

Additional file 7 - Best likelihood models of sequence evolution for each codon position and combined positions.

Models were selected by AIC score and were used to inform the likelihood parameters of the MrBayes phylogenetic analysis. For the Bayesian phylogenetic analyses, the best model for *Cytb* was with position 1, 2 and 3 separate. The best model for *Rag1* was also with position 1, 2 and 3 separate.

	position 1	position 2	position 1+2 combined	position 3	position 1+2+3 combined
cyt b	HKY+I	TVM+I	TrN+I+G	SYM+G	HKY+I+G
rag1	TVM	F81+I	TVM+I	TVM+G	TVMef+I+G