Supplemental Table S1. Functionally confirmed TFBSs in *AP1* and *CAL* regulatory regions.

							AP1	
No.	**Name**	**Position**	**Sequence**	**Putative *cis*-element**	**Binding TF**	**Gene family**	**Gene expression pattern**	**Gene function**
1	LFY"	-255 — -250	CCACTG	LFY binding site	LEAFY		*LFY* is weakly expressed in young leaves during the vegetative phase, and strongly expressed in young primordia surrounding the inflorescence apex.	*LFY* controls the production of the flowers, and activates the floral homeotic genes that specify the identity of organs in the flower.
2	LFY	-289 — -284	CCAATG	LFY binding site	LEAFY		*LFY* is weakly expressed in young leaves during the vegetative phase, and strongly expressed in young primordia surrounding the inflorescence apex.	*LFY* controls the production of the flowers, and activates the floral homeotic genes that specify the identity of organs in the flower.
3	SPL9	-301 — -298	GTAC	GTAC box	SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE 9	SPL	*SPL9* is strongly expressed in leaf primordia and provascular strands of young leaves. Its expression is transiently upregulated in floral anlagen and very early floral primordia, but declined again by stage 2 of flower development.	*SPL9* promotes flowering in an FT/FD-independent manner.
		—	—					
4	TCP4	-316 — -309	ATGGACCC	TCP4 binding site	TCP FAMILY TRANSCRIPTION FACTOR 4	TCP	*TCP4* is broadly expressed in stems, leaves and flowers.	Nag et al., (2009) found that miR319a targeting of TCP4 is critical for petal growth and development.
		—	—					
5	PAN	-376 — -373	ACGT	TGA binding site	PERIANTHIA	bZIP	*PAN* RNA is present in the inflorescence meristem, the floral meristem, and in developing petals, stamens, and carpels.	*PAN* plays roles in the control of perianth organ number specification, and the regulation of floral determinacy. It mediates BOP1 and 2 to the promoter of *AP1*, which activates expression of *AP1* to control floral trasition and patterning.
5	FD	-377 — -372	GACGTC	C-box	FLOWERING LOCUS D	bZIP	*FD* is highly expressed at the shoot apex. Specifically, *FD* is expressed in leaf and floral anlagen. Its levels decrease soon after floral primordia start to express *AP1*.	*FD* could integrate temporal and spatial information that is already expressed at the shoot apex before floral induction, and promote flowering. A complex of FT and FD proteins can activate *AP1*.
6	LMI2	-399 — -393	ACTTACC	R2R3 MYB binding site	LATE MERISTEM IDENTITY 2	R2R3 MYB	*LMI2* is expressed throughout the shoot apical meristem of primary inflorescences, with the highest expression observed in the young flower primordia.	*LMI2* plays a role in the meristem identiry transition .
7	SPL3/9	-411 — -404	CCGTACAA	GTAC box	TCP FAMILY TRANSCRIPTION FACTOR 3/9	SPL	*SPL3* is expersssed in vegetative and inflorescence apical meristems, floral meristems, leaf and flower organ primordia, and inflorescence stem tissue. *SPL9* is strongly expressed in leaf primordia and provascular strands of young leaves. The expression of *SPL9* is transiently upregulated in floral anlagen and very early floral primordia, but declined again by stage 2 of flower development.	*SPL3* controls the timing of flower formation. *SPL9* promotes flowering in an FT/FD-independent manner.
8	LFY"	-419 — -414	CCAGTG	LFY binding site	LEAFY		*LFY* is weakly expressed in young leaves during the vegetative phase, and strongly expressed in young primordia surrounding the inflorescence apex.	*LFY* controls the production of the flowers, and activates the floral homeotic genes that specify the identity of organs in the flower.
9	bHLH	-433 — -428	CACTTG	E-box	bHLH genes	bHLH		
10	AP2/SMZ'	-487— -482	TTTGTT		APETALA 2/SCHLAFMUTZE	AP2	*AP2* is expressed in the inflorescence meristem and in all four types of floral organs. *SMZ* is expressed in hypocotyl, cotyledons, merstematic region of 7-d-old seedlings, and seeds.	*AP2* plays a central role in the establishment of the floral meristem, the specification of floral organ identity and the regulation of floral homeotic gene expression. *SMZ* is a repressor of flowering.

11	PI	-603 — -594	GCAAATTTGA	CArG-box	PISTILLATA	MADS-box	*PI* is expressed at inner three whorls of floral organs at stage 3, its expression in the whorl 4 region dissappeared by stage 5. It remains present at high levels in the developing second and third whorls till stages 10 and 11.	PI determines the identity of petals and stamens, by interacting with AP3.
12	Dof	-658 — -651	AAAGAAAG	AAAG motif	Dof genes	Dof domain proteins		
13	SPL3	-733 — -727	CGTACAA	GTAC box	SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE 3	SPL	*SPL3* is experssed in vegetative and inflorescence apical meristems, floral meristems, leaf and flower organ primordia, and inflorescence stem tissues.	*SPL3* controls the timing of flower formation.
14	AP1	-805 — -796	CTATTTTTGG	CArG-box	APETALA1	MADS-box	*AP1* is expressed in young floral primordia, sepals and petals.	*AP1* plays roles in the formation of floral meristems, and specification of sepals and petals.
15	SPL3	-948 — -942	CGTACAA	GTAC box	SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE 3	SPL	*SPL3* is experssed in vegetative and inflorescence apical meristems, floral meristems, leaf and flower organ primordia, and inflorescence stem tissues.	*SPL3* controls the timing of flower formation.
15	PAN	-949 — -946	ACGT	TGA binding site	PERIANTHIA	bZIP	*PAN* RNA is present in the inflorescence meristem, the floral meristem, and in developing petals, stamens, and carpels.	*PAN* plays roles in the control of perianth organ number specification, and the regulation of floral determinacy. It mediates BOP1 and 2 to the promoter of *AP1* , which activates expression of *AP1* to control floral trasition and patterning.
16	AP2/SMZ	-1858— -1853	TTTGTT		APETALA 2/SCHLAFMUTZE	AP2	*AP2* is expressed in the inflorescence meristem and in all four types of floral organs. *SMZ* is expressed in hypocotyl, cotyledons, merstematic region of 7-d-old seedlings, and seeds.	*AP2* plays a central role in the establishment of the floral meristem, the specification of floral organ identity and the regulation of floral homeotic gene expression.*SMZ* is a repressor of flowering.
		—	—					
17	WRKY	1044 — 1049	TTGACC	W-box	WRKY genes	WRKY		
		—	—					
18	SPL8	1253 — 1268	TTTTCTGTACC TAATT	GTAC box	SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE 8	SPL	*SPL8* is lowly expressed in vegetative growth and highly expressed in inflorescences formed after the floral transition. It is also expressed in the developing pollen sacs of the anthers, the placental tissue of the developing gynoecium, and the margins of the petals.	*SPL8* is required for proper development of sporogenic tissues.
		—	—					
		—	—					
19	SPL4/7	3358 — 3364	TTGTACG	GTAC box	SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE 4/7	SPL		

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									CAL
Evidence	References	**No.**	**Name**	**Position**	**Sequence**	**Putative *cis* - element**	**Binding TF**	**Gene family**	**Gene expression pattern**
LFY directely induces expression of *AP1* , as evidenced by EMSA, LFY-GR system, and ChIP-qPCR.	(Weigel et al., 1992; Parcy et al., 1998; Wagner et al., 1999; William et al., 2004; Benlloch et al., 2011; Winter et al., 2011)			—	—				
LFY directely induces expression of *AP1* , as evidenced by EMSA, LFY-GR system, and ChIP-qPCR.	(Weigel et al., 1992; Parcy et al., 1998; Wagner et al., 1999; William et al., 2004; Benlloch et al., 2011; Winter et al., 2011)	1	LFY	-231 — -226	CCAATG	LFY binding site	LEAFY		*LFY* is weakly expressed in young leaves during the vegetative phase, and strongly expressed in young primordia surrounding the inflorescence apex.
SPL9 directly activates *AP1* , as evidenced by sequence prediction and ChIP-qPCR.	(Wang et al., 2009)			—	—				
		2	MYB	-252 — -247	GGCAAT	MYB binding site	MYB genes	MYB	
TCP4 could bind to the DNA sequence TGGTCCC, as revealed by EMSA. The putative TCP4 binding site is predicted based on the sequence similarity.	(Yao et al., 2007; Nag et al., 2009; Aggarwal et al., 2010)			—	—				
		3	LMI1	-326 — -318	CAATTATTG	HD-Zip binding site	LATE MERISTEM IDENTITY 1	HD-Zip1	*LMI1* is expressed in leaves of young seedlings during the vegetative stage, strongly expressed in the incipient flower primordia, and developing flowers.
PAN mediates BOP1 and 2 to the promoter of *AP1* , as evidenced by sequence prediction and ChIP-qPCR.	(Foster et al., 1994; Chuang et al., 1999; Hepworth et al., 2005; Maier et al., 2009; Xu et al., 2010)	4	PAN	-337 — -334	ACGT	TGA binding site	PERIANTHIA	bZIP	
Wigg et al., (2005) proposed this site as potential FD-binding site based on the evidence of sequence prediction and ChIP-qPCR, but Benlloch et al., (2011) indicated that this C-box is not needed for *AP1* activation based on the EMSA analysis.	(Wigge et al., 2005; Benlloch et al., 2011)	4	FD	-338 — -333	GACGTC	C-box	FLOWERING LOCUS D	bZIP	
LMI2 directely activates expression of AP1, as evidenced by sequence predication and ChIP-qPCR.	(Pastore et al., 2011; Prouse and Campbell, 2012)			—	—				
SP3 directly promotes expression of *AP1* , as evidenced by EMSA and ChIP-qPCR. SPL9 directly activates expression of *AP1* , as evidenced by sequence prediction and ChIP-qPCR.	(Cardon et al., 1997; Yanagisawa, 2004; Wang et al., 2009)			—	—				
LFY directely induces expression of *AP1* , as evidenced by EMSA, LFY-GR system, and CHIP-qPCR, and this site has been demonstrated to be the most functionally important LFY binding site in the *AP1* promoter.	(Weigel et al., 1992; Parcy et al., 1998; Wagner et al., 1999; William et al., 2004; Benlloch et al., 2011)			—	—				
This site is predicted based on the sequence similarity.	(Toledo-Ortiz et al., 2003)	5	bHLH	-411 — -406	CACTTG	E-box	bHLH genes	bHLH	
AP2 and SMZ directly bind to the promoter region of *AP1* and repress its expression, as evidenced by sequence prediction and ChIP-qPCR.	(Jofuku et al., 1994; Fujimoto et al., 2000; Mathieu et al., 2009; Yant et al., 2010; Dinh et al., 2012)			—	—				

PI could bind to this site, and restrict the expression of *AP1* during early stages of floral development by interacting with AP3 and other factors, as evidenced by sequence prediction and ChIP-qPCR.	(Goto and Meyerowitz, 1994; Sundstrom et al., 2006; Wuest et al., 2012)			—	—				
This site is predicted based on the sequence similarity.	(Yamaguchi et al., 2009)			—	—				
SP3 directly promotes expression of *AP1* , as evidenced by EMSA and ChIP-qPCR.	(Cardon et al., 1997; Yamaguchi et al., 2009)			—	—				
AP1 controls the onset of flowering by activating itself, as evidenced by sequence prediction and ChIP-qPCR.	(Mandel et al., 1992; Kaufmann et al., 2010; Benlloch et al., 2011)			—	—				
SPL3 directly promotes expression of *AP1* , as evidenced by EMSA and ChIP-qPCR.	(Cardon et al., 1997; Yamaguchi et al., 2009)	6	SPL3	-911 — -905	CGTACTA	GTAC box	SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE 3	SPL	
PAN mediates BOP1 and 2 to the promoter of *AP1* , as evidenced by sequence prediction and ChIP-qPCR.	(Foster et al., 1994; Chuang et al., 1999; Hepworth et al., 2005; Maier et al., 2009; Xu et al., 2010)	6	PAN	-912 — -909	ACGT	TGA binding site	PERIANTHIA	bZIP	
AP2 and SMZ directly bind to the promoter region of *AP1* and repress its expression, as evidenced by sequence prediction and ChIP-qPCR.	(Jofuku et al., 1994; Fujimoto et al., 2000; Mathieu et al., 2009; Yant et al., 2010; Dinh et al., 2012)	7	AP2/SMZ	-1486 — -1481	TTTGTT		AP2/SMZ	AP2	*AP2* is expressed in the inflorescence meristem and in all four types of floral organs. *SMZ* is expressed in hypocotyl, cotyledons, merstematic region of 7-d-old seedlings, and seeds.
		8	LFY	319 — 324	CCACTG	LFY binding site	LEAFY	LFY	*LFY* is weakly expressed in young leaves during the vegetative phase, and strongly expressed in young primordia surrounding the inflorescence apex.
This site is predicted based on the sequence similarity.	(Rushton et al., 2010)	9	WRKY	795 — 800	TTGACC	W-box	WRKY genes	WRKY	
		10	SPL3/9	851 — 856	CCGTAC	GTAC box	SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE 3/9	SPL	
This site is predicted based on the sequence similarity.	(Unte et al., 2003; Birkenbihl et al., 2005)			—	—				
		11	MYB98	1375 — 1383	TTTAACATA	MYB binding site	MYB98	R2R3-MYB	
		12	ARR1/2	3065 — 3073	TATGATTGT		*Arabidopsis* response regulators 1/2	ARR	
This site is predicted based on AthaMap.				—	—				

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Gene function	**Evidence**	References
LFY controls the production of the flowers, and activates the floral homeotic genes that specify the identity of organs in the flower.	LFY directly induces expression of *CAL* , as evidenced by LFY-GR system and CHIP-qPCR.	(Weigel et al., 1992; William et al., 2004)
	This site is predicted based on the sequence similarity.	(Rosinski and Atchley, 1998)
LMI1 is a meristem identity regulator and acts together with LFY to induce the expression of CAL. *LMI1* may also play roles in bracts and leaves.	*LMI1* directly promotes expression of CAL, as evidenced by sequence prediction and ChIP-PCR.	(Saddic et al., 2006)
	This site is predicted based on the sequence similarity.	(Foster et al., 1994; Hepworth et al., 2005; Maier et al., 2009; Xu et al., 2010)
	This site is predicted based on the sequence similarity to *AP1*.	
	This site is predicted based on the sequence similarity.	(Toledo-Ortiz et al., 2003)

	This site is predicted based on the sequence similarity to *AP1*.	
	This site is predicted based on the sequence similarity.	(Foster et al., 1994; Xu et al., 2010)
AP2 plays a central role in the establishment of the floral meristem, the specification of floral organ identity and the regulation of floral homeotic gene expression.*SMZ* is a repressor of flowering.	AP2 directly binds to the promoter region of *CAL* and represses its expression, as evidenced by sequence prediction and ChIP-qPCR.	(Jofuku et al., 1994; Fujimoto et al., 2000; Mathieu et al., 2009; Dinh et al., 2012)
LFY controls the production of the flowers, and activates the floral homeotic genes that specify the identity of organs in the flower.	This site is predicted based on the sequence similarity.	(Benlloch et al., 2011)
	This site is predicted based on the sequence similarity.	(Rushton et al., 2010)
	This site is predicted based on AthaMap.	
	This site is predicted based on AthaMap.	
	This site is predicted based on AthaMap.	