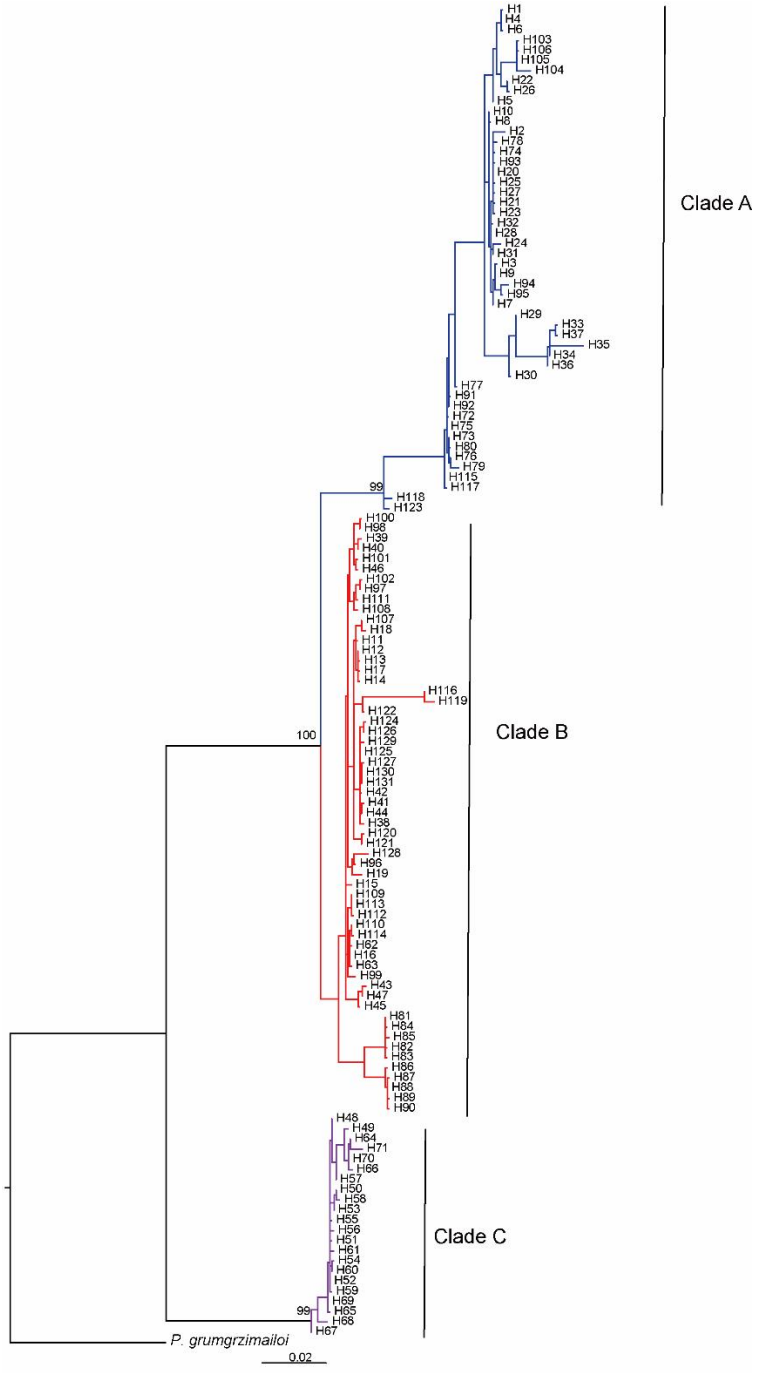


FIGURE S1 | Maximum-likelihood phylogeny of *P. przewalskii* mitochondrial haplotypes based on concatenated COI and cyt *b* sequences, using *P. grumgrzimailoi* as the outgroup. This tree recovered three major divergent clades (A, B, and C) consistent with the topology inferred from the Bayesian phylogenetic analysis. Node values indicate ultrafast bootstrap support, with only values ≥ 90 displayed. The scale bar represents 0.02 nucleotide substitutions per site.