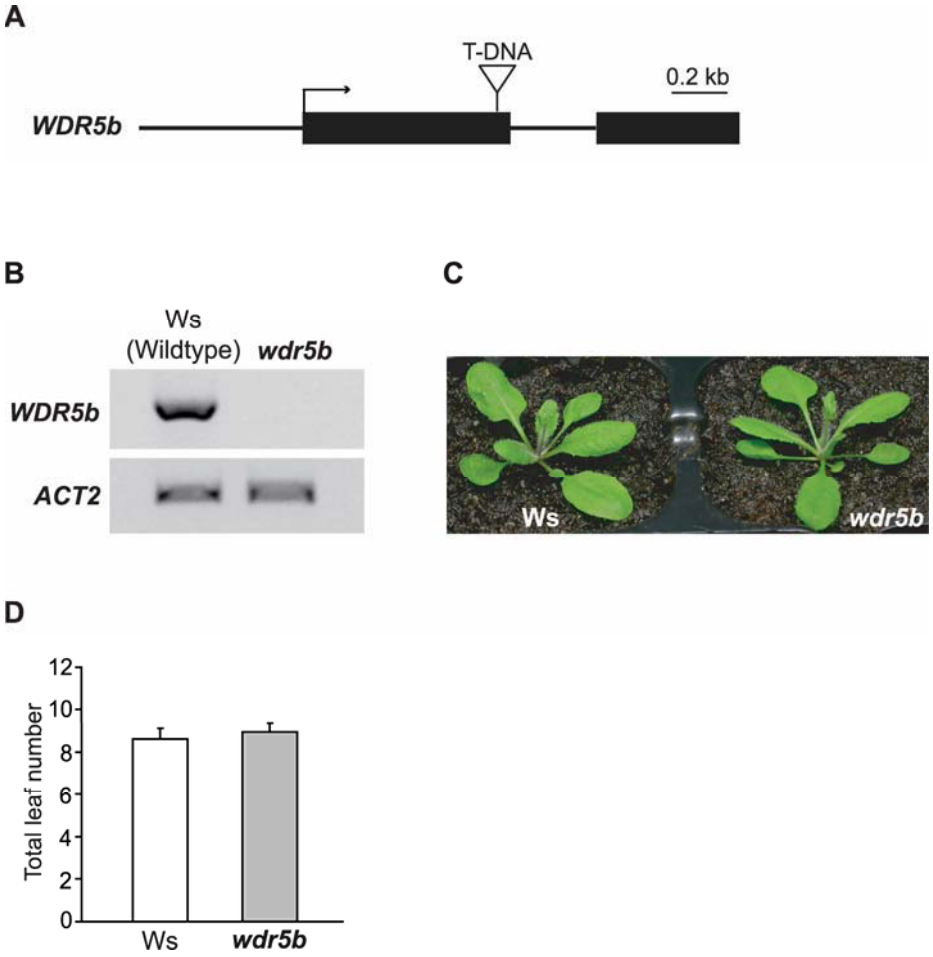
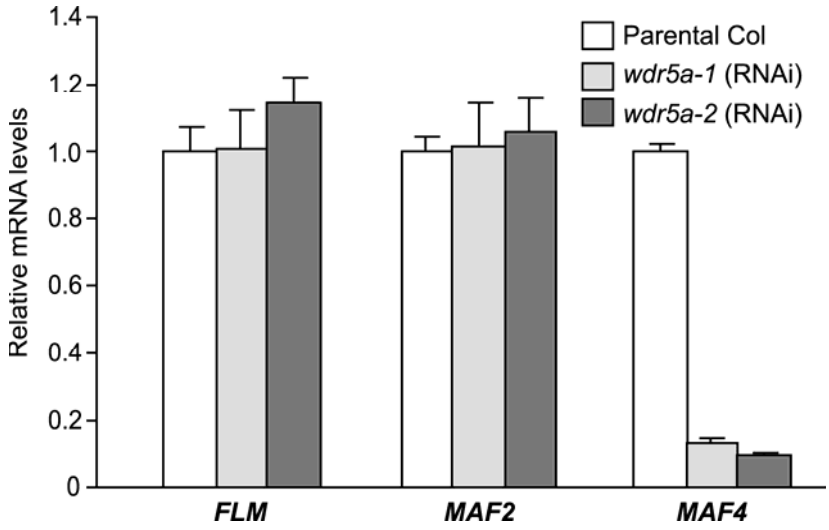
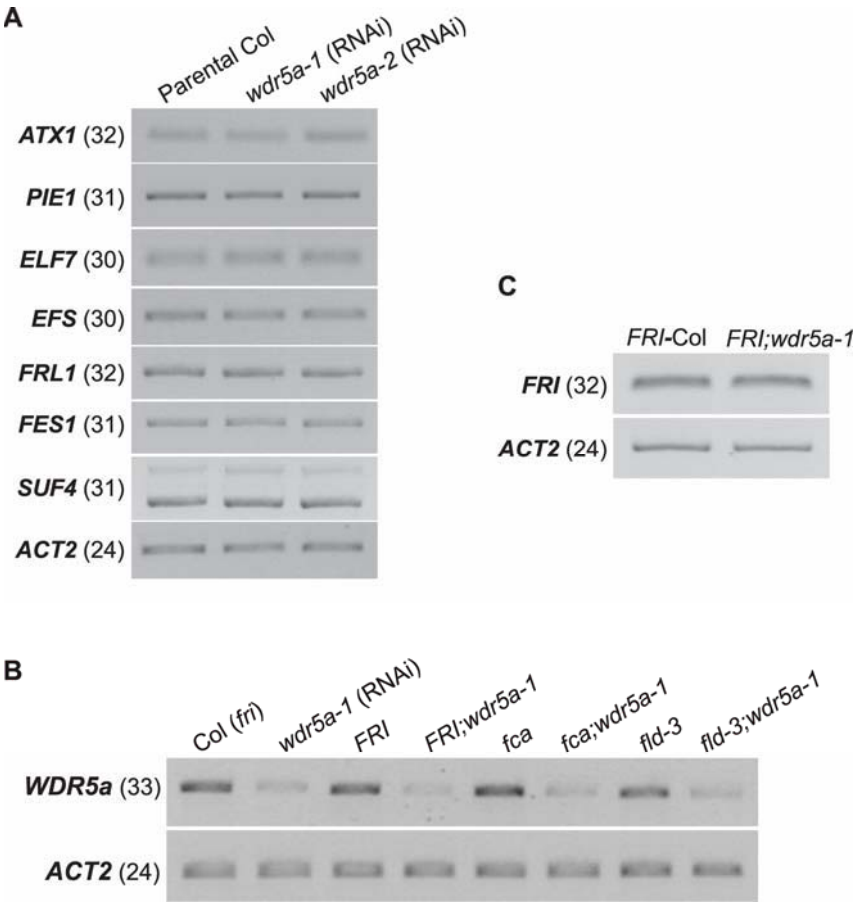
Supplemental Data Jiang et al., (2009) Establishment of the Winter-Annual Growth Habit via FRIGIDA-Mediated Histone Methylation at FLOWERING LOCUS C in Arabidopsis.



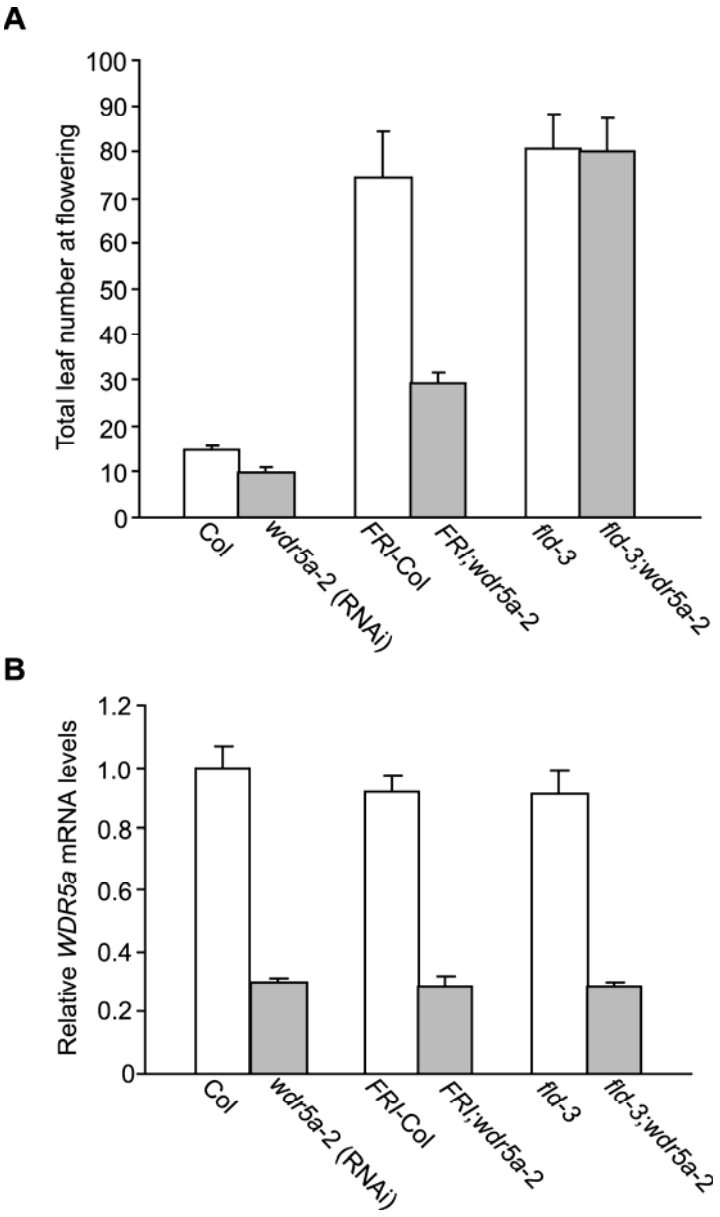
Supplemental Figure 1. Analyses of a Loss-of-Function *wdr5b* Mutant. (**A**) *WDR5b* structure. Exons are represented by filled boxes. The arrow indicates the transcription start site, and the triangle indicates a *T-DNA* insertion. (**B**) Analysis of *WDR5b* expression in *wdr5b* mutant seedlings by RT-PCR. The constitutively expressed *ACTIN 2* (*ACT2*) served as a control. (**C**) A *wdr5b* mutant grown in LDs. The *wdr5b* mutant is phenotypically indistinguishable from wild-type Ws. (**D**) Flowering times of *wdr5b* grown in LDs. The total number of primary rosette and cauline leaves at flowering was counted, and 18 and 17 plants were scored for Ws and *wdr5b* respectively. The values shown are means ± SD.



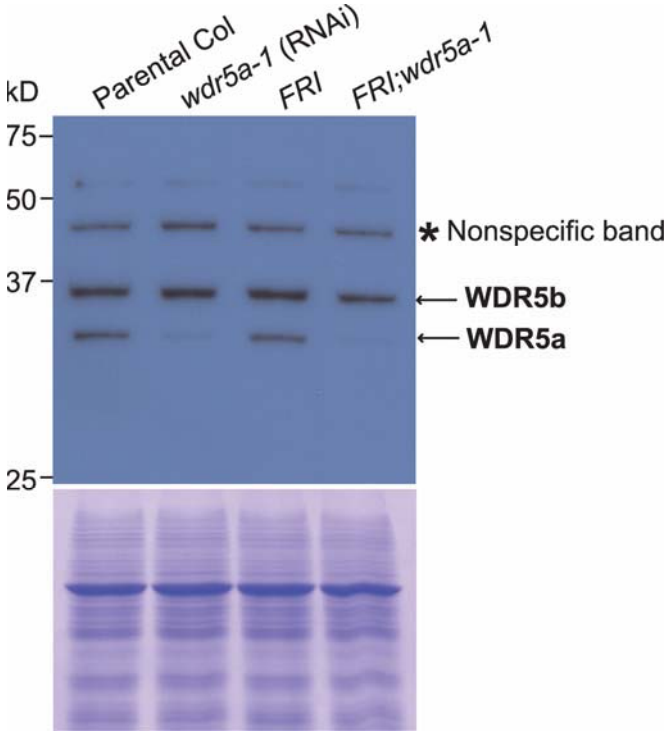
Supplemental Figure 2. Relative mRNA Levels of *FLM*, *MAF2* and *MAF4* in Seedlings of *wdr5a* (RNAi) Lines Quantified by Real-Time PCR. Relative expression to parental Col is presented, with standard deviation for three qPCR replicates.



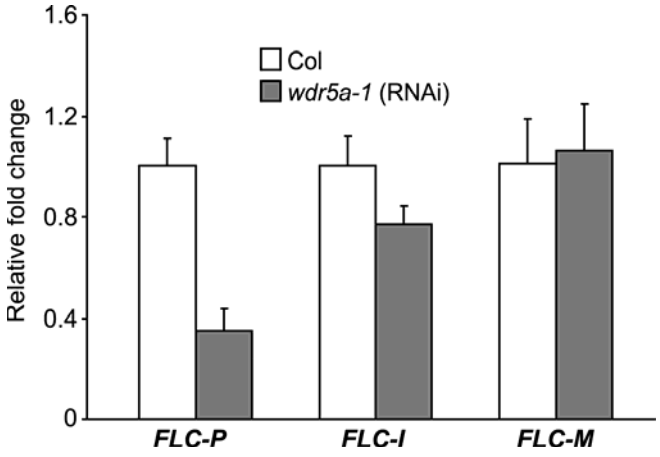
Supplemental Figure 3. Analysis of the Expression of the Indicated Genes upon *WDR5a* Knockdown. (**A**) Analysis of the expression of *FLC* regulators in *wdr5a* (RNAi) lines. The constitutively expressed *ACT2* served as a control. These RT-PCR experiments were performed twice with similar results; the numbers in parentheses represent the PCR cycles ([A], [B] and [C]). The amplifications were optimized to be in the linear range; the gels were stained with ethidium bromide ([A], [B] and [C]). (**B**) Analysis of *WDR5a* expression in the indicated genotypes. (**C**) Analysis of *FRI* expression in *FRI* and *FRI;wdr5a-1* seedlings.



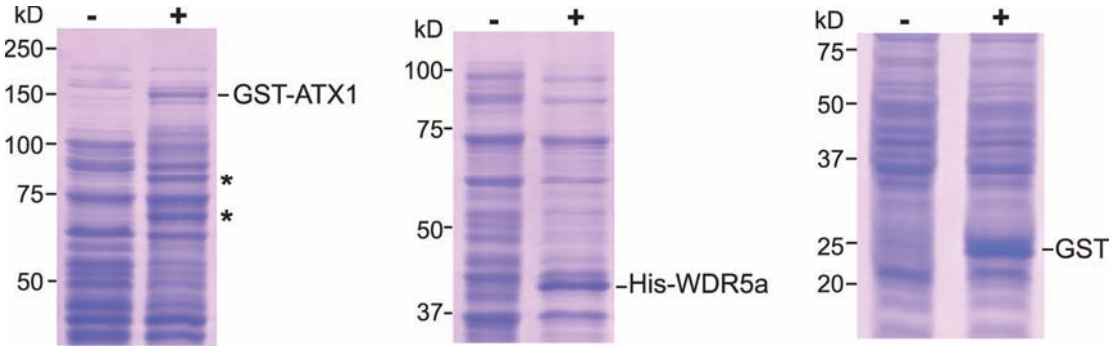
Supplemental Figure 4. Effect of *WDR5a* Knockdown on the Late-Flowering Phenotypes of *FRI*-Col and *fld* Grown in LDs. (**A**) Flowering times of the indicated genotypes. The total number of primary rosette and cauline leaves at flowering was scored, and 7 to 12 plants were counted for each line. The values shown are means ± SD. (**B**) Relative *WDR5a* mRNA levels in seedlings of the indicated genotypes quantified by real-time PCR. Relative expression to Col is presented, with standard deviation for three qPCR replicates.



Supplemental Figure 5. Immunoblot Analysis of Arabidopsis WDR5a in the Indicated Lines Using an Antibody Raised Against the Human WDR5. WDR5a (34.8 kD) and WDR5b (36.3 kD) are indicated by arrows in the top panel, and the non-specific immunoreactive band is indicated by an asterisk (*). The bottom panel shows the total protein extracts separated in a duplicated SDS-PAGE gel and stained with Coomassie blue, and serves as the loading control.



Supplemental Figure 6. *WDR5a* Knockdown Leads to Decreased WDR5a Binding to *FLC* Chromatin. The amounts of *FLC* fragments immunoprecipitated from seedlings of Col and the *wdr5a-1* line were quantified by real-time PCR and subsequently normalized to an internal control (*TUB2*). The fold changes of *wdr5a-1* over Col at the indicated regions are shown. Data in the graphs are average values from two ChIP experiments (each quantified in triplicate), and error bars represent standard deviations. The examined regions are as illustrated in Figure 6A.



Supplemental Figure 7. SDS-PAGE Analysis of Total Protein Extracts from *E. coli* Harboring *GST-ATX1*, *His-WDR5a* or *GST* Plasmids. Total proteins were extracted from *E. coli* before (-) and after (+) induction of respective protein expression. Induced proteins are indicated with their respective names. Immunoblot analysis with anti-GST revealed that the GST-ATX1 fusion protein in *E. coli* was partially degraded (data not shown); the apparent degradation products are marked with *. Molecular weight markers are indicated on the left.

Supplemental Table 1. Total Leaf Number at Flowering of *wdr5a* (RNAi) Lines Grown in Long Days

Line name	Total leaf number (Mean ± SD)	Number of the T_2 plants scored
Col	13.6 ± 0.8	12
wdr5a-3	10.1± 0.9	11
wdr5a-4	9.5 ± 1.0	12
wdr5a-5	9.9 ± 1.1	12
wdr5a-6	10.8 ± 1.1	12
wdr5a-7	8.8 ± 0.8	12
wdr5a-8	9.0 ± 0.8	11
wdr5a-9	10.1 ± 1.1	11

Supplemental Table 2. Sequences of Primers Used in RT-PCR and ChIP-PCR Experiments

Amplified regions	Sequences
WDR5a	Forward: AATGGCAAGTTTATCCTCGTTGGTA Reverse: TTTCTGTAGCAGTTTCTTGGAGTTTAGC
WDR5b	Forward: GGGATGCTAAAGAAGGAACTTGCT Reverse: AACTTCCCCGTCGCATAGTTCG
FRI	Forward: AGTTGCTTGTTTTGGTGTTCCTTC Reverse: TCCACGCTTGATACTTGATTCAAC
ATX1	Forward: TGGGTGAAGAACTAAATGGATCTGG Reverse: TGGCAGACATTGCACTTATCGAGA
EFS	Forward: AGCTGTGAACCAAACTGCCGTACTG Reverse: TTCAAAGCTCTGTGGCATTTGCTC
PIE1	Forward: AGTGATGAGGAGAGGGCAGAACAG Reverse: AAGGTCATGTGAATGGGTCTCGG
SUF4	Forward: CGCATCGATTGGGTAAGAAGAAGAAGAGAGCTACAG Reverse: GCCCTCGAGCTAAAACGCCATCCGCCCAG
ELF7	Forward: CAGGTATGTGCCAGGATCGTTTG Reverse: TTCTGGCGTACATGGTTCCTTCC
FLC-I	Forward: GAAGCAGTCTTCCACTATTTGCTATTGT Reverse: ACGCAGCCCCAATCTTAAATGC
FLC-M	Forward: CCTTCTTGGCTCTAGTCACGGAGA Reverse: GGCAGGATCATCAGTCAAAAGCTCT