

Electronic supplementary material: Supplementary Table 3

Title: Genetic dissection of growth, wood basic density and gene expression in interspecific backcrosses of *Eucalyptus grandis* and *E. urophylla*

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Supplementary Table 3a. eQTLs identified for the top 10 most positively correlated genes (transcript abundance correlated with wood basic density) under the epistatic QTL region on LG8 of the F₁ hybrid (*E. urophylla* BC family). A total of three and eight genes share trans-eQTLs on LG4 (10-22 cM) and LG10 (52-88 cM) that correspond to wood basic density QTLs on the same linkage groups. A putative trans-eQTL was also detected for six genes on LG6 (85-120 cM), but no wood density QTL was detected in this region.

Gene identification	Physical position (bp)	At. identification	At. description	eQTL on linkage group	eQTL position (cM)	Correlation with wood density (R ²)
Eucgr.H03646.1	53,552,147	AT3G21550.1	DUF679 domain membrane protein 2	6, 10	85, 54	0.54
Eucgr.H03652.1	53613563	AT5G18910.1	Protein kinase superfamily protein	6, 10	101, 52	0.52
Eucgr.H04339.1	62373141	AT5G28840.1	GDP-D-mannose 3',5'-epimerase	4, 6, 10	14, 101, 54	0.52
Eucgr.H04134.1	59247365	AT1G62290.1	Sapogenin-like aspartyl protease family protein	6, 10	120, 70	0.51
Eucgr.H04474.1	64015570	AT5G19090.1	Heavy metal transport/detoxification superfamily protein	4, 6, 10	10, 93, 52	0.49
Eucgr.H04133.1	59246267	AT4G04460.1	Sapogenin-like aspartyl protease family protein	4, 6, 10	22, 99, 54	0.48
Eucgr.H04329.1	62264300	AT3G04720.1	pathogenesis-related 4	-	-	0.46
Eucgr.H03914.1	56889409	AT5G13930.1	Chalcone and stilbene synthase family protein	10	72	0.45
Eucgr.H03673.1	53833668		Unknown	8	65	0.43
Eucgr.H04139.1	59277899	AT1G48320.1	Thioesterase superfamily protein	7, 10	46, 88	0.42

At., *Arabidopsis thaliana*; eQTL, Expression quantitative trait locus; Eucgr., *Eucalyptus grandis*; QTL, Quantitative trait locus.

Supplementary Table 3b: eQTLs identified for the top 10 genes (whose transcript abundance were negatively correlated with wood density trait variation) located in the wood basic density QTL intervals on LG8 and LG9 (F₁ hybrid map, *E. urophylla* backcross family).

Gene identification	Linkage group (LG)	Physical position (bp)	At. identification	At. description	eQTL on linkage group	eQTL position (cM)	Correlation with wood density (R ²)
Eucgr.H03971.1	LG8	57716920	AT1G06330.1	Heavy metal transport/detoxification superfamily protein	4, 8	39, 71	0.42
Eucgr.H04207.1	LG8	60095955	AT5G18460.1	Protein of Unknown Function (DUF239)	9	2.0	0.40
Eucgr.H03952.1	LG8	57402958	AT5G49130.1	MATE efflux family protein	10	72	0.35
Eucgr.H04141.1	LG8	59329525	AT3G17600.1	indole-3-acetic acid inducible 31	10	72	0.33
Eucgr.H04476.1	LG8	64030893	AT1G08970.1	nuclear factor Y, subunit C9	4, 8, 10	18, 90, 73	0.33
Eucgr.H04042.1	LG8	58287114	AT3G17040.2	high chlorophyll fluorescent 107	2, 8	74, 77	0.33
Eucgr.H04058.1	LG8	58443103	-	Unknown	4, 8	27, 63	0.32
Eucgr.H04118.1	LG8	59125445	AT1G56720.1	Protein kinase superfamily protein	8	88	0.32
Eucgr.H04336.1	LG8	62350663	AT5G43700.1	AUX/IAA transcriptional regulator family protein	5, 8	44, 88	0.30
Eucgr.H04045.1	LG8	58315064	AT5G49460.1	ATP citrate lyase subunit B 2	10	51	0.30
Eucgr.I02511.1	LG9	36197592	AT2G14520.1	CBS domain-containing protein with a domain of unknown function (DUF21)	9	70	0.34
Eucgr.I02585.1	LG9	37144011	AT5G64410.1	oligopeptide transporter 4	8, 9, 10	88, 70, 54	0.32
Eucgr.I02426.1	LG9	34863154	AT2G18260.1	syntaxin of plants 112	-	-	0.31

Eucgr.I02587.1	LG9	37175082	AT5G64410.1	oligopeptide transporter 4	9	70	0.30
Eucgr.I01897.1	LG9	28902234	AT3G28480.1	Oxoglutarate/iron-dependent oxygenase	9	58	0.30
Eucgr.I02119.1	LG9	30935715	AT5G15900.1	TRICHOME BIREFRINGENCE-LIKE 19	9	61	0.29
Eucgr.I02091.1	LG9	30613087	AT3G02350.1	galacturonosyltransferase 9	-	-	0.29
Eucgr.I01898.1	LG9	28908553	AT5G40020.1	Pathogenesis-related thaumatin superfamily protein	9	52	0.29
Eucgr.I02197.1	LG9	31874363	AT1G76520.1	Auxin efflux carrier family protein	9	60	0.27
Eucgr.I02308.1	LG9	33653685	AT4G35840.1	RING/U-box superfamily protein	10	72	0.27

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