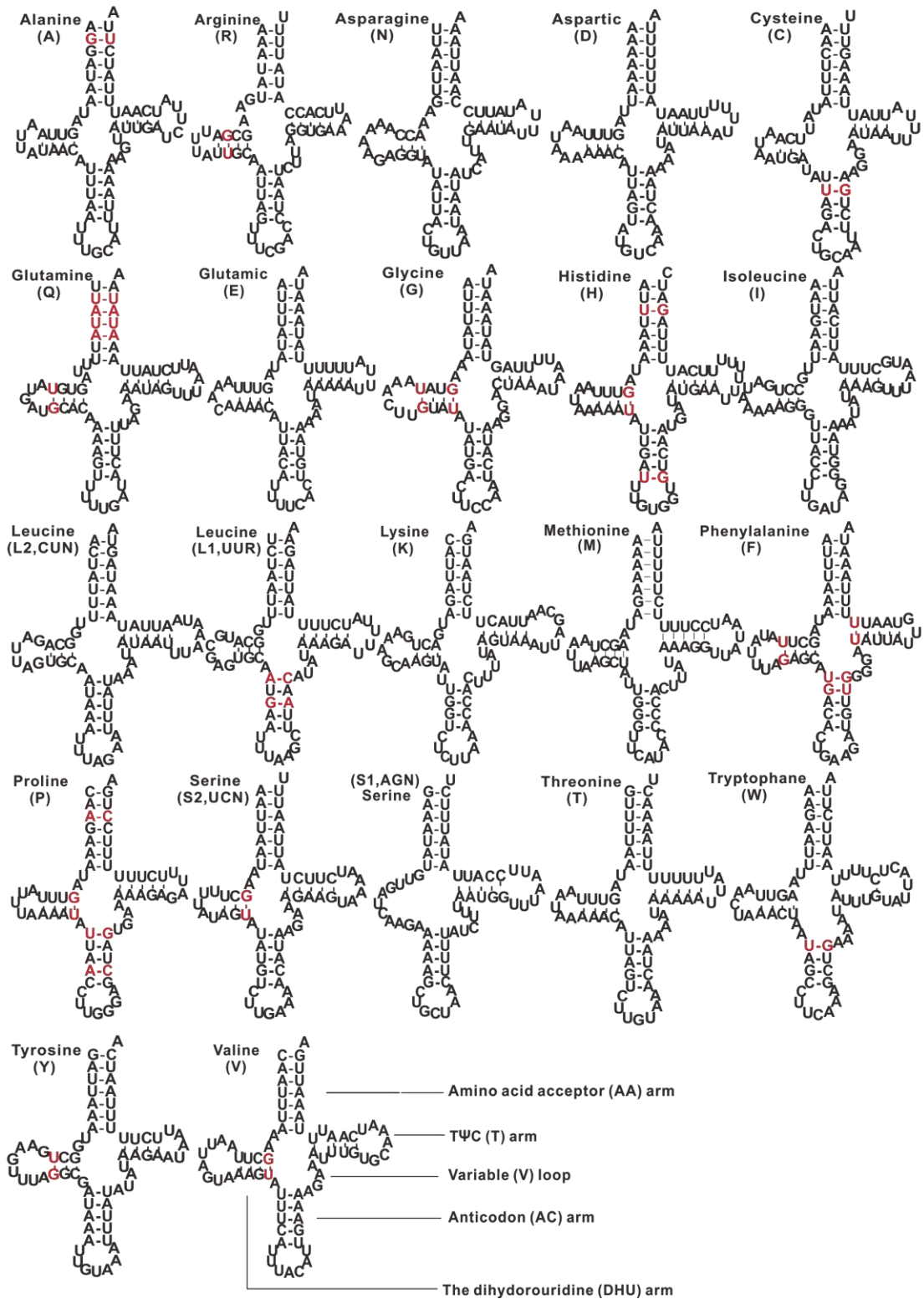
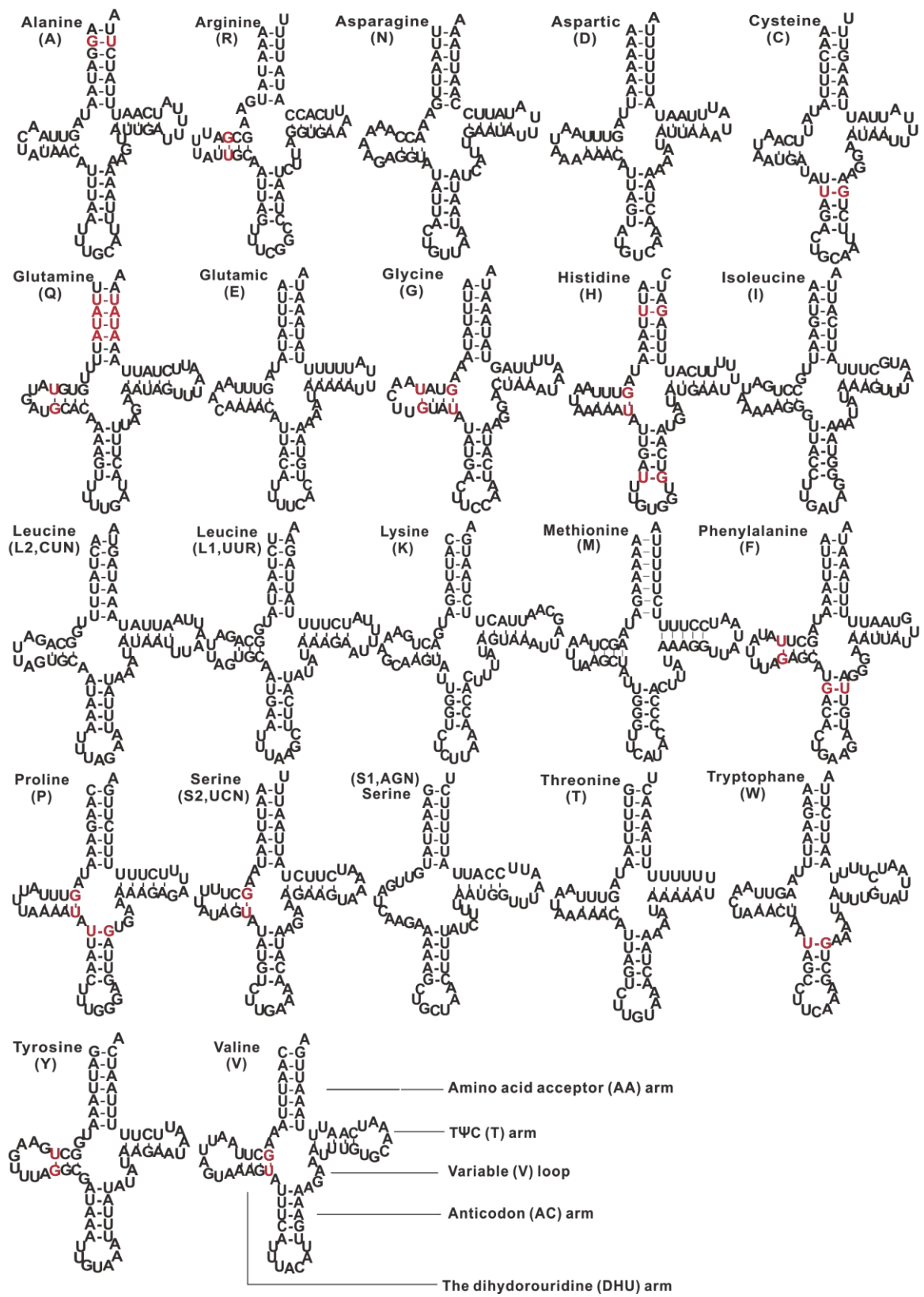


Figure S1. Predicted secondary structures for 22 tRNAs in *Lt. fuscans* (A), *Lt. halifaxia* (B) and *Cx. pallidothorax* (C) mt genomes. Nucleotides highlighted in red indicate mismatch.

A



B



C

