

**Table S2.** Statistics of WGS and assembly summary for *P. ginseng* mitogenome

Sequencing platform	Sequencing data			
	Input reads	Trimmed reads	Total bases (bp)	Trimmed bases (bp)
ONT	1,489,463	1,350,258 (90.65 %)	6,780,920,988	6,298,153,130 (92.88 %)
GridION				
Illumina	18,549,540	17,960,262 (96.82 %)	5,583,411,540	4,990,695,283 (89.38 %)
Miseq				

ONT, oxford nanopore technologies, WGS, whole-genome sequence.

<b>Assembly data</b>		
Genome length (bp)	Aligned reads	Coverage (x)
464,705	29,150 (1.96 %)	110.81
	293,142 (1.58 %)	165.41