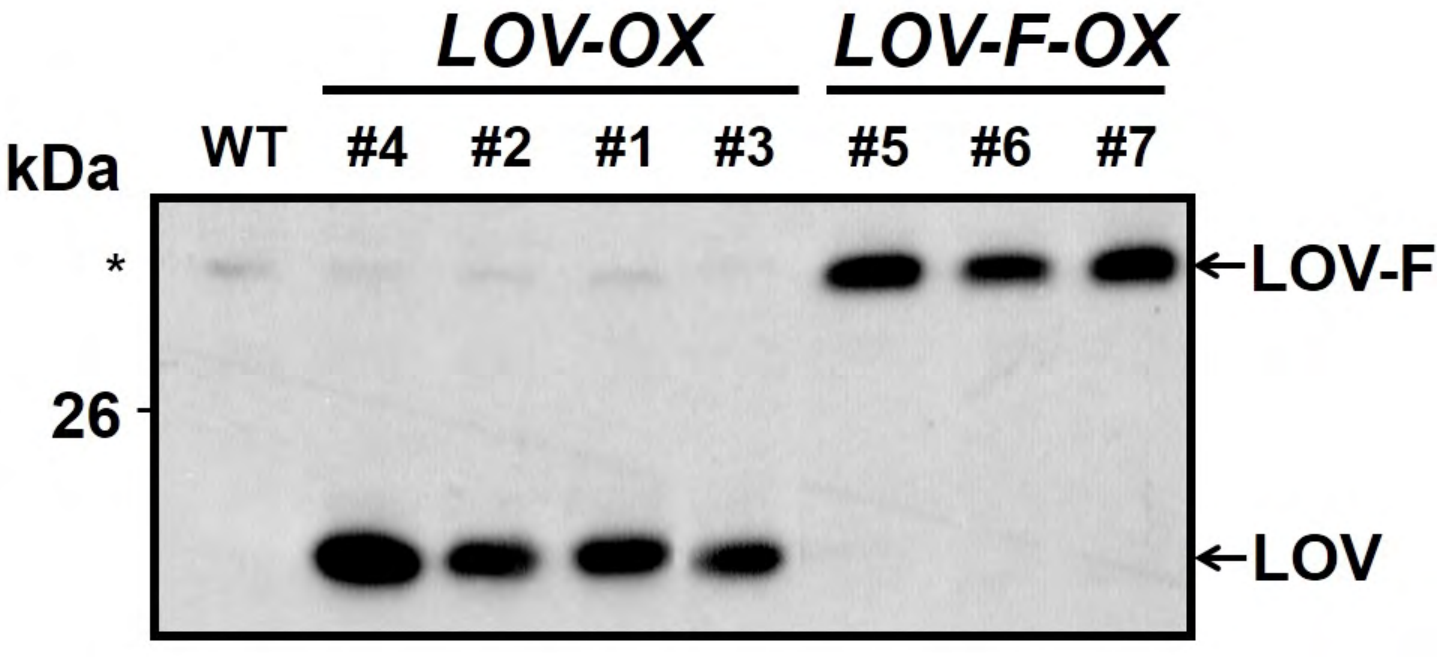

Fig. S1. Identification of independent transgenic lines expressing LOV and LOV-F domains of ZTL. The accumulation of LOV and LOV-F polypeptides was detected using anti-ZTL antibody from total protein extracts of four LOV-expressing lines (#4, #2, #1, and #3) and three LOV-F expressing lines (#5, #6, and #7). A weak band (*) was occasionally detected in WT extracts at the same running position as that of LOV-F polypeptide.

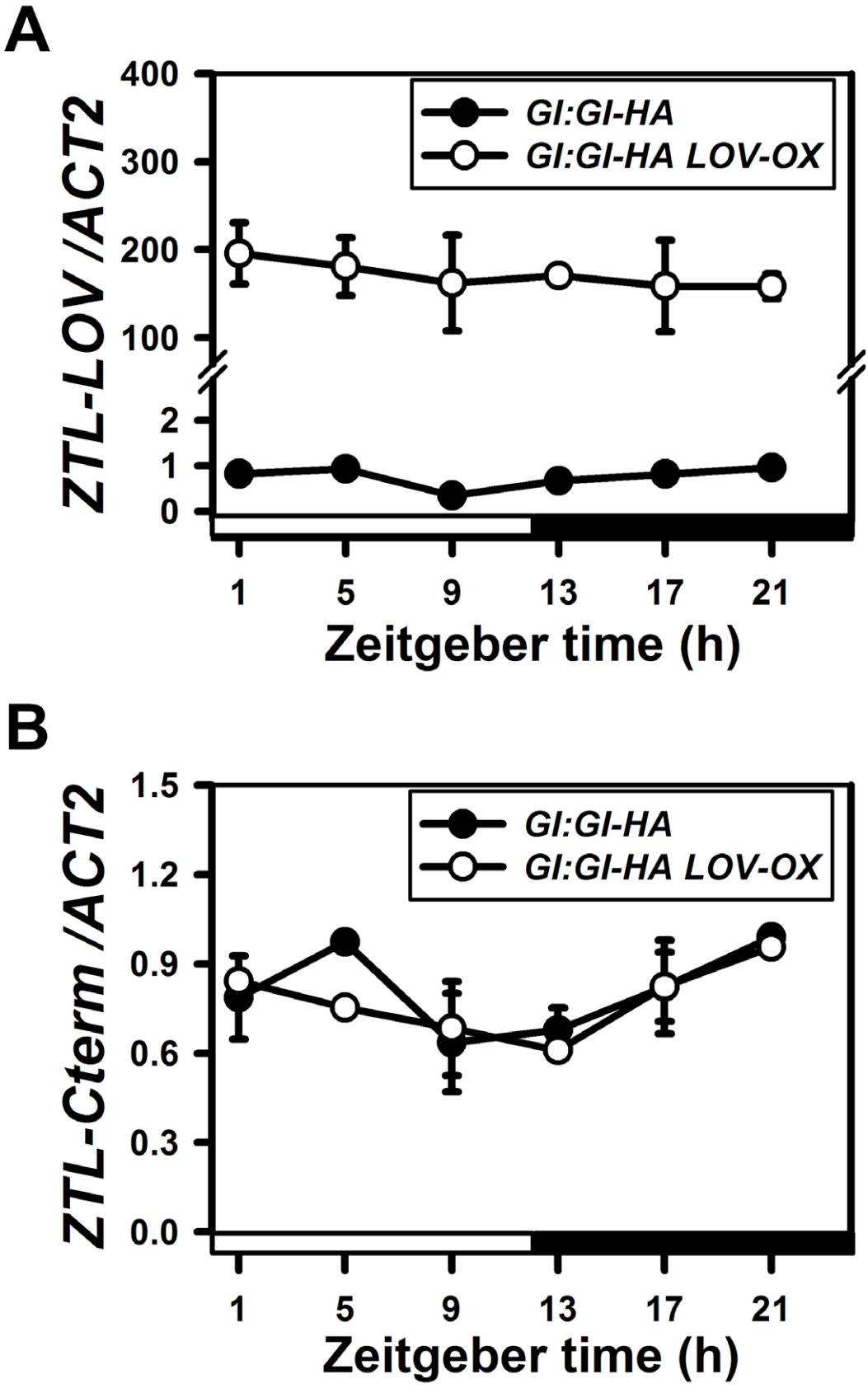

Fig. S2. Accumulation of endogenous *ZTL* mRNA is unchanged in *GI:GI-HA x LOV-OX*. Expression of LOV (**A**) and endogenous *ZTL* (**B**) mRNA levels in *GI:GI-HA x LOV-OX* and *GI:GI-HA* plants. Expression of introduced LOV and endogenous ZTL transcripts was monitored from the same cDNAs used in Fig 3B using primer sets detecting the LOV and KELCH domains of ZTL, respectively. Relative expression was calculated by normalization to ACT2 and then normalized to highest level among WT samples within a trial. Data indicate means±SEM of two independent trials.

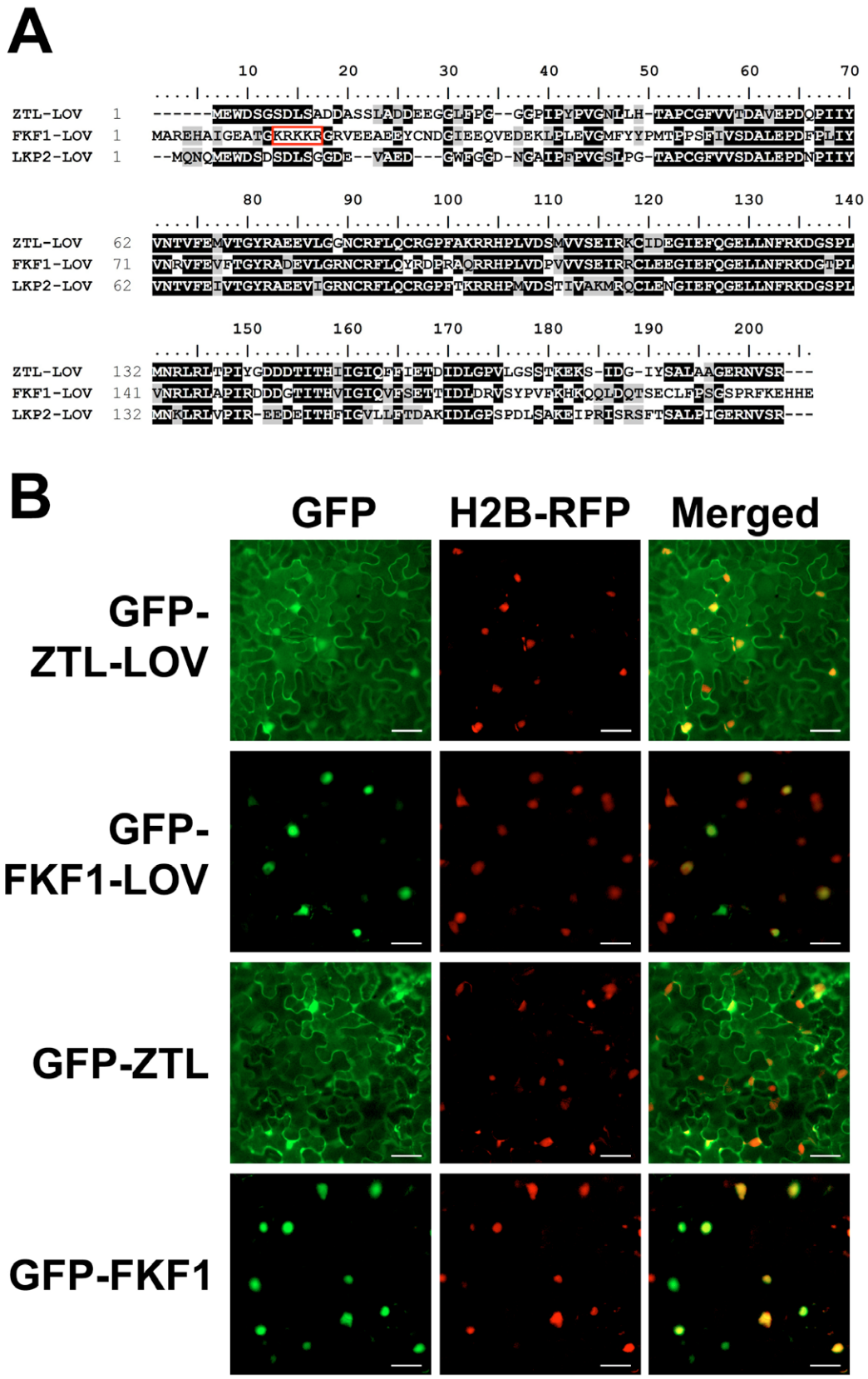

Fig. S3. Subcellular localization of full length or the LOV domain of ZTL and FKF1. (**A**) Sequence alignment of ZTL and FKF1 LOV domains. Putative NLS is marked with a box. (**B**) Localization of full length or LOV domain of ZTL and FKF1. GFP-ZTL-LOV, GFP-FKF1-LOV, GFP-ZTL or GFP-FKF1 were co-expressed with H2B-RFP transiently in *N. benthamina* and GFP and RFP fluorescent signals were monitored with a fluorescent microscope. Signals from GFP, RFP, and the merged signals are shown. Scale bars = 30 um. These are representative of three independent experiments.

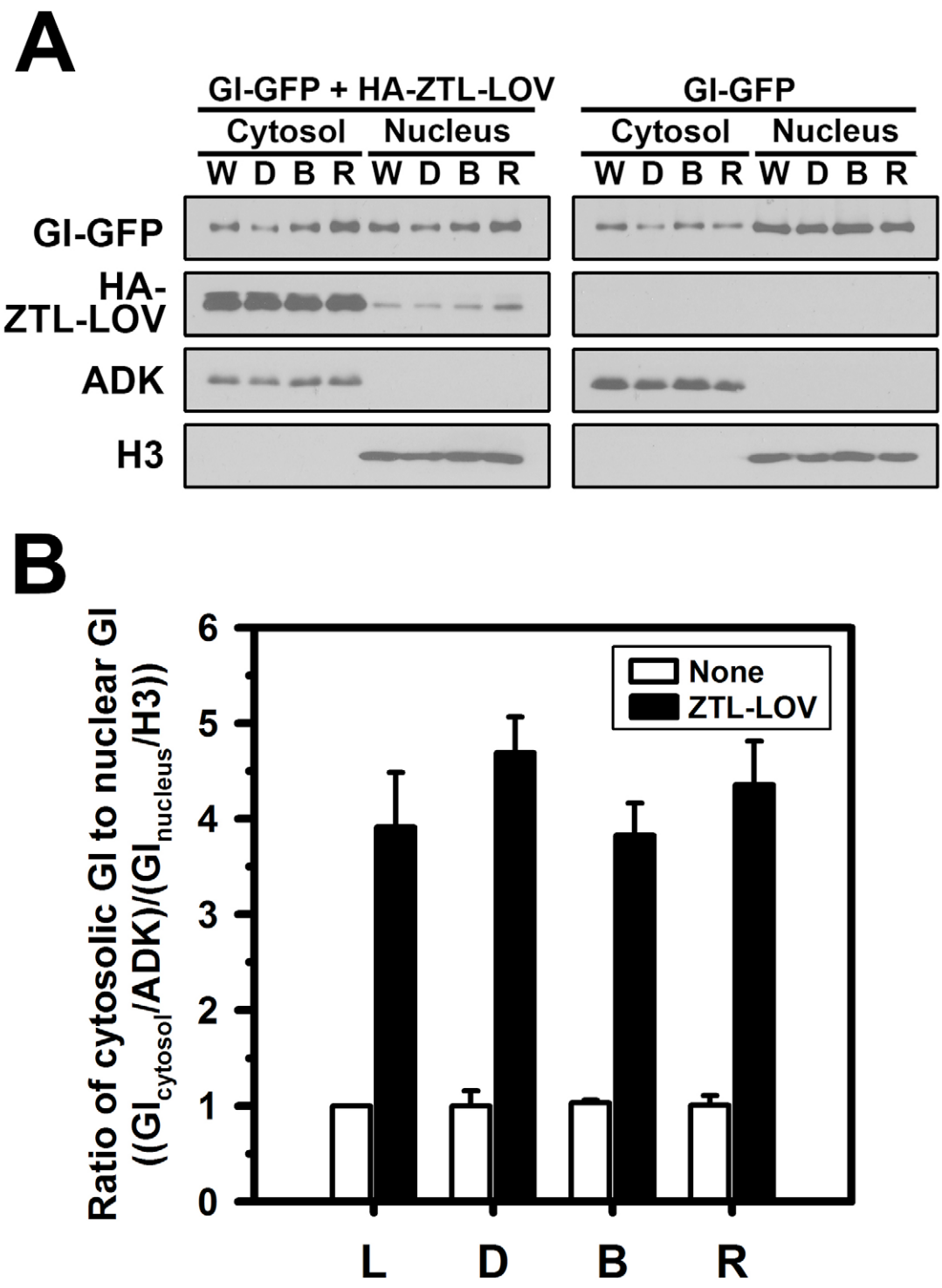

Fig. S4. Light quality has no effect on ZTL-LOV-dependent GI localization. (**A**) Cytosolic and nuclear GI-GFP protein levels in *N. benthamiana* transiently expressing GI-GFP along HA-ZTL-LOV as effectors in the different light conditions. *35S:GI-GFP* was expressed alone or co-expressed with *CsVMV:HA-ZTL-LOV* plasmids in *N. benthamiana*. After 48 h incubation, plants were shifted to chambers with irradiations as indicated (L: White light; D: Dark; B: Blue; R Red) for 6 hours from ZT0. Data are representative of two trials. (**B**) Quantification of ratios of cytosolic to nuclear GI level from (A). Levels of cytosolic and nuclear GI protein normalized to ADK and H3, respectively and further normalized to a non-effector sample (None) within a trial. Bars show means ± SEM of two independent trials.

Table S1. Primers used in this study

1. Plasmid construction

Primer name	Sequences (5′ to 3′)*	R.E.	Vector
ZTL-F	TCCGGATCCTTATGGAGTGGGACAGTGGT	*Bam*HI	pCR-CCD-F
ZTL-R	TCCAGGCCTTTACGTGAGATAGCTCGCTA	*Stu*I	
FKF1-F	TCCACTAGTGTCGACATGGCGAGAGAACATGC	*Spe*I	pCR-CCD-F
FKF1-R	TCCAGGCCTTTACAGATCCGAGTCTTG	*Stu*I	
FKF1-LOV-F	CTTCTGCAGATGGCGAGAGAACATGCGATC	*Pst*I	pCR-CCD-F
FKF1-LOV-R	CTTAGGCCTTCATTCATGATGCTCCTTAAACCT	*Stu*I	
ZTL-LOV-F	CTTCTGCAGATGGAGTGGGACAGTGGTTCC	*Pst*I	pCR-CCD-F
ZTL-LOV-R	CTTAGGCCTTCATCGGGAAACATTCCGCTCCC	*Stu*I	
ZTL-Kelch-F	CTTGGATCCATGACCACCCTTGAAGCT	*Bam*HI	pCR-CCD-F
ZTL-Kelch-R	CTTAGGCCTTTACGTGAGATAGCTCGCTA	*Stu*I	

*Annealing temperature for all primers is 56℃
R.E., restriction enzyme sites

2. RT-PCR or real-time PCR

Primer name	Sequences (5′ to 3′)	Annealing temperature
CO-RT-F	ACGCCATCAGCGAGTTCC	48℃
CO-RT-R	AAATGTATGCGTTATGGTTAATGG	
FT-RT-F	ACAACTGGAACAACCTTTGGCAATG	60℃
FT-RT-R	ACTACTATAGGCATCATCACCGTTCGTTACTCG	
ACT2-RT-F	AAAACCACTTACAGAGTTCGTTCG	55℃
ACT2-RT-R	GTTGAACGGAAGGGATTGAGAGT	
HA-qPCR-F	GGACTACGCTTCTTTGGGTGG	60℃
HA-qPCR-R	GGATAGCCCGCATAGTCAGGAAC	
ZTL-LOV-qPCR-F	TCCGGATCCTTATGGAGTGGGACAGTGGT	60℃
ZTL-LOV-qPCR-R	CCTCCGAGAACTTCCTCAG	
ZTL-KELCH-qPCR-F	TCTTGATATTTGGCGGCTCAGT	60℃
ZTL-KELCH-qPCR-R	TTGTCCTCCGTTGGGTCAAGTA	
ACT2-qPCR-F	CAGTGTCTGGATCGGAGGAT	60℃
ACT2-qPCR-R	TGAACAATCGATGGACCTGA	