

**S2 Table. Information on the dataset used for the phylogenetic analyses.** Composition, length, partitions, models and run- specifications for the dataset used for phylogenetic analyses.

Dataset	Genes	N° seq	bp	Subst. model (unlinked) & partitions	Clock model (unlinked)	Tree model (linked)	Alignments	Other prior parameters	Run specifications
146 taxa 14,454 bp	12S	125	329	GTR + G	Uncorrelated relaxed Lognormal		<b>Geneious</b> Muscle alignment		
	16S	108	442						
	COI	52	1.605	GTR + G					
	CYTb	118	1.167	GTR + G					
	ND2	75	1.056	GTR + G					
	ND4	69	1.383	GTR + G					
	CMOS	120	945	GTR + G	Strict clock	Yule process User-specified tree: RaxML tree	<b>TranslatorX</b> Muscle protein alignment	<b>Partition Finder</b> Branch length: linked Models of evolution: BEAST Model selection: BIC Greedy search algorithm	<b>RaxML</b> Generations: 100 Reps: 1,000
	RAG2	52	720						
	RAG1	91	2.934						
	ACM4	41	444						
	NT3	66	669						
	PDC	23	441						
	BDNF	74	714						
MC1R	34	861	GTR + G						
R35	57	744	GTR + G						