**Table S4 The best partitioning scheme selected by PartitionFinder for the BI and ML analyses**

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| --- | --- | --- |
| **Phylogenetic methods** | **Subset Partitions** | **Best Model** |
| BI: 5 partitions | P1: (12srRNA, 16srRNA, tRNA-Arg, tRNA-His, tRNA-Ile, tRNA-Phe, tRNA-Tyr) | GTR+G |
|  | P2: (ATP6, COI, COII, COIII, CytB) | GTR+I |
|  | P3: (ATP8, ND2, ND3, ND6, tRNA-Ala, tRNA-Asn, tRNA-Asp, tRNA-Cys, tRNA-Glu) | HKY+G |
|  | P4: (ND1, ND4, ND4L, ND5) | HKY+I |
|  | P5: (tRNA-Gln, tRNA-Gly, tRNA-Leu1, tRNA-Leu2, tRNA-Lys, tRNA-Met, tRNA-Pro, tRNA-Ser1, tRNA-Ser2, tRNA-Thr, tRNA-Trp, tRNA-Val) | HKY+I |
| ML: 4 partition | P1: (12srRNA, 16srRNA, tRNA-Arg, tRNA-Cys, tRNA-Gln, tRNA-Gly, tRNA-His, tRNA-Ile, tRNA-Leu1, tRNA-Leu2, tRNA-Lys, tRNA-Met, tRNA-Phe, tRNA-Pro, tRNA-Ser1, tRNA-Ser2, tRNA-Thr, tRNA-Trp, tRNA-Tyr, tRNA-Val) | GTR+G |
|  | P2: (ATP6, COI, COII, COIII, CytB) | GTR+G |
|  | P3: (ATP8, ND2, ND3, ND6, tRNA-Ala, tRNA-Asn, tRNA-Asp, tRNA-Glu) | GTR+G |
|  | P4: (ND1, ND4, ND4L, ND5) | GTR+G |