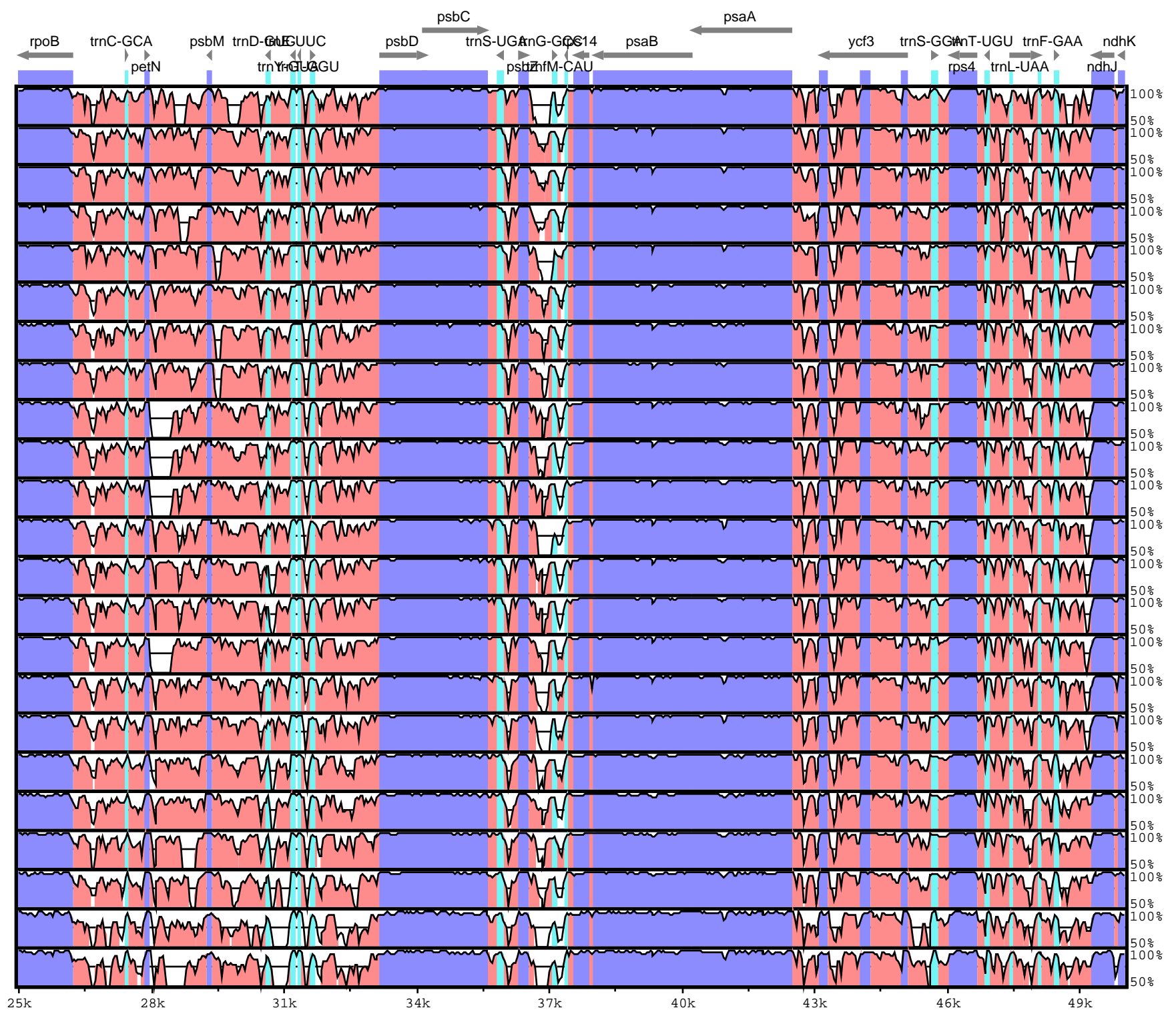
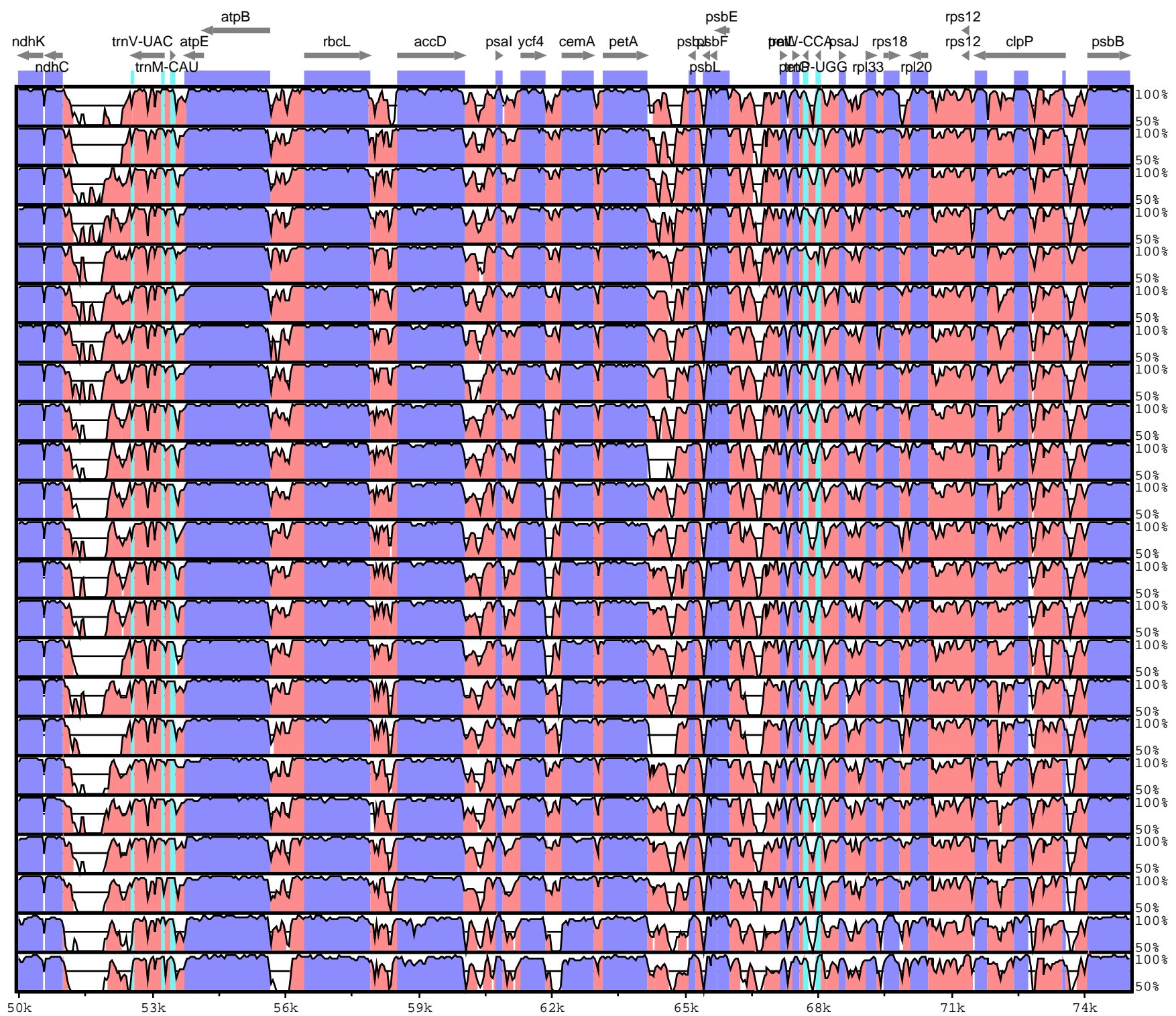
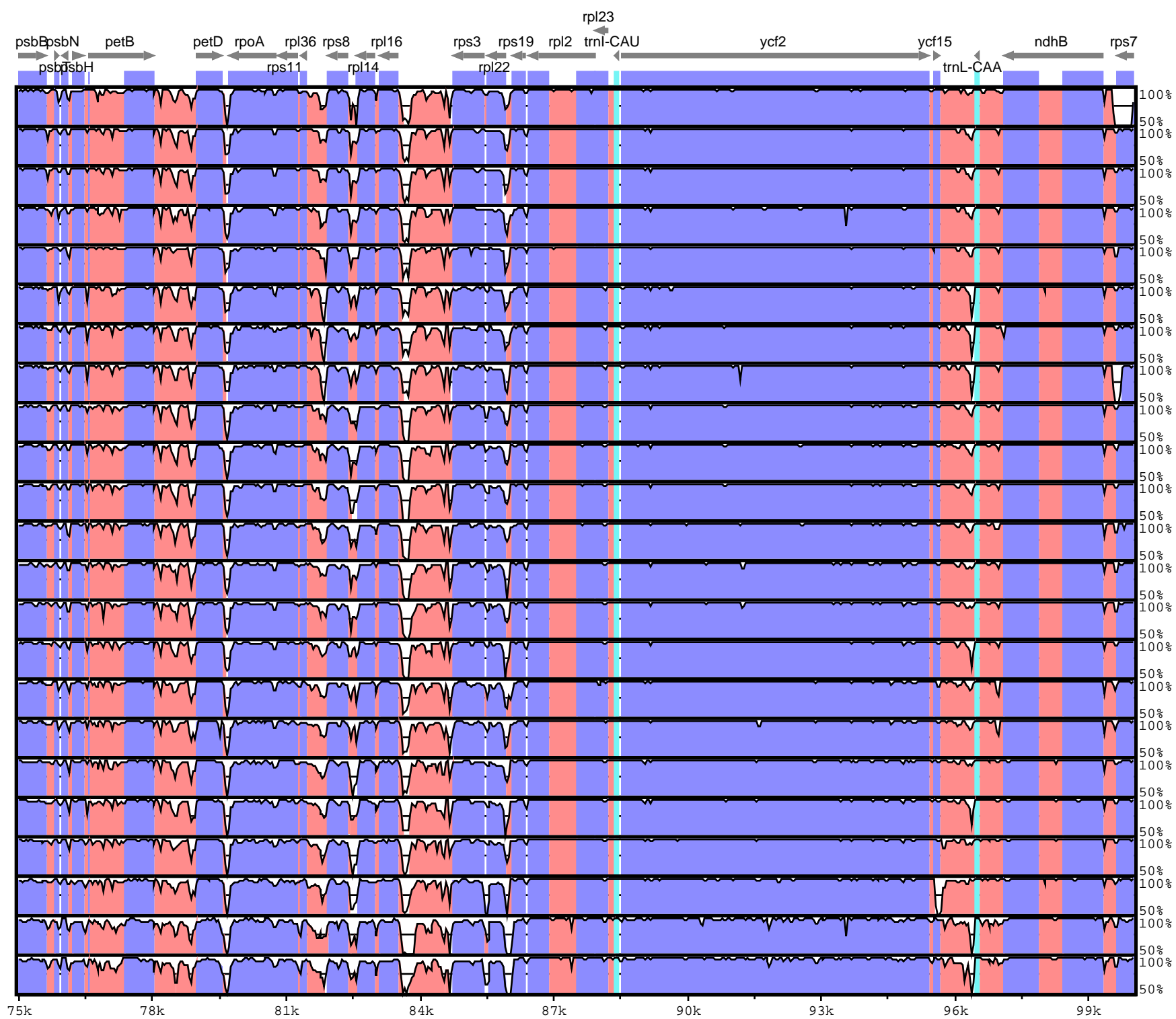
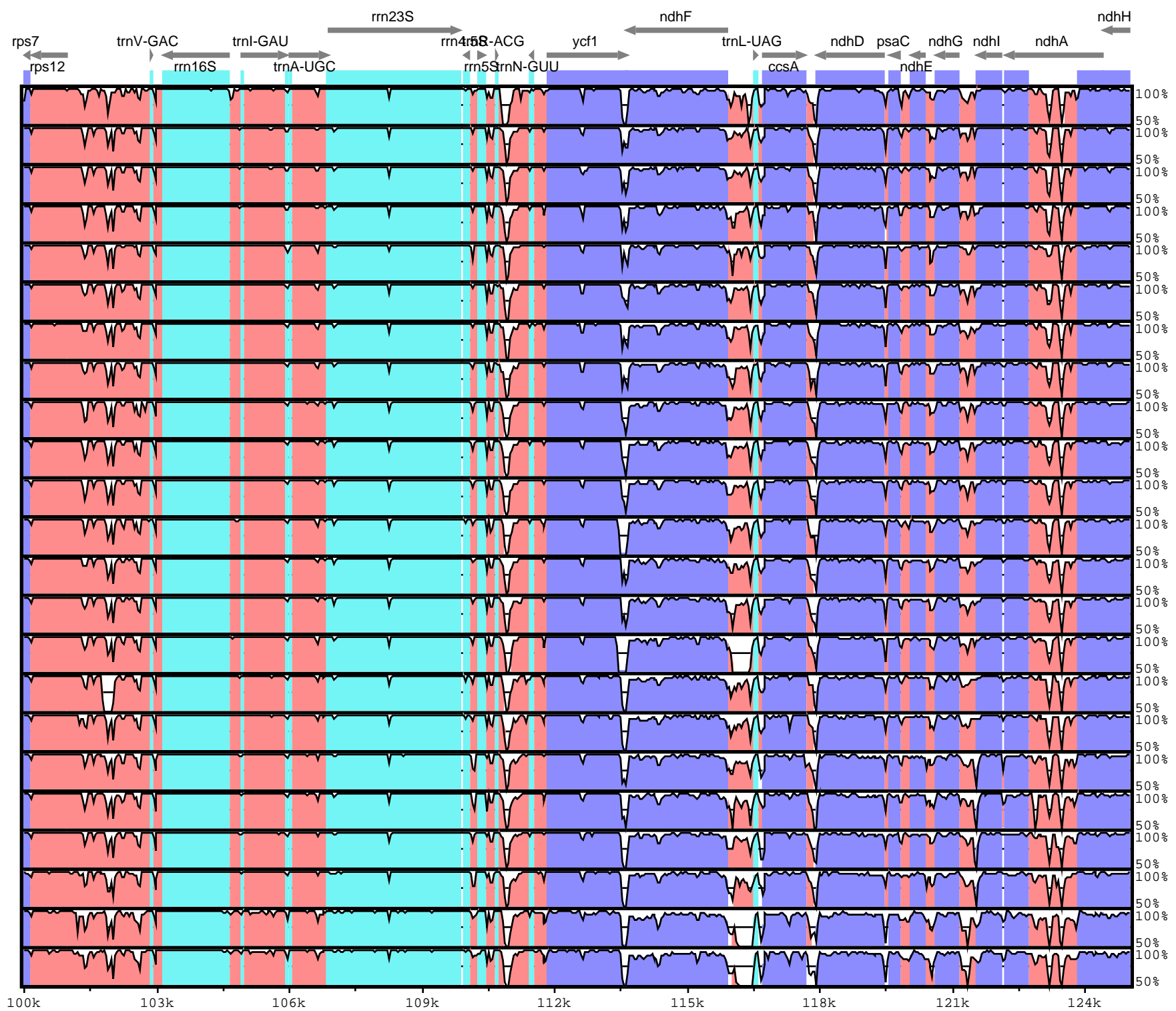


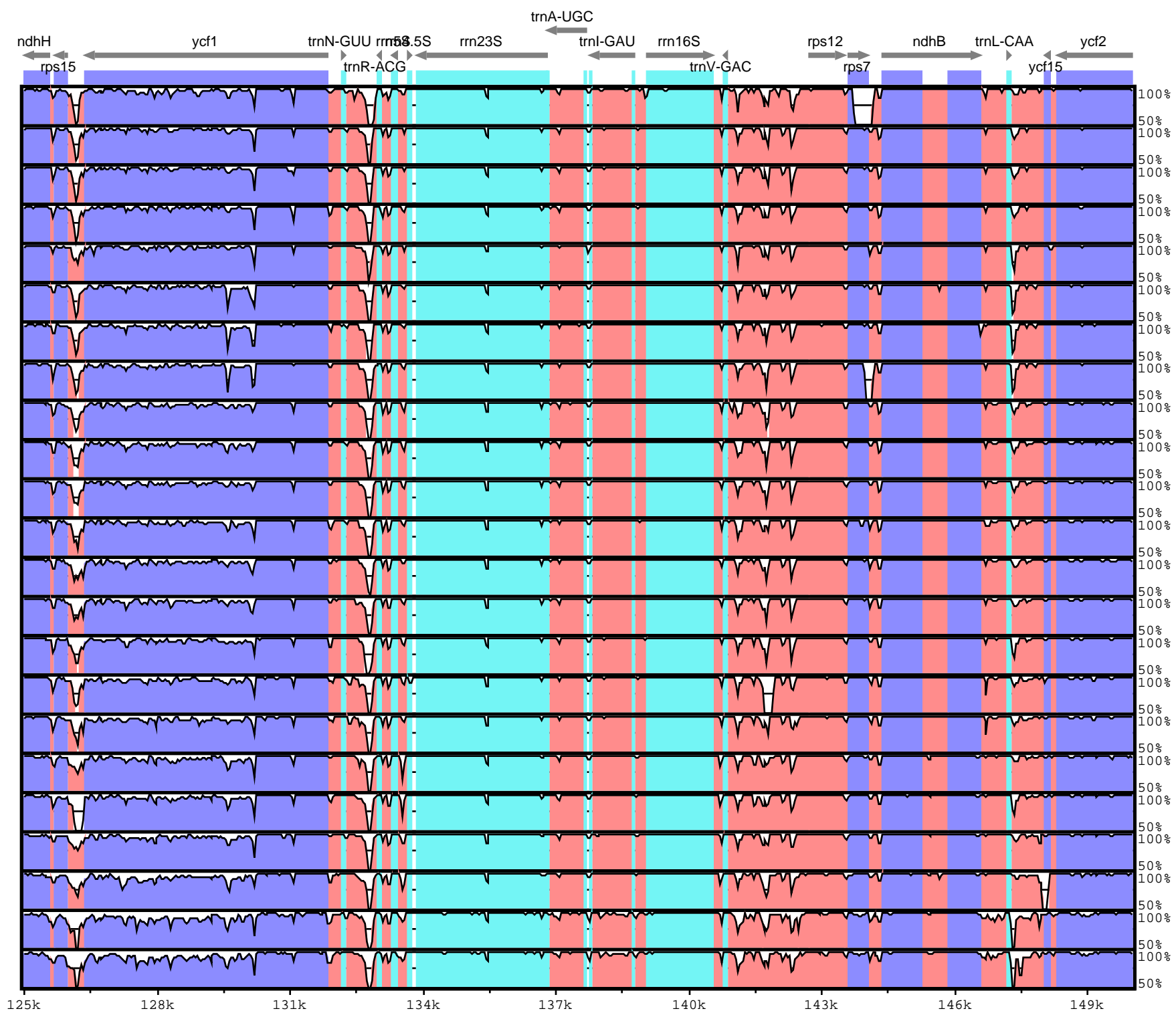
→ gene
exon
UTR
CNS
mRNA











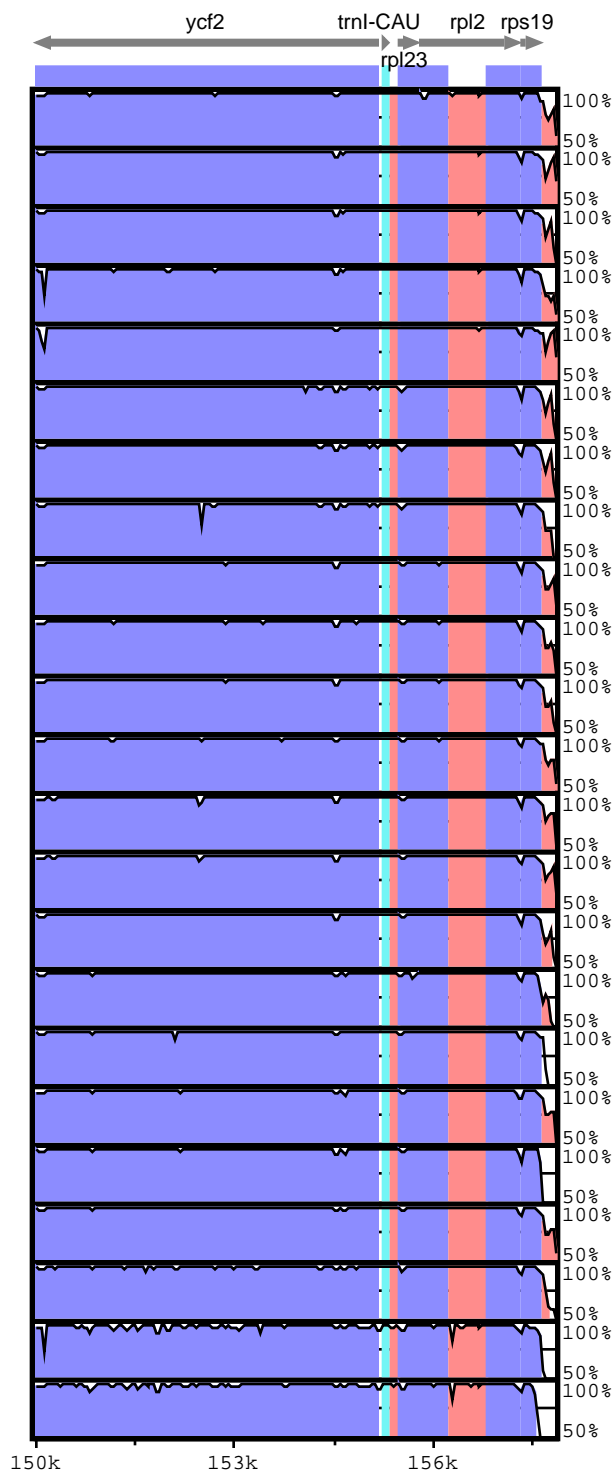


Figure S1. Sequence alignment of plastid genomes from twenty-four Salicaceae *s.l.* species. Sequences of plastid genomes were aligned and compared using the mVISTA program. The horizontal axis(x) indicates the coordinates within the plastid genome. The vertical scale (y axis) indicates the percentage identity, ranging from 50 to 100%. The grey arrows indicates the direction of each gene. Purple bars represent exons, orange bars show conserved non-coding sequences.