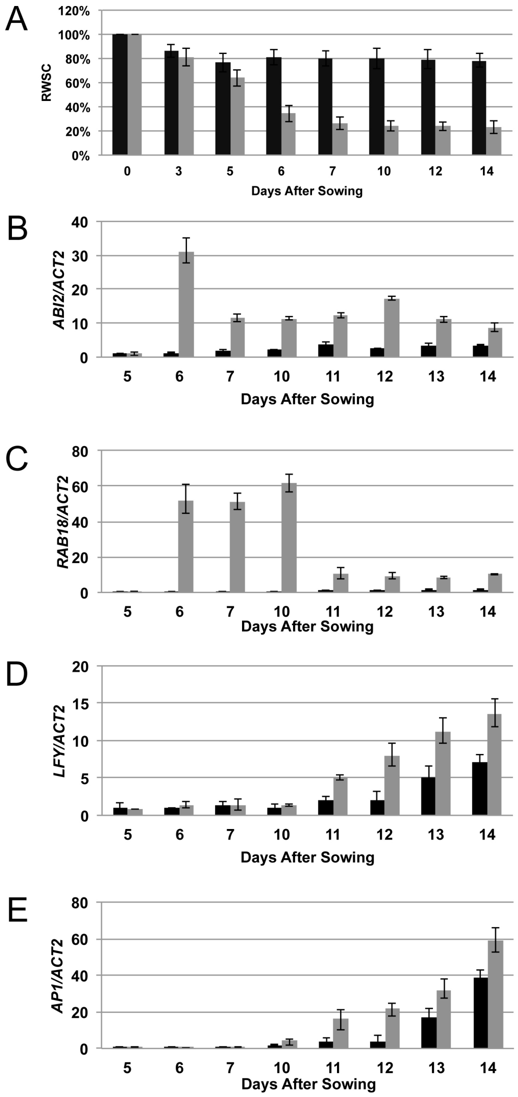

Figure S1. DE Response Induction in Arabidopsis.

(A) Mean relative soil water content (RSWC) values in Arabaskets pots of plants undergoing normal watering (NW, black bar) and low watering (LW, grey bar) treatments. Pots (n = 17) were weighed at the indicated days in 16 h light / 8 h dark photoperiod.

(B) to **(E)** Real-time qPCR transcript analyses of ABA and floral markers in wild-type (Col-0) plants grown under a 16 h light / 8 h dark photoperiod as detailed in (**A**). At least 20 seedlings from 3 different pots were harvested at the indicated days after sowing at Zeitgeber time 8. Values represent fold change variations of *ABI2* (**B**), *RAB18* (**C**), *LFY* (**D**) and *AP1* (**E**) transcript levels relatively to day 5. *ACTIN2* expression (*ACT2*) was used for normalization; error bars represent SE of two technical replicates. A representative experiment of two biological replicates is shown.

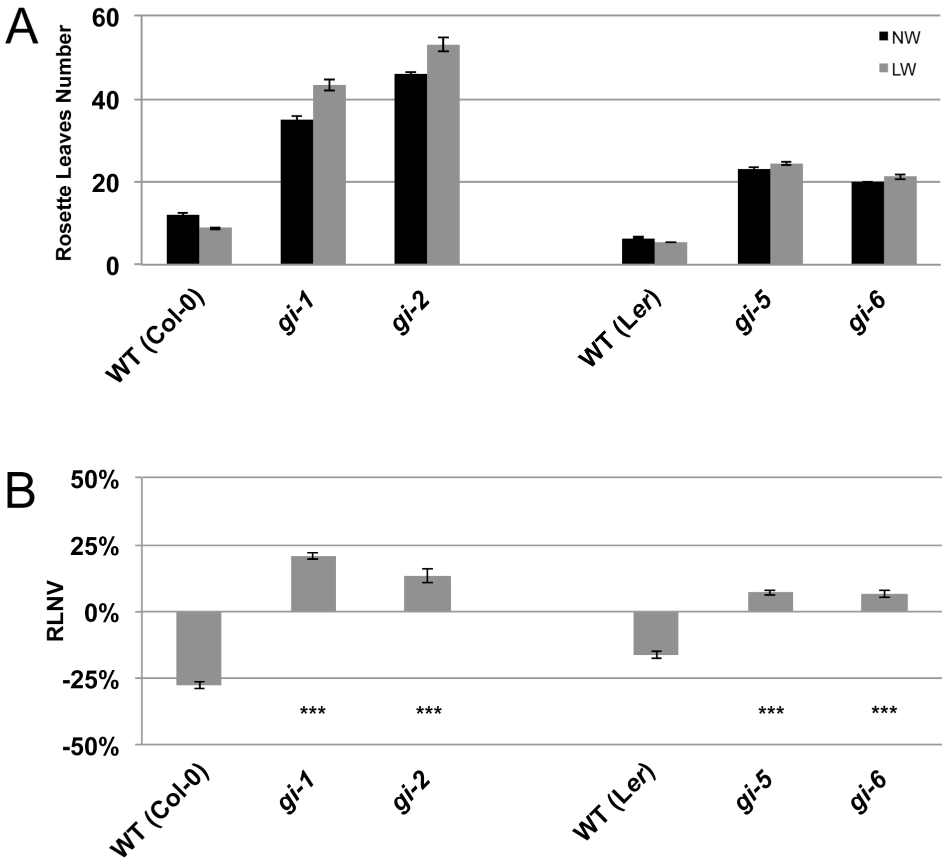

Figure S2. Absence of DE Response in Independent *gi* Alleles.

(A) Rosette leaves mean number of wild type and *gi* mutants grown under LDs. Plants were subjected to NW (black bars) or LW (grey bars) regimes. Error bars represent ± SE n = 15.

(B) Quantification of DE response for each genotype detailed in (**A**) expressed as relative leaves number variation (RLNV). Error bars represent ± SE, Student's t test P values ≤ 0.001 (***).

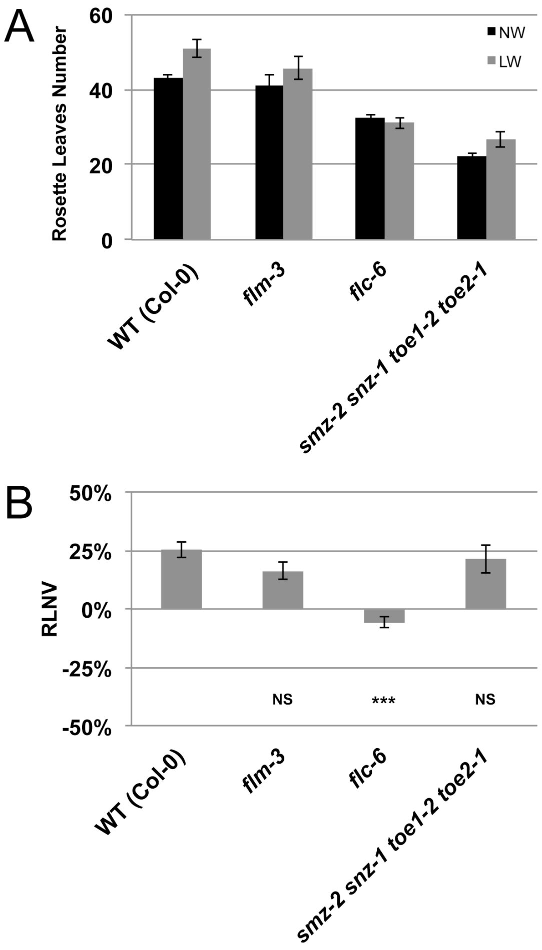

Figure S3. DE Response in Floral Repressors Mutants Under SDs.

(A) Rosette leaves mean number of wild-type and the indicated floral repressor mutants grown under SDs (10 h light / 14 h dark). Plants were subjected to NW (black bars) or LW (grey bars) regimes. Error bars represent ± SE n = 17.

(B) Quantification of DE response for each genotype detailed in (**A**) expressed as RLNV. Error bars represent ± SE, Student’s t test P values ≤ 0.001 (***), > 0.05

not significant (NS).

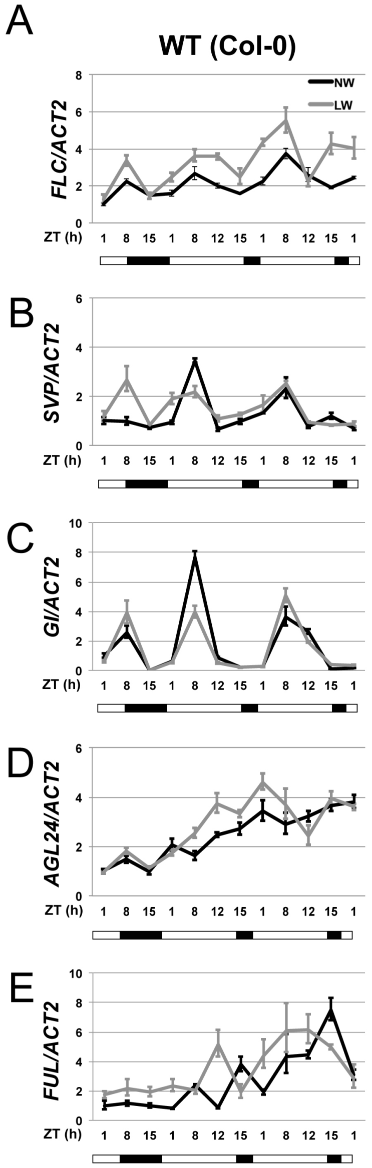

Figure S4. Floral Genes Regulation Under Drought Stress Upon SDs to LDs Shifts.

(A) to **(E)** Real-time qPCR of floral genes transcripts in 3 week-old wild-type seedlings. Plants were subjected to NW (black lines) or LW (grey lines) regimes and harvested at the indicated time points (Zeitgeber, ZT) in coincidence with the light phase (open bar) or in the dark (black bar) during a SDs to LDs shift. At each time point, values represent fold change variations of transcript levels of *FLC* **(A)**, *SVP* **(B)**, *GI* **(C)**, *AGL24* **(D)** and *FUL* **(E)** relatively to the first ZT1 (arbitrarily set at 1 in normal watering control). *ACT2* expression was used for normalization; error bars represent SD of two technical replicates. A representative experiment of two biological replicates is shown.

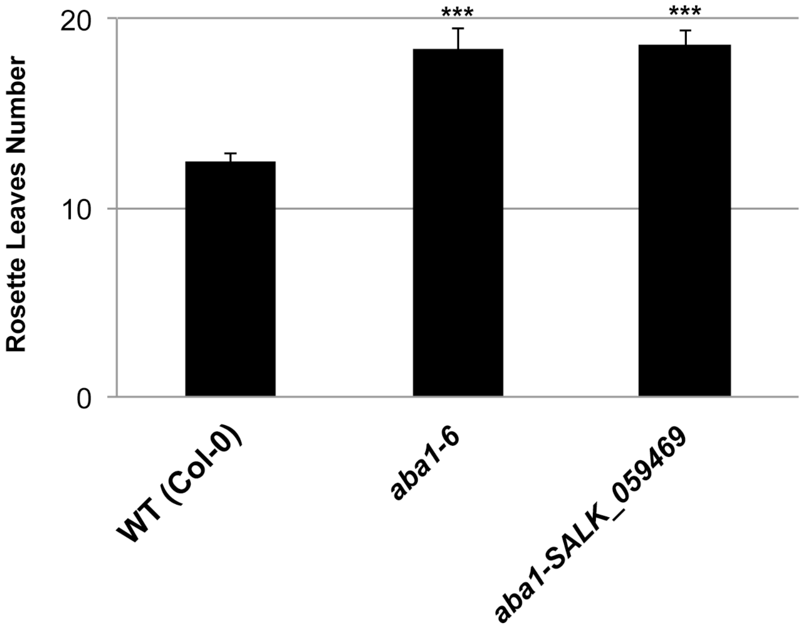

Figure S5. Mean Rosette Leaves Number in *aba1* mutants.

Rosette leaves mean number of wild-type and the indicated *aba1* alleles grown under LDs (16 h light / 8 h dark). Error bars represent ± SE n = 9 to 17. *** indicate Student's t test P values ≤ 0.001.

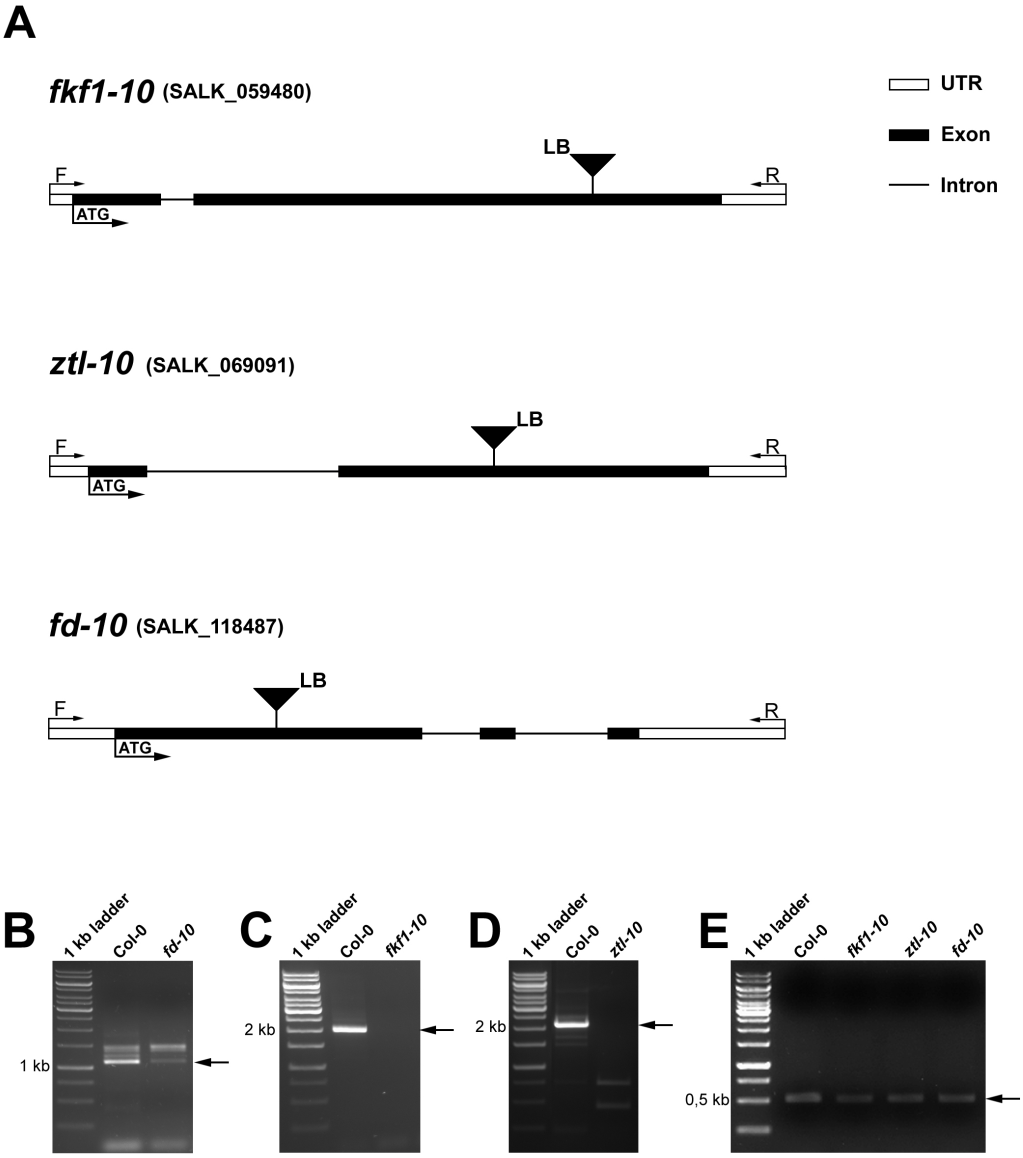

Figure S6. Characterization of T-DNA Insertion Alleles of *FD*, *FKF1* and *ZTL*.

(A) Diagram illustrating the T-DNA insertion alleles of *FD*, *FKF1* and *ZTL*. The positions of the forward (F) and reverse (R) primers used for RT-PCR and the T-DNA Left Board (LB) orientation are shown. **(B)** to **(E)** RT-PCR analysis from total cDNA derived from wild-type and the indicated mutant plants. Gene–specific primers illustrated in **(A)** were used to amplify *FD* **(B)**, *FKF1* **(C)**, *ZTL* **(D)** and *ACT2* **(E)**. Arrows indicate the expected size band. PCR was conducted for 40 cycles except for *ACT2* (25 cycles). PCR products were visualized with Ethidium Bromide on an Agarose gel.

Table S1

Figure	Genotype	Normal Watering			Low Watering			
		VL	SE	range	VL	SE	range	*P* (NW vs. LW)
1 A	**WT (Col–0)**	**12.6**	±0.3	11–15	**9.4**	±0.3	8–12	< .0001
	cry2–1	**32.1**	±1.1	28–44	**28.5**	±0.6	23–31	= .009781
	fkf1–10	**44.0**	±0.8	41–49	**36.0**	±0.7	33–41	< .0001
	ztl–10	**15.1**	±0.4	13–19	**10.8**	±0.2	10–12	< .0001
	gi–100	**54.6**	±0.6	51–59	**65.4**	±1.3	56–72	< .0001
	gi–100 soc1–2	**75.3**	±1.2	67–84	**94.6**	±1.0	88–103	< .0001
	co–10	**44.6**	±0.5	41–49	**35.6**	±0.4	33–38	< .0001
	ft–10	**39.7**	±0.8	33–44	**29.7**	±0.7	23–34	< .0001
	tsf–1	**14.6**	±0.4	13–18	**10.5**	±0.5	8–14	< .0001
	ft–10 tsf–1	**55.2**	±0.8	51–62	**60.2**	±0.8	53–64	= .000228
	smz–D	**50.2**	±0.5	47–53	**34.8**	±0.9	29–43	< .0001
	soc1–2	**20.8**	±0.4	18–24	**20.8**	±0.9	17–26	= .992085
	agl24–2	**14.8**	±0.4	12–18	**10.6**	±0.4	9–13	< .0001
	soc1–2 agl24–2	**34.0**	±0.5	31–37	**32.0**	±0.4	30–35	= .014153
	fd–10	**28.9**	±0.6	25–34	**21.1**	±0.5	18–24	< .0001
	ld–1	**78.4**	±1.7	67–88	**68.0**	±1.4	60–75	= .000317

Figure	Genotype	VL	SE	range	VL	SE	range	*P* (NW vs. LW)
1 C	**WT (L*er*)**	**6.7**	±0.1	6–7	**5.7**	±0.1	5–6	< .0001
	fha–3	**10.2**	±0.3	8–13	**8.7**	±0.3	7–11	= .007010
	phyA–205	**7.8**	±0.3	6–10	**6.3**	±0.2	5–8	= .001191
	gi–4	**27.4**	±0.5	24–31	**29.7**	±1.0	26–32	= .046167
	co–2	**22.2**	±0.5	18–26	**17.5**	±0.5	12–22	< .0001
	ft–1	**21.3**	±0.3	19–25	**18.2**	±0.2	16–20	< .0001
	soc1–1	**15.2**	±0.2	14–17	**15.1**	±0.3	13–17	= .866151
	ful–1	**8.8**	±0.2	8–10	**6.7**	±0.2	6–8	< .0001
	ga1–3	**11.4**	±0.4	9–14	**8.7**	±0.3	7–11	< .0001
	fy–1	**13.8**	±0.5	12–17	**10.4**	±0.3	9–12	< .0001
	fve–1	**19.2**	±0.4	17–22	**16.2**	±0.4	14–19	< .0001
	fca–1	**31.4**	±1.0	23–44	**25.2**	±0.5	20–28	= .001037
2 A	**WT (Col–0)**	**79.5**	±0.8	77–87	**86.7**	±1.7	79–97	= .003456
	gi–2	**99.2**	±1.9	81–111	**108.9**	±3.4	88–130	= .0021275
	flc–6	**74.6**	±1.0	68–81	**74.5**	±1.0	69–77	= .952723
	smz–2 snz–1 toe1–2 toe2–1	**45.5**	±0.6	41–49	**53.6**	±1.5	48–59	< .0001
	svp–41	**22.9**	±0.6	19–27	**18.3**	±0.6	13–22	< .0001
	35S:HA–GI	**42.2**	±2.6	28–51	**32.9**	±2.9	18–41	= .020842
2 A	**WT (L*er*)**	**49.6**	±0.6	44–52	**48.2**	±0.5	44–52	= .063810
	35S:GI	**17.1**	±0.3	15–19	**14.5**	±0.3	13–16	< .0001
	35S:SOC1	**15.1**	±0.5	13–19	**16.1**	±0.8	12–23	= .288215
	35S:GI / - 35S:SOC1 / -	**10.4**	±0.4	8–14	**9.9**	±0.4	7–13	= .297334

	fve–1	**60.6**	±0.8	54–65	**74.5**	±1.4	69–84	< .0001
	fca–1	**89.6**	±0.9	85–95	**100.8**	±1.5	86–106	= .000309
2 B	**WT (Col–0)**	**12.9**	±0.5	10–16	**9.4**	±0.3	7–12	< .0001
	flc–6	**10.9**	±0.1	10–11	**7.6**	±0.2	7–9	< .0001
	flm–3	**11.5**	±0.4	8–14	**8.6**	±0.3	7–10	< .0001
	svp–41	**5.9**	±0.1	5–7	**5.3**	±0.1	5–6	= .000327
	35S:SVP	**24.3**	±0.5	22–28	**19.9**	±0.5	18–23	< .0001
	WT (L*er*)	**7.7**	±0.1	6–7	**6.4**	±0.1	5–6	= .000353
	35S:SOC1	**5.3**	±0.2	4–6	**5.4**	±0.2	4–6	= .500149
	35S:GI	**5.5**	±0.1	5–6	**5.8**	±0.1	5–6	= .170316
3 A	**WT (Col–0)**	**12.9**	±0.3	11–15	**9.7**	±0.2	9–11	< .0001
	aba1–6	**15.5**	±0.3	13–17	**13.9**	±0.5	11–17	= .021215
	aba2–4	**14.5**	±0.3	13–16	**11.7**	±0.3	10–14	< .0001
	hab1–1 abi1–2 pp2ca–1	**10.7**	±0.2	10–11	**8.2**	±0.3	7–9	< .0001
	hab1–1 abi1–2 abi2–2	**9.8**	±0.4	6–15	**7.6**	±0.2	6–10	< .0001
3 E	**WT (Col–0)**	**80.5**	±1.3	62–84	**87.5**	±1.7	81–103	= .002435
	aba1–6	**85.3**	±2.3	71–96	**92.0**	±1.6	81–99	= .025848
	hab1–1 abi1–2 pp2ca–1	**99.7**	±1.3	88–106	**103.4**	±2.0	95–119	= .023857

Figure	**Genotype**	**VL**	**SE**	**range**	***P***	**vs.**
4 G	**WT (Col–0)**	**12.5**	±0.4	10–16		
	aba1–6	**16.4**	±0.3	15–18	< .0001	Col–0
	soc1–2	**25.4**	±0.8	23–29	< .0001	Col–0
	soc1–2 aba1–6	**29.5**	±0.7	26–33	= .00057	*soc1–2*
	svp–41	**5.7**	±0.2	5–6	< .0001	
	svp–41 aba1–6	**6.5**	±0.2	5–8	= .02488	*svp–41*
4 H	**WT (Col-0)**	**81.5**	±0.9	77–87		
	aba1–6	**83.8**	±2.6	71–99	= .102985	Col–0
	svp–41	**20.5**	±0.8	16–26		
	svp–41 aba1–6	**32.6**	±1.2	25–40	< .0001	*svp–41*

		Normal Watering			**Low Watering**			
Figure	**Genotype**	**VL**	**SE**	**range**	**VL**	**SE**	**range**	***P* (NW vs. LW)**
S2	**WT (Col-0)**	**12.2**	±0.4	10–15	**8.8**	±0.3	7–11	< .0001
	gi–1	**35.1**	±1.0	29–41	**43.4**	±1.5	32–58	< .0001
	gi–2	**46.1**	±0.6	43–50	**53.1**	±1.6	44–65	= .000208
	WT (L*er*)	**6.1**	±0.1	6–7	**5.5**	±0.1	5–6	< .0001

	gi–5	**23.1**	±0.5	21–27	**24.4**	±0.4	21–27	= .026375
	gi–6	**19.8**	±0.3	18–22	**21.1**	±0.5	18–26	= .025683
S3	**WT (Col-0)**	**43.0**	±0.9	38–52	**50.9**	±2.4	33–69	= .008682
	flm-3	**41.0**	±3.1	22–59	**45.7**	±3.0	34–64	= .024636
	flc-6	**32.4**	±0.8	27–39	**31.1**	±1.4	24–43	= .412885
	smz-2 snz-1 toe1-2 toe2-1	**22.2**	±0.8	20–25	**26.7**	±2.0	17–39	= .012685

Figure	**Genotype**	**VL**	**SE**	**range**	***P***	**vs.**
S5	**WT (Col-0)**	**12.4**	±0.5	10–14		
	aba1–6	**18.4**	±1.1	14–23	< .0001	Col–0
	aba1-SALK_059469	**18.6**	±0.8	14–25	< .0001	Col–0

Table S1. Flowering time of mutant and transgenic plants used in this study.

Mean values of vegetative leaves (VL) and standard error (SE) of plants undergoing normal watering and low watering conditions. Two tailed Student's *t* test values (*P*) are shown.

Table S2

Allele	Background	Reference
ld–1	Col–1	(Lee et al., 1994)
fca–1	L*er*	(Koornneef et al., 1991)
fve–1	L*er*	(Koornneef et al., 1991)
fy–1	L*er*	(Koornneef et al., 1991)
cry2–1	Col–4	(Guo et al., 1999)
fha–3	L*er*	(Koornneef et al., 1991)
fkf–10	Col–0	This work
ztl–10	Col–0	This work
gi–100	Col–0	(Huq et al., 2000)
gi–1	Col–1	(Fowler et al., 1999)
gi–2	Col–1	(Fowler et al., 1999)
gi–4	L*er*	(Fowler et al., 1999)
gi–5	L*er*	(Fowler et al., 1999)
gi–6	L*er*	(Fowler et al., 1999)
35S:GI gi–3	L*er*	(Mizoguchi et al., 2005)
35S:HA–GI gi–2	Col–0	(David et al., 2006)
phyA–205	L*er*	(Reed et al., 1994)
co–2	L*er*	(Koornneef et al., 1991)
co–10	Col–0	(Laubinger et al., 2006)
ft–1	L*er*	(Koornneef et al., 1991)
ft–10	Col–0	(Yoo et al., 2005)
tsf–1	Col–0	(Yamaguchi et al., 2005)
ft–10 tsf–1	Col–0	(Jang et al., 2009)
fd–10	Col–0	This work
soc1–2	Col–0	(Lee et al., 2000)
soc1–1	L*er*	(Onouchi et al., 2000)
gi–100 soc1–2	Col–0	This work
35S:SOC1	L*er*	Samach et al. 2000
35S:GI -/35S:SOC1 -	Col–0	This work
agl24–2	Col–0	(Michaels Scott D et al., 2003)
soc1–2 agl24–2	Col–0	This work
ful–1	L*er*	(Gu et al., 1998)
svp–41	Col–0	(Hartmann et al., 2000)
35S:SVP	Col–0	(Gregis et al., 2009)
flc–6	Col–0	(Bouveret, 2006)
flm–3	Col–0	(Bouveret, 2006)
smz–2 snz–1 toe1–2 toe2–1	Col–0	(Mathieu et al., 2009)
smz–D	Col–0	(Mathieu et al., 2009)
***aba1*–SALK_059469**	Col–0	(Morris et al., 2006)
aba1–6	Col–0	(Niyogi et al., 1998; Barrero et al., 2005)
aba2–4	Col–0	(Laby et al., 2001)
hab1–1 abi1–2 pp2ca–1	Col–0	(Rubio et al., 2009)
hab1–1 abi1–2 abi2–2	Col–0	(Rubio et al., 2009)

Table S3

Gene	**Forward**	**Reverse**	**Use**
ACT	CTCTCCCGCTATGTATGTCGCCA	GTGAGACACACCATCACCAG	**qPCR**
GI	AATTCAGCACGCGCCTATTG	GTTGCTTCTGCTGCAGGAACTT	**qPCR**
FT	CTAGCAACCCTCACCTCCGAGAATA	CTGCCAAGCTGTCGAAACAATATAA	**qPCR**
TSF	CTCGGGAATTCATCGTATTG	CCCTCTGGCAGTTGAAGTAA	**qPCR**
SOC1	ATCGAGGAGCTGCAACAGAT	GCTACTCTCTTCATCACCTCTTCC	**qPCR**
FLC	TGTGGATAGCAAGCTTGTGG	TAGTCACGGAGAGGGCAGTC	**qPCR**
SVP	CCGGAAAACTGTTCGAGTTC	TGACTGCAAGTTATGCCTCTCT	**qPCR**
AGL24	GAGGCTTTGGAGACAGAGTCGGTGA	AGATGGAAGCCCAAGCTTCAGGGAA	**qPCR**
FD	GCTCACTTGCAGGCAGAAAA	CCTTTTCTCTTTCCGGGTCT	**qPCR**
FUL	TTGCAAGATCACAACAATTCGCTTCT	GAGAGTTTGGTTCCGTCAACGACGAT	**qPCR**
LFY	ACGTGGCAAAAAGAACGGCTTAGA	CGCGTACCTGAATACTTGGTTCGTC	**qPCR**
AP1	AGGGAAAAAATTCTTAGGGCTCAACAG	GCGGCGAAGCAGCCAAGGTTGCAGTTG	**qPCR**
RAB18	ATGGCGTCTTACCAGAACCGT	CCAGATCCGGAGCGGTGAAGC	**qPCR**
ABI2	GGAGTGACTTCGATTTGTGGTAGACG	GTCAAAGCCAGATGCATCCTCTCACG	**qPCR**
ZTL	CCACTCGTTTCTTTGTCCACC	TGAACACAAATGCACTTCTCAA	**RT-PCR**
FKF1	AGGCTGAGAGCTTATCAGAGA	TGTACACACGCTTCTAGCTTCT	**RT-PCR**
FD	AGCTGTGTTGTTGGTTCACT	GACAGGTGTTCCTGTGCCTT	**RT-PCR**
ACT	GTGTTGGACTCTGGAGATGGTGTG	GCCAAAGCAGTGATCTCTTTGCTC	**RT-PCR**
SOC1	ACTAAAGAAGAAGATATGGTGAGG	ATATCACAAACCGTTTAGAAGCTTCGAGTTGTTCA	**genotype**
soc1-2	TGGTTCACGTAGTGGGCCATCG	ATATCACAAACCGTTTAGAAGCTTCGAGTTGTTCA	**genotype**
aba1–6	GCTCGGAGTAAAGGCGGCGA	CAGGAAGTCCCCGTGACGCC	**genotype**

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