

**Table S2 Putative eucalypt homologs of key genes involved in vegetative and reproductive phase-change transitions in Arabidopsis, and their position in the *Eucalyptus grandis* genome and Lighthouse *E. globulus* F<sub>2</sub> linkage map.**

Gene <sup>a</sup>	TAIR accession	<i>E. grandis</i> v1.1 locus <sup>b</sup>	Position (v1.1)	LG	cM
<b>miR156 precursors</b>					
<i>EgrMIR156.1</i>		na	scaffold_3:6,875,645..6,875,558	3	1.41
<i>EgrMIR156.2</i>		na	scaffold_3:11,870,361..11,870,270	3	7.61
<i>EgrMIR156.3</i>		na	scaffold_3:11,879,442..11,879,528	3	7.63
<i>EgrMIR156.4</i>		na	scaffold_3:33,774,484..33,774,404	3	50.11
<i>EgrMIR156.5</i>		na	scaffold_3:50,822,714..50,822,639	3	64.76
<i>EgrMIR156.6</i>		na	scaffold_3:57,552,911..57,552,994	3	75.18
<i>EgrMIR156.7</i>		na	scaffold_3:57,574,796..57,574,878	3	75.18
<i>EgrMIR156.8</i>		na	scaffold_3:57,594,656..57,594,739	3	75.18
<i>EgrMIR156.9</i>		na	scaffold_3:57,604,491..57,604,574	3	75.18
<i>EgrMIR156.10</i>		na	scaffold_3:64,630,889..64,630,798	3	85.26
<i>EgrMIR156.11</i>		na	scaffold_3778:2795_2874		
<b>miR157 precursors</b>					
<i>EgrMIR157.1</i>		na	scaffold_2:10,262,540..10,262,626	2	33.15
<i>EgrMIR157.2</i>		na	scaffold_6:37,685,287..37,685,385	6	84.48
<i>EgrMIR157.3</i>		na	scaffold_10:28,534,316..28,534,229	10	70.07
<i>EgrMIR157.4</i>		na	scaffold_11:29,604,562..29,604,654	11	64.76
<b>miR172 precursors</b>					
<i>EgrMIR172.1</i>		na	scaffold_2:47,463,700..47,463,718	2	76.81
<i>EgrMIR172.2</i>		na	scaffold_7:46,895,298..46,895,316	7	73.69
<i>EgrMIR172.3</i>		na	scaffold_7:48,069,802..48,069,820	7	77.54
<i>EgrMIR172.4</i>		na	scaffold_10:9,766,042..9,766,060	10	28.06
<i>EgrMIR172.5</i>		na	scaffold_10:11,654,521..11,654,539	10	33.87
<i>EgrMIR172.6</i>		na	scaffold_10:14,042,402..14,042,420	10	39.63
<b>miR156/157 targets</b>					
<i>SPL2</i>	AT5G43270	Eucgr.B03500	scaffold_2:59,707,186..59,711,577	2	109.34
<i>SPL3</i>	AT2G33810	na			
<i>SPL4</i>	AT1G53160	Eucgr.F03303	scaffold_6:42,095,464..42,096,829	6	101.61
<i>SPL5</i>	AT3G15270	Eucgr.E03260	scaffold_5:55,297,144..55,300,470	5	77.32
<i>SPL5</i>	AT3G15270	Eucgr.K01046	scaffold_11:13,198,982..13,200,949	11	21.65
<i>SPL9</i>	AT2G42200	Eucgr.A02441	scaffold_1:35,069,324..35,074,597	1	85.53
<i>SPL9</i>	AT2G42200	Eucgr.K01828	scaffold_11:22,648,024..22,650,837	11	48.8
<i>SPL10</i>	AT1G27370	na			
<i>SPL11</i>	AT1G27360	na			
<i>SPL15</i>	AT3G57920	na			
<b>miR172 targets</b>					
<i>TOE1</i>	AT2G28550	Eucgr.A01182	scaffold_1:18,327,635..18,329,322	1	26.97

<i>TOE1</i>	AT2G28550	Eucgr.B02453	scaffold_2:46,666,684..46,670,642	2	71.43
<i>TOE1</i>	AT2G28550	Eucgr.G02793	scaffold_7:46,189,542..46,193,511	7	71.39
<i>TOE1</i>	AT2G28550	Eucgr.J02113	scaffold_10:27,123,430..27,127,595	10	65.12
<i>SMZ</i>	AT3G54990	na			
<i>SNZ</i>	AT2G39250	na			
<i>AP2</i>	AT4G36920	Eucgr.I00892	scaffold_9:18,318,869..18,322,920	9	24.3
<b>Flowering genes</b>					
<i>AP1</i>	AT1G69120	na			
<i>FD</i>	AT4G35900	Eucgr.F01674	scaffold_6:21,180,795..21,182,560	6	44.75
<i>FD</i>	AT4G35900	Eucgr.J02482	scaffold_10:30,908,543..30,909,313	10	78.83
<i>EgFLC.1</i>	AT5G10140	Eucgr.H04618	scaffold_8:66,300,089..66,316,194	8	116.26
<i>EgFT</i>	AT1G65480	Eucgr.B01458	scaffold_2:23,917,879..23,919,338	2	48.49
<i>EgFUL.1</i>	AT5G60910	Eucgr.B00634	scaffold_2:8,088,480..8,094,596	2	24.35
<i>EgFUL.2</i>	AT5G60910	Eucgr.K02547	scaffold_11:32,650,033..32,656,017	11	68.51
<i>LFY</i>	AT5G61850	Eucgr.K02192	scaffold_11:29,183,297..29,184,533	11	63.8
<i>SOC1</i>	AT2G45660	na			
<i>EgSVP.1</i>	AT2G22540	Eucgr.I00556	scaffold_9:11,461,709..11,470,322	9	17.11
<i>EgSVP.2</i>	AT2G22540	Eucgr.F00420	scaffold_6:5,336,346..5,346,958	6	14.24
<i>EgTFL1</i>	AT5G03840	Eucgr.A01505	scaffold_1:23,524,373..23,525,501	1	35.33

<sup>a</sup>The miR156, miR157 and miR172 precursors were identified by performing BLAST searches. Putative homologues of genes targeted by miR156 and miR172 were identified using the *E. grandis* genome annotations. Putative homologues of key flowering genes were identified by Vining et al (in prep); genes with “Eg” prefix are *E. grandis* orthologs confirmed by phylogenetic analyses (Vining et al in prep). See methods for details of gene identification.

<sup>b</sup>na, not annotated.