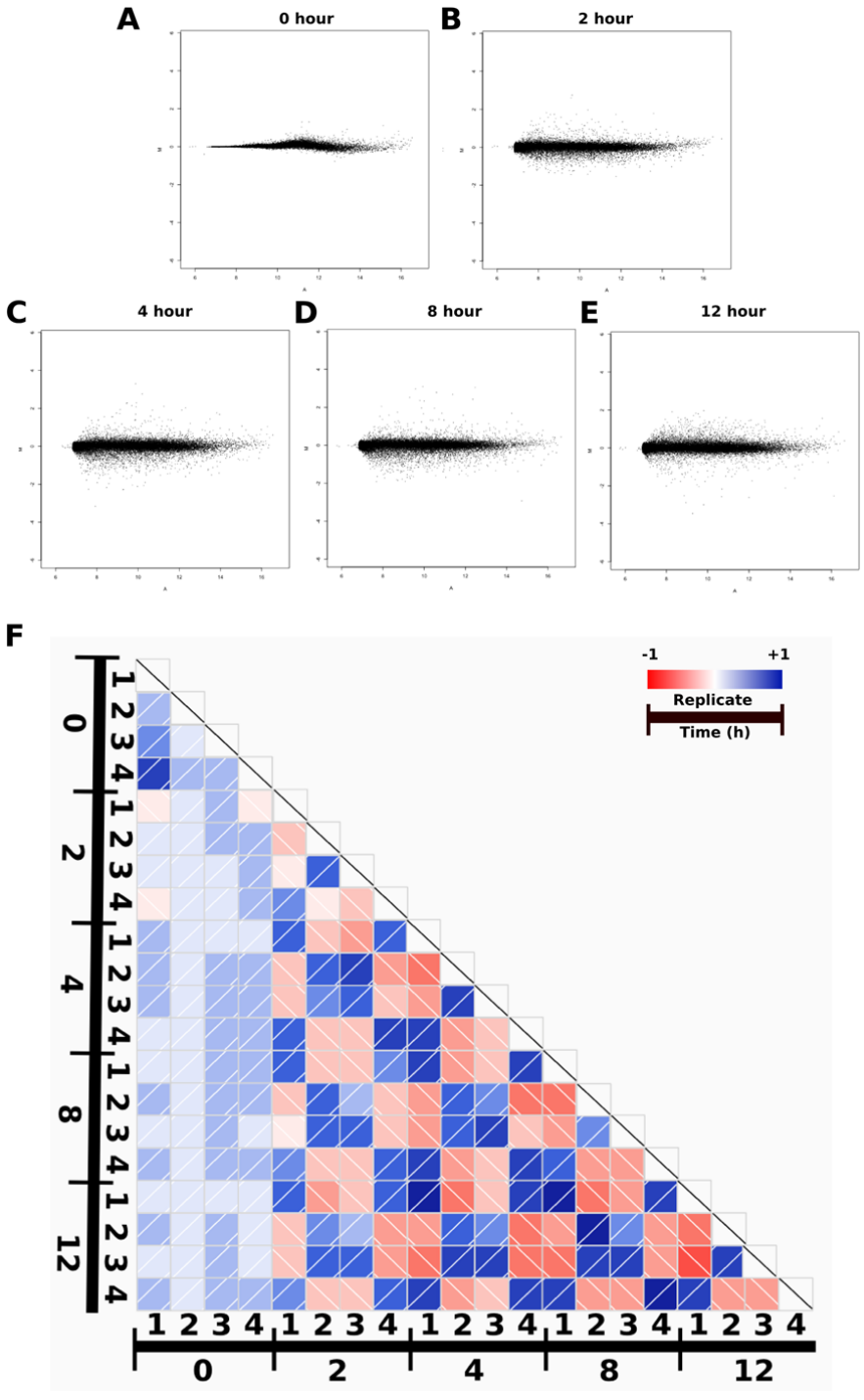
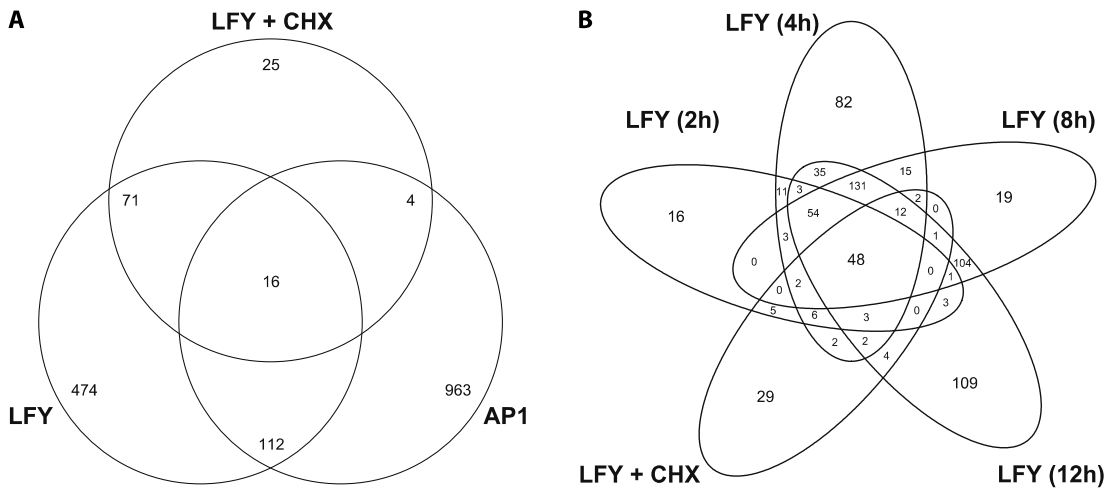
Supplemental Figures



Supplemental Figure S1: Microarray analysis of LFY-GR time-course experiment.

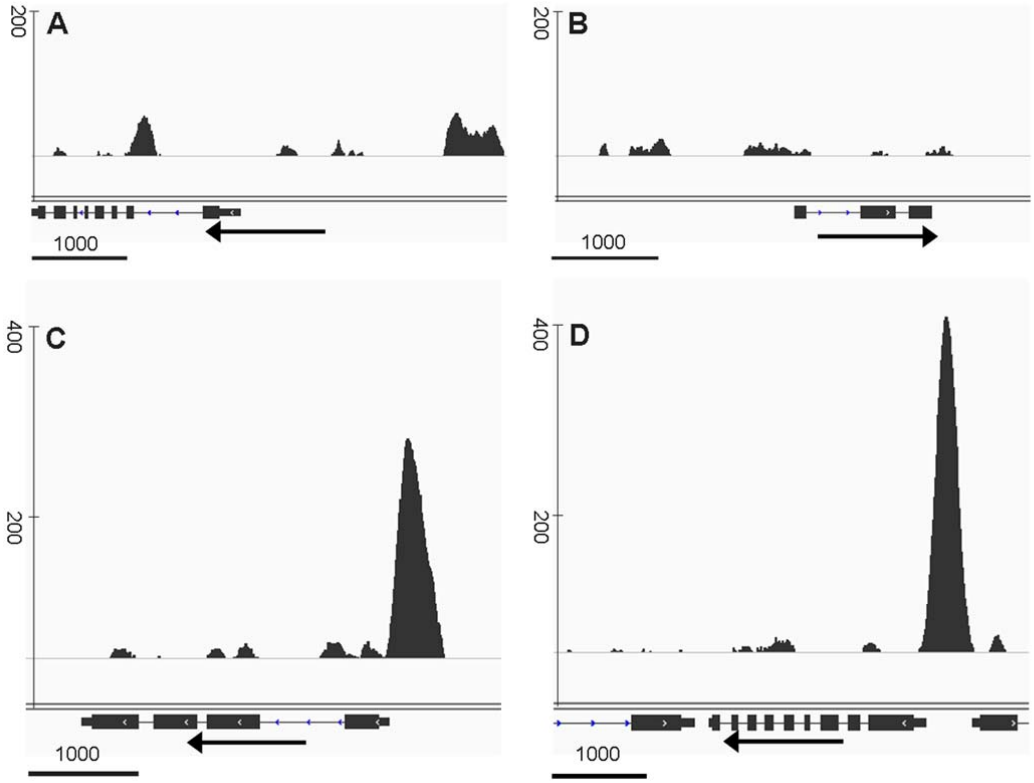
(**A-E**) MA plots for each time-point (as indicated) of the p35S:LFY-GR *ap1 cal* time-course experiment. (**F**) Correlelogram indicating correlation between M-values from the different

replicate experiments for each time-point. Due to dye-swaps being conducted for replicate experiments, both positive and negative correlation values were obtained. Slashed boxes at the end of each row indicate self/self comparisons.



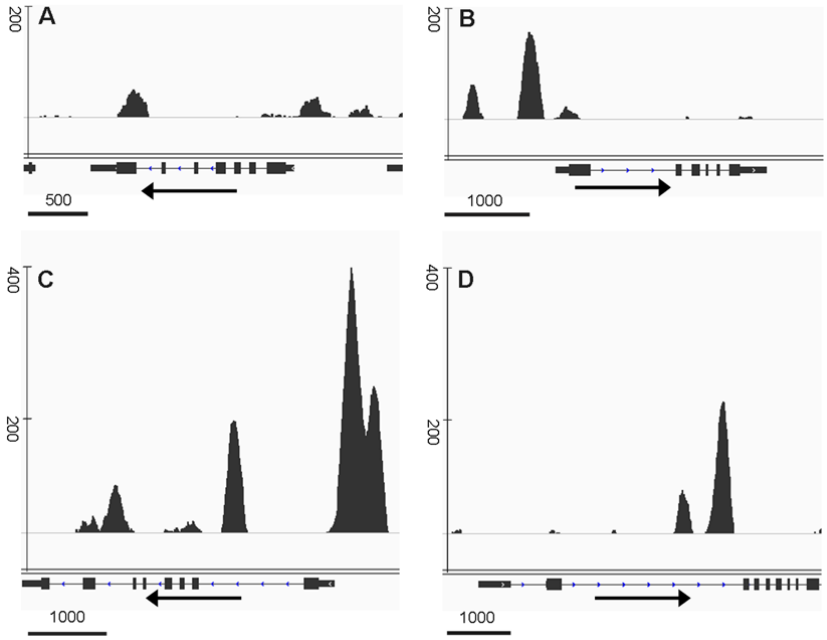
Supplemental Figure S2: Activation of LFY-GR in the presence of cycloheximide.

(**A**) Overlap between DEGs identified in the p35S:LFY-GR *ap1 cal* (LFY) and p35S:AP1-GR *ap1 cal* (AP1) time-course experiments, and the p35S:LFY-GR *ap1 cal* experiment where LFY-GR was activated in the presence of cycloheximide (LFY+CHX). (**B**) Overlap between DEGs identified in each time-point (as indicated) of the p35S:LFY-GR *ap1 cal* (LFY) time-course experiment, and the p35S:LFY-GR *ap1 cal* experiment where LFY-GR was activated in the presence of cycloheximide (LFY+CHX).



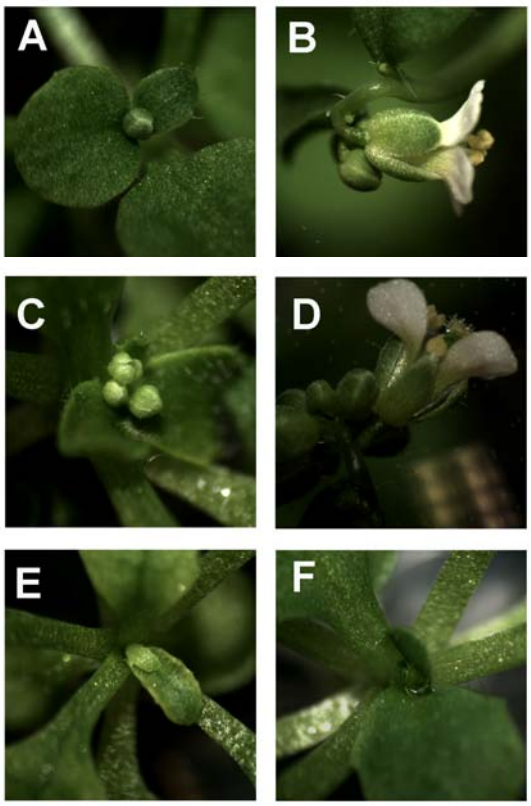
Supplemental Figure S3: ChIP-seq results for known LFY target genes.

Using a LFY-specific antiserum, ChIP-seq experiments were conducted with p35S:LFY-GR *ap1 cal* plants 4 h after treatment with a dexamethasone-containing solution. Results for (**A**) *SEP3*, (**B**) *LMI1*, (**C**) *ELA1*, and (**D**) *LMI5* are shown. Scale bars indicate sequence lengths (in base pairs), and arrows indicate gene orientations.



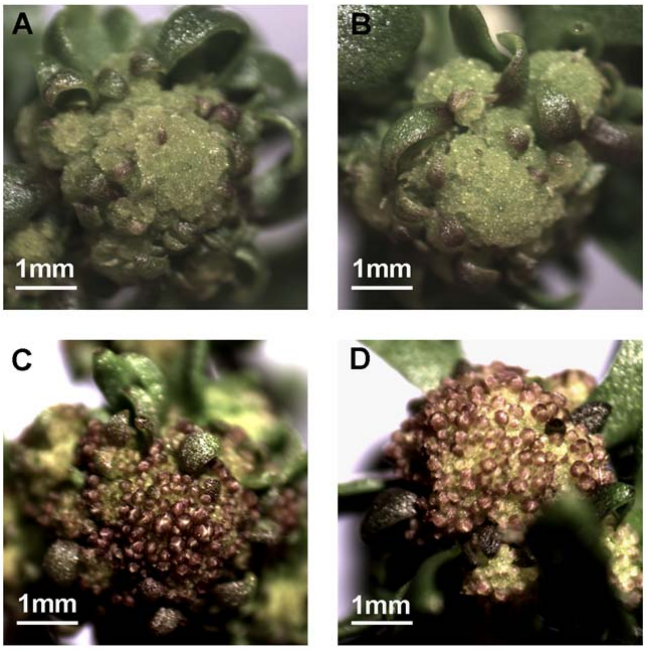
Supplemental Figure S4: ChIP-seq results for floral organ identity genes.

Using a LFY-specific antiserum, ChIP-seq experiments were conducted with p35S:LFY-GR *ap1 cal* plants 4 h after treatment with a dexamethasone-containing solution. Results for (**A**) *AP3*, (**B**) *PI*, (**C**) *AP1*, and (**D**) *AG* are shown. Scale bars indicate sequence lengths (in base pairs), and arrows indicate gene orientations.



Supplemental Figure S5: Flowering after LFY-GR activation in wild-type and *ap1 cal* double-mutant plants.

Seeds of different genotypes were germinated on plates with a medium containing 50 nM dexamethasone. (**A**, **B**) Wild type. (**C**, **D**) p35S:LFY-GR. (**E**, **F**) p35S:LFY-GR *ap1 cal*. Representative images of approximately 5 week-old plants selected from three independent experiments are shown. Note the absence of inflorescences in panels E and F.



Supplemental Figure S6: Activation of AP1 rescues the late flowering phenotype of *ap1 cal* plants observed after LFY-GR activation.

Ap1 cal plants carrying the p35S:LFY-GR transgene as well as a construct that mediates expression of a fusion between AP1 and the hormone binding domain of the androgen receptor (AR) from the AP1 promoter (pAP1:AP1-AR; O'Maoileidigh et al., 2015) were treated with the following solutions: **(A)** A mock solution (containing no steroid hormones). **(B)** A solution containing 10 µM dexamethasone (to activate LFY-GR). **(C)** A solution containing 500 µM dihydrotestosterone (to activate AP1-AR). **(D)** A solution containing 10 µM dexamethasone and 500 µM dihydrotestosterone (to activate both LFY-GR and AP1-AR). Images were taken 6 d after the treatments. Note the formation of (brownish; most likely caused by anthocyanin accumulation) floral buds in panels C and D.

Supplemental Tables

Supplemental Table S1: **Differentially expressed genes identified in the p35S:LFY-GR *ap1 cal* time-course experiment.**

For each time-point, the number of differentially expressed genes (No. DEGs), and the numbers of genes that were up- or down-regulated relative to mock-treated control plants are shown.

Time-point [h]	**0**	**2**	**4**	**8**	**12**
No. DEGs	0	202	465	456	537
Up-regulated	0	63	114	120	134
Down-regulated	0	139	351	336	403

Supplemental Table S2: Primers used for PCR genotyping and the generation of constructs.

Primer names and sequences are shown.

Primer Name	**Sequence (5'->3')**
DM400	TCCGACAAGATCCTTTGAGCAC
DM494	AGTACATTAAAAACGTCCGCAATGTG
KG2	CCTCGTCTCTCTATTTGGTATGTTC
KG14	TAATTCAGAGGAGACAAACAGCAT
LR177	CGTCATATGGGAGGTAGTGGTTTGGGG
LR178	CGGGATCCCTAGAAACGCAAGTCGTCGC

Supplemental Table S3: Primers used for qRT-PCR analysis.

Gene identifiers ('AGI'), gene aliases and primer sequences are shown.

AGI	Alias	Forward Primer (5'->3')	Reverse Primer (5'->3')
At4g36920	AP2	GGAATCCTACTACTCCACAAGATCACAA	GGTTCATCCTGAGCCGCATA
At4g35900	FD	GCCAAGATTCCAATGAAGGTTCAGG	AAGTGAGCAACTTCAAGTTCTAACTCGTT
At5g03790	LMI1	CACGTCAGATAGCAGTTTGGTTCC	CCCTGGTCTCTTAGTAAAGCTCTC
At5g03840	TFL1	TCCTTCTTCTGTTTCCTCCAAG	ACATCTGGGTCTATCATCACCA
At1g13320	REF1	AAGCGGTTGTGGAGAACATGATACG	TGGAGAGCTTGATTTGCGAAATACCG

Supplemental Table S4: Primers used for ChIP-qPCR analysis.

Gene identifiers ('AGI'), gene aliases and primer sequences are shown.

AGI	Alias	Forward Primer (5'->3')	Reverse Primer (5'->3')
At1g69120	AP1	GGAAATCTCCGCCGTCAAT	TGGTCCTTCCCCAAGTGTCA
At5g03840	TFL1	CGAAGCCGCAAACCTGGTG	AGAGTCGTTCTAAACCGAAGTATGG
At1g16070	LMI5/TLP8	GTGTCTTTGGTTCTGTGCTCG	CAGGTGTTTGACAATGGTACTGAG
At4g21870	-	CCACATGAACCATTTGAGCAAGTTGC	CGTGAGTGAGTCGACACAATTCGTGAGTGAGTCGACACAATTGTTGGCGTGAGTGAGTCGACACAATTGTTGG
At3g05220	-	GGTCAAGGTGGTCCGATGGGTATG	GCAAGCCTTGAACCGCTGG
At5g09810	ACTIN	CGTTTCGCTTTCCTTAGTGTTAGCT	AGCGAACGGATCTAGAGACTCACCTTG
At4g03870	TUBULIN	ATCCGTGAAGAGTACCCAGAT	AAGAACCATGCACTCATCAGC
At4g03870	Mu	GATTTACAAGGAATCTGTTGGTGGT	CATAACATAGGTTTAGAGCATCTG C
At4g39400	BRI1	ACCCAGCACTAAACAGAAGATCAG	CCCAACCACCTATCTCTTGATTCTC
At4g26930	REF1	TCTCCGACCTTTCTTCACACCCATTCC	GTCTCCGCTTAGGAGCACGAAAGCTATC

Supplemental Datasets

Supplemental Dataset 1: DEGs identified in LFY-GR *ap1 cal* time-course experiment.

For each DEG, the identifier (Locus), description and alias is provided. Log_2-transformed fold-change values, *P*-values and adjusted *P*-values are listed for each time-point. The column 'In AP1 dataset?' indicates whether or not a given DEG was also found among genes identified as differentially expressed after activation of AP1-GR in *ap1 cal* inflorescences (Kaufmann et al., 2010). The column 'Antagonistic?' indicates genes with opposite expression changes after LFY-GR and AP1-GR activation, respectively.

Supplemental Dataset 2: DEGs identified after activating LFY-GR in *ap1 cal* inflorescences in the presence of cycloheximide.

List of 116 DEGs identified after activation of LFY-GR in the presence of cycloheximide. For each DEG, the identifier (Locus), description and alias is provided. Log_2-transformed fold-change values, *P*-values and adjusted *P*-values are also listed. The column 'Also in LFY-GR time-course?' indicates whether or not a given DEG was also found among genes identified as differentially expressed in the p35S:LFY-GR in *ap1 cal* time-course experiment.

Supplemental Dataset 3: DEGs with LFY binding sites and results of ChIP-seq experiments.

The sheet 'DEGs bound' lists the DEGs and data provided in Supplemental Dataset 1. The columns on the right indicate whether a LFY binding peak was found be associated with a given DEG in the genome-wide localization studies by Winter et al. (2011), Moyroud et al. (2011), and the present study.

The sheet ‘LFY ChIP-seq’ lists the results of the LFY ChIP-seq experiment conducted for this study. A standard output file for *MACS* version 1.4 is provided (see Material and Methods for details).