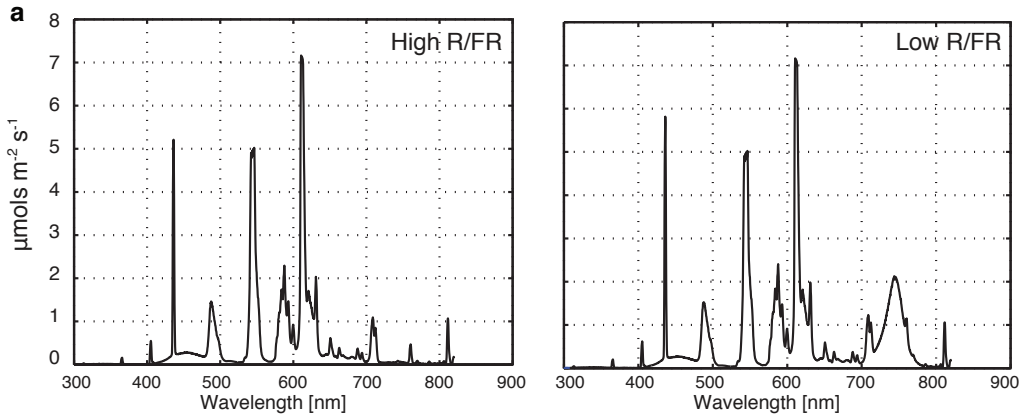
a

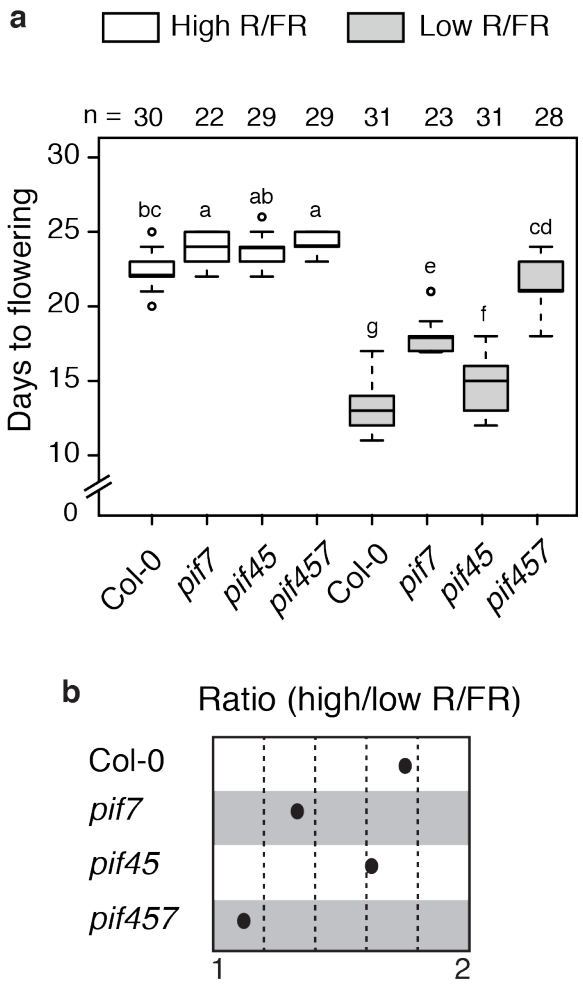


b

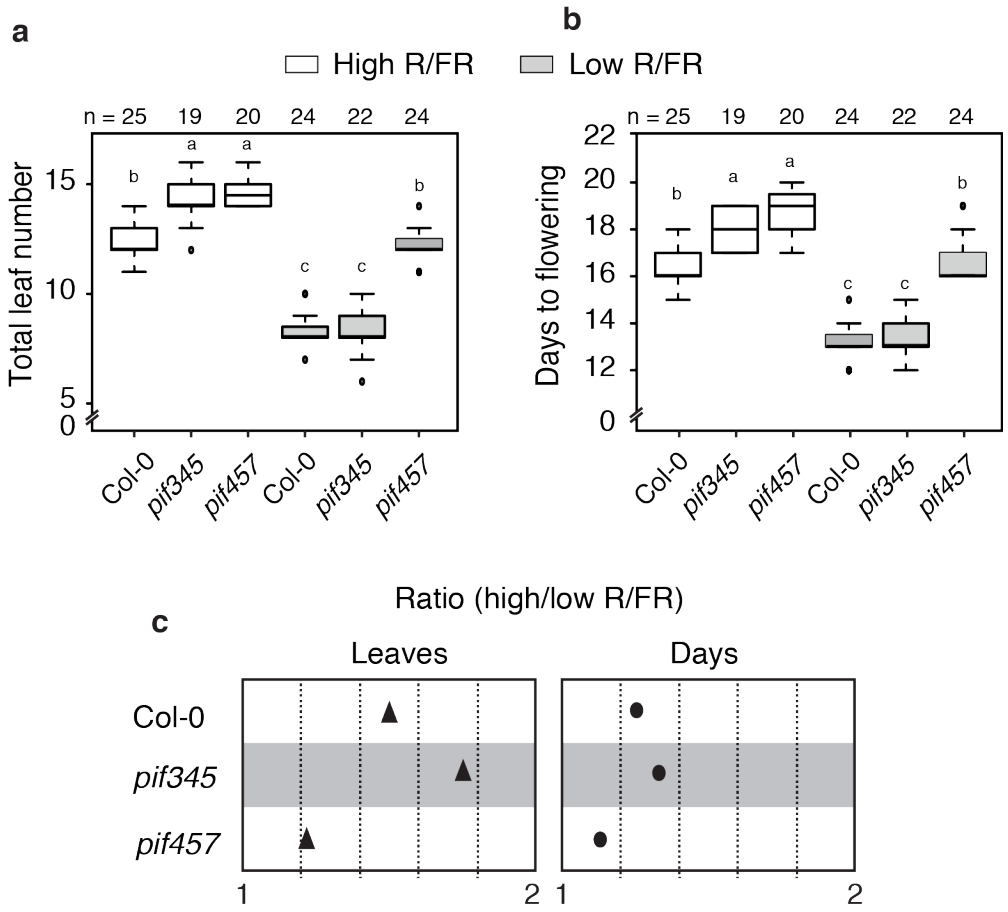
Condition	PAR	Blue	Red	Far-Red	R/FR ratio
High R/FR	212	69.1	13.2	10.7	1.231
Low R/FR	215	69.0	13.3	65.9	0.201

Supplementary Figure 1

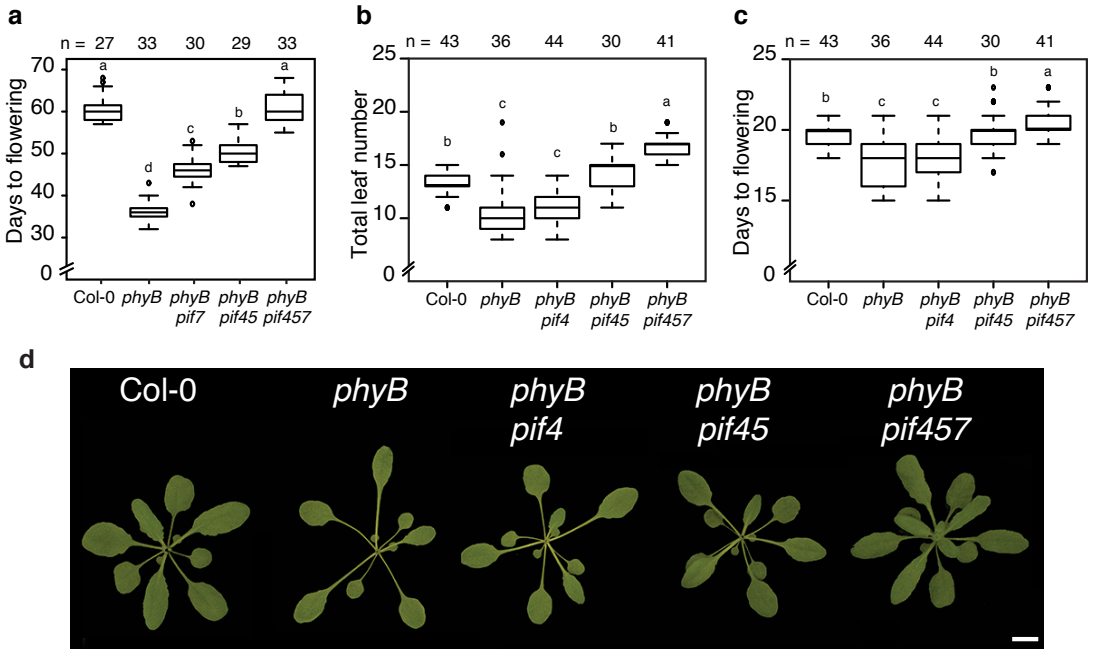
a Light spectra and fluence rate of high R/FR ratio and low R/FR ratio light conditions obtained with OceanOptics USB2000+ spectrometer in CLF plant growth incubator model AR-41L equipped with fluorescent light bulbs and supplemental far-red light-emitting diodes (LED). **b** Light intensities (µmoles m^{-2} s^{-1}) of photosynthetically active radiation (PAR, between 400-700 nm), blue (400-500 nm), red (640-700 nm), far-red (700-760 nm) are listed on the table.



Supplementary Figure 2
PIFs mediate flowering in low R/FR. Flowering time represented as number of days to flowering after sowing of plants growing under LD at 22°C in high and low R/FR **a** and the ratio of days to flowering in high *vs* low R/FR **b**. Plants were grown for 5 days high R/FR for complete de-etiolation and either kept in high R/FR or shifted to low R/FR on day 6 until the onset of flowering. Letters represent the significance groups at p-value < 0.01 using ANOVA followed by Tukey honestly significant difference (HSD) test. n represent the number of plants phenotyped. Boxplots were created using the online BoxPlotR [1]; center line, median; box limits, upper and lower quartiles; whiskers, 1.5x interquartile range (IQR); dots, outliers. n represents the number of plants phenotyped.

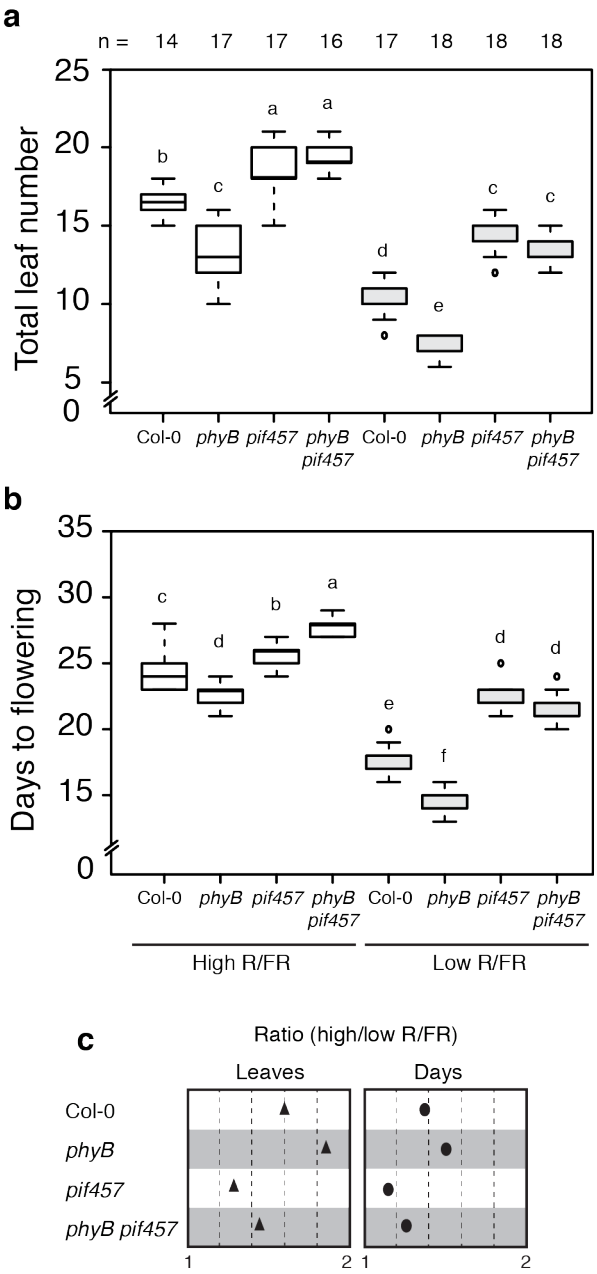


Supplementary Figure 3
Flowering time phenotype represented as total leaf number **a** and days to flowering **b** after bolting. Plants were grown under LD at 22°C in high R/FR for 5 days and either kept in the same condition or shifted to low R/FR on day 6 until the onset of flowering. **c** Ratio of total leaf number and days to flowering in high *vs* low R/FR represented in **a** and **b**. Letters represent the significance groups at p-value < 0.01 using ANOVA followed by Tukey honestly significant difference (HSD) test. n represent the number of plants phenotyped. Boxplots were created using the online BoxPlotR [1]; center line, median; box limits, upper and lower quartiles; whiskers, 1.5x interquartile range (IQR); dots, outliers.



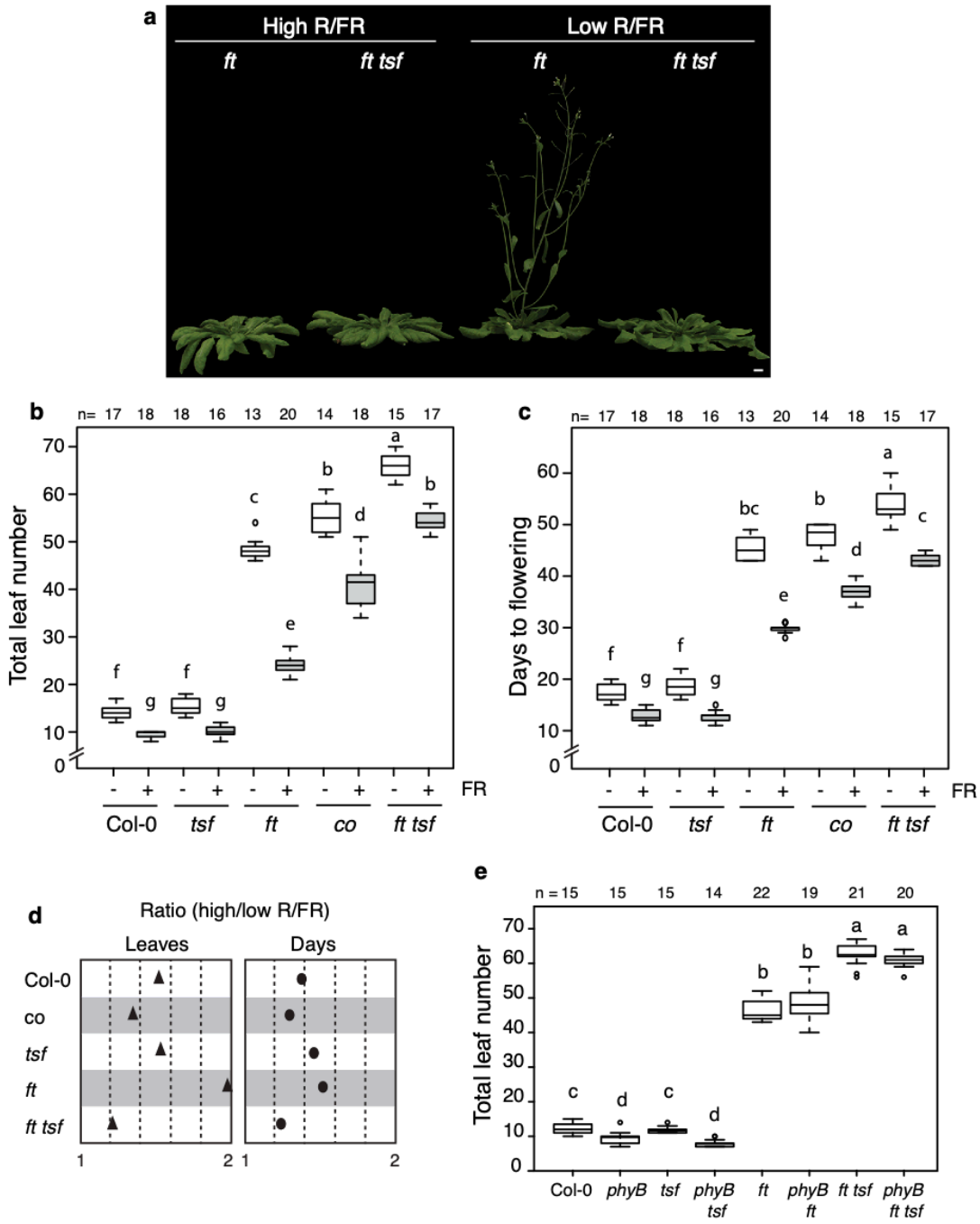
Supplementary Figure 4

a Days to flowering after sowing of Col-0, *phyB*, *phyB pif7*, *phyB pif4 pif5* and *phyB pif4 pif5 pif7* growing under SD at 22°C in high R/FR. Total leaf number **b** and days to flowering after sowing **c** of Col-0, *phyB*, *phyB pif4*, *phyB pif4 pif5* and *phyB pif4 pif5 pif7* mutants growing under LD at 22°C in high R/FR. **d** 25-day-old representative plants grown under LD. Scale bar correspond to 1 cm. Letters represent the significance groups at p-value < 0.01 using ANOVA followed by Tukey honestly significant difference (HSD) test. n represent the number of plants phenotyped. Boxplots were created using the online BoxPlotR [1]; center line, median; box limits, upper and lower quartiles; whiskers, 1.5x interquartile range (IQR); dots, outliers.



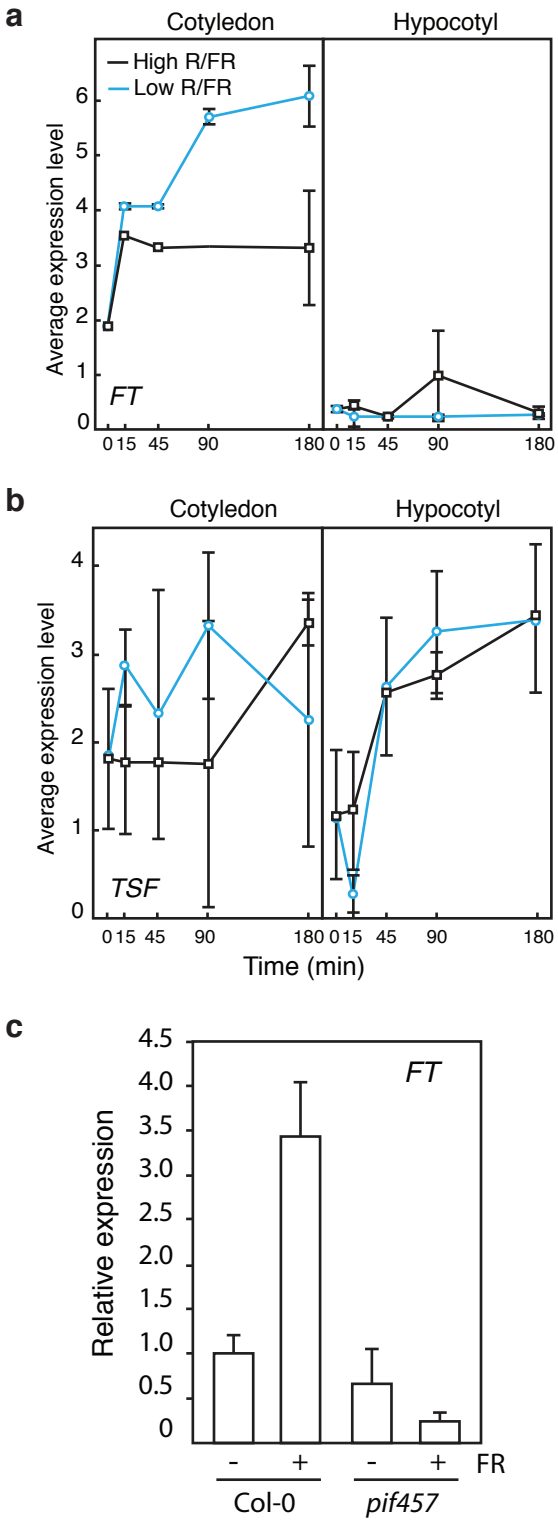
Supplementary Figure 5

PIF4, PIF5 and PIF7 mediate flowering transition downstream of phyB in high and low R/FR. The flowering time phenotype is represented as total leaf number **a** and days to flowering **b** after bolting. Plants were grown under LD at 22°C in high R/FR for 5 days and either kept in the same condition or shifted to low R/FR until the onset of flowering. **c** Ratio of total leaf number and days to flowering in high *vs* low R/FR represented in **a** and **b**. Letters represent the significance groups at p-value < 0.01 using ANOVA followed by Tukey honestly significant difference (HSD) test. n represent the number of plants phenotyped. Boxplots were created using the online BoxPlotR [1]; center line, median; box limits, upper and lower quartiles; whiskers, 1.5x interquartile range (IQR); dots, outliers.



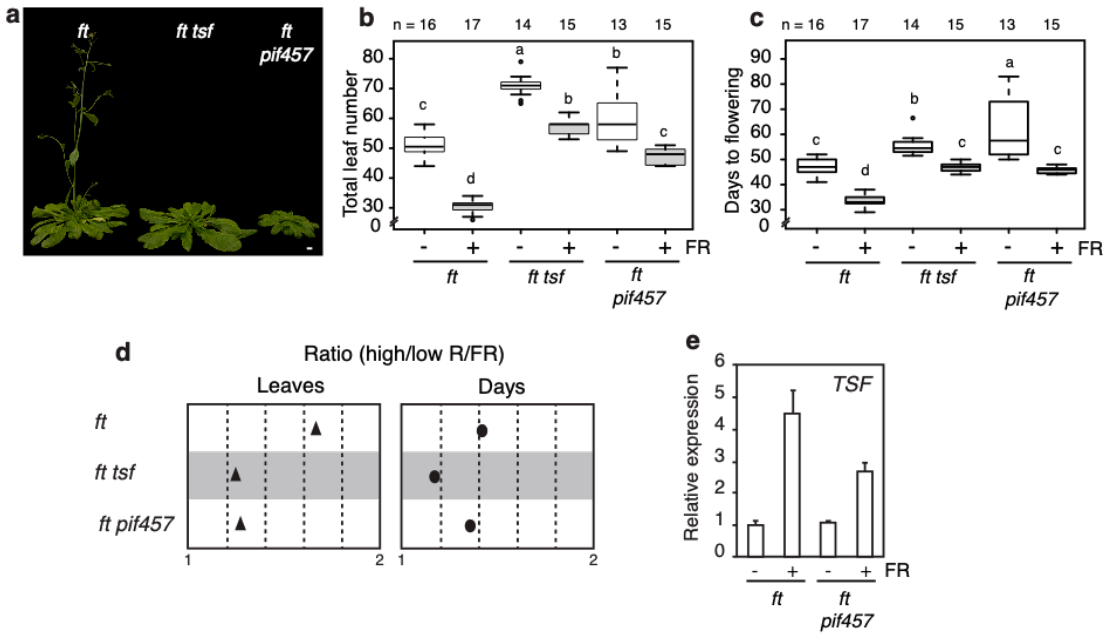
Supplementary Figure 6

a Representative plants of *ft* single and *ft tsf* double mutant genotypes grown under LD at 22°C in high R/FR and low R/FR. Plants were grown under LD at 22°C in high R/FR for 5 days and either kept in the same condition or shifted to low R/FR until the onset of flowering. Flowering time phenotype was represented as total leaf number **b** and days to flowering after sowing **c**. **d** Ratio of total leaf number and days to flowering in high *vs* low R/FR represented in **b** and **c**. **e** Flowering time phenotype of Col-0, *phyB*, *tsf*, *phyB tsf*, *ft*, *phyB ft*, *ft tsf* and *phyB ft tsf* under LD at 22°C in high R/FR was represented as total leaf number after bolting. FR, supplemental far-red light. Letters represent the significance groups at p-value < 0.01 using ANOVA followed by Tukey honestly significant difference (HSD) test. n represent the number of plants phenotyped. Boxplots were created using the online BoxPlotR [1]; center line, median; box limits, upper and lower quartiles; whiskers, 1.5x interquartile range (IQR); dots, outliers. Scale bar correspond to 1 cm.



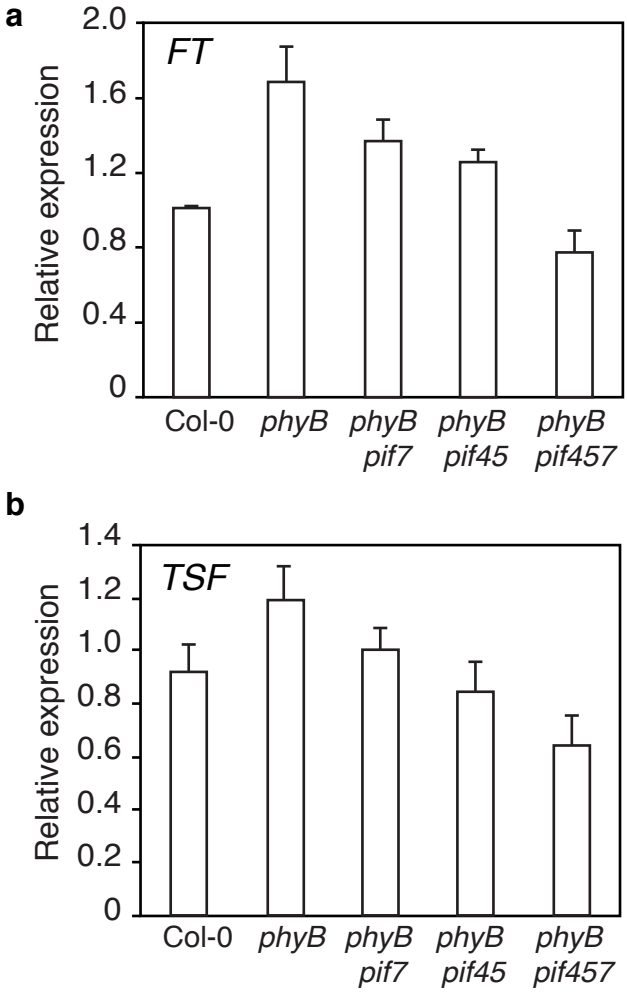
Supplementary Figure 7

Short-term *FT* up-regulation in low R/FR. *FT* **a** and *TSF* **b** RNA-seq data of relative expression in hypocotyl and cotyledon samples before (0) and 15, 45, 90 and 180 minutes after shift from high to low R/FR. RNA-seq expression data was obtained from [2]. **c** *FT* transcript level using quantitative real-time PCR (RT-qPCR) of Col-0 and *pif4 pif5 pif7* plants growing under LD at 22°C. Plants were grown for 5 days in high R/FR and on day 6 either kept in standard high R/FR or shifted to low R/FR at ZT2. Samples were harvested 180 minutes after shift to low R/FR (ZT 5). FR, supplemental far-red light. Error bars represent the standard deviation of three biological and three technical replicates.

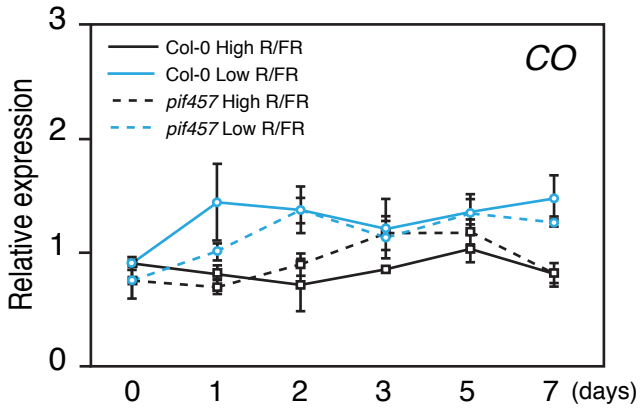


Supplementary Figure 8

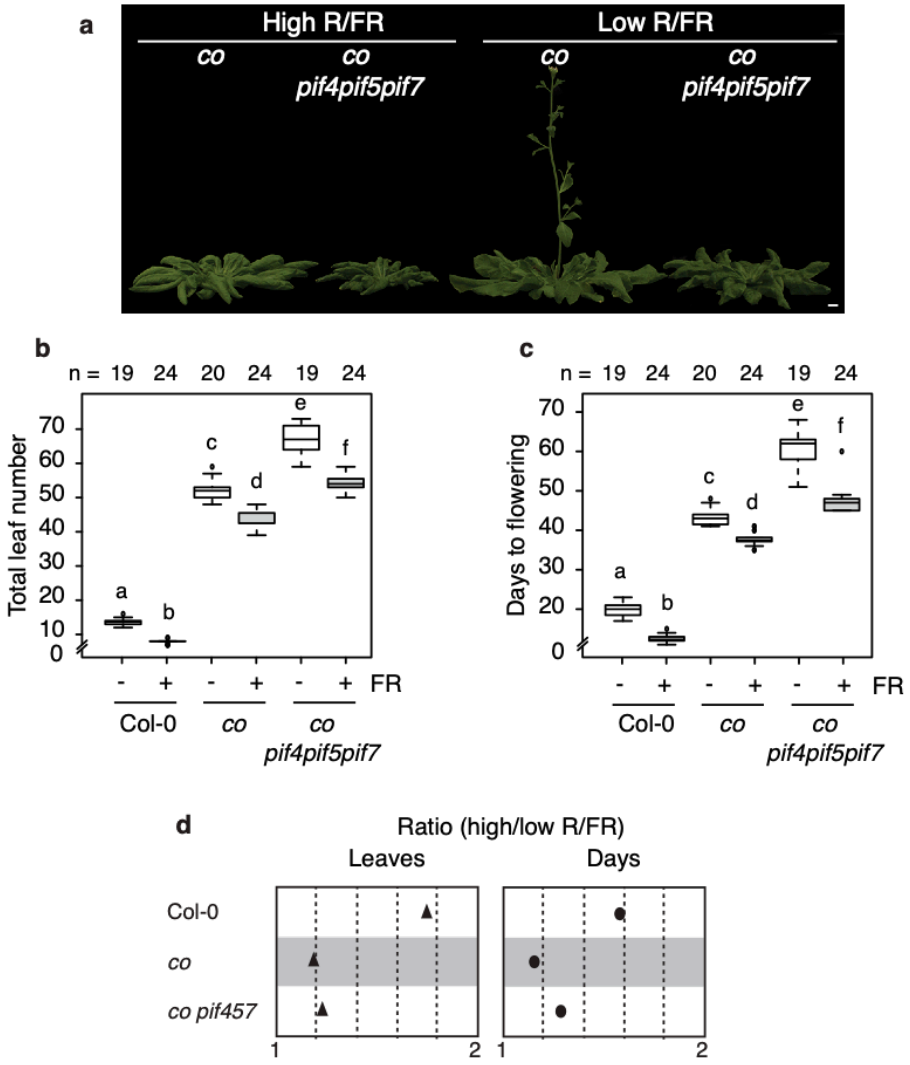
a Representative 50-day-old *ft*, *ft tsf* and *ft pif4 pif5 pif7* plants grown under LD at 22°C in low R/FR. Plants were grown under LD at 22°C in high R/FR for 5 days and either kept in the same condition or shifted to low R/FR on day 6 until the onset of flowering. Flowering time was represented as total leaf number **b** and days to flowering after sowing **c** in high and low R/FR. FR, supplemental far-red light. **d** Ratio of total leaf number and days to flowering after sowing in high *vs* low R/FR. **e** *TSF* mRNA levels in *ft* and *ft pif4 pif5 pif7* 19 days after sowing. Plants were grown under LD at 22°C in high R/FR for 5 days and either kept in the same condition or shifted to low R/FR on day 6. Letters represent the significance groups at p-value < 0.01 using ANOVA followed by Tukey honestly significant difference (HSD) test. n represent the number of plants phenotyped. Boxplots were created using the online BoxPlotR [1]; center line, median; box limits, upper and lower quartiles; whiskers, 1.5x interquartile range (IQR); dots, outliers. Scale bar correspond to 1 cm.



Supplementary Figure 9
FT **a** and *TSF* **b** mRNA quantification using quantitative real-time PCR (RT-qPCR) of Col-0, *phyB*, *phyB pif7*, *phyB pif4 pif5* and *phyB pif4 pif5 pif7* plants growing under LD at 22°C. Plants were grown high R/FR at 22°C and samples were harvested 10 days after sowing at ZT 15-16. Error bars represent the standard deviation of three biological and three technical replicates.

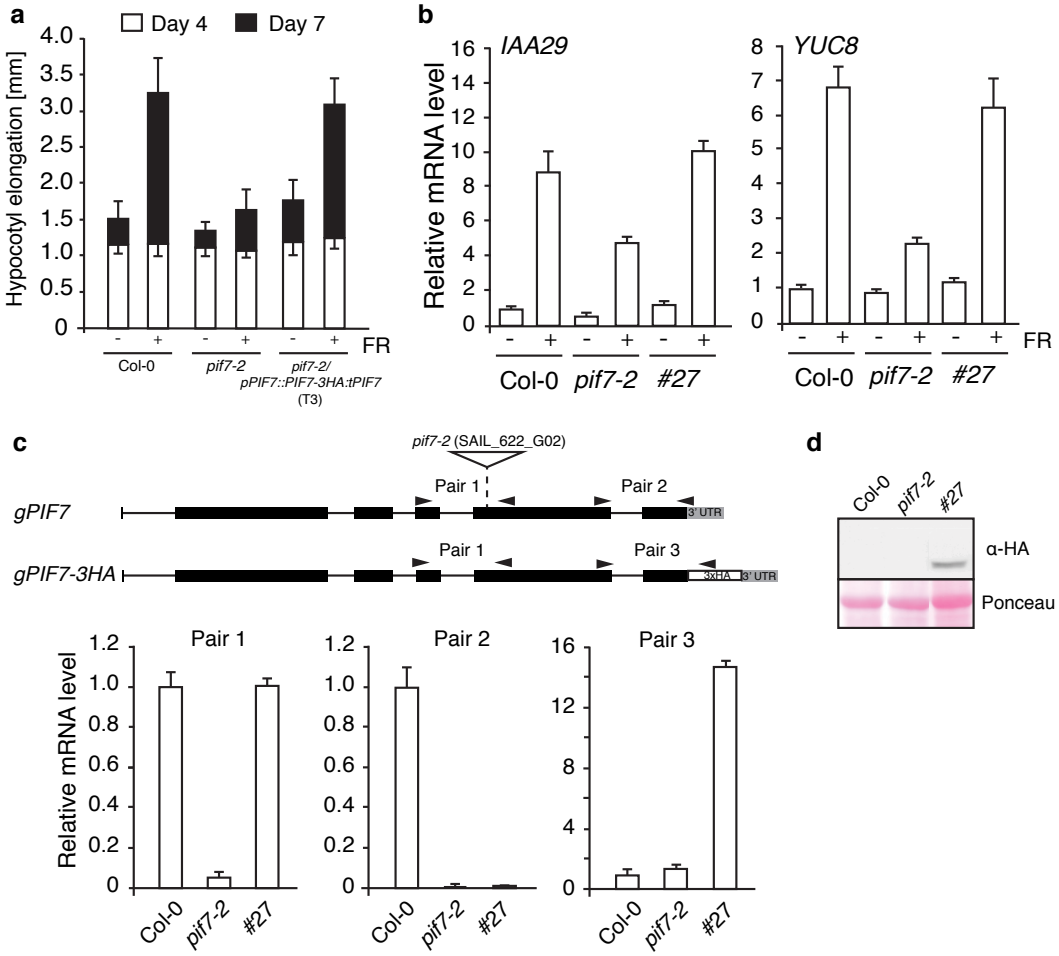


Supplementary Figure 10
CO mRNA level using quantitative real-time PCR (RT-qPCR) after shift from high to low R/FR in Col-0 and *pif4 pif5 pif7*. Plants were grown on soil for 5 days under LD at 22°C in high R/FR and samples were harvested at ZT 15-16 before (0) and 1, 2, 3, 5, and 7 days after shift to low R/FR. Error bars represent 2x SEM.

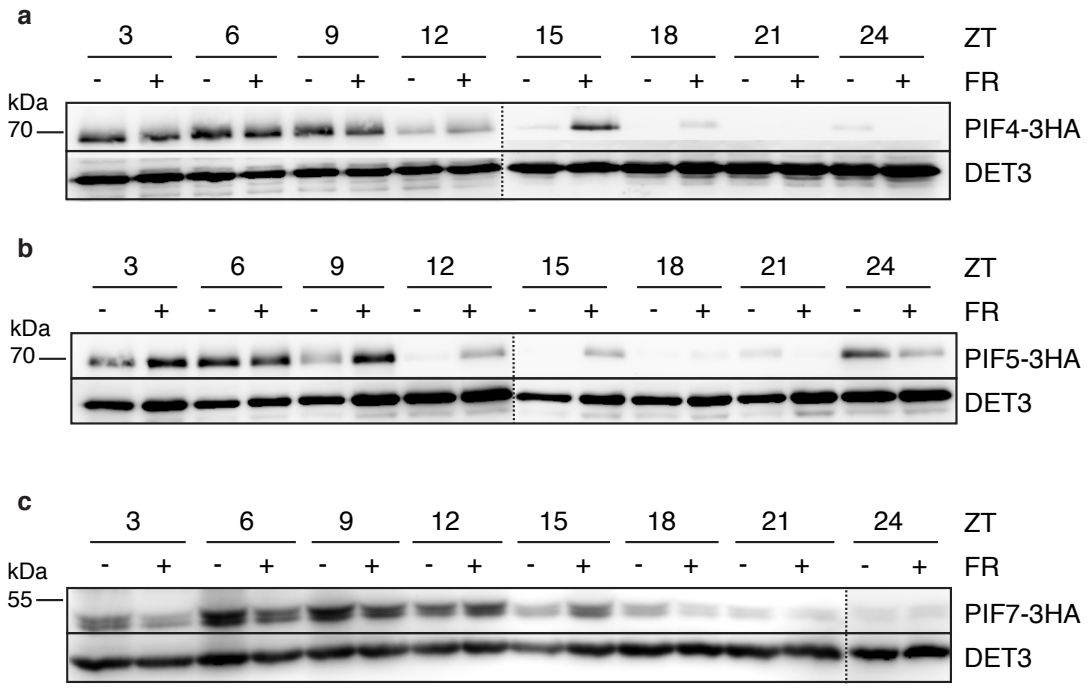


Supplementary Figure 11

a Representative plants of *co* single and *co pif4 pif5 pif7* quadruple mutant were grown under LD at 22°C in high R/FR and low R/FR. Plants were grown under LD at 22°C in high R/FR for 5 days and either kept in the same condition or shifted to low R/FR on day 6 until the onset of flowering. Flowering time phenotype was represented as total leaf number **b** and days to flowering after bolting **c**. **d** Ratio of total leaf number and days to flowering of plants growing under high *vs* low R/FR represented in **b** and **c**. FR, supplemental far-red light. Letters represent the significance groups at p-value < 0.01 using ANOVA followed by Tukey honestly significant difference (HSD) test. n represent the number of plants phenotyped. Boxplots were created using the online BoxPlotR [1]; center line, median; box limits, upper and lower quartiles; whiskers, 1.5x interquartile range (IQR); dots, outliers. Scale bar correspond to 1 cm.

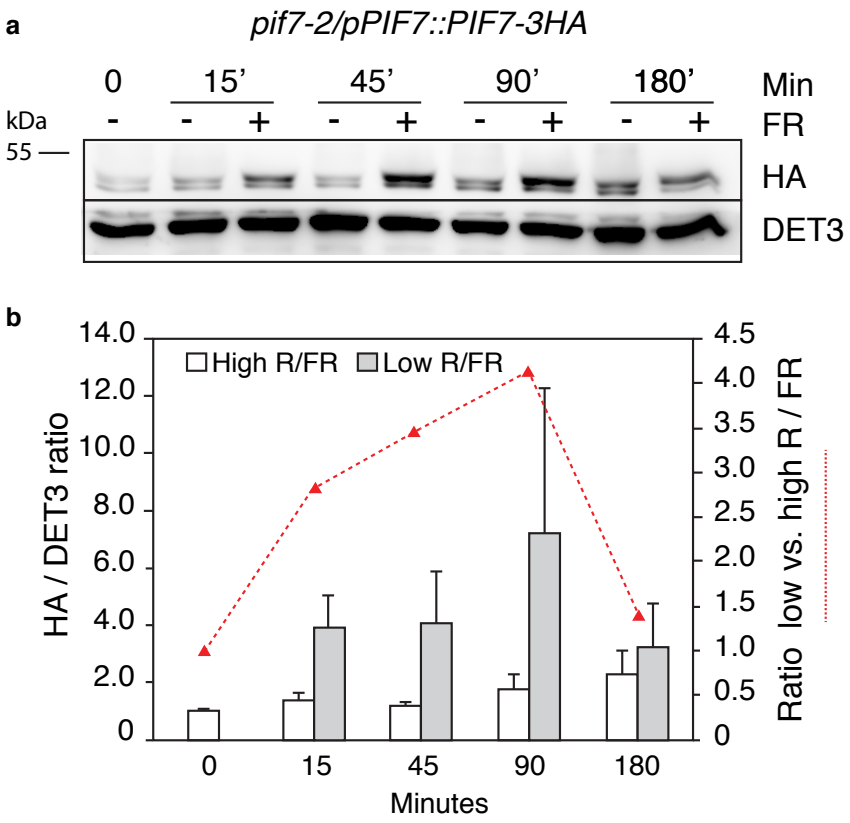


Supplementary Figure 12
pPIF7::PIF7-3HA-tPIF7 (*gPIF7*, labelled #27 on the figure) recues the *pif7-2* short hypocotyl phenotype **a** and the expression of marker genes *IAA29* and *YUC8* **b** in low R/FR. Transgene *gPIF7* expression was confirmed both using quantitative real time PCR (RT-qPCR) with both gene- and transgene-specific oligonucleotides **c** and western blot probed against α-HA **d**. Error bars represent standard deviation of three biological replicates. FR, supplemental far-red light.



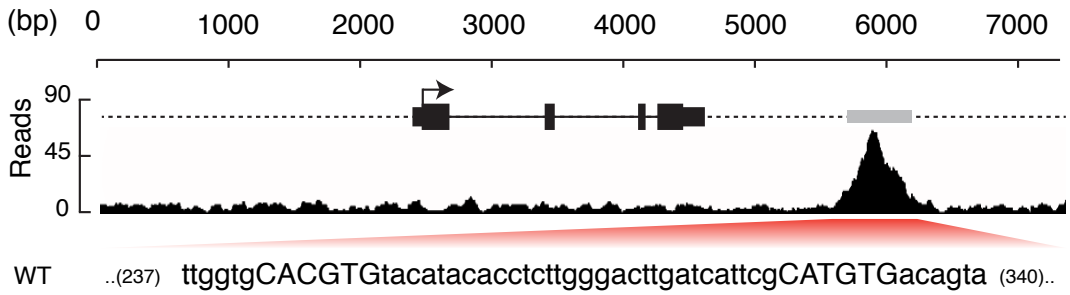
Supplementary Figure 13

PIF4, PIF5 and PIF7 protein accumulation in high and low R/FR. Western-blot of *pif4-101/pPIF4::PIF4-3HA* **a**, *pif5-3/pPIF5::PIF5-3HA* **b** and *pif7-2/pPIF7::PIF7-3HA* **c**. Plants were grown on soil for 5 days in high R/FR and either kept in control high R/FR or shifted to low R/FR in day 6. Samples were harvested every 3 hours in high and low R/FR of 10-day-old plants for 24 hours. Western-blots were performed using anti-DET3 and anti-HA antibodies.

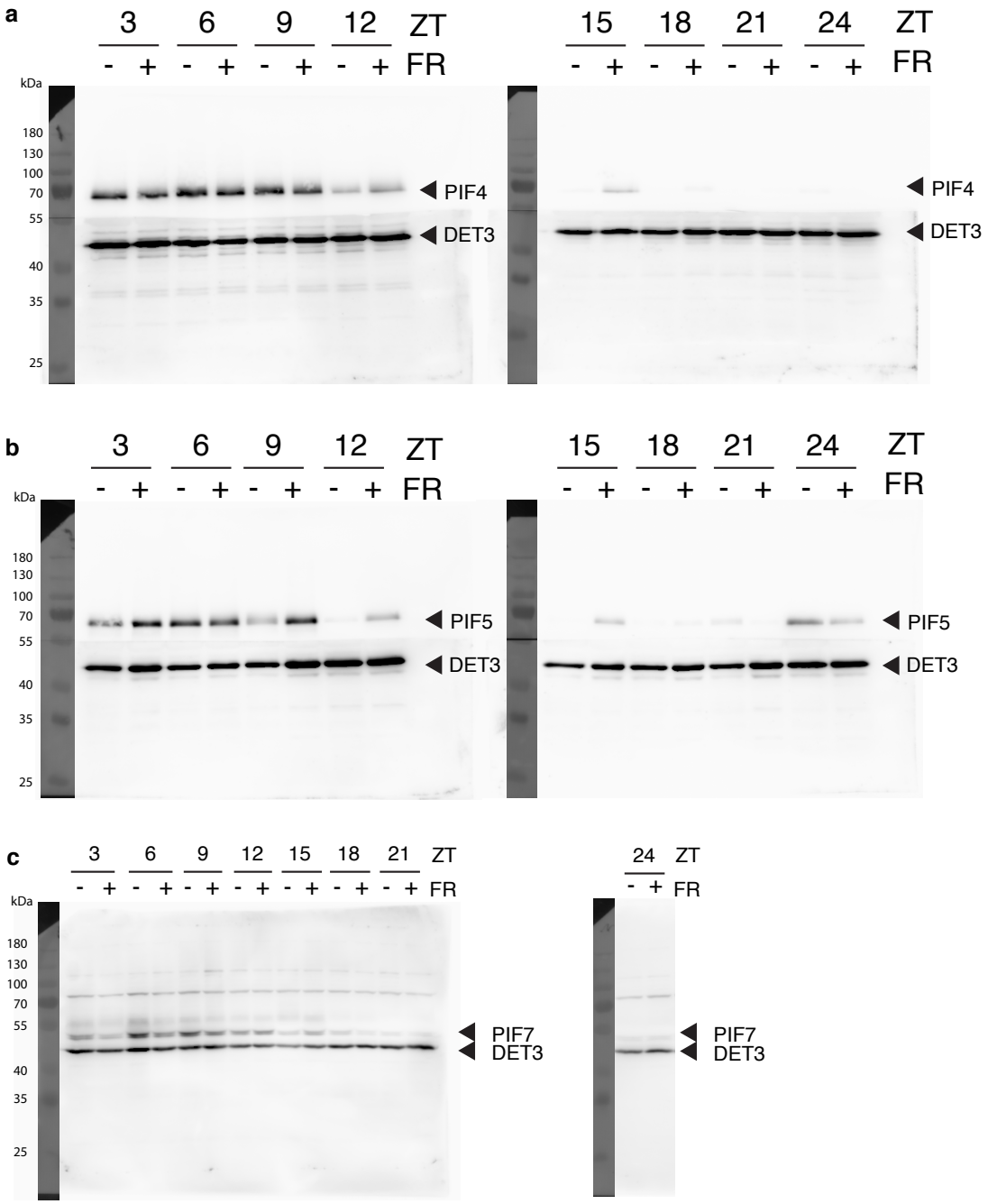


Supplementary Figure 14

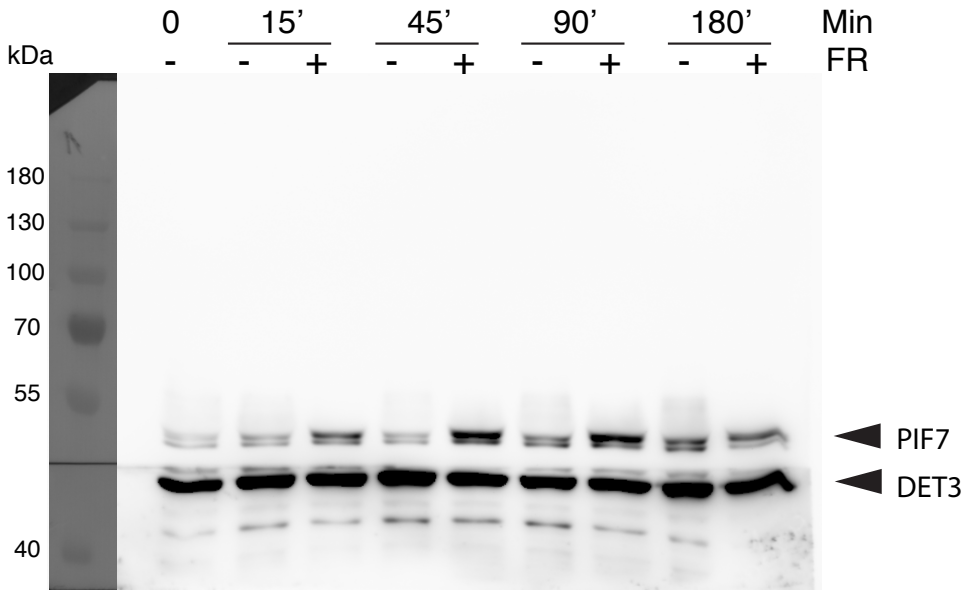
Short-term PIF7-HA protein accumulation by western-blot in 6-day-old *pif7-2/pPIF7::PIF7-3HA* plants in high and low R/FR **a**, and quantitative analysis over DET3 protein levels **b**. Plants were grown for 5 days in high R/FR and in day 6 either kept in control high R/FR or shifted to low R/FR at ZT2. Samples were harvested before (0) and 15, 45, 90 and 180 minutes after shift to low R/FR. White (high R/FR) and grey (low R/FR) bars correspond to the average protein levels of 3 biological replicates and at least 3 technical replicates relative to DET3. Red dashed line represent the PIF protein level ratio of low/high R/FR. Error bars represent standard deviation. FR, supplemental far-red light. Note that we observe 2 isoforms for PIF7 with more of the slower migrating one present after transfer to low R/FR.



Supplementary Figure 15
Representation of PIF4 ChIP-seq reads mapped to the *FT* locus (At1g65480) [3]. Grey box represents high confidence PIF4 binding peak at the *FT* terminator and nucleotide sequence represent the WT DNA sequence. G-box (CACGTG) and PBE-box (CATGTG) are represented in uppercase.



Supplementary Figure 16
Full western-blots shown in supplementary Figure 13a-c. **a.** PIF4-HA and DET3 loading control. **b.** PIF5-HA and DET3 loading control. **c.** PIF7-HA and DET3 loading control.



Min - Minutes after shift
FR - Supplemental far-red light

Supplementary Figure 17
Full western-blot shown in supplementary Figure 14a.

Supplementary Table 1 – List of oligonucleotides used in this study.

Oligos used for cloning			
Construct	**Backbone/Description**	**Oligonucleotide**	**Sequence (5'>3')**
pASF-02	*pBGW/pPIF7::PIF7-3HA:tPIF7*	oASF-25	AGCATGCGACGTCGGGCCCTAATCAAAATTACTTATATCAATGAAACTATATTTG
		oVCG-165	CTGGAACGTCGTATGGGTAGTCATCTCTTTTCTCATGATTCGAAG
		oVCG-166	CTTCGAATCATGAGAAAAGAGATGACTACCCATACGACGTTCCAG
		oVCG-167	CAATAATACTAGGTCGCTAGACTATCCTGCATAGTCCGGGAC
		oVCG-168	GTCCCGGACTATGCAGGATAGtctagcgacctagtattattg
		oASF-26	CGAGGGTACCCGGGGATCCTGTGCATATGATCTATTAACATTGAAG
pVG-24	*pMAL-c2 TEV/MBP-PIF7_bHLH*	oVCG-226 (SacI)	CGAGCTCGAATGGACGACGGGGACGAGCAG
		oVCG-192 (XbaI)	CCTCTAGACTTCATTGTTGGTGTTGGATGCTG
pVG-55	*pGREENII-0800/pTSF::fLUC*	oVCG-440 (XhoI)	CCCCCCTCGAGGTCGACGGGTTTTTTTCTCGGTCATAAACG
		oVCG-441 (NotI)	GGTGGCGGCCGCTCTAATTTATCTTGGATCTCAAGTATCTC
pVG-84	*pGREENII-0800/pTSF 1xmut::fLUC*	..	..
		..	..
pVG-87	*pGREENII-0800/pTSF 3xmut::fLUC*	oVCG-374	CAATGCCCGGATTTATCTCTCTGT
		oVCG-559	GACCAGTTTCATTTGCTGACCAC
		oVCG-378	GTGGTCAGCAAATGAAACTG
		oASF-73	TTCTTATTCCAAAACCCACCAG
		oVCG-560	CTGGTGGGTTTTGGAATAAG
		oVCG-381	ATTTATCTTGGATCTCAAGTATCTC
		oVCG-440 (XhoI)	CCCCCCTCGAGGTCGACGGGTTTTTTTCTCGGTCATAAACG
		oVCG-441 (NotI)	GGTGGCGGCCGCTCTAATTTATCTTGGATCTCAAGTATCTC
pAM-01	*pCB308/pPIF4::GUS*	SL-128 (BamHI)	ATCGGATCCGCCGCCAATCTGCCGACAAG
		SL-129 (BamHI)	ATCGGATCCGCTAGCGTCAGATCTCTGGAGACAT
pAM-03	*pCB308/pPIF5::GUS*	SL-132 (BamHI)	ATCGGATCCAAATACAACGACATCATTTG
		SL-133 (BamHI)	ATCGGATCCGCTAGCGTCAGATCTGTAAAGACACT
pMK-09	*pCB308/pPIF7::GUS*	MK-207 (XbaI)	CCGTCTAGAAAAGAGTCGAACAGGGAAAGTTC
		MK-208 (BamHI)	CCGGGATCCGTGTTACTTAGGCCGCACG

Oligos used for genotyping			
Allele	**Collection**	**Oligonucleotide**	**Sequence**
phyB-9	Point mutation	PB9	GTGTCTGCGTTCTCAAAACG
		B9dCAPS	GTGGAAGAAGCTCGACCAGGCTTTG
ft-10	GK-290E08	oVCG-53	CCCATTTGGACGTGAATGTAGACAC
		oVCG-417	CGAGCAACATGTTTGAGCTAT
co-101	SAIL_24_H04	oVCG-61	TAGCATCTGAATTTCATAACCAATCTCGATACAC
		oVCG-143	AGCTCCCACACCATCAAACTTACTACATC
tsf-1	SALK_087522	oVCG-55	ACGTGGACTCTCGTAGCACAC
		oVCG-56	ATTTTGCCGATTTCGGAAC
pif3-1	SALK_030753	CF-230	AGGCATTCCCATACCCATTG
		oVCG-56	ATTTTGCCGATTTCGGAAC
pif4-101	SAIL_114_G06	SL-43	CAGACGGTTGATCATCTG
		oVCG-61	TAGCATCTGAATTTCATAACCAATCTCGATACAC
pif5-3 (pil6-1)	SALK_087012	SL-46	TCGCTCACTCGCTTACTTAC
		oVCG-56	ATTTTGCCGATTTCGGAAC

pif7-1	CS68809	SL-195	GTGGCAAGTTGGCTCTTAGG
		SL-169	TGATAGTGACCTTAGGCGACTTTTGAACGC
pif7-2	SAIL_622_G02	oASF-27	GGAGAGCCATAGAGTTGG
		oVCG-61	TAGCATCTGAATTTCATAACCAATCTCGATACAC

Oligos used for RT-qPCR			
Target	**Primer Efficiency**	**Oligonucleotide**	**Sequence**
FT	2.00	oVCG-27	CCCTGCTACAACTGGAACAAC
		oVCG-28	CACCCTGGTGCATACACTG
TSF	2.00	MT-608	TGGAGATGTTCTTGATCCTTTC
		MT-609	TAGATCCAAGCCATTAGTAACC
CO	2.05	MT-596	AACGCCTGCACCGTGTATTG
		MT-597	ACGCGATTGGCAGAGTGAAC
PIF4	2.02	oVCG-246	TACCTCGATTTCCGGTTATGGATC
		oVCG-247	GTTGTTGACTTTGCTGTCCCGC
PIF5	2.01	oVCG-588	GAGCAGCTCGCTAGGTACATG
		oVCG-589	GTTGTTGTTGCACGGTCTG
PIF7	1.99	SL-194	AAAGGAGACGGCGTGATAGG
		SL-195	GTGGCAAGTTGGCTCTTAGG
PIL1	1.92	MT-125	TCAGACTCAGGCTACTTCTTTTACTCA
		MT-126	TCCTCTATATTGCATTGCATCTTCTAA
IAA29	1.94	MT-157	CTTCCAAGGGAAAGAGGGTGA
		MT-158	TTCCGCAAAGATCTTCCATGTAAC
YUC8	2.00	MT-271	GGCGGCTTGTCTCCATGAAC
		MT-171	ACTGTTGACCTCGACGTTGTTG
UBC	1.94	UBC-F	CAGTCTGTGTGTAGAGCTATCATAGCAT
		UBC-R	AGAAGATTCCCTGAGTCGCAGTT
YSL8	2.00	YSL8-F	TCATTCGTTTCGGCCATGA
		YSL8-R	CTCAGCAACAGACGCAAGCA
PIF7 - Pair 1	1.99	SL-194	AAAGGAGACGGCGTGATAGG
		SL-195	GTGGCAAGTTGGCTCTTAGG
PIF7 - Pair 2	1.97	oASF-52	GAACCACCCAAAGAAGCGTA
		oASF-53	CTGATCCATACAGCGCCTTT
PIF7 - Pair 3	1.94	oASF-63	TAGGTCGCTAGACTAATCTC
		oASF-53	CTGATCCATACAGCGCCTTT

Supplementary Table 2 – DNA sequences.

pTSF_3xmut synthesis
tttttgtggtcagcaaatgaaactggtctgcaatagtttttagaagtctttatcggtttatttct**catg**G**g**ttttgtcagaaatttcttagaa attttttgtcttccaaacttggggaactaaatttgtttggagtgtaagaatacacggttgagcttttaggtaatacacttgtttttgaaaggt ataatgaatttttaaaaaaattactttatcaacatttaagatttggagacaattttgaaatcacgtttgaaaacgaatttttttggccaattgtt cacttttctgtcgttattatacttctgttaccttgtgtctatttgttaatttacttgttttatttgatttactccattgttttaaaagttttactggttt gttttgttaaattgatatttttgatggtattaattaagtttagtactacattaagaaaagaaaaaaaagagtctagtacgtatgtacacac caaccagatatgtgaacaattatggcgtcaatttatctggagcatatatacttttatatgatggtttaggttgaaggagttattctaaaat gcattaacatcatacataatcggtgtaatgtagtgtccttaactatttaaatgagtga**catg**G**g**acgcaaaatgcgtgacgtacgca aatatgcagcatattatatgcttgtgacattattttaaatagttcatgaagttacaatgataagtcagaataaattacatactagtggcta gcaagaaa**caag**G**g**gatgatgtataatttggaatatgattatttctgttttatactggtgggttttggaataagaatactataaatttag aaaaaaggaaagaaaaaaaaaacatg

PIF7_bHLH

aatggacgacggggacgagcagcagcgattcacaacgagtccgaaaggagacggcgtgataggataaaccagaggatgag
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gcatccaacaccaacaa

References

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