**Supplementary Table III. Descriptive statistics of tissue gene expression in different structures of the central nervous system.**

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| --- | --- |
| **CNS structure** | **Mean [range]; SD** |
| Amygdala | -8.33e-008 [-1.81,1.64]; 1.00 |
| Anterior cingulate cortex | 1.08e-006 [-1.83, 1.40]; 1.00 |
| Caudate nucleus | 7.50e-007 [-0.22, 0.22]; 0.14 |
| Cerebellum | 8.33e-008 [-0.22, 0.32]; 0.14 |
| Frontal cortex | -5.00e-007 [-2.83, 1.10]; 1.00 |
| Hippocampus | -3.33e-007 [-0.30, 0.24]; 0.16 |
| Hypothalamus | 8.33e-008 [-2.16, 1.18]; 1.00 |
| Nucleus accumbens | -1.67e-007 [-0.79, 0.35]; 0.33 |
| Putamen | 6.67e-007 [-0.60, 0.31]; 0.29 |
| Spinal cord | -3.33e-007 [-0.25, 0.37]; 0.17 |
| Substantia nigra | -7.50e-007 [-0.65, 0.37]; 0.31 |

**Footnote:** Mean, range (minimum, maximum), and standard deviation (SD) of normalized (z-scores) gene expression data are given per each central nervous system (CNS) structure. Values were calculated based on the means individual expression data of the 12 DCD-associated genes. Gene expression data were available as transcript per million.