**Supplementary File 5.** **Numbers of genes showing different magnitudes of TE changes between uORFs and CDS at the interspecific level, *H. sapiens* and *M. mulatta*.**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Tissues** | **# of expressed uORFs** | **βu ≠ 1**  **(%)** | **# of expressed CDSs** | **βc ≠ 1**  **(%)** | **uORF-CDS pairs with βu > 1** | | | **uORF-CDS pairs with βu < 1** | | |
| **Total** | **γ > 1** | **γ < 1** | **Total** | **γ > 1** | **γ < 1** |
| **Brain** | 7,380 | 80  (1.08) | 15,086 | 507  (3.36) | 51 | 0 | 27 | 29 | 14 | 0 |
| **Liver** | 4,429 | 28  (0.63) | 13,246 | 149  (1.24) | 10 | 0 | 4 | 18 | 10 | 0 |
| **Testis** | 7,384 | 53  (0.72) | 15,134 | 272  (1.80) | 33 | 0 | 9 | 20 | 5 | 0 |

Only uORFs and CDSs with an mRNA RPKM > 0.1 in both *H. sapiens and* *M. mulatta* were considered in each sample pair in the analysis. = / , is the fold change in TEuORF in *M. mulatta* relative to *H. sapiens* for each sample. = /, is the fold change in TECDS in *M. mulatta* relative to *H. sapiens* for each sample. =. For each CDS-uORF pair, >1 and < 1 or <1 and > 1 means that the magnitude of TE change is lower for a CDS than a uORF. The statistical significance of , , and were all determined at an FDR < 0.05.