

SNP and haplotype-based genomic selection of quantitative traits in *Eucalyptus globulus*

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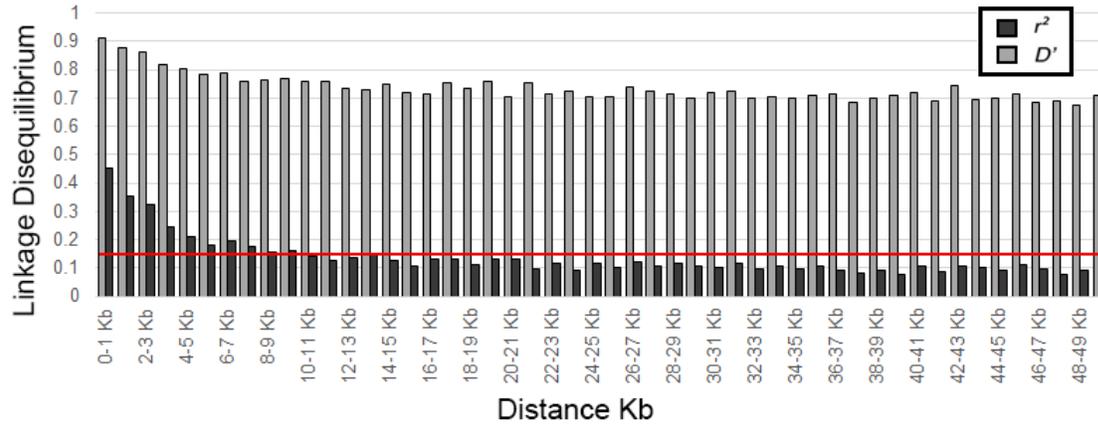


Figure S1. Genome-wide average linkage disequilibrium (LD) decay plot estimated across all chromosomes of *Eucalyptus* for the studied population. The LD values correspond to the average of the correlation between alleles at two loci (r^2) and the normalized disequilibrium coefficient (D') for each 1 Kpb. The LD threshold of $r^2=0.14$ is indicated with a red line.

Table S1. Summary of phenotypic information for quantitative traits related to wood quality and tree growth measured in a six-year-old breeding population of *E. globulus*.

Trait	Minimum	Maximum	Mean	Standard Deviation
Tree Height (m)	4.4	16.6	9.3	2.1
Diameter at breast height (cm)	3.3	25.3	11.6	3.1
Stem straightness (0 – 6)	0	6	-	-
Branch quality (0 – 6)	0	6	-	-
Wood density (mm)	10	23	16	2.0

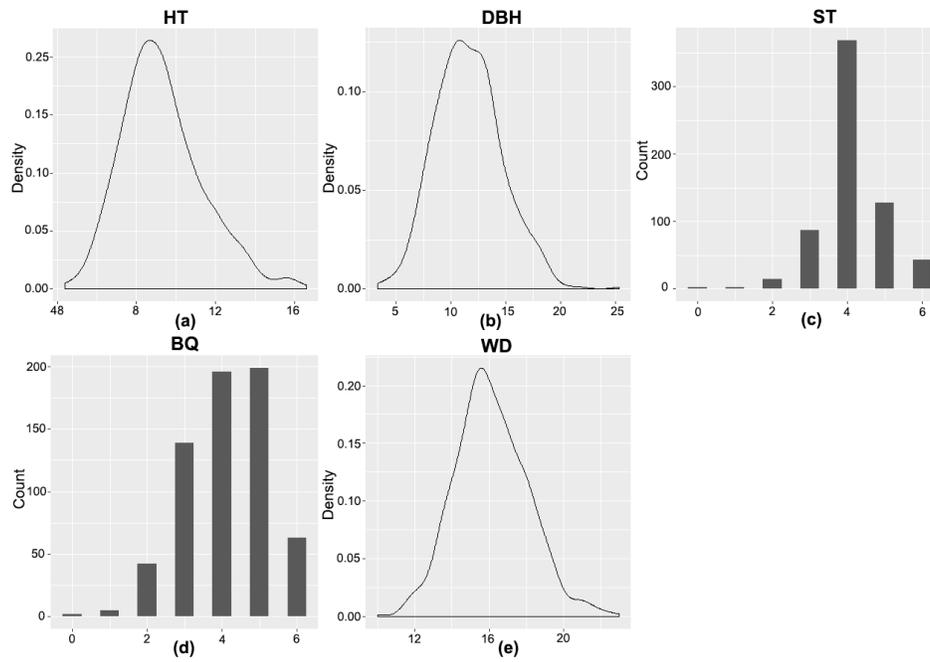


Figure S2. Distributions and histograms of the studied traits: (a) tree height (HT) in m, (b) diameter at breast height (DBH) in cm, (c) stem straightness (ST), (d) branch quality (BQ) and (e) wood density (WD) in mm.