

Figure S1 Manhattan plots of genome-wide association analyses of tree heights at time points T1-T8 separately. The horizontal dashed lines indicate the genome-wide significant threshold of 6.36, a base 10 logarithm of p -value based on the Bonferroni correction at the 0.01 significant level.

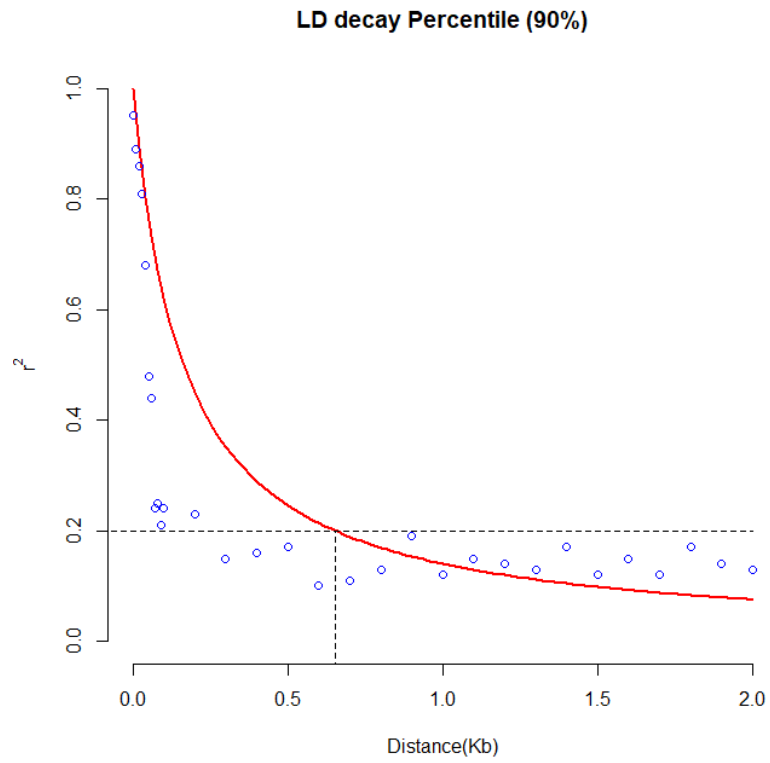


Figure S2 LD decay in the hybrid F₁ population of *Populus deltoides* and *Populus simonii*. The red curve was fitted on the basis of the equation of Sved (1971) with the 90% percentile of LDs (r^2) within a short range of 10-100 bp against the distance of pairwise SNPs. The dashed lines indicate a threshold of $r^2 = 0.2$ could be used, corresponding to a decay distance of ~650 bp.