

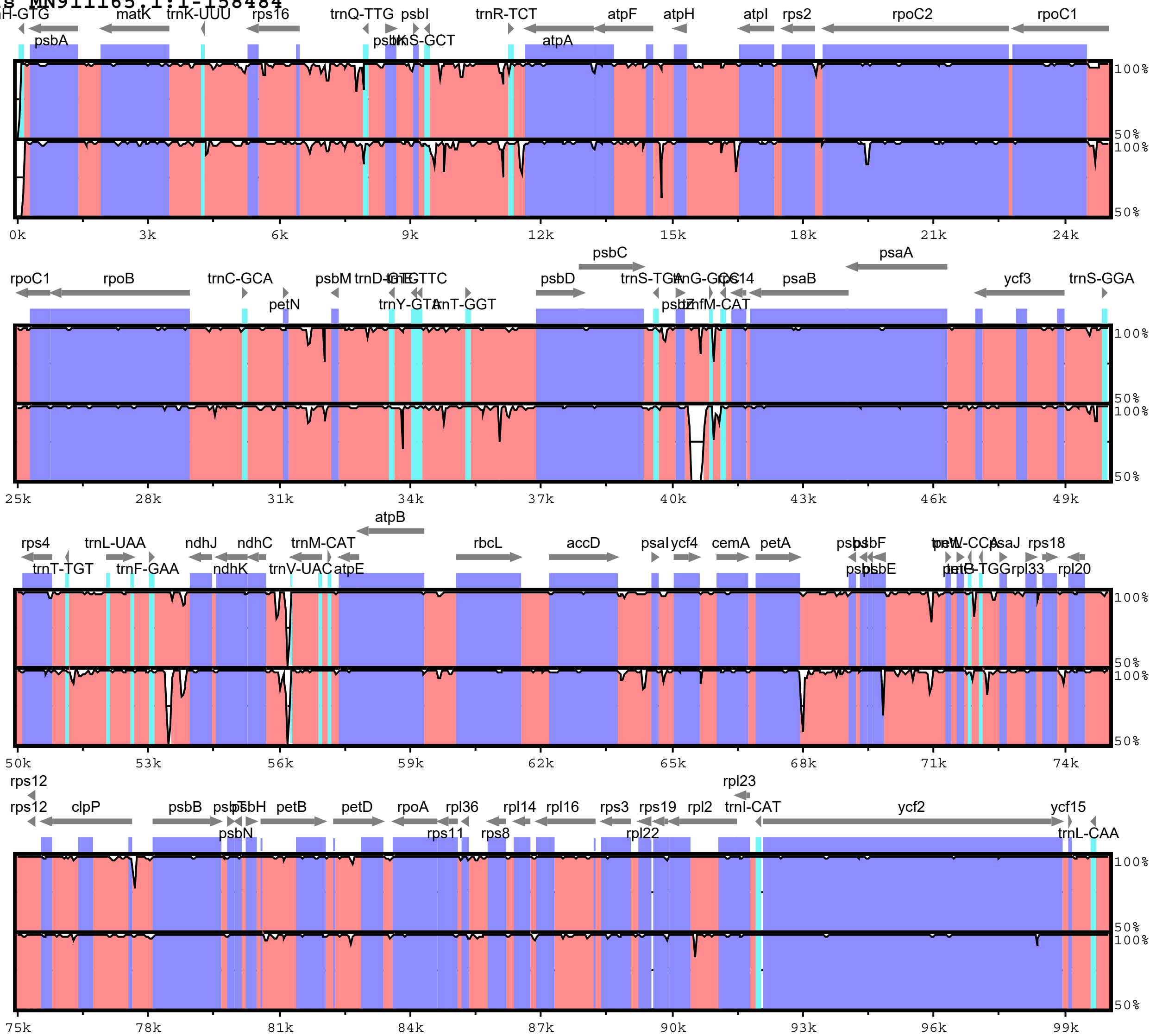
**Annamocarya sinensis\_MN911165.1:1-158484**

Alignment 1  
Carya\_kweichowensis  
NC\_040864.1 (+)  
1-175313  
Criteria: 70%, 100 bp  
Regions: 277

Alignment 2  
Carya\_cathayensis  
NC\_046572.1 (+)  
1-160666  
Criteria: 70%, 100 bp  
Regions: 281

X-axis: *Annamocarya\_sinensis*  
Resolution: 39  
Window size: 100 bp

gene  
exon  
UTR  
CNS  
mRNA



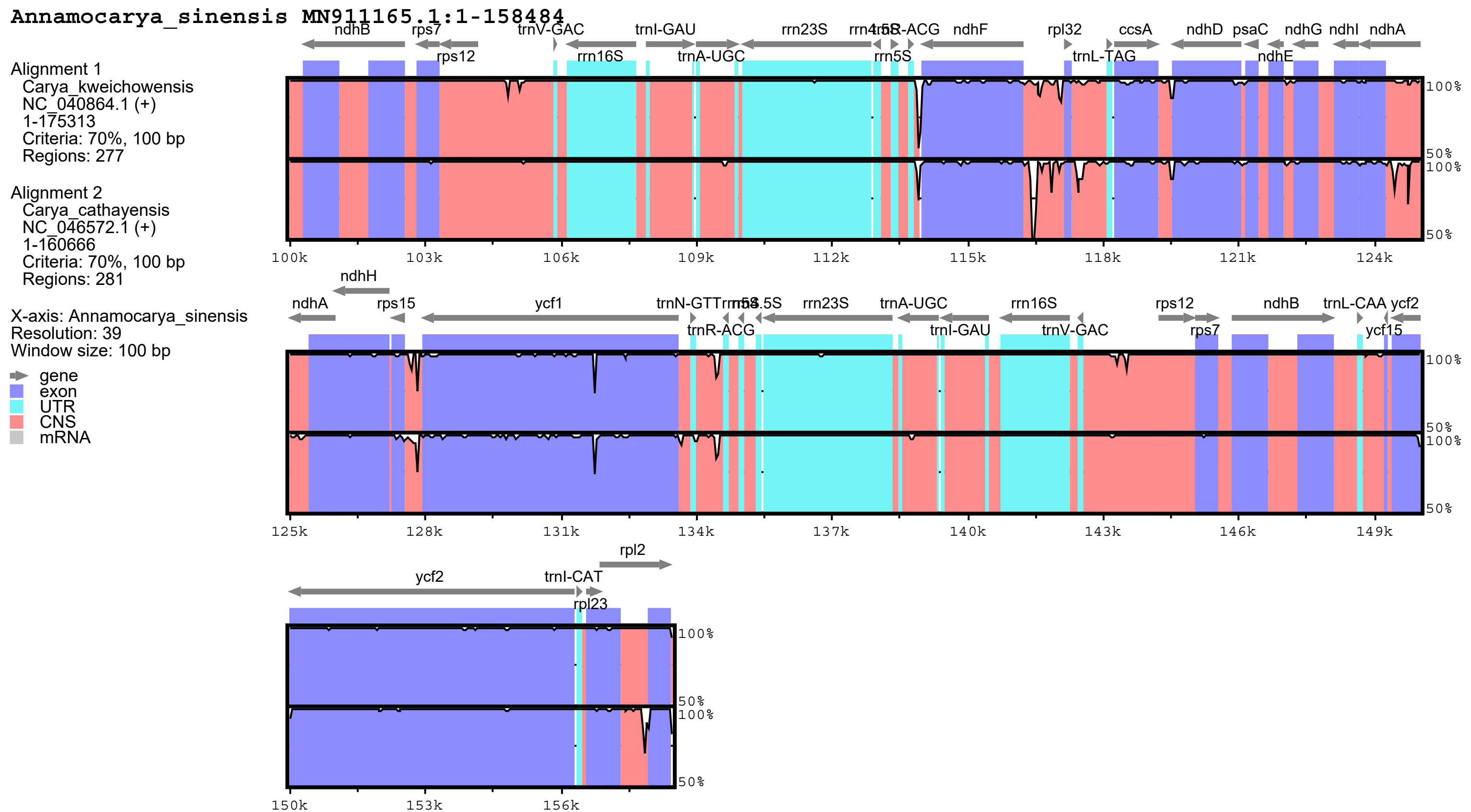


Figure S4: The alignment of chloroplast genomes of *A.sinensis*, *C.cathayensis* and *C.kweichowensis*. This result was constructed using mVISTA web tool (<https://genome.lbl.gov/vista/index.shtml>). The first row (alignment 1) was the alignment between *C.kwichowensis* and *A.sinensis*. And the second row (alignment 2) was the alignment between *C.cathayensis* and *A.sinensis*. The "valleys" in this graph indicated the non-conservation percentage between the two alignment genomes. The dark blue regions are exon. Untranslated regions (UTR) are marked in light blue, while conservative non-coding sequences (CNS) are marked in pink. The arrows signify the direction of the gene.