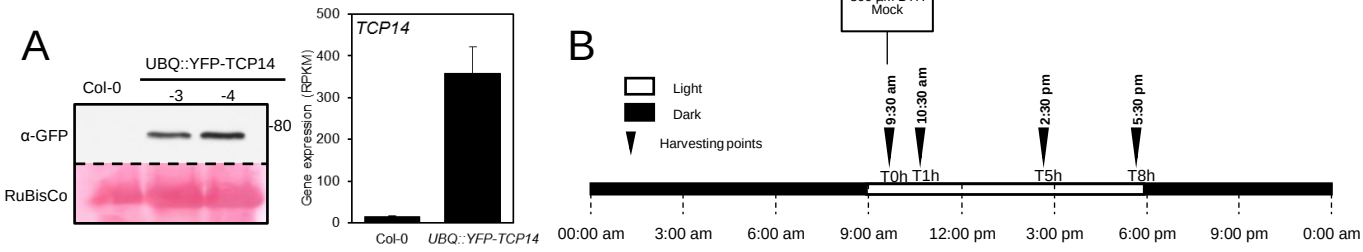
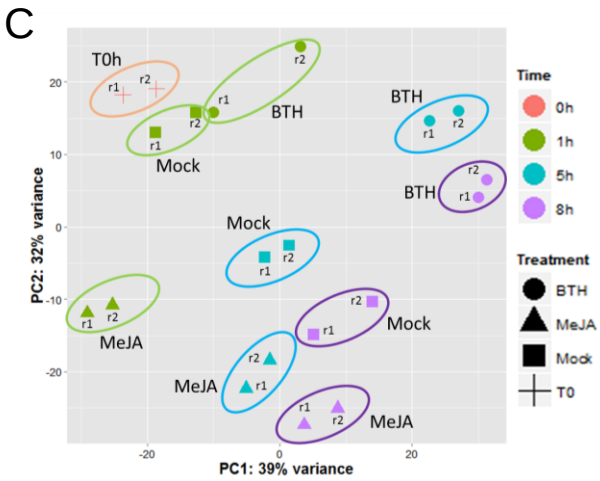
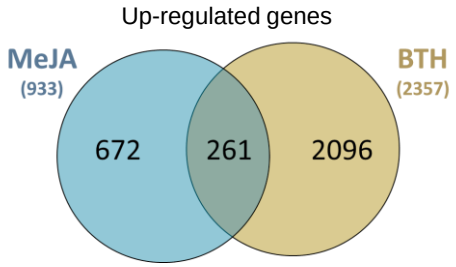
sFigure 1



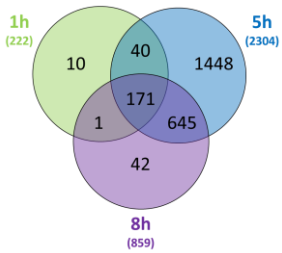


D

	Up-regulated	Down-regulated
MeJA	933	1054
BTH	2357	1593



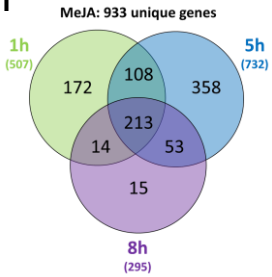
E



Top10 enriched GO terms

Gene Set Name(NO. Genes)	FDR
DEFENSE_RESPONSE(1644)	9.67E-158
RESPONSE_TO_BIOTIC_STIMULUS(1675)	3.40E-151
INNATE_IMMUNE_RESPONSE(926)	1.15E-150
IMMUNE_SYSTEM_PROCESS(980)	6.89E-149
IMMUNE_RESPONSE(980)	6.89E-149
RESPONSE_TO_OTHER_ORGANISM(1411)	2.41E-140
RESPONSE_TO_STRESS(4037)	2.61E-131
RESPONSE_TO_STIMULUS(6222)	1.89E-123
DEFENSE_RESPONSE,_INCOMPATIBLE_INTERACTION(535)	5.07E-123
MULTI-ORGANISM_PROCESS(1804)	3.98E-122

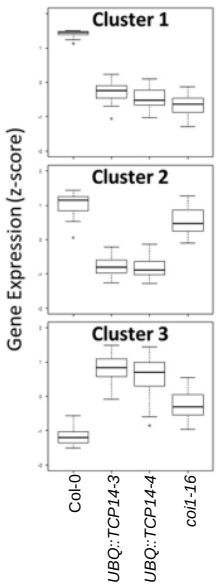
F



Top10 enriched GO terms

Gene Set Name(NO. Genes)	FDR
RESPONSE_TO_JASMONIC_ACID_STIMULUS(471)	1.46E-74
RESPONSE_TO_STIMULUS(6222)	1.46E-64
RESPONSE_TO_WOUNDING(340)	3.02E-64
JASMONIC_ACID_METABOLIC_PROCESS(159)	3.02E-64
OXYLIPIN_METABOLIC_PROCESS(167)	4.12E-64
RESPONSE_TO_STRESS(4037)	1.99E-58
RESPONSE_TO_CHEMICAL_STIMULUS(3953)	2.06E-52
JASMONIC_ACID_BIOSYNTHETIC_PROCESS(135)	9.12E-52
OXYLIPIN_BIOSYNTHETIC_PROCESS(141)	7.85E-51
SMALL_MOLECULE_BIOSYNTHETIC_PROCESS(1859)	1.01E-50

G

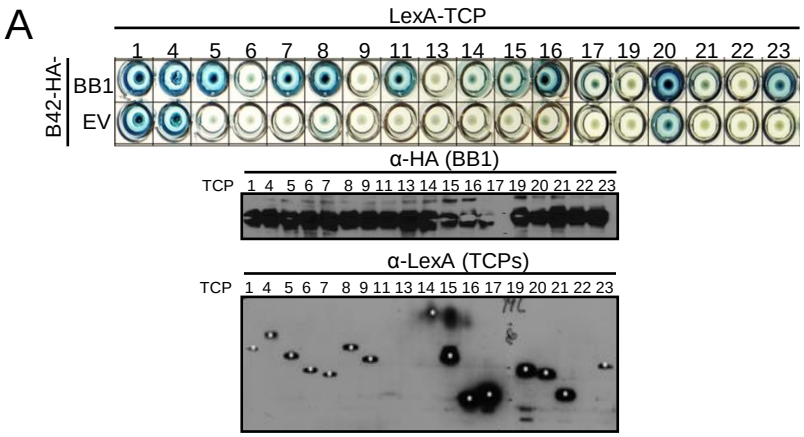


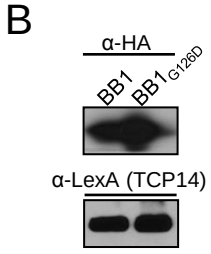
GO Term	Description	FDR
GO:0009718	anthocyanin biosynthetic process	1.78E-05
GO:0009753	response to jasmonic acid stimulus	1.78E-05
GO:0046283	anthocyanin metabolic process	3.47E-05
GO:0009611	response to wounding	8.74E-04
GO:0019762	glucosinolate catabolic process	8.74E-04

No enriched terms

GO:0010467	gene expression	1.63E-05
GO:0034645	cell. macromolecule bios. process	4.99E-05
GO:0009059	macromolecule bios. process	3.47E-05
GO:0044260	cell. macromolecule metabolic process	1.00E-03
GO:0090304	nucleic acid metabolic process	1.30E-03

sFigure 2





D

```
TCP14:          180-PANFTSLNISLRSSGSSMSLPSHFRSAASTFSPNNI-216
TCP14-PANFTS:   180-NAAIRSLNISLRSSGSSMSLPSHFRSAASTFSPNNI-216
TCP14-LNISLR:   180-PANFTSNAAIRSSGSSMSLPSHFRSAASTFSPNNI-216
TCP14-SSGSSM:   180-PANFTSLNISLRNAAIRSSLPSHFRSAASTFSPNNI-216
TCP14-SLPSHF:   180-PANFTSLNISLRSSGSSMNAAIRSRSAASTFSPNNI-216
TCP14-RSAAST:   180-PANFTSLNISLRSSGSSMSLPSHFNAAIRSFSPNNI-216
TCP14-FSPNNI:   180-PANFTSLNISLRSSGSSMSLPSHFRSAASTNAAIRS-216
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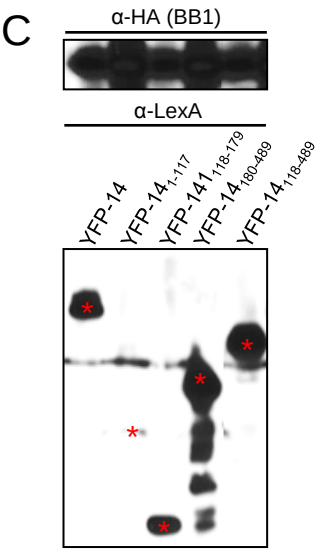
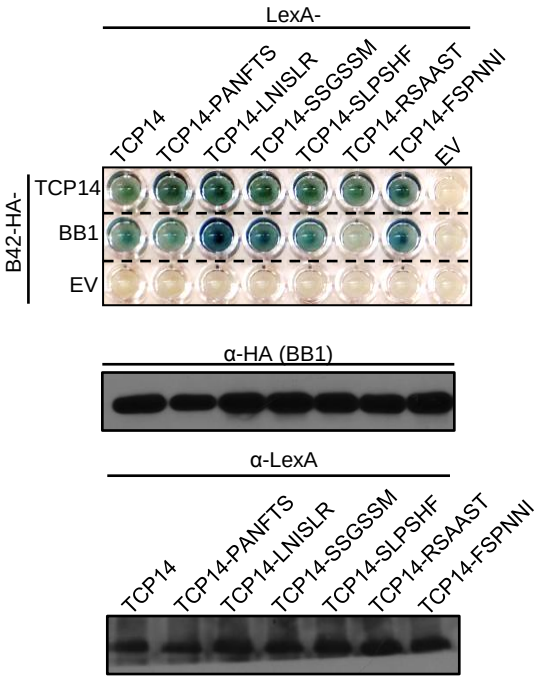
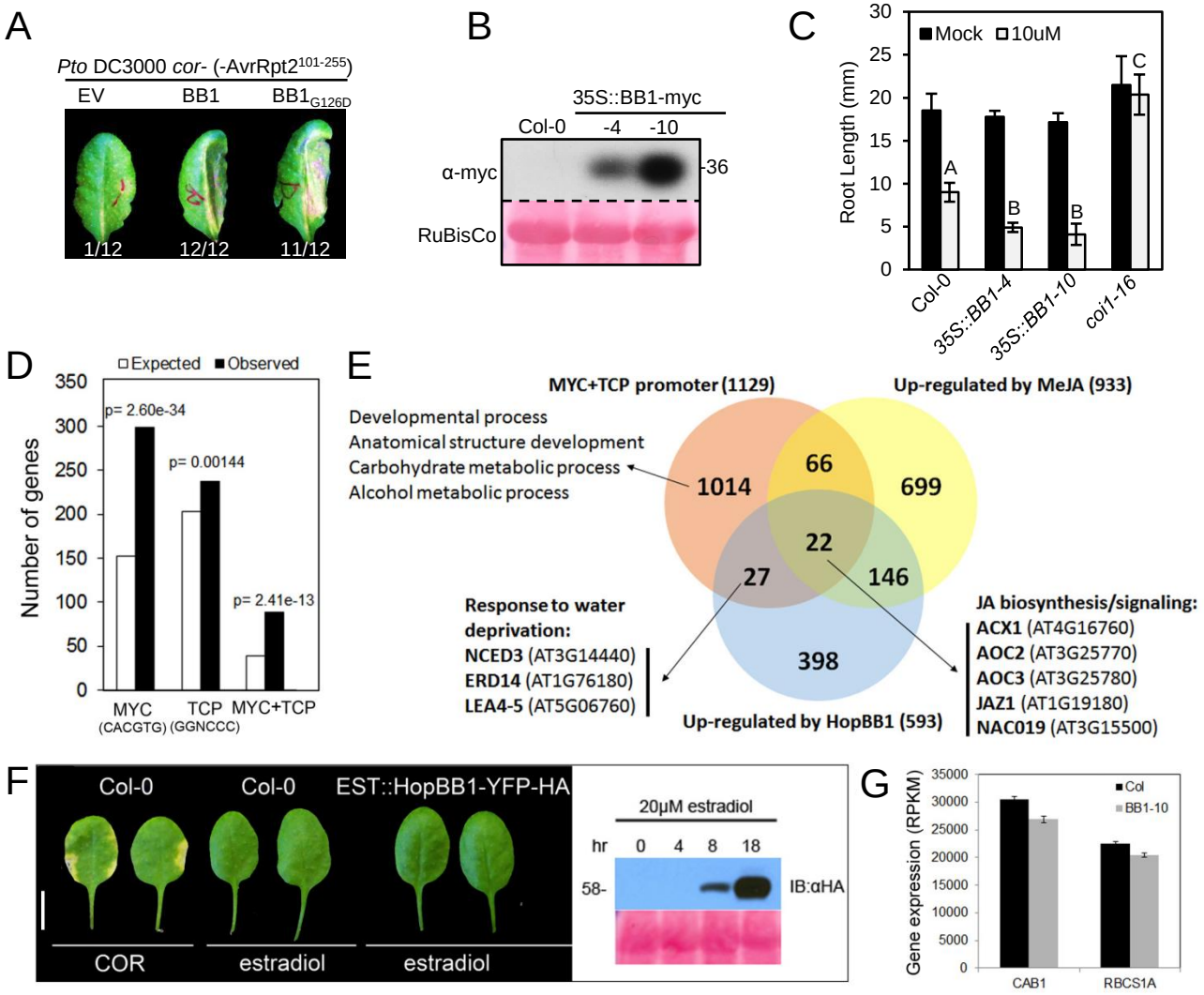
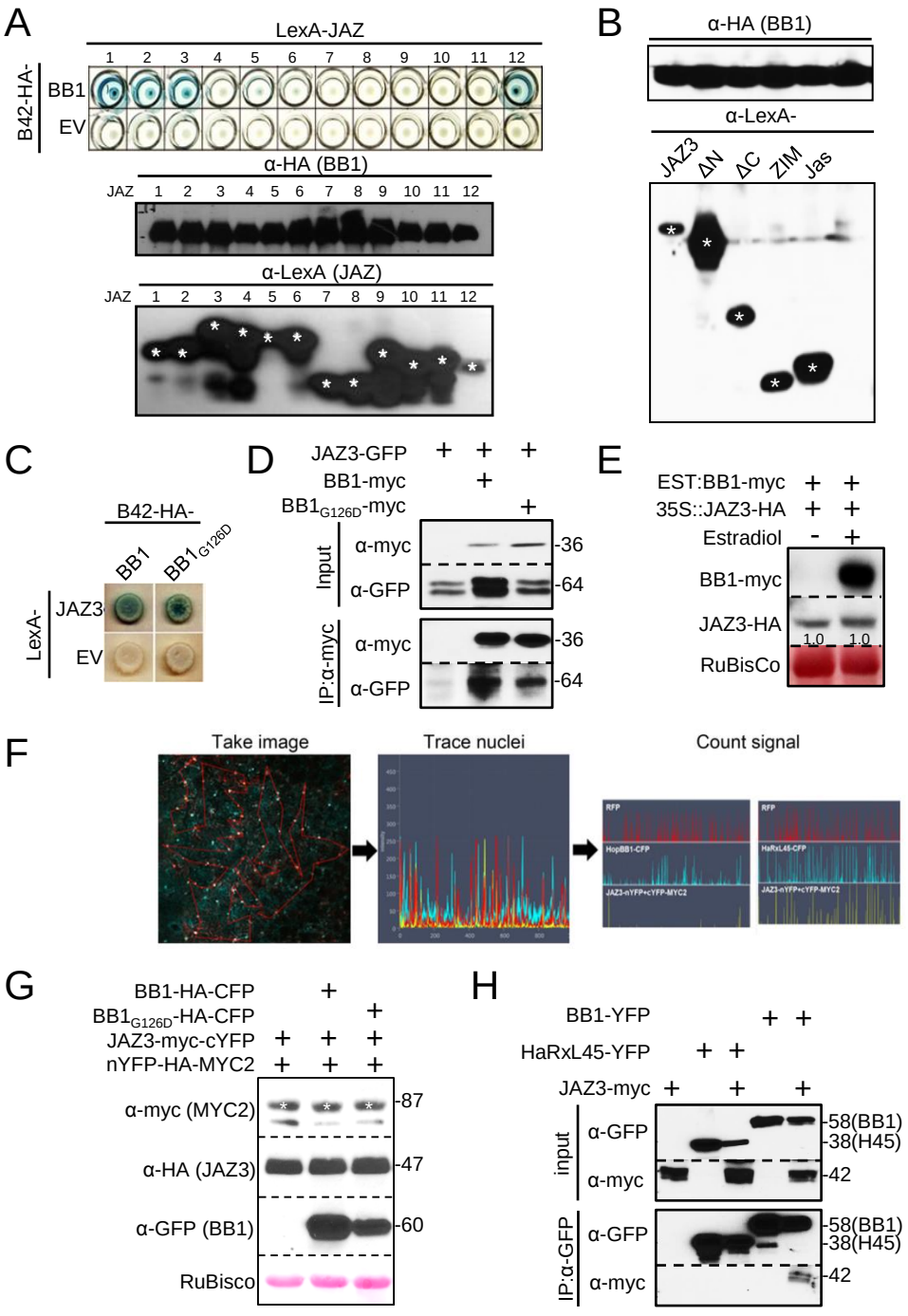




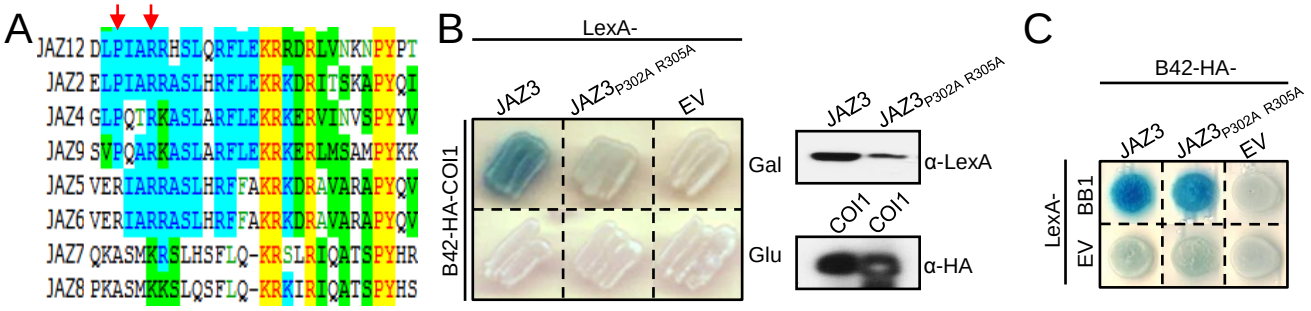
sFigure 3


A
Pto DC3000 cor- (-AvrRpt2101-255)
EV
BB1
BB1G126D
1/12
12/12
11/12
B
35S::BB1-myc
Col-0
-4
-10
α-myc
-36
RuBisCo
C
Mock
10uM
Root Length (mm)
A
B
B
C
Col-0
35S::BB1-4
35S::BB1-10
coi1-16
D
Expected
Observed
Number of genes
p= 2.60e-34
p= 0.00144
p= 2.41e-13
MYC (CACGTG)
TCP (GGNCCC)
MYC+TCP
E
MYC+TCP promoter (1129)
Up-regulated by MeJA (933)
Developmental process
Anatomical structure development
Carbohydrate metabolic process
Alcohol metabolic process
1014
66
699
22
27
146
398
Response to water deprivation:
NCED3 (AT3G14440)
ERD14 (AT1G76180)
LEA4-5 (AT5G06760)
JA biosynthesis/signaling:
ACX1 (AT4G16760)
AOC2 (AT3G25770)
AOC3 (AT3G25780)
JAZ1 (AT1G19180)
NAC019 (AT3G15500)
Up-regulated by HopBB1 (593)
F
Col-0
Col-0
EST::HopBB1-YFP-HA
COR
estradiol
estradiol
20μM estradiol
hr
0
4
8
18
58-
IB:αHA
G
Col
BB1-10
Gene expression (RPKM)
CAB1
RBCS1A

sFigure 4


A
LexA-JAZ
1 2 3 4 5 6 7 8 9 10 11 12
B42-HA-
BB1
EV
α-HA (BB1)
JAZ 1 2 3 4 5 6 7 8 9 10 11 12
α-LexA (JAZ)
JAZ 1 2 3 4 5 6 7 8 9 10 11 12
B
α-HA (BB1)
α-LexA-
JAZ3 ΔN ΔC ZIM Jas
C
B42-HA-
BB1
BB1G126D
LexA-
JAZ3
EV
D
JAZ3-GFP + + +
BB1-myc +
BB1G126D-myc +
Input
α-myc
α-GFP
IP:α-myc
α-myc
α-GFP
-36
-64
-36
-64
E
EST:BB1-myc + +
35S::JAZ3-HA + +
Estradiol - +
BB1-myc
JAZ3-HA
RuBisCo
1.0 1.0
F
Take image
Trace nuclei
Count signal
RFP
HopBB1-CFP
JAZ3-nYFP+cYFP-MYC2
RFP
HaRxL45-CFP
JAZ3-nYFP+cYFP-MYC2
G
BB1-HA-CFP +
BB1G126D-HA-CFP +
JAZ3-myc-cYFP + + +
nYFP-HA-MYC2 + + +
α-myc (MYC2)
α-HA (JAZ3)
α-GFP (BB1)
RuBisco
-87
-47
-60
H
BB1-YFP + +
HaRxL45-YFP + +
JAZ3-myc + + +
input
α-GFP
α-myc
IP:α-GFP
α-GFP
α-myc
-58(BB1)
-38(H45)
-42
-58(BB1)
-38(H45)
-42

sFigure 5


A
JAZ12 DLPIARRHSLQRFLEKRRDRLVNKNPYPT
JAZ2 ELPIARRASLHRFLEKRKDRITSKAPYQI
JAZ4 GLPQTRKASLARFLEKRKERVINVSPYYV
JAZ9 SVPQARKASLARFLEKRKERLMSAMPYKK
JAZ5 VERIARRASLHRFFAKRKDRAVARAPYQV
JAZ6 VERIARRASLHRFFAKRKDRAVARAPYQV
JAZ7 QKASMKRSLHSFLQ-KRSLRIQATSPYHR
JAZ8 PKASMKKSLQSFLQ-KRKIRIQATSPYHS
B
LexA-
JAZ3
JAZ3P302A R305A
EV
B42-HA-COI1
Gal
Glu
JAZ3
JAZ3P302A R305A
α-LexA
COI1
COI1
α-HA
C
B42-HA-
JAZ3
JAZ3P302A R305A
EV
LexA-
BB1
EV

sFigure 6

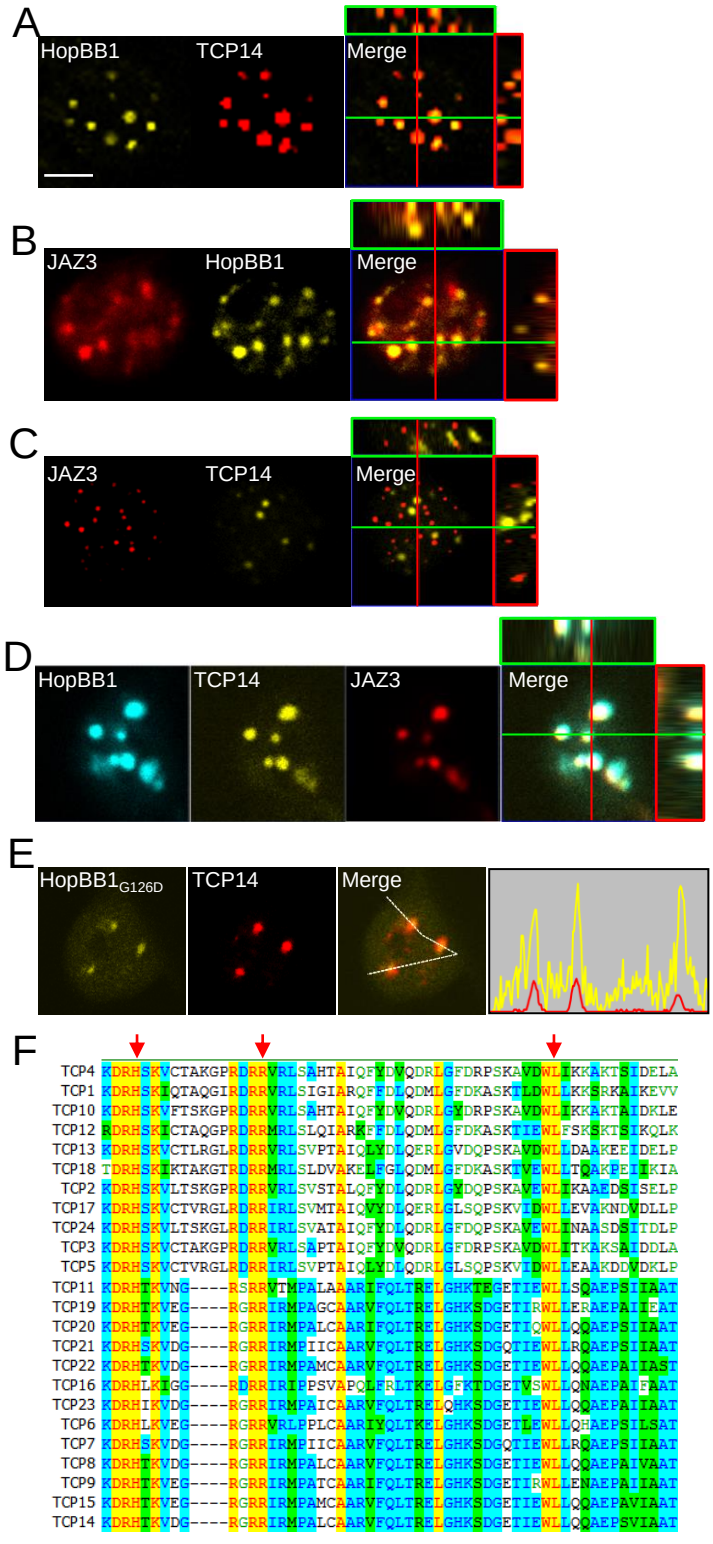

A
HopBB1
TCP14
Merge
B
JAZ3
HopBB1
Merge
C
JAZ3
TCP14
Merge
D
HopBB1
TCP14
JAZ3
Merge
E
HopBB1G126D
TCP14
Merge
F
TCP4 KDRHSKVCTAKGPRDRRVRLSAHTAIQFYDVQDRLGFDRPSKAVDWLIKKAKTSIDELA
TCP1 KDRHSKIQTAQGIRDRRVRLSIGIARQFFDLQDMLGFDKASKTLDWLLKKSRKAIKEVV
TCP10 KDRHSKVFTSKGPRDRRVRLSAHTAIQFYDVQDRLGYDRPSKAVDWLIKKAKTAIDKLE
TCP12 RDRHSKICTAQGPRDRRMRLSLQIARRFFDLQDMLGFDKASKTIEWLFSKSKTSIKQLK
TCP13 KDRHSKVCTLRGLRDRRVRLSVPTAIQLYDLQERLGVDQPSKAVDWLLDAAKEEIDELP
TCP18 TDRHSKIKTAKGTRDRRMRLSLDVAKELFGLQDMLGFDKASKTVEWLLTQAKPEIIKIA
TCP2 KDRHSKVLTSKGPRDRRVRLSVSTALQFYDLQDRLGYDQPSKAVEWLIKAAEDSISELP
TCP17 KDRHSKVCTVRGLRDRRIRLSVMTAIQVYDLQERLGLSQPSKVIDWLLEVAKNDVDLLP
TCP24 KDRHSKVLTSKGLRDRRIRLSVATAIQFYDLQDRLGFDQPSKAVEWLINAASDSITDLP
TCP3 KDRHSKVCTAKGPRDRRVRLSAPTAIQFYDVQDRLGFDRPSKAVDWLITKAKSAIDDLA
TCP5 KDRHSKVCTVRGLRDRRIRLSVPTAIQLYDLQDRLGLSQPSKVIDWLLEAAKDDVDKLP
TCP11 KDRHTKVNG----RSRRVTMPALAAARIFQLTRELGHKTEGETIEWLLSQAEPSIIAAT
TCP19 KDRHTKVEG----RGRRIRMPAGCAARVFQLTRELGHKSDGETIRWLLERAEPAIIEAT
TCP20 KDRHTKVEG----RGRRIRMPALCAARIFQLTRELGHKSDGETIQWLLQQAEPSIIAAT
TCP21 KDRHSKVDG----RGRRIRMPIICAARVFQLTRELGHKSDGQTIEWLLRQAEPSIIAAT
TCP22 KDRHTKVDG----RGRRIRMPAMCAARVFQLTRELGHKSDGETIEWLLQQAEPAIIAST
TCP16 KDRHLKIGG----RDRRIRIPPSVAPQLFRLTKELGFKTDGETVSWLLQNAEPAIFAAT
TCP23 KDRHIKVDG----RGRRIRMPAICAARVFQLTRELQHKSDGETIEWLLQQAEPAIIAAT
TCP6 KDRHLKVEG----RGRRVRLPPLCAARIYQLTKELGHKSDGETLEWLLQHAEPSILSAT
TCP7 KDRHSKVDG----RGRRIRMPIICAARVFQLTRELGHKSDGQTIEWLLRQAEPSIIAAT
TCP8 KDRHTKVDG----RGRRIRMPALCAARVFQLTRELGHKSDGETIEWLLQQAEPAIVAAT
TCP9 KDRHTKVEG----RGRRIRMPATCAARIFQLTRELGHKSDGETIRWLLENAEPAIIAAT
TCP15 KDRHTKVEG----RGRRIRMPAMCAARVFQLTRELGHKSDGETIEWLLQQAEPAVIAAT
TCP14 KDRHTKVDG----RGRRIRMPALCAARVFQLTRELGHKSDGETIEWLLQQAEPSVIAAT
G
LexA-
TCP14
TCP14H121Q R130K L161N
EV
B42-HA-
TCP14
BB1
EV
H
BB1-YFP + + +
TCP14-HA + + +
TCP14H121Q R130K L161N-HA + +
input
α-GFP
α-HA
IP:α-GFP
α-GFP
α-HA
60
56
60
56
I
TCP14H121Q R130K L161N-GFP + +
TCP14H121Q R130K L161N-HA + +
input
α-GFP
α-HA
IP:α-GFP
α-GFP
α-HA
80
56
80
56

Figure S1 (Related to Figure 1)

(A) Accumulation of YFP-TCP14 protein (left) and transcripts (right) in transgenic plants.

(B)–(F) Defining JA and SA responsive genes in Col-0. (B) Overview of the experimental conditions used to define genes responsive to MeJA and BTH by RNA-seq. (C) Principal Component Analysis (PCA) showing the overall relationship of the RNA-seq libraries used to define MeJA and BTH/SA markers. Colors represent different time-points and symbols represent treatments. Biological replicates are labeled r1 and r2. (D) Number of genes up- and down-regulated by each treatment defined using the edgeR package (FDR ≤ 0.01; 1.5 fold-change difference). While 261 genes were up-regulated by both hormones, 672 and 2096 genes were up-regulated specifically by MeJA and BTH, respectively, which define our set of marker genes. Table S1 shows the complete RNA-seq results for all Arabidopsis genes. (E) Overview of genes up-regulated by BTH at each time-point. The table shows Gene Ontology terms (biological processes) enriched in this set of genes. (F) Overview of the genes up-regulated by MeJA at each time-point. The table shows Gene Ontology terms (biological processes) enriched in this set of genes.

(G) Gene Ontology terms (biological processes) enriched in the set of genes identified as differentially expressed in the *UBQ::YFP-TCP14-3* line. The three clusters correspond to the hierarchical clustering analysis presented in Figure 1D.

Figure S2 (Related to Figure 2)

(A) Protein interaction between HopBB1 and 18 of 24 Arabidopsis TCP family members in yeast.

(B) Protein accumulation in Figure 2B.

(C) Protein accumulation in Figure 2D.

(D) NAAIRS-scanning mutagenesis in the $TCP14_{180\text{-}216}$ region. $TCP14_{RSAAST/NAAIRS}$ cannot interact with HopBB1.

Figure S3 (Related to Figure 3)

(A) HopBB1 and $HopBB1_{G126D}$ were delivered into plant cells when expressed in *Pto* DC3000 *cor-*. HopBB1 or $HopBB1_{G126D}$ were cloned upstream of $AvrRpt2^{101\text{-}255}$. The chimeric proteins were expressed under the control of NPTII promoter (Vinatzer et al., 2005).

(B) Protein accumulation in transgenic plants expressing HopBB1-myc.

(C) Plants expressing HopBB1 are hypersensitive to JA-mediated inhibition of root elongation. One-week-old seedlings grown on vertical plates were transferred to mock plates or plates with 10μM MeJA. Root length was measured one week after transfer. Error bars indicate ±SD. Statistics were performed using one-way ANOVA test with Tukey-Kramer HSD with 95% confidence. Similar results were obtained from two independent experiments.

(D) Co-occurrence of consensus MYC (CACGTG) and TCP (GGNCCC) binding sites is enriched in the promoters of MeJA-regulated genes from Figure S1F,

Table S1 (88/933, p=2.41e-13; hypergeometric test). We searched for these motifs in the 1kb upstream region relative to the start codon of 27206 nuclear protein-coding genes (TAIR10). The observed number of promoters containing each or both motifs was contrasted to the expected number in each category, given the motif's frequency in the entire genome and tested for over-representation using the hypergeometric test.

(E) The overlap between genes up-regulated by MeJA and HopBB1, and with the co-occurrence of TCP14 and MYC binding sites in their promoters. We verified that 22 (25%) of the 88 JA-responsive genes containing both MYC and TCP binding sites in their promoters are also up-regulated by HopBB1, which is more than expected by random sampling (2.18%; p=1.49e-16; hypergeometric test). Importantly, this list includes genes required for JA biosynthesis and signaling.

(F) Induced expression of HopBB1 does not trigger chlorosis (left). Four-week old plants were either treated with 50μM of coronatine or 20μM of estradiol for five days. The fifth leaves from three representative plants were photographed. Bar=5mm. The protein accumulation of conditionally expressed HopBB1 is shown in the right panel.

(G) The expression of representative photosynthesis genes is not altered in HopBB1-myc expressing plants.

Figure S4 (Related to Figure 5)

(A) Protein interaction between HopBB1 and 12 Arabidopsis JAZ family members in yeast. HopBB1 interacts with a subset of JAZ proteins.

(B) Protein accumulation for Figure 5C.

(C) $HopBB1_{G126D}$ retains interaction with JAZ3 in yeast.

(D) $HopBB1_{G126D}$ retains interaction with JAZ3 in *N. benthamiana*.

(E) HopBB1 does not promote JAZ3 degradation in Arabidopsis. Conditional expression of HopBB1-myc in transgenic plants expressing 35S::JAZ3-HA does not alter the accumulation of JAZ3.

(F) Quantification of the HopBB1-mediated disruption of MYC2-JAZ3 association. Proteins were transiently co-expressed in *N. benthamiana*. HaRxL45-CFP, HopBB1-CFP or $HopBB1_{G126D}$-CFP was induced 6 hrs after Agrobacteria infiltration. Microscopy was conducted 18 hrs after induction. Eight to ten confocal images with 1 mm^2 field of view were taken from four randomly sampled leaf discs on each leaf. Images were taken from YFP, CFP and RFP channels. Nuclei were traced only in the RFP channel. Following that, the nucleus signal peaks in each individual channel were counted, and the degree of overlap was compared. Four independent experiments were pooled for the summary presented in Figure 5F.

(G) HopBB1 does not alter MYC2 level in *N. benthamiana*. Proteins were transiently co-expressed in *N. benthamiana.*

(H) JAZ3 does not associate with HaRxL45 *in planta*. Proteins were transiently co-expressed in *N. benthamiana* from a constitutive 35S promoter.

Figure S5 (Related to Figure 6)

(A) Alignment of the conserved Jas motifs from 12 Arabidopsis JAZ proteins. The P302 and R305 are highlighted with a red arrow.

(B) $JAZ3_{P302A\ R305A}$ cannot interact with COI1 in the presence of coronatine. 50μM of coronatine was added to yeast medium. Protein accumulation is shown in the right panel.

(C) $JAZ3_{P302A\ R305A}$ interacts with HopBB1 in yeast.

Figure S6 (related to Figure 7)

(A) Orthogonal slices of TCP14-RFP and HopBB1-YFP co-localization in sub-nuclear foci. Bar=5 μM. For all orthogonal slices in (A)-(D), the “Merge” panel is the xy plane, right panel (red) is the yz plane, and top panel (green) is the xz plane. The crosshairs indicate the location of the yz and xz planes.

(B) Orthogonal slices view of JAZ3-RFP and HopBB1-YFP co-localization in sub-nuclear foci.

(C) Orthogonal slices view of the distinct sub-nuclear localization of TCP14-YFP and JAZ3-RFP in a nucleus.

(D) Orthogonal slices view of the co-localization of TCP14-YFP, HopBB1-CFP and JAZ3-RFP in sub-nuclear foci.

(E) $HopBB1_{G126D}$ co-localizes with TCP14 when transiently co-expressed in *N.benthamiana*.

(F) Alignment of the TCP domain from 24 Arabidopsis TCP family members. The mutated H121, R130 and L161 were highlighted with a red arrow. These

residues are conserved in TCP14. Mutation in each individual residue significantly reduced the ability of TCP4 protein to bind DNA (Kosugi and Ohashi, 2002).

(G) $TCP14_{H121Q\ R130K\ L161N}$ retains the ability to interact with HopBB1 and TCP14 in yeast.

(H) $TCP14_{H121Q\ R130K\ L161N}$ retains the ability to interact with HopBB1 in *N. benthamiana*.

(I) $TCP14_{H121Q\ R130K\ L161N}$ homo-dimerizes.

A-E, H-I: Proteins were transiently expressed from the 35S promoter in *N. benthamiana*.

Table S1 (related to Figure 1): Transcriptional response to MeJA or BTH in Col-0.

Table S2 (related to Figure 1): Transcriptional changes induced by *TCP14* mutation or overexpression.

Table S3 (related to Figure 3): Transcriptional changes induced by bacteria delivered HopBB1 or heterologous HopBB1 expression in Arabidopsis.

Table S4 (related to Figure 3): Comparison between genes expression altered by HopBB1 and TCP14 expression.

Table S5 (related to Figure 3): Distribution of JA-activating virulence factors in 287 *Psy* genomes.

Table S6 (related to experimental procedures): Primers, seed stocks, constructs, sequences and core genes for phylogenetic analysis.

Extended Experimental Procedures

Plants

Arabidopsis Col-0, *tcp14-6* (SAIL_1145_H03, backcrossed to Col-0 four times) (Mukhtar et al., 2011), *tcp14-7* (cs108688, backcrossed to Col-0 twice) (Wessling et al., 2014), *coi1-16* (Ellis and Turner, 2002; He et al., 2012), and all transgenics were sown and grown as described (Boyes et al., 1998). Primers for genotyping and constructs for generating transgenic Arabidopsis were listed in Table S6.

Yeast two hybridization

HopBB1, JAZ3, TCP14, COI1 and mutant derivatives were cloned into gateway-compatible pJG4-5 (-Trp) or pEG202 (-His) vectors. pJG4-5 and pEG202 constructs were transformed into competent yeast strains EGY48 and RFY206, respectively following manufacturer's protocol (Frozen-EZ Yeast Transformation II ^{TM}, Zymo Research) and selected on plates with dropout media. Each strain also carries the GAL4 reporter on psH18-34 (-Ura). Positive colonies were verified by yeast colony PCR. After mating the strain EGY48 and RFY206, diploid yeasts were plated on selective medium (-H-W-U) supplied with 100μM X-Gal for developing blue color from 2-6 days. To measure protein accumulation, yeast colonies were suspended in 50 μl 0.2N NaOH for 10 minutes. Cells were then collected by centrifugation and re-suspended in 1 x loading buffer. Protein levels were examined by western blotting.

RNA sequencing

In order to define a comprehensive set of marker genes for the JA and SA responses, we used RNA-seq to assess the transcriptome of the Arabidopsis Col-0 ecotype over a time-course hormone treatment (Figure S1B). Two-week-old seedlings were sprayed with 50 µM MeJA (Sigma), 300 µM BTH (Actigard 50WG) or a mock solution (0.02% Silwet, 0.1% ethanol). Samples were harvested 1h, 5h and 8h after spraying. This experiment was repeated twice. The experiments shown in Figures 1D, 1E and 1F were performed using steady-state seedlings grown under the same conditions as the ones used in the hormone treatment experiment. Lines Col-0 (4 replicates), UBQ10::YFP-TCP14-3 (4 replicates), UBQ10::YFP-TCP14-4 (1 replicate), and *coi1-16* (2 replicates) were used in the experiment presented in Figures 1D and E; whereas Col-0 (3 replicates), *tcp14-6* (3 replicates) and *tcp14-7* (3 replicates) were used in the experiment shown in Figure 1F. Bacteria-infected plants were used in the experiments shown in Figures 1G, 1H and 1I. For this, the strain *Pto* DC3000 *cor-* (at OD_{600}=0.2 with 10mM $MgCl_2$ and 0.04% Silwet L-77) was sprayed onto Col-0 (3 replicates), *tcp14-6* (3 replicates), UBQ10::YFP-TCP14-4 (3 replicates) and *coi1-16* (3 replicates). Samples were harvested for RNA preparation 24 hours post infection.

We also evaluated the effect of bacteria-delivered HopBB1 on the transcriptome of wild-type plants (shown in Figures 3B, 3C and 3D). For this, two-week-old Col-0 seedlings were sprayed with a mock solution (10 mM $MgCl_2$) or bacteria [*Pto*

DC3000 (EV), *Pto* DC3000 *cor*- (EV); *Pto* DC3000 *cor*- (HopBB1); *Pto* DC3000 *cor*- ($HopBB1_{G126D}$)] at OD_{600}=0.2 with 10mM $MgCl_2$ and 0.04% Silwet L-77. Samples were harvested 24 hours after infection. This experiment included three biological replicates. The transcriptome of the transgenic line HopBB1-myc-10 (3 replicates) was also compared to the one of Col-0 seedlings at steady-state conditions (shown in Figure 3G). In all experiments, each biological replicate corresponds to approximately 30 seedlings grown on the same pot.

For RNA isolation, plant tissue was ground to a fine powder using the Qiashredder tissue homogenizer (Qiagen) and total RNA was extracted using the RNeasy Plant Mini kit (Qiagen). Illumina-based RNA-seq libraries were prepared from 1000ng total RNA. Library quality control and quantification were performed using a 2100 Bioanalyzer instrument (Agilent) and the Quant-iT PicoGreen dsDNA Reagent (Invitrogen), respectively. The Illumina HiSeq2500 sequencer was used to generate single-end reads. Raw sequencing data are available at the NCBI Gene Expression Omnibus accession GSE90606.

RNA-seq reads were mapped against the TAIR10 reference genome using Tophat (Trapnell et al., 2009). Alignment parameters were set to allow only one mismatch and to discard reads mapping to multiple positions in the reference. HTSeq (Anders et al., 2015) was then used to count reads mapping to each one of the 27,206 nuclear protein-coding genes. Differential gene expression analyses were performed with the edgeR package (Robinson et al., 2010) using the False Discovery Rate (FDR) method for correction of multiple comparisons (Benjamini and Hochberg, 1995). Genes with FDR below 0.01 and a fold-change

variation greater than 1.5X were considered differentially expressed between conditions. Gene Ontology enrichment analyses were performed with the PlantGSEA toolkit (Yi et al., 2013) and with the Cytoscape plugin ClueGO (Bindea et al., 2009) .

We identified a total of 933 and 2357 genes that were significantly up-regulated (FDR≤0.01; 1.5 fold-change difference relative to the mock control) in at least one of the three time-points analyzed after treatment with MeJA or BTH, respectively (Figure S1D; Table S1). As expected, these sets of genes were strongly enriched for biological processes related to JA and SA responses (Figures S1E and S1F). After filtering out the 261 genes upregulated by both hormones, we defined a set of 672 and 2096 markers of the JA and SA responses, respectively.

Confocal microscopy

Microscopy was conducted 16-24 hours after infiltration using a LSM 7 DUO (Carl Zeiss). Leaf disc samples were imaged with a 40x water objective. Between 5 and 15 nuclei were observed in each repetition. The confocal images were edited with Zen 2009 (Zeiss) and Adobe Photoshop CS2. Zen 2009 (Zeiss) and Excel (Microsoft) were used to create histograms. For the HopBB1-TCP14-JAZ3 co-localization assay, JAZ3-RFP and TCP14-YFP were driven under 35S promoter, HopBB1-CFP or $HopBB1_{G126D}$-CFP was driven by estradiol-inducible promoter. Estradiol was applied 6 hours after the co-infiltration of Agrobacteria.

The primers and constructs used for confocal analysis are listed in Table S6. GV3101 carrying 35S promoter-driven p19 protein was co-infiltrated at OD_{600}=0.05 in each experiment to prevent the onset of post-transcriptional gene silencing and improve the efficiency of transient expression (Lindbo, 2007).

For transient protein expression in *N. benthamiana*, Agrobacteria at annotated concentration were suspended in 10mM $MgCl_2$, 10mM MES and 100μM acetosyringone, and hand infiltrated into *N. benthamiana* leaves. For the HopBB1-mediated disruption of the JAZ3-MYC2 interaction, rBiFC (JAZ3+MYC2) and EST::HopBB1-CFP-HA, EST::HopBB1$_{G126D}$-CFP-HA or EST::HaRxL45-CFP-HA were co-inoculated at OD_{600}=0.1 and OD_{600}=0.2, respectively (Grefen and Blatt, 2012). Six hours after inoculation, 20μM estradiol was infiltrated. Samples were collected 20-24 hours after inoculation. 4-6 images of 50-80 cells/per field were taken in each repetition.

Disease resistance assay

Pto DC3000 *and Pto* DC3000 *cor-* were described in (He et al., 2012). *Pto* DC3000 *cor-* (EV), *Pto* DC3000 *cor-* (HopBB1) and *Pto* DC3000 *cor-* (HopBB1$_{G126D}$) were generated by transforming *Pto* DC3000 *cor-* with either pJC531 (empty vector), pJC531 (HopBB1) or pJC531 (HopBB1$_{G126D}$). HopBB1 or HopBB1$_{G126D}$ were expressed from the native promoter. Bacterial growth assays in *Arabidopsis* were performed by spray or dipping inoculation as described. Bacterial cultures were resuspended in 10 mM $MgCl_2$ with 0.04% Silwet L-77.

Plants were sprayed or dipped with a bacterial suspension at OD_{600}=0.2. Results displayed in Figures 1C, 3A and 3F were performed independently a minimum of 3 times with similar results. Hpa infection was performed as described in (Mukhtar et al., 2011).

Bacterial colony formation units (CFU) were measured after three days. Dashed line indicates the CFU at day 0. Statistics in Figures 1C, 3A and 3F were performed using one-way ANOVA test with Tukey-Kramer HSD with 95% confidence.

Effector Delivery Assay

The coding regions of HopBB1 or $HopBB1_{G126D}$ were cloned into pBAV178 (proNPTII:: Gateway cassette-$AvrRpt2^{101-255}$) (Vinatzer et al., 2005). pBAV178 (HopBB1) and pBAV178 ($HopBB1_{G126D}$) were transformed into *Pto* DC3000 *cor-.* Bacteria were infiltrated into leaves of four-week-old Col-0 plants at OD_{600}=0.01 with 10mM $MgCl_2$, and cell death was scored after 16-20 hours.

Phylogenetic Analysis

The phylogenetic history of *Pseudomonas* was inferred by multi-locus alignment using MUSCLE (Edgar, 2004) to align amino acid sequences of 31 single copy core genes from the 2681 *Pseudomonas* genomes available for download on the PATRIC database (Wattam et al., 2014) . Using the resulting tree, *P. syringae* genomes were identified by selecting the smallest monophyletic group containing

all genomes annotated as *P. syringae*. This analysis resulted in a dataset 287 *P. syringae* genomes (Table S5). Pan genome analysis was performed on this subset using Roary (Page et al., 2015) with default parameters. The nucleotide sequences of the resulting 84 core genes (Table S6) were used to construct a new phylogenetic tree. Trees were constructed using a Maximum Likelihood method (Jones et al., 1992) implemented in MEGA7 (Tamura et al., 2013) with 100 bootstrap iterations. The HopBB1 (from *Pseudomonas syringae pv. mori str.* 301020), HopX1 (from *Pseudomonas syringae pv. tabaci str. ATCC* 11528), HopZ1a (from *Pseudomonas syringae pv. syringae* strain A2) and the coronatine biosynthesis pathway genes (from *Pseudomonas syringae pv. tomato str.* DC3000) were used as blast queries to search for homologous proteins in these 287 *P. syringae* genomes. A hit with over 80% protein sequence identity was considered positive. For HopZ1a, the difference between HopZ1a and HopZ1b annotated in (Ma et al., 2006) was used as guideline. Each homologue was manually checked for the integrity of reading frame. The tree was visualized using iTOL (http://itol.embl.de/) (Letunic and Bork, 2007) . A newick file is available for download and interactive viewing at http://itol.embl.de/shared/HopBB1.

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