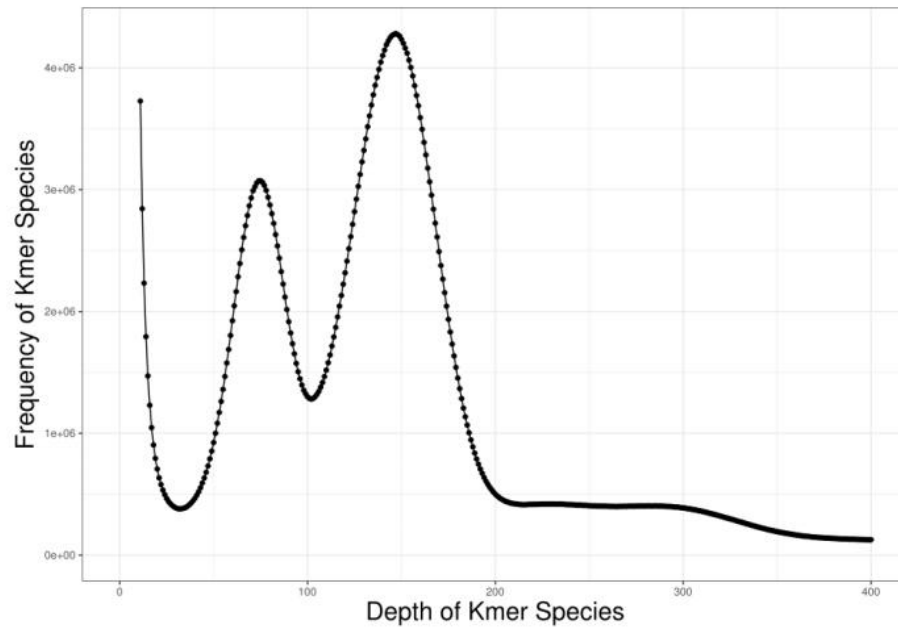


Sample	K-mer number	K-mer Depth	Genome Size(Mb)	Heterozygous Ratio (%)	Repeat (%)
Fraxinus_mandshurica	119996908612	147	786.75	1.07	53.53



Supplementary Figure S1. K-mer analysis for estimating the genome size and complexity of *Fraxinus mandshurica*.

The distribution of k-mer frequency shows a distinct heterozygous peak and a main homozygous peak. The table above summarizes the estimated genomic characteristics, indicating an estimated genome size of ~786.75 Mb, a heterozygosity rate of 1.07%, and a high repetitive sequence content of 53.53%.