**Extended Experimental Procedures**

*Plants*

Arabidopsis Col-0, *tcp14-6* (cs108688, backcrossed to Col-0 4 times) ([Mukhtar et al., 2011](#_ENREF_10)), *tcp14-7* (SAIL\_1145\_H03, backcrossed to Col-0 twice) ([Wessling et al., 2014](#_ENREF_14)), *coi1-16* ([Ellis and Turner, 2002](#_ENREF_5); [He et al., 2012](#_ENREF_6)), and all transgenics were sown and grown as described ([Boyes et al., 1998](#_ENREF_3)). 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 S1C). 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 using UBQ10::YFP-TCP14-3 (4 replicates), UBQ10::YFP-TCP14-4 (1 replicate), 35S::HopBB1-myc-10 (3 replicates) and *coi1-16* (2 replicates) were performed using steady-state seedlings grown under the same conditions as the ones used in the hormone treatment experiment. In all experiments, each biological replicate corresponds to approximately 30 seedlings grown on the same pot.

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 50bp single-end reads. Raw sequencing data are available at the NCBI Sequence Read Archive under accession number SRAXXXXXX.

RNA-seq reads were mapped against the TAIR10 reference genome using Tophat ([Trapnell et al., 2009](#_ENREF_13)). 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](#_ENREF_1)) was then used to count reads mapping to each one of the 27,208 nuclear protein-coding genes. Differential gene expression analyses were performed with the edgeR package ([Robinson et al., 2010](#_ENREF_11)) using the False Discovery Rate (FDR) method for correction of multiple comparisons ([Benjamini and Hochberg, 1995](#_ENREF_2)) . Genes with FDR below 0.01 and a fold-change variation greater than 1.5X were considered differentially expressed between conditions. The scripts used to process the data and generate the figures (Heatmap, Boxplot) were deposited in GitHub.

*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 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.

For the HopBB1-mediated disruption of JAZ3-MYC2 interaction, rBiFC (JAZ3+MYC2) and EST::HopBB1-CER-HA were co-inoculated at OD600=0.1 and OD600=0.2, respectively. Six hours after inoculation, 20µM estradiol was infiltrated. Samples were collected 20-24 hours after inoculation. 12-15 images of 50-100 cells/per field were taken in each repetition.

*Disease resistance assay*

*Pto DC3000 and Pto* DC3000 *cor-* were described in ([He et al., 2012](#_ENREF_6)). *Pto* DC3000 *cor-* (EV) and *Pto* DC3000 *cor-* (*HopBB1*) were generated by transforming *Pto* DC3000 *cor-* with either pJC531 (empty vector) or pJC531 (HopBB1). HopBB1 is expressed under its native promoter. Plant inoculations and bacterial growth assays were performed as described ([He et al., 2012](#_ENREF_6)). All assays were performed independently a minimum of 3 times with similar results.

*Phylogenetic Analysis*

Phylogenetic history of *Pseudomonas* was inferred by multi-locus alignment using MUSCLE ([Edgar, 2004](#_ENREF_4)) to align 20 single copy conserved COGs (Table S6) from all 850 *Pseudomonas* genomes that included a complete set of these genes, extracted from the Integrated Microbial Genomes (IMG) system http://img.jgi.doe.gov/; ([Markowitz et al., 2012](#_ENREF_9)). A phylogenetic tree was constructed using the Maximum Likelihood method ([Jones et al., 1992](#_ENREF_7)) implemented in MEGA6 ([Tamura et al., 2013](#_ENREF_12)). The branch that included all *P. syringae* was extracted from this tree, including its nearest outgroup. This branch included 162 genomes, 143 of which were annotated as *P. syringae.* There were no genomes annotated as *P. syringae* in other branches of the larger tree. The tree was visualized using iTOL (http://itol.embl.de/) ([Letunic and Bork, 2007](#_ENREF_8)).

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