

**Table S1.** Shapiro-Wilks test in 8 wood property traits.

**Table S2.** Populus clones re-sequencing raw reads, clean reads, mapping reads, raw depth, clean depth, and mapping depth.

**Table S3.** The statistics and average (Mbp) densities of SNP and InDel on each chromosome.

**Table S4.** Corresponding gene of Significant SNP in eight poplar traits, with the significance threshold level of  $p < 0.0005$ .

**Table S5.** Genome-wide significant candidate genes associated with more than one trait.

**Table S6.** Information on the GO annotated from the corresponding gene with eight poplar traits.

**Table S7.** Information on the KEGG annotated from the Corresponding gene with 8 wood property traits.

**Table S8.** Expression level of the candidate genes in CL290 and CL33.

**Table S9.** Differential expression of candidate genes between CL290 and CL33.

**Table S10.** miRNA related to the candidate genes.

**Figure S1.** The number of indels within 1Mb window size.

**Figure S2.** The number of SNPs within 1Mb window size.

**Figure S3.** Alternative splicing sites.

**Figure S4.** Expression of CL290 and CL33.