**Table S4.** The base substitution models selected by ModelTest-NG. The Bayesian information criterion (BIC) is used as the criterion for model selection. Numbers in parentheses after the gene names represent one of the three codon positions.

|  |  |
| --- | --- |
| **Model** | **Partitions** |
| GTR+I+G4 | CAD(part2: 1), EF-1a(part2: 2) |
| JC+I+G4 | EF-1a(part2: 1) |
| TIM1+I+G4 | COI(2) |
| TIM1ef+I+G4 | CAD(part1: 3) |
| TIM2+I+G4 | COI(3), EF-1a(part2: 3) |
| TIM3+I+G4 | RpS5(2) |
| TPM1+I+G4 | EF-1a(part1: 3) |
| TPM1uf+I+G4 | CAD(part2: 2), EF-1a(part1: 2) |
| TPM2uf+I+G4 | CAD(part2: 3), RpS5(1), |
| TrN+I+G4 | COI(1), CAD(part1: 1, 2) |
| TrNef+I+G4 | RpS5(3) |
| TVM+I+G4 | EF-1a(part1: 1) |