



Figure S3. Results of traditional dN/dS estimates for the entire set of 13 mitochondrial protein-coding genes 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 GTR Γ I model. Estimates of dN/dS are from codon model-based analyses conducted HyPhy (See Supplementary Methods).