SUPPLEMENTARY INFORMATION FOR:

*Shared in planta* population and transcriptomic features of non-pathogenic members of endophytic phyllosphere microbiota

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SUPPLEMENTARY TEXT

SUPPLEMENTARY MATERIALS AND METHODS

In vitro bacterial growth and antibiotics used
Table S10 lists the bacterial strains used in this study. *Escherichia coli* strains were grown in LB (Lennox) medium at 37 °C, while all other strains were grown in either a modified LB medium (LM: 10 g L⁻¹ tryptone, 6 g L⁻¹ yeast extract, 1.5 g L⁻¹ KH₂PO₄, 0.6 g NaCl, and 0.4 g MgSO₄•7H₂O) or King’s B medium at 30 °C.

Antibiotics and derivatives were used at the following concentrations: 10⁰ µg mL⁻¹ ampicillin, 67–80 ng mL⁻¹ anhydrotetracycline, 400 µg mL⁻¹ carbenicillin, 400 µg mL⁻¹ cefotaxime, 75 µg mL⁻¹ cycloheximide (to prevent fungal growth), 1–15 µg mL⁻¹ gentamycin, 50 µg mL⁻¹ kanamycin, 100 µg mL⁻¹ rifampicin, and 50 µg mL⁻¹ spectinomycin. Diaminopimelic acid (DAP) was used at a concentration between 200–400 µg mL⁻¹.

To evaluate the response of logarithmic-phase *Pseudomonas syringae* pv. *tomato* (Pst) ∆hrcC∆CFA and stationary-phase Pst ∆hrcC∆CFA, *Pandoraea* sp. Col-0-28, and *Rhodococcus* sp. 964 cultures to the β-lactam antibiotics carbenicillin or cefotaxime, bacteria were grown in liquid LM overnight at 30 °C. For logarithmic-phase samples, overnight bacterial suspensions were diluted with LM to 10⁸ CFU mL⁻¹, and grown for 4 hours before antibiotic treatment. Stationary-phase samples were not diluted. H₂O control or 400 µg mL⁻¹ carbenicillin or cefotaxime were added to the cultures and grown for over 3 days. Before plating serial dilutions of the samples to determine population densities, cultures were washed twice with 10 mM MgCl₂ to remove any trace of the antibiotic from the bacterial suspension.

Plant growth conditions
Arabidopsis plants were grown in a growth chamber with the following conditions: 12-hour day length, 80 µmoles m⁻² s⁻¹ of photon flux, a temperature of 24.5 °C during the day and 23.0 °C during the night, and a relative humidity between 65% and 75%. Table S11 lists the plant material used for this study. For some experiments (Figure S2B, and for the in planta RNA-Seq samples of *Achromobacter xylosoxidans* and *Pandoraea*), the relative humidity was increased to be higher than 99% after bacterial inoculation. Seeds were stratified for 2 to 5 days before sowing. Plants were watered with one-half strength Hoagland’s solution when needed. All plants were grown partially covered under a plastic transparent dome.

Bacterial population density quantification assays
Bacterial inoculum suspensions were prepared from cultures grown in LM or KB agar plates to stationary phase. Bacteria were resuspended in 0.25 mM MgCl₂ to an appropriate OD₆₀₀, after which they were infiltrated using a needleless syringe into the abaxial side of Arabidopsis leaves. To determine the in planta population density numbers, leaf-disc punches were collected from plants and ground in 250 µL of 10 mM MgCl₂ using a TissueLyser II (QIAGEN; 2 cycles of 30 seconds at 25 Hz) and 3-mm zirconium oxide beads (Glen Mills Inc.). Serial dilutions of the ground tissue were spotted onto LM plates with appropriate antibiotics...
and grown overnight. Colony forming units (CFUs) per cm\(^2\) were determined for each sample, while CFUs per mL were determined for each inoculum.

To determine endophytic bacterial populations, leaves were placed in a 0.825% sodium hypochlorite solution for 1 minute, and then washed twice in distilled H\(_2\)O, each for a minute. Leaves were blotted dry, after which leaf discs were collected as described above.

As described before (1), the *in planta* transcriptome analysis requires an inoculum greater than \(10^9\) CFU mL\(^{-1}\); otherwise the sequencing would be overwhelmed by mostly plant RNAs. The observed slight decrease in population densities between 6 and 24 hours (Figure S4A, S4B, and S4C) could be caused by a strong initial PTI response due to the overabundance of MAMPs in the inoculum.

For *in planta* antibiotic treatments, 400 \(\mu\)g mL\(^{-1}\) of a β-lactam antibiotic, carbenicillin or cefotaxime, was infiltrated into plants every day until the end of the experiment starting at 1 day post-inoculation with the bacterial endophytes. H\(_2\)O was used as a mock control. To calculate the percentage of cells that attempted to divide, we divided the average CFU cm\(^{-2}\) treated with the β-lactam antibiotic by the average CFU cm\(^{-2}\) mock-treated with H\(_2\)O, multiplied this by 100, and subtracted the result from 100.

**Cloning**

The dual fluorescent division reporter construct pUC18-mini-Tn7T-Gm::tetR(BD)-\(P\_tet\)mCitrine\(_m\)Cerulean3-BCD2-\(P\_14g\) was created in two steps. In the first step, a DNA fragment containing a strong transcriptional terminator, TpheA-1 (2), repressor tetR(BD) [sequence is the fusion of two alleles of tetR, carrying 50 codons of tetR(B) and the last 158 codons of tetR(D) (3)], the tetracycline promoter from *E. coli* Tn10 (which controls expression of both tetR(BD) and mCitrine; GenBank accession number AF162223), fluorescent protein mCitrine (4), and two strong transcriptional terminators in opposite orientation, ECK125109870 and L3S2P56 (2), was synthesized by GenScript®. This DNA fragment was cloned into pUC18-mini-Tn7T-Gm (5) (cut with Nsil and Stul [New England Biolabs®, Inc.]) using Gibson assembly.

In the second step, two DNA fragments were PCR amplified using primer pairs AVL001 and AVL002, and AVL003 and AVL004 (Table S12): one amplicon included the promoter P14g and translational coupler BCD2 from plasmid pBG42 (6), while the other amplicon included the gene coding for the fluorescent protein mCerulean3 (7). These fragments were introduced into the previously generated intermediate plasmid (after cutting the plasmid with SpeI [New England Biolabs®, Inc.]) by Gibson assembly to generate the division reporter pUC18-mini-Tn7T-Gm::tetR(BD)-\(P\_tet\)mCitrine\(_m\)Cerulean3-BCD2-\(P\_14g\) (Figure 3A).

**Gene integration into the *P. syringae* genome**

Integration into the *Pst* genome was performed by site-specific transposition by Tn7 into the unique attTn7 site of *Pst* DC3000. For this, triparental mating was set up between the *Pst* recipient strain, the strain containing the transposase helper plasmid pTNS3 (8), and the *E. coli* RHO5 donor strain (9) (carrying plasmid pUC18-mini-Tn7T-Gm with the genes to be integrated). Three to six days after conjugation and selection in plates containing 1.5 \(\mu\)g mL\(^{-1}\) of gentamycin, colony PCRs were set up to identify the putative
transconjugants using three primer pairs: AVL005 and AVL006, AVL007 and AVL008, and AVL005 and AVL007 (Table S12).

Confocal microscopy
Images were taken using the Nikon A1Rsi confocal microscope with a 20X objective (numerical aperture of 0.7 and a pinhole of 1.2 airy units). The CFP and YFP channels are detected using gallium arsenide phosphide photomultiplier (PMT) detectors. For the CFP channel, an excitation of 443.6 nm and an emission between 467 to 502 nm were used. For the YFP channel, an excitation of 513.9 nm and an emission of 530 to 600 nm were used. Images were acquired at a gain and offset at which the negative control (Arabidopsis plants infected with Pst DC3000 or Pst ΔhrcΔCFA without the fluorescent division reporter) had no signal being detected.

To determine the distribution of the overlap in signal intensity between mCitrine and mCerulean in segmented regions of interest, we used ImageJ (version 2.3.0/1.53f).

RNA extraction
For A. xylosoxidans, we used only the endophytic bacteria by eliminating the surface-inhabiting bacteria with sodium hypochlorite before RNA extraction. Frozen plant tissue was ground using a TissueLyser II (QIAGEN; 2 cycles of 30 seconds at 27 Hz) and 3-mm zirconium oxide beads (Glen Mills Inc.). RNA was extracted using TRizol™ (Thermo Fisher Scientific) and the Direct-zol RNA miniprep kit (Zymo Research), using a 30-minute on-column treatment with 12 U of DNase I. A second DNase I treatment to remove all residual genomic DNA was performed using 30 U of recombinant DNase I (Roche) and 10 U of Protector RNase inhibitor (Roche) for 1 hour at 37 °C. RNA was purified a second time using TRizol™ and the Direct-zol RNA miniprep kit.

To prepare logarithmic- and stationary-phase Pst ΔhrcΔCFA cultures for RNA extraction, bacteria were grown in liquid KB overnight at 30 °C. For logarithmic-phase samples, overnight bacterial suspensions were diluted with KB to 10⁸ CFU mL⁻¹ and grown for 6 hours. Stationary-phase samples were not diluted and grown for 6 additional hours.

To extract RNA from bacterial cultures grown in vitro, 10⁹ CFUs of bacteria were resuspended in 150 µL of buffer TE (10 mM Tris-HCl, 1 mM EDTA, pH 8.0) with 5 mg mL⁻¹ of lysozyme (Roche) for 5 minutes at room temperature. For the in vitro liquid-grown logarithmic- and stationary-phase bacteria, an extra step that used the RNA stabilizer RNAprotect Bacteria Reagent (QIAGEN) was used before the addition of lysozyme. After incubation with lysozyme, 400 µL of buffer RLT (QIAGEN) were added to the suspension, which was then applied through QIA shredder columns (QIAGEN). The eluate was used for RNA purification using the RNeasy mini kit (QIAGEN). The only modification to the protocol of the kit was the extension of the on column DNase I (QIAGEN) digestion to 30 minutes. After RNA purification, a second DNase I treatment and purification using the Direct-zol RNA miniprep kit was performed as described above.

To check for the presence of genomic DNA (gDNA) contamination in the RNA samples, a PCR using 50–100 ng of RNA was performed using primers AVL009 and AVL010 (to check for Pst gDNA
contamination), AVL011 and AVL012 (to check for *Pandoraea* sp. Col-0-28 gDNA contamination), AVL013 and AVL014 (to check for *A. xylosoxidans* sp. Col-0-50 gDNA contamination), and AVL015 and AVL016 (to check for *Arabidopsis thaliana* gDNA contamination; Table S12).

**cDNA preparation and quantitative reverse transcription-PCR (qRT-PCR)**

Three-hundred ng to two µg of RNA were used to prepare cDNA using 2.5 µM of random hexamer primers (Integrated DNA Technologies, Inc.), 40 U of Protector RNase inhibitor and 200 U of M-MLV reverse transcriptase (Invitrogen™), following the protocol described by the manufacturer. Between 0.4 and 1 µL of cDNA was used with appropriate primers (Table S12) and SYBR® Green PCR master mix (Applied Biosystems) for qRT-PCR. Two technical replicates were done per sample. PCR was performed on the 7500 Fast Real-Time PCR System (Applied Biosystems™) using automatic C₅ threshold detection. Bacterial transcripts were normalized to the *leuB* (*PSPTO_2175*) reference gene using the ∆C₅ method (10). In test RNA-Seq experiments, *leuB* showed very little variability in expression under multiple conditions. *rpoD*, one of our evaluated genes, has been used in the past as a qPCR reference gene (11); however, its expression, at least under certain conditions, is too variable for this purpose (Figures 6B and 6C). The efficiency of all primer pairs was validated to be between 90 to 110%. Amplicon melting curves had a single predominant peak.

For qRT-PCR of *Pst* DC3000 genes under ETI-inducing conditions (in Bu-22 plants; Figures 6C, S7C and S7D), we initially tried using a high bacterial inoculum, similar to the inoculum that had been used in previous *in planta* transcriptomic studies (1, 12). However, even though a faster hypersensitive response is observed at a high inoculum in Bu-22 plants (13), ETI restriction of bacterial multiplication is compromised (Figure S7E). As such, we decided to use a lower inoculum for evaluating gene expression in an incompatible interaction (Figure S7F). Samples for ETI-inducing *Pst* DC3000 were collected starting at 24 hours post-inoculation, once population density became static (Figure S7F).

**RNA-Sequencing and bioinformatic analysis**

RNA integrity was evaluated using the 2100 BioAnalyzer (Agilent Technologies, Inc.) and RNA concentration was determined with the Qubit™ RNA HS assay kit (Thermo Fisher Scientific). Libraries for RNA-Seq were prepared using the protocol described in Nobori *et al.* (1), but using the newest iteration of the library preparation kit from NuGEN® (Tecan Genomics, Inc.), the Universal RNA-Seq with NuQuant® kit, and skipping the use of the MICROBEnrich kit. This protocol allows the removal of plant and bacterial rRNAs and of the most abundant *Arabidopsis* transcripts. Libraries were pooled and sequenced in the Illumina® HiSeq 4000 using HiSeq 4000 SBS reagents to obtain single 50-bp reads. Base calling was done by Illumina Real Time Analysis (RTA version 2.7.7). RNA-Seq reads were deposited under BioProject PRJNA738276 of the Sequence Read Archive (SRA) (14).

The read quality was evaluated with FASTQC (version 0.11.7) (15), while adapters and low quality sequences were trimmed with Cutadapt (version 2.9) (16). Three different pipelines were used to calculate differential gene expression (DGE), as DGE varies depending on the models used for transcript estimation
In the first pipeline, reads were aligned to the reference genomes using HISAT2 (version 2.1.0) (18). Aligned reads were processed using SAMTools (version 1.9) (19), after which StringTie (version 2.1.3) (20) was used to calculate transcript frequency, to finally estimate DGE using DESeq2 (average expression per treatment is shown on Datasets S1, S2, and S3) (21). On the second pipeline, reads were also aligned with HISAT2, but this time DGE was calculated directly using Cuffdiff (version 2.2.1) (17). In the third pipeline, reads were pseudo-aligned using Salmon (version 0.11.3 for *Pst ΔhrcCΔCFA* or 1.2.1 for the other two endophytes) (22), after which DESeq2 was performed for DGE. Differentially expressed genes present in at least one of the three analyses were used for subsequent analysis. Comparison of the three pipelines for each endophyte is shown in Tables S13, S14 and S15.

Principal component analysis (PCA) of transcript reads after DESeq2 analysis used the `rlog` and `plotPCA` functions of DESeq2 in Rstudio (version 1.3.1093). Significantly up- or down-regulated genes were identified as those in any of the three pipelines in which the absolute value of the logarithm (in base 2) of the fold change was greater than 0.58, and the adjusted false discovery rate *p* value of the statistical test was less than 0.05. GO (gene ontology) enrichment analysis used the Cytoscape application BINGO (version 3.0.4) (23). For *Pst ΔhrcCΔCFA*, we used the default database incorporated into the bioinformatics tool, while for *A. xylosoxidans* and *Pandoraea*, we created reference databases using InterProScan (version 5.47-82.0). GO results were summarized with REVIGO to remove GO term redundancies (24), after which manual curation of the enriched pathways was done. A complete list of biological pathways enriched in differentially expressed up- or down-regulated genes is shown in Tables S1, S2, and S3. PaintOmics 3 (version 0.4.5) (25) was used for initial visualization of *Pst ΔhrcCΔCFA* gene expression in biological pathways. We used antiSMASH (version 6.0.0) (26) to identify clusters of genes predicted to be involved in the production of secondary metabolites.

STEM (Short-Time series Expression Miner; version 1.3.13) (27) analysis was used to look for enriched patterns of expression over time between the samples collected at 0 (the inoculum), 6, 24, and 168 hours post-inoculation (hpi) into Col-0 plants, to identify sets of genes whose expression increased or decreased once phyllosphere bacteria were inside plants. Analysis used the logarithmically (in base 2) normalized expression data obtained from StringTie. GO pathway enrichment analysis used the BINGO application, and summarization of the results was done as described above (Table S4, S5, and S6).

Orthologous gene groups between bacterial strains were identified using OrthoMCL (28). Each orthologous group may have more than one gene from each strain, and were identified as having an expected value of less than $10^{-5}$. Genes that had the same pattern of differential up- or down-regulation for a comparison between two treatments in one, two or all three strains were identified (Figure S8). We only compared the inoculum or 6 hpi with 168 hpi, as we expected these two comparisons to be the most significant for the long-term adaptation of phyllosphere microbiota to plants. Biological process enrichment analysis of orthologous groups used the *Pst ΔhrcCΔCFA* genes as references.

Plant-associated genes (PA) were retrieved from Levy et al. (29) using the PA protein sequences provided. *Pst DC3000* PA proteins were directly retrieved from such publication. To identify PA proteins in *Achromobacter xylosoxidans* Col-0-50, proteins from 11 strains that belonged to the genus *Achromobacter*
(29) were used to identify PA proteins in *A. xylosoxidans* Col-0-50, using the program CD-HIT (version 4.8.1) (30). The same program was used to identify PA proteins in *Pandoraea* sp. Col-0-28, this time using the PA proteins from 5 *Pandoraea* strains, plus three closely related strains isolated from plants from the genus *Burkholderia* (*Burkholderia andropogonis Ba3549*, *Burkholderia* sp. JPY347, and *Burkholderia* sp. YR520) (29). Proteins were considered orthologous if they had at least 80% amino acid identity and coverage with a protein from Levy *et al.* (29). PA gene enrichment was calculated using a hypergeometric test and a Bonferroni-Hochberg correction (*p* < 0.05).

The reference genomes used for analysis are those from *Pst* DC3000: GenBank accession AE016853.1 for the genomic DNA, and GenBank accessions AE016855.1 and AE016854.1 for the two plasmids. For *A. xylosoxidans* Col-0-50 and *Pandoraea* sp. Col-0-28, the genome sequences are under the BioProject PRJNA555902 deposited in the SRA (sample runs SRR9732406 and SRR9732397, respectively).

Graphs and statistical analysis were performed using Prism (version 6.0b) or Rstudio (Bubble graphs and Venn diagrams). Upset plots and the heatmaps for Figures 4D and 4E were graphed using TBTools (version 1.0) (31). Figure 6D and part of Figure S5 were created with BioRender.com.
Fig. S1. Endophytic bacterial populations experience stasis inside plants. (A) Bacterial population density of gram-negative and gram-positive microbiota members Achromobacter xylosoxidans Col-0-50 (inoculum: $10^7$ CFU mL$^{-1}$) and Rhodococcus sp. 964 (inoculum: $10^6$ CFU mL$^{-1}$) over the course of 20 days after infection of Col-0 plants. (B) Bacterial population density of Pst ΔhrcCΔCFA inoculated at $5 \times 10^4$ CFU mL$^{-1}$ into Arabidopsis leaves. (C) Photographs of Col-0 leaves inoculated with non-pathogenic Pseudomonas syringae pv. tomato (Pst) ΔhrcCΔCFA at two different inoculum levels 22 days after infiltration. Leaves infiltrated at the higher inoculum were chlorotic and barely grew over the course of 22 days. Scale bar represents 1 cm. (D) Population density of Rhodococcus sp. 964 (inoculum: $5 \times 10^5$ CFU mL$^{-1}$) over the course of 2 weeks after infiltration into leaves of Col-0 and PTI-compromised triple mutant bak1 bkk1 cerk1 (bbc).

Individual biological repetitions for each treatment are shown as open circles. Error bars indicate the standard error of the mean. When appropriate, different letters indicate differences in means, as judged by a Tukey HSD test ($p < 0.05$). dpi indicates days post-inoculation.
Fig. S2. Equilibrium in bacterial multiplication and death underlies bacterial population stasis. (A) Bacterial population density of virulent *Pseudomonas syringae* pv. *tomato* (*Pst*) DC3000 (inoculum: $10^5$ CFU mL$^{-1}$) in Col-0 plants after infiltration with 400 µg mL$^{-1}$ of carbenicillin, an antibiotic that kills dividing bacteria. Note the dramatic reduction in population density after carbenicillin treatment to 0.001% of the water control. (B) Same experiment as in Fig. 2B, but, using a relative humidity of over 99% throughout the experiment. *Pst ΔhrcC ΔCFA* was inoculated at $10^7$ CFU mL$^{-1}$, and 400 µg mL$^{-1}$ of carbenicillin was infiltrated daily starting at 24 hours post-inoculation. Over 98% of the population is killed over the course of 5 days. (C) *In vitro* β-lactam antibiotic effect of 400 µg mL$^{-1}$ of carbenicillin or cefotaxime on stationary-phase *Rhodococcus* sp. 964 and *Pandoraea* sp. Col-0-28. The y-axis is in logarithmic scale. (D) *In planta* population density of *Rhodococcus* sp. 964 (inoculum: $2 \times 10^7$ CFU mL$^{-1}$) after addition of 400 µg mL$^{-1}$ of carbenicillin. Over 87% of the population was killed after 5 days.

Individual biological repetitions for each treatment are shown as circles. Error bars indicate the standard error of the mean. Different letters indicate differences in means, as judged by a Tukey HSD test ($p < 0.05$). dpi indicates days post-inoculation.
**Fig. S3.** *In planta* visualization of bacterial endophytes. (A) Visualization of pathogenic *Pseudomonas syringae* (*Pst*) carrying the fluorescent division reporter on the surface of Arabidopsis leaves. Confocal images of virulent *Pst* DC3000 carrying the $P_{tet\cdot mCitrine\cdot P_{14g}\cdot mCerulean3} + aTc$ division reporter (inoculum: $5 \times 10^7$ CFU mL$^{-1}$; grown with 80 ng mL$^{-1}$ anhydrotetracycline [aTc]) 2 days after inoculation of Col-0 plants. Images were taken at the leaf surface, where individual fluorescent bacteria can be observed. Note that no mCitrine signal is observed in the samples, as it was diluted out during *in planta* bacterial multiplication. Cyan represents signal from mCerulean3. Yellow represents signal from mCitrine. Composite image of both fluorescent proteins and the transmitted light image is shown. Scale bars represent 10 µm. (B) Relative frequency of median mCitrine signal intensity (in arbitrary units) in areas in which there was detection of constitutive mCerulean3 signal from endophytic *Pst ΔhrcCΔCFA* carrying the division reporter $P_{tet\cdot mCitrine\cdot P_{14g}\cdot mCerulean3}$ after 5 days post-inoculation into Arabidopsis leaves. Quantification was performed on the confocal image presented on Fig. 3D.
Fig. S4

A. \( Pst \Delta hrcC\Delta CFA \) vs. Pandoraea

B. \( Pst \Delta hrcC\Delta CFA \) vs. Pandoraea

C. \( A. \ xylosoxidans \)

D. \( \Delta hrcC\Delta CFA \ t_6 \ vs. \ t_{168} \)

DESalmon

DEStringTie

Cuffdiff

E. \( Pst \Delta hrcC\Delta CFA \)

A. \( Pst \Delta hrcC\Delta CFA \)

Pandoraea sp.
Fig. S4. Transcriptome and population analysis of three phyllosphere-inhabiting bacteria. (A) Bacterial population density of non-pathogenic *Pseudomonas syringae* pv. *tomato* (*Pst*) Δ*hrcC*Δ*CFA* mutant (inoculum: 2 × 10⁹ CFU mL⁻¹) over the course of 7 days in Col-0 plants. These samples were used for the bacterial RNA-Seq analysis presented in Fig. S4G. (B) Bacterial population density of *Pandoraea* sp. Col-0-28 (inoculum: 2 × 10⁹ CFU mL⁻¹) over the course of 7 days in Col-0 plants. These samples were used for the bacterial RNA-Seq analysis presented in Fig. S4H. (C) Total and endophytic bacterial population density of *Achromobacter xylosoxidans* Col-0-50 (inoculum: 2 × 10⁹ CFU mL⁻¹) over the course of 7 days in Col-0 plants. Endophytic samples were used for the bacterial RNA-Seq analysis presented in Fig. S4I. (D) Venn diagram showing the number of differentially expressed *Pst* Δ*hrcC*Δ*CFA* genes between 6 (t₀) and 168 (t₁₆₈) hpi into Arabidopsis leaves after using one of three methods: DESeq2 after pseudo-alignment with Salmon (DESalmon), DESeq2 after alignment with HISAT2 and analysis with StringTie (DEStringTie), and Cuffdiff after alignment with HISAT2 (Cuffdiff). (E) Principal component analysis (PCA) of transcript reads pseudo-aligned with Salmon, and then analyzed with DESeq2 with the rog and plotPCA functions in R. There were three experiments: Col-0 plants were inoculated with *Pst* Δ*hrcC*Δ*CFA*, *A. xylosoxidans* Col-0-50, or *Pandoraea* sp. Col-0-28 at 6 (t₀), 24 (t₂₄), and 168 (t₁₆₈, 7 days) hpi, while their respective inoculum was grown in King’s (KB) or modified LB (LM) medium. *In vitro* logarithmic (Log) or stationary (Stat) phase treatments were also included for *Pst* Δ*hrcC*Δ*CFA*. (F) PCA of transcript reads aligned with HISAT2, and then analyzed with StringTie and DESeq2. Same experiments as in Fig. S4E were analyzed. (G) Long-term *in planta* transcriptome heatmap of gene expression of select enriched biological processes in non-pathogenic *Pst* Δ*hrcC*Δ*CFA* and microbiota strains (H) *Achromobacter xylosoxidans* Col-0-50 and (I) *Pandoraea* sp. Col-0-28. Gene expression values of select categories were graphed in ascending order of their log₂ fold change (FC) of the ratio between 6 (t₀), 24 (t₂₄) or 168 (t₁₆₈) hpi and the expression in the inoculum (KB or LM). FC was color coded for repression (magenta), no change (white), and induction (cyan). Individual biological repetitions for each treatment are shown as circles. Error bars indicate the standard error of the mean. Different letters indicate differences in means, as judged by a Tukey HSD test (p < 0.05). hpi indicates hours post-inoculation. TCA = tricarboxylic acid cycle.
C

Pentose phosphate pathway

Glucose
  \( \xrightarrow{glk} \)
  Glucose-6P
  \( \xrightarrow{zwf-1} \)
  \( \xrightarrow{zwf-2} \)
  6P-Gluconolactone
  \( \xrightarrow{pgl} \)
  \( \xrightarrow{2765} \)
  6P-Gluconate
  \( \xrightarrow{gnd} \)
  Ribulose-5P
  \( \xrightarrow{rpiA} \)
  \( \xrightarrow{rpe} \)
  Ribose-5P
  \( \xrightarrow{tkt} \)
  \( \xrightarrow{2401} \)
  \( \xrightarrow{2402} \)
  Xylulose-5P
  \( \xrightarrow{tal} \)
  Sedoheptulose-7P
  \( \xrightarrow{tkt} \)
  \( \xrightarrow{2401} \)
  \( \xrightarrow{2402} \)
  Glycerladehyde-3P
  \( \xrightarrow{tal} \)
  Erythrose-4P
  \( \xrightarrow{tkt} \)
  \( \xrightarrow{2401} \)
  \( \xrightarrow{2402} \)
  Fructose-6P
  \( \xrightarrow{tal} \)
  Glycerladehyde-3P

log\(_2 FC(t_x/KB)\)

-2.8  5.4
### Fig. S5

#### Aminoacyl-tRNA Processing

|       | $t_6$ | $t_{24}$ | $t_{168}$ | Log | Stat |
|-------|-------|----------|-----------|-----|------|
| tRNA-Arg-1 |       |          |           |     |      |
| tRNA-Met-1  |       |          |           |     |      |
| tRNA-Tyr-1  |       |          |           |     |      |
| tRNA-Gly-1  |       |          |           |     |      |
| tRNA-Thr-1  |       |          |           |     |      |
| tRNA-Trp-1  |       |          |           |     |      |
| tRNA-Met-2  |       |          |           |     |      |
| tRNA-Gln-1  |       |          |           |     |      |
| tRNA-Leu-1  |       |          |           |     |      |
| tRNA-Ser-1  |       |          |           |     |      |
| tRNA-Arg-4  |       |          |           |     |      |
| tRNA-Ser-2  |       |          |           |     |      |
| tRNA-Pro-3  |       |          |           |     |      |
| tRNA-Leu-2  |       |          |           |     |      |
| tRNA-Cys-1  |       |          |           |     |      |
| tRNA-Ser-3  |       |          |           |     |      |
| tRNA-Leu-3  |       |          |           |     |      |
| tRNA-His-1  |       |          |           |     |      |
| tRNA-Arg-5  |       |          |           |     |      |
| tRNA-Val-3  |       |          |           |     |      |
| tRNA-Ser-4  |       |          |           |     |      |
| tRNA-Gly-5  |       |          |           |     |      |
| tRNA-Leu-4  |       |          |           |     |      |
| tRNA-Phe-5  |       |          |           |     |      |
| tRNA-Thr-2  |       |          |           |     |      |

#### Log2 FC ($t_x/KB$)

- $-10.9$
- $5.4$

### Gene Symbols

- fmt
- glyQ
- glyS
- tyrS
- ileS
- pth
- hisS
- lysS
- alaS
- gltX
- thrS
- pheS
- pheT
- 2964
- 3192
- serS
- cysS
- glnS
- aspS
- proS
- metG
- 4204
- trpS
- gatC
- gatA
- gatB
- leuS
- argS
Fig. S5

Flagellum

| t_6 | t_24 | t_168 | Log   | Stat   |
|-----|------|-------|-------|--------|
|     |      |       | flgM  |        |
|     |      |       | flgA  |        |
|     |      |       | flgB  |        |
|     |      |       | flgC  |        |
|     |      |       | flgD  |        |
|     |      |       | flgE-1|        |
|     |      |       | flgE-2|        |
|     |      |       | flgF  |        |
|     |      |       | flgG  |        |
|     |      |       | flgH  |        |
|     |      |       | flgl  |        |
|     |      |       | flgJ  |        |
|     |      |       | flgK  |        |
|     |      |       | flgL  |        |
|     |      |       | fiIC  |        |
|     |      |       | fiAG  |        |
|     |      |       | fiID  |        |
|     |      |       | fiIS  |        |
|     |      |       | fiIT  |        |
|     |      |       | fleQ  |        |
|     |      |       | fleS  |        |
|     |      |       | fleR  |        |
|     |      |       | fleE  |        |
|     |      |       | fleF  |        |
|     |      |       | fleG  |        |
|     |      |       | fleH  |        |
|     |      |       | fleI  |        |
|     |      |       | fleJ  |        |
|     |      |       | fleK  |        |
|     |      |       | fleL  |        |
|     |      |       | fleM  |        |
|     |      |       | fleN  |        |
|     |      |       | fleO  |        |
|     |      |       | fleP  |        |
|     |      |       | fleQ  |        |
|     |      |       | fleR  |        |
|     |      |       | fleN  |        |
|     |      |       | fleA  |        |
|     |      |       | motA-1|        |
|     |      |       | motD  |        |
|     |      |       | aprF  |        |
|     |      |       | aprE  |        |
|     |      |       | aprD  |        |
|     |      |       | aprI  |        |
|     |      |       | aprA  |        |
|     |      |       | motY  |        |
|     |      |       | motB  |        |
|     |      |       | motA-2|        |
|     |      |       | 5230  |        |

log_{2}FC(t_{x}/KB)

-10.6  1.5
Fig. S5. Expression of genes from select biological pathways for *Pseudomonas syringae pv. tomato* ΔhrcCΔCFA. Pathways represented were (A) the Entner-Doudoroff pathway (with the addition in the pathway of the conversion of pyruvate to acetyl-CoA), (B) the tricarboxylic acid cycle (TCA), (C) the pentose phosphate pathway, (D) ribosome biogenesis genes, (E) tRNAs and genes involved in tRNA aminoacylation, (F) flagellar biosynthesis genes, and (G) and (H) virulence-promoting genes encoding structural and regulatory components of the type III secretion system (T3SS), effectors, and coronatine biosynthesis genes.

Expression of each gene was calculated as the average log₂ fold change (FC) of the ratio between the treatment and the inoculum. Expression of each gene is represented by five rectangles corresponding to each treatment in the following order: 6, 24, and 168 hours post-inoculation, and *in vitro* logarithmic and stationary phase populations. FC was color coded for repression (magenta), no change (white), and induction (cyan). When locus names are shown, “PSPTO_” is omitted from the name.
Fig. S6. Enriched biological processes in up-regulated differentially expressed genes (DEGs). Bubble graphs compared 168 hours post-inoculation (hpi; $t_{168}$) or in vitro stationary-phase populations with in vitro logarithmic-phase populations, or $t_{168}$ with stationary-phase. Processes found in at least two comparisons are highlighted in light blue. The fold-enrichment, number of significant DEGs, and the $-\log_{10}(q)$ of the adjusted $p$-value ($q$) are shown for each biological process. Only processes with at least 4 genes are shown. Refers to Fig. 5B.
**Fig. S7.** Similar *in planta* gene expression patterns for non-pathogenic and effector triggered immunity-inducing bacteria. *(A)* Bacterial population density of three effector-triggered immunity-inducing strains (inoculum: $5 \times 10^5$ – $2 \times 10^6$ CFU mL$^{-1}$) over the course of 3 weeks after infection of Col-0 plants. In Col-0 plants, effector AvrRpt2 is recognized by RPS2, AvrPphB is recognized by RPS5, whereas AvrRps4 is recognized by RPS4. *(B)* *In planta* gene expression of the RNA polymerase sigma factor controlling virulence in *Pseudomonas syringae* tomato (*Pst*) DC3000 (*hrlP*) after inoculation of *Pst* ∆*hrcC*∆*CFA* into Col-0 plants. *(C)* An experimental repeat of *ftsZ* expression. Related to Fig. 6B and 6C. *Pst* ∆*hrcC*∆*CFA* was inoculated into Col-0 plants, whereas *Pst* DC3000 was inoculated into Bu-22 plants. *(D)* *In planta* gene expression of the virulence master regulator *hrlP*, a gene involved in the biosynthesis of the phytotoxin coronatine (coronafacate ligase, *cfl*), a gene involved in mRNA translation (tRNA$^{fMet}$formyl transferase, *fmt*), and a gene involved in the final step of the Entner-Doudoroff pathway (pyruvate kinase, *pyk*) after inoculation of *Pst* DC3000 into Bu-22 plants. *(E)* Bacterial population density after high inoculum infiltration of *Pst* DC3000 (inoculum: $10^7$ CFU mL$^{-1}$) into Arabidopsis Bu-22 plants. Note the loss of containment of bacterial growth at high inoculum. *(F)* Bacterial population density after infiltration of *Pst* DC3000 at a low inoculum ($4 \times 10^5$ CFU mL$^{-1}$) into Arabidopsis Bu-22 plants. The same plants were also used to collect samples for qRT-PCR. Individual biological repetitions for each treatment are shown as circles. Error bars indicate the standard error of the mean. When appropriate, different letters indicate differences in means, as judged by a Tukey HSD test ($p < 0.05$, which was performed between the ∆Ct values for qRT-PCR). For qRT-PCR, gene expression was evaluated using *leuB* as the reference gene and the ∆Ct method. *hpi* indicates hours post-inoculation. *dpi* indicates days post-inoculation.
**Fig. S8.** Number of shared and unique differentially expressed genes between three phyllosphere-inhabiting endophytes. (A) Upset graph showing the number of unique and shared orthologous gene groups in the genomes of *Pseudomonas syringae* pv. *tomato* (Pst) ΔhrcΔCFA (ΔCΔCFA), *Achromobacter xylosoxidans* Col-0-50 (Achr), and *Pandoraea* sp. Col-0-28 (Pand). The core genome encompasses 1,610 gene groups shared by all three bacterial strains. (B) Upset graphs showing the number of unique and shared orthologous up-regulated and down-regulated differentially expressed gene (DEG) groups in Pst ΔhrcΔCFA, *A. xylosoxidans* Col-0-50, and *Pandoraea* sp. Col-0-28 in the inoculum or 6 hours post-inoculation (hpi; t_6) of Col-0 plants, when compared to 168 hpi (t_168).
Table S1. Enriched up- and down-regulated biological processes of differentially expressed genes (DEG) in Pseudomonas syringae pv. tomato (Ps) str. C6CFR.

### Up-regulated processes in Ps str. C6CFR vs. Pst (hrcC)

| Process                                      | q-value | Log2 vs. t | Log2 vs. ∆t | q-value | Log2 vs. t | Log2 vs. ∆t | q-value | Log2 vs. t | Log2 vs. ∆t | q-value | Log2 vs. t | Log2 vs. ∆t | q-value
|----------------------------------------------|---------|------------|-------------|---------|------------|-------------|---------|------------|-------------|---------|------------|-------------|---------|
| Protein translation                          | 1.61E-11| 2.25E-04   | 1.31E-03    | 2.25E-04| 1.31E-03   | 2.25E-04    | 1.31E-03| 3.00E-10   | 1.31E-03    | 3.00E-10| 1.31E-03   | 3.00E-10    | 3.00E-10|
| Nucleotide metabolism                        | 3.32E-02| 2.25E-04   | 1.31E-03    | 2.25E-04| 1.31E-03   | 2.25E-04    | 1.31E-03| 3.00E-10   | 1.31E-03    | 3.00E-10| 1.31E-03   | 3.00E-10    | 3.00E-10|
| Nucleotide metabolism                        | 3.32E-02| 2.25E-04   | 1.31E-03    | 2.25E-04| 1.31E-03   | 2.25E-04    | 1.31E-03| 3.00E-10   | 1.31E-03    | 3.00E-10| 1.31E-03   | 3.00E-10    | 3.00E-10|
| NDG-1                                        | 3.75E-02| 2.25E-04   | 1.31E-03    | 2.25E-04| 1.31E-03   | 2.25E-04    | 1.31E-03| 3.00E-10   | 1.31E-03    | 3.00E-10| 1.31E-03   | 3.00E-10    | 3.00E-10|

### Up-regulated processes in Ps str. C6CFR vs. KB

| Process                                      | q-value | Log2 vs. t | Log2 vs. ∆t | q-value | Log2 vs. t | Log2 vs. ∆t | q-value | Log2 vs. t | Log2 vs. ∆t | q-value | Log2 vs. t | Log2 vs. ∆t | q-value
|----------------------------------------------|---------|------------|-------------|---------|------------|-------------|---------|------------|-------------|---------|------------|-------------|---------|
| Protein translation                          | 1.61E-11| 2.25E-04   | 1.31E-03    | 2.25E-04| 1.31E-03   | 2.25E-04    | 1.31E-03| 3.00E-10   | 1.31E-03    | 3.00E-10| 1.31E-03   | 3.00E-10    | 3.00E-10|
| Nucleotide metabolism                        | 3.32E-02| 2.25E-04   | 1.31E-03    | 2.25E-04| 1.31E-03   | 2.25E-04    | 1.31E-03| 3.00E-10   | 1.31E-03    | 3.00E-10| 1.31E-03   | 3.00E-10    | 3.00E-10|
| Nucleotide metabolism                        | 3.32E-02| 2.25E-04   | 1.31E-03    | 2.25E-04| 1.31E-03   | 2.25E-04    | 1.31E-03| 3.00E-10   | 1.31E-03    | 3.00E-10| 1.31E-03   | 3.00E-10    | 3.00E-10|
| NDG-1                                        | 3.75E-02| 2.25E-04   | 1.31E-03    | 2.25E-04| 1.31E-03   | 2.25E-04    | 1.31E-03| 3.00E-10   | 1.31E-03    | 3.00E-10| 1.31E-03   | 3.00E-10    | 3.00E-10|

### Up-regulated processes in Ps str. C6CFR vs. tomato

| Process                                      | q-value | Log2 vs. t | Log2 vs. ∆t | q-value | Log2 vs. t | Log2 vs. ∆t | q-value | Log2 vs. t | Log2 vs. ∆t | q-value | Log2 vs. t | Log2 vs. ∆t | q-value
|----------------------------------------------|---------|------------|-------------|---------|------------|-------------|---------|------------|-------------|---------|------------|-------------|---------|
| Protein translation                          | 1.61E-11| 2.25E-04   | 1.31E-03    | 2.25E-04| 1.31E-03   | 2.25E-04    | 1.31E-03| 3.00E-10   | 1.31E-03    | 3.00E-10| 1.31E-03   | 3.00E-10    | 3.00E-10|
| Nucleotide metabolism                        | 3.32E-02| 2.25E-04   | 1.31E-03    | 2.25E-04| 1.31E-03   | 2.25E-04    | 1.31E-03| 3.00E-10   | 1.31E-03    | 3.00E-10| 1.31E-03   | 3.00E-10    | 3.00E-10|
| Nucleotide metabolism                        | 3.32E-02| 2.25E-04   | 1.31E-03    | 2.25E-04| 1.31E-03   | 2.25E-04    | 1.31E-03| 3.00E-10   | 1.31E-03    | 3.00E-10| 1.31E-03   | 3.00E-10    | 3.00E-10|
| NDG-1                                        | 3.75E-02| 2.25E-04   | 1.31E-03    | 2.25E-04| 1.31E-03   | 2.25E-04    | 1.31E-03| 3.00E-10   | 1.31E-03    | 3.00E-10| 1.31E-03   | 3.00E-10    | 3.00E-10|
Table S1 (Continued).

| Comparisons | t⁶ vs. t⁶ | q-value | t⁶ vs. KB | q-value | t⁶ vs. Stat | q-value | t⁶ vs. t⁶ | q-value | t⁶ vs. KB | q-value | t⁶ vs. Stat | q-value | t⁶ vs. t⁶ | q-value |
|--------------|-----------|---------|----------|---------|-----------|---------|----------|---------|----------|---------|-----------|---------|----------|---------|
| Locomotion and flagellum | 5.30E-19 | – | – | – | Locomotion and flagellum | 5.30E-19 | – | – | Locomotion and flagellum | 5.30E-19 | – | – | Locomotion and flagellum | 5.30E-19 |
| Locomotion and flagellum | 3.87E-23 | – | – | – | Locomotion and flagellum | 3.87E-23 | – | – | Locomotion and flagellum | 3.87E-23 | – | – | Locomotion and flagellum | 3.87E-23 |
| Locomotion and flagellum | 3.95E-02 | – | – | – | Locomotion and flagellum | 3.95E-02 | – | – | Locomotion and flagellum | 3.95E-02 | – | – | Locomotion and flagellum | 3.95E-02 |
| Locomotion and flagellum | 1.20E-16 | – | – | – | Locomotion and flagellum | 1.20E-16 | – | – | Locomotion and flagellum | 1.20E-16 | – | – | Locomotion and flagellum | 1.20E-16 |
| Fatty acid biosynthesis | 4.97E-02 | – | – | – | Fatty acid biosynthesis | 4.97E-02 | – | – | Fatty acid biosynthesis | 4.97E-02 | – | – | Fatty acid biosynthesis | 4.97E-02 |
| LPS biosynthesis* | 4.81E-02 | – | – | – | LPS biosynthesis* | 4.81E-02 | – | – | LPS biosynthesis* | 4.81E-02 | – | – | LPS biosynthesis* | 4.81E-02 |
| Siderophore biosynthesis | 7.47E-03 | – | – | – | Siderophore biosynthesis | 7.47E-03 | – | – | Siderophore biosynthesis | 7.47E-03 | – | – | Siderophore biosynthesis | 7.47E-03 |

Comparisons for enrichment of biological processes were done between the inoculum (KB), 6 (t⁶), 24 (t²⁴) and 168 (t¹⁶⁸) hours post-inoculation into Arabidopsis leaves, and in vitro cultures grown to logarithmic (Log) or stationary (Stat) phase. An asterisk denotes that a biological process had less than 5 DEGs. False discovery rate adjusted p-values (q-values) calculated by BINGO for each comparison are shown.
### Table S2. Enriched up- and down-regulated biological processes of differentially expressed genes (DEG) in *Achromobacter xylosoxidans* Col-0-50.

| Up-regulated processes in *Achromobacter xylosoxidans* Col-0-50 | t<sub>6</sub> vs. t<sub>24</sub> | | | t<sub>6</sub> vs. t<sub>168</sub> | | t<sub>24</sub> vs. t<sub>168</sub> | | t<sub>6</sub> vs. LM | | t<sub>24</sub> vs. LM | | t<sub>168</sub> vs. LM | q-value |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| t<sub>6</sub> vs. t<sub>24</sub> | q-value | t<sub>6</sub> vs. t<sub>168</sub> | q-value | t<sub>6</sub> vs. LM | q-value | t<sub>24</sub> vs. t<sub>168</sub> | q-value | t<sub>24</sub> vs. LM | q-value | t<sub>168</sub> vs. LM | q-value |
| Primary metabolism | 6.36E-08 | 7.21E-18 | Osmyolyte (ectoine) biosynthesis* | 3.30E-02 | Primary metabolism | 4.85E-11 | 4.36E-02 | Protein translation | 5.63E-22 | 3.01E-02 | ATP biosynthesis | 7.89E-03 | 4.36E-02 |
| Protein translation | 1.05E-02 | 6.37E-04 | RNA primer synthesis for DNA replication* | 1.21E-12 | Protein translation | 4.36E-02 | 3.55E-02 | RNA primer synthesis for DNA replication* | 1.34E-03 | 3.14E-02 | ATP biosynthesis | 1.34E-03 | 3.55E-02 |
| Protein folding | 1.05E-02 | 6.37E-04 | Protein translation | 1.21E-12 | Protein translation | 4.36E-02 | 3.55E-02 | Protein translation | 1.34E-03 | 3.14E-02 | ATP biosynthesis | 1.34E-03 | 3.55E-02 |
| Glutathione metabolism | 4.36E-02 | 4.36E-02 | Glutathione metabolism | 4.36E-02 | Glutathione metabolism | 4.36E-02 | 4.36E-02 | Glutathione metabolism | 4.36E-02 | 4.36E-02 | Glutathione metabolism | 4.36E-02 | 4.36E-02 |
| Amino acid metabolism | 3.30E-02 | 3.30E-02 | Amino acid metabolism | 3.30E-02 | Amino acid metabolism | 3.30E-02 | 3.30E-02 | Amino acid metabolism | 3.30E-02 | 3.30E-02 | Amino acid metabolism | 3.30E-02 | 3.30E-02 |
| Serine family amino acid metabolism* | 1.05E-02 | 1.05E-02 | Serine family amino acid metabolism* | 1.05E-02 | Serine family amino acid metabolism* | 1.05E-02 | 1.05E-02 | Serine family amino acid metabolism* | 1.05E-02 | 1.05E-02 | Serine family amino acid metabolism* | 1.05E-02 | 1.05E-02 |
| Sulfate transport | 1.28E-02 | 1.28E-02 | Sulfate transport | 1.28E-02 | Sulfate transport | 1.28E-02 | 1.28E-02 | Sulfate transport | 1.28E-02 | 1.28E-02 | Sulfate transport | 1.28E-02 | 1.28E-02 |

Comparisons for enrichment of biological processes were done between the inoculum (LM), 6 (t<sub>6</sub>), 24 (t<sub>24</sub>) and 168 (t<sub>168</sub>) hours post-inoculation into Arabidopsis leaves. An asterisk denotes that a biological process had less than 5 DEGs. False discovery rate adjusted p-values (q-values) calculated by BINGO for each comparison are shown.
Table S3. Enriched up- and down-regulated biological processes of differentially expressed genes (DEG) in Pandoraea sp. Col-0-28.

### Up-regulated processes in Pandoraea sp. Col-0-28

| Comparison | q-value | Comparison | q-value | Comparison | q-value | Comparison | q-value |
|------------|---------|------------|---------|------------|---------|------------|---------|
| t<sub>6</sub> vs. t<sub>24</sub> | 9.29E-04 | t<sub>6</sub> vs. t<sub>168</sub> | 4.22E-02 | t<sub>24</sub> vs. t<sub>168</sub> | 5.57E-03 | t<sub>6</sub> vs. LM | 1.53E-06 |
| t<sub>6</sub> vs. t<sub>24</sub> | 2.76E-02 | t<sub>6</sub> vs. t<sub>168</sub> | 5.71E-03 | t<sub>24</sub> vs. t<sub>168</sub> | 4.66E-02 | t<sub>6</sub> vs. LM | 1.32E-02 |
| t<sub>24</sub> vs. t<sub>168</sub> | 9.29E-04 | t<sub>24</sub> vs. LM | 5.93E-03 | t<sub>168</sub> vs. LM | 3.97E-02 |

### Down-regulated processes in Pandoraea sp. Col-0-28

| Comparison | q-value | Comparison | q-value | Comparison | q-value | Comparison | q-value | Comparison | q-value |
|------------|---------|------------|---------|------------|---------|------------|---------|------------|---------|
| t<sub>6</sub> vs. t<sub>24</sub> | 3.39E-03 | t<sub>6</sub> vs. t<sub>168</sub> | 1.04E-02 | t<sub>24</sub> vs. t<sub>168</sub> | 4.41E-02 | t<sub>6</sub> vs. LM | 4.66E-02 |
| t<sub>6</sub> vs. t<sub>24</sub> | 3.78E-02 | t<sub>6</sub> vs. t<sub>168</sub> | 3.97E-02 | t<sub>24</sub> vs. t<sub>168</sub> | 5.71E-03 | t<sub>6</sub> vs. LM | 1.32E-02 |
| t<sub>24</sub> vs. t<sub>168</sub> | 5.80E-02 | t<sub>24</sub> vs. LM | 1.51E-05 | t<sub>168</sub> vs. LM | 2.05E-02 |

Comparisons for enrichment of biological processes were done between the inoculum (LM), 6 (t<sub>6</sub>), 24 (t<sub>24</sub>) and 168 (t<sub>168</sub>) hours post-inoculation into Arabidopsis leaves. An asterisk denotes that a biological process had less than 5 DEGs. False discovery rate adjusted p-values (q-values) calculated by BINGO for each comparison are shown.
Table S4. Enriched biological processes based on significantly different expression profiles after STEM (Short-Time series Expression Miner) analysis in Pseudomonas syringae pv. tomato (Pst) ∆hrcC∆CFA.

| Enriched Pst ∆hrcC∆CFA biological processes in Profile: | 1  | 11 | 26 | 39 | 44 | 45 | 47 |
|----------------------------------------------------------|----|----|----|----|----|----|----|
| Flagellum and locomotion                                 | 1.03E-16 | 1.24E-03 | 1.68E-02 | 1.25E-03 | 4.62E-03 | 1.35E-10 | 1.36E-03 |
| Nucleoside transport                                     | 2.64E-02 | 3.47E-02 | 1.71E-02 | 2.04E-02 | 2.04E-02 | 7.88E-13 | 8.31E-03 |
| Transcriptional regulation                              | 1.68E-02 | 1.31E-02 | 4.57E-02 |                |                |                |                |
| Virulence family amino acid metabolism                  | 1.25E-03 | 4.40E-03 |                |                |                |                |                |
| Lysine metabolism                                        | 1.71E-02 | 1.31E-02 |                |                |                |                |                |
| Carbohydrate transport*                                   | 6.47E-02 | 1.71E-02 |                |                |                |                |                |
| Vitamin biosynthesis                                     | 4.57E-02 | 1.71E-02 |                |                |                |                |                |
| Primary metabolism                                       | 2.04E-02 | 1.31E-02 |                |                |                |                |                |
| Glutamine family amino acid metabolism                  | 1.25E-03 | 4.40E-03 |                |                |                |                |                |
| Purine ribonucleotide biosynthesis                       | 2.04E-02 | 1.31E-02 |                |                |                |                |                |
| Virulence                                               | 8.04E-03 | 1.71E-02 |                |                |                |                |                |
| Nucleotide metabolism                                   | 2.04E-02 | 1.31E-02 |                |                |                |                |                |
| Ribosome biogenesis                                      | 2.04E-02 | 1.31E-02 |                |                |                |                |                |
| RNA aminoacylation                                       | 6.47E-02 | 1.71E-02 |                |                |                |                |                |
| Glutamine family amino acid metabolism                  | 1.25E-03 | 4.40E-03 |                |                |                |                |                |
| Lysine metabolism                                        | 1.71E-02 | 1.31E-02 |                |                |                |                |                |
| Carbohydrate transport*                                   | 6.47E-02 | 1.71E-02 |                |                |                |                |                |
| Vitamin biosynthesis                                     | 4.57E-02 | 1.71E-02 |                |                |                |                |                |
| Primary metabolism                                       | 2.04E-02 | 1.31E-02 |                |                |                |                |                |
| Glutamine family amino acid metabolism                  | 1.25E-03 | 4.40E-03 |                |                |                |                |                |
| Purine ribonucleotide biosynthesis                       | 2.04E-02 | 1.31E-02 |                |                |                |                |                |
| Virulence                                               | 8.04E-03 | 1.71E-02 |                |                |                |                |                |
| Nucleotide metabolism                                   | 2.04E-02 | 1.31E-02 |                |                |                |                |                |
| Ribosome biogenesis                                      | 2.04E-02 | 1.31E-02 |                |                |                |                |                |
| RNA aminoacylation                                       | 6.47E-02 | 1.71E-02 |                |                |                |                |                |
| Glutamine family amino acid metabolism                  | 1.25E-03 | 4.40E-03 |                |                |                |                |                |
| Lysine metabolism                                        | 1.71E-02 | 1.31E-02 |                |                |                |                |                |
| Carbohydrate transport*                                   | 6.47E-02 | 1.71E-02 |                |                |                |                |                |
| Vitamin biosynthesis                                     | 4.57E-02 | 1.71E-02 |                |                |                |                |                |
| Primary metabolism                                       | 2.04E-02 | 1.31E-02 |                |                |                |                |                |

An image of the expression profile is shown below the list of processes, starting from the zero time point (the inoculum; the x-axis denotes time [not to scale], while the y-axis indicates gene expression). The time points used for the analysis were the inoculum, 6, 24, and 168 hours post-inoculation into Arabidopsis leaves. An asterisk denotes that a biological process had less than 5 genes. False discovery rate adjusted p-values (q-values) for biological process enrichment for each expression profile as calculated by BINGO are shown.
Table S5. Enriched biological processes based on significantly different expression profiles after STEM (Short-Time series Expression Miner) analysis in _Achromobacter xylosoxidans_ Col-0-50.

| Process                                      | q-value  |
|----------------------------------------------|----------|
| 9                                            | 2.82E-02 |
| 26                                           | 1.94E-04 |
| 34                                           | 2.50E-02 |
| 39                                           | 7.70E-04 |
| 47                                           | 6.18E-06 |

An image of the expression profile is shown below the list of processes, starting from the zero time point (the inoculum; the x-axis denotes time [not to scale], while the y-axis indicates gene expression). The time points used for the analysis were the inoculum, 6, 24, and 168 hours post-inoculation into Arabidopsis leaves. An asterisk denotes that a biological process had less than 5 genes. False discovery rate adjusted p-values (q-values) for biological process enrichment for each expression profile as calculated by BINGO are shown.
Table S6. Enriched biological processes based on significantly different expression profiles after STEM (Short-Time series Expression Miner) analysis in *Pandoraea* sp. Col-0-28.

| Process                                      | q-value  |
|----------------------------------------------|----------|
| Transcriptional regulation                   | 3.10E-02 |
| Two-component system                         | 1.45E-02 |
| Transposition                                | 4.82E-03 |
| Primary metabolism                           | 5.02E-10 |
| Nucleotide metabolism                        | 4.08E-02 |
| RNA aminoacylation                            | 2.32E-02 |
| RNA processing                                | 7.04E-03 |
| Amino acid biosynthesis                       | 1.31E-03 |
| Vitamin biosynthesis                          | 1.61E-02 |
| Ubiquinone biosynthesis                       | 1.86E-02 |
| Protein translation                           | 5.92E-15 |
| Tricarboxylic acid cycle                     | 1.32E-02 |
| ATP biosynthesis                              | 6.10E-03 |
| Inositol phosphate dephosphorylation*        | 3.74E-02 |

An image of the expression profile is shown below the list of processes, starting from the zero time point (the inoculum; the x-axis denotes time [not to scale], while the y-axis indicates gene expression). The time points used for the analysis were the inoculum, 6, 24, and 168 hours post-inoculation into Arabidopsis leaves. An asterisk denotes that a biological process had less than 5 genes. False discovery rate adjusted *p*-values (*q*-values) for biological process enrichment for each expression profile as calculated by BINGO are shown.
| Locus name   | Gene name | log$_2$(t$_6$/KB) | < 0.05 | log$_2$(t$_{168}$/KB) | < 0.05 | log$_2$(t$_6$/t$_{168}$) | < 0.05 | Annotation description |
|-------------|-----------|------------------|--------|----------------------|--------|------------------------|--------|------------------------|
| PSPTO_1627  | PSPTO_1627| -1.01            | yes    | -1.53                | yes    | 0.52                   | yes    | Short chain dehydrogenase |
| PSPTO_1631  | PSPTO_1631| 3.26             | yes    | 3.60                 | yes    | -0.34                  | yes    | Coronafacic acid synthetase, acyl carrier protein component; deleted in Pst ΔhrcC ΔCFA. |
| PSPTO_1632  | PSPTO_1632| 3.21             | yes    | 2.35                 | yes    | 0.86                   | yes    | GNAT family acetyltransferase |
| PSPTO_1633  | asnB      | 2.50             | yes    | 2.33                 | yes    | 0.17                   | yes    | Asparagine synthetase |
| PSPTO_4671  |           | -0.60            | yes    | -0.97                | yes    | 0.37                   |        | Alkaline D-peptidase |
| PSPTO_4680  | cfl       |                  |        |                      |        |                        |        | Coronafacic acid synthetase, ligase component; deleted in Pst ΔhrcC ΔCFA. |
| PSPTO_4681  | cfa1      |                  |        |                      |        |                        |        | Coronafacic acid synthetase, acyl carrier protein component; deleted in Pst ΔhrcC ΔCFA. |
| PSPTO_4682  | cfa2      |                  |        |                      |        |                        |        | Coronafacic acid synthetase, dehydratase component; deleted in Pst ΔhrcC ΔCFA. |
| PSPTO_4683  | cfa3      |                  |        |                      |        |                        |        | Coronafacic acid beta-ketoacyl synthetase component; deleted in Pst ΔhrcC ΔCFA. |
| PSPTO_4684  | cfa4      |                  |        |                      |        |                        |        | Coronafacic acid synthetase component; deleted in Pst ΔhrcC ΔCFA. |
| PSPTO_4685  | cfa5      |                  |        |                      |        |                        |        | Coronafacic acid synthetase, ligase component; deleted in Pst ΔhrcC ΔCFA. |
| PSPTO_4686  | cfa6      |                  |        |                      |        |                        |        | Coronafacic acid polyketide synthase I; deleted in Pst ΔhrcC ΔCFA. |
| PSPTO_4687  | cfa7      |                  |        |                      |        |                        |        | Coronafacic acid polyketide synthetase II; deleted in Pst ΔhrcC ΔCFA. |
| PSPTO_4688  | cfa8      |                  |        |                      |        |                        |        | Crotonyl-CoA reductase; deleted in Pst ΔhrcC ΔCFA. |
| PSPTO_4689  | cfa9      |                  |        |                      |        |                        |        | CFA synthetase, thioesterase component; deleted in Pst ΔhrcC ΔCFA. |
| PSPTO_4699  |           | -0.85            | yes    | -1.05                | yes    | 0.20                   |        | Non-ribosomal peptide synthetase, terminal component |
| PSPTO_4704  | corR      | 0.69             | yes    | -0.59                | yes    | 1.28                   |        | DNA-binding response regulator CorR |
| PSPTO_4705  | corS      | 0.00             | yes    | -0.05                | yes    | 0.04                   |        | Sensor histidine kinase CorS |
| PSPTO_4706  | corP      | -1.18            | yes    | -0.59                | yes    | -0.59                  |        | Response regulator CorP |
| PSPTO_4707  | cmaD      | 3.25             | yes    | -0.45                | yes    | 3.70                   | yes    | Coronamic acid synthetase CmaD |
| PSPTO_4708  | cmaE      | 1.92             | yes    | -0.31                | yes    | 2.23                   | yes    | Coronamic acid synthetase CmaE |
| PSPTO_4709  | cmaA      | 3.21             | yes    | 0.56                 | yes    | 2.66                   | yes    | Coronamic acid synthetase CmaA |
| PSPTO_4710  | cmaB      | 3.52             | yes    | 1.13                 | yes    | 2.39                   | yes    | Coronamic acid synthetase CmaB |
| PSPTO_4711  | cmaC      | 3.19             | yes    | -2.36                | yes    | 5.56                   | yes    | Coronamic acid synthetase CmaC |
| PSPTO_4712  | cmaT      | 2.63             | yes    | 0.98                 | yes    | 1.65                   | yes    | Coronamic acid synthetase, thioesterase component |
| PSPTO_4714  | cmaU      | 0.05             | yes    | -2.20                | yes    | 2.25                   | yes    | CmaU protein |
| PSPTO_4723  | cmaL      | 4.11             | yes    | 1.12                 | yes    | 3.00                   | yes    | Coronafacic ligase CmaL |

Table S7. Secondary metabolite biosynthetic gene clusters in *Pseudomonas syringae pv. tomato* ΔhrcC ΔCFA whose expression is differentially regulated in planta.
Table S7 (Continued).

| Locus name  | Gene name      | $\log_{2}(t_6/KB)$ | $< 0.05$ | $\log_{2}(t_{168}/KB)$ | $< 0.05$ | $\log_{2}(t_6/t_{168})$ | $< 0.05$ | Annotation description                                      |
|-------------|----------------|--------------------|----------|------------------------|----------|------------------------|----------|------------------------------------------------------------|
| PSPTO_2120  | PSPTO_2120     | -1.09              | yes      | -2.69                  | yes      | 1.61                   | yes      | Peptidase, M20/M25/M40 family                                |
| PSPTO_2123  | PSPTO_2123     | -0.88              | yes      | 0.70                   | yes      | -1.58                  | yes      | Sensor histidine kinase                                     |
| PSPTO_2128  | PSPTO_2128     | 2.63               | yes      | 1.11                   | yes      | 1.52                   | yes      | Response regulator                                          |
| PSPTO_2130  | PSPTO_2130     | 2.88               | yes      | 2.28                   | yes      | 0.60                   | yes      | LuxR family DNA-binding response regulator                  |
| PSPTO_2131  | PSPTO_2131     | 2.11               | yes      | 0.59                   | yes      | 1.51                   | yes      | Sensor histidine kinase                                     |
| PSPTO_2133  | sigX           | 2.37               | yes      | 1.64                   | yes      | 0.73                   | yes      | RNA polymerase sigma-70 family protein                      |
| PSPTO_2134  | pvdG           | -3.71              | yes      | -2.47                  |          |                       |          | Pyoverdin synthetase, thioesterase component                |
| PSPTO_2135  | pvsA, pvdL     | -2.24              | yes      | -1.01                  | yes      | -1.23                  | yes      | Pyoverdin chromophore precursor synthetase                  |
| PSPTO_2136  | daT, pvdH      | -0.68              | yes      | 0.30                   |          | -0.98                  |          | 2,4-diaminobutyrate 4-transaminase                          |
| PSPTO_2137  | PSPTO_2137     | -0.50              | yes      | -1.91                  | yes      | 1.41                   |          | MBH-like protein                                            |
| PSPTO_2140  | PSPTO_2140     | -1.50              | yes      | 0.50                   |          | -1.99                  |          | Cation ABC transporter ATP-binding protein                  |
| PSPTO_2141  | PSPTO_2141     | -1.57              | yes      | -1.74                  | yes      | 0.17                   |          | Cation ABC transporter substrate-binding protein             |
| PSPTO_2146  | PSPTO_2146     | -0.65              | yes      | -4.92                  | yes      | 4.27                   | yes      | Pyoverdin biosynthesis regulatory gene                      |
| PSPTO_2147  | PSPTO_2147     | -0.16              | yes      | -0.15                  | yes      | -0.02                  |          | Pyoverdin sidechain peptide synthetase I, epsilon-Lys module|
| PSPTO_2148  | PSPTO_2148     | -0.75              | yes      | -0.17                  |          | -0.58                  |          | Pyoverdin sidechain peptide synthetase II, D-Asp-L-Thr component|
| PSPTO_2149  | pvdD           | -0.52              | yes      | 0.49                   |          | -1.00                  |          | Pyoverdin sidechain peptide synthetase III, L-Thr-L-Ser component|
| PSPTO_2150  | PSPTO_2150     | -0.81              | yes      | -0.12                  |          | -0.69                  |          | Pyoverdin sidechain peptide synthetase IV, D-Asp-L-Ser component|
| PSPTO_2151  | fjaA           | 0.99               | yes      | 0.65                   | 1.64     | yes                    |          | TonB-dependent siderophore receptor                         |
| PSPTO_2152  | PSPTO_2152     | -0.80              | yes      | -0.53                  |          | -0.27                  |          | TonB-dependent siderophore receptor                         |
| PSPTO_2153  | pvdE           | -0.22              | yes      | -0.36                  |          | 0.14                   |          | Pyoverdin ABC transporter, ATP-binding/permease protein      |
| PSPTO_2154  | pvdO           | -0.07              | yes      | -1.24                  |          | 1.17                   | yes      | Class V aminotransferase                                    |
| PSPTO_2155  | pvdN           | -1.92              | yes      | -0.09                  | yes      | -1.83                  | yes      | Class V aminotransferase                                    |
| PSPTO_2156  | pvdM           | 0.51               | yes      | -3.80                  | yes      | 4.31                   | yes      | Renal dipeptidase family protein                            |
| PSPTO_2158  | PSPTO_2158     | 0.10               | yes      | 0.26                   |          | -0.17                  |          | Outer membrane efflux protein                               |
| PSPTO_2159  | PSPTO_2159     | -1.18              | yes      | -1.53                  | yes      | 0.35                   |          | Macrolide ABC efflux protein                                |
| PSPTO_2160  | PSPTO_2160     | -3.15              | yes      | -0.02                  | yes      | -3.13                  |          | RND family efflux transporter MFP subunit                   |
| PSPTO_2161  | pvdQ           | -1.07              | yes      | -0.55                  | yes      | -0.51                  |          | Penicillin amidase family protein                            |
Table S7 (Continued).

| Locus name | Gene name | log₂(t₆/KB) | log₂(t₁₆₈/KB) | log₂(t₆/t₁₆₈) | Annotation description |
|------------|-----------|------------|----------------|----------------|------------------------|
| PSPTO_2583 | -1.88     | -3.05      | 1.17           |                | Glutamine amidotransferase, class-II protein |
| PSPTO_2590 | 1.59      | yes        | 2.75           | -1.16          | yes                    | Luciferase family protein |
| PSPTO_2591 | -0.69     | yes        | 0.34           | -1.03          | yes                    | Diguanylate cyclase |
| PSPTO_2592 | saxG      | 0.10       | 0.45           | -0.35          |                        | Aliphatic isothiocyanate resistance protein SaxG; AcrB/AcrD/AcrF family |
| PSPTO_2593 | 0.77      | yes        | -3.34          | 4.11           | yes                    | Multidrug resistance protein, AcrA/AcrE family |
| PSPTO_2595 | pchA      | -0.42      | 0.14           | -0.56          |                        | Isochorismate synthase |
| PSPTO_2596 | pchB      | -0.62      | -0.96          | 0.34           |                        | Isochorismate pyruvate-lyase |
| PSPTO_2597 | irp5, ybtE| 0.28       | -0.15          | 0.43           |                        | Yersiniabactin synthetase, salycilate ligase component |
| PSPTO_2598 | irp4, ybtT| -0.57      | -0.50          | -0.07          |                        | Yersiniabactin synthetase, thioesterase component |
| PSPTO_2599 | irp3, ybtU| -1.32      | -0.71          | -0.61          |                        | Yersiniabactin synthetase, thiazolinyl reductase component |
| PSPTO_2600 | irp1, hmwp1| -0.64     | -0.48          | -0.15          |                        | Yersiniabactin polyketide/non-ribosomal peptide synthetase |
| PSPTO_2601 | ybtX      | -0.09      | -1.52          | 1.43           | yes                    | Membrane protein |
| PSPTO_2602 | hmwp2     | -0.57      | -1.13          | 0.55           |                        | Yersiniabactin non-ribosomal peptide synthetase |
| PSPTO_2603 | ybtQ      | -1.09      | -1.25          | 0.16           |                        | ABC transporter ATP-binding protein/permease |
| PSPTO_2604 | ybtP      | -0.84      | -1.73          | 0.89           |                        | ABC transporter ATP-binding protein/permease |
| PSPTO_2605 | fyuA      | -0.99      | -0.18          | -0.81          | yes                    | TonB-dependent siderophore receptor |
| PSPTO_2606 | yblA      | -0.87      | -1.37          | 0.50           | yes                    | Arac family transcriptional regulator |
| PSPTO_2607 | -0.80     | 0.18       | -0.99          |                |                        | TonB-dependent siderophore receptor |
| PSPTO_2612 | -0.97     | -1.61      | 0.64           |                |                        | GNAT family acetyltransferase |
| PSPTO_2614 | 1.43      | yes        | -0.38          | 1.81           | yes                    | Dioxygenase, TauD/TfdA family |
| PSPTO_2617 | 0.84      | 0.93       | -0.09          |                |                        | LysR family transcriptional regulator |
| PSPTO_2618 | argD-2    | -0.48      | -1.90          | 1.42           |                        | Acetyltomithine aminotransferase |

Gene expression used the logarithm in base 2 fold-change values calculated by DESeq2 after aligning the reads with StringTie when comparing the inoculum (KB) with 6 (t₆) and 168 (t₁₆₈) hours post-inoculation (hpi) into Arabidopsis leaves, and 6 with 168 hpi. Genes that are up-regulated are highlighted in cyan, while those that are down-regulated are highlighted in magenta. A column indicating if a gene was differentially regulated, as determined by DESeq2 or Cuffdiff (false discovery rate adjusted p < 0.05), is also shown. Gene clusters were identified as enriched using a hypergeometric enrichment test. The yersiniabactin gene cluster did not show differential expression, but is included as it is a cluster already known to be associated with secondary metabolite biosynthesis.
**Table S8.** Secondary metabolite biosynthetic gene clusters in *Achromobacter xylosoxidans* Col-0-50 whose expression is differentially regulated in planta.

| Locus name | Gene name | log₂(t168/LM) | < 0.05 | log₂(t168/Col-0-50) | < 0.05 | log₂(t168/Col-0-50) | < 0.05 | Annotation description |
|------------|-----------|---------------|--------|----------------------|--------|----------------------|--------|----------------------|
| **Siderophore, similar to desferrioxamine** | | | | | | | | |
| FLPKDCGK_00714 | bcr_1 | -4.39 | yes | -2.87 | yes | -1.52 | yes | Bicyclomycin resistance protein |
| FLPKDCGK_00715 | pchR_3 | -4.22 | yes | -2.31 | yes | -1.91 | yes | Regulatory protein PchR |
| FLPKDCGK_00718 | lucC | -5.23 | yes | -3.00 | yes | -2.23 | yes | Aerobactin synthase |
| FLPKDCGK_00719 | lucB | -4.04 | yes | -3.53 | yes | -0.50 | yes | N(II)-hydroxyllysine O-acetyltransferase |
| FLPKDCGK_00720 | lucD | -5.42 | yes | -3.15 | yes | -2.27 | yes | L-lysine N6-monoxygenase |
| FLPKDCGK_00721 | ftaA | -0.46 | -0.85 | 0.39 | | | | Putative iron export ATP-binding protein FtaA |
| FLPKDCGK_00722 | ftbB | -0.92 | -5.36 | yes | 4.43 | | | Putative iron export permease protein FtbB |
| **Ectoine** | | | | | | | | |
| FLPKDCGK_01732 | ectD_1 | 6.13 | yes | 4.58 | yes | 1.55 | yes | Ectoine dioxygenase |
| FLPKDCGK_01733 | ectC | 6.68 | yes | 5.20 | yes | 1.48 | yes | L-ectoine synthase |
| FLPKDCGK_01734 | ectB | 7.33 | yes | 5.45 | yes | 1.88 | yes | Diaminopimelate-2-oxoglutarate transaminase |
| FLPKDCGK_01735 | ectA | 5.67 | yes | 3.05 | yes | 2.62 | yes | L-2,4-diaminobutyric acid acetyltransferase |
| FLPKDCGK_01736 | yusO | 2.59 | yes | 1.26 | yes | 1.32 | yes | Putative HTH-type transcriptional regulator YusO |
| **Non-ribosomal peptide synthase-like** | | | | | | | | |
| FLPKDCGK_01927 | livH_6 | -0.83 | | 0.88 | yes | -1.71 | yes | High-affinity branched-chain amino acid transport system permease protein LivH |
| FLPKDCGK_01928 | livF_6 | 0.80 | yes | 2.66 | yes | -1.66 | yes | High-affinity branched-chain amino acid transport ATP-binding protein LivF |
| FLPKDCGK_01929 | lptB_3 | -1.98 | yes | 3.24 | yes | -0.20 | yes | Lipopolysaccharide export system ATP-binding protein LptB |
| FLPKDCGK_01930 | gro_1 | -0.59 | yes | 2.50 | yes | -3.09 | yes | Glucosamine 5-dehydrogenase |
| FLPKDCGK_01932 | - | -1.08 | yes | 2.14 | yes | -3.23 | yes | |
| FLPKDCGK_01933 | fabG2 | -0.23 | yes | 0.27 | yes | -0.50 | yes | Putative oxidoreductase |
| FLPKDCGK_01934 | kipR_2 | -0.31 | yes | -0.23 | yes | -0.08 | yes | HTH-type transcriptional regulator KipR |
| FLPKDCGK_01947 | dhbF | -0.69 | yes | 0.13 | yes | -0.82 | yes | Diamino acid nonribosomal peptide synthase |
| FLPKDCGK_01952 | tctD_1 | -0.54 | yes | 0.13 | yes | -0.67 | yes | Transcriptional regulatory protein tctD |
| FLPKDCGK_01953 | qaeC_2 | 0.11 | yes | 1.27 | yes | -1.16 | yes | Sensor protein QaeC |
| FLPKDCGK_01954 | proP_3 | 2.39 | yes | 2.91 | yes | -0.52 | yes | Proline/betaine transporter |
| FLPKDCGK_01957 | dosC_2 | 0.24 | yes | -1.01 | yes | 1.25 | yes | Diguanylate cyclase DosC |
| FLPKDCGK_01958 | pyrB_1 | -1.52 | yes | -0.63 | yes | -0.89 | yes | Aspartate carbamoyltransferase catalytic subunit |
| **Resorcinol** | | | | | | | | |
| FLPKDCGK_03746 | yaJ_2 | 0.83 | yes | -0.56 | yes | 1.39 | yes | Inner membrane transport protein YaJ |
| FLPKDCGK_03748 | biC_1 | 0.44 | yes | -0.21 | yes | 0.66 | yes | Malonyl-[acyl-carrier protein] O-methyltransferase |
| FLPKDCGK_03751 | acuR | -0.13 | yes | -0.37 | yes | 0.24 | yes | Transcriptional regulator AcuR |
| FLPKDCGK_03754 | - | -2.51 | yes | -2.94 | yes | 0.43 | yes | |
| FLPKDCGK_03756 | gIC_2 | 0.40 | yes | -0.64 | yes | 1.04 | yes | Glic operon transcriptional activator |
| FLPKDCGK_03766 | fabI2 | 0.46 | yes | -0.30 | yes | 0.76 | yes | 3-oxoacyl-[acyl-carrier-protein] synthase 3 protein 2 |
| FLPKDCGK_03774 | yjE_8 | 0.95 | yes | 0.09 | yes | 1.04 | yes | Putative cystine transporter YjE |
| FLPKDCGK_03775 | bmc_3 | 0.82 | yes | 0.60 | yes | 0.23 | yes | Multidrug resistance protein 3 |
| FLPKDCGK_03777 | rkpK_2 | 0.51 | yes | 0.19 | yes | 0.32 | yes | UDP-glucose 6-dehydrogenase |
| FLPKDCGK_03778 | - | 0.68 | yes | 0.48 | yes | 0.20 | yes | UDP-glucose 4-epimerase |
| FLPKDCGK_03779 | pseB | 0.45 | yes | 0.24 | yes | 0.20 | yes | UDP-N-acetylglucosamine 4,6-dehydratase (inverting) |
| FLPKDCGK_03780 | pseC | 0.92 | yes | 0.41 | yes | 0.51 | yes | UDP-4-amino-4,6-dideoxy-N-acetyl-beta-L-altrosamine transaminase |

Gene expression used the logarithm in base 2 fold-change values calculated by DESeq2 after aligning the reads with StringTie when comparing the inoculum (LM) with 6 (t4) and 168 (t168) hours post-inoculation (hpi) into Arabidopsis leaves, and 6 with 168 hpi. Genes that are up-regulated are highlighted in cyan, while those that are down-regulated are highlighted in magenta. A column indicating if a gene was differentially regulated, as determined by DESeq2 or Cuffdiff (false discovery rate adjusted p < 0.05), is also shown. Gene clusters were identified as enriched using a hypergeometric enrichment test.
Table S9. Enrichment of plant-associated genes that were up-regulated within the differentially expressed genes in the transcriptome analysis.

| Strains                  | Comparison          | q-value |
|--------------------------|---------------------|---------|
| *Pseudomonas syringae*  | Up t<sub>6</sub> vs. KB | 1.000   |
| pv. *tomato* △hrcC△CFA  | Up t<sub>24</sub> vs. KB | 1.000   |
|                          | Up t<sub>168</sub> vs. KB | 1.000   |
|                          | Up Log vs. KB       | 1.000   |
|                          | Up Stat vs. KB      | 1.000   |
|                          | Up t<sub>6</sub> vs. t<sub>24</sub> | 0.015   |
|                          | Up t<sub>6</sub> vs. t<sub>168</sub> | 4.84E-05 |
|                          | Up t<sub>24</sub> vs. t<sub>168</sub> | 2.67E-05 |
|                          | Up t<sub>6</sub> vs. Log   | 4.32E-09 |
|                          | Up t<sub>6</sub> vs. Stat   | 0.003   |
|                          | Up t<sub>24</sub> vs. Log   | 2.86E-09 |
|                          | Up t<sub>24</sub> vs. Stat   | 1.99E-05 |
|                          | Up t<sub>168</sub> vs. Log  | 5.37E-07 |
|                          | Up t<sub>168</sub> vs. Stat  | 0.049   |
|                          | Up Log vs. Stat      | 1.000   |
| *Achromobacter xylosoxidans* Col-0-50 | Up t<sub>6</sub> vs. LM | 0.998   |
|                          | Up t<sub>24</sub> vs. LM  | 0.998   |
|                          | Up t<sub>168</sub> vs. LM | 0.998   |
|                          | Up t<sub>6</sub> vs. t<sub>24</sub> | 0.220   |
|                          | Up t<sub>6</sub> vs. t<sub>168</sub> | 0.658   |
|                          | Up t<sub>24</sub> vs. t<sub>168</sub> | 0.228   |
| *Pandoraea* sp. Col-0-28 | Up t<sub>6</sub> vs. LM | 0.072   |
|                          | Up t<sub>24</sub> vs. LM  | 0.182   |
|                          | Up t<sub>168</sub> vs. LM | 0.182   |
|                          | Up t<sub>6</sub> vs. t<sub>24</sub> | 0.002   |
|                          | Up t<sub>6</sub> vs. t<sub>168</sub> | 0.002   |
|                          | Up t<sub>24</sub> vs. t<sub>168</sub> | 0.002   |

The Benjamini-Hochberg adjusted p-value (q-value) for each hypergeometric enrichment test for up-regulated plant-associated genes is shown. Comparisons were performed between the inoculum (KB or LM), 6 (t<sub>6</sub>), 24 (t<sub>24</sub>), and 168 (t<sub>168</sub>) hours post-inoculation into Col-0 plants, and in vitro logarithmic (Log) and stationary (Stat) populations. Adjusted p-values that were significant (p < 0.05) are highlighted in cyan.
| Strains                          | Comments                                                                                     | References |
|--------------------------------|----------------------------------------------------------------------------------------------|------------|
| *Achromobacter xylosoxidans* Col-0–50 | Non-pathogenic Betaproteobacteria isolated from Arabidopsis Col-0 leaves. Kanamycin-resistant strain. | (32)       |
| *Escherichia coli* DH5α          | *E. coli* strain used for cloning of most constructs.                                         | (33)       |
| *E. coli* DH5α pUC18-mini-Tn7T-Gm | Strain used for integration of genes into the attTn7 site of *Pseudomonas*.                    | (5)        |
| *E. coli* MaH1                    | Strain is a derivative of *E. coli* DH5α with attTn7::pir116 integrated into the genome for expression of the \(\pi\) protein, which is necessary for R6K plasmid replication. | (9)        |
| *E. coli* PIR2 pBG42             | Strain used for integration of msfGFP into the attTn7 site of *Pseudomonas*.                   | (6)        |
| *E. coli* RH03 pTNS3             | Tn7 transposase helper strain, site-specific TnsD pathway only.                                | (8)        |
| *E. coli* RH05                    | *E. coli* SM10 derivative carrying the pir116 gene for replication of R6K plasmids. Used for conjugation of plasmids into *Pseudomonas*. | (9)        |
| *E. coli* RH05 pUC18-mini-Tn7T-Gm::tetR(BD)-\(\Pi_{tet}\)mCitrine_mCerulean3-BCD2-P\(_{14g}\) | Strain used for integration of a dual fluorescent reporter for cell division into the attTn7 site of *Pseudomonas*. \(mCitrine\) is under the control of a tetracycline inducible promoter, while \(mCerulean3\) is under the control of the constitutive promoter \(P_{14g}\) and the translational enhancer BCD2. | This study |
| *Pandoraea* sp. Col-0–28         | Non-pathogenic Betaproteobacteria isolated from Arabidopsis Col-0 leaves. Ampicillin-resistant strain. | (32)       |
| *Pseudomonas syringae* pv. *tomato* DC3000 | Rifampicin-resistant derivative from *Pseudomonas syringae* pv. *tomato* strain DC52. | (34)       |
| *Pst* DC3000 attTn7::tetR(BD)-\(\Pi_{tet}\)mCitrine_mCerulean3-BCD2-P\(_{14g}\) | *Pst* DC3000 strain carrying the cell division reporter: \(mCitrine\) expressed under the control of a tetracycline inducible promoter and \(mCerulean3\) under the control of the constitutive promoter \(P_{14g}\) and the translational enhancer BCD2. | This study |
| *Pst* DC3000 pDSK600::avrPphB     | *Pst* DC3000 expressing \(avrPphB\) effector from plasmid pPPY3031 (pDSK600::avrPphB). \(avrPphB\) is expressed under the control of a triple lacUV5 promoter. | (35)       |
| *Pst* DC3000 pDSK600::avrRpt2     | *Pst* DC3000 expressing \(avrRpt2\) effector from plasmid pDSK600.                             | (36)       |
| *Pst* DC3000 pVSP61::avrRps4     | *Pst* DC3000 expressing \(avrRps4\) effector from plasmid pVSP61.                            | (37)       |
| *Pst* \(\Delta hrcC\)\(\Delta CFA\) | Non-pathogenic *Pseudomonas syringae* strain with the coronafacic acid cluster (CFA; 11 genes are deleted) and a gene necessary for type III secretion system formation (hrcC) deleted. | (38)       |
| *Pst* \(\Delta hrcC\)\(\Delta CFA\) attTn7::tetR(BD)-\(\Pi_{tet}\)mCitrine_mCerulean3-BCD2-P\(_{14g}\) | Non-pathogenic *Pst* \(\Delta hrcC\)\(\Delta CFA\) strain carrying the cell division reporter: \(mCitrine\) expressed under the control of a tetracycline inducible promoter and \(mCerulean3\) under the control of the constitutive promoter \(P_{14g}\) and the translational enhancer BCD2. | This study |
| *Rhodococcus sp.* 964          | Non-pathogenic Actinobacteria strain isolated from Arabidopsis leaves. Rifampicin-resistant strain. | (39)       |
Table S11. Plant genotypes used in this study.

| Plant genotypes                        | Comments                                                                 | References |
|----------------------------------------|--------------------------------------------------------------------------|------------|
| *A. thaliana* Bu-22                    | Carries *RPS7*, a resistance locus that recognizes the *AvrPto* effector. | (13)       |
| *Arabidopsis thaliana* Col-0            |                                                                          |            |
| *A. thaliana* Col-0 *bak1-5 bkk1-1 cerk1* | Three genes involved in pattern recognition receptor signaling are mutated: *bak1*, *bkk1*, and *cerk1*. | (40)       |
Table S12. Primer sequences used in this study.

| Primer name | Primer sequence (5’ to 3’) | Comments | References |
|-------------|----------------------------|----------|------------|
| AVL001      | GCCTGCAAGGGAGCTCAGTGAATTAAGGCCATG   | Used with primer AVL002 to amplify the 14g promoter and BCD2 translational enhancer from pBG42 for Gibson assembly of pUC18-mini-Tn7T-Gm::tetR(BD)-P<sub>isr</sub>-mCitrine_mCerulean3-BCD2-P<sub>14g</sub>. In bold, sequence complementary to pUC18-mini-Tn7T-Gm. Used with primer AVL001 to amplify the 14g promoter and BCD2 translational enhancer from pBG42 for Gibson assembly of pUC18-mini-Tn7T-Gm::tetR(BD)-P<sub>isr</sub>-mCitrine_mCerulean3-BCD2-P<sub>14g</sub>. In bold, sequence complementary to mCerulean3. | This study |
| AVL002      | CCTCGCCCTTGCTCACCATTAGAAAACCTCCTTAGCATG | Used with primer AVL001 to amplify the 14g promoter and BCD2 translational enhancer from pBG42 for Gibson assembly of pUC18-mini-Tn7T-Gm::tetR(BD)-P<sub>isr</sub>-mCitrine_mCerulean3-BCD2-P<sub>14g</sub>. In bold, sequence complementary to mCerulean3. | This study |
| AVL003      | CATGCTAAGGAGCTTTCTAATGTCGAGGAGG     | Used with primer AVL004 for Gibson assembly of pUC18-mini-Tn7T-Gm::tetR(BD)-P<sub>isr</sub>-mCitrine_mCerulean3-BCD2-P<sub>14g</sub>. In bold, sequence complementary to the BCD2 translational enhancer. | This study |
| AVL004      | CCGAGAcCGAAGGCACTA                   | Used with primer AVL003 for Gibson assembly of pUC18-mini-Tn7T-Gm::tetR(BD)-P<sub>isr</sub>-mCitrine_mCerulean3-BCD2-P<sub>14g</sub>. | This study |
| AVL005      | GTTACGCGAGCAGACAATCCT                | Used with primer AVL006 to check for transposants while with primer AVL007, it is used to check for bacteria in which transposition has not occurred. Primer hybridizes near the 5’ end of the CDS of PSPTO_5594. | Kvitko lab (University of Georgia) |
| AVL006      | ATTACGCGAGCAGCTACACCC                | Used with primer AVL005 to check for transposants. | Kvitko lab (University of Georgia) |
| AVL007      | GCAGCGCCTTTCTGATATTG                 | Used with primer AVL008 to check for transposants while with primer AVL005, it is used to check for bacteria in which transposition has not occurred. Primer hybridizes near the 3’ end of glmS (PSPTO_5595). | Kvitko lab (University of Georgia) |
| AVL008      | CACAGCATAACTGAGCTGATTTC              | Used with primer AVL007 to check for transposants. | Kvitko lab (University of Georgia) |
| AVL009      | TGTGACTcatATGGTCGATTTGCCAGG          | Used with primer AVL010 to amplify hpa (PSPTO_1381) from Pseudomonas syringae pv. tomato (Pst) DC3000 to check for genomic DNA contamination in RNA samples. In lowercase, an added NdeI site. | This study |
| AVL010      | GCGagaattcTTAGTAACTGATACCTTTAGCG    | Used with primer AVL009 to amplify hpa (PSPTO_1381) from Pst DC3000 to check for genomic DNA contamination in RNA samples. In lowercase, an added EcoRI site. | This study |
| Primer name | Primer sequence (5’ to 3’) | Comments | References |
|-------------|----------------------------|----------|------------|
| AVL011      | GAAACTGATCGACTTGCAGG       | Used with primer AVL012 to amplify rpoD (FEPFGCPE_00166) of *Pandoraea* sp. Col-0-28 to check for genomic DNA contamination in RNA samples. | This study |
| AVL012      | ATGTGCACCGGAATAACGGAT      | Used with primer AVL011 to amplify rpoD (FEPFGCPE_00166) of *Pandoraea* sp. Col-0-28 to check for genomic DNA contamination in RNA samples. | This study |
| AVL013      | TGCAGTGGGTCGTCGACGAA       | Used with primer AVL014 to amplify rpoD1 (FLPKDCKG_00166) of *Achromobacter xylosoxidans* Col-0-50 to check for genomic DNA contamination in RNA samples. | This study |
| AVL014      | CGACGGTGACTCGAATTTGTC      | Used with primer AVL013 to amplify rpoD1 (FLPKDCKG_00166) of A. *xylosoxidans* Col-0-50 to check for genomic DNA contamination in RNA samples. | This study |
| AVL015      | ATCTCATACTGACCCATATGTTCC   | Used with primer AVL016 to amplify microsatellite marker nga151a from *Arabidopsis thaliana* to check for genomic DNA contamination in RNA samples. | (41) |
| AVL016      | ATTGTACAGTCTAAAACGGAGAG    | Used with primer AVL015 to amplify microsatellite marker nga151a from A. *thaliana* to check for genomic DNA contamination in RNA samples. | (41) |
| AVL017      | CTGACCGGTCGACATCATATT      | Used with primer AVL018 for quantitative real-time PCR (qRT-PCR) of reference *Pst* DC3000 gene leuB (PSPTO_2175). | This study |
| AVL018      | ATTTGCCTCTCGCTGATGACG     | Used with primer AVL017 for qRT-PCR of reference *Pst* DC3000 gene leuB (PSPTO_2175). | This study |
| AVL019      | GTCTCCAGAGCGATTTGTTG       | Used with primer AVL020 for qRT-PCR of *Pst* DC3000 effector gene avrPto (PSPTO_4001). | (42) |
| AVL020      | GGGCTAGAGAAAAGTGTGGA     | Used with primer AVL019 for qRT-PCR of *Pst* DC3000 effector gene avrPto (PSPTO_4001). | (42) |
| AVL021      | TGCTCGTCTCGCTGCAAGG      | Used with primer AVL022 for qRT-PCR of *Pst* DC3000 cfl (PSPTO_4680); a coronafacic acid ligase involved in the biosynthesis of the toxin coronatine. | (38) |
| AVL022      | CGATACCTTATGTTAGTCTCGG    | Used with primer AVL021 for qRT-PCR of *Pst* DC3000 cfl (PSPTO_4680); a coronafacic acid ligase involved in the biosynthesis of the toxin coronatine. | (38) |
| AVL023      | CAACATGACATCCCGGTCA      | Used with primer AVL024 for qRT-PCR of *Pst* DC3000 fmt (PSPTO_0178), a tRNA<sup>Met</sup>-formyl transferase involved in formylating the methionine of the initiator tRNA. | This study |
| Primer name | Primer sequence (5' to 3') | Comments | References |
|-------------|-----------------------------|----------|------------|
| AVL024      | CGGAATATCCAGACCACACTT       | Used with primer AVL023 for qRT-PCR of Pst DC3000 fmt (PSPTO_0178), a tRNA<sup>™</sup>-formyl transferase involved in formylating the methionine of the initiator tRNA. | This study |
| AVL025      | TCACCATTCCCAACGAGAAG         | Used with primer AVL026 for qRT-PCR of Pst DC3000 cell division gene ftsZ (PSPTO_4403). | This study |
| AVL026      | CGCTTGATGATGTCGGAGATA        | Used with primer AVL025 for qRT-PCR of Pst DC3000 cell division gene ftsZ (PSPTO_4403). | This study |
| AVL027      | AGATGCTCAGGGCGTTTATC         | Used with primer AVL028 for qRT-PCR of Pst DC3000 hrsL RNA polymerase sigma factor (PSPTO_1404). | This study |
| AVL028      | ACGCAGGGCTTCAAGAAA           | Used with primer AVL027 for qRT-PCR of Pst DC3000 hrsL RNA polymerase sigma factor (PSPTO_1404). | Kvitko lab (University of Georgia) |
| AVL029      | TGAAGGTCGTTGACAAATTC         | Used with primer AVL030 for qRT-PCR of Pst DC3000 gene PSPTO_4337, which encodes a pyruvate kinase involved in the Entner-Doudoroff pathway. | This study |
| AVL030      | CCGCAATCCTTGACCAGAT          | Used with primer AVL029 for qRT-PCR of Pst DC3000 gene PSPTO_4337, which encodes a pyruvate kinase involved in the Entner-Doudoroff pathway. | This study |
| AVL031      | CAACTCGGTTGACGAAGATAAC       | Used with primer AVL032 for qRT-PCR of Pst DC3000 housekeeping RNA polymerase sigma factor rpoD (PSPTO_0537). | This study |
| AVL032      | GCTTTGAGGTGCTTGTTACTA        | Used with primer AVL031 for qRT-PCR of Pst DC3000 housekeeping RNA polymerase sigma factor rpoD (PSPTO_0537). | This study |
| AVL033      | TACAACGCCATCCACCGCAA         | Primer specific for mCerulean3 that will not hybridize with the sequence of mCitrine. Used for sequencing. | This study |
| AVL034      | GAACCTTCAAGATCCGCACCA        | Primer specific for mCitrine that will not hybridize with the sequence of mCerulean3. Used for sequencing. | This study |
Table S13. Comparison of the three different methods used to determine differential gene expression in *Pseudomonas syringae pv. tomato ΔhrcCΔCFA*.

| Comparison                     | Unique to DESStringTie | Unique to DESalmon | Unique to Cuffdiff | DESStringTie and DESalmon | DESStringTie and Cuffdiff | DESalmon and Cuffdiff | Shared by all methods | Total DEGs |
|--------------------------------|------------------------|--------------------|--------------------|---------------------------|---------------------------|--------------------------|-----------------------|-------------|
| t<sub>6</sub> vs. t<sub>24</sub> | 90                     | 158                | 18                 | 177                       | 9                         | 5                        | 58                    | 425         |
| t<sub>6</sub> vs. t<sub>168</sub> | 284                    | 289                | 7                  | 701                       | 11                        | 1                       | 229                   | 1,238       |
| t<sub>6</sub> vs. Inoculum    | 148                    | 388                | 224                | 343                       | 118                       | 76                       | 1,505                 | 2,654       |
| t<sub>6</sub> vs. Logarithmic | 205                    | 184                | 220                | 336                       | 160                       | 67                       | 1,684                 | 2,651       |
| t<sub>24</sub> vs. Stationary | 171                    | 192                | 203                | 258                       | 162                       | 58                       | 1,247                 | 2,120       |
| t<sub>24</sub> vs. t<sub>168</sub> | 275                    | 285                | 9                  | 674                       | 6                         | 2                        | 146                   | 1,122       |
| t<sub>24</sub> vs. Inoculum   | 203                    | 269                | 125                | 436                       | 91                        | 46                       | 1,311                 | 2,278       |
| t<sub>24</sub> vs. Logarithmic | 222                    | 176                | 131                | 464                       | 112                       | 32                       | 1,595                 | 2,510       |
| t<sub>24</sub> vs. Stationary | 215                    | 189                | 111                | 378                       | 113                       | 45                       | 1,106                 | 1,942       |
| t<sub>168</sub> vs. Inoculum  | 292                    | 468                | 14                 | 985                       | 17                        | 18                       | 926                   | 2,428       |
| t<sub>168</sub> vs. Logarithmic | 415                    | 291                | 24                 | 1,077                      | 37                        | 12                       | 1,017                 | 2,458       |
| t<sub>168</sub> vs. Stationary | 286                    | 320                | 23                 | 870                       | 34                        | 12                       | 624                   | 1,883       |
| Inoculum vs. Logarithmic      | 77                     | 89                 | 1,221              | 79                        | 223                       | 243                      | 2,326                 | 4,181       |
| Inoculum vs. Stationary       | 57                     | 196                | 1,308              | 50                        | 155                       | 259                      | 1,548                 | 3,516       |
| Logarithmic vs. Stationary    | 38                     | 34                 | 2,077              | 18                        | 354                       | 150                      | 1,434                 | 4,067       |

Differential gene expression was determined by either of three methods: DESeq2 after pseudo-alignment with Salmon (DESalmon), DESeq2 after alignment with HISAT2 and analysis with StringTie (DEStringTie), and Cuffdiff after alignment with HISAT2 (Cuffdiff), when comparing the inoculum, 6 (t<sub>6</sub>), 24 (t<sub>24</sub>) and 168 (t<sub>168</sub>) hours post-inoculation into Arabidopsis leaves, and *in vitro* cultures grown to logarithmic or stationary phase. The number of differentially expressed genes (false discovery rate adjusted *p*-value less than 0.05) unique or shared by these analyses is shown.
Table S14. Comparison of the three different methods used to determine differential gene expression in *Achromobacter xylosoxidans* Col-0-50.

| Comparison        | Unique to DEStringTie | Unique to DESalmon | Unique to Cuffdiff | DEStringTie and DESalmon | DEStringTie and Cuffdiff | DESalmon and Cuffdiff | Shared by all methods | Total DEGs |
|-------------------|------------------------|--------------------|--------------------|--------------------------|--------------------------|------------------------|------------------------|-------------|
| t6 vs. t24        | 55                     | 34                 | 67                 | 65                       | 18                       | 7                      | 128                    | 319         |
| t6 vs. t168       | 167                    | 122                | 23                 | 344                      | 32                       | 3                      | 459                    | 983         |
| t6 vs. Inoculum   | 46                     | 32                 | 567                | 145                      | 153                      | 36                     | 938                    | 1,871       |
| t24 vs. t168      | 145                    | 74                 | 10                 | 252                      | 19                       | 6                      | 216                    | 577         |
| t24 vs. Inoculum  | 71                     | 57                 | 382                | 227                      | 140                      | 37                     | 996                    | 1,839       |
| t168 vs. Inoculum | 147                    | 105                | 132                | 404                      | 68                       | 23                     | 909                    | 1,641       |

Differential gene expression was determined by either of three methods: DESeq2 after pseudo-alignment with Salmon (DESalmon), DESeq2 after alignment with HISAT2 and analysis with StringTie (DEStringTie), and Cuffdiff after alignment with HISAT2 (Cuffdiff), when comparing the inoculum, 6 (t6), 24 (t24), and 168 (t168) hours post-inoculation into Arabidopsis leaves. The number of differentially expressed genes (false discovery rate adjusted p-value less than 0.05) unique or shared by these analyses is shown.
**Table S15.** Comparison of the three different methods used to determine differential gene expression in *Pandoraea* sp. Col-0-28.

| Comparison          | Unique to DEStringTie | Unique to DESalmon | Unique to Cuffdiff | DEStringTie and DESalmon | DEStringTie and Cuffdiff | DESalmon and Cuffdiff | Shared by all methods | Total DEGs |
|---------------------|-----------------------|--------------------|--------------------|--------------------------|--------------------------|------------------------|------------------------|------------|
| \(t_6\) vs. \(t_{24}\) | 32                    | 40                 | 29                 | 68                       | 9                        | 14                     | 169                    | 329        |
| \(t_6\) vs. \(t_{168}\) | 157                   | 131                | 26                 | 260                      | 40                       | 13                     | 513                    | 983        |
| \(t_6\) vs. Inoculum | 25                    | 36                 | 422                | 35                       | 66                       | 85                     | 670                    | 1,314      |
| \(t_{24}\) vs. \(t_{168}\) | 111                   | 99                 | 25                 | 192                      | 28                       | 5                      | 221                    | 570        |
| \(t_{24}\) vs. Inoculum | 25                    | 34                 | 302                | 49                       | 62                       | 102                    | 715                    | 1,264      |
| \(t_{168}\) vs. Inoculum | 129                   | 115                | 105                | 175                      | 77                       | 40                     | 843                    | 1,355      |

Differential gene expression was determined by either of three methods: DESeq2 after pseudo-alignment with Salmon (DESalmon), DESeq2 after alignment with HISAT2 and analysis with StringTie (DEStringTie), and Cuffdiff after alignment with HISAT2 (Cuffdiff), when comparing the inoculum, 6 (\(t_6\)), 24 (\(t_{24}\)) and 168 (\(t_{168}\)) hours post-inoculation into Arabidopsis leaves. The number of differentially expressed genes (false discovery rate adjusted \(p\)-value less than 0.05) unique or shared by these analyses is shown.
**Dataset S1.** Average gene expression in *Pseudomonas syringae* pv. *tomato ΔhrcCΔCFA*. (A) Average gene expression in *Pseudomonas syringae* pv. *tomato ΔhrcCΔCFA* calculated using DESeq2 after StringTie read alignment. Gene expression used the logarithm in base 2 fold-change values calculated by DESeq2 after aligning the reads with StringTie, when comparing the inoculum (KB), 6 (t₆), 24 (t₂₄) and 168 (t₁₆₈) hours post-inoculation into Arabidopsis leaves, and in vitro cultures grown to logarithmic or stationary phase. Each treatment had four biological replicates. p-values and false discovery rate adjusted p-values (q-values) calculated by DESeq2 for each comparison are shown. Extreme outliers and zero read counts cause DESeq2 to not perform statistical analyses and set the p-values to NA. When available, gene name for each locus is shown. DNA template strand, coordinates for the start and end of each gene, and a brief annotation are also shown. (B) Average gene expression in *Pseudomonas syringae* pv. *tomato ΔhrcCΔCFA* calculated using DESeq2 after Salmon read alignment. Gene expression used the logarithm in base 2 fold-change values calculated by DESeq2 after aligning the reads with Salmon, when comparing the inoculum (KB), 6 (t₆), 24 (t₂₄) and 168 (t₁₆₈) hours post-inoculation into Arabidopsis leaves, and in vitro cultures grown to logarithmic or stationary phase. Each treatment had four biological replicates. p-values and false discovery rate adjusted p-values (q-values) calculated by DESeq2 for each comparison are shown. Extreme outliers and zero read counts cause DESeq2 to not perform statistical analyses and set the p-values to NA. When available, gene name for each locus is shown. DNA template strand, coordinates for the start and end of each gene, and a brief annotation are also shown. (C) Average gene expression in *Pseudomonas syringae* pv. *tomato ΔhrcCΔCFA* calculated using Cuffdiff. Gene expression used the logarithm in base 2 fold-change values calculated by Cuffdiff, when comparing the inoculum (KB), 6 (t₆), 24 (t₂₄) and 168 (t₁₆₈) hours post-inoculation into Arabidopsis leaves, and in vitro cultures grown to logarithmic or stationary phase. Each treatment had four biological replicates. p-values and false discovery rate adjusted p-values (q-values) calculated by Cuffdiff for each comparison are shown. Zero read counts cause Cuffdiff to set the log₂ fold-change values to −Inf (−) or Inf. When available, gene name for each locus is shown. DNA template strand, coordinates for the start and end of each gene, and a brief annotation are also shown.

**Dataset S2.** Average gene expression in *Achromobacter xylosoxidans* Col-0-50. (A) Average gene expression in *Achromobacter xylosoxidans* Col-0-50 calculated using DESeq2 after StringTie read alignment. Gene expression used the logarithm in base 2 fold-change values calculated by DESeq2 after aligning the reads with StringTie, when comparing the inoculum (LM), 6 (t₆), 24 (t₂₄) and 168 (t₁₆₈) hours post-inoculation into Arabidopsis leaves. Each treatment had four biological replicates. p-values and false discovery rate adjusted p-values (q-values) calculated by DESeq2
for each comparison are shown. Extreme outliers and zero read counts causes DESeq2 to not perform statistical analyses and set the \( p \)-values to NA. When available, gene name for each locus is shown. DNA template strand, coordinates for the start and end of each gene, and a brief annotation are also shown. (B) Average gene expression in *Achromobacter xylosoxidans* Col-0-50 calculated using DESeq2 after Salmon read alignment. Gene expression used the logarithm in base 2 fold-change values calculated by DESeq2 after aligning the reads with Salmon, when comparing the inoculum (LM), 6 (\( t_6 \)), 24 (\( t_{24} \)) and 168 (\( t_{168} \)) hours post-inoculation into Arabidopsis leaves. Each treatment had four biological replicates. \( p \)-values and false discovery rate adjusted \( p \)-values (\( q \)-values) calculated by DESeq2 for each comparison are shown. Extreme outliers and zero read counts causes DESeq2 to not perform statistical analyses and set the \( p \)-values to NA. When available, gene name for each locus is shown. DNA template strand, coordinates for the start and end of each gene, and a brief annotation are also shown. (C) Average gene expression in *Achromobacter xylosoxidans* Col-0-50 calculated using Cuffdiff. Gene expression used the logarithm in base 2 fold-change values calculated by Cuffdiff, when comparing the inoculum (LM), 6 (\( t_6 \)), 24 (\( t_{24} \)) and 168 (\( t_{168} \)) hours post-inoculation into Arabidopsis leaves. Each treatment had four biological replicates. \( p \)-values and false discovery rate adjusted \( p \)-values (\( q \)-values) calculated by Cuffdiff for each comparison are shown. Zero read counts causes Cuffdiff to set the log\(_2\) fold-change values to \(-\infty\) \((-\)\) or \(\infty\). When available, gene name for each locus is shown. DNA template strand, coordinates for the start and end of each gene, and a brief annotation are also shown.

**Dataset S3.** Average gene expression in *Pandoraea* sp. Col-0-28. (A) Average gene expression in *Pandoraea* sp. Col-0-28 calculated using DESeq2 after StringTie read alignment. Gene expression used the logarithm in base 2 fold-change values calculated by DESeq2 after aligning the reads with StringTie, when comparing the inoculum (LM), 6 (\( t_6 \)), 24 (\( t_{24} \)) and 168 (\( t_{168} \)) hours post-inoculation into Arabidopsis leaves. Each treatment had four biological replicates. \( p \)-values and false discovery rate adjusted \( p \)-values (\( q \)-values) calculated by DESeq2 for each comparison are shown. Extreme outliers and zero read counts causes DESeq2 to not perform statistical analyses and set the \( p \)-values to NA. When available, gene name for each locus is shown. DNA template strand, coordinates for the start and end of each gene, and a brief annotation are also shown. (B) Average gene expression in *Pandoraea* sp. Col-0-28 calculated using DESeq2 after Salmon read alignment. Gene expression used the logarithm in base 2 fold-change values calculated by DESeq2 after aligning the reads with Salmon, when comparing the inoculum (LM), 6 (\( t_6 \)), 24 (\( t_{24} \)) and 168 (\( t_{168} \)) hours post-inoculation into Arabidopsis leaves. Each treatment had four biological replicates. \( p \)-values and false discovery rate adjusted \( p \)-values (\( q \)-values) calculated by DESeq2
for each comparison are shown. Extreme outliers and zero read counts causes DESeq2 to not perform statistical analyses and set the p-values to NA. When available, gene name for each locus is shown. DNA template strand, coordinates for the start and end of each gene, and a brief annotation are also shown. (C) Average gene expression in Pandoraea sp. Col-0-28 calculated using Cuffdiff. Gene expression used the logarithm in base 2 fold-change values calculated by Cuffdiff, when comparing the inoculum (LM), 6 (t₆), 24 (t₂₄) and 168 (t₁₆₈) hours post-inoculation into Arabidopsis leaves. Each treatment had four biological replicates. p-values and false discovery rate adjusted p-values (q-values) calculated by Cuffdiff for each comparison are shown. Zero read counts causes Cuffdiff to set the log₂ fold-change values to –Inf (–) or Inf. When available, gene name for each locus is shown. DNA template strand, coordinates for the start and end of each gene, and a brief annotation are also shown.

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