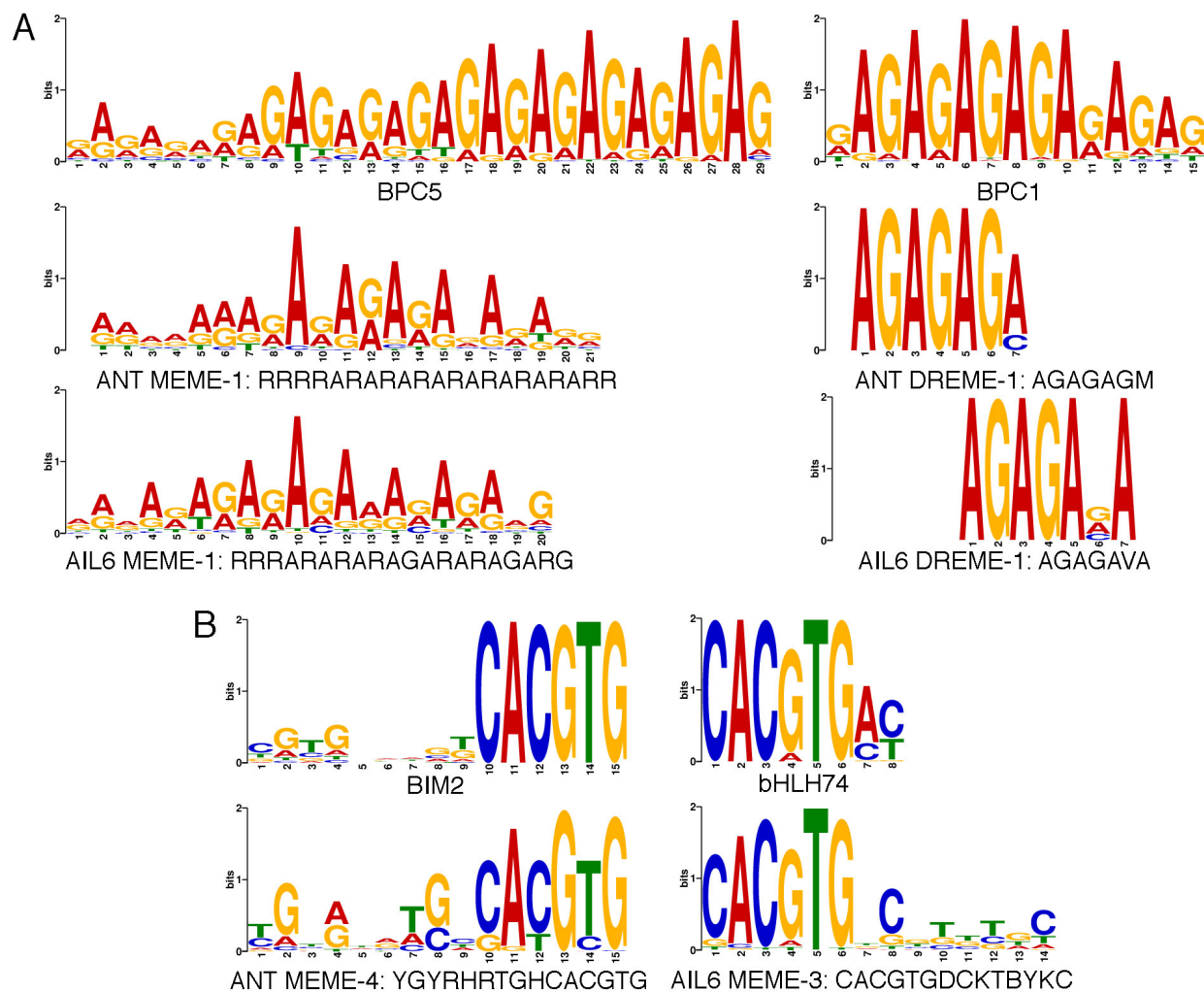
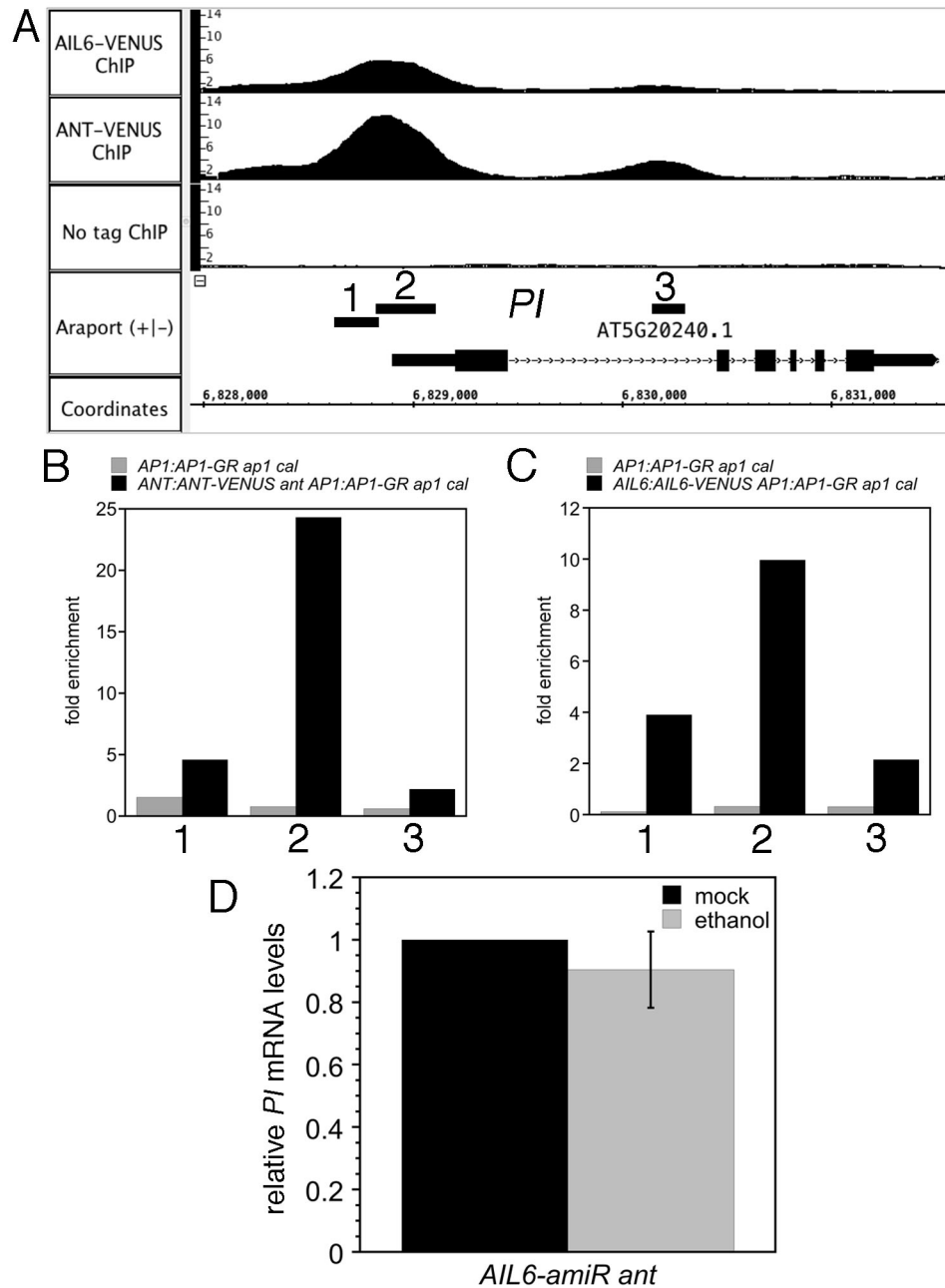


Supplementary Figures and Tables

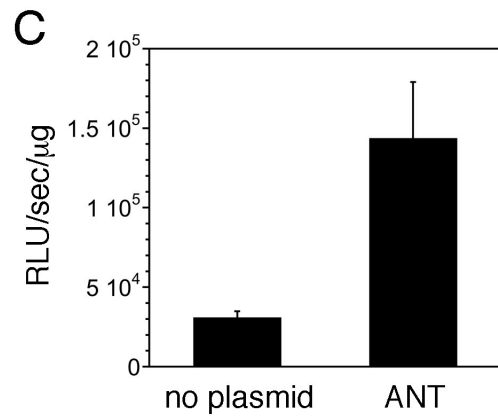
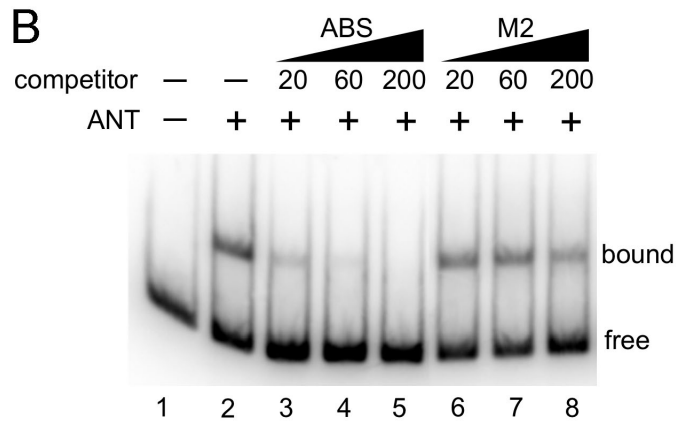


**Supplementary Figure S1. DNA motifs with similarity to BBR/BPC and bHLH binding motifs are over-represented in ANT and AIL6 ChIP-Seq binding peaks.** A. Sequence logos for the BPC5 and BPC1 binding motifs and motifs overrepresented in ANT binding peaks (ANT MEME-1 and ANT DREME-1) and AIL6 binding peaks (AIL6 MEME-1 and AIL6 DREME-1) that have similarity to the BPC motif. B. Sequence logos for the BIM2 and bHLH74 binding motifs and motifs overrepresented in ANT binding peaks (ANT MEME-4) and AIL6 binding peaks (AIL6 MEME-3) that have similarity to the bHLH motifs.

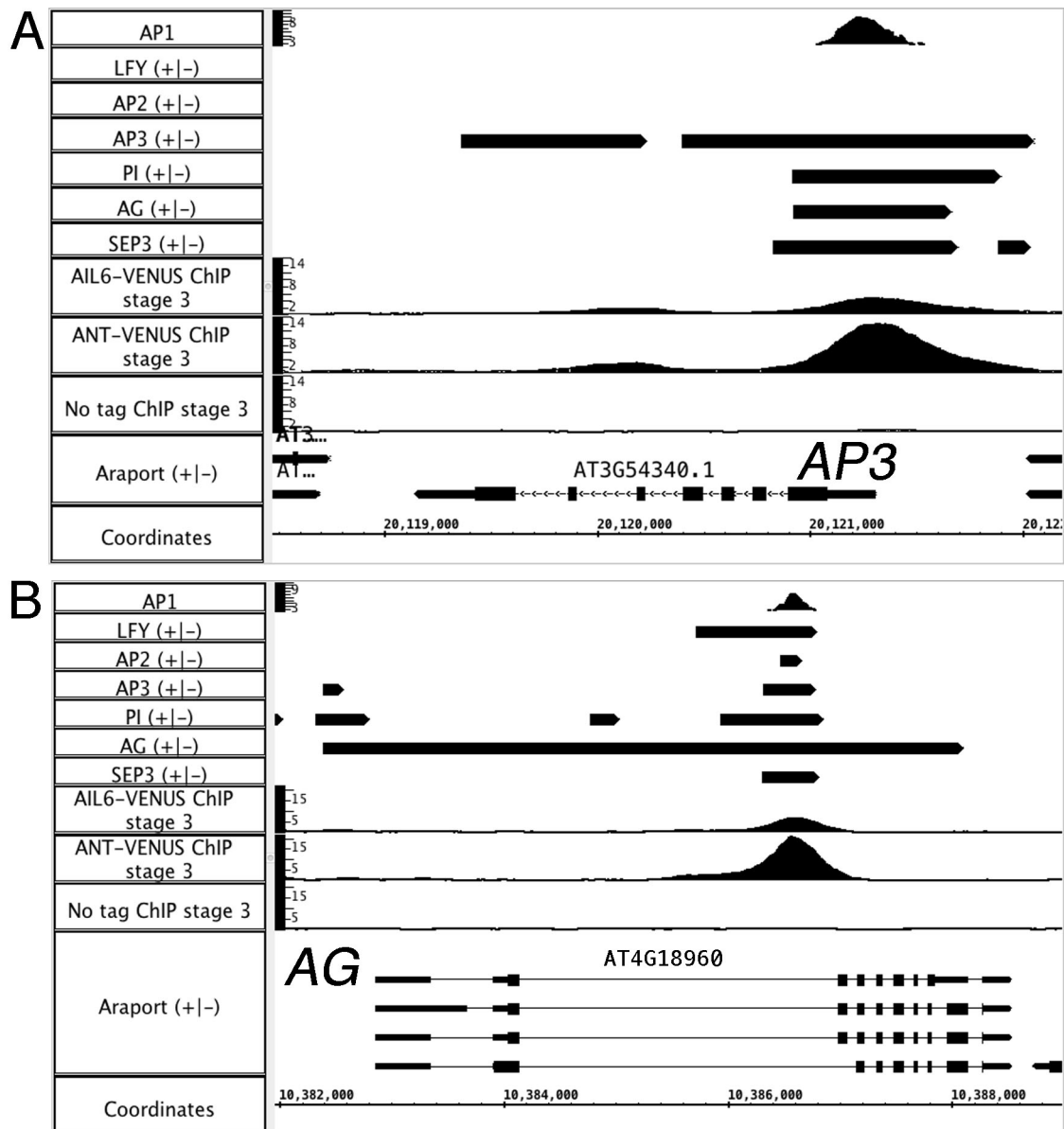


**Supplementary Figure S2. ANT and AIL6 bind directly to regulatory regions associated with the floral organ identity gene *PI*, but *PI* expression is not altered after downregulation of *AIL6* expression in *35S:ALCR/AlcA:AIL6-amiR ant* inflorescences.** A. ChIP-Seq of ANT and AIL6 binding to *PI* genomic region. 1, 2, and 3 are genomic regions tested for binding using ChIP-qPCR in B and C. B. ChIP-qPCR of ANT binding to *PI* genomic region 2. C. ChIP-qPCR of AIL6 binding to *PI* genomic region 2. D. Expression of *PI* is not reduced in *35S:ALCR/AlcA:AIL6-amiR ant* inflorescences after an eight-hour ethanol treatment.

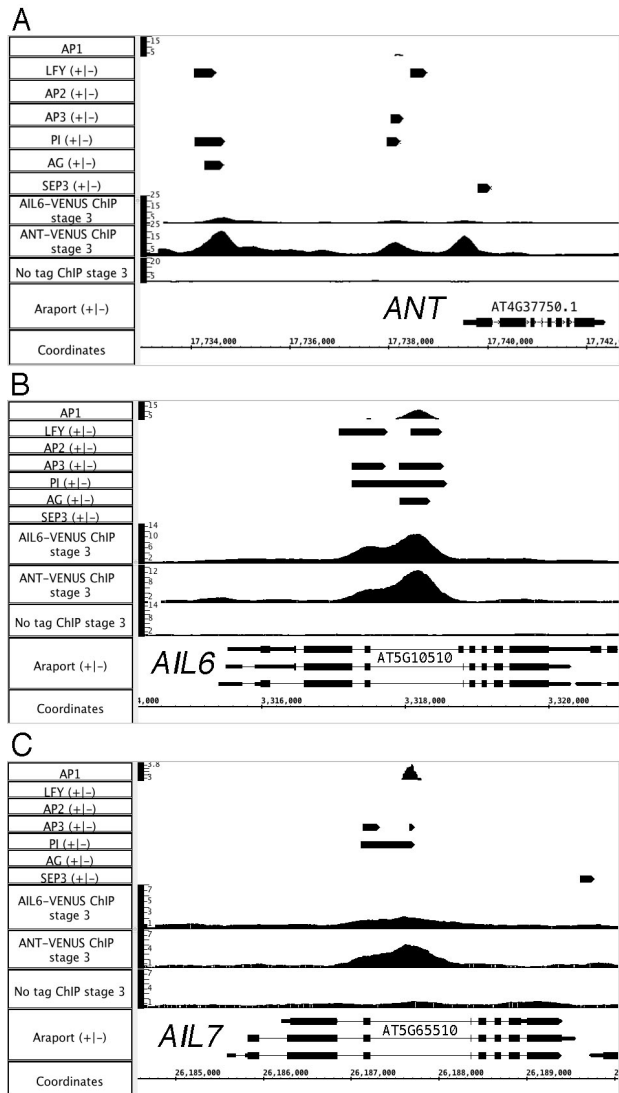
**A** 10,368,485 10,368,557  
 CAGGAAACTCAAGAAAAAAGAATAAATGGTAAATTTAATTATATTCCAAATAAGGAAAAGTATGGAACGTTGTG



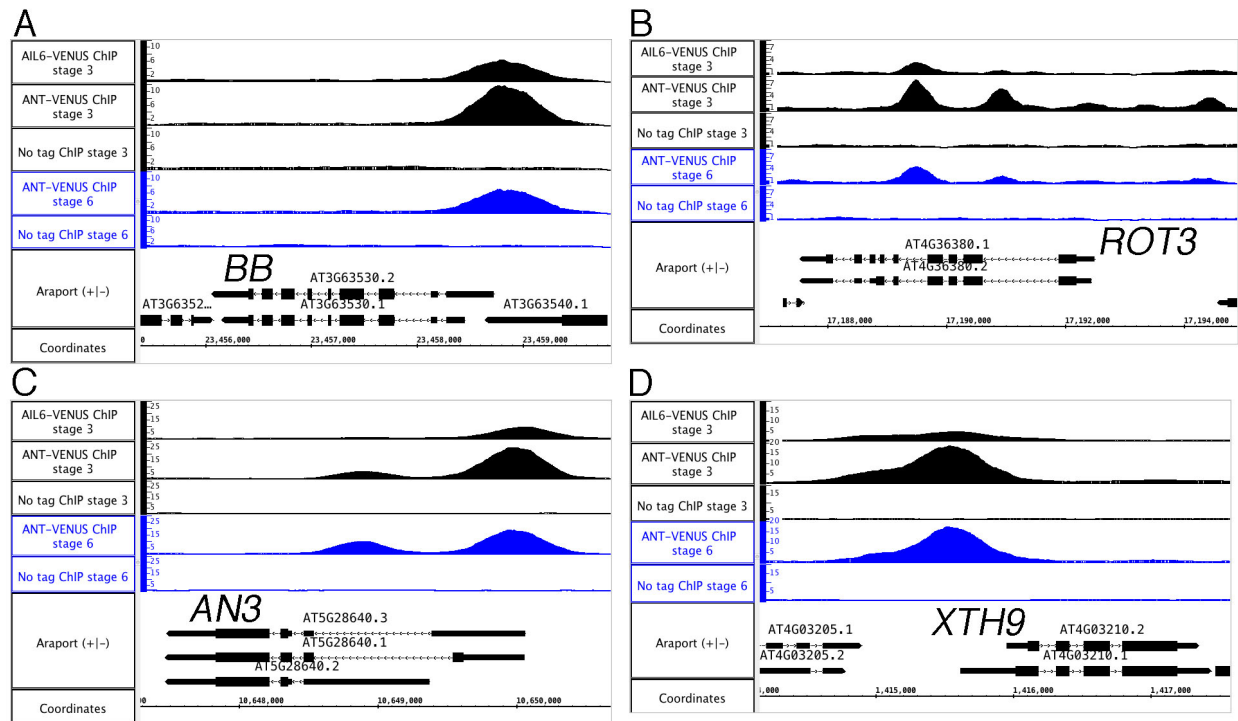
**Supplementary Figure S3. ANT binds to the *AG* intron *in vitro* and can activate transcription through this binding site in yeast.** A. Two overlapping sequence within the *AG* intron (genomic coordinates 10,368,485-10,368,557) with weak similarity to the ANT binding motif. One motif is shown in red and the other motif is highlighted in yellow. A central GGAA (reverse complement TTCC) in these two motifs is underlined. An overlapping CArG box is shown in bold type. LFY binding sites are located at 10,368,608-10,368,614 and 10,368,655-10,368,661. WUS binding sites are located at 10,368,603-10,368,609 and 10,368,663-10,368,669. B. Gel mobility shift of ANT binding to a probe corresponding to the *AG* intron sequence shown in A. The binding is competed away by addition of the consensus ANT binding site (ABS) but not by addition of a mutated version of this site (M2) (Nole-Wilson and Krizek, 2000). C. ANT can activate transcription in a yeast strain containing the *lacZ* reporter gene under the control of this *AG* intron sequence and the TATA portion of the *CYC1* gene.



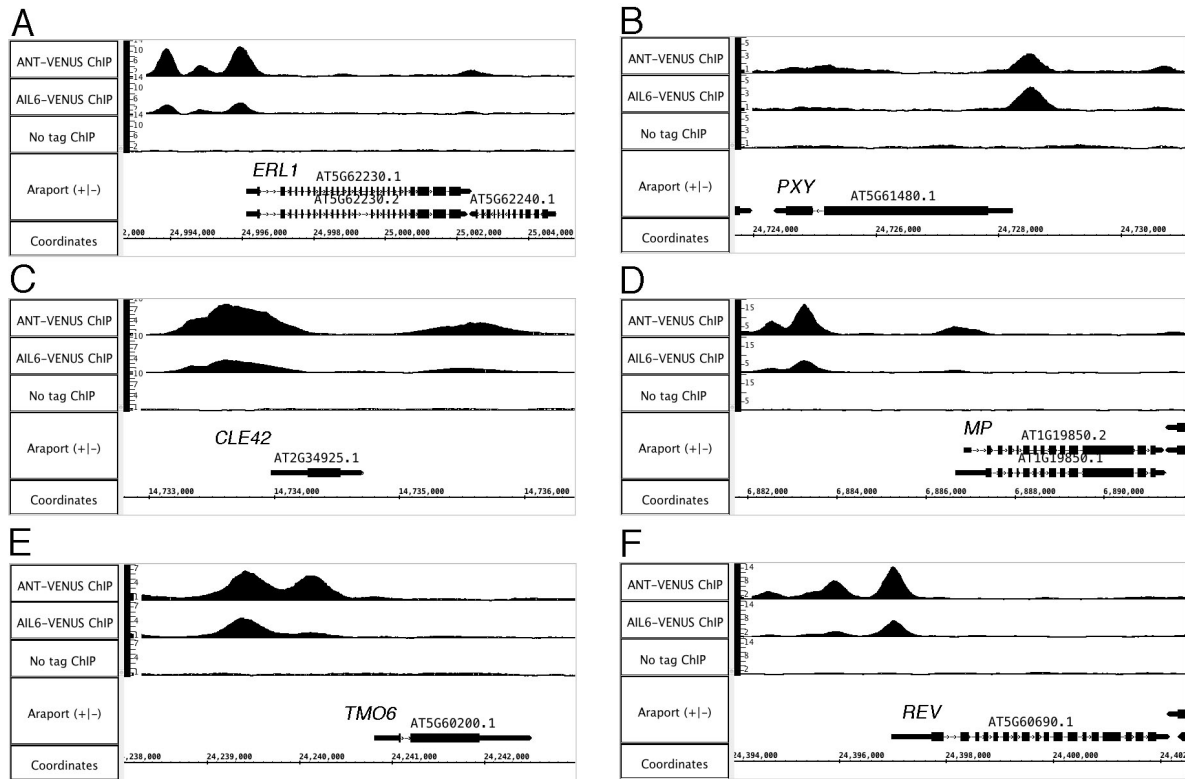
**Supplementary Figure S4. ANT and AIL6 binding peaks within *AP3* and *AG* regulatory regions overlap those of other floral regulators.** A. ANT and AIL6 binding peaks overlap those of AP1, AP3, PI, AG and SEP3 in the *AP3* promoter. B. ANT and AIL6 binding peaks overlap those of LFY, AP1, AP2, AP3, PI, AG and SEP3 in the *AG* intron.



**Supplementary Figure S5. ANT and AIL6 binding peaks within *ANT*, *AIL6* and *AIL7* regulatory regions overlap those of other floral regulators.** A. ANT and AIL6 binding peaks overlap those of LFY, AP1, AP3, PI, and AG in the *ANT* promoter. B. ANT and AIL6 binding peaks overlap those of LFY, AP1, AP3, PI, and AG in the *AIL6* intron. C. ANT and AIL6 binding peaks overlap those of AP1, AP3, and PI in the *AIL7* intron.



**Supplementary Figure S6. ANT and AIL6 ChIP-Seq binding peaks in *BB*, *ROT3*, *AN3* and *XTH9* genomic regions.** A. Binding of ANT and AIL6 in stage 3 flowers and ANT in stage 6/7 flowers to a region near the TSS of *BB*. B. Binding of ANT and AIL6 in stage 3 flowers and ANT in stage 6/7 flowers to regions inside *ROT3*. C. Binding of ANT and AIL6 in stage 3 flowers and ANT in stage 6/7 flowers to a region overlapping the TSS of *AN3*. D. Binding of ANT and AIL6 in stage 3 flowers and ANT in stage 6/7 flowers to a region near the TSS of *XTH9*.



**Supplementary Figure S7. ANT and AIL6 ChIP-Seq binding peaks in *ERL1*, *PXY*, *CLE42*, *MP*, *TMO6*, and *REV* genomic regions.** A. Binding of ANT and AIL6 in stage 3 flowers to regions upstream and near the TSS of *ERL1*. B. Binding of ANT and AIL6 in stage 3 flowers to region upstream of *PXY*. C. Binding of ANT and AIL6 in stage 3 flowers to a region upstream of *CLE42*. D. Binding of ANT and AIL6 in stage 3 flowers to a region upstream of *MP*. D. Binding of ANT and AIL6 in stage 3 flowers to a region upstream of *MP*. E. Binding of ANT and AIL6 in stage 3 flowers to a region upstream of *TMO6*. F. Binding of ANT and AIL6 in stage 3 flowers to a region near the TSS of *REV*.

**Supplementary Table S1. Primers used in this study**

| <b>ChIP-qPCR primers</b> | <b>Primer sequence (5' to 3')</b>                                     |
|--------------------------|---|
| <i>AP3</i>               |   |
| fragment 1               | AP3 Pro7: CGATCATACGGCTGGGTGAT<br>AP3 Pro8: AAGGCATTCCCCGTATCTGC      |
| fragment 2               | AP3 Pro3: TGATTTGATGGACTGTTTGGAG<br>AP3 Pro4: TTTGGATTAATCGTCACTTCCA  |
| fragment 3               | AP3 Pro5: CATCGATGTCCGTTGATTTA<br>AP3 Pro6: TTTGGTGGAGAGGACAAGAGA     |
| <i>AG</i>                |   |
| fragment 1               | AG INT-1: AGAGAGTCCCACGTGATTACTT<br>AG INT-2: AATCTTGCGCTCAATTCCAACC  |
| fragment 2               | AG INT-5: TGGGTACTGAGAGGAAAGTGAG<br>AG INT-6: TGGTCTGAACATGTCTAGGGTT  |
| fragment 3               | AG A3F: AGACCAAACCGCTCTCCAGT<br>AG A3R: TTGCTTGCTCAACCCAATTC          |
| <i>PI</i>                |   |
| fragment 1               | PI Pro1: GCTAAATAAAAGTTTGACCACATTC<br>PI Pro2: CACTCTTTGCATGTGATTGATG |
| fragment 2               | PI Pro3: TGCAAAGAGTGTTCAATTAAGCAA<br>PI Pro4: GAACAAGAAGAGGAGCATTGGT  |
| fragment 3               | PI I-1: AGGGTAATAAGCATAACAGAGGC<br>PI I-2: GCATATAACACACACACACACTG    |
| <b>RT-qPCR primers</b>   |   |
| <i>AIL6</i>              | RTAIL6-4: CGAGTTGCTGGGAACAAAG<br>RTAIL6-5: TCATACGCTTCAGCTGCTTC       |
| <i>AP3</i>               | AP3-F: CGAATGCAAGAAACCAAGAGG<br>AP3-R: GAATGTCAAGCTCGTCCAAC           |
| <i>AG</i>                | AG-F: GTTCTTTGTGATGCTGAAGTCG<br>AG-R: TGTACCTCTCAATAGTCCCTTTTAC       |
| <i>PI</i>                | PI-F: AATGAGAAGATGATGGCGGAG<br>PI-R: CATTCTCTTGCGTTGCTTG              |
| <i>ANT</i>               | RTANT-7: AAGGAAGAGCAGTGGTTTCTC<br>RTANT-8: ACTCTACCAATCCGTGCTTG       |
| <i>BB</i>                | BB-F: AAATCGGAGACACAGATGAGC<br>BB-R: GATCAATGTCATCTTGCCAGG            |
| <i>AN3</i>               | AN3-RT1: CCAAGTGTGCATAGCCAGTA<br>AN3-RT2: GTTGCTGTTGAGTCGCTTG         |
| <i>XTH9</i>              | XTH9-F: TGGGCTATGGATCATTGTGTC<br>XTH9-R: TGATTCAAACCCAGCTCCAG         |
| <i>ERL1</i>              | ERL1-F: GTTCATGTGCAGCCTTGAATC<br>ERL1-R: CAGATAAGTCAAGCTCCCGAG        |
| <i>PXY</i>               | PXY-F: AAGCCAAAGAGGAAGACAGTAG<br>PXY-R: ACCAACATCAACACTACAAACATC      |
| <i>CLE42</i>             | CLE42-F: GAGAGGTTTAGAGTTCGGCG   |



|                        |  |
|------------------------|--|
|                        | CLE42-R: TGGGACTCCATGTTTCATTGG               |
| <i>TMO6</i>            | TMO6-F: AAGCCAAAGAGGAAGACAGTAG               |
|                        | TMO6-R: ACCAACATCAACACTACAAACATC             |
| <i>REV</i>             | REV-F: GCTTAGAGATGCGAATAGTCCTG               |
|                        | REV-R: CAGTTCCTGTAGCCTTGGATAG                |
| <i>MP</i>              | MP-F: CTTCTCACAAGGTCATAGCGAG                 |
|                        | MP-R: AACTGAGATGGAAGGTTCCGG                  |
| <i>AT5G15710</i>       | RTFbox-1: TTTCGGCTGAGAGGTTTCGAGT             |
|                        | RTFbox-2: GATTCCAAGACGTAAAGCAGATCAA          |
| <b>Cloning primers</b> |  |
| <i>ANT-IR</i>          | ANTIR-5: CTCGAGGGATCCATGAAGTCTTTTTGTGATAATG  |
|                        | ANTIR-6: GGTACCATCGATTTCGTCTCAAACCCAACGCTTGT |