

Supplementary Information for
Comparative mitogenomics of *Perilla frutescens* and relative species
provides cytoplasmic genomic resources for germplasm improvement

Additional file 1: Supplementary Figures
Figures S1–S6

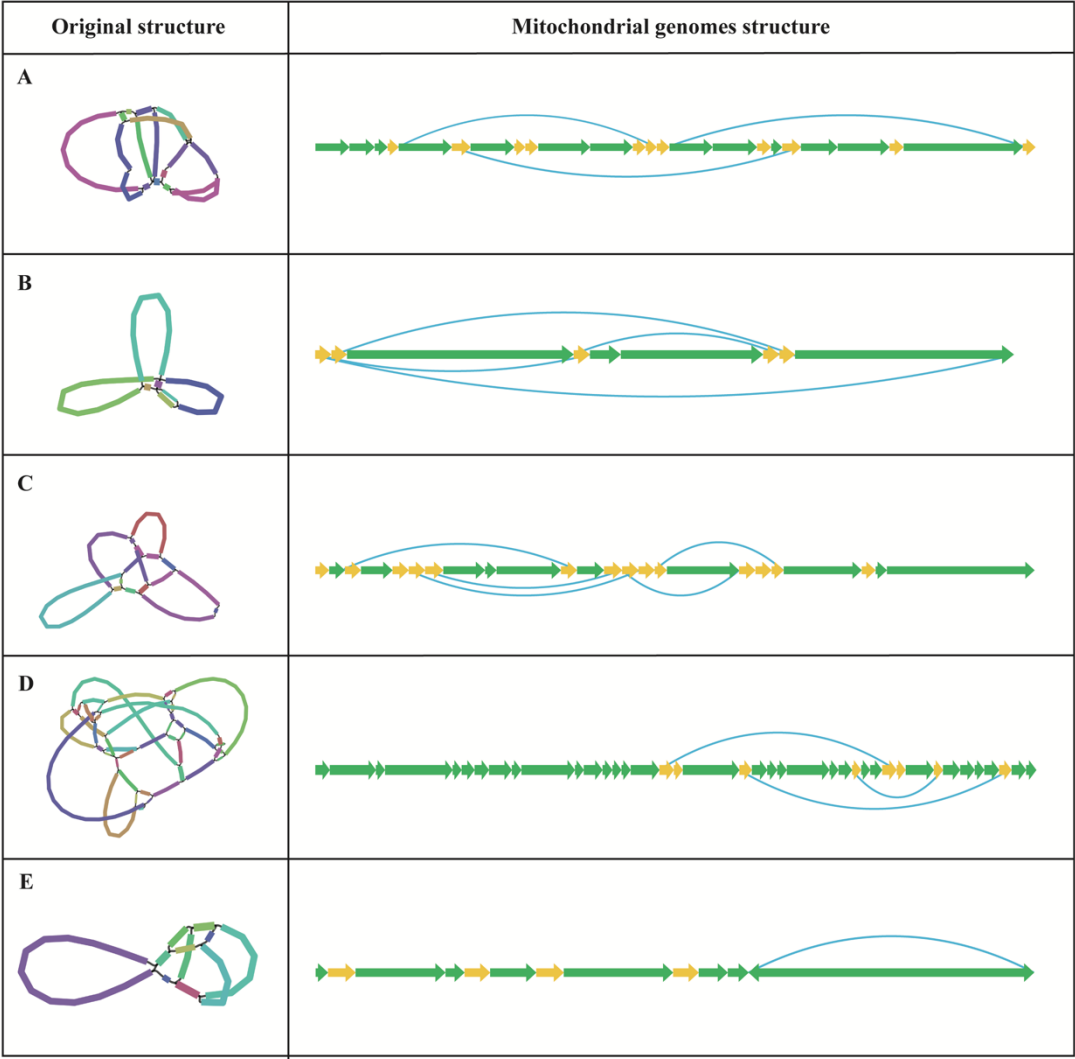


Figure S1. Schematic representation of mitogenome structures in *P. frutescens* and its close relatives.

Original assembly structures and reconstructed mitogenome structures of the five taxa. The left panels show the original structures, and the right panels show the mitogenome structures, illustrating gene distribution and repeat-associated structural connections. (A) *K. sinensis* (B) *P. frutescens* (C) *M. soochouensis* (D) *M. chinensis* (E) *M. chinensis* ‘Jiangxiangru’.

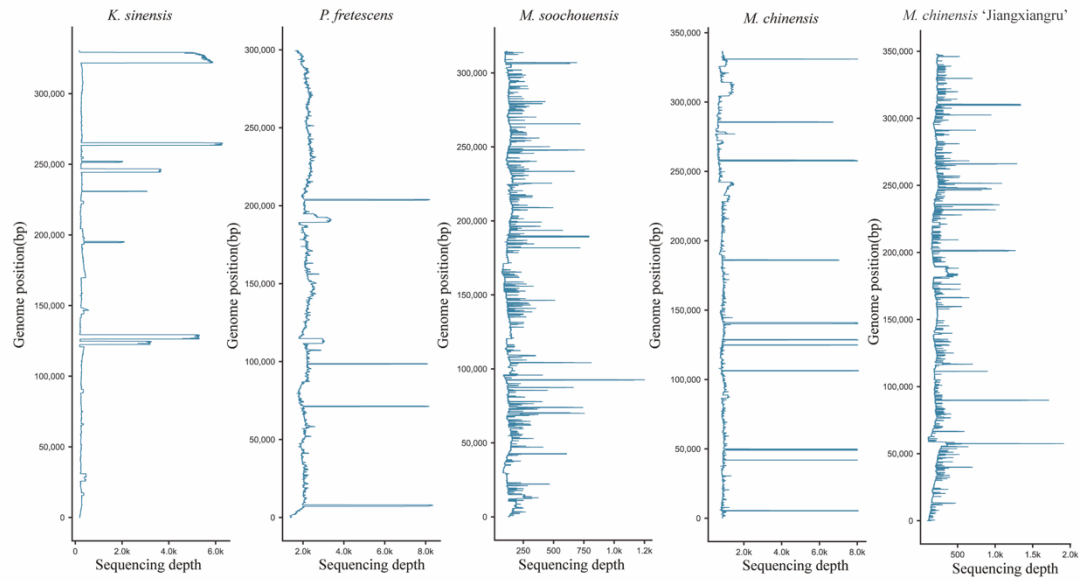


Figure S2. Sequencing depth profiles of mitogenomes in *Perilla frutescens* and its close relatives.

Genome-wide sequencing depth distributions of the five mitogenomes, showing coverage variation across genome positions and supporting the reliability of mitogenome assemblies. The x-axis indicates sequencing depth, and the y-axis indicates genome position.

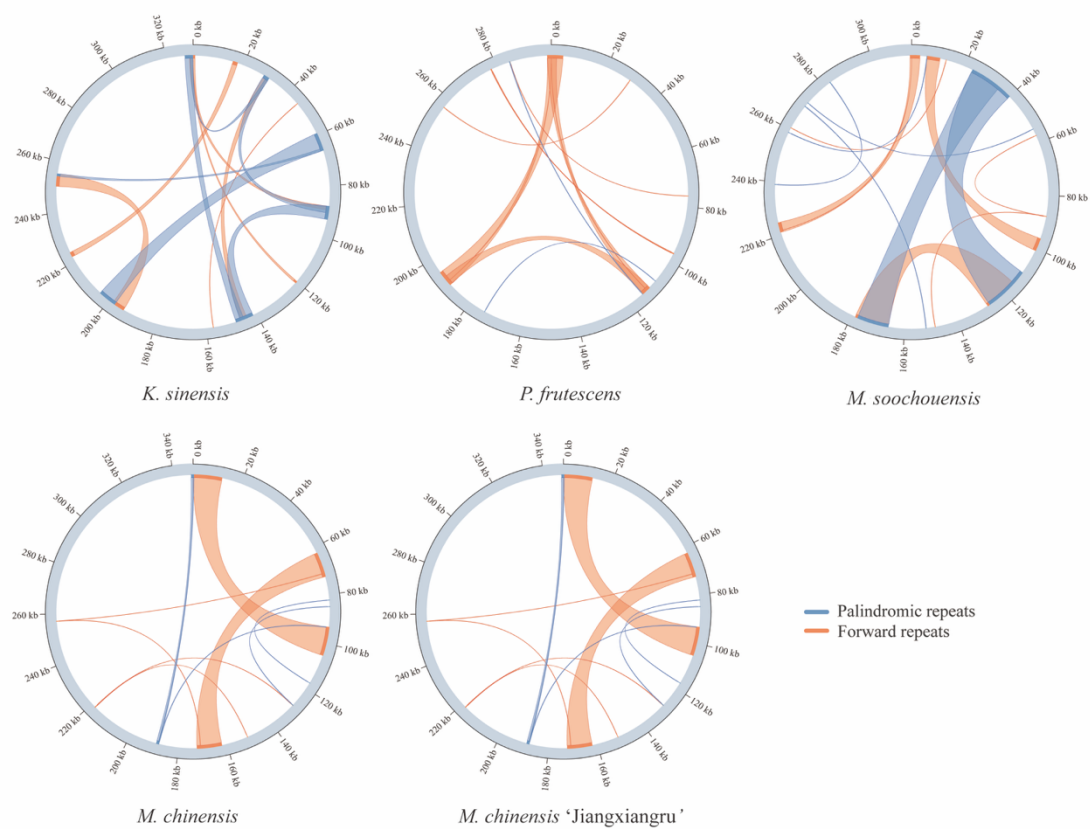


Figure S3. Distribution of dispersed repeats in the mitogenomes of *Perilla frutescens* and its close relatives.

Genomic positions and connections of forward and palindromic repeats in the five mitogenomes, showing differences in repeat distribution patterns among taxa.

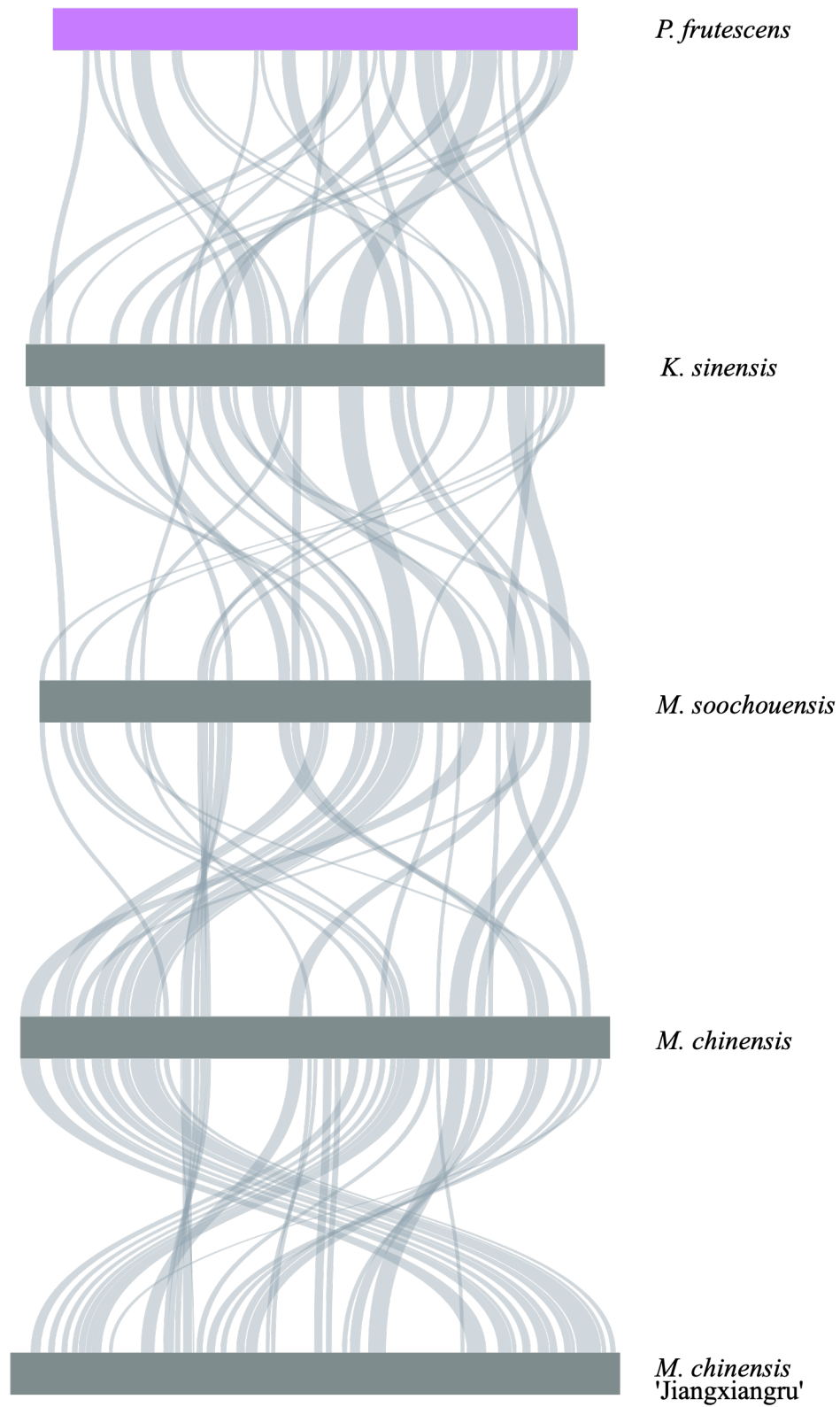


Figure S4. Overall mitogenome collinearity among *Perilla frutescens* and its close relatives.

Multiple-genome collinearity comparison of the five mitogenomes, showing conserved homologous blocks and extensive structural rearrangements among closely related taxa. The purple bar indicates the *P. frutescens* mitogenome.

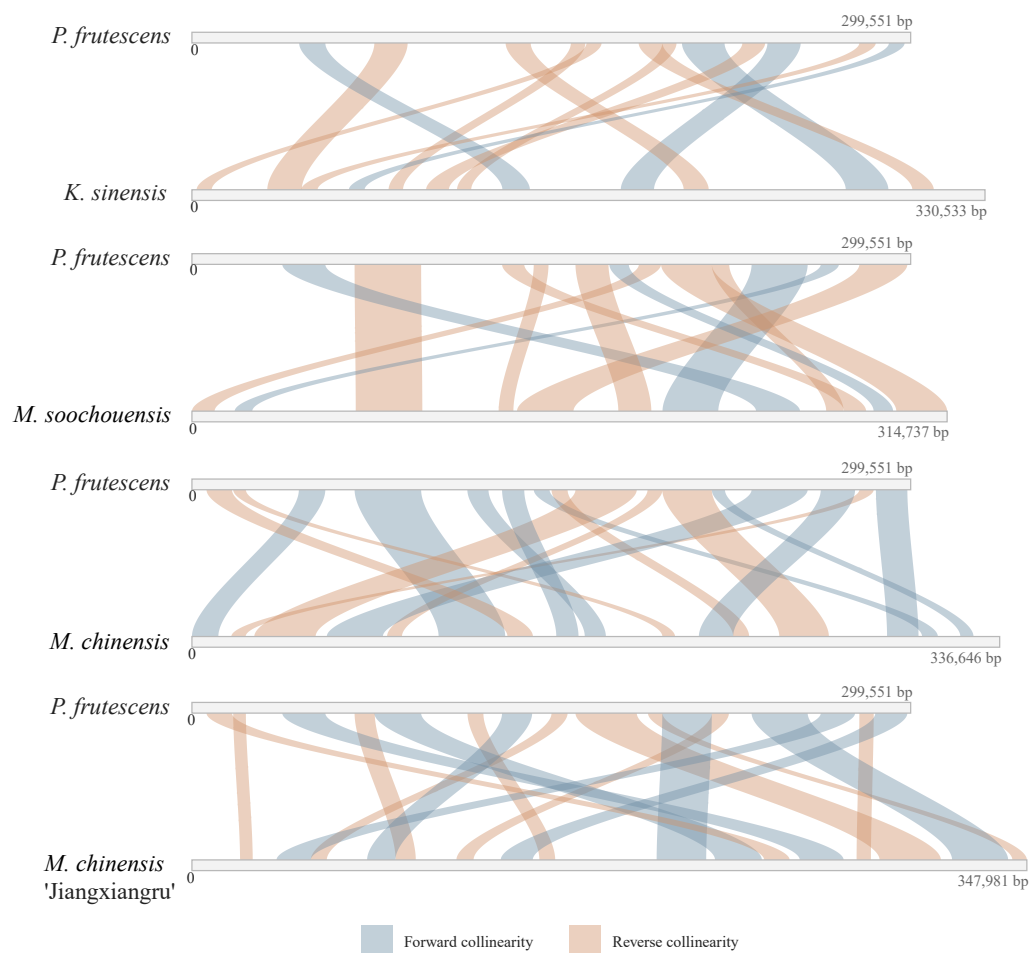


Figure S5. *Perilla frutescens*-centered pairwise mitogenome collinearity. Pairwise collinearity comparisons of *P. frutescens* with *K. sinensis*, *M. soochouensis*, *M. chinensis*, and *M. chinensis* 'Jiangxiangru', showing conserved homologous fragments and forward or reverse collinear relationships between *P. frutescens* and its close relatives.

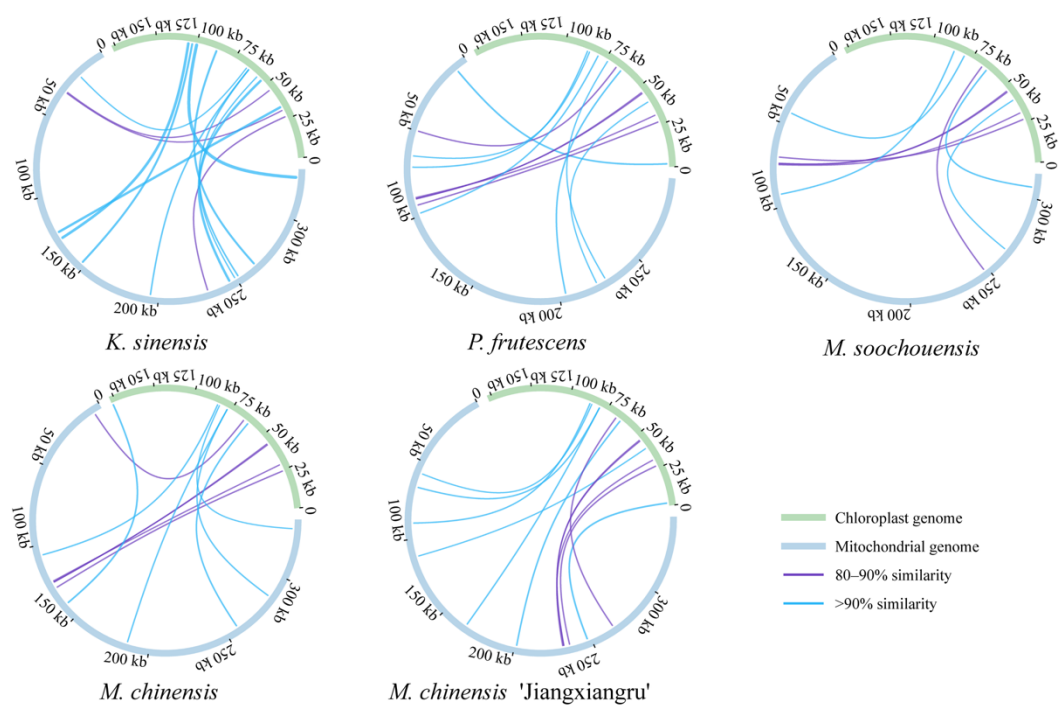


Figure S6. Plastid-derived transferred fragments in the mitogenomes of *Perilla frutescens* and its close relatives.

Distribution of homologous fragments between chloroplast and mitochondrial genomes in the five taxa, showing interorganellar sequence transfer and variation in sequence similarity.