

## Supplementary Online Data

**Title: CRYPTIC PRECOCIOUS/MED12 is a novel flowering regulator with multiple target steps in *Arabidopsis***

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**Supplementary Table S1.** Effect of *crp-1D* mutation on flowering time of transgenic plants over-expressing *FT*, *TSF*, *SOC1*, *LFY* and *API*.

Genotype	Number of rosette	Number of cauline	n
	leaves	leaves	
Col	10.4 ± 1.1	2.8 ± 0.6	12
Col × <i>crp-1D</i> F1	8.7 ± 0.9	3.1 ± 0.5	11
<i>crp-1D</i>	8.1 ± 0.8	2.8 ± 0.7	13
35S:: <i>FT</i> #11-1	3.7 ± 0.5	1.4 ± 0.5	15
<i>crp-1D</i> × 35S:: <i>FT</i> #11-1 F1	0.7 ± 0.8 *	1.9 ± 0.5	18
35S:: <i>FT</i> #1-5C	4.3 ± 0.5	1.1 ± 0.6	15
<i>crp-1D</i> × 35S:: <i>FT</i> #1-5C F1	2.1 ± 0.3 *	1.5 ± 0.5	13
<i>SULTR2;1</i> :: <i>FT</i>	4.7 ± 0.5	1.3 ± 0.5	15
<i>crp-1D</i> × <i>SULTR2;1</i> :: <i>FT</i> F1	2.6 ± 0.5 *	1.4 ± 0.5	10
35S:: <i>TSF</i> #4-1	7.7 ± 0.5	2.3 ± 0.5	13
<i>crp-1D</i> × 35S:: <i>TSF</i> #4-1 F1	3.9 ± 0.4 *	1.5 ± 0.5	14
Col	10.3 ± 1.0	2.3 ± 0.5	12
<i>crp-1D</i>	6.4 ± 0.8	3.0 ± 0.4	14
Col × <i>soc1-101D</i> F1	5.4 ± 0.6	2.6 ± 0.5	16
<i>crp-1D</i> × <i>soc1-101D</i> F1	4.9 ± 0.5	2.9 ± 0.7	27
Col	10.4 ± 0.7	2.4 ± 0.5	12
<i>crp-1D</i>	7.6 ± 0.8	3.1 ± 0.4	14
35S:: <i>LFY</i>	7.7 ± 1.3	4.0 ± 1.8	8
<i>crp-1D</i> × 35S:: <i>LFY</i> F1	6.0 ± 0.7 *	2.8 ± 0.8	14
35S:: <i>API</i>	5.8 ± 0.5	2.1 ± 0.6	13
<i>crp-1D</i> × 35S:: <i>API</i> F1	5.4 ± 0.6	2.6 ± 0.5	19
Ler	7.6 ± 0.7	3.3 ± 0.5	14
<i>crp-1D</i> Ler	5.8 ± 0.8	3.3 ± 0.5	16
35S:: <i>FT</i> #1-5L	2.9 ± 0.6	2.7 ± 0.5	19
<i>crp-1D</i> × 35S:: <i>FT</i> #1-5L F1	1.3 ± 0.9 *	3.4 ± 1.1	11

**(Supplementary Table S1 continued)**

Statistics for results presented in Fig. 1E, 4A and 4E.

The number of leaves is presented as the average  $\pm$  SD.

Plants were grown on 1/2MS medium under long-day conditions.

\* Statistically significant difference (Student's *t*-test,  $P < 0.005$ ) from the respective parental transgenic line.

**Supplementary Table S2.** Flowering time of *crp* and *mab2* single mutants under long-day and short-day conditions.

Genotype	Number of rosette leaves	Number of cauline leaves	n
Long day			
Col	12.5 ± 0.9	2.9 ± 0.5	15
<i>crp-1D</i>	8.8 ± 0.9 *	2.6 ± 0.5	12
<i>crp-3</i>	29.1 ± 1.7 *	8.5 ± 0.8	11
<i>crp-4</i>	28.1 ± 2.5 *	8.6 ± 1.7	12
Ler	6.3 ± 0.5	2.4 ± 0.5	15
<i>crp-2</i>	10.9 ± 0.7 *	5.9 ± 0.7	14
<i>mab2-1</i>	10.0 ± 0.8 *	3.4 ± 0.7	10
Short day			
Col	52.9 ± 4.2	8.6 ± 0.5	14
<i>crp-1D</i>	42.8 ± 1.8 *	7.8 ± 0.8	14
<i>crp-3</i>	53.9 ± 6.0	16 ± 3.0	7
<i>crp-4</i>	46.6 ± 4.5 *	16.9 ± 1.2	10
Ler	16.6 ± 0.7	5.8 ± 1.0	14
<i>crp-2</i>	18.3 ± 1.5	14.7 ± 0.6	3
<i>mab2-1</i>	18.8 ± 2.0	10.4 ± 2.4	9

Statistics for results presented in Fig. 1E, 2A, 2B, 5A and 5B.

The number of leaves is presented as the average ± SD.

Plants were grown on soil.

\* Statistically significant difference (Student's *t*-test,  $P < 0.005$ ) between marked genotypes and the respective wild types.

**Supplementary Table S3.** Effect of *crp-3* and *crp-4* mutation on flowering time of *SULTR2;1::FT*.

Genotype	Number of rosette leaves	Number of cauline leaves	n
Col	9.3 ± 0.5	2.7 ± 0.5	12
<i>crp-3</i>	31.5 ± 3.6	8.9 ± 1.4	10
<i>crp-4</i>	30.9 ± 2.4	7.9 ± 2.4	9
<i>SULTR2;1::FT</i>	4.2 ± 0.4	1.2 ± 0.4	14
<i>SULTR2;1::FT; crp-3</i>	5.4 ± 0.7 *	1.6 ± 0.5	13
<i>SULTR2;1::FT; crp-4</i>	7.2 ± 1.0 *	1.9 ± 0.6	20

Statistics for results presented in Fig. 2E.

The number of leaves is presented as the average ± SD.

Plants were grown on soil under long-day conditions.

\* Statistically significant difference (Student's *t*-test,  $P < 0.005$ ) from *SULTR2;1::FT*.

**Supplementary Table S4.** Genetic interaction between *crp* loss-of function mutants and flowering mutants.

Genotype	Number of rosette leaves	Number of cauline leaves	n
Col	12.5 ± 0.9	2.9 ± 0.5	15
<i>crp-3</i>	29.1 ± 1.7	8.5 ± 0.8	11
<i>crp-4</i>	31.5 ± 2.0	9.7 ± 2.3	14
<i>ft-2</i>	30.9 ± 2.5	6.7 ± 1.3	12
<i>ft-2; crp-3</i>	39.6 ± 4.0 *	15.9 ± 3.3	19
<i>ft-2; crp-4</i>	41.2 ± 3.6 *	17.3 ± 3.6	11
Col	9.6 ± 0.7	2.7 ± 0.5	12
<i>crp-3</i>	31.0 ± 2.0	7.6 ± 1.4	14
<i>crp-4</i>	30.9 ± 3.0	7.5 ± 2.2	12
<i>tsf-1</i>	9.5 ± 0.5	2.8 ± 0.5	14
<i>tsf-1; crp-3</i>	30.7 ± 3.0 **	8.4 ± 1.4	15
<i>tsf-1; crp-4</i>	31.4 ± 2.6 **	8.4 ± 1.3	18
Col	10.4 ± 0.5	2.4 ± 0.5	12
<i>crp-3</i>	29.5 ± 2.4	7.1 ± 1.6	15
<i>crp-4</i>	32.5 ± 3.0	9.7 ± 1.7	20
<i>fd-1</i>	16.9 ± 0.8	4.6 ± 0.8	12
<i>fd-1; crp-3</i>	34.5 ± 2.3 *	12.1 ± 3.7	11
<i>fd-1; crp-4</i>	35.6 ± 2.7 *	12.0 ± 2.7	17
Col	9.5 ± 0.7	2.7 ± 0.5	15
<i>crp-3</i>	29.1 ± 2.9	7.6 ± 0.9	8
<i>crp-4</i>	29.5 ± 2.0	6.7 ± 1.1	11
<i>soc1-2</i>	18.4 ± 1.4	3.6 ± 0.7	12
<i>soc1-2; crp-3</i>	39.8 ± 2.5 *	14.6 ± 4.2	16
<i>soc1-2; crp-4</i>	38.6 ± 3.9 *	13.3 ± 3.9	16

(Supplementary Table S4 continued)

Genotype	Number of rosette leaves	Number of cauline leaves	n
Col	9.9 ± 0.7	2.7 ± 0.5	12
<i>crp-3</i>	34.3 ± 2.2	6.3 ± 1.0	12
<i>crp-4</i>	35.9 ± 3.1	6.7 ± 1.6	10
<i>flc-3</i>	7.7 ± 0.5	2.3 ± 0.5	12
<i>flc-3; crp-3</i>	24.2 ± 1.8 *	4.9 ± 1.3	16
<i>flc-3; crp-4</i>	25.1 ± 3.0 *	6.2 ± 1.2	18

Statistics for results presented in Fig. 2A.

The number of leaves is presented as the average ± SD.

Plants were grown on soil under long-day conditions.

\* Statistically significant difference (Student's *t*-test,  $P < 0.005$ ) from the corresponding *crp* single mutants in the same group.

\*\* No statistically significant difference (Student's *t*-test,  $P > 0.5$ ) from the corresponding *crp* single mutants in the same group.

**Supplementary Table S5.** Flowering time of *35S::CRP* under long-day and short-day conditions.

Genotype	Number of rosette leaves	Number of cauline leaves	n
Long day			
Col	10.2 ± 0.7	2.5 ± 0.5	12
<i>crp-1D</i>	7.6 ± 0.9	2.8 ± 0.4	12
<i>35S::CRP</i> #11	12.0 ± 1.0 *	3.8 ± 0.8	12
<i>35S::CRP</i> #12	11.1 ± 0.8	3.1 ± 0.5	12
<i>35S::CRP</i> #14	10.8 ± 0.6	3.0 ± 0.6	12
<i>35S::CRP</i> #15	9.8 ± 0	2.8 ± 0.4	12
Short day			
Col	52.3 ± 3.4	8.4 ± 1.0	10
<i>crp-1D</i>	48.8 ± 4.8	8.3 ± 1.5	12
<i>35S::CRP</i> #11	54.8 ± 3.9	8.0 ± 0.5	10
<i>35S::CRP</i> #12	54.5 ± 2.2	8.6 ± 1.1	10
<i>35S::CRP</i> #14	52.9 ± 3.1	9.1 ± 1.0	11
<i>35S::CRP</i> #15	52.1 ± 4.3	8.4 ± 0.5	10

Statistics for results presented in Fig. 3B and 3C.

The number of leaves is presented as the average ± SD.

Plants were grown on soil.

\* Statistically significant difference (Student's *t*-test,  $P < 0.005$ ) from Col.



**Supplementary Table S6.** Effect of *35S::CRP* on flowering time of *crp-1D* plants.

Genotype	Number of rosette leaves	Number of cauline leaves	n
Col	9.8 ± 0.8	2.4 ± 0.5	12
<i>crp-1D</i>	6.0 ± 0.9	2.9 ± 0.3	12
<i>35S::CRP</i> #11	11.0 ± 0.9	3.1 ± 0.3	12
<i>crp-1D</i> × <i>35S::CRP</i> #11 F1	8.6 ± 0.7 *	3.4 ± 0.6	18

Statistics for results presented in Fig. 3D.

The number of leaves is presented as the average ± SD.

Plants were grown on soil under long-day conditions.

\* Statistically significant difference (Student's *t*-test,  $P < 0.005$ ) from *crp-1D*.

**Supplementary Table S7.** Effect of loss-of-function mutation of flowering genes on flowering time of *crp-1D* plants.

Genotype	Number of rosette leaves	Number of cauline leaves	n
Col	11.5 ± 0.8	3.2 ± 0.6	12
<i>crp-1D</i>	7.6 ± 0.8	3.3 ± 0.5	12
<i>ft-2</i>	26.1 ± 1.1	4.9 ± 0.8	15
<i>ft-2; crp-1D</i>	25.9 ± 0.8 *	6.0 ± 1.2	14
Col	10.2 ± 0.7	2.3 ± 0.5	12
<i>crp-1D</i>	7.2 ± 0.4	2.9 ± 0.5	12
<i>tsf-1</i>	11.0 ± 1.2	2.6 ± 0.5	10
<i>tsf-1; crp-1D</i>	7.4 ± 0.7	2.9 ± 0.3	12
<i>fd-1</i>	18.1 ± 1.0	4.8 ± 0.8	11
<i>fd-1; crp-1D</i>	8.7 ± 0.8 *	3.4 ± 0.7	12
Col	9.6 ± 0.7	2.5 ± 0.5	8
<i>crp-1D</i>	6.1 ± 0.6	3.3 ± 0.5	8
<i>soc1-2</i>	19.3 ± 0.9	3.3 ± 0.5	8
<i>soc1-2; crp-1D</i>	15.3 ± 1.8 *	4.1 ± 1.0	17
Col	9.8 ± 0.9	3.0 ± 0.4	12
<i>crp-1D</i>	6.7 ± 0.5	3.1 ± 0.4	15
<i>ful-2</i>	10.2 ± 0.9	3.9 ± 0.6	10
<i>ful-2; crp-1D</i>	7.2 ± 0.8	4.2 ± 0.4	12
Col	9.4 ± 0.9	2.9 ± 0.5	12
<i>crp-1D</i>	6.4 ± 0.8	3.0 ± 0.4	14
<i>lfy-1</i>	14.2 ± 1.3	25.2 ± 6.5	14
<i>lfy-1; crp-1D</i>	6.2 ± 0.7	4.8 ± 0.7	12

Statistics for results presented in Fig. 4C.

The number of leaves is presented as the average ± SD.

Plants were grown on soil under long-day conditions.

\* Statistically significant difference (Student's *t*-test,  $P < 0.005$ ) from *crp-1D* in the same group.

**Supplementary Table S8.** Effect of *fd-1* and *soc1-2* mutation on flowering time of *SULTR2;1::FT/-; crp-1D/+* plants.

Genotype	Number of rosette leaves	Number of cauline leaves	n
Col	10.7 ± 0.8	2.6 ± 0.5	12
<i>crp-1D</i>	6.9 ± 0.7	3.1 ± 0.7	12
<i>SULTR2;1::FT/-</i>	4.7 ± 0.5	1.4 ± 0.5	12
<i>SULTR2;1::FT/-; crp-1D/+</i>	2.0 ± 0.0	2.0 ± 0.0	15
<i>SULTR2;1::FT/-; fd-1</i>	9.0 ± 0.4	2.9 ± 0.3	15
<i>SULTR2;1::FT/-; fd-1; crp-1D/+</i>	3.0 ± 0.5 *	2.4 ± 0.5	8
<i>SULTR2;1::FT/-; soc1-2</i>	8.6 ± 0.8	0.6 ± 0.5	22
<i>SULTR2;1::FT/-; soc1-2; crp-1D/+</i>	5.2 ± 0.8 *	1.5 ± 0.5	13

Statistics for results presented in Fig. 4E.

The number of leaves is presented as the average ± SD.

Plants were grown on soil under long-day conditions.

\* Statistically significant difference (Student's *t*-test,  $P < 0.005$ ) from *SULTR2;1::FT/-; crp-1D/+*.

**Supplementary Table S9.** Flowering time of *crp-2; mab2-1* plants.

Genotype	Number of rosette leaves	Number of cauline leaves	n
Ler	5.4 ± 0.5	2.2 ± 0.4	10
<i>mab2-1</i>	12.4 ± 0.8 *	7.1 ± 1.2	7
<i>crp-2</i>	12.4 ± 1.3 *	7.7 ± 1.0	9
<i>crp-2; mab2-1</i>	12.7 ± 1.5 *	9.3 ± 1.8	6

Statistics for results presented in Fig. 5C.

The number of leaves is presented as the average ± SD.

Plants were grown on soil under long-day conditions.

\* No statistically significant difference (Student's *t*-test,  $P > 0.5$ ) from among the genotypes.

**Supplementary Table S10.** Effects of *mab2-1* on flowering time of *crp-1D L* plants.

Genotype	Number of rosette leaves	Number of cauline leaves	n
Experiment 1			
Ler	5.9 ± 0.5	2.0 ± 0.4	15
<i>mab2-1</i>	12, 13	6, 10	2
<i>crp-1D L</i>	4.1 ± 0.4	2.4 ± 0.5	14
<i>crp-1D L; mab2-1</i>	11.9 ± 1.3	7.4 ± 2.1	9
Experiment 2			
Ler	6.3 ± 0.8	3.4 ± 0.5	7
<i>crp-1D L</i>	4.3 ± 0.8	3.0 ± 0.8	7
<i>35S::FT #1-5L</i>	2.4 ± 0.5	2.4 ± 0.6	16
<i>35S::FT #1-5L; mab2-1/ mab2-1</i>	4.8 ± 0.7 **	3.9 ± 1.2	10
<i>35S::FT #1-5L/-; crp-1DL/+</i>	1.1 ± 0.5 *	2.8 ± 1.1	18
<i>35S::FT #1-5L/-; crp-1DL/+;</i> <i>mab2-1/ mab2-1</i>	4.6 ± 0.5 *,**	3.6 ± 1.1	5

Statistics for results presented in Fig. 5D and 5E.

The number of leaves is presented as the average ± SD.

Plants were grown on soil (Experiment 1) or on 1/2MS medium (Experiment 2) under long-day conditions.

\* Statistically significant difference (Student's *t*-test,  $P < 0.005$ ) between marked genotypes.

\*\* No statistically significant difference (Student's *t*-test,  $P > 0.5$ ) between marked genotypes.

**Supplementary Table S11.** Plant materials used in this study.

Name	Background	References	Note
<b>Wild-type</b>			
Col-0	Col		CS6673 (stock name)
Ler-2	Ler		CS8581 (stock name)
<b>EMS mutation</b>			
<i>crp-1D</i>	Col	this study	S99F missense
<i>crp-1D L</i>	Ler	this study	introgression line
<i>fd-1</i>	Col	Abe et al. 2005	introgression line
<i>ft-2</i>	Col	this study	introgression line
<i>ful-2</i>	Col	Ferrández et al. 2000	W91stop nonsense
<i>lfy-1</i>	Col	Schultz and Haughn 1991	CS6228 (stock name)
<i>mab2-1</i>	Ler	Ito et al. 2011	W1833stop nonsense
<i>pid-2</i>	Ler	Bennett et al. 1995	CS8063 (stock name)
<i>pid-3</i>	Col	Bennett et al. 1995	CS8064 (stock name)
<b>Fast neutron deletion</b>			
<i>flc-3</i>	Col	Michaels and Amasino 1999	104-bp deletion that removes the start codon
<b>T-DNA/transposon insertion (loss-of-function)</b>			
<i>crp-2</i>	Ler	this study	Ds-transposon insertion (SET_3.701) <sup>1</sup>
<i>crp-3</i>	Col	this study	SALK_108241 described as <i>cct-2</i> <sup>2</sup>
<i>crp-4</i>	Col	this study	SALK_124276 described as <i>cct-3</i> <sup>2</sup>
<i>soc1-2</i>	Col	Lee et al. 2000	T-DNA insertion
<i>tsf-1</i>	Col	Yamaguchi et al. 2005	SALK_087522
<b>Transgenic (gain-of-function)</b>			
<i>35S::FT #1-5C</i>	Col	Kobayashi et al. 1999	weak line
<i>35S::FT #1-5L</i>	Ler	Kobayashi et al. 1999	introgression line
<i>35S::FT #11-1</i>	Col	Kobayashi et al. 1999	strong line
<i>35S::TSF #4-1</i>	Col	Kobayashi et al. 1999	weak line
<i>SULTR2;1::FT #1-a</i>	Col	Abe et al. 2005	
<i>soc1-101D</i>	Col	Lee et al. 2000	activation-tagging line
<i>35S::LFY</i>	Col	Weigel and Nilsson 1995	DW151.2.5C
<i>35S::API</i>	Col	Mandel and Yanofsky 1995	

1: Parinov et al. 1999      2: Gilmor et al. 2010

**Supplementary Table S12.** Primer sets used in quantitative RT-PCR.

Gene	Sequence (5' to 3')		References
	Forward	Reverse	
<i>ACT2</i>	GCTGAGAGATTCAGATGCCCA	GTGGATTCCAGCAGCTTCCAT	Kim et al. 2008
<i>API</i>	GAAGGCCATACAGGAGCAAA	ACTGCTCCTGTTGAGCCCTA	Yamaguchi et al. 2009
<i>CO</i>	CTACAACGACAATGGTTCCATTAAC	CAGGGTCAGGTTGTTGCTC	Nakamichi et al. 2007
<i>CRP</i>	ATACAAGGAAACTGTTGATGGACTT	GCAATCGTTTGTGCTGTTGTG	in this study
<i>FD</i>	TGTTTCTCTTTGGGGATTGA	CCTTTTCTCTTTCCGGGTCT	Yamaguchi et al. 2009
<i>FLC</i>	CCGAACTCATGTTGAAGCTTGTGAG	CGGAGATTGTCCAGCAGGTG	Jiang et al. 2007
<i>FT</i>	CTAGCAACCCTCACCTCCGAGAATA	CTGCCAAGCTGTCGAAACAATATAA	Wang et al. 2009
<i>FUL</i>	TTGCAAGATCACAACAATTCGTTCT	GAGAGTTGGTTCCGTCACGACGAT	Yamaguchi et al. 2009
<i>LFY</i>	ACGCCGTCATTTGCTACTCT	CTTTCTCCGCTCTGCTGCT	Yamaguchi et al. 2009
<i>NRT1.7</i>	CAACAGTCAGTTCCAGAGCACAT	CGACAGTCACAAGGAACTACTAAGGTA	Fan et al. 2009
<i>SOCI</i>	ATAGGAACATGCTCAATCGAGGAGCTG	TTTCTGAAGAACAAGGTAACCCAATG	Wang et al. 2009
<i>STM</i>	CTCTTGCGCAAGTACAGTGG	GGTGAGGATGTGTTGCGTC	Takami et al. 2010
<i>TSF</i>	GAGTCCAAGCAACCCTCACCAA	CACAATACGATGAATTCCCGAG	Yamaguchi et al. 2005

**Supplementary Table S13.** Primer sets used in semi-quantitative RT-PCR.

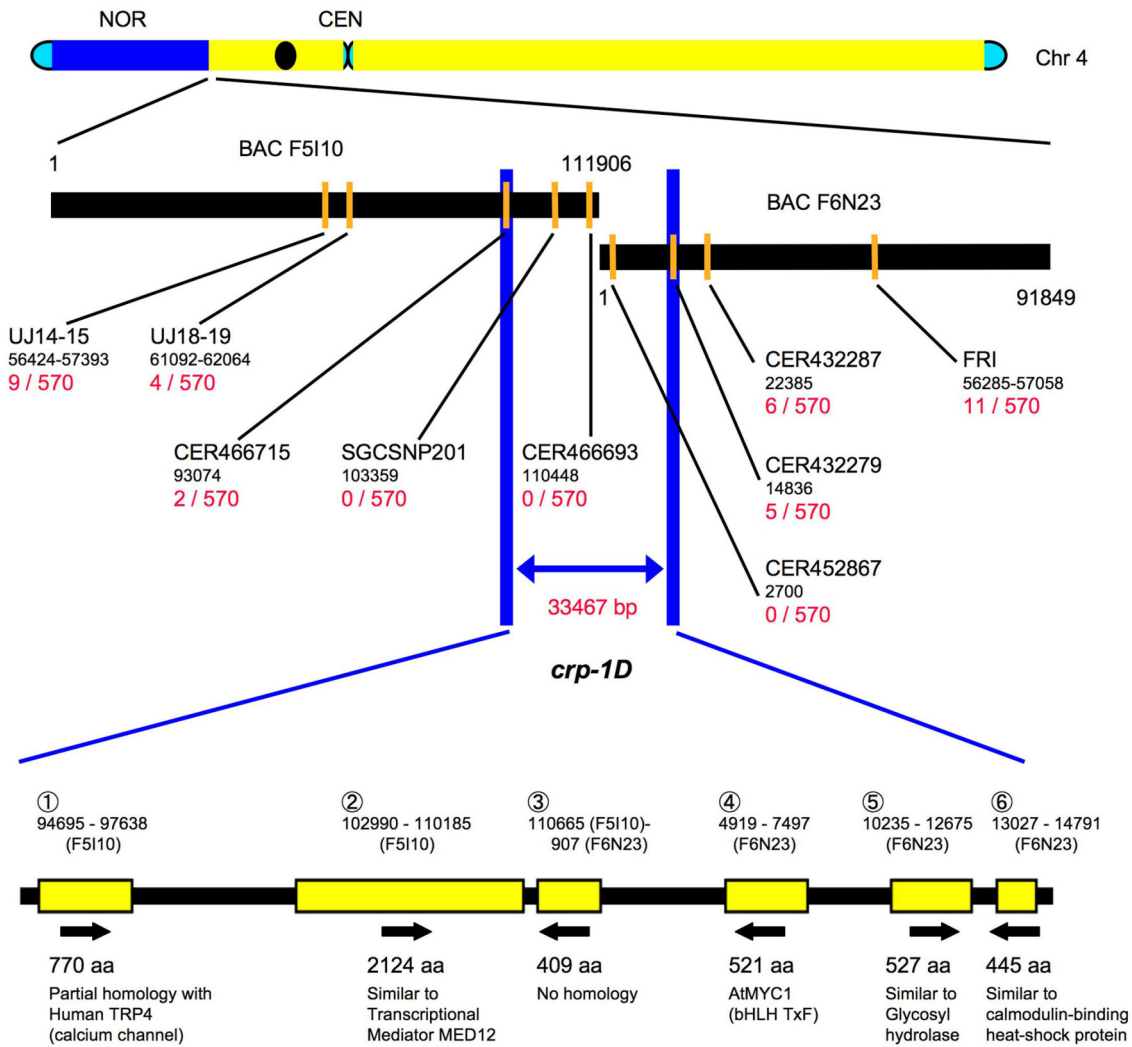
Gene	Sequence (5' to 3')		References
	Forward	Reverse	
<i>ACT2</i>	AGAGATTCAGATGCCCAGAAGTCTTGTCC	AACGATTCTGGACCTGCCTCATCATACTC	Abe et al. 2005
<i>CRP</i>	CATGAAGGAGTTAGTGAAGC	AGTCCTTTGCTTTCACCTAC	in this study

**Supplementary Table S14.** Primer sets used in constructs.

Primer	Sequence (5' to 3')	Experiment
CRP pro. 1	ATAATAAAATGAATGAAAGTAATAATAAT	<i>CRP::GUS</i>
CRP pro. 2	TTCTCCCAACTATATCCAGCATACT	<i>CRP::GUS</i>
CRP ATG	gtcgacATGCAAAGGTATCATGCTGCCAACTG	<i>CRP-GFP, crp-1D-GFP</i>
CRP stop	ttctcgagCCTCAGCTGTCGTCGCTACTG	<i>CRP::GFP, crp-1D-GFP</i>

**Supplementary Table S15.** Accession numbers of *Arabidopsis* genes used in this study.

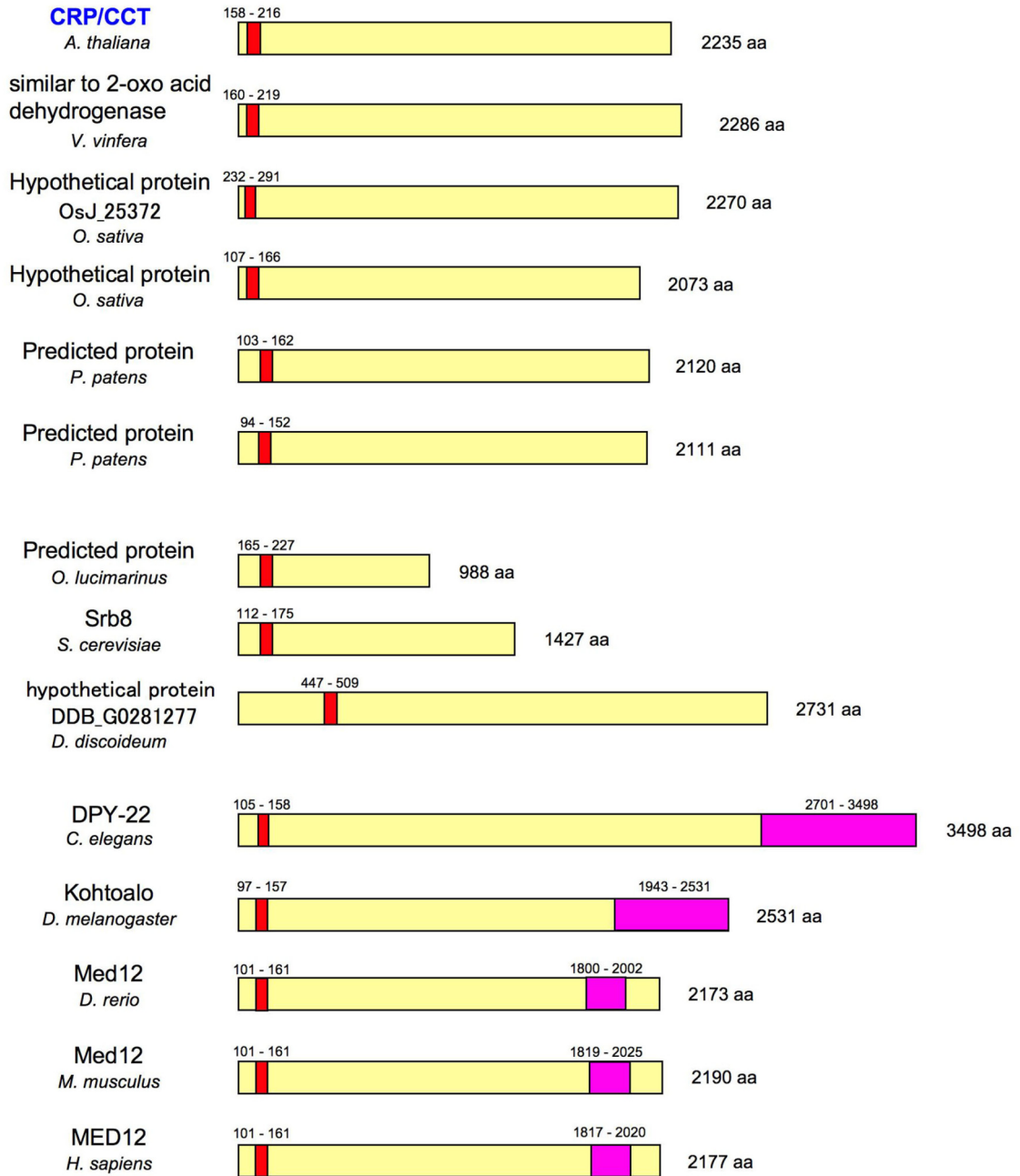
	Gene	AGI code
ACT2	ACTIN2	At3g18780
AG	AGAMOUS	At4g18960
AP1	APETALA 1	At1g69120
CLF	CURLY LEAF	At2g23380
CO	CONSTANS	At5g15840
CRP	CRYPTIC PRECOCIOUS	At4g00450
CYC1;1	Cyclin C 1;1	At5g48640
CYC1;2	Cyclin C 1;2	At5g48630
ETT	ETTIN	At2g33860
FD	FD	At4g35900
FLC	FLOWERING LOCUS C	At5g10140
FT	FLOWERING LOCUS T	At1g65480
FUL	FRUITFULL	At5g60910
HEN3	HUA ENHANCER 3	At5g63610
LFY	LEAFY	At5g61850
LUG	LEUNIG	At4g32551
NRT1.7	NITRATE TRANSPORTER 1.7	At1g69870
MAB2	MACCHI-BOU 2	At1g55325
MED8	MEDIATOR COMPLEX SUBUNIT 8	At5g63480
PFT1	PHYTOCHROME AND FLOWERING TIME 1	At1g25540
PID	PINOID	At2g34650
SEU	SEUSS	At1g43850
SOC1	SUPPRESSOR OF OVEREXPRESSION OF CO 1	At2g45660
STM	SHOOT MERISTEMLESS	At1g62360
SULTR2;1	SULFATE TRANSPORTER 2;1	At5g10180
TSF	TWIN SISTER OF FT	At4g20370



### Supplementary Figure S1. Mapping and identification of the *CRP* gene.

The *CRP* locus was mapped to a 33,467-bp region between CER466715 (BAC F5110) and CER432279 (BAC F6N23) markers on the top arm of chromosome 4 by analyzing *CRP*<sup>+</sup>/*CRP*<sup>+</sup> progeny from a cross between *crp-1D* (Col) and *35S::FT* (Ler). Six genes were predicted in the region. No significant change in expression level of these genes was observed in *crp-1D* relative to wild type. A C-to-T substitution in the coding region of gene 2 (At4g00450) was the found by sequence analysis of these six genes in *crp-1D* mutant.

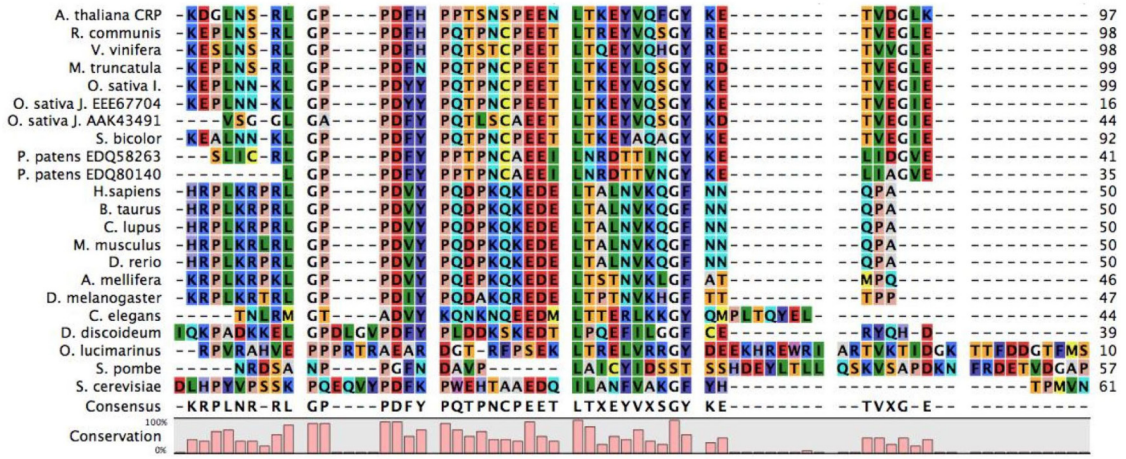




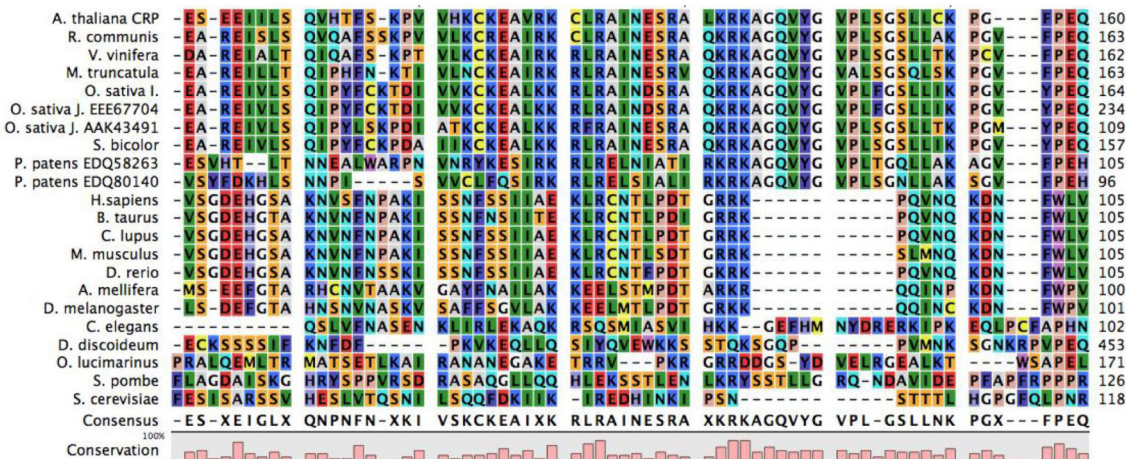
**Supplementary Figure S2. The domain structure of MED12 orthologues.**

Red and pink boxes represent MED12 domain and PQL region, respectively.

SSM#1

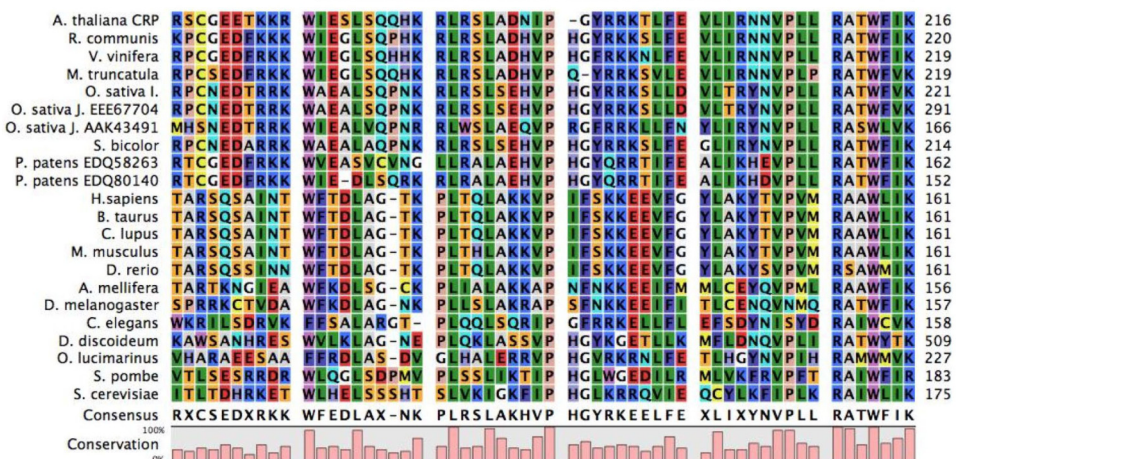


SSM#2



SSM#3

SSM#4

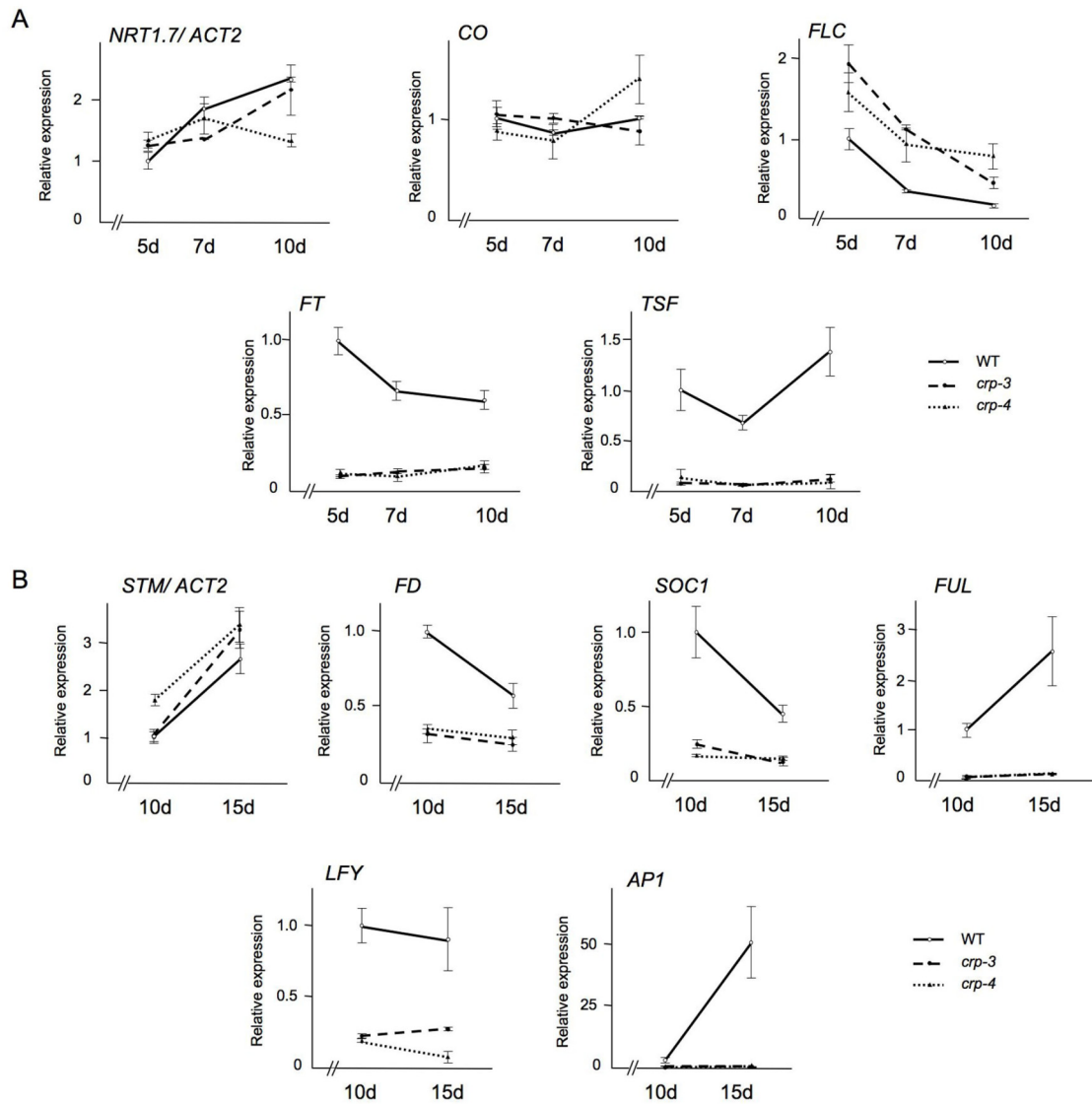


### Supplementary Figure S3. Sequence alignment of MED12 proteins.

Sequence alignment of MED12 domain of CRP and MED12 orthologues. Alignment was done with the CLC sequence viewer 6 for the twenty-two sequences summarized in Table below. Thick lines indicate signature sequence motif (SSM) (Bourbon 2008). Arrowheads indicate the position of *crp-ID* mutation. Arrows indicate from start and end positions of the MED12 domain.

#### MED12 orthologues.

Name		Length	MED12 domain
Arabidopsis thaliana	CRP	2235	158 - 216
Ricinus communis	XP_002511863	2264	161 - 220
Vitis vinifera	XM_002274443	2286	160 - 219
Medicago truncatula	ABD32834	2270	161 - 219
Oryza sativa Indica	EEC82567	2094	162 - 221
Oryza sativa. japonica	EEE67704	2270	232 - 291
Oryza sativa. japonica	AAK43491	2073	107 - 166
Sorghum bicolor	XP_002466024	2201	155 - 214
Physcomitrella patens	EDQ58263	2120	103 - 162
Physcomitrella patens	EDQ80140	2111	94 - 152
Homo sapiens	NM_005120.2	2177	101 - 161
Bos taurus	XP_599229	2176	101 - 161
Canis lupus	XP_538072	2186	101 - 161
Mus musculus	NP_067496	2190	101 - 161
Danio rerio	NP_001034550	2173	101 - 161
Apis mellifera	XP_392792	2243	97 - 157
Drosophila melanogaster	NP_524786	2531	97 - 157
Caenorhabditis elegans	NP_509645	3498	105 - 158
Dictyostelium discoideum	XP_640927	2731	447 - 509
Ostreococcus lucimarinus	XP_001420511	988	165 - 227
Schizosaccharomyces pombe	NP_594066	1134	120 - 183
Saccharomyces cerevisiae	NP_010004	1427	112 - 175

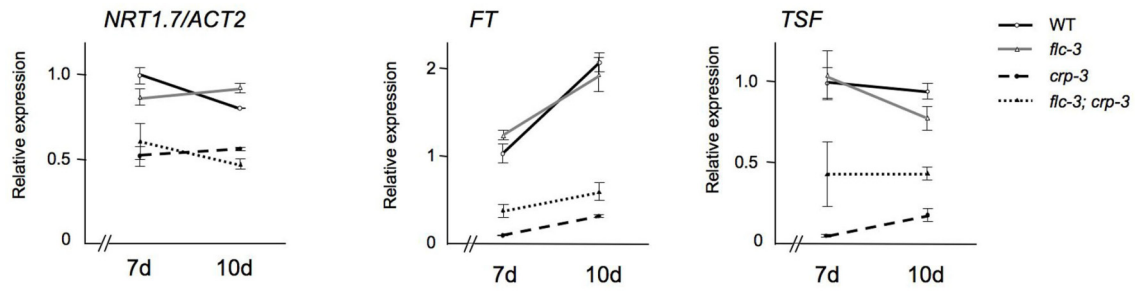


**Supplementary Figure S4. Expression level of *NRT1.7* and *STM* in *crp* mutant plants.**

(A) *NRT1.7* expression level (relative to *ACT2*) and expression levels of *CO*, *FLC*, *FT* and *TSF* (normalized by *NRT1.7*) in wild-type Col and *crp* mutants. Aerial parts of seedlings grown under long-day conditions were harvested on days 5, 7, and 10 for qRT-PCR analysis.

(B) *STM* expression (relative to *ACT2*) and expression levels of *FD*, *SOC1*, *FUL*, *LFY*, and *AP1* (normalized by *STM*) in wild-type Col and *crp* mutants. Shoot apical region of seedlings grown under long-day conditions was harvested on days 10 and 15 for qRT-PCR analysis.

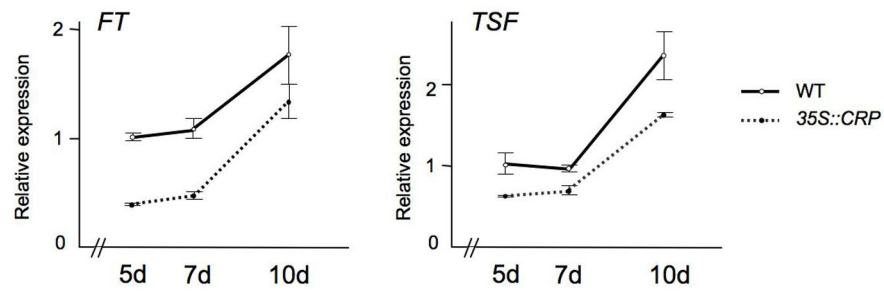
Error bars indicate SE (n=9).



**Supplementary Figure S5. Effect of *flc* loss-of-function mutation on expression levels of *FT* and *TSF* in *crp-3*.**

*NRT1.7* expression level (relative to *ACT2*) and expression levels of *FT* and *TSF* (normalized by *NRT1.7*) in wild-type Col, *flc-3*, *crp-3* and *flc-3; crp-3* plants. Aerial parts of seedlings grown under long-day conditions were harvested on days 7 and 10 for qRT-PCR analysis.

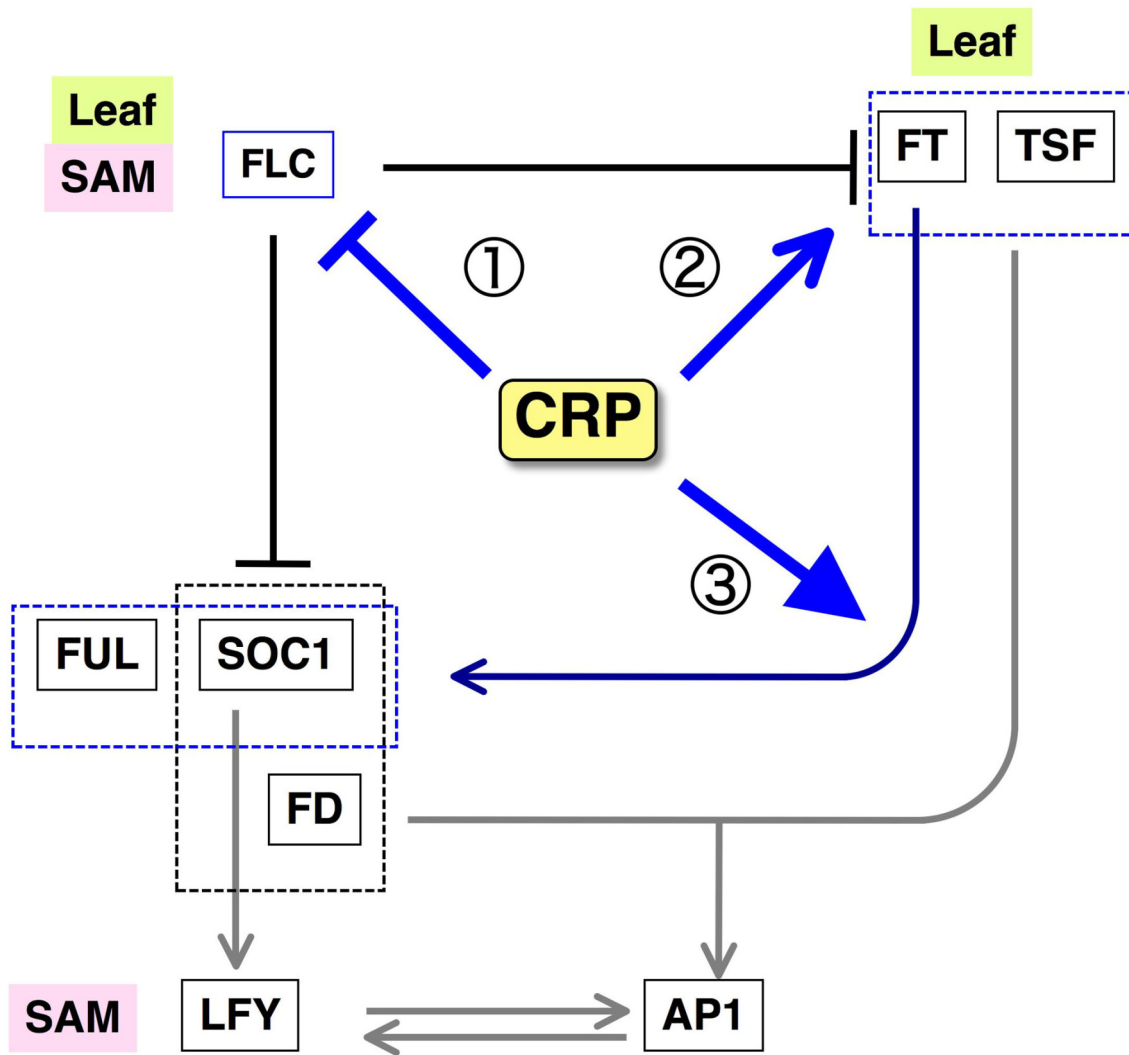
Error bars indicate SE (n=9).



**Supplementary Figure S6. Effects of *CRP* over-expression on expression levels of *FT* and *TSF*.**

*FT* and *TSF* expression levels (normalized by *NRT1.7*) in wild-type Col and *35S::CRP* #11 plants. Aerial parts of seedlings grown under long-day conditions were harvested on days 5, 7 and 10 for qRT-PCR analysis.

Error bars indicate SE (n=9).



**Supplementary Figure S7. Genetic framework of feed-forward regulation by *CRP*.** Arrows indicate transcriptional activation. T-bars indicate transcriptional repression. See text for detailed explanation.

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