



**Figure S8.** Results of traditional  $dN/dS$  estimates for the CytB gene 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).