



Figure S6. Bayesian maximum clade credibility tree from all mitochondrial coding regions, partitioned by codon position, of the 59-tip dataset (i.e., lacking *Gymnomyza aubryana*). Node support is given as posterior probabilities if less than 1. Clades A–H are referenced in the text. Only genus names are given, except for instances of where we sampled multiple, paraphyletic genera.