Intermittent Hypoxia Mobilizes Bone Marrow-Derived Very Small Embryonic-Like Stem Cells and Activates Developmental Transcriptional Programs in Mice

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Background: Obstructive sleep apnea is a prevalent disorder associated with cognitive dysfunction and cardiovascular and metabolic morbidity and is characterized by recurrent episodes of hypoxia during sleep. Bone marrow-derived very small embryonic-like (VSEL) pluripotent stem cells represent a recruitable pool that may play an important role in organ repair after injury. We hypothesized that exposure to intermittent hypoxia (IH) can mobilize VSELs from the bone marrow (BM) to peripheral blood (PB) in mice and can activate distinct transcriptional programs.

Methods: Adult mice were exposed to IH or normoxia for 48 hours. VSELs were sorted from BM and PB using flow cytometry. Plasma levels of stem cell chemokines, stromal cell derived factor-1 (SDF-1), hepatocyte growth factor (HGF), and leukemia inhibitory factor (LIF) were measured. Transcriptional profiling of VSELs was performed, and differentially expressed genes were mapped to enriched functional categories and genetic networks.

Results: Exposure to IH elicited migration of VSELs from BM to PB and elevations in plasma levels of chemokines. More than 1100 unique genes were differentially expressed in VSELs in response to IH. Gene Ontology and network analysis revealed the activation of organ-specific developmental programs among these genes.

Conclusions: Exposure to IH mobilizes VSELs from the BM to PB and activates distinct transcriptional programs in VSELs that are enriched in developmental pathways, including central nervous system development and angiogenesis. Thus, VSELs may serve as a reserve mobile pool of pluripotent stem cells that can be recruited into PB and may play an important role in promoting end-organ repair during IH.

Keywords: Stem cells, sleep apnea, intermittent hypoxia

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OBSTRUCTIVE SLEEP APNEA (OSA) IS A PREVALENT DISORDER IN CHILDREN[1] AND ADULTS[2,3] AND IS CHARACTERIZED BY THE OCCURRENCE OF repetitive episodes of airflow obstruction during sleep, leading to intermittent hypoxia (IH) and reoxygenation.[4] The morbid consequences of OSA are substantial and include cardiovascular, neurocognitive, and metabolic dysfunction.[5-11] For example, patients with OSA exhibit substantial memory and executive functional losses, have increased circulating markers of oxidative stress and inflammation, and develop regional gray matter loss.[12-14] In children, sleep apnea is associated with significant neurocognitive abnormalities, including attention deficits and poor school performance.[15]

Exposure to IH has now been widely used to model sleep apnea in animals,[16,17] and, while such model does not mimic all aspects of OSA, it recapitulates many of the pathophysiologic sequelae of OSA in humans, such as increased oxidative stress, hypertension and endothelial dysfunction, insulin resistance, and cognitive deficits.[18-22] To more closely approximate human

OSA, we and others have developed mouse models in which exposure to IH is applied only during periods of sleep and removed upon either arousal or wakefulness.[17,23-25] However, although recurrent hypoxia during sleep is a key characteristic of OSA, the molecular mechanisms by which IH promotes end-organ injury and, importantly, the responses mounted by the host to mitigate this effect remain poorly understood.

Accumulating evidence suggests that pluripotent stem cells residing in the bone marrow (BM) play an important role in the homeostasis and turnover of peripheral tissues and can be mobilized from the BM into the circulation during tissue injury and stress.[26-30] Recruitment of BM-derived stem-cell niches have been proposed as a major endogenous source for facilitation of structural and functional recovery, as well as promotion of the regeneration of damaged organs.[31,32] Ratajczak et al.[33] have recently identified a homogenous population of rare, small (~3.7 µm) pluripotent stem cells residing in murine BM that express cellular markers characteristic for embryonic lineage and have shown that such stem cells can differentiate into lineage-committed cells from all 3 germ layers. Indeed, Sca-1+ Lin− CD45− very small embryonic-like stem cells (VSELs) can be mobilized from the BM to peripheral blood (PB) in response to specific chemokine gradients, including stromal cell–derived factor-1 (SDF-1), hepatocyte growth factor (HGF), and leukemia inhibitory factor (LIF).[33,34] We have previously reported on the recruitment of VSELs from BM to PB following tissue-specific injury, including stroke[30,35] and myocardial infarction.[27,29] In the present study, we hypothesized that mice

exposed to IH will increase plasma levels of stem cell–specific chemoattractants and mobilize BM-derived VSELs into the PB. Furthermore, since these pluripotent stem cells possess the ability to differentiate into any cell type, we performed gene expression profiling to systematically map the transcriptional architecture of activated programs within VSELs in response to IH.

MATERIALS AND METHODS

Animals

Adult male mice (2 months old), C57BL/J6, were purchased from Jackson Laboratory (Jackson Laboratory, Bar Harbor, ME). All animal experiments were performed according to protocols approved by Institutional Animal Care and Use Committee of the University of Louisville and complied with the American Physiological Society Guidelines for Animal Studies.

Exposure to IH

Mice were placed in 4 identical commercially designed chambers (30 × 20 × 20 in.; Oxycycler model A44XO; Biospherix, Redfield, NY) that were operated under a 12-hour:12-hour light-dark cycle (07:00 -19:00) for 48 hours. Gas was circulated around each of the chambers, attached tubing, and other units at 60 L/min (i.e., 1 complete change/10 s). The O_2 concentration was measured continuously by an O_2 analyzer and was changed using a computerized system controlling the gas valve outlets such that the moment-to-moment desired O_2 concentration of the chamber was programmed and adjusted automatically. Deviations from the desired concentration were met by addition of N_2 or O_2 through solenoid valves. Ambient CO_2 in the chamber was monitored periodically and maintained at less than 0.01% by adjusting overall chamber basal ventilation. Humidity was measured and maintained at 40% to 50% by circulating the gas through a freezer and silica gel. Ambient temperature was kept at 22°C to 24°C.

The IH profile consisted of alternating 21.0% and 5.7% O_2 every 180 seconds for the 12-hour light period. Such a profile is associated with reproducible nadir oxyhemoglobin saturations in the 73% to 77% range. Control animals were exposed to circulating room air in 1 of the chambers. Animals were exposed to IH or normoxia for a period of 48 hours and sacrificed immediately after exposure.

Measurement of Plasma Chemokines

Stromal cell–derived factor-1 (SDF-1), hepatocyte growth factor (HGF), and leukemia inhibitory factor (LIF) levels were measured using commercially available ELISA kits according to the manufacturer's instructions (R&D Systems, Minneapolis, MN). For each exposure condition, i.e., IH and normoxia, 30 independent measurements were performed. For each of these measurements, plasma was pooled from 3 to 4 mice. The SDF-1 assay had a sensitivity of 40 pg/mL and is linear between 100 and 20,000 pg/mL. The interassay and intraassay of coefficients of variability were 3.9% and 7.1%, respectively. The HGF assay had a sensitivity of 55 pg/mL and is linear between 60 and 15,000 pg/mL. The interassay and intraassay of coefficients of variability were 7.7% and 7.1%, respectively. The LIF had a sensitivity of 18 pg/mL and was linear between 20 and 2000 pg/

mL. In our experiments, the interassay and intraassay of coefficients of variability were 6.8% and 4.1%, respectively.

Statistical Analysis

Comparison of chemokine levels and VSEL counts between IH and normoxia were performed using unpaired, 2-tailed student t-tests, with P values adjusted for unequal variances when appropriate (GraphPad Prism version 5, San Diego CA). Values are reported as mean ± standard error of mean (SEM).

Isolation of VSEL stem cells from BM and PB

VSELs were sorted from a full population of murine BM cells and PB mononuclear cells using multicolor fluorescence-activated cell sorting (FACS), as we have previously described.[26,33] Briefly, mouse BM mononuclear cells were flushed from tibias and femurs, and erythrocytes were removed by a hypotonic solution (Pharm Lyse Buffer; BD Pharmingen, San Jose, CA). Cells were resuspended for staining in medium, containing 2% heat-inactivated FBS (GIBCO). The following rat antimouse antibodies (BD Pharmingen) were employed to detect Sca-1^{+} Lin^{–} CD45^{–} VSEL-SC: anti-CD45 (APC-Cy7; clone 30-F11), anti-Ly-6A/E (Sca-1) (biotin; clone E13-161.7, with streptavidin conjugated with PE-Cy5), "lineage cocktail", including anti-CD45R/B220 (PE; clone RA3-6B2), anti-Gr-1 (PE; clone RB6-8C5), anti-TCR α β (PE; clone H57-597), anti-TCR γ δ (PE; clone GL3), anti-CD11b (PE; clone M1/70), and anti-Ter119 (PE; clone TER-119). Cells were sorted based on size, estimated using bead particles (Flow Cytometry Size Calibration Kit, Invitrogen, Carlsbad, CA) employing MoFlo sorter (DAKO, Carpinteria, CA).

Given the scarcity of VSELs in PB and BM, we performed 6 independent measurements per exposure condition (IH, normoxia), each based on pooled samples from 10 mice (for a total of 120 animals).

RNA Isolation and Amplification

BM-derived VSELs were isolated from 30 additional mice exposed to IH (pooled into 3 groups of n = 10), and 30 mice were exposed to room air (pooled into 3 groups of n = 10). Total RNA was isolated using PicoPure RNA Isolation Kit (Arcturus Bioscience Inc., Mountain View, CA) following the manufacturer's instructions. RNA amplification was performed using Low-RNA Input Fluorescent Linear Amplification kit (Agilent Technologies, Santa Clara, CA) with modifications. To produce sufficient amount of amplified RNA (cRNA), 2 rounds of RNA amplification were employed using random and T7 primers, respectively, followed by labeling with cyanine 3-dCTP (Cy3-dCTP; Perkin Elmer, Boston, MA).

Microarray Experiments

For each VSEL-pooled group (n = 10 mice per group), labeled cRNA was hybridized to an Agilent murine whole-genome 60-mer oligo microarray (Agilent Technologies) comprised of more than 45,000 probes. Six independent hybridizations (3 pooled samples from mice exposed to IH and 3 pooled samples from normoxic mice) were performed. Microarrays were scanned using SureScan technology and images processed with Feature Extraction 9.5 software (Agilent Technologies). Background-subtracted intensities were normalized across all microarrays using the quantile method.[36]
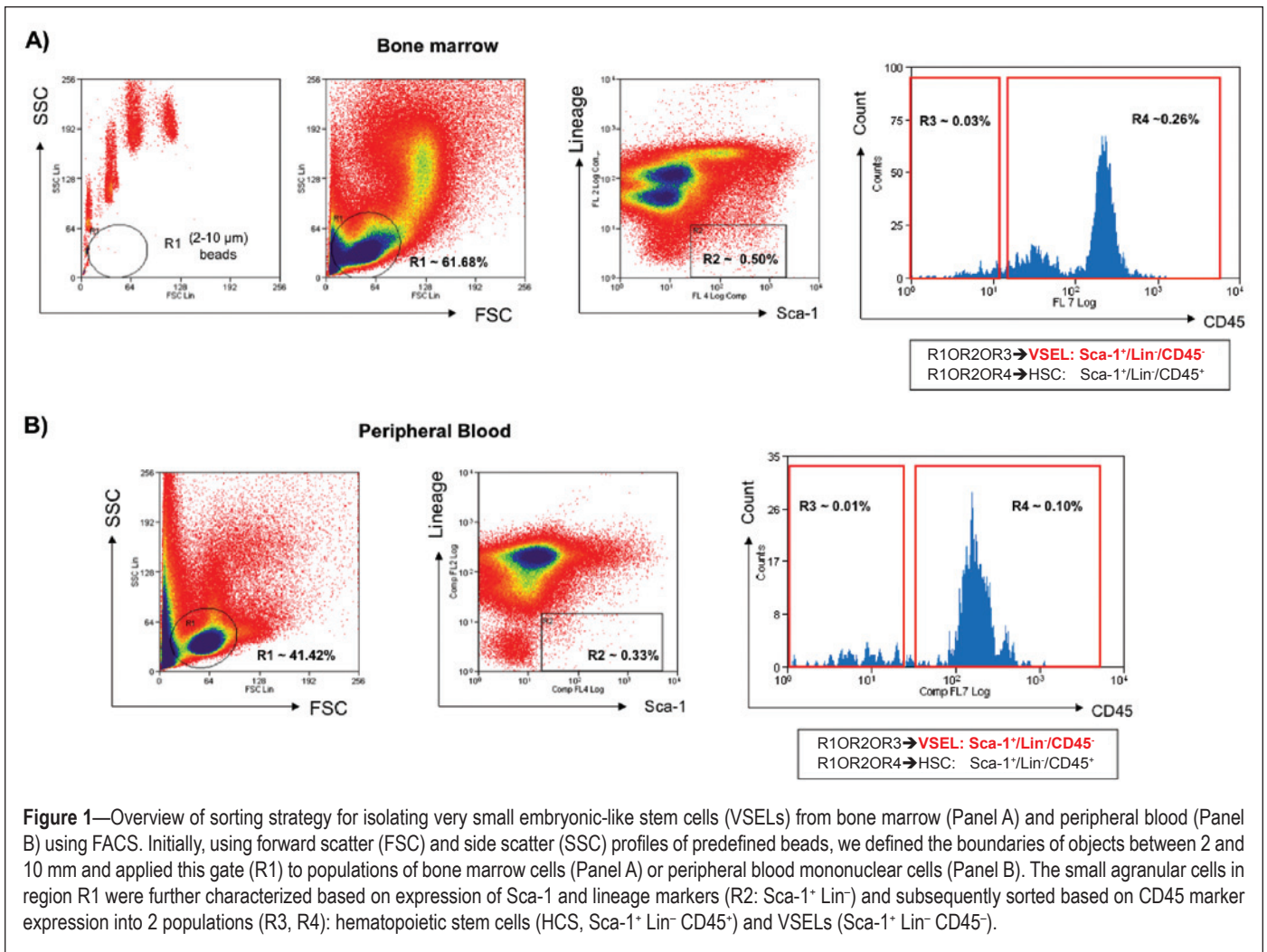
Figure 1—Overview of sorting strategy for isolating very small embryonic-like stem cells (VSELs) from bone marrow (Panel A) and peripheral blood (Panel B) using FACS. Initially, using forward scatter (FSC) and side scatter (SSC) profiles of predefined beads, we defined the boundaries of objects between 2 and 10 mm and applied this gate (R1) to populations of bone marrow cells (Panel A) or peripheral blood mononuclear cells (Panel B). The small agranular cells in region R1 were further characterized based on expression of Sca-1 and lineage markers (R2: Sca-1$^+$ Lin$^-$) and subsequently sorted based on CD45 marker expression into 2 populations (R3, R4): hematopoietic stem cells (HCS, Sca-1$^+$ Lin$^-$ CD45$^+$) and VSELs (Sca-1$^+$ Lin$^-$ CD45$^-$).

Gene-Expression Analysis

Multidimensional scaling using principal components analysis (PCA) was performed based on the covariance matrix of approximately 45,000 normalized gene-expression values.[37] Differential gene expression in VSELs exposed to IH versus normoxia was determined using a Bayesian implementation of the parametric t-test designed for robust analysis of microarray experiments with modest replicates.[38] Multiple-hypothesis testing was addressed by false discovery rate (FDR) analysis using the Q-value[39] method. A cutoff Q value of less than 0.05 was used for significant differential gene expression.

Functional Pathway and Network Analyses

Differentially expressed genes in VSELs (Q value < 0.05) underwent Gene Ontology analysis using the Database for Annotation, Visualization and Integrated Discovery (DAVID) program.[40] Enrichment of functional processes was determined using P values derived from a modified Fisher exact test. Functional annotation clustering of enriched categories was used to identify and group biologic modules with similar gene members based on the κ coefficient.[40] A permutation-based FDR analysis was employed to correct for multiple-hypothesis testing (FDR cutoff < 5%).

We then constructed a gene product interaction network of differentially expressed genes in VSELs during exposure to IH based on previously published direct and indirect interactions using Ingenuity knowledge base[41] and several publicly available databases. The topologic characteristic of the resulting network was studied by using its connectivity matrix. To assess whether the network possessed "scale-free" properties, i.e., followed a power-law distribution, the degree distribution of its nodes, N_k, was plotted against the connectivity of the nodes, k.[42] Next, we extracted a subnetwork from the original network, and limited the subnetwork to nodes involved in developmental processes, as determined by our Gene Ontology analysis.

RESULTS

VSELs Can Be Isolated and Quantified from Murine BM and PB

Employing a systematic gating strategy using FACS, based on size, granularity, and specific antibody staining, we isolated rare populations of VSELs from PB and BM of mice exposed to normoxia and IH (Figure 1).

Exposure to IH Mobilizes VSELs from the BM into PB

Isolation of VSELs from BM and PB of mice exposed to either normoxia or IH revealed a significant increase in the peripheral count of these pluripotent stem cells during IH (Figure 2A) and a concomitant reduction in the BM reserve pool (Figure 2B). The relative effect of IH in mobilizing VSELs

from BM to PB in response to IH is shown in Figure 2C. Furthermore, IH was associated with a significant increase in plasma levels of the stem cell chemoattractants SDF-1, HGF, and LIF (Figure 2D-F), providing further evidence that exposure to IH promotes a favorable gradient for recruitment of VSELs from BM to PB.

Exposure to IH Induces a Distinct Transcriptional Response in VSELs

Differential variability in genome-wide expression profiles of BM-derived VSELs exposed to IH and normoxia was assessed using PCA. This analysis robustly segregated the 2 exposure groups (Figure 3), implying that IH causes a global perturbation in the VSEL transcriptome. We then statistically identified 1113 differentially expressed genes in VSELs exposed to IH versus normoxia at a Q-value cutoff of less than 0.05. (See supplementary section, Table S1. Supplementary material is available online only at www.journalsleep.org.) These differentially expressed genes underwent further computational analyses as described below.

IH Activates Organ-Specific Developmental Programs in VSELs

To determine whether genes differentially expressed during IH map to coherent biologic processes, we performed Gene Ontology analysis followed by functional annotation clustering.[40] The most significant functional cluster was "multicellular organismal development" (enrichment P value 9.7×10^{-11}, FDR 1.7×10^{-11}), but several other developmental processes were also highly overrepresented, including those involved in angiogenesis, central nervous system (CNS) development, and tube/lung development (supplementary section, Table S2). Figure 4 depicts a wiring-diagram representation of these enriched developmental modules and highlights the intermodular connections resulting from the genes that are shared among them. These findings demonstrate that a brief exposure to IH induces a transcriptional response in BM-derived VSELs that is highly enriched in multi-organ developmental programs.

Network Analysis of VSEL Transcriptome Reveals the Interaction of Key Developmental Regulators During IH

Because biologic processes are often orchestrated by co-regulated changes among many genes, we created a gene product interaction network, or interactome, of IH-induced differentially expressed genes in VSELs (Figure 5A). This network consisted of 387 genes (nodes) and 620 connections (edges). Topologic analysis of this interactome demonstrated that, consistent with many biologic networks, it is scale free and follows a power law distribution—i.e., $N_k \sim k^{-\gamma}$ ($\gamma = 1.39$, $R^2 = 0.98$)
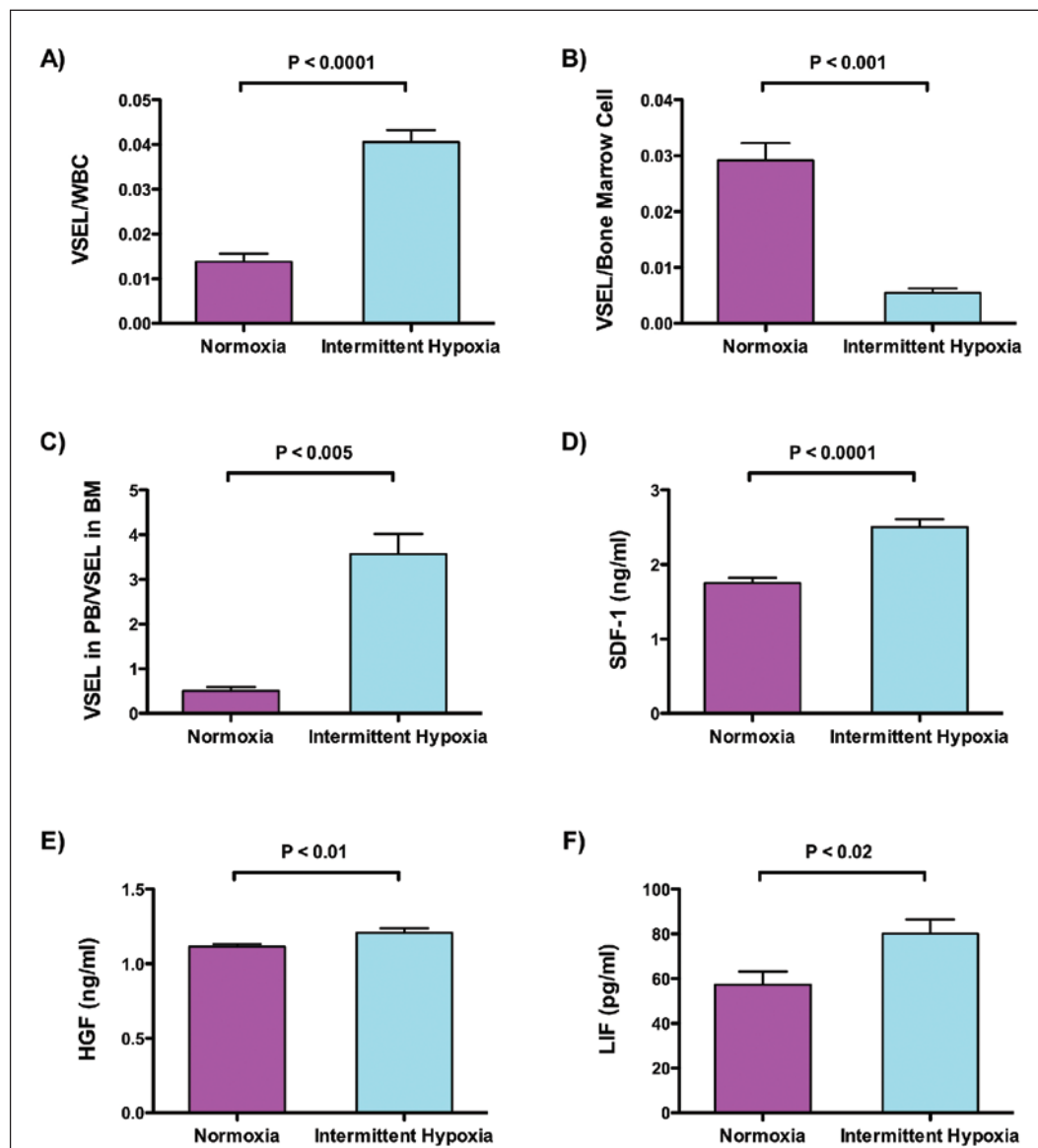
Figure 2—Mobilization of very small embryonic-like stem cells (VSEL) from bone marrow (BM) to peripheral blood (PB) and development of chemokine gradients in plasma after exposure to intermittent hypoxia profile for 48 hours. Panels A-C demonstrate significant increases in PB counts of VSEL (normalized for total leukocyte numbers) and concomitant decrease in the relative ratio of these stem cells in BM. Panels D-F show significant elevation in protein levels of 3 stem cell chemoattractants in response to intermittent hypoxia: stromal cell–derived factor-1 (SDF-1), hepatocyte growth factor (HGF), and leukemia inhibitory factor (LIF). The values displayed are means ± standard error of mean (SEM). P values were calculated using unpaired student t-test.

where N_k is the degree distribution and k is the nodal connectivity (Figure 5B). Network nodes mapping to the "development module" are highlighted in a darker shade, confirming that this functional module comprises a significant proportion of the membership of the interactome. To better evaluate the links among members of this highly enriched module, we extracted a subnetwork limited to these genes (Figure 6). This "developmental interactome" captures the complex relationships among genes mapping to the "development module" in Figure 4. Members of the network involved in CNS, blood vessel, or tube/lung development are highlighted in different colors for illustration purposes. A select number of representative nodes regulating these processes are labeled in Figure 6, including vascular endothelial growth factor receptor-1 (*Flt1*), angiopoietin-1 (*Angpt1*), epidermal growth factor (*Egf*), peroxisome proliferator activated receptor-γ (*Pparg*), glucose transporter type-4 (*Glut4*), stromal cell-derived factor-1 (*Sdf1*), dishevelled-1 (*Dvl1*), and vang-like 1 and 2 (*Vangl1*, *Vangl2*). A fully labeled network is available in the supplementary section (Figure S1).

DISCUSSION

In this study, we show that exposure to IH during the circadian rest period (i.e., daylight hours) promotes induction of distinct stem cell chemoattractant gradients in PB of mice and robustly mobilizes pluripotent VSELs from BM to the peripheral circulation. Since IH is a key pathophysiologic feature of OSA, our findings raise the possibility that this phenomenon also occurs in the clinical setting. Recent studies by Carreras et al. showed that mesenchymal stem cells are released into the peripheral circulation of anesthetized rats exposed to recurrent apneas for 6 hours[43] and that injection of mesenchymal stem cells can reduce markers of inflammation.[44] Despite similar findings, there are important differences between our approaches. Firstly, we studied different stem cell populations. VSELs are very rare pluripotent cells occupying the highest level in the hierarchical organization of stem cells because they can self renew and differentiate into all 3 germ layers, whereas mesenchymal stem cells represent a more populous and lineage-committed stem cell pool that differentiate only into mesenchymal tissues, such as bone, adipose tissue, and muscle. Secondly, our experimental exposure to IH occurred during the natural sleep cycle of mice and without instrumentation or anesthesia. Notwithstanding, the consistency between our findings supports the proposition that recurrent hypoxia promotes recruitment of various stem cell populations from the BM into the PB and that such recruitment should be apparent in patients with OSA as well. Indeed, we and others have shown that OSA is associated with alterations in the levels of circulating endothelial progenitor cells in adult[45] and pediatric[46] populations, thereby further lending support to the notion that OSA and/or IH will not only activate organ injury-related processes, but also recruit repair mechanisms that may mitigate the magnitude of morbidity or facilitate recovery upon treatment and cessation of IH.

Although we found that VSELs were activated and mobilized during in vivo exposure to IH, the genetic programs orchestrating this response remained unexplored. We therefore proceeded to systematically explore the transcriptional consequences of IH on these unique rare clusters of pluripotent stem cells using expression profiling followed by functional and network analysis. Initial analysis revealed that exposure to IH induces a distinct global transcriptional signature in VSELs. More than 1000 unique genes were differentially expressed in BM-derived VSELs in response to IH, and their interacting network possessed scale-free properties characteristic of complex biologic networks.[47,48] Importantly, functional analysis of the differentially expressed genes revealed that multiple, organ-specific developmental programs were enriched during IH exposure (Figure 4). Consistent with the pluripotent embryonic-like properties of VSELs, these modules encompassed developmental processes originating from the differentiation of distinct germ lines, including ectoderm (CNS CNS development), me-
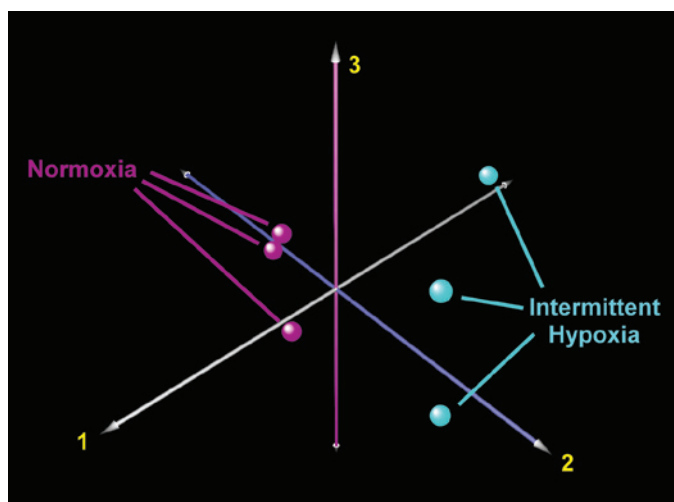
Figure 3—Principal component analysis of bone marrow-derived very small embryonic-like stem cells (VSELs) gene expression from mice exposed to intermittent hypoxia and normoxia. The clear segregation and prominent clustering of the experiments into 2 groups implies that exposure to intermittent hypoxia elicits a distinct genome-wide transcriptional perturbation in these pluripotent stem cells.
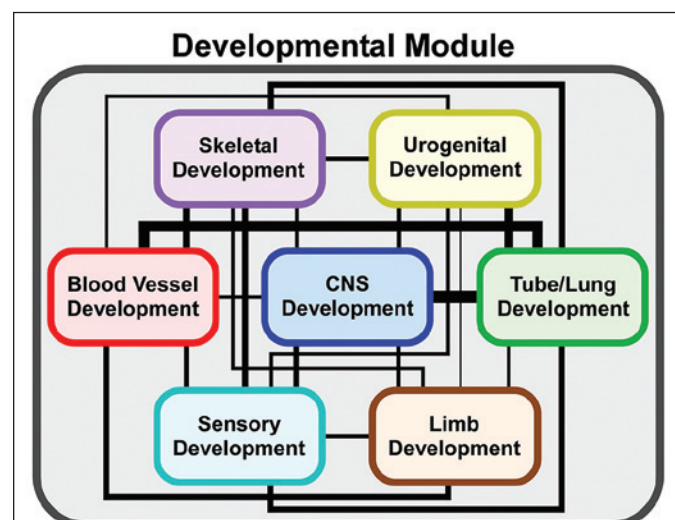
Figure 4—Enriched biologic processes involved in specific organ development are depicted using a wiring diagram. The intermodular connections reflect the fact that some genes map to multiple modules, whereas the line thickness is proportional to the number of shared genes. CNS refers to central nervous system.

Figure 5—Gene product interaction network of differentially expressed genes in very small embryonic-like stem cells (VSELs) after in vivo exposure to intermittent hypoxia. Panel (A) highlights genes annotated to developmental processes in a darker shade. Panel (B) shows that the topology of this network is scale free and follows a power-law distribution. N_k refers to degree distribution; k, the nodal connectivity.

Figure 6—A "developmental" subnetwork of differentially expressed genes in very small embryonic-like stem cells after exposure to intermittent hypoxia. This network was extracted from the larger interactome of Figure 5A, and was limited to genes mapping to developmental processes. To better visualize selected network components, genes involved in central nervous system (CNS) development (blue), vessel development (red), and tube/lung development (green) have been highlighted in primary colors. Genes shared by 2 of these modules are shown using secondary colors (magenta, yellow, and cyan), whereas genes common to all 3 are depicted in rainbow color. Genes include vascular endothelial growth factor receptor-1 (*Flt1*), angiopoietin-1 (*Angpt1*), epidermal growth factor (*Egf*), peroxisome proliferator activated receptor-γ (*Pparg*), glucose transporter type-4 (*Glut4*), stromal cell-derived factor-1 (*Sdf1*), dishevelled-1 (*Dvl1*), and vang-like 1 and 2 (*Vangl1, Vangl2*).

soderm (blood vessel and skeletal development), and endoderm (tube/lung development).

To further understand the gene-product relationships within the highly enriched developmental module, we extracted a genetic interaction network from the large network of differentially expressed genes (Figure 6). This analysis attributed functional roles for specific differentially expressed candidate genes. It was reassuring to find among such highly enriched genes within this interactome—the stem cell chemoattractant *Sdf1*, which also mapped to multiple developmental processes. Other members of this developmental network in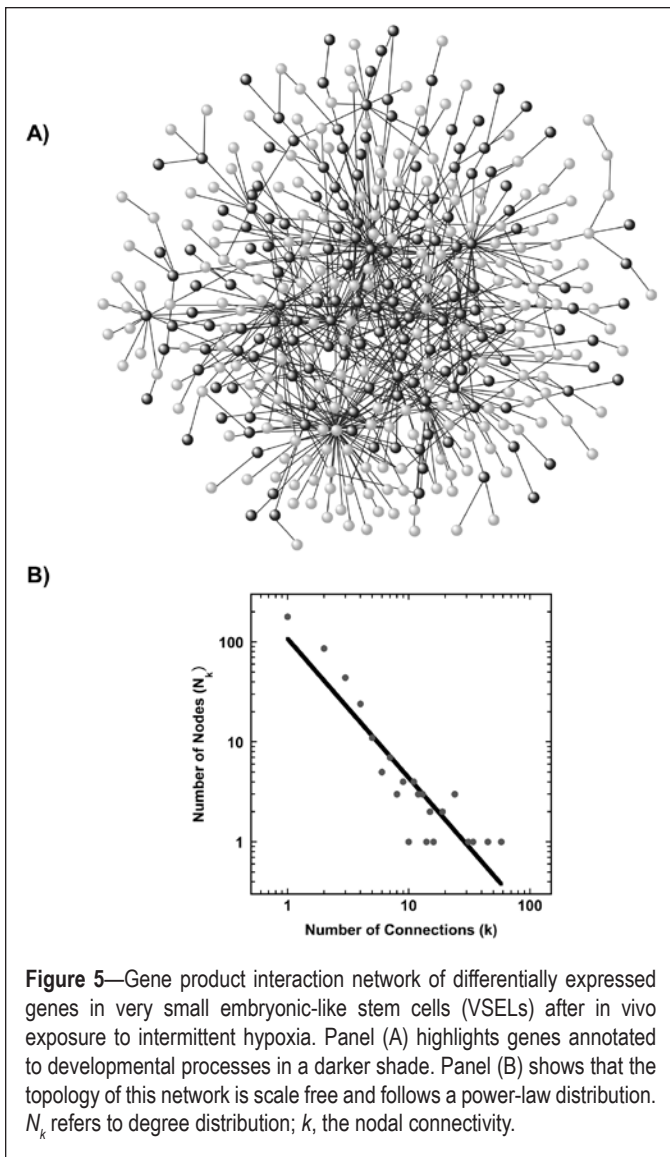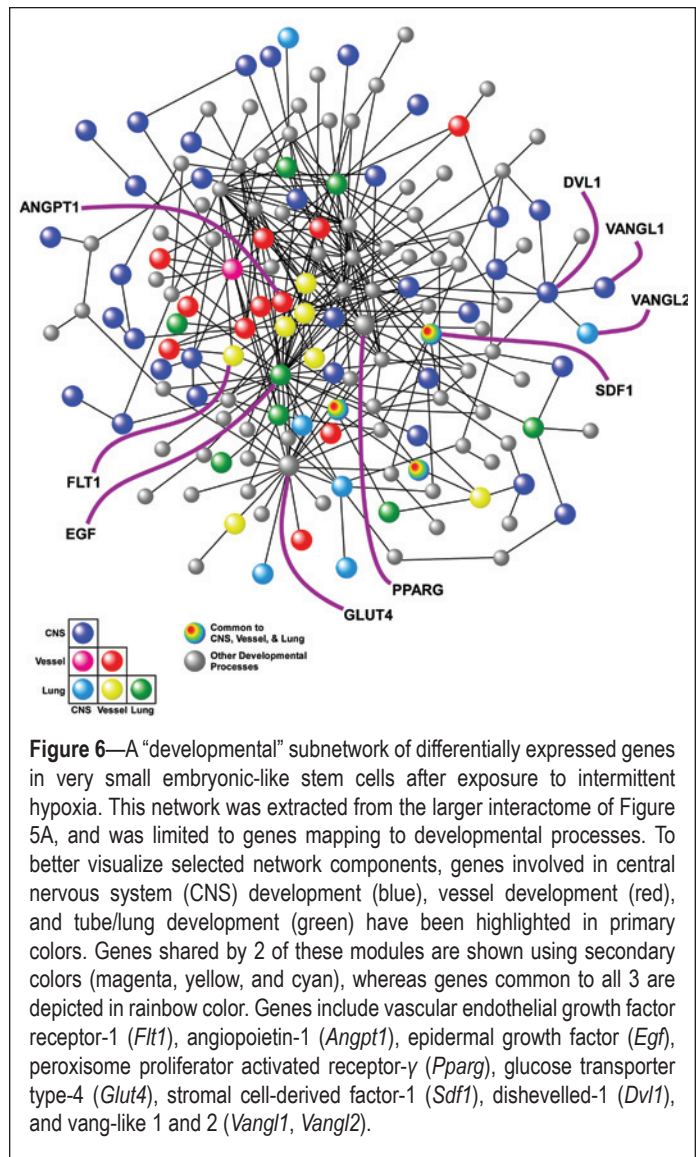cluded vascular *Flt1* and *Angpt1*—2 critical regulators of angiogenesis.[49,50] The most densely connected node within the network was *Egf*, a controller of branching morphogenesis[51] and a key ligand in the EGFR signaling cascade regulating many developmental, proliferative, and transformative processes.[52] Several interacting gene products—including *Dvl1, Vangl1*, and *Vangl2*—were members of the CNS development module. Mutations in *Vangl1* and *Vangl2* have been linked to neural-tube defects in mice[53] and humans,[54] whereas *Dvl1* functionally interacts with these genes during CNS development.[55] Interestingly, transgenic mice lacking *Dvl1* exhibit abnormality in their social behavior, sensorimotor gat-

ing, and sleep patterns.[56] A number of the nodes (shown in gray, Figure 6) did not map to enriched developmental submodules (as depicted in Figure 4) but were, nevertheless, members of the developmental network. Prominent examples included *Pparg* and *Glut4*. The products of these genes play critical roles in adipogenesis[57] and maintenance of glucose homeostasis.[58]

Taken together, these results imply that in vivo exposure to IH activates distinct and selective transcriptional programs in BM-derived pluripotent stem cells. Intriguingly, many of these differentially enriched developmental processes map to organs or pathways known to be adversely affected in OSA, including the CNS, vascular system, and metabolism.[59] This finding raises the possibility that, in response to IH, VSELs activate regenerative programs tailored for end organs that are either injured or at increased risk for injury.

Our study has a number of limitations. The murine model of IH does not capture the pathophysiologic complexity of OSA, since it does not incorporate sleep fragmentation, recurrent hypercapnia, and increased intrathoracic pressure swings. Furthermore, we have restricted our studies to the effects of short-term exposure to IH—chronic exposure to IH, as seen in OSA, may result in different patterns of VSEL recruitment

and the activation of different transcriptional programs. Our animal-based findings may not be generalizable to humans, although previous studies on VSEL recruitment during stroke and myocardial infarction reported similar responses in humans[35,60] and in mice.[27,30] Our functional and network analysis of the VSEL transcriptome is limited by the current state of knowledge and can yield different results in future iterations. Additionally, components of this interactome may represent a generalized response of VSELs to other pathophysiologic perturbations and, therefore, may not be specific to IH exposures. Although compelling, our results do not unequivocally prove that recruited VSELs in PB originated from the BM, since it is possible that some of these stem cells were mobilized from other tissue depots. However, BM is the predominant repository of VSELs and likely the primary source of the increased numbers observed during IH in PB. Finally, we have not demonstrated that mobilized populations of BM-derived VSELs are recruited to specific target organs in response to IH, where they undergo lineage differentiation and proliferation. Further studies are clearly required to elucidate the fate of these IH-activated pluripotent stem cells in circulating blood and to investigate their role within specific tissue compartments.

In summary, we report that exposure to IH during sleep for 48 hours alters stem cell chemoattractant gradients in plasma and mobilizes VSELs from BM to the peripheral circulation. A systematic analysis of the VSEL transcriptome further reveals selective activation of developmental programs in response to IH, including those involved in CNS development and angiogenesis. Future work is needed to establish the regenerative mechanisms initiated by these transcriptional programs upon recruitment of pluripotent stem cells to at-risk organs.

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Table S1

Differentially Expressed Genes in Bone Marrow-derived VSELs Exposed to Intermittent Hypoxia

Gene Symbol	Entrez ID	P-value	Q-value	Log$_2$[IH/Normoxia]	Description
Abl2	11352	2.35E-03	4.30E-02	-1.871	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene) (Abl2), transcript variant 2,
Acp2	11432	3.51E-04	1.14E-02	-1.619	8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730407E21 product:acid phosphatas
Acr	11434	1.32E-04	5.66E-03	1.838	acrosin prepropeptide (Acr), mRNA [NM_013455]
Adipoq	11450	4.54E-06	4.01E-04	1.580	adiponectin, C1Q and collagen domain containing (Adipoq), mRNA [NM_009605]
Actb	11461	1.46E-04	6.19E-03	1.965	actin, beta (Actb), mRNA [NM_007393]
Adamts1	11504	9.10E-06	6.92E-04	1.698	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1 (Adamts1), mRNA [N
Adh1	11522	3.65E-06	3.42E-04	1.782	alcohol dehydrogenase 1 (class I) (Adh1), mRNA [NM_007409]
Gpr182	11536	1.52E-05	1.05E-03	1.374	G protein-coupled receptor 182 (Gpr182), mRNA [NM_007412]
Afp	11576	3.33E-04	1.10E-02	-1.719	alpha fetoprotein (Afp), mRNA [NM_007423]
Ager	11596	2.40E-03	4.36E-02	-1.629	advanced glycosylation end product-specific receptor (Ager), mRNA [NM_007425]
Angpt1	11600	6.11E-07	8.05E-05	-2.230	angiopoietin 1 (Angpt1), mRNA [NM_009640]
Ahsg	11625	1.18E-03	2.74E-02	-3.153	alpha-2-HS-glycoprotein (Ahsg), mRNA [NM_013465]
Alas1	11655	1.57E-03	3.27E-02	0.694	aminolevulinic acid synthase 1 (Alas1), mRNA [NM_020559]
Alas2	11656	1.49E-07	2.64E-05	2.046	aminolevulinic acid synthase 2, erythroid (Alas2), nuclear gene encoding mitochondrial protein, transcript variant
Aldh2	11669	5.51E-04	1.55E-02	1.176	adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230105J09 product:aldehyde
Prdx6	11758	1.21E-05	8.68E-04	-2.813	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130091B17 product:peroxiredoxin 5, rela
Fabp4	11770	7.54E-09	2.16E-06	1.732	fatty acid binding protein 4, adipocyte (Fabp4), mRNA [NM_024406]
Apbb2	11787	3.98E-04	1.25E-02	1.303	amyloid beta (A4) precursor protein-binding, family B, member 2 (Apbb2), mRNA [NM_009686]
Speg	11790	3.18E-05	1.90E-03	3.353	SPEG complex locus (Speg), transcript variant 3, mRNA [NM_001085371]
Apoc1	11812	1.50E-03	3.17E-02	1.289	apolipoprotein C-I (Apoc1), transcript variant 1, mRNA [NM_007469]
Apoe	11816	2.81E-05	1.72E-03	0.974	apolipoprotein E (Apoe), mRNA [NM_009696]
Aqr	11834	2.46E-14	9.89E-11	-3.830	aquarius (Aqr), mRNA [NM_009702]
Rplp0	11837	3.65E-05	2.10E-03	1.089	ribosomal protein, large, P0 (Rplp0), mRNA [NM_007475]
Rhoc	11853	2.73E-04	9.69E-03	0.905	ras homolog gene family, member C (Rhoc), mRNA [NM_007484]
Arvcf	11877	2.09E-03	3.95E-02	-2.058	armadillo repeat gene deleted in velo-cardio-facial syndrome (Arvcf), mRNA [NM_033474]
Atm	11920	1.53E-05	1.05E-03	-2.259	ataxia telangiectasia mutated homolog (human) (Atm), mRNA [NM_007499]
Barx2	12023	1.53E-05	1.05E-03	-2.655	BarH-like homeobox 2 (Barx2), mRNA [NM_013800]
Bcl2l11	12125	9.29E-04	2.27E-02	1.281	BCL2-like 11 (apoptosis facilitator) (Bcl2l11), transcript variant 1, mRNA [NM_207680]
Fabp7	12140	6.01E-04	1.64E-02	-6.486	fatty acid binding protein 7, brain (Fabp7), mRNA [NM_021272]
Bnip3l	12177	2.28E-03	4.20E-02	0.696	BCL2/adenovirus E1B interacting protein 3-like (Bnip3l), mRNA [NM_009761]
Serping1	12258	1.14E-03	2.65E-02	1.286	serine (or cysteine) peptidase inhibitor, clade G, member 1 (Serping1), mRNA [NM_009776]
C4b	12268	9.36E-04	2.28E-02	1.723	complement component 4B (Childo blood group) (C4b), mRNA [NM_009780]
Calb1	12307	2.80E-10	1.53E-07	-2.589	calbindin 1 (Calb1), mRNA [NM_009788]
Aspm	12316	8.23E-05	3.98E-03	-1.835	asp (abnormal spindle)-like, microcephaly associated (Drosophila) (Aspm), mRNA [NM_009791]
Camk4	12326	9.78E-06	7.39E-04	4.137	calcium/calmodulin-dependent protein kinase IV (Camk4), mRNA [NM_009793]
Car2	12349	9.18E-04	2.25E-02	0.732	carbonic anhydrase 2 (Car2), mRNA [NM_009801]
Casp12	12364	6.76E-04	1.79E-02	3.049	caspase 12 (Casp12), mRNA [NM_009808]
Casp3	12367	1.42E-03	3.07E-02	-2.188	ICE-like cysteine protease (Lice) mRNA, complete cds. [U49929]
Cbln1	12404	4.42E-07	6.20E-05	3.306	cerebellin 1 precursor protein (Cbln1), mRNA [NM_019626]
Serpinh1	12406	1.06E-05	7.82E-04	1.746	serine (or cysteine) peptidase inhibitor, clade H, member 1 (Serpinh1), transcript variant 1, mRNA [NM_009825]
Cbx2	12416	6.75E-06	5.49E-04	-2.744	chromobox homolog 2 (Drosophila Pc class) (Cbx2), mRNA [NM_007623]
Cd36	12491	7.53E-04	1.94E-02	1.305	CD36 antigen mRNA, complete cds. [L23108]
Cd48	12506	3.93E-06	3.59E-04	-2.467	CD48 antigen (Cd48), mRNA [NM_007649]
Cd72	12517	5.66E-04	1.58E-02	-1.175	CD72 antigen (Cd72), transcript variant 2, mRNA [NM_007654]
Cdgap	12549	1.14E-03	2.65E-02	1.294	CDC42 GTPase-activating protein (Cdgap), mRNA [NM_020260]
Cdh5	12562	1.95E-04	7.71E-03	1.511	cadherin 5 (Cdh5), mRNA [NM_009868]
Cdkn2b	12579	2.83E-05	1.72E-03	-2.146	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (Cdkn2b), mRNA [NM_007670]
Cenpb	12616	3.07E-04	1.05E-02	-3.449	centromere protein B (Cenpb), mRNA [NM_007682]
Ch25h	12642	8.91E-07	1.09E-04	-3.542	cholesterol 25-hydroxylase (Ch25h), mRNA [NM_009890]
Chd1	12648	6.89E-04	1.81E-02	-1.067	chromodomain helicase DNA binding protein 1 (Chd1), mRNA [NM_007690]
Clca1	12722	7.38E-06	5.83E-04	1.618	chloride channel calcium activated 1 (Clca1), mRNA [NM_009899]
Cldn5	12741	1.27E-04	8.98E-04	1.468	claudin 5 (Cldn5), mRNA [NM_013805]
Il8rb	12765	3.85E-04	1.22E-02	-1.195	interleukin 8 receptor, beta (Il8rb), mRNA [NM_009909]
Cxcr7	12778	8.57E-08	1.67E-05	3.817	chemokine (C-X-C motif) receptor 7 (Cxcr7), mRNA [NM_007722]
Cnn1	12797	1.47E-03	3.13E-02	-1.789	calponin 1 (Cnn1), mRNA [NM_009922]
Col11a1	12814	1.95E-04	2.10E-04	3.616	collagen, type XI, alpha 1 (Col11a1), mRNA [NM_007729]
Col3a1	12825	3.38E-06	3.23E-04	2.364	collagen, type III, alpha 1 (Col3a1), mRNA [NM_009930]
Col4a1	12826	4.83E-05	2.65E-03	1.818	collagen, type IV, alpha 1 (Col4a1), mRNA [NM_009931]
Col4a2	12827	2.51E-03	4.53E-02	1.984	collagen, type IV, alpha 2 (Col4a2), mRNA [NM_009932]
Col8a1	12837	5.66E-05	2.95E-03	1.883	collagen, type VIII, alpha 1 (Col8a1), mRNA [NM_007739]
Col1a2	12843	1.93E-03	3.75E-02	0.932	collagen, type I, alpha 2 (Col1a2), mRNA [NM_007743]
Cox6a2	12862	4.08E-04	1.27E-02	-0.861	cytochrome c oxidase, subunit VI a, polypeptide 2 (Cox6a2), nuclear gene encoding mitochondrial protein, mRN/
Cp	12870	3.91E-04	1.24E-02	1.680	ceruloplasmin (Cp), transcript variant 2, mRNA [NM_007752]
Cpne6	12891	8.23E-04	2.09E-02	1.629	copine VI (Cpne6), mRNA [NM_009947]
Bcar1	12927	1.48E-03	3.15E-02	1.084	breast cancer anti-estrogen resistance 1 (Bcar1), mRNA [NM_009954]
Dmbt1	12945	2.84E-04	9.92E-03	2.165	deleted in malignant brain tumors 1 (Dmbt1), mRNA [NM_007769]
Crym	12971	1.31E-03	2.93E-02	2.656	crystallin, mu (Crym), mRNA [NM_016669]
Csf1r	12978	1.65E-03	3.37E-02	-1.269	colony stimulating factor 1 receptor (Csf1r), mRNA [NM_001037859]
Csf2	12981	2.72E-04	9.69E-03	-1.824	colony stimulating factor 2 (granulocyte-macrophage) (Csf2), mRNA [NM_009969]
Cux1	13047	1.16E-06	1.36E-04	-2.880	cut-like homeobox 1 (Cux1), transcript variant 2, mRNA [NM_198602]
Cyb561	13056	3.17E-04	1.06E-02	2.061	cytochrome b-561 (Cyb561), mRNA [NM_007805]
Cyp4b1	13120	1.56E-06	1.75E-04	2.344	cytochrome P450, family 4, subfamily b, polypeptide 1 (Cyp4b1), mRNA [NM_007823]
Dab2	13132	1.05E-05	7.79E-04	1.624	disabled homolog 2 (Drosophila) (Dab2), transcript variant 3, mRNA [NM_001037905]
Dck	13178	2.79E-12	3.06E-09	-3.207	deoxycytidine kinase (Dck), mRNA [NM_007832]
Dcn	13179	6.57E-13	1.16E-09	3.939	decorin (Dcn), mRNA [NM_007833]
Des	13346	3.39E-04	1.11E-02	0.617	desmin (Des), mRNA [NM_010043]
Darc	13349	8.87E-06	6.77E-04	1.791	Duffy blood group, chemokine receptor (Darc), mRNA [NM_010045]

Dlg1	13383	2.12E-04	8.08E-03	-2.486	discs, large homolog 1 (Drosophila) (Dlg1), mRNA [NM_007862]
Dnase2a	13423	2.77E-06	2.79E-04	3.703	ES cells cDNA, RIKEN full-length enriched library, clone:2410038B05 product:unclassifiable, full insert sequence
Dpep1	13479	1.60E-06	1.79E-04	2.420	dipeptidase 1 (renal) (Dpep1), mRNA [NM_007876]
Slc26a3	13487	5.41E-09	1.67E-06	-2.648	solute carrier family 26, member 3, mRNA (cDNA clone IMAGE:4989186), complete cds. [BC037066]
Dvl1	13542	6.71E-13	1.16E-09	-3.330	dishevelled, dsh homolog 1 (Drosophila) (Dvl1), mRNA [NM_010091]
Dyrk1a	13548	2.65E-03	4.71E-02	0.784	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a (Dyrk1a), transcript variant 1, mRNA [NM_0078]
Ebf1	13591	2.26E-03	4.17E-02	-1.503	adult male bone cDNA, RIKEN full-length enriched library, clone:9830166E18 product:unclassifiable, full insert se
Ebf3	13593	1.50E-04	6.32E-03	1.311	early B-cell factor 3 (Ebf3), transcript variant 3, mRNA [NM_010096]
Ecel1	13599	2.68E-04	9.58E-03	1.887	endothelin converting enzyme-like 1 (Ecel1), mRNA [NM_021306]
S1pr3	13610	1.09E-05	7.99E-04	1.623	sphingosine-1-phosphate receptor 3 (S1pr3), mRNA [NM_010101]
Edn1	13614	4.01E-04	1.26E-02	2.947	endothelin 1 (Edn1), mRNA [NM_010104]
Ednra	13617	3.54E-05	2.06E-03	1.353	endothelin receptor type A (Ednra), mRNA [NM_010332]
Ednrb	13618	1.70E-03	3.43E-02	-2.923	endothelin receptor type B (Ednrb), mRNA [NM_007904]
Eed	13626	1.06E-03	2.50E-02	-1.812	adult male testis cDNA, RIKEN full-length enriched library, clone:4930565G20 product:hypothetical protein, full in
Efna5	13640	3.74E-04	1.20E-02	2.123	ephrin A5 (Efna5), transcript variant 1, mRNA [NM_207654]
Egf	13645	6.51E-07	8.49E-05	-1.647	epidermal growth factor (Egf), mRNA [NM_010113]
Egr4	13656	1.69E-05	1.14E-03	-2.539	early growth response 4 (Egr4), mRNA [NM_020596]
Eif3a	13669	1.23E-13	3.71E-10	-3.407	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130093N16 product:EUKARYOTIC TRAN
Elk3	13713	2.15E-03	4.02E-02	0.706	ELK3, member of ETS oncogene family (Elk3), transcript variant 1, mRNA [NM_013508]
Epas1	13819	6.00E-08	1.27E-05	1.494	endothelial PAS domain protein 1 (Epas1), mRNA [NM_010137]
Epb4.1l1	13821	2.29E-03	4.21E-02	1.656	erythrocyte protein band 4.1-like 1 (Epb4.1l1), transcript variant 2, mRNA [NM_001003815]
Epb4.1l4a	13824	1.15E-04	5.18E-03	2.748	erythrocyte protein band 4.1-like 4a (Epb4.1l4a), mRNA [NM_013512]
Erg	13876	1.80E-03	3.58E-02	-1.680	avian erythroblastosis virus E-26 (v-ets) oncogene related (Erg), mRNA [NM_133659]
Fabp3	14077	3.71E-06	3.46E-04	1.668	fatty acid binding protein 3, muscle and heart (Fabp3), mRNA [NM_010174]
Fabp1	14080	1.03E-05	7.67E-04	3.337	fatty acid binding protein 1, liver (Fabp1), mRNA [NM_017399]
Fbln2	14115	1.26E-03	2.85E-02	-2.487	fibulin 2 (Fbln2), transcript variant 1, mRNA [NM_007992]
Lgr5	14160	1.95E-03	3.77E-02	-2.500	leucine rich repeat containing G protein coupled receptor 5 (Lgr5), mRNA [NM_010195]
Fgf8	14179	4.71E-04	1.39E-02	1.700	fibroblast growth factor 8 (Fgf8), mRNA [NM_010205]
Fgf9	14180	2.21E-04	8.33E-03	2.597	fibroblast growth factor 9 (Fgf9), mRNA [NM_013518]
Fgfr1	14182	1.67E-03	3.40E-02	-1.471	Mouse basic fibroblast growth factor receptor (bFGF-R) mRNA, complete cds. [M28998]
Fgfr4	14186	2.83E-03	4.90E-02	1.162	fibroblast growth factor receptor 4 splice variant 17b (Fgfr4) mRNA, partial cds. [AF127140]
Akr1b8	14187	1.84E-04	7.36E-03	1.235	aldo-keto reductase family 1, member B8 (Akr1b8), mRNA [NM_008012]
Fgl2	14190	2.06E-03	3.91E-02	-1.100	fibrinogen-like protein 2 (Fgl2), mRNA [NM_008013]
Fhl1	14199	1.25E-04	5.45E-03	1.155	four and a half LIM domains 1 (Fhl1), transcript variant 1, mRNA [NM_001077361]
Ctgf	14219	1.49E-11	1.28E-08	3.058	connective tissue growth factor (Ctgf), mRNA [NM_010217]
Fkbp10	14230	9.23E-04	2.26E-02	1.562	FK506 binding protein 10 (Fkbp10), mRNA [NM_010221]
Fkbp7	14231	1.08E-03	2.55E-02	1.407	FK506 binding protein 7 (Fkbp7), mRNA [NM_010222]
Flt1	14254	5.11E-04	1.47E-02	1.004	FMS-like tyrosine kinase 1 (Flt1), mRNA [NM_010228]
Fnbp1	14269	7.77E-05	3.80E-03	-1.853	formin binding protein 1 (Fnbp1), transcript variant 2, mRNA [NM_019406]
Fpr2	14289	1.80E-03	3.58E-02	-0.914	formyl peptide receptor 2 (Fpr2), mRNA [NM_008039]
Fstl1	14314	3.58E-07	5.23E-05	2.341	follistatin-like 1 (Fstl1), mRNA [NM_008047]
Fxc1	14356	1.65E-03	3.37E-02	-1.569	fractured callus expressed transcript 1 Gene [Source:MGI (curated)
Fzd9	14371	9.94E-05	4.61E-03	-2.146	frizzled homolog 9 (Drosophila) (Fzd9), mRNA [NM_010246]
Gabrd	14403	8.43E-04	2.12E-02	1.589	gamma-aminobutyric acid (GABA-A) receptor, subunit delta (Gabrd), mRNA [NM_008072]
Gad1	14415	6.24E-10	2.89E-07	-2.805	glutamic acid decarboxylase 1 (Gad1), mRNA [NM_008077]
Gas6	14456	1.91E-04	7.58E-03	1.039	growth arrest specific 6 (Gas6), mRNA [NM_019521]
Gcg	14526	1.57E-03	3.27E-02	1.742	adult pancreas islet cells cDNA, RIKEN full-length enriched library, clone:C820012C23 product:unclassifiable, full
Kat2a	14534	3.65E-07	5.27E-05	-2.650	K(lysine) acetyltransferase 2A (Kat2a), transcript variant 1, mRNA [NM_020004]
Arhgdig	14570	1.70E-03	3.43E-02	-1.706	Rho GDP dissociation inhibitor (GDI) gamma (Arhgdig), mRNA [NM_008113]
Gem	14579	6.74E-04	1.78E-02	-1.826	GTP binding protein (gene overexpressed in skeletal muscle) (Gem), mRNA [NM_010276]
Ggt1	14598	1.88E-05	1.24E-03	-1.974	gamma-glutamyltransferase 1 (Ggt1), mRNA [NM_008116]
Ghrh	14601	1.00E-04	4.64E-03	-2.012	growth hormone releasing hormone (Ghrh), mRNA [NM_010285]
Gjc1	14615	3.11E-04	1.05E-02	2.838	gap junction protein, gamma 1 (Gjc1), mRNA [NM_008122]
Gjb2	14619	1.18E-05	8.52E-04	-2.234	gap junction protein, beta 2 (Gjb2), mRNA [NM_008125]
Slc6a9	14664	1.29E-08	3.24E-06	1.929	solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (Slc6a9), mRNA [NM_008135]
Gna13	14674	1.10E-03	2.58E-02	-1.810	guanine nucleotide binding protein, alpha 13 (Gna13), mRNA [NM_010303]
Gnai1	14677	7.10E-06	5.65E-04	-2.214	guanine nucleotide binding protein (G protein), alpha inhibiting 1 (Gnai1), mRNA [NM_010305]
Gng12	14701	4.24E-04	1.30E-02	0.878	guanine nucleotide binding protein (G protein), gamma 12 (Gng12), mRNA [NM_025278]
Gpc4	14735	3.95E-04	1.25E-02	-2.278	glypican 4 (Gpc4), mRNA [NM_008150]
Nr3c1	14815	1.27E-03	2.85E-02	1.768	nuclear receptor subfamily 3, group C, member 1 (Nr3c1), mRNA [NM_008173]
Gstm1	14862	8.34E-04	2.11E-02	0.788	glutathione S-transferase, mu 1 (Gstm1), mRNA [NM_010358]
Gstm3	14864	5.72E-05	2.97E-03	0.920	glutathione S-transferase, mu 3 (Gstm3), mRNA [NM_010359]
Magi1	14924	1.36E-03	2.99E-02	1.935	membrane associated guanylate kinase, WW and PDZ domain containing 1 (Magi1), transcript variant 1, mRNA
H13	14950	1.27E-03	2.85E-02	-1.562	histocompatibility 13, mRNA (cDNA clone MGC:66829 IMAGE:6818912), complete cds. [BC056977]
Hba-a1	15122	3.75E-06	3.46E-04	1.572	hemoglobin alpha, adult chain 1 (Hba-a1), mRNA [NM_008218]
Hbb-b1	15129	1.64E-08	4.04E-06	1.689	hemoglobin, beta adult major chain (Hbb-b1), mRNA [NM_008220]
Mst1	15235	1.82E-03	3.59E-02	1.404	macrophage stimulating 1 (hepatocyte growth factor-like) (Mst1), mRNA [NM_008243]
Hic1	15248	2.07E-03	3.91E-02	1.099	hypermethylated in cancer 1 (Hic1), transcript variant 1, mRNA [NM_010430]
Hira	15260	7.27E-08	1.47E-05	-2.576	histone cell cycle regulation defective homolog A (S. cerevisiae) (Hira), mRNA [NM_010435]
Hmg20b	15353	5.48E-05	2.90E-03	-1.233	high mobility group 20 B (Hmg20b), mRNA [NM_010440]
Foxa2	15376	2.66E-03	4.72E-02	-0.620	forkhead box A2 (Foxa2), mRNA [NM_010446]
Hnrnpab	15384	1.14E-03	2.65E-02	-2.571	12 days embryo head cDNA, RIKEN full-length enriched library, clone:3010025C11 product:unclassifiable, full ins
Hoxb6	15414	1.90E-04	7.56E-03	1.302	Murine HOX 2.2 mRNA for a homeobox protein. [X56459]
Eif2ak1	15467	1.45E-03	3.10E-02	-1.199	eukaryotic translation initiation factor 2 alpha kinase 1 (Eif2ak1), mRNA [NM_013557]
Hsf1	15499	9.26E-04	2.27E-02	1.249	mRNA for heat shock factor 1-alpha. [Z49206]
Hsph1	15505	2.21E-04	8.32E-03	-0.914	heat shock 105kDa/110kDa protein 1 (Hsph1), mRNA [NM_013559]
Hspg2	15530	1.09E-07	2.04E-05	2.025	perlecan (heparan sulfate proteoglycan 2) (Hspg2), mRNA [NM_008305]
Ifi203	15950	7.60E-05	3.73E-03	-1.152	interferon activated gene 203 (Ifi203), transcript variant 1, mRNA [NM_001045481]
Ifnb1	15977	5.23E-05	2.81E-03	-3.589	interferon beta 1, fibroblast (Ifnb1), mRNA [NM_010510]
Ifng	15978	2.90E-04	1.01E-02	-1.232	interferon gamma (Ifng), mRNA [NM_008337]
Ifngr2	15980	1.19E-03	2.75E-02	0.885	interferon gamma receptor 2 (Ifngr2), mRNA [NM_008338]

Cyr61	16007	5.92E-06	4.94E-04	2.913	cysteine rich protein 61 (Cyr61), mRNA [NM_010516]
Igfbp5	16011	4.42E-05	2.47E-03	1.451	insulin-like growth factor binding protein 5 (Igfbp5), mRNA [NM_010518]
Igh-VJ558	16061	9.84E-05	4.57E-03	-1.190	J558+ IgM heavy chain mRNA, hybridoma clone ME2B7, partial cds. [U39781]
Igll1	16136	1.89E-06	2.06E-04	-2.359	adult male bone cDNA, RIKEN full-length enriched library, clone:9830138N18 product:immunoglobulin lambda ch
Igl-V1	16142	1.01E-12	1.52E-09	2.687	adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010004G10 product:immunoglobulin l
Il10	16153	5.87E-05	3.02E-03	-1.688	interleukin 10 (Il10), mRNA [NM_010548]
Il1rap	16180	4.88E-04	1.43E-02	-3.388	interleukin 1 receptor accessory protein (Il1rap), transcript variant 1, mRNA [NM_008364]
Il1rn	16181	2.23E-03	4.14E-02	-1.024	interleukin 1 receptor antagonist (Il1rn), transcript variant 2, mRNA [NM_001039701]
Il2rg	16186	2.45E-05	1.54E-03	-3.373	interleukin 2 receptor, gamma chain (Il2rg), mRNA [NM_013563]
Inhbc	16325	1.24E-03	2.82E-02	-3.158	inhibin beta-C (Inhbc), mRNA [NM_010565]
Invs	16348	2.68E-03	4.75E-02	-1.735	adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330415L19 product:inversin, full insert
Irf1	16362	2.51E-04	9.16E-03	-0.877	interferon regulatory factor 1 (Irf1), mRNA [NM_008390]
Irg1	16365	1.17E-06	8.47E-04	-1.095	immune-responsive gene 1 (Irg1) mRNA, 3' end of cds. [L38281]
Irf9	16391	1.28E-03	2.86E-02	-0.976	interferon regulatory factor 9 (Irf9), mRNA [NM_008394]
Itga5	16402	8.60E-07	1.05E-04	-2.748	integrin alpha 5 (fibronectin receptor alpha) (Itga5), mRNA [NM_010577]
Itgav	16410	5.45E-05	2.89E-03	-2.177	integrin alpha V (Itgav), mRNA [NM_008402]
Itgb3	16416	2.34E-03	4.30E-02	1.849	integrin beta3 subunit mRNA, complete cds. [AF026509]
Jup	16480	5.48E-04	1.55E-02	2.897	junction plakoglobin (Jup), mRNA [NM_010593]
Kcnj8	16523	1.17E-06	1.36E-04	2.201	potassium inwardly-rectifying channel, subfamily J, member 8 (Kcnj8), mRNA [NM_008428]
Kcnj9	16524	4.80E-04	1.41E-02	1.859	adult male testis cDNA, RIKEN full-length enriched library, clone:1700085N21 product:unclassifiable, full insert se
Kcnk7	16530	2.09E-04	8.07E-03	-2.004	potassium channel, subfamily K, member 7 (Kcnk7), transcript variant 2, mRNA [NM_001004138]
Kcnq1	16535	2.26E-04	8.47E-03	1.816	potassium voltage-gated channel, subfamily Q, member 1 (Kcnq1), mRNA [NM_008434]
Kif13b	16554	1.02E-04	4.69E-03	-2.101	kinesin family member 13B (Kif13b), mRNA [NM_001081177]
Kif1c	16562	4.38E-07	6.18E-05	-2.514	kinesin family member 1C (Kif1c), mRNA [NM_153103]
Klra8	16639	2.63E-06	2.71E-04	-2.160	killer cell lectin-like receptor, subfamily A, member 8 (Klra8), transcript variant 2, mRNA [NM_010650]
Kpna4	16649	5.08E-06	4.41E-04	-2.945	karyopherin (importin) alpha 4 (Kpna4), mRNA [NM_008467]
Hivep3	16656	2.65E-04	9.53E-03	1.288	adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900056N03 product:hypothetical prote
Krt8	16691	2.01E-03	3.85E-02	-1.674	keratin 8 (Krt8), mRNA [NM_031170]
Lamb2	16779	9.28E-05	4.39E-03	3.012	laminin, beta 2 (Lamb2), mRNA [NM_008483]
Anpep	16790	4.62E-04	1.37E-02	1.192	alanyl (membrane) aminopeptidase (Anpep), mRNA [NM_008486]
Lbx2	16815	6.49E-04	1.74E-02	1.764	ladybird homeobox homolog 2 (Drosophila) (Lbx2), mRNA [NM_010692]
Lfng	16848	2.15E-03	4.01E-02	-2.059	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase (Lfng), mRNA [NM_008494]
Lhx1	16869	6.16E-13	1.16E-09	-3.387	LIM homeobox protein 1 (Lhx1), mRNA [NM_008498]
Psmb9	16912	8.96E-04	2.21E-02	-0.696	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) (Psmb9), mRNA [NM_
Psmb8	16913	1.74E-03	3.49E-02	-0.679	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7) (Psmb8), mRNA [NM_
Lmx1b	16917	2.77E-03	4.84E-02	2.066	LIM homeobox transcription factor 1 beta (Lmx1b), mRNA [NM_010725]
Lrp5	16973	3.33E-04	1.10E-02	1.073	low density lipoprotein receptor-related protein 5 (Lrp5), mRNA [NM_008513]
Lrp6	16974	3.91E-05	2.21E-03	-1.936	adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030016K15 product:unclassifiable, fi
Lrp8	16975	7.88E-15	4.34E-11	-3.680	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (Lrp8), transcript variant 1, mRNA [NM
Ltbp2	16997	1.12E-03	2.61E-02	1.318	latent transforming growth factor beta binding protein 2 (Ltbp2), mRNA [NM_013589]
Lum	17022	1.08E-03	2.53E-02	2.512	lumican (Lum), mRNA [NM_008524]
Ly6f	17071	2.72E-03	4.79E-02	-1.609	lymphocyte antigen 6 complex, locus F (Ly6f), mRNA [NM_008530]
Ly96	17087	2.22E-04	8.35E-03	0.921	lymphocyte antigen 96 (Ly96), mRNA [NM_016923]
Lyz2	17105	6.26E-04	1.69E-02	0.825	osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:I420013M05 product:lysozyme, full insert sequ
Tm4sf1	17112	1.96E-05	1.28E-03	1.487	transmembrane 4 superfamily member 1 (Tm4sf1), mRNA [NM_008536]
Smad5	17129	1.57E-03	3.27E-02	0.852	MAD homolog 5 (Drosophila) (Smad5), mRNA [NM_008541]
Maf	17132	7.57E-04	1.95E-02	0.896	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog Gene [Source:MGI (curated)
Mfap2	17150	1.14E-05	8.28E-04	1.681	microfibrillar-associated protein 2 (Mfap2), mRNA [NM_008546]
Mbp	17196	5.51E-06	2.91E-03	-2.327	myelin basic protein (Mbp), transcript variant 7, mRNA [NM_010777]
Mc3r	17201	2.62E-04	9.43E-03	1.407	melanocortin 3 receptor (Mc3r), mRNA [NM_008561]
Mcf2l	17207	4.60E-04	1.36E-02	-2.476	mcf.2 transforming sequence-like (Mcf2l), mRNA [NM_178076]
Mdfi	17240	6.99E-05	3.50E-03	2.308	MyoD family inhibitor (Mdfi), transcript variant 1, mRNA [NM_010783]
Mdm4	17248	1.21E-04	5.32E-03	1.757	adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230385P13 product:inferred: t
Mest	17294	2.95E-08	6.71E-06	3.243	mesoderm specific transcript (Mest), mRNA [NM_008590]
Foxc1	17300	1.83E-04	7.35E-03	1.722	forkhead box C1 (Foxc1), mRNA [NM_008592]
Mgat1	17308	1.21E-03	2.77E-02	1.321	mannoside acetylglucosaminyltransferase 1 (Mgat1), transcript variant 2, mRNA [NM_010794]
Mgp	17313	2.51E-09	9.17E-07	3.298	matrix Gla protein (Mgp), mRNA [NM_008597]
Mgmt	17314	1.25E-03	2.84E-02	1.758	adult male gall bladder cDNA, RIKEN full-length enriched library, clone:G630095K06 product:0-6-methylguanine-
Mid1	17318	8.69E-05	4.17E-03	1.292	midline 1, mRNA (cDNA clone MGC:69759 IMAGE:6810837), complete cds. [BC059027]
Mllt4	17356	8.79E-04	2.18E-02	3.014	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (Mllt4), mRNA [NM
Ndst2	17423	5.87E-04	1.61E-02	0.972	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 (Ndst2), mRNA [NM_010811]
Grap2	17444	2.37E-03	4.32E-02	1.180	GRB2-related adaptor protein 2 (Grap2), mRNA [NM_010815]
COX2	17709	4.97E-05	2.69E-03	1.130	mitochondrially encoded cytochrome c oxidase II Gene [Source:MGI Symbol
Mtap7	17761	2.11E-05	1.35E-03	-2.375	microtubule-associated protein 7 (Mtap7), mRNA [NM_008635]
Mx2	17858	2.78E-03	4.85E-02	-1.059	myxovirus (influenza virus) resistance 2 (Mx2), mRNA [NM_013606]
Myl4	17896	6.11E-04	1.66E-02	-1.384	myosin, light polypeptide 4 (Myl4), mRNA [NM_010858]
Myo10	17909	1.11E-06	1.31E-04	-3.058	B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730038D06 product:hypoth
Myo6	17920	2.06E-04	7.99E-03	1.516	myosin VI (Myo6), mRNA [NM_001039546]
Nbl1	17965	1.78E-03	3.55E-02	1.129	neuroblastoma, suppression of tumorigenicity 1 (Nbl1), mRNA [NM_008675]
Neurod2	18013	5.64E-04	1.57E-02	1.980	neurogenic differentiation 2 (Neurod2), mRNA [NM_010895]
Nfatc2ip	18020	8.18E-05	3.96E-03	1.531	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein (Nfatc2ip), mRNA [NM
Nfib	18028	3.31E-05	1.95E-03	1.807	nuclear factor I/B (Nfib), transcript variant 1, mRNA [NM_001113209]
Nefl	18039	6.79E-08	1.41E-05	-2.452	neurofilament, light polypeptide (Nefl), mRNA [NM_010910]
Nid1	18073	4.00E-06	3.63E-04	1.579	nidogen 1 (Nid1), mRNA [NM_010917]
Nppc	18159	1.58E-09	6.35E-07	-2.855	natriuretic peptide precursor type C (Nppc), mRNA [NM_010933]
Nrap	18175	1.72E-03	3.46E-02	-2.299	nebulin-related anchoring protein (Nrap), transcript variant 2, mRNA [NM_008733]
Nrp2	18187	3.13E-06	3.08E-04	1.457	neuropilin 2 (Nrp2), transcript variant 1, mRNA [NM_001077403]
Nrxn2	18190	1.63E-04	6.71E-03	2.785	neurexin II (Nrxn2), mRNA [NM_020253]
Nsf	18195	3.96E-04	1.25E-02	-2.271	N-ethylmaleimide sensitive fusion protein (Nsf), mRNA [NM_008740]
Odf2	18286	8.64E-08	1.67E-05	-2.699	outer dense fiber of sperm tails 2 (Odf2), transcript variant 1, mRNA [NM_001113213]
Olfr32	18331	6.14E-04	1.67E-02	1.741	olfactory receptor 32 (Olfr32), mRNA [NM_010980]

Olfr48	18347	1.26E-06	1.45E-04	-2.515	olfactory receptor 48 (Olfr48), mRNA [NM_010990]
Osm	18413	2.01E-04	7.84E-03	-2.420	oncostatin M (Osm), mRNA [NM_001013365]
Osmr	18414	3.62E-07	5.26E-05	1.949	oncostatin M receptor (Osmr), mRNA [NM_011019]
Pafah1b3	18476	1.96E-03	3.79E-02	-0.916	platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit (Pafah1b3), mRNA [NM_008776]
Pam	18484	1.59E-11	1.32E-08	-3.218	peptidylglycine alpha-amidating monooxygenase (Pam), mRNA [NM_013626]
Pax2	18504	2.43E-04	8.93E-03	1.619	paired box gene 2 (Pax2), mRNA [NM_011037]
Pax6	18508	2.53E-03	4.55E-02	-0.129	paired box gene 6 (Pax6), mRNA [NM_013627]
Pcolce	18542	2.89E-06	2.88E-04	1.503	procollagen C-endopeptidase enhancer protein (Pcolce), mRNA [NM_008788]
Pcsk2	18549	2.47E-08	5.78E-06	-2.446	proprotein convertase subtilisin/kexin type 2 (Pcsk2), mRNA [NM_008792]
Pcsk6	18553	5.73E-06	4.85E-04	3.645	PREDICTED: proprotein convertase subtilisin [XM_355911]
Pctk3	18557	5.66E-05	2.95E-03	1.162	PCTAIRE-motif protein kinase 3 (Pctk3), mRNA [NM_008795]
Pdgfrb	18596	3.08E-04	1.05E-02	1.118	platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA [NM_008809]
Padi2	18600	8.23E-04	2.09E-02	-1.193	peptidyl arginine deiminase, type II (Padi2), mRNA [NM_008812]
Peg3	18616	2.02E-04	7.85E-03	2.228	0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130105D15 product:unclassifiable, full in
Per3	18628	9.40E-04	2.28E-02	-1.889	period homolog 3 (Drosophila) (Per3), mRNA [NM_011067]
Pfn1	18643	1.78E-04	7.18E-03	-1.244	profilin 1 (Pfn1), mRNA [NM_011072]
Abcb1b	18669	1.35E-03	2.99E-02	1.159	ATP-binding cassette, sub-family B (MDR/TAP), member 1B (Abcb1b), mRNA [NM_011075]
Prkcz	18762	1.92E-12	2.44E-09	-3.380	protein kinase C, zeta (Prkcz), transcript variant 1, mRNA [NM_008860]
Prl3d1	18775	1.44E-04	6.13E-03	1.751	Mouse placental lactogen I (PL-I) mRNA, complete cds. [M35662]
Papola	18789	1.78E-04	7.18E-03	-2.160	poly (A) polymerase alpha (Papola), mRNA [NM_011112]
Pa2g4	18813	5.83E-04	1.61E-02	-1.257	proliferation-associated 2G4 (Pa2g4), mRNA [NM_011119]
Plp1	18823	1.52E-03	3.20E-02	-1.842	proteolipid protein (myelin) 1 (Plp1), mRNA [NM_011123]
Plxna3	18846	1.83E-04	7.35E-03	-2.074	plexin A3 (Plxna3), mRNA [NM_008883]
Prrx1	18933	1.61E-03	3.32E-02	2.472	paired related homeobox 1 (Prrx1), transcript variant 2, mRNA [NM_175686]
Pou2f2	18987	6.66E-04	1.77E-02	2.493	POU domain, class 2, transcription factor 2 (Pou2f2), mRNA [NM_011138]
Pou5f1	18999	8.89E-04	2.20E-02	2.053	POU domain, class 5, transcription factor 1 (Pou5f1), mRNA [NM_013633]
Pparg	19016	9.39E-05	4.43E-03	1.049	peroxisome proliferator activated receptor gamma (Pparg), transcript variant 2, mRNA [NM_011146]
Ppic	19038	1.92E-04	7.60E-03	0.986	peptidylprolyl isomerase C (Ppic), mRNA [NM_008908]
Ppt1	19063	1.71E-03	3.45E-02	-1.858	B16 F10Y cells cDNA, RIKEN full-length enriched library, clone:G370087F11 product:palmitoyl-protein thioestera
Prkg1	19091	3.27E-05	1.93E-03	-2.487	protein kinase, cGMP-dependent, type I (Prkg1), transcript variant 2, mRNA [NM_011160]
Mapk8ip1	19099	1.28E-05	9.02E-04	-2.245	0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130310D04 product:unclassifiable, full in
Ptch2	19207	2.80E-03	4.87E-02	-2.017	patched homolog 2 (Ptch2), mRNA [NM_008958]
Pter	19212	2.71E-03	4.78E-02	-1.732	phosphotriesterase related (Pter), mRNA [NM_008961]
Ptrf	19285	3.22E-06	3.13E-04	1.372	polymerase I and transcript release factor (Ptrf), mRNA [NM_008986]
Aldh1a2	19378	1.88E-03	3.68E-02	1.687	aldehyde dehydrogenase family 1, subfamily A2 (Aldh1a2), mRNA [NM_009022]
Rapsn	19400	8.64E-04	2.15E-02	-1.761	receptor-associated protein of the synapse (Rapsn), mRNA [NM_009023]
Rara	19401	1.05E-03	2.49E-02	-1.646	retinoic acid receptor, alpha (Rara), mRNA [NM_009024]
Rbbp4	19646	6.22E-04	1.68E-02	1.410	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930061B17 product:unclassifiable,
Renbp	19703	2.71E-03	4.78E-02	0.885	renin binding protein (Renbp), mRNA [NM_023132]
Rfx2	19725	2.92E-05	1.76E-03	-2.209	6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430432H19 product:hypothetical protein, f
Rfx3	19726	2.38E-03	4.34E-02	-1.873	adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530084A02 product:regulatory factor
Rgl1	19731	2.56E-04	9.29E-03	1.062	ral guanine nucleotide dissociation stimulator,-like 1 (Rgl1), mRNA [NM_016846]
Rgs9	19739	4.92E-05	2.68E-03	2.659	regulator of G-protein signaling 9 (Rgs9), mRNA [NM_011268]
Mst1r	19882	9.03E-05	4.30E-03	-1.863	macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (Mst1r), mRNA [NM_009074]
Polr2a	20020	4.06E-04	1.26E-02	0.680	polymerase (RNA) II (DNA directed) polypeptide A (Polr2a), mRNA [NM_009089]
Trim30	20128	5.60E-05	2.93E-03	-1.376	tripartite motif-containing 30 (Trim30), mRNA [NM_009099]
Rtn2	20167	4.09E-04	1.27E-02	-2.740	reticulon 2 (Z-band associated protein) (Rtn2), transcript variant B, mRNA [NM_013648]
Prrx2	20204	3.77E-04	1.20E-02	-2.295	Mouse homeobox gene Prx2 mRNA [X52875]
Saa1	20208	6.79E-05	3.40E-03	1.552	serum amyloid A 1 (Saa1), mRNA [NM_009117]
Sag	20215	8.51E-05	4.09E-03	7.092	retinal S-antigen (Sag), mRNA [NM_009118]
Sap18	20220	5.27E-05	2.82E-03	-2.563	Sin3-associated polypeptide 18 (Sap18), mRNA [NM_009119]
Ccl2	20296	1.72E-03	3.47E-02	0.663	chemokine (C-C motif) ligand 2 (Ccl2), mRNA [NM_011333]
Ccl20	20297	1.41E-03	3.06E-02	1.957	chemokine (C-C motif) ligand 20 (Ccl20), mRNA [NM_016960]
Sdf1	20315	5.77E-08	1.23E-05	1.427	stromal cell-derived factor-1 (Sdf1), or, chemokine (C-X-C motif) ligand 12 (Cxcl12), transcript variant 3, mRNA [N
Sdpr	20324	2.84E-06	2.85E-04	1.370	serum deprivation response (Sdpr), mRNA [NM_138741]
Sel1l	20338	1.01E-03	2.43E-02	-1.653	adult female placenta cDNA, RIKEN full-length enriched library, clone:1600026C08 product:Sel1 (suppressor of li
Sema5b	20357	1.83E-04	7.35E-03	-2.213	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cy
Sema6b	20359	1.51E-03	3.19E-02	1.143	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), transcript vari
Sgce	20392	1.55E-03	3.25E-02	1.054	sarcoglycan, epsilon (Sgce), transcript variant 4, mRNA [NM_011360]
Itsn2	20403	4.08E-09	1.37E-06	-2.865	intersectin 2 (Itsn2), mRNA [NM_011365]
Siah1a	20437	3.12E-04	1.06E-02	-2.422	seven in absentia 1A (Siah1a), mRNA [NM_009172]
St6galnac2	20446	9.12E-05	4.33E-03	1.620	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2 (S
St6galnac3	20447	1.08E-03	2.54E-02	1.695	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3 (S
Ski	20481	1.62E-03	3.33E-02	0.817	ski sarcoma viral oncogene homolog (avian) (Ski), mRNA [NM_011385]
Glut4	20528	1.99E-04	7.80E-03	0.921	solute carrier family 2 (facilitated glucose transporter), member 4 (Glut4, Slc2a4), mRNA [NM_009204]
Slc31a2	20530	4.87E-04	1.42E-02	0.960	solute carrier family 31, member 2 (Slc31a2), mRNA [NM_025286]
Slc4a1	20533	2.70E-06	2.76E-04	1.224	solute carrier family 4 (anion exchanger), member 1 (Slc4a1), mRNA [NM_011403]
Slfn1	20555	2.18E-04	8.25E-03	-1.833	schlafen 1 (Slfn1), mRNA [NM_011407]
Hltf	20585	9.77E-05	4.56E-03	-1.772	helicase-like transcription factor (Hltf), transcript variant 2, mRNA [NM_144959]
Smarca4	20586	1.10E-03	2.57E-02	-0.803	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (Smarca4),
Snca	20617	4.38E-04	1.32E-02	1.553	synuclein, alpha (Snca), transcript variant 1, mRNA [NM_001042451]
Sod1	20655	1.24E-06	1.44E-04	-2.985	superoxide dismutase 1, soluble, mRNA (cDNA clone IMAGE:5697222), with apparent retained intron. [BC05707
Sorl1	20660	3.00E-04	1.03E-02	-0.800	hybrid receptor gp250 precursor, mRNA, partial cds. [AF031816]
Sparc	20692	2.63E-08	6.10E-06	2.094	secreted acidic cysteine rich glycoprotein (Sparc), mRNA [NM_009242]
Spint1	20732	4.94E-05	2.69E-03	-1.973	serine protease inhibitor, Kunitz type 1 (Spint1), mRNA [NM_016907]
Strbp	20744	5.19E-04	1.48E-02	1.769	Spnr mRNA for RNA binding protein [X84692]
Spp1	20750	5.12E-06	4.41E-04	1.557	secreted phosphoprotein 1 (Spp1), mRNA [NM_009263]
Srpk1	20815	6.04E-04	1.65E-02	-1.743	serine/arginine-rich protein specific kinase 1 (Srpk1), mRNA [NM_016795]
Stag1	20842	3.76E-06	3.46E-04	-2.269	stromal antigen 1 (Stag1), mRNA [NM_009282]
Star	20845	1.40E-07	2.52E-05	-2.677	steroidogenic acute regulatory protein (Star), nuclear gene encoding mitochondrial protein, mRNA [NM_011485]
Stfa3	20863	1.98E-04	7.80E-03	1.548	stefin A3 (Stfa3), mRNA [NM_025288]

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Gene	ID	p-val	q-val	FC	Description
Sts	20905	2.52E-04	9.20E-03	1.254	steroid sulfatase (Sts), mRNA [NM_009293]
Abcc9	20928	3.29E-07	4.90E-05	2.251	ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (Abcc9), transcript variant 2, mRNA [NM_021041]
Surf2	20931	3.26E-04	1.09E-02	1.111	surfeit gene 2 (Surf2), mRNA [NM_013678]
Swap70	20947	1.76E-05	1.17E-03	1.423	SWA-70 protein (Swap70), mRNA [NM_009302]
Syt1	20979	8.49E-04	2.13E-02	-2.192	synaptotagmin I (Syt1), mRNA [NM_009306]
Taf1a	21339	1.17E-04	5.21E-03	-1.692	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, A (Taf1a), mRNA [NM_021466]
Slc6a6	21366	3.91E-05	2.21E-03	-2.314	solute carrier family 6 (neurotransmitter transporter, taurine), member 6 (Slc6a6), mRNA [NM_009320]
Tcf7l2	21416	2.06E-03	3.91E-02	-1.796	transcription factor 7-like 2, T-cell specific, HMG-box (Tcf7l2), transcript variant 3, mRNA [NM_009333]
Tcfeb	21425	3.05E-04	1.04E-02	-1.891	transcription factor EB (Tcfeb), mRNA [NM_011549]
Tcra	21473	2.34E-10	1.31E-07	-2.912	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130010C18 product:unclassifiable, full
Dntt	21673	5.68E-06	4.82E-04	-1.534	deoxynucleotidyltransferase, terminal (Dntt), transcript variant 1, mRNA [NM_009345]
Tef	21685	7.34E-04	1.91E-02	-1.850	thyrotroph embryonic factor (Tef), transcript variant 2, mRNA [NM_153484]
Tekt1	21689	3.72E-09	1.26E-06	-2.925	tektin 1 (Tekt1), mRNA [NM_011569]
Tfpi	21788	9.78E-05	4.56E-03	1.307	tissue factor pathway inhibitor, mRNA (cDNA clone MGC:37332 IMAGE:4975683), complete cds. [BC036146]
Tgfa	21802	2.74E-03	4.80E-02	0.161	transforming growth factor alpha (Tgfa), mRNA [NM_031199]
Tgif1	21815	4.57E-05	2.53E-03	-2.086	TGFB-induced factor homeobox 1 (Tgif1), mRNA [NM_009372]
Thbs1	21825	4.61E-04	1.36E-02	-1.044	thrombospondin 1 (Thbs1), mRNA [NM_011580]
Thbs3	21827	1.72E-05	1.15E-03	1.767	thrombospondin 3 (Thbs3), mRNA [NM_013691]
Timeless	21853	7.55E-04	1.95E-02	-0.968	timeless homolog (Drosophila) (Timeless), transcript variant 2, mRNA [NM_011589]
Timm17b	21855	3.72E-12	3.61E-09	-3.248	translocase of inner mitochondrial membrane 17b (Timm17b), nuclear gene encoding mitochondrial protein, mRN
Timp1	21857	5.55E-07	7.56E-05	2.648	tissue inhibitor of metalloproteinase 1 (Timp1), transcript variant 1, mRNA [NM_001044384]
Timp3	21859	1.15E-04	5.17E-03	1.566	tissue inhibitor of metalloproteinase 3 (Timp3), mRNA [NM_011595]
Tle2	21886	2.82E-03	4.89E-02	1.348	transducin-like enhancer of split 2, homolog of Drosophila E(spl) (Tle2), mRNA [NM_019725]
Tspan7	21912	4.86E-06	4.26E-04	1.457	tetraspanin 7 (Tspan7), mRNA [NM_019634]
Clec3b	21922	6.19E-04	1.68E-02	1.827	C-type lectin domain family 3, member b (Clec3b), mRNA [NM_011606]
Cd27	21940	1.62E-03	3.33E-02	1.118	CD27 antigen (Cd27), transcript variant 1, mRNA [NM_001033126]
Tns1	21961	1.79E-09	7.08E-07	-3.281	PREDICTED: tensin 1 (Tns1), mRNA [XM_619639]
Hsp90b1	22027	3.17E-04	1.06E-02	-0.749	heat shock protein 90, beta (Grp94), member 1 (Hsp90b1), mRNA [NM_011631]
Trp73	22062	4.37E-04	1.32E-02	-2.160	transformation related protein 73 (Trp73), transcript variant 1, mRNA [NM_011642]
Tsn	22099	5.94E-06	4.94E-04	-2.709	10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2600015M20 product:translin, full ins
Ttf1	22130	1.53E-03	3.21E-02	-2.401	transcription termination factor, RNA polymerase I (Ttf1), mRNA [NM_009442]
Tubb2a	22151	1.64E-03	3.36E-02	-0.789	tubulin, beta 2a (Tubb2a), mRNA [NM_009450]
Ubr1	22222	3.60E-04	1.16E-02	-2.231	ubiquitin protein ligase E3 component n-recognin 1 (Ubr1), mRNA [NM_009461]
Slc35a2	22232	2.89E-04	1.01E-02	1.415	solute carrier family 35 (UDP-galactose transporter), member A2 (Slc35a2), transcript variant 1, mRNA [NM_078]
Umps	22247	1.42E-04	6.10E-03	-1.809	adult male testis cDNA, RIKEN full-length enriched library, clone:1700095D23 product:unclassifiable, full insert se
Nr1h3	22259	1.98E-03	3.81E-02	1.654	nuclear receptor subfamily 1, group H, member 3 (Nr1h3), mRNA [NM_013839]
Vamp2	22318	1.43E-12	2.03E-09	-3.526	vesicle-associated membrane protein 2 (Vamp2), mRNA [NM_009497]
Vav1	22324	2.63E-03	4.70E-02	-0.909	vav 1 oncogene (Vav1), mRNA [NM_011691]
Vpreb1	22362	3.25E-06	3.15E-04	-1.533	pre-B lymphocyte gene 1 (Vpreb1), mRNA [NM_016982]
Vpreb3	22364	1.61E-04	6.66E-03	-0.914	pre-B lymphocyte gene 3 (Vpreb3), mRNA [NM_009514]
Wnt5b	22419	3.59E-04	1.16E-02	2.318	wingless-related MMTV integration site 5B (Wnt5b), mRNA [NM_009525]
Siae	22619	1.76E-03	3.53E-02	-2.172	sialic acid acetylesterase (Siae), mRNA [NM_011734]
Zfp161	22666	2.42E-07	3.98E-05	-2.611	zinc finger protein 161 (Zfp161), mRNA [NM_009547]
Sf1	22668	1.05E-04	4.82E-03	-1.377	splicing factor 1 (Sf1), transcript variant 1, mRNA [NM_001110791]
Zfp2	22678	1.95E-03	3.77E-02	-1.705	zinc finger protein 2 (Zfp2), transcript variant 4, mRNA [NM_001044698]
Hs2st1	23908	9.34E-04	2.28E-02	-2.067	heparan sulfate 2-O-sulfotransferase 1 (Hs2st1), mRNA [NM_011828]
Kel	23925	2.65E-04	9.53E-03	0.994	Kell blood group (Kel), mRNA [NM_032540]
Mmp17	23948	1.25E-07	2.30E-05	-2.503	matrix metallopeptidase 17 (Mmp17), mRNA [NM_011846]
Nek4	23955	8.66E-04	2.15E-02	-1.627	NIMA (never in mitosis gene a)-related expressed kinase 4 (Nek4), mRNA [NM_011849]
Nt5e	23959	6.14E-04	1.67E-02	-2.626	5' nucleotidase, ecto (Nt5e), mRNA [NM_011851]
Oasl2	23962	1.40E-03	3.05E-02	-1.130	2'-5' oligoadenylate synthetase-like 2 (Oasl2), mRNA [NM_011854]
2-Sep	24050	2.14E-03	4.01E-02	-1.667	septin 3 (Sept3), mRNA [NM_011889]
Synj2bp	24071	8.28E-08	1.64E-05	-2.569	activin receptor-interacting protein 2b (Arip2b) mRNA, complete cds, alternatively spliced. [AY071903]
Tnfsf13b	24099	3.74E-12	3.61E-09	-3.222	tumor necrosis factor (ligand) superfamily, member 13b Gene [Source:MGI Symbol;Acc:MGI:1344376] [ENSMUS
Ubd	24108	4.50E-04	1.35E-02	1.079	ubiquitin D (Ubd), mRNA [NM_023137]
Axl	26362	3.62E-04	1.17E-02	-1.926	AXL receptor tyrosine kinase (Axl), mRNA [NM_009465]
Fto	26383	1.33E-05	9.32E-04	-2.120	fat mass and obesity associated (Fto), mRNA [NM_011936]
Ror2	26564	1.31E-03	2.92E-02	1.149	receptor tyrosine kinase-like orphan receptor 2 (Ror2), mRNA [NM_013846]
Rcn2	26611	1.98E-07	3.33E-05	-2.263	taipoxin-associated calcium binding protein 49 mRNA, complete cds. [AF049125]
B3galt1	26877	3.36E-04	1.11E-02	-3.918	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3galt1), mRNA [NM_020283]
B3galnt1	26879	3.77E-04	1.20E-02	-2.397	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 1 (B3galnt1), mRNA [NM_020026]
Polr3e	26939	1.60E-10	9.95E-08	-2.973	0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833431M21 product:sex-lethal interactor ho
Asns	27053	2.72E-03	4.78E-02	0.700	asparagine synthetase (Asns), mRNA [NM_012055]
Trp53bp1	27223	1.97E-03	3.80E-02	-2.333	transformation related protein 53 binding protein 1 (Trp53bp1), mRNA [NM_013735]
Dnajb9	27362	1.39E-03	3.03E-02	-1.152	DnaJ (Hsp40) homolog, subfamily B, member 9 (Dnajb9), mRNA [NM_013760]
Srr	27364	1.31E-03	2.92E-02	-1.768	adult male kidney cDNA, RIKEN full-length enriched library, clone:0610015N12 product:serine racemase, full inse
Mmel1	27390	1.25E-03	2.84E-02	2.581	membrane metallo-endopeptidase-like 1 (Mmel1), mRNA [NM_013783]
Pign	27392	1.92E-06	2.09E-04	-2.309	phosphatidylinositol glycan anchor biosynthesis, class N (Pign), mRNA [NM_013784]
Mrpl15	27395	6.10E-05	3.10E-03	1.225	NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630108O13 product:mit
Skp2	27401	8.47E-04	2.13E-02	-1.756	S-phase kinase-associated protein 2 (p45) (Skp2), transcript variant 2, mRNA [NM_145468]
Snf8	27681	2.32E-05	1.46E-03	-2.426	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae), mRNA (cDNA clone IMAGE:5372918) [BC030490]
Ubfd1	28018	9.10E-04	2.24E-02	-1.819	ubiquitin family domain containing 1 (Ubfd1), mRNA [NM_138589]
D5Wsu178e	28042	4.09E-04	1.27E-02	-1.718	DNA segment, Chr 5, Wayne State University 178, expressed (D5Wsu178e), mRNA [NM_027652]
Ndrg3	29812	2.69E-07	4.17E-05	-2.332	N-myc downstream regulated gene 3 (Ndrg3), mRNA [NM_013865]
Igfbp7	29817	2.43E-07	3.98E-05	1.744	insulin-like growth factor binding protein 7 (Igfbp7), mRNA [NM_008048]
Mapk12	29857	1.20E-05	8.64E-04	1.785	mitogen-activated protein kinase 12 (Mapk12), mRNA [NM_013871]
Ulk2	29869	3.16E-04	1.06E-02	1.452	0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030037L18 product:unclassifiable, full inser
Pdlim4	30794	1.86E-03	3.66E-02	2.456	adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530058N05 product:PDZ and LIM do
Fbxl17	50758	3.01E-04	1.04E-02	-2.202	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930017P15 product:unclassifiable, full ins
Rgs3	50780	2.91E-05	1.76E-03	1.585	regulator of G-protein signaling 3 (Rgs3), transcript variant 1, mRNA [NM_019492]
Olig2	50913	5.75E-04	1.59E-02	2.109	oligodendrocyte transcription factor 2 (Olig2), mRNA [NM_016967]

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Gene	ID	p-value	q-value	FC	Description
Pdcd7	50996	5.78E-05	3.00E-03	-2.408	programmed cell death 7 (Pdcd7), mRNA [NM_016688]
Bok	51800	1.46E-04	6.19E-03	1.080	apoptosis activator Mtd (Mtd) mRNA, complete cds. [AF027707]
Rnf24	51902	5.48E-06	4.69E-04	-2.698	ring finger protein 24 (Rnf24), mRNA [NM_178607]
Rab11fip5	52055	1.77E-04	7.18E-03	2.950	RAB11 family interacting protein 5 (class I) (Rab11fip5), transcript variant 1, mRNA [NM_001003955]
Coq5	52064	5.11E-06	1.47E-02	-1.914	coenzyme Q5 homolog, methyltransferase (yeast) (Coq5), mRNA [NM_026504]
Pvr	52118	5.55E-04	1.56E-02	-1.887	poliovirus receptor (Pvr), mRNA [NM_027514]
Klhl7	52323	1.53E-03	3.22E-02	-2.640	kelch-like 7 (Drosophila) (Klhl7), mRNA [NM_026448]
Atxn1l	52335	1.34E-03	2.97E-02	0.902	ataxin 1-like (Atxn1l), mRNA [NM_001080930]
Ddx56	52513	1.43E-06	1.62E-04	-2.312	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56 (Ddx56), mRNA [NM_026538]
Ncald	52589	1.18E-04	5.25E-03	-2.653	neurocalcin delta (Ncald), mRNA [NM_134094]
Cd300lg	52685	2.89E-03	4.99E-02	1.123	CD300 antigen like family member G (Cd300lg), mRNA [NM_027987]
Dbndd2	52840	4.55E-04	1.36E-02	1.018	dysbindin (dystrobrevin binding protein 1) domain containing 2 (Dbndd2), transcript variant 2, mRNA [NM_02679...
Sgsm1	52850	1.02E-03	2.45E-02	1.927	small G protein signaling modulator 1 (Sgsm1), mRNA [NM_172718]
Plrg1	53317	2.41E-03	4.38E-02	-0.912	pleiotropic regulator 1, PRL1 homolog (Arabidopsis) (Plrg1), mRNA [NM_016784]
Gosr1	53334	2.45E-03	4.44E-02	0.800	golgi SNAP receptor complex member 1 (Gosr1), mRNA [NM_016810]
Tsnax	53424	4.36E-08	9.56E-06	-2.431	translin-associated factor X (Tsnax), mRNA [NM_016909]
Pcdh12	53601	3.95E-04	1.25E-02	1.067	protocadherin 12 (Pcdh12), mRNA [NM_017378]
Map3k6	53608	2.78E-04	4.85E-02	0.953	mitogen-activated protein kinase kinase kinase 6 (Map3k6), mRNA [NM_016693]
Rcan2	53901	1.21E-04	5.32E-03	2.046	regulator of calcineurin 2 (Rcan2), transcript variant 1, mRNA [NM_207649]
Nell2	54003	1.27E-03	2.85E-02	-1.547	NEL-like 2 (chicken) (Nell2), mRNA [NM_016743]
Diap2	54004	2.35E-03	4.30E-02	-1.634	diaphanous homolog 2 (Drosophila) (Diap2), transcript variant 1, mRNA [NM_017398]
Uevld	54122	1.17E-07	2.17E-05	-2.584	UEV and lactate/malate dehydrogenase domains (Uevld), mRNA [NM_001040695]
Ccrl2	54199	3.05E-04	1.04E-02	-1.213	chemokine (C-C motif) receptor-like 2 (Ccrl2), mRNA [NM_017466]
Ramp2	54409	4.14E-04	1.28E-02	1.560	receptor (calcitonin) activity modifying protein 2 (Ramp2), mRNA [NM_019444]
Barhl1	54422	2.13E-04	8.10E-03	1.811	BarH-like 1 (Drosophila) (Barhl1), mRNA [NM_019446]
Calcrl	54598	3.97E-05	2.24E-03	-1.924	calcitonin receptor-like (Calcrl), mRNA [NM_018782]
Abhd2	54608	2.77E-03	4.84E-02	-2.332	abhydrolase domain containing 2 (Abhd2), mRNA [NM_018811]
Ubqln2	54609	1.27E-03	2.85E-02	-1.929	ubiquilin 2 (Ubqln2), mRNA [NM_018798]
Npff	54615	7.26E-04	1.89E-02	1.132	neuropeptide FF-amide peptide precursor (Npff), mRNA [NM_018787]
Pdgfc	54635	1.77E-08	4.31E-06	-2.648	platelet-derived growth factor, C polypeptide (Pdgfc), mRNA [NM_019971]
Praf2	54637	2.07E-06	2.18E-04	-2.461	PRA1 domain family 2 (Praf2), mRNA [NM_138602]
Sh3glb1	54673	1.65E-03	3.36E-02	-2.524	melanocyte cDNA, RIKEN full-length enriched library, clone:G270052F16 product:unclassifiable, full insert seque...
Pigb	55981	1.72E-03	3.47E-02	-1.709	phosphatidylinositol glycan anchor biosynthesis, class B (Pigb), mRNA [NM_018889]
Ccnl2	56036	1.31E-04	5.66E-03	-1.956	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130042P04 product:similar to CYCLIN A...
Pdss1	56075	3.91E-05	2.21E-03	-2.108	prenyl (solanesyl) diphosphate synthase, subunit 1 (Pdss1), mRNA [NM_019501]
Prodh2	56189	6.78E-06	5.49E-04	-2.175	proline dehydrogenase (oxidase) 2 (Prodh2), mRNA [NM_019546]
Htra1	56213	2.49E-05	1.55E-03	1.383	HtrA serine peptidase 1 (Htra1), mRNA [NM_019564]
Fam69b	56279	1.53E-04	6.42E-03	-2.495	family with sequence similarity 69, member B (Fam69b), mRNA [NM_019833]
Ptpn9	56294	5.64E-06	4.81E-04	-2.172	protein tyrosine phosphatase, non-receptor type 9 (Ptpn9), mRNA [NM_019651]
Fam60a	56306	7.48E-04	1.94E-02	-2.038	family with sequence similarity 60, member A (Fam60a), mRNA [NM_019643]
Eif3c	56347	1.08E-04	4.93E-03	-0.869	eukaryotic translation initiation factor 3, subunit C (Eif3c), mRNA [NM_146200]
Arid3b	56380	1.84E-03	3.63E-02	0.652	AT rich interactive domain 3B (BRIGHT-like) (Arid3b), mRNA [NM_019689]
Kcnip3	56461	1.22E-03	2.78E-02	-1.779	Kv channel interacting protein 3, calsenilin (Kcnip3), transcript variant 1, mRNA [NM_019789]
Pias1	56469	2.55E-07	4.07E-05	-2.965	protein inhibitor of activated STAT 1 (Pias1), mRNA [NM_019663]
Cldn18	56492	2.52E-03	4.53E-02	2.364	claudin 18 (Cldn18), mRNA [NM_019815]
Habp4	56541	8.73E-10	3.83E-07	-2.839	hyaluronic acid binding protein 4 (Habp4), mRNA [NM_019986]
Adam21	56622	1.81E-03	3.59E-02	-1.712	a disintegrin and metallopeptidase domain 21 (Adam21), mRNA [NM_020330]
Nfu1	56748	2.49E-03	4.49E-02	2.947	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130089D18 product:unclassifiable, full ins...
Cxcl14	57266	9.14E-07	1.11E-04	1.845	chemokine (C-X-C motif) ligand 14 (Cxcl14), mRNA [NM_019568]
S3-12	57435	2.47E-03	4.47E-02	1.691	plasma membrane associated protein, S3-12 (S3-12), mRNA [NM_020568]
Golga7	57437	5.51E-04	1.55E-02	-2.952	activated spleen cDNA, RIKEN full-length enriched library, clone:F830033L24 product:hypothetical protein, MNC...
Angptl4	57875	2.78E-04	9.82E-03	0.884	angiopoietin-like 4 (Angptl4), mRNA [NM_020581]
Zbp1	58203	3.03E-04	1.04E-02	-1.183	Z-DNA binding protein 1 (Zbp1), transcript variant 1, mRNA [NM_021394]
Fam184b	58227	1.83E-06	2.02E-04	-2.246	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230091O15 product:unclassifiable, fu...
Slc35b4	58246	1.63E-03	3.34E-02	1.180	solute carrier family 35, member B4 (Slc35b4), mRNA [NM_021435]
Rnase4	58809	4.06E-04	1.26E-02	1.335	ribonuclease, RNase A family 4 (Rnase4), transcript variant 1, mRNA [NM_021472]
Tssk3	58864	8.29E-07	1.03E-04	-2.122	testis-specific serine kinase 3 (Tssk3), mRNA [NM_080442]
Jph2	59091	1.04E-07	1.96E-05	-2.402	activated spleen cDNA, RIKEN full-length enriched library, clone:F830204M13 product:junctophilin 2, full insert se...
Fxyd6	59095	4.97E-05	2.69E-03	-2.174	FXYD domain-containing ion transport regulator 6 (Fxyd6), mRNA [NM_022004]
Nek6	59126	1.44E-03	3.09E-02	0.985	NIMA (never in mitosis gene a)-related expressed kinase 6 (Nek6), mRNA [NM_021606]
Ccbp2	59289	1.41E-03	9.83E-04	1.764	chemokine binding protein 2 (Ccbp2), mRNA [NM_021609]
Emcn	59308	3.29E-06	3.16E-04	1.545	endomucin (Emcn), mRNA [NM_016885]
Fn3k	63828	3.10E-08	6.99E-06	1.735	fructosamine 3 kinase (Fn3k), transcript variant 1, mRNA [NM_022014]
Trpv4	63873	1.46E-04	6.19E-03	1.312	transient receptor potential cation channel, subfamily V, member 4 (Trpv4), mRNA [NM_022017]
Rbp7	63954	1.26E-03	2.85E-02	-2.228	retinol binding protein 7, cellular (Rbp7), mRNA [NM_022020]
Nrgn	64011	1.57E-03	3.27E-02	-1.224	neurogranin (Nrgn), mRNA [NM_022029]
Ptges	64292	4.53E-04	1.35E-02	1.465	prostaglandin E synthase (Ptges), mRNA [NM_022415]
Tsc1	64930	4.29E-06	3.85E-04	-2.404	tuberous sclerosis 1 (Tsc1), mRNA [NM_022887]
Arl6ip6	65103	1.95E-03	3.77E-02	1.881	ADP-ribosylation factor-like 6 interacting protein 6 (Arl6ip6), mRNA [NM_022989]
Slc9a3r2	65962	6.21E-06	5.15E-04	1.386	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2 (Slc9a3r2), transcript variant B, mRN...
B230120H23Rik	65964	1.82E-03	3.59E-02	-2.025	RIKEN cDNA B230120H23 gene (B230120H23Rik), transcript variant 2, mRNA [NM_178084]
Gng11	66066	3.47E-07	5.10E-05	1.234	guanine nucleotide binding protein (G protein), gamma 11 (Gng11), mRNA [NM_025331]
Gtpbp8	66067	9.26E-05	4.39E-03	-2.059	13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430011P07 product:unclassifiable, full ins...
Ndufa3	66091	4.40E-06	3.93E-04	-3.028	adult male testis cDNA, RIKEN full-length enriched library, clone:1700022J01 product:weakly similar to NADH-UB...
Smpx	66106	5.08E-04	1.47E-02	3.232	small muscle protein, X-linked (Smpx), mRNA [NM_025357]
Tspan13	66109	1.26E-03	2.85E-02	-0.753	tetraspanin 13 (Tspan13), mRNA [NM_025359]
Mosc1	66112	5.76E-04	1.59E-02	3.155	MOCO sulphurase C-terminal domain containing 1 (Mosc1), mRNA [NM_001081361]
Anapc11	66156	3.36E-05	1.98E-03	-2.116	anaphase promoting complex subunit 11 (Anapc11), transcript variant 2, mRNA [NM_001038230]
Eif1ay	66235	1.96E-03	3.79E-02	-0.736	eukaryotic translation initiation factor 1A, Y-linked (Eif1ay), mRNA [NM_025437]
Isoc1	66307	2.98E-04	1.03E-02	-1.967	isochorismatase domain containing 1 (Isoc1), mRNA [NM_025478]
2810021B07Rik	66308	6.02E-05	3.08E-03	-2.149	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130054I08 product:unclassifiable, full i...

Table S1 continues on the following page

Table S1 (continued)

Gene	ID				Description
Wdr61	66317	3.83E-05	2.19E-03	-1.943	adult male testis cDNA, RIKEN full-length enriched library, clone:4932422L05 product:MEIOTIC RECOMBINATIO
Alkbh7	66400	1.03E-03	2.46E-02	-1.885	alkB, alkylation repair homolog 7 (E. coli) (Alkbh7), mRNA [NM_025538]
Golph3	66629	8.62E-04	2.15E-02	1.558	golgi phosphoprotein 3 (Golph3), mRNA [NM_025673]
Tmem186	66690	2.12E-03	3.99E-02	1.082	transmembrane protein 186 (Tmem186), mRNA [NM_025708]
Speer4c	66773	3.19E-04	1.07E-02	2.422	PREDICTED: spermatogenesis associated glutamate (E)-rich protein 4c (Speer4c), mRNA [XM_904193]
Atg10	66795	2.22E-03	4.12E-02	-1.933	autophagy-related 10 (yeast) (Atg10), mRNA [NM_025770]
Nacc1	66830	1.16E-04	5.20E-03	-2.278	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing (Nacc1), mRNA [NM_025788]
0610007N19Rik	66835	7.60E-05	3.73E-03	2.848	PREDICTED: RIKEN cDNA 0610007N19 gene (0610007N19Rik), mRNA [XM_001475347]
0610009O20Rik	66839	2.18E-08	5.15E-06	-2.955	9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030019G05 product:hypothetical Se
Slc16a9	66859	3.11E-04	1.05E-02	1.136	solute carrier family 16 (monocarboxylic acid transporters), member 9 (Slc16a9), mRNA [NM_025807]
1300014I06Rik	66895	9.18E-04	2.25E-02	1.153	RIKEN cDNA 1300014I06 gene (1300014I06Rik), mRNA [NM_025831]
Nudt16l1	66911	2.19E-03	4.08E-02	-1.838	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1 (Nudt16l1), mRNA [NM_025839]
1700010I14Rik	66931	6.65E-04	1.77E-02	1.283	RIKEN cDNA 1700010I14 gene (1700010I14Rik), mRNA [NM_025851]
Cdk5rap1	66971	3.60E-14	1.24E-10	-3.613	CDK5 regulatory subunit associated protein 1 (Cdk5rap1), mRNA [NM_025876]
Zcchc18	66995	9.52E-04	2.30E-02	-1.520	zinc finger, CCHC domain containing 18 (Zcchc18), transcript variant 1, mRNA [NM_001035510]
Tmem88	67020	1.48E-04	6.25E-03	1.368	transmembrane protein 88 (Tmem88), mRNA [NM_025915]
Mon2	67074	9.42E-06	7.14E-04	-2.729	MON2 homolog (yeast) (Mon2), mRNA [NM_153395]
2510048L02Rik	67119	1.89E-03	3.69E-02	2.379	RIKEN cDNA 2510048L02 gene (2510048L02Rik), mRNA [NM_025977]
Mastl	67121	2.36E-03	4.31E-02	2.571	microtubule associated serine (BC086483]
Lrrc40	67144	5.89E-05	3.03E-03	-2.023	leucine rich repeat containing 40 (Lrrc40), mRNA [NM_024194]
Pdzk1ip1	67182	8.54E-06	6.56E-04	1.620	PDZK1 interacting protein 1 (Pdzk1ip1), mRNA [NM_026018]
Zswim6	67263	1.22E-03	2.78E-02	-0.894	zinc finger, SWIM domain containing 6 (Zswim6), mRNA [NM_145456]
2900092E17Rik	67278	5.52E-04	1.55E-02	-0.960	RIKEN cDNA 2900092E17 gene (2900092E17Rik), mRNA [NM_030240]
Rpl37	67281	1.44E-11	1.28E-08	-3.035	ribosomal protein L37 (Rpl37), mRNA [NM_026069]
3110021A11Rik	67289	1.36E-03	2.99E-02	-1.653	13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110021A11 product:hypothetical protein, f
3110049J23Rik	67307	1.39E-03	3.04E-02	1.908	RIKEN cDNA 3110049J23 gene (3110049J23Rik), mRNA [NM_026085]
1700086P04Rik	67349	3.51E-04	1.14E-02	-2.658	BY707078 RIKEN full-length enriched, adult male testis cDNA clone 1700086P04 5'. [BY707078]
1700084E18Rik	67350	2.70E-03	4.77E-02	-1.745	PREDICTED: RIKEN cDNA 1700084E18 gene (1700084E18Rik), mRNA [XM_977942]
Ppil4	67418	1.61E-03	3.33E-02	-1.720	12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530010C12 product:unclassifiable,
Entpd4	67464	1.04E-03	2.47E-02	2.343	ectonucleoside triphosphate diphosphohydrolase 4 (Entpd4), mRNA [NM_026174]
Tmem167b	67495	2.82E-03	4.90E-02	-1.813	transmembrane protein 167B (Tmem167b), mRNA [NM_026198]
Tctn3	67590	1.62E-10	9.95E-08	-2.671	adult male testis cDNA, RIKEN full-length enriched library, clone:4930521E07 product:hypothetical DENN (AEX-3
Fibin	67606	1.64E-03	3.36E-02	2.708	fin bud initiation factor homolog (zebrafish) (Fibin), mRNA [NM_026271]
4930558C23Rik	67654	3.59E-05	2.08E-03	1.459	PREDICTED: RIKEN cDNA 4930558C23 gene (4930558C23Rik), mRNA [XM_001473262]
Slc25a37	67712	2.24E-03	4.15E-02	1.631	solute carrier family 25, member 37 (Slc25a37), nuclear gene encoding mitochondrial protein, mRNA [NM_02633
Dnajc19	67713	2.41E-03	4.38E-02	1.261	adult male testis cDNA, RIKEN full-length enriched library, clone:4921531D08 product:weakly similar to CG7394
Asprv1	67855	3.54E-04	1.15E-02	0.917	aspartic peptidase, retroviral-like 1 (Asprv1), mRNA [NM_026414]
Zfp169	67911	1.17E-10	7.62E-08	-3.001	zinc finger protein 169 (Zfp169), mRNA [NM_026450]
Ppap2b	67916	5.47E-04	1.55E-02	1.154	phosphatidic acid phosphatase type 2B (Ppap2b), mRNA [NM_080555]
Mak16	67920	8.55E-04	2.14E-02	-1.608	MAK16 homolog (S. cerevisiae) (Mak16), mRNA [NM_026453]
Slc25a39	68066	1.05E-06	1.15E-04	-2.336	solute carrier family 25, member 39 (Slc25a39), mRNA [NM_026542]
Upf3b	68134	2.87E-03	4.96E-02	2.335	UPF3 regulator of nonsense transcripts homolog B (yeast), mRNA (cDNA clone IMAGE:6491218, with apparent
Cgnl1	68178	5.19E-04	1.48E-02	1.431	cingulin-like 1 (Cgnl1), mRNA [NM_026599]
Fam98b	68215	3.56E-05	2.07E-03	-1.690	family with sequence similarity 98, member B (Fam98b), mRNA [NM_026620]
2410066E13Rik	68235	2.14E-12	2.58E-09	-3.274	RIKEN cDNA 2410066E13 gene (2410066E13Rik), mRNA [NM_026629]
Ccdc88c	68339	9.81E-10	4.22E-07	-2.658	coiled-coil domain containing 88C (Ccdc88c), mRNA [NM_026681]
Gpihbp1	68453	5.00E-11	3.35E-08	2.512	GPI-anchored HDL-binding protein 1 (Gpihbp1), mRNA [NM_026730]
Dhrs7c	68460	6.29E-04	1.70E-02	-1.748	dehydrogenase/reductase (SDR family) member 7C (Dhrs7c), mRNA [NM_001013013]
Rmnd5a	68477	1.35E-03	2.99E-02	-1.737	required for meiotic nuclear division 5 homolog A (S. cerevisiae), mRNA (cDNA clone IMAGE:4458681), with appa
1110018H23Rik	68509	7.15E-06	5.67E-04	-2.204	18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110018H23 product:hypothetical Pe
Caly	68566	4.10E-04	1.27E-02	1.346	calcyon neuron-specific vesicular protein (Caly), mRNA [NM_026769]
Ppm1f	68606	1.80E-03	3.58E-02	0.803	protein phosphatase 1F (PP2C domain containing) (Ppm1f), mRNA [NM_176833]
1110012J17Rik	68617	5.29E-06	4.54E-04	2.927	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130071O13 product:hypothetic
Myct1	68632	5.59E-05	2.93E-03	1.412	myc target 1 (Myct1), mRNA [NM_026793]
Tm2d3	68634	1.99E-07	3.33E-05	-2.440	TM2 domain containing 3 (Tm2d3), transcript variant 1, mRNA [NM_026795]
Abhd14a	68644	5.13E-10	2.43E-07	-3.069	abhydrolase domain containing 14A (Abhd14a), transcript variant 2, mRNA [NM_145919]
Fndc1	68655	3.64E-10	1.87E-07	4.296	fibronectin type III domain containing 1 (Fndc1), mRNA [NM_001081416]
Scgb3a1	68662	1.26E-07	2.30E-05	3.070	secretoglobin, family 3A, member 1 (Scgb3a1), transcript variant B, mRNA [NM_170727]
Arl8a	68724	2.66E-03	4.72E-02	0.831	ADP-ribosylation factor-like 8A (Arl8a), mRNA [NM_026823]
Dus1l	68730	1.94E-03	3.77E-02	1.862	melanocyte cDNA, RIKEN full-length enriched library, clone:G270120D15 product:hypothetical Dihydrouridine sy
Angel1	68737	3.99E-04	1.26E-02	1.736	angel homolog 1 (Drosophila) (Angel1), mRNA [NM_144524]
Flnc	68794	7.44E-04	1.93E-02	2.939	filamin C, gamma (Flnc), mRNA [NM_001081185]
Pdgfrl	68797	8.81E-04	2.18E-02	2.573	platelet-derived growth factor receptor-like (Pdgfrl), mRNA [NM_026840]
Tmcc2	68875	7.91E-07	9.88E-05	3.476	transmembrane and coiled-coil domains 2 (Tmcc2), mRNA [NM_178874]
Rasl11b	68939	2.57E-03	4.60E-02	-2.624	RAS-like, family 11, member B (Rasl11b), mRNA [NM_026878]
Spcs1	69019	6.86E-04	1.81E-02	-0.774	signal peptidase complex subunit 1 homolog (S. cerevisiae) (Spcs1), mRNA [NM_026911]
1810011O10Rik	69068	1.33E-03	2.95E-02	1.150	RIKEN cDNA 1810011O10 gene (1810011O10Rik), mRNA [NM_026931]
1810031K17Rik	69171	1.08E-03	2.54E-02	-1.688	RIKEN cDNA 1810031K17 gene (1810031K17Rik), mRNA [NM_026977]
Tmem110	69179	2.13E-03	4.00E-02	-1.866	transmembrane protein 110 (Tmem110), mRNA [NM_028839]
Tmem121	69195	2.80E-04	9.87E-03	-1.388	transmembrane protein 121 (Tmem121), mRNA [NM_153776]
Sat2	69215	4.78E-04	1.40E-02	2.710	spermidine/spermine N1-acetyl transferase 2 (Sat2), mRNA [NM_026991]
2610034M16Rik	69239	3.72E-06	3.46E-04	-2.185	RIKEN cDNA 2610034M16 gene (2610034M16Rik), mRNA [NM_027001]
1700008P20Rik	69301	1.76E-04	7.13E-03	1.846	RIKEN cDNA 1700008P20 gene (1700008P20Rik), non-coding RNA [NR_003638]
1700007K09Rik	69318	2.01E-03	3.85E-02	4.346	RIKEN cDNA 1700007K09 gene (1700007K09Rik), mRNA [NM_027037]
Glrx2	69367	2.25E-03	4.16E-02	-0.984	glutaredoxin 2 (thioltransferase) (Glrx2), transcript variant 1, mRNA [NM_001038592]
1700023A16Rik	69371	2.34E-04	8.71E-03	2.707	adult male testis cDNA, RIKEN full-length enriched library, clone:1700023A16 product:hypothetical protein, full ins
1700024P04Rik	69382	7.13E-05	3.55E-03	-2.007	adult male testis cDNA, RIKEN full-length enriched library, clone:1700024P04 product:HISTONE H2B, full insert s
1700021K14Rik	69398	4.91E-04	1.43E-02	1.167	RIKEN cDNA 1700021K14 gene (1700021K14Rik), mRNA [NM_001122635]
1700023F06Rik	69441	6.70E-04	1.78E-02	1.165	adult male testis cDNA, RIKEN full-length enriched library, clone:1700023F06 product:hypothetical protein, full ins
1700030C10Rik	69513	1.17E-04	5.21E-03	-1.808	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630001I11 product:KIAA0400 PROTEIN
Esam	69524	7.59E-06	5.94E-04	1.941	endothelial cell-specific adhesion molecule (Esam), mRNA [NM_027102]

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Mrps9	69527	2.01E-04	7.84E-03	-1.973	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430067C05 product:hypothetical protein,
Hemk1	69536	1.43E-03	3.08E-02	-1.842	HemK methyltransferase family member 1 (Hemk1), mRNA [NM_133984]
2300002D11Rik	69539	7.48E-06	5.89E-04	1.736	RIKEN cDNA 2300002D11 gene (2300002D11Rik), mRNA [NM_001081156]
Klhdc2	69554	2.20E-03	4.08E-02	-1.706	12 days embryo male wolffian region cDNA, RIKEN full-length enriched library, clone:6
Mfsd3	69572	4.57E-04	1.36E-02	-1.659	major facilitator superfamily domain containing 3 (Mfsd3), mRNA [NM_027122]
Gpx8	69590	3.98E-04	1.25E-02	1.635	glutathione peroxidase 8 (putative) (Gpx8), mRNA [NM_027127]
Clybl	69634	2.82E-03	4.89E-02	-2.139	citrate lyase beta like (Clybl), mRNA [NM_029556]
2310046K01Rik	69698	1.22E-04	5.34E-03	1.845	RIKEN cDNA 2310046K01 gene (2310046K01Rik), mRNA [NM_027172]
1810065E05Rik	69864	9.27E-04	2.27E-02	-1.915	RIKEN cDNA 1810065E05 gene (1810065E05Rik), mRNA [NM_027239]
2810011L19Rik	69952	3.28E-04	1.09E-02	-2.085	RIKEN cDNA 2810011L19 gene, mRNA (cDNA clone IMAGE:6810678), partial cds [BC059025]
1700026L06Rik	69987	4.41E-04	1.33E-02	-1.277	RIKEN cDNA 1700026L06 gene (1700026L06Rik), mRNA [NM_027283]
Trnt1	70047	1.37E-04	5.89E-03	-2.775	ES cells cDNA, RIKEN full-length enriched library, clone:2410043H24 product:tRNA nucleotidyl transferase, CCA
Nol7	70078	7.46E-05	3.69E-03	-2.149	nucleolar protein 7 (Nol7), mRNA [NM_023554]
Mllt3	70122	3.80E-04	1.21E-02	1.946	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (Mllt3), transcript
3000004C01Rik	70218	7.14E-07	9.06E-05	-2.991	RIKEN cDNA 3000004C01 gene (3000004C01Rik), mRNA [NM_197959]
Ufsp1	70240	1.48E-03	3.14E-02	1.066	UFM1-specific peptidase 1 (Ufsp1), mRNA [NM_027356]
2510049J12Rik	70291	1.55E-04	6.50E-03	-2.147	RIKEN cDNA 2510049J12 gene (2510049J12Rik), mRNA [NM_001101431]
Ndufab1	70316	2.01E-03	3.85E-02	-0.948	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1 (Ndufab1), mRNA [NM_028177]
2210416O15Rik	70393	1.72E-03	3.47E-02	-2.005	adult male stomach cDNA, RIKEN full-length enriched library, clone:2210416O15 product:hypothetical protein, fu
Wdr77	70465	1.61E-04	6.66E-03	-2.775	WD repeat domain 77 (Wdr77), mRNA [NM_027432]
Bbx	70508	1.33E-03	2.96E-02	-2.618	bobby sox homolog (Drosophila) (Bbx), mRNA [NM_027444]
Btf3l4	70533	1.64E-03	3.36E-02	1.319	basic transcription factor 3-like 4 (Btf3l4), mRNA [NM_027453]
5730442P18Rik	70559	3.16E-11	2.31E-08	-3.034	RIKEN cDNA 5730442P18 gene (5730442P18Rik), mRNA [NM_183288]
5730469M10Rik	70564	1.98E-05	1.28E-03	1.261	RIKEN cDNA 5730469M10 gene (5730469M10Rik), mRNA [NM_027464]
Ankrd24	70615	1.61E-03	3.32E-02	0.799	ankyrin repeat domain 24 (Ankrd24), mRNA [NM_027480]
5730575I04Rik	70649	1.32E-03	2.95E-02	-1.790	8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730575I04 product:unclassifiable, fu
Tspan2	70747	1.09E-08	2.83E-06	-2.807	tetraspanin 2 (Tspan2), mRNA [NM_027533]
Kynu	70789	2.88E-13	7.72E-10	-3.292	kynureninase (L-kynurenine hydrolase) (Kynu), mRNA [NM_027552]
Stox2	71069	1.28E-03	2.86E-02	1.680	storkhead box 2 (Stox2), transcript variant 2, mRNA [NM_175162]
Tssk4	71099	2.15E-04	8.16E-03	2.277	testis-specific serine kinase 4 (Tssk4), mRNA [NM_027673]
4933407L21Rik	71141	3.07E-09	1.07E-06	-3.087	adult male testis cDNA, RIKEN full-length enriched library, clone:4933407L21 product:4933407L21RIK PROTEIN
4933425L03Rik	71169	2.87E-07	4.33E-05	-2.586	RIKEN cDNA 4933425L03 gene, mRNA (cDNA clone MGC:67140 IMAGE:6822193), complete cds. [BC057020]
1700012M01Rik	71184	6.55E-05	3.31E-03	-2.167	adult male testis cDNA, RIKEN full-length enriched library, clone:4933411J23 product:hypothetical protein, full ins
Otud1	71198	7.02E-08	1.45E-05	-2.609	adult male testis cDNA, RIKEN full-length enriched library, clone:4933428L19 product:hypothetical protein, full ins
Pex1	71382	1.02E-03	2.44E-02	1.501	2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330005K07 product:hypothe
Chd6	71389	1.60E-05	1.08E-03	-2.262	chromodomain helicase DNA binding protein 6 (Chd6), mRNA [NM_173368]
Ankrd40	71452	7.89E-06	6.12E-04	-2.639	ankyrin repeat domain 40 (Ankrd40), transcript variant 1, mRNA [NM_027799]
9030409G11Rik	71529	2.82E-03	4.89E-02	1.761	RIKEN cDNA 9030409G11 gene (9030409G11Rik), transcript variant 3, mRNA [NM_001109685]
9030425E11Rik	71566	3.10E-05	1.85E-03	1.625	RIKEN cDNA 9030425E11 gene (9030425E11Rik), mRNA [NM_133733]
Myo1e	71602	3.50E-06	3.31E-04	-2.165	myosin IE (Myo1e), mRNA [NM_181072]
Rarres2	71660	2.71E-09	9.75E-07	2.078	retinoic acid receptor responder (tazarotene induced) 2 (Rarres2), mRNA [NM_027852]
Acy3	71670	6.74E-06	5.49E-04	2.013	aspartoacylase (aminoacylase) 3 (Acy3), mRNA [NM_027857]
0610010F05Rik	71675	8.34E-04	2.11E-02	-1.817	RIKEN cDNA 0610010F05 gene (0610010F05Rik), mRNA [NM_027860]
Galnt14	71685	2.16E-03	4.03E-02	-1.938	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (Galnt14), mRNA [NM_0
Esm1	71690	5.83E-07	7.81E-05	2.021	endothelial cell-specific molecule 1 (Esm1), mRNA [NM_023612]
Cic	71722	1.67E-07	2.90E-05	-2.686	capicua homolog (Drosophila), mRNA (cDNA clone IMAGE:4953397). [BC035474]
Vps11	71732	9.07E-09	2.46E-06	-2.882	vacuolar protein sorting 11 (yeast) (Vps11), mRNA [NM_027889]
Pdgfd	71785	1.30E-04	5.62E-03	-2.400	adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C630020I23 product:platelet-derived gro
Gtf2a1l	71828	4.95E-11	3.35E-08	-2.990	general transcription factor IIA, 1-like (Gtf2a1l), mRNA [NM_023630]
Nupl1	71844	2.08E-03	3.93E-02	-2.079	nucleoporin like 1 (Nupl1), mRNA [NM_170591]
Serpinb12	71869	1.24E-03	2.82E-02	-1.836	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12 (Serpinb12), mRNA [NM_027971]
Noxo1	71893	2.70E-05	1.66E-03	1.589	NADPH oxidase organizer 1, mRNA (cDNA clone MGC:28618 IMAGE:4220018), complete cds. [BC019525]
Rpap3	71919	1.73E-03	3.47E-02	-1.453	RNA polymerase II associated protein 3 (Rpap3), mRNA [NM_028003]
Scand3	71970	2.15E-03	4.02E-02	1.622	SCAN domain containing 3 (Scand3), mRNA [NM_183088]
Prmt3	71974	4.14E-04	1.28E-02	1.259	adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C630002L24 product:hypothetical protei
Tdrd12	71981	8.81E-05	4.22E-03	-1.906	tudor domain containing 12 (Tdrd12), transcript variant 2, mRNA [NM_028034]
Cyb5r1	72017	6.88E-06	5.54E-04	-2.250	cytochrome b5 reductase 1 (Cyb5r1), mRNA [NM_028057]
Tsc22d2	72033	1.39E-03	3.04E-02	-1.798	TSC22 domain family, member 2 (Tsc22d2), mRNA [NM_001081229]
Zbed3	72114	2.73E-04	9.69E-03	-1.908	zinc finger, BED domain containing 3 (Zbed3), mRNA [NM_028106]
Zfp157	72154	3.97E-07	5.70E-05	-2.368	mRNA for mszf12, partial cds. [AB010313]
Mms19	72199	1.59E-03	3.31E-02	-1.797	adult male testis cDNA, RIKEN full-length enriched library, clone:4931409L11 product:MMS19 (MET18 S. cerevis
1700001P01Rik	72215	4.55E-05	2.53E-03	3.769	RIKEN cDNA 1700001P01 gene (1700001P01Rik), mRNA [NM_028156]
1700021J08Rik	72235	1.15E-04	5.17E-03	2.403	adult male testis cDNA, RIKEN full-length enriched library, clone:1700021J08 product:unclassifiable, full insert se
Cyth4	72318	1.75E-04	7.11E-03	1.481	cytohesin 4 (Cyth4), mRNA [NM_028195]
Plxdc1	72324	1.92E-03	3.74E-02	-0.885	plexin domain containing 1 (Plxdc1), mRNA [NM_028199]
Palld	72333	2.06E-08	4.92E-06	1.825	13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430036A13 product:ACTIN-ASSOCIATED
Kcnmb2	72413	4.76E-04	1.40E-02	2.076	potassium large conductance calcium-activated channel, subfamily M, beta member 2 (Kcnmb2), mRNA [NM_02
Rnf219	72486	5.00E-06	4.35E-04	-2.221	adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230113H14 product:hypotheti
Atxn7l2	72522	2.89E-03	4.98E-02	0.779	ataxin 7-like 2 (Atxn7l2), mRNA [NM_175183]
Utp14a	72554	1.53E-09	6.25E-07	-2.701	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast) (Utp14a), mRNA [NM_028276]
Uaca	72565	2.11E-03	3.96E-02	2.696	uveal autoantigen with coiled-coil domains and ankyrin repeats (Uaca), mRNA [NM_028283]
Anks3	72615	4.54E-13	9.95E-10	-3.499	ankyrin repeat and sterile alpha motif domain containing 3 (Anks3), mRNA [NM_028301]
B3gat3	72727	9.71E-04	2.34E-02	-2.738	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I) (B3gat3), mRNA [NM_024256]
Prdm4	72843	5.88E-06	4.92E-04	-2.153	PR domain containing 4 (Prdm4), mRNA [NM_181650]
Hepacam	72927	4.96E-04	1.44E-02	-2.700	hepatocyte cell adhesion molecule (Hepacam), mRNA [NM_175189]
Insig2	72999	1.86E-06	2.04E-04	1.532	insulin induced gene 2 (Insig2), mRNA [NM_133748]
Slc22a23	73102	2.42E-03	4.39E-02	0.881	solute carrier family 22, member 23 (Slc22a23), mRNA [NM_001033167]
3110021N24Rik	73133	4.78E-05	2.63E-03	2.537	10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610002D03 product:hypothetical pr
Pear1	73182	5.35E-07	7.37E-05	-2.592	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630081A16 product:similar to MEGF12
Setd7	73251	1.46E-06	1.65E-04	-2.456	SET domain containing (lysine methyltransferase) 7 (Setd7), mRNA [NM_080793]
1700026J12Rik	73255	1.34E-03	2.96E-02	2.491	adult male testis cDNA, RIKEN full-length enriched library, clone:1700026J12 product:hypothetical INTEGRIN CD

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1700055N04Rik	73458	3.29E-04	1.09E-02	-1.657	adult male testis cDNA, RIKEN full-length enriched library, clone:1700055N04 product:hypothetical Aldehyde red
Rnf38	73469	5.44E-07	7.45E-05	-2.863	ring finger protein 38 (Rnf38), transcript variant 1, mRNA [NM_175201]
1700080E11Rik	73532	5.36E-04	1.52E-02	1.915	RIKEN cDNA 1700080E11 gene (1700080E11Rik), mRNA [NM_028562]
1700106N22Rik	73582	4.44E-04	1.33E-02	-1.886	adult male testis cDNA, RIKEN full-length enriched library, clone:1700106N22 product:similar to CDNA: FLJ2345
Trp53tg5	73603	1.12E-03	2.62E-02	-3.237	adult male testis cDNA, RIKEN full-length enriched library, clone:1700126L10 product:weakly similar to CLG01 [D
Tex19.1	73679	3.48E-06	3.31E-04	-2.445	testis expressed gene 19.1 (Tex19.1), mRNA [NM_028602]
2410089E03Rik	73692	8.39E-05	4.04E-03	-3.153	RIKEN cDNA 2410089E03 gene, mRNA (cDNA clone IMAGE:6824838), complete cds. [BC058107]
Zfp383	73729	9.81E-05	4.57E-03	-2.494	zinc finger protein 383, mRNA (cDNA clone IMAGE:6813023) [BC064456]
Whrn	73750	5.55E-15	4.34E-11	-3.864	adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230098N07 product:hypothetical prote
Lyrm1	73919	1.03E-05	7.67E-04	-2.223	LYR motif containing 1 (Lyrm1), mRNA [NM_029610]
Rftn2	74013	2.58E-04	9.35E-03	2.115	raftlin family member 2 (Rftn2), mRNA [NM_028713]
Pex26	74043	1.58E-07	2.76E-05	-2.620	peroxisomal biogenesis factor 26 (Pex26), mRNA [NM_028730]
Arpp21	74100	1.29E-08	3.24E-06	-2.619	cyclic AMP-regulated phosphoprotein, 21 (Arpp21), transcript variant 2, mRNA [NM_033264]
Iqwd1	74106	9.40E-04	2.28E-02	-2.125	adult male lung cDNA, RIKEN full-length enriched library, clone:1200006M05 product:similar to PC326 PROTEIN
Acoxl	74121	1.11E-08	2.85E-06	-3.573	acyl-Coenzyme A oxidase-like (Acoxl), mRNA [NM_028765]
Syvn1	74126	2.47E-05	1.54E-03	-2.419	synovial apoptosis inhibitor 1, synoviolin (Syvn1), mRNA [NM_028769]
Robo4	74144	1.83E-09	7.12E-07	1.963	roundabout homolog 4 (Drosophila) (Robo4), mRNA [NM_028783]
Nfx1	74164	3.62E-04	1.17E-02	-1.898	nuclear transcription factor, X-box binding 1 (Nfx1), mRNA [NM_023739]
Prei4	74182	2.77E-04	9.81E-03	0.878	adult male tongue cDNA, RIKEN full-length enriched library, clone:2310004G06 product:weakly similar to KIAA14
1200009I06Rik	74190	8.66E-08	1.67E-05	1.558	RIKEN cDNA 1200009I06 gene (1200009I06Rik), mRNA [NM_028807]
Klrg2	74253	1.80E-03	3.58E-02	1.432	killer cell lectin-like receptor subfamily G, member 2 (Klrg2), mRNA [NM_001033171]
Wdr33	74320	3.43E-07	5.07E-05	-2.457	WD repeat domain 33 (Wdr33), mRNA [NM_028866]
Ranbp10	74334	8.99E-05	4.29E-03	1.212	RAN binding protein 10 (Ranbp10), mRNA [NM_145824]
4931428F04Rik	74356	1.77E-07	3.03E-05	-2.400	RIKEN cDNA 4931428F04 gene (4931428F04Rik), mRNA [NM_028888]
4932417H02Rik	74370	1.19E-03	2.75E-02	-1.693	adult male testis cDNA, RIKEN full-length enriched library, clone:4932417H02 product:hypothetical ARM repeat s
Ubap2l	74383	7.07E-04	1.85E-02	-1.115	ubiquitin associated protein 2-like (Ubap2l), transcript variant 2, mRNA [NM_153489]
Zfp819	74400	2.26E-03	4.17E-02	0.725	zinc finger protein 819 (Zfp819), mRNA [NM_028913]
Exoc3l2	74463	9.49E-04	2.30E-02	1.063	adult male testis cDNA, RIKEN full-length enriched library, clone:4933417E01 product:hypothetical protein, full in
Samd4	74480	1.68E-03	3.41E-02	-1.669	adult male testis cDNA, RIKEN full-length enriched library, clone:1700111L17 product:unclassifiable, full insert se
8430428J23Rik	74534	6.69E-04	1.78E-02	1.205	16 days embryo lung cDNA, RIKEN full-length enriched library, clone:8430428J23 product:hypothetical protein, fu
Elovl7	74559	4.90E-06	4.28E-04	-2.557	adult female vagina cDNA, RIKEN full-length enriched library, clone:9930019E07 product:Weakly similar to elong
Glb1l	74577	1.68E-03	3.41E-02	1.091	galactosidase, beta 1-like, mRNA (cDNA clone MGC:28635 IMAGE:4222994), complete cds. [BC021773]
Mrpl47	74600	1.25E-03	2.85E-02	1.129	mitochondrial ribosomal protein L47, mRNA (cDNA clone IMAGE:4954230), partial cds [BC029173]
Trim14	74735	3.07E-04	1.05E-02	-2.572	tripartite motif-containing 14 (Trim14), mRNA [NM_029077]
Usp38	74841	1.11E-04	5.04E-03	-2.570	ubiquitin specific peptidase 38 (Usp38), mRNA [NM_027554]
Zcchc13	75064	1.32E-03	2.95E-02	2.009	zinc finger, CCHC domain containing 13 (Zcchc13), mRNA [NM_029158]
Sv2c	75209	3.49E-06	3.31E-04	-2.198	adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330582C22 product:unclassifiable
Rnf121	75212	1.02E-04	4.69E-03	-2.080	activated spleen cDNA, RIKEN full-length enriched library, clone:F830010E14 product:unclassifiable, full insert se
4930534B04Rik	75216	4.04E-07	5.76E-05	-3.037	RIKEN cDNA 4930534B04 gene (4930534B04Rik), mRNA [NM_181815]
3200002M19Rik	75430	2.91E-05	1.76E-03	-2.424	adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330414C15 product:hypothetical A
1700001C19Rik	75462	1.74E-10	1.02E-07	-3.010	RIKEN cDNA 1700001C19 gene (1700001C19Rik), mRNA [NM_029296]
Zbtb4	75580	1.69E-03	3.42E-02	1.000	zinc finger and BTB domain containing 4 (Zbtb4), mRNA [NM_029348]
2310035P21Rik	75683	3.01E-04	1.04E-02	-1.815	adult male tongue cDNA, RIKEN full-length enriched library, clone:2310035P21 product:unclassifiable, full insert s
Anks6	75691	1.72E-05	1.15E-03	-2.580	12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6
4933415A04Rik	75727	4.80E-04	1.41E-02	2.099	adult male testis cDNA, RIKEN full-length enriched library, clone:4933415A04 product:hypothetical protein, full ins
Mpp7	75739	5.98E-05	3.06E-03	-2.180	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230053G20 product:Similar to memb
Them4	75778	1.07E-03	2.51E-02	-2.039	thioesterase superfamily member 4 (Them4), mRNA [NM_029431]
5830417I10Rik	76022	5.62E-08	1.21E-05	-3.566	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230095N02 product:hypothetical pro
Arhgap15	76117	1.89E-03	3.69E-02	-1.887	Rho GTPase activating protein 15 (Arhgap15), transcript variant 1, mRNA [NM_153820]
6230409E13Rik	76132	6.66E-04	1.77E-02	-2.800	RIKEN cDNA 6230409E13 gene (6230409E13Rik), mRNA [NM_175234]
Jakmip2	76217	3.59E-05	2.08E-03	-2.244	12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230008E15 product:unclassifiable, full
6530402F18Rik	76220	1.34E-03	2.97E-02	2.028	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:6530402F18 product:hypothetical pr
Grhpr	76238	2.27E-04	8.49E-03	0.807	glyoxylate reductase/hydroxypyruvate reductase (Grhpr), mRNA [NM_080289]
Ndfip2	76273	1.62E-03	3.33E-02	1.525	10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810436B12 product:unclassifial
Prss23	76453	1.49E-04	6.29E-03	2.396	protease, serine, 23 (Prss23), mRNA [NM_029614]
Ly6k	76486	1.46E-04	6.19E-03	-2.344	lymphocyte antigen 6 complex, locus K (Ly6k), mRNA [NM_029627]
Mib2	76580	2.10E-04	8.07E-03	0.999	mindbomb homolog 2 (Drosophila) (Mib2), mRNA [NM_145124]
Ipo11	76582	1.18E-04	5.24E-03	-2.030	importin 11 (Ipo11), mRNA [NM_029665]
Srxn1	76650	2.10E-04	8.07E-03	-1.880	sulfiredoxin 1 homolog (S. cerevisiae) (Srxn1), mRNA [NM_029688]
Ttc18	76670	1.01E-03	2.43E-02	2.778	adult male testis cDNA, RIKEN full-length enriched library, clone:4921518C22 product:hypothetical TPR repeat c
Clasp1	76707	1.63E-03	3.35E-02	-1.807	CLIP associating protein 1 (Clasp1), transcript variant 1, mRNA [NM_001081276]
Rab36	76877	1.86E-06	2.04E-04	-2.260	RAB36, member RAS oncogene family (Rab36), mRNA [NM_029781]
Fam81a	76886	2.55E-03	4.58E-02	1.977	family with sequence similarity 81, member A (Fam81a), mRNA [NM_029784]
Adck4	76889	1.99E-03	3.83E-02	1.398	aarF domain containing kinase 4 (Adck4), mRNA [NM_133770]
Ifi27	76933	2.53E-04	9.20E-03	-1.343	interferon, alpha-inducible protein 27 (Ifi27), mRNA [NM_029803]
Psapl1	76943	1.02E-03	2.45E-02	-2.247	prosaposin-like 1 (Psapl1), mRNA [NM_175249]
Mpped2	77015	1.75E-04	7.11E-03	-1.947	metallophosphoesterase domain containing 2 (Mpped2), transcript variant 1, mRNA [NM_001143683]
4931408D14Rik	77059	2.10E-04	8.07E-03	-2.758	adult male testis cDNA, RIKEN full-length enriched library, clone:4931408D14 product:weakly similar to 2900054
9430040K09Rik	77280	4.54E-11	3.22E-08	-3.769	0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630032C06 product:hypothetical protein,
Fam162b	77296	8.91E-08	1.69E-05	-2.649	family with sequence similarity 162, member B (Fam162b), mRNA [NM_029894]
Ppp4r1l	77310	3.57E-06	3.36E-04	-2.166	0 day neonate head cDNA, RIKEN full-length enriched library, clone:4831403I15 product:unclassifiable, full insert
C030014I23Rik	77381	1.38E-03	3.02E-02	2.342	adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030014I23 product:hypothetical prot
Rbm35b	77411	2.13E-03	4.00E-02	-2.334	17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:I920028B02 product:Hypo
9230112J17Rik	77749	4.49E-04	1.35E-02	1.423	adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230052I24 product:unclassifiable, full
Lrrc42	77809	2.60E-04	9.40E-03	-2.107	leucine rich repeat containing 42 (Lrrc42), mRNA [NM_029985]
9430065F17Rik	77857	2.67E-04	9.57E-03	2.713	0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130110G22 product:unclassifiable, full in
Lbh	77889	2.04E-06	2.17E-04	-2.603	limb-bud and heart (Lbh), mRNA [NM_029999]
Yipf6	77929	1.86E-04	7.41E-03	-2.379	Yip1 domain family, member 6 (Yipf6), mRNA [NM_207633]
Nuak1	77976	2.09E-07	3.48E-05	-2.336	NUAK family, SNF1-like kinase, 1 (Nuak1), mRNA [NM_001004363]
Prr15	78004	6.77E-06	5.49E-04	1.652	proline rich 15 (Prr15), mRNA [NM_030024]
4930430O22Rik	78154	2.35E-03	4.30E-02	2.034	adult male testis cDNA, RIKEN full-length enriched library, clone:4930430O22 product:hypothetical protein, full in

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Ng23	78376	1.16E-03	2.70E-02	-1.912	Ng23 protein (Ng23), mRNA [NM_023893]
C330024D12Rik	78444	2.11E-04	8.08E-03	2.236	ES cells cDNA, RIKEN full-length enriched library, clone:C330024D12 product:hypothetical Pyrrolidone carboxyl
1700065I16Rik	78462	7.51E-05	3.70E-03	2.257	adult male testis cDNA, RIKEN full-length enriched library, clone:1700065I16 product:unclassifiable, full insert se
Htra3	78558	1.70E-07	2.93E-05	3.423	HtrA serine peptidase 3 (Htra3), transcript variant 1, mRNA [NM_030127]
A330105O20Rik	78590	2.07E-06	2.18E-04	-2.416	adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330105O20 product:unclassifiable, full in
Nrip3	78593	2.47E-05	1.54E-03	-2.168	nuclear receptor interacting protein 3 (Nrip3), mRNA [NM_020610]
Tnrc4	78784	6.92E-04	1.82E-02	1.671	trinucleotide repeat containing 4 (Tnrc4), mRNA [NM_172434]
5830407P18Rik	78818	1.56E-05	1.06E-03	-2.627	6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430437C10 product:unclassifiable, full ins
Pus7l	78895	1.73E-03	3.47E-02	2.537	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430080N03 product:hypothetical protein,
Spnb4	80297	9.53E-04	2.31E-02	1.513	spectrin beta 4 (Spnb4), mRNA [NM_032610]
Rhoj	80837	1.05E-04	4.82E-03	1.337	ras homolog gene family, member J (Rhoj), mRNA [NM_023275]
Ghdc	80860	9.62E-07	1.15E-04	-2.146	GH3 domain containing (Ghdc), mRNA [NM_031871]
Ifitm2	80876	2.62E-03	4.69E-02	-0.833	interferon induced transmembrane protein 2 (Ifitm2), mRNA [NM_030694]
Kank3	80880	4.68E-07	6.52E-05	1.446	KN motif and ankyrin repeat domains 3 (Kank3), mRNA [NM_030697]
Ntng1	80883	8.22E-09	2.30E-06	-2.563	PREDICTED: hypothetical protein LOC100046244 (LOC100046244), mRNA [XM_001475857]
Ankrd17	81702	3.50E-04	1.14E-02	1.169	13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030410M12 product:unclassifiable,
Tlr9	81897	3.82E-04	1.22E-02	1.040	toll-like receptor 9 (Tlr9), mRNA [NM_031178]
Glis2	83396	3.68E-04	1.18E-02	2.944	GLIS family zinc finger 2 (Glis2), mRNA [NM_031184]
Gimap3	83408	6.76E-09	1.99E-06	-2.875	GTPase, IMAP family member 3 (Gimap3), nuclear gene encoding mitochondrial protein, mRNA [NM_031247]
Tdrd1	83561	6.71E-09	1.99E-06	-2.520	tudor domain containing 1 (Tdrd1), transcript variant 3, mRNA [NM_001002241]
Bicc1	83675	4.43E-06	3.94E-04	1.789	bicaudal C homolog 1 (Drosophila) (Bicc1), mRNA [NM_031397]
Kremen1	84035	5.87E-05	3.02E-03	2.719	kringle containing transmembrane protein 1 (Kremen1), mRNA [NM_032396]
Plvap	84094	1.55E-07	2.73E-05	1.874	plasmalemma vesicle associated protein (Plvap), mRNA [NM_032398]
Zfp192	93681	1.98E-08	4.77E-06	-3.066	zinc finger protein 192 (Zfp192), mRNA [NM_139141]
Narg2	93697	7.75E-05	3.80E-03	-2.803	NMDA receptor-regulated gene 2 (Narg2), mRNA [NM_145618]
Rnf111	93836	1.56E-03	3.26E-02	1.142	ring finger 111 (Rnf111), mRNA [NM_033604]
Vangl2	93840	1.49E-03	3.16E-02	-1.881	vang-like 2 (van gogh, Drosophila) (Vangl2), mRNA [NM_033509]
Wwtr1	97064	5.34E-05	2.85E-03	1.979	WW domain containing transcription regulator 1 (Wwtr1), mRNA [NM_133784]
B3gnt9	97440	7.84E-08	1.56E-05	-2.592	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 (B3gnt9), mRNA [NM_178879]
Wdr42a	98193	1.98E-03	3.81E-02	-1.651	WD repeat domain 42A (Wdr42a), mRNA [NM_153555]
1190005F20Rik	98685	1.38E-03	3.03E-02	-2.010	RIKEN cDNA 1190005F20 gene (1190005F20Rik), mRNA [NM_026876]
Obsl1	98733	1.71E-04	7.01E-03	-2.110	obscurin-like 1 (Obsl1), mRNA [NM_178884]
Cul4a	99375	2.77E-04	9.79E-03	-1.788	cullin 4A (Cul4a), mRNA [NM_146207]
9630041G16Rik	100223	2.59E-04	9.37E-03	-2.754	16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630041G16 product:unclassifiable,
Smpdl3b	100340	1.97E-05	1.28E-03	3.004	sphingomyelin phosphodiesterase, acid-like 3B (Smpdl3b), mRNA [NM_133888]
1110008J03Rik	100764	4.19E-08	9.27E-06	-2.477	RIKEN cDNA 1110008J03 gene (1110008J03Rik), mRNA [NM_029096]
Ttll3	101100	7.09E-09	2.06E-06	-2.780	tubulin tyrosine ligase-like family, member 3, mRNA (cDNA clone IMAGE:3597662), complete cds. [BC006830]
Fbxl14	101358	2.08E-03	3.93E-02	1.066	F-box and leucine-rich repeat protein 14 (Fbxl14), mRNA [NM_133940]
Adamts9	101401	1.13E-03	2.65E-02	-1.803	10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810011L16 product:similar to ADAMT
Dhx32	101437	3.06E-04	1.04E-02	1.036	DEAH (Asp-Glu-Ala-His) box polypeptide 32 (Dhx32), mRNA [NM_133941]
Wtip	101543	5.86E-07	7.81E-05	1.849	WT1-interacting protein (Wtip), mRNA [NM_207212]
Agpat6	102247	2.01E-06	2.15E-04	-3.231	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) (Agpat6), mRNA [N
Slc6a8	102857	1.74E-05	1.16E-03	1.704	solute carrier family 6 (neurotransmitter transporter, creatine), member 8 (Slc6a8), transcript variant 1, mRNA [NM
Pls3	102866	4.73E-04	1.39E-02	1.230	plastin 3 (T-isoform) (Pls3), mRNA [NM_145629]
B630019K06Rik	102941	9.04E-05	4.30E-03	-2.668	RIKEN cDNA B630019K06 gene (B630019K06Rik), mRNA [NM_175327]
Upb1	103149	8.13E-04	2.07E-02	-0.884	ureidopropionase, beta (Upb1), mRNA [NM_133995]
Chchd10	103172	2.10E-03	3.96E-02	-0.632	coiled-coil-helix-coiled-coil-helix domain containing 10 (Chchd10), mRNA [NM_175329]
4932439E07Rik	103405	1.17E-03	2.71E-02	-1.802	adult male testis cDNA, RIKEN full-length enriched library, clone:4932439E07 product:unclassifiable, full insert se
Mgat4b	103534	2.64E-03	4.70E-02	-1.702	mannoside acetylglucosaminyltransferase 4, isoenzyme B (Mgat4b), mRNA [NM_145926]
AI449309	103727	1.99E-04	7.80E-03	2.026	UI-M-BH1-amc-g-06-0-UI.r1 NIH_BMAP_M_S2 cDNA clone UI-M-BH1-amc-g-06-0-UI 5'. [BE647330]
Cyp27a1	104086	1.63E-06	1.81E-04	-2.754	cytochrome P450, family 27, subfamily a, polypeptide 1 (Cyp27a1), nuclear gene encoding mitochondrial protein,
Adcy4	104110	1.18E-04	5.23E-03	1.278	adenylate cyclase 4 (Adcy4), mRNA [NM_080435]
Cdc42ep1	104445	3.19E-04	1.07E-02	1.392	CDC42 effector protein (Rho GTPase binding) 1 (Cdc42ep1), mRNA [NM_027219]
Ccdc117	104479	2.39E-05	1.50E-03	-3.019	coiled-coil domain containing 117 (Ccdc117), mRNA [NM_134033]
Iars	105148	7.81E-06	6.09E-04	-2.055	isoleucine-tRNA synthetase (Iars), mRNA [NM_172015]
Nhlrc1	105193	5.06E-04	1.46E-02	-2.158	NHL repeat containing 1 (Nhlrc1), mRNA [NM_175340]
Golm1	105348	1.64E-03	3.36E-02	0.650	golgi membrane protein 1 (Golm1), transcript variant 1, mRNA [NM_027307]
Fam149b	105428	1.97E-03	3.80E-02	2.419	family with sequence similarity 149, member B (Fam149b), transcript variant 1, mRNA [NM_001024512]
Slain1	105439	3.28E-06	3.16E-04	-2.149	SLAIN motif family, member 1 (Slain1), mRNA [NM_198014]
Dock9	105445	1.40E-06	1.59E-04	-2.391	dedicator of cytokinesis 9 (Dock9), transcript variant 3, mRNA [NM_001128307]
Mmrn2	105450	1.06E-05	7.82E-04	1.356	multimerin 2 (Mmrn2), mRNA [NM_153127]
Ppif	105675	2.20E-04	8.32E-03	-2.063	peptidylprolyl isomerase F (cyclophilin F) (Ppif), nuclear gene encoding mitochondrial protein, mRNA [NM_13408
Slc38a1	105727	2.22E-05	1.41E-03	-2.425	solute carrier family 38, member 1 (Slc38a1), mRNA [NM_134086]
Zc3h7a	106205	1.80E-03	3.58E-02	-1.452	zinc finger CCCH type containing 7 A (Zc3h7a), mRNA [NM_145931]
Eaf2	106389	1.81E-03	3.59E-02	-1.350	ELL associated factor 2 (Eaf2), transcript variant 1, mRNA [NM_134111]
Ift140	106633	4.80E-05	2.64E-03	3.301	intraflagellar transport 140 homolog (Chlamydomonas) (Ift140), mRNA [NM_134126]
Ttbk1	106763	1.97E-04	7.77E-03	1.619	PREDICTED: tau tubulin kinase 1 (Ttbk1), mRNA [XM_001480065]
Kctd1	106931	2.71E-03	4.78E-02	-1.877	10 days neonate olfactory brain cDNA, RIKEN full-length enriched library, clone:E530017G24 product:weakly sim
Arap3	106952	2.09E-04	8.06E-03	1.329	0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030006K04 product:PHOSPHOINOSITIDE-
Unc5b	107449	3.21E-05	1.91E-03	-2.291	unc-5 homolog B (C. elegans) (Unc5b), mRNA [NM_029770]
Tm6sf2	107770	1.45E-03	3.10E-02	1.881	transmembrane 6 superfamily member 2, mRNA (cDNA clone MGC:37441 IMAGE:4982620), complete cds. [BC(
Bfsp2	107993	1.13E-05	8.23E-04	-1.585	beaded filament structural protein 2, phakinin (Bfsp2), mRNA [NM_001002896]
Ap1s2	108012	1.92E-05	1.26E-03	-2.496	adaptor-related protein complex 1, sigma 2 subunit (Ap1s2), mRNA [NM_026887]
Lin7a	108030	7.98E-05	3.89E-03	-1.894	lin-7 homolog A (C. elegans) (Lin7a), transcript variant 1, mRNA [NM_001039354]
Ltbp4	108075	1.20E-03	2.76E-02	1.243	latent transforming growth factor beta binding protein 4 (Ltbp4), transcript variant 1, mRNA [NM_175641]
4933403F05Rik	108654	7.90E-05	3.86E-03	-1.847	RIKEN cDNA 4933403F05 gene (4933403F05Rik), mRNA [NM_153794]
Foxp1	108655	1.69E-03	3.42E-02	-2.089	adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330416B21 product:forkhead box
Mex3b	108797	5.59E-05	2.93E-03	2.225	premature mRNA for mKIAA2009 protein [AK173330]
Jmjd1c	108829	2.84E-03	4.92E-02	-1.932	mRNA for mKIAA1380 protein. [AK173162]
Cdca2	108912	6.87E-07	8.81E-05	2.241	13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930403H17 product:hypothetical prote
Obfc2a	109019	2.71E-03	4.78E-02	-1.830	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630084H02 product:unclassifiable, full i

Prkcdbp	109042	2.09E-05	1.34E-03	1.250	protein kinase C, delta binding protein (Prkcdbp), mRNA [NM_028444]
Ints5	109077	6.78E-07	8.74E-05	-2.485	integrator complex subunit 5 (Ints5), mRNA [NM_176843]
Kif24	109242	6.43E-06	5.29E-04	-2.541	kinesin family member 24 (Kif24), mRNA [NM_024241]
Tspan9	109246	1.41E-07	2.52E-05	1.777	tetraspanin 9 (Tspan9), mRNA [NM_175414]
Itga1	109700	1.96E-03	3.78E-02	-1.882	integrin alpha 1 (Itga1), mRNA [NM_001033228]
Hba-a2	110257	6.30E-09	1.90E-06	1.684	Mouse alpha-globin mRNA. [M10466]
Bcr	110279	3.93E-13	9.48E-10	-3.362	breakpoint cluster region (Bcr), mRNA [NM_001081412]
Acat2	110460	1.67E-04	6.86E-03	1.334	acetyl-Coenzyme A acetyltransferase 2 (Acat2), mRNA [NM_009338]
Fntb	110606	1.26E-04	5.49E-03	-2.799	farnesyltransferase, CAAX box, beta (Fntb), mRNA [NM_145927]
Igh	111507	1.44E-05	1.00E-03	2.909	Mouse IgMk rearranged heavy-chain mRNA variable region (V-D-J) anti-DNA autoantibody [M20831]
V1rb8	113856	2.73E-03	4.79E-02	2.201	vomeronasal 1 receptor, B8 (V1rb8), mRNA [NM_053229]
Aipl1	114230	1.14E-03	2.65E-02	2.603	aryl hydrocarbon receptor-interacting protein-like 1 (Aipl1), mRNA [NM_053245]
Dcun1d1	114893	2.30E-03	4.23E-02	-1.706	RP42 mRNA, complete cds [AF198092]
Prelp	116847	6.11E-07	8.05E-05	1.541	proline arginine-rich end leucine-rich repeat (Prelp), mRNA [NM_054077]
Slc2a9	117591	3.54E-05	2.06E-03	-2.032	solute carrier family 2 (facilitated glucose transporter), member 9 (Slc2a9), transcript variant 2, mRNA [NM_0010
Man2a2	140481	2.58E-05	1.60E-03	-2.642	mannosidase 2, alpha 2 (Man2a2), mRNA [NM_172903]
Ppp1r3a	140491	2.17E-03	4.05E-02	1.954	protein phosphatase 1, regulatory (inhibitor) subunit 3A (Ppp1r3a), mRNA [NM_080464]
Eri3	140546	2.01E-09	7.57E-07	-2.620	exoribonuclease 3 (Eri3), mRNA [NM_080469]
Sesn1	140742	2.93E-12	3.07E-09	-3.161	sestrin 1 (Sesn1), mRNA [NM_001013370]
Lnx2	140887	4.38E-04	1.32E-02	-1.965	ligand of numb-protein X 2 (Lnx2), mRNA [NM_080795]
Slc2a10	170441	2.86E-03	4.95E-02	2.644	solute carrier family 2 (facilitated glucose transporter), member 10 (Slc2a10), mRNA [NM_130451]
Grin3b	170483	7.68E-09	2.18E-06	-3.830	glutamate receptor, ionotropic, NMDA3B (Grin3b), mRNA [NM_130455]
Tmem37	170706	5.64E-04	1.57E-02	0.901	transmembrane protein 37 (Tmem37), mRNA [NM_019432]
Rac3	170758	8.45E-04	2.12E-02	1.255	RAS-related C3 botulinum substrate 3 (Rac3), mRNA [NM_133223]
Ripply3	170765	4.26E-04	1.30E-02	1.480	ripply3 homolog (zebrafish) (Ripply3), mRNA [NM_133229]
AY036118	170798	1.42E-03	3.07E-02	1.891	ETS-related transcription factor ERF (Erf1) mRNA, complete cds. [AY036118]
Usp33	170822	4.17E-04	1.28E-02	-1.996	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930083N20 product:hypothetical p
Zfp617	170938	9.29E-04	2.27E-02	-2.422	zinc finger protein 617 (Zfp617), mRNA [NM_133358]
V1rh7	171250	3.10E-05	1.85E-03	2.842	vomeronasal 1 receptor, H7 (V1rh7), mRNA [NM_134216]
Creld1	171508	1.98E-03	3.81E-02	-2.567	cysteine-rich with EGF-like domains 1 (Creld1), mRNA [NM_133930]
Stab1	192187	1.16E-04	5.20E-03	1.579	stabilin 1 (Stab1), mRNA [NM_138672]
Stab2	192188	5.94E-05	3.05E-03	1.441	stabilin 2 (Stab2), mRNA [NM_138673]
Tmlhe	192289	4.41E-04	1.33E-02	-1.874	trimethyllysine hydroxylase, epsilon (Tmlhe), mRNA [NM_138758]
Zfp286	192651	2.32E-12	2.66E-09	-3.237	zinc finger protein 286 (Zfp286), mRNA [NM_138949]
Wdr81	192652	6.22E-04	1.68E-02	0.703	PREDICTED: WD repeat domain 81 (Wdr81), mRNA [XM_001002633]
Pcdhg@	192682	1.21E-04	5.32E-03	-1.883	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930087D19 product:protocadherin
Itgb4	192897	1.42E-03	3.07E-02	1.166	integrin beta 4 (Itgb4), transcript variant 1, mRNA [NM_001005608]
BC049762	193286	2.42E-03	4.39E-02	1.775	cDNA sequence BC049762 (BC049762), mRNA [NM_177567]
Fam65b	193385	1.20E-03	2.77E-02	-1.054	family with sequence similarity 65, member B (Fam65b), transcript variant 2, mRNA [NM_001080381]
Rbms3	207181	1.59E-04	6.61E-03	-2.147	RNA binding motif, single stranded interacting protein (Rbms3), mRNA [NM_178660]
Zbtb7c	207259	6.10E-05	3.10E-03	1.232	zinc finger and BTB domain containing 7C (Zbtb7c), mRNA [NM_145356]
Kctd12b	207474	1.47E-03	3.14E-02	1.240	potassium channel tetramerisation domain containing 12b (Kctd12b), mRNA [NM_175429]
BC004728	207818	6.78E-05	3.40E-03	1.412	cDNA sequence BC004728 (BC004728), transcript variant 1, mRNA [NM_174992]
Aph1b	208117	1.90E-03	3.71E-02	-1.372	anterior pharynx defective 1b homolog (C. elegans) (Aph1b), mRNA [NM_177583]
Eif4g1	208643	8.34E-07	1.03E-04	-2.326	eukaryotic translation initiation factor 4, gamma 1 (Eif4g1), transcript variant 1, mRNA [NM_145941]
Cblb	208650	2.12E-04	8.08E-03	-1.928	9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130018P07 product:hypotheti
Aqp12	208760	2.55E-03	4.58E-02	2.415	aquaporin 12 (Aqp12), mRNA [NM_177587]
Cpeb3	208922	3.18E-04	1.07E-02	-1.977	cytoplasmic polyadenylation element binding protein 3 (Cpeb3), mRNA [NM_198300]
Npb	208990	7.79E-04	2.00E-02	-1.856	neuropeptide B (Npb), mRNA [NM_153288]
EG211331	211331	2.76E-03	4.83E-02	-0.722	BY724721 RIKEN full-length enriched, adult male aorta and vein cDNA clone A530011I23 5'. [BY724721]
Arfgef1	211673	1.26E-03	2.85E-02	-1.920	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited) (Arfgef1), mRNA [NM_00110
2810046L04Rik	212127	7.76E-04	1.99E-02	-1.776	RIKEN cDNA 2810046L04 gene (2810046L04Rik), mRNA [NM_173382]
Zswim4	212168	1.42E-03	3.07E-02	-1.715	zinc finger, SWIM domain containing 4 (Zswim4), mRNA [NM_172503]
A530054K11Rik	212281	5.75E-04	1.59E-02	-2.587	RIKEN cDNA A530054K11 gene (A530054K11Rik), mRNA [NM_183146]
2700007P21Rik	212772	1.33E-03	2.95E-02	1.037	RIKEN cDNA 2700007P21 gene (2700007P21Rik), transcript variant 1, mRNA [NM_001025102]
Kctd7	212919	1.45E-04	6.19E-03	-1.940	potassium channel tetramerisation domain containing 7 (Kctd7), mRNA [NM_172509]
Nudt18	213484	2.03E-03	3.86E-02	-1.874	nudix (nucleoside diphosphate linked moiety X)-type motif 18 (Nudt18), mRNA [NM_153136]
Efcab4a	213573	6.05E-05	3.08E-03	1.469	EF-hand calcium binding domain 4A (Efcab4a), mRNA [NM_001025103]
Tmem82	213989	1.57E-04	6.57E-03	2.430	transmembrane protein 82 (Tmem82), mRNA [NM_145987]
Crygn	214301	6.94E-04	1.82E-02	1.918	crystallin, gamma N (Crygn), mRNA [NM_153076]
2700050L05Rik	214764	4.94E-04	1.44E-02	-1.935	RIKEN cDNA 2700050L05 gene (2700050L05Rik), transcript variant 1, mRNA [NM_145995]
Zfp609	214812	1.41E-03	3.07E-02	2.737	zinc finger protein 609 (Zfp609), mRNA [NM_172536]
Cecr5	214932	2.20E-03	4.08E-02	-1.640	cat eye syndrome chromosome region, candidate 5 homolog (human) (Cecr5), mRNA [NM_144815]
Vezt	215008	1.37E-06	1.57E-04	-2.304	vezatin, adherens junctions transmembrane protein (Vezt), mRNA [NM_172538]
Rhbdd2	215160	2.84E-04	9.92E-03	-2.025	rhomboid domain containing 2 (Rhbdd2), mRNA [NM_146002]
Traf3ip3	215243	1.03E-03	2.46E-02	0.859	TRAF3 interacting protein 3 (Traf3ip3), mRNA [NM_153137]
Il1f9	215257	6.87E-04	1.81E-02	-2.010	interleukin 1 family, member 9 (Il1f9), mRNA [NM_153511]
Slc36a3	215332	2.38E-03	4.34E-02	-1.759	solute carrier family 36 (proton/amino acid symporter), member 3 (Slc36a3), mRNA [NM_172258]
Fcgbp	215384	1.38E-03	3.03E-02	2.111	Fc fragment of IgG binding protein (Fcgbp), mRNA [NM_001122603]
Rassf2	215653	2.74E-03	4.81E-02	1.096	Ras association (RalGDS/AF-6) domain family member 2 (Rassf2), mRNA [NM_175445]
Mfsd6l	215723	1.22E-03	2.80E-02	1.296	major facilitator superfamily domain containing 6-like (Mfsd6l), mRNA [NM_146004]
Pdxk	216134	2.10E-03	3.96E-02	-1.863	pyridoxal (pyridoxine, vitamin B6) kinase (Pdxk), mRNA [NM_172134]
Shc2	216148	6.72E-04	1.78E-02	1.062	src homology 2 domain-containing transforming protein C2 (Shc2), mRNA [NM_001024539]
Gls2	216456	5.31E-05	2.84E-03	1.499	glutaminase 2 (liver, mitochondrial) (Gls2), nuclear gene encoding mitochondrial protein, mRNA [NM_001033264
Chd3	216848	3.38E-05	1.98E-03	-2.090	chromodomain helicase DNA binding protein 3 (Chd3), mRNA [NM_146019]
Unc45b	217012	1.53E-05	1.05E-03	1.787	unc-45 homolog B (C. elegans) (Unc45b), mRNA [NM_178680]
Heatr6	217026	2.46E-04	9.04E-03	-1.257	HEAT repeat containing 6 (Heatr6), mRNA [NM_145432]
Myo15b	217328	9.87E-07	1.18E-04	-3.731	mRNA for mKIAA1783 protein [AK173262]
6030408C04Rik	217558	1.34E-03	2.96E-02	-1.732	RIKEN cDNA 6030408C04 gene (6030408C04Rik), mRNA [NM_001015099]
Gm527	217648	4.21E-04	1.29E-02	-1.824	gene model 527, (NCBI) (Gm527), mRNA [NM_001025605]
4933426M11Rik	217684	2.11E-11	1.70E-08	-3.272	RIKEN cDNA 4933426M11 gene (4933426M11Rik), mRNA [NM_178682]

Table S1 continues on the following page

Gene	ID				Description
Mlh3	217716	2.95E-08	6.71E-06	-2.639	mutL homolog 3 (E coli) (Mlh3), mRNA [NM_175337]
2310044G17Rik	217732	2.68E-04	9.57E-03	-1.804	RIKEN cDNA 2310044G17 gene (2310044G17Rik), mRNA [NM_173735]
BC002230	217827	2.47E-07	4.00E-05	-2.259	PREDICTED: cDNA sequence BC002230, transcript variant 1 (BC002230), mRNA [XM_484171]
Mylip	218203	1.92E-03	3.74E-02	1.142	myosin regulatory light chain interacting protein (Mylip), mRNA [NM_153789]
Ankrd34b	218440	1.95E-03	3.77E-02	-1.794	ankyrin repeat domain 34B (Ankrd34b), mRNA [NM_175455]
BC025446	223631	8.36E-04	2.11E-02	-1.880	cDNA sequence BC025446, mRNA (cDNA clone MGC:29251 IMAGE:5053382), complete cds [BC025446]
Zc3h3	223642	1.25E-05	8.89E-04	-2.162	zinc finger CCCH type containing 3 (Zc3h3), mRNA [NM_172121]
Nrbp2	223649	1.78E-05	1.18E-03	2.222	nuclear receptor binding protein 2, mRNA (cDNA clone IMAGE:6419290) [BC068117]
5031439G07Rik	223739	1.81E-03	3.59E-02	1.149	RIKEN cDNA 5031439G07 gene (5031439G07Rik), mRNA [NM_001033273]
Rnd1	223881	9.66E-05	4.52E-03	-2.043	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430040J04 product:similar to RHO-RELA
Atf7	223922	2.35E-03	4.30E-02	-1.881	NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630037N13 product:hyp
Dirc2	224132	2.02E-03	3.85E-02	0.919	disrupted in renal carcinoma 2 (human) (Dirc2), mRNA [NM_153550]
Ktelc1	224143	6.72E-08	1.41E-05	-2.445	KTEL (Lys-Tyr-Glu-Leu) containing 1 (Ktelc1), mRNA [NM_172380]
Cldnd1	224250	4.05E-04	1.26E-02	-1.487	claudin domain containing 1 (Cldnd1), mRNA [NM_171826]
Acat3	224530	3.19E-04	1.07E-02	1.697	acetyl-Coenzyme A acetyltransferase 3 (Acat3), mRNA [NM_153151]
D17Wsu92e	224647	1.35E-03	2.98E-02	-1.796	DNA segment, Chr 17, Wayne State University 92, expressed (D17Wsu92e), transcript variant 2, mRNA [NM_00
Gpr116	224792	2.86E-03	4.95E-02	1.142	G protein-coupled receptor 116 (Gpr116), mRNA [NM_001081178]
Sfrs7	225027	1.21E-03	2.77E-02	-3.114	splicing factor, arginine/serine-rich 7 (Sfrs7), mRNA [NM_146083]
Lims2	225341	2.54E-04	9.23E-03	1.670	LIM and senescent cell antigen like domains 2 (Lims2), mRNA [NM_144862]
Cep120	225523	4.43E-10	2.14E-07	-2.589	centrosomal protein 120 (Cep120), mRNA [NM_178686]
Slmo1	225655	2.03E-03	3.86E-02	1.223	10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830096K14 product:hypothetical protein
BC021614	225884	1.90E-05	1.25E-03	-2.316	cDNA sequence BC021614 (BC021614), mRNA [NM_144869]
Myof	226101	7.89E-04	2.02E-02	1.103	myoferlin (Myof), mRNA [NM_001099634]
Taf5	226182	1.94E-05	1.27E-03	-2.385	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor (Taf5), mRNA [NM_177342]
Ahctf1	226747	5.06E-05	2.74E-03	-2.007	AT hook containing transcription factor 1 (Ahctf1), mRNA [NM_026375]
Gm106	226866	2.65E-03	4.71E-02	-3.280	gene model 106, (NCBI) (Gm106), mRNA [NM_001033288]
Plcl1	227120	1.38E-08	3.43E-06	-2.791	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230017K02 product:similar to CDNA
Usp40	227334	1.61E-03	3.32E-02	2.934	ubiquitin specific peptidase 40 (Usp40), mRNA [NM_001033291]
Phyhd1	227696	2.37E-04	8.78E-03	1.053	phytanoyl-CoA dioxygenase domain containing 1 (Phyhd1), mRNA [NM_172267]
Ccdc148	227933	1.28E-03	2.87E-02	-1.759	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430070N18 product:unclassifiable, full in
Vps18	228545	3.20E-06	3.12E-04	-2.287	vacuolar protein sorting 18 (yeast) (Vps18), mRNA [NM_172269]
Prkcbp1	228880	2.47E-04	9.05E-03	-1.266	protein kinase C binding protein 1 (Prkcbp1), mRNA [NM_027230]
Tm4sf4	229302	3.49E-04	1.14E-02	1.976	transmembrane 4 superfamily member 4 (Tm4sf4), mRNA [NM_145539]
D930015E06Rik	229473	2.63E-07	4.14E-05	-3.074	2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430020C19 product:hypoth
Fhdc1	229474	2.67E-07	4.17E-05	2.153	FH2 domain containing 1 (Fhdc1), mRNA [NM_001033301]
Isg20l2	229504	5.51E-05	2.91E-03	1.368	interferon stimulated exonuclease gene 20-like 2 (Isg20l2), mRNA [NM_177663]
Smg5	229512	1.56E-03	3.26E-02	-1.717	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans), mRNA (cDNA clone MGC:118167 IMAGE
Adamtsl4	229595	5.52E-04	1.55E-02	2.833	ADAMTS-like 4 (Adamtsl4), mRNA [NM_144899]
Vangl1	229658	9.53E-05	4.49E-03	1.492	vang-like 1 (van gogh, Drosophila), mRNA (cDNA clone IMAGE:3669388), partial cds [BC024687]
Ak5	229949	2.65E-06	2.72E-04	-2.728	adenylate kinase 5 (Ak5), mRNA [NM_001081277]
Ddx58	230073	6.61E-04	1.77E-02	-1.294	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (Ddx58), mRNA [NM_172689]
Galnt12	230145	1.06E-03	2.51E-02	-2.672	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (Galnt12), mRNA [NM_
Aldob	230163	6.53E-06	5.36E-04	1.361	aldolase B, fructose-bisphosphate (Aldob), mRNA [NM_144903]
E130308A19Rik	230259	1.89E-03	3.69E-02	-1.055	RIKEN cDNA E130308A19 gene (E130308A19Rik), transcript variant 1, mRNA [NM_153158]
Atpaf1	230649	2.40E-04	8.84E-03	1.130	adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330547J17 product:unclassifiable
Fam176b	230752	3.01E-05	1.81E-03	1.051	family with sequence similarity 176, member B (Fam176b), mRNA [NM_172145]
Fam167b	230766	1.67E-03	3.39E-02	1.240	family with sequence similarity 167, member B (Fam167b), mRNA [NM_182783]
Iqcc	230767	1.48E-03	3.14E-02	-2.346	IQ motif containing C (Iqcc), mRNA [NM_198026]
Fam76a	230789	2.12E-03	3.98E-02	0.735	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130052N11 product:hypothetical prote
Nppa	230899	8.20E-04	2.09E-02	1.169	natriuretic peptide precursor type A (Nppa), mRNA [NM_008725]
Plekhn1	231002	4.32E-04	1.31E-02	1.482	pleckstrin homology domain containing, family N member 1 (Plekhn1), mRNA [NM_001008233]
Mll3	231051	1.10E-03	2.58E-02	-1.853	15 days embryo male testis cDNA, RIKEN full-length enriched library, clone:8030497B12 product:unclassifiable, f
Agbl5	231093	4.59E-04	1.36E-02	1.854	ATP/GTP binding protein-like 5 (Agbl5), transcript variant 5, mRNA [NM_174849]
Sh3tc1	231147	1.39E-04	5.95E-03	0.857	SH3 domain and tetratricopeptide repeats 1 (Sh3tc1), mRNA [NM_194344]
Guf1	231279	1.55E-04	6.50E-03	-1.957	GUF1 GTPase homolog (S. cerevisiae) (Guf1), mRNA [NM_172711]
Paqr3	231474	1.89E-03	3.69E-02	-2.167	adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330440B03 product:Bmp2-inducible ki
Fbxo21	231670	3.06E-04	1.04E-02	-1.891	F-box protein 21 (Fbxo21), mRNA [NM_145564]
Cyp26b1	232174	5.36E-05	2.85E-03	-2.028	cytochrome P450, family 26, subfamily b, polypeptide 1 (Cyp26b1), mRNA [NM_175475]
Ankrd26	232339	1.06E-04	4.86E-03	-2.387	ankyrin repeat domain 26 (Ankrd26), mRNA [NM_001081112]
Wnk1	232341	2.48E-03	4.48E-02	-1.841	adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430573H23 product:unclassifiable, ful
Gprc5a	232431	6.42E-04	1.73E-02	1.300	G protein-coupled receptor, family C, group 5, member A (Gprc5a), mRNA [NM_181444]
Lrfn3	233067	4.41E-04	1.33E-02	1.992	leucine rich repeat and fibronectin type III domain containing 3 (Lrfn3), mRNA [NM_175478]
Tbc1d17	233204	2.37E-03	4.33E-02	1.940	2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330015O10 product:interleu
Lrrk1	233328	1.16E-03	2.69E-02	-1.374	leucine-rich repeat kinase 1 (Lrrk1), mRNA [NM_146191]
Frag1	233575	2.34E-03	4.30E-02	-1.004	FGF receptor activating protein 1 (Frag1), mRNA [NM_145583]
Palb2	233826	7.33E-05	3.63E-03	-1.870	10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732427B05 product:hypothetical protein, f
Fbxl19	233902	4.18E-04	1.28E-02	1.323	F-box and leucine-rich repeat protein 19 (Fbxl19), mRNA [NM_172748]
Adprhl1	234072	1.27E-06	1.46E-04	2.058	ADP-ribosylhydrolase like 1 (Adprhl1), mRNA [NM_172750]
Whsc1l1	234135	2.44E-07	3.98E-05	-3.044	Wolf-Hirschhorn syndrome candidate 1-like 1 (human) (Whsc1l1), transcript variant 2, mRNA [NM_001081269]
Fgl1	234199	2.04E-03	3.88E-02	1.783	2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920030L09 product:hypoth
Neil3	234258	5.84E-04	1.61E-02	0.894	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630055A13 product:similar to CDNA FL
Gpm6a	234267	2.22E-16	5.35E-12	-4.293	membrane glycoprotein M6=major CNS myelin protein PLP/DM20 homolog {clone M6a} [mice, brain, mRNA, 127
Ushbp1	234395	2.71E-07	4.17E-05	3.551	Usher syndrome 1C binding protein 1 (Ushbp1), mRNA [NM_181418]
BC015286	234669	4.00E-04	1.26E-02	2.910	cDNA sequence BC015286 (BC015286), mRNA [NM_198171]
Tat	234724	5.88E-06	4.92E-04	-2.401	tyrosine aminotransferase (Tat), nuclear gene encoding mitochondrial protein, mRNA [NM_146214]
Rfwd3	234736	3.76E-04	1.20E-02	-1.715	adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230214I19 product:hypothetic
Slc38a8	234788	1.60E-03	3.31E-02	-3.660	solute carrier family 38, member 8 (Slc38a8), mRNA [NM_001009950]
Mthfsd	234814	9.15E-04	2.25E-02	-2.716	methenyltetrahydrofolate synthetase domain containing (Mthfsd), mRNA [NM_172761]
Fam38a	234839	3.26E-04	1.09E-02	2.035	premature mRNA for mKIAA0233 protein [AK129095]
Rnf214	235315	2.36E-04	8.78E-03	-1.916	ring finger protein 214 (Rnf214), mRNA [NM_178709]

Table S1 continues on the following page

Dlat	235339	7.73E-04	1.99E-02	-1.138	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) (Dlat), mRNA [NM_14
Atp2c1	235574	1.11E-05	8.11E-04	-2.194	ATPase, Ca++-sequestering (Atp2c1), mRNA [NM_175025]
Als2cl	235633	1.82E-03	3.59E-02	-1.754	ALS2 C-terminal like (Als2cl), mRNA [NM_146228]
Zfp445	235682	4.03E-06	3.64E-04	-2.554	zinc finger protein 445 (Zfp445), mRNA [NM_173364]
Alms1	236266	3.07E-06	3.03E-04	-2.449	Alstrom syndrome 1 homolog (human) (Alms1), mRNA [NM_145223]
Usp11	236733	1.24E-03	2.83E-02	1.007	ubiquitin specific peptidase 11 (Usp11), mRNA [NM_145628]
Stac3	237611	1.73E-03	3.47E-02	0.965	SH3 and cysteine rich domain 3 (Stac3), mRNA [NM_177707]
Smcr8	237782	7.24E-05	3.59E-03	-1.965	Smith-Magenis chromosome region, candidate 8 homolog (human) (Smcr8), transcript variant 2, mRNA
Usp32	237898	2.89E-06	2.88E-04	2.081	adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900074J03 product:UBIQUITIN SPECI
Cdr2l	237988	8.56E-04	2.14E-02	1.057	cerebellar degeneration-related protein 2-like (Cdr2l), mRNA [NM_001080929]
Mtr	238505	7.07E-06	5.65E-04	-1.966	5-methyltetrahydrofolate-homocysteine methyltransferase (Mtr), mRNA [NM_001081128]
Phf20l1	239510	1.03E-03	2.46E-02	-1.694	PHD finger protein 20-like 1, mRNA (cDNA clone IMAGE:4019308), complete cds. [BC052212]
Slc4a9	240215	2.73E-04	9.69E-03	1.610	solute carrier family 4, sodium bicarbonate cotransporter, member 9 (Slc4a9), mRNA [NM_172830]
Ythdc2	240255	4.59E-04	1.36E-02	-2.222	PREDICTED: YTH domain containing 2 (Ythdc2), mRNA [XM_140310]
Ccdc85b	240514	2.99E-04	1.03E-02	1.040	coiled-coil domain containing 85B (Ccdc85b), mRNA [NM_198616]
9930021J03Rik	240613	6.54E-04	1.75E-02	-2.563	RIKEN cDNA 9930021J03 gene (9930021J03Rik), mRNA [NM_172836]
EG240921	240921	2.63E-03	4.69E-02	-2.535	PREDICTED: predicted gene, EG240921 (EG240921), mRNA [XM_136331]
Ypel4	241525	1.49E-03	3.15E-02	2.783	10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830009I03 product:unclassifiable, full in
Fermt1	241639	6.44E-15	4.34E-11	-3.683	adult male colon cDNA, RIKEN full-length enriched library, clone:9030204L13 product:unclassifiable, full insert se
Bank1	242248	5.13E-04	1.47E-02	-1.533	B-cell scaffold protein with ankyrin repeats 1 (Bank1), mRNA [NM_001033350]
Lingo2	242384	1.24E-05	8.85E-04	-2.324	leucine rich repeat and Ig domain containing 2 (Lingo2), mRNA [NM_175516]
Zfp462	242466	8.30E-04	2.10E-02	-1.659	zinc finger protein 462 (Zfp462), mRNA [NM_172867]
Atg4c	242557	2.82E-04	9.90E-03	-1.949	autophagy-related 4C (yeast) (Atg4c), mRNA [NM_175029]
Adc	242669	1.66E-04	6.80E-03	3.573	arginine decarboxylase (Adc), mRNA [NM_172875]
9530096D07Rik	242681	4.26E-09	1.40E-06	-2.641	adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530096D07 product:unclassifiable, fu
Rsbn1l	242860	1.26E-03	2.85E-02	1.086	BB635789 RIKEN full-length enriched, 0 day neonate thymus cDNA clone A430085L23 5', mRNA sequence [BB6
H1fx	243529	1.37E-03	3.01E-02	1.004	AGENCOURT_10129125 NIH_MGC_134 cDNA clone IMAGE:6506165 5', mRNA sequence [BU511373]
Plxna4	243743	1.55E-03	3.25E-02	2.533	plexin A4 (Plxna4), mRNA [NM_175750]
Gp6	243816	1.20E-03	2.76E-02	1.934	PREDICTED: glycoprotein 6 (platelet) (Gp6), mRNA [XM_145298]
Gm505	244666	2.75E-03	4.82E-02	-1.537	16 days embryo lung cDNA, RIKEN full-length enriched library, clone:8430404H04 product:hypothetical protein, f
Fam70a	245386	9.63E-05	4.52E-03	-1.909	family with sequence similarity 70, member A (Fam70a), mRNA [NM_172930]
Cd207	246278	9.13E-09	2.46E-06	4.169	CD207 antigen (Cd207), mRNA [NM_144943]
Lgi2	246316	2.63E-07	4.14E-05	-2.579	mRNA for mKIAA1916 protein. [AK122570]
Oas3	246727	2.52E-03	4.53E-02	-1.615	2'-5' oligoadenylate synthetase 3 (Oas3), mRNA [NM_145226]
Olfr95	258506	2.42E-03	4.39E-02	-1.483	olfactory receptor 95 (Olfr95), mRNA [NM_146513]
Olfr1368	258527	1.93E-03	3.75E-02	0.280	olfactory receptor 1368 (Olfr1368), mRNA [NM_146534]
Olfr700	258593	1.22E-03	2.78E-02	-3.203	olfactory receptor 700 (Olfr700), mRNA [NM_146600]
Olfr611	258722	1.70E-05	1.14E-03	-2.220	olfactory receptor 611 (Olfr611), mRNA [NM_146727]
Cadm4	260299	4.74E-07	6.57E-05	2.590	cell adhesion molecule 4 (Cadm4), mRNA [NM_153112]
Acsf2	264895	2.13E-04	8.09E-03	-1.980	acyl-CoA synthetase family member 2 (Acsf2), mRNA [NM_153807]
Irak4	266632	8.40E-04	2.12E-02	-1.728	interleukin-1 receptor-associated kinase 4 (Irak4), mRNA [NM_029926]
Cpne1	266692	1.20E-04	5.28E-03	-2.215	copine I (Cpne1), transcript variant 1, mRNA [NM_170588]
Zbtb24	268294	2.09E-05	1.34E-03	-2.024	zinc finger and BTB domain containing 24 (Zbtb24), mRNA [NM_153398]
Rapgefl1	268480	1.41E-03	3.07E-02	-2.556	Rap guanine nucleotide exchange factor (GEF)-like 1 (Rapgefl1), mRNA [NM_001080925]
4930503L19Rik	269033	2.00E-03	3.84E-02	-1.539	RIKEN cDNA 4930503L19 gene (4930503L19Rik), mRNA [NM_172967]
C030048B08Rik	269623	4.03E-05	2.27E-03	-2.225	RIKEN cDNA C030048B08 gene (C030048B08Rik), mRNA [NM_172991]
Mphosph9	269702	7.23E-05	3.59E-03	-2.049	M-phase phosphoprotein 9 (Mphosph9), mRNA [NM_001081323]
Zfp384	269800	3.78E-05	2.17E-03	1.722	zinc finger protein 384 (Zfp384), mRNA [NM_175557]
Tspan12	269831	8.51E-06	6.56E-04	1.852	tetraspanin 12 (Tspan12), mRNA [NM_173007]
AW121567	270028	9.38E-07	1.13E-04	-2.428	expressed sequence AW121567 (AW121567), mRNA [NM_173446]
Pcnxl2	270109	1.32E-05	9.28E-04	-2.313	pecanex-like 2 (Drosophila) (Pcnxl2), transcript variant 2, mRNA [NM_175561]
Myo9a	270163	2.87E-03	4.95E-02	-1.890	10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732465J09 product:MYOSIN-IXA homolog
Pfkfb4	270198	8.29E-04	2.10E-02	0.646	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (Pfkfb4), mRNA [NM_173019]
Zbtb11	271377	3.16E-10	1.66E-07	-2.796	PREDICTED: zinc finger and BTB domain containing 11 (Zbtb11), mRNA [XM_001481121]
Shc4	271849	1.00E-04	4.64E-03	1.811	SHC (Src homology 2 domain containing) family, member 4 (Shc4), mRNA [NM_199022]
A630047E20Rik	271981	1.33E-09	5.63E-07	-2.789	RIKEN cDNA A630047E20 gene (A630047E20Rik), mRNA [NM_173032]
Tbcel	272589	1.81E-04	7.28E-03	1.068	tubulin folding cofactor E-like (Tbcel), mRNA [NM_173038]
C530036F05Rik	319355	2.62E-04	9.44E-03	1.982	12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530036F05 product:unclassifiable,
C920008N22Rik	319366	4.42E-05	2.47E-03	-2.276	2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920008N22 product:unclas
D230002A01Rik	319388	1.05E-03	2.49E-02	-2.131	12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230002A01 product:hypothetical protei
Itga11	319480	2.65E-03	4.71E-02	1.922	integrin alpha 11 (Itga11), mRNA [NM_176922]
Nrcam	319504	1.81E-03	3.59E-02	1.922	neuron-glia-CAM-related cell adhesion molecule (Nrcam), mRNA [NM_176930]
Fam113a	319513	1.76E-12	2.36E-09	-3.539	family with sequence similarity 113, member A (Fam113a), transcript variant 1, mRNA [NM_178762]
A430010J10Rik	319665	4.09E-04	1.27E-02	-1.767	2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920008P08 product:hypoth
Mpzl3	319742	3.72E-05	2.14E-03	-1.969	myelin protein zero-like 3 (Mpzl3), transcript variant 1, mRNA [NM_176993]
Zcchc7	319885	2.10E-03	3.96E-02	-2.209	zinc finger, CCHC domain containing 7 (Zcchc7), transcript variant 2, mRNA [NM_177027]
Fstl4	320027	9.59E-05	4.51E-03	-1.936	follistatin-like 4 (Fstl4), mRNA [NM_177059]
Zdhhc17	320150	2.07E-05	1.33E-03	1.952	zinc finger, DHHC domain containing 17 (Zdhhc17), mRNA [NM_172554]
Lrrc58	320184	1.55E-03	3.25E-02	-2.047	leucine rich repeat containing 58 (Lrrc58), mRNA [NM_177093]
Tmem91	320208	5.13E-04	1.47E-02	1.808	transmembrane protein 91 (Tmem91), mRNA [NM_177102]
2-Mar	320253	1.38E-07	2.50E-05	-2.534	membrane-associated ring finger (C3HC4) 3 (March3), mRNA [NM_177115]
A930041I02Rik	320271	1.36E-03	2.99E-02	-1.940	RIKEN cDNA A930041I02 gene (A930041I02Rik), mRNA [NM_178778]
A430035B10Rik	320312	1.47E-03	3.13E-02	1.380	adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330071G13 product:unclassifiable, full in
Fry	320365	2.13E-03	3.99E-02	-2.489	mRNA for mKIAA4143 protein. [AK220506]
A430057L12Rik	320372	3.11E-04	1.05E-02	1.276	adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330442C03 product:unclassifiable
D930030O05Rik	320387	7.09E-04	1.86E-02	-1.726	9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030028K24 product:unclassifiable, f
Klri2	320407	5.85E-06	4.92E-04	-2.543	killer cell lectin-like receptor family I member 2 (Klri2), mRNA [NM_177155]
Heatr5a	320487	6.06E-06	1.65E-02	-2.692	HEAT repeat containing 5A (Heatr5a), mRNA [NM_177171]
9830001H06Rik	320706	2.78E-04	9.82E-03	1.732	PREDICTED: RIKEN cDNA 9830001H06 gene (9830001H06Rik), mRNA [XM_283804]
Tmem117	320709	2.64E-03	4.71E-02	2.992	transmembrane protein 117 (Tmem117), mRNA [NM_178789]
Ipo8	320727	5.82E-04	1.61E-02	-1.907	importin 8 (Ipo8), mRNA [NM_001081113]

Table S1 continues on the following page

B230217O12Rik	320879	1.03E-05	7.67E-04	-2.257	9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030014C21 product:unclassifiable, f
Wscd2	320916	6.37E-07	8.35E-05	-2.403	WSC domain containing 2 (Wscd2), mRNA [NM_177292]
Tmem26	327766	8.38E-04	2.11E-02	-2.968	transmembrane protein 26 (Tmem26), mRNA [NM_177794]
Ppfia2	327814	7.30E-04	1.90E-02	3.180	adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330438O12 product:hypothetical prote
Slc39a9	328133	2.23E-04	8.37E-03	-2.916	solute carrier family 39 (zinc transporter), member 9, mRNA (cDNA clone IMAGE:30536025), partial cds. [BC072
Mast4	328329	1.43E-04	6.13E-03	3.192	bone marrow stroma cell CRL-2028 SR-4987 cDNA, RIKEN full-length enriched library, clone:G431004F08 produ
Apol11b	328563	2.16E-03	4.03E-02	-2.068	apolipoprotein L 11b (Apol11b), mRNA [NM_001143686]
D430006K04	328861	4.68E-04	1.38E-02	-1.693	13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430006K04 product:hypothetical protein, f
AI847670	330050	2.71E-06	2.76E-04	-2.226	expressed sequence AI847670 (AI847670), mRNA [NM_177869]
BC038925	330216	5.47E-04	1.55E-02	-1.217	cDNA sequence BC038925 (BC038925), mRNA [NM_177878]
Fbxo41	330369	1.05E-03	2.49E-02	-2.155	F-box protein 41 (Fbxo41), mRNA [NM_001001160]
Lphn1	330814	3.58E-04	1.16E-02	-1.744	latrophilin 1 (Lphn1), mRNA [NM_181039]
Slc7a6	330836	8.91E-08	1.69E-05	-2.887	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (Slc7a6), mRNA [NM_178798]
Hcn4	330953	1.73E-03	3.47E-02	1.331	hyperpolarization-activated, cyclic nucleotide-gated K+ 4 (Hcn4), mRNA [NM_001081192]
Cntln	338349	5.69E-04	1.58E-02	-1.781	centlein, centrosomal protein (Cntln), transcript variant 1, mRNA [NM_175275]
Ust	338362	2.35E-04	8.73E-03	3.231	uronyl-2-sulfotransferase (Ust), mRNA [NM_177387]
A730011L01Rik	338371	2.71E-03	4.78E-02	0.894	RIKEN cDNA A730011L01 gene (A730011L01Rik), mRNA [NM_177394]
Egfl7	353156	8.57E-04	2.14E-02	0.852	EGF-like domain 7 (Egfl7), transcript variant a, mRNA [NM_178444]
Muc6	353328	4.20E-04	1.29E-02	2.038	mucin 6, gastric (Muc6), mRNA [NM_181729]
Trim46	360213	1.61E-04	6.66E-03	1.624	tripartite motif-containing 46 (Trim46), transcript variant 2, mRNA [NM_183037]
Txlnb	378431	1.97E-10	1.13E-07	-2.984	taxilin beta (Txlnb), mRNA [NM_138628]
Fastkd5	380601	1.22E-05	8.73E-04	-2.045	FAST kinase domains 5 (Fastkd5), mRNA [NM_198176]
Intu	380614	5.14E-05	2.77E-03	1.574	inturned planar cell polarity effector homolog (Drosophila) (Intu), mRNA [NM_175515]
Ccnjl	380694	2.00E-04	7.82E-03	1.728	cyclin J-like (Ccnjl), mRNA [NM_001045530]
AI324046	380795	2.43E-06	2.54E-04	-3.425	mRNA for mFLJ00385 protein [AK131185]
Fam82a1	381110	9.71E-09	2.54E-06	-3.138	family with sequence similarity 82, member A1 (Fam82a1), mRNA [NM_201361]
Tmem151a	381199	4.11E-04	1.27E-02	1.545	transmembrane protein 151A (Tmem151a), mRNA [NM_001001885]
Als2cr4	381259	1.11E-11	1.03E-08	-4.077	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4 (Als2cr4), transcript variant 2, mRNA [
Tbc1d2	381605	8.32E-04	2.11E-02	1.313	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630005A06 product:hypothetical Plecks
Ssbp1	381760	1.50E-03	3.16E-02	-1.967	single-stranded DNA binding protein 1 (Ssbp1), transcript variant 1, mRNA [NM_212468]
4922501C03Rik	382090	1.58E-05	1.07E-03	1.922	RIKEN cDNA 4922501C03 gene (4922501C03Rik), mRNA [NM_199316]
A830080D01Rik	382252	2.45E-06	2.55E-04	-2.163	RIKEN cDNA A830080D01 gene (A830080D01Rik), mRNA [NM_001033472]
Wdr51b	382406	1.70E-04	6.94E-03	3.480	WD repeat domain 51B (Wdr51b), mRNA [NM_027740]
383196	383196	5.86E-04	1.61E-02	2.761	Immunoglobulin Kappa light chain V gene segment [Source:IMGT/GENE-DB
384261	384261	6.35E-05	3.22E-03	-2.032	PREDICTED: hypothetical LOC384261 (LOC384261), mRNA [XM_986220]
Map4k5	399510	1.61E-04	6.66E-03	0.973	mitogen-activated protein kinase kinase kinase kinase 5 (Map4k5), mRNA [NM_201519]
Plcxd1	403178	4.69E-09	1.47E-06	-2.870	phosphatidylinositol-specific phospholipase C, X domain containing 1 (Plcxd1), mRNA [NM_207279]
Iqgap3	404710	2.57E-03	4.60E-02	-0.984	IQ motif containing GTPase activating protein 3 (Iqgap3), mRNA [NM_001033484]
Bex4	406217	3.30E-04	1.09E-02	1.058	brain expressed gene 4 (Bex4), mRNA [NM_212457]
Specc1	432572	5.08E-04	1.47E-02	1.547	sperm antigen with calponin homology and coiled-coil domains 1 (Specc1), mRNA [NM_001029936]
EG434025	434025	6.75E-05	3.40E-03	-1.959	anti-DNA antibody light chain variable region mRNA, partial cds [U88675]
Gpr62	436090	2.73E-06	2.77E-04	3.407	BY714829 RIKEN full-length enriched, adult male testis cDNA clone 4930431J04 5'. [BY714829]
Ccin	442829	3.78E-06	3.47E-04	1.933	calicin (Ccin), mRNA [NM_001002787]
Cep170	545389	1.92E-03	3.73E-02	-2.016	centrosomal protein 170 (Cep170), mRNA [NM_001099637]
Zfp551	619331	7.16E-08	1.46E-05	-2.737	zinc fingr protein 551 (Zfp551), mRNA [NM_001033820]
Igk-V21-4	626347	6.92E-07	8.83E-05	-4.867	immunoglobulin kappa chain variable 21 (V21)-4, mRNA (cDNA clone MGC:118186 IMAGE:4989625), complete
631105	631105	1.03E-03	2.46E-02	2.795	PREDICTED: similar to fimbriae-associated protein Fap1, transcript variant 1 (LOC631105), mRNA [XM_904722]
ENSMUSG0000(	632737	2.42E-03	4.39E-02	3.745	PREDICTED: predicted gene, EG666638 (EG666638), mRNA [XM_985112]
Sbpl	638345	3.48E-04	1.14E-02	3.104	spermine binding protein-like (Sbpl), mRNA [NM_001077421]
LOC639988	639988	2.03E-06	2.17E-04	-1.829	PREDICTED: similar to immunoglobulin gamma-chain (LOC639988), mRNA [XM_916675]
LOC640979	640979	5.83E-07	7.81E-05	-2.284	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE-DB
EG665317	665317	1.07E-05	7.87E-04	-2.330	PREDICTED: predicted gene, EG665317, transcript variant 1 (EG665317), mRNA [XM_979163]
Hmcn2	665700	7.71E-04	1.99E-02	2.569	9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030068H01 product:inferred: hemic
EG665756	665756	8.97E-04	2.21E-02	1.872	PREDICTED: predicted gene, EG665756 (EG665756), mRNA [XM_979235]
EG668139	668139	5.74E-04	1.59E-02	-0.958	PREDICTED: predicted gene, EG668139 (EG668139), misc RNA [XR_001627]
Zfp507	668501	2.14E-05	1.36E-03	3.010	zinc finger protein 507 (Zfp507), mRNA [NM_177739]
RP23-212C14.7	670533	1.49E-03	3.15E-02	1.272	keratin associated protein 9 family member (LOC670533), mRNA [NM_001101613]
4732444A12Rik	100015211	3.11E-10	1.66E-07	-3.284	21 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:G630051C23 product:hypothetical p
ENSMUSG0000	100038553	4.41E-10	2.14E-07	-3.215	predicted gene, ENSMUSG00000073540, mRNA (cDNA clone MGC:14005 IMAGE:3660311), complete cds. [BC
100042757	100042757	1.89E-04	7.54E-03	2.379	PREDICTED: hypothetical protein LOC100046917 (LOC100046917), mRNA [XM_001477379]
100043468	100043468	5.09E-04	1.47E-02	-1.967	predicted gene, 100043468 (100043468), mRNA [NM_001142957]
LOC100047628	100047628	4.28E-04	1.30E-02	-2.270	Immunoglobulin Kappa light chain V gene segment [Source:IMGT/GENE-DB
LOC100048021	100048021	3.95E-04	1.25E-02	0.731	PREDICTED: similar to Guanine nucleotide-binding protein alpha-12 subunit (G alpha-12) (LOC100048021), mR
ENSMUSG0000(	100126228	7.57E-06	5.94E-04	1.253	adult male testis cDNA, RIKEN full-length enriched library, clone:4933429E06 product:hypothetical protein, full in

Table S2

Functional Clustering of Differentially Expressed Genes in VSELs Exposed to Intermittent Hypoxia

Annotation Cluster 1   Enrichment Score: 6.410687762258607

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0007275~multicellular organismal development	204	9.74E-11	1.520
Biological Process	GO:0032502~developmental process	217	1.54E-10	1.486
Biological Process	GO:0048856~anatomical structure development	176	2.88E-09	1.523
Biological Process	GO:0048731~system development	164	1.50E-08	1.520
Biological Process	GO:0048513~organ development	135	3.59E-07	1.525
Biological Process	GO:0009653~anatomical structure morphogenesis	96	2.30E-06	1.619
Biological Process	GO:0030154~cell differentiation	119	5.04E-05	1.425
Biological Process	GO:0048869~cellular developmental process	123	5.46E-05	1.412
Biological Process	GO:0032501~multicellular organismal process	245	1.37E-01	1.063

Annotation Cluster 2   Enrichment Score: 4.409348996268908

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0001568~blood vessel development	32	6.00E-06	2.463
Biological Process	GO:0001944~vasculature development	32	9.81E-06	2.404
Biological Process	GO:0048514~blood vessel morphogenesis	27	1.83E-05	2.561
Biological Process	GO:0001525~angiogenesis	20	7.68E-05	2.825

Annotation Cluster 3   Enrichment Score: 3.8059194810335697

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0009790~embryonic development	63	1.35E-05	1.766
Biological Process	GO:0043009~chordate embryonic development	45	1.39E-05	2.008
Biological Process	GO:0048598~embryonic morphogenesis	40	1.80E-05	2.093
Biological Process	GO:0048568~embryonic organ development	27	4.84E-04	2.104
Biological Process	GO:0001701~in utero embryonic development	27	2.17E-03	1.899
Biological Process	GO:0009887~organ morphogenesis	43	3.66E-02	1.360

Annotation Cluster 4   Enrichment Score: 2.6233303269471335

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0048598~embryonic morphogenesis	40	1.80E-05	2.093
Biological Process	GO:0035113~embryonic appendage morphogenesis	14	1.83E-03	2.711
Biological Process	GO:0030326~embryonic limb morphogenesis	14	1.83E-03	2.711
Biological Process	GO:0035108~limb morphogenesis	14	8.02E-03	2.287
Biological Process	GO:0035107~appendage morphogenesis	14	8.02E-03	2.287
Biological Process	GO:0060173~limb development	14	1.06E-02	2.210
Biological Process	GO:0048736~appendage development	14	1.06E-02	2.210

Annotation Cluster 5   Enrichment Score: 2.5479907939308135

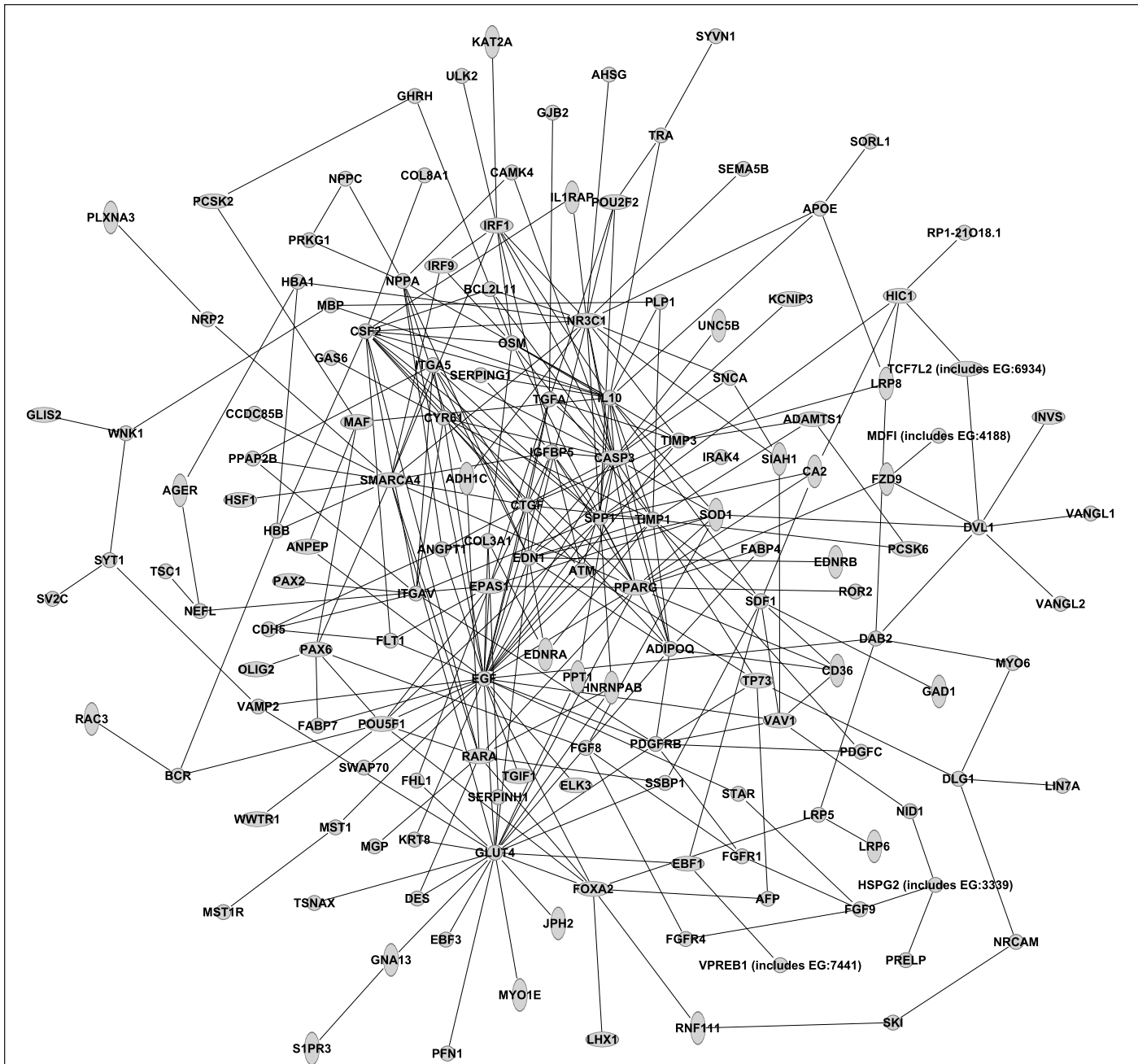| Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0001822~kidney development	17	1.61E-04	2.984
Biological Process	GO:0001655~urogenital system development	18	1.93E-03	2.316
Biological Process	GO:0001657~ureteric bud development	8	6.18E-03	3.578
Biological Process	GO:0001656~metanephros development	8	3.33E-02	2.591

Table S2 continues on the following page

Table S2 (continued)

Annotation Cluster 6   Enrichment Score: 2.512425848615364

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0048598~embryonic morphogenesis	40	1.80E-05	2.093
Biological Process	GO:0048568~embryonic organ development	27	4.84E-04	2.104
Biological Process	GO:0043583~ear development	14	3.42E-03	2.529
Biological Process	GO:0048562~embryonic organ morphogenesis	18	5.35E-03	2.100
Biological Process	GO:0042471~ear morphogenesis	11	6.76E-03	2.719
Biological Process	GO:0048839~inner ear development	12	6.81E-03	2.561
Biological Process	GO:0042472~inner ear morphogenesis	10	8.71E-03	2.803
Biological Process	GO:0007423~sensory organ development	24	1.05E-02	1.754
Biological Process	GO:0009887~organ morphogenesis	43	3.66E-02	1.360

Annotation Cluster 7   Enrichment Score: 2.432221052606057

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0007155~cell adhesion	48	1.35E-03	1.607
Biological Process	GO:0022610~biological adhesion	48	1.40E-03	1.604
Biological Process	GO:0016337~cell-cell adhesion	21	2.68E-02	1.671

Annotation Cluster 8   Enrichment Score: 2.3347226255726903

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0035295~tube development	31	7.20E-05	2.206
Biological Process	GO:0001569~patterning of blood vessels	6	7.66E-03	4.696
Biological Process	GO:0035239~tube morphogenesis	18	9.63E-03	1.977
Biological Process	GO:0001763~morphogenesis of a branching structure	14	1.55E-02	2.104
Biological Process	GO:0048754~branching morphogenesis of a tube	11	2.57E-02	2.222

Annotation Cluster 9   Enrichment Score: 2.2522030394510346

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0007420~brain development	29	1.53E-03	1.891
Biological Process	GO:0007399~nervous system development	64	4.83E-03	1.408
Biological Process	GO:0007417~central nervous system development	32	8.12E-03	1.629
Biological Process	GO:0030900~forebrain development	17	1.63E-02	1.912

Annotation Cluster 10   Enrichment Score: 2.0995523296663214

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0019216~regulation of lipid metabolic process	10	3.31E-03	3.239
Biological Process	GO:0019218~regulation of steroid metabolic process	6	5.18E-03	5.123
Biological Process	GO:0050810~regulation of steroid biosynthetic process	5	8.64E-03	5.870
Biological Process	GO:0046890~regulation of lipid biosynthetic process	5	2.70E-02	4.269

Annotation Cluster 11   Enrichment Score: 2.0748660760971993

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0035295~tube development	31	7.20E-05	2.206
Biological Process	GO:0030324~lung development	13	1.48E-02	2.200
Biological Process	GO:0030323~respiratory tube development	13	1.69E-02	2.161
Biological Process	GO:0060541~respiratory system development	13	3.23E-02	1.969
Biological Process	GO:0008543~fibroblast growth factor receptor signaling pathway	5	7.26E-02	3.131

Table S2 continues on the following page

Table S2 (continued)

Annotation Cluster 12   Enrichment Score: 1.8887932893479804

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0001558~regulation of cell growth	15	3.39E-04	3.063
Biological Process	GO:0045792~negative regulation of cell size	9	6.52E-03	3.190
Biological Process	GO:0030308~negative regulation of cell growth	8	1.15E-02	3.197
Biological Process	GO:0045926~negative regulation of growth	9	3.42E-02	2.381
Biological Process	GO:0008361~regulation of cell size	11	6.13E-02	1.913
Biological Process	GO:0032535~regulation of cellular component size	14	8.76E-02	1.633

Annotation Cluster 13   Enrichment Score: 1.8348372706488445

Category	Term	Number of Genes	P-value	Fold Enrichment
GOTERM_MF_ALL	GO:0008034~lipoprotein binding	6	4.64E-03	5.239
GOTERM_MF_ALL	GO:0005041~low-density lipoprotein receptor activity	4	1.06E-02	8.150
GOTERM_MF_ALL	GO:0030169~low-density lipoprotein binding	4	3.06E-02	5.642
GOTERM_MF_ALL	GO:0030228~lipoprotein receptor activity	4	3.06E-02	5.642

Annotation Cluster 14   Enrichment Score: 1.830345700823631

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0007389~pattern specification process	28	2.54E-03	1.852
Biological Process	GO:0003002~regionalization	20	1.98E-02	1.755
Biological Process	GO:0009952~anterior/posterior pattern formation	14	6.41E-02	1.719

Annotation Cluster 15   Enrichment Score: 1.5577264652830227

Category	Term	Number of Genes	P-value	Fold Enrichment
Biological Process	GO:0001501~skeletal system development	26	9.88E-03	1.714
Biological Process	GO:0060348~bone development	13	2.30E-02	2.069
Biological Process	GO:0001503~ossification	12	2.52E-02	2.126
Biological Process	GO:0001649~osteoblast differentiation	6	1.03E-01	2.398

Figure S1