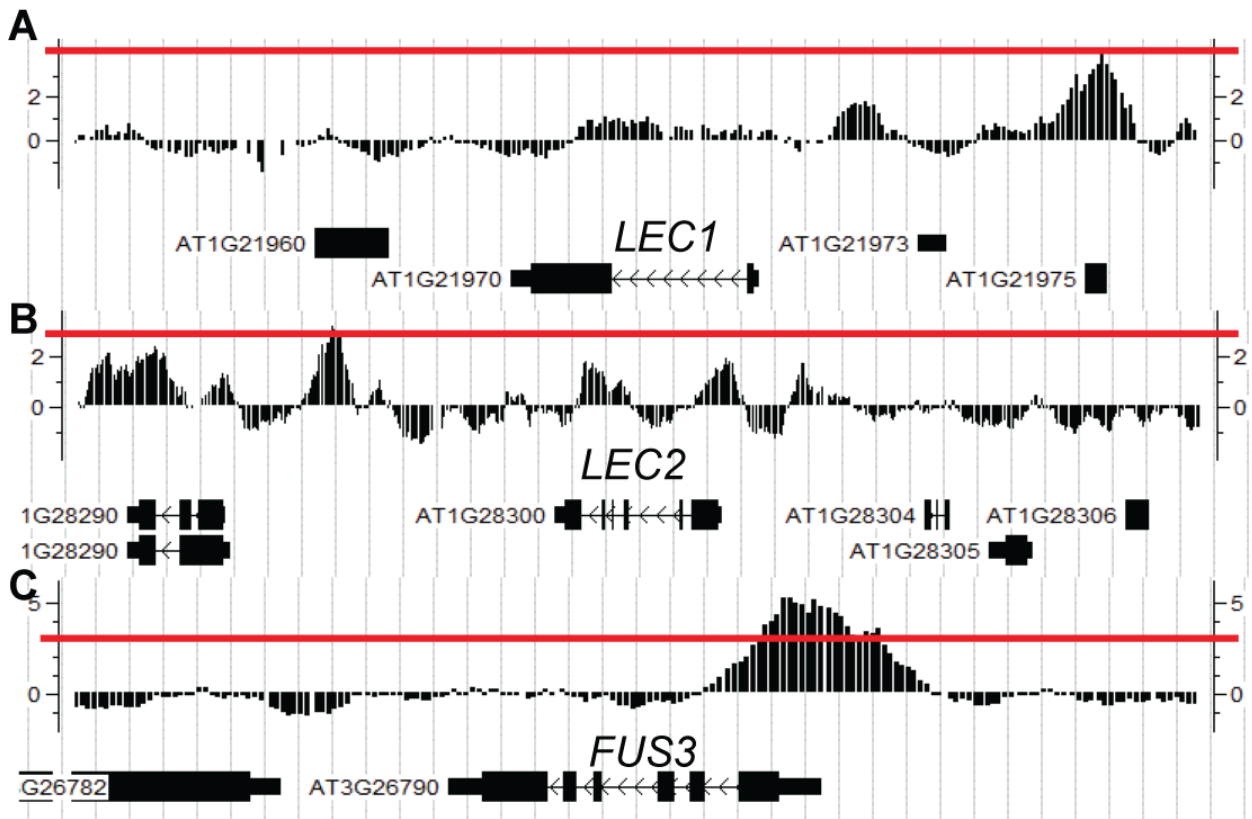
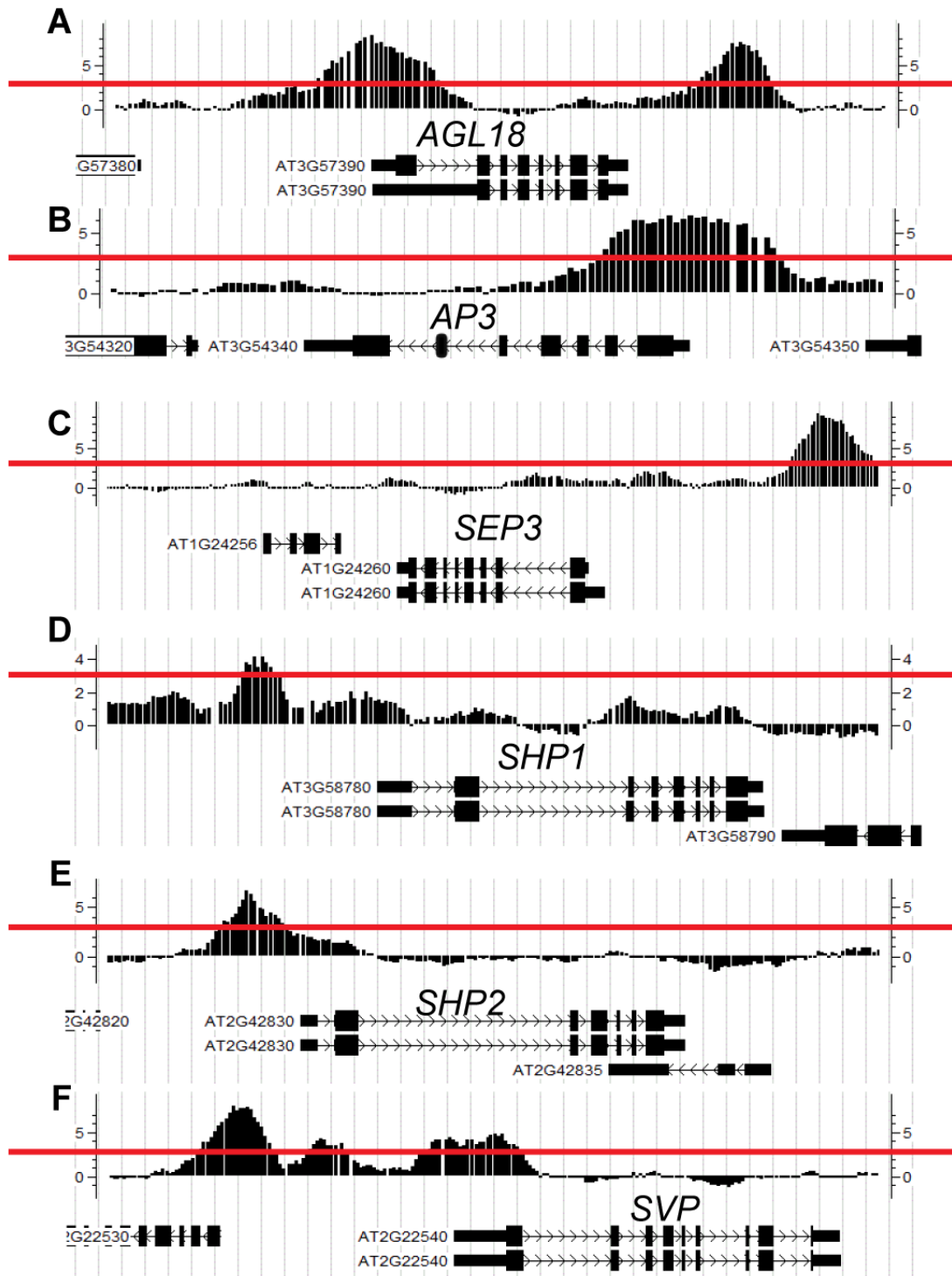


**Table S1.** Oligonucleotides used for qRT-PCR. All oligonucleotides are written 5' to 3'.

<b>AGI</b>	<b>Gene Name</b>	<b>Forward</b>	<b>Reverse</b>
AT5G19770	<i>TUA3</i>	TGG TGC CCA ACT GGG TTC AAA T	ACC TCT GCA ACT GCT GTG TTG T
AT5G13790	<i>AGL15</i>	TGC AAA GCC TTG AGC AGC AAC T	AAC CTG TCT ACG CAA GGT CTC GTT
	<i>AGL15-LLL</i>	GAC ACA ACT TTG CAA TTA GGG TT	GTT TCG CTG CTC GTG TTT G
	<i>AGL15-AAA</i>	TGC GCA AGC AGG GGC	GTT TCG CTG CTC GTG TTT G
AT1G21970	<i>LEC1</i>	AAC GTG GAG CTC CCT TCT CTC ACT AT	TTG GGT TGT TGC TGT GCT GGT
AT1G28300	<i>LEC2</i>	ATC CTC AGA TCC CGG TTA CGC AAA	ACC ACC TCT CTC TTG CCA CAA AC
AT3G54340	<i>AP3</i>	CAT ACA TGA GCT GGA ACT AAG A	ACG TGA CCC TTC GAT TTG
AT3G58780	<i>SHP1</i>	GTA CCT GCG AGC AAA GAT AG	GAA GAT ACA CCG GAT TCG TAA A
AT2G42830	<i>SHP2</i>	CGC TCC AAG ATT ACT GAA AGA	CGA CTG GTG AGA AGA AGT AAC
AT1G24260	<i>SEP3</i>	TTC GAG CAT GCT TCG GAC ACT	AGG GTC CGA AGC ATG CTC GAA
AT3G57390	<i>AGL18</i>	ACC AGT TGA ACG AGA GCT TG	TCT CAA CCT GTT TGC GCA AG
AT3G26790	<i>FUS3</i>	TCA TCA TGG GTT ATC GGC GT	AGT TGG CAC GTG GGA AAT AGG A
AT2G22540	<i>SVP</i>	ACA GTC GTC GGA GTC TAT T	CTA ACC ACC ATA CGG TAA GC



**Figure S1:** CisGenome traces showing association of AGL15 with promoter regions of (A) *LEAFY COTYLEDON1* (B) *LEAFY COTYLEDON2*, and (C) *FUSCA3*. The red line indicates the moving average cutoff of 3 for peak determination as used in Zheng et al., (2009).



**Figure S2:** CisGenome traces showing association of AGL15 with promoter regions of (A) *AGAMOUS-Like18* (B) *APETALA3*, (C) *SEPALLATA3*, (D) *SHATTERPROOF1*, (E) *SHATTERPROOF2*, and (F) *SHORT VEGETATIVE PHASE*. The red line indicates the moving average cutoff of 3 for peak determination as used in Zheng et al., (2009). In all cases, the binding region(s) is 5' of and/or within the 5' end of the gene, with the exception of *AGL18* that also shows association with AGL15 3' of the gene.