



Figure S1

Method used for exogenous application of ABA. The ABA or mock solutions are applied in soil using a pipette tip as a funnel. Treatments started early in development (3 days post germination), thus before the floral transition.

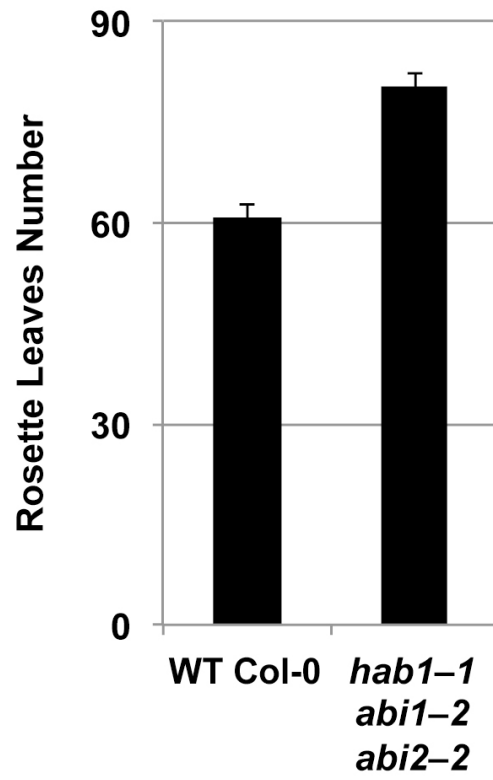


Figure S2

Activated ABA signaling inhibits flowering under SDs. Rosette leaves mean number at flowering of wild type (Col-0) and mutant *hab1-1 abi1-2 abi2-2* grown under SDs. Student's t test P value ≤ 0.001 (***) compared to Wild Type.

Supplemental Table S1

Fig 1	A	Genotype	MOCK			ABA 25µM			t-test MOCK vs ABA 25µM
			Rosette leaves	SE	range	Rosette leaves	SE	range	
		WT Col-0	10.3	0.3	9-12	8.6	0.6	5-10	P< 0.001
		<i>aba1-6</i>	17.8	0.7	16-22	11.9	0.9	8-17	P< 0.001
		<i>aba2-1</i>	16.9	0.7	13-21	8.8	0.5	7-13	P< 0.001
		One-Way ANOVA with post-HOC Tukey HSD Test							
		MOCK Genotype pair	p-value	inference					
		WT Col vs <i>aba1-6</i>	1.01E-03	** p<0.01					
		WT Col vs <i>aba2-1</i>	1.01E-03	** p<0.01					
		<i>aba1-6</i> vs <i>aba2-1</i>	2.77E-01	NS					
		Normal Watering							
	B	Genotype	Rosette leaves	SE	range	t-test			
		WT Col-0	13.9	0.5	12-16				
		<i>aba1-6</i>	17.1	0.3	16-18	P<0.001			
		<i>ft-10</i>	40.9	1.4	36-48				
		<i>ft-10 aba1-6</i>	53.3	1.3	40-63	P<0.001			
		<i>ft-10 tsf-1</i>	53.9	0.6	51-55				
		<i>ft-10 tsf-1 aba1-6</i>	58.4	1.4	53-64	P=0.018			
		<i>gi-2</i>	61.9	1.0	59-67				
		<i>gi-2 aba1-6</i>	62.0	1.2	54-73	P=0.945			
		Normal Watering							
	C	Genotype	Rosette leaves	SE	range	t-test			
		WT Col-0	6.5	0.2	5-8				
		<i>aba1-6</i>	7.8	0.2	7-9	P<0.001			
		<i>ft-10</i>	20.8	0.5	19-23				
		<i>ft-10 aba1-6</i>	24.9	0.5	24-28	P<0.001			
		<i>co-10</i>	36.0	0.7	31-40				
		<i>co-10 aba1-6</i>	36.5	1.0	28-43	P=0.484			
Fig 3	A	Genotype	Normal Watering			Low Watering			t-test NW vs LW
			Rosette leaves	SE	range	Rosette leaves	SE	range	
		WT Col-0	15.9	0.4	14-18	11.7	0.5	9-15	P<0.001
		<i>cdf1-R cdf2-1 cdf3-1 cdf5-1</i>	7.8	0.2	6-9	5.8	0.1	5-7	P<0.001
		<i>cdf1-R cdf2-1 cdf3-1 cdf5-1 gi-100</i>	9.2	0.2	8-11	8.9	0.2	8-10	P=0.311
		Normal Watering							
	B	Genotype	Rosette leaves	SE	range	Low Watering			t-test NW vs LW
			Rosette leaves	SE	range	Rosette leaves	SE	range	
		WT Col-0	55.7	0.9	51-62	63.4	2.4	55-75	P=0.003
		<i>co-10</i>	57.5	1.3	51-65	73.2	2.8	54-85	P<0.001
		<i>cdf1-R cdf2-1 cdf3-1 cdf5-1</i>	10.5	0.4	8-14	10.2	0.8	7-15	P=0.729
		Normal Watering							
	G	Genotype	Rosette leaves	SE	range	t-test			
		WT Col-0	14.0	0.0	14				
		<i>aba1-6</i>	22.7	4.0	16-27	P<0.001			
		<i>elf3-1</i>	4.1	0.4	4-5				
		<i>elf3-1 aba1-6</i>	6.5	1.6	4-9	P<0.001			

Fig 4

A	Genotype	Normal Watering			Low Watering			t-test NW vs LW
		Rosette leaves	SE	range	Rosette leaves	SE	range	
	WT Ler	8.2	0.2	7-9	6.9	0.1	6-8	P<0.001
	<i>aba1-1</i>	9.4	0.3	8-11	9.0	0.3	8-10	P=0.365
	<i>aba1-3</i>	9.3	0.2	8-11	9.3	0.2	8-10	P=0.446
	<i>abi1-1</i>	8.5	0.3	7-9	9.5	0.3	8-10	P<0.001
One-Way ANOVA with post-HOC Tukey HSD Test								
	Normal Watering Genotype pair	p-value	inference					
	WT Ler vs <i>aba1-1</i>	1.01E-03	** p<0.01					
	WT Ler vs <i>aba1-3</i>	3.98E-03	** p<0.01					
	WT Ler vs <i>abi1-1</i>	8.56E-01	NS					
	<i>aba1-1</i> vs <i>aba1-3</i>	9.00E-01	NS					
	<i>aba1-1</i> vs <i>abi1-1</i>	5.83E-02	NS					
	<i>aba1-3</i> vs <i>abi1-1</i>	1.30E-01	NS					
B	Genotype	Normal Watering						
		Rosette leaves	SE	range				
	WT Ler	37.9	0.7	33-41				
	<i>aba1-3</i>	37.0	1.2	27-42				
	<i>abi1-1</i>	27.0	1.0	20-32				
One-Way ANOVA with post-HOC Tukey HSD Test								
	Normal Watering Genotype pair	p-value	inference					
	WT Ler vs <i>aba1-3</i>	7.76E-01	NS					
	WT Ler vs <i>abi1-1</i>	1.01E-03	** p<0.01					
	<i>aba1-3</i> vs <i>abi1-1</i>	1.01E-03	** p<0.01					

Fig 5

F	Genotype	Normal Watering			Low Watering			t-test NW vs LW
		Rosette leaves	SE	range	Rosette leaves	SE	range	
	WT Ler	35.9	0.5	32-38	38.4	0.8	35-44	P=0.016
	<i>abi1-1</i>	27.6	0.8	23-32	31.9	1.3	21-36	P=0.019
	35S::<i>GI</i>	13.6	0.3	12-16	11.8	0.2	11-13	P<0.001
	35S::<i>GI abi1-1</i>	12.6	0.5	10-17	17.5	0.5	15-20	P<0.001
One-Way ANOVA with post-HOC Tukey HSD Test								
	Normal Watering Genotype pair	p-value	inference					
	WT Ler vs <i>abi1-1</i>	1.01E-03	** p<0.01					
	WT Ler vs 35S::<i>GI</i>	1.01E-03	** p<0.01					
	WT Ler vs 35S::<i>GI abi1-1</i>	1.01E-03	** p<0.01					
	<i>abi1-1</i> vs 35S:: <i>GI</i>	1.01E-03	** p<0.01					
	<i>abi1-1</i> vs 35S:: <i>GI abi1-1</i>	1.01E-03	** p<0.01					
	35S:: <i>GI</i> vs 35S:: <i>GI abi1-1</i>	5.07E-01	NS					

Fig 6

C	Genotype	Normal Watering						
		Rosette leaves	SE	range				
	WT Ler	28.9	1.4	25-37				
	<i>abi1-1</i>	17.0	0.4	16-19				
	<i>soc1-1</i>	50.3	1.9	42-59				
	<i>abi1-1 soc1-1</i>	53.7	1.3	39-61				
One-Way ANOVA with post-HOC Tukey HSD Test								
	Genotype pair	p-value	inference					
	WT Ler vs <i>abi1-1</i>	1.01E-03	** p<0.01					
	WT Ler vs <i>soc1-1</i>	1.01E-03	** p<0.01					
	WT Ler vs <i>abi1-1 soc1-1</i>	1.01E-03	** p<0.01					
	<i>abi1-1</i> vs <i>soc1-1</i>	1.01E-03	** p<0.01					
	<i>abi1-1</i> vs <i>abi1-1 soc1-1</i>	1.01E-03	** p<0.01					
	<i>soc1-1</i> vs <i>abi1-1 soc1-1</i>	3.25E-01	NS					

6	D	Genotype	Normal Watering		
			Rosette leaves	SE	range
		WT Ler	8.3	0.2	8-9
		<i>abi1-1</i>	8.4	0.2	8-9
		<i>soc1-1</i>	12.5	0.2	12-13
		<i>abi1-1 soc1-1</i>	15.0	0.2	14-16
One-Way ANOVA with post-HOC Tukey HSD Test					
		Genotype pair	p-value	inference	
		WT Ler vs <i>abi1-1</i>	7.96E-01	NS	
		WT Ler vs <i>soc1-1</i>	5.69E-06	*** p<0.001	
		WT Ler vs <i>abi1-1 soc1-1</i>	6.88E-15	*** p<0.001	
		<i>abi1-1</i> vs <i>soc1-1</i>	7.08E-05	*** p<0.001	
		<i>abi1-1</i> vs <i>abi1-1 soc1-1</i>	2.80E-14	*** p<0.001	
		<i>soc1-1</i> vs <i>abi1-1 soc1-1</i>	3.62E-10	*** p<0.001	

Fig Supp 2	Genotype	Normal Watering			t-test
		Rosette leaves	SE	range	
	WT Col-0	60.6	2.1	49-80	
	<i>hab1-1 abi1-2 abi2-2</i>	80.4	1.9	68-101	P<0.001

Flowering time of mutant and transgenic plants used in this study. Mean values of vegetative leaves and standard error (SE) of plants under different watering conditions. Two tailed Student's *t* test values (*P*) and One-Way ANOVA (*P*) are shown, NS (Not Significant).

Supplemental Table S2

Fig 3	H	GI expression Genotype pair	Tukey HSD	
			p-value	inference
		WT Col-0 vs <i>aba1-6</i>	9.00E-01	NS
		WT Col-0 vs <i>elf3-1</i>	1.01E-03	** p<0.01
		WT Col-0 vs <i>elf3-1 aba1-6</i>	1.01E-03	** p<0.01
		<i>aba1-6</i> vs <i>elf3-1</i>	1.01E-03	** p<0.01
		<i>aba1-6</i> vs <i>elf3-1 aba1-6</i>	1.01E-03	** p<0.01
		<i>elf3-1</i> vs <i>elf3-1 aba1-6</i>	9.00E-01	NS
	I	CO expression Genotype pair	Tukey HSD	
		WT Col-0 vs <i>aba1-6</i>	1.29E-01	NS
		WT Col-0 vs <i>elf3-1</i>	8.99E-01	NS
		WT Col-0 vs <i>elf3-1 aba1-6</i>	8.96E-01	NS
		<i>aba1-6</i> vs <i>elf3-1</i>	3.57E-02	* p<0.05
		<i>aba1-6</i> vs <i>elf3-1 aba1-6</i>	3.76E-01	NS
		<i>elf3-1</i> vs <i>elf3-1 aba1-6</i>	5.19E-01	NS
	J	FT expression Genotype pair	Tukey HSD	
		WT Col-0 vs <i>aba1-6</i>	9.00E-01	NS
		WT Col-0 vs <i>elf3-1</i>	1.46E-02	* p<0.05
		WT Col-0 vs <i>elf3-1 aba1-6</i>	9.00E-01	NS
		<i>aba1-6</i> vs <i>elf3-1</i>	6.89E-03	** p<0.01
		<i>aba1-6</i> vs <i>elf3-1 aba1-6</i>	9.00E-01	NS
		<i>elf3-1</i> vs <i>elf3-1 aba1-6</i>	1.08E-02	* p<0.05
	K	TSF expression Genotype pair	Tukey HSD	
		WT Col-0 vs <i>aba1-6</i>	7.44E-02	NS
		WT Col-0 vs <i>elf3-1</i>	4.35E-01	NS
		WT Col-0 vs <i>elf3-1 aba1-6</i>	1.49E-01	NS
		<i>aba1-6</i> vs <i>elf3-1</i>	3.44E-03	** p<0.01
		<i>aba1-6</i> vs <i>elf3-1 aba1-6</i>	9.00E-01	NS
		<i>elf3-1</i> vs <i>elf3-1 aba1-6</i>	7.37E-03	** p<0.01

One-Way ANOVA (*P*) for the expression analysis of Fig 3H-K are shown, NS (Not Significant).

Supplemental Table S3

Allele	Reference	Background
<i>aba1-6</i>	(Niyogi et al., 1998)	Col-0
<i>aba2-1</i>	(Léon-Kloosterziel et al., 1996)	Col-0
<i>ft-10</i>	(Yoo et al., 2005)	Col-0
<i>ft-10 aba1-6</i>	This Work	Col-0
<i>ft-10 tsf-1</i>	(Jang et al., 2009)	Col-0
<i>ft-10 tsf-1 aba-6</i>	This Work	Col-0
<i>gi-2</i>	(Fowler et al., 1999)	Col-1
<i>gi-2 aba1-6</i>	This Work	Col-1
<i>co-10</i>	(Laubinger et al., 2006)	Col-0
<i>co-10 aba1-6</i>	This Work	Col-0
<i>elf3-1</i>	(Zagotta et al., 1992)	Col-0
<i>elf3-1 aba1-6</i>	This Work	Col-0
<i>cdf1-R cdf2-1 cdf3-1 cdf5-1</i>	(Fornara et al., 2009)	Col-0
<i>gi-100 cdf1-R cdf2-1 cdf3-1 cdf5-1</i>	(Fornara et al., 2009)	Col-0
<i>aba1-1</i>	(Koornneef et al. 1982)	Ler
<i>aba1-3</i>	(Koornneef et al. 1982)	Ler
<i>abil-1</i>	(Koornneef et al., 1984)	Ler
<i>soc1-1</i>	(Onouchi et al., 2000)	Ler
<i>abil-1 soc1-1</i>	This Work	Ler
<i>35S::GI</i>	(Mizoguchi et al., 2005)	Ler
<i>abil-1 35S::GI</i>	This Work	Ler
<i>hab1-1 abil-2 pp2ca-1</i>	(Rubio et al., 2009)	Col-0
<i>hab1-1 abil-2 abi2-2</i>	(Rubio et al., 2009)	Col-0

Genotypes used in this study

Fornara F, Panigrahi KCS, Gissot L, Sauerbrunn N, RUhl M, Jarillo JA, Coupland G (2009) Arabidopsis DOF Transcription Factors Act Redundantly to Reduce CONSTANS Expression and Are Essential for a Photoperiodic Flowering Response. *Dev Cell* **17**: 75–86

Fowler S, Lee K, Onouchi H, Samach A, Richardson K, Morris B, Coupland G, Putterill J (1999) GIGANTEA: a circadian clock-controlled gene that regulates photoperiodic flowering in Arabidopsis and encodes a protein with several possible membrane-spanning domains. *EMBO J* **18**: 4679–4688

Jang S, Torti S, Coupland G (2009) Genetic and spatial interactions between FT, TSF and SVP during the early stages of floral induction in Arabidopsis. *The Plant Journal* **60**: 614–625

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- Yoo SK, Chung KS, Kim J, Lee JH, Hong SM, Yoo SJ, Yoo SY, Lee JS, Ahn JH** (2005) CONSTANS activates SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1 through FLOWERING LOCUS T to promote flowering in Arabidopsis. *Plant Physiol* **139**: 770–778
- Zagotta MT, Shannon S, Jacobs C, Meeks-Wagner DR** (1992) Early-Flowering Mutants of Arabidopsis thaliana. *Australian Journal of Plant Physiology* **19**: 411–418

Supplemental Table S4

Gene	Forward	Use
<i>aba1-6</i>	GCTCGGAGTAAAGGCGGCGA CAGGAAGTCCCCGTGACGCC	Genotyping
<i>abil-1</i>	ATGGAGGAAGTATCTCCGGCG TCAGTTCAAGGGTTTGCTCTTGAG	Genotyping
<i>CO WT</i>	atgttgaacaagagagtaac tcattgtgtactgtatcatctg	Genotyping
<i>co-10</i>	atgttgaacaagagagtaac gcctttcagaatggataaatgccttgcttcc	Genotyping
<i>atb pAB11</i>	GGGGACAAGTTTGTACAAAAAAGCAGGCTCTCTTATCCACTTGCCCCG GGGGACCACTTGTACAAGAAAGCTGGGTGCGATCGCCGGAGATACTC	Cloning
<i>ACT</i>	CTCTCCCGCTATGTATGTCGCCA GTGAGACACACCATCACCAG	qPCR
<i>CO</i>	CTACAACGACAATGGTTCCATTAAC CAGGGTCAGGTTGTTGC	qPCR
<i>FT</i>	CTAGCAACCCTCACCTCCGAGAATA CTGCCAAGCTGTCGAAACAATATAA	qPCR
<i>TSF</i>	CTCGGGAATTCATCGTATTG CCCTCTGGCAGTTGAAGTAA	qPCR
<i>SOC1</i>	ATCGAGGAGCTGCAACAGAT GCTACTCTCTTCATCACCTCTCC	qPCR
<i>GI</i>	AATTCAGCACGCGCCTATTG GTTGCTTCTGCTGCAGGAACTT	qPCR

Primers used in this study