

On-line Suppl. Tab. 1. Details of genes selected for high resolution melting (HRM) analysis and the position of variants (SNPs/InDel/SSRs). Gene IDs referred are from *Eucalyptus grandis* genome hosted in Phytozome portal (Goodstein et al. 2012). The position of the marker in the gene is presented in parentheses. CDS: Coding Domain Sequence; UTR: Un-translated region; SNP: Single Nucleotide Polymorphism; InDel: Insertion or Deletion; SSR: Simple Sequence Repeat.

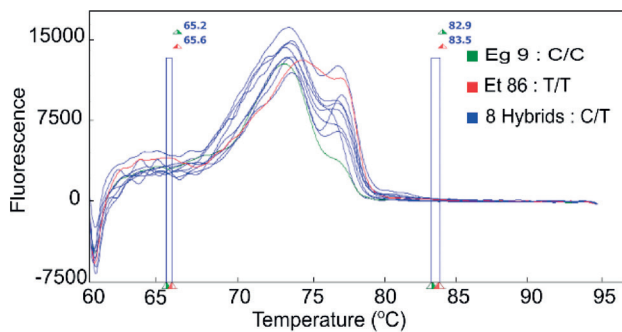
Gene ID	Gene Name	Gene Product	CDS length (bp)	Transcript length (bp)	SNP/ InDel/ SSR Position (bp)	Biological Function	Xylogenesi s-related function
SNPs							
Eucgr.F00106.1	<i>BP</i>	KNAT Knotted like Homeobox TF	1164	1820	1105 (CDS)	Regulates secondary cell wall biosynthesis	Secondary cell wall biogenesis
Eucgr.C00175.1	<i>XTH</i>	Xyloglucanendo-transglycosylase/hydrolase	894	1223	694 (CDS)	Cell wall extensibility	Regulates cell growth by strengthening or weakening xyloglucan – cellulose microfibril network
Eucgr.D01413.1	<i>PAAPA</i>	Hydroxyproline-rich glycoprotein (HRGP) and ‘PAAPA’ motif	519	1189	1047 (5’UTR)	Probable role in cell wall development	Probable role in cell wall development
Eucgr.F02243.1	<i>LIM1</i>	Homeodomain TF	567	1421	917 (CDS)	Developmental regulators in basic cellular processes such as organizing of cytoskeleton	Lignin biosynthesis
InDel							
Eucgr.G03380.2	<i>CesA4</i>	Cellulose synthase 4	3243	3951	3516 (CDS)	Cellulose deposition in primary cell wall	Primary cell wall formation
SSRs							
Eucgr.A01318.1	<i>MUR3</i>	Xyloglucan galactosyl transferase Exostosin family	1854	2347	67 – 80 ^{Eg9} 71 – 80 ^{Et86} (Upstream)	Xyloglucan biosynthesis	Xyloglucan biosynthesis
Eucgr.B03551.1	<i>ARF4</i>	Auxin response factor	2394	3040	197 – 214 ^{Eg9} 197 – 208 ^{Et86} (Upstream)	Transcription factors that bind to auxin response elements in promoters of early auxin response genes	Auxin signaling

On-line Suppl. Tab. 2. Details of primer pairs used for high resolution melting (HRM) analysis. Gene IDs referred are from *Eucalyptus grandis* genome hosted in Phytozome portal (Goodstein et al. 2012). SNP: Single Nucleotide Polymorphism; InDel: Insertion Deletion; SSR: Simple Sequence Repeat; bp: base pair.

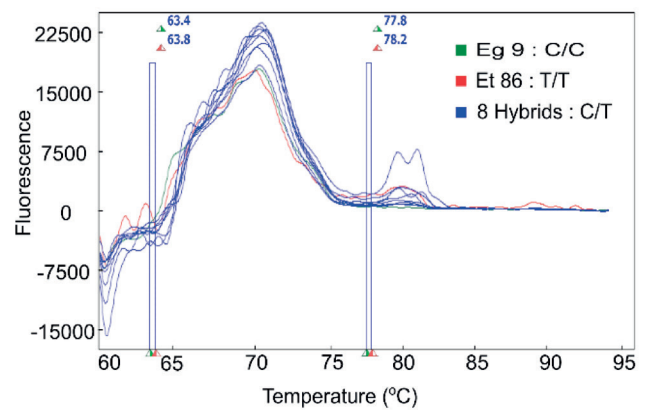
Gene ID	Gene Name	Forward Primer	Reverse Primer	Amplicon size (in bp)	Annealing Temperature (°C)
SNPs					
Eucgr.F00106.1	<i>BP</i>	CAGCATCAGCAGCTACAA	CAAGAGGTTGGAATACTGAG	96	60
Eucgr.C00175.1	<i>XTH</i>	CGACTAAAGCGTTTGCCAAT	GCCATCTCCGAAAGTGACAT	153	55
Eucgr.D01413.1	<i>PAAPA</i>	GAAGTGGACGTGCCTGCT	CTTGGCTGGAGTCTCCTCAG	120	60
Eucgr.F02243.1	<i>LIM1</i>	ACAGACACAATCACAGAGA	GCTTGTCCACCAGATAGA	112	60
INDELs					
Eucgr.G03380.2	<i>CesA4</i>	GAGCAGTGTGGAATCAAC	GGAGTAACCAATTTTCGGATC	71	55
SSRs					
Eucgr.A01318.1	<i>MUR3</i>	CAGCACCTTCCTCCACAC	ACAAGGAAGCAGCCGATG	81–85	60
Eucgr.B03551.1	<i>ARF4</i>	TTAAGCCC GTTCTTG GTG	CTGGAAGAAGCAATCACTG	82–90	60

On-line Suppl. Tab. 3. Melting temperatures (°C) of the parents (*Eucalyptus tereticornis* clone Et86 and *Eucalyptus grandis* clone Eg9) and eight hybrids (H13, H48, H137, H160, H190, H218, H265, and H275) for the genes used in high resolution melting (HRM) analysis. Data presented are mean of triplicate values ± standard deviation.

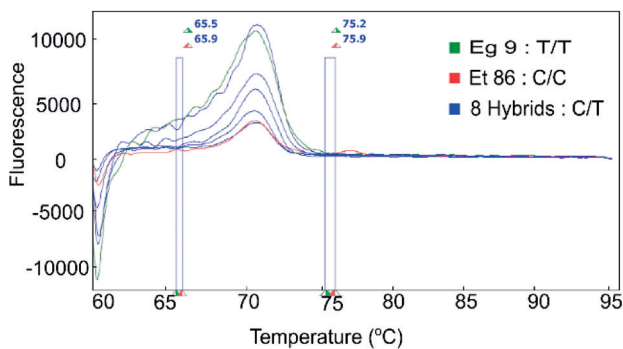
Gene Name	Eg9	Et86	H13	H 48	H 137	H 160	H 190	H 218	H 265	H275
BP	72.7 ± 0.35	74.5 ± 0.21	73.2 ± 0.14	73.3 ± 0.21	73.3 ± 0.07	73.4 ± 0.21	73.3 ± 0.21	73.4 ± 0.14	73.4 ± 0.15	73.3 ± 0.14
PAAPA	70.2 ± 0.14	70.9 ± 0.14	70.6 ± 0.14	70.7 ± 0.07	70.6 ± 0.14	70.7 ± 0.07	70.5 ± 0.14	70.6 ± 0.07	70.7 ± 0.07	70.6 ± 0.07
XTH	70.7 ± 0.14	70.5 ± 0.07	70.9 ± 0.07	70.9 ± 0.07	70.8 ± 0.07	70.8 ± 0.07	70.7 ± 0.07	70.6 ± 0.14	70.7 ± 0.07	70.9 ± 0.07
LIM1	81.1 ± 0.07	80.6 ± 0.07	81.2 ± 0.07	81.3 ± 0.07	80.6 ± 0.14	80.8 ± 0.21	80.8 ± 0.14	81.2 ± 0.07	80.6 ± 0.14	81.1 ± 0.14
CesA4	75.2 ± 0.14	74.7 ± 0.14	74.9 ± 0.07	74.9 ± 0.07	74.6 ± 0.07	74.9 ± 0.07	74.6 ± 0.07	74.8 ± 0.07	74.6 ± 0.07	74.8 ± 0.07
MUR3	79.8 ± 0.07	80.4 ± 0.28	79.7 ± 0.07	79.6 ± 0.14	79.7 ± 0.07	79.7 ± 0.07	79.7 ± 0.07	79.7 ± 0.14	79.7 ± 0.14	79.8 ± 0.07
ARF4	83.3 ± 0.21	84.4 ± 0.14	83.7 ± 0.28	83.7 ± 0.21	84.0 ± 0.14	83.9 ± 0.14	83.3 ± 0.07	84.0 ± 0.21	82.8 ± 0.14	83.4 ± 0.21



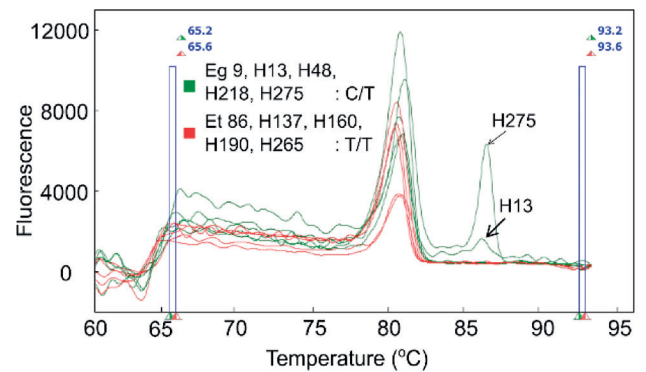
On-line Suppl. Fig. 1. Derivative melt curve of SNP marker in BP



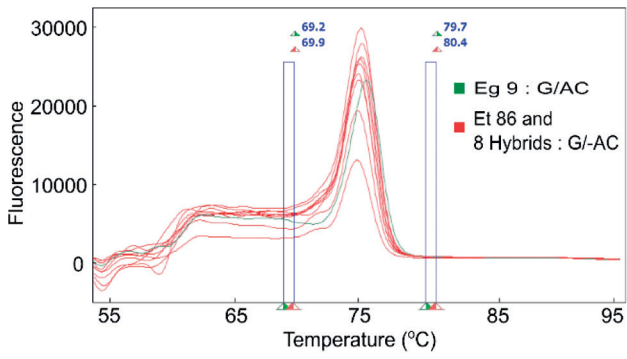
On-line Suppl. Fig. 3. Derivative melt curve of SNP marker in XTH



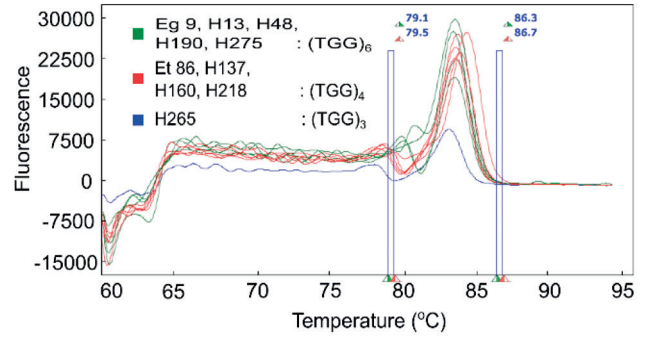
On-line Suppl. Fig. 2. Derivative melt curve of SNP marker in PAAPA



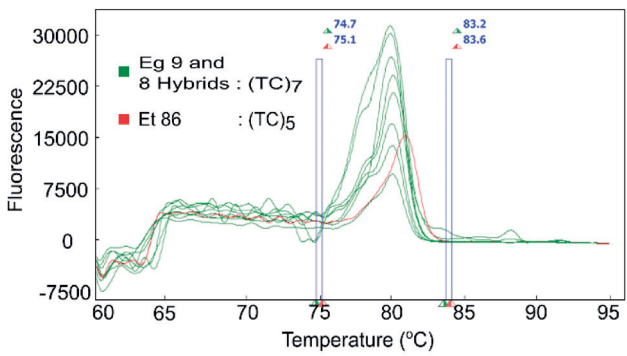
On-line Suppl. Fig. 4. Derivative melt curve of SNP marker in Lim1



On-line Suppl. Fig. 5. Derivative melt curve of InDel marker in *Cesa4*



On-line Suppl. Fig. 7. Derivative melt curve of SSR marker in *Arf4*



On-line Suppl. Fig. 6. Derivative melt curve of SSR marker in *Mur3*