

TABLE S2 | The partitions by position and by gene for Cytochrome-*b* and concatenated dataset (Cyt-*b*, ND2, and RAG1), including the total length in base pairs and number of parsimony informative sites (PI). The best-fit substitution models under the Bayesian Information Criterion evaluated in the program Partition Finder are also provided.

Partition	Length, PI	Pos 1	Pos 2	Pos 3	Gene
Cyt <i>b</i>	1140, 306	K80+I +G	HKY+I	GTR+I	GTR+I+G
All genes	3748,619	Gene1_pos1: K80+I+G; Gene1_pos2, Gene2_pos2: HKY+I; Gene1_pos3, Gene2_pos3: GTR+I+G; Gene2_pos1: HKY+G; Gene3_pos1: HKY+G; Gene3_pos2, Gene3_pos3: JC+I			



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