

Table S3. Partition schemes and best-fitting models for phylogenetic analyses

Datasets		Phylogenetic Reconstruction Approaches	
		Maximum Likelihood	Bayesian Inference
		Best-fitting model	Best-fitting model
Amino acid datasets 43taxa 2,043 sites	<i>cox1</i>	mtART+I+G+F	RtREV+I+G+F
	<i>cox2</i>	mtART+I +G+F	mtART+I+G+F
	<i>cox3</i>	mtART+I +G+F	mtREV+I+G+F
	<i>cytb</i>	mtART+I +G +F	mtREV+I+G+F
	<i>atp6</i>	mtART+I +G+F	RtREV+I+G+F
	<i>nad1</i>	mtART+I +G+F	mtREV+I+G
	<i>nad3</i>	mtART+I +G	mtREV+I+G+F
Nucleotide datasets 43taxa 3,464 sites	The 1 st codon of <i>cox1</i>	SYM+G+I	SYM+G+I
	The 2 nd codon of <i>cox1</i>	GTR+G+I	GTR+G+I
	The 1 st codon of <i>cox2</i>	GTR +G+I	GTR+G+I
	The 2 nd codon of <i>cox2</i>	GTR +G+I	GTR+G+I
	The 1 st codon of <i>cox3</i>	GTR+G+I	GTR+G+I
	The 2 nd codon of <i>cox3</i>	GTR+G+I	GTR+G+I
	The 1 st codon of <i>cytb</i>	GTR+G+I	GTR +G+I
	The 2 nd codon of <i>cytb</i>	GTR+G+I	GTR+G+I
	The 1 st codon of <i>atp6</i>	GTR+G+I	GTR+G+I
	The 2 nd codon of <i>atp6</i>	GTR+G+I	GTR+G+I
	The 1 st codon of <i>nad3</i>	HKY+G+I	HKY+G+I
	The 2 nd codon of <i>nad3</i>	GTR+G+I	GTR+G+I