**Table S1.** Best models were calculated by Modelfinder of cds\_faa, cds12\_fna, cds12\_rrna datasets used in analysis.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Dataset** | **starting partitions** | **Subset** | **SubsetPartitions** | **BestModel** |
| cds\_faa | ATP6 = 1-217; ATP8 = 218-252; COX1 = 253-763; COX2 = 764-989; COX3 = 990-1248; CYTB = 1249-1626; ND1 = 1627-1936; ND2 = 1937-2256; ND3 = 2257-2372; ND4L = 2373-2465; ND4 = 2466-2905;  ND5 = 2906-3459; ND6 = 3460-3612; | P1 | ATP6, ATP8, ND2, ND3, ND6 | mtMet+F+I+G4 |
| P2 | COX1 | mtART+I+G4 |
| P3 | COX2, COX3, CYTB | mtART+F+R3 |
| P4 | ND1, ND4L, ND4, ND5 | mtZOA+F+R4 |
| cds12\_fna | COX1=1-1024; ND1=1025-1646; COX2=1647-2098; ND2=2099-2746; COX3=2747-3266; ND3=3267-3498; ND4=3499-4380; ND5=4381-5496; ATP6=5497-5932; ND6=5933-6248; ATP8=6249-6350; CYTB=6351-7108; ND4L=7109-7296; | P1 | COX1, COX2, COX3, CYTB | TIM+F+I+G4 |
| P2 | ND1, ND4, ND5, ND4L | TVM+F+I+G4 |
| P3 | ND2, ATP8, | TVM+F+I+G4 |
|  | P4 | ND3, ATP6, ND6 | TIM+F+I+G4 |
| cds12\_rrna | COX1=1-1024; ND1=1025-1646; COX2=1647-2098; ND2=2099-2746; COX3=2747-3266; ND3=3267-3498; ND4=3499-4380; ND5=4381-5496; ATP6=5497-5932; ND6=5933-6248; ATP8=6249-6350; CYTB=6351-7108; ND4L=7109-7296; l-rRNA = 7297-8403; s-rRNA = 8404-9065; | P1 | COX1, COX2, COX3, CYTB | TIM+F+I+G4 |
| P2 | ND1, ND4, ND5, ND4L | TVM+F+I+G4 |
| P3 | ND2, ATP8 | TVM+F+I+G4 |
| P4 | ND3, ATP6, ND6 | TIM+F+I+G4 |
| P5 | l-rRNA, s-rRNA | TVM+F+R2 |

cds\_faa: amino acid sequences of the protein-coding genes (PCGs); cds12\_fna: first and second codon positions of PCGs; cds12\_rrna: the first and the second codon positions of the PCGs and two rRNA genes.