Supplemental Table S2. Sequences and positions of the TFBSs shown in Supplemental Figure S5.

Name	*AP1*	*AlyAP1*	*CruAP1*	*TpaAP1*	*AarAP1*	*CAL*	*AlyCAL*	*CruCAL*	*TpaCAL*	*AarCAL*	*Tha01189*	*Tha13754*	*CpaAP1*
LFY"	CCACTG (-255/-250)	/	/	/	/	/	/	/	/	/	/	/	/
LFY	CCAATG (-289/-284)	CCAATG (-289/-284)	CCAATG (-297/-292)	CCAATG (-288/-283)	CCAATG (-284/-279)	CCAATG (-231/-226)	CCAATG (-262/-257)	CCAATG (-263/-258)	/	/	CCAATG (-339/-334)	CCAATG (-357/-352)	CCAGTG (-409/-404)
SPL9	GTAC (-301/-298)	GTAC (-301/-298)	GTAC (-309/-306)	GTAC (-299/-296)	GTAC (-296/-293)	/	/	/	/	/	GTAC (-350/-347)	GTAC (-367/-364)	/
MYB	/	/	/	/	/	GGCAAT (-252/-247)	GGCAAT (-283/-278)	GGCAAT (-284/-279)	GGCAAT (-307/-302)	/	/	/	/
TCP4	ATGGACCC (-316/-309)	ATGGACCC (-316/-309)	ATGGACCC (-324/-317)	GTGGACCC (-314/-307)	/	/	/	/	/	/	GTGGACCC (-365/-358)	GTGGACCA (-391/-384)	/
LMI1	/	/	/	/	/	CAATTATTG (-326/-318)	CAATTACTG (-354/-346)	CAATTATTT (-370/-362)	CAATTACTG (-375/-367)	/	/	/	/
PAN	ACGT (-376/-373)	/	ACGT (-384/-381)	ACGT (-400/-397)	ACGT (-360/-357)	ACGT (-337/-334)	ACGT (-365/-362)	ACGT (-382/-379)	ACGT (-386/-383)	/	/	/	/
FD	GACGTC (-377/-372)	/	GACGTC (-385/-380)	GACGTC (-401/-396)	GACGTC (-361/-356)	GACGTC (-338/-333)	GACGTC (-366/-361)	GACGTT (-383/-378)	GACGTC (-387/-382)	/	/	/	/
LMI2	ACTTACC (-399/-393)	ACTTACC (-398/-392)	/	/	/	/	/	/	/	/	ACTGACC (-454/-448)	ACTGACC (-476/-470)	/
SPL3/9	GTCCGTACAA (-413/-404)	GTCCGTACAA (-412/-403)	GTCCGTACAA (-431/-422)	GTCCGTACAA (-431/-422)	/	/	/	GTCCGTACAC (-445/-436)	/	CTCCGTACAA (-307/-298)	GTCCGTACCA (-475/-466)	GTCCGTACAA (-501/-492)	/
LFY'	CCAGTG (-419/-414)	CCAGTG (-418/-413)	CCAGTG (-437/-432)	CCACTG (-437/-432)	/	/	/	/	/	/	/	/	/
bHLH	CACTTG (-433/-428)	CACTTG (-432/-427)	CACTTG (-451/-446)	CACTTG (-451/-446)	CACTTG (-404/ -399)	CACTTG (-411/-406)	CACTTG (-432/-427)	CACTTG (-467/-462)	CACTTG (-453/-448)	CACTTG (-326/-321)	CACTTG (-494/-489)	CACTTG (-520/-515)	CACTTG (-506/-501)
AP2/ SMZ'	TTTGTT (-487/-482)	TTTGTT (-486/-481)	/	TTTGTT (-505/-500)	TTTGTT (-458/-453)	/	/	/	/	/	/	/	/
PI	GCAAATTTGA (-603/-594)	GCAAATTTGA (-602/-593)	ACAAATTTGA (-617/-608)	/	/	/	/	/	/	/	/	/	/
Dof	AAAGAAAG (-658/-651)	AAAGAAAG (-654/-647)	AAAAAAAG (-675/-668)	AAAAAAAG (-666/-659)	AAAGAAAG (-598/-591)	/	/	/	/	/	AAGAAAG (-667/-661)	/	AGAAAAAG (-754/-747)
SPL3	CGTACAA (-733/-727)	CGTACAA (-729/-723)	CGTACAA (-757/-751)	/	/	/	/	/	/	/	/	/	/
AP1	CTATTTTTGG (-805/-796)	CTATTTTTGG (-800/-791)	/	/	/	/	/	/	/	/	/	CTATTTTAGG (-868/-859)	/
SPL3	CGTACAA (-948/-942)	AGTACAA (-919/-913)	AGTACCA (-954/-948)	CGTACGA (-913/-907)	AGTACTA (-940/-934)	CGTACTA (-911/-905)	/	TGTACAA (-905/-898)	AGTACAG (-1189/-1183)	/	GTACAG (-896/-890)	/	AGTACTT (-1180/-1174)
PAN	ACGT (-949/-946)	/	/	ACGT (-914/-911)	/	ACGT (-912/-909)	/	/	/	/	/	/	/
AP2/ SMZ	TTTGTT (-1858/-1853)	TTTGTT (-1747/-1742)	TTTGTT (-1857/-1852)	TTTGTT (-1767/-1762)	AACAAA (-1713/-1708)	TTTGTT (-1486/-1481)	TTTGTT (-1349/-1344)	AACAAA (-1361/-1359)	TTTGTT (-1290/-1285)	AACAAA (-1372/-1367)	TTTGTT (-1847/-1842)	TTTGTT (-1873/-1868)	AACAAA (-1929/-1924)

Supplemental Table S3. *AP1*- and *CAL*-like genes included in this study.

Taxon	**Gene**	**Accession No.**	**Source**
Arabidopsis thaliana	*AP1*	At1g69120	TAIR10
	CAL	At1g26310	TAIR10
Arabidopsis lyrata	*AlyAP1*	476039	Phytozome 9.1
	AlyCAL	921628	Phytozome 9.1
Capsella rubella	*CruAP1*	Carubv10022005m.g	Phytozome 9.1
	CruCAL	Carubv10011954m.g	Phytozome 9.1
Thellungiella parvula	*TpaAP1*	AFAN01000026.1:1131966/1128287	GenBank
	TpaCAL	AFAN01000001.1: 8231573/8235104	GenBankI
Aethionema arabicum	*AarAP1*	KE153490.1:210765/224506	GenBank
	AarCAL	KE150702.1:473531/469589	GenBank
Tarenaya hassleriana	*Tha13754*	KE705813.1: 564960/560792	GenBank
	Tha01189	KE705860.1: 102975/98186	GenBank
Carica Papaya	*CpaAP1*	evm.TU.supercontig_1.16	Phytozome 9.1

Supplemental Table S4. Primer sequences used in this study.

Purpose	**Primer name**	**Forward primer (5′-3′)**	**Reverse primer (5′-3′)**
In situ hybridization	*AthAP1*	ATGTACGAGTCCATCAATGAGC	T7-AAGCAGCCAAGGTTGCAGTTG
	AthCAL	AATGAGTCCCTCAACCACCTCC	T7-CGTAACAGCCAAGGTAATT
qRT-PCR	*AthAP1*	CAGCAGCACCAAATCCAGC	GAGCCTAGCCACTATTTATATG
	AthCAL	CCATTTCAACACCCCCATC	TCATGAGTAGAGGATCGATC
	AthACTIN	CATGCCATCCTCCGTCTTG	GCTCTGCTGTTGTGGTGAAC
	CruAP1	CAGCAACACCAAATCCAGC	CGTTTCTCCTCATTGCCATTGG
	CruCAL	CAACCGCAACAGTTTCAACC	GGTACATTCCACCCATATTTAGG
	CruACTIN	GACTACGAGCAAGAGATGG	GGAACAAGACTTCTGGGC
	GUS	CCTGCGTCAATGTAATGTTC	GTGATGATAATCGGCTGATG
Genotyping	*GUS*	GCGTGGTGATGTGGAGTATTG	GATCCCTTTCTTGTTACCGCC
AP1 constructs	AP1$_{intr1}$	CTCCACTGAAGCTTGGTAACTTC	CATAGCGTTCAAGTATCTTCTCGAGACTG
	AP1$_{pro2887}$	AGGTACCTGTGTGTAGCTGCGTAT	TGAACCCTACCCCTTAAGCTTTTG
	AP1$_{pro2887(mut805-796)+intr1}$-up	CAATTCAGTCGACTGGATCC	TTTCAAACGGTTAATTAAGTATTTTGTCAAAGATTTGTTCAATGT
	AP1$_{pro2887(mut805-796)+intr1}$-down	CAAAATACTTAATTAACCGTTTGAAATTTTGAATACTTACAATTATTC	GCGGGATATCACCACTTTGTAC
	AP1$_{pro1163}$	GCCTTAAGCAAATGCCGGATCCG	TTCCCATTCTCGAGCCTTTTTTA
	AP1$_{pro855}$	CCGGATCCTCTACAACTTAATAAG	TTCCCATTCTCGAGCCTTTTTTA
	AP1$_{pro755}$	CTTCTGGATCCTCCTCTCTTTCC	TTCCCATTCTCGAGCCTTTTTTA
	AP1$_{pro577}$	AGGGTACCCACCTTATTCC	TTCCCATTCTCGAGCCTTTTTTA
	AP1$_{pro276}$	ACCAATGAGGATCCGACACGC	TTCCCATTCTCGAGCCTTTTTTA
CAL constructs	CAL$_{intr1}$	GTTCGAGTACTCCTCGGTACCTTGG	CGTTCGAGCTCCTTCTCGAGGCTAC
	CAL$_{pro1210}$	GACGGATCCACAACACTCAAAAC	TTCAACCCTACCGGTACCCTGTTCTC
	CAL$_{pro1210(mut703-693)+intr1}$-up	CAATTCAGTCGACTGGATCC	ATTTTGAAGTTTGCCAAAAATAGGAAATATCCAAAATACAAATTACCATAAGTTT
	CAL$_{pro1210(mut703-693)+intr1}$-down	TTCTATTTTTGGCAAACTTCAAAATTAATTTTCTTCTGCT	GCGGGATATCACCACTTTGTAC
	CAL$_{pro1109}$	ATGGACAAAGGAGGAGGTACCGC	CCCATTTCTCTCGAGATAAC
	CAL$_{pro850}$	GGTCTGCTTAAAGGTACCATGG	CCCATTTCTCTCGAGATAAC
	CAL$_{pro521}$	CCTCTATAACTACTTGGATCCATT	CCCATTTCTCTCGAGATAAC
	CAL$_{pro340}$	CCATTTTCAGGTACCTAGACGTCG	CCCATTTCTCTCGAGATAAC
	CAL$_{pro240}$	AGGCAATGGTACCCTAATCAGACC	CCCATTTCTCTCGAGATAAC
EMSA	*AthAP1*	AAAGGATCAACCATGGGAAGG	TATATGGAAATCTCGAGTGCG
	AthCAL	GTTATTTTAAGAGCCATGGGAAG	GATGTAGTCCTCGAGAGCGG
	CruAP1	ACCATGGGAAGGGGTAGGGTTC	CTCGAGTGCAGCGAAGCAGCCAAGGTTG
	CruCAL	ACCATGGGAAGGGGTAGGGTTG	CTCGAGTGCAGCGTAACAACCAAGG

Note: Sequences underlined represent the restriction enzyme sites.

Supplemental Table S5. Independent transgenic lines examined by GUS-staining analyses.

construct name	**No. of independent lines examined by GUS staining**	**No. of lines showing the representative spatiotemporal expression pattern**
$AP1_{pro2887+intr1}$	47	40(85%)
$AP1_{pro1163}$	33	27(81.8%)
$AP1_{pro855}$	34	26(76.5%)
$AP1_{pro755}$	65	65(100%)
$AP1_{pro577}$	97	70(72.2%)
$AP1_{pro276}$	30	30(100%)
$AP1_{pro2887(mut805-796)+intr1}$	31	24(77.4%)
$CAL_{pro1210+intr1}$	47	39(83%)
$CAL_{pro1109}$	53	40(75.5%)
CAL_{pro850}	57	49(86%)
CAL_{pro521}	48	48(100%)
CAL_{pro340}	60	47(78.3%)
CAL_{pro240}	41	29(70.7%)
$CAL_{pro1210(mut703-693)+intr1}$	55	53(93.4%)