Table S1. Terms in the Gene Ontology and KEGG pathway databases enriched among genes that decreased expression with advancing age in brain (1450 genes in total 13,216)

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<th>HGeom</th>
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<td>38 17% 8.0(10^1)</td>
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<td>1.8(10^{-6})</td>
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<td>2%</td>
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<td>2.6(10^{-6})</td>
<td>4.9(10^{-6})</td>
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<td>14</td>
<td>31%</td>
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<td>23</td>
<td>22%</td>
<td>3.2(10^{-6})</td>
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<td>8</td>
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<td>6.2(10^{-6})</td>
<td>3.73</td>
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</table>

**KEGG**

- **Oxidative phosphorylation**: 41 | 35% | 1.9(10^{-6}) | 3.8(10^{-6}) | 5.3(10^{-6}) | 2.66 | 0.25 | 1.4(10^{-6}) |
- **Gap junction**: 20 | 27% | 2.2(10^{-6}) | 3.6(10^{-6}) | 8.9(10^{-6}) | 2.06 | 0.79 | 2.9(10^{-6}) |
Overall set of over-represented terms (PValue < 0.01; 5th column) are listed here. Every term is followed by the complementary terms of final descendants or ones inbetween which are enriched even excluding genes in descendants. The over-represented terms for themselves are listed first. *The proportion of genes within group in total 13,216 genes which were annotated with the specific term †EASE score ‡Hypergeometric test for overrepresentation §Fold enrichment of the term in the gene group ¶Fold enrichment of the term in the opposite gene group (Table S2, genes expression of which increases as age) ‖Hypergeometric test for underrepresentation of genes in the opposite group