**Supplementary Table S3. The optimal evolutionary models for gene and codon partitions as estimated in PartitionFinder v1.0.1.**

The optimal partitioning scheme and model fit was estimated as suggested by the Akaike information criterion (AIC).

|  |  |
| --- | --- |
| **Gene** | **Substitution Model** |
| 12S rRNA | GTR+I+G |
| tRNA-Val | JC+G |
| 16S rRNA | GTR+I+G |
| BDNF codon position 1 | K2P+I |
| BDNF codon position 2 | K2P+G |
| BDNF codon position 3 | HKY+I+G |