Figure S2 | Flowchart depicting study design. This study first conducted HiFi sequencing and de novo assembly to generate a complete circular mitogenome of *O. vulgare*. Subsequent annotation characterized the genomic features, including PCGs, tRNAs, rRNAs and repeat elements. Computational predictions were then performed to identify RNA-editing sites. In parallel, the chloroplast genome was assembled and analyzed to detect MTPTs. Finally, phylogenetic analysis was carried out using mitochondrial PCGs from multiple species to resolve evolutionary relationships.