Table S2: Best fit model for sequence evolution and partitioning scheme selected in PartitionFInder for assessing phylogenetic relationships using maximum likelihood in RAxML and Bayesian inference in MrBayes.

|  |  |  |  |
| --- | --- | --- | --- |
| **RAxML** | | **MrBayes** | |
| rag\_pos1  pdc\_pos2, pdc\_pos3, rag\_pos2  pdc\_pos1, rag\_pos3  nd\_pos1  nd\_pos2  nd\_pos3 | GTR+I+G | rag\_pos1  pdc\_pos2, rag\_pos2  rag\_pos3  nd\_pos1  nd\_pos2  nd\_pos3  pdc\_pos1  pdc\_pos3 | HKY+I  GTR+I  HKY+I+G  GTR+G  GTR+I+G  GTR+I+G  GTR+G  GTR+G |