**Supplementary Information:** Hüttenrauch M. et al.

**Physical activity delays hippocampal neurodegeneration and rescues memory deficits in an Alzheimer disease mouse model**

Supplementary Figure S1:
Spatial working memory was evaluated using the cross-maze task (a, b). (a) Tg4-42<sup>het</sup> EE mice displayed significantly higher alternation rates in the cross-maze task. The dotted line represents chance level. (b) The enhanced alternation is not due to higher explorative behavior as there is no difference in total arm entries between SH and EE mice. (c) Enriched housed Tg4-42<sup>het</sup> mice spent more time in the center of the open field compared with Tg4-42<sup>het</sup> SH mice. (d) No differences in activity levels could be detected between standard and enriched housed Tg4-42<sup>het</sup> mice during the open field task. All data were given as means ± standard error of the mean (SEM) (**p < 0.01; *p < 0.05).

**Cross-Maze:** Working memory was assessed by analyzing spontaneous alternation behavior in the Cross-Maze task. The Cross-Maze consists of 4 arms, constructed from black plastic material with arm sizes of 30 cm x 8 cm. During 10 min test sessions, each mouse was randomly placed in one arm and allowed to move freely through the maze. Alternation was defined as successive entries into the four arms in overlapping quadruple sets. An entry was defined to be successive as soon as a mouse enters an arm with all four paws. The percent alternation was calculated as the ratio of actual to possible alternations. In order to diminish odor cues, the maze was cleaned with a solution containing 30% ethanol, 60% water and 10% odorless soap (Cotel et al., Neurobiol Aging 33: 96-107 (2012)).

**Open Field:** The open field test was used to assess both exploratory behavior and locomotor activity. The mice were tested using an open field box made of grey plastic with 50 x 50 cm surface area and 38 cm-high walls. Monitoring was done by an automated tracking system (AnyMaze, Stoelting). The percentage of time spent in the central part (20 x 20 cm) and the total active time was recorded (Jawhar et al., Neurobiol Aging 33: 196.e29–196.e40 (2012)).
Supplementary Figure S2:

(a, d) In the cued training phase of the Morris water maze test, Tg4-42$^{\text{het}}$ SH or EE mice did not show any differences in the swimming speed, while Tg4-42$^{\text{hom}}$ EE mice swam significantly faster compared to SH mice. (b, e) Tg4-42$^{\text{het}}$ SH and EE mice showed similar swimming speeds during the acquisition training trials while Tg4-42$^{\text{hom}}$ EE mice again swam faster compared to standard housed mice. (c, f) During the probe trial, Tg4-42$^{\text{het}}$ EE mice showed a slightly increased swimming speed compared to Tg4-42$^{\text{hom}}$ SH mice while there was no speed difference between groups in Tg4-42$^{\text{hom}}$ mice. All data were given as means ± standard error of the mean (SEM) (***p < 0.001; *p < 0.05).
Supplementary Figure S3:

(a) Overview of voluntary wheel running performance of Tg4-42 hom mice in the recording period of 11 weeks. The average distance (km) per week is represented. (b) Exemplary picture of the tail hyperflexion phenotype due to the regular running wheel usage. All data were given as means ± standard error of the mean (SEM).

During the weeks of running wheel training mice were housed in single cages with food and water ad libitum. All animals had continuous voluntary access to a running wheel with a diameter of 11.3 cm placed inside the cage. A rotation sensor connected to the running wheel axis transmitted running activity with a resolution of 1/16 revolution and a sampling rate of 1/0.48 s to a customized recording device (Boenig und Kallenbach oHG, Dortmund, Germany). From this raw data, the average weekly running distance (km) was calculated and visualized using a custom-designed Matlab (The MathWorks, Inc., Natick, MA, USA) program. Animals were divided into two groups of equal size (n = 9). The running wheels of one group were freely movable whereas the running wheels of the other group were blocked, preventing the animals from running activity while providing the same enrichment of the environment.
Supplementary Figure S4:
(a) Schematic drawing of the counting area. The dentate gyrus was quantified from Bregma -1.34 to -3.80. Figures were created using the mouse atlas by Paxinos and Franklin [57]. (b) New-born doublecortin (DCX)-positive neurons were stained in the subgranular zone (SGZ) of the dentate gyrus (DG). Adult neurogenesis was found to be marginal in 12-month-old Tg4-42\textsuperscript{het} mice which could not be restored by enriched living conditions at that age. However, 6-months-old Tg4-42\textsuperscript{hom} mice showed profound neurogenesis which was increased after 4 months of EE. A higher magnification shows that new-born neurons in enriched Tg4-42\textsuperscript{hom} mice are longer and more branched compared to standard housed controls. Scale bar: 100 µm.
Supplementary Figure S5:

Housing condition has no impact on Aβ levels in Tg4-42<sup>het</sup> mice. (a) Immunostaining in the hippocampus using the 4G8 antibody against Aβ (Aβ<sub>17-14</sub>, Covance) showed a comparable staining in the CA1 region of standard and enriched housed Tg4-42<sup>het</sup> mice. (b) Aβ levels of whole brain hemispheres were quantified using an electrochemiluminescence assay. No difference could be detected in Tg4-42<sup>het</sup> SH and EE mice (n = 6 per group). Scale bar: 200 µm. Data were given as means ± standard error of the mean (SEM).

Electrochemiluminescence Assay

Whole brain hemispheres were homogenized with 10 strokes of a glass-teflon homogenizer (800 rpm, CAT) in 700 µl lysis buffer (120 mM NaCl, 50 mM Tris, 1 % Triton X-100, 1 x Complete Mini-Protease Inhibitor, 1 x Complete Mini-Phosphatase inhibitor, dissolved in 10 ml ddH<sub>2</sub>O, pH 7.5) per 100 mg brain tissue. After centrifugation at 17000 x g at 4°C for 20 min, the supernatant containing the protein was stored at -80 °C until further use.

Protein concentrations of lysates were determined using the Roti®-Quant universal kit according to the instructions of the supplier (Carl Roth).

For determination of Aβ levels in whole brain hemispheres, an electrochemiluminescence total Aβ assay obtained from Meso Scale Discovery (Gaithersburg, MD, USA) was used. The Aβ assay is based on the Human (6E10) Abeta 40 Ultra-Sensitive kit. Here, the Aβ40 detection antibody is replaced by anti-Aβ 4G8 monoclonal antibody. Therefore, the total Aβ assay employs monoclonal antibody 6E10 (directed against an aminoterminal epitope of Aβ) for capture and the monoclonal antibody 4G8 (directed against Aβ17-26) for detection. As previously shown, 6E10 detects Aβ4-42 equally well compared to full-length Aβ1-42 or other N-truncated variants like Aβ2-42 or Aβ3-42 (Vanderstichele et al., Clin Chem 51(9): 1650-1660 (2005)).

The assay was performed according to the protocol of the manufacturer and readout on a MSD QuickPLex SQ 120. In brief, a 96-well plate pre-coated with an Aβ antibody (6E10) was blocked with 3% BSA under shaking conditions at room temperature for 1 h. After 3 washing steps with 150 µl/well of 1X Tris Wash Buffer, 25µl of 2mg/ml protein lysates or calibrator was added per well and incubated under shaking conditions at room temperature for 1 h. After 3 additional washing steps, 25 µl of detection antibody solution (4G8) was added and again incubated with shaking for 1 h at room temperature in the dark. Upon 3 more washing steps, 150 µl of 1X Read Buffer T was added to each well and plate was read on MSD instrument.
Supplementary Figure S6:
Volcano plots of the significantly differentially expressed genes showing log2-fold-change (x-axis) and p-value (y-axis) of DEGs comparing Tg4-42het SH versus EE. Significantly down-regulated genes (n = 75) are depicted in dark blue and up-regulated genes (n = 80) in yellow.

Supplementary Figure S7:
Analysis of members of the HSP70 (HSPA1B) or HSP40 (DNAJA4) family revealed that these candidate genes are not per se altered in standard housed heterozygous Tg4-42 mice compared to standard housed WT mice. No significant differences in expression levels were detected (n = 6 per group).
**Supplementary Table 1:** Primer sequences used in the present study

| Name      | Forward 5’ – 3’                         | Reverse 3’ - 5’                         | Amplicon size |
|-----------|----------------------------------------|----------------------------------------|---------------|
| DNAJA4    | ATTGCCTGTTTCTCCACCTTG                  | CAAGTACCACCCGGACAAGA                  | 123           |
| OCIAD2    | GATTTGGGGGAAAAACACAG                   | ACGGCAATAGAAGAAAACGC                  | 118           |
| BFSP2     | GCGTTTTCCTAGGACAGCTTC                 | GAACCTGGAACACAAACTGCG                 | 125           |
| HSPH1     | GGCTTCTACAGGCAGCTCAA                   | CAGAAGAAAGCAAACCCCA                   | 116           |
| NDN       | GTGTGGAGATTGGTCTAGCT                  | AAAGAGGTCATGCGGCACTTA                 | 110           |
| STIP1     | AGCACTGTAAGGCATCATCAA                  | GAATCGATTCAACGGGGT                    | 111           |
| HSP90AB1  | ACGGACCTTCTAAGTTGGAC                  | TCAGGCTTGGTCATGCAAATG                 | 113           |
| CRYAB     | GATCCGGTTACTTCCTGTGGA                 | TCTCTCCGGAGGAACCTCAA                  | 122           |
| HSPA1B    | ATGACCTCCTGGCATTGTC                   | GCTCGAATCCTATGCGTCTCA                 | 111           |
| BDNF      | GCCTTCATGCAACCGAAGTA                  | TGAGTCCAGGACAGCAA                     | 103           |
Supplementary Table 2: Significantly regulated genes identified by RNA-Sequencing in Tg4-42<sup>SH</sup> SH vs Tg4-42<sup>EE</sup>:

| ID          | Gene name | Gene description                                                                 | log2 Fold change | Adjusted p-value |
|-------------|-----------|----------------------------------------------------------------------------------|------------------|------------------|
| MGI: 88516  | Cryab     | crystallin, alpha B                                                              | 0.154            | 1.2E-03          |
| MGI: 105053 | Hsph1     | heat shock 105kDa/110kDa protein 1                                               | 0.134            | 3.6E-03          |
| MGI: 1916377| Ociad2    | OCIA domain containing 2                                                         | 0.127            | 3.4E-03          |
| MGI: 1927638| Dnaja4    | Dnaj (Hsp40) homolog, subfamily A, member 4                                      | 0.125            | 8.4E-03          |
| MGI: 1933155| Arel4d    | ADP-ribosylation factor-like 4D                                                  | 0.118            | 1.3E-02          |
| MGI: 1933972| Tra2a     | transformer 2 alpha homolog (Drosophila)                                         | 0.116            | 1.5E-02          |
| MGI: 1343180| Vgf       | VGF nerve growth factor inducible                                                | 0.116            | 1.3E-02          |
| MGI: 1933972| Tra2a     | transformer 2 alpha homolog (Drosophila)                                         | 0.116            | 1.3E-02          |
| MGI: 1333828| Bfsp2     | beaded filament structural protein 2, phakinin                                   | 0.116            | 3.6E-03          |
| MGI: 1916133| Ahsa2     | AHA1, activator of heat shock 90kDa protein ATPase homolog 2                    | 0.115            | 1.4E-02          |
| MGI: 1919715| Zfp131    | zinc finger protein 131                                                          | 0.112            | 1.9E-02          |
| MGI: 1916523| Metli7a1  | methyltransferase like 7A1                                                       | 0.110            | 1.9E-02          |
| MGI: 97314  | Nefm      | neurofilament, medium polypeptide                                                | 0.110            | 1.6E-02          |
| MGI: 1914167| Chordc1   | cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1    | 0.109            | 2.0E-02          |
| MGI: 1917814| Fam213a   | family with sequence similarity 213, member A                                   | 0.109            | 1.5E-02          |
| MGI: 1923691| Daam2     | dishevelled associated activator of morphogenesis 2                              | 0.109            | 1.4E-02          |
| MGI: 1914662| Soga3     | SOGA family member 3                                                             | 0.108            | 1.7E-02          |
| MGI: 2443958| A330023F24Rik | RIKEN cDNA A330023F24 gene                                                   | 0.108            | 2.5E-02          |
| MGI: 1328308| Scrg1     | scrapie responsive gene 1                                                         | 0.107            | 2.4E-02          |
| MGI: 1309528| Ppp1r12a  | protein phosphatase 1, regulatory (inhibitor) subunit 12A                       | 0.107            | 2.6E-02          |
| MGI: 1916216| Ngdn      | neuroguidin, EIF4E binding protein                                               | 0.106            | 2.7E-02          |
| MGI: 1922985| Pank1     | pantothenate kinase 1                                                            | 0.105            | 2.9E-02          |
| MGI: 1353450| Aldh1a1   | aldehyde dehydrogenase family 1, subfamily A1                                    | 0.105            | 2.1E-02          |
| MGI: 2181202| Pfkb3     | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3                           | 0.105            | 2.5E-02          |
| MGI: 1890410| Acss2     | acyl-CoA synthetase short-chain family member 2                                 | 0.104            | 2.4E-02          |
| MGI: 1928760| Ruvbl1    | RuvB-like protein 1                                                              | 0.104            | 2.9E-02          |
| MGI: 1921450| 2810403A07Rik | RIKEN cDNA 2810403A07 gene                                           | 0.104            | 2.4E-02          |
| MGI: 1919103| Pdia6     | protein disulfide isomerase associated 6                                         | 0.103            | 3.0E-02          |
| MGI: 97463  | P4ha1     | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide | 0.103            | 3.3E-02          |
| MGI: 1914538| Srek1ip1  | splicing regulatory glutamine/lysine-rich protein interacting protein 1          | 0.102            | 3.4E-02          |
| MGI: 1914228| Luc7l     | Luc7 homolog (S. cerevisiae)-like                                                | 0.101            | 2.6E-02          |
| MGI: 109130 | Stip1     | stress-induced phosphoprotein 1                                                 | 0.101            | 2.4E-02          |
| MGI: 104680 | Hspe1     | heat shock protein 1 (chaperonin 10)                                            | 0.101            | 3.3E-02          |
| MGI: 1923429| Usp31     | ubiquitin specific peptidase 31                                                 | 0.100            | 2.4E-02          |
| Gene ID   | Gene Name          | Description                                                                 | Freq. | Log2 Fold Change |
|----------|--------------------|-----------------------------------------------------------------------------|-------|-----------------|
| MGI:95834 | Pdia3              | protein disulfide isomerase associated 3                                   | 0,100 | 2,9E-02         |
| MGI:1917581 | Shprh             | SNF2 histone linker PHD RING helicase                                      | 0,100 | 3,8E-02         |
| MGI:2682254 | Zbtb40            | zinc finger and BTB domain containing 4                                     | 0,099 | 2,3E-02         |
| MGI:1929658 | Tbk1              | TANK-binding kinase 1                                                       | 0,099 | 3,7E-02         |
| MGI:95739  | Glul               | glutamate-ammonia ligase (glutamine synthetase)                             | 0,099 | 1,9E-02         |
| MGI:104864 | Pdia4              | protein disulfide isomerase associated 4                                   | 0,099 | 4,0E-02         |
| MGI:1926176 | Gas2l1            | growth arrest-specific 2 like 1                                            | 0,098 | 3,7E-02         |
| MGI:2445356 | Smox              | spermine oxidase                                                           | 0,098 | 3,8E-02         |
| MGI:2443430 | Dgki              | diacylglycerol kinase, iota                                                | 0,097 | 4,0E-02         |
| MGI:2136381 | Hadhb             | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A hydratase (trifunctional protein), beta subunit tensin 3 | 0,097 | 3,3E-02         |
| MGI:2443012 | Tns3              | TBC1 domain family, member 4                                               | 0,095 | 4,5E-02         |
| MGI:1355331 | Olig2             | oligodendrocyte transcription factor 2                                     | 0,096 | 4,5E-02         |
| MGI:1918764 | Sfpq               | splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) | 0,096 | 3,9E-02         |
| MGI:2429660 | Tbc1d4            | TBC1 domain family, member 4                                               | 0,095 | 4,5E-02         |
| MGI:1931874 | Dnajb1            | DnaJ (Hsp40) homolog, subfamily B, member 1                                | 0,095 | 4,6E-02         |
| MGI:1914436 | Rplp2             | ribosomal protein, large P2                                                | 0,094 | 4,5E-02         |
| MGI:1926462 | Hnrrnph3          | heterogeneous nuclear ribonucleoprotein H3                                 | 0,094 | 4,8E-02         |
| MGI:95640  | Gapdh              | glyceraldehyde-3-phosphate dehydrogenase                                   | 0,094 | 4,6E-02         |
| MGI:1925496 | Phf23             | PHD finger protein 23                                                       | 0,093 | 5,0E-02         |
| MGI:1928739 | Dnajb2            | DnaJ (Hsp40) homolog, subfamily B, member 2                                | 0,093 | 4,2E-02         |
| MGI:1927406 | Herpud1           | homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 | 0,093 | 4,3E-02         |
| MGI:98341  | Snrnp70           | small nuclear ribonucleoprotein 70 (U1)                                    | 0,092 | 2,5E-02         |
| MGI:107380 | Spag7             | sperm associated antigen 7                                                  | 0,092 | 4,9E-02         |
| MGI:109522 | Ugt8a             | UDP galactosyltransferase 8A                                               | 0,091 | 4,2E-02         |
| MGI:1923013 | Dcaf17            | DDB1 and CUL4 associated factor 17                                          | 0,090 | 4,6E-02         |
| MGI:1891824 | Acin1             | apoptotic chromatin condensation inducer 1                                 | 0,090 | 4,6E-02         |
| MGI:1353499 | Baz1b             | bromodomain adjacent to zinc finger domain, 1B                              | 0,090 | 4,5E-02         |
| MGI:96247  | Hsp90ab1          | heat shock protein 90 alpha (cytosolic), class B member 1                   | 0,090 | 2,4E-02         |
| MGI:1923686 | Tufm              | Tu translation elongation factor, mitochondrial                            | 0,090 | 3,6E-02         |
| MGI:106014 | Nudc              | nuclear distribution gene C homolog (Aspergillus)                          | 0,088 | 4,7E-02         |
| MGI:88025  | Ank2              | ankyrin 2, brain                                                           | 0,088 | 3,4E-02         |
| MGI:95524  | Fgfr3             | fibroblast growth factor receptor 3                                        | 0,082 | 4,9E-02         |
| MGI:1922942 | Nr2c2ap           | nuclear receptor 2C2-associated protein                                     | 0,080 | 2,4E-02         |
| MGI:99517  | Hspa1b            | heat shock protein 1B                                                       | 0,078 | 3,0E-02         |
| MGI:1921997 | Ddit4             | DNA-damage-inducible transcript 4                                          | 0,077 | 4,6E-02         |
| MGI:1203481 | Map3k19 | mitogen-activated protein kinase kinase 19 | 0,074 | 4,4E-02 |
| MGI:3643804 | Gm5499 | predicted pseudogene 5499 | 0,067 | 4,7E-02 |
| MGI:1859388 | Dll4 | delta-like 4 (Drosophila) | 0,061 | 4,0E-02 |
| MGI:2685450 | Rtp1 | receptor transporter protein 1 | 0,059 | 8,3E-03 |
| MGI:1930153 | Popdc3 | popeye domain containing 3 | 0,058 | 2,6E-02 |
| MGI:2685841 | Mamdc4 | MAM domain containing 4 | 0,058 | 2,7E-02 |
| MGI:5504060 | Gm26945 | predicted gene, 26945 | 0,053 | 8,1E-03 |
| MGI:109619 | Neurog2 | neurogenin 2 | 0,046 | 3,5E-02 |
| MGI:3646759 | Zfp947 | zinc finger protein 947 | 0,032 | 2,3E-02 |
| MGI:3704330 | Gm10177 | predicted gene 10177 | 0,029 | 1,8E-02 |
| MGI:1915594 | Tmem174 | transmembrane protein 174 | 0,027 | 3,1E-02 |
| MGI:96090 | Asmt | acetylserotonin O-methyltransferase | -0,014 | 4,8E-02 |
| MGI:96177 | Hoxa5 | homeobox A5 | -0,020 | 2,1E-02 |
| MGI:3649000 | Gm8104 | predicted gene 8104 | -0,024 | 4,8E-02 |
| MGI:2443002 | A330032B11Rik | RIKEN cDNA A330032B11 gene | -0,026 | 4,8E-02 |
| MGI:3045296 | Efhb | EF hand domain family, member B | -0,026 | 2,5E-02 |
| MGI:1923110 | Tex26 | testis expressed 26 | -0,027 | 4,1E-02 |
| MGI:1196234 | Ccde69 | coiled-coil domain containing 69 | -0,040 | 3,5E-02 |
| MGI:3649668 | Gm13544 | predicted gene 13544 | -0,040 | 1,5E-02 |
| MGI:4439718 | Gm16794 | predicted gene, 16794 | -0,051 | 4,5E-02 |
| MGI:1346063 | Ggt5 | gamma-glutamyltransferase 5 | -0,063 | 4,8E-02 |
| MGI:95557 | Flnc | filamin C, gamma | -0,069 | 4,8E-02 |
| MGI:1855694 | Isg15 | ISG15 ubiquitin-like modifier | -0,069 | 4,6E-02 |
| MGI:2441897 | Gpr151 | G protein-coupled receptor 151 | -0,078 | 4,6E-02 |
| MGI:1921330 | Nmnat3 | nicotinamide nucleotide adenyllyltransferase 3 | -0,078 | 3,8E-02 |
| MGI:1915025 | Rtp4 | receptor transporter protein 4 | -0,080 | 2,5E-02 |
| MGI:1926263 | Gbp3 | guanylate binding protein 3 | -0,083 | 9,7E-03 |
| MGI:1913292 | Sostdc1 | sclerostin domain containing 1 | -0,084 | 3,3E-02 |
| MGI:1929063 | Copz1 | coatomer protein complex, subunit zeta 1 | -0,084 | 4,9E-02 |
| MGI:1888992 | Msln | mesothelin | -0,088 | 1,6E-03 |
| MGI:102643 | Myh11 | myosin, heavy polypeptide 11, smooth muscle | -0,089 | 1,2E-02 |
| MGI:1914500 | Ube2l6 | ubiquitin-conjugating enzyme E2L 6 | -0,089 | 4,7E-02 |
| MGI:894315 | Rap1b | RAS related protein 1b | -0,089 | 4,1E-02 |
| MGI:1915288 | Chid1 | chitinase domain containing 1 | -0,090 | 4,5E-02 |
| MGI:1859682 | Slc23a2 | solute carrier family 23 (nucleobase transporters), member 2 | -0,091 | 3,6E-02 |
| MGI:97386 | Ntsr1 | neurotensin receptor 1 | -0,091 | 4,8E-02 |
| MGI:88501 | Crip1 | cysteine-rich protein 1 (intestinal) | -0,092 | 3,4E-02 |
| MGI:104745 | Sez6 | seizure related gene 6 | -0,093 | 2,8E-02 |
| MGI:2148924 | Clic1 | chloride intracellular channel 1 | -0,093 | 4,8E-02 |
| MGI:2145316 | Txndc5 | thioredoxin domain containing 5 | -0,094 | 3,0E-02 |
| MGI:1344344 | Dazap2 | DAZ associated protein 2 | -0,095 | 2,2E-02 |
| MGI:95895 | H2-Aa | histocompatibility 2, class II antigen A, alpha | -0,095 | 2,4E-02 |
| MGI:1913625 | Dhrs7 | dehydrogenase/reductase (SDR family) | -0,095 | 4,8E-02 |
MGI:1353596 Tor2a torsin family 2, member A -0,095 4,6E-02
MGI:97742 Pomc pro-opiomelanocortin-alpha -0,095 5,3E-03
MGI:106214 Jrk jerky -0,095 4,2E-02
MGI:103156 Gabrg1 gamma-aminobutyric acid (GABA) A receptor, subunit gamma 1 -0,096 4,6E-02
MGI:98476 Tac2 tachykinin 2 -0,096 4,4E-02
MGI:97168 Msx1 msh homeobox 1 -0,097 1,9E-02
MGI:127719 Pde9a phosphodiesterase 9A -0,097 4,4E-02
MGI:1914164 Vps28 Vacular protein sorting 28 -0,097 3,5E-02
MGI:2157946 Cacng5 calcium channel, voltage-dependent, gamma subunit 5 -0,098 4,2E-02
MGI:2386741 Slc30a6 solute carrier family 30 (zinc transporter), member 6 -0,098 4,1E-02
MGI:2685790 Gabem GRB2 associated, regulator of MAPK1 -0,098 3,8E-02
MGI:2146851 Tfb1m transcription factor B1, mitochondrial -0,099 2,1E-02
MGI:97168 Msx1 msh homeobox 1 -0,099 3,5E-02
MGI:106214 Jrk jerky -0,100 3,7E-02
MGI:102709 Cav1 caveolin 1, caveolae protein -0,100 3,6E-02
MGI:2138915 Myl9 myosin, light polypeptide 9, regulatory -0,100 3,7E-02
MGI:3045495 Tmem205 transmembrane protein 205 -0,100 3,4E-02
MGI:103017 Fcgt Fc receptor, IgG, alpha chain transporter -0,100 3,7E-02
MGI:1913951 Cab39l calcium binding protein 39-like -0,101 2,9E-02
MGI:1913391 Ifitm3 interferon induced transmembrane protein 3 -0,101 2,0E-02
MGI:1913301 0610012G03Rik RIKEN cDNA 0610012G03 gene -0,107 2,5E-02
MGI:3582583 Sprn shadow of prion protein -0,107 1,0E-02
MGI:95904 Ephx1 epoxide hydrolase 1, microsomal -0,111 2,1E-02
MGI:1096574 Car4 carbonic anhydrase 4 -0,113 1,8E-02
MGI:1913974 Tab3 TGF-beta activated kinase 1/MAP3K7 binding protein 3 -0,114 1,7E-02
MGI:1915376 Fahd2a fumarylacetoacetate hydrolase domain containing 2A -0,115 1,7E-02
MGI:1860292 Ramp3 receptor (calcitonin) activity modifying protein 3 -0,115 1,6E-02
MGI:2147570 Marveld1 MARVEL (membrane-associating) domain containing 1 -0,117 1,1E-02
MGI:1341868 Rfc2 replication factor C (activator 1) 2 -0,118 1,2E-02
MGI:95904 H2-K1 histocompatibility 2, K1, K region -0,119 1,3E-02
MGI:98822 Tfcc transferrin receptor -0,120 1,3E-02
MGI:1101771 Kl klotho -0,121 1,0E-02
MGI:1351317 Podxl podocalyxin-like -0,122 1,1E-02
MGI:894696 Serping1 serine (or cysteine) peptidase inhibitor, clade G, member 1 -0,126 6,0E-03
MGI:99554 Lgals3bp lectin, galactoside-binding, soluble, 3 binding protein -0,128 6,8E-03
MGI:88498 Crhr1 corticotropin releasing hormone receptor 1 -0,129 7,3E-03
MGI:98865 Ttr transthyretin -0,130 5,7E-03
MGI:1352480 Igfbp7 insulin-like growth factor binding protein 7 -0,130 6,5E-03
| MGI   | Symbol | Description                                           | Log2 | p-value |
|-------|--------|-------------------------------------------------------|------|---------|
| MGI:99261 | Ptgsd  | prostaglandin D2 synthase (brain)                     | -0.131 | 1.3E-03 |
| MGI:106012 | Tagln  | transgelin                                            | -0.146 | 1.9E-03 |
| MGI:106679 | Zic2   | zinc finger protein of the cerebellum 2               | -0.152 | 1.6E-03 |
| MGI:97290 | Ndn    | necdin                                                | -0.165 | 1.6E-04 |