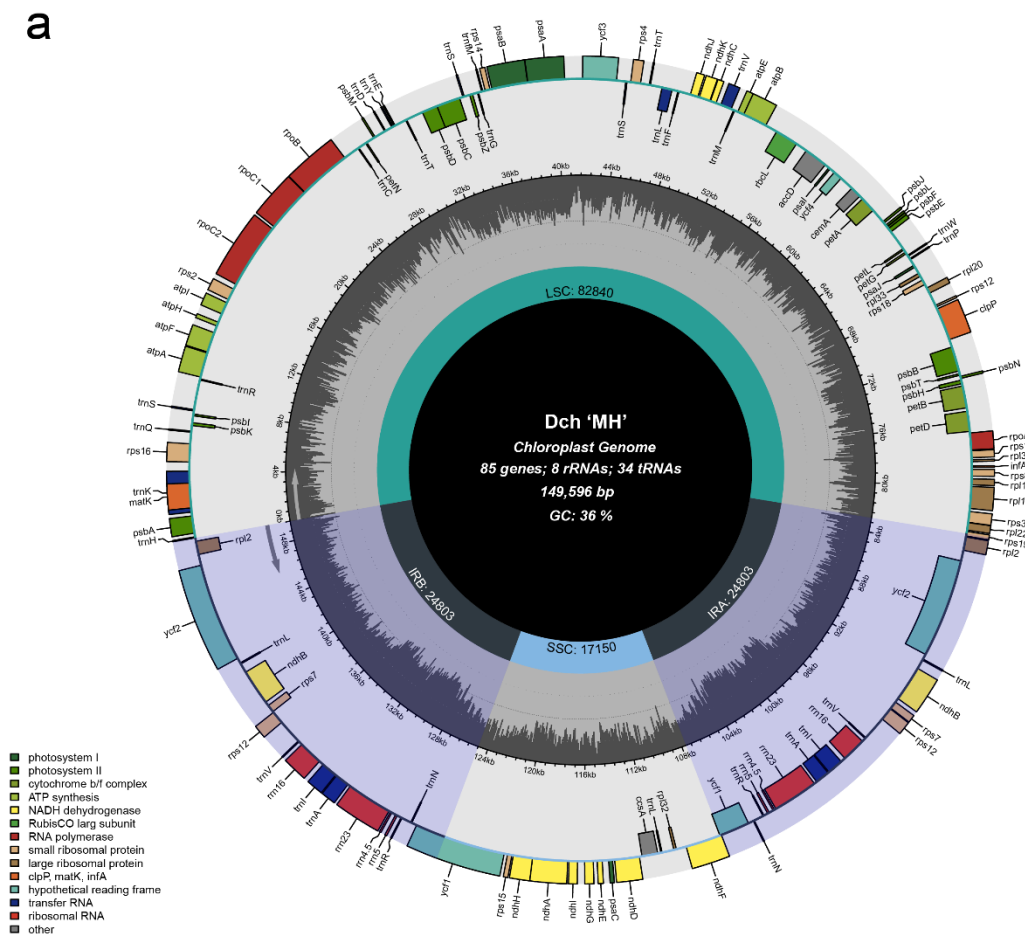
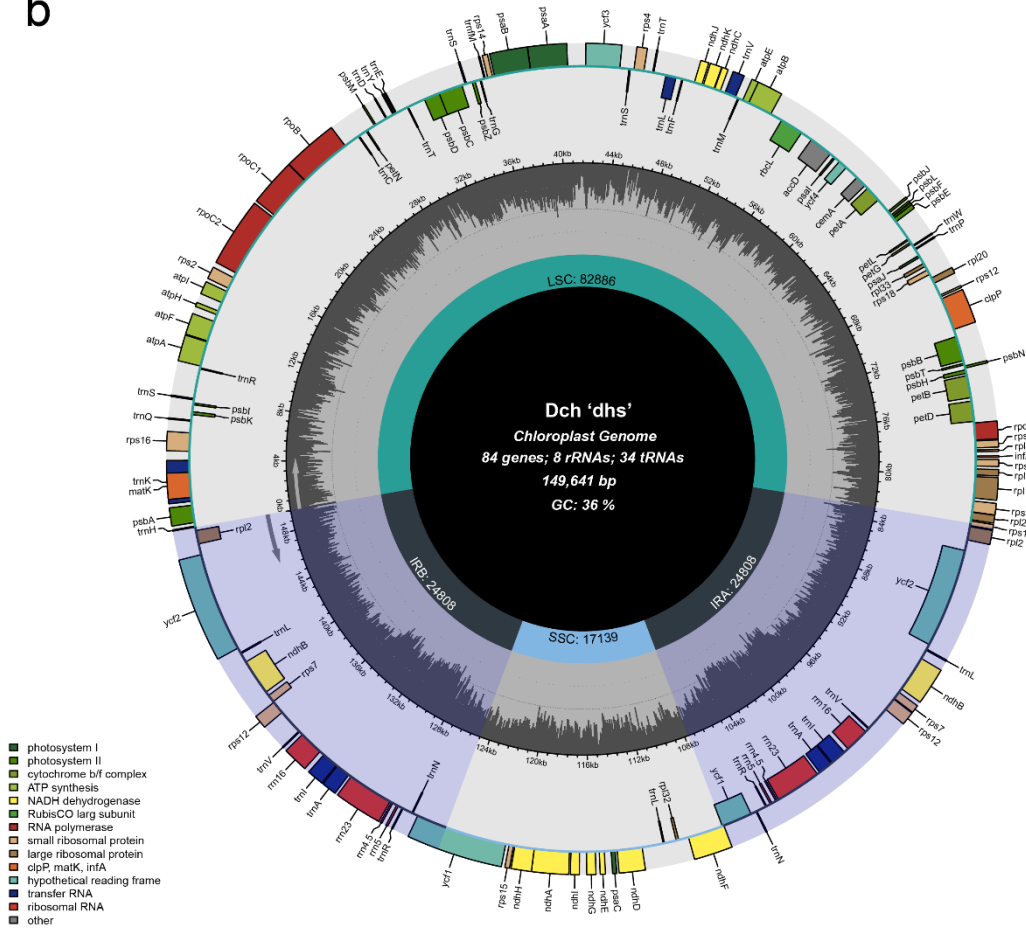


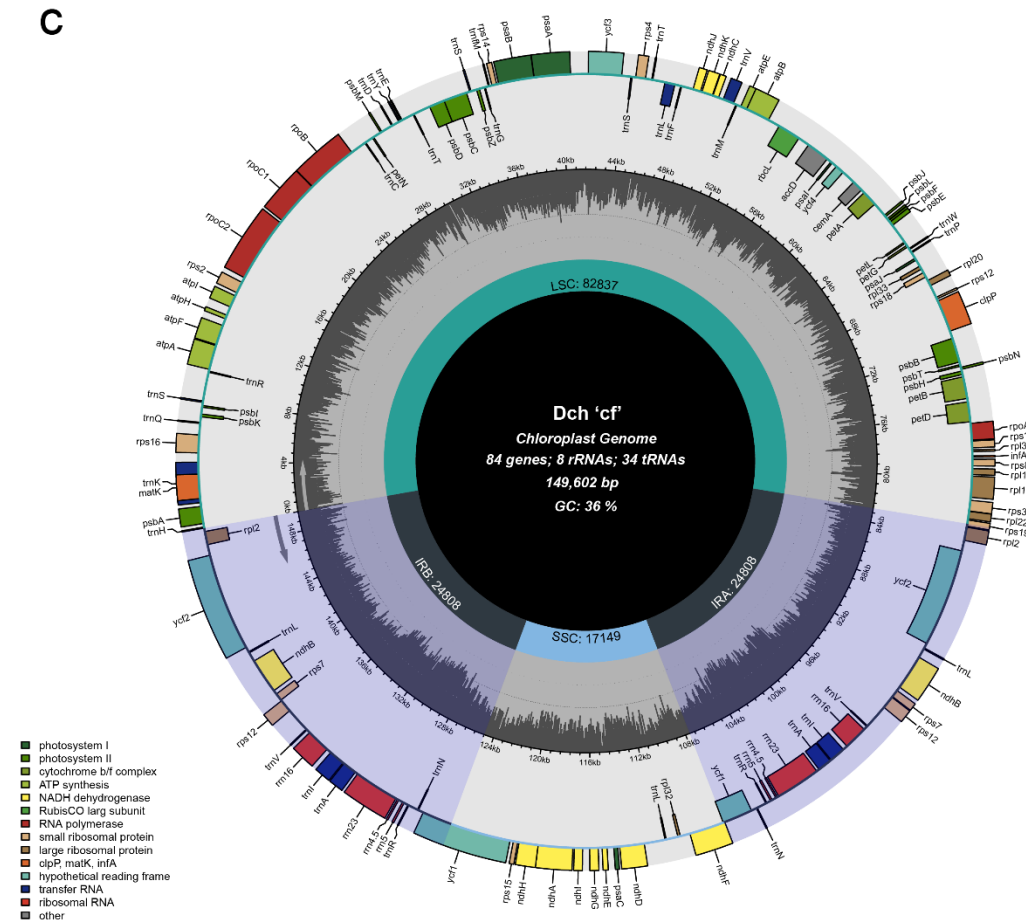
Figure S1. The gel electrophoresis results of the amplification of gaps in Dch 'X' sample using designed primers. (a) The result of X-1. r1-r5 were five repetitions. (b) The result of X-2. r1-r2 were two repetitions. Lane M was the marker of DL2000.



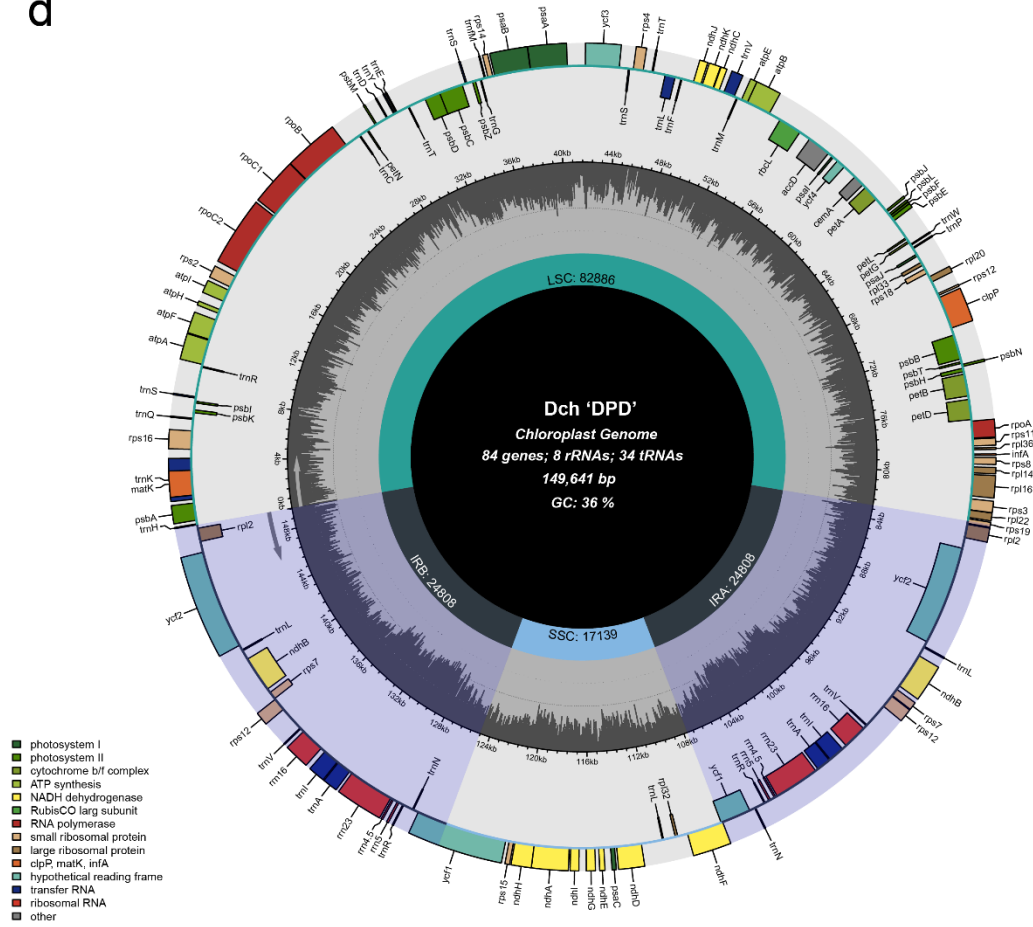
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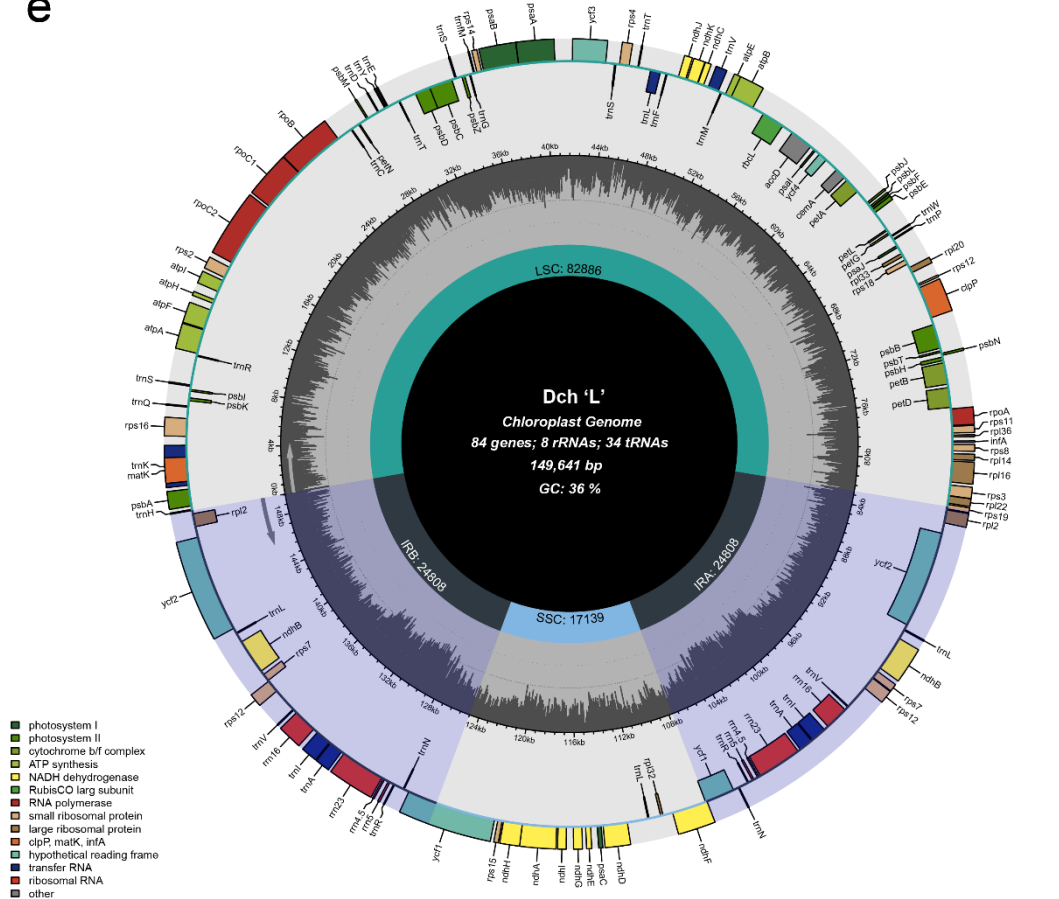
c



d



e



Dch 'X'
Chloroplast Genome
84 genes; 8 rRNAs; 34 tRNAs
149,641 bp
GC: 36 %

Legend:

- photosystem I
- photosystem II
- cytochrome b6/f complex
- ATP synthase
- NADH dehydrogenase
- Rubisco large subunit
- RNA polymerase
- small ribosomal protein
- large ribosomal protein
- clpP, matK, infA
- hypothetical reading frame
- transfer RNA
- ribosomal RNA
- other

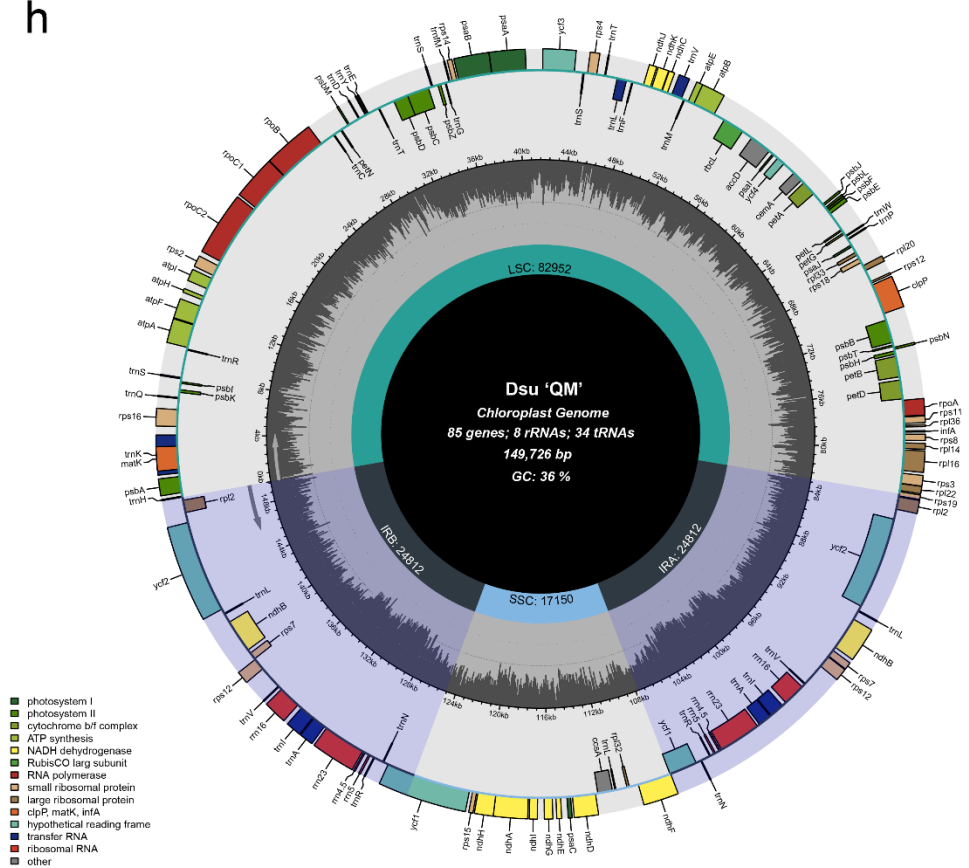
'HY'
Chloroplast Genome
85 genes; 8 rRNAs; 34 tRNAs
149,800 bp
GC: 36 %

Genomic Regions:
LSC: 82963
IRB: 24805
IRA: 24805
SSC: 17227

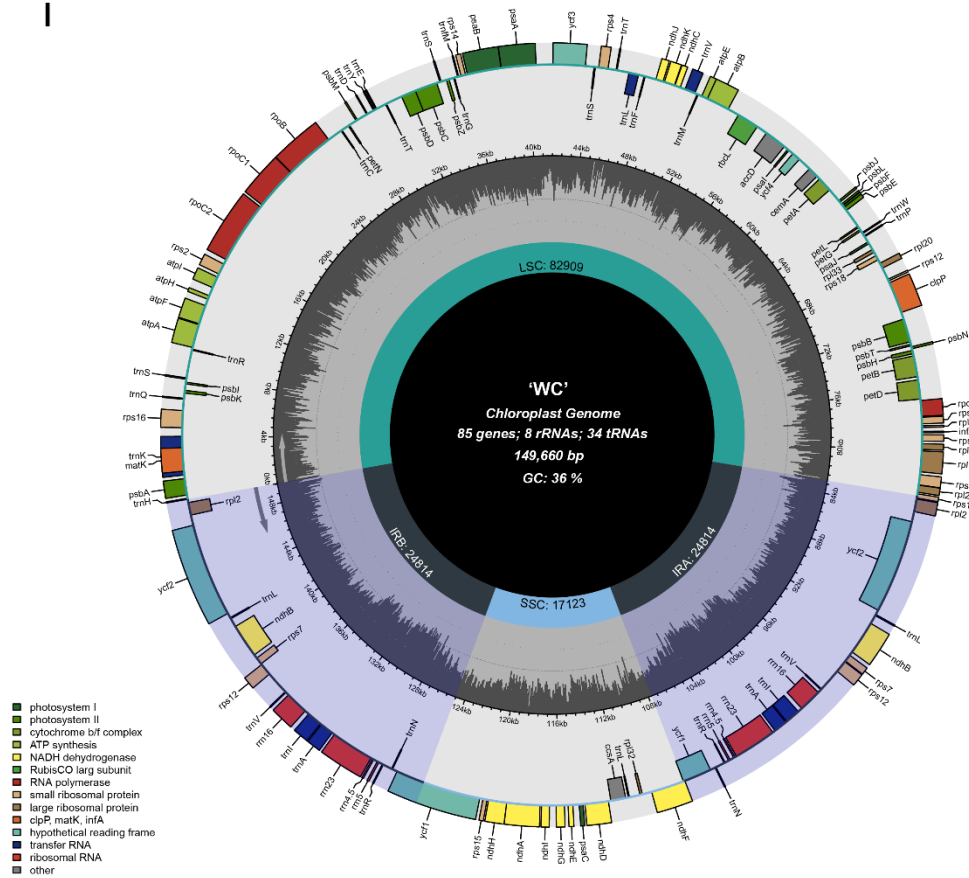
Legend:
 ■ photosystem I
 ■ photosystem II
 ■ cytochrome b/f complex
 ■ ATP synthase
 ■ NADH dehydrogenase
 ■ RubisCO large subunit
 ■ RNA polymerase
 ■ small ribosomal protein
 ■ large ribosomal protein
 ■ clpP, matK, infA
 ■ hypothetical reading frame
 ■ transfer RNA
 ■ ribosomal RNA
 ■ other

The circular map displays the chloroplast genome of 'HY' with a total size of 149,800 bp and 36% GC content. The genome is organized into four main regions: LSC (82,963 bp), IRB (24,805 bp), IRA (24,805 bp), and SSC (17,227 bp). The LSC region contains the majority of the genes, including photosystem I and II, cytochrome b/f complex, ATP synthase, NADH dehydrogenase, RubisCO large subunit, RNA polymerase, small ribosomal protein, large ribosomal protein, clpP, matK, infA, and hypothetical reading frames. The IRB and IRA regions contain transfer RNA and ribosomal RNA genes. The SSC region contains other genes. The map also shows the locations of 85 genes, 8 rRNAs, and 34 tRNAs. The genes are color-coded according to the legend, and the map includes a scale bar in kb (kilobases) and a GC content scale.

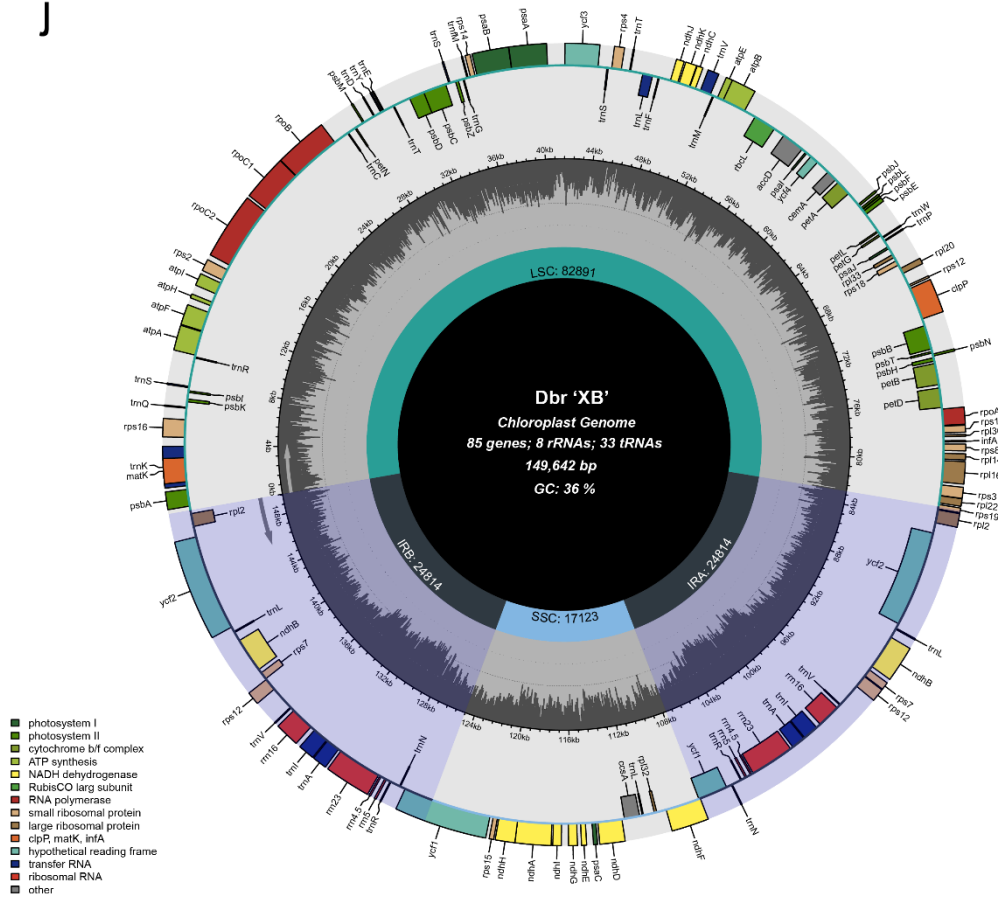
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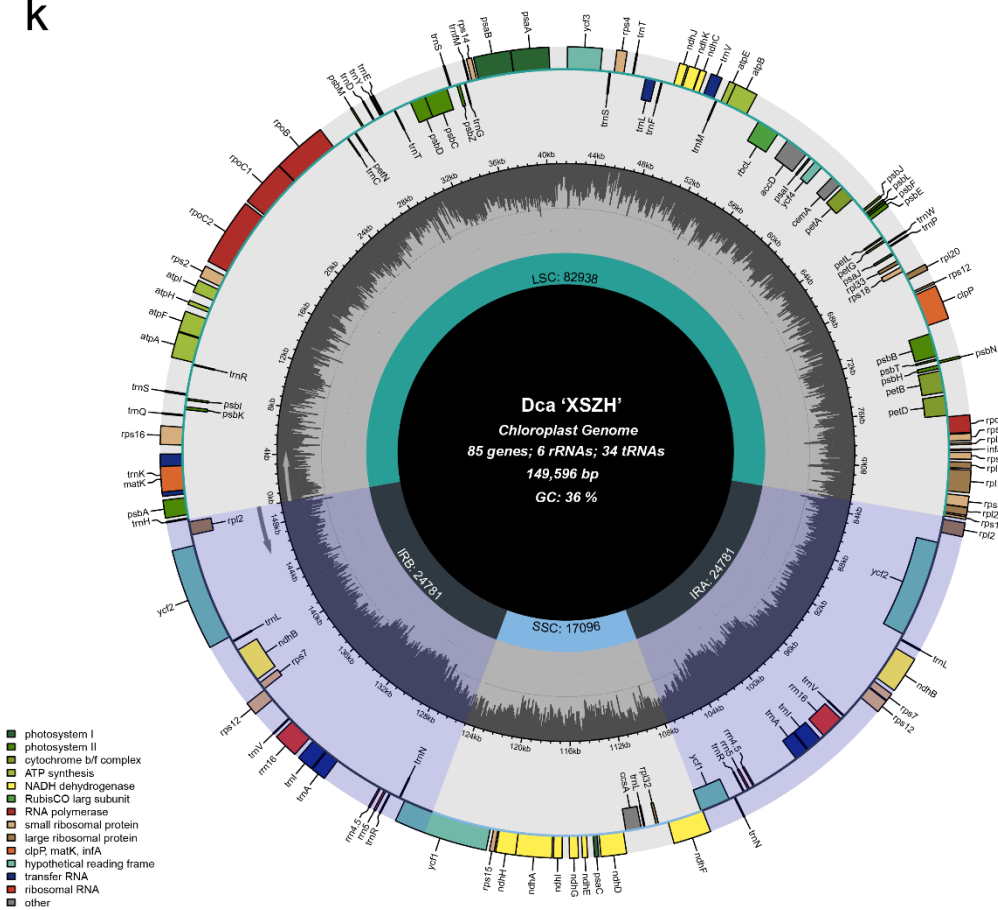
i



j



k



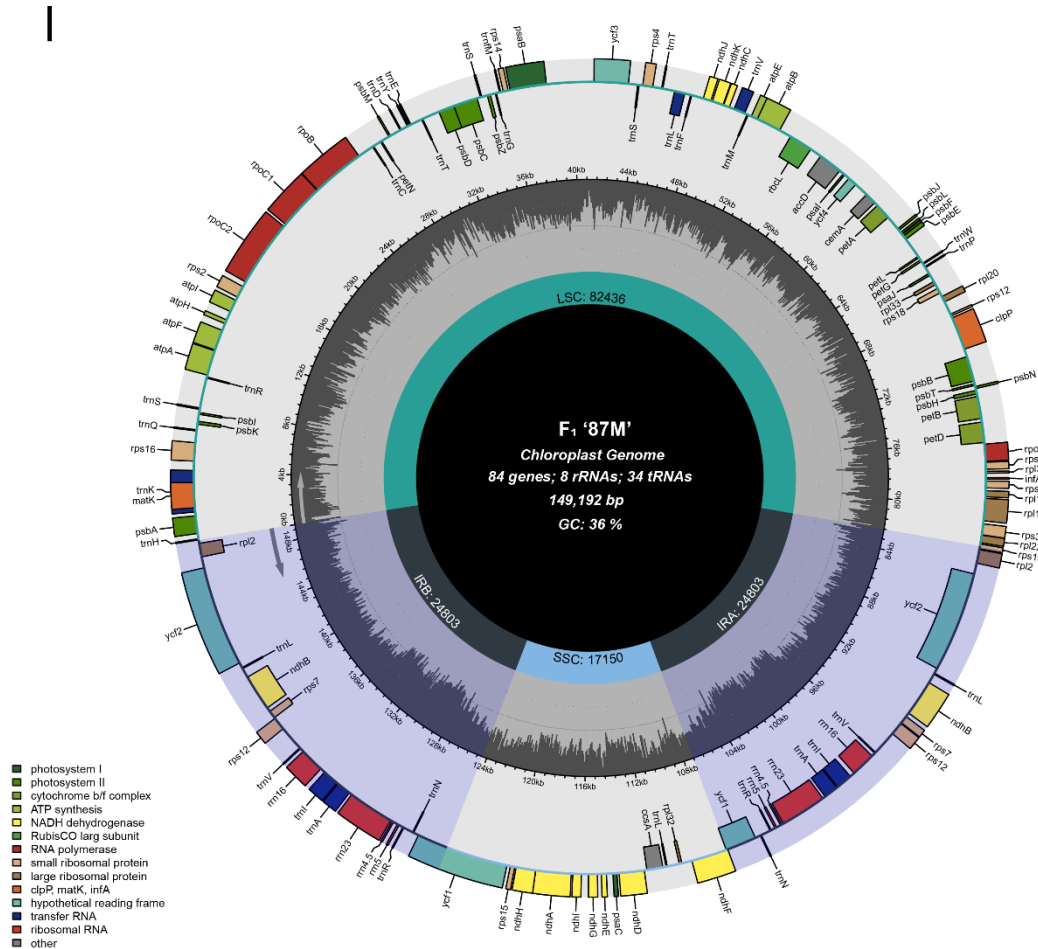
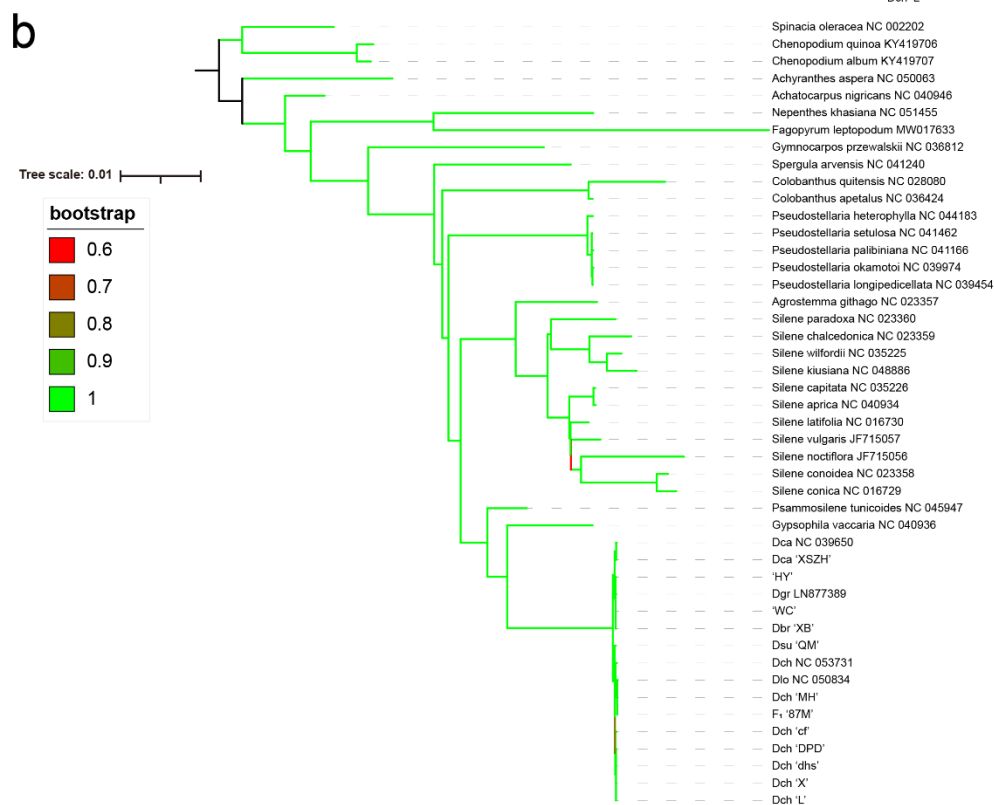
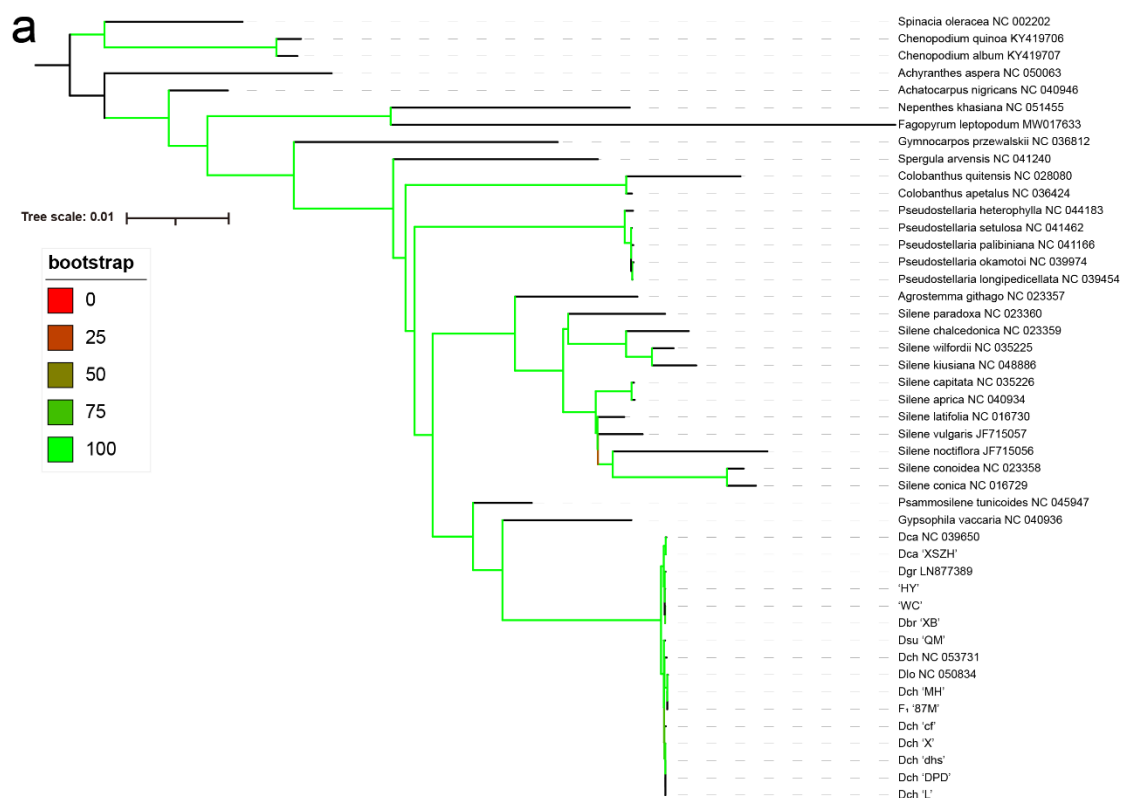
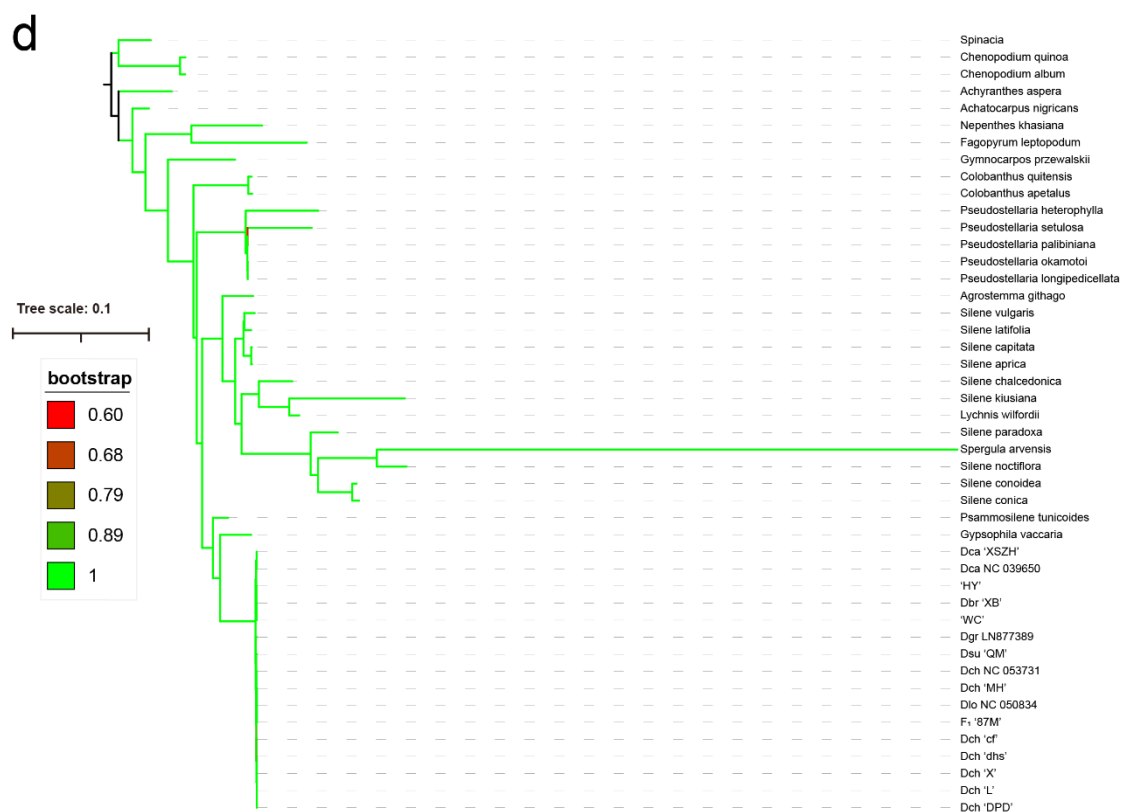
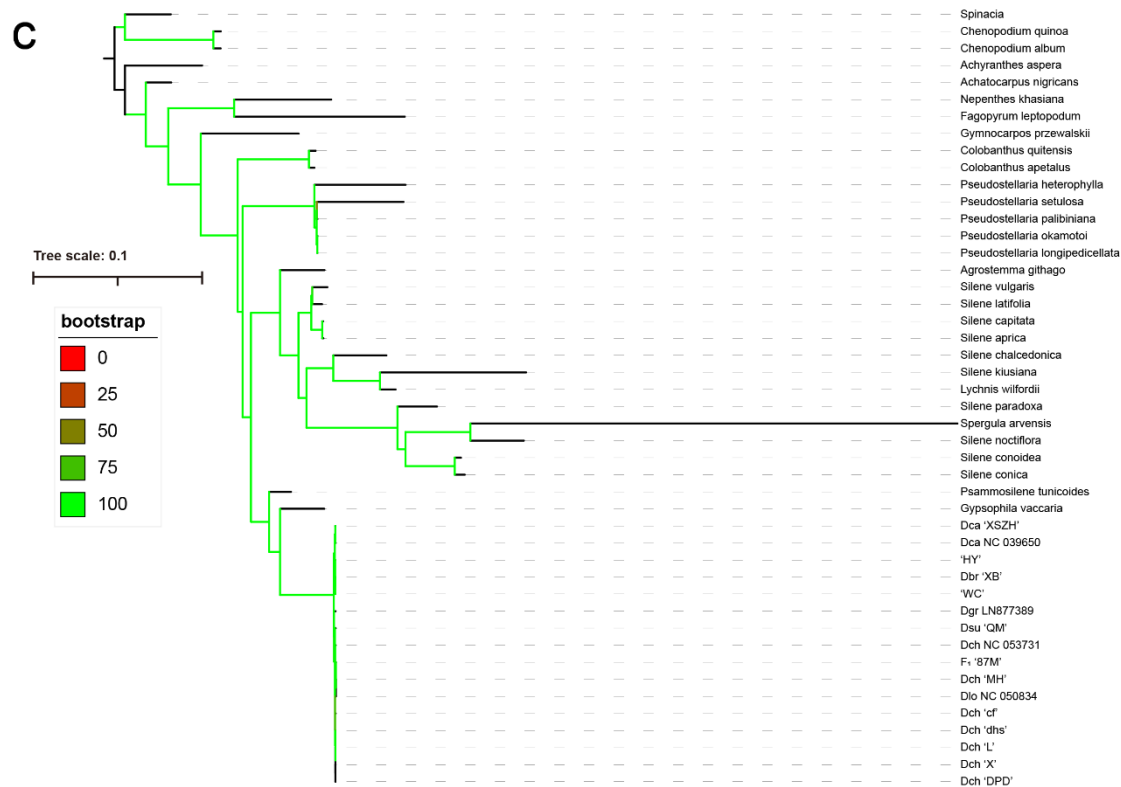
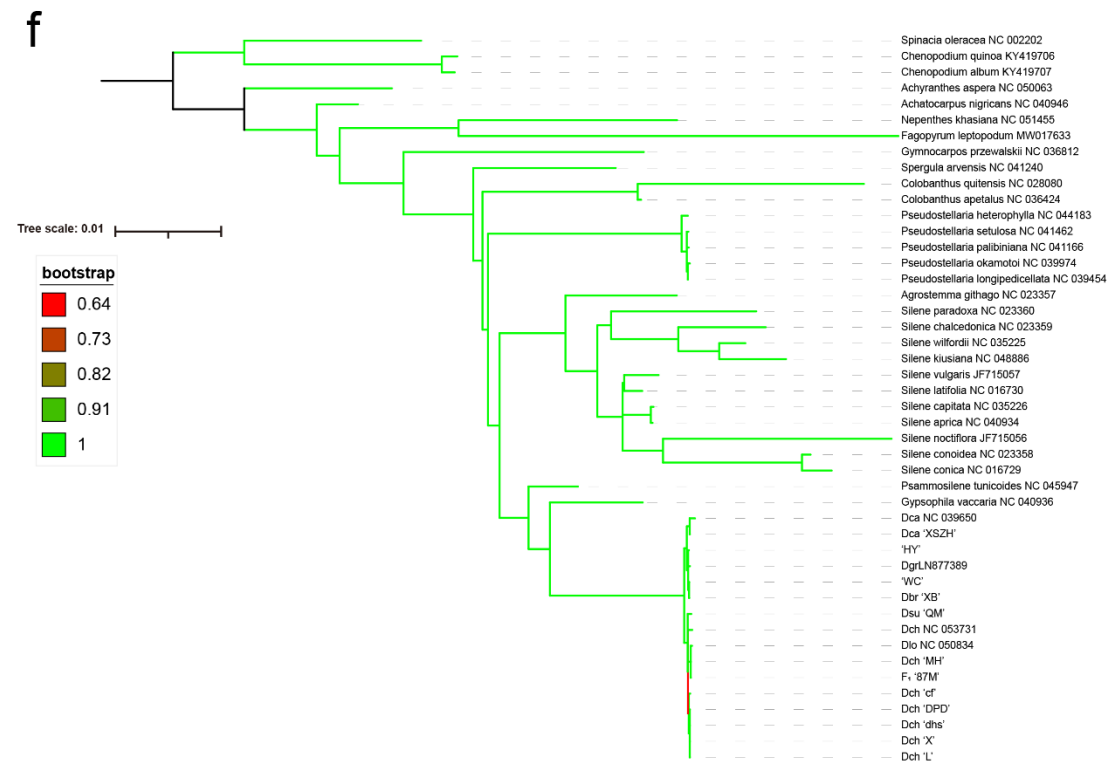
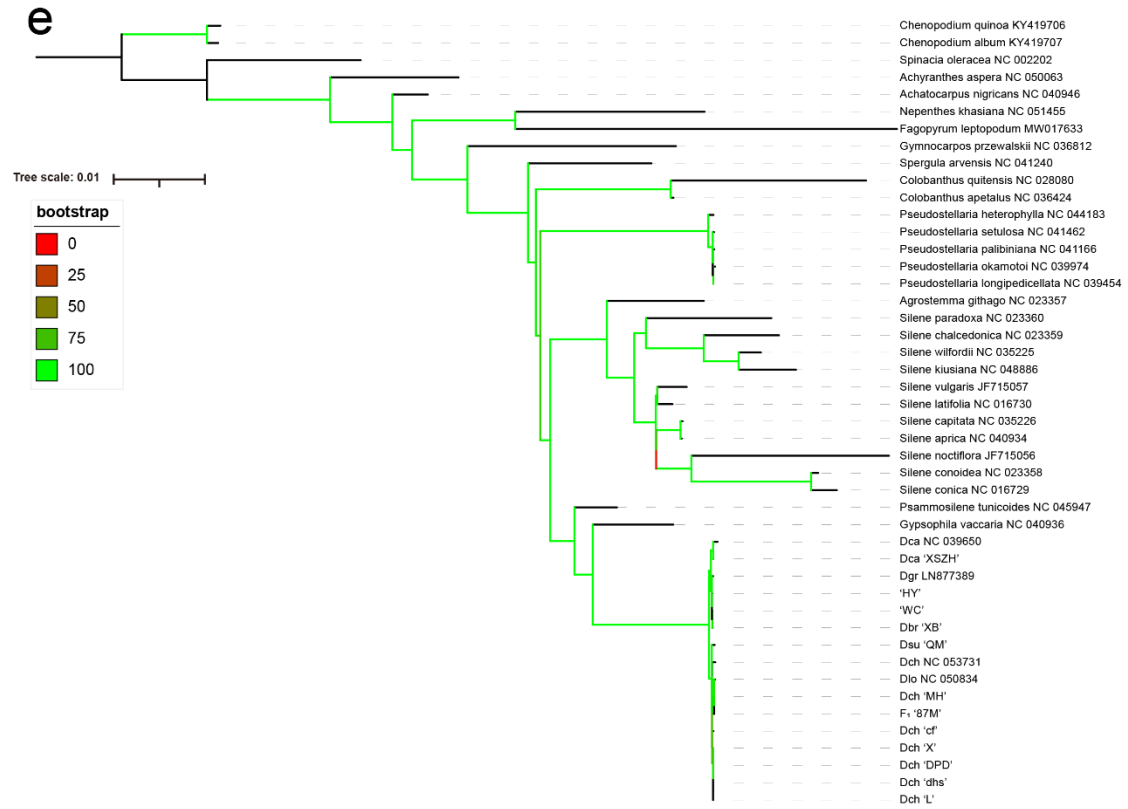


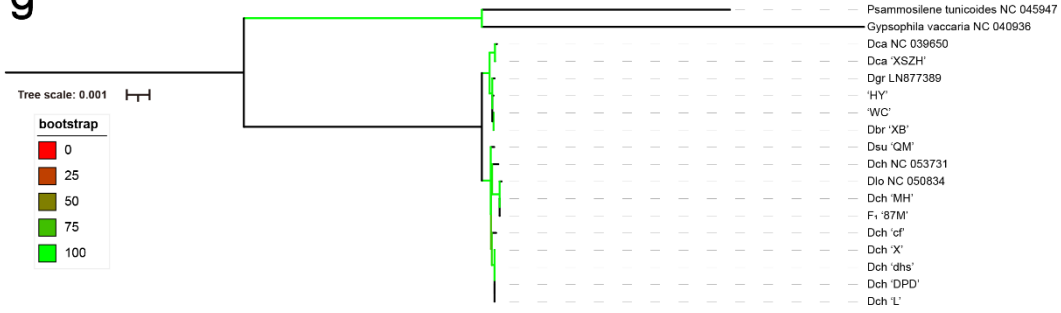
Figure S2. Gene maps of the 12 assembled *Dianthus* chloroplast genomes in this study. Genes shown inside the circle are transcribed clockwise, and those outside are transcribed counterclockwise. Different genes are color coded. The inner circle also indicates that the chloroplast genome contains a large single copy region (LSC), a small single copy region (SSC), and two copies of the inverted repeat (IRA and IRB). (a) The chloroplast genome of Dch 'MH'. (b) The chloroplast genome of Dch 'dhs'. (c) The chloroplast genome of Dch 'cf'. (d) The chloroplast genome of Dch 'DPD'. (e) The chloroplast genome of Dch 'L'. (f) The chloroplast genome of Dch 'X'. (g) The chloroplast genome of 'HY'. (h) The chloroplast genome of Dsu 'QM'. (i) The chloroplast genome of 'WC'. (j) The chloroplast genome of Dbr 'XB'. (k) The chloroplast genome of Dca 'XSZH'. (l) The chloroplast genome of F₁ '87M'.



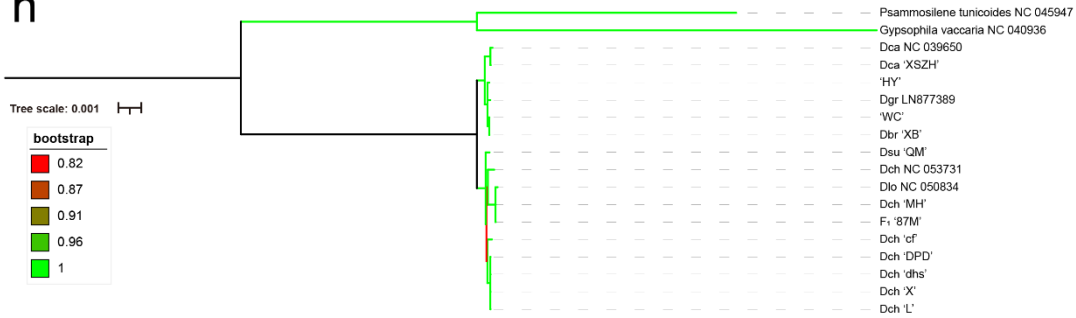




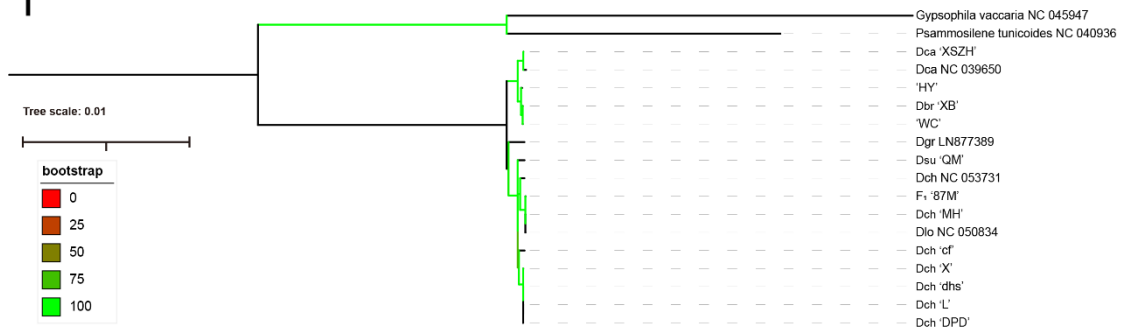
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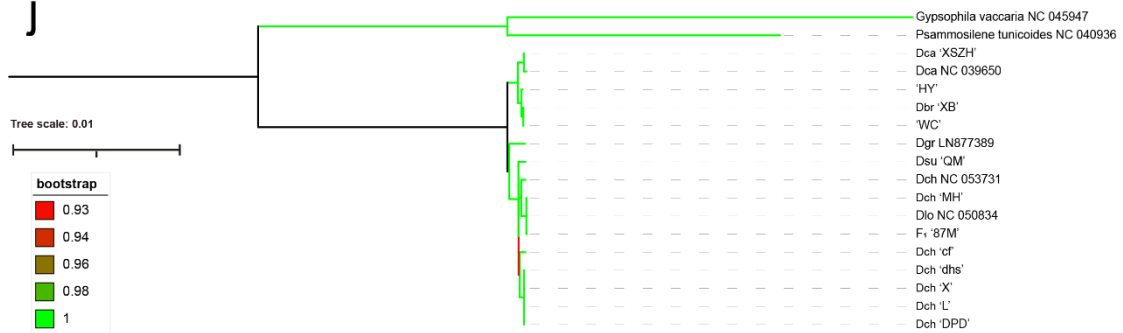
h



i



j



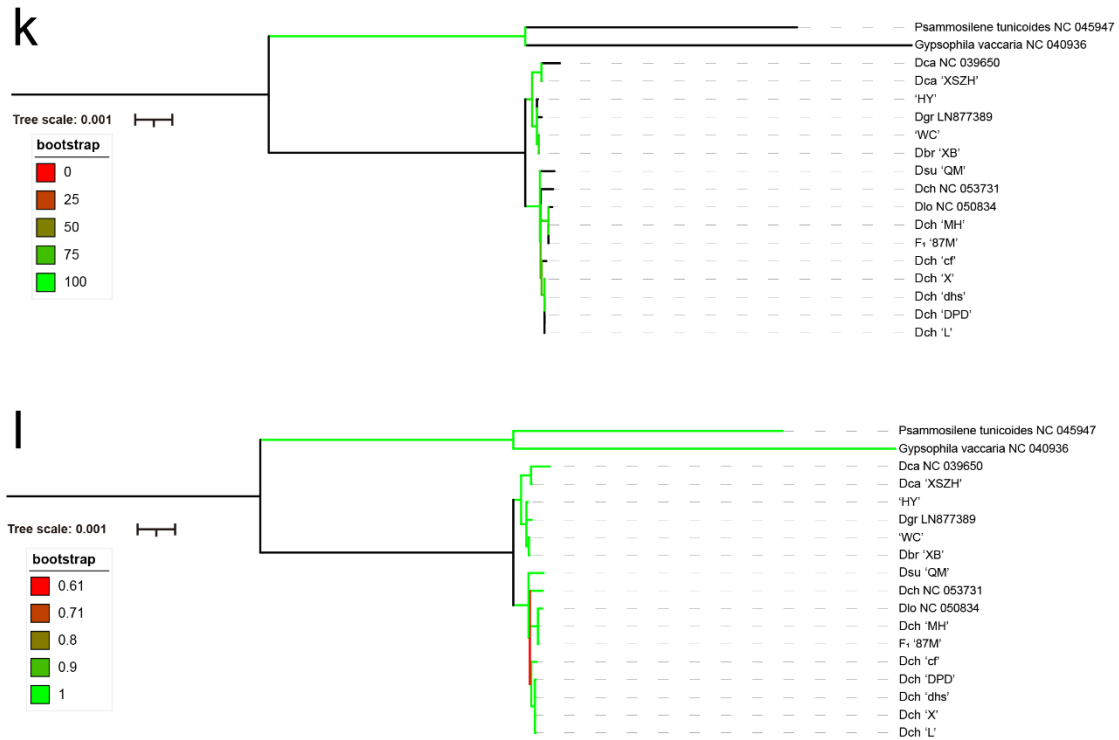
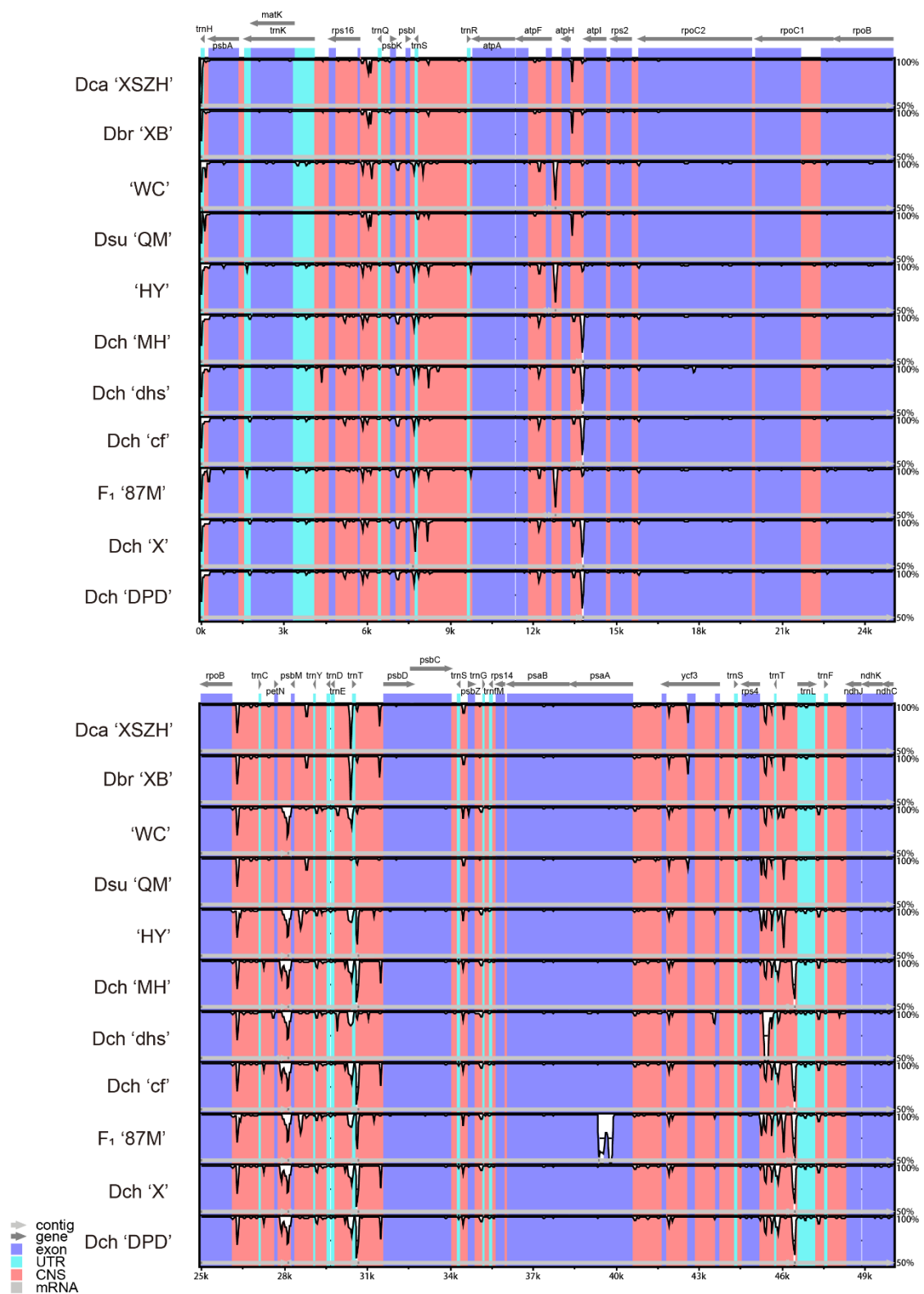
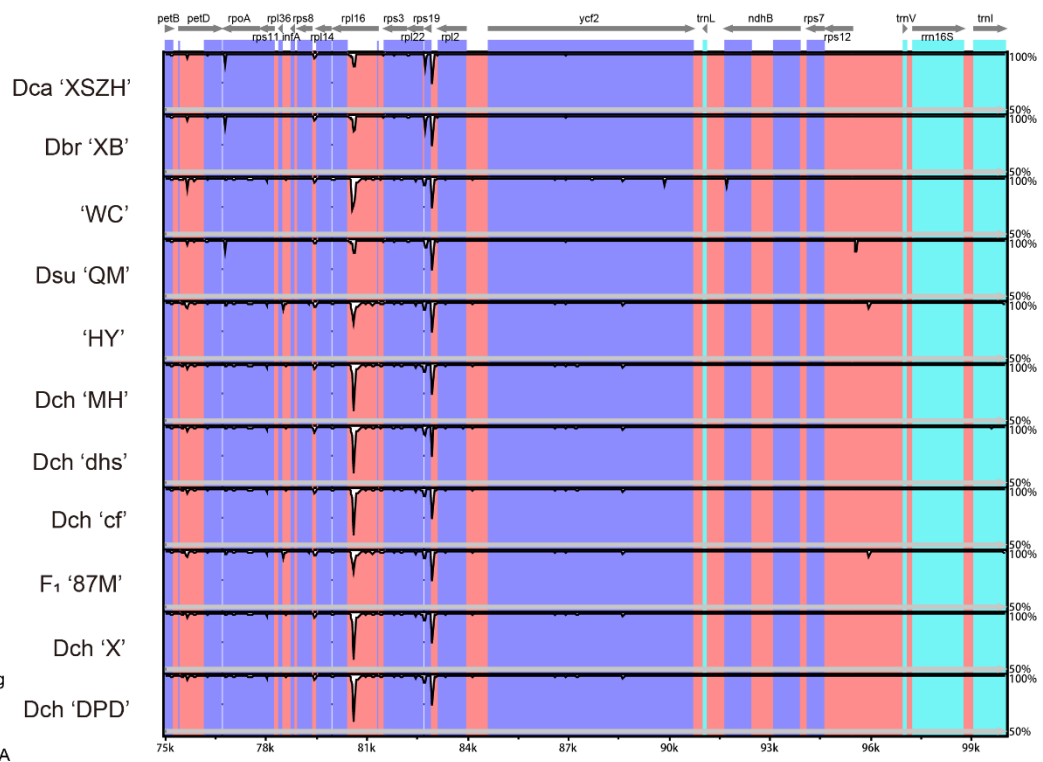
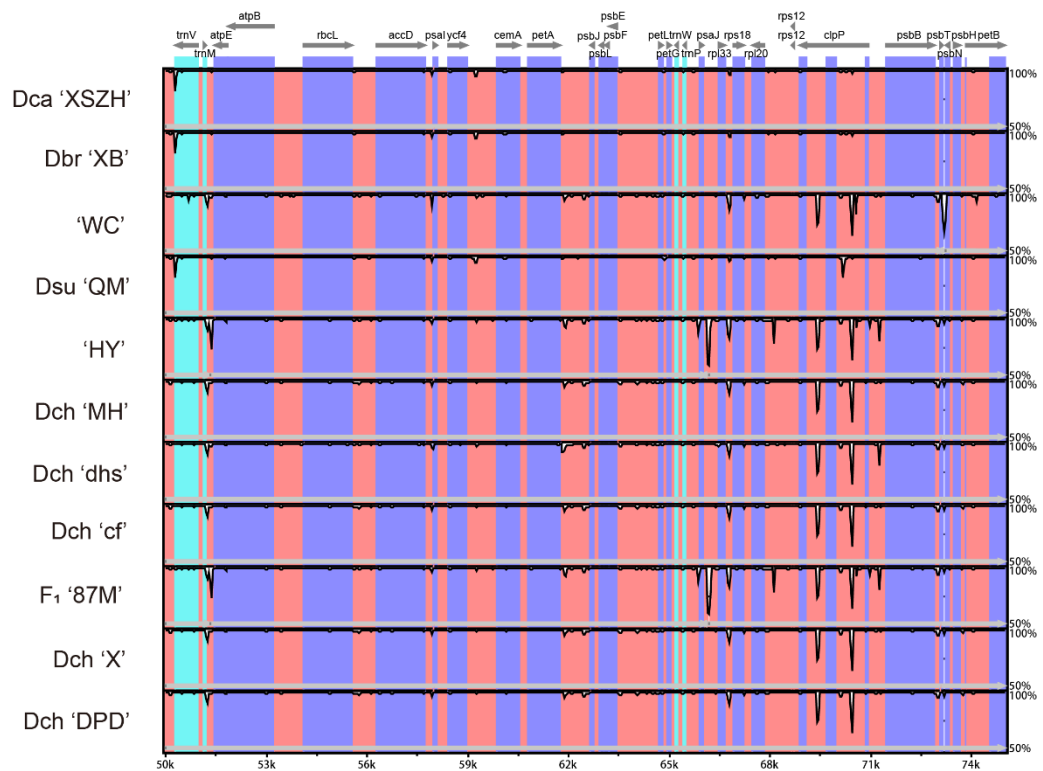


Figure S3. Phylogenetic tree based on the six datasets from Caryophyllales and *Dianthus* chloroplast genomes. (a-f) Phylogenetic tree based on the three datasets from 46 Caryophyllales chloroplast genomes. a. Phylogenetic tree based on all shared CDS from 46 Caryophyllales chloroplast genomes by maximum likelihood (ML); b. Phylogenetic tree based on all shared CDS from 46 Caryophyllales chloroplast genomes by Bayesian inference (BI); c. Phylogenetic tree based on whole chloroplast genomes from 46 Caryophyllales chloroplast genomes by maximum likelihood (ML); d. Phylogenetic tree based on whole chloroplast genomes from 46 Caryophyllales chloroplast genomes by Bayesian inference (BI); e. Phylogenetic tree based on exclude-third-codon-site matrix with deleting the terminal base of each codon from 46 Caryophyllales chloroplast genomes by maximum likelihood (ML); f. Phylogenetic tree based on exclude-third-codon-site matrix with deleting the terminal base of each codon from 46 Caryophyllales chloroplast genomes by Bayesian inference (BI). (g-l) Phylogenetic tree based on the three datasets from 16 *Dianthus* and two outgroups. g. Phylogenetic tree based on all shared CDS from 16 *Dianthus* and two outgroups by maximum likelihood (ML); h. Phylogenetic tree based on all shared CDS from 16 *Dianthus* and two outgroups by Bayesian inference (BI); i. Phylogenetic tree based on whole chloroplast genomes from 16 *Dianthus* and two outgroups by maximum likelihood (ML); j. Phylogenetic tree based on whole chloroplast genomes from 16 *Dianthus* and two outgroups by Bayesian inference (BI); k. Phylogenetic tree based on exclude-third-codon-site matrix with deleting the terminal base of each codon from 16 *Dianthus* and two outgroups by maximum likelihood (ML); l. Phylogenetic tree based on exclude-third-codon-site matrix with deleting the terminal base of each codon from 16 *Dianthus* and two outgroups by Bayesian inference (BI).





← contig
 → gene
 ■ exon
 ■ UTR
 ■ CNS
 ■ mRNA

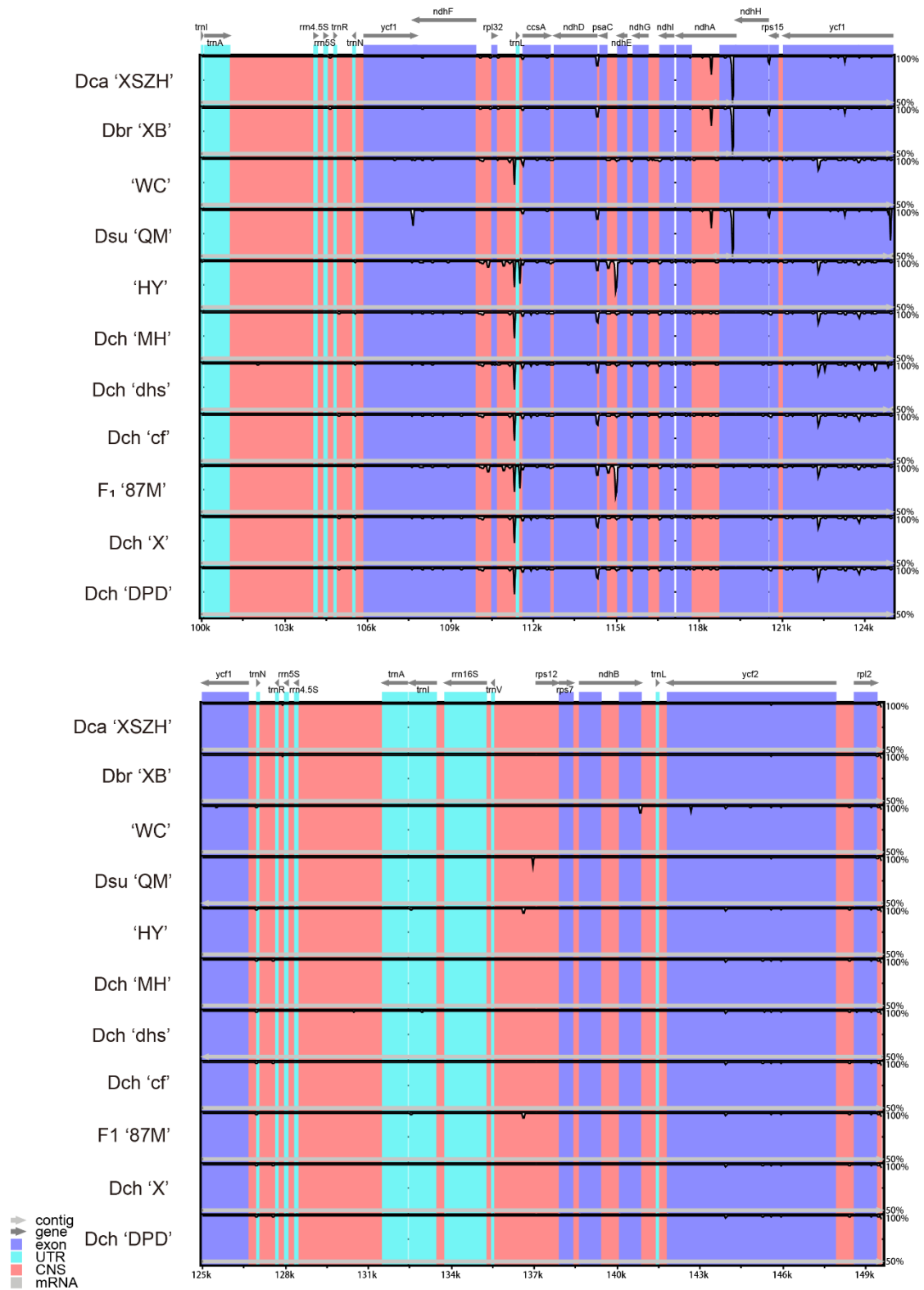


Figure S4. Sequence identity plot of the 12 *Dianthus* chloroplast genomes with 'XSZH' as a reference by mVISTA. The species names are shown to the left. The grey arrows above the alignment indicate the transcription direction of genes. In the alignment box, the blue color box indicates protein-coding, the pink color box shows the conserved noncoding sequence, and the light green box indicates tRNAs and rRNAs. The x-axis represents the positions in the chloroplast genomes, and the Y-scale represents the percent identity ranging from 50-100%.