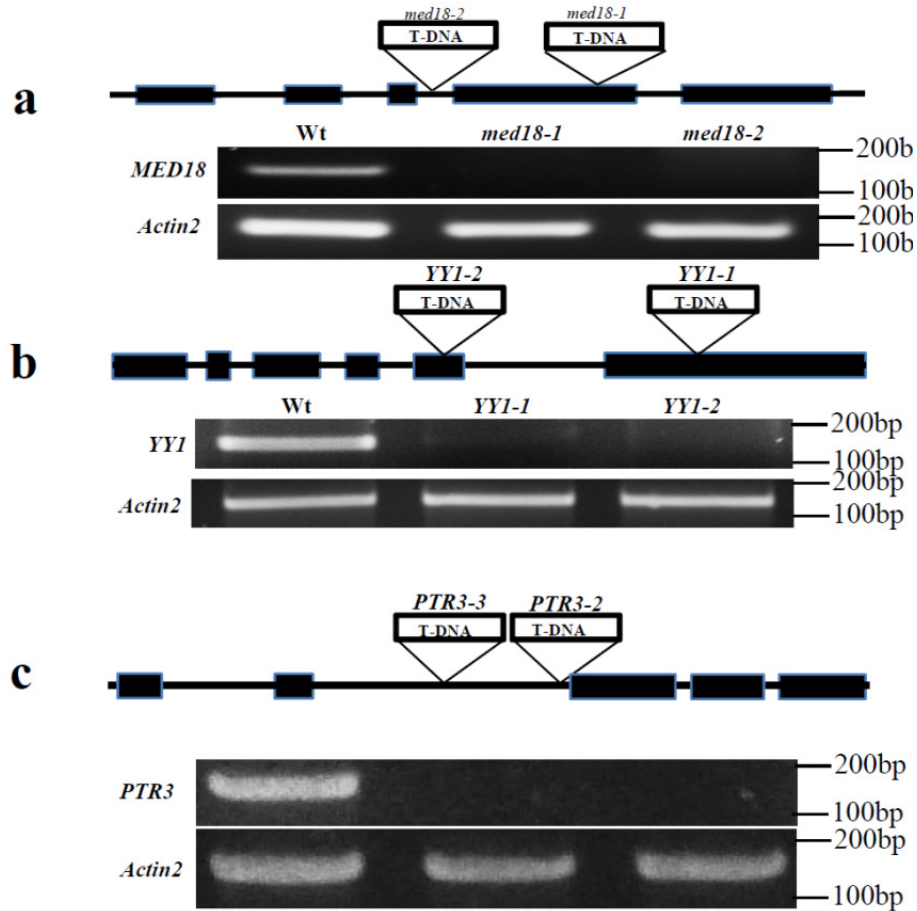
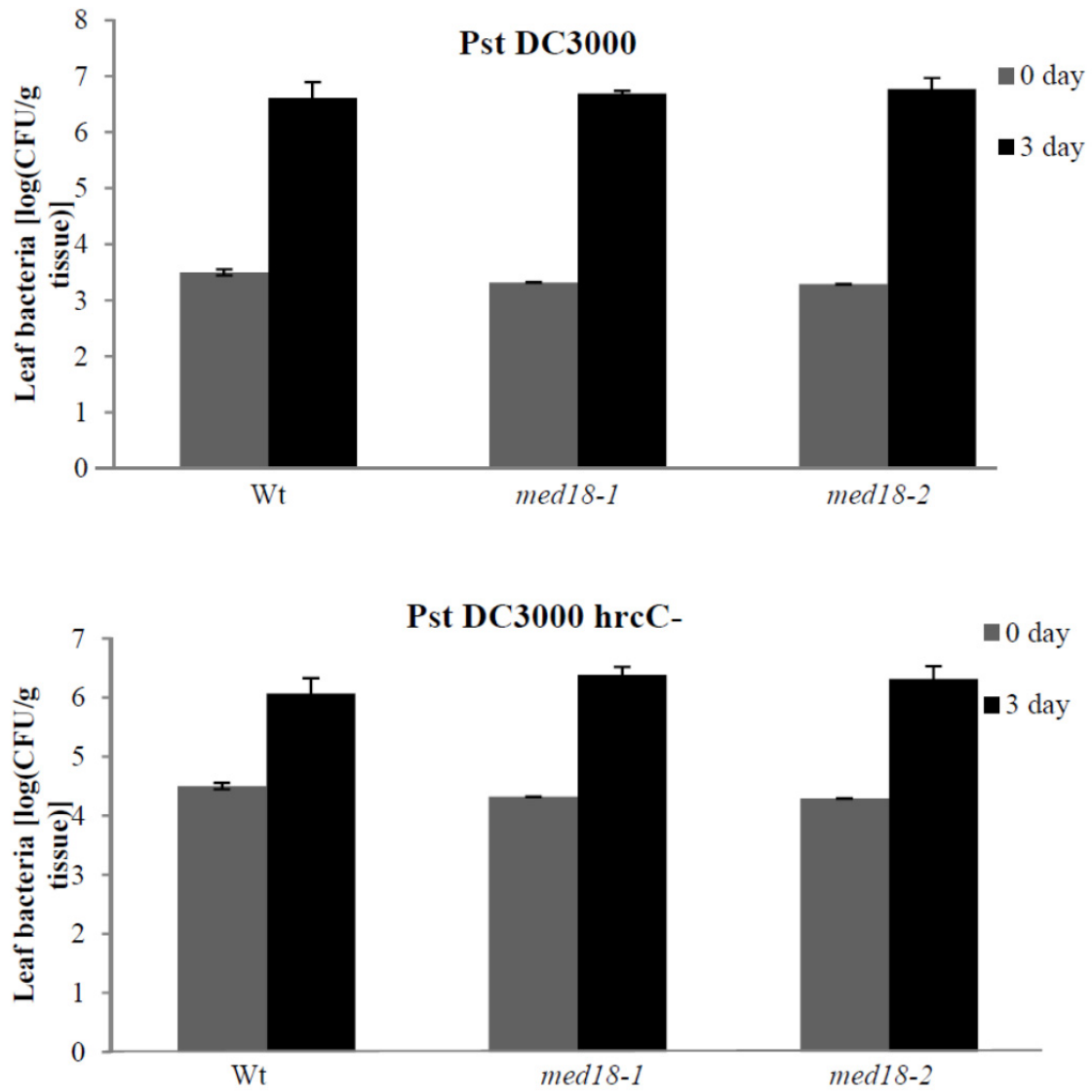


Supplementary Information

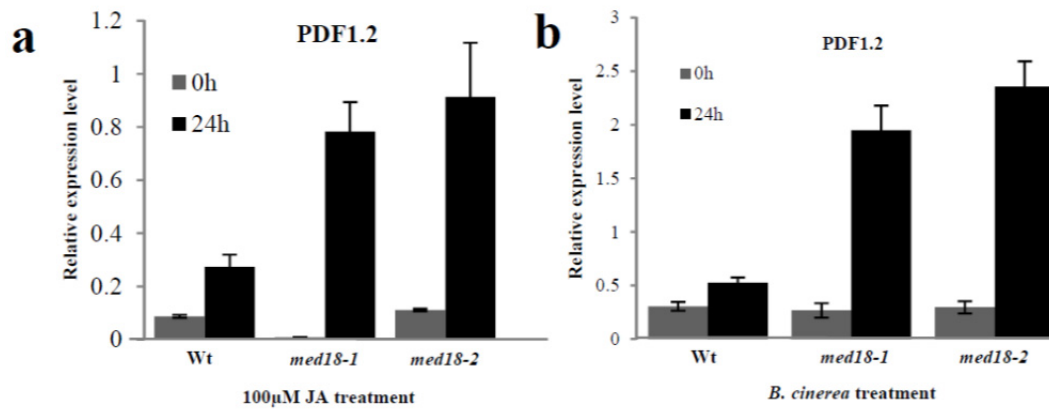
MED18 interaction with distinct transcription factors regulates plant immunity, flowering time and responses to hormones



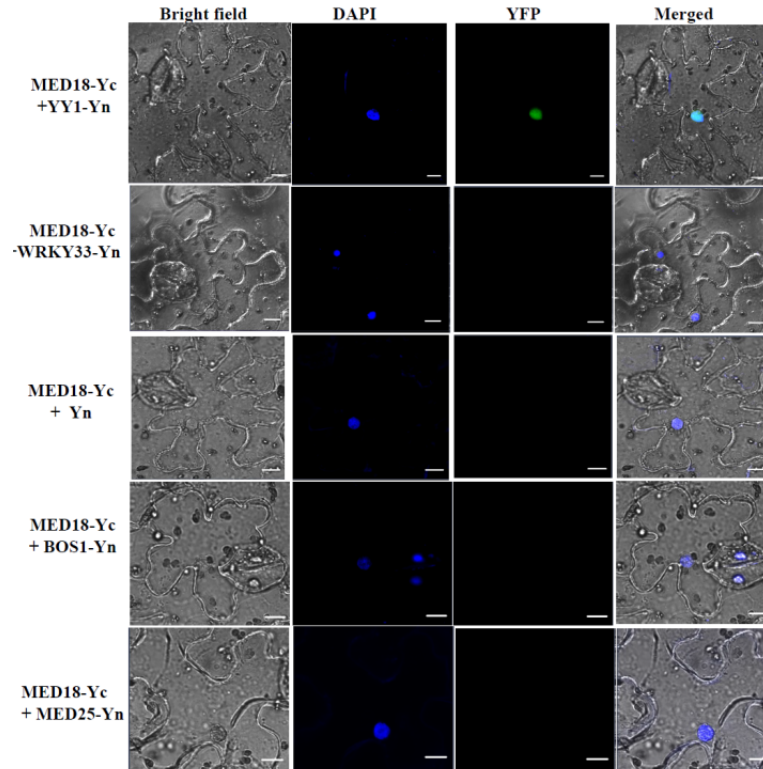
Supplementary Figure 1. Diagram showing T-DNA insertion in *MED18*, *YY1* and *PTR3* genes generating mutant alleles (top) and RT-PCR analysis of *MED18*, *YY1* and *PTR3* expression in *med18*, *yy1*, and *ptr3* mutants. Black rectangles represent exons, lines represent introns, and triangles represent T-DNA insertions. *Arabidopsis Actin 2* was used as a loading control for RT-PCR.



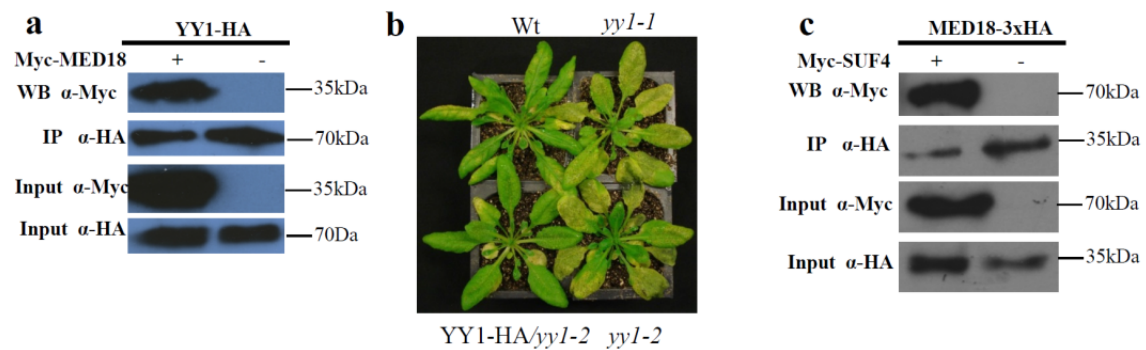
Supplementary Figure 2. MED18 is not required for plant responses to *P. syringae* pv. *tomato* DC3000 (virulent strain) and *P. syringae* pv. *tomato* DC3000 *hrcC*⁻ (non-pathogenic strain). The experiments were repeated at least three times with similar results. Error bars indicate SE from three replicates.



Supplementary Figure 3. The expression of the *PDF1.2* gene in response to MeJA and *B. cinerea*. *PDF1.2* gene expression in response to
(a) 100 μM MeJA treatment or
(b) *B. cinerea* infection in wild-type and *med18* mutant plants.



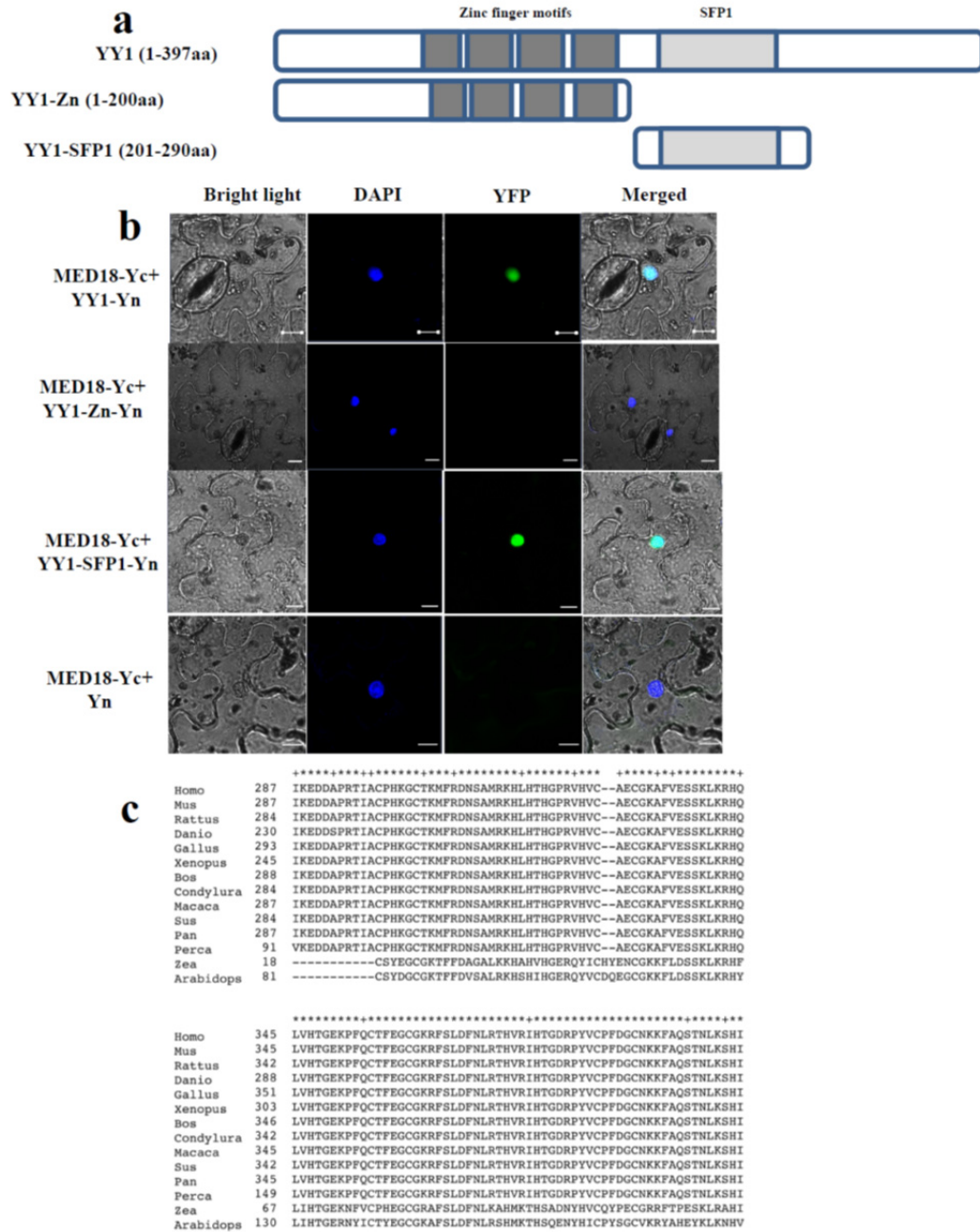
Supplementary Figure 4. BiFC analysis showing lack of interaction between MED18 and BOS1, WRKY33 or MED25 proteins. MED18-Yc was transiently co-expressed with BOS1-Yn, WRKY33-Yn, MED25-Yn or a respective empty vector in *Nicotiana benthamiana* leaf cells. No YFP fluorescence was detected. Cells were examined under brightfield (left column), fluorescence (YFP), and as a merged image (right) showing no interaction. The nucleus was stained with DAPI (4,6, diamidino-2-phenylindole). Scale bars, 10 μ m.



Supplementary Figure 5. Complementation of Arabidopsis *yy1* mutant by the constitutive expression of YY1 and MED18 interactions with Myc-YY1 or Myc-SUF4 proteins.

- (a) Co-immunoprecipitation of MYC-MED18 and YY1-HA.
- (b) Epitope tagged YY1 rescues the disease susceptibility of the *yy1* mutant.
- (c) Co-immunoprecipitation of Myc-SUF4 and MED18-HA in *Nicotiana benthamiana*.

YY1-HA and MED18-Myc or Myc-SUF4 and MED18-HA were co-expressed in *N. benthamiana* leaf tissue for the co-IP experiments. The control experiments involved expression of empty vector containing Myc tag.



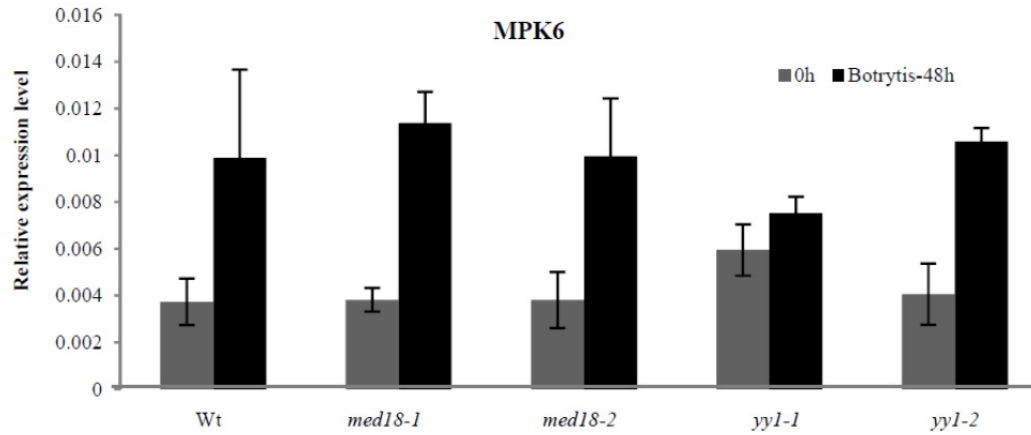
Supplementary Figure 6. The *Arabidopsis* YY1 protein structure and sequence alignment of YY1 proteins from different animal and plant species.

(a) Overall protein structure of the *Arabidopsis* YY1 protein showing four C₂H₂ type zinc finger motifs and one SFP1 motif.

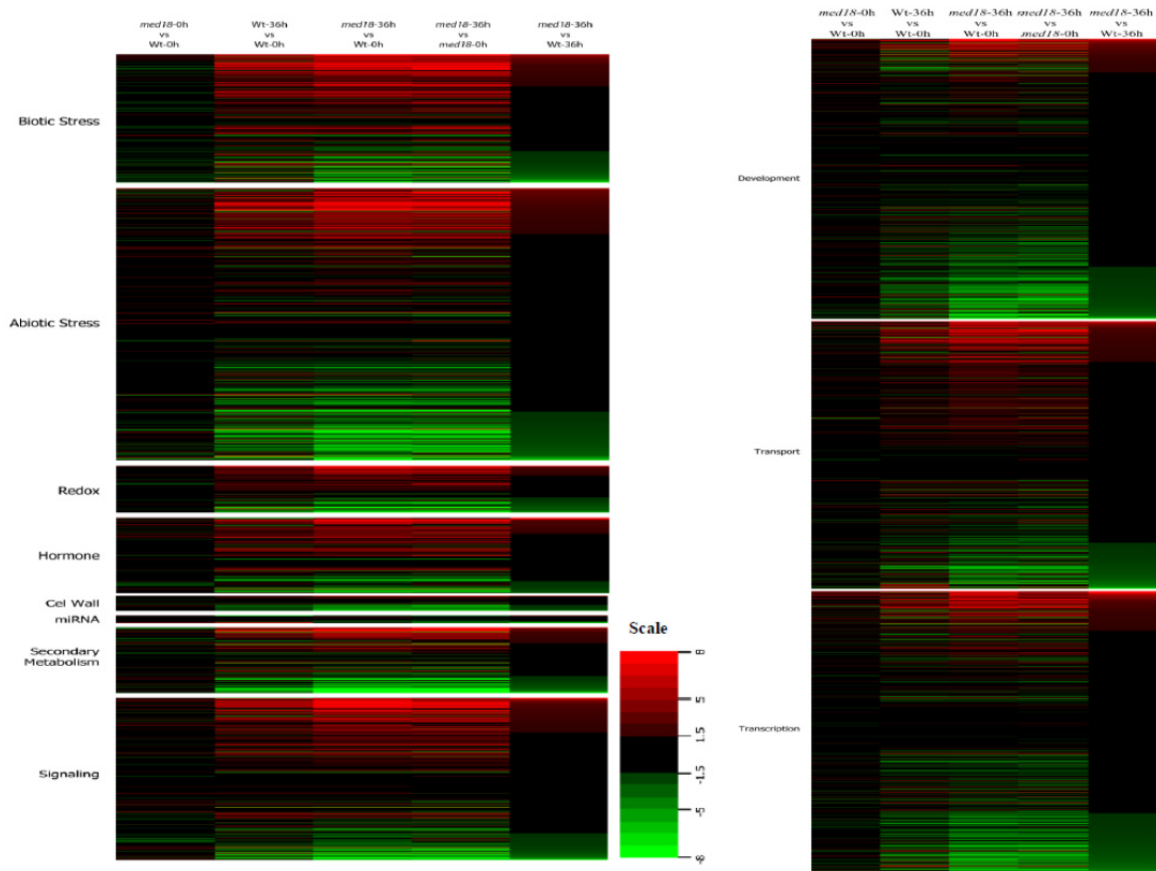
(b) The SFP1 domain but not the zinc finger domain of YY1 is required for interaction with MED18.

(c) Sequence comparisons between Metazoan, maize and *Arabidopsis* YY1 proteins.

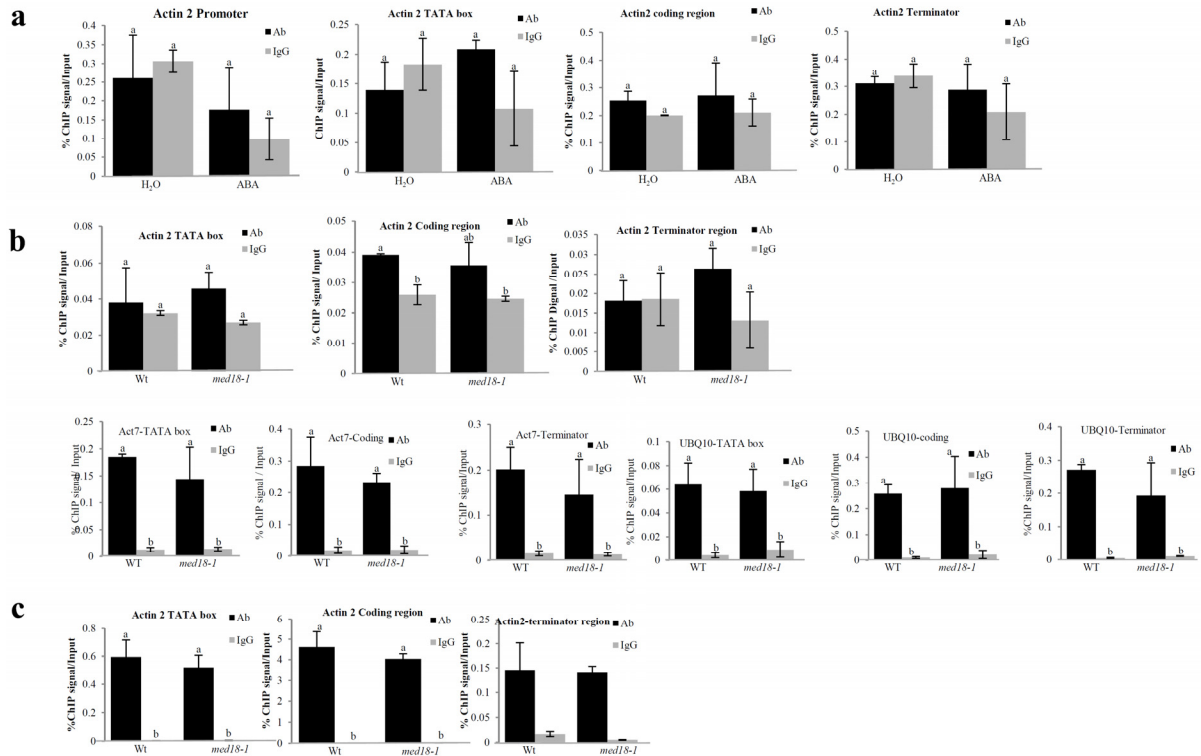
Scale bars, 10 µm.



Supplementary Figure 7. MPK6 expression in wild type, *med18* and *yy1* mutants in response to *B. cinerea* infection. The experiments were repeated at least three times with similar results. Error bars indicate SE



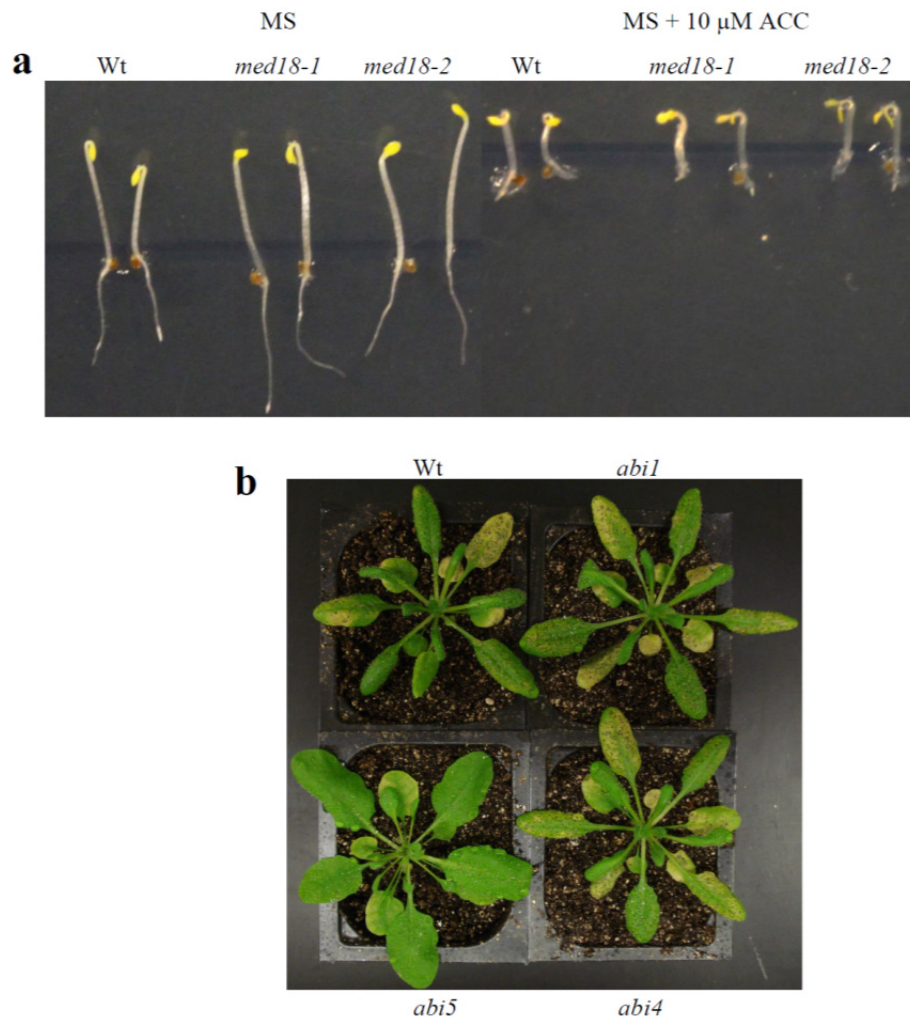
Supplementary Figure 8. Heat map showing altered expression of genes (fold change relative to the wild type) by functional categories in *med18* mutant and wild-type plants before and after infection. The heat map was generated based on 2-fold changes in gene expression on RPKM transcript counts ($p \leq 0.05$) with the non-inoculated wild type as a reference. A subset of functional categories that are MED18-dependent before and after *B. cinerea* inoculation were used based on GO annotations. Statistically significant changes were determined by R-software V3.16.5 ($P < 0.05$, t- test).



Supplementary Figure 9. MED18-HA, RNA polymerase II and H3K36 me3 levels on Arabidopsis Actin 2 gene.

- (a) MED18-HA association on Arabidopsis Actin2 promoter, TATA box, coding and terminator regions.
- (b) RNA polymerase II occupancy on the TATA box, coding and terminator regions of Arabidopsis Actin2, Actin7 and UBQ10.
- (c) Histone H3K36 me3 level on Arabidopsis Actin2 TATA box, coding and terminator regions.

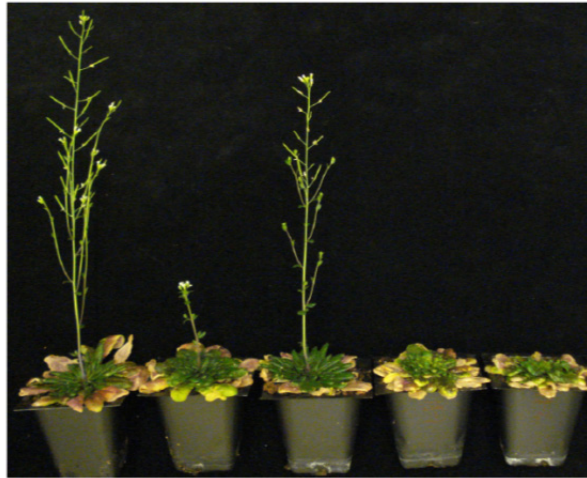
ChIP-qPCR was performed as described in legend for Figures 4 and in the methods section. Error bars show mean $\pm$ SE from at least three technical repeats. The means followed by different letters are significantly different from each other. ($p < 0.01$, student's t-test)



Supplementary Figure 10. The *hookless* phenotype of the *med18* mutant and the disease responses of the ABA response mutants

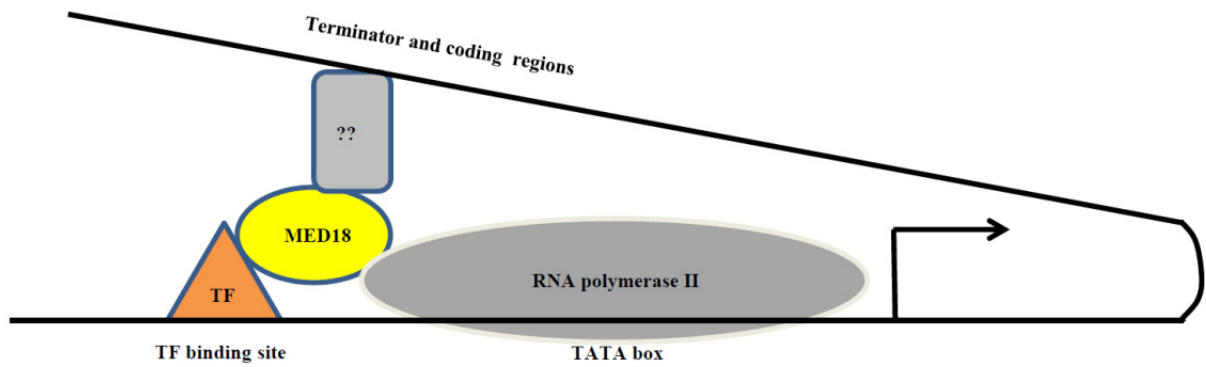
(a) *med18* mutant displays loss of the apical hook in response to ACC

(b) *B. cinerea* disease assays on Arabidopsis *abi1*, *abi4*, and *abi5* mutants. Four-week-old plants were treated with *B. cinerea* and the pictures are from plants at 4 days after inoculation.

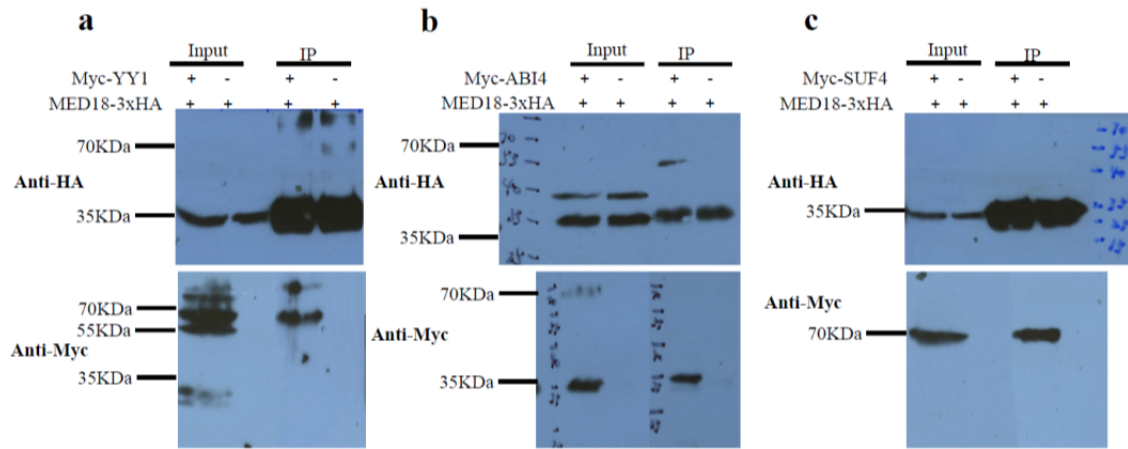


Col *med8* *med17* *med18-1* *med18-2*

Supplementary Figure 11. Delayed flowering in *med17*, *med8*, *med18*, and *med20a* plants under short day conditions. Plants were germinated and grown in a short day growth room (6 h light and 18 h dark).



Supplementary Figure 12. MED18 interacts with TFs and is required for RNA polymerase II on the promoter of target genes. MED18 also likely associates with yet unknown proteins in the terminator and coding regions of target genes.



Supplementary Figure 13. Full Western blots corresponding to Figures 2b, 5g and 6f.

Western blots showing Co-IP of MED18 with **(a)** YY1 in Arabidopsis transgenic plants,

(b) ABI4 after transient expression in *N. benthamiana* leaves, and

(c) SUF4 in Arabidopsis transgenic plants.

Supplementary Table 1: Primers used in this study.

Sequences read from 5' to 3'.

Primers for Constructs
MED18-HA
PL85: ATCCGCGGTATGTCAATGGAGTGTGTGGT
PL86: ATGAATTCCAATGTAGTACCTCCTCCATC
Myc-MED18
PM185: GGAATTCCATATGATGTCAATGG AGTGTGTGGT
PM293: CGGGATCCTTACAATGTAGTACCTCCTCC
MED18-Yc
PL235: AT TCTAGAATGTCAATGG AGTGTGTGGT
PL236: AT GGATCCCAATGTAGTACCTCCTCCAT
MED18-GFP
PM201: CCGCTCGAGATGTCAATGGAGTGTGTGGT
PM202: CGGGATCCCAATGTAGTACCTCCTCCATCC
MYC-YY1
PL897: CGGGATCCTAATGGATCATCAAAATTATCA
PL898: GGACTAGTCTAATCTTCATACTCGGTCTC
YY1-Yn
PL828: ACGAGCTCATGGATCATCAAAATTATCAATACCAA
PL829: CTAGTCTAGAATCTTCATACTCGGTCTCTTC
YY1-GFP
PM203: CCGCTCGAGATGGATCATCAAAATTATCA
PM204: CGGGATCCATCTTCATACTCGGTCTCTTC
YY1-HA
PL828: ACGAGCTCATGGATCATC AAAATTATCAATACCAA
PL829: CTAGTCTAGAATCTTCATACTCGGTCTCTTC
ABI4-N-YFP
PL756: ACATGGACCCTTTAGCTTCCCA
PL757: TGCTCTAGAATAGAATTCCCCCAAGATGG
SUF4-Yn
PM197: ACGAGCTCATGGGTAAGAAGAAGAAGAG
PM198: GCTCTAGAAAACGCCATCCGCCAGCAAGC
Myc-SUF4
PM299: CGGGATCCTAATGGGTAAGAAGAAGAAGAG
PM300: GGACTAGTCTAAAACGCCATCCGCCAGC
Myc-ABI4
PM199: TCCCCCGGGTTATGGACCCTTTAGCTTCCCA

PM200: GGACTAGTTTAATAGAATTCCCCCAAGATGG
Primers for mutant identification
yy1-1
PL166: GACTCCCAAATATACACCACCAGC SALK_071311C
PL167: CTCTTCATCGTCGTCATCATCCTC SALK_071311C
yy1-2
PL168: GATCAGGAAGGATGTGGAAAGG
PL169: TGGAGCTAGACTCTGACTAAGGAG SALK_040806C
med18-1
LP: aagaagcaagtggaggaagatg
RP: cccacatggtacagcttcttc
med18-2
LP: TCCATCCGACATAAGAGATGC
RP: TTCGGATTTGGTCTTGTTGAG
med17
AAACACATGAAAACTGAGCAAG
AGTGGTGGTGAAGGATGATTG
med8
AATGTAAAGAATGGGCCAGG
CTCAGCAAAAGTTTCAGACGG
ptr3-2
PM127 : TAAGCTAGAAGCGATCGGTTG
PM128 : GAACAGTGTTGGCGAAGAGAG
ptr3-3
PM129 : GAAGCTTTTTTCGCAATTTTCC
PM130 : AACCAATAAGCCTCATGCATG
Primers for qPCR
ACT 2
PL23: GACCTTTAACTCTCCCGCTATG
PL24: AAACCCTCGTAGATTGGCAC
PDF1.2
qPDF1.2-F: TTCTCTTTGCTGCTTTCGACGCA
qPDF1.2-R: TTGCATGATCCATGTTTGGCTCCTT
YY1
PL808: TTATGAAGGATGTGGAAAGGCA
PL809: GCAACGTGGTTCTTTAGCTTG
MED18
PL806: TTCCTGTAACACCTGGTATGC

PL807: GGAGATAGACGGTTTCGACAAG
Botrytis ActinA
PL507: 5'-ACTCATATGTTGGAGATGAAGCGCA-3'
PL508: 5'-AATGTTACCATACAAATCCTTACGGA-3'
PTR3
PM23: TGCTGATCATGGTCTCATCCACCA
PM24: TTCCCAATCGCCAAACTCGTTGTC
A. brassicicola CutA
FP (5'-CACTGCGCCCAATGATGAAC-3')
RP (5'-GTAGCCGAACAACACGACACC-3')
TRX-h5
PM452: ATGGCCGGTGAAGGAGAAGT
PM453: GCAATGAAACGGCAAGGTGG
GRXS13
PM454: TGGTGTTTGCAAGGAGAGGC
PM455: AACCACCACTGGATTCACGC
GRX480
PM488: GAATCCGGCGGTCCTTGAGA
PM489: AACTTCACCGTACCTCCGCC
Primers for ChIP qPCR assays
PTR3 promoter region
PM379: AAGTCCTGCATTTTGTGACTCTG
PM380: TCCAAACGGATCCTCCTACATC
PTR3 TATA box
PM302: AGTGCCGACTCTCTTGACATT
PM303: GCCTTGAAGATCAACTGTTCCAT
PTR3 coding region
PM304: ATGTTGGCTGGACCTTGGGT
PM305: ATGGCGGTAAAACGGAGTGC
PTR3 terminator region
PM306: TCGTTTTGTTCTTGGTCGTGGT
PM307: TCCACCTCTTTCACATCAACCGA
ABI4 binding site on ABI5 promoter
PL838: ctccggcggttttaactatgt
PL839: ttatttaacagtcttctaataccaagatc
ABI5 TATA box
PM265: TGTTGACCTTCACGCCTCTC
PM266: AAAGCCGCCGGAGAATTTTG

ABI5 coding region
PM267: GAGGGTGGTGTGTTGGTGTCTT
PM268: CCTACAAAGCGGAGCTGGAA
ABI5 terminator region
PM269: TCGGAGACAGAACGAGGGAA
PM270: GGTGTTCTCCTACCAACACA
SUF4 binding site on FLC promoter
PM296: CAAGCTGATACAAGCATTTCACC
PM297: GTCCACACATATGGCAATAGCTC
FLC TATA box
PM322: ATCTCCGGCGACTTGAACC
PM323: TCCCATGGCTTCTCTCCGA
FLC coding region
PM324: TGGTGGCTCCACATGCATTA
PM325: AAAGGGACAGAAGAAGCGGT
FLC terminator region
PM326: TGGCCAAGAGACTTTGTGTGT
PM327: ATCTCGATGCAATTCTCACACG
TRX-h5 promoter: -250 bp from Transcription site
PM492: CGTGCACACAAAACATGCGT
PM493: GGTCAACGGCGTGATGATGG
TRX-h5 promoter: -750 bp from Transcription site
PM494: TGAACAATTCGTTGACCTGACCA
PM495: CAGTCACTAACGGATAATAACGGGT
GRXS13 promoter: -75 bp from Transcription site
PM496: TACGGTGACATGGCTTCGGAT
PM497: GCATTTGGCTTTGGGGGTCAA
GRXS13 promoter: -400 bp from Transcription site
PM498: TGACATCAGCCTTGTCGTAA
PM499: ATTGTCGGA ACTCAAATGCG
GRXS13 promoter: -800 bp from Transcription site
PM500: GTGCAACGTATTTTCGACCA
PM501: ACTACCCAGTACACGTCCTA
Actin2 promoter -500bp from Transcription site
PM586: GCCAACCACGACGACGACTA
PM587: CTGCTCGATCCGCGTGTTAC
Actin2 TATA box region
PM588: TGTAACACGCGGATCGAGCA
PM589: AACGTGACCTGGCTGTCAGA

Actin2 coding region
PM590: ACTGTGCCAATCTACGAGGGT
PM591: AAGGTCACGTCCAGCAAGGT
Actin2 terminator region
PM592: TGTGTGTGACAACTCTCTGGGT
PM593: ACTAAAACGCAAAACGAAAGCGG
Actin7 TATA box region
PM622: CGGCTCCCGGGCTAATTCAT
PM623: ACCGACGCGTCTATGTTGCC
Actin7 coding region
PM624: GGTGTGTCTCACACTGTGCC
PM625: GTCTGTGAGATCCCGACCCG
Actin7 terminator region
PM626: TGGTTGTGTCAAGAAGTCTTGTGT
PM627: CAGCATCATCACAAGCATCCTAAAG
UBQ10 TATA box region
PM628: TTGCGTGTAACAACGCTCAA
PM629: ACGAGAAAGCTAAGGCGGTG
UBQ10 coding region
PM630: TGGCAGAACTTTGGCCGACT
PM631: ATACCTCCACGCAGACGCAA
UBQ10 terminator region
PM632: CGCCTGCAAAGTGACTCGAC
PM633: CCAACAGCTCAACACTTTTCGCT