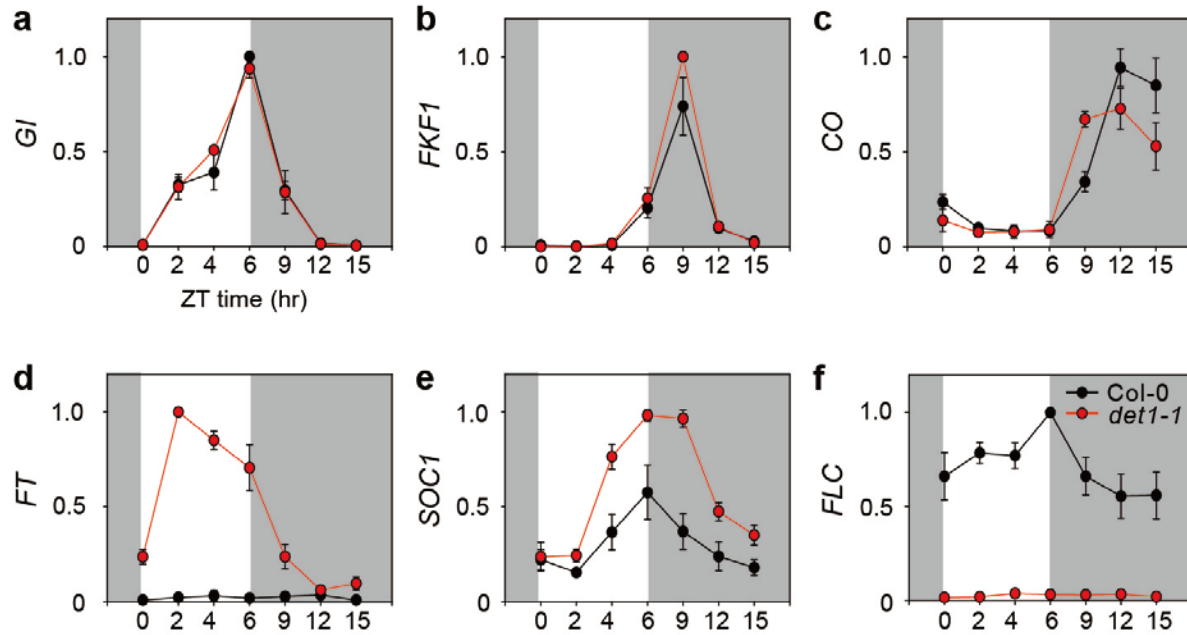


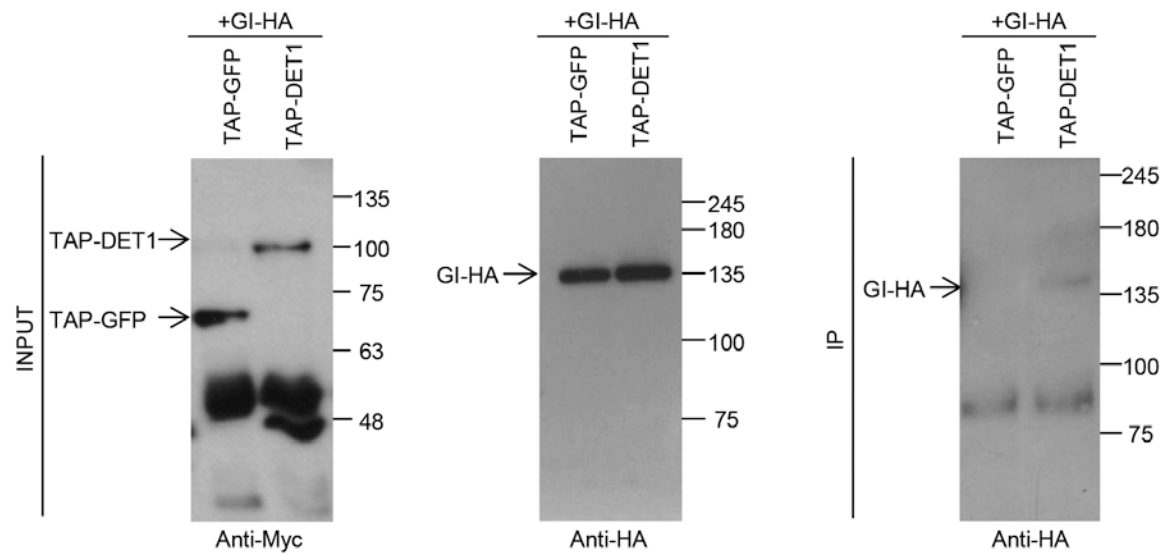
# Supplementary Information

## Negative regulatory roles of *DE-ETIOLATED1* in flowering time in *Arabidopsis*

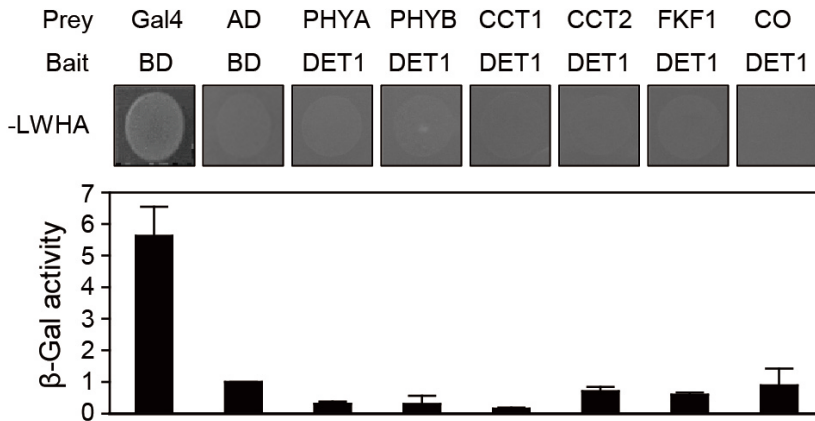
Min-Young Kang, Soo-Cheul Yoo, Hye-Young Kwon, Byoung-Doo Lee, Jung-Nam Cho, Yoo-Sun Noh & Nam-Chon Paek



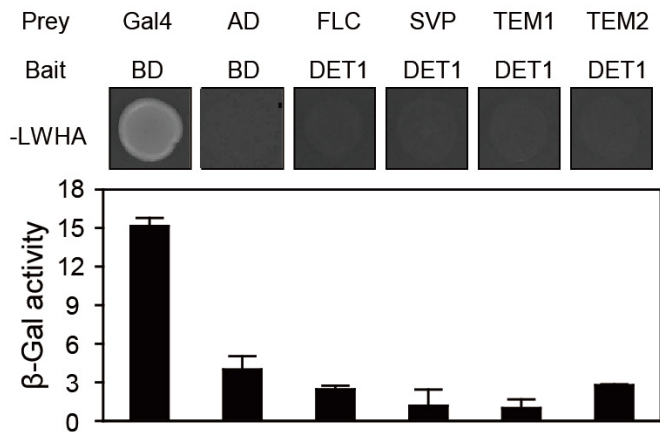
**Figure S1 | Effect of *det1-1* mutation on *GI*, *FKF1*, *CO*, *FT*, *SOC1*, and *FLC* expression under 18T (6-h light:12-h dark).** (a-f) The expression of *GI* (a), *FKF1* (b), *CO* (c), *FT* (d), *SOC1* (e), and *FLC* (f) genes was analyzed in Col-0 and *det1-1* mutants by real-time PCR using 10-day-old plants. Plants were grown at 22°C under SD (6-h light:12-h dark) conditions, and plant tissues were harvested every 2 h during daytime and every 3 h during nighttime. *ACT2* expression was used for normalization. Means and standard deviations were obtained from three biological replicates.



**Figure S2 | DET1 directly interacts with GI.** Uncropped immunoblot images of Fig. 4c.



**Figure S3 | DET1 does not interact with circadian clock-related proteins in a yeast-2-hybrid assay.** DET1 does not interact with PHYA, PHYB, CCT1, CCT2, CO, and FKF1 in yeast-2-hybrid assays. DET1 was used as bait in the pGBK vector. For preys, PHYA, PHYB, CCT1, CCT2, CO, and FKF1 were used. Gal4 indicates a positive control. Empty pGBKT7 (BD) and pGADT7 (AD) vectors were a negative control. SD medium (-LWHA; lacking medium of tryptophan, leucine, histidine, and adenine) was used for selection of the interaction between bait and prey proteins.  $\beta$ -Galactosidase ( $\beta$ -Gal) activity assays were performed according to the manufacturer's protocol. Means and standard deviations were obtained from three biological replicates. This experiment was replicated at least three times with similar results.



**Figure S4 | DET1 does not interact with repressors of *FT* in a yeast-2-hybrid assay.** DET1 does not interact with FLC, SVP, TEM1, and TEM2 in yeast-2-hybrid assays. DET1 was used as bait in pGBK vector. For preys, FLC, SVP, TEM1, and TEM2 were used. Gal4 indicates a positive control. Empty pGBKT7 (BD) and pGADT7 (AD) vectors were a negative control. SD medium (-LWHA; lacking medium of tryptophan, leucine, histidine, and adenine) was used for selection of the interaction between bait and prey proteins.  $\beta$ -Galactosidase ( $\beta$ -Gal) activity assays were performed according to the manufacturer's protocol. Means and standard deviations were obtained from three biological replicates.

**Table S1. Effect of *det1* mutation on flowering time in different mutant backgrounds.**

Genotype	Rosette leaves at bolting	
	LD (16L:8D)	SD (10L:14D)
Wild type (Col-0)	12.1 ± 0.9	37.7 ± 3.3
<i>det1-1</i>	9.0 ± 1.3	12.9 ± 2.2
<i>cry2-1</i>	19.4 ± 2.4	42.1 ± 7.8
<i>cry2-1 det1-1</i>	11.4 ± 0.9	17.9 ± 3.5
<i>gi-1</i>	35.5 ± 1.8	52.2 ± 4.0
<i>gi-1 det1-1</i>	29.9 ± 1.7	40.3 ± 4.4
<i>fkf1-t</i>	20.1 ± 1.0	43.0 ± 4.4
<i>fkf1-t det1-1</i>	12.6 ± 1.1	24.3 ± 2.2
<i>co-101</i>	31.8 ± 2.2	48.8 ± 3.6
<i>co-101 det1-1</i>	21.8 ± 1.6	25.6 ± 4.9
<i>ft-1</i>	31.7 ± 1.2	51.7 ± 4.3
<i>ft-1 det1-1</i>	29.0 ± 1.5	40.3 ± 3.0
<i>soc1-2</i>	18.2 ± 1.1	56.2 ± 2.9
<i>soc1-2 det1-1</i>	14.0 ± 2.1	27.0 ± 2.6

Genotype	Rosette leaves at bolting	
	LD (16L:8D)	SD (8L:16D)
Wild type(Col-0)	11.8 ± 0.8	44.9 ± 3.7
<i>det1-1</i>	10.4 ± 0.5	16.8 ± 1.0
<i>ft-1</i>	40.8 ± 3.8	69.0 ± 3.9
<i>soc1-2</i>	20.6 ± 1.5	63.1 ± 2.9
<i>ft-1 soc1-2</i>	48.4 ± 4.5	79.8 ± 5.3
<i>ft-1 soc1-2 det1-1</i>	52.4 ± 3.6	85.9 ± 6.6

**Table S2. Primer sequences used in this study.**

Construct	Primer	Sequence (5' → 3')
<b>Real-time PCR</b>		
<i>ACT2</i>	ACT_F	TGGGATGAACCAGAAGGATG
	ACT_R	AAGAATACCTCTCTTGGATTGTGC
<i>CO</i>	CO_F	GCCTACTTGTGCATGAGCTG
	CO_R	GTTTATGGCGGGAAGCAAC
<i>FT</i>	FT_F	GGTGGAGAAGACCTCAGGAA
	FT_R	GGTTGCTAGGACTTGGAACATC
<i>FKF1</i>	FKF1_F	GTTGTACCGCCTCCAAGACT
	FKF1_R	AGATGATGACCCTACCACACG
<i>GI</i>	GI_F	TGCATCTGGTGTAAGGCTACC
	GI_R	CCTATAGCCCGCAAGAAGTG
<i>SOC1</i>	SOC1_F	AACAACCTCGAAGCTTCTAAACGTAA
	SOC1_R	CCTCGATTGAGCATGTTCT
<i>FLC</i>	FLC_F	GCTACTTGAACCTTGTGGATAGCAA
	FLC_R	GGAGAGGGCAGTCTCAAGGT
<b><i>FT</i> promoters</b>		
I region	pFT_I_F	CTGCGACTGCGACCTATTTT
	pFT_I_R	GCCACTGTTCTACACGTCCA
II region	pFT_II_F	ACTTGGCGGTACCCTACTT
	pFT_II_R	ATATCTCCCACTTGGTAG
III region	pFT_III_F	GTCGAGAGAGGTATCTTGTTAAAG
	pFT_III_R	ATCATAGGCATGAACCCTCTACAC
IV region	pFT_IV_F	TATGTGTAGAGGGTTCATGCCTATG
	pFT_IV_R	TGGCCATAACCTTTAGAGTG
V region	pFT_V_F	CCAAGAGTTGAGATTGGTGGA

	pFT_V_R	CCAAGAGTTGAGATTGGTGGA
VI region	pFT_VI_F	TCCACCAACTTCTTGCATAA
	pFT_VI_R	CCACAACAGAAATTCATCAA
<i>UBI10</i>	UBI10_F	TTGCCAATTTTCAGCTCCAC
	UBI10_R	TGACTCGTCGACAACCACAA
<b><i>FLC promoters</i></b>		
I region	pFLC_I_F	TGTCCACACATATGGCAATAGCTCAA
	pFLC_I_R	CAAGCTGATACAAGCATTTACCAA
II region	pFLC_II_F	CCTAATTTGATCCTCAGGTTTGGG
	pFLC_II_R	CCGACGAAGAAAAAGTAGATAGGCAC
III region	pFLC_III_F	GTCATTCACGATTTGTTTGATACGATCTG
	pFLC_III_R	GATCTCCCGTAAGTGCATTGCA
<i>FUS3</i>	FUS3_F	ATGTGGCACGTGGGAAATAG
	FUS3_R	GTGGCAAGTGTTGATCATGG

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