



Figure S6. Results of traditional dN/dS estimates for all 13 protein-coding mitochondrial genes using the alternative (mitochondrial gene-based) topology from Fig. S1, with branches colored based on dN/dS ratios. Branch lengths are based on all mitochondrial protein-coding genes, optimized on this topology in PAUP* under a GTRFI model. Estimates of dN/dS are from codon model-based analyses conducted HyPhy (See Supplementary Methods).