**Table S2.** Maximum Composite Likelihood estimate of the pattern of nucleotide substitutions in Cer-SERV-1 and Cer-SERV-2.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Cer-SERV-1 1 | **A** | **T/U** | **C** | **G** |
| A | - | 2.50 | 2.28 | **15.25** |
| T/U | 2.98 | - | **19.29** | 1.80 |
| C | 2.98 | **21.15** | - | 1.80 |
| G | **25.22** | 2.50 | 2.28 | - |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Cer-SERV-2 2 | **A** | **T/U** | **C** | **G** |
| A | - | 2.82 | 2.69 | **14.54** |
| T/U | 3.48 | - | **18.95** | 2.06 |
| C | 3.48 | **19.88** | - | 2.06 |
| G | **24.53** | 2.82 | 2.69 | - |

Each entry is the probability of substitution (*r*) from one base (row) to another base (column). Transitions are in shown in **bold**. Substitution pattern and rates were estimated under the Hasegawa-Kishino-Yano (1985) model (+G) [1]. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories, [+*G*], parameter = 0.2006). For estimating ML values, a tree topology was automatically computed. Relative values of instantaneous *r* should be considered when evaluating them. For simplicity, the sum of the *r* values is made equal to 100. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA6 [2]. There were a total of 8629 positions in the final dataset.

1 The nucleotide frequencies are A = 31.17%, T/U = 26.14%, C = 23.84%, and G = 18.85%. The maximum Log likelihood for the ML tree was -40321.529. The analysis involved 55 nucleotide sequences.

2 The nucleotide frequencies are A = 31.49%, T/U = 25.52%, C = 24.32%, and G = 18.67%. The maximum Log likelihood for the ML tree was -26259.835. The analysis involved 26 nucleotide sequences.

References

1. Hasegawa, M.; Kishino, H.; Yano, T. Dating of the human-ape splitting by a molecular clock of mitochondrial DNA. *Journal of molecular evolution* **1985**, *22*, 160-174, doi:10.1007/bf02101694.

2. Tamura, K.; Stecher, G.; Peterson, D.; Filipski, A.; Kumar, S. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular biology and evolution* **2013**, *30*, 2725-2729, doi:10.1093/molbev/mst197.