**Table S5.** The base substitution models selected by Kakusan4. 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.

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| **Model** | **Partitions** |
| GTR+G | COI(1, 2, 3), RpS5(1), CAD(part1: 3), CAD(part2: 1, 3), EF-1a(part1: 2, 3), EF-1a(part2: 2, 3) |
| SYM+G | RpS5(2), CAD(part2: 2) |
| K80+G | RpS5(3) |
| HKY85+G | CAD(part1: 1, 2), EF-1a(part1: 1) |
| JC69+G | EF-1a(part2: 1) |