

# Haplotype- and SNP-based GWAS for growth and wood quality traits in *Eucalyptus cladocalyx* trees under arid conditions

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**Table S1.** Candidate genes associated with SNPs or haplotype blocks for the 6 traits related to growth and wood quality, assessed in adult trees of *E. cladocalyx*.

Trait <sup>a</sup>	MTA	Chr <sup>c</sup>	Location <sup>d</sup>	Distance <sup>e</sup>	ID <sup>f</sup>	Gene annotation	Mutation
HT	SNP112	1	Upstream	1.12	Eucgr.B02728	Major facilitator superfamily protein (MFS)	-
	SNP3721	7	Exon	0.20	Eucgr.G02044	Magnesium protoporphyrin ix methyltransferase (CHLM)	Missense <sup>h</sup>
	SNP901	2	Intron	1.34	Eucgr.B02601	Lipoyltransferase 2 (LPT2)	Silent
	SNP2690	5	Downstream	2.72	Eucgr.E00620	Phosphoglycerate dehydrogenase 3 (PGDH3)	-
DBH	SNP112	1	Upstream	1.12	Eucgr.B02728	Major facilitator superfamily protein (MFS)	-
SLD	SNP2880	6	Exon	1.50	Eucgr.F00721	Rnase three-like protein 2 (RT2)	Missense <sup>h</sup>
						Double-stranded RNA binding motif <sup>g</sup>	
	SNP5245	10	Exon	1.03	Eucgr.J02998	Receptor like protein 54 (RLP54)	Missense <sup>h</sup>
	SNP1146	3	Upstream	1.30	Eucgr.C00778	Beta-ketoacyl- <i>acp</i> synthetase 2 (KASII)	-
	SNP2976	6	Upstream	1.22	Eucgr.F01050	S-locus lectin protein kinase	-
SNP3215	6	Upstream	1.34	Eucgr.F02674	Laccase-like 15 (TT10)	-	
BHT	SNP4880	9	Downstream	0.93	Eucgr.I01832.1	Xyloglucan O-acetyltransferase (TBL)	-
	SNP4591	8	Upstream	3.35	Eucgr.H04806	Nuclear localized protein, Unknown	-
	C7HB2 <sup>b</sup>	7	Exon	0.75	Eucgr.G00060	Methionine S-methyltransferase (MMT)	Missense <sup>h</sup>
STR	SNP3832	7	Downstream	3.46	Eucgr.G03051	Leucine-rich repeat protein kinase family protein	-
	SNP4141	8	Upstream	3.48	Eucgr.H02411	Cinnamyl-alcohol dehydrogenase 8 (CAD8)	-
	SNP1382	3	Exon	1.07	Eucgr.C01907	Gem-related 5 (GER5)	Missense <sup>h</sup>
PIL	SNP4981	9	Intron	0.80	Eucgr.I02798	LSM motif, RRM_1 domain	Missense <sup>h</sup>
	SNP3906	8	Intron	2.37	Eucgr.H00774	Fatty acyl-ACP thioesterase A (FATA)	Missense <sup>h</sup>
	SNP3991	8	Downstream	0.78	Eucgr.H01244	Coniferyl-alcohol glucosyltransferase /UDP-Glucosyl transferase 72E1 (UGT72E)	-
	SNP3995	8	Upstream	1.47	Eucgr.H01620	Serine carboxypeptidase-LIKE 20-RELATED	-

<sup>a</sup> HT, DBH, SLD, BHT, STR and PIL correspond to the total tree height, diameter at breast height, slenderness coefficient, 1st bifurcation height, stem straightness and pilodyn penetration, respectively. <sup>b</sup> Haplotype block; <sup>c</sup> Chromosome; <sup>d</sup> MTA location with respect to gene; <sup>e</sup> Physical distance

between MTA and candidate gene; <sup>f</sup> Transcript name in Phytozome and EucGenIE databases; <sup>g</sup> Additional sequence variants in the candidate genes;  
<sup>h</sup> Conservative or non-Conservative missense mutation.