

## SUPPORTING INFORMATION

### Spermine deficiency shifts the balance between Jasmonic Acid and Salicylic Acid-mediated defense responses in Arabidopsis

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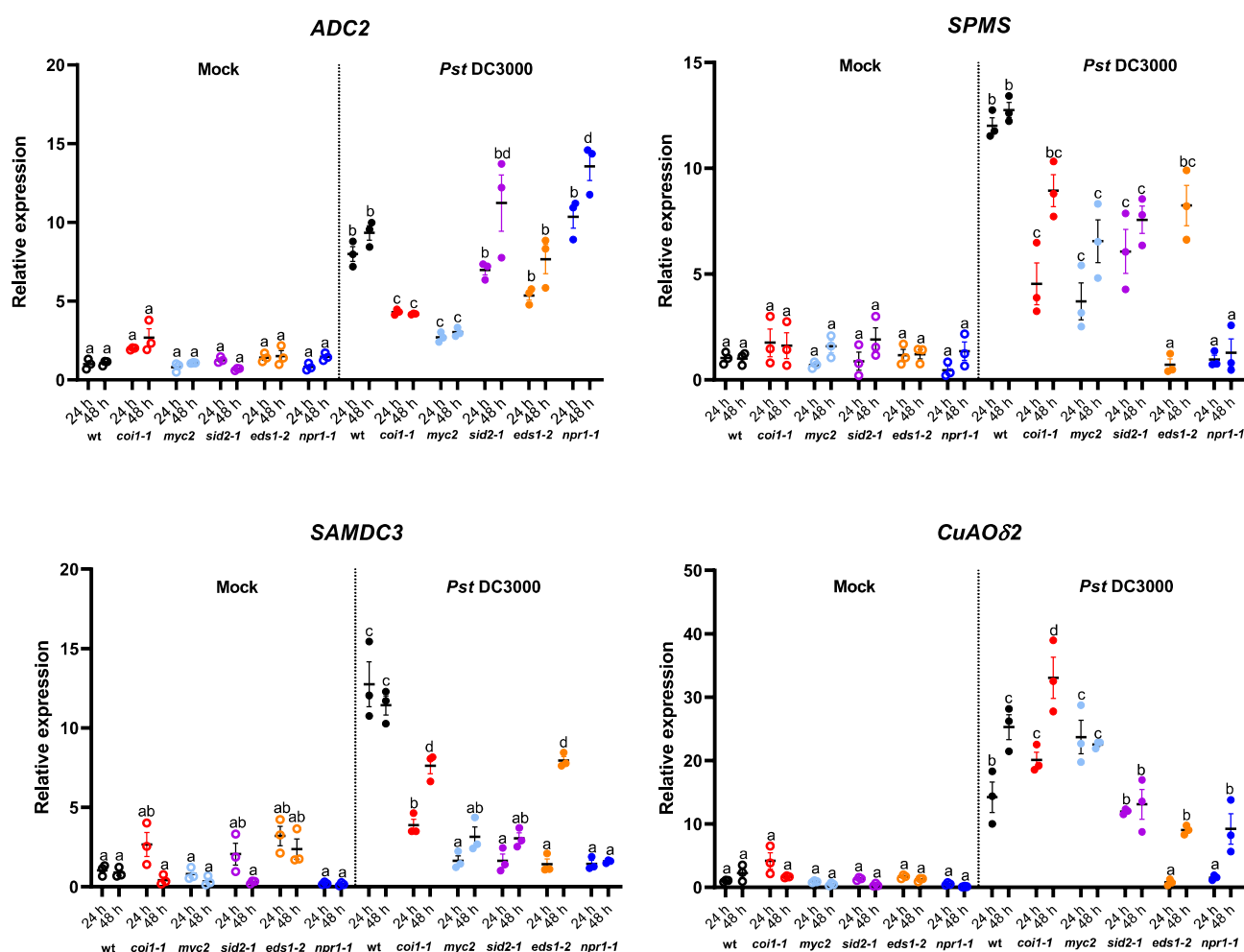
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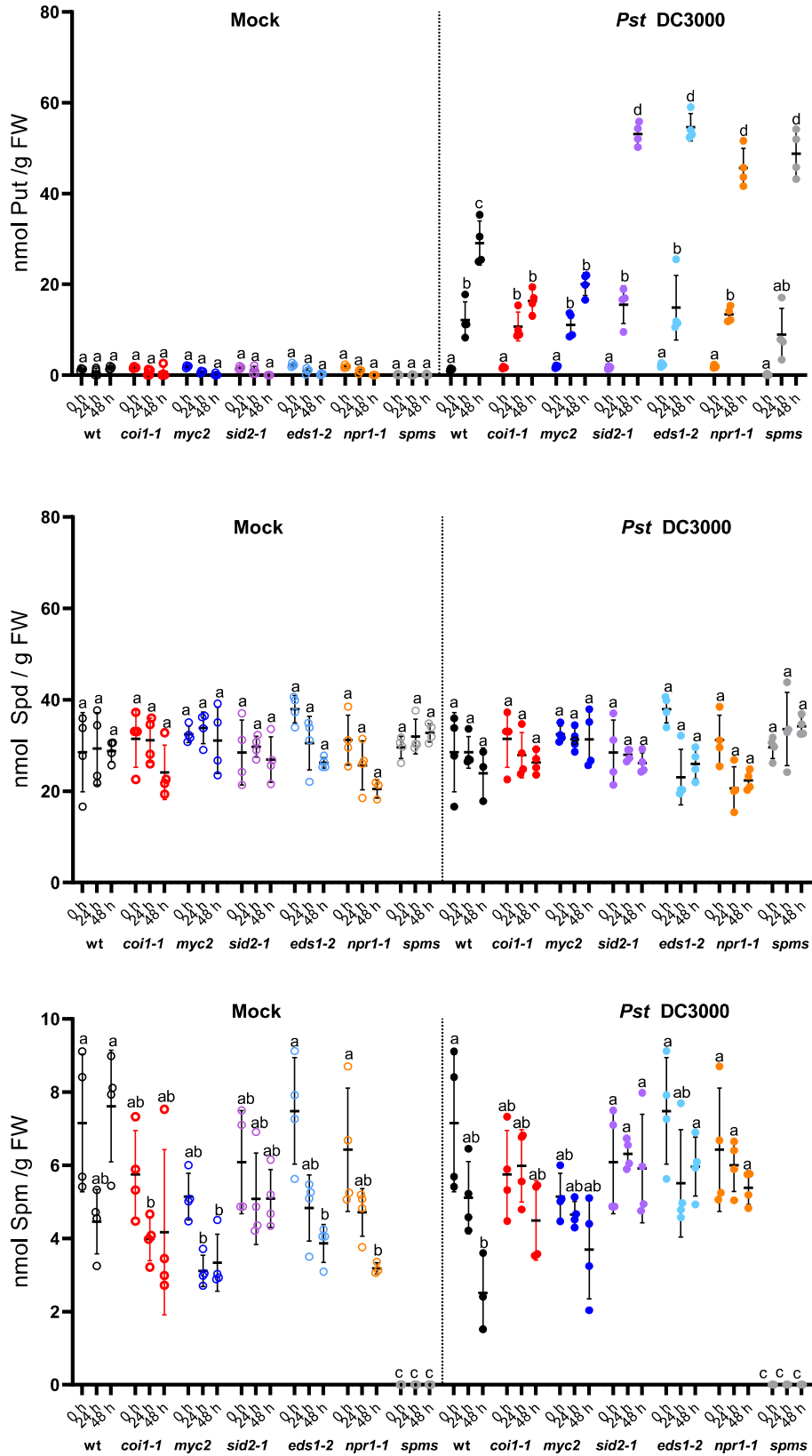
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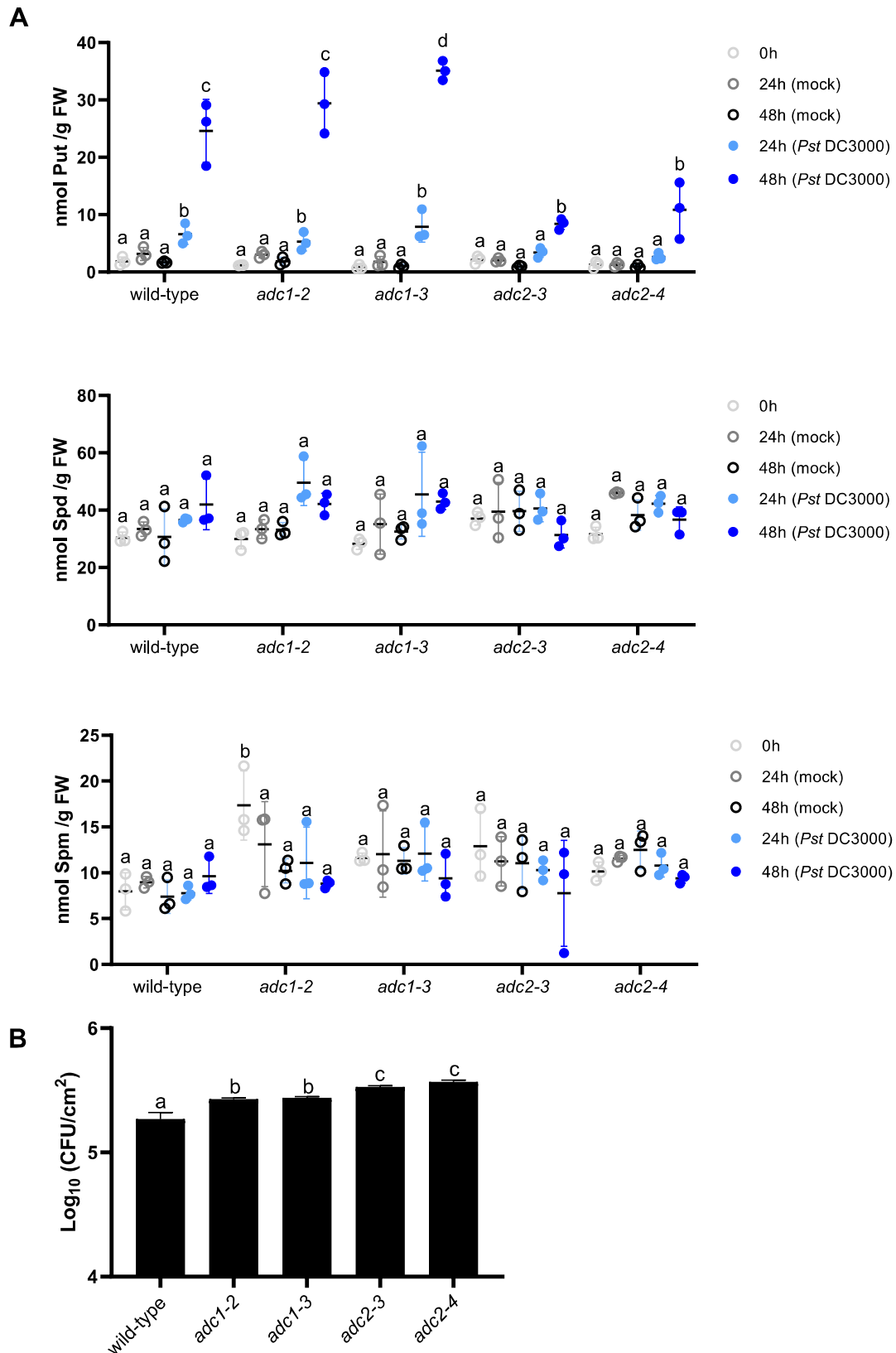
## SUPPLEMENTARY FIGURES



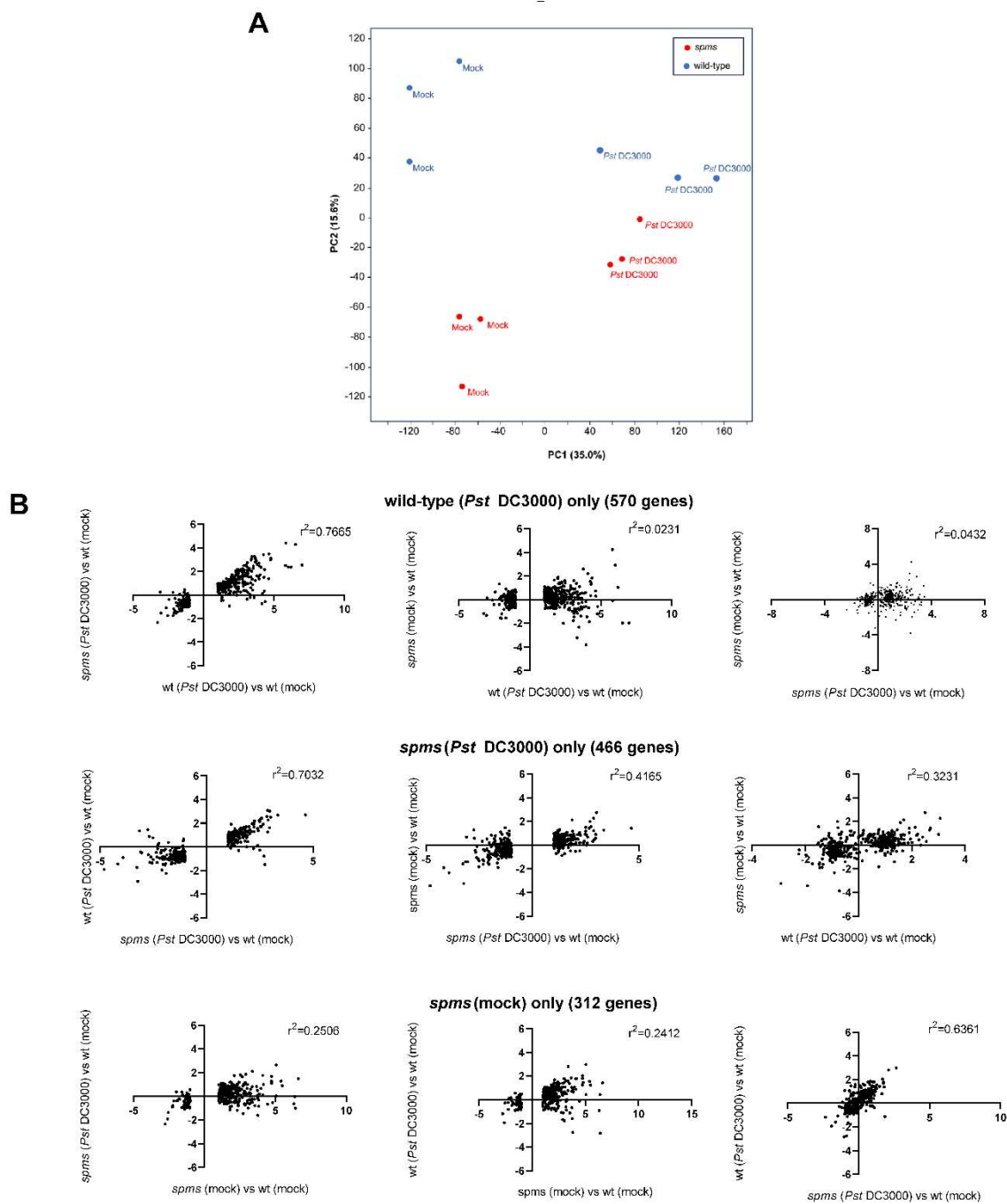
**Figure S1.** Expression analyses of *ADC2*, *SPMS*, *SAMDC3* and *CuAOδ2* in wild-type, *coil-1*, *myc2*, *sid2-1*, *eds1-2* and *npr1-1* mutants in response to *Pst* DC3000 (OD<sub>600</sub>=0.001) and mock (10 mM MgCl<sub>2</sub>) infiltration at 24 h and 48 h of treatment. Expression values are relative to wild-type (mock) treatment and represent the mean ± standard deviation from three biological replicates per genotype and treatment. Different letters indicate significant differences (p < 0.05) according to two-way ANOVA followed by Tukey's post-hoc test.



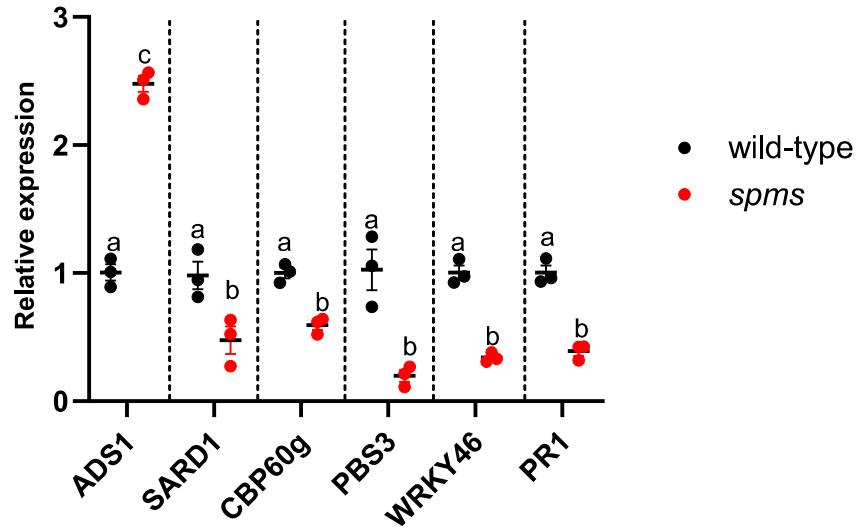
**Figure S2.** Determination of polyamine contents in wild-type (wt), *coi1-1*, *myc2*, *sid2-1*, *eds1-2* and *npr1-1* mutants in response to *Pst* DC3000 (OD<sub>600</sub>=0.001) and mock (10 mM MgCl<sub>2</sub>) infiltration at 0 h, 24 h and 48 h of treatment. Values represent the mean ± standard deviation from four biological replicates per genotype. Different letters indicate significant differences (p<0.05) according to two-way ANOVA followed by Tukey's post-hoc test.



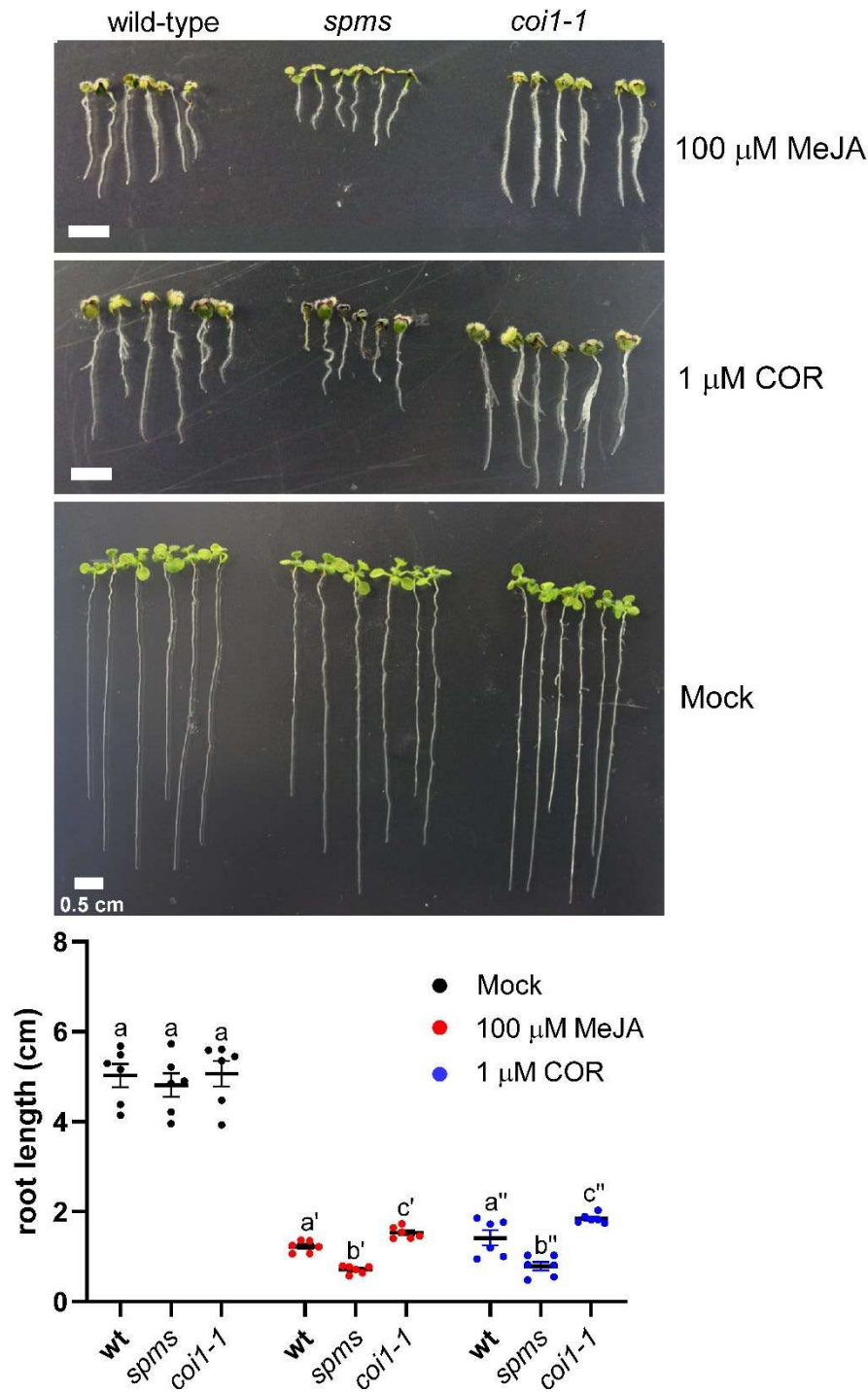
**Figure S3. (A)** Determination of polyamine contents in wild-type, *adc1-2*, *adc1-3*, *adc2-3* and *adc2-4* mutants in response to *Pst* DC3000 (OD<sub>600</sub>=0.001) and mock (10 mM MgCl<sub>2</sub>) infiltration at 0 h, 24 h and 48 h of treatment. Values represent the mean  $\pm$  standard deviation from three biological replicates per genotype. **(B)** Determination of *Pst* DC3000 growth in wild-type, *adc1* and *adc2* mutants at 48 h of infiltration. Bacterial numbers are expressed as colony forming units (CFU) per cm<sup>2</sup> of leaf area. Values are the mean from six biological replicates  $\pm$  SD. Different letters indicate significant differences (p<0.05) according to two-way ANOVA followed by Tukey's post-hoc test.



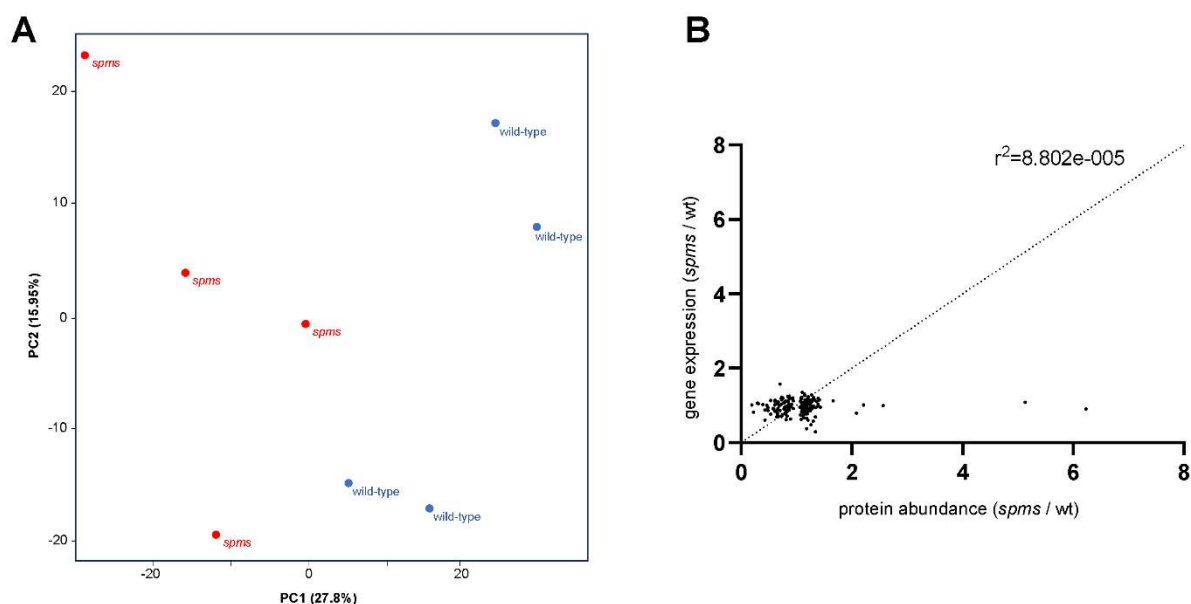
**Figure S4. (A)** Principal component analysis (PCA) of RNA-seq gene expression data at 24 h of *Pst* DC3000 ( $OD_{600}=0.001$ ) and mock (10 mM  $MgCl_2$ ) inoculation in *spms* and wild-type plants. **(B)** Expression correlation analyses between wild-type (wt) and *spms* in the ‘wild-type (*Pst* DC3000) only’ sector (genes deregulated only in the comparison between wt *Pst* DC3000 vs wt mock), ‘*spms* (*Pst* DC3000) only’ sector (genes deregulated only in the comparison between *spms* *Pst* DC3000 vs wt mock) and ‘*spms* (mock) only’ sector (genes deregulated only in the comparison between *spms* mock vs wt mock).



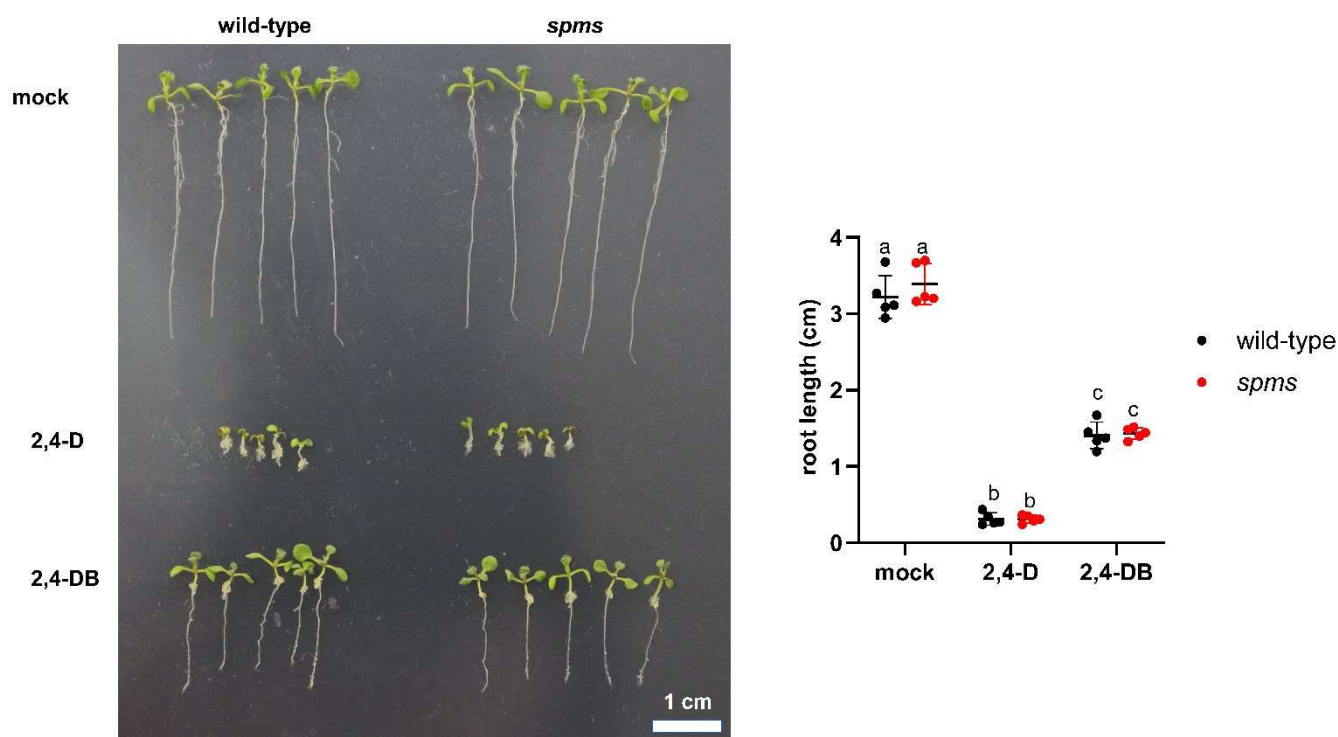
**Figure S5.** Basal expression of *ADS1*, *SARD1*, *CBP60g*, *PBS3*, *WRKY46* and *PR1* in wild-type and *spms* mutant plants determined by qRT-PCR. Expression values are relative to the wild-type and represent the mean  $\pm$  standard deviation from three biological replicates per genotype. Different letters indicate significant differences ( $p < 0.05$ ) according to two-way ANOVA followed by Tukey's post-hoc test.



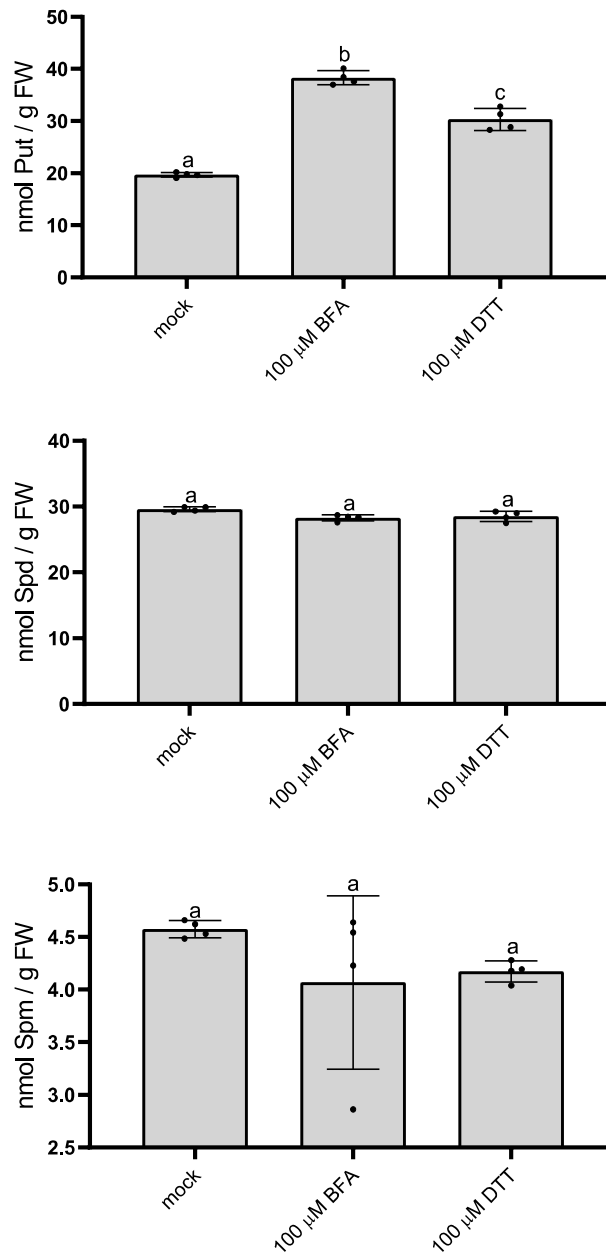
**Figure S6.** Root growth inhibition assays in response to MeJA and COR. Wild-type (wt), *spms* and *coi1-1* seeds were germinated and grown on vertical plates containing half-strength MS supplemented with 1% sucrose and 100  $\mu$ M methyl jasmonate (MeJA), 1  $\mu$ M coronatine (COR) or mock (0.1% DMSO in water) at 16 h light/8 h dark cycles, 20 – 22  $^{\circ}$ C and 100–125  $\mu$ mol photons  $m^{-2} s^{-1}$  of light intensity. Pictures were taken 12 days after germination for the measurement of the primary root length. Different letters indicate significant differences ( $p < 0.05$ ) according to two-way ANOVA followed by Tukey's post-hoc test.



**Figure S7. (A)** Principal component analysis (PCA) of the proteomics data in *spms* and wild-type under basal conditions. **(B)** Correlation analysis between protein abundance and gene expression in *spms* under basal conditions. Values of proteins exhibiting >1.3-fold difference between *spms* and wild-type are shown.



**Figure S8.** Root growth phenotypes of 12-day-old wild-type and *spms* seedlings germinated and grown on half-strength MS supplemented with 1 % sucrose and 0.05  $\mu\text{g/ml}$  2,4-dichlorophenoxyacetic acid (2,4-D), 0.2  $\mu\text{g/ml}$  2,4-dichlorophenoxybutyric acid (2,4-DB) or mock (0.1% DMSO in water). Different letters indicate significant differences ( $p < 0.05$ ) according to two-way ANOVA followed by Tukey's post-hoc test.



**Figure S9.** Polyamine levels (Put, putrescine; Spd, spermidine; Spm, spermine) in 10-day-old wild-type seedlings at 6 h of treatment with 100 μM Brefeldin A (BFA), 100 μM DTT (dithiothreitol) or mock (0.1% DMSO in water). Values represent the mean ± standard deviation from four biological replicates per treatment. Different letters indicate significant differences ( $p < 0.05$ ) according to two-way ANOVA followed by Tukey's post-hoc test.



## SUPPLEMENTARY TABLES

**Table S1.** List of oligonucleotides used in this work.

**Table S2.1.** List of 1867 differentially expressed genes (fold-change>2; Bonferroni corrected p-value <0.05) in the comparison between wild-type inoculated with *Pst* DC3000 and wild-type inoculated with mock (10 mM MgCl<sub>2</sub>) at 24 h of treatment.

**Table S2.2.** List of 1793 differentially expressed in the comparison between *spms* inoculated with *Pst* DC3000 and wild-type inoculated with mock (10 mM MgCl<sub>2</sub>) at 24 h of treatment.

**Table S2.3.** List of 1078 common differentially expressed genes between [*spms* (*Pst* DC3000) vs wild-type (mock)] and [wild-type (*Pst* DC3000) vs wild-type (mock)] at 24 h of treatment.

**Table S2.4.** Gene ontology (GO) enrichment analysis of genes in Table S1.3

**Table S2.5.** List of 570 genes differentially expressed only in the wild-type inoculated with *Pst* DC3000 at 24 h of treatment ('wild-type *Pst* DC3000 only')

**Table S2.6.** Gene ontology (GO) enrichment analysis of genes in Table S1.5

**Table S2.7.** List of 466 genes differentially expressed only in the *spms* mutant inoculated with *Pst* DC3000 at 24 h of treatment ('*spms Pst* DC3000 only')

**Table S2.8.** Gene ontology (GO) enrichment analysis of genes in Table S1.7

**Table S2.9.** List of 608 differentially expressed in the comparison between *spms* inoculated with mock (10 mM MgCl<sub>2</sub>) vs wild-type inoculated with mock (10 mM MgCl<sub>2</sub>) at 24 h of treatment.

**Table S2.10.** Gene ontology (GO) enrichment analysis of genes in Table S1.9

**Table S2.11.** List of 312 genes differentially expressed only in the *spms* mutant inoculated with mock (10 mM MgCl<sub>2</sub>) at 24 h of treatment ('*spms* mock only').

**Table S2.12.** Gene ontology (GO) enrichment analysis of genes in Table S1.11

**Table S2.13.** List of 172 common differentially expressed genes in the comparisons between [*spms* (*Pst* DC3000) vs wild-type (mock)], [wild-type (*Pst* DC3000) vs wild-type (mock)] and [*spms* (mock) vs wild-type (mock)] at 24 h of treatment.

**Table S2.14.** List of 77 common differentially expressed genes in the comparisons between [*spms* (*Pst* DC3000) vs wild-type (mock)] and [*spms* (mock) vs wild-type (mock)] at 24 h of treatment.

**Table S2.15.** List of 47 common differentially expressed genes in the comparisons between [wild-type (*Pst* DC3000) vs wild-type (mock)] and [*spms* (mock) vs wild-type (mock)] at 24 h of treatment.

**Table S2.16.** Complete list of genes and their expression in the comparison between [*spms* (*Pst* DC3000) vs wild-type (mock)] at 24 h of treatment.

**Table S2.17.** Complete list of genes and their expression in the comparison between [*spms* (mock) vs wild-type (mock)] at 24 h of treatment.

**Table S2.18.** Complete list of genes and their expression in the comparison between [wild-type (*Pst* DC3000) vs wild-type (mock)] at 24 h of treatment.

**Table S3.1.** List of differentially expressed genes (fold-change>2; Bonferroni corrected p-value <0.05) in the comparison between *spms* and wild-type under basal conditions.

**Table S3.2.** Gene ontology (GO) enrichment analysis of genes in Table S2.1

**Table S4.1.** List of differentially accumulating proteins between *spms* and the wild-type.

**Table S4.2.** GO terms of differentially accumulating proteins in Table S3.1.

**Table S5.** Untargeted lipidomics analysis of *spms* and wild-type plants under basal conditions.