

**Table S1:** Genes with introns in the *Shizhenia pinguicula* chloroplast genome and the length of introns and exons;

**Table S2:** The relative synonymous codon usage of the *Shizhenia pinguicula* chloroplast genome;

**Table S3:** The GC content of the 69 CDS genes within the chloroplast genome of *Shizhenia pinguicula*;

**Table S4:** Dispersed repeat sequence statistics data and distribution;

**Table S5:** SSRs in the chloroplast genome of *Shizhenia pinguicula*;

**Figure S1:** Sequence similarity between *Shizhenia pinguicula* and its five closely related species was analyzed using mVISTA with the chloroplast genome of *Hemipilia yajiangensis* as the reference genome. The horizontal axis represents the gene position of the reference sequence, while the vertical axis indicates the similarity ranging from 50% to 100%. Exons, t/rRNAs, and conserved noncoding sequences (CNS) are represented by different colors in the lower left corner.

**Figure S2:** The coverage depth of the chloroplast genome of *Shizhenia pinguicula*. The horizontal axis represents the base of the chloroplast genome, while the vertical axis indicates the sequencing depth corresponding to that base.