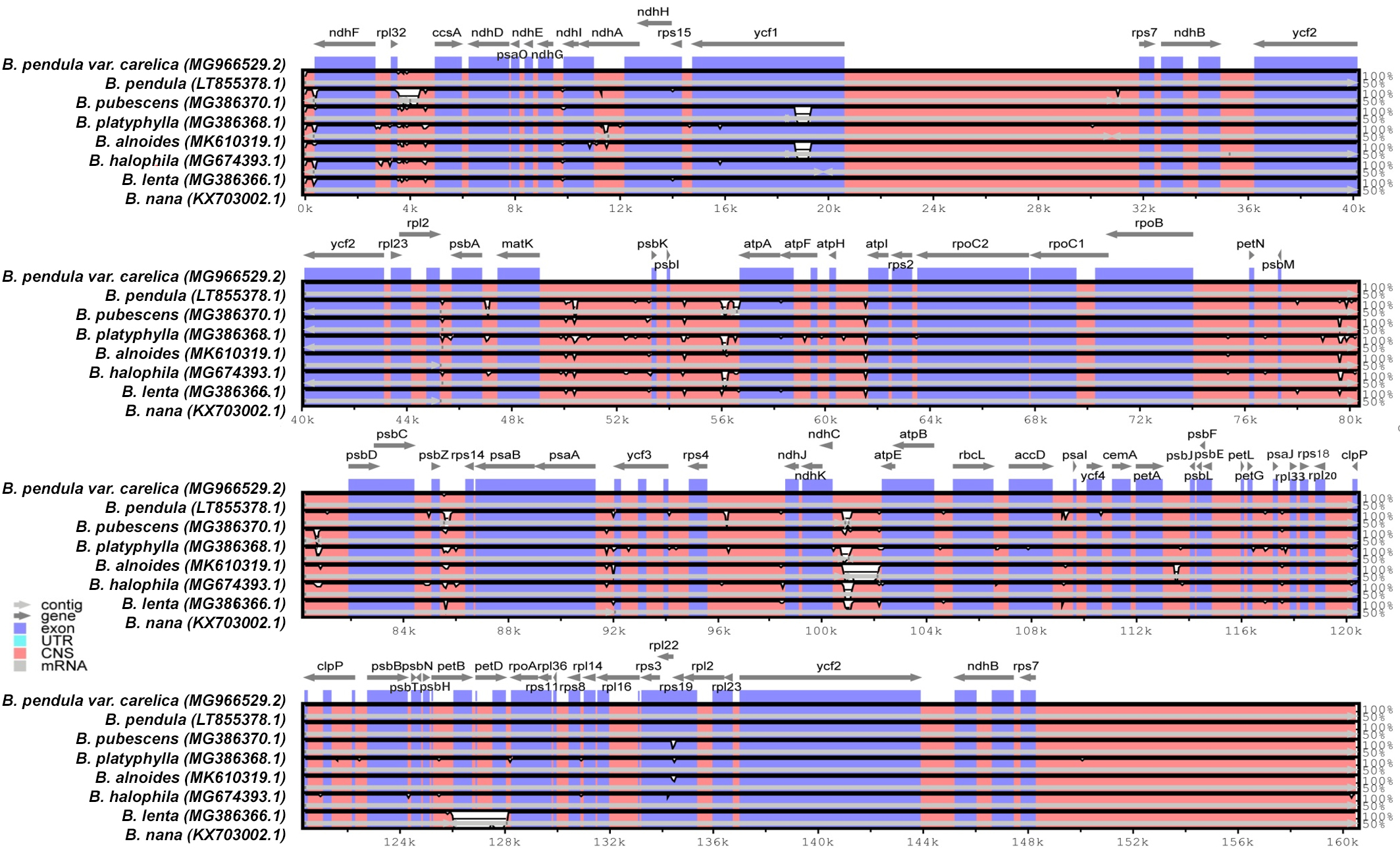
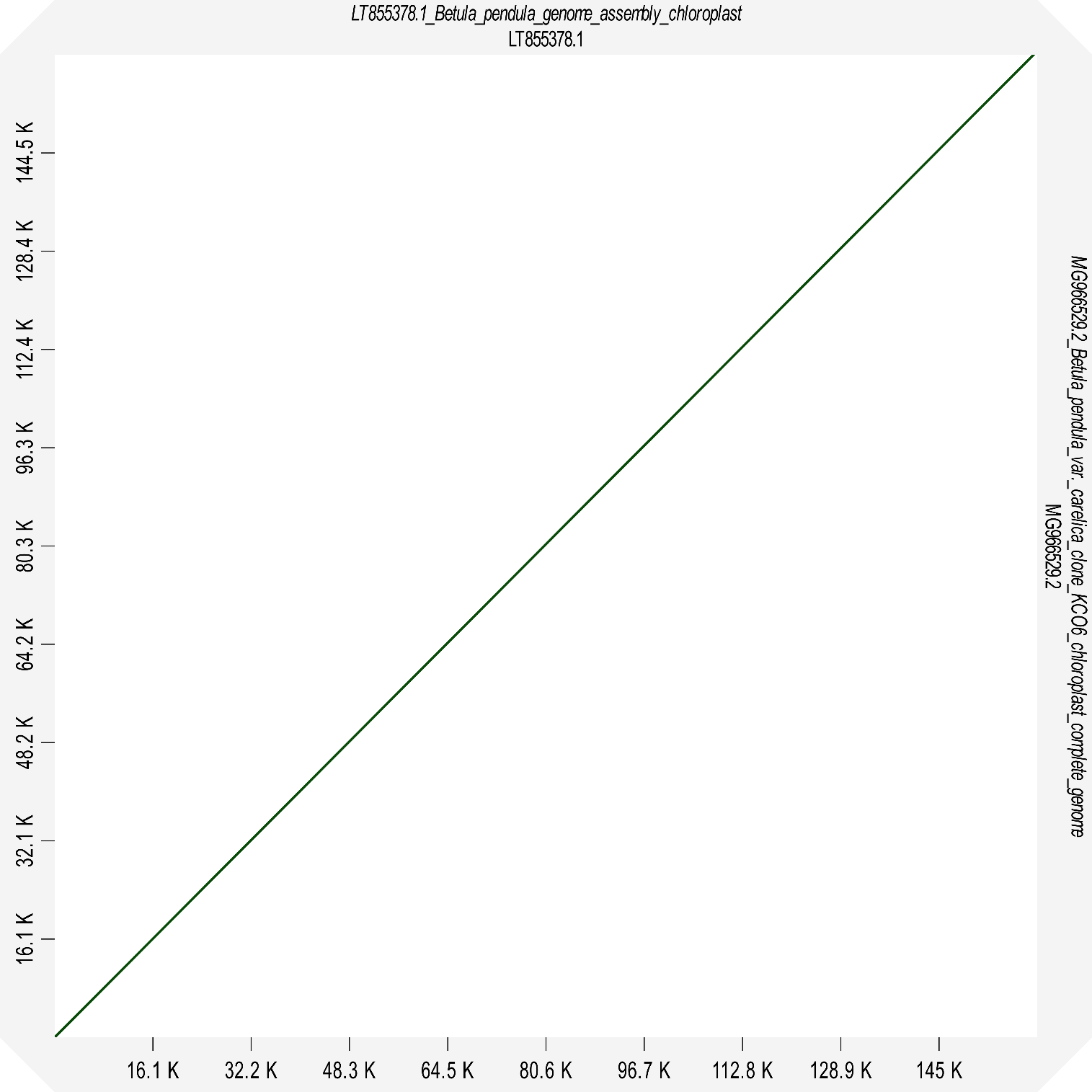
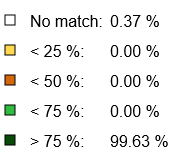
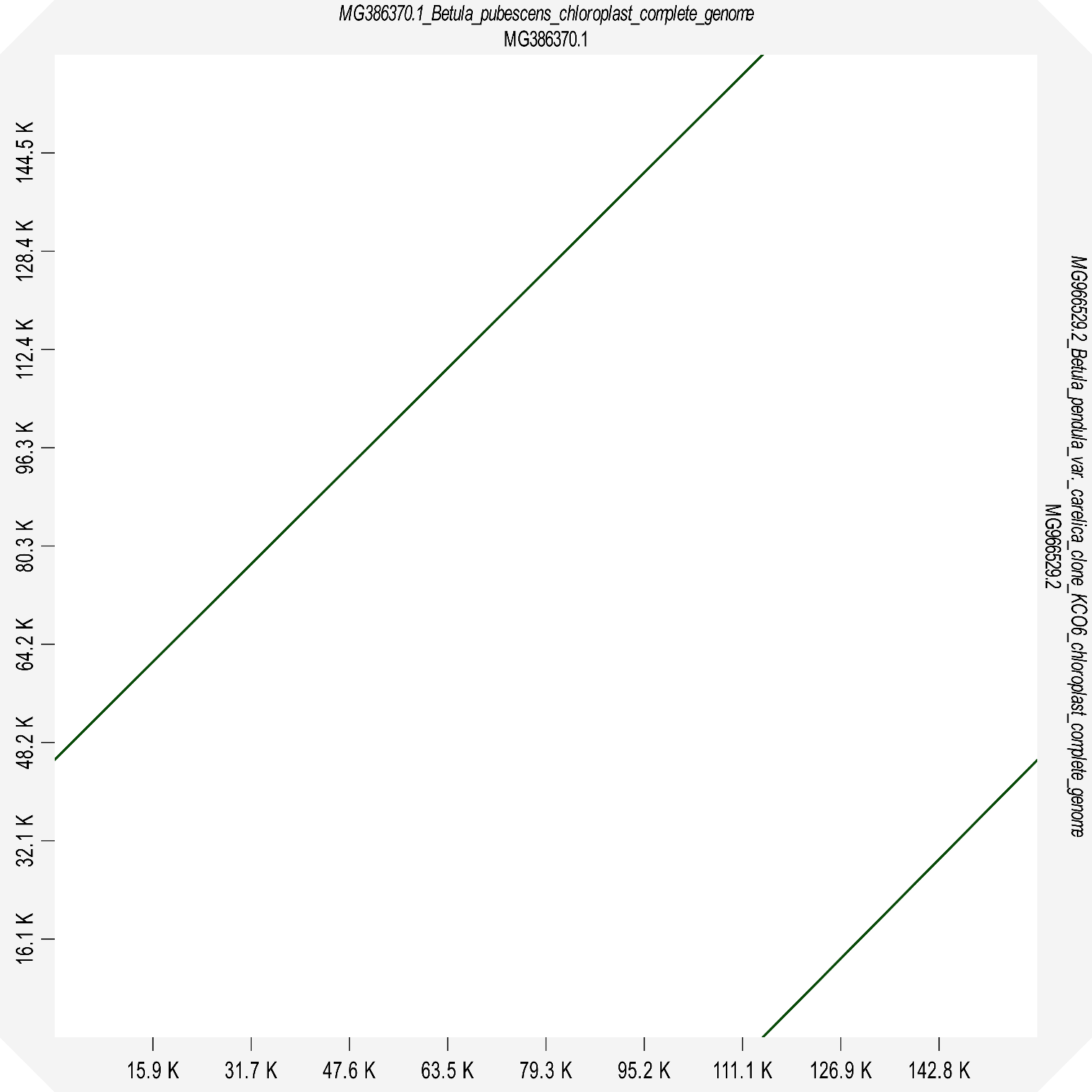
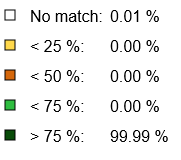
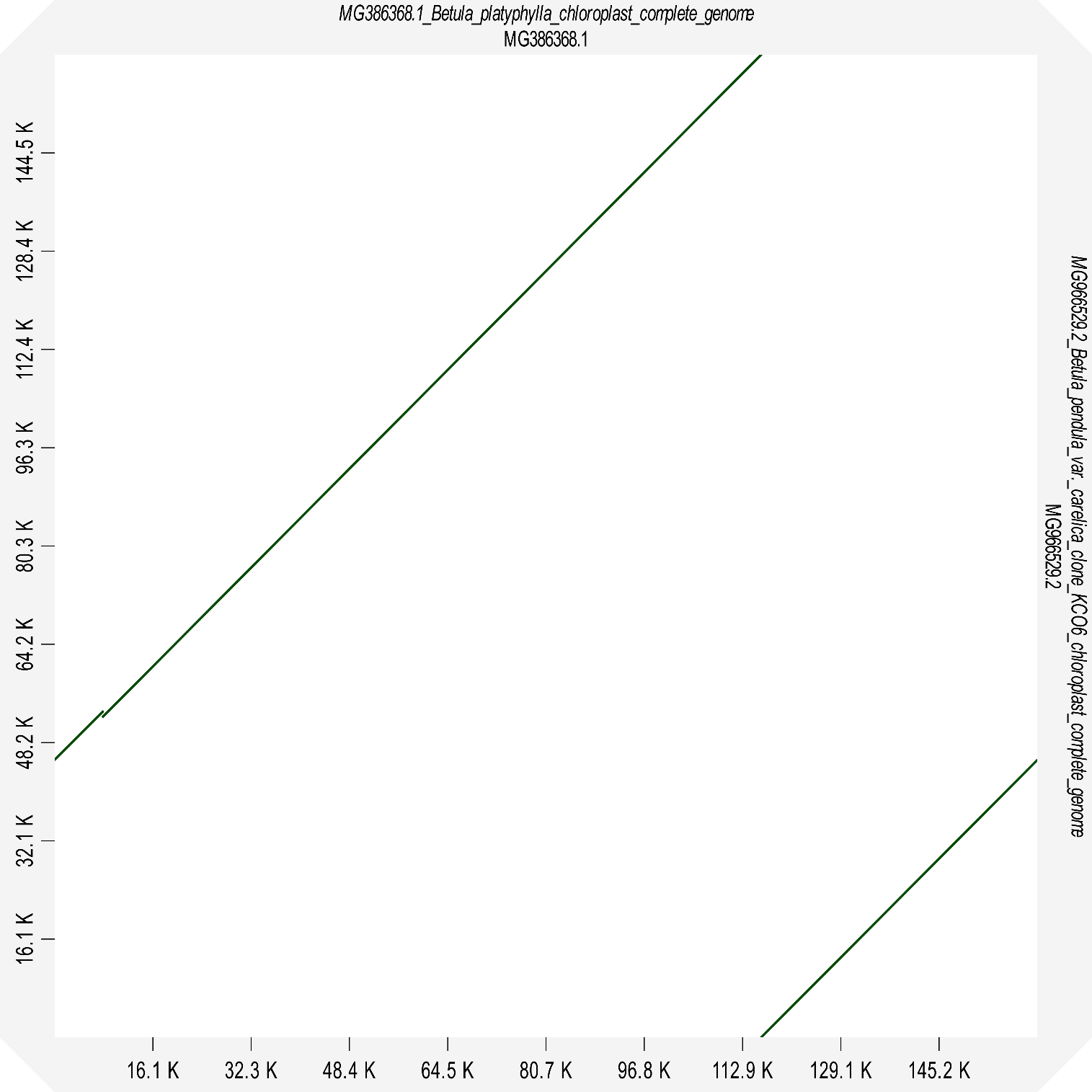
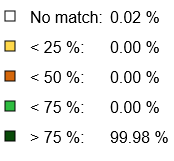
Supplementary Material

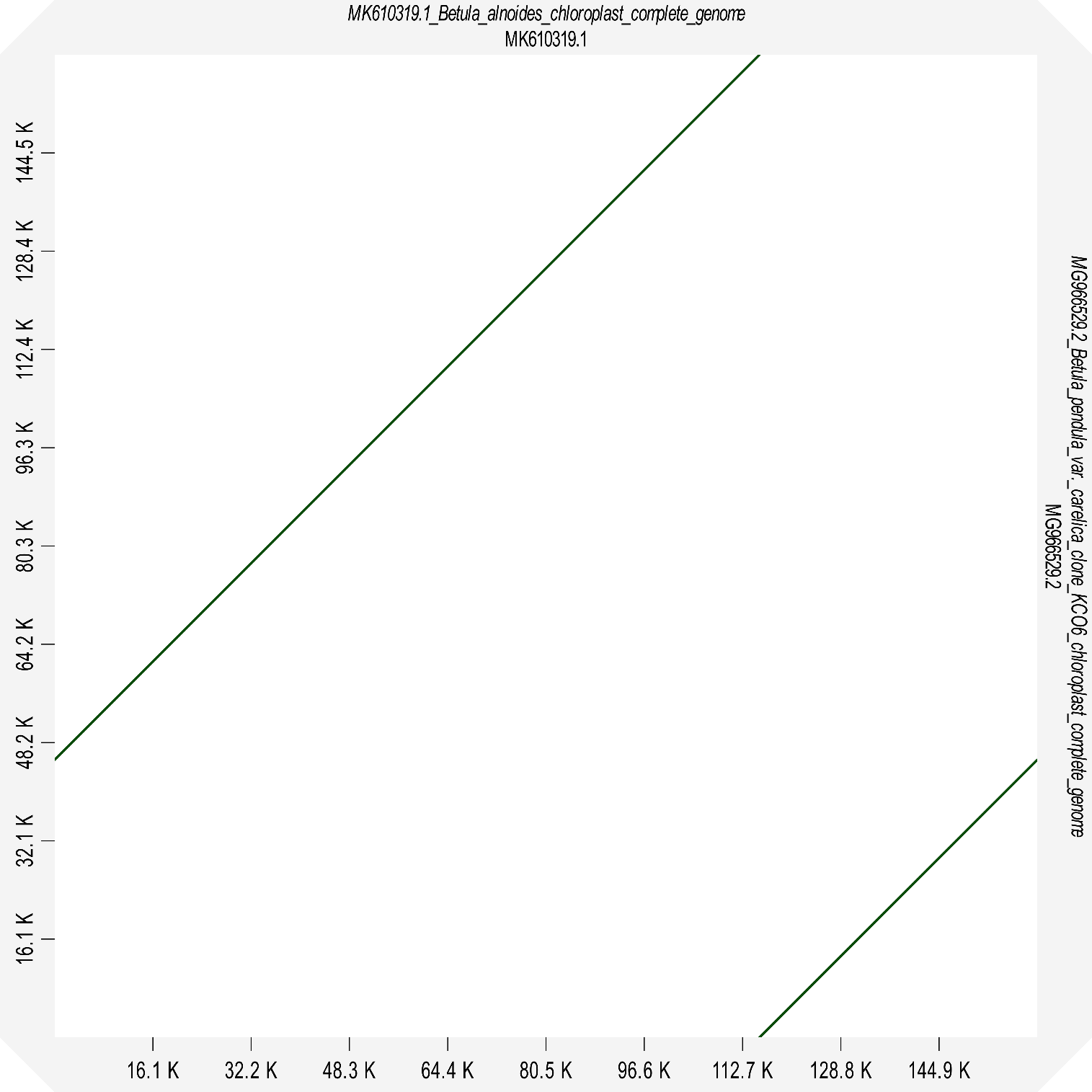
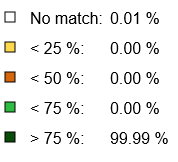
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| |  | | --- | |  | |  | |  |   **Supplementary Figure S1.** Multiple nucleotide sequence alignment of nine woody plant species plastomes from *Spermatophyta* (mVISTA). *B. pendula var. carelica* was used as a reference. Grey arrows above the alignment indicate the transcriptional directions of genes. Genome regions are color-coded as exon (violet) and conserved non-coding sequences (CNS) (red). A cut-off of 50% identity was used for the plots. The Y-axis indicates the percent identity between 50 and 100%. |

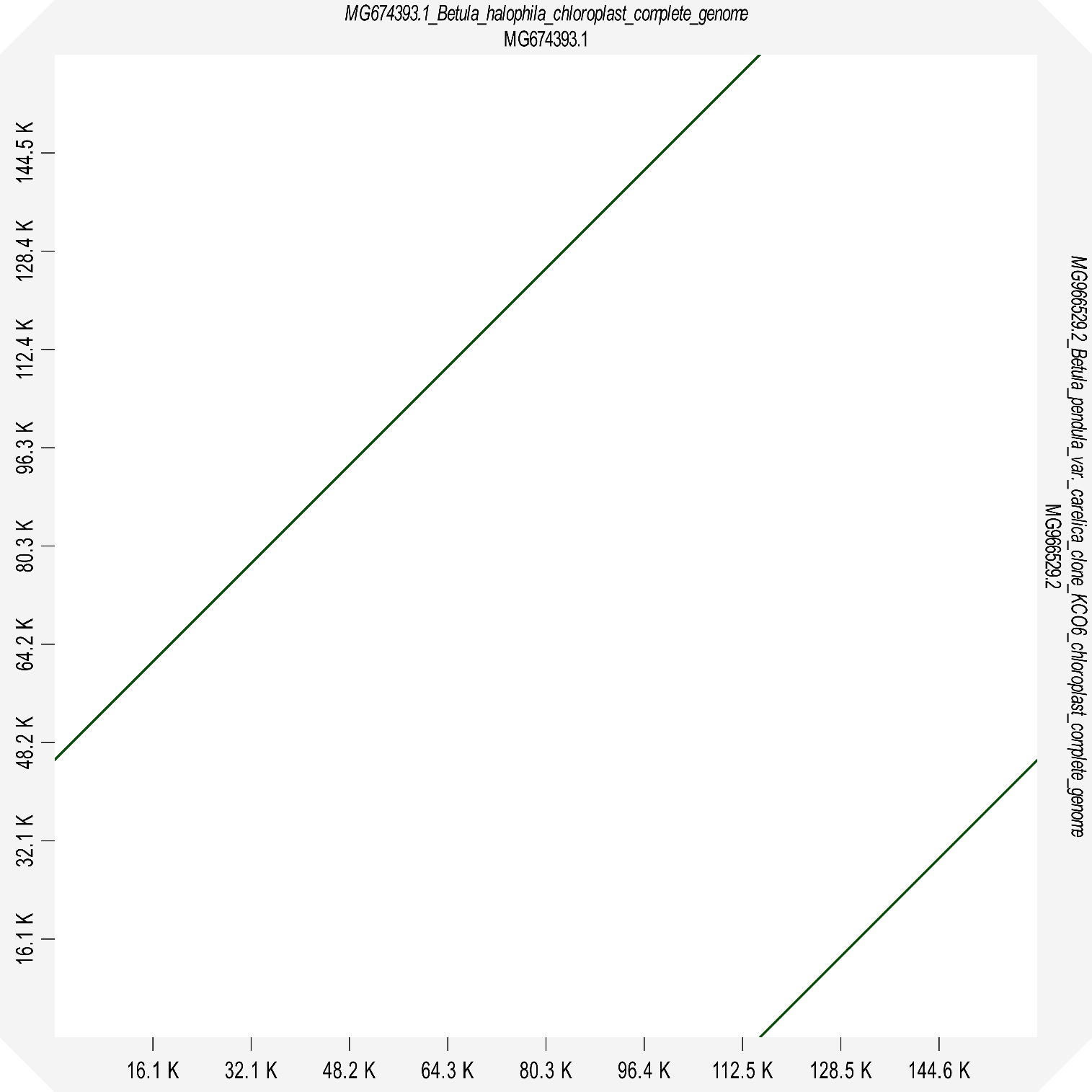
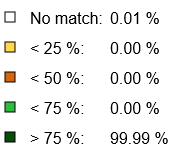
**Supplementary Figure S2.** Multiple whole-plastome sequence alignment of eight birch species. Grey arrows above the alignment indicate the transcriptional directions of genes. Genome regions are color-coded.

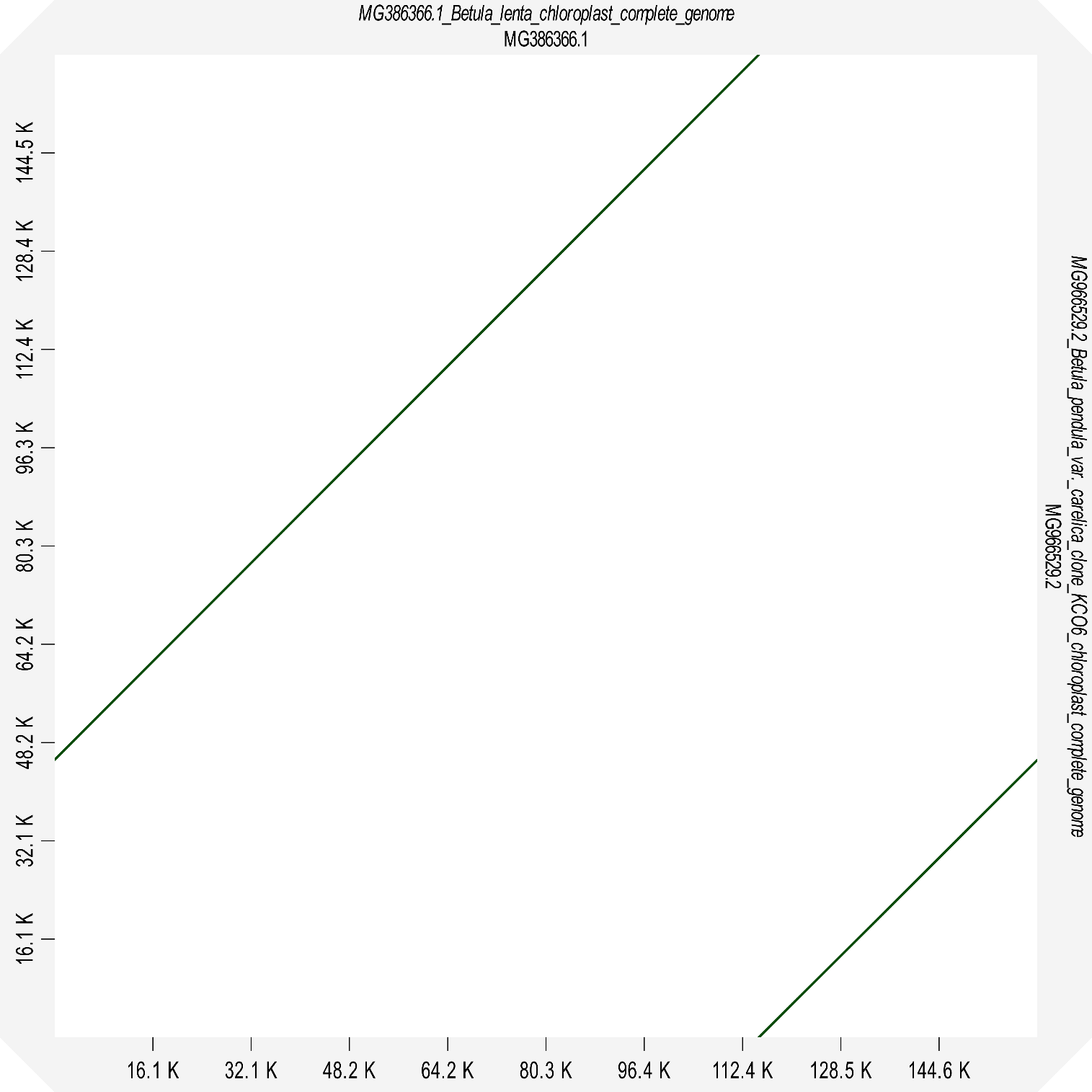
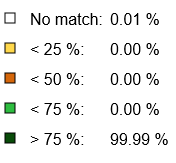


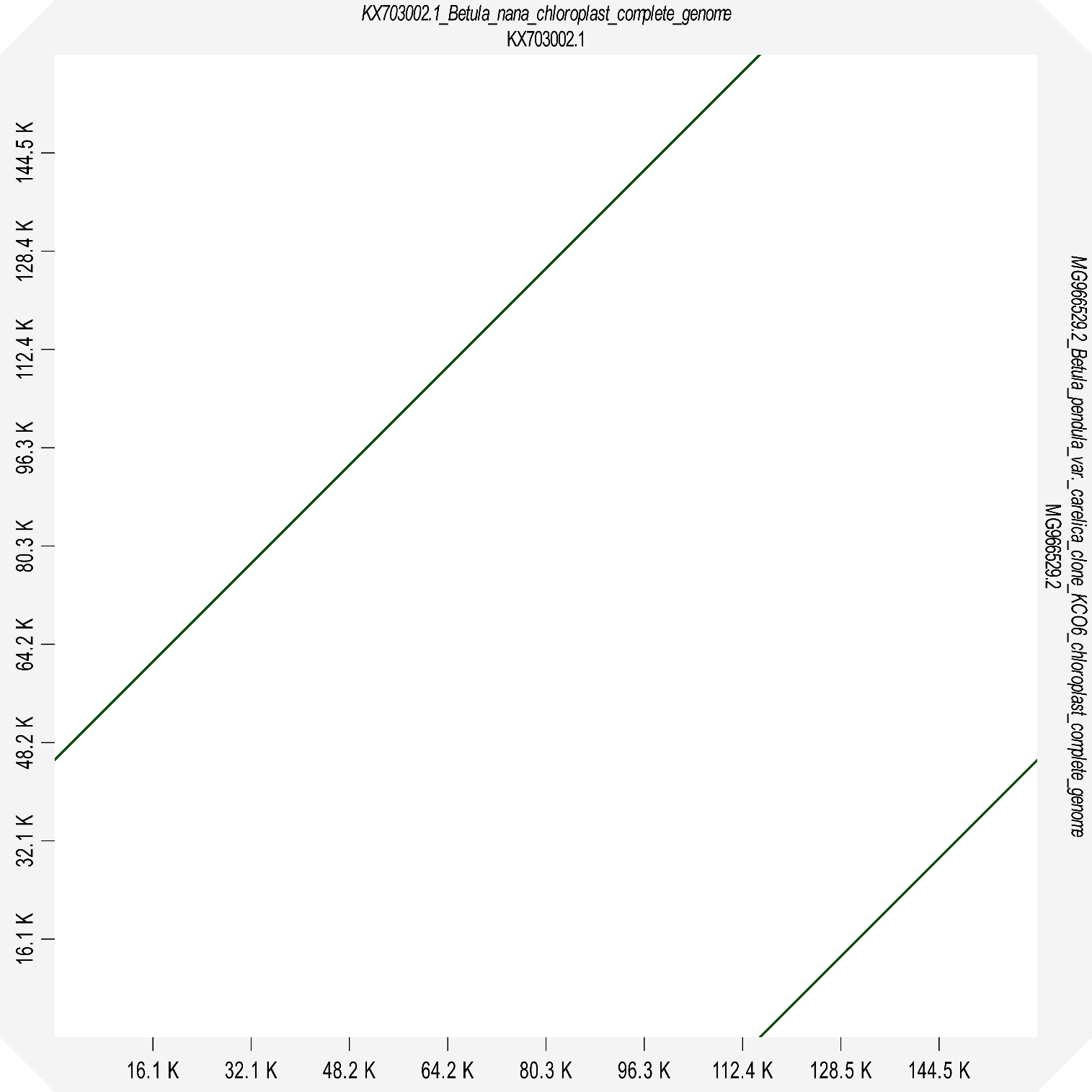
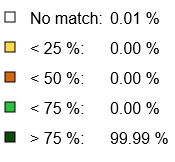












**Supplementary Figure S3.** Dot plots of pairwise alignments of the *B. pendula var. carelica* (MG966529.2) complete plastome sequence vs. plastomes of eight birch species.