

**Table S1.** The partition schemes and best-fitting models selected.

| Nucleotide Sequence Alignments |   |            |
|--------------------------------|---|------------|
| Subset                         | Subset Partitions   | Best Model |
| Partition 1                    | ND3_pos1, ND1_pos1, ND4L_pos1, ATP6_pos1, ATP8_pos1, ND2_pos1, ND4_pos1 | GTR+I+G    |
| Partition 2                    | ND3_pos2, ND1_pos2, ATP6_pos2, ATP8_pos2, ND2_pos2, ND4L_pos2, ND4_pos2 | TVM+I+G    |
| Partition 3                    | ND2_pos3, ND4_pos3, ND4L_pos3, ATP6_pos3, ATP8_pos3                     | TRN+I+G    |
| Partition 4                    | COII_pos1, Cytb_pos1, COIII_pos1, COI_pos1                              | SYM+I+G    |
| Partition 5                    | COI_pos2, Cytb_codon2, COIII_codon2, COII_pos2                          | HKY+I+G    |
| Partition 6                    | COI_pos3, ND3_pos3, ND1_pos3, COIII_pos3, COII_pos3                     | TIM+I+G    |
| Partition 7                    | Cytb_pos3   | TRN+I+G    |
| Partition 8                    | ND6_pos1, ND6_pos2  | HKY+G      |
| Partition 9                    | ND6_pos3  | TRN+G      |

**Note:** The full names of all abbreviations are as follows: pos1: first codon; pos2: second codon; GTR: general time reversible; I: unchanged site proportion; G: Gamma distribution.