SUPPLEMENTAL MATERIAL

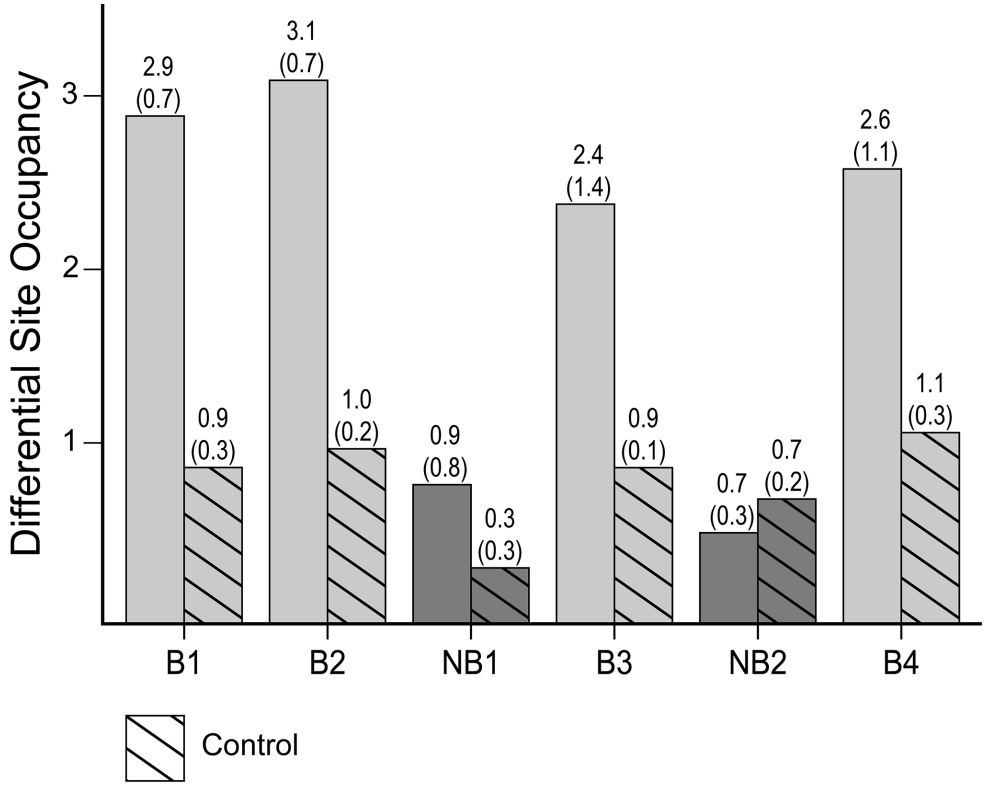

Figure S1. Co-precipitation of select DNA fragments using IgG-Sepharose to isolate complexes via the protein A domain in a TAP-tag added to the C-terminal end of AGL15 (35S:AGL15-TAP, solid bars). Nontagged tissue served as a control (*35S:AGL15*, hatched bars). DSO calculations from three independent experiments comparing recovery of target to nonbound control (*TUA3*) in the same immune precipitation is shown. The averages (standard deviations) are shown.

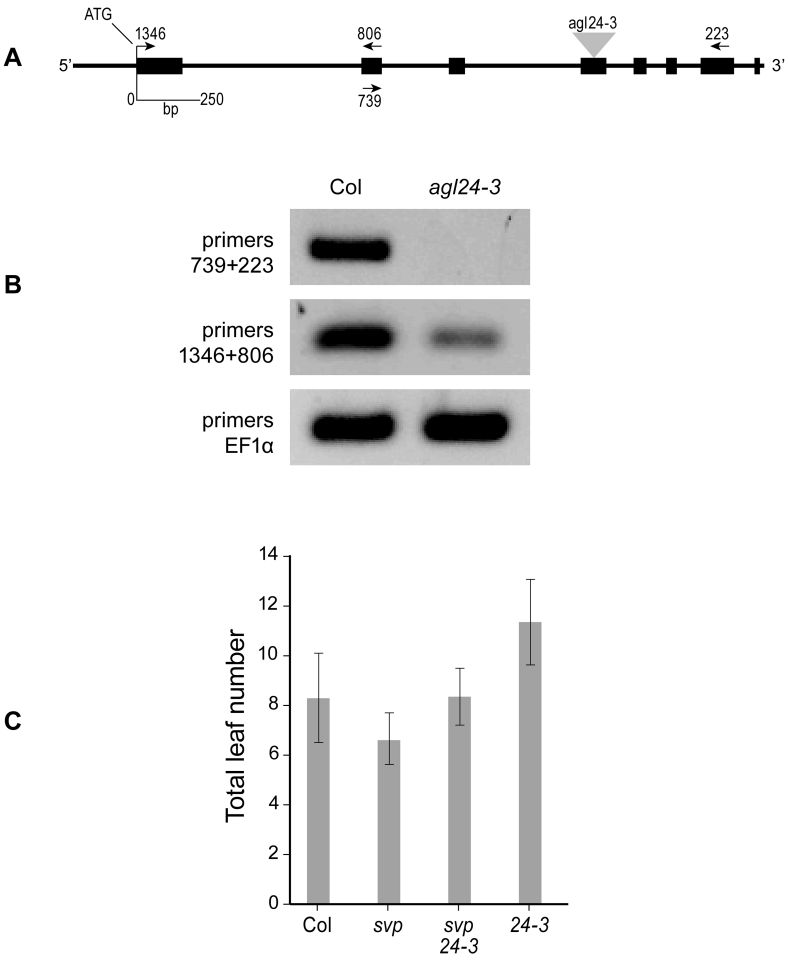

Figure S2. Analysis of the *agl24-3* mutant allele. (A) Gene diagram showing positions of the T-DNA insertion in the *agl24-3* (SALK_095007) mutant and RT-PCR primers. Black boxes indicate exons in the coding sequence. (B) RT-PCR of wild type Columbia and homozygous *agl24-3* seedlings with gene-specific primers (primer 223: AAGTGTCGGAGTCATCCTCAAG, primer 739: CAAATTGATGGATCCACCTTC, primer 806: CGGAGATGAGTAGAAGGTGGA, primer 1346: AAAATGGCGAGAGAGAAGATAAGG). Although transcripts that encode the region upstream of the insertion accumulate at reduced levels, no full-length transcripts can be detected in *agl24-3* plants. (C) Flowering time under LD conditions of the *agl24-3* allele alone and in combination with *svp* mutations. The means ± 1 standard deviation are shown (n ≥ 24 plants).

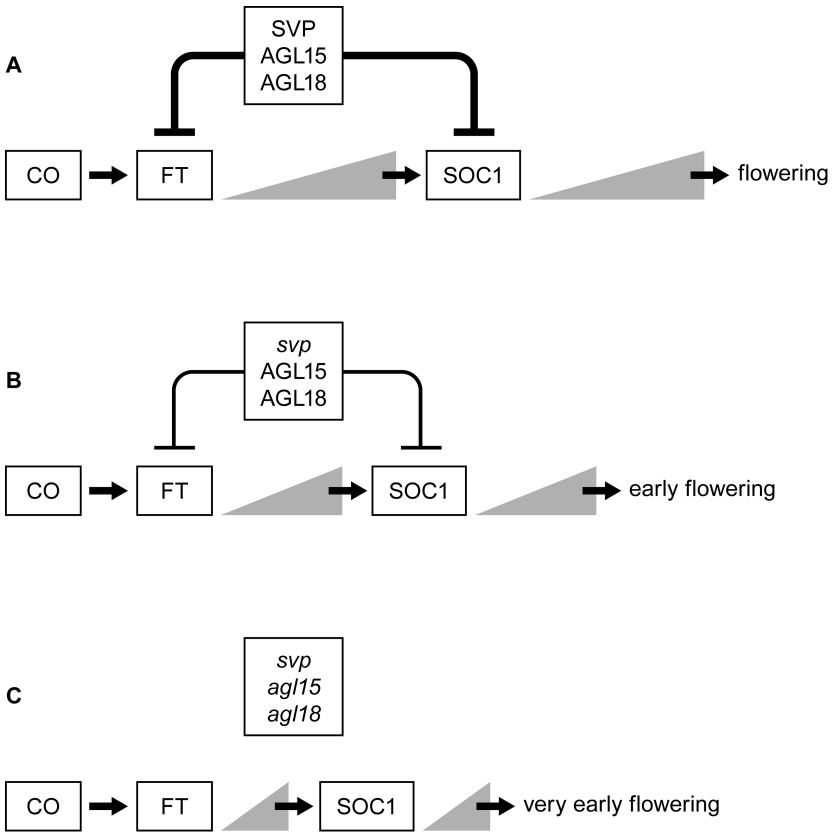

Figure S3. Model summarizing the effects of *agl15*, *agl18*, and *svp* mutations on *FT* and *SOC1* expression and flowering time under inductive conditions. (A) *FT* and *SOC1* serve as floral integrators and are direct targets of the floral repressors, including SVP, AGL15 and AGL18. (B) In the absence of SVP, FT and SOC1 reach levels necessary to induce flowering more quickly, resulting in earlier flowering. (C) *agl15 agl18* mutations enhance the effect of *svp* mutations, allowing FT and SOC1 levels to increase even more quickly, resulting in very early flowering.

Table SI. Oligonucleotides used for PCR genotyping

allele	Forward	Reverse
agl15-3	TTATCTAGATGGGTCGTGGAAAAATCGAG	GCGTGGACCGCTTGCTGCAACT
AGL15	TTATCTAGATGGGTCGTGGAAAAATCGAG	AATATCCACCTCTGCACAATCCTCCT
agl18-1	GCGTGGACCGCTTGCTGCAACT	TGCATCTCCCAAATTCTGATAC
AGL18	CCACAGAGCCCAGGTTGATT	TGCATCTCCCAAATTCTGATAC
agl24-3	GCGTGGACCGCTTGCTGCAACT	AAGTGTCGGAGTCATCCTCAAG
AGL24	CAAATTGATGGATCCACCTTC	AAGTGTCGGAGTCATCCTCAAG
KNAT1p: AGL15	GGTGCAACTTCACCTCACAA	ACCGTATCTGGAAAGTGTTTGCTTCATT
sep3-2	AAAGTGTTGGTGAGAGTGGAA	GAGCGTCGGTCCCCACACTTCTATAC
SEP3	AAAGTGTTGGTGAGAGTGGAA	AACCCTAATTTCATATCAGATAGATTG
soc1-2	TTGGGTGATGGTTCACGTAGTGGG	ATATCACAAACCGTTTAGAAGCTTCGAGTTGTTCA
SOC1	TGTGCTCTTTCGTAGCCAAT	ATATCACAAACCGTTTAGAAGCTTCGAGTTGTTCA
SUC2p: AGL15	CACGTGTCACGAAGATACCC	ACCGTATCTGGAAAGTGTTTGCTTCATT
svp-32	GAAGGAAGTCCTAGAGAGGCATAAC	GCGTGGACCGCTTGCTGCAACT
SVP	GAAGGAAGTCCTAGAGAGGCATAAC	CGTTAGTAATAGACTCCGACGACTG

Table SII. Oligonucleotides used for qPCR analyses

Gene	Forward	Reverse
AG	AGATTAGAGAGAAGTATTACCCGAATC	GTCTTGGCGACCCGCGGATGAGTAATG
AGL15	GCAAACACTTTCCAGATACGG	CTTGCCCTGCAGTTGTAAATG
AP1	GCAAGCAATGAGCCCTAAAG	ACTGCTCCTGTTGAGCCCTA
AP3	ATACAAAAGAATCTCATACATGAGCTG	AATGATGTCAGAGGCAGAGGGTGCATG
CN1 *At2g28390*	CCCCCAGTAACTAGTCACAGACA	TGATTGCATATCTTTATCGCCATC
FT	CTGGAACAACCTTTGGCAAT	AGCCACTCTCCCTCTGACAA
FT-IB	CGTTGATGATAGTGAAGTGAGACATCTTGGC	CGTCTCGATACTTTGCACTCATCCAATCC
FT-2B	GCCAAAGAGAGGTGACTAATGGCT	AGTTCCTGAGGTCTTCTCCACCAA
FT-3B	CATTGGTGCACGTGTACATACACCTCTTGG	GGTTTGACAAGACTGTCCGTATGATGGAG
FT-4B	CAGTCACAACGACGAATTCATTTGAGCTCTG	GAGAGGTTCTTTAGGGTTTATTGGGTCTAGT
FT-NB1	AGCATAGCTCAAACATGTTGCTCG	GGGAGACAAATTGATGCATCGCAC
FT-NB2	CGCCTCTAGGTATGTATAGAAGGTTGACCAC	CATGTTTACACACGGAAGTGGAAGCACTCG
FUL	TGCGTAACCTCCTCCAGAGAT	GTTCTACTCGTTCGTAGTGGTAGGAC
PI	AAGAAAGAGAATGATAGCTTACAACTG	CACTCTATATCCAAACTGCCCATCATG
SEP3	CTAAGACTAAGGTTAGCTGATGGGTA	ATGATGACGACCGTAGTGATCAA
TUA3 *At5g19770*	AGGGCTTACCACGAGCAGCTATCA	ACAGGCCATGTACTTTCCGTGTCT
β-tubulin *At5g62690*	AAACTCACTACCCCCAGCTTTG	CACCAGACATAGTAGCAGAAATCAAGT