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\_pos1pdc\_pos2, pdc\_pos3, rag\_pos2pdc\_pos1, rag\_pos3nd\_pos1nd\_pos2nd\_pos3 | GTR+I+G | rag\_pos1pdc\_pos2, rag\_pos2rag\_pos3 nd\_pos1nd\_pos2nd\_pos3pdc\_pos1pdc\_pos3 | HKY+IGTR+IHKY+I+GGTR+GGTR+I+GGTR+I+GGTR+GGTR+G |