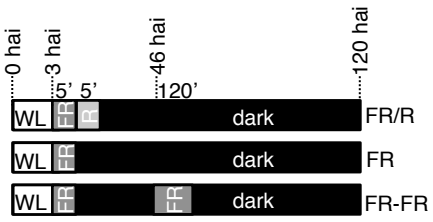

Fig. S1 Schematic representation of the experimental set-up: After-ripened seeds were imbibed for 3 h under white light (WL); then treated with (i) two consecutive 5 minute (5') FR and R light pulses (FR/R); (ii) only one 5' FR pulse (FR); and (iii) an initial 5' FR pulse followed (46-hours-after-imbibition, hai) by a second 120' FR pulse (FR-FR). At all other times seeds were kept in the dark. Seed germination was scored 5 days-after-imbibition (120 hai).

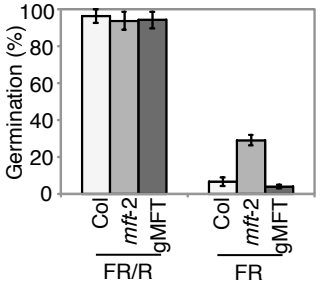

Fig. S2. Germination of complemented *mft-2* seeds. Wild-type (Col), *mft-2* and *mft-2* complemented with the wild-type *MFT* gene (gMFT). After-ripened seeds were treated with FR/R and FR light as indicated in Fig. S1. Germination was scored 5 days-after-imbibition. Data are the means of four biological replicates and error bars represent standard deviation. Asterisk indicates statistically significant difference (*t*-test, p <0.01).

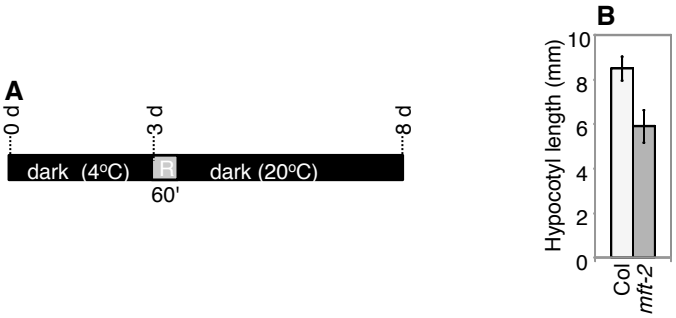

Fig. S3. Hypocotyl length of *mft*-2 seedlings. (*A*) Schematic representation of the experimental set-up: Imbibed seeds were kept for 3 d in the dark at 4ºC, then treated with red light (R) for 60 minutes (60'), and finally kept for 5 days in the dark at 20ºC before scoring hypocotyl length. (*B*) Hypocotyl length of wild-type (Col) and *mft-2* seedlings. Data are means of ten biological replicas and error bars represent standard deviation. Asterisk indicates statistically significant difference (*t*-test, p <0.01).

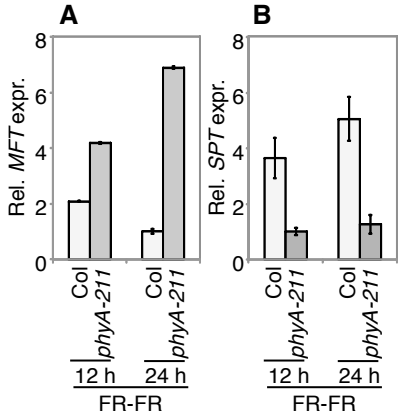

Fig. S4. Gene expression in *phyA-211* mutant seeds. (*A-B*) Relative *MFT* and *SPT* transcript accumulation in FR-FR treated seeds 12 and 24 h after the second FR-treatment. Error bars represent standard error of three qPCR replicates.

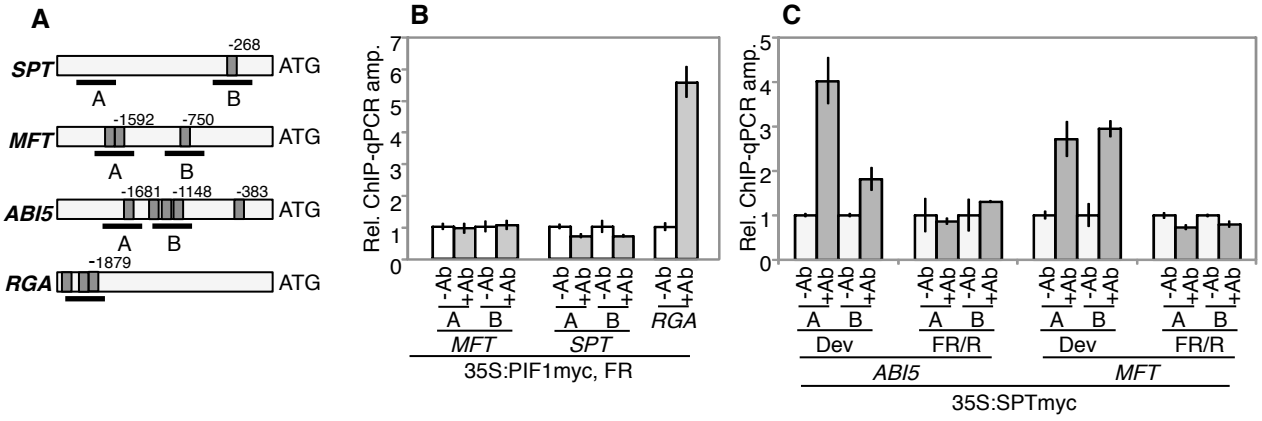

Fig. S5. Characterisation of interactions of PIF1 and MFT with selected gene promoters. (*A*) Schematic diagram of *SPT*, *MFT*, *ABI5* and *RGA* promoters. Dark gray boxes represent G-box motifs (CACGTG). Negative numbers indicates G-box positions with respect to the ATG start codon. Horizontal black lines indicate regions assessed (as previously described; (1)) for protein-DNA interactions by chromatin immuno-precipitations (ChIP) followed by quantitative PCR (qPCR). (*B-C*) ChIP-qPCR analyses of imbibed seeds (24 hai) of epitope-tagged FR-treated 35S:PIF1myc (*B*) and FR/R-treated 35S:SPTmyc (*C*) transgenic seeds. ChIPs were performed with anti-Myc Ab (+Ab) or anti-HA (-Ab) as negative controls. qPCR amplifications were normalized to an internal unrelated control region (*UBQ11*) and plotted relative to the -Ab negative control. The PIF1-*RGA* interaction (in *B*) and SPT-*MFT* in developing seeds (Dev; in *C*) were used as a positive ChIP-qPCR controls. Error bars represent standard error of three qPCR replicates.

Name	Sequence
qMFT-For	ATCACTAACGGCTGCGAGAT
qMFT-Rev	CGGGAATATCCACGACAATC
qABI5-For	CAATAAGAGAGGGATAGCGAACGAG
qABI5-Rev	CGTCCATTGATGTCTCCTCCA
qSPT-For	TGCTTGATGAAGCCATTGAG
qSPT-Rev	TGATCATTTCCGGTGCATTA
qUBQ11-For	TTCATTTGGTCTTGCGTCTG
qUBQ11-Rev	GAAGATGAGACGCTGCTGGT
chipMFT-A-For	CCAATCGATCGAGTACCACA
chipMFT-A-Rev	GCCATTTGAAACTCCTTTGC
chipMFT-B-For	CGACCGACCATAAATCATACG
chipMFT-B-Rev	CACGTGTTGCATGATTAGCC
chipSPT-A-For	TCGATTTCATCCGATGCAGA
chipSPT-A-Rev	TCCCAAAACTTTTCCTCGTC
chipSPT-B-For	GGTTGTATATTATTTGTTACCCCAAAA
chipSPT-B-Rev	AGCATGAGCTTGTGTAGC
chipABI5-A-For	TTAGGTCGCTGGTTCGATTC
chipABI5-A-Rev	CATGATTCCGAACTTCCATTG
chipABI5-B-For	TGTGTAGCCGAAGTCACACGTG
chipABI5-B-Rev	CTTTCGACCAATGGAATGCT
chipRGA-For	CAGACTCGGTCCCTACCGTTT
chipRGA-Rev	GCCGTCATTAACGGCCTCTTTCT

Table S1. Sequence of primers used in tis study.

sample	file	raw_count	minus_rRNA	percentage_rRNA	mapped_reads_Q20	percentage_mapped_Q20
Col FR (24hai) #1	./F1_S69_L008_R1_001.fastq.gz	14299154	13274012	7.17	18531949	69.81
	./F1_S69_L008_R2_001.fastq.gz	14299154	13274012	7.17		
Col FR (24hai) #2	./F2_S70_L008_R1_001.fastq.gz	26511193	24502415	7.58	39539111	80.68
	./F2_S70_L008_R2_001.fastq.gz	26511193	24502415	7.58		
Col FR (24hai) #3	./F3_S71_L008_R1_001.fastq.gz	16749808	15883995	5.17	24608385	77.46
	./F3_S71_L008_R2_001.fastq.gz	16749808	15883995	5.17		
Col FR/R (24hai) #1	./F4_S72_L008_R1_001.fastq.gz	22553178	21758137	3.53	34415602	79.09
	./F4_S72_L008_R2_001.fastq.gz	22553178	21758137	3.53		
Col FR/R (24hai) #2	./F5_S73_L008_R1_001.fastq.gz	12343199	11659903	5.54	19442635	83.37
	./F5_S73_L008_R2_001.fastq.gz	12343199	11659903	5.54		
Col FR/R (24hai) #3	./F6_S74_L008_R1_001.fastq.gz	13980663	12577893	10.03	17776434	70.67
	./F6_S74_L008_R2_001.fastq.gz	13980663	12577893	10.03		
mft-2 FR (24hai) #1	./F7_S75_L008_R1_001.fastq.gz	17475160	16582783	5.11	25079694	75.62
	./F7_S75_L008_R2_001.fastq.gz	17475160	16582783	5.11		
mft-2 FR (24hai) #2	./F8_S76_L008_R1_001.fastq.gz	20302816	19049813	6.17	29691651	77.93
	./F8_S76_L008_R2_001.fastq.gz	20302816	19049813	6.17		
mft-2 FR (24hai) #3	./F9_S77_L008_R1_001.fastq.gz	20458216	18789459	8.16	29997949	79.83
	./F9_S77_L008_R2_001.fastq.gz	20458216	18789459	8.16		

Table S2. RNAseq reads statistics.

REFERENCES

1. Vaistij FE, *et al*. (2013) Differential control of seed primary dormancy in Arabidopsis ecotypes by the transcription factor SPATULA. *Proc Natl Acad Sci U S A* 110 (26):10866-10871.