), mRNA [NM_001243238]
52 Mus musculus START domain containing 10 (Stard10), mRNA [NM_019990]
53 Mus musculus serine/threonine kinase 38 like (Stk38l), mRNA [NM_172734]
54 Mus musculus RIKEN cDNA 1700001C19 gene (1700001C19Rik), transcript variant 1, mRNA [NM_02929
55 Mus musculus predicted gene 13298 (Gm13298), mRNA [NM_001085530]
56 Mus musculus peptidase D (Pepd), mRNA [NM_008820]
57 Mus musculus polyadenylate binding protein-interacting protein 1 (Paip1), transcript variant 1, mRNA [NM_
58 Mus musculus Smith-Magenis syndrome chromosome region, candidate 8 homolog (human) (Smcr8), tran:
59 PREDICTED: Mus musculus pregnancy specific glycoprotein 16 (Psg16), transcript variant X2, mRNA [XM

1 Mus musculus growth factor receptor bound protein 14 (Grb14), mRNA [NM_016719]
2 Mus musculus predicted gene 10845 (Gm10845), long non-coding RNA [NR_033535]
3 Mus musculus ribosomal protein L15 (Rpl15), mRNA [NM_025586]
4 Mus musculus cDNA clone IMAGE:5065404. [BC029971]
5 Mus musculus dedicator of cytokinesis 4 (Dock4), mRNA [NM_172803]
6 Mus musculus retinal degeneration 3 (Rd3), transcript variant 1, mRNA [NM_023727]
7 Mus musculus vimentin-type intermediate filament associated coiled-coil protein (Vmac), transcript variant
8 Mus musculus predicted gene, 547127, mRNA (cDNA clone IMAGE:577088), complete cds. [BC096660]
9 Mus musculus predicted gene 3448 (Gm3448), mRNA [NM_001123367]
10 Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430517C21 prod
11 Mus musculus four and a half LIM domains 2 (Fhl2), transcript variant 1, mRNA [NM_010212]
12 Mus musculus fibronectin type III domain containing 1 (Fndc1), mRNA [NM_001081416]
13 Mus musculus zinc finger, B-box domain containing (Zbbx), mRNA [NM_172515]
14 Mus musculus predicted gene 13157 (Gm13157), mRNA [NM_001127189]
15 Mus musculus ribosomal protein L31 (Rpl31), transcript variant 3, mRNA [NM_053257]
16 Mus musculus ring finger protein 41 (Rnf41), transcript variant 1, mRNA [NM_001164237]
17 Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530041D01 proc
18 Mus musculus galactosidase, beta 1 (Glb1), transcript variant 1, mRNA [NM_009752]
19 Mus musculus zinc finger protein 420 (Zfp420), mRNA [NM_172740]
20 Mus musculus ribosomal protein S13 (Rps13), mRNA [NM_026533]
21 Mus musculus maestro (Mro), mRNA [NM_027741]
22 Mus musculus myocilin (Myoc), mRNA [NM_010865]
23 Mus musculus peptidylprolyl isomerase domain and WD repeat containing 1 (Ppwd1), mRNA [NM_172807]
24 Mus musculus tubulin tyrosine ligase-like family, member 2 (Ttl2), mRNA [NM_001098267]
25 Mus musculus WD repeat domain 60 (Wdr60), mRNA [NM_146039]
26 Mus musculus OCIA domain containing 1 (Ociad1), transcript variant 1, mRNA [NM_023429]
27 Mus musculus SPEG complex locus (Speg), transcript variant 3, mRNA [NM_001085371]
28 Mus musculus actin-binding LIM protein 1 (Ablim1), transcript variant 1, mRNA [NM_178688]
29 Mus musculus autophagy related 16-like 2 (S. cerevisiae) (Atg16l2), mRNA [NM_001111111]
30 Mus musculus 4 days neonate thymus cDNA, RIKEN full-length enriched library, clone:B630008G01 produ
31 Mus musculus autophagy related 16-like 2 (S. cerevisiae) (Atg16l2), mRNA [NM_001111111]
32 Mus musculus tripartite motif-containing 16 (Trim16), mRNA [NM_053169]
33 Mus musculus coiled-coil domain containing 65 (Ccdc65), mRNA [NM_153518]
34 Mus musculus solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1 (Slc9a3r1), mRN
35 Mus musculus period circadian clock 1 (Per1), transcript variant 1, mRNA [NM_011065]
36 Mus musculus protein kinase, cAMP dependent regulatory, type II alpha (Prkar2a), mRNA [NM_008924]
37 Mus musculus predicted gene 10516 (Gm10516), long non-coding RNA [NR_033536]
38 Mus musculus vomeronasal 2, receptor 121 (Vmn2r121), mRNA [NM_001100616]
39 Mus musculus ets variant gene 3 (Etv3), transcript variant 1, mRNA [NM_001286844]
40 Mus musculus nuclear receptor 2C2-associated protein (Nr2c2ap), transcript variant 1, mRNA [NM_001025
41 Mus musculus hormonally upregulated Neu-associated kinase (Hunk), mRNA [NM_015755]
42 Mus musculus asunder, spermatogenesis regulator (Asun), mRNA [NM_138757]
43 Mus musculus potassium voltage-gated channel, subfamily H (eag-related), member 5 (Kcnh5), mRNA [NM
44 Mus musculus chemokine (C-X-C motif) ligand 14 (Cxcl14), mRNA [NM_019568]
45 Mus musculus insulin-like growth factor binding protein 3 (Igfbp3), mRNA [NM_008343]
46 Mus musculus serine/threonine kinase 38 like (Stk38l), mRNA [NM_172734]
47 Mus musculus epidermal growth factor receptor pathway substrate 8 (Eps8), transcript variant 1, mRNA [NI
48 PREDICTED: Mus musculus uncharacterized LOC102639358 (LOC102639358), transcript variant X1, ncR
49 Mus musculus signal peptidase complex subunit 3 homolog (S. cerevisiae) (Spcs3), mRNA [NM_029701]
50 Mus musculus distal-less homeobox 2 (Dlx2), mRNA [NM_010054]
51 Mus musculus docking protein 7 (Dok7), mRNA [NM_172708]
52 Mus musculus musashi RNA-binding protein 1 (Msi1), mRNA [NM_008629]
53 Mus musculus zinc finger protein 386 (Kruppel-like) (Zfp386), transcript variant 1, mRNA [NM_001004066]
54 Mus musculus ATPase, class V, type 10A (Atp10a), mRNA [NM_009728]
55 Mus musculus matrix-remodelling associated 7 (Mxra7), mRNA [NM_026280]
56 Mus musculus dynein, axonemal, heavy chain 7A (Dnah7a), mRNA [NM_001252070]
57 Mus musculus frizzled homolog 6 (Drosophila) (Fzd6), transcript variant 1, mRNA [NM_008056]
58 Mus musculus serine/threonine kinase 36 (Stk36), mRNA [NM_175031]
59 Mus musculus Parkinson disease (autosomal recessive, juvenile) 2, parkin (Park2), mRNA [NM_016694]

1 Mus musculus 2 cells egg cDNA, RIKEN full-length enriched library, clone:B020040A10 product:unclassifia
2 PREDICTED: Mus musculus RIKEN cDNA C230072F16 gene (C230072F16Rik), transcript variant X3, ncF
3 Mus musculus dual adaptor for phosphotyrosine and 3-phosphoinositides 1 (Dapp1), mRNA [NM_011932]
4 Mus musculus LYR motif containing 5 (Lyrm5), transcript variant 1, mRNA [NM_001163628]
5 Mus musculus serine/threonine kinase 38 like (Stk38l), mRNA [NM_172734]
6 Mus musculus DNA segment, Chr 7, ERATO Doi 143, expressed (D7Ert43e), long non-coding RNA [NR
7 Mus musculus RIKEN cDNA 5830444B04 gene (5830444B04Rik), transcript variant 1, long non-coding RN
8 Mus musculus dynein light chain Tctex-type 1C (Dyntl1c), mRNA [NM_001166630]
9 Mus musculus CDGSH iron sulfur domain 2 (Cisd2), mRNA [NM_025902]
10 Mus musculus camello-like 5 (Cml5), mRNA [NM_023493]
11 BB001409 RIKEN full-length enriched, 13 days embryo head Mus musculus cDNA clone 3110026C13 3'. [I
12 Mus musculus ATP-binding cassette, sub-family D (ALD), member 1 (Abcd1), mRNA [NM_007435]
13 Mus musculus phosphatidylserine decarboxylase (Pisd), mRNA [NM_177298]
14 Mus musculus cat eye syndrome chromosome region, candidate 5 (Cecr5), mRNA [NM_144815]
15 Mus musculus NFkB inhibitor interacting Ras-like protein 1 (Nkiras1), mRNA [NM_023526]
16 Mus musculus FH2 domain containing 1 (Fhdc1), transcript variant 1, mRNA [NM_001205355]
17 Mus musculus zinc finger protein 14 (Zfp14), transcript variant 1, mRNA [NM_011748]
18 Mus musculus predicted gene 13298 (Gm13298), mRNA [NM_001085530]
19 Mus musculus Yip1 domain family, member 4 (Yipf4), mRNA [NM_026417]
20 Mus musculus kelch-like 26 (Kihl26), transcript variant 2, mRNA [NM_178771]
21 Mus musculus Williams-Beuren syndrome chromosome region 17 homolog (human) (Wbscr17), mRNA [N
22 Mus musculus sperm associated antigen 1 (Spag1), mRNA [NM_012031]
23 Mus musculus cytochrome c oxidase assembly protein 18 (Cox18), transcript variant 1, mRNA [NM_00116
24 Mus musculus DAZ interacting protein 1 (Dzip1), mRNA [NM_025943]
25 Mus musculus trinucleotide repeat containing 18 (Tnrc18), transcript variant A, mRNA [NM_001122730]
26 Mus musculus NLR family, pyrin domain containing 5 (Nlrp5), transcript variant 1, mRNA [NM_011860]
27 Mus musculus septin 9 (Sept9), transcript variant 2, mRNA [NM_001113487]
28 Mus musculus nicotinamide nucleotide transhydrogenase (Nnt), transcript variant 1, mRNA [NM_008710]
29 Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130026C10 prod
30 Mus musculus transmembrane protein 242 (Tmem242), mRNA [NM_027457]
31 Mus musculus transmembrane protein 242 (Tmem242), mRNA [NM_027457]
32 Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130009K03 prodi
33 Mus musculus biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) binding prot
34 Mus musculus predicted gene, OTTMUSG00000016609 (OTTMUSG00000016609), mRNA [NM_0011004
35 Mus musculus dual specificity phosphatase 8 (Dusp8), mRNA [NM_008748]
36 Mus musculus purine rich element binding protein B (Purb), mRNA [NM_011221]
37 Mus musculus tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (Tnfrsf11b), mRN
38 Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E4300C
39 Mus musculus phosphatidylserine decarboxylase, pseudogene 1 (Pisd-ps1), non-coding RNA [NR_003517
40 Mus musculus mitochondrial ribosomal protein S7 (Mrps7), mRNA [NM_025305]
41 Mus musculus polymerase (DNA directed), delta 2, regulatory subunit (Pold2), mRNA [NM_008894]
42 Mus musculus trans-golgi network vesicle protein 23A (Tvp23a), mRNA [NM_001013778]
43 Mus musculus F-box protein 44 (Fbxo44), transcript variant 1, mRNA [NM_173401]
44 Mus musculus expressed sequence A1661453 (A1661453), mRNA [NM_145489]
45 Mus musculus purine rich element binding protein B (Purb), mRNA [NM_011221]
46 Mus musculus coxsackie virus and adenovirus receptor (Cxadr), transcript variant 1, mRNA [NM_0010251:
47 Mus musculus a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 5
48 Mus musculus INO80 homolog (S. cerevisiae) (Ino80), mRNA [NM_026574]
49 Mus musculus insulin receptor (Insr), mRNA [NM_010568]
50 Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2600006K01 pi
51 BC009829 Sin3A associated protein p30-like {Homo sapiens} (exp=-1; wgp=0; cg=0), complete [TC161034
52 Mus musculus SPEG complex locus (Speg), transcript variant 2, mRNA [NM_001085370]
53 Mus musculus nicotinamide nucleotide transhydrogenase (Nnt), transcript variant 1, mRNA [NM_008710]
54 Mus musculus exostoses (multiple)-like 2 (Extl2), transcript variant 1, mRNA [NM_021388]
55 Mus musculus striatin, calmodulin binding protein (Strn), mRNA [NM_011500]
56 Mus musculus armadillo repeat containing 6 (Armc6), mRNA [NM_133972]
57 Mus musculus glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (Qpct), mRNA [NM_027455]
58 Mus musculus aryl hydrocarbon receptor nuclear translocator 2 (Arnt2), mRNA [NM_007488]
59 PREDICTED: Mus musculus uncharacterized LOC102633020 (LOC102633020), ncRNA [XR_382000]
60

1 Mus musculus dispatched homolog 2 (*Drosophila*) (*Disp2*), mRNA [NM_170593]
2 Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130101M22 produc
3 Mus musculus NME/NM23 nucleoside diphosphate kinase 6 (*Nme6*), mRNA [NM_018757]
4 PREDICTED: Mus musculus RIKEN cDNA 3830406C13 gene (3830406C13Rik), transcript variant X1, mR
5 Mus musculus prolylcarboxypeptidase (angiotensinase C) (*Prpc*), mRNA [NM_028243]
6 Mus musculus DNA segment, Chr 16, ERATO Doi 472, expressed (D16Ert472e), transcript variant 2, mRl
7 coiled-coil domain containing 107 [Source:MGI Symbol;Acc:MGI:1913423] [ENSMUST00000107922]
8 Mus musculus ribonuclease, RNase K (*Rnasek*), mRNA [NM_173742]
9 Mus musculus vacuolar protein sorting 4a (yeast) (*Vps4a*), mRNA [NM_126165]
10 Mus musculus STT3, subunit of the oligosaccharyltransferase complex, homolog B (*S. cerevisiae*) (*Stt3b*),
11 Mus musculus solute carrier family 4, sodium bicarbonate cotransporter, member 7 (*Slc4a7*), mRNA [NM_C
12 Mus musculus ezrin (*Ezr*), mRNA [NM_009510]
13 Mus musculus predicted gene 14326 (*Gm14326*), transcript variant 2, mRNA [NM_001282028]
14 Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length en
15 predicted gene 9949 [Source:MGI Symbol;Acc:MGI:3647947] [ENSMUST00000067743]
16 Mus musculus caspase 7 (*Casp7*), mRNA [NM_007611]
17 Mus musculus post-GPI attachment to proteins 2 (*Pgap2*), transcript variant 1, mRNA [NM_001291358]
18 Mus musculus STAR-related lipid transfer (START) domain containing 6 (*Stard6*), transcript variant 1, mRN
19 Mus musculus zinc finger protein 74 (*Zfp74*), mRNA [NM_178384]
20 Mus musculus dual adaptor for phosphotyrosine and 3-phosphoinositides 1 (*Dapp1*), mRNA [NM_011932]
21 Mus musculus zinc finger protein 868 (*Zfp868*), transcript variant 1, mRNA [NM_172754]
22 Mus musculus zyg-II family member B, cell cycle regulator (*Zyg11b*), mRNA [NM_001033634]
23 Mus musculus regulatory factor X-associated ankyrin-containing protein (*Rfxank*), transcript variant 1, mRN
24 Mus musculus cysteine-serine-rich nuclear protein 1 (*Csrnp1*), mRNA [NM_153287]
25 Mus musculus KDEL (Lys-Asp-Glu-Leu) containing 1 (*Kdelc1*), mRNA [NM_023645]
26 Mus musculus vacuolar protein sorting 33A (yeast) (*Vps33a*), mRNA [NM_029929]
27 Mus musculus coiled-coil domain containing 144B (*Ccdc144b*), mRNA [NM_178418]
28 Mus musculus alpha tubulin acetyltransferase 1 (*Atat1*), transcript variant 1, mRNA [NM_001142744]
29 Mus musculus 3-oxoacyl-ACP synthase, mitochondrial (*Oxsm*), mRNA [NM_027695]
30 Mus musculus glycerol kinase (*Gyk*), transcript variant 1, mRNA [NM_008194]
31 Mus musculus D17Mia10e clone c7 mRNA, partial sequence. [U49252]
32 Mus musculus neuroepithelial cell transforming gene 1 (*Net1*), transcript variant 1, mRNA [NM_019671]
33 Mus musculus DNA segment, Chr 16, ERATO Doi 472, expressed (D16Ert472e), transcript variant 1, mRl
34 Mus musculus potassium channel, subfamily K, member 2 (*Kcnk2*), transcript variant 2, mRNA [NM_01060
35 Mus musculus regulator of microtubule dynamics 3 (*Rmdn3*), mRNA [NM_001033136]
36 Mus musculus galanin receptor 2 (*Galr2*), mRNA [NM_010254]
37 Mus musculus N(alpha)-acetyltransferase 30, NatC catalytic subunit (*Naa30*), mRNA [NM_001081430]
38 Mus musculus Rho guanine nucleotide exchange factor (GEF) 39 (*Arhgef39*), mRNA [NM_001013377]
39 Mus musculus src homology three (SH3) and cysteine rich domain (*Stac*), mRNA [NM_016853]
40 Mus musculus prostate stem cell antigen (*Pzca*), mRNA [NM_028216]
41 Mus musculus testis expressed 33 (*Tex33*), transcript variant 1, mRNA [NM_001163612]
42 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930439M07 product:uncl
43 Mus musculus FERM domain containing 4A (*Frmd4a*), transcript variant 2, mRNA [NM_001177843]
44 Mus musculus tubulin, delta 1 (*Tubd1*), transcript variant 1, mRNA [NM_001199045]
45 Mus musculus ribokinase (*Rbks*), mRNA [NM_153196]
46 Mus musculus suppressor of Ty 16 (*Supt16*), mRNA [NM_033618]
47 Mus musculus zinc finger protein 882 (*Zfp882*), mRNA [NM_001166645]
48 Mus musculus netrin G1 (*Ntng1*), transcript variant a, mRNA [NM_030699]
49 Mus musculus dehydrogenase/reductase (SDR family) X chromosome (*Dhrsx*), mRNA [NM_001033326]
50 Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833419G08 product:u
51 Mus musculus tripartite motif-containing 16 (*Trim16*), mRNA [NM_053169]
52 Mus musculus *Emx2* opposite strand/antisense transcript (non-protein coding) (*Emx2os*), long non-coding l
53 Mus musculus antizyme inhibitor 1 (*Azin1*), transcript variant 2, mRNA [NM_018745]
54 tripartite motif-containing 5 [Source:MGI Symbol;Acc:MGI:3646853] [ENSMUST00000138557]
55 Mus musculus ADAMTS-like 2 (*Adamtsl2*), mRNA [NM_029981]
56 Mus musculus WD repeat domain 52 (*Wdr52*), mRNA [NM_001033247]
57 Mus musculus amyloid beta (A4) precursor protein-binding, family B, member 2 (*Apbb2*), transcript variant
58 Mus musculus zinc finger protein 931 (*Zfp931*), mRNA [NM_001162922]
59 Mus musculus predicted gene 14326 (*Gm14326*), transcript variant 1, mRNA [NM_001190302]

1 Mus musculus platelet-derived growth factor, C polypeptide (Pdgfc), mRNA [NM_019971]
2 PREDICTED: Mus musculus predicted gene 7967 (Gm7967), misc_RNA [XR_387291]
3 Mus musculus triosephosphate isomerase 1 (Tpi1), mRNA [NM_009415]
4 Mus musculus ubiquitin specific peptidase 36 (Usp36), mRNA [NM_001033528]
5 Mus musculus transforming growth factor, beta receptor associated protein 1 (Tgfbrap1), mRNA [NM_0010
6 Mus musculus hormonally upregulated Neu-associated kinase (Hunk), mRNA [NM_015755]
7 Mus musculus MLX interacting protein (Mlxip), transcript variant 2, mRNA [NM_133917]
8 Mus musculus tropomyosin 1, alpha (Tpm1), transcript variant 1, mRNA [NM_001164248]
9 Mus musculus mannosidase, beta A, lysosomal (Manba), mRNA [NM_027288]
10 Mus musculus insulin receptor (Insr), mRNA [NM_010568]
11 Mus musculus MIF4G domain containing (Mif4gd), transcript variant 3, mRNA [NM_001243586]
12 Mus musculus potassium voltage gated channel, Shaw-related subfamily, member 1 (Kcnc1), transcript var
13 Mus musculus cDNA sequence BC100451 (BC100451), mRNA [NM_021440]
14 Mus musculus coiled-coil domain containing 65 (Ccdc65), mRNA [NM_153518]
15 Mus musculus OTU domain containing 7A (Otud7a), mRNA [NM_130880]
16 Mus musculus cleavage stimulation factor, 3' pre-RNA, subunit 3 (Cstf3), transcript variant 1, mRNA [NM_1
17 Mus musculus 2-oxoglutarate and iron-dependent oxygenase domain containing 1 (Ogfod1), transcript vari
18 Mus musculus RIKEN cDNA 2610305D13 gene (2610305D13Rik), mRNA [NM_145078]
19 Mus musculus F-box protein 3 (Fbxo3), transcript variant 2, mRNA [NM_020593]
20 Mus musculus SMAD family member 7 (Smad7), mRNA [NM_001042660]
21 Mus musculus collagen, type XII, alpha 1 (Col12a1), mRNA [NM_001290308]
22 insulin-like growth factor binding protein 3 [Source:MGI Symbol;Acc:MGI:96438] [ENSMUST00000135887]
23 Mus musculus migration and invasion inhibitory protein (Miip), mRNA [NM_001025365]
24 Mus musculus family with sequence similarity 45, member A (Fam45a), transcript variant 1, mRNA [NM_02
25 Mus musculus p21 protein (Cdc42/Rac)-activated kinase 6 (Pak6), transcript variant 1, mRNA [NM_001033
26 Mus musculus tumor necrosis factor receptor superfamily, member 1b (Tnfrsf1b), mRNA [NM_011610]
27 Mus musculus RIKEN cDNA 2010107G23 gene (2010107G23Rik), mRNA [NM_027251]
28 Mus musculus predicted pseudogene 5523 (Gm5523), non-coding RNA [NR_004447]
29 Mus musculus asparagine-linked glycosylation 8 (alpha-1,3-glucosyltransferase) (Alg8), mRNA [NM_19903
30 Mus musculus single stranded DNA binding protein 4 (Ssbp4), mRNA [NM_133772]
31 Mus musculus RIKEN cDNA 1500015A07 gene (1500015A07Rik), long non-coding RNA [NR_029432]
32 Mus musculus transforming growth factor, beta 3 (Tgfb3), mRNA [NM_009368]
33 Mus musculus transmembrane protein 62 (Tmem62), mRNA [NM_175285]
34 Mus musculus UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4 (B4galt4), transcript var
35 Mus musculus RAB4A, member RAS oncogene family (Rab4a), mRNA [NM_009003]
36 Mus musculus predicted gene 14325 (Gm14325), mRNA [NM_001024849]
37 Mus musculus myocyte enhancer factor 2D (Mef2d), mRNA [NM_133665]
38 Mus musculus transcription elongation factor A (SII) N-terminal and central domain containing 2 (Tceanc2),
39 Mus musculus amylo-1,6-glucosidase, 4-alpha-glucanotransferase (AgI), mRNA [NM_001081326]
40 Mus musculus fragile X mental retardation, autosomal homolog 2 (Fxr2), mRNA [NM_011814]
41 Y box protein 2 [Source:MGI Symbol;Acc:MGI:1096372] [ENSMUST00000018698]
42 Mus musculus inhibitor of DNA binding 1 (Id1), mRNA [NM_010495]
43 Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, c
44 Mus musculus rcd1 (required for cell differentiation) homolog 1 (S. pombe) (Rqcd1), mRNA [NM_021383]
45 Mus musculus family with sequence similarity 129, member C (Fam129c), mRNA [NM_001166213]
46 Mus musculus RNA polymerase II associated protein 1 (Rpap1), transcript variant 1, mRNA [NM_177294]
47 Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830223B06 product:hypo
48 Mus musculus mitogen-activated protein kinase 1 interacting protein 1-like (Mapk1ip1l), mRNA [NM_17868
49 Mus musculus integrator complex subunit 10 (Ints10), mRNA [NM_027590]
50 Mus musculus mitogen-activated protein kinase 8 (Mapk8), mRNA [NM_016700]
51 Mus musculus ankyrin repeat and LEM domain containing 1 (Ankle1), mRNA [NM_172756]
52 Mus musculus ADAMTS-like 4 (Adamtsl4), mRNA [NM_144899]
53 Mus musculus jerky (Jrk), mRNA [NM_008415]
54 Mus musculus vacuolar protein sorting 13B (yeast) (Vps13b), mRNA [NM_177151]
55 PREDICTED: Mus musculus predicted gene 6410 (Gm6410), misc_RNA [XR_378684]
56 Mus musculus predicted gene 14305 (Gm14305), mRNA [NM_001099327]
57 Mus musculus insulin receptor (Insr), mRNA [NM_010568]
58 Mus musculus trafficking protein particle complex 5 (Trappc5), mRNA [NM_025701]
59 Mus musculus tropomyosin 1, alpha (Tpm1), transcript variant 1, mRNA [NM_001164248]

1 Mus musculus neuroepithelial cell transforming gene 1 (Net1), transcript variant 1, mRNA [NM_019671]
2 Mus musculus asparaginyl-tRNA synthetase (Nars), transcript variant 2, mRNA [NM_027350]
3 Mus musculus protein O-fucosyltransferase 2 (Pofut2), mRNA [NM_030262]
4 Mus musculus mediator complex subunit 29 (Med29), mRNA [NM_026042]
5 Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130203P04 product
6 Mus musculus RIKEN cDNA 4930539J05 gene (4930539J05Rik), long non-coding RNA [NR_030689]
7 Mus musculus STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae) (Stt3b),
8 Mus musculus gap junction protein, gamma 2 (Gjc2), transcript variant 2, mRNA [NM_175452]
9 Mus musculus NME/NM23 nucleoside diphosphate kinase 6 (Nme6), mRNA [NM_018757]
10 Mus musculus MAD2 mitotic arrest deficient-like 2 (Mad2l2), mRNA [NM_027985]
11 Mus musculus Kell blood group precursor (McLeod phenotype) homolog (Xk), mRNA [NM_023500]
12 Mus musculus predicted gene 3893 (Gm3893), long non-coding RNA [NR_033506]
13 Mus musculus vomeronasal 2, receptor 121 (Vmn2r121), mRNA [NM_001100616]
14 Mus musculus sine oculis-related homeobox 4 (Six4), mRNA [NM_011382]
15 Mus musculus mechanistic target of rapamycin (serine/threonine kinase) (Mtor), mRNA [NM_020009]
16 Mus musculus PET112 homolog (S. cerevisiae) (Pet112), mRNA [NM_144896]
17 Mus musculus predicted gene 14484 (Gm14484), mRNA [NM_001025260]
18 Mus musculus vomeronasal 2, receptor 88 (Vmn2r88), mRNA [NM_011686]
19 Mus musculus RIKEN cDNA 6030419C18 gene (6030419C18Rik), mRNA [NM_176921]
20 Mus musculus NudC domain containing 3 (Nudcd3), mRNA [NM_173748]
21 Mus musculus STAR-related lipid transfer (START) domain containing 6 (Stard6), transcript variant 1, mRNA
22 Mus musculus RIKEN cDNA 2410141K09 gene (2410141K09Rik), transcript variant 1, mRNA [NM_00129C
23 Mus musculus haloacid dehalogenase-like hydrolase domain containing 2 (Hdhd2), transcript variant 3, mF
24 Mus musculus cysteinyl leukotriene receptor 1 (Cysltr1), transcript variant 1, mRNA [NM_021476]
25 Mus musculus nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, beta (Nfkbib), ml
26 myosin XVIIIa [Source:MGI Symbol;Acc:MGI:2667185] [ENSMUST00000100795]
27 Mus musculus predicted gene 10825 (Gm10825), long non-coding RNA [NR_028580]
28 Mus musculus NADH dehydrogenase (ubiquinone) 1 alpha subcomplex assembly factor 7 (Ndufaf7), mRN
29 Mus musculus epidermal growth factor receptor pathway substrate 8 (Eps8), transcript variant 1, mRNA [NI
30 PREDICTED: Mus musculus anoctamin 3 (Ano3), transcript variant X3, mRNA [XM_006499262]
31 Mus musculus CREB/ATF bZIP transcription factor (Crebzf), transcript variant 1, mRNA [NM_145151]
32 Mus musculus tubulin, gamma complex associated protein 4 (Tubgcp4), transcript variant 1, mRNA [NM_1:
33 Mus musculus transmembrane protein 181A (Tmem181a), mRNA [NM_001033178]
34 Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830048115 product:hypotl
35 Mus musculus RAB4A, member RAS oncogene family (Rab4a), mRNA [NM_009003]
36 Mus musculus kin of IRRE like (Drosophila) (Kirrel), transcript variant 1, mRNA [NM_001170985]
37 Mus musculus EF-hand calcium binding domain 11 (Efcab11), mRNA [NM_030172]
38 Mus musculus ceramide synthase 2 (Cers2), mRNA [NM_029789]
39 family with sequence similarity 227, member A [Source:MGI Symbol;Acc:MGI:1922979] [ENSMUST00000C
40 Mus musculus spermine synthase (Sms), mRNA [NM_009214]
41 Mus musculus eukaryotic translation initiation factor 3, subunit J1 (Eif3j1), mRNA [NM_144545]
42 Mus musculus small nuclear ribonucleoprotein N (Snrpn), transcript variant 3, mRNA [NM_001082962]
43 Mus musculus IQ motif containing GTPase activating protein 2 (Iqgap2), mRNA [NM_027711]
44 Mus musculus transmembrane protein 62 (Tmem62), mRNA [NM_175285]
45 Mus musculus ferrochelatase (Fech), mRNA [NM_007998]
46 Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630006J12 produc
47 Mus musculus L-2-hydroxyglutarate dehydrogenase (L2hgdh), mRNA [NM_145443]
48 Mus musculus sulfatase modifying factor 2 (Sumf2), mRNA [NM_026445]
49 Mus musculus RIKEN cDNA 1700104L18 gene (1700104L18Rik), long non-coding RNA [NR_108033]
50 Mus musculus staufer (RNA binding protein) homolog 1 (Drosophila) (Stau1), transcript variant 3, mRNA [f
51 Mus musculus contactin 6 (Cntn6), mRNA [NM_017383]
52 Mus musculus synaptic vesicle glycoprotein 2c (Sv2c), mRNA [NM_029210]
53 Mus musculus valosin containing protein (Vcp), mRNA [NM_009503]
54 Mus musculus 13 days embryo stomach cDNA, RIKEN full-length enriched library, clone:D530006I24 produ
55 Mus musculus biogenesis of lysosomal organelles complex-1, subunit 6, pallidin (Bloc1s6), mRNA [NM_01
56 Mus musculus transmembrane and coiled-coil domains 6 (Tmco6), mRNA [NM_028036]
57 Mus musculus RIKEN cDNA 4933406C10 gene (4933406C10Rik), long non-coding RNA [NR_044986]
58 Mus musculus glucosaminyl (N-acetyl) transferase 2, l-branching enzyme (Gcnt2), transcript variant 3, mRI
59 Mus musculus fibroblast growth factor receptor 2 (Fgfr2), transcript variant 1, mRNA [NM_010207]

1 Mus musculus cDNA sequence BC026513, mRNA (cDNA clone IMAGE:4909841), partial cds. [BC039787]
2 Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110040I23 product:f
3 Mus musculus WW, C2 and coiled-coil domain containing 1 (Wwc1), mRNA [NM_170779]
4 Mus musculus ataxin 2 (Atxn2), mRNA [NM_009125]
5 Mus musculus RAB8A, member RAS oncogene family (Rab8a), mRNA [NM_023126]
6 PREDICTED: Mus musculus RIKEN cDNA G630016G05 gene (G630016G05Rik), transcript variant X2, mi
7 Mus musculus zinc finger protein 868 (Zfp868), transcript variant 1, mRNA [NM_172754]
8 Mus musculus coenzyme Q5 homolog, methyltransferase (yeast) (Coq5), mRNA [NM_026504]
9 leucine zipper, putative tumor suppressor 1 [Source:MGI Symbol;Acc:MGI:2684762] [ENSMUST00000185]
10 Mus musculus C-type lectin domain family 2, member f (Clec2f), mRNA [NM_001277202]
11 eukaryotic translation initiation factor 2 alpha kinase 4 [Source:MGI Symbol;Acc:MGI:1353427] [ENSMUST
12 Mus musculus coenzyme Q5 homolog, methyltransferase (yeast) (Coq5), mRNA [NM_026504]
13 sideroflexin 5 [Source:MGI Symbol;Acc:MGI:2137681] [ENSMUST00000138489]
14 Mus musculus apolipoprotein O (ApoO), transcript variant 2, mRNA [NM_001199337]
15 Mus musculus cathepsin O (Ctso), mRNA [NM_177662]
16 Mus musculus MAX gene associated (Mga), transcript variant 1, mRNA [NM_013720]
17 Mus musculus nicotinamide riboside kinase 1 (Nmrk1), mRNA [NM_145497]
18 Mus musculus 2 days neonate sympathetic ganglion cDNA, RIKEN full-length enriched library, clone:71204
19 PREDICTED: Mus musculus predicted gene 5785 (Gm5785), mRNA [XM_974939]
20 Mus musculus RIKEN cDNA 2900026A02 gene (2900026A02Rik), mRNA [NM_172884]
21 Mus musculus adipogenesis associated Mth938 domain containing (Aamdc), transcript variant 1, mRNA [N
22 Mus musculus lysocardiolipin acyltransferase 1 (Lclat1), transcript variant 1, mRNA [NM_001081071]
23 Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310007J06 product:uncl
24 Mus musculus predicted gene 14325 (Gm14325), mRNA [NM_001024849]
25 Mus musculus transmembrane protein 18 (Tmem18), mRNA [NM_172049]
26 Mus musculus leucine carboxyl methyltransferase 2 (Lcmt2), mRNA [NM_177846]
27 Mus musculus transcription elongation factor A (SII) N-terminal and central domain containing 2 (Tceanc2),
28 Mus musculus churchill domain containing 1 (Churc1), mRNA [NM_206534]
29 Mus musculus lysine (K)-specific demethylase 4C (Kdm4c), transcript variant 1, mRNA [NM_144787]
30 Mus musculus adult inner ear cDNA, RIKEN full-length enriched library, clone:F930115A20 product:hypoth
31 Mus musculus excision repair/ross-complementing rodent repair deficiency, complementation group 8 (Ercc8
32 Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610312K03 pi
33 immunoglobulin kappa variable 16-104 [Source:MGI Symbol;Acc:MGI:2685913] [ENSMUST00000103323]
34 Q8BSH3_MOUSE (Q8BSH3) 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEI
35 Mus musculus solute carrier organic anion transporter family, member 5A1 (Slco5a1), mRNA [NM_172841]
36 Mus musculus solute carrier family 30 (zinc transporter), member 7 (Slc30a7), mRNA [NM_023214]
37 Mus musculus serine/threonine kinase 38 (Stk38), mRNA [NM_134115]
38 T cell receptor alpha variable 13N-3 [Source:MGI Symbol;Acc:MGI:3645598] [ENSMUST00000179580]
39 Mus musculus asparagine-linked glycosylation 2 (alpha-1,3-mannosyltransferase) (Alg2), mRNA [NM_0195
40 Mus musculus RCB-1283 B16 melanoma cDNA, RIKEN full-length enriched library, clone:G430107107 pro
41 Mus musculus dynein, axonemal, heavy chain 7A (Dnah7a), mRNA [NM_001252070]
42 Mus musculus acetyl-Coenzyme A carboxylase beta (Acacb), mRNA [NM_133904]
43 Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830143P17 product:uncla
44 Mus musculus coiled-coil domain containing 88C (Ccdc88c), mRNA [NM_026681]
45 Mus musculus predicted gene 14499 (Gm14499), mRNA [NM_001277184]
46 Mus musculus zinc finger and BTB domain containing 34 (Zbtb34), transcript variant 1, mRNA [NM_001085
47 Mus musculus myosin, light chain 12A, regulatory, non-sarcomeric (My12a), mRNA [NM_026064]
48 REM2 and RAB-like small GTPase 1 [Source:MGI Symbol;Acc:MGI:1923416] [ENSMUST00000097813]
49 Mus musculus vomeronasal 2, receptor 86 (Vmn2r86), mRNA [NM_001103365]
50 Mus musculus vomeronasal 2, receptor 10 (Vmn2r10), mRNA [NM_009491]
51 Mus musculus predicted gene 5132 (Gm5132), mRNA [NM_001085517]
52 osteopetrosis associated transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:2655574] [ENSMUST00
53 Mus musculus Emx2 opposite strand/antisense transcript (non-protein coding) (Emx2os), long non-coding I
54 Mus musculus zinc fingers and homeoboxes 2 (Zhx2), mRNA [NM_199449]
55 Mus musculus patched domain containing 2 (Ptchd2), mRNA [NM_001083342]
56 Mus musculus Fas apoptotic inhibitory molecule 2 (Faim2), transcript variant 1, mRNA [NM_028224]
57 Mus musculus cyclin B1 interacting protein 1 (Ccnb1ip1), mRNA [NM_001111119]
58 Mus musculus adenosine deaminase-like (Adal), transcript variant 1, mRNA [NM_029475]
59 Mus musculus TBC1 domain family, member 5 (Tbc1d5), transcript variant 1, mRNA [NM_001285991]

1 Mus musculus lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730040L14 product:h
2 Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:4022436C10 product:
3 Mus musculus citrate lyase beta like (Clybl), mRNA [NM_029556]
4 Mus musculus predicted gene 13298 (Gm13298), mRNA [NM_001085530]
5 Mus musculus CD84 antigen (Cd84), transcript variant 1, mRNA [NM_013489]
6 Mus musculus glutamate receptor, ionotropic, NMDA2B (epsilon 2) (Grin2b), mRNA [NM_008171]
7 Mus musculus ankyrin repeat and IBR domain containing 1 (Ankib1), transcript variant 2, mRNA [NM_0010
8 Mus musculus DEAD (Asp-Glu-Ala-Asp) box polypeptide 51 (Ddx51), mRNA [NM_027156]
9 PREDICTED: Mus musculus RIKEN cDNA 2810407A14 gene (2810407A14Rik), transcript variant X1, mis
10 Mus musculus congenital dyserythropoietic anemia, type I (human) (Cdan1), mRNA [NM_026891]
11 Mus musculus angiopoietin-like 7 (Angptl7), mRNA [NM_001039554]
12 Mus musculus zinc finger protein 72 (Zfp72), mRNA [NM_001081680]
13 Mus musculus mesoderm development candidate 1 (Mesdc1), mRNA [NM_030705]
14 Mus musculus nucleus accumbens associated 2, BEN and BTB (POZ) domain containing (Nacc2), transcri
15 Mus musculus Rho guanine nucleotide exchange factor (GEF) 26 (Arhgef26), mRNA [NM_001081295]
16 Mus musculus ethanol induced 1 (Etohi1), transcript variant 1, mRNA [NM_001177399]
17 Mus musculus calpain 15 (Capn15), mRNA [NM_015830]
18 Mus musculus mitofusin 2 (Mfn2), transcript variant 2, mRNA [NM_133201]
19 Mus musculus solute carrier family 25, member 37 (Slc25a37), mRNA [NM_026331]
20 Mus musculus glucose phosphate isomerase 1 (Gpi1), mRNA [NM_008155]
21 Mus musculus cyclin L2 (Ccnl2), mRNA [NM_207678]
22 Mus musculus glucose phosphate isomerase 1 (Gpi1), mRNA [NM_008155]
23 Mus musculus kinesin light chain 2 (Klc2), transcript variant 1, mRNA [NM_008451]
24 Mus musculus homeobox D8 (Hoxd8), transcript variant 1, mRNA [NM_008276]
25 Mus musculus CREB/ATF bZIP transcription factor (Crebzf), transcript variant 1, mRNA [NM_145151]
26 Mus musculus 4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. ele
27 Mus musculus membrane associated guanylate kinase, WW and PDZ domain containing 1 (Magi1), transc
28 Mus musculus PHD finger protein 13 (Phf13), mRNA [NM_172705]
29 Mus musculus ribonuclease P 14 subunit (Rpp14), mRNA [NM_025938]
30 Mus musculus importin 11 (Ipo11), mRNA [NM_029665]
31 Mus musculus LanC lantibiotic synthetase component C-like 3 (bacterial) (Lancl3), mRNA [NM_173414]
32 Mus musculus potassium voltage-gated channel, subfamily Q, member 5 (Kcnq5), transcript variant 1, mRN
33 Mus musculus mRNA for mKIAA0996 protein. [AK129256]
34 Mus musculus RAB37, member RAS oncogene family (Rab37), transcript variant 2, mRNA [NM_00116375]
35 Mus musculus predicted gene 5382 (Gm5382), mRNA [NM_001034100]
36 Mus musculus microfibrillar-associated protein 3 (Mfap3), transcript variant 1, mRNA [NM_145426]
37 Mus musculus predicted gene 14137 (Gm14137), mRNA [NM_001039223]
38 Mus musculus heat shock factor binding protein 1-like 1 (Hsbp111), mRNA [NM_001136181]
39 Mus musculus desumoylating isopeptidase 1 (Desi1), mRNA [NM_134095]
40 Mus musculus toll-like receptor 1 (Tlr1), transcript variant 1, mRNA [NM_030682]
41 Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330167E06 produ
42 Mus musculus Rho guanine nucleotide exchange factor (GEF) 38 (Arhgef38), mRNA [NM_029953]
43 Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430528A12 prod
44 Mus musculus ubiquitin-conjugating enzyme E2E 1 (Ube2e1), mRNA [NM_009455]
45 Mus musculus SR-related CTD-associated factor 8 (Scaf8), mRNA [NM_134123]
46 Mus musculus adenylate cyclase 6 (Adcy6), mRNA [NM_007405]
47 Mus musculus expressed sequence AI593442 (AI593442), transcript variant 1, mRNA [NM_001286641]
48 Mus musculus phosphatidic acid phosphatase type 2A (Ppap2a), transcript variant 1, mRNA [NM_008247]
49 Mus musculus nuclear fragile X mental retardation protein interacting protein 1 (Nufip1), mRNA [NM_01374
50 Mus musculus transmembrane protein 135 (Tmem135), mRNA [NM_028343]
51 Mus musculus RIKEN cDNA 1700012L04 gene (1700012L04Rik), mRNA [NM_029588]
52 Mus musculus SEC63-like (S. cerevisiae) (Sec63), mRNA [NM_153055]
53 Mus musculus RAS-like, estrogen-regulated, growth-inhibitor (Rerg), transcript variant 1, mRNA [NM_0011
54 Mus musculus USO1 vesicle docking factor (Uso1), mRNA [NM_019490]
55 Mus musculus guanosine diphosphate (GDP) dissociation inhibitor 2 (Gdi2), mRNA [NM_008112]
56 Mus musculus vomeronasal 2, receptor 16 (Vmn2r16), mRNA [NM_001104627]
57 Mus musculus NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (Ndufc2), mRNA [NM_0242
58 Mus musculus RAD23b homolog (S. cerevisiae) (Rad23b), mRNA [NM_009011]
59 UI-M-GI0-cek-h-17-0-UI.r1 NIH_BMAP_GI0 Mus musculus cDNA clone IMAGE: 6840738 5', mRNA sequer

1 Mus musculus ATP synthase, H⁺ transporting mitochondrial F1 complex, beta subunit (Atp5b), mRNA [NM_023418]
2 Mus musculus phosphoglycerate mutase 1 (Pgam1), mRNA [NM_023418]
3 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921515G04 product:uncl
4 Mus musculus UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9 (Ga
5 Mus musculus Kell blood group precursor (McLeod phenotype) homolog (Xk), mRNA [NM_023500]
6 Mus musculus RAB37, member RAS oncogene family (Rab37), transcript variant 2, mRNA [NM_00116375
7 Mus musculus jagunal homolog 1 (Drosophila) (Jagn1), transcript variant 1, mRNA [NM_026365]
8 Mus musculus natriuretic peptide type A (Nppa), mRNA [NM_008725]
9 Mus musculus mitochondrial ribosomal protein L34 (Mrpl34), mRNA [NM_053162]
10 PREDICTED: Mus musculus predicted gene, 20764 (Gm20764), mRNA [XM_003688790]
11 Mus musculus multivesicular body subunit 12A (Mvb12a), mRNA [NM_028617]
12 Mus musculus family with sequence similarity 114, member A2 (Fam114a2), transcript variant 2, mRNA [N
13 PREDICTED: Mus musculus predicted gene 3693 (Gm3693), transcript variant X2, misc_RNA [XR_38175
14 Mus musculus superkiller viralicidic activity 2-like 2 (S. cerevisiae) (Skiv2l2), mRNA [NM_028151]
15 Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 3E (Ppp1r3e), mRNA [NM_001167908]
16 Mus musculus TNFRSF1A-associated via death domain (Tradd), mRNA [NM_001033161]
17 Mus musculus ankyrin repeat and sterile alpha motif domain containing 1B (Anks1b), transcript variant 4, r
18 Mus musculus abhydrolase domain containing 5 (Abhd5), mRNA [NM_026179]
19 Mus musculus ribosomal protein L36 (Rpl36), mRNA [NM_018730]
20 Mus musculus trafficking protein particle complex 5 (Trappc5), mRNA [NM_025701]
21 Mus musculus RIKEN cDNA 2810408A11 gene (2810408A11Rik), mRNA [NM_027419]
22 Mus musculus G protein-coupled receptor 158 (Gpr158), mRNA [NM_001004761]
23 Mus musculus spastic paraplegia 11 (Spg11), mRNA [NM_145531]
24 Mus musculus ribosomal protein L36 (Rpl36), mRNA [NM_018730]
25 PREDICTED: Mus musculus predicted gene 6404 (Gm6404), mRNA [XM_006517804]
26 Mus musculus RAB3 GTPase activating protein subunit 2 (Rab3gap2), mRNA [NM_001163754]
27 Mus musculus THO complex 7 homolog (Drosophila) (Thoc7), transcript variant 3, mRNA [NM_001285780]
28 Mus musculus piggyBac transposable element derived 5 (Pgbd5), mRNA [NM_171824]
29 Mus musculus bone morphogenetic protein 8a (Bmp8a), transcript variant 1, mRNA [NM_001256019]
30 Mus musculus ribosomal protein L13A (Rpl13a), mRNA [NM_009438]
31 Mus musculus ubiquitin specific peptidase 37 (Usp37), mRNA [NM_176972]
32 Mus musculus SHC (Src homology 2 domain containing) transforming protein 2 (Shc2), mRNA [NM_00102
33 Mus musculus DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae) (Dclre1c), transcript variant 2, mRN
34 Mus musculus neuroguidin, EIF4E binding protein (Ngdn), mRNA [NM_026890]
35 Mus musculus folliculin (Flcn), transcript variant 2, mRNA [NM_146018]
36 PREDICTED: Mus musculus zinc finger protein 74 (Zfp74), transcript variant X1, mRNA [XM_006540384]
37 Mus musculus caspase 3 (Casp3), transcript variant 2, mRNA [NM_009810]
38 Mus musculus protocadherin beta 7 (Pcdhb7), mRNA [NM_053132]
39 Mus musculus EFR3 homolog B (S. cerevisiae) (Efr3b), mRNA [NM_001082483]
40 Mus musculus Ras interacting protein 1 (Rasip1), mRNA [NM_028544]
41 Mus musculus tubulin, beta 6 class V (Tubb6), mRNA [NM_026473]
42 Mus musculus G protein-coupled receptor 135 (Gpr135), mRNA [NM_181752]
43 Mus musculus REC8 meiotic recombination protein (Rec8), mRNA [NM_020002]
44 Mus musculus SAP30-like (Sap30l), mRNA [NM_001081168]
45 Mus musculus nucleotide binding protein-like (Nubpl), mRNA [NM_029760]
46 Mus musculus chemokine (C-C motif) ligand 28 (Ccl28), mRNA [NM_020279]
47 Mus musculus SLIT and NTRK-like family, member 3 (Slitrk3), mRNA [NM_198864]
48 Mus musculus unconventional SNARE in the ER 1 homolog (S. cerevisiae) (Use1), transcript variant 3, mR
49 Mus musculus G patch domain containing 1 (Gpatch1), mRNA [NM_026181]
50 Mus musculus F-box and leucine-rich repeat protein 21 (Fbxl21), mRNA [NM_178674]
51 Mus musculus SIVA1, apoptosis-inducing factor (Siva1), transcript variant 1, mRNA [NM_013929]
52 Mus musculus small G protein signaling modulator 1 (Sgsm1), transcript variant 3, mRNA [NM_001162965]
53 Mus musculus RIKEN cDNA 1700049G17 gene (1700049G17Rik), mRNA [NM_028538]
54 Mus musculus family with sequence similarity 160, member B1 (Fam160b1), mRNA [NM_145505]
55 Mus musculus mitogen-activated protein kinase kinase kinase 1 (Map4k1), mRNA [NM_008279]
56 Mus musculus RIKEN cDNA 6330416G13 gene (6330416G13Rik), mRNA [NM_144905]
57 Mus musculus coiled-coil domain containing 71 (Ccdc71), mRNA [NM_133744]
58 Mus musculus monoglyceride lipase (Mgll), transcript variant 1, mRNA [NM_001166251]
59 leucine-rich and death domain containing [Source:MGI Symbol;Acc:MGI:1889507] [ENSMUST0000013806
60

1 Mus musculus phosphopantothenoylcysteine decarboxylase (Ppcdc), mRNA [NM_176831]
2 Mus musculus RIKEN cDNA D130040H23 gene (D130040H23Rik), mRNA [NM_172491]
3 Mus musculus small integral membrane protein 7 (Smim7), mRNA [NM_172396]
4 Mus musculus thioredoxin-like 4A (Txnl4a), transcript variant 1, mRNA [NM_025299]
5 synaptosomal-associated protein 23 [Source:MGI Symbol;Acc:MGI:109356] [ENSMUST00000110711]
6 Mus musculus N-acetyltransferase 9 (GCN5-related, putative) (Nat9), mRNA [NM_025400]
7 Mus musculus pleckstrin homology domain containing, family A member 7 (Plekha7), mRNA [NM_172743]
8 Mus musculus RIKEN cDNA 4930563E22 gene (4930563E22Rik), mRNA [NM_001163728]
9 Mus musculus myelin basic protein (Mbp), transcript variant 7, mRNA [NM_010777]
10 Mus musculus prion protein (Prnp), transcript variant 2, mRNA [NM_001278256]
11 Mus musculus mutS homolog 3 (E. coli) (Msh3), mRNA [NM_010829]
12 Mus musculus TBC1 domain family, member 2 (Tbc1d2), mRNA [NM_198664]
13 Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430410E06 product:
14 zinc finger protein 81 [Source:MGI Symbol;Acc:MGI:1890752] [ENSMUST00000054072]
15 Mus musculus slingshot homolog 1 (Drosophila) (Ssh1), mRNA [NM_198109]
16 Mus musculus Sh3 domain YSC-like 1 (Sh3yl1), transcript variant 1, mRNA [NM_013709]
17 Mus musculus spastin (Spast), transcript variant 2, mRNA [NM_016962]
18 Mus musculus RAB26, member RAS oncogene family (Rab26), mRNA [NM_177375]
19 Mus musculus F-box protein 6 (Fbxo6), transcript variant 1, mRNA [NM_015797]
20 Mus musculus MEF2 activating motif and SAP domain containing transcriptional regulator (Mamstr), mRNA
21 Mus musculus patatin-like phospholipase domain containing 3 (Pnpla3), mRNA [NM_054088]
22 Mus musculus serine hydroxymethyltransferase 1 (soluble) (Shmt1), mRNA [NM_009171]
23 PREDICTED: Mus musculus predicted pseudogene 7241 (Gm7241), mRNA [XM_006543539]
24 Mus musculus solute carrier organic anion transporter family, member 2b1 (Slco2b1), transcript variant 1, n
25 Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130094KC
26 Mus musculus RIKEN cDNA 4930570G19 gene (4930570G19Rik), transcript variant 2, long non-coding RN
27 Mus musculus wingless-type MMTV integration site 9A (Wnt9a), mRNA [NM_139298]
28 Mus musculus transmembrane protein 192 (Tmem192), transcript variant 1, mRNA [NM_028427]
29 Mus musculus leucine rich repeat containing 73 (Lrrc73), mRNA [NM_001111142]
30 Mus musculus serine peptidase inhibitor, Kazal type 2 (Spink2), transcript variant 2, mRNA [NM_183284]
31 Mus musculus oxytocin receptor (Oxtr), mRNA [NM_001081147]
32 Mus musculus transmembrane emp24 protein transport domain containing 4 (Tmed4), mRNA [NM_13402C
33 Mus musculus cytochrome c oxidase assembly factor 4 (Coa4), mRNA [NM_183270]
34 Mus musculus glutathione S-transferase kappa 1 (Gstk1), mRNA [NM_029555]
35 Mus musculus tripartite motif-containing 12C (Trim12c), transcript variant 1, mRNA [NM_001146007]
36 Mus musculus CDP-diacylglycerol synthase 1 (Cds1), mRNA [NM_173370]
37 Mus musculus fibroblast activation protein (Fap), mRNA [NM_007986]
38 Mus musculus nodal modulator 1 (Nomo1), mRNA [NM_153057]
39 Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530073P05 pro
40 Mus musculus T cell activation GTPase activating protein 1 (Tagap1), mRNA [NM_147155]
41 Mus musculus BCL2-like 12 (proline rich) (Bcl2l12), mRNA [NM_029410]
42 Mus musculus immunoglobulin superfamily, member 10 (Igsf10), mRNA [NM_001162884]
43 Mus musculus high mobility group box transcription factor 1 (Hbp1), transcript variant 2, mRNA [NM_1779C
44 Mus musculus NEL-like 1 (Nell1), mRNA [NM_001037906]
45 Mus musculus synergin, gamma (Synrg), mRNA [NM_194341]
46 Mus musculus protein phosphatase 2 (formerly 2A), regulatory subunit B", delta (Ppp2r3d), transcript varia
47 Mus musculus putative homeodomain transcription factor 1 (Phtf1), transcript variant 1, mRNA [NM_01362
48 Mus musculus progesterin and adipoQ receptor family member VI (Paqr6), mRNA [NM_198410]
49 Mus musculus tRNA splicing endonuclease 54 homolog (S. cerevisiae) (Tsen54), mRNA [NM_029557]
50 PREDICTED: Mus musculus predicted gene 6306 (Gm6306), mRNA [XM_006500499]
51 PREDICTED: Mus musculus predicted gene 5093 (Gm5093), mRNA [XM_006543383]
52 Mus musculus RAS-like, family 10, member A (Rasl10a), mRNA [NM_145216]
53 Mus musculus SURP and G patch domain containing 1 (Sugp1), mRNA [NM_027481]
54 Mus musculus DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 (Ddx55), transcript variant 1, mRNA [NM_026
55 Mus musculus ubiquitin specific peptidase 53 (Usp53), mRNA [NM_133857]
56 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930522L14 product:simila
57 Mus musculus coiled-coil domain containing 91 (Ccdc91), mRNA [NM_025911]
58 Mus musculus oligonucleotide/oligosaccharide-binding fold containing 1 (Obfc1), mRNA [NM_175360]
59 Mus musculus cytokine receptor-like factor 2 (Crfl2), transcript variant 1, mRNA [NM_001164735]

1 Mus musculus centromere protein K (Cenpk), transcript variant 1, mRNA [NM_021790]
2 Mus musculus zinc finger protein 608 (Zfp608), mRNA [NM_175751]
3 Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630055C05 produ
4 Mus musculus solute carrier family 10 (sodium/bile acid cotransporter family), member 3 (Slc10a3), transcr
5 Mus musculus Holliday junction recognition protein (Hjrp), mRNA [NM_198652]
6 Mus musculus D-tyrosyl-tRNA deacylase 2 (Dtd2), mRNA [NM_029545]
7 Mus musculus progesterin and adipoQ receptor family member VI (Paqr6), mRNA [NM_198410]
8 Mus musculus palmdelphin (Palmd), mRNA [NM_023245]
9 Mus musculus ferritin light chain 1 (Ftl1), mRNA [NM_010240]
10 Mus musculus THAP domain containing 6 (Thap6), non-coding RNA [NR_028429]
11 PREDICTED: Mus musculus uncharacterized LOC102634598 (LOC102634598), misc_RNA [XR_386205]
12 Mus musculus monoglyceride lipase (Mgll), transcript variant 1, mRNA [NM_001166251]
13 Mus musculus RIKEN cDNA 1810009N02 gene (1810009N02Rik), mRNA [NM_026939]
14 Mus musculus solute carrier family 25, member 41 (Slc25a41), mRNA [NM_175333]
15 Mus musculus aldo-keto reductase family 1, member C19 (Akr1c19), mRNA [NM_001013785]
16 Mus musculus transmembrane protein 173 (Tmem173), transcript variant 1, mRNA [NM_028261]
17 Mus musculus ubiquitin C (Ubc), mRNA [NM_019639]
18 predicted gene 10654 [Source:MGI Symbol;Acc:MGI:3643366] [ENSMUST00000098653]
19 Mus musculus histocompatibility 2, M region locus 3 (H2-M3), mRNA [NM_013819]
20 Mus musculus NIM1 serine/threonine protein kinase (Nim1k), mRNA [NM_175538]
21 Mus musculus beaded filament structural protein 2, phakinin (Bfsp2), mRNA [NM_001002896]
22 Mus musculus alkB, alkylation repair homolog 6 (E. coli) (Alkbh6), mRNA [NM_198027]
23 Mus musculus CaM kinase-like vesicle-associated (Camkv), mRNA [NM_145621]
24 Mus musculus polymerase (DNA directed), iota (Poli), transcript variant 2, mRNA [NM_011972]
25 Mus musculus zinc finger protein 566 (Zfp566), mRNA [NM_152814]
26 Mus musculus retinol binding protein 7, cellular (Rbp7), mRNA [NM_022020]
27 PREDICTED: Mus musculus predicted gene 8013 (Gm8013), transcript variant X4, ncRNA [XR_389350]
28 Mus musculus synaptogyrin 2 (Syngr2), mRNA [NM_009304]
29 Mus musculus LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae) (Lsm4), mRNA [NM_0158]
30 Mus musculus FXD domain-containing ion transport regulator 6 (Fxd6), mRNA [NM_022004]
31 Mus musculus solute carrier family 2 (facilitated glucose transporter), member 9 (Slc2a9), transcript variant
32 Mus musculus SERTA domain containing 3 (Sertad3), mRNA [NM_133210]
33 Mus musculus acyl-CoA synthetase long-chain family member 5 (Acsl5), mRNA [NM_027976]
34 Mus musculus SLIT and NTRK-like family, member 5 (Slitrk5), mRNA [NM_198865]
35 cut-like homeobox 2 [Source:MGI Symbol;Acc:MGI:107321] [ENSMUST00000111752]
36 BEN domain containing 7 [Source:MGI Symbol;Acc:MGI:2443100] [ENSMUST00000115022]
37 Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:C330018M05 product:similar to ZF
38 Mus musculus myosin, light polypeptide 2, regulatory, cardiac, slow (Myl2), mRNA [NM_010861]
39 Mus musculus telomeric repeat binding factor 1 (Terf1), transcript variant 1, mRNA [NM_009352]
40 Mus musculus predicted gene 13247 (Gm13247), transcript variant 1, mRNA [NM_001243138]
41 Mus musculus polymerase (DNA directed), epsilon (Pole), mRNA [NM_011132]
42 Mus musculus Holliday junction recognition protein (Hjrp), mRNA [NM_198652]
43 Mus musculus coiled-coil domain containing 91 (Ccdc91), mRNA [NM_025911]
44 Mus musculus G2/M-phase specific E3 ubiquitin ligase (G2e3), transcript variant 2, mRNA [NM_00116796:
45 Mus musculus PTPRF interacting protein, binding protein 2 (liprin beta 2) (Ppfbp2), transcript variant 1, mF
46 Mus musculus methyltransferase like 3 (Mettl3), mRNA [NM_019721]
47 Mus musculus thyroid hormone responsive (Thrsp), mRNA [NM_009381]
48 Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130019E
49 Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130072N09 prod
50 Mus musculus CD1d2 antigen (Cd1d2), transcript variant 1, mRNA [NM_007640]
51 Mus musculus phosphatidylinositol glycan anchor biosynthesis, class P (Pigg), transcript variant 5, mRNA [
52 Mus musculus germ cell-specific gene 2 (Gsg2), mRNA [NM_010353]
53 Mus musculus huntingtin interacting protein K (Hypk), mRNA [NM_026318]
54 Mus musculus apolipoprotein L 7b (Apol7b), mRNA [NM_001024848]
55 Mus musculus apoptotic chromatin condensation inducer 1 (Acin1), transcript variant 2, mRNA [NM_02319
56 Mus musculus methyltransferase like 17 (Mettl17), mRNA [NM_001029990]
57 Mus musculus Friend virus susceptibility 1 (Fv1), mRNA [NM_010244]
58 Mus musculus churchill domain containing 1 (Churc1), mRNA [NM_206534]
59 Mus musculus predicted gene 15698 (Gm15698), non-coding RNA [NR_003564]
60

1 Mus musculus microsomal triglyceride transfer protein (Mttp), transcript variant 1, mRNA [NM_001163457]
2 Mus musculus adrenergic receptor kinase, beta 2 (Adrbk2), transcript variant 1, mRNA [NM_177078]
3 Mus musculus RIKEN cDNA 4930515G01 gene (4930515G01Rik), long non-coding RNA [NR_027872]
4 ribosomal protein S3A3 [Source:MGI Symbol;Acc:MGI:3643406] [ENSMUST00000074680]
5 Mus musculus Ca²⁺-dependent secretion activator (Cadps), transcript variant 1, mRNA [NM_012061]
6 Mus musculus RIKEN cDNA 2410006H16 gene (2410006H16Rik), long non-coding RNA [NR_030738]
7 Mus musculus RWD domain containing 3 (Rwdd3), transcript variant 2, mRNA [NM_028456]
8 Mus musculus cortistatin (Cort), mRNA [NM_007745]
9 Mus musculus kinesin light chain 4 (Klc4), mRNA [NM_029091]
10 Mus musculus G2/M-phase specific E3 ubiquitin ligase (G2e3), transcript variant 3, mRNA [NM_00116796]
11 Mus musculus 4HAUS augmin-like complex, subunit 8 (Haus8), transcript variant 1, mRNA [NM_00116304]
12 Mus musculus EH-domain containing 4 (Ehd4), mRNA [NM_133838]
13 Mus musculus interleukin 17 receptor D (Il17rd), mRNA [NM_134437]
14 regulating synaptic membrane exocytosis 3 [Source:MGI Symbol;Acc:MGI:2443331] [ENSMUST00000071]
15 Mus musculus RAB19, member RAS oncogene family (Rab19), mRNA [NM_011226]
16 Mus musculus FXYD domain-containing ion transport regulator 2 (Fxyd2), transcript variant b, mRNA [NM_]
17 Mus musculus creatine kinase, mitochondrial 1, ubiquitous (Ckmt1), mRNA [NM_009897]
18 Mus musculus dehydrogenase/reductase (SDR family) member 7 (Dhrs7), mRNA [NM_025522]
19 Mus musculus zinc finger protein 286 (Zfp286), mRNA [NM_138949]
20 Mus musculus polymerase (DNA directed), kappa (Polk), mRNA [NM_012048]
21 Mus musculus cysteine-rich PDZ-binding protein (Cript), mRNA [NM_019936]
22 mp78f05.y1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:575361 5'. [AI530666]
23 Mus musculus G protein-coupled receptor 180 (Gpr180), mRNA [NM_021434]
24 Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, c
25 Mus musculus neuron-glia-CAM-related cell adhesion molecule (Nrcam), transcript variant 1, mRNA [NM_1]
26 Mus musculus RIKEN cDNA 2810459M11 gene (2810459M11Rik), transcript variant 1, mRNA [NM_00114]
27 Mus musculus asparaginase homolog (S. cerevisiae) (Aspg), mRNA [NM_001081169]
28 Mus musculus uncharacterized LOC100862268 (LOC100862268), transcript variant 1, long non-coding RN
29 Mus musculus DEAD (Asp-Glu-Ala-Asp) box polypeptide 4 (Ddx4), transcript variant 2, mRNA [NM_01002]
30 Mus musculus ATPase, class I, type 8B, member 5 (Atp8b5), mRNA [NM_177195]
31 Mus musculus dynein, axonemal, intermediate chain 2 (Dnaic2), mRNA [NM_001034878]
32 Mus musculus kelch repeat and BTB (POZ) domain containing 11 (Kbtbd11), mRNA [NM_029116]
33 Mus musculus nudix (nucleoside diphosphate linked moiety X)-type motif 7 (Nudt7), transcript variant 4, mF
34 Mus musculus predicted gene 7120 (Gm7120), transcript variant 2, mRNA [NM_001177666]
35 Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330442E02
36 Mus musculus Iroquois related homeobox 1 (Drosophila) (Irx1), mRNA [NM_010573]
37 Mus musculus ribosomal protein L34, pseudogene 1 (Rpl34-ps1), mRNA [NM_001199350]
38 Mus musculus doublecortin domain containing 2a (Dcdc2a), transcript variant 1, mRNA [NM_177577]
39 Mus musculus parathyroid hormone 1 receptor (Pth1r), transcript variant 1, mRNA [NM_011199]
40 Mus musculus synaptotagmin IX (Syt9), mRNA [NM_021889]
41 Mus musculus glutathione S-transferase, mu 6 (Gstm6), mRNA [NM_008184]
42 Mus musculus gem (nuclear organelle) associated protein 5 (Gemin5), transcript variant 1, mRNA [NM_00
43 Mus musculus RUN and FYVE domain containing 3 (Rufy3), transcript variant 3, mRNA [NM_001289776]
44 Q8NFW1_HUMAN (Q8NFW1) Alpha 1 type XXII collagen, partial (33%) [TC1681647]
45 Mus musculus protein tyrosine phosphatase, receptor type, R (Ptpr), transcript variant 1, mRNA [NM_0112
46 Mus musculus microtubule-associated protein 1S (Map1s), mRNA [NM_173013]
47 Mus musculus cDNA sequence BC005764 (BC005764), transcript variant 1, mRNA [NM_181681]
48 Mus musculus zinc finger protein 536 (Zfp536), mRNA [NM_172385]
49 Mus musculus RALBP1 associated Eps domain containing protein 2 (Reps2), transcript variant 1, mRNA [N
50 Mus musculus family with sequence similarity 83, member G (Fam83g), mRNA [NM_178618]
51 Mus musculus guanine nucleotide binding protein, alpha 14 (Gna14), mRNA [NM_008137]
52 Mus musculus teashirt zinc finger family member 1 (Tshz1), mRNA [NM_001081300]
53 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930532K22 product:hypoi
54 Mus musculus RIKEN cDNA 4930515G01 gene (4930515G01Rik), long non-coding RNA [NR_027872]
55 Mus musculus oxysterol binding protein-like 10 (Osbp10), mRNA [NM_148958]
56 Mus musculus periaxin (Prx), transcript variant 2, mRNA [NM_019412]
57 Mus musculus Rap guanine nucleotide exchange factor (GEF) 3 (Rapgef3), transcript variant 2, mRNA [NM
58 Mus musculus Rho GTPase activating protein 22 (Arhgap22), mRNA [NM_153800]
59 Mus musculus RIKEN cDNA 2010109A12 gene (2010109A12Rik), mRNA [NM_029363]

1 Mus musculus carbonyl reductase 3 (Cbr3), mRNA [NM_173047]
2 BB713741 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA clone B020049A06 3', mRNA sequ
3 predicted gene 6816 [Source:MGI Symbol;Acc:MGI:3648347] [ENSMUST00000059737]
4 Mus musculus transmembrane protein 65 (Tmem65), mRNA [NM_175212]
5 Mus musculus pleckstrin homology domain containing, family B (evectins) member 1 (Plekhb1), transcript v
6 Mus musculus histamine receptor H1 (Hrh1), transcript variant 1, mRNA [NM_001252643]
7 PREDICTED: Mus musculus ADP-ribosylation factor 1-like (LOC102632770), misc_RNA [XR_399117]
8 Mus musculus M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (Mphosph10), mRNA [N
9 Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830106C12 product:hypo
10 Mus musculus centromere protein K (Cenpk), transcript variant 1, mRNA [NM_021790]
11 histone cluster 3, H2ba [Source:MGI Symbol;Acc:MGI:1925553] [ENSMUST00000078267]
12 Mus musculus cation channel, sperm associated 2 (Catsper2), mRNA [NM_153075]
13 Mus musculus microtubule-associated protein 1 A (Map1a), transcript variant 1, mRNA [NM_032393]
14 Mus musculus TRAF-interacting protein (Traip), mRNA [NM_011634]
15 Mus musculus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), transcript variant 1, mRNA [NM_
16 Mus musculus seven in absentia homolog 3 (Drosophila) (Siah3), mRNA [NM_001128093]
17 Mus musculus heparanase (Hpse), mRNA [NM_152803]
18 Mus musculus iduronidase, alpha-L- (Idua), transcript variant 1, mRNA [NM_008325]
19 Mus musculus predicted gene 2696 (Gm2696), mRNA [NM_001205009]
20 Mus musculus mannan-binding lectin serine peptidase 2 (Masp2), transcript variant 2, mRNA [NM_010767.
21 Mus musculus ferritin light chain 1 (Ftl1), mRNA [NM_010240]
22 Mus musculus bisphosphate 3'-nucleotidase 1 (Bpnt1), mRNA [NM_011794]
23 Mus musculus synaptoporin (Synpr), transcript variant 2, mRNA [NM_001163032]
24 Mus musculus synuclein, gamma (Sncg), mRNA [NM_011430]
25 PREDICTED: Mus musculus uncharacterized LOC102634215 (LOC102634215), ncRNA [XR_386425]
26 Mus musculus H2A histone family, member J (H2afj), mRNA [NM_177688]
27 Mus musculus coiled-coil domain containing 184 (Ccdc184), mRNA [NM_177716]
28 Mus musculus transmembrane emp24 protein transport domain containing 5 (Tmed5), mRNA [NM_028876
29 Mus musculus solute carrier family 6 (neurotransmitter transporter), member 17 (Slc6a17), mRNA [NM_17:
30 Mus musculus carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 14 (Chst14), mRNA [NM_02811
31 Mus musculus C-type lectin domain family 16, member A (Clec16a), transcript variant 1, mRNA [NM_1775t
32 Mus musculus GATA zinc finger domain containing 2A (Gatad2a), transcript variant 1, mRNA [NM_145596
33 Mus musculus inositol 1,4,5-trisphosphate 3-kinase A (Itpka), mRNA [NM_146125]
34 Mus musculus synaptotagmin 2 (Synj2), transcript variant 1, mRNA [NM_001113353]
35 Mus musculus RIKEN cDNA 2310045N01 gene (2310045N01Rik), mRNA [NM_001145552]
36 Mus musculus L-3-hydroxyproline dehydratase (trans-) (L3hypdh), mRNA [NM_026038]
37 Mus musculus UbiA prenyltransferase domain containing 1 (Ubiad1), mRNA [NM_027873]
38 Mus musculus integrin beta 4 (Itgb4), transcript variant 1, mRNA [NM_001005608]
39 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) [Source:MGI Symbol;Acc:MGI:104771] [E
40 Mus musculus solute carrier family 27 (fatty acid transporter), member 3 (Slc27a3), mRNA [NM_011988]
41 Mus musculus HscB iron-sulfur cluster co-chaperone homolog (E. coli) (Hscb), mRNA [NM_153571]
42 Mus musculus solute carrier family 48 (heme transporter), member 1 (Slc48a1), mRNA [NM_026353]
43 Mus musculus meiotic nuclear divisions 1 homolog (S. cerevisiae) (Mnd1), mRNA [NM_029797]
44 Mus musculus alcohol dehydrogenase, iron containing, 1 (Adhfe1), transcript variant 1, mRNA [NM_17523t
45 Mus musculus solute carrier family 35, member E1 (Slc35e1), mRNA [NM_177766]
46 Mus musculus late endosomal/lysosomal adaptor, MAPK and MTOR activator 3 (Lamtor3), mRNA [NM_01
47 Mus musculus a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1
48 Mus musculus Holliday junction recognition protein (Hjrp), mRNA [NM_198652]
49 Mus musculus fatty acid binding protein 5, epidermal (Fabp5), transcript variant 2, mRNA [NM_001272097]
50 Mus musculus calmodulin binding transcription activator 1 (Camta1), transcript variant 1, mRNA [NM_0010
51 Mus musculus RIKEN cDNA E330013P04 gene (E330013P04Rik), long non-coding RNA [NR_026942]
52 Mus musculus ChaC, cation transport regulator 1 (Chac1), mRNA [NM_026929]
53 Mus musculus selenium binding protein 1 (Selenbp1), mRNA [NM_009150]
54 Mus musculus protocadherin beta 4 (Pcdhb4), mRNA [NM_053129]
55 Mus musculus solute carrier family 13 (sodium-dependent citrate transporter), member 5 (Slc13a5), mRNA
56 Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810451K1
57 Mus musculus acid phosphatase 1, soluble (Acp1), transcript variant 1, mRNA [NM_001110239]
58 Mus musculus predicted gene 7120 (Gm7120), transcript variant 2, mRNA [NM_001177666]
59 Mus musculus islet cell autoantigen 1-like (Ica1l), mRNA [NM_027407]

1 Mus musculus ribonuclease T2A (Rnaset2a), mRNA [NM_001083938]
2 Mus musculus RIKEN cDNA 1700010I14 gene (1700010I14Rik), mRNA [NM_025851]
3 Mus musculus predicted gene 13157 (Gm13157), mRNA [NM_001127189]
4 Mus musculus intraflagellar transport 27 (Ift27), mRNA [NM_025931]
5 Mus musculus RIKEN cDNA 3110070M22 gene (3110070M22Rik), long non-coding RNA [NR_027974]
6 Mus musculus CD1d1 antigen (Cd1d1), mRNA [NM_007639]
7 Mus musculus synaptotagmin XV (Syt15), transcript variant a, mRNA [NM_181529]
8 Mus musculus pannexin 1 (Panx1), mRNA [NM_019482]
9 Mus musculus small nuclear RNA activating complex, polypeptide 1 (Snapc1), mRNA [NM_178392]
10 Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E33002
11 Mus musculus protein kinase, cAMP dependent regulatory, type II beta (Prkar2b), mRNA [NM_011158]
12 Mus musculus EF-hand calcium binding domain 12 (Efcab12), mRNA [NM_001110506]
13 Mus musculus olfactomedin-like 3 (Olfml3), mRNA [NM_133859]
14 Mus musculus lectin, galactose-binding, soluble 2 (Lgals2), mRNA [NM_025622]
15 Mus musculus cysteine-rich protein 1 (intestinal) (Crip1), mRNA [NM_007763]
16 Mus musculus Ly6/neurotoxin 1 (Lynx1), mRNA [NM_011838]
17 Mus musculus transmembrane protein 140 (Tmem140), mRNA [NM_197986]
18 Mus musculus RIKEN cDNA 4932415M13 gene (4932415M13Rik), long non-coding RNA [NR_073205]
19 Mus musculus microfibrillar-associated protein 1A (Mfap1a), mRNA [NM_026220]
20 Mus musculus eukaryotic translation initiation factor 2-alpha kinase 2 (Eif2ak2), mRNA [NM_011163]
21 Mus musculus RIKEN cDNA 6720483E21 gene (6720483E21Rik), long non-coding RNA [NR_040492]
22 Mus musculus leukocyte specific transcript 1 (Lst1), mRNA [NM_010734]
23 Mus musculus malic enzyme 3, NADP(+)-dependent, mitochondrial (Me3), mRNA [NM_181407]
24 Mus musculus calmodulin binding transcription activator 1 (Camta1), transcript variant 1, mRNA [NM_0010
25 Mus musculus guanine nucleotide binding protein (G protein), beta 4 (Gnb4), mRNA [NM_013531]
26 Mus musculus ribosomal protein S4-like (Rps4l), non-coding RNA [NR_003634]
27 Mus musculus transmembrane protein 132B (Tmem132b), mRNA [NM_001190352]
28 Mus musculus a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1
29 Mus musculus ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (Abcc4), transcript variant 1, m
30 Mus musculus malic enzyme 3, NADP(+)-dependent, mitochondrial (Me3), mRNA [NM_181407]
31 Mus musculus apoptotic chromatin condensation inducer 1 (Acin1), transcript variant 2, mRNA [NM_02319
32 Mus musculus calcium channel, voltage-dependent, alpha2/delta subunit 3 (Cacna2d3), mRNA [NM_00978
33 Mus musculus proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) (F
34 Mus musculus minichromosome maintenance deficient 3 (S. cerevisiae) (Mcm3), mRNA [NM_008563]
35 Mus musculus solute carrier family 26 (sulfate transporter), member 1 (Slc26a1), mRNA [NM_174870]
36 Mus musculus solute carrier family 13 (sodium-dependent citrate transporter), member 5 (Slc13a5), mRNA
37 Mus musculus ring finger protein 43 (Rnf43), mRNA [NM_172448]
38 Mus musculus zinc finger protein 930 (Zfp930), mRNA [NM_001013379]
39 Mus musculus solute carrier family 29 (nucleoside transporters), member 4 (Slc29a4), mRNA [NM_146257
40 Mus musculus ataxia telangiectasia mutated homolog (human) (Atm), mRNA [NM_007499]
41 Mus musculus purinergic receptor P2X, ligand-gated ion channel, 7 (P2rx7), transcript variant 2, mRNA [N
42 Mus musculus strain ICR clone Li(i)01 endogenous retrovirus U3 region, partial sequence. [FJ654066]
43 Mus musculus meiotic nuclear divisions 1 homolog (S. cerevisiae) (Mnd1), mRNA [NM_029797]
44 Mus musculus zinc finger homeobox 3 (Zfhx3), mRNA [NM_007496]
45 Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930032C08 product
46 Mus musculus RIKEN cDNA 6330403K07 gene (6330403K07Rik), mRNA [NM_134022]
47 Mus musculus DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae) (Dclre1c), transcript variant 2, mRN
48 Mus musculus RNA polymerase II associated protein 2 (Rpap2), transcript variant 3, mRNA [NM_0011634
49 Mus musculus inhibitor of four 1 (Mif1) mRNA, complete cds. [DQ459435]
50 Mus musculus RIKEN cDNA 2010315B03 gene (2010315B03Rik), transcript variant 1, mRNA [NM_001243
51 Mus musculus zinc finger protein 619 (Zfp619), mRNA [NM_001004139]
52 Mus musculus olfactomedin-like 1 (Olfml1), mRNA [NM_172907]
53 Mus musculus RIKEN cDNA A730008H23 gene (A730008H23Rik), mRNA [NM_172505]
54 Mus musculus dynein regulatory complex subunit 1 (Drc1), mRNA [NM_001033460]
55 Mus musculus RIKEN cDNA 1600014C10 gene (1600014C10Rik), transcript variant 1, mRNA [NM_001083
56 Mus musculus chordin-like 1 (Chrdl1), transcript variant 1, mRNA [NM_001114385]
57 Mus musculus NLR family, CARD domain containing 5 (Nlr5), mRNA [NM_001033207]
58 Mus musculus hydroxyprostaglandin dehydrogenase 15 (NAD) (Hpgd), mRNA [NM_008278]
59 Mus musculus T cell activation Rho GTPase activating protein (Tagap), mRNA [NM_145968]
60

1 Mus musculus immunoglobulin superfamily, member 21 (Igsf21), mRNA [NM_198610]
2 Mus musculus growth differentiation factor 15 (Gdf15), mRNA [NM_011819]
3 Mus musculus potassium large conductance calcium-activated channel, subfamily M, beta member 4 (Kcnr
4 Mus musculus BH3 interacting domain death agonist (Bid), mRNA [NM_007544]
5 Mus musculus chloride channel Kb (Clcnkb), mRNA [NM_019701]
6 Mus musculus fibulin 2 (Fbln2), transcript variant 1, mRNA [NM_007992]
7 Mus musculus LIM domain and actin binding 1 (Lima1), transcript variant a, mRNA [NM_001113545]
8 Mus musculus lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730026111 product:u
9 Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length en
10 Mus musculus cDNA clone IMAGE:40090117. [BC128469]
11 Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E33003
12 Mus musculus tubulin, beta 3 class III (Tubb3), mRNA [NM_023279]
13 Mus musculus potassium voltage-gated channel, Shal-related family, member 2 (Kcnd2), mRNA [NM_019
14 Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130022E09 product:hyp
15 Mus musculus CDC42 effector protein (Rho GTPase binding) 1 (Cdc42ep1), mRNA [NM_027219]
16 Mus musculus myosin, heavy polypeptide 1, skeletal muscle, adult (Myh1), mRNA [NM_030679]
17 PREDICTED: Mus musculus predicted gene, 20746 (Gm20746), mRNA [XM_006542883]
18 Mus musculus small nucleolar RNA host gene 6 (Snhg6), long non-coding RNA [NR_024067]
19 Mus musculus ring finger protein 41 (Rnf41), transcript variant 2, mRNA [NM_026259]
20 Mus musculus A kinase (PRKA) anchor protein 5 (Akap5), mRNA [NM_001101471]
21 Mus musculus membrane-associated ring finger (C3HC4) 8 (March8), mRNA [NM_027920]
22 Mus musculus RNA polymerase II associated protein 3 (Rpap3), mRNA [NM_028003]
23 Mus musculus UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15 (G
24 Mus musculus N-myristoyltransferase 2 (Nmt2), transcript variant 1, mRNA [NM_008708]
25 Mus musculus 13 days embryo whole body cDNA, RIKEN full-length enriched library, clone:3930401B19 pi
26 Mus musculus 2-phosphoxoylose phosphatase 1 (Pxylp1), transcript variant 1, mRNA [NM_001289645]
27 Mus musculus mitochondrial ribosomal protein S12 (Mrps12), mRNA [NM_011885]
28 Mus musculus transmembrane protein 254a (Tmem254a), transcript variant 1, mRNA [NM_026679]
29 Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530030H05 pro
30 Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B430105A11
31 Mus musculus dynein light chain LC8-type 1 (Dylnl1), mRNA [NM_019682]
32 Mus musculus chemokine (C-C motif) ligand 25 (Ccl25), transcript variant 2, long non-coding RNA [NR_03:
33 Mus musculus transmembrane protein 178 (Tmem178), mRNA [NM_026516]
34 Mus musculus cell adhesion molecule with homology to L1CAM (Ch1), mRNA [NM_007697]
35 Mus musculus transmembrane protein 254c (Tmem254c), transcript variant 1, mRNA [NM_001270498]
36 Mus musculus lipoma HMGIC fusion partner-like 3 (Lhfp13), transcript variant 2, mRNA [NM_001081231]
37 Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900019G23 prodi
38 Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900019G23 prodi
39 Mus musculus BMP2 inducible kinase (Bmp2k), mRNA [NM_080708]
40 Mus musculus leucine rich repeat and sterile alpha motif containing 1 (Lrsam1), mRNA [NM_199302]
41 Mus musculus collagen, type IV, alpha 6 (Col4a6), mRNA [NM_053185]
42 Mus musculus serine/threonine kinase receptor associated protein (Strap), mRNA [NM_011499]
43 Mus musculus purine-nucleoside phosphorylase 2 (Pnp2), mRNA [NM_001123371]
44 Mus musculus dehydrogenase/reductase (SDR family) member 7C (Dhrs7c), mRNA [NM_001013013]
45 Mus musculus RIKEN cDNA A930005H10 gene (A930005H10Rik), transcript variant 2, long non-coding RT
46 Mus musculus pituitary tumor-transforming gene 1 (Pttg1), transcript variant 2, mRNA [NM_013917]
47 Mus musculus anaphase-promoting complex subunit 5 (Anapc5), transcript variant 1, mRNA [NM_021505]
48 PREDICTED: Mus musculus RIKEN cDNA A030001D20 gene (A030001D20Rik), misc_RNA [XR_105107]
49 Mus musculus stathmin-like 3 (Stmn3), mRNA [NM_009133]
50 Mus musculus S100 calcium binding protein, zeta (S100z), mRNA [NM_001081159]
51 Mus musculus LIM domain only 1 (Lmo1), mRNA [NM_057173]
52 Mus musculus tissue inhibitor of metalloproteinase 4 (Timp4), mRNA [NM_080639]
53 Mus musculus integrin alpha 9 (Itga9), transcript variant 1, mRNA [NM_133721]
54 Mus musculus complement component 2 (within H-2S) (C2), mRNA [NM_013484]
55 Mus musculus EH-domain containing 3 (Ehd3), mRNA [NM_020578]
56 Mus musculus potassium intermediate/small conductance calcium-activated channel, subfamily N, member
57 Mus musculus doubl homeobox B-like 2 (Duxbl2), mRNA [NM_001177538]
58 Mus musculus lectin, galactose binding, soluble 4 (Lgals4), mRNA [NM_010706]
59 Mus musculus lectin, galactose binding, soluble 4 (Lgals4), mRNA [NM_010706]

1 Mus musculus GATA zinc finger domain containing 2A (Gatad2a), transcript variant 1, mRNA [NM_145596]
2 Mus musculus nuclear receptor subfamily 1, group D, member 2, mRNA (cDNA clone MGC:106146 IMAGE
3 Mus musculus F-box protein 17 (Fbxo17), mRNA [NM_015796]
4 Mus musculus glutamate receptor, metabotropic 5 (Grm5), transcript variant b, mRNA [NM_001143834]
5 Mus musculus ribosomal protein S3A1 (Rps3a1), mRNA [NM_016959]
6 Mus musculus endothelial cell-specific molecule 1 (Esm1), mRNA [NM_023612]
7 Mus musculus RIKEN cDNA 4833420G17 gene (4833420G17Rik), transcript variant 1, mRNA [NM_02612]
8 Mus musculus nicotinamide nucleotide adenyltransferase 3 (Nmnat3), mRNA [NM_144533]
9 Mus musculus exonuclease 3'-5' domain containing 1 (Exd1), mRNA [NM_172857]
10 Q3J0L9_RHOS4 (Q3J0L9) Hydrogenase maturation factor F, partial (3%) [TC1616199]
11 Mus musculus cell adhesion molecule with homology to L1CAM (Chl1), mRNA [NM_007697]
12 Mus musculus protein arginine N-methyltransferase 8 (Prmt8), mRNA [NM_201371]
13 Mus musculus KN motif and ankyrin repeat domains 1 (Kank1), mRNA [NM_181404]
14 Mus musculus hydroxyprostaglandin dehydrogenase 15 (NAD) (Hpgd), mRNA [NM_008278]
15 Mus musculus leucine rich repeat and sterile alpha motif containing 1 (Lrsam1), mRNA [NM_199302]
16 Mus musculus collagen, type II, alpha 1 (Col2a1), transcript variant 2, mRNA [NM_001113515]
17 Mus musculus growth associated protein 43 (Gap43), mRNA [NM_008083]
18 Mus musculus translocase of outer mitochondrial membrane 22 homolog (yeast) (Tomm22), mRNA [NM_1
19 Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830138L07 product:uncla:
20 Mus musculus histocompatibility 2, Q region locus 5 (H2-Q5), non-coding RNA [NR_051981]
21 Mus musculus pyruvate dehydrogenase (lipoamide) beta (Pdhb), mRNA [NM_024221]
22 Mus musculus amyloid beta (A4) precursor protein-binding, family A, member 2 (Apba2), transcript variant
23 Mus musculus stathmin-like 4 (Stmn4), mRNA [NM_019675]
24 Mus musculus Ly6/neurotoxin 1 (Lynx1), mRNA [NM_011838]
25 Mus musculus butyrylcholinesterase (Bche), mRNA [NM_009738]
26 Mus musculus SH3-domain GRB2-like 3 (Sh3gl3), transcript variant 1, mRNA [NM_017400]
27 Mus musculus uncoupling protein 3 (mitochondrial, proton carrier) (Ucp3), mRNA [NM_009464]
28 Mus musculus stathmin-like 4 (Stmn4), mRNA [NM_019675]
29 Mus musculus peptidyl arginine deiminase, type II (Padi2), mRNA [NM_008812]
30 Mus musculus G protein-coupled receptor, family C, group 5, member A (Gprc5a), mRNA [NM_181444]
31 Mus musculus lipoprotein lipase (Lpl), mRNA [NM_008509]
32 Mus musculus lipoprotein lipase (Lpl), mRNA [NM_008509]
33 Mus musculus peptidyl arginine deiminase, type II (Padi2), mRNA [NM_008812]
34 Mus musculus uncoupling protein 2 (mitochondrial, proton carrier) (Ucp2), mRNA [NM_011671]
35 Mus musculus abhydrolase domain containing 1 (Abhd1), mRNA [NM_021304]
36 Mus musculus RIKEN cDNA 4833420G17 gene (4833420G17Rik), transcript variant 1, mRNA [NM_02612]
37 Mus musculus serine (or cysteine) peptidase inhibitor, clade A, member 3N (Serpina3n), mRNA [NM_0092
38 Mus musculus complement component factor i (Cfi), mRNA [NM_007686]
39 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15 [Source:MGI Sym
40 Mus musculus purinergic receptor P2X, ligand-gated ion channel, 7 (P2rx7), transcript variant 1, mRNA [NM
41 Mus musculus phosphatidylethanolamine binding protein 2 (Pbp2), mRNA [NM_029595]
42 Mus musculus olfactory receptor 224 (Olfr224), mRNA [NM_207695]
43 Mus musculus processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae) (Pop4), mRNA [NM_(
44 Mus musculus POU domain, class 6, transcription factor 1 (Pou6f1), mRNA [NM_010127]
45 Mus musculus protocadherin 17 (Pcdh17), mRNA [NM_001013753]
46 Mus musculus family with sequence similarity 183, member B (Fam183b), transcript variant 1, mRNA [NM_
47 Mus musculus RIKEN cDNA 1810037I17 gene (1810037I17Rik), mRNA [NM_024461]
48 Mus musculus RIKEN cDNA 1810037I17 gene (1810037I17Rik), mRNA [NM_024461]
49 Mus musculus sterile alpha motif domain containing 4 (Samd4), transcript variant 1, mRNA [NM_00103722
50 Mus musculus serine (or cysteine) peptidase inhibitor, clade A, member 3I (Serpina3i), mRNA [NM_001195
51 Mus musculus collagen, type IV, alpha 6 (Col4a6), mRNA [NM_053185]
52 Mus musculus XIAP associated factor 1 (Xaf1), transcript variant 1, mRNA [NM_001037713]
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27	0.632936888	10.47605776	8.88541E-06
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30	0.629777447	9.01476485	0.008859233
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56	-1.374346569	10.16522609	1.02537E-05
57	-1.382825841	9.054592244	0.000124631
58	-1.384107062	8.150682833	2.57183E-07
59	-1.384406462	9.160897964	0.011447725
60	-1.394429143	9.083050324	0.009286241

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2	-1.417803996	10.06687358	1.11591E-09
3	-1.418944898	9.618498483	1.10279E-05
4	-1.431784462	9.098136864	8.79673E-09
5	-1.445020115	7.754319196	0.029882996
6	-1.46036708	14.50307495	1.29869E-07
7	-1.476230322	7.936182419	0.001772617
8	-1.485576479	8.419571885	1.17782E-08
9	-1.491097654	8.464035327	4.59997E-05
10	-1.525678034	8.520248792	3.00086E-06
11	-1.53256524	11.03368948	6.69066E-07
12	-1.534507736	10.44255926	0.001739455
13	-1.54223841	7.044327945	0.003583798
14	-1.562962584	11.84753693	8.03792E-08
15	-1.568266039	7.811720919	0.004381404
16	-1.595495677	11.18370501	0.000514259
17	-1.60138222	10.26377656	0.030428182
18	-1.608736505	10.06212415	0.002286646
19	-1.623250362	12.76321099	5.03003E-15
20	-1.6590401	7.042019248	1.12499E-07
21	-1.663988464	9.535892008	0.005659542
22	-1.683490724	12.85410198	1.47938E-09
23	-1.686820938	9.225208525	6.98037E-05
24	-1.693097435	9.25076796	0.032298961
25	-1.71821413	11.50331263	8.90582E-07
26	-1.719959388	10.67728495	1.00373E-08
27	-1.728042937	9.346406711	1.20027E-10
28	-1.732205788	8.742824015	0.005579854
29	-1.765390964	9.267843384	0.016968618
30	-1.825424764	12.92514476	9.79076E-06
31	-1.882880186	10.6940361	4.87063E-05
32	-1.961023445	10.53863681	0.002138263
33	-1.966798117	8.512458682	0.000396451
34	-1.981559202	13.12004985	2.85216E-06
35	-2.008925416	9.278059744	0.003448159
36	-2.028719361	9.154942083	1.9464E-13
37	-2.135137596	11.72763205	2.19306E-10
38	-2.257787149	11.293936	0.022418234
39	-2.283011075	7.59612213	0.00086345
40	-2.327912086	10.82348441	1.10279E-05
41	-2.566482682	9.918835431	1.55236E-05
42	-2.708851464	7.72208074	5.32555E-10
43	-2.853577013	8.061203017	2.76734E-14
44	-2.990439512	11.37800517	1.19839E-16
45	-3.085193903	8.567395379	1.53107E-11
46	-3.096400623	9.286752712	4.62079E-09
47	-3.146347755	10.8863997	4.37739E-06
48	-3.150307147	11.50210939	8.73791E-16
49	-3.218676372	12.76378133	9.75281E-16
50	-3.381084819	9.712777677	3.4835E-12
51	-3.517707117	8.237049671	0.00111415
52	-4.328433054	11.49218277	1.68799E-16
53	-6.156879098	9.98739195	1.65288E-09
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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 probe 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
A_55_P2016647	1448314_at
A_55_P1955457	1425458_a_at
A_52_P470466	1434685_at
A_52_P24308	1448260_at
A_55_P2085142	1449254_at
A_51_P366061	1416514_a_at
A_52_P105537	1426852_x_at
A_55_P2056325	1460330_at
A_51_P455997	1452905_at
A_55_P2031021	1448595_a_at
A_52_P569023	1454926_at
A_66_P101600	1424113_at
A_55_P1954221	1416529_at
A_52_P667287	1434418_at
A_55_P2100475	1455980_a_at
A_55_P1991016	1428572_at
A_51_P455997	1439380_x_at
A_51_P404463	1423261_at
A_51_P394997	1418047_at
A_55_P2065424	1422256_at

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2	A_51_P200561	1429055_at
3	A_55_P2032412	1436329_at
4	A_52_P203316	1454768_at
5	A_51_P112734	1417929_at
6	A_52_P502577	1438658_a_at
7	A_55_P2151388	1449340_at
8	A_55_P2011436	1448113_at
9	A_55_P1966204	1448823_at
10	A_51_P405606	1456174_x_at
11	A_55_P2215880	1425016_at
12	A_51_P100208	1435612_at
13	A_55_P2017418	1450876_at
14	A_52_P87839	1429348_at
15	A_51_P295085	1419663_at
16	A_55_P1959748	1451095_at
17	A_55_P2006629	1420798_s_at
18	A_51_P484111	1455978_a_at
19	A_51_P163953	1416107_at
20	A_55_P2000521	1455665_at
21	A_55_P2003813	1435767_at
22	A_52_P462472	1440910_at
23	A_51_P107362	1418507_s_at
24	A_55_P2042486	1454613_at
25	A_55_P2006629	1424341_s_at
26	A_51_P278653	1422552_at
27	A_55_P2052062	1448788_at
28	A_52_P599317	1450047_at
29	A_51_P353252	1427042_at
30	A_51_P230098	1448627_s_at
31	A_55_P2026530	1434582_at
32	A_55_P2074736	1434325_x_at
33	A_52_P568235	1439904_at
34	A_52_P628915	1415844_at
35	A_55_P2031836	1424896_at
36	A_55_P2041828	1415978_at
37	A_52_P331727	1460627_at
38	A_55_P2110512	1455056_at
39	A_55_P2031836	1437618_x_at
40	A_55_P2007155	1418979_at
41	A_52_P162486	1416405_at
42	A_51_P105709	1429295_s_at
43	A_55_P2017636	1421811_at
44	A_51_P254855	1417262_at
45	A_52_P49042	1435050_at
46	A_55_P2025033	1452242_at
47	A_51_P126437	1450061_at
48	A_55_P2031836	1424897_at
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2	A_55_P2085060	1436094_at
3	A_52_P263518	1428156_at
4	A_51_P127738	1435933_at
5	A_55_P2111302	1448735_at
6	A_55_P1980631	1451246_s_at
7	A_52_P351925	1452124_at
8	A_51_P317031	1418778_at
9	A_55_P2024525	1455925_at
10	A_55_P2084646	1455516_at
11	A_55_P2158251	1440177_at
12	A_51_P465128	1452092_at
13	A_52_P925277	1435227_at
14	A_55_P1964638	1427321_s_at
15	A_51_P405606	1420760_s_at
16	A_51_P494293	1453245_at
17	A_51_P247157	1438988_x_at
18	A_51_P389156	1420994_at
19	A_52_P413646	1450759_at
20	A_55_P2063462	1449286_at
21	A_55_P2412847	1426016_a_at
22	A_55_P2100555	1450435_at
23	A_51_P366207	1418046_at
24	A_66_P114461	1443119_at
25	A_55_P2128511	1435917_at
26	A_51_P398037	1439204_at
27	A_55_P2380970	1448083_at
28	A_51_P360492	1438852_x_at
29	A_55_P2013336	1416558_at
30	A_55_P2033362	1427683_at
31	A_51_P289889	1452107_s_at
32	A_55_P2003216	1460214_at
33	A_52_P263518	1428157_at
34	A_51_P427663	1450981_at
35	A_55_P2102385	1426880_at
36	A_52_P470466	1427247_at
37	A_55_P2044587	1436662_at
38	A_52_P21	1436237_at
39	A_51_P455997	1452183_a_at
40	A_55_P2082653	1432750_at
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3 **Autely isolated astrocytes**

4 AGILENT Gene Symbol	5 AFFY Gene Symbol	6 q-value
7 Cd24a	Cd24a	0
8 Stmn2	Stmn2	0
9 Cd24a	Cd24a	0
10 Stmn2	Stmn2	0
11 Asns	Asns	0
12	0 Tmsb10	0
13 B3galnt1	B3galnt1	0
14 Pak3	Pak3	0
15 1500015O10Rik	1500015O10Rik	0
16 Nov	Nov	0
17 Cd24a	Cd24a	0
18 Top2a	Top2a	0
19 Map1b	Ints6	0
20 Gap43	Gap43	2.38E-04
21 Cxadr	Cxadr	2.38E-04
22 Enc1	Enc1	2.38E-04
23 Slc6a15	Slc6a15	2.38E-04
24 Mme	Mme	2.38E-04
25 Tmsb10	Tmsb10	2.38E-04
26 Egr2	Egr2	2.38E-04
27 Gpr27		0 2.38E-04
28 Tmeff2	Tmeff2	2.38E-04
29 Sertad4	Sertad4	2.38E-04
30 Lpl	Lpl	2.38E-04
31 Cdk1	Cdk1	2.38E-04
32 Grb10	Grb10	2.38E-04
33 D3Bwg0562e	D3Bwg0562e	2.38E-04
34 Uchl1	Uchl1	2.38E-04
35 Spp1	Spp1	2.38E-04
36 Fscn1	Fscn1	2.38E-04
37 Nov	Nov	2.38E-04
38 Anxa3	Anxa3	2.08E-04
39 Meg3	Meg3	3.03E-04
40 Bex1	Bex1	3.92E-04
41 Sphkap	Sphkap	3.92E-04
42 Lamb1	Lamb1	3.92E-04
43 Emp1	Emp1	3.92E-04
44 Cers6	Cers6	6.14E-04
45 Gas2l3	Gas2l3	7.69E-04
46 Basp1	Basp1	8.33E-04
47 Meg3	Meg3	8.94E-04
48 1500015O10Rik	1500015O10Rik	8.94E-04
49 Neurod6	Neurod6	8.94E-04
50 Sstr2	Sstr2	9.09E-04

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2	4930506M07Rik	4930506M07Rik	9.09E-04
3	Egr3	Egr3	9.09E-04
4	Kcnf1	Kcnf1	9.22E-04
5	Slc7a8	Slc7a8	9.72E-04
6	S1pr3	S1pr3	9.72E-04
7	Sostdc1	Sostdc1	9.72E-04
8	Gm11223	Stmn1	0.001045752
9	Cxcl12	Cxcl12	0.001045752
10	Ndr1	Ndr1	0.001069182
11	Ephb2	Ephb2	0.00117284
12	Opcml	Opcml	0.001212121
13	Cfh	Cfh	0.001212121
14	Sema3c	Sema3c	0.001212121
15	Ogn	Ogn	0.001206897
16	Asns	Asns	0.001206897
17		0 Pcdha1 Pcdha10 Pcdha11	0.001206897
18	Matn2	Matn2	0.001206897
19	Nsg2	Nsg2	0.001290323
20	Lonrf1	Lonrf1	0.001640212
21	Scn3b	Scn3b	0.001666667
22	C77370	C77370	0.001666667
23	Socs2	Socs2	0.001666667
24	Dpysl3	Dpysl3	0.001666667
25		0 Pcdha1 Pcdha10 Pcdha11	0.001666667
26	Rprm	Rprm	0.001642512
27	Cd200	Cd200	0.001642512
28	Hs6st2	Hs6st2	0.001642512
29	Mal2	Mal2	0.00162037
30	Pbk	Pbk	0.00162037
31	Erc2	Erc2	0.001621622
32	Prkar1b	Prkar1b	0.002044444
33	Fstl5	Fstl5	0.002061404
34	Syt4	Syt4	0.002061404
35	Gpr85	Gpr85	0.002094017
36	Tubb3	Tubb3	0.002109705
37	Thsd7b	Thsd7b	0.002333333
38	Lmo7	Lmo7	0.002333333
39	Gpr85	Gpr85	0.002333333
40	Akr1c14	Akr1c14	0.002329317
41	Bgn	Bgn	0.002329317
42	Trip13	Trip13	0.002329317
43	Thbs1	Pald1 Thbs1	0.00248062
44	Ptgs2	Ptgs2	0.00248062
45	D10Bwg1379e	D10Bwg1379e	0.00248062
46	Cep55	Cep55	0.002509363
47	Enc1	Enc1	0.002555556
48	Gpr85	Gpr85	0.002857143
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2	Vgf	Vgf	0.002857143
3	Gng2	Gng2	0.003046595
4	Scn2a1	Scn2a1	0.003046595
5	Cp	Cp	0.003017544
6	Aurkb	Aurkb	0.003125
7	Ank3	Ank3	0.003127148
8	Ccdc109b	Ccdc109b	0.003127148
9	Prdm8	Prdm8	0.003127148
10	Csrnp3	Csrnp3	0.003266667
11	Grik3	Grik3	0.003432343
12	Chst15	Chst15	0.00372549
13	Bcl11b	Bcl11b	0.003883495
14	Cxadr	Cxadr	0.003942308
15	Ndrgr1	Ndrgr1	0.003942308
16	9130024F11Rik	9130024F11Rik	0.004025157
17	Hn1	Hn1	0.004049844
18	B3gnt5	B3gnt5	0.004290124
19	Bmp6	Bmp6	0.00440367
20		0 Ntng1	0.00440367
21	Tro	Tro	0.004384385
22	L1cam	L1cam	0.004375
23	Nap112	Nap112	0.004483776
24	Grm7	Grm7	0.004473684
25	Ociad2	Ociad2	0.004550725
26	Scn3a	Scn3a	0.00454023
27	Nalcn	Nalcn	0.004586895
28	Mcm6	Mcm6	0.004661017
29	Melk	Melk	0.00464986
30	Egr2	Egr2	0.004833333
31	Npnt	Npnt	0.004903582
32	Igsf5	Pcp4	0.004903582
33	Gng2	Gng2	0.004850949
34	Cnn2	Cnn2	0.004850949
35	Etl4	Etl4	0.0048
36	D3Bwg0562e	D3Bwg0562e	0.00489418
37	Sorcs1	Sorcs1	0.00488189
38	Ttc9	Ttc9	0.00488189
39	Meg3	Meg3	0.004909561
40	Zfp711	Zfp711	0.004948718
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4	RP-value
5	34.223267
6	39.382553
7	41.796303
8	58.87709
9	78.59536
10	118.15399
11	130.00249
12	130.11092
13	142.4315
14	145.698
15	147.38728
16	153.62456
17	155.22014
18	164.82515
19	168.33496
20	169.44853
21	170.17828
22	173.7218
23	175.71043
24	178.14516
25	179.20235
26	181.67484
27	183.20612
28	191.8282
29	193.05821
30	195.35397
31	196.87836
32	196.96948
33	200.75273
34	201.90858
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36	205.22661
37	210.77614
38	218.74706
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40	223.22322
41	225.10469
42	235.67517
43	244.70367
44	256.50943
45	263.50482
46	263.89993
47	263.93997
48	275.0427
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For Review Only

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2 275.65512
3 276.24673
4 277.1194
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6 279.0203
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8 281.23773
9 282.6501
10 284.16025
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12 290.9738
13 291.76346
14 293.47815
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16 296.6824
17 296.96982
18 298.0942
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21 324.035
22 325.75204
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24 327.51932
25 327.8075
26 329.64703
27 331.24893
28 336.4755
29 338.52478
30 340.3146
31 341.4727
32 349.87045
33 351.45538
34 355.1068
35 358.2844
36 359.173
37 366.26736
38 367.05988
39 371.30234
40 378.1268
41 378.5343
42 378.63394
43 382.84604
44 383.13834
45 383.91983
46 385.2477
47 386.46875
48 399.72336
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For Review Only

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2	399.76904
3	407.29984
4	407.35904
5	409.69595
6	
7	412.1374
8	413.18622
9	413.26825
10	
11	413.3775
12	423.0475
13	426.3158
14	432.8777
15	438.29535
16	439.4035
17	
18	439.8584
19	444.10327
20	445.91617
21	450.83182
22	455.31924
23	
24	456.33588
25	457.64203
26	458.6556
27	461.70532
28	
29	462.412
30	463.3562
31	464.0969
32	464.66165
33	465.9082
34	
35	467.39966
36	470.19315
37	472.44604
38	472.52155
39	473.28952
40	
41	473.4576
42	474.54385
43	476.9111
44	477.72067
45	478.11398
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47	480.9673
48	482.90833
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For Review Only

Ranked list of genes down-regulated in non-Tg compared to Tg**AGILENT SurePrint G3 GE 8x60k probe set 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
A_51_P391616	1452975_at
A_51_P268193	1421093_at
A_55_P1955412	1451627_a_at
A_55_P2427900	1455304_at
A_51_P127297	1449038_at
A_55_P1971599	1416718_at
A_51_P207988	1424208_at
A_55_P2013701	1427284_a_at
A_51_P468260	1434342_at
A_55_P1955627	1424945_at
A_55_P2003266	1435918_at
A_51_P431543	1429647_at
A_51_P443819	1425408_a_at
A_55_P1955627	1456722_at
A_55_P1961913	1448602_at
A_55_P2054673	1418050_at
A_51_P321341	1427345_a_at
A_55_P2162712	1435314_at
A_52_P177847	1428922_at
A_51_P285077	1424553_at
A_66_P109397	1457373_at
A_55_P2033312	1434121_at
A_52_P177847	1452961_at
A_55_P2002849	1434742_s_at
A_66_P109368	1436569_at
A_51_P504354	1417985_at
A_55_P2123484	1442917_at
A_55_P2007447	1417946_at
A_51_P140641	1424652_at

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2	A_55_P2003266	1434202_a_at
3	A_52_P532227	1423571_at
4	A_55_P2056483	1422315_x_at
5	A_52_P622850	1456010_x_at
6	A_55_P2156304	1435094_at
7	A_55_P2391065	1441867_x_at
8	A_55_P2036392	1436611_at
9	A_51_P124126	1419040_at
10	A_51_P375558	1450468_at
11	A_55_P2056483	1425164_a_at
12	A_51_P396883	1460408_at
13	A_51_P216702	1434492_at
14	A_51_P156857	1423306_at
15	A_55_P1955437	1430600_at
16	A_55_P2108599	1426616_at
17	A_55_P2070992	1424714_at
18	A_55_P2391065	1429229_s_at
19	A_55_P2029721	1432922_at
20	A_55_P2003266	1434203_at
21	A_55_P2108599	1452132_at
22	A_52_P85174	1422782_s_at
23	A_66_P139666	1434136_at
24	A_66_P114784	1430700_a_at
25	A_55_P1963508	1435936_at
26	A_55_P2036392	1447248_at
27	A_51_P169516	1452922_at
28	A_52_P883557	1438751_at
29	A_66_P124091	1434201_at
30	A_66_P105046	1417932_at
31	A_55_P2105472	1418212_at
32	A_66_P119457	1434727_at
33	A_55_P2027900	1455444_at
34	A_51_P396883	1427227_at
35	A_55_P2103225	1428964_at
36	A_52_P141687	1424146_at
37	A_51_P268697	1426341_at
38	A_51_P207988	1421073_a_at
39	A_51_P302566	1434354_at
40	A_52_P496956	1422428_at
41	A_51_P404077	1418532_at
42	A_51_P334942	1416468_at
43	A_51_P392005	1427482_a_at
44	A_55_P2034067	1439708_at
45	A_55_P1955412	1439940_at
46	A_66_P139666	1455963_at
47	A_51_P312336	1428114_at
48	A_55_P2002849	1431923_at
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2	A_52_P376169	1454969_at
3	A_52_P368306	1449533_at
4	A_55_P1973033	1448870_at
5	A_51_P330044	1424677_at
6	A_52_P681391	1448700_at
7	A_51_P216702	1454678_s_at
8	A_51_P404077	1418533_s_at
9	A_52_P401504	1449388_at
10	A_55_P2396370	1439894_at
11	A_55_P2025228	1455703_at
12	A_55_P2388118	1438132_at
13	A_51_P268697	1426340_at
14	A_55_P2427900	1437319_at
15	A_55_P1961014	1450699_at
16	A_51_P276235	1451361_a_at
17	A_55_P2002572	1448499_a_at
18	A_55_P1964363	1455451_at
19	A_55_P1996674	1449123_at
20	A_55_P1972192	1422743_at
21	A_55_P1996578	1421841_at
22	A_55_P1972192	1435567_at
23	A_55_P2080021	1434510_at
24	A_55_P1964960	1416200_at
25	A_51_P510764	1434191_at
26	A_52_P655687	1419332_at
27	A_51_P209327	1451038_at
28	A_55_P1971889	1417408_at
29	A_55_P1972981	1429651_at
30	A_55_P2030373	1455136_at
31	A_51_P479230	1419520_at
32	A_51_P117477	1435658_at
33	A_55_P2096043	1429267_at
34	A_55_P2000369	1425382_a_at
35	A_55_P2018666	1424737_at
36	A_55_P2156304	1436163_at
37	A_55_P2133007	1419429_at
38	A_55_P1960416	1451174_at
39	A_30_P01022245	1455799_at
40	A_55_P2009752	1434736_at
41	A_66_P101835	1433741_at
42	A_55_P1952638	1435467_at
43	A_52_P457567	1434096_at
44	A_51_P496309	1436931_at
45	A_52_P376169	1456138_at
46	A_52_P174915	1415801_at
47	A_55_P2051885	1421221_at
48	A_52_P382886	1423271_at
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2	A_52_P309166	1419420_at
3	A_30_P01017882	1456523_at
4	A_55_P2061620	1449147_at
5	A_51_P204715	1435870_at
6	A_55_P1959923	1426243_at
7	A_55_P1972192	1422744_at
8	A_55_P1982454	1422823_at
9	A_52_P116264	1424393_s_at
10	A_55_P1961014	1417580_s_at
11	A_55_P2000369	1434449_at
12	A_55_P2024669	1435559_at
13	A_52_P309166	1440973_at
14	A_52_P622850	1423146_at
15	A_55_P2112270	1457143_at
16	A_55_P2062737	1416444_at
17	A_55_P1964363	1426633_s_at
18	A_51_P502150	1438115_a_at
19	A_55_P2055854	1449051_at
20	A_66_P112684	1455636_at
21	A_51_P125842	1424383_at
22	A_52_P586944	1437312_at
23	A_51_P426739	1426502_s_at
24	A_51_P258690	1420764_at
25	A_52_P571371	1426362_at
26	A_51_P131216	1428731_at
27	A_55_P2049752	1433529_at
28	A_66_P119457	1429023_at
29	A_55_P1996578	1425796_a_at
30	A_55_P1965616	1436669_at
31	A_52_P175376	1418091_at
32	A_51_P242201	1452068_at
33	A_55_P2078670	1423844_s_at
34	A_51_P216702	1433671_at
35	A_55_P2106901	1422596_at
36	A_52_P520495	1415989_at
37	A_55_P2168823	1437621_x_at
38	A_52_P62121	1450875_at
39	A_55_P2091858	1424863_a_at
40	A_51_P488991	1424086_at
41	A_51_P337523	1455462_at
42	A_51_P455647	1448752_at
43	A_51_P173709	1451411_at
44	A_52_P465886	1428736_at
45	A_55_P2009752	1434735_at
46	A_55_P2000148	1437094_x_at
47	A_51_P309854	1448927_at
48	A_52_P488427	1424530_at
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2 A_51_P211793 1418310_a_at
3 A_55_P1964363 1455452_x_at
4 A_55_P2423586 1457424_at
5 A_51_P242201 1452067_at
6 A_51_P455866 1419555_at
7 A_55_P2117119 1448507_at
8 A_51_P437135 1421100_a_at
9 A_52_P376169 1457843_at
10 A_55_P2091858 1425983_x_at
11 A_52_P598634 1429260_at
12 A_55_P1960108 1437418_at
13 A_52_P250400 1424701_at
14 A_51_P355427 1450974_at
15 A_66_P139785 1448908_at
16 A_55_P2027900 1421738_at
17 A_51_P352452 1443525_at
18 A_51_P170463 1456833_at
19 A_55_P2100884 1422733_at
20 A_55_P2030373 1452308_a_at
21 A_51_P436727 1460444_at
22 A_51_P481159 1427912_at
23 A_55_P1982454 1422824_s_at
24 A_55_P2094831 1423343_at
25 A_52_P288251 1436698_x_at
26 A_52_P12877 1431182_at
27 A_55_P1965931 1418013_at
28 A_51_P185247 1424007_at
29 A_55_P1991164 1448139_at
30 A_51_P355427 1435833_at
31 A_55_P1974645 1418259_a_at
32 A_55_P2003483 1416049_at
33 A_52_P249424 1420909_at
34 A_30_P01021563 1457257_x_at
35 A_51_P224042 1453310_at
36 A_55_P2010871 1455717_s_at
37 A_51_P171288 1455154_at
38 A_52_P85174 1422781_at
39 A_55_P1963154 1450154_at
40 A_55_P2027083 1419601_at
41 A_55_P2012241 1433501_at
42 A_55_P1965616 1436670_x_at
43 A_51_P255682 1420911_a_at
44 A_52_P195881 1428536_at
45 A_52_P512575 1451776_s_at
46 A_51_P434670 1425597_a_at
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AGILENT Gene Symbol	AFFY Gene Symbol	q-value
Gjb6	Gjb6	0
Dio2	Dio2	0
Ppp1r3g	Ppp1r3g	0
Grin2c	Grin2c	0
Etnppl		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

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2	Fam107a	Fam107a	5.85E-05
3	S1pr1	S1pr1	5.85E-05
4	Phkg1	Phkg1	5.85E-05
5	Hes5	Hes5	5.85E-05
6	Kcnj16	Kcnj16	5.85E-05
7	Cep128	Cep128	5.85E-05
8	Slc39a12	Slc39a12	5.85E-05
9	Cyp2d22	Cyp2d22	5.85E-05
10	Myoc	Myoc	5.85E-05
11	Phkg1	Phkg1	5.85E-05
12	Gabrg1	Gabrg1	5.85E-05
13	Eogt	Eogt	5.85E-05
14	Smim3	Smim3	1.67E-04
15	Cmtm5	Cmtm5	1.67E-04
16	Tlcd1	Tlcd1	1.67E-04
17	Aldoc	Aldoc	1.99E-04
18	Cep128	Cep128	1.99E-04
19		0 4933416E14Rik	1.99E-04
20	Fam107a	Fam107a	1.99E-04
21	Tlcd1	Tlcd1	1.99E-04
22	Tlr3	Tlr3	1.99E-04
23	Tmem229a	Tmem229a	1.99E-04
24	Pla2g7	Pla2g7	2.94E-04
25	Slc13a5	Slc13a5	3.38E-04
26	Slc39a12	Slc39a12	3.70E-04
27	Ppp1r3d	Ppp1r3d	3.70E-04
28	Slc30a10	Slc30a10	3.70E-04
29	Chrdl1	Chrdl1	3.85E-04
30	Il18	Il18	3.85E-04
31	Omg	Omg	3.85E-04
32	Hepacam	Hepacam	3.85E-04
33	Gabra2	Gabra2	3.85E-04
34	Gabrg1	Gabrg1	3.85E-04
35	Slc25a18	Slc25a18	4.17E-04
36	Gpr37l1	Gpr37l1	4.17E-04
37	Slc1a3	Slc1a3	4.37E-04
38	Ptger4	Ptger4	4.37E-04
39	Maob	Maob	4.37E-04
40	Acsbg1	Acsbg1	4.37E-04
41	Fzd2	Fzd2	4.71E-04
42	Aldh1a1	Aldh1a1	6.13E-04
43	Car8	Car8	6.13E-04
44	Myom3	Myom3	6.44E-04
45	Slc1a2	Slc1a2	6.74E-04
46	Tmem229a	Tmem229a	7.41E-04
47	Slc14a1	Slc14a1	7.69E-04
48	Aifm3	Aifm3	8.16E-04
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2	Lypd6	Lypd6	8.16E-04
3	Tmem100	Tmem100	8.16E-04
4	Ltbp1	Ltbp1	9.03E-04
5	Cyp2j9	Cyp2j9	9.03E-04
6	G0s2	G0s2	9.15E-04
7	Eogt	Eogt	9.15E-04
8	Fzd2	Fzd2	9.15E-04
9	Thbs4	Thbs4	9.15E-04
10			
11	A730056I06Rik	A730056I06Rik	9.15E-04
12	Akt2	Akt2	9.15E-04
13	Gm5089	Gm5089	9.94E-04
14	Slc1a3	Slc1a3	9.94E-04
15	Unc13c	Unc13c	9.97E-04
16	Selenbp1	Selenbp1	9.97E-04
17	Pnpla7	Pnpla7	9.97E-04
18	Ephx2	Ephx2	0.00100295
19	Kctd14	Kctd14	0.00100295
20	Itih3	Itih3	0.00100295
21	Phka1	Phka1	0.00100295
22	Fgfr3	Fgfr3	0.00100295
23	Phka1	Phka1	0.00100295
24	Papss2	Papss2	0.001014493
25	Il33	Il33	0.001014493
26	Agmo	Agmo	0.001016949
27	Egfl6	Egfl6	0.001016949
28	Apln	Apln	0.001016949
29	F3	F3	0.001288515
30	Phactr3	Phactr3	0.001305556
31	Atp1a2	Atp1a2	0.001338798
32	Nat8	Nat8	0.001338798
33	Slc27a1	Slc27a1	0.001490515
34	Acot11	Acot11	0.001435897
35	Aqp4	Aqp4	0.001435897
36	Thrsp	Thrsp	0.001435897
37	Kcnj16	Kcnj16	0.001435897
38	Cntfr	Cntfr	0.001435897
39	Nrros	Nrros	0.001435897
40		0 Rorb	0.001435897
41	Hlf	Hlf	0.001450382
42	Cd38	Cd38	0.001464646
43	Fgd6	Fgd6	0.001519608
44	Slc4a4	Slc4a4	0.001519608
45	Rfx4	Rfx4	0.001519608
46	Lypd6	Lypd6	0.001519608
47	Gja1	Gja1	0.001545894
48	Bco2	Bco2	0.001545894
49	Gjb2	Gjb2	0.001558753
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2	St6galnac5	St6galnac5	0.001571429
3		0 Gm2115	0.001619718
4	Chst1	Chst1	0.001619718
5		0 Chpt1	0.001757991
6	Cth	Cth	0.001757991
7	Phka1	Phka1	0.001757991
8	Eps8	Eps8	0.001757991
9	Adhfe1	Adhfe1	0.001756757
10	Selenbp1	Selenbp1	0.001756757
11	Aqp4	Aqp4	0.001834452
12	Myo6	Myo6	0.00187638
13	St6galnac5	LOC552874 St6galnac5	0.00187638
14	Hes5	Hes5	0.001873638
15	Gm6556	Gm6556	0.001873638
16	Elovl2	Elovl2	0.001991342
17	Kctd14	Kctd14	0.002086022
18	Slc9a3r1	Slc9a3r1	0.002067511
19	Ppara	Ppara	0.002067511
20	Lsamp	Lsamp	0.002067511
21	Tmem51	Tmem51	0.002180293
22	Bmpr1b	Bmpr1b	0.0021875
23	Gpt	Gpt	0.002283951
24	Scrg1	Scrg1	0.002283951
25	Tmem144	Tmem144	0.002357724
26	Usp54	Usp54	0.002357724
27	Pamr1	Pamr1	0.002383838
28	Hepacam	Hepacam	0.002409639
29	Fgfr3	Fgfr3	0.00247505
30	1700019G17Rik	1700019G17Rik	0.002480159
31	Tfcp2l1	Tfcp2l1	0.002509804
32	Naaa	Naaa	0.002509804
33	Cbs	Cbs	0.002534113
34	Eogt	Eogt	0.00253876
35	Nkain4	Nkain4	0.002681992
36	Vcam1	Vcam1	0.002681992
37		0 Phgdh	0.002685714
38	Gpr37	Gpr37	0.002689394
39	Hipk2	Hipk2	0.002749529
40	Oaf	Oaf	0.002752809
41	Adcy2	Adcy2	0.002811918
42	Car2	Car2	0.002799264
43	Gprc5b	Gprc5b	0.002799264
44	Gramd3	Gramd3	0.002893773
45	Hlf	Hlf	0.003005465
46	Dnaic1	Dnaic1	0.003007246
47	Kcnn2	Kcnn2	0.003028674
48	Sec14l2	Sec14l2	0.003028674
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2	Rlbp1	Rlbp1	0.003065954
3	Kctd14	Kctd14	0.003191489
4	Eya1	Eya1	0.003227513
5	Naaa	Naaa	0.003245614
6	Elf5	Elf5	0.003246073
7	Efh1	Efh1	0.00328125
8	Dab1	Dab1	0.00338488
9	Lypd6	Lypd6	0.00338488
10	Hipk2	Hipk2	0.003434856
11	1190007I07Rik	1810014B01Rik	0.003434856
12		0 Gm3515 Rmst Rmst	0.003434856
13	Pcdh20	Pcdh20	0.003451179
14	Timp4	Timp4	0.003500838
15	Ppap2b	Ppap2b	0.003582089
16	Gabra2	Gabra2	0.003582089
17	Dbx2	Dbx2	0.003596059
18	Gpr17	Gpr17	0.003596059
19	Fjx1	Fjx1	0.003788618
20	Atp1a2	Atp1a2	0.003788618
21	Arrb1	Arrb1	0.00381877
22	Cbr3	Cbr3	0.003864734
23	Eps8	Eps8	0.003974359
24	Slco1c1	Slco1c1	0.004051037
25	Tmem204	Tmem204	0.004063492
26	Hspa8	Hspa8	0.004060031
27	Cml1	Cml1	0.004166667
28	Gdf10	Gdf10	0.004178404
29	Mlc1	Mlc1	0.004205607
30	Timp4		0.004178187
31	Entpd2	Entpd2	0.004178187
32	Gldc	Gldc	0.004178187
33	Vegfa	Vegfa	0.004272727
34		0 Pvrl3	0.004272727
35	Ppil6	Ppil6	0.004272727
36	Daam2	Daam2	0.004519519
37	Gli3	Gli3	0.004519519
38	Tlr3	Tlr3	0.004538691
39	Folh1	Folh1	0.004538691
40	Kcnj10	Kcnj10	0.004592592
41	Ctso	Ctso	0.004631268
42	1700019G17Rik	1700019G17Rik	0.004625551
43	Mfge8	Mfge8	0.004649123
44	Kcng4	Kcng4	0.004905386
45	Hopx	Hopx	0.004942029
46	Qk	Qk	0.004978355
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RP-value

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5 24.644915
6 26.695889
7 27.522926
8 33.58823
9 43.206196
10 61.288677
11 62.309135
12 62.836388
13 64.41103
14 69.695885
15 69.91839
16 71.759315
17 72.41244
18 73.50246
19 75.417435
20 83.77455
21 94.02736
22 94.02997
23 103.75071
24 106.39344
25 108.31859
26 112.75734
27 113.002426
28 116.54206
29 124.52192
30 125.80281
31 127.0251
32 136.35811
33 139.29944
34 141.49802
35 142.41406
36 142.93747
37 143.23853
38 147.61919
39 149.85312
40 152.98512
41 158.6776
42 166.2588
43 167.47302
44 168.47269
45 169.36873
46 171.65129
47 172.2331
48 175.3014
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For Review Only

1	
2	177.39088
3	182.10867
4	186.31653
5	186.81396
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10	201.91025
11	202.76529
12	202.9588
13	202.9588
14	203.4925
15	204.7286
16	204.7286
17	209.87178
18	211.39044
19	211.7252
20	213.88184
21	214.17499
22	215.81322
23	217.67305
24	217.67305
25	219.32573
26	222.31761
27	224.37596
28	232.59555
29	234.4146
30	234.4146
31	240.17686
32	242.47684
33	242.71936
34	244.18542
35	244.18542
36	244.7931
37	247.11661
38	247.49614
39	249.8631
40	249.8631
41	250.66602
42	252.1773
43	255.6293
44	258.95258
45	266.3059
46	269.01913
47	269.01913
48	269.74008
49	276.63492
50	280.38712
51	281.23877
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54	286.58472
55	290.4159
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For Review Only

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2 302.3299
3 303.2233
4 307.74292
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25 338.11765
26 338.93024
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For Review Only

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3	386.04007
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9	400.7253
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11	404.258
12	407.03204
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14	408.72513
15	409.5564
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17	418.4479
18	419.91495
19	419.9687
20	421.51254
21	425.69516
22	428.70026
23	431.65393
24	431.71558
25	433.46893
26	434.47955
27	435.32947
28	438.09555
29	439.92416
30	441.28415
31	443.32953
32	444.2281
33	444.37793
34	446.0623
35	451.50034
36	451.54767
37	453.3818
38	454.6325
39	457.33798
40	458.19244
41	461.158
42	461.62555
43	462.0157
44	463.79324
45	466.17126
46	467.1176
47	468.19165
48	468.2247
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For Review Only

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17 496.7033
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21 503.03995
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34 523.8691
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38 533.3345
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40 536.3649
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42 537.97784
43 538.7643
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45 546.1528
46 548.8445
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For Review Only

Ranked list of genes up-regulated in non-Tg astrocytes com|**AGILENT SurePrint G3 GE 8x60k probe AFFY Mouse430 2 probe**

A_52_P622850	1456010_x_at
A_52_P150950	1452090_a_at
A_55_P2045299	1457536_at
A_51_P274488	1417051_at
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
A_52_P515880	1420955_at
A_66_P108810	1449465_at
A_55_P1972981	1429651_at
A_55_P1997525	1419028_at
A_52_P568235	1439904_at
A_55_P2057132	1423515_at
A_52_P229959	1420877_at
A_51_P394997	1418047_at
A_55_P2027900	1455444_at
A_52_P298394	1423183_at
A_55_P1954486	1424719_a_at
A_55_P1990309	1428741_at
A_55_P2164629	1416211_a_at
A_51_P509643	1436853_a_at
A_52_P38208	1424248_at
A_55_P1977431	1419473_a_at
A_55_P2062737	1416444_at
A_55_P2075298	1433965_at
A_55_P1962303	1428361_x_at
A_51_P396883	1427227_at
A_55_P1984307	1440225_at
A_52_P560006	1455374_at
A_52_P179068	1420872_at
A_55_P1954034	1441317_x_at
A_51_P187352	1455554_at
A_55_P2143688	1458492_x_at
A_52_P124472	1422835_at

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2	A_55_P1954486	1455028_at
3	A_51_P154379	1436656_at
4	A_51_P256384	1433888_at
5	A_51_P359173	1460081_at
6	A_51_P259603	1429022_at
7	A_51_P249193	1436013_at
8	A_55_P1976278	1460419_a_at
9	A_55_P1993777	1436450_at
10	A_55_P2011290	1457273_at
11	A_55_P2143688	1426282_at
12	A_52_P356093	1423084_at
13	A_52_P250400	1424701_at
14	A_55_P2132512	1448978_at
15	A_55_P2037662	1427481_a_at
16	A_55_P1953753	1434172_at
17	A_55_P1969650	1434295_at
18	A_51_P463401	1456480_at
19	A_52_P309166	1440973_at
20	A_51_P270355	1435940_at
21	A_55_P2013601	1456786_at
22	A_52_P655687	1419332_at
23	A_52_P377537	1436889_at
24	A_52_P26357	1424482_at
25	A_51_P268193	1421093_at
26	A_66_P112684	1435895_at
27	A_52_P531731	1436575_at
28	A_66_P112684	1455636_at
29	A_55_P2001793	1421175_at
30	A_55_P2020602	1449380_at
31	A_51_P187352	1424848_at
32	A_52_P883557	1439934_at
33	A_55_P2105472	1418212_at
34	A_55_P1962303	1452757_s_at
35	A_51_P222993	1428525_at
36	A_55_P2027900	1421738_at
37	A_55_P2094831	1423343_at
38	A_52_P282500	1435772_at
39	A_55_P2009752	1434735_at
40	A_51_P189814	1417839_at
41	A_55_P2143688	1426283_at
42	A_52_P72965	1434989_at
43	A_51_P477458	1435487_at
44	A_52_P201558	1437559_at
45	A_55_P1965694	1437147_at
46	A_55_P1956567	1435047_at
47	A_52_P309166	1449468_at
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2	A_55_P1982454	1422823_at
3	A_51_P237255	1436275_at
4	A_52_P40695	1435308_at
5	A_55_P2046744	1450713_at
6	A_66_P118059	1450466_at
7	A_52_P136782	1417466_at
8	A_52_P221756	1435026_at
9	A_51_P233153	1451499_at
10	A_55_P1953391	1418314_a_at
11	A_55_P2143499	1460570_at
12	A_55_P2013888	1438782_at
13	A_55_P2001793	1436483_at
14	A_52_P66226	1417529_at
15	A_55_P2427900	1455304_at
16	A_52_P8324	1429175_at
17	A_52_P622850	1423146_at
18	A_55_P1982454	1422824_s_at
19	A_52_P628915	1415844_at
20	A_55_P2014229	1448110_at
21	A_55_P2108151	1417184_s_at
22	A_51_P509643	1418493_a_at
23	A_55_P2164629	1448254_at
24	A_51_P438657	1439808_at
25	A_51_P337523	1455462_at
26	A_55_P2075298	1454728_s_at
27	A_51_P488180	1434759_at
28	A_55_P2057132	1457412_at
29	A_55_P1954693	1416783_at
30	A_55_P2075298	1423597_at
31	A_52_P494622	1455034_at
32	A_66_P123643	1423471_at
33	A_55_P2086213	1435957_at
34	A_52_P265937	1450683_at
35	A_55_P2332926	1428866_at
36	A_51_P359173	1441927_at
37	A_55_P2148748	1446190_at
38	A_55_P2012572	1456392_at
39	A_52_P201558	1457743_at
40	A_55_P2078040	1460608_at
41	A_52_P298394	1435851_at
42	A_55_P2018176	1455161_at
43	A_55_P2013601	1439557_s_at
44	A_51_P109840	1420484_a_at
45	A_51_P477458	1421436_at
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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

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2	Mapt	Mapt	6.82E-04
3	Tmem150c	Tmem150c	8.70E-04
4	Atp2b2	Atp2b2	0.00106383
5	Syt7	Syt7	0.00106383
6	Adcyap1r1	Adcyap1r1	0.00106383
7	Gsg1l	Gsg1l	0.001133333
8	Prkcb	Prkcb	0.001133333
9	Rbfox3	Rbfox3	0.001133333
10	Tenm2	Tenm2	0.001133333
11	Ntm	Ntm	0.001133333
12	B3galt2	B3galt2	0.001133333
13	Pcdh20	Pcdh20	0.001133333
14	Ngef	Ngef	0.001133333
15	Atp1a3	Atp1a3	0.001133333
16	Cnr1	Cnr1	0.001073446
17	Rasgrp1	Rasgrp1	0.001222222
18	Fry	Fry	0.001256831
19	St6galnac5	LOC552874 St6galnac5	0.001290323
20	Dclk1	Dclk1	0.001290323
21	Ldb2	Ldb2	0.001302083
22	Egfl6	Egfl6	0.001302083
23	Gabra1	Gabra1	0.001302083
24	Arhgef7	Arhgef7	0.001302083
25	Slc7a10	Slc7a10	0.00127451
26	Lsamp	Lsamp	0.00127451
27	Grin3a	Grin3a	0.001476191
28	Lsamp	Lsamp	0.001690141
29	Myt1l	Myt1l	0.001851852
30	Pacsin1	Pacsin1	0.001851852
31	Kcnma1	Kcnma1	0.001936937
32	Slc30a10	Slc30a10	0.001955556
33	Omg	Omg	0.002017544
34	Hba-a1	Hba-a1 Hba-a2	0.002207792
35	Pnmal1	4930488B01Rik Pnmal1	0.002350427
36	Gabra2	Gabra2	0.002489452
37	Slco1c1	Slco1c1	0.002541667
38	Kif21b	Kif21b	0.00255144
39	Hlf	Hlf	0.00255144
40	Cldn5	Cldn5	0.002570281
41	Ntm	Ntm	0.002570281
42	Unc80	Unc80	0.002570281
43	Grid2	Grid2	0.00251938
44	Rgs7bp	Rgs7bp	0.002528736
45	Gabrg2	Gabrg2	0.002528736
46	Rab3c	Rab3c	0.00258427
47	St6galnac5	St6galnac5	0.00258427
48	Syt16	Syt16	0.002564103
49			
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1			
2	Eps8	Eps8	0.002572464
3	Kcnip2	Kcnip2	0.002724014
4	Fut9	Fut9	0.003049645
5	Cspg5	Cspg5	0.003087719
6	Cdk5r2	Cdk5r2	0.003090278
7	Rgs5	Rgs5	0.003090278
8	Spock2	Spock2	0.003061225
9	Cadps2	Cadps2	0.003131313
10	Rbfox1	Rbfox1	0.003166667
11	Pgbd5	Pgbd5	0.003168317
12	Cntn4	Cntn4	0.003168317
13	Myt1l	Myt1l	0.003139159
14	Rab33a	Rab33a	0.003141026
15	Unc13c	Unc13c	0.003141026
16	Tmem178	Tmem178	0.003144654
17	Hes5	Hes5	0.003302181
18	Eps8	Eps8	0.003487654
19	Syt4	Syt4	0.00351682
20	Sema4a	Sema4a	0.00351682
21	Hbb-b1	Hbb-b1 Hbb-b2 Hbb-bs Hbb-bt	0.00351682
22	Snca	Snca	0.003452381
23	Ptn	Ptn	0.00359882
24	Ipcef1	Ipcef1	0.00371345
25	Adcy2	Adcy2	0.00371345
26	Atp8a1	Atp8a1	0.003706896
27	Lrrtm3	Lrrtm3	0.003732194
28	Scn8a	Scn8a	0.0040113
29	Tac1	Tac1	0.0040113
30	Atp8a1	Atp8a1	0.004194445
31	Nr4a2	Nr4a2	0.004269972
32	Ptbp2	Ptbp2	0.004371585
33	Kcnq3	B830032F12 Kcnq3	0.004371585
34	Tagln3	Tagln3	0.004354839
35	2810037O22Rik	2810037O22Rik	0.0044
36	Syt7	Syt7	0.004417989
37	Dclk1	Dclk1	0.004435696
38	Negr1	Negr1	0.004427083
39	Rgs7bp		0
40	Cacna1b	Cacna1b	0.004435897
41	Lgi1	Lgi1	0.004435897
42	A1504432	A1504432	0.004671717
43	Ldb2	Ldb2	0.004786967
44	Vtn	Vtn	0.004900497
45	Grid2	Grid2	0.005
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4	RP-value
5	38.228867
6	40.14826
7	45.530594
8	62.825222
9	63.489967
10	70.426056
11	72.795235
12	75.77436
13	77.42768
14	77.601295
15	78.4775
16	79.4883
17	85.087296
18	85.21892
19	86.613976
20	86.902824
21	94.64061
22	107.83927
23	108.764145
24	110.133865
25	110.722885
26	113.11523
27	113.57372
28	120.68429
29	124.78282
30	124.88154
31	128.00078
32	129.13066
33	129.43092
34	131.86943
35	132.60532
36	135.56566
37	138.43987
38	138.47098
39	139.53728
40	143.77821
41	153.75385
42	156.69489
43	157.85565
44	162.09242
45	163.97165
46	167.04994
47	169.75223
48	176.13744
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For Review Only

1
2 179.00458
3 186.50255
4 189.62704
5 190.53268
6 190.71278
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8 195.93103
9 197.03783
10 197.31279
11 197.84146
12 198.58455
13 201.48653
14 202.16022
15 202.53145
16 203.75371
17 206.5847
18 209.93912
19 211.64128
20 212.32985
21 213.5691
22 213.70602
23 215.07327
24 216.10878
25 217.23347
26 217.45518
27 233.61598
28 243.20815
29 247.11243
30 247.14339
31 249.70981
32 251.43748
33 253.3812
34 257.16528
35 268.65164
36 275.85614
37 277.00516
38 277.91016
39 278.34482
40 281.2168
41 281.3428
42 282.6356
43 284.27158
44 287.12534
45 287.5331
46 289.21994
47 291.4899
48 293.7496
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1
2 295.9357
3 299.10336
4 307.84622
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6 311.68964
7 311.8501
8 311.99994
9 312.87704
10 314.05276
11 315.99564
12 316.35825
13 317.2488
14 319.63144
15 319.81186
16 321.23337
17 324.1635
18 329.6535
19 330.8359
20 330.9058
21 332.35577
22 333.18903
23 336.3066
24 339.2922
25 340.9835
26 341.86188
27 343.79172
28 349.89343
29 349.94983
30 353.92282
31 355.45477
32 356.17947
33 356.44672
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35 358.854
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37 360.94888
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39 363.14523
40 364.91345
41 364.97015
42 370.66614
43 374.21698
44 375.81137
45 382.1414
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Ranked list of genes down-regulated in non-Tg astrocytes c**AGILENT SurePrint G3 GE 8x60k probe AFFY Mouse430 2 probe**

A_55_P2007155	1418979_at
A_55_P2092826	1448213_at
A_51_P295085	1419663_at
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

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2	A_51_P404463	1423261_at
3	A_55_P2087607	1448734_at
4	A_55_P2110713	1419091_a_at
5	A_51_P131408	1418572_x_at
6	A_51_P465281	1455439_a_at
7	A_51_P515605	1427883_a_at
8	A_66_P111562	1448698_at
9	A_55_P2055487	1451969_s_at
10	A_51_P342567	1419706_a_at
11	A_51_P222657	1438948_x_at
12	A_55_P2064043	1423760_at
13	A_66_P104815	1448613_at
14	A_55_P2016647	1448314_at
15	A_55_P2459897	1434719_at
16	A_51_P414889	1445897_s_at
17	A_55_P1952379	1416125_at
18	A_52_P263095	1452217_at
19	A_51_P315682	1439764_s_at
20	A_55_P1980631	1451246_s_at
21	A_52_P304720	1418476_at
22	A_51_P376238	1416625_at
23	A_55_P2033997	1439096_at
24	A_51_P222657	1456251_x_at
25	A_55_P2003033	1446951_at
26	A_51_P405606	1450976_at
27	A_55_P2025033	1452242_at
28	A_55_P1997604	1448558_a_at
29	A_30_P01030135	1424768_at
30	A_51_P131408	1418571_at
31	A_55_P2154709	1417667_a_at
32	A_55_P1995205	1454694_a_at
33	A_55_P2104894	1422437_at
34	A_52_P413646	1450759_at
35	A_52_P602847	1424825_a_at
36	A_52_P372151	1420930_s_at
37	A_51_P157042	1416953_at
38	A_52_P223127	1435399_at
39	A_55_P2086949	1422033_a_at
40	A_51_P222657	1416695_at
41	A_52_P52303	1440142_s_at
42	A_51_P484111	1455978_a_at
43	A_55_P2002577	1422438_at
44	A_51_P464387	1417013_at
45	A_30_P01029470	1460603_at
46	A_55_P2108837	1448232_x_at
47	A_51_P392687	1456292_a_at
48	A_55_P2004781	1416239_at
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2	A_52_P679105	1437671_x_at
3	A_55_P2171116	1426808_at
4	A_52_P35048	1416168_at
5	A_52_P114905	1455239_at
6	A_51_P392687	1450641_at
7	A_51_P411271	1416543_at
8	A_51_P168613	1438684_at
9	A_55_P1978060	1423061_at
10	A_55_P2028015	1426910_at
11	A_66_P111562	1417420_at
12	A_51_P237752	1424130_a_at
13	A_55_P2105025	1455872_at
14	A_51_P321341	1427345_a_at
15	A_52_P426870	1438233_at
16	A_55_P2087607	1417496_at
17	A_55_P2007713	1448276_at
18	A_55_P2013948	1456312_x_at
19	A_51_P255456	1416613_at
20	A_55_P2056241	1422861_s_at
21	A_55_P2213209	1448475_at
22	A_51_P128876	1423754_at
23	A_30_P01017425	1434845_at
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60**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
Ndr1	Ndr1	0
Col8a1	Col8a1	1.19E-04
Tfcp2l1	Tfcp2l1	1.19E-04
Tagln	Tagln	1.19E-04
Thbs1	Pald1 Thbs1	1.19E-04
Ndr1	Ndr1	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
Ndr1	Ndr1	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

1			
2	1500015O10Rik	1500015O10Rik	8.70E-04
3	Cp	Cp	0.001020408
4	Anxa2	Anxa2	0.001020408
5	Tnfrsf12a	Tnfrsf12a	0.001020408
6	Lgals1	Lgals1	0.001069182
7	Col3a1	Col3a1	0.001069182
8	Col3a1	Col3a1	0.001069182
9	Ccnd1	Ccnd1	0.001069182
10	Parp3	Parp3	0.001069182
11	Akap12	Akap12	0.001358025
12	Tspo	Tspo	0.001369048
13	Cd44	Cd44	0.001369048
14	Cd44	Cd44	0.001369048
15	Ecm1	Ecm1	0.001637427
16	Cdk1	Cdk1	0.001724138
17	A2m	A2m	0.001777778
18	Ifi35	Ifi35	0.001777778
19	Ifi35	Ifi35	0.001777778
20	Fkbp5	Fkbp5	0.001912568
21	Ahnak	Ahnak	0.002239583
22	Igf2bp2	Igf2bp2	0.002239583
23	Aurkb	Aurkb	0.002239583
24	Aurkb	Aurkb	0.002239583
25	Crlf1	Crlf1	0.002575758
26	Serping1	Serping1	0.002575758
27	Ddo	Ddo	0.00254902
28	Tspo	Tspo	0.00254902
29	P4ha3	P4ha3	0.002560386
30	P4ha3	P4ha3	0.002560386
31	Ndrgr1	Ndrgr1	0.002571429
32	Cep55	Cep55	0.002676056
33	Pla2g4a	Pla2g4a	0.002685185
34		0 Cald1	0.002844445
35		0 Cald1	0.002844445
36	Tnfrsf12a	Tnfrsf12a	0.002844445
37	Pter	Pter	0.002844445
38	Top2a	Top2a	0.002850877
39	Col5a2	Col5a2	0.00278481
40	Col5a2	Col5a2	0.00278481
41	Bmp6	Bmp6	0.00278481
42	Glycam1	Glycam1	0.00278481
43	Ctnnal1	Ctnnal1	0.002705882
44	Ctgf	Ctgf	0.002705882
45	Synpo2	Synpo2	0.002705882
46	Cntf	Cntf Zfp91 Zfp91Cntf	0.002705882
47	Cntf	Cntf Zfp91 Zfp91Cntf	0.002705882
48	Tspo	Tspo	0.002705882
49	Gfap	Gfap	0.002705882
50	Matn2	Matn2	0.002720307
51	Ephx1	Ephx1	0.002720307
52	Ephx1	Ephx1	0.002720307
53	Hspb8	Hspb8	0.002954545
54		0 Samd9l	0.003183521
55	Tuba1c	Gm6682 Tuba1c	0.003333333
56	Vim	Vim	0.003443223
57	Ass1	Ass1 Gm5424	0.003514493
58	Ass1	Ass1 Gm5424	0.003514493
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1			
2	Prss23	Prss23	0.003942652
3	Lgals3	Lgals3	0.00393617
4	Serpinf1	Serpinf1	0.003964912
5	Ifitm10	Ifitm10	0.00395189
6	Vim	Vim	0.00395189
8	Nfe2l2	Nfe2l2	0.003973064
9	Nuak1	Nuak1	0.003973064
10	Arvcf	Arvcf	0.004125413
11	Pawr	Pawr	0.004125413
12	Ccnd1	Ccnd1	0.004150327
14	Ptrf	Ptrf	0.004174757
15	Fam167a	Fam167a	0.004285714
16	Sult1a1	Sult1a1	0.004285714
17	Fam178a	Fam178a	0.004299066
18	Cp	Cp	0.004299066
20	Tspan4	Tspan4	0.004567901
21	Gsn	Gsn	0.004617737
22	Cyp1b1	Cyp1b1	0.004761905
23	Pdlim5	Pdlim5	0.004761905
24	LOC269472	Olfml3	0.004761905
25	Ifitm3	Ifitm3	0.004778761
26		0 Gm20204 Gm20204	1.1075892
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RP-value

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5 17.760506
6 21.299797
7 44.875797
8 45.48008
9 46.285477
10 46.47518
11 61.248623
12 69.88809
13 71.779144
14 76.01784
15 79.818085
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17 83.2879
18 86.75464
19 98.28696
20 101.41915
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22 104.86032
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26 118.08096
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38 158.77759
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43 164.54904
44 164.72581
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48 184.028
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2	185.64188
3	189.1975
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5	191.00963
6	193.47166
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8	194.40431
9	194.40431
10	201.44685
11	207.14667
12	208.84042
13	208.84042
14	209.04135
15	225.9906
16	230.59737
17	235.13782
18	235.81168
19	235.81168
20	240.1142
21	248.59438
22	248.6939
23	248.80313
24	248.80313
25	258.99164
26	259.13593
27	260.77747
28	263.60544
29	265.3935
30	265.3935
31	267.84378
32	272.88193
33	274.96954
34	280.0921
35	280.35248
36	280.35248
37	280.7766
38	283.7272
39	286.75015
40	287.31424
41	287.31424
42	287.33698
43	289.6153
44	289.66763
45	290.13354
46	292.6118
47	292.6118
48	293.02707
49	293.23822
50	294.50955
51	294.90085
52	294.90085
53	299.7972
54	305.96927
55	312.11148
56	313.82053
57	313.82053
58	317.18402
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2 326.07068
3 327.4596
4 329.2706
5 330.53345
6 332.79706
7 333.51178
8 333.60986
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10 337.49805
11 339.68878
12 343.50995
13 344.82422
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16 347.7488
17 352.6393
18 354.39297
19 356.665
20 357.09262
21 357.35934
22 358.40176
23 8950.983
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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-cc	Mus musculus tripa	1.832444376	8.366008201
A_55_P2085142	Spp1	secreted phospho	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 MAM	1.503395436	9.872073547
A_52_P209484	Tmem88	transmembrane p	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 tumc	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	Adamts4	ADAMTS-like 4	Mus musculus ADAI	0.52369464	11.96438562
A_52_P363216	Gcnt2	glucosaminyl (N-a	Mus musculus glucc	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 adult	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
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3	A_52_P267391	Trim12a	tripartite motif-coi	Mus musculus tripa	5.326621277	7.971349421
4	A_55_P1974432	Gm5067	predicted gene 50i	Mus musculus 13 d	4.706882168	7.941454285
5	A_55_P2070576	Ccl27a	chemokine (C-C m	Mus musculus chen	3.159607921	8.528529626
6	A_55_P2205650	2610507101Rik	RIKEN cDNA 2610	Mus musculus RIKEI	2.76634258	8.199204967
7	A_55_P2064659	Trim12a	tripartite motif-coi	Mus musculus tripa	2.625034338	7.006201591
8	A_55_P2256646	C130078N14	uncharacterized pi	Mus musculus 16 d	2.576144419	6.975926163
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10	A_55_P2068731	Gm20878	predicted gene, 2C	Mus musculus pred	2.535424208	9.5022869
11	A_52_P360330	Map1b	microtubule-assoc	Mus musculus micr	2.528377361	9.568691036
12	A_55_P2068733	Gm20878	predicted gene, 2C	Mus musculus pred	2.4557783	8.486798968
13	A_55_P2092750	Car9	carbonic anhydras	Mus musculus carb	2.227984321	11.43046767
14	A_55_P1981756	Vmn2r123	vomeronasal 2, rei	Mus musculus vome	2.222558264	6.863824084
15	A_51_P349888	Ang2	angiogenin, ribon	Mus musculus angic	2.221223649	7.455657139
16	A_52_P88793	Zfp933	zinc finger protein	Mus musculus zinc f	2.187870963	8.102504202
17	A_52_P238846	Bpnt1	bisphosphate 3'-ni	Mus musculus bispt	2.17951172	8.499105459
18	A_51_P288549	Jmjd7	jumonji domain co	Mus musculus jumc	2.155696224	9.038758021
19	A_66_P130730	Zfp963	zinc finger protein	Mus musculus zinc f	2.142761169	7.714208648
20	A_55_P2112986	Klk1b22	kallikrein 1-relatec	Mus musculus kallik	2.141524133	6.950826515
21	A_55_P2134591	BC049715	cDNA sequence BC	Mus musculus cDN/	2.123548403	7.11520769
22	A_55_P2097151	Ptchd2	patched domain c	Mus musculus patcl	2.000964933	7.331541801
23	A_55_P2073965	BC049715	cDNA sequence BC	Mus musculus cDN/	1.994500273	6.927881761
24	A_51_P217498	Slc2a4	solute carrier fami	Mus musculus solut	1.966656603	8.572006753
25	A_55_P2045886	Stk3	serine/threonine k	Mus musculus serin	1.91680325	9.198570422
26	A_55_P2108773	4930427A07Rik	RIKEN cDNA 4930	Mus musculus RIKEI	1.903303041	6.870745089
27	A_66_P134474	Ang3	angiogenin, ribon	Mus musculus angic	1.797567531	7.969980889
28	A_55_P1964628	LOC102633627	tropomyosin alph	Mus musculus PREDICTED: Mus m	1.763559756	13.64296854
29	A_51_P293069	Mfsd7b	major facilitator s	Mus musculus majo	1.750158707	9.743132096
30	A_55_P2154387	Bmp4	bone morphogene	Mus musculus bone	1.725246422	12.829438
31	A_51_P413147	Klk1b3	kallikrein 1-relatec	Mus musculus kallik	1.701860019	6.732605311
32	A_51_P112627	St6galnac2	ST6 (alpha-N-acety	Mus musculus ST6 (1.692648894	10.18934601
33	A_51_P512820	Dera	2-deoxyribose-5-p	Mus musculus 2-dei	1.680832596	8.494281435
34	A_55_P2095603	Ccdc65	coiled-coil domain	Mus musculus coile	1.680817626	10.32761111
35	A_51_P477121	Pmaip1	phorbol-12-myrist:	Mus musculus phor	1.661805686	9.694988353
36	A_55_P2373852	2310058N22Rik	RIKEN cDNA 2310	Mus musculus adult	1.602415256	8.177045633
37	A_55_P2144597	9030025P20Rik	RIKEN cDNA 9030	Mus musculus RIKEI	1.574018429	10.33013058
38	A_51_P180724	Mlh1	mutL homolog 1 (E	Mus musculus mutL	1.554543727	10.33206306
39	A_51_P142896	Cd59a	CD59a antigen	Mus musculus CD5	1.5382424	11.07205551
40	A_55_P2003561	Luzp2	leucine zipper prot	Mus musculus leuci	1.53117695	10.52421298
41	A_51_P417321	Zfp236	zinc finger protein	Mus musculus zinc f	1.517239691	7.995104458
42	A_51_P115953	Ctxn3	cortexin 3	Mus musculus corte	1.515844412	7.480665769
43	A_55_P2068723	Ccl27a	chemokine (C-C m	Mus musculus chen	1.506485285	9.878089363
44	A_55_P2068734	Ccl27a	chemokine (C-C m	Mus musculus chen	1.501278472	10.14705428
45	A_55_P2015912	Zfp961	zinc finger protein	Mus musculus zinc f	1.460709523	7.978713091
46	A_55_P1961395	Pdpn	podoplanin	Mus musculus podc	1.408511896	15.4731878
47	A_51_P358722	Lancl3	LanC lantibiotic sy	Mus musculus LanC	1.403818102	7.624333535
48	A_55_P2053551	Mast4	microtubule assoc	Mus musculus micr	1.383573947	9.459809864
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2	A_55_P2019577	1500011B03Rik	RIKEN cDNA 1500C	Mus musculus RIKEI	1.382367568	11.13618528
3	A_52_P532687	Ermard	ER membrane assc	Mus musculus ER m	1.374998141	9.208882095
4	A_52_P490207	Ermard	ER membrane assc	Mus musculus ER m	1.288727894	8.746606738
5	A_55_P2059357	Myo7a	myosin VIIA	Mus musculus myo:	1.280346209	7.864933543
6	A_51_P507899	Ttc8	tetratricopeptide r	Mus musculus tetra	1.276939334	10.06822585
8	A_55_P2194064	BC023969	cDNA sequence BC	Mus musculus lung	1.267825845	7.04159718
9	A_55_P2067727	Mxra7	matrix-remodellin	Mus musculus matr	1.262225358	11.32684755
10	A_55_P2197338	Tnfsf13os	tumor necrosis fac	PREDICTED: Mus mi	1.258335257	7.508009275
11	A_51_P345316	Cep76	centrosomal prote	Mus musculus centi	1.257149573	7.422795425
12	A_55_P2065726	Snx29	sorting nexin 29	sorting nexin 29 [So	1.257094651	7.59703769
14	A_55_P2179793		0	0 GAG_IPMAE (P3179	1.25413714	11.05468172
15	A_52_P642012	BC006965	cDNA sequence BC	Mus musculus cDN/	1.25400917	7.4799979
16	A_52_P616332	Atp10d	ATPase, class V, ty	Mus musculus ATPa	1.247972291	7.18748402
17	A_51_P179504	Ang3	angiogenin, ribon	Mus musculus angic	1.243578938	7.705143143
18	A_55_P2169963	Gm13152	predicted gene 13	Mus musculus pred	1.236720209	6.482225328
19	A_52_P559545	Cercam	cerebral endotheli	Mus musculus cerel	1.218979981	8.680124663
20	A_55_P2180196	Ccdc32	coiled-coil domain	coiled-coil domain c	1.210677001	6.693191129
21	A_52_P135707	Creb3	cAMP responsive ϵ	Mus musculus cAMI	1.208699556	11.79138848
22	A_52_P598634	1190007I07Rik	RIKEN cDNA 1190C	Mus musculus RIKEI	1.196215216	10.74842945
23	A_52_P587738	P2ry2	purinergic recepto	Mus musculus purir	1.195637072	10.79148861
24	A_55_P2380428	5430416G10Rik	RIKEN cDNA 5430C	Mus musculus 6 day	1.190354222	6.615967993
25	A_66_P122158	Pisd-ps3	phosphatidylserine	Mus musculus phos	1.175927068	9.074216706
26	A_52_P592909	Dgat2	diacylglycerol O-ac	Mus musculus diacy	1.173956077	10.39327982
27	A_52_P549977	Fam32a	family with sequer	Mus musculus famil	1.173692938	11.4060602
28	A_51_P125368	Hars	histidyl-tRNA synt	Mus musculus histic	1.172348692	11.44773653
29	A_55_P2019054	Acacb	acetyl-Coenzyme β	Mus musculus acety	1.168117595	8.899943125
30	A_55_P1987196	Gm3448	predicted gene 34	Mus musculus pred	1.167901495	9.058289041
31	A_55_P1960167	Bcat2	branched chain an	Mus musculus bran	1.149749383	9.932383882
32	A_51_P480013	Car11	carbonic anhydras	Mus musculus carb	1.147119938	10.42364956
33	A_55_P2120866	Gm7120	predicted gene 71	Mus musculus pred	1.137640533	9.945520617
34	A_51_P418908	Larp1	La ribonucleoprote	Mus musculus La rik	1.137191779	9.48531631
35	A_55_P1975874	Bcl2l15	BCL2-like 15	Mus musculus BCL2	1.121558908	6.994147168
36	A_51_P286814	Ncor2	nuclear receptor c	Mus musculus nucle	1.109882524	14.09285663
37	A_55_P2108883	AV356131	expressed sequen	Mus musculus adult	1.104483644	10.05893668
38	A_55_P2083213	Purb	purine rich elemer	Mus musculus purir	1.07740577	10.71629864
39	A_51_P490747	AI593442	expressed sequen	Mus musculus expri	1.075390771	7.060184729
40	A_52_P311853	Ddit4l	DNA-damage-indu	Mus musculus DNA-	1.07360728	11.17332195
41	A_55_P2065059	Wnt2	wingless-related β	Mus musculus wing	1.071997776	6.654513312
42	A_55_P1998401	Eif2ak4	eukaryotic translat	eukaryotic translati	1.065720732	7.579710465
43	A_55_P2079158	Fam154b	family with sequer	Mus musculus famil	1.060527374	7.097166998
44	A_55_P2153941	Zfp386	zinc finger protein	Mus musculus zinc f	1.059050992	10.08765784
45	A_55_P1974602	Map2k7	mitogen-activated	Mus musculus mito;	1.042915394	7.206717795
46	A_51_P155174	Zfp672	zinc finger protein	Mus musculus zinc f	1.034852851	9.47375292
47	A_55_P2097156	Ptchd2	patched domain c	Mus musculus patcl	1.034050443	6.365934281
48	A_52_P295104	Smim5	small integral men	Mus musculus smal	1.026324687	7.028001519
49	A_55_P2151138	Dynlt1f	dynein light chain	Mus musculus dyne	1.011748282	15.31604468
50	A_55_P2201612	Slc30a7	solute carrier fami	Mus musculus solut	1.003319035	6.695524338

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2	A_55_P2109544	Trnt1	tRNA nucleotidyl t	Mus musculus tRNA	1.001272322	8.431184682
3	A_66_P120770	Ywhaz	tyrosine 3-monoox	Mus musculus tyros	0.997607559	9.774694003
4	A_55_P1983268	4930444P10Rik	RIKEN cDNA 49304	Mus musculus RIKEI	0.994940226	9.194778744
5	A_51_P191520	Stard10	START domain con	Mus musculus STAR	0.994448253	10.48259345
6	A_66_P130366	Stk38l	serine/threonine k	Mus musculus serin	0.993625574	7.328617183
7	A_55_P2293414	1700001C19Rik	RIKEN cDNA 17000	Mus musculus RIKEI	0.990165687	7.960315863
8	A_55_P2018330	Gm13298	predicted gene 13	Mus musculus pred	0.986638051	6.426310477
9	A_51_P470989	Paip1	polyadenylate bin	Mus musculus poly	0.972419001	10.13248007
10	A_55_P2127587	Smcr8	Smith-Magenis syr	Mus musculus Smitl	0.96794916	6.547066031
11	A_55_P1972490	Psg16	pregnancy specific	PREDICTED: Mus mi	0.96746518	12.66758381
12	A_55_P1955483	Grb14	growth factor rece	Mus musculus grow	0.961537973	10.67699007
13	A_66_P123055	Gm10845	predicted gene 10	Mus musculus pred	0.961441464	12.63602144
14	A_51_P275496	BC026762	cDNA sequence BC	Mus musculus cDN/	0.956225426	10.39653181
15	A_52_P682745	Dock4	dedicator of cytoki	Mus musculus dedic	0.953245847	10.42480206
16	A_52_P20639	Rd3	retinal degenerati	Mus musculus retin	0.952385121	6.56148348
17	A_51_P494863	Vmac	vimentin-type inte	Mus musculus vime	0.951203788	9.571912151
18	A_55_P2021094	Tmem181b-ps	transmembrane pi	Mus musculus pred	0.950888888	7.161708914
19	A_55_P2149382	Gm3448	predicted gene 34	Mus musculus pred	0.949503743	8.596002824
20	A_55_P2221647	AI605517	expressed sequenc	Mus musculus adult	0.946454699	7.987944032
21	A_55_P1989524	Fndc1	fibronectin type III	Mus musculus fibro	0.939270273	9.499426291
22	A_51_P159293	Zbbx	zinc finger, B-box c	Mus musculus zinc f	0.938960672	7.015945354
23	A_55_P1995924	Gm13157	predicted gene 13	Mus musculus pred	0.936224377	8.820762873
24	A_51_P452820	Rpl31	ribosomal protein	Mus musculus ribos	0.935299927	9.628451691
25	A_52_P123738	Rnf41	ring finger protein	Mus musculus ring f	0.934464172	9.579431688
26	A_52_P222230		0	Mus musculus adult	0.932941732	10.09808608
27	A_51_P327564	Glb1	galactosidase, bet	Mus musculus galac	0.930537406	12.02546985
28	A_51_P422335	Zfp420	zinc finger protein	Mus musculus zinc f	0.926862021	7.796718242
29	A_55_P2146749	Rps13	ribosomal protein	Mus musculus ribos	0.926468304	15.57163982
30	A_51_P375558	Myoc	myocilin	Mus musculus myoc	0.91987638	7.037334081
31	A_51_P123604	Ppwd1	peptidylprolyl ison	Mus musculus pepti	0.918453225	7.857252107
32	A_55_P1962756	Ttll2	tubulin tyrosine lig	Mus musculus tubu	0.915979939	6.474892893
33	A_51_P316801	Wdr60	WD repeat domain	Mus musculus WD r	0.91300515	9.671748455
34	A_51_P228193	Ociad1	OCIA domain cont	Mus musculus OCIA	0.902626422	12.05023919
35	A_55_P1998995	Speg	SPEG complex loc	Mus musculus SPEG	0.890537687	9.842623979
36	A_52_P489778	Ablim1	actin-binding LIM j	Mus musculus actin	0.888374228	10.72166376
37	A_52_P512553	Atg16l2	autophagy related	Mus musculus autoj	0.884566919	10.25934981
38	A_65_P08864	Dph5	DPH5 homolog (S.	Mus musculus 4 da	0.882305084	6.622110984
39	A_55_P1985428	Atg16l2	autophagy related	Mus musculus autoj	0.878149304	11.34750968
40	A_52_P325477	Trim16	tripartite motif-co	Mus musculus tripa	0.875770007	7.500056636
41	A_66_P108434	Ccdc65	coiled-coil domain	Mus musculus coile	0.8752307	6.761612792
42	A_55_P1970033	Per1	period circadian cl	Mus musculus peric	0.87102614	11.30179325
43	A_51_P409893	Prkar2a	protein kinase, cA	Mus musculus prote	0.870456096	8.073370053
44	A_55_P2161465	Gm10516	predicted gene 10	Mus musculus pred	0.869660084	8.602021347
45	A_55_P2031547	Vmn2r121	vomer nasal 2, rei	Mus musculus vom	0.868193142	6.340248683
46	A_55_P2062133	Etv3	ets variant gene 3	Mus musculus ets v	0.865016273	8.229462351
47	A_51_P314153	Nr2c2ap	nuclear receptor 2	Mus musculus nucl	0.857212287	10.25241127
48	A_51_P140607	Asun	asunder, spermatc	Mus musculus asun	0.854600958	11.24260127
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2	A_55_P2012694	Kcnh5	potassium voltage Mus musculus pota:	0.853264496	8.804906186
3	A_52_P253179	Igfbp3	insulin-like growth Mus musculus insul	0.843238604	11.69049314
4	A_55_P1968977	Stk38l	serine/threonine k Mus musculus serin	0.839143396	9.521077412
5	A_55_P1982454	Eps8	epidermal growth Mus musculus epide	0.83854701	8.848665964
6	A_55_P2000007	LOC102639358	uncharacterized LC PREDICTED: Mus mi	0.837915964	8.84202077
7	A_51_P481821	Spcs3	signal peptidase cc Mus musculus signa	0.834205312	11.87147738
8	A_51_P480202	Dlx2	distal-less homeot Mus musculus dista	0.831967305	8.505777767
9	A_55_P2062688	Msi1	musashi RNA-bind Mus musculus musa	0.824555268	7.664091488
10	A_55_P2023697	Zfp386	zinc finger protein Mus musculus zinc f	0.824299376	11.04881999
11	A_51_P320022	Atp10a	ATPase, class V, ty Mus musculus ATPa	0.823382272	9.570566289
12	A_51_P356579	Mxra7	matrix-remodellin Mus musculus matr	0.821065949	7.115904662
13	A_55_P1967514	Dnah7a	dynein, axonemal, Mus musculus dyne	0.816310076	7.747422009
14	A_52_P217710	Fzd6	frizzled homolog 6 Mus musculus frizzl	0.813851943	8.487905687
15	A_55_P2036723	Stk36	serine/threonine k Mus musculus serin	0.812564111	6.839913205
16	A_55_P1978226	Park2	Parkinson disease Mus musculus Parki	0.809691701	9.930960787
17	A_55_P1999958		0 0 Mus musculus 2 cell	0.805965228	9.252652714
18	A_66_P112301	C230072F16Rik	RIKEN cDNA C230(PREDICTED: Mus mi	0.80311273	7.553472865
19	A_51_P244824	Dapp1	dual adaptor for pl Mus musculus dual	0.802564631	8.572185508
20	A_55_P1969431	Lym5	LYR motif containi Mus musculus LYR r	0.79913581	11.07024261
21	A_55_P2145521	Stk38l	serine/threonine k Mus musculus serin	0.798266378	10.21390203
22	A_55_P2259125	D7Erted143e	DNA segment, Chr Mus musculus DNA	0.796972973	7.136638653
23	A_55_P2206605	5830444B04Rik	RIKEN cDNA 5830(Mus musculus RIKEI	0.79643716	6.400644648
24	A_55_P2151143	Dynlt1c	dynein light chain Mus musculus dyne	0.795550998	14.87675664
25	A_51_P333965	Cisd2	CDGSH iron sulfur Mus musculus CDG	0.792549929	8.447908953
26	A_52_P456561	Abcd1	ATP-binding casset Mus musculus ATP-	0.789316322	8.448857429
27	A_55_P2183735	Pisd	phosphatidylserine Mus musculus phos	0.785035418	11.98425589
28	A_52_P565279	Cecr5	cat eye syndrome Mus musculus cat e	0.784649746	7.912325413
29	A_51_P448391	Nkiras1	NFKB inhibitor inte Mus musculus NFKE	0.783418591	9.121554978
30	A_55_P1985693	Fhdc1	FH2 domain conta Mus musculus FH2	0.782106906	11.3884465
31	A_51_P269634	Zfp14	zinc finger protein Mus musculus zinc f	0.776997444	8.491684404
32	A_55_P2033480	Gm13298	predicted gene 13: Mus musculus pred	0.774332816	6.342741632
33	A_55_P2170509	Yipf4	Yip1 domain famil Mus musculus Yip1	0.772816822	11.90136956
34	A_51_P143468	Klhl26	kelch-like 26 Mus musculus kelch	0.77198704	10.29776949
35	A_52_P436590	Wbscr17	Williams-Beuren s Mus musculus Willi	0.769558866	12.28938237
36	A_52_P547589	Spag1	sperm associated Mus musculus sperr	0.769269498	8.242367136
37	A_55_P1990134	Cox18	cytochrome c oxid Mus musculus cytoc	0.76750367	10.11076173
38	A_55_P2002226	Dzip1	DAZ interacting pr Mus musculus DAZ	0.767356331	6.538813239
39	A_66_P101108	Tnrc18	trinucleotide repe: Mus musculus trinu	0.76600373	11.76838989
40	A_55_P1987151	Nlrp5	NLR family, pyrin c Mus musculus NLR	0.762876701	7.174930312
41	A_55_P1988882	Sept9	septin 9 Mus musculus septi	0.760689134	13.17396197
42	A_55_P2144280	Nnt	nicotinamide nucl Mus musculus nicot	0.755399056	6.408132733
43	A_55_P2255737		0 0 Mus musculus 16 d	0.751739655	7.646039652
44	A_55_P2045114	Tmem242	transmembrane pi Mus musculus trans	0.746315876	12.40287643
45	A_55_P2186558	Tmem242	transmembrane pi Mus musculus trans	0.745602274	11.74115813
46	A_55_P2212498	C030005K06Rik	RIKEN cDNA C030(Mus musculus 16 d	0.744696963	7.496432326
47	A_55_P2067652	Boc	biregional cell adh Mus musculus bireg	0.744606754	10.68001093
48	A_55_P1995992	Gm14432	predicted gene 14: Mus musculus pred	0.734175842	10.19189597
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2	A_51_P263246	Dusp8	dual specificity phosphatase 8	Mus musculus dual	0.729339237 8.550859775
3	A_51_P433091	Purb	purine rich element	Mus musculus purin	0.729313164 14.36585406
4	A_52_P106620	Tnfrsf11b	tumor necrosis factor receptor superfamily class 1 member 11b	Mus musculus tumc	0.724063196 9.178956716
5	A_51_P324934	Mcm3	minichromosome maintenance complex component 3	Mus musculus 2 day	0.723982874 11.08620242
6	A_51_P193302	Mrps7	mitochondrial ribosomal protein S7	Mus musculus mitcl	0.719882585 10.07382699
7	A_51_P342707	Pold2	polymerase (DNA directed) delta	Mus musculus polyr	0.718347678 10.00505646
9	A_55_P2163729	Tvp23a	trans-golgi network protein 23A	Mus musculus trans	0.714329056 10.78639596
10	A_55_P2085333	Fbxo44	F-box protein 44	Mus musculus F-bo	0.711686096 8.802084472
11	A_55_P1967820	Al661453	expressed sequence tag	Mus musculus expri	0.707301965 7.567482964
12	A_55_P1980292	Purb	purine rich element	Mus musculus purir	0.70306024 12.08650609
13	A_55_P1964638	Cxadr	coxsackievirus and adenovirus receptor	Mus musculus coxsa	0.702794142 10.81708985
14	A_55_P1956918	Adamts5	a disintegrin-like and metalloprotease with thrombospondin type 1 motifs 5	Mus musculus a disi	0.701754973 8.144140925
15	A_55_P2037883	Ino80	INO80 homolog (S. pombe)	Mus musculus INO8	0.693705043 7.913768321
16	A_55_P2173927	Insr	insulin receptor	Mus musculus insul	0.691688622 7.865164283
17	A_51_P487913	2600006K01Rik	RIKEN cDNA 2600006K01	Mus musculus 10 d	0.69118068 7.997964919
18	A_55_P2028370				
19	A_55_P2028370				
20	A_55_P2028370				
21	A_55_P1991851	Speg	SPEG complex locus	Mus musculus SPEG	0.687259254 9.934616638
22	A_55_P2144285	Nnt	nicotinamide nucleotide transhydrogenase	Mus musculus nicot	0.68724313 12.56592392
23	A_55_P1955568	Extl2	exostosin 2	Mus musculus exosi	0.685268426 11.19675553
24	A_55_P1976993	Strn	striatin, calmodulin-binding domain protein	Mus musculus striat	0.680102547 7.201136783
25	A_55_P2140118	Qpct	glutaminyl-peptidyl transferase	Mus musculus gluta	0.678864447 8.702572561
26	A_52_P260696	Arnt2	aryl hydrocarbon receptor nuclear translocator 2	Mus musculus aryl t	0.677915652 11.15522419
27	A_55_P2154943	LOC102633020	uncharacterized LOC102633020	PREDICTED: Mus mi	0.676814658 6.813185302
28	A_52_P627068	Disp2	dispatched homolog	Mus musculus disp	0.674397108 7.74997714
29	A_55_P2211937	E130101M22	uncharacterized protein	Mus musculus 0 day	0.671839525 7.244348901
30	A_55_P2045658	Nme6	NME/NM23 nucleoside diphosphate kinase 6	Mus musculus NME	0.671023993 9.369172174
31	A_55_P2322029	3830406C13Rik	RIKEN cDNA 3830406C13	PREDICTED: Mus mi	0.66786877 6.852701833
32	A_55_P1979929	Prcp	prolylcarboxypeptidase	Mus musculus proly	0.66627182 7.089942414
33	A_52_P646979	D16Erd472e	DNA segment, Chromosome 16	Mus musculus DNA	0.664518727 8.526185962
34	A_55_P2146500	Ccdc107	coiled-coil domain containing 107	coiled-coil domain c	0.664242439 9.312354149
35	A_51_P127915	Rnasek	ribonuclease K	Mus musculus ribor	0.660400658 11.60556053
36	A_51_P383629	Vps4a	vacuolar protein sorting 4A	Mus musculus vacu	0.659040627 8.892115274
37	A_52_P67200	Stt3b	STT3, subunit of the vacuolar protein sorting 3 complex	Mus musculus STT3	0.65786142 12.59516264
38	A_55_P2026818	Slc4a7	solute carrier family 4 member 7	Mus musculus solut	0.65742112 11.80618119
39	A_55_P1995874	Gm14326	predicted gene 14	Mus musculus pred	0.655155313 9.473693824
40	A_55_P2122633	Airn	antisense Igf2r RNA	Mus musculus 12 d	0.655073738 9.447841546
41	A_66_P110742				
42	A_66_P110742				
43	A_66_P110742				
44	A_51_P414548	Casp7	caspase 7	Mus musculus casp	0.652297056 9.262799375
45	A_55_P2035717	Pgap2	post-GPI attachment protein 2	Mus musculus post-	0.649830054 11.01902213
46	A_55_P1974088	Stard6	StAR-related lipid transfer domain containing 6	Mus musculus StAR	0.644654813 7.252685872
47	A_55_P2044982	Zfp74	zinc finger protein 74	Mus musculus zinc f	0.643862306 8.623261586
48	A_55_P1974855	Zfp868	zinc finger protein 868	Mus musculus zinc f	0.642298042 9.44786431
49	A_52_P14526	Zyg11b	zyg-11 family member 11b	Mus musculus zyg-ll	0.6399025 8.984744753
50	A_52_P484838	Rfxank	regulatory factor X	Mus musculus regul	0.638156992 10.24113363
51	A_55_P2161695	Kdelc1	KDEL (Lys-Asp-Glu) receptor 1	Mus musculus KDEL	0.633604449 8.732323513
52	A_51_P102507	Vps33a	vacuolar protein sorting 33A	Mus musculus vacu	0.632936888 10.47605776
53	A_55_P2000798	Ccdc144b	coiled-coil domain containing 144b	Mus musculus coile	0.630687382 8.797090317
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2	A_55_P2049095	Atat1	alpha tubulin acet	Mus musculus alph	0.630435448	9.141766982
3	A_51_P312748	Oxsm	3-oxoacyl-ACP syn	Mus musculus 3-ox	0.629777447	9.01476485
4	A_55_P2035667	Gyk	glycerol kinase	Mus musculus glyce	0.628787466	8.648364662
5	A_55_P2048483	D17Zt10e	DNA segment, Chr	Mus musculus D17	0.628777962	6.992196756
6	A_66_P105736	Net1	neuroepithelial cel	Mus musculus neur	0.6286504	8.454326837
7	A_52_P244463	D16Ertd472e	DNA segment, Chr	Mus musculus DNA	0.628406852	9.597217161
8	A_51_P487027	Kcnk2	potassium channe	Mus musculus pota	0.626168174	9.661418919
9	A_51_P233027	Rmdn3	regulator of micro	Mus musculus regul	0.625932519	8.988246549
10	A_51_P310676	Galr2	galanin receptor 2	Mus musculus galar	0.622724432	7.162505651
11	A_51_P119031	Naa30	N(alpha)-acetyltra	Mus musculus N(al	0.621554593	9.624039204
12	A_55_P2133220	Arhgef39	Rho guanine nucle	Mus musculus Rho	0.616734048	8.642150922
13	A_55_P2028522	Stac	src homology thre	Mus musculus src h	0.616010766	7.041364257
14	A_51_P253897	Psca	prostate stem cell	Mus musculus prost	0.615881617	6.42562448
15	A_51_P261560	Tex33	testis expressed 3	Mus musculus testi	0.615386339	7.329209425
16	A_51_P186798		0	0 Mus musculus adult	0.61322874	9.016423032
17	A_55_P2030383	Frmd4a	FERM domain con	Mus musculus FERN	0.612959998	10.90964601
18	A_55_P2098578	Tubd1	tubulin, delta 1	Mus musculus tubu	0.612758828	8.954822571
19	A_51_P181722	Rbks	ribokinase	Mus musculus ribok	0.61159276	9.245800439
20	A_51_P280532	Supt16	suppressor of Ty 1	Mus musculus supp	0.61157395	8.530965999
21	A_55_P2118891	Zfp882	zinc finger protein	Mus musculus zinc f	0.610913984	8.294079552
22	A_55_P1989341	Ntng1	netrin G1	Mus musculus netri	0.60958472	8.476360633
23	A_52_P644534	Dhrsx	dehydrogenase/re	Mus musculus dehy	0.609560651	9.25671223
24	A_66_P138585	4833419G08Rik	RIKEN cDNA 48334	Mus musculus 0 day	0.607587363	6.595782617
25	A_55_P1998947	Trim16	tripartite motif-co	Mus musculus tripa	0.604488449	7.155449916
26	A_51_P234544	Azin1	antizyme inhibitor	Mus musculus antiz	0.602800226	11.96811488
27	A_52_P1187949	Trim5	tripartite motif-co	tripartite motif-con	0.599764892	6.187168827
28	A_51_P367780	Adamts2	ADAMTS-like 2	Mus musculus ADAI	0.599729357	7.341050691
29	A_55_P2146996	Wdr52	WD repeat domair	Mus musculus WD r	0.597251838	7.020264708
30	A_55_P2173073	Zfp931	zinc finger protein	Mus musculus zinc f	0.595265308	8.866986993
31	A_51_P283292	Gm14326	predicted gene 14	Mus musculus pred	0.595082261	9.015347234
32	A_52_P376360	Pdgfc	platelet-derived gr	Mus musculus plate	0.594601426	10.96578443
33	A_55_P1954436	Gm7967	predicted gene 79	PREDICTED: Mus m	0.594041539	9.155739992
34	A_55_P1988424	Tpi1	triosephosphate is	Mus musculus triosi	0.593343466	12.72558299
35	A_65_P02321	Usp36	ubiquitin specific	Mus musculus ubiq	0.591697254	7.853283573
36	A_51_P343851	Tgfbra1	transforming grow	Mus musculus trans	0.589821522	7.554407441
37	A_55_P1967538	Hunk	hormonally upregu	Mus musculus horr	0.588246584	11.69706941
38	A_51_P246727	Mlxip	MLX interacting pr	Mus musculus MLX	0.588227683	8.368515877
39	A_55_P2187043	Tpm1	tropomyosin 1, al	Mus musculus trop	0.585164286	15.06169489
40	A_51_P454103	Manba	mannosidase, bet	Mus musculus mani	0.584351312	9.614489926
41	A_52_P494514	Insr	insulin receptor	Mus musculus insul	0.583352015	8.423305987
42	A_55_P2057994	Mif4gd	MIF4G domain cor	Mus musculus MIF4	0.5807349	11.5472407
43	A_55_P2007243	Kcnc1	potassium voltage	Mus musculus pota	0.578759804	9.232521563
44	A_51_P441494	BC100451	cDNA sequence BC	Mus musculus cDN	0.576549426	7.490033464
45	A_52_P74576	Ccdc65	coiled-coil domain	Mus musculus coile	0.575074749	7.18473457
46	A_55_P1993876	Otud7a	OTU domain conta	Mus musculus OTU	0.56755514	6.807269488
47	A_51_P382928	Cstf3	cleavage stimulat	Mus musculus cleav	0.567207944	11.55214483
48	A_52_P259558	Ogfod1	2-oxoglutarate anc	Mus musculus 2-ox	0.564501633	8.350975048
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2	A_55_P2037081	2610305D13Rik	RIKEN cDNA 2610305D13Rik	Mus musculus RIKEI	0.564272206 6.91795213
3	A_52_P412529	Fbxo3	F-box protein 3	Mus musculus F-box protein 3	0.56094732 9.33493547
4	A_51_P403636	Smad7	SMAD family member 7	Mus musculus SMAD7	0.558336877 8.78753881
5	A_55_P2062469	Col12a1	collagen, type XII, alpha 1	Mus musculus collagen, type XII, alpha 1	0.555681636 11.31206825
6	A_55_P1992715	Igfbp3	insulin-like growth factor binding protein 3	insulin-like growth factor binding protein 3	0.554260468 7.33220213
7	A_55_P2113356	Miip	migration and invasion protein 1	Mus musculus migration and invasion protein 1	0.552280288 8.129275828
8	A_55_P2060278	Fam45a	family with sequence similarity 45A	Mus musculus family with sequence similarity 45A	0.549155306 10.93484853
9	A_55_P2039556	Pak6	p21 protein (Cdc42 binding protein kinase 6)	Mus musculus p21 protein (Cdc42 binding protein kinase 6)	0.547684608 6.8612788
10	A_51_P308029	2010107G23Rik	RIKEN cDNA 2010107G23Rik	Mus musculus RIKEI	0.54748727 9.996108859
11	A_55_P2034600	Gm5523	glyceraldehyde-3-phosphate dehydrogenase	Mus musculus glyceraldehyde-3-phosphate dehydrogenase	0.546447402 9.212421977
12	A_55_P2241204	1500015A07Rik	RIKEN cDNA 1500015A07Rik	Mus musculus RIKEI	0.54219336 8.26476772
13	A_66_P113662	Tmem62	transmembrane protein 62	Mus musculus transmembrane protein 62	0.538267077 9.893821557
14	A_55_P1985554	B4galt4	UDP-Gal:beta-GlcNAc 4-epimerase	Mus musculus UDP-Gal:beta-GlcNAc 4-epimerase	0.537628446 10.83785546
15	A_55_P2148641	Rab4a	RAB4A, member RAB4 subfamily	Mus musculus RAB4A, member RAB4 subfamily	0.537243189 9.172580706
16	A_55_P1996086	Gm14325	predicted gene 14325	Mus musculus predicted gene 14325	0.537186059 9.111250799
17	A_55_P1966958	Mef2d	myocyte enhancer factor 2D	Mus musculus myocyte enhancer factor 2D	0.536620471 7.75838435
18	A_52_P144794	Tceanc2	transcription elongation factor A class 2	Mus musculus transcription elongation factor A class 2	0.53455295 7.249346109
19	A_55_P1969166	Fxr2	fragile X mental retardation protein 2	Mus musculus fragile X mental retardation protein 2	0.531489988 12.34194972
20	A_55_P1973447	Ybx2	Y box protein 2	Y box protein 2 [Somatomedin B]	0.531057305 7.109701064
21	A_55_P2052563	Id1	inhibitor of DNA binding 1	Mus musculus inhibitor of DNA binding 1	0.53033599 13.47147372
22	A_55_P2078213	1700020I14Rik	RIKEN cDNA 1700020I14Rik	Mus musculus 11 days embryonic	0.530002687 6.877639522
23	A_52_P110068	Rqcd1	rcd1 (required for cell division)	Mus musculus rcd1	0.529942113 8.065464761
24	A_55_P2147791	Fam129c	family with sequence similarity 129C	Mus musculus family with sequence similarity 129C	0.529236236 7.217970946
25	A_55_P2026109	Rpap1	RNA polymerase II	Mus musculus RNA polymerase II	0.527509786 11.77046652
26	A_55_P2354336		0	Mus musculus activator protein 1	0.526987573 8.20102921
27	A_66_P125212	Mapk1ip1	mitogen-activated protein kinase 1 interacting protein 1	Mus musculus mitogen-activated protein kinase 1 interacting protein 1	0.526302456 11.42316344
28	A_55_P2076927	Ints10	integrator complex subunit 10	Mus musculus integrator complex subunit 10	0.525810261 10.3795043
29	A_52_P558382	Mapk8	mitogen-activated protein kinase 8	Mus musculus mitogen-activated protein kinase 8	0.525327826 6.850921359
30	A_55_P2030721	Ankle1	ankyrin repeat domain containing 1	Mus musculus ankyrin repeat domain containing 1	0.525007257 7.995435084
31	A_52_P505143	Jrk	jerky	Mus musculus jerky	0.522539156 8.542489357
32	A_51_P144648	Vps13b	vacuolar protein sorting 13B	Mus musculus vacuolar protein sorting 13B	0.519678366 6.7346537
33	A_55_P2147457	Gm6410	predicted gene 6410	PREDICTED: Mus musculus predicted gene 6410	0.519481968 6.166119882
34	A_55_P2013396	Gm14305	predicted gene 14305	Mus musculus predicted gene 14305	0.517683154 7.864612391
35	A_55_P2172566	Insr	insulin receptor	Mus musculus insulin receptor	0.515697068 7.323745759
36	A_52_P137691	Trappc5	trafficking protein associated with cilia 5	Mus musculus trafficking protein associated with cilia 5	0.513420389 9.062810254
37	A_55_P2187038	Tpm1	tropomyosin 1, alpha	Mus musculus tropomyosin 1, alpha	0.51307192 15.71376893
38	A_52_P662098	Net1	neuroepithelial cell adhesion molecule 1	Mus musculus neuroepithelial cell adhesion molecule 1	0.512228233 6.892396013
39	A_51_P315555	Nars	asparaginyl-tRNA synthetase	Mus musculus asparaginyl-tRNA synthetase	0.509016823 10.21166179
40	A_55_P2144075	Pofut2	protein O-fucosyltransferase 2	Mus musculus protein O-fucosyltransferase 2	0.506738417 9.580876216
41	A_65_P17492	Med29	mediator complex subunit 29	Mus musculus mediator complex subunit 29	0.506204122 11.08044267
42	A_51_P213099	Ntng1	netrin G1	Mus musculus 0 days embryonic	0.504996564 9.917510525
43	A_55_P2212259	4930539J05Rik	RIKEN cDNA 4930539J05Rik	Mus musculus RIKEI	0.504221596 6.774963856
44	A_51_P149621	Stt3b	STT3, subunit of the Golgi apparatus	Mus musculus STT3	0.50217731 10.53780671
45	A_55_P2047962	Gjc2	gap junction protein gamma 2	Mus musculus gap junction protein gamma 2	0.501911712 8.075503933
46	A_55_P1966863	Mad2l2	MAD2 mitotic arrest protein 2	Mus musculus MAD2	0.497055694 12.22692429
47	A_52_P6828	Xk	Kell blood group protein	Mus musculus Kell blood group protein	0.49681471 6.75218636
48	A_55_P2102998	Gm3893	predicted gene 3893	Mus musculus predicted gene 3893	0.496695 6.443091727
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2	A_55_P2090152	Vmn2r121	vomeronasal 2, rei	Mus musculus vomer	0.496549998 6.426258453
3	A_55_P2041095	Six4	sine oculis-related	Mus musculus sine o	0.496515097 8.936492814
4	A_51_P282179	Mtor	mechanistic target	Mus musculus mecl	0.49615176 9.600335943
5	A_51_P397375	Pet112	PET112 homolog (:	Mus musculus PET1	0.491822478 10.63703531
6	A_55_P1953226	Gm14484	predicted gene 14:	Mus musculus pred	0.490968565 6.890348424
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8	A_55_P2017140	Vmn2r88	vomeronasal 2, rei	Mus musculus vomer	0.489958584 6.596218494
9	A_55_P2121344	Nudcd3	NudC domain cont	Mus musculus NudC	0.486613312 14.48644209
10	A_52_P85765	Stard6	StAR-related lipid i	Mus musculus StAR	0.485532131 7.245921317
11	A_55_P2161958	2410141K09Rik	RIKEN cDNA 24101	Mus musculus RIKEI	0.483897201 8.944749485
12	A_55_P2167160	Hdhd2	haloacid dehaloge	Mus musculus halo:	0.483636246 8.721553593
13	A_55_P2023818	Cysltr1	cysteinyl leukotrie	Mus musculus cyste	0.482200122 6.913667873
14	A_55_P2051666	Nfkbib	nuclear factor of k	Mus musculus nucle	0.481825109 6.924766802
15	A_55_P2154049	Myo18a	myosin XVIIIIA	myosin XVIIIIA [Sou	0.481029403 9.351451737
16	A_55_P2121038	Gm10825	predicted gene 10:	Mus musculus pred	0.480494615 6.490948216
17	A_52_P180826	Ndufaf7	NADH dehydrogen	Mus musculus NADH	0.478197332 12.06995123
18	A_55_P2155479	Eps8	epidermal growth	Mus musculus epid	0.477778391 6.329612776
19	A_55_P2169775	Ano3	anoctamin 3	PREDICTED: Mus m	0.477457485 6.133871034
20	A_55_P2341950	Crebzf	CREB/ATF bZIP tra	Mus musculus CREB	0.477145148 8.496257562
21	A_55_P2108808	Tubgcp4	tubulin, gamma co	Mus musculus tubu	0.476459195 9.030731709
22	A_55_P2021099	Tmem181a	transmembrane pi	Mus musculus trans	0.475629474 11.52617749
23	A_52_P329314		0	0 Mus musculus activ	0.474168018 8.776230772
24	A_55_P2015715	Rab4a	RAB4A, member R	Mus musculus RAB4	0.472820882 11.89110055
25	A_55_P2266880	Kirrel	kin of IRRE like (Dr	Mus musculus kin o	0.469979146 11.97410603
26	A_51_P215190	Efcab11	EF-hand calcium b	Mus musculus EF-h:	0.468088991 6.530560013
27	A_51_P517381	Cers2	ceramide synthase	Mus musculus cerar	0.467385174 11.93577959
28	A_55_P2134645	Fam227a	family with sequer	family with sequenc	0.466809009 6.952928892
29	A_55_P2115995	Sms	spermine synthase	Mus musculus sperr	0.46670616 10.36200694
30	A_51_P211341	Eif3j1	eukaryotic translat	Mus musculus euka	0.465694432 10.78643735
31	A_55_P1998194	Snrpn	small nuclear ribor	Mus musculus smal	0.465682748 9.972197283
32	A_52_P65494	Iqgap2	IQ motif containin	Mus musculus IQ m	0.465013328 7.800658437
33	A_52_P404895	Tmem62	transmembrane pi	Mus musculus trans	0.463251515 7.426336173
34	A_55_P2042146	Fech	ferrochelata	Mus musculus ferro	0.458340686 12.87623246
35	A_55_P2081398		0	0 Mus musculus 3 day	0.457982439 6.874884315
36	A_51_P221132	L2hgdh	L-2-hydroxyglutar:	Mus musculus L-2-h	0.457098176 9.207769539
37	A_55_P1974442	Sumf2	sulfatase modifyin	Mus musculus sulfa	0.456851178 10.3700016
38	A_55_P2105563	1700104L18Rik	RIKEN cDNA 17001	Mus musculus RIKEI	0.454910321 6.389015679
39	A_51_P257684	Stau1	staufen (RNA bindi	Mus musculus stauf	0.453790437 10.17502422
40	A_52_P412452	Cntn6	contactin 6	Mus musculus cont:	0.452227075 6.28573148
41	A_55_P2187171	Sv2c	synaptic vesicle gly	Mus musculus synaj	0.451273743 6.044621352
42	A_55_P1961645	Vcp	valosin containing	Mus musculus valos	0.44903777 15.30971961
43	A_55_P1955172	Camk2d	calcium/calmoduli	Mus musculus 13 d:	0.447763023 7.272524621
44	A_55_P2433218	Bloc1s6	biogenesis of lysos	Mus musculus bioge	0.44500213 11.46295795
45	A_51_P292368	Tmco6	transmembrane ar	Mus musculus trans	0.444879683 8.843225584
46	A_55_P2168118	4933406C10Rik	RIKEN cDNA 49334	Mus musculus RIKEI	0.444090327 6.470058176
47	A_55_P2094881	Fgfr2	fibroblast growth f	Mus musculus fibro	0.440891409 9.97808478
48	A_55_P2326337	BC026513	cDNA sequence BC	Mus musculus cDN/	0.440689436 6.983094672
49	A_66_P111216	4632427E13Rik	RIKEN cDNA 46324	Mus musculus 13 d:	0.438953046 9.873997921
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2	A_55_P1962174	Rab8a	RAB8A, member R Mus musculus RAB8	0.424137876	10.59066735
3	A_55_P2018681	G630016G05Rik	RIKEN cDNA G630(PREDICTED: Mus mi	0.42271889	6.292352942
4	A_52_P417990	Zfp868	zinc finger protein Mus musculus zinc f	0.42043698	6.57986675
5	A_51_P125183	Coq5	coenzyme Q5 hom Mus musculus coen	0.419476387	8.945056584
6	A_55_P2261772	Lzts1	leucine zipper, put leucine zipper, puta	0.419198928	7.577093736
7	A_55_P2163363	Clec2f	C-type lectin domæ Mus musculus C-tyr	0.41913221	6.343168511
8	A_55_P1998392	Eif2ak4	eukaryotic translat eukaryotic translati	0.417164393	7.420248711
9	A_55_P2098305	Coq5	coenzyme Q5 hom Mus musculus coen	0.416936983	8.769634807
10	A_55_P2032478	Sfxn5	sideroflexin 5 sideroflexin 5 [Sour	0.416637414	7.721938883
11	A_55_P2092776	Apoo	apolipoprotein O Mus musculus apoli	0.415844374	11.68965048
12	A_55_P2012241	Ctso	cathepsin O Mus musculus cathe	0.41559322	7.125120729
13	A_55_P2452384	Mga	MAX gene associat Mus musculus MAX	0.415243264	8.932685792
14	A_52_P663526	Nmrk1	nicotinamide ribos Mus musculus nicot	0.414414455	8.003857616
15	A_55_P1974063	Gm2545	predicted gene 25 Mus musculus 2 day	0.413708974	6.218528632
16	A_55_P2050592	Gm5785	predicted gene 57 PREDICTED: Mus mi	0.413684181	8.461838113
17	A_55_P1970578	Aamdc	adipogenesis asso Mus musculus adipc	0.411471092	11.92703754
18	A_52_P299358	Lclat1	lysocardiolipin acy Mus musculus lysoc	0.409296709	9.949768884
19	A_55_P2288285	2310007J06Rik	RIKEN cDNA 2310 Mus musculus adult	0.408617418	6.306220274
20	A_55_P2115968	Gm14325	predicted gene 14 Mus musculus pred	0.406099667	10.10361514
21	A_51_P336391	Tmem18	transmembrane pi Mus musculus trans	0.40553698	12.25146122
22	A_52_P67983	Lcmt2	leucine carboxyl m Mus musculus leuci	0.405340924	10.26010917
23	A_51_P114456	Tceanc2	transcription elong Mus musculus trans	0.404316557	8.001395018
24	A_55_P1962384	Churc1	churchill domain c Mus musculus churi	0.40263635	13.35054757
25	A_55_P2053206	Kdm4c	lysine (K)-specific c Mus musculus lysin	0.402091708	10.49093052
26	A_55_P1979246	Cep192	centrosomal prote Mus musculus adult	0.401581925	6.726663181
27	A_51_P341010	Ercc8	excision repaiross- Mus musculus excis	0.398522876	9.191087781
28	A_55_P2388687	1700003G18Rik	RIKEN cDNA 1700 Mus musculus 10 d	0.397935551	6.495699396
29	A_55_P2043430		0 0 immunoglobulin kaj	0.397025619	6.260679891
30	A_55_P2078675		0 0 Q8BSH3_MOUSE (Q	0.394629866	10.55175122
31	A_55_P2174273	Slco5a1	solute carrier orga Mus musculus solut	0.394162375	6.254228174
32	A_52_P147666	Slc30a7	solute carrier fami Mus musculus solut	0.392889528	8.867834981
33	A_55_P2085731	Stk38	serine/threonine k Mus musculus serin	0.392477146	7.244947197
34	A_55_P2160737		0 0 T cell receptor alph	0.392156901	6.228406796
35	A_55_P2170911	Gm10366	predicted gene 10 Mus musculus RCB-	0.391173241	6.982595294
36	A_52_P425510	Dnah7a	dynein, axonemal, Mus musculus dyne	0.39117049	6.474571593
37	A_55_P2104532	Acacb	acetyl-Coenzyme / Mus musculus acety	0.390395955	6.37202715
38	A_52_P600946	Ccdc88c	coiled-coil domain Mus musculus coile	0.389765394	6.700200388
39	A_55_P1999883	Gm14499	predicted gene 14 Mus musculus pred	0.387386265	6.58660119
40	A_52_P916539	Zbtb34	zinc finger and BTE Mus musculus zinc f	0.38576947	7.042352643
41	A_55_P2045535	Rsg1	REM2 and RAB-like REM2 and RAB-like	0.383686004	6.568754731
42	A_55_P1973896	Vmn2r86	vomer nasal 2, rei Mus musculus vom	0.381511625	6.091046043
43	A_55_P2012107	Vmn2r10	vomer nasal 2, rei Mus musculus vom	0.379830315	6.27031141
44	A_52_P151905	Gm5132	predicted gene 51 Mus musculus pred	0.379563561	6.283761675
45	A_55_P2169909	Ostm1	osteopetrosis asso osteopetrosis assoc	0.378501009	6.99491057
46	A_55_P2186460	Emx2os	Emx2 opposite str: Mus musculus Emx2	0.376192058	6.496326483
47	A_51_P381230	Zhx2	zinc fingers and hc Mus musculus zinc f	0.375666934	6.692151172
48	A_55_P2161485	Ptchd2	patched domain c Mus musculus patcl	0.372827738	6.5520809

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2	A_55_P2160910	Faim2	Fas apoptotic inhib	Mus musculus Fas a	0.371593115 6.831524973
3	A_55_P1986208	Ccnb1ip1	cyclin B1 interactir	Mus musculus cyclir	0.369710291 6.103756239
4	A_52_P622694	Adal	adenosine deamin	Mus musculus aden	0.365872239 7.522421143
5	A_55_P2293967	Tbc1d5	TBC1 domain fami	Mus musculus TBC1	0.365251988 9.774149604
6	A_55_P1953984	Gm11033	predicted gene 11i	Mus musculus lung	0.36350122 7.161944693
8	A_66_P130911	Proser2	proline and serine	Mus musculus 15 d	0.362276281 6.964030088
9	A_52_P88818	Clybl	citrate lyase beta l	Mus musculus citrat	0.361906265 9.542409873
10	A_55_P2033481	Gm13298	predicted gene 13i	Mus musculus pred	0.361137232 6.680187468
11	A_66_P122377	Cd84	CD84 antigen	Mus musculus CD84	0.360506202 6.583811787
12	A_51_P320357	Grin2b	glutamate recepto	Mus musculus gluta	0.360280168 6.359031467
13	A_52_P504330	Ankib1	ankyrin repeat anc	Mus musculus anky	0.360250064 11.36207192
14	A_51_P394154	Ddx51	DEAD (Asp-Glu-Ala	Mus musculus DEAI	0.359877757 10.16927723
15	A_55_P2055642	2810407A14Rik	RIKEN cDNA 28104	Mus musculus PREDICTED: Mus mi	0.358951156 6.040017011
16	A_52_P219913	Cdan1	congenital dyseryt	Mus musculus cong	0.358850754 8.473046024
17	A_51_P220150	Angptl7	angiopoietin-like 7	Mus musculus angic	0.357228462 6.165392545
18	A_51_P228865	Zfp72	zinc finger protein	Mus musculus zinc f	0.355300342 7.847411318
19	A_55_P1993094	Mesdc1	mesoderm develo	Mus musculus meso	0.350713908 6.76590339
20	A_55_P2005853	Nacc2	nucleus accumben	Mus musculus nucle	0.348924514 15.54803706
21	A_55_P2057247	Etohi1	ethanol induced 1	Mus musculus ethai	0.348267114 7.063109429
22	A_51_P226962	Capn15	calpain 15	Mus musculus calpa	0.344518115 6.57454886
23	A_51_P343429	Slc25a37	solute carrier fami	Mus musculus solut	0.337178716 10.60161225
24	A_55_P2025363	Ccnl2	cyclin L2	Mus musculus cyclir	0.334404589 9.599327514
25	A_55_P2002918	Klc2	kinesin light chain	Mus musculus kines	0.328100484 11.33603232
26	A_55_P1977649	Hoxd8	homeobox D8	Mus musculus homi	0.328027082 6.093584714
27	A_55_P2031382	Crebzf	CREB/ATF bZIP tra	Mus musculus CREB	0.327529398 10.64772186
28	A_55_P2124016	Nipsnap1	4-nitrophenylphos	Mus musculus 4-nit	0.327066316 11.36759244
29	A_55_P2057268	Magi1	membrane associa	Mus musculus mem	0.32681088 12.32067837
30	A_55_P2139713	Phf13	PHD finger protein	Mus musculus PHD	0.325865291 7.367699171
31	A_65_P10433	Rpp14	ribonuclease P 14	Mus musculus ribor	0.321284724 9.956294104
32	A_55_P2005680	Ipo11	importin 11	Mus musculus impo	0.319029262 12.22021613
33	A_55_P2134351	Lancl3	LanC lantibiotic syi	Mus musculus LanC	0.318940372 6.245579756
34	A_66_P122053	Kcnq5	potassium voltage	Mus musculus pota:	0.312625093 6.374769691
35	A_55_P2002220	Dzip1	DAZ interacting pr	Mus musculus mRN	0.310498076 7.108950154
36	A_55_P1956687	Rab37	RAB37, member R.	Mus musculus RAB3	0.308690405 6.946824503
37	A_52_P221588	Gm5382	predicted gene 53i	Mus musculus pred	0.30857958 6.411918635
38	A_55_P2062787	Mfap3	microfibrillar-asso	Mus musculus micr	0.308502076 11.29521395
39	A_55_P2094484	Gm14137	predicted gene 14	Mus musculus pred	0.307841674 6.249040867
40	A_52_P18765	Hsbp111	heat shock factor l	Mus musculus heat	0.305411046 6.175418302
41	A_55_P1983999	Desi1	desumoylating iso	Mus musculus desu	0.305050921 9.223225353
42	A_51_P495581	Tlr1	toll-like receptor 1	Mus musculus toll-li	0.304755981 6.483885608
43	A_55_P2197134	A930018M24Rik	RIKEN cDNA A9300	Mus musculus adult	0.303146333 6.14613498
44	A_52_P146403	Arhgef38	Rho guanine nucle	Mus musculus Rho g	0.297713631 6.022117917
45	A_55_P2066219	Gm3455	predicted gene 34i	Mus musculus adult	0.292306122 6.846252621
46	A_51_P390775	Ube2e1	ubiquitin-conjugat	Mus musculus ubiq	0.288261272 12.4664347
47	A_51_P494006	Scaf8	SR-related CTD-ass	Mus musculus SR-re	0.287834928 11.40734343
48	A_51_P243134	Adcy6	adenylate cyclase	Mus musculus aden	0.286563466 10.60793854
49	A_55_P1955851	AI593442	expressed sequenc	Mus musculus expri	0.285949357 6.264288781
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2	A_55_P2024555	Ppap2a	phosphatidic acid Mus musculus phos	0.28340742	12.70854687
3	A_55_P2108868	Nufip1	nuclear fragile X m Mus musculus nucle	0.28340483	8.406819665
4	A_51_P375693	Tmem135	transmembrane p1 Mus musculus trans	0.282838866	10.08696021
5	A_55_P1982494	1700012L04Rik	RIKEN cDNA 17000 Mus musculus RIKEI	0.280394525	6.499018685
6	A_51_P129100	Sec63	SEC63-like (S. cere Mus musculus SEC6	0.279371698	9.600818144
7	A_55_P2003228	Rerg	RAS-like, estrogen- Mus musculus RAS-	0.278174735	6.186459568
8	A_55_P2060722	Uso1	USO1 vesicle docki Mus musculus USO:	0.27386441	11.79810942
9	A_55_P2052210	Gdi2	guanosine diphosç Mus musculus guan	0.268127974	15.07008493
10	A_55_P1970887	Vmn2r16	vomeronasal 2, rei Mus musculus vom	0.267919866	5.980558817
11	A_65_P10180	Rad23b	RAD23b homolog (Mus musculus RAD:	0.266502634	11.43165245
12	A_55_P2049483		0 UI-M-GI0-cek-h-17-i	0.265694877	5.93789424
13	A_52_P328078	Atp5b	ATP synthase, H+ t Mus musculus ATP :	0.26256479	16.25543189
14	A_55_P2217548	4921515G04Rik	RIKEN cDNA 49215 Mus musculus adult	0.261423553	6.071820881
15	A_51_P263290	Galnt9	UDP-N-acetyl-alph Mus musculus UDP-	0.260345438	6.151726529
16	A_55_P2078815	Xk	Kell blood group p Mus musculus Kell t	0.254480206	6.21155289
17	A_55_P2107447	Rab37	RAB37, member R. Mus musculus RAB3	0.244140291	7.029616615
18	A_51_P150608	Jagn1	jagunal homolog 1 Mus musculus jagur	0.2368731	13.19987516
19	A_52_P580582	Nppa	natriuretic peptide Mus musculus natri	0.227610422	6.588381243
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	adj.P.Val	Orre-Log_FC	Orre-adj.P.Val
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3	1.5155E-21	0.494015964	0.101276807
4	4.18232E-23	-0.208741888	0.86222962
5	2.51609E-15	0.509514034	0.173245869
6	1.89631E-15	-0.721426483	0.168073428
7	6.07388E-14	0.706101378	0.198794714
8	4.55163E-12	-0.645492101	0.561180497
9	5.66539E-10	0.382869744	0.300412533
10	2.68489E-12	1.530274252	0.10751908
11	5.03003E-15	0.607561951	0.180640491
12	0.011383754	0.708072732	0.095841743
13	6.99163E-09	0.417157621	0.732697156
14	1.00373E-08	0.348358531	0.722818593
15	1.76297E-14	-0.461955973	0.69554264
16	7.34401E-09	-0.265301426	0.85895072
17	9.52423E-12	0.132054376	0.806731065
18	2.51609E-15	-0.319929586	0.487450339
19	1.26452E-13	-0.30277199	0.776862477
20	3.81067E-16	0.423154735	0.751201622
21	1.71376E-13	-0.511838677	0.522961414
22	1.32742E-15	-0.104540487	0.937077956
23	8.45076E-09	1.128015324	0.251670799
24	6.39585E-07	0.393027073	0.583894548
25	5.0348E-13	-0.042822396	0.97312979
26	1.87675E-06	-0.077991108	0.910601338
27	1.62674E-08	0.700674909	0.157310536
28	9.79076E-06	-0.346039523	0.750752793
29	0.002006738	0.363396889	0.739710744
30	1.20027E-10	-0.321280956	0.739926932
31	9.90908E-05	1.089900036	0.110643562
32	1.34408E-05	-0.328214025	0.839521089
33	1.10036E-06	0.437062716	0.598329105
34	0.00193586	0.689481662	0.092676384
35	1.9256E-09	0.861615264	0.251034963
36	4.0172E-06	-0.363493756	0.486203135
37	1.77247E-14	-0.184267324	0.609527127
38	3.00086E-06	1.268073293	0.059985475
39	0.002874148	-1.61715276	0.065441134
40	1.94892E-09	-0.181696617	0.81968488
41	0.000172194	-0.157933401	0.719679153
42	0.000877619	-0.128163665	0.838921279
43	0.001129742	-0.086616262	0.918491027
44	2.92927E-08	-0.489734962	0.595972008
45	3.00086E-06	-1.135394748	0.284746979
46	6.62656E-06	1.171930897	0.186324197
47	6.70599E-07	0.056053329	0.955954662
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2	1.13328E-08	-0.113275734	0.894025902
3	7.54693E-07	-0.227365388	0.707333422
4	3.00779E-07	-0.088017319	0.938485136
5	0.000151278	-0.100899014	0.849011492
6	3.2388E-06	-0.349722197	0.719898927
7	6.28876E-05	-0.664151751	0.338510783
8	0.001641709	0.742797052	0.080935733
9	4.49879E-06	-0.135059276	0.882935769
10	1.0619E-08	-0.169947384	0.892526632
11	1.65847E-12	-0.307697854	0.641328681
12	3.32214E-07	-0.424691967	0.444760948
13	0.001489104	-1.157946462	0.330185942
14	8.45947E-07	0.845414186	0.365791074
15	0.000101522	0.707672554	0.168664396
16	3.57358E-09	0.553731131	0.647569617
17	1.34579E-06	-0.320991989	0.516380365
18	2.60497E-08	0.213144118	0.725963984
19	1.9256E-09	-0.204806123	0.573717182
20	5.21515E-09	-0.481573263	0.072468507
21	0.000396451	-0.127132138	0.878705558
22	1.14267E-07	-0.845345713	0.302189147
23	0.011911037	-0.436640002	0.425322426
24	6.61822E-08	0.12927286	0.907153397
25	2.33153E-08	0.28379144	0.580809949
26	0.002800997	-0.145749407	0.784052969
27	4.13642E-05	0.226120011	0.69554264
28	0.000407261	0.086866091	0.887775569
29	0.001686638	-0.63980779	0.082399826
30	0.000808174	-0.121826605	0.820857056
31	8.79673E-09	-0.536393529	0.698553736
32	0.000189232	-0.175484885	0.809427246
33	2.63238E-05	-0.013684635	0.992257293
34	6.28876E-05	0.029962335	0.948802911
35	1.11737E-05	0.22137264	0.824760267
36	0.016323043	0.470246434	0.601138648
37	2.84266E-07	-0.067080822	0.964389247
38	9.61673E-06	-0.339238132	0.790694488
39	5.55739E-06	0.059781564	0.975871464
40	1.9168E-05	-0.013439338	0.990510763
41	0.000427139	0.447834803	0.738308088
42	1.43E-09	0.000976591	0.999393864
43	2.43926E-06	-0.680573205	0.1180523
44	9.88697E-06	-0.519690316	0.070583758
45	2.75871E-10	-1.035950628	0.39089491
46	0.013270961	1.792970376	0.152119333
47	8.16187E-07	0.536623925	0.067094894
48	1.0803E-06	-0.402527074	0.714474121
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2	9.10813E-08	-0.0884533	0.944831525
3	0.017215445	0.214479384	0.728038356
4	0.000426641	-0.350065867	0.568731758
5	0.000396451	0.350261399	0.700220974
6			
7	5.39858E-08	-0.000770162	0.999311806
8	0.002746233	0.518897284	0.531876039
9	5.32555E-10	-0.523888849	0.455688565
10	2.66649E-05	-0.082641617	0.901318559
11	2.33153E-08	-0.067664713	0.944831525
12			
13	0.003856341	-0.311484797	0.644089282
14	0.032023049	0.801679878	0.272374934
15	9.25444E-05	-0.533474707	0.197890713
16	0.000580121	-0.694080695	0.335852093
17	0.000245655	-0.445709032	0.40001535
18			
19	6.56904E-05	0.090970165	0.946152468
20	6.41213E-05	0.145174467	0.855871263
21	0.000200769	-0.46867821	0.647058366
22	0.000226702	0.122331107	0.860951268
23			
24	0.004185517	1.215372159	0.133330557
25	0.037876068	-0.289080588	0.654741331
26	0.00732291	0.255868136	0.796533306
27	9.48239E-05	0.485161194	0.724124183
28	0.009804102	0.271313713	0.438743872
29			
30	7.88421E-07	-0.359228447	0.540486499
31	0.000228528	0.1005591	0.923754161
32	2.70552E-05	-0.479348533	0.066856402
33	9.56544E-07	-0.473266278	0.656861723
34	1.46332E-08	0.419511615	0.06877729
35			
36	0.000484742	0.461133994	0.435461001
37	0.000186626	-0.189919105	0.979780693
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39	2.54921E-07	-0.154880818	0.887577752
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41	0.001153761	0.045572013	0.937286143
42	0.000797911	0.822685256	0.164250851
43	6.2652E-05	0.854454407	0.210081543
44	4.05156E-05	0.18406571	0.853191719
45	7.2128E-07	-0.614345578	0.612173152
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47	0.000826698	0.040459997	0.965681273
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57	3.24393E-06	-0.245466726	0.736884352
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5	0.022055148	-0.917940314	0.133641052
6	7.47489E-09	-0.694356039	0.078477358
7	0.005950991	0.222865538	0.713806716
8	0.00411945	-0.509013023	0.465995005
9	6.18358E-05	-0.927245633	0.240098905
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21	0.003231136	0.094367677	0.880089213
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23	5.14628E-07	-0.072300221	0.964362185
24	8.79832E-05	0.269129185	0.306411953
25	0.00131247	-0.152166942	0.887775569
26	0.034321854	0.047372976	0.944629072
27	0.001106059	-0.657205133	0.107121807
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29	7.31445E-05	-0.283027394	0.739465708
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28	0.022276408	0.280191903	0.328943221
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30	0.004503427	1.966160529	0.112804984
31	0.042907697	-0.091797784	0.90348464
32	0.016323043	0.348195883	0.556938943
33	0.00438292	-0.149724691	0.805316244
34	0.013741568	0.334509501	0.53737695
35	0.014616597	-0.465638588	0.216701127
36	0.031632846	-0.042794899	0.952185198
37			
38	0.04111064	0.9322916	0.12538621
39	0.022577663	0.376433338	0.748119776
40	0.038259174	-0.700573535	0.461646396
41	0.013829316	-0.007444889	0.994595766
42	0.019963223	0.193461308	0.748151145
43			
44	0.045020123	-0.463016025	0.231343292
45	0.008896115	-0.071720797	0.958254307
46	0.002139643	-0.246673356	0.917846987
47	0.045313536	-0.202359587	0.724238845
48	0.037458535	0.655697306	0.389624379
49	0.000922085	-0.6213534	0.471845336
50	0.021502423	-0.498189824	0.642314642
51	0.043087117	-0.174642245	0.806563934
52	0.029254681	-0.282875435	0.478335484
53	0.047302553	-0.190999745	0.726889473
54	0.045840929	1.240114553	0.080677841
55	0.023205635	-0.067376118	0.944315462
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2	0.026533243	0.35946619	0.345679794
3	0.043648966	-0.311143834	0.723711472
4	0.038215668	-0.60975336	0.112666331
5	0.00638709	0.301275366	0.74330113
6	0.03373804	0.269081489	0.636054626
7	0.037622926	1.104599641	0.167841309
8	0.029406977	-0.07133184	0.926678896
9	0.022126019	0.019095725	0.972308321
10	0.025922503	-0.183055671	0.804321056
11	0.014394077	-0.042228316	0.957896512
12	0.045460992	0.38651112	0.77894764
13	0.04557964	-0.193157067	0.588569274
14	0.004203953	-0.67525574	0.478371423
15	0.048646043	0.908993348	0.074897277
16	0.04557964	0.362902411	0.499762677
17	0.03366818	-0.031770126	0.969956952
18	0.04580648	-0.534179197	0.10751908
19	0.021502423	-0.306600745	0.961860984
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	ProbeName	GeneSymbol	GeneName	Description	logFC	AveExpr
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3	A_51_P277006	Chst8	carbohydrate (N-a	Mus musculus carbo	1.998798403	9.506990359
4	A_51_P155458	Dok7	docking protein 7	docking protein 7 [S	1.099704047	10.92169511
5	A_55_P2054350	Fbxo44	F-box protein 44	Mus musculus F-bo	1.094375528	11.4403973
6	A_55_P2005055	Pepd	peptidase D	Mus musculus pept	0.978903734	14.00742747
7	A_66_P116461	Mro	maestro	Mus musculus mae	0.919902196	8.853408542
8	A_51_P502150	Slc9a3r1	solute carrier fami	Mus musculus solut	0.874304136	11.64877569
9	A_55_P1967539	Hunk	hormonally upregi	Mus musculus horn	0.856801394	12.39458915
10	A_51_P209183	Cxcl14	chemokine (C-X-C	Mus musculus chen	0.84718745	11.79136499
11	A_55_P2127258	Dok7	docking protein 7	Mus musculus dock	0.831719821	7.804274362
12	A_52_P2710	Cml5	camello-like 5	Mus musculus cam	0.791982403	6.561499522
13	A_55_P2049211	Pisd-ps1	phosphatidylserin	Mus musculus phos	0.722973556	12.65183916
14	A_51_P475228	Armc6	armadillo repeat c	Mus musculus arm	0.679278376	10.62667145
15	A_55_P1955548	Ezr	ezrin	Mus musculus ezrin	0.656022612	14.14145509
16	A_55_P1979330	Dapp1	dual adaptor for pl	Mus musculus dual	0.642553318	9.285773136
17	A_55_P1994062	Emx2os	Emx2 opposite str	Mus musculus Emx	0.603575825	6.937128745
18	A_55_P2054300	Alg8	asparagine-linked	Mus musculus aspa	0.546261365	10.05023853
19	A_55_P2427685	Agf	amylo-1,6-glucosic	Mus musculus amyl	0.533416528	11.83440315
20	A_55_P2158866	Nme6	NME/NM23 nuclei	Mus musculus NME	0.497635144	11.57278217
21	A_55_P2181334	6030419C18Rik	RIKEN cDNA 60304	Mus musculus RIKE	0.487781402	7.659255264
22	A_55_P2133165	Wwc1	WW, C2 and coilec	Mus musculus WW,	0.43524986	14.53699509
23	A_55_P2086983	Atxn2	ataxin 2	Mus musculus ataxi	0.427666332	13.23524556
24	A_55_P1965674	Alg2	asparagine-linked	Mus musculus aspa	0.3917772	12.77511628
25	A_51_P473953	Arhgef26	Rho guanine nucle	Mus musculus Rho	0.348289958	12.24174198
26	A_55_P2022434	Gpi1	glucose phosphate	Mus musculus glucc	0.336512554	16.14117805
27	A_55_P2030433	Gpi1	glucose phosphate	Mus musculus glucc	0.331171618	15.58858241
28	A_55_P2061809	Ndufc2	NADH dehydrogen	Mus musculus NAD	0.267545274	14.98538925
29	A_51_P342669	Pgam1	phosphoglycerate	Mus musculus phos	0.26250287	15.53968412
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	adj.P.Val	Orre-Log_FC	Orre-adj.P.Val
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3	0.000527398	-1.020809588	0.001347252
4	0.007527662	-1.84709202	0.009582176
5	3.56729E-05	-1.227709635	0.015712097
6	1.69542E-06	-0.729933657	0.028285973
7	0.001379325	-1.030168616	0.011926881
8	0.001417212	-1.376082523	0.003271452
9	5.70527E-07	-0.773139893	0.041430647
10	0.008896115	-1.724736378	0.001170971
11	0.017565766	-1.582479166	0.007184006
12	1.34579E-06	-1.652541234	0.017572167
13	0.001443363	-0.883124413	0.033965586
14	0.001789253	-0.676496203	0.045520561
15	0.001756325	-1.66632014	0.022479083
16	0.04355309	-0.862129878	0.036372988
17	0.003464519	-1.089412003	0.004521647
18	0.001092598	-1.123162944	0.003275647
19	0.00106005	-0.931225482	0.007552042
20	0.000808174	-0.481070518	0.049567233
21	0.031413191	-0.919446508	0.019012689
22	0.037393167	-1.066002187	0.038947926
23	0.007459508	-0.812278155	0.035762889
24	0.023798032	-0.822906418	0.00479841
25	0.033356178	-1.226972592	0.016222111
26	0.022431714	-0.53157885	0.025429949
27	0.03292527	-0.476276205	0.04722026
28	0.029039158	-0.875073385	0.005907455
29	0.02976617	-0.761186395	0.006498149
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	ProbeName	GeneSymbol	GeneName	Description	logFC	AveExpr
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2						
3	A_52_P393314	P2rx7	purinergic receptor	Mus musculus puriner	-2.566483	9.918835431
4	A_55_P2091359	Padi2	peptidyl arginine de	Mus musculus peptidy	-1.825425	12.92514476
5	A_55_P2212603	Apba2	amyloid beta (A4) p	Mus musculus amyloid	-1.686821	9.225208525
6	A_51_P355427	Timp4	tissue inhibitor of r	Mus musculus tissue ir	-1.339929	9.342884771
7	A_66_P125862	A930005H10Rik	RIKEN cDNA A93000	Mus musculus RIKEN c	-1.307057	10.74695408
8	A_51_P337944	Bmp2k	BMP2 inducible kin	Mus musculus BMP2 ir	-1.289259	10.84824895
9	A_55_P2123683	Chrdl1	chordin-like 1	Mus musculus chordin	-1.06929	9.614315788
10	A_55_P2044242	Slc13a5	solute carrier family	Mus musculus solute c	-0.979917	8.652415373
11	A_51_P474422	Ift27	intraflagellar transp	Mus musculus intraflag	-0.888869	14.3953448
12	A_55_P1961014	Selenbp1	selenium binding pr	Mus musculus seleniur	-0.846845	10.7388478
13	A_55_P1953387	Fabp5	fatty acid binding pr	Mus musculus fatty aci	-0.83057	14.93510115
14	A_51_P331661	Ubiad1	UbiA prenyltransfer	Mus musculus UbiA pr	-0.803178	11.61194832
15	A_55_P2097178	Idua	iduronidase, alpha-	Mus musculus iduronic	-0.749596	9.374207676
16	A_55_P2045007	Hrh1	histamine receptor	Mus musculus histami	-0.709332	7.351788502
17	A_51_P481159	Cbr3	carbonyl reductase	Mus musculus carbony	-0.692289	12.81832935
18	A_55_P2075213	Kbtbd11	kelch repeat and BT	Mus musculus kelch re	-0.631394	8.672056845
19	A_55_P2003541	Nrcam	neuron-glia-CAM-re	Mus musculus neuron-	-0.62582	12.7418749
20	A_51_P312437	Dhrs7	dehydrogenase/red	Mus musculus dehydr	-0.621441	13.58264256
21	A_51_P108581	Adrbk2	adrenergic receptor	Mus musculus adrener	-0.593173	9.552982166
22	A_55_P2018666	Thrsp	thyroid hormone re	Mus musculus thyroid	-0.558281	12.163245
23	A_55_P1961140	Mettl3	methyltransferase I	Mus musculus methylt	-0.557766	11.63462664
24	A_66_P104309	Myl2	myosin, light polype	Mus musculus myosin,	-0.539752	7.415807899
25	A_55_P2063316	Mgl1	monoglyceride lipa	Mus musculus monogl	-0.50398	13.43596113
26	A_55_P1971025	Paqr6	progesterin and adip	Mus musculus progest	-0.501593	9.802427856
27	A_51_P475628	Paqr6	progesterin and adip	Mus musculus progest	-0.470051	8.884532746
28	A_55_P2114863	Mgl1	monoglyceride lipa	Mus musculus monogl	-0.396421	12.14565961
29	A_55_P1967648	Fln	folliculin	Mus musculus folliculir	-0.346075	11.043084
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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
1						
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3	A_55_P1966838	Xaf1	XIAP associated fa	Mus musculus XIAP	-6.156879098	9.98739195
4	A_52_P516409	Col4a6	collagen, type IV, i	Mus musculus colla	-4.328433054	11.49218277
5	A_55_P1966774	Serpina3i	serine (or cysteine	Mus musculus serir	-3.517707117	8.237049671
6	A_66_P130813	Samd4	sterile alpha motil	Mus musculus steri	-3.381084819	9.712777677
7	A_52_P303176	1810037I17Rik	RIKEN cDNA 1810	Mus musculus RIKE	-3.218676372	12.76378133
8	A_55_P2132207	1810037I17Rik	RIKEN cDNA 1810	Mus musculus RIKE	-3.150307147	11.50210939
9	A_55_P2137527	Fam183b	family with seque	Mus musculus fami	-3.146347755	10.8863997
10	A_52_P111031	Pcdh17	protocadherin 17	Mus musculus prot	-3.096400623	9.286752712
11	A_55_P2026420	Pou6f1	POU domain, clas	Mus musculus POU	-3.085193903	8.567395379
12	A_52_P206492	Pop4	processing of prec	Mus musculus proc	-2.990439512	11.37800517
13	A_55_P2105944	Olf22a	olfactory receptor	Mus musculus olfac	-2.853577013	8.061203017
14	A_55_P1952482	Pbp2	phosphatidyletha	Mus musculus phos	-2.708851464	7.72208074
15	A_51_P462428	Galnt15	UDP-N-acetyl-alf	UDP-N-acetyl-alpha	-2.327912086	10.82348441
16	A_55_P2026270	Cfi	complement com	Mus musculus com	-2.283011075	7.59612213
17	A_51_P159453	Serpina3n	serine (or cysteine	Mus musculus serir	-2.257787149	11.293936
18	A_52_P613498	4833420G17Rik	RIKEN cDNA 4833	Mus musculus RIKE	-2.135137596	11.72763205
19	A_52_P157450	Abhd1	abhydrolase dom	Mus musculus abhy	-2.028719361	9.154942083
20	A_51_P297105	Ucp2	uncoupling protei	Mus musculus uncc	-2.008925416	9.278059744
21	A_55_P2074656	Padi2	peptidyl arginine	Mus musculus pept	-1.981559202	13.12004985
22	A_52_P257812	Lpl	lipoprotein lipase	Mus musculus lipo	-1.966798117	8.512458682
23	A_52_P597775	Gprc5a	G protein-coupled	Mus musculus G pr	-1.882880186	10.6940361
24	A_55_P2045642	Stmn4	stathmin-like 4	Mus musculus statf	-1.765390964	9.267843384
25	A_66_P108247	Ucp3	uncoupling protei	Mus musculus uncc	-1.732205788	8.742824015
26	A_55_P2176792	Sh3gl3	SH3-domain GRB2	Mus musculus SH3-	-1.728042937	9.346406711
27	A_66_P105175	Bche	butyrylcholinester	Mus musculus buty	-1.719959388	10.67728495
28	A_51_P128667	Lynx1	Ly6/neurotoxin 1	Mus musculus Ly6/	-1.71821413	11.50331263
29	A_51_P194249	Stmn4	stathmin-like 4	Mus musculus statf	-1.693097435	9.25076796
30	A_55_P1953972	Pdhb	pyruvate dehydro	Mus musculus pyru	-1.683490724	12.85410198
31	A_55_P2315012	4930458D05Rik	RIKEN cDNA 4930	Mus musculus adul	-1.6590401	7.042019248
32	A_55_P1968276	Tomm22	translocase of out	Mus musculus tran	-1.623250362	12.76321099
33	A_55_P2004179	Col2a1	collagen, type II, a	Mus musculus colla	-1.60138222	10.26377656
34	A_55_P2162344	Lrsam1	leucine rich repea	Mus musculus leuci	-1.595495677	11.18370501
35	A_51_P458778	Hpgd	hydroxyprostagla	Mus musculus hydr	-1.568266039	7.811720919
36	A_55_P2014304	Kank1	KN motif and ank	Mus musculus KN n	-1.562962584	11.84753693
37	A_52_P165773	Prmt8	protein arginine N	Mus musculus prot	-1.54223841	7.044327945
38	A_55_P2093774	Chl1	cell adhesion mol	Mus musculus cell	-1.534507736	10.44255926
39	A_55_P2140212		0	0 Q3J0L9_RHOS4 (Q3	-1.53256524	11.03368948
40	A_55_P2040600	Exd1	exonuclease 3'-5'	Mus musculus exor	-1.525678034	8.520248792
41	A_55_P2106525	Nmnat3	nicotinamide nucl	Mus musculus nico	-1.491097654	8.464035327
42	A_55_P2058791	4833420G17Rik	RIKEN cDNA 4833	Mus musculus RIKE	-1.485576479	8.419571885
43	A_52_P257625	Esm1	endothelial cell-s	Mus musculus endc	-1.476230322	7.936182419
44	A_55_P2033425	Grm5	glutamate recept	Mus musculus gluta	-1.445020115	7.754319196
45	A_55_P2010936	Fbxo17	F-box protein 17	Mus musculus F-bo	-1.431784462	9.098136864
46	A_55_P2148534	Nr1d2	nuclear receptor s	Mus musculus nucl	-1.418944898	9.618498483
47	A_51_P129149	Gatad2a	GATA zinc finger c	Mus musculus GAT	-1.417803996	10.06687358
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2	A_51_P497100	Lgals4	lectin, galactose b	Mus musculus lecti	-1.394429143 9.083050324	
3	A_55_P2063256	Lgals4	lectin, galactose b	Mus musculus lecti	-1.384406462 9.160897964	
4	A_66_P125035	Duxbl2	doubl homeobox l	Mus musculus douk	-1.384107062 8.150682833	
5	A_51_P309854	Kcnn2	potassium interm	Mus musculus pota	-1.382825841 9.054592244	
6	A_51_P360918	Ehd3	EH-domain contai	Mus musculus EH-d	-1.374346569 10.16522609	
7	A_51_P497985	C2	complement com	Mus musculus com	-1.354036194 9.530156157	
8	A_52_P331762	Lmo1	LIM domain only 1	Mus musculus LIM	-1.330942564 7.548138306	
9	A_55_P2013223	S100z	S100 calcium bind	Mus musculus S100	-1.326491423 6.933102342	
10	A_51_P140690	Stmn3	stathmin-like 3	Mus musculus statf	-1.321998206 9.494028319	
11	A_55_P2213214	A030001D20Rik	RIKEN cDNA A030	PREDICTED: Mus m	-1.312346267 8.010692055	
12	A_55_P2011659	Anapc5	anaphase-promot	Mus musculus anap	-1.310212874 11.35954614	
13	A_55_P1987499	Pttg1	pituitary tumor-tr	Mus musculus pitui	-1.308267592 13.17460908	
14	A_55_P1994339	Dhrs7c	dehydrogenase/r	Mus musculus dehy	-1.305209065 6.754466092	
15	A_55_P1976898	Pnp2	purine-nucleoside	Mus musculus purit	-1.301681346 6.985190238	
16	A_52_P650379	Strap	serine/threonine l	Mus musculus serir	-1.299661285 10.59363689	
17	A_52_P447196	Col4a6	collagen, type IV,	Mus musculus colla	-1.292810345 8.244840928	
18	A_55_P2007673	Lrsam1	leucine rich repea	Mus musculus leuci	-1.290806296 11.45712366	
19	A_55_P1954724		0	0 Mus musculus adul	-1.287861539 10.32515557	
20	A_55_P2029746		0	0 Mus musculus adul	-1.285958826 11.11618368	
21	A_51_P241210	Lhfp13	lipoma HMGIC fus	Mus musculus lipor	-1.284340644 8.019613107	
22	A_55_P1967553	Tmem254c	transmembrane p	Mus musculus tran	-1.277819902 12.04771936	
23	A_52_P441294	Chl1	cell adhesion mol	Mus musculus cell a	-1.27532299 11.41555856	
24	A_52_P8324	Tmem178	transmembrane p	Mus musculus tran	-1.273076613 7.695362808	
25	A_55_P2027852	Ccl25	chemokine (C-C m	Mus musculus chen	-1.259566696 7.416547542	
26	A_52_P250555	Dynl1	dynein light chain	Mus musculus dyne	-1.249217853 8.532070831	
27	A_55_P2209258	B430105A11Rik	RIKEN cDNA B430	Mus musculus 4 da	-1.246870514 9.199220507	
28	A_55_P2088720		0	0 Mus musculus adul	-1.241041739 9.778383825	
29	A_55_P2110290	Tmem254a	transmembrane p	Mus musculus tran	-1.240039813 10.20028868	
30	A_51_P506937	Mrps12	mitochondrial rib	Mus musculus mito	-1.237578376 13.28474287	
31	A_55_P2115151	Pxylp1	2-phosphoxylose	Mus musculus 2-ph	-1.232574717 9.952113468	
32	A_55_P1957213	3930401B19Rik	RIKEN cDNA 3930	Mus musculus 13 d	-1.217322024 10.06362884	
33	A_55_P2133205	Nmt2	N-myristoyltransf	Mus musculus N-m	-1.216097007 8.675213006	
34	A_55_P2006035	Galnt15	UDP-N-acetyl-alf	Mus musculus UDP	-1.210849447 7.273377309	
35	A_55_P2154977	Rpap3	RNA polymerase I	Mus musculus RNA	-1.208079308 12.74712555	
36	A_55_P2076303	March8	membrane-associ	Mus musculus men	-1.204814812 12.02120848	
37	A_52_P1042732	Akap5	A kinase (PRKA) a	Mus musculus A kir	-1.204530816 8.904980631	
38	A_52_P48546	Rnf41	ring finger protein	Mus musculus ring	-1.200195931 8.519484927	
39	A_66_P122415	Snhg6	small nucleolar R	Mus musculus smal	-1.186454912 12.55778235	
40	A_55_P1983958	Gm20746	predicted gene, 2l	PREDICTED: Mus m	-1.176907362 14.13568133	
41	A_55_P2147280	Myh1	myosin, heavy pol	Mus musculus myo	-1.176209151 8.320743949	
42	A_52_P573255	Cdc42ep1	CDC42 effector pr	Mus musculus CDC	-1.175193414 13.7926044	
43	A_55_P2334927		9.13002E+15	uncharacterized 9	Mus musculus adul	-1.17230089 10.08795111
44	A_52_P124472	Kcnd2	potassium voltage	Mus musculus pota	-1.161813793 7.390531663	
45	A_55_P2041828	Tubb3	tubulin, beta 3 cla	Mus musculus tubu	-1.154640221 9.179596699	
46	A_55_P2057622	Ocel1	occludin/ELL dom	Mus musculus 2 da	-1.118246162 6.968431276	
47	A_55_P2079116		0	0 Mus musculus cDN	-1.104652911 9.549861633	
48	A_55_P2056557		0	0 Mus musculus 12 d	-1.104080784 7.188119824	
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2	A_65_P01834	Lima1	LIM domain and a Mus musculus LIM	-1.097432887	9.4342313
3	A_52_P590535	Fbln2	fibulin 2 Mus musculus fibul	-1.093996254	12.94250986
4	A_55_P2080880	Clcnkb	chloride channel k Mus musculus chlo	-1.093432417	7.365545407
5	A_52_P574653	Bid	BH3 interacting d Mus musculus BH3	-1.093040424	9.627188001
6	A_55_P2090330	Kcnmb4	potassium large c Mus musculus pota	-1.089176143	9.227035955
7	A_52_P305230	Igsf21	immunoglobulin s Mus musculus imm	-1.084637957	7.380111698
8	A_55_P2059090	Tagap	T cell activation RI Mus musculus T cel	-1.083238495	8.716056759
9	A_55_P2035424	Hpgd	hydroxyprostaglar Mus musculus hydr	-1.074317003	7.136480655
10	A_55_P2016034	Nlrc5	NLR family, CARD Mus musculus NLR	-1.072914512	7.882077667
11	A_55_P2073642	1600014C10Rik	RIKEN cDNA 1600 Mus musculus RIKE	-1.066481948	7.714238037
12	A_52_P481279	Drc1	dynein regulatory Mus musculus dyne	-1.055443982	13.18253392
13	A_55_P2018181	A730008H23Rik	RIKEN cDNA A730 Mus musculus RIKE	-1.054299776	7.487791722
14	A_55_P2048478	Olfml1	olfactomedin-like Mus musculus olfac	-1.047088892	10.54004959
15	A_55_P2075313	Zfp619	zinc finger protein Mus musculus zinc	-1.046286275	7.246426253
16	A_55_P2155644	2010315B03Rik	RIKEN cDNA 2010 Mus musculus RIKE	-1.043721456	7.702890424
17	A_55_P2062593	Gm4924	predicted gene 49 Mus musculus inhi	-1.025819062	9.365154479
18	A_65_P03606	Rpap2	RNA polymerase I Mus musculus RNA	-1.015013348	7.598731978
19	A_55_P2067116	Dclre1c	DNA cross-link re Mus musculus DNA	-1.012283165	6.842454651
20	A_51_P417251	6330403K07Rik	RIKEN cDNA 6330 Mus musculus RIKE	-1.011200848	13.89378848
21	A_55_P2370160	C130009A20Rik	RIKEN cDNA C130 Mus musculus 15 d	-1.010625441	8.214180271
22	A_55_P2008417	Mnd1	meiotic nuclear di Mus musculus meic	-1.001459002	9.396695121
23	A_55_P1973352		0 0 Mus musculus strai	-1.001231056	6.997009656
24	A_51_P506733	P2rx7	purinergic recept Mus musculus puri	-0.99870721	6.940510888
25	A_52_P400509	Atm	ataxia telangiecta Mus musculus atax	-0.997462528	8.427413446
26	A_55_P2048119	Slc29a4	solute carrier fam Mus musculus solut	-0.992982222	8.686096717
27	A_55_P1959076	Zfp930	zinc finger protein Mus musculus zinc	-0.992804216	7.209102318
28	A_55_P2079619	Rnf43	ring finger protein Mus musculus ring	-0.980674207	8.064939843
29	A_55_P2115567	Slc26a1	solute carrier fam Mus musculus solut	-0.969683986	7.481536136
30	A_55_P1953087	Mcm3	minichromosome Mus musculus mini	-0.968129022	11.14341804
31	A_51_P502437	Cacna2d3	calcium channel, \ Mus musculus calci	-0.962221758	8.022540062
32	A_55_P2105321	Acin1	apoptotic chroma Mus musculus apo	-0.95576469	12.63445814
33	A_55_P1953920	Me3	malic enzyme 3, N Mus musculus mali	-0.953796608	12.11485534
34	A_52_P630867	Abcc4	ATP-binding casse Mus musculus ATP-	-0.95071448	9.199235192
35	A_51_P283968	Adamts18	a disintegrin-like ε Mus musculus a dis	-0.94559252	7.148584453
36	A_52_P38908	Tmem132b	transmembrane p Mus musculus tran	-0.943684784	12.32166788
37	A_51_P446796	Camta1	calmodulin bindin Mus musculus calm	-0.938806673	8.029084983
38	A_55_P1953919	Me3	malic enzyme 3, N Mus musculus mali	-0.938219484	12.78076322
39	A_55_P2356736	6720483E21Rik	RIKEN cDNA 6720 Mus musculus RIKE	-0.934845512	7.048698444
40	A_52_P559919	Eif2ak2	eukaryotic transla Mus musculus euka	-0.932749376	10.38326438
41	A_55_P2023864	Mfap1a	microfibrillar-asso Mus musculus micr	-0.929622826	10.59280982
42	A_51_P477736	4932415M13Rik	RIKEN cDNA 4932 Mus musculus RIKE	-0.927067258	6.697441234
43	A_55_P1969497	Lynx1	Ly6/neurotoxin 1 Mus musculus Ly6/	-0.91552837	6.878404826
44	A_52_P563375	Lgals2	lectin, galactose-b Mus musculus lecti	-0.914295845	8.245668406
45	A_52_P167535	Efcab12	EF-hand calcium b Mus musculus EF-h	-0.90932356	10.96212449
46	A_55_P2055087	Prkar2b	protein kinase, cA Mus musculus prot	-0.908929989	10.02342185
47	A_55_P2329298	Gm12758	predicted gene 12 Mus musculus 2 da	-0.908030723	7.239072622
48	A_51_P282268	Snapc1	small nuclear RNA Mus musculus smal	-0.902064505	9.180275957
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2	A_51_P517430	Cd1d1	CD1d1 antigen	Mus musculus CD1d	-0.895878116	10.1105168
3	A_55_P1986639	3110070M22Rik	RIKEN cDNA 3110	Mus musculus RIKE	-0.89528171	7.824256532
4	A_55_P2008722	Gm13157	predicted gene 13	Mus musculus pred	-0.883596352	9.60656173
5	A_51_P116687	1700010I14Rik	RIKEN cDNA 1700	Mus musculus RIKE	-0.87477972	7.97858127
6	A_55_P2040371	Rnaset2a	ribonuclease T2A	Mus musculus ribo	-0.869114138	13.71026659
7	A_51_P147034	Ica1l	islet cell autoantig	Mus musculus islet	-0.868364731	8.69777082
8	A_55_P2183914	Gm7120	predicted gene 71	Mus musculus pred	-0.864147811	7.927760277
9	A_55_P2072391	Acp1	acid phosphatase	Mus musculus acid	-0.852700759	8.912448535
10	A_55_P1963508	Slc13a5	solute carrier fam	Mus musculus solut	-0.850735708	8.000988516
11	A_52_P529195	Pcdhb4	protocadherin bet	Mus musculus prot	-0.849945399	7.043555936
12	A_51_P134812	Chac1	ChaC, cation trans	Mus musculus ChaC	-0.844774071	10.36841888
13	A_51_P497240	E330013P04Rik	RIKEN cDNA E330	Mus musculus RIKE	-0.844765396	8.72807961
14	A_55_P2023707	Camta1	calmodulin bindin	Mus musculus calm	-0.835058655	8.292413142
15	A_65_P01247	Hjurp	Holliday junction	Mus musculus Holli	-0.829270832	7.395492019
16	A_55_P2095909	Lamtor3	late endosomal/ly	Mus musculus late	-0.827157354	8.550491325
17	A_52_P650325	Slc35e1	solute carrier fam	Mus musculus solut	-0.82154184	8.104474982
18	A_52_P116264	Adhfe1	alcohol dehydroge	Mus musculus alcol	-0.820653163	8.914064684
19	A_66_P138584	Mnd1	meiotic nuclear di	Mus musculus meic	-0.815750524	8.886104688
20	A_55_P2059179	Slc48a1	solute carrier fam	Mus musculus solut	-0.81004159	13.10075273
21	A_55_P2105220	Hscb	HscB iron-sulfur cl	Mus musculus HscE	-0.807694136	12.28189497
22	A_55_P1958597	Slc27a3	solute carrier fam	Mus musculus solut	-0.806533897	10.39221354
23	A_55_P2119892	Erbp4	v-erb-a erythrobla	v-erb-a erythroblas	-0.805175492	7.44387188
24	A_55_P1998299	Itgb4	integrin beta 4	Mus musculus inte	-0.804716433	8.351358579
25	A_51_P408989	L3hypdh	L-3-hydroxyprolin	Mus musculus L-3-h	-0.797873579	9.429268854
26	A_51_P348617	2310045N01Rik	RIKEN cDNA 2310	Mus musculus RIKE	-0.796333366	13.13596643
27	A_55_P2124026	Synj2	synaptojanin 2	Mus musculus syna	-0.791329143	9.277978073
28	A_51_P273609	Itpka	inositol 1,4,5-trisp	Mus musculus inosi	-0.788523626	7.336973459
29	A_55_P2179834	Gatad2a	GATA zinc finger c	Mus musculus GAT	-0.782587668	11.70726936
30	A_52_P558609	Clec16a	C-type lectin dom	Mus musculus C-ty	-0.774440114	9.135758847
31	A_55_P2059986	Chst14	carbohydrate (N-a	Mus musculus carb	-0.773816524	10.15616747
32	A_51_P215374	Slc6a17	solute carrier fam	Mus musculus solut	-0.773417223	7.374150143
33	A_55_P2105362	Tmed5	transmembrane e	Mus musculus tran	-0.771893147	9.178735545
34	A_55_P2169227	Ccdc184	coiled-coil domair	Mus musculus coile	-0.771250879	6.917791641
35	A_55_P2099540	H2afj	H2A histone famil	Mus musculus H2A	-0.769429041	9.782121086
36	A_55_P2121156	LOC102634215	uncharacterized L	PREDICTED: Mus m	-0.766437171	6.673007895
37	A_55_P2187076	Sncg	synuclein, gamma	Mus musculus synu	-0.76410798	7.636786619
38	A_55_P2088223	Synpr	synaptoporin	Mus musculus syna	-0.760669861	6.512934163
39	A_55_P2185950	Bpnt1	bisphosphate 3'-n	Mus musculus bispl	-0.756583454	8.664448436
40	A_55_P1983959	Ftl1	ferritin light chain	Mus musculus ferri	-0.753556952	15.30605533
41	A_55_P2185504	Masp2	mannan-binding li	Mus musculus man	-0.753143511	6.990580432
42	A_55_P1999240	Gm2696	predicted gene 26	Mus musculus pred	-0.750089216	10.2949764
43	A_55_P2021266	Hpse	heparanase	Mus musculus hepa	-0.747821613	6.970430604
44	A_55_P2044602	Siah3	seven in absentia	Mus musculus seve	-0.733318565	7.304939267
45	A_55_P1955726	Ptpn5	protein tyrosine p	Mus musculus prot	-0.726347174	6.546976015
46	A_51_P254045	Traip	TRAF-interacting	Mus musculus TRAI	-0.721879342	9.180452669
47	A_55_P2157966	Map1a	microtubule-assoc	Mus musculus micr	-0.721370838	9.367794738
48	A_55_P2007771	Catsper2	cation channel, sp	Mus musculus catic	-0.71932791	8.371543358
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2	A_55_P2036813		0	0 histone cluster 3, H	-0.714894858	10.43484322
3	A_55_P2106150	Cenpk		centromere prote Mus musculus cent	-0.714021248	10.33973892
4	A_55_P1975120	Gm10777		predicted gene 10 Mus musculus activ	-0.713805022	9.633629823
5	A_55_P2115127	Mphosph10		M-phase phospho Mus musculus M-pl	-0.71194352	7.574959028
6	A_55_P2096368	LOC102632770		ADP-ribosylation f PREDICTED: Mus m	-0.710643542	12.49347357
7	A_51_P451588	Plekhhb1		pleckstrin homolo Mus musculus plecl	-0.709050858	14.22405549
8	A_55_P1979027	Tmem65		transmembrane p Mus musculus tran:	-0.701847616	10.42426536
9	A_55_P1954092		0	0 BB713741 RIKEN fu	-0.698752868	12.30346033
10	A_51_P413507	2010109A12Rik		RIKEN cDNA 2010 Mus musculus RIKE	-0.688651928	6.812251
11	A_55_P2108784	Arhgap22		Rho GTPase activ Mus musculus Rho	-0.688137356	11.21104891
12	A_51_P116906	Rapgef3		Rap guanine nucle Mus musculus Rap	-0.685272422	13.75316692
13	A_55_P2149951	Prx		periaxin Mus musculus peria	-0.684956015	10.13531086
14	A_51_P461108	Osbpl10		oxysterol binding Mus musculus oxys	-0.682059235	7.962313068
15	A_55_P2169311	4930515G01Rik		RIKEN cDNA 4930 Mus musculus RIKE	-0.681579817	6.703695122
16	A_51_P477019	Rnaset2a		ribonuclease T2A Mus musculus adul	-0.680902955	7.43885386
17	A_51_P394833	Tshz1		teashirt zinc finge Mus musculus teasl	-0.678681382	10.80255508
18	A_66_P106611	Gna14		guanine nucleotid Mus musculus guar	-0.677677589	8.386191975
19	A_55_P1956812	Fam83g		family with seque Mus musculus fami	-0.675928149	6.64692581
20	A_55_P1985410	Reps2		RALBP1 associater Mus musculus RALF	-0.674603957	8.042257813
21	A_51_P218953	Zfp536		zinc finger protein Mus musculus zinc	-0.674028528	10.56982114
22	A_55_P2060991	BC005764		cDNA sequence B Mus musculus cDN,	-0.66926502	7.535671867
23	A_51_P431870	Map1s		microtubule-asso Mus musculus micr	-0.667960126	12.34555259
24	A_55_P1984690	Ptprr		protein tyrosine p Mus musculus prot	-0.667881529	6.581299389
25	A_52_P434306		0	0 Q8NFW1_HUMAN	-0.667355779	9.649754062
26	A_55_P2031496	Rufy3		RUN and FYVE do Mus musculus RUN	-0.663256388	10.86869213
27	A_55_P2111148	Gemin5		gem (nuclear orga Mus musculus gem	-0.65688668	10.40659555
28	A_55_P2031692	Gstm6		glutathione S-tran Mus musculus gluta	-0.655180632	9.210465339
29	A_52_P348031	Syt9		synaptotagmin IX Mus musculus syna	-0.654460663	8.327190519
30	A_51_P327874	Pth1r		parathyroid horm Mus musculus para	-0.650364411	8.882151868
31	A_52_P640922	Dcdc2a		doublecortin dom Mus musculus douk	-0.649492628	7.587100373
32	A_55_P2045085	Rpl34-ps1		ribosomal protein Mus musculus ribos	-0.648502424	14.32799093
33	A_52_P1092823	Irx1		Iroquois related h Mus musculus Iroq1	-0.646761588	7.349592041
34	A_55_P2108820	Adamts3		a disintegrin-like Mus musculus adul	-0.638849777	6.65699864
35	A_55_P2014100	Gm7120		predicted gene 71 Mus musculus pred	-0.638107189	6.806996401
36	A_55_P1953103	Nudt7		nudix (nucleoside Mus musculus nudi	-0.637864703	10.25545194
37	A_55_P2064257	Dnaic2		dynein, axonemal Mus musculus dyne	-0.630274633	8.390636213
38	A_55_P1974487	Atp8b5		ATPase, class I, ty Mus musculus ATPa	-0.629303175	6.822180076
39	A_51_P223569	Ddx4		DEAD (Asp-Glu-Al Mus musculus DEAl	-0.62905002	6.622449063
40	A_66_P131169	LOC100862268		uncharacterized L Mus musculus uncl	-0.628680049	6.69161194
41	A_52_P338956	Aspg		asparaginase hom Mus musculus aspa	-0.628241548	10.06611532
42	A_51_P310164	2810459M11Rik		RIKEN cDNA 2810 Mus musculus RIKE	-0.626909774	11.89244788
43	A_55_P2028936	5033425G24Rik		RIKEN cDNA 5033 Mus musculus 11 d	-0.625547854	6.890613452
44	A_55_P2181009	Gpr180		G protein-coupled Mus musculus G pr	-0.624550444	6.798522375
45	A_55_P2417936	AW125324		expressed sequen mp78f05.y1 Soares	-0.623425317	7.849930106
46	A_51_P353392	Cript		cysteine-rich PDZ- Mus musculus cyste	-0.622867594	10.81794644
47	A_55_P2000533	Polk		polymerase (DNA Mus musculus poly	-0.622037502	9.398512501
48	A_52_P664404	Zfp286		zinc finger protein Mus musculus zinc	-0.622037367	10.36518427
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2	A_55_P2072656	Ckmt1	creatine kinase, m	Mus musculus crea	-0.61884061 11.75980585
3	A_55_P2137941	Fxyd2	FXYP domain-con	Mus musculus FXYP	-0.611672447 8.641529844
4	A_55_P2143251	Rims3	regulating synapti	regulating synaptic	-0.607351966 8.439466739
5	A_51_P253732	Il17rd	interleukin 17 rec	Mus musculus inter	-0.607331836 8.923142563
6	A_55_P2457154	G2e3	G2/M-phase speci	Mus musculus G2/M	-0.603883427 9.938832239
7	A_51_P101573	Klc4	kinesin light chain	Mus musculus kine	-0.601913768 11.14096031
8	A_55_P2167323	Cort	cortistatin	Mus musculus corti	-0.601224344 7.784270421
9	A_52_P257686	Rwdd3	RWD domain cont	Mus musculus RWD	-0.599845312 8.583303218
10	A_66_P111430	2410006H16Rik	RIKEN cDNA 2410	Mus musculus RIKE	-0.598883168 12.43387167
11	A_55_P1968858	Cadps	Ca ²⁺ -dependent s	Mus musculus Ca ²⁺	-0.594774845 9.341019473
12	A_52_P67270	4930515G01Rik	RIKEN cDNA 4930	Mus musculus RIKE	-0.593215762 6.518906201
13	A_55_P1970299	Mttp	microsomal triglyc	Mus musculus micr	-0.5865943 8.981610299
14	A_55_P2061371	Gm15698	transcription elon	Mus musculus pred	-0.584142169 7.129086897
15	A_55_P2131340	Churc1	churchill domain c	Mus musculus chur	-0.583044972 11.95122776
16	A_51_P421223	Fv1	Friend virus susce	Mus musculus Frier	-0.581308579 6.783421774
17	A_51_P465273	Mettl17	methyltransferase	Mus musculus metl	-0.579305966 8.739388881
18	A_52_P367675	Acin1	apoptotic chroma	Mus musculus apo	-0.579116752 9.293635462
19	A_55_P2019113	Apol7b	apolipoprotein L 7	Mus musculus apol	-0.572998316 8.668444439
20	A_55_P1968908	Hypk	huntingtin interac	Mus musculus hunt	-0.572592964 11.62842225
21	A_51_P151586	Gsg2	germ cell-specific	Mus musculus gern	-0.57106147 8.077335091
22	A_55_P2084332	Pigp	phosphatidylinosi	Mus musculus phos	-0.569703885 8.212483905
23	A_55_P1971174	Cd1d2	CD1d2 antigen	Mus musculus CD1	-0.567292844 7.798990811
24	A_55_P2227580	A130072N09Rik	RIKEN cDNA A130	Mus musculus 16 d	-0.559844118 6.673560482
25	A_55_P2223282	B130019D13Rik	RIKEN cDNA B130	Mus musculus 9.5 c	-0.558378263 7.195029296
26	A_51_P230439	Ppfbp2	PTPRF interacting	Mus musculus PTPF	-0.55630513 10.34894026
27	A_52_P211418	G2e3	G2/M-phase speci	Mus musculus G2/M	-0.554271362 7.792367244
28	A_52_P357055	Ccdc91	coiled-coil domair	Mus musculus coile	-0.553942714 7.770909696
29	A_55_P1968200	Hjurp	Holliday junction r	Mus musculus Holli	-0.55155621 7.033226409
30	A_55_P2007273	Pole	polymerase (DNA	Mus musculus poly	-0.550291814 10.13382839
31	A_55_P2137701	Gm13247	predicted gene 13	Mus musculus pred	-0.546813814 7.656052718
32	A_55_P2000304	Terf1	telomeric repeat t	Mus musculus telor	-0.546075343 9.872026358
33	A_51_P192139	Zfp74	zinc finger protein	Mus musculus ES c	-0.539117791 6.409237197
34	A_66_P128445	Bend7	BEN domain cont	BEN domain contain	-0.538424509 7.861391583
35	A_66_P122699	Cux2	cut-like homeobo	cut-like homeobox	-0.53739685 7.345768936
36	A_55_P1998872	Slitrk5	SLIT and NTRK-like	Mus musculus SLIT	-0.535909484 8.610305633
37	A_52_P71105	Sertad3	SERTA domain cor	Mus musculus SERT	-0.532389964 9.861783381
38	A_55_P2008936	Slc2a9	solute carrier fam	Mus musculus solut	-0.532021351 7.214637148
39	A_51_P116487	Lsm4	LSM4 homolog, U	Mus musculus LSM	-0.530560598 13.57404857
40	A_55_P2106235	Syngn2	synaptogyrin 2	Mus musculus syna	-0.529964886 13.79897881
41	A_66_P126415	Gm8013	predicted gene 80	PREDICTED: Mus m	-0.528496734 6.685350041
42	A_52_P343627	Rbp7	retinol binding pr	Mus musculus retin	-0.528055686 6.853990708
43	A_51_P437478	Zfp566	zinc finger protein	Mus musculus zinc	-0.525914817 9.49558264
44	A_55_P2053497	Poli	polymerase (DNA	Mus musculus poly	-0.523897824 11.47795665
45	A_55_P2097340	Camkv	CaM kinase-like v	Mus musculus CaM	-0.523781288 7.664345723
46	A_51_P468762	Alkbh6	alkB, alkylation re	Mus musculus alkB	-0.523356552 12.08819889
47	A_51_P298802	Bfsp2	beaded filament s	Mus musculus beac	-0.522173308 7.956404228
48	A_55_P2057127	Nim1k	NIM1 serine/thre	Mus musculus NIM	-0.521263457 6.49076766
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2	A_55_P2145139		0	0 predicted gene 106	-0.517379933	6.649375349
3	A_55_P2143075	Ubc		ubiquitin C Mus musculus ubiq	-0.515250808	16.61461059
4	A_51_P240801	Tmem173		transmembrane p Mus musculus tran:	-0.513561067	9.911571688
5	A_55_P2007919	Akr1c19		aldo-keto reducta Mus musculus aldo	-0.512737911	6.304006357
6	A_51_P331827	Slc25a41		solute carrier fam Mus musculus solut	-0.509338122	6.456710962
7	A_55_P1975832	1810009N02Rik		RIKEN cDNA 1810 Mus musculus RIKE	-0.506346906	10.81241498
8	A_55_P1961241	LOC102634598		uncharacterized L PREDICTED: Mus m	-0.503420231	9.192490397
9	A_55_P2123831	Thap6		THAP domain con Mus musculus THAI	-0.50292242	9.608058208
10	A_55_P1968245	Ftl1		ferritin light chain Mus musculus ferri	-0.502896156	17.27428723
11	A_55_P2037812	Palmd		palmdelphin Mus musculus palr	-0.502660256	7.526994087
12	A_55_P1974233	Dtd2		D-tyrosyl-tRNA de Mus musculus D-ty	-0.498511647	8.995692324
13	A_55_P2045096	Hjulp		Holliday junction r Mus musculus Holli	-0.496971605	6.68312203
14	A_55_P2067513	Slc10a3		solute carrier fam Mus musculus solut	-0.495867287	10.35448148
15	A_55_P2021892	Ccdc114		coiled-coil domair Mus musculus 3 da	-0.495838288	8.738892753
16	A_51_P382369	Zfp608		zinc finger protein Mus musculus zinc	-0.493057428	10.15897212
17	A_55_P2077263	Cenpk		centromere prote Mus musculus cent	-0.491159912	9.796181967
18	A_55_P2018847	Crif2		cytokine receptor Mus musculus cyto	-0.487538832	12.22311955
19	A_55_P1991500	Obfc1		oligonucleotide/o Mus musculus oligc	-0.48748131	11.17769638
20	A_51_P487547	Ccdc91		coiled-coil domair Mus musculus coile	-0.486825904	11.34420614
21	A_55_P2032318	4930522L14Rik		RIKEN cDNA 4930 Mus musculus adul	-0.486588132	7.441660797
22	A_52_P640386	Usp53		ubiquitin specific j Mus musculus ubiq	-0.481768787	7.753841713
23	A_66_P137383	Ddx55		DEAD (Asp-Glu-Al; Mus musculus DEAI	-0.481484634	7.7673737
24	A_51_P341789	Sugp1		SURP and G patch Mus musculus SURI	-0.480862132	12.83928633
25	A_51_P302942	Ras10a		RAS-like, family 1(Mus musculus RAS-	-0.479764409	7.097069326
26	A_66_P133993	Gm5093		predicted gene 50 PREDICTED: Mus m	-0.478687639	7.624410673
27	A_66_P128927	Gm6306		predicted gene 63 PREDICTED: Mus m	-0.473064458	7.780634724
28	A_55_P1963687	Tsen54		tRNA splicing endi Mus musculus tRNA	-0.472348364	12.43909794
29	A_55_P2049448	Phtf1		putative homeodc Mus musculus puta	-0.467956686	11.76027675
30	A_55_P2153496	Ppp2r3d		protein phosphat: Mus musculus prot	-0.464874953	7.113971128
31	A_51_P245546	Synrg		synergyn, gamma Mus musculus syne	-0.463458339	10.42186201
32	A_55_P1967500	Nell1		NEL-like 1 Mus musculus NEL-	-0.461407325	6.769094052
33	A_51_P216605	Hbp1		high mobility grou Mus musculus high	-0.460215485	8.599211577
34	A_55_P2157902	Igsf10		immunoglobulin s Mus musculus imm	-0.457935852	8.96305814
35	A_51_P239286	Bcl2l12		BCL2-like 12 (proli Mus musculus BCL2	-0.45634682	9.648729447
36	A_55_P2157360	Tagap1		T cell activation G Mus musculus T cel	-0.456021568	8.846243503
37	A_55_P2308743	A430106A12Rik		RIKEN cDNA A430 Mus musculus adul	-0.455161398	7.933766962
38	A_55_P2115225	Fap		fibroblast activati Mus musculus fibrc	-0.452820717	6.722753058
39	A_52_P327402	Cds1		CDP-diacylglycero Mus musculus CDP-	-0.451307076	6.871725015
40	A_55_P2039061	Trim12c		tripartite motif-co Mus musculus tripa	-0.448747311	8.022101966
41	A_55_P2051313	Gstk1		glutathione S-tran Mus musculus glut:	-0.447816462	11.34736659
42	A_52_P434841	Coa4		cytochrome c oxic Mus musculus cyto	-0.446903622	9.46071069
43	A_51_P291682	Tmed4		transmembrane e Mus musculus tran:	-0.443998054	10.73423118
44	A_55_P2013203	Oxtr		oxytocin receptor Mus musculus oxyt	-0.442780027	8.023385113
45	A_55_P2000027	Spink2		serine peptidase i Mus musculus serir	-0.442537681	6.96804014
46	A_52_P734742	Lrrc73		leucine rich repea Mus musculus leuci	-0.442136942	8.936830228
47	A_55_P2003951	Tmem192		transmembrane p Mus musculus tran:	-0.440106598	12.66518165
48	A_55_P2032147	Wnt9a		wingless-type MV Mus musculus wing	-0.439482762	10.92706414
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2	A_55_P1977454	4930570G19Rik	RIKEN cDNA 4930 Mus musculus RIKE	-0.435903908	7.161056162
3	A_55_P2011692		0 0 Mus musculus 12 d	-0.434179405	8.677359589
4	A_52_P73559	Gm7241	predicted pseudo; PREDICTED: Mus m	-0.430169066	9.586233165
5	A_52_P673499	Shmt1	serine hydroxyme Mus musculus serir	-0.430087668	7.142456297
6	A_55_P2025514	Pnpla3	patatin-like phosph Mus musculus pata	-0.428814069	6.700148086
7	A_51_P122141	Mamstr	MEF2 activating r Mus musculus MEF	-0.427829791	6.52676216
8	A_55_P2074291	Fbxo6	F-box protein 6 Mus musculus F-bo	-0.425180806	13.84031149
9	A_52_P448870	Rab26	RAB26, member R Mus musculus RAB	-0.424956589	8.087186472
10	A_51_P348652	Spast	spastin Mus musculus spas	-0.424725762	12.20201077
11	A_55_P1970676	Sh3yl1	Sh3 domain YSC-li Mus musculus Sh3	-0.424228425	9.598710633
12	A_55_P2027152	Ssh1	slingshot homolog Mus musculus sling	-0.422795069	6.834679035
13	A_55_P2330545	Zfp81	zinc finger protein zinc finger protein	-0.422072903	8.529420477
14	A_55_P1981461	5430410E06Rik	RIKEN cDNA 5430 Mus musculus 6 da	-0.420509947	6.602185969
15	A_55_P2183597	Tbc1d2	TBC1 domain fam Mus musculus TBC1	-0.420158886	10.38577948
16	A_55_P1974477	Msh3	mutS homolog 3 (Mus musculus mut!	-0.420019862	10.7021489
17	A_55_P2153797	Prnp	prion protein Mus musculus prior	-0.416155848	10.31468171
18	A_51_P372156	4930563E22Rik	RIKEN cDNA 4930 Mus musculus RIKE	-0.411011206	7.679272315
19	A_55_P2109585	Plekha7	pleckstrin homolo Mus musculus plecl	-0.40841751	10.278925
20	A_55_P2167898	Nat9	N-acetyltransfera; Mus musculus N-ac	-0.407279096	7.689265574
21	A_55_P2471798	Snap23	synaptosomal-ass synaptosomal-asso	-0.407062662	10.13514035
22	A_52_P179729	Txn14a	thioredoxin-like 4 Mus musculus thior	-0.406120836	12.55293121
23	A_52_P595642	Smim7	small integral mer Mus musculus smal	-0.406112892	10.50763342
24	A_51_P517001	D130040H23Rik	RIKEN cDNA D130 Mus musculus RIKE	-0.400511742	6.338211044
25	A_52_P409457	Ppcdc	phosphopantothe Mus musculus phos	-0.398509715	6.177407482
26	A_55_P2069012	Pidd1	p53 induced deatl leucine-rich and de	-0.397772469	9.97175954
27	A_52_P108321	Ccdc71	coiled-coil domair Mus musculus coile	-0.396032959	8.637270977
28	A_55_P2104572	6330416G13Rik	RIKEN cDNA 6330 Mus musculus RIKE	-0.394704756	8.641996503
29	A_52_P552589	Map4k1	mitogen-activatec Mus musculus mito	-0.3923582	8.471880485
30	A_52_P561377	Fam160b1	family with seque Mus musculus fami	-0.38798432	12.37367207
31	A_55_P2057941	1700049G17Rik	RIKEN cDNA 1700 Mus musculus RIKE	-0.383331981	7.964018539
32	A_55_P2088711	Sgsm1	small G protein sig Mus musculus smal	-0.3821107	6.60586313
33	A_51_P456838	Fbxl21	F-box and leucine Mus musculus F-bo	-0.379835667	6.874468646
34	A_51_P167374	Gpatch1	G patch domain c; Mus musculus G pa	-0.37911143	9.9860935
35	A_55_P1967983	Use1	unconventional S; Mus musculus uncc	-0.3789746	13.46950848
36	A_52_P47781	Slitrk3	SLIT and NTRK-like Mus musculus SLIT	-0.376113158	6.396932242
37	A_55_P2175915	Ccl28	chemokine (C-C m Mus musculus cher	-0.374930748	6.151763833
38	A_51_P234627	Nubpl	nucleotide binding; Mus musculus nucl	-0.373125451	10.36569262
39	A_51_P241943	Sap30l	SAP30-like Mus musculus SAP	-0.373063734	14.28047258
40	A_51_P246677	Rec8	REC8 meiotic reco Mus musculus REC	-0.367071601	8.342925093
41	A_52_P275678	Gpr135	G protein-couplec Mus musculus G pr	-0.36573505	6.810300528
42	A_51_P421140	Tubb6	tubulin, beta 6 cla Mus musculus tubu	-0.364131056	14.78805775
43	A_51_P268843	Rasip1	Ras interacting pr; Mus musculus Ras i	-0.361460853	6.858814738
44	A_55_P1956418	Efr3b	EFR3 homolog B (; Mus musculus EFR	-0.360229036	9.792465029
45	A_51_P184223	Pcdhb7	protocadherin bet Mus musculus prot	-0.356613104	7.918822651
46	A_52_P117576	Casp3	caspase 3 Mus musculus casp	-0.351742878	8.091329134
47	A_55_P2044967	Zfp74	zinc finger protein PREDICTED: Mus m	-0.350202078	6.389182029
48	A_51_P131025	Ngdn	neuroguidin, EIF4I Mus musculus neur	-0.340262798	13.42970696
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2	A_55_P2067131	Dclre1c	DNA cross-link re	Mus musculus DNA	-0.338402188 6.315412162
3	A_55_P2027077	Shc2	SHC (Src homolog	Mus musculus SHC	-0.33820507 7.375840756
4	A_55_P2026054	Usp37	ubiquitin specific	Mus musculus ubiq	-0.333676116 6.919608859
5	A_55_P2012096	Bmp8a	bone morphogen	Mus musculus bone	-0.330118616 7.33400305
6	A_55_P2143499	Pgbd5	piggyBac transpos	Mus musculus piggy	-0.32667779 6.992213644
7	A_55_P1999829	Thoc7	THO complex 7 hc	Mus musculus THO	-0.324738732 13.25310654
8	A_51_P244558	Rab3gap2	RAB3 GTPase acti	Mus musculus RAB3	-0.320028198 11.01221532
9	A_55_P2002113	Rpl36	ribosomal protein	Mus musculus ribos	-0.308280506 16.65947439
10	A_51_P289414	Spg11	spastic paraplegia	Mus musculus spas	-0.306241068 11.47302291
11	A_52_P133578	Gpr158	G protein-coupled	Mus musculus G pr	-0.302885456 6.416264013
12	A_66_P130612	2810408A11Rik	RIKEN cDNA 2810	Mus musculus RIKE	-0.30270723 7.686468818
13	A_51_P208377	Trappc5	trafficking protein	Mus musculus traff	-0.297651608 13.16186953
14	A_55_P2177233	Abhd5	abhydrolase dom	Mus musculus abhy	-0.276226719 9.274185661
15	A_55_P1968683	Anks1b	ankyrin repeat an	Mus musculus anky	-0.275841965 6.319708996
16	A_51_P288505	Tradd	TNFRSF1A-associa	Mus musculus TNFI	-0.27415141 11.49981129
17	A_51_P133747	Ppp1r3e	protein phosphat	Mus musculus prot	-0.272996573 6.29524283
18	A_51_P476711	Skiv2l2	superkiller viralici	Mus musculus supe	-0.270984564 11.41603014
19	A_55_P2041372	Gm3693	predicted gene 36	PREDICTED: Mus m	-0.2646902 6.199455621
20	A_51_P242356	Fam114a2	family with seque	Mus musculus fami	-0.262671874 12.80714837
21	A_51_P146303	Mvb12a	multivesicular boc	Mus musculus mult	-0.260071046 12.17524294
22	A_55_P1960621	Gm20764	predicted gene, 2l	PREDICTED: Mus m	-0.258454404 15.49930838
23	A_51_P107433	Mrpl34	mitochondrial ribc	Mus musculus mito	-0.248200928 12.30902572
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	adj.P.Val	Orre-Log_FC	Orre-adj.P.Val
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3	1.65288E-09	1.142724869	0.160126428
4	1.68799E-16	1.678279674	0.148286687
5	0.00111415	0.276521938	0.856285005
6	3.4835E-12	0.849713018	0.247609338
7	9.75281E-16	0.065397702	0.920220832
8	8.73791E-16	0.032101359	0.971052049
9	4.37739E-06	1.601979349	0.136939403
10	4.62079E-09	-1.246342593	0.095148351
11	1.53107E-11	-0.4348927	0.346208983
12	1.19839E-16	-0.29463285	0.553202296
13	2.76734E-14	-0.227918918	0.76436986
14	5.32555E-10	-0.565335125	0.64712269
15	1.10279E-05	0.963523397	0.221847465
16	0.00086345	0.372087289	0.620916602
17	0.022418234	1.275249124	0.081367361
18	2.19306E-10	-0.399166545	0.510246289
19	1.9464E-13	-0.671109095	0.1423435
20	0.003448159	0.710352137	0.080953995
21	2.85216E-06	-1.037247785	0.050508329
22	0.000396451	1.606931711	0.058847733
23	4.87063E-05	0.057324928	0.930977484
24	0.016968618	0.665876263	0.227829936
25	0.005579854	0.288125691	0.591016158
26	1.20027E-10	0.852487476	0.203223242
27	1.00373E-08	0.87696271	0.228263976
28	8.90582E-07	0.177948445	0.737984738
29	0.032298961	0.680503994	0.232991983
30	1.47938E-09	-0.612991048	0.078478102
31	1.12499E-07	0.619121571	0.164250851
32	5.03003E-15	0.191531928	0.600619589
33	0.030428182	-0.154790328	0.854360891
34	0.000514259	-0.421653429	0.122025146
35	0.004381404	0.725679062	0.37780821
36	8.03792E-08	0.147025135	0.90705714
37	0.003583798	0.9132766	0.171140015
38	0.001739455	-0.273496341	0.863827852
39	6.69066E-07	-0.091756023	0.893142157
40	3.00086E-06	-1.012174185	0.25474915
41	4.59997E-05	-0.757915491	0.066325331
42	1.17782E-08	-0.353650207	0.70042947
43	0.001772617	-0.112859725	0.962512328
44	0.029882996	0.594754598	0.427097363
45	8.79673E-09	-0.265966628	0.529308318
46	1.10279E-05	-0.675059016	0.223691543
47	1.11591E-09	0.421854979	0.289475858
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2	0.009286241	-0.295782195	0.686189715
3	0.011447725	-0.305899627	0.691832878
4	2.57183E-07	-0.613424673	0.283946905
5	0.000124631	-1.584282679	0.053011793
6	1.02537E-05	0.628280133	0.408457847
7	0.030972985	-0.559354504	0.187239299
8	0.02720596	-1.230463843	0.186703471
9	0.004452627	0.051163701	0.969437555
10	0.026361683	0.545463528	0.417027811
11	3.1151E-07	-0.364747065	0.56625963
12	4.60298E-08	0.662787674	0.052881943
13	8.90883E-09	-0.14863164	0.756692535
14	0.000380425	0.088500281	0.969964566
15	2.95281E-10	-0.526342386	0.511302615
16	2.0813E-07	0.044819377	0.953255298
17	1.23069E-07	-0.071202692	0.882404727
18	0.004785393	-0.403521443	0.091993005
19	1.29869E-07	0.04377789	0.9628957
20	1.87675E-06	-0.11163067	0.888541003
21	0.038078984	-0.360765364	0.681260954
22	9.48239E-05	-0.502842706	0.160623939
23	0.006661276	-0.528933679	0.707697644
24	1.24605E-05	0.616650301	0.144912553
25	0.000338177	-0.570124245	0.474083165
26	8.64891E-08	0.27076903	0.802552215
27	6.28876E-05	-0.539482757	0.457925459
28	0.000177844	-0.083079696	0.925518302
29	6.73139E-05	-0.346003991	0.778235249
30	8.02961E-12	-0.265245317	0.354709911
31	1.13328E-08	0.295428837	0.90816598
32	1.12499E-07	0.03003259	0.973326255
33	2.22782E-06	-0.093002614	0.949245873
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35	8.8279E-07	-0.026648062	0.964173244
36	2.82752E-06	0.416415697	0.24076864
37	3.56596E-07	0.113710815	0.932303384
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39	2.89973E-05	0.21152987	0.456262298
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46	0.000989719	0.181901546	0.865463843
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5	0.00045366	0.269147757	0.620916602
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7	0.029919663	-0.801326888	0.221233965
8	8.1122E-08	0.327987134	0.529096273
9	0.021399671	0.212515961	0.816645104
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22	4.0172E-06	0.868287968	0.462835421
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25	0.000797786	-0.251777072	0.876023417
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39	0.031178225	-0.327333102	0.250189628
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42	0.025807202	0.476032164	0.361728506
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18	0.024400901	0.269695413	0.588960812
19	0.013472871	0.988885315	0.446051422
20	0.046805456	0.293560558	0.28906354
21	0.032215926	-0.112124245	0.783414487
22	0.019807083	0.480621118	0.086088543
23	0.026179106	-0.45390268	0.134324512
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	ProbeName	GeneSymbol	GeneName	Description	logFC	AveExpr
1						
2						
3	A_51_P259296	Lpl	lipoprotein lipase	Mus musculus lipoproc	-1.961023445	10.53863681
4	A_55_P1978465	H2-Q5	histocompatibility 2	Mus musculus histococ	-1.663988464	9.535892008
5	A_55_P2096867	Gap43	growth associated p	Mus musculus growth	-1.608736505	10.06212415
6	A_51_P292357	Rps3a1	ribosomal protein S	Mus musculus riboso	-1.46036708	14.50307495
7	A_51_P382970	Itga9	integrin alpha 9	Mus musculus integri	-1.351976919	8.757361984
8	A_55_P2116650		0	0 Mus musculus lung R	-1.10377111	8.828398051
9						
10	A_55_P1960735	Gdf15	growth differentiat	Mus musculus growth	-1.088687615	10.28319672
11	A_55_P2106459	Zfxh3	zinc finger homeobc	Mus musculus zinc fir	-1.010052712	8.340668201
12	A_51_P369803	Psmb9	proteasome (prosor	Mus musculus protea	-0.963065252	10.67436193
13	A_55_P2001628	Rps4l	ribosomal protein S	Mus musculus riboso	-0.939220016	12.10141308
14	A_51_P464308	Gnb4	guanine nucleotide	Mus musculus guanin	-0.9391572	8.637065817
15	A_55_P2052834	Lst1	leukocyte specific tr	Mus musculus leukoc	-0.935420349	9.52643648
16	A_52_P463977	Tmem140	transmembrane pro	Mus musculus transnr	-0.919020928	9.96346538
17	A_55_P2163774	Crip1	cysteine-rich proteir	Mus musculus cysteir	-0.915395828	12.97283366
18	A_51_P191782	Olfml3	olfactomedin-like 3	Mus musculus olfactc	-0.914211713	8.602884528
19	A_51_P135340	Panx1	pannexin 1	Mus musculus panne	-0.89971548	10.51056148
20	A_55_P2000973	Syt15	synaptotagmin XV	Mus musculus synapt	-0.899192384	6.884006593
21	A_55_P2004960	9130017K11Rik	RIKEN cDNA 913001	Mus musculus 10, 11	-0.852685098	7.532819994
22	A_52_P489295	Adamts1	a disintegrin-like an	Mus musculus a disin	-0.827379384	12.74595804
23	A_66_P112024		0	0 predicted gene 6816	-0.70174101	11.68203967
24	A_51_P414126	Rab19	RAB19, member RA	Mus musculus RAB19	-0.609561157	8.039804732
25	A_51_P455807	Ehd4	EH-domain containi	Mus musculus EH-doi	-0.606539442	11.96303719
26	A_55_P2035951	Haus8	4HAUS augmin-like	Mus musculus 4HAUS	-0.604556892	12.67961674
27	A_55_P2121846		0	0 ribosomal protein S3	-0.593846476	16.01148154
28	A_52_P593037	Acsl5	acyl-CoA synthetase	Mus musculus acyl-Co	-0.535221942	9.966696844
29	A_52_P472302	Fxyd6	FXYP domain-contai	Mus musculus FXYP c	-0.531319508	15.21101819
30	A_51_P469968	H2-M3	histocompatibility 2	Mus musculus histococ	-0.519228813	8.643048954
31	A_51_P105520	Nomo1	nodal modulator 1	Mus musculus nodal	-0.452860024	13.6108246
32	A_55_P2079009	Slco2b1	solute carrier organi	Mus musculus solute	-0.433713878	6.892808091
33	A_55_P1992160	Mbp	myelin basic proteir	Mus musculus myelin	-0.413993257	6.478592337
34	A_55_P2056186	Siva1	SIVA1, apoptosis-inc	Mus musculus SIVA1,	-0.380111236	12.3637751
35	A_55_P2058953	Rpl13a	ribosomal protein L	Mus musculus riboso	-0.330979256	15.77584397
36	A_55_P2041893	Gm6404	predicted gene 640	PREDICTED: Mus mus	-0.31280088	15.50642516
37	A_55_P2071326	Rpl36	ribosomal protein L	Mus musculus riboso	-0.285050556	15.50237923
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	adj.P.Val	Orre-Log_FC	Orre-adj.P.Val
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3	0.002138263	2.300310172	0.020588553
4	0.005659542	1.095400427	0.010853939
5	0.002286646	1.534549449	0.020310107
6			
7	1.30E-07	1.159248599	0.022479083
8	9.24E-09	1.432290312	0.030984266
9	0.002824029	1.103008775	0.035505379
10			
11	0.00234358	1.475890823	0.029959263
12	6.68E-05	1.571058738	0.04406641
13	0.021316806	1.195568717	0.009768585
14	0.000466592	0.7724143	0.022479083
15	0.003570734	1.462830423	0.043323509
16	0.008269886	0.855486614	0.014706557
17	0.006768385	1.194912543	0.01368295
18	0.013328699	1.479869423	0.020679583
19	0.005752664	1.314593295	0.015213125
20	0.024043042	0.703522655	0.011848366
21			
22	7.61E-05	1.206623188	0.042870119
23	0.002774688	0.863387317	0.010153149
24	0.002352939	1.18883491	0.028313328
25	0.015404752	0.843857777	0.009585061
26	0.007993662	0.975357457	0.021980244
27	0.032697401	1.880255118	0.001780435
28	0.011775353	0.850035903	0.023924257
29	0.01463281	1.09546824	0.001887175
30	0.011511499	1.283903087	0.006122076
31	0.04119468	1.031697808	0.026852476
32	0.008188084	0.786736671	0.027384624
33	0.017975634	0.690060618	0.005963268
34	0.01463281	1.097696112	0.023980247
35	0.00429445	1.146770973	0.004021838
36	0.010471067	0.943997477	0.013463823
37	0.008188084	0.85748709	0.002800163
38	0.028012031	0.758588	0.015596586
39	0.001807237	0.72597553	0.008348755
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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	NDUF7, !
GOTERM_MF_DIRECT	GO:0016740~transferase activ	67	0.002022	STK38, DP
UP_KEYWORDS	ATP-binding	59	0.002958	STK38, NAF
UP_KEYWORDS	Mitochondrion	51	6.38E-04	NDUF7, !
GOTERM_CC_DIRECT	GO:0042995~cell projection	39	7.83E-04	LZTS1, SSH
UP_KEYWORDS	Cell projection	37	4.93E-04	LZTS1, CRIF
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-associate	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, KC
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 associ	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
1					
2					
3	UP_KEYWORDS	Membrane	19	0.008025	9130017K1
4	GOTERM_CC_DIRECT	GO:0005730~nucleolus	6	0.007182	RPL13A, RP
5	UP_KEYWORDS	Ribosomal protein	4	0.002175	RPL13A, RP
6	GOTERM_MF_DIRECT	GO:0003735~structural constituent of ribosome	4	0.00485	RPL13A, RP
7	UP_KEYWORDS	Ribonucleoprotein	4	0.006979	RPL13A, RP
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For Review Only

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

For Review Only

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

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

Supplementary table 10. Comparison with human AD dataset

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