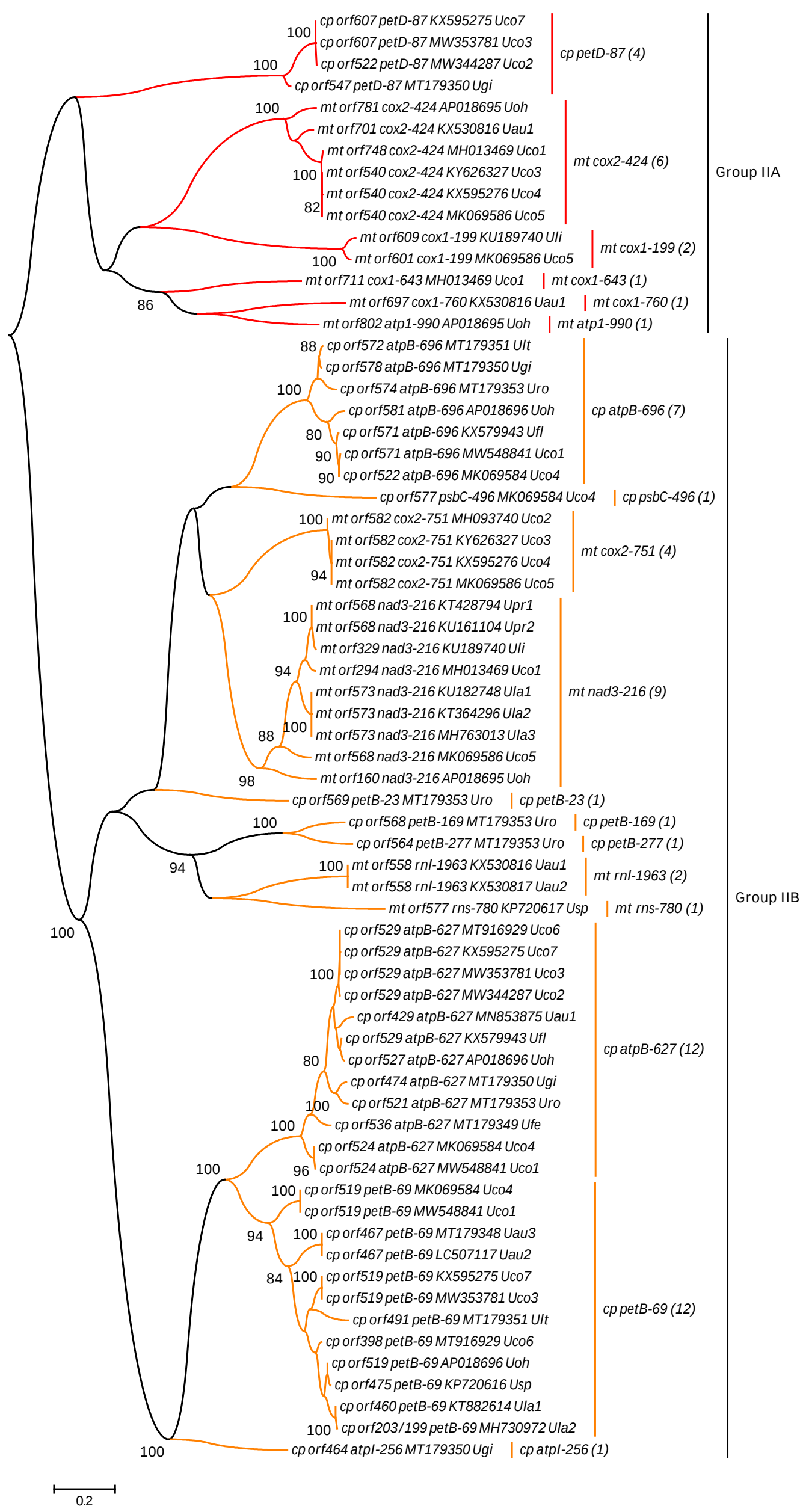




0.2

Supplementary Fig. S2 Phylogenetic tree based on Maximum Likelihood (ML) analysis of amino acid (aa) sequences of 67 reverse transcriptase (RT) domains (40 in cpDNAs and 27 in mtDNAs) from group IIA and IIB introns. The ML analysis was conducted with 1,000 bootstrap replicates using MEGA 7.0. The bootstrap support values greater than 80% were displayed at branches. Branch lengths were proportional to the amount of sequence change, which were indicated by the scale bar below the trees.