

Table S7 Partition schemes and best-fitting models selected in PR dataset.

Nucleotide sequence alignment		
Partition	Partition name	Best model
1	ATP6_codon1, COIII_codon1, COII_codon1, Cytb_codon1	SYM+G
2	COI_codon2, COIII_codon2, COII_codon2, Cytb_codon2, ATP6_codon2	GTR+I
3	COI_codon3, ATP6_codon3, COII_codon3, ATP8_codon3	HKY+I+G
4	ND3_codon1, ATP8_codon1, ND2_codon1, ND6_codon1	HKY+I+G
5	ATP8_codon2, ND2_codon2, ND6_codon2	GTR+I+G
6	COI_codon1	SYM+G
7	COIII_codon3, Cytb_codon3, ND2_codon3, ND3_codon3, ND6_codon3	GTR+I+G
8	ND4L_codon1, ND1_codon1, ND5_codon1, ND4_codon1	GTR+I+G
9	ND4L_codon2, ND1_codon2, ND4_codon2, ND5_codon2, ND3_codon2	GTR+I+G
10	ND4L_codon3, ND1_codon3, ND4_codon3, ND5_codon3	GTR+G
11	rrnaS, rrnaL	GTR+I+G