Table S2. Best Partition Scheme (BPS) and best-fit models of molecular evolution for the subsets partitions of the mitochondrial protein-coding genes alignment. The likelihood score (lnL) and the Bayesian Information Criterion (BIC) value were -123862 and 248843 respectively.

|  |  |  |
| --- | --- | --- |
| **Subset** | **Partition for codon position** | **Model** |
| 1 | Cox1\_1, Cox2\_1, Cox3\_1, Cytb\_1, Nadh1\_1 | GTR+I+G |
| 2 | Cox1\_2, Cox2\_2, Cox3\_2, Cytb\_2 | GTR+G |
| 3 | Cox1\_3, Cox2\_3, Cytb\_3 | HKY+G |
| 4 | ATP6\_3, ATP8\_3, Cox3\_3, Nadh3\_3 | HKY+G |
| 5 | ATP6\_2, Nadh1\_2, Nadh3\_2, Nadh4\_2, Nadh5\_2 | GTR+I+G |
| 6 | Nadh1\_3, Nadh4\_3, Nadh5\_3 | HKY+G |
| 7 | ATP6\_1, Nadh2\_1, Nadh3\_1, Nadh4L\_1, Nadh4\_1, Nadh5\_1, Nadh6\_1 | GTR+I+G |
| 8 | Nahd2\_2, Nadh4L\_2, Nadh6\_2 | GTR+G |
| 9 | Nahd2\_3, Nadh4L\_3, Nadh6\_3 | HKY+G |
| 10 | ATP8\_1, ATP8\_2 | F81+G |