<table>
<thead>
<tr>
<th>No.</th>
<th>Name</th>
<th>Position</th>
<th>Sequence</th>
<th>Putative cis-element</th>
<th>Binding TF</th>
<th>Gene family</th>
<th>Gene expression pattern</th>
<th>Gene function</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>LFY</td>
<td>-255 — -250</td>
<td>CCACTG</td>
<td>LFY binding site</td>
<td>LEAFY</td>
<td>LEAFY</td>
<td>LFY is weakly expressed in young leaves during the vegetative phase, and strongly expressed in young primordia surrounding the inflorescence apex.</td>
<td>LFY controls the production of the flowers, and activates the floral homeotic genes that specify the identity of organs in the flower.</td>
</tr>
<tr>
<td>2</td>
<td>LFY</td>
<td>-289 — -284</td>
<td>CCAATG</td>
<td>LFY binding site</td>
<td>LEAFY</td>
<td>LEAFY</td>
<td>LFY is weakly expressed in young leaves during the vegetative phase, and strongly expressed in young primordia surrounding the inflorescence apex.</td>
<td>LFY controls the production of the flowers, and activates the floral homeotic genes that specify the identity of organs in the flower.</td>
</tr>
<tr>
<td>3</td>
<td>SPL9</td>
<td>-301 — -298</td>
<td>GTAC</td>
<td>SPL box</td>
<td>SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE 9</td>
<td>SPL</td>
<td>FLAVIN</td>
<td>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.</td>
</tr>
<tr>
<td>4</td>
<td>TCP4</td>
<td>-316 — -309</td>
<td>ATGGACCC</td>
<td>TCP binding site</td>
<td>TCP FAMILY TRANSCRIPTION FACTOR 4</td>
<td>TCP</td>
<td>TCPV is broadly expressed in stems, leaves and flowers.</td>
<td>Nag et al., (2009) found that miR319a targeting of TCP4 is critical for petal growth and development.</td>
</tr>
<tr>
<td>5</td>
<td>PAN</td>
<td>-376 — -373</td>
<td>ACCGTC</td>
<td>TLG box</td>
<td>PERIANTHIA</td>
<td>SPL</td>
<td>PANN RNA is present in the inflorescence meristem, the floral meristem, and in developing petals, stamens, and carpels.</td>
<td>PAN plays a role in the control of petal number and specification, and the regulation of floral development. It mediates BOP1 and 2 to the promoter of AP1, which activates expression of AP1 to control flower transition and patterning.</td>
</tr>
<tr>
<td>6</td>
<td>FD</td>
<td>-377 — -372</td>
<td>GACGTC</td>
<td>C-box</td>
<td>FLOWERING LOCUS D</td>
<td>SPL</td>
<td>FD is highly expressed at the shoot apex. Specifically, FD is expressed in leaf and floral anlagen. It declines when floral primordia are initiated.</td>
<td>FD could integrate temporal and spatial information that is already expressed at the shoot apex before floral induction, and promotes flowering. A complex of FT and FD proteins can activate AP1.</td>
</tr>
<tr>
<td>7</td>
<td>LMI2</td>
<td>-399 — -393</td>
<td>ACTTACC</td>
<td>R2R3 MYB box</td>
<td>LATE MERISTEM IDENTITY 2</td>
<td>R2R3 MYB</td>
<td>LMI2 is expressed throughout the shoot apical meristem of primary inflorescences, with the highest expression observed in the young flower primordia.</td>
<td>LMI2 plays a role in the meristem identity transition.</td>
</tr>
<tr>
<td>8</td>
<td>LFY</td>
<td>-419 — -414</td>
<td>CCACTG</td>
<td>LFY binding site</td>
<td>LEAFY</td>
<td>LEAFY</td>
<td>LFY is weakly expressed in young leaves during the vegetative phase, and strongly expressed in young primordia surrounding the inflorescence apex.</td>
<td>LFY controls the production of the flowers, and activates the floral homeotic genes that specify the identity of organs in the flower.</td>
</tr>
<tr>
<td>9</td>
<td>MHL2</td>
<td>-433 — -428</td>
<td>CACTGC</td>
<td>MHL box</td>
<td>MHL genes</td>
<td>MHL</td>
<td>MHL2 is expressed throughout the inflorescence meristem of primary inflorescences, with the highest expression observed in the young flower primordia.</td>
<td>MHL2 plays a role in the meristem identity transition.</td>
</tr>
<tr>
<td>10</td>
<td>AP2</td>
<td>-487 — -482</td>
<td>TGTGTT</td>
<td>E-box</td>
<td>APETALA 2 AND HAPLOIDIZE</td>
<td>AP2</td>
<td>AP2 is expressed in the inflorescence meristem and in all four types of floral organs. MAZ is expressed in hypocotyl, cotyledons, meristematic region of 7-d-old seedlings, and seeds.</td>
<td>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. MAZ is a repressor of flowering.</td>
</tr>
</tbody>
</table>
PI is expressed at inner three whorls of floral organs at stage 5. Its expression is the whorl 4 region disappeared 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 API.

P.1

Supplemental References


Cardon GH, Hohmann S, Nettesheim K, Saedler H, Huijser P

Kramer EM, Dorit RL, Irish VF

Jofuku KD, Denboer BGW, Vanmontagu M, Okamuro JK

Foster R, Izawa T, Chua NH

Hepworth SR, Zhang YL, McKim S, Li X, Haughn G

Dinh TT, Girke T, Liu X, Yant L, Schmid M, Chen X

Goto K, Meyerowitz EM

Chuang CF, Running MP, Williams RW, Meyerowitz EM


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 petal organ number specification, and the regulation of floral determinacy. It mediates BOP1 and 2 to the promoter of API, which activates expression of API to control floral transition and patterning.

API plays the role in the establishment of the floral meristem, the specification of floral organ identity and the regulation of floral homeotic gene expression. API is required for proper development of epidermal tissues.

SPL8 is highly expressed in vegetative growth and highly expressed in inflorescences formed after the floral transition. It is also expressed in the developing petals, leaves of the anthers, the placental region of the developing gynoecium, and the margins of the petals.

SPL6 is expressed in vegetative and inflorescence apical meristems, floral meristems, leaf and flower organ primordia, and in meristem stem tissues. SPL6 controls the timing of flower formation.

SPL5 is expressed in vegetative and inflorescence apical meristems, floral meristems, leaf and flower organ primordia, and in meristem stem tissues. SPL5 controls the timing of flower formation.

SPL4/7 is expressed in hypophyll, cotyledons, meristematic region of 7-8-old seedlings, and seeds.

SPL3 is expressed in young floral primordia, sepals, petals, and carpels. SPL3 plays role in the formation of floral meristem, and specification of sepals and petals.

SPL2 is expressed in the inflorescence meristem, the floral meristem, and in developing petals, stamens, and carpels. SPL2 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. SPL2 is required for proper development of epidermal tissues.

SPL1 is expressed in vegetative and inflorescence apical meristems, floral meristems, leaf and flower organ primordia, and in meristem stem tissues. SPL1 controls the timing of flower formation.

SPL0 is expressed in vegetative and inflorescence apical meristems, floral meristems, leaf and flower organ primordia, and in meristem stem tissues. SPL0 controls the timing of flower formation.

SPL-7

SPL-8

SPL-3

SPL-2

SPL-1

SPL-0

SPL-9

SPL-10

SPL-11

SPL-12

Supplementary References


<table>
<thead>
<tr>
<th>Evidence References</th>
<th>No.</th>
<th>Name</th>
<th>Position</th>
<th>Sequence</th>
<th>Putative cis - element</th>
<th>Binding TF</th>
<th>Gene family</th>
<th>Gene expression pattern</th>
</tr>
</thead>
<tbody>
<tr>
<td>LFY directly induces expression of AP1, as evidenced by EMBSA, LFY-GR system, Wagner et al., 1999; William et al., 2004; Bennett et al., 2011; Winter et al., 2011</td>
<td>1</td>
<td>LFY</td>
<td>-231 — -226</td>
<td>CCAATG</td>
<td>LFY binding site</td>
<td>LEAFY</td>
<td>LFY</td>
<td>LFY is weakly expressed in young leaves during the vegetative phase, and strongly expressed in young primordia surrounding the inflorescence axis.</td>
</tr>
<tr>
<td>LFY directly induces expression of AP1, as evidenced by EMBSA, LFY-GR system, Wagner et al., 1999; William et al., 2004; Bennett et al., 2011; Winter et al., 2011</td>
<td>2</td>
<td>MYB</td>
<td>-252 — -247</td>
<td>GGCAAT</td>
<td>MYB binding site</td>
<td>MYB</td>
<td>MYB genes</td>
<td>MYB</td>
</tr>
<tr>
<td>TCP1 could bind to the DNA sequence TGATCC, as revealed by EMBSA. The putative TCP1 binding site is predicted based on the sequence similarity.</td>
<td>3</td>
<td>LMI1</td>
<td>-326 — -318</td>
<td>CAATTATTG</td>
<td>HD-Zip binding site</td>
<td>LATE MERISTEM IDENTITY 1</td>
<td>HD-Zip</td>
<td>LMI1 is expressed in leaves of young seedlings during the vegetative stage, strongly expressed in the incipient flower primordia, and developing flowers.</td>
</tr>
<tr>
<td>PAN interacts with BOP1 and 2 to the promoter of AP1, as evidenced by sequence prediction and ChIP-qPCR.</td>
<td>4</td>
<td>PAN</td>
<td>-337 — -334</td>
<td>ACGT</td>
<td>TGA binding site</td>
<td>PERIANTHIA</td>
<td>bZIP</td>
<td></td>
</tr>
<tr>
<td>SP1 directly activates AP1, as evidenced by sequence prediction and ChIP-qPCR.</td>
<td>5</td>
<td>bHLH</td>
<td>-411 — -406</td>
<td>CACTTG</td>
<td>E-box</td>
<td>bHLH genes</td>
<td>bHLH</td>
<td></td>
</tr>
</tbody>
</table>

Note: The table entries are based on the provided information, which includes references to various studies. The gene family and expression patterns are highlighted for clarity.
PI could bind to this site, and restrict the expression of AP1 during early stages of floral development by interacting with AP1 and other factors, as evidenced by sequence prediction and ChIP-qPCR. (Eisen and Meyerson, 1994; Sundstrom et al., 2000; Wienecke et al., 2012)

This site is predicted based on the sequence similarity. (Yamaguchi et al., 2009)

<table>
<thead>
<tr>
<th>Site</th>
<th>Location</th>
<th>Sequence</th>
<th>Gene Product</th>
<th>Refs</th>
</tr>
</thead>
<tbody>
<tr>
<td>SPL3</td>
<td>-911—-905</td>
<td>GTGACTA</td>
<td>SPL</td>
<td>Goto and Meyerowitz, 1994; Sundstrom et al., 2006; Wuest et al., 2012</td>
</tr>
<tr>
<td>AP1</td>
<td>-912—-909</td>
<td>ACUT</td>
<td>SPLA1</td>
<td>Cardon et al., 1997; Yamaguchi et al., 2009</td>
</tr>
<tr>
<td>AP1</td>
<td>-1486—-1481</td>
<td>TTGTT</td>
<td>AP2/SMZ</td>
<td>Jofuku et al., 1994; Fujimoto et al., 2000; Mathieu et al., 2009; Yant et al., 2010; Dinh et al., 2012</td>
</tr>
<tr>
<td>LFY</td>
<td>319—324</td>
<td>CCACTG</td>
<td>LFY</td>
<td>Foster et al., 1994; Chuang et al., 1999; Hepworth et al., 2005; Maier et al., 2009; Xu et al., 2010</td>
</tr>
<tr>
<td>WRKY</td>
<td>795—800</td>
<td>TTGGACCC</td>
<td>W-box</td>
<td>Raschid et al., 2010</td>
</tr>
<tr>
<td>SPL3/9</td>
<td>851—856</td>
<td>CCCTAC</td>
<td>SPLA1</td>
<td>Unte et al., 2003; Birkenbihl et al., 2005</td>
</tr>
<tr>
<td>MYB8</td>
<td>1375—1383</td>
<td>TTTACATA</td>
<td>MYB binding site</td>
<td>Ume et al., 2003; Britschiger et al., 2005</td>
</tr>
<tr>
<td>ARR1/2</td>
<td>3065—3073</td>
<td>TATGATTGT</td>
<td>ARR</td>
<td>Arabidopsis response regulators 1/2</td>
</tr>
</tbody>
</table>

This site is predicted based on the sequence similarity. (Raschid et al., 2010)

This site is predicted based on the sequence similarity. (Unte et al., 2003; Britschiger et al., 2005)

This site is predicted based on AthaMap.

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; Benitez et al., 2011)

SPL3 directly promotes expression of AP1, as evidenced by EMSA and ChIP-qPCR. (Cardon et al., 1997; Yamaguchi et al., 2009)

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)

PAN mediates BOP1 and 2 to the promoter of AP1, as evidenced by sequence prediction and ChIP-qPCR. (Towe et al., 1996; Chuang et al., 1999; Hepworth et al., 2005; Mair et al., 2009; Xia et al., 2010)

AP2/SMZ AP2

AP2 is expressed in the inflorescence meristem and in all four types of floral organs. SMZ is expressed in hypocotyl, cotyledons, meristematic region of 7-d-old seedlings, and seeds.

LFY is weakly expressed in young leaves during the vegetative phase, and strongly expressed in young primordia surrounding the inflorescence apex.
Development 136: 1613-1620.

Development 136: 3189-3198.

Development 133: 1673–1682.

Plant J 59: 987–1000.

6–41.

Dev Cell 20: 430-443.


2156-2170.

**Gene function**

- **LFY** controls the production of the flowers, and activates the floral homeotic genes that specify the identity of organs in the flower.
- **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.

**Evidence**

- LFY directly induces expression of CAL, as evidenced by LFY-GR system and CHIP-qPCR. ([Weigel et al., 1992; William et al., 2004])
- 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. ([Rosinski and Atchley, 1998])
- 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. ([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 to AP2.

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.

(Foster et al., 1994; Xu et al., 2010)

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.

(Jofuku et al., 1994; Fujimoto et al., 2000; Mathieu et al., 2009; Dinh et al., 2012)

This site is predicted based on AthaMap.