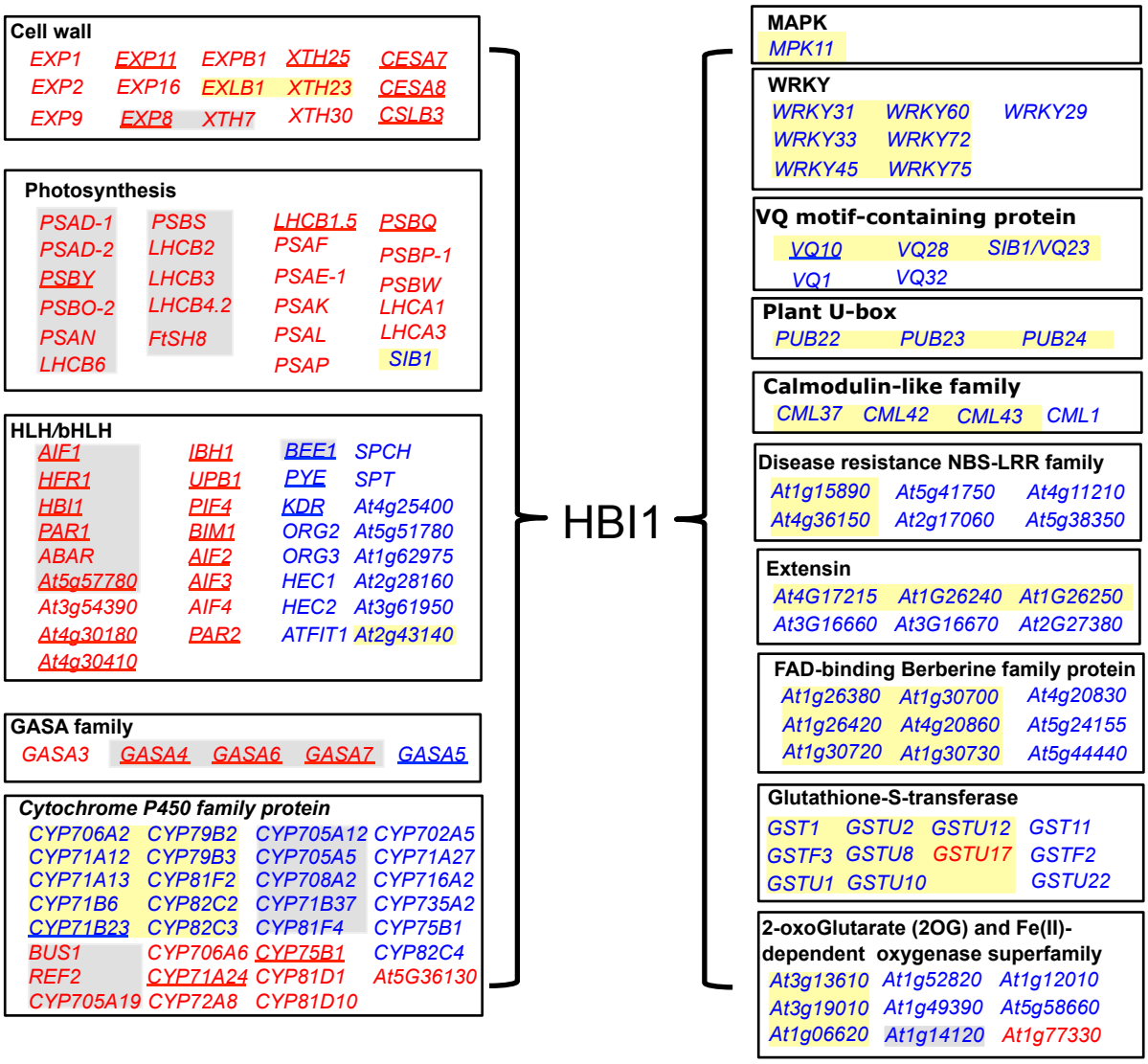
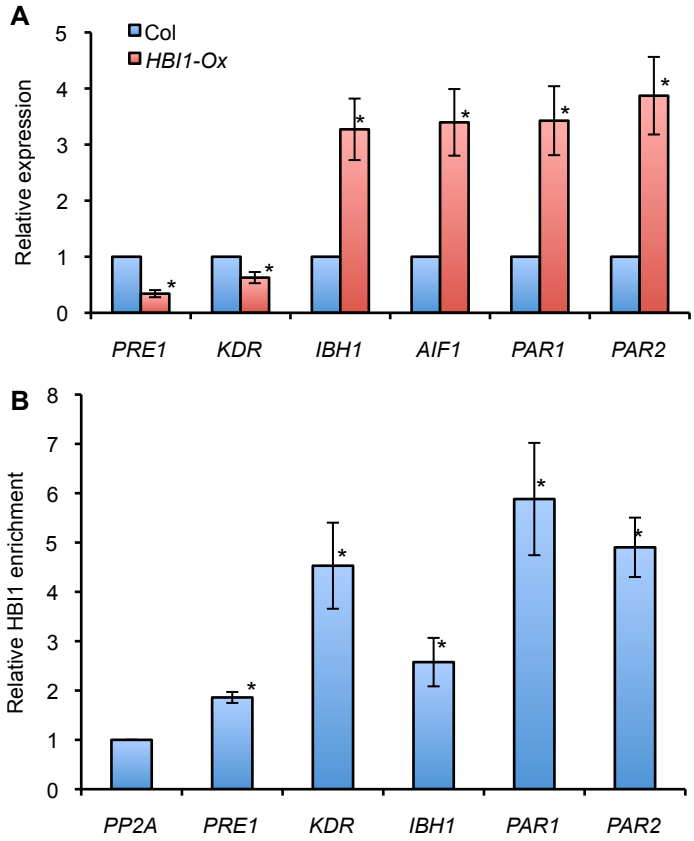


Supplemental Figure 1. Representative HBI1-binding and HBI1-regulated genes with known functions in various developmental and cellular processes.

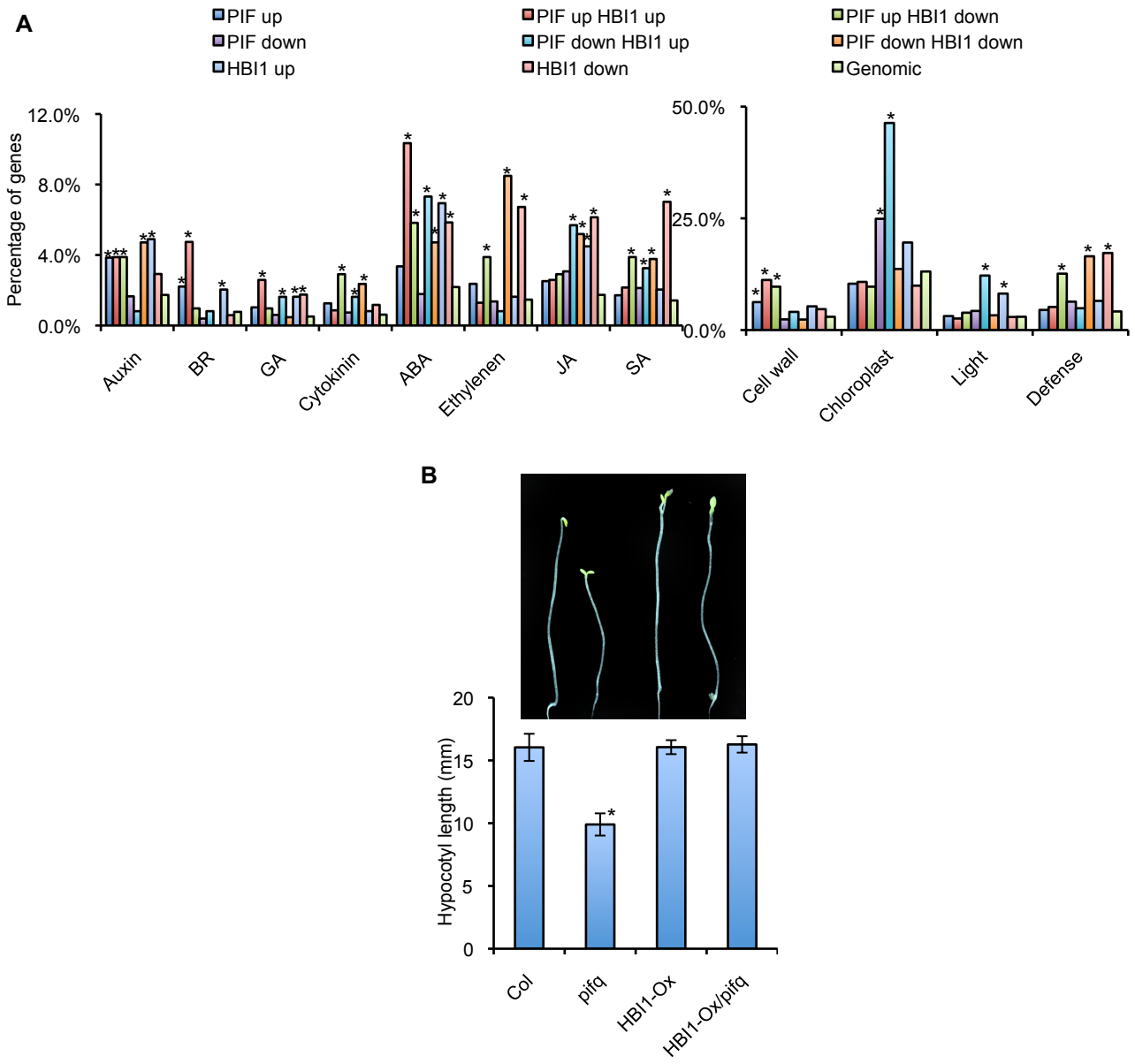
Genes induced or repressed by HBI1 are in red or blue, respectively. Direct HBI1-binding target genes are underlined. Genes induced or repressed by flg22 are in yellow or gray background, respectively.



Supplemental Figure 2. Growth-promoting and growth-inhibiting HLH factors are directly repressed and induced by HBI1, respectively.

(A) Quantitative RT-PCR analysis of the expression of *PRE1, KDR, IBH1, AIF1, PAR1* and *PAR2*. *PP2A* was used as the internal control. The wild-type and *HBI1-Ox* plants were grown in half-strength MS medium under constant light for five days. Error bars indicate SD from three biological repeats. Asterisk indicates significant difference from wild-type (*t* test; *P<0.05).

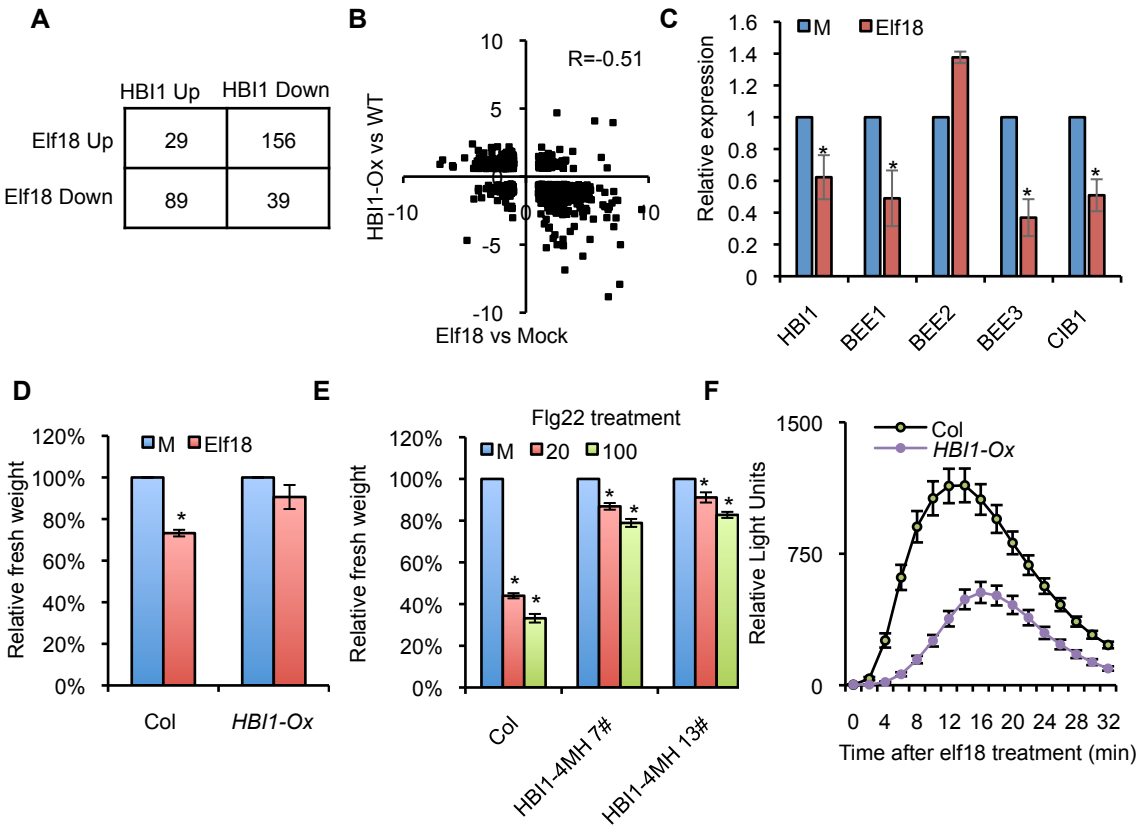
(B) Quantitative ChIP-PCR analysis of HBI1 binding to the promoter of selected genes. The chromatin of *pHBI1::HBI1-YFP* and *35S::YFP* transgenic plants was immunoprecipitated with anti-YFP antibody, and the precipitated DNA was quantified by qPCR. Enrichment of DNA was calculated as the ratio between *pHBI1::HBI1-YFP* and *35S::YFP*, normalized to that of the *PP2A* coding region. Error bars indicate SD of three biological repeats. Asterisk indicates significant difference from control gene *PP2A* (*t* test; *P<0.05).



Supplemental Figure 3. HBI1 and PIF have overlapping and distinct functions

(A) GO analyses of HBI1- and PIF-regulated genes. Numbers indicate the percentage of genes belonging to each GO category. Asterisk indicates significant difference from genomic random (Fisher exact test; *P<0.05).

(B) Growth of wild-type, *pifq, HBI1-Ox* and *HBI1-Ox/pifq* in the dark for 6 days. Bottom graph shows the quantification of hypocotyl lengths. Asterisk indicates significant difference from wild-type (*t* test; *P<0.05). Error bars indicate SD from three biological repeats.



Supplemental Figure 4. HBI1 negatively regulates elf18- and flg22-mediated PTI responses.

(A) Table shows the overlaps between gene sets regulated by HBI1 and elf18.

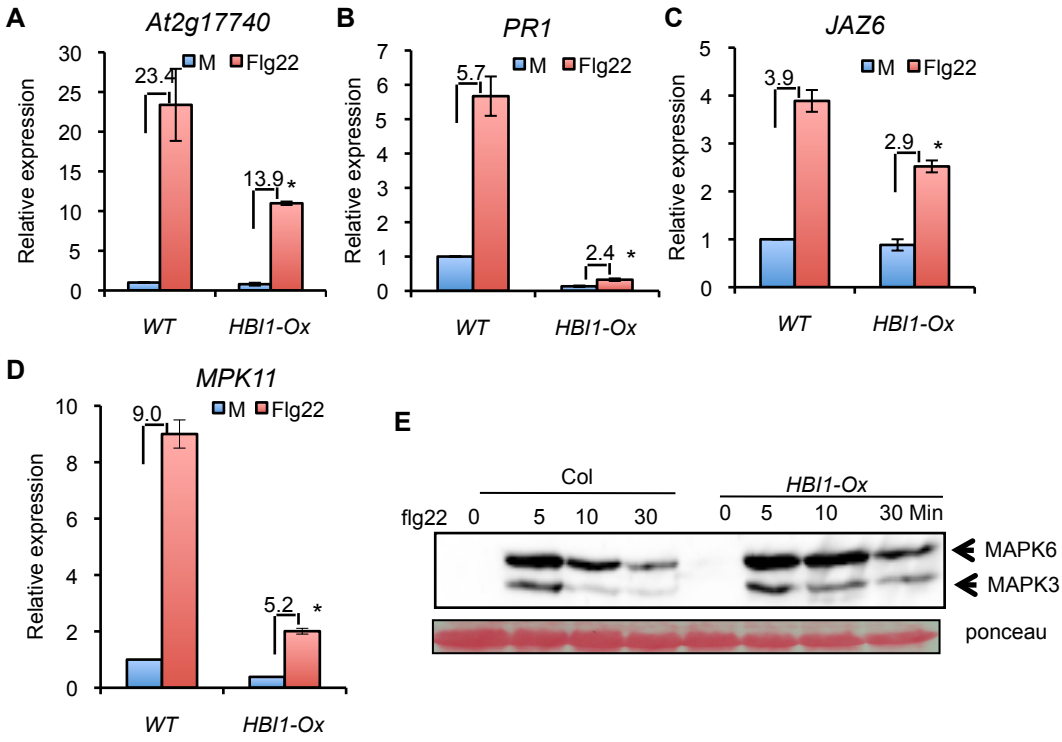
(B) Scatter plot of log2 fold change values of the genes co-regulated by HBI1 and elf18.

(C) Quantitative RT-PCR analysis of RNA levels of *HBI1* and its homologs in 4-week old plants treated with mock (M) or 1μM elf18 for 3 hours. *PP2A* was used as the internal control. Error bars indicate SD from three biological repeats. Asterisk indicates significant difference from Col with mock treatment. (*t* test; *P<0.05).

(D) Elf18-dependent inhibition of wild-type (Col) and *HBI1-Ox* seedling growth. Seedlings were grown in half-strength MS medium for 5 days, then transferred to liquid half-strength MS medium without (M) or with 1μM elf18 for another 8 days. Growth is represented relative to untreated plants. Error bars indicate SD from three biological repeats. Asterisk indicates significant difference from wild-type (*t* test; *P<0.05).

(E) Growth of wild-type (Col) and two independent lines of Ox-*HBI1-4MH* in the absence (M) or presence of flg22 (20 and 100 nM). Growth is represented as fresh weight relative to untreated plants. Error bars indicate SD from three biological repeats.

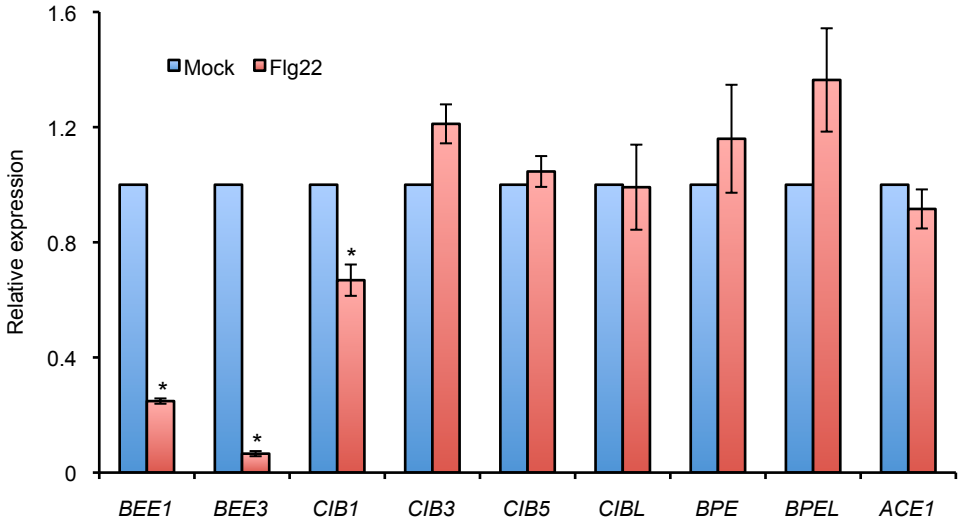
(F) Oxidative burst triggered by 1μM elf18 in leaf discs of wild-type and *HBI1-Ox* plants. Error bars indicate SD from twelve biological repeats.



Supplemental Figure 5. Activation of HBI1 results in the suppression of PTI marker gene expression, but not MAPK activation.

(A-D) Quantitative RT-PCR analyses of flg22 effects on the expression of defense-related genes in wild type and *HBI1-Ox*. The wild-type and *HBI1-Ox* plants were grown in half-strength MS medium under constant light for 2 weeks, and then treated with mock (M) or 1μM flg22 for 3 hours. *PP2A* was used as the internal control. Error bars indicate SD from three biological repeats. Asterisk indicates significant difference from flg22 treatment between wild-type and *HBI1-Ox* (*t* test; *P<0.05).

(E) Immunoblot analysis of flg22-induced (1 uM) MAPK phosphorylation in 2-week-old Col and *HBI1-Ox* seedlings. Arrowheads indicate phosphorylated MPK3 and MPK6. Blot stained with ponsceau S is presented to show equal loading. Immunoblots were probed with anti-phospho-p44/42 MAPK (Erk1/2) (Thr202/Tyr204) antibody (Cell signaling).



Supplemental Figure 6. Quantitative RT-PCR analyses of flg22 effects on the expression of HBI1 homologous genes.

The wild-type plants were grown in half-strength MS medium under constant light for 2 weeks, and then treated with mock or 1μM flg22 for 3 hours. *PP2A* was used as the internal control. Error bars indicate SD from three biological repeats. Asterisks indicate significant difference from the mock treatment (*t* test; *P<0.05).

Gene	HBI1-Ox vs WT	
	RT-qPCR	RNA-Seq
At1g26380	-8.25 ±0.54*	-8.83
At1g26420	-3.96 ±0.06*	-5
WRKY33	-2.65 ±0.05*	-2.5
At4g26120	-2.22 ±0.27*	-2.69
VQ28	-1.91 ±0.08*	-2.24
MPK11	-2.35 ±0.12*	-3.12
KDR	-1.78 ±0.1*	-1.63
BEE1	-1.44 ±0.08*	-1.29
IBH1	0.79 ±0.04*	1.04
AIF1	0.80 ±0.03*	1.02
EXP8	1.00 ±0.05*	1.34
EXP1	1.06 ±0.1*	1.04
PIF4	1.04 ±0.07*	1.24

Supplemental Table 1. Quantitative RT-PCR validation of the RNA-Seq data.

Seedlings of wild-type (WT) and *HBI1-Ox* plants were grown in half-strength MS medium under constant light for 5 days. The RT-qPCR data were normalized to PP2A, and the average ratio (in log2) between *HBI1-Ox* and WT and the standard deviation were calculated from three biological repeats. *Significant difference between *HBI1-Ox* and WT ($p<0.05$). RNA-Seq data are from Supplemental Table 2.

RT-PCR primers	
PP2A RTF	tatcggatgacgattcttcgtgcag
PP2A RTR	gcttggtcgactatcggaatgagag
EXP1RTF	GCTTACCGAAGGCTTACCGAAG
EXP1RTR	CTTGACATCGCTTGCCATCCAG
EXP8RTF	tcctcctcttcagcatttcgacct
EXP8RTR	cttgccacgactgtgtttttgagc
CPDRTF	TTGCTCAACTCAAGGAAGAG
CPDRTR	TGATGTTAGCCACTCGTAGC
DWF4RTF	cataaagctcttcagtcacga
DWF4RTR	cgtctgttctttgtttcctaa
BR6OX1RTF	TCGGGTTACGAAACTGTCTCTACG
BR6OX1RTR	CCTGAATGCCAAATGCTCAGCTC
FRK1RTF	ATCTTCGCTTGGAGCTTCTC
FRK1RTR	TGCAGCGCAAGGACTAGAG
At2g17740 RTF	TGCTCCATCTCTCTTTGTGC
At2g17749 RTR	ATGCGTTGCTGAAGAAGAGG
PR1RTF	AAGGGTTCACAACCAGGCAC
PR1RTR	CACTGCATGGGACCTACGC
JAZ6RTF	cgtggtgattcccgatcttaacgag
JAZ6RTR	tgggaggaagatgactaccgtgttg
HBI1RTF	TGCCTGGATGCAATAAGGTCACAG
HBI1RTR	TGGAGCTTCGATAGATGTCGTTTGG
BEE2RTF	CAGTTTCAGGCTTACTTCACAGGT
BEE2RTR	CTTTAGCGCCGAGAGATGTGGT
BEE1RTF	TGGTGCCCGGATGTTATAAGGC
BEE1RTR	GCTGCAGTGAGTTTCATCGAGAGG
BEE3RTF	TGCTGTGGAATCCATGCAGAAG
BEE3RTR	AGGGTCCACGATGATGAATGGAAG
CIB1RTF	aggccggattttgatatggatgac
CIB1RTR	ttgctgcattggattgacatgaagg
CIB5RTF	TGTCCACATGAACCATGAAACCG
CIB5RTR	CTCCACCTTCATGTCAGCTGTTG
ACE1RTF	GCAACTGTGAACCCACAAATGGAC
ACE1RTR	ACCAGCTCGTAGTTGAAGTGCATC
ChIP-PCR primers	
PP2A ChIP-F	CGGCTTTCATGATTCCCTCT
PP2A ChIP-R	GCCTTAAGCTCCGTTTCCTACTT
EXP1ChIPF	TGTATGCGAAGCACACAAAGACATC
EXP1ChIPR	GATGGAGGTGCCTTAATATAAACGC
EXP8ChIPF	CACAACCTTCAAAGTCCCT
EXP8ChIPR	CAACAATGTATGCCACCG
DWF4ChIPF	acgagaaaacggcatgtgaaattgg
DWF4ChIPR	gatactttgggcacgtccatgtgttc
CPDChIPF	gagagacatgtgaagtgttcatag
CPDChIPR	gttcgatgaatgtagtcagtgttagattc
BR6OX1ChIPF	accgtaatcatggttatgcctagagc
BR6OX1ChIPR	tgccttgtgatgattgagcgcacg

Supplemental Table 2. Oligonucleotide sequences used in this paper