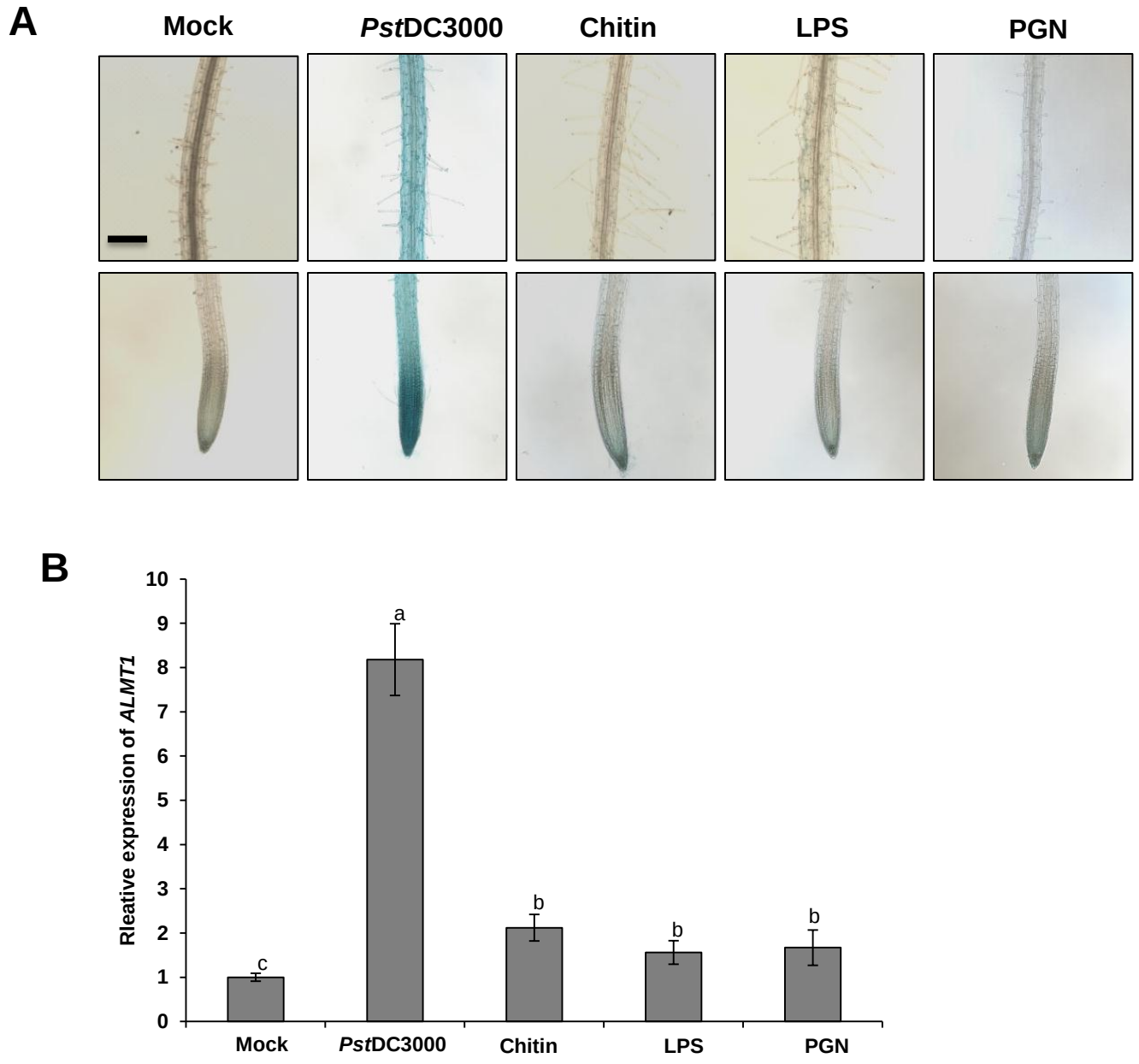
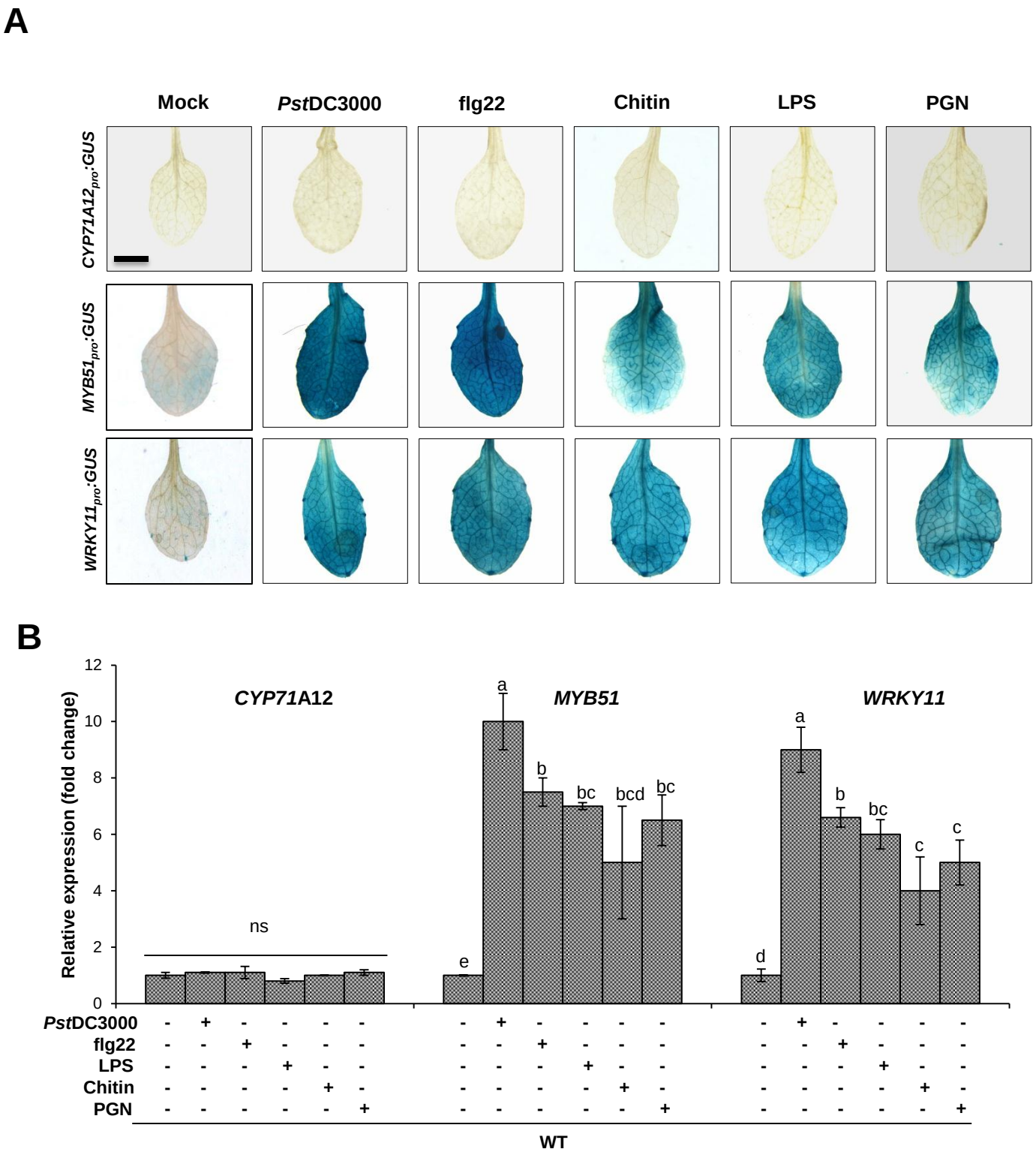
SOM Fig. 1
Lakshmanan et al., 2012



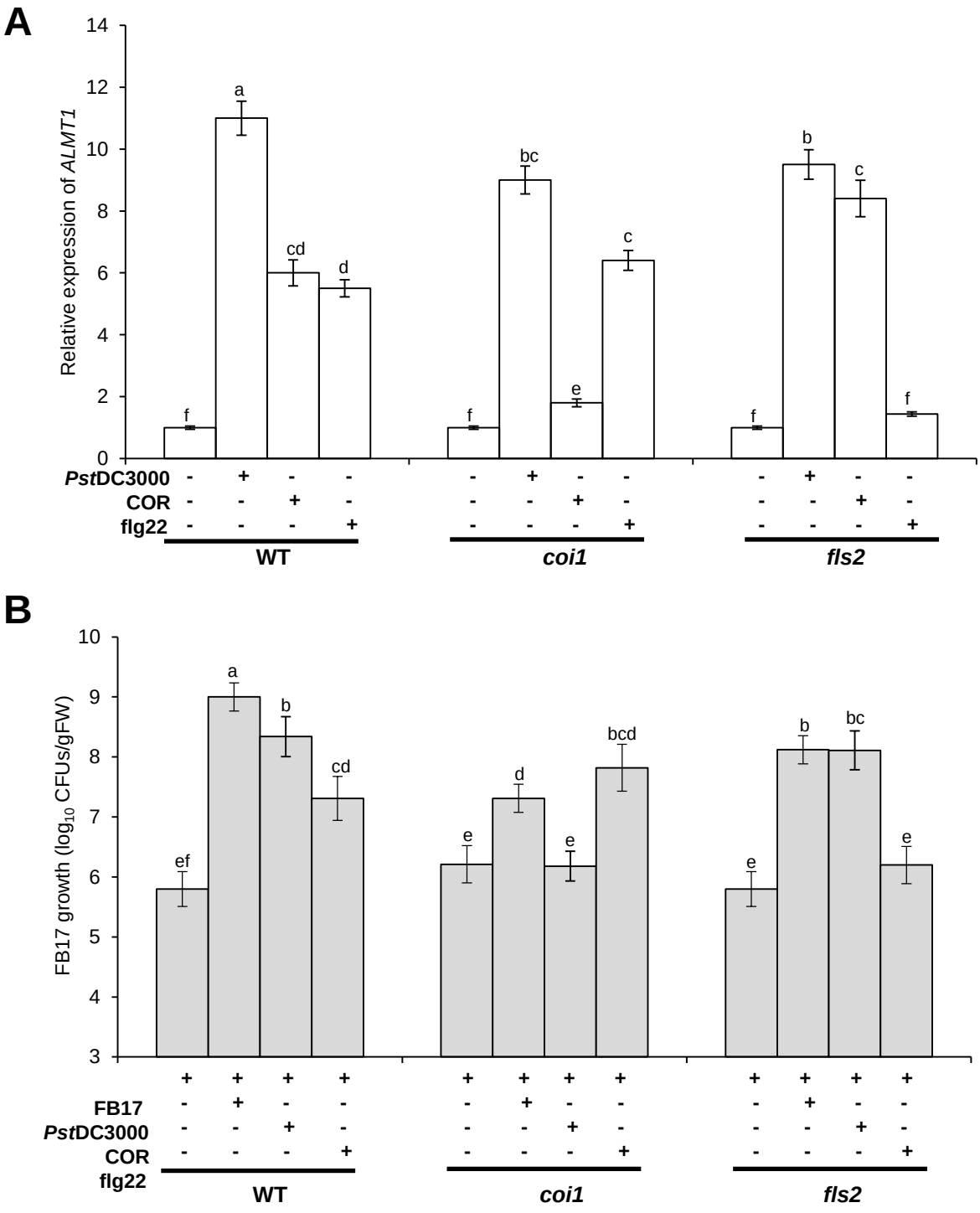
Supplementary Figure 1: (A) Three-week-old *in vitro* grown transgenic seedlings carrying *ALMT1*$_{pro}$*:GUS* promoter were foliar sprayed with LPS (500 µg mL^{-1}), chitin (500 µg mL^{-1}), PGN (500 µg mL^{-1}), an equal volume of water (mock control) or *Pst*DC3000 (OD_{600}=0.1). GUS staining of *ALMT1*$_{pro}$*:GUS* seedlings were performed 24 h post-treatment. Scale bars: 4 mm, common to all panels. **(B)** Measurement of *ALMT1* expression in the roots of plants foliar sprayed with MAMPs: LPS (500 µg mL^{-1}), chitin (500 µg mL^{-1}), PGN (500 µg mL^{-1}), an equal volume of water (mock control) or *Pst*DC3000 (OD_{600}=0.1). Total RNA was isolated and semi-quantitative RT-PCR performed. Lower case letters indicate the statistical significance among different treatments according to DMRT at $p \leq 0.05$, ($_{SE}$ values are three technical replicates of one experiment, repeated twice with similar results).

SOM Fig. 2
Lakshmanan et al., 2012



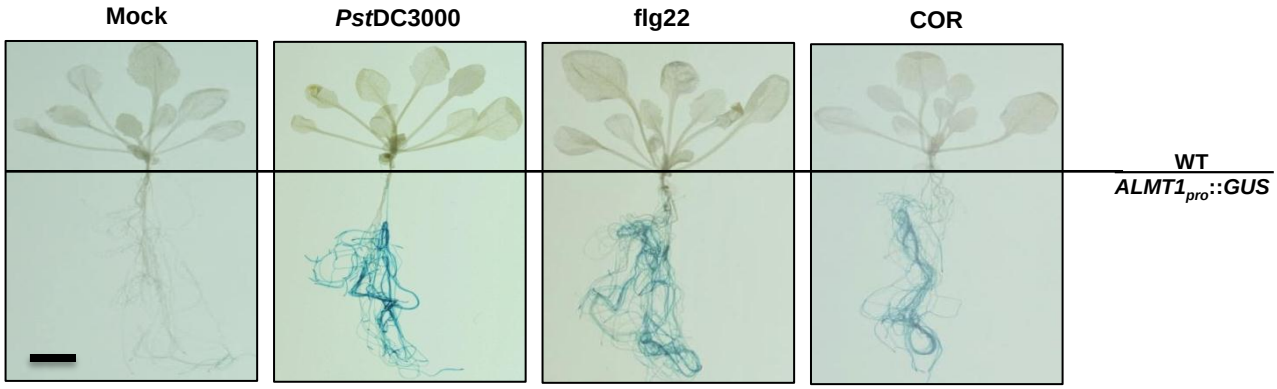
Supplementary Figure 2: (A) Three-week-old *in vitro* grown transgenic seedlings carrying *CYP71A12*$_{pro}$*:GUS, MYB51*$_{pro}$*:GUS,* and *WRKY11*$_{pro}$*:GUS* promoter were foliar sprayed with flg22 (1 µM), LPS (500 µg mL^{-1}), chitin (500 µg mL^{-1}), PGN (500 µg mL^{-1}), an equal volume of water (mock control), or *Pst*DC3000 (OD_{600}=0.1. GUS staining of treated leaf was performed 24 h post-treatment. Scale bars: 4 mm, common to all panels. **(B)** Measurement of *ALMT1* expression in the roots of WT plants after foliar spraying with flg22 (1 µM), LPS (500 µg mL^{-1}), chitin (500 µg mL^{-1}), PGN (500 µg mL^{-1}), or an equal volume of water (mock control) or *Pst*DC3000 (OD_{600}=0.1). Total RNA was isolated and semi-quantitative RT-PCR performed. Lower case letters indicate the statistical significance among different treatments according to DMRT at *p≤0.05*, ($_{SE}$ values are three technical replicates of one experiment, repeated twice with similar results).

SOM Fig. 3
Lakshmanan et al., 2012



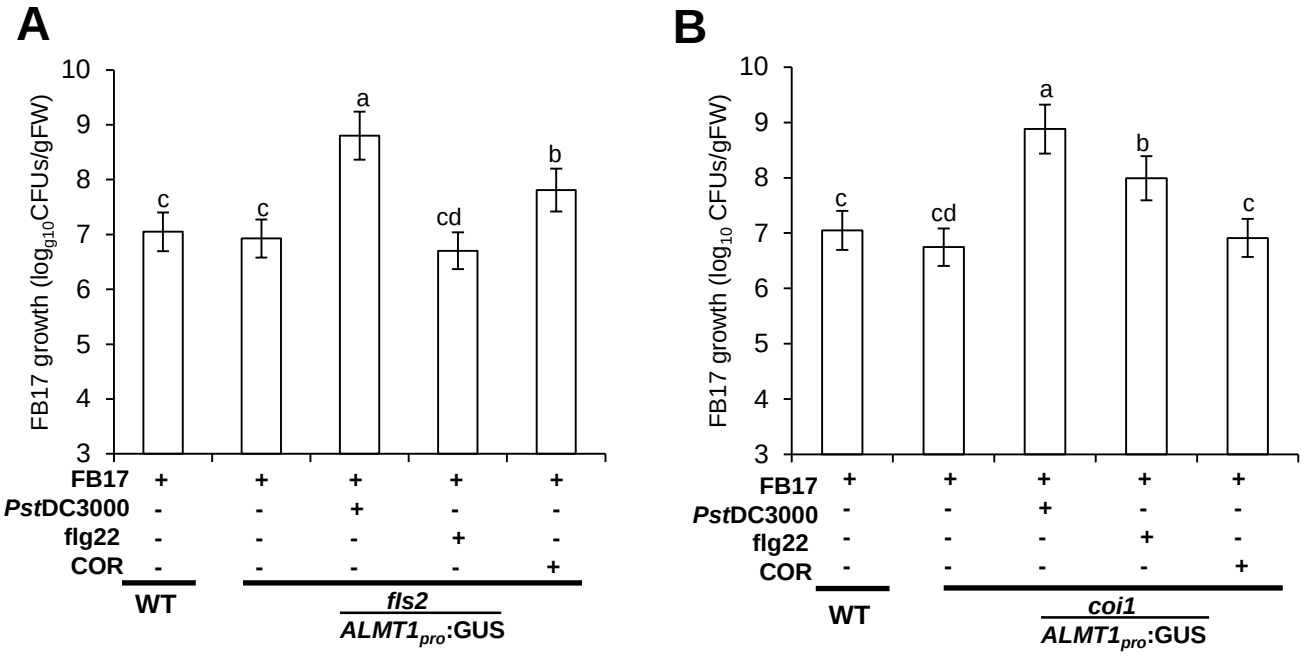
Supplementary Figure 3: (A) Measurement of *ALMT1* expression by semi-quantitative RT-PCR in WT and mutant's *fls2* and *coi1*. Three-week-old WT, *coi1* and *fls2* plants were foliar sprayed with flg22 (1 µM), COR (5 µM) or *Pst*DC3000 (OD_{600}=0.1), an equal volume of water as control and incubated for 24 h. The total root RNA was isolated and was subsequently analyzed for relative expression level of *ALMT1*. **(B)** FB17 growth quantification in the roots by CFUs in WT and mutant's *fls2* and *coi1*. Three-week-old pellet-grown plants of WT, *coi1* and *fls2* were foliar sprayed with flg22 (1 µM), COR (5 µM), *Pst*DC3000 (OD_{600}=0.1), or an equal volume of water (mock control) and then rhizo-inoculated with 4 mL of FB17 (OD_{600}=0.5) and incubated for 72 h. FB17 growth was quantified as CFUs by serial dilution method. For both panels, data presented as mean ± SE. The lower case letters represent statistical difference at $p \leq 0.05$ according to DMRT, ($_{SE}$ values are three technical replicates of one experiment, repeated twice with similar results).

SOM Fig. 4
Lakshmanan et al., 2012



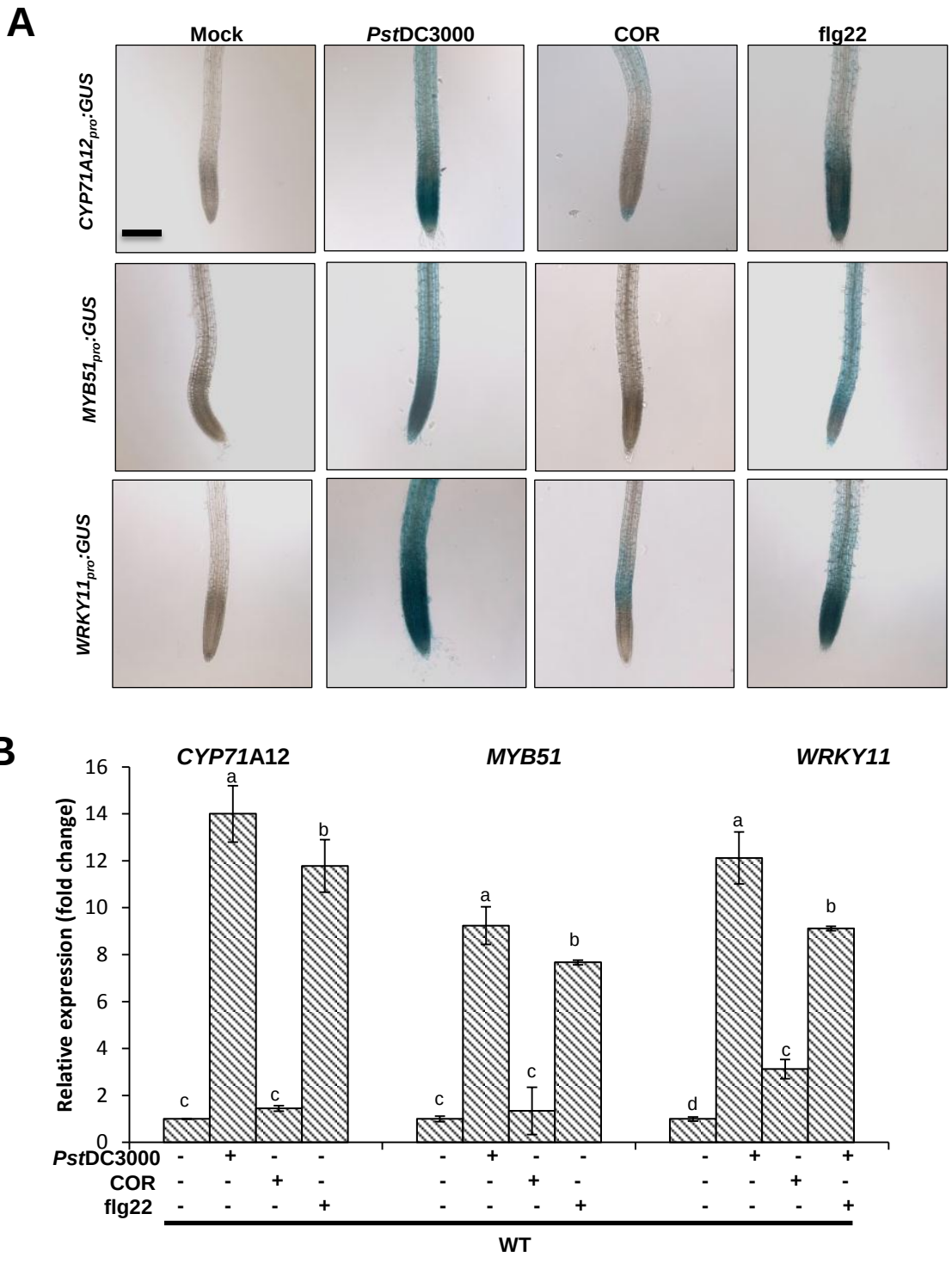
Supplementary Figure 4: Two-weeks-old micrografts post maturation were transferred to liquid medium for 4 d and foliar sprayed with flg22 (1 µM), COR (5 µM) or *Pst*DC3000 (OD_{600}=0.1). Plants incubated for 24 h were subjected to GUS staining. The images are a representative sample of six plants. Scale bars: 4 mm, common to all panels. Graft notation is WT/*ALMT1*$_{pro}$*:GUS,* where WT is scion and *ALMT1*$_{pro}$*:GUS* is rootstock.

SOM Fig. 5
Lakshmanan et al., 2012



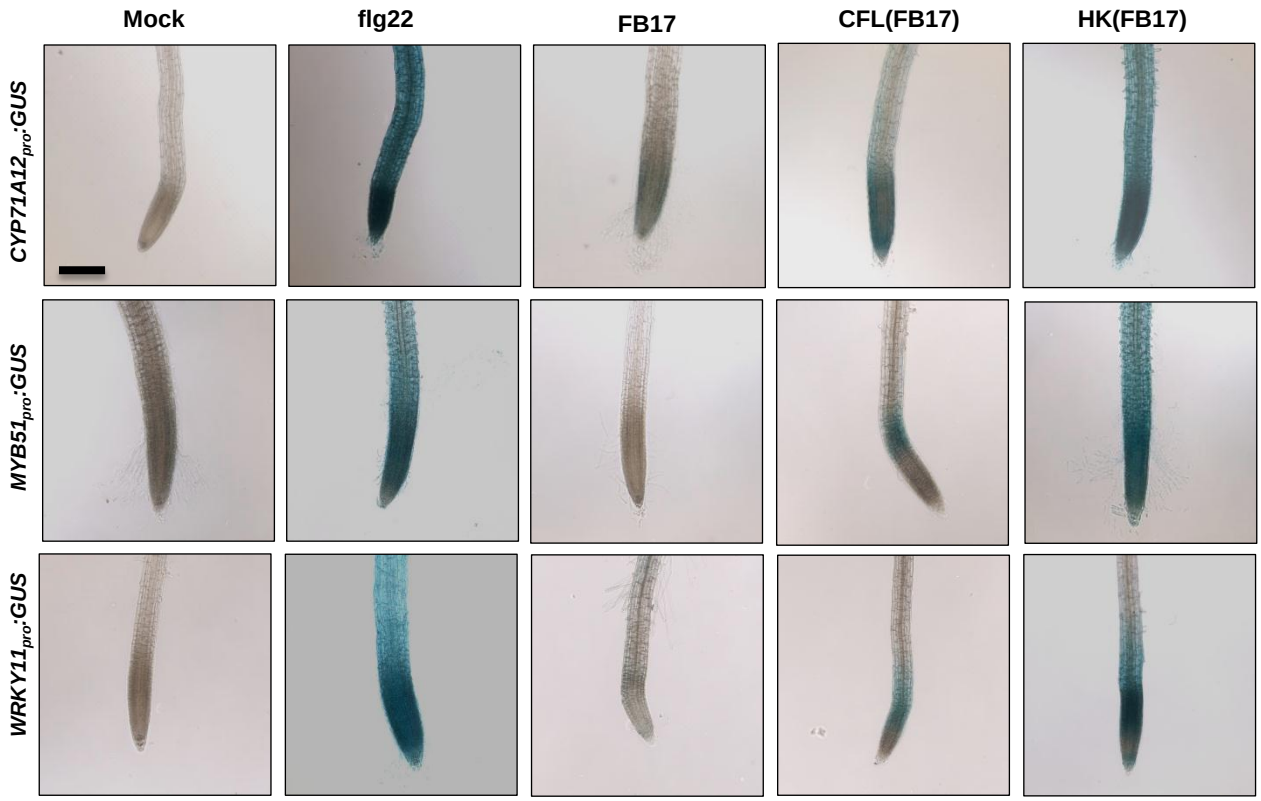
Supplementary Figure 5: (**A** and **B**) FB17 growth quantification on the roots by colony forming units (CFUs). Micrografts *fls2*/*ALMT1*$_{pro}$*:GUS* and *coi1*/*ALMT1*$_{pro}$*:GUS* foliar sprayed with flg22 (1 µM), COR (5 µM), *Pst*DC3000 (OD_{600}=0.1), an equal volume of water (mock control) and then rhizo-inoculated with FB17 (OD_{600}=0.5) of 4mL/pellet, and incubated for 72 h. Graft notation is *fls2*/*ALMT1*$_{pro}$*:GUS,* where *fls2* is scion and *ALMT1*$_{pro}$*:GUS* is rootstock and for *coi1*/*ALMT1*$_{pro}$*:GUS,* where *coi1* is scion and *ALMT1*$_{pro}$*:GUS* is rootstock. Lower case letters indicate the statistical significance among different treatments according to DMRT at $p \leq 0.05$, ($_{SE}$ values are 12 technical replicates of one experiment).

SOM Fig. 6
Lakshmanan et al., 2012



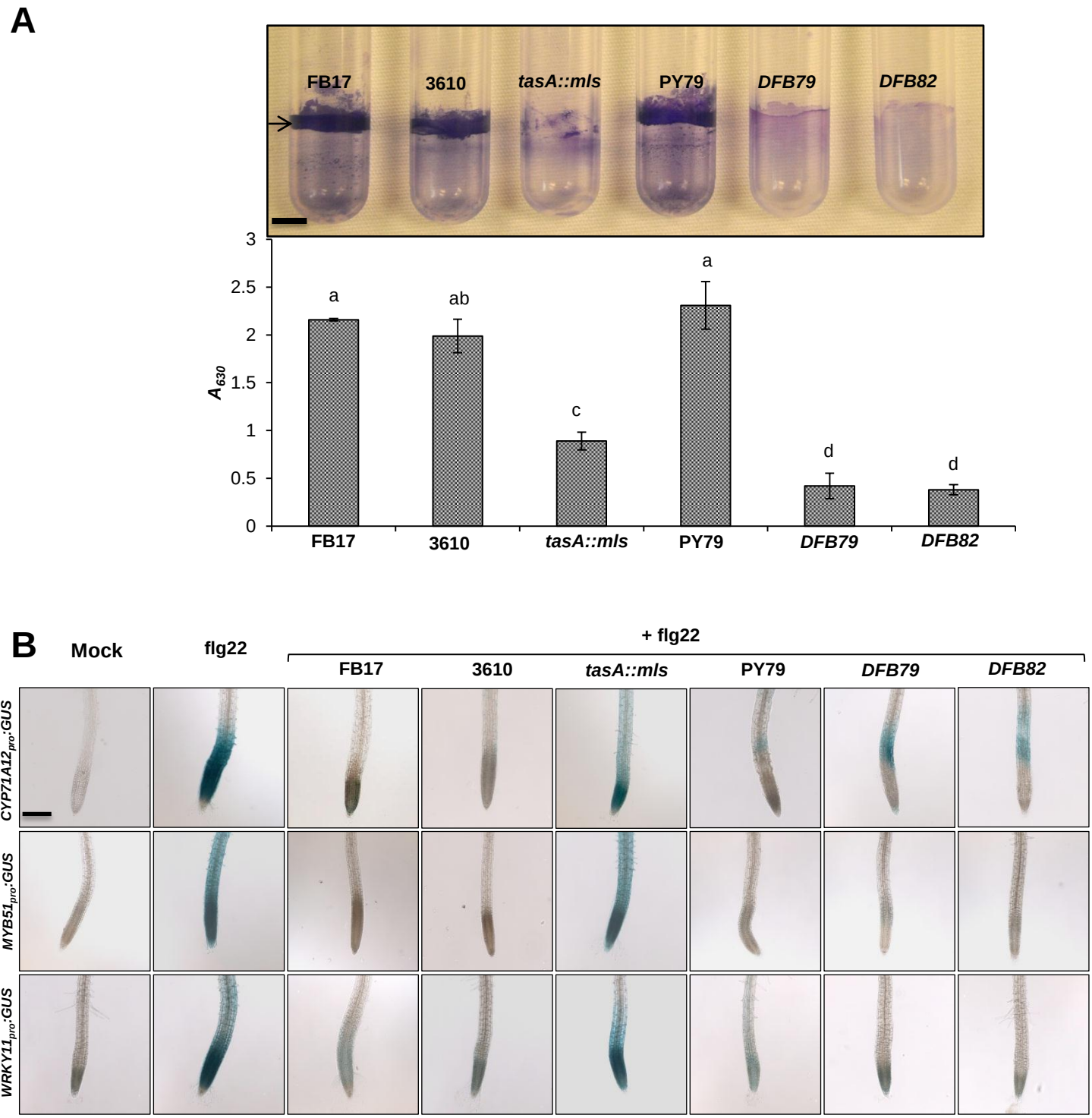
Supplementary Figure 6: (A) Transgenic seedlings carrying a *CYP71A12$_{pro}$:GUS*, *MYB51$_{pro}$:GUS,* and *WRKY11$_{pro}$:GUS* reporter construct in WT background were grown *in vitro* and treated with flg22 (1 µM), COR (5 µM), *Pst*DC3000 (OD_{600}=0.1), with equal volume of water (mock control). Plants were incubated for 24 h before GUS staining. Scale bars: 50 µm, common to all panels. **(B)** Measurement of *CYP71A12, MYB51, WRKY11* expression in WT plants treated with flg22 (1 µM), COR (5 µM), *Pst*DC3000 (OD_{600}=0.1) or equal volume of water (mock control). Total RNA was collected from roots after 24 h of incubation. sqRT-PCR was performed and relative expression of *CYP71A12, MYB5* and *WRKY11* was quantified. Data represents the mean ± SE. The lower case letters represent statistical difference at $p \leq 0.05$ according to DMRT ($_{SE}$ values are three technical replicates of one experiment, repeated twice with similar results).

SOM Fig. 7
Lakshmanan et al., 2012



Supplementary Figure 7: Transgenic seedlings carrying a *CYP71A12$_{pro}$:GUS, MYB51$_{pro}$:GUS,* or *WRKY11$_{pro}$:GUS* reporter construct in WT background were grown *in vitro* and co-treated with flg22 (1 µM) + FB17 (OD_{600}=0.001), flg22 (1 µM) + culture-free lysate (CFL) from FB17 and flg22 (1 µM) + heat killed FB17 and incubated for 24 h before GUS staining. Scale bars: 4mm, common to all panels.

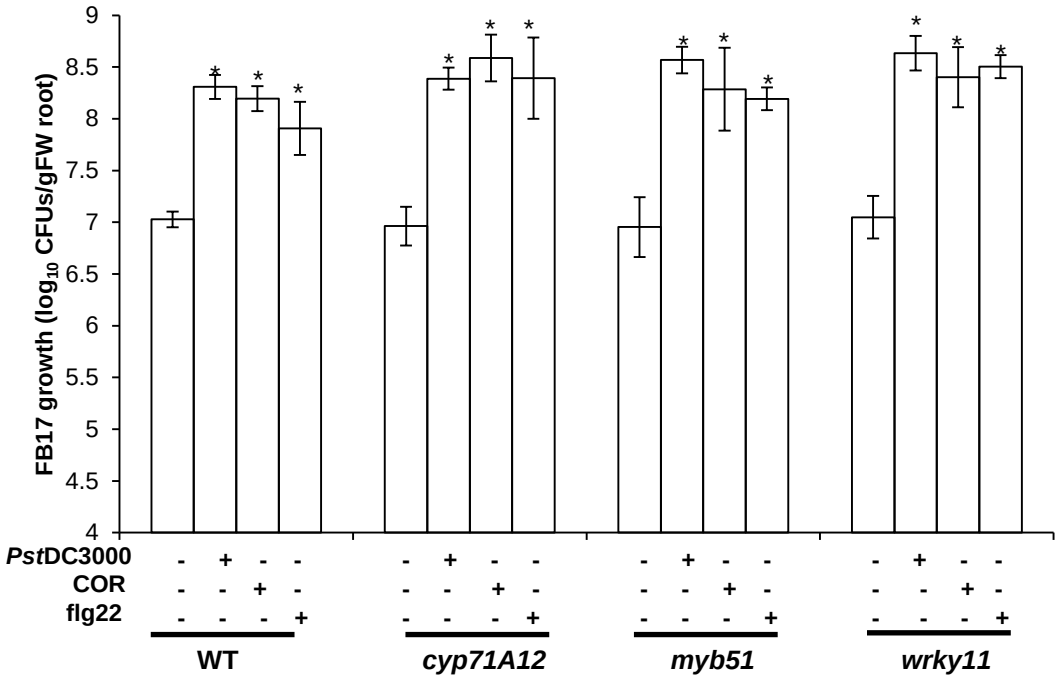
SOM Fig. 8
Lakshmanan et al., 2012



Supplementary Figure 8: (A) Evaluation of surface attachment properties on solid surface by FB17, 3610 wild-type, *tasA::mls* mutant, PY79 wild type, biofilm deficient mutants *DFB79,* and *DFB82* strains. OD_{630} of solubilized crystal violet (CV) from tube assays over time for tested *B. subtilis* strains. Data presented as mean ± SE. The lower case letters represent statistical difference at $p \leq 0.05$ according to DMRT ($_{SE}$ values are three technical replicates of one experiment, repeated twice with similar results). Insert: Photograph of surface attachment of different strains of *Bacillus.*

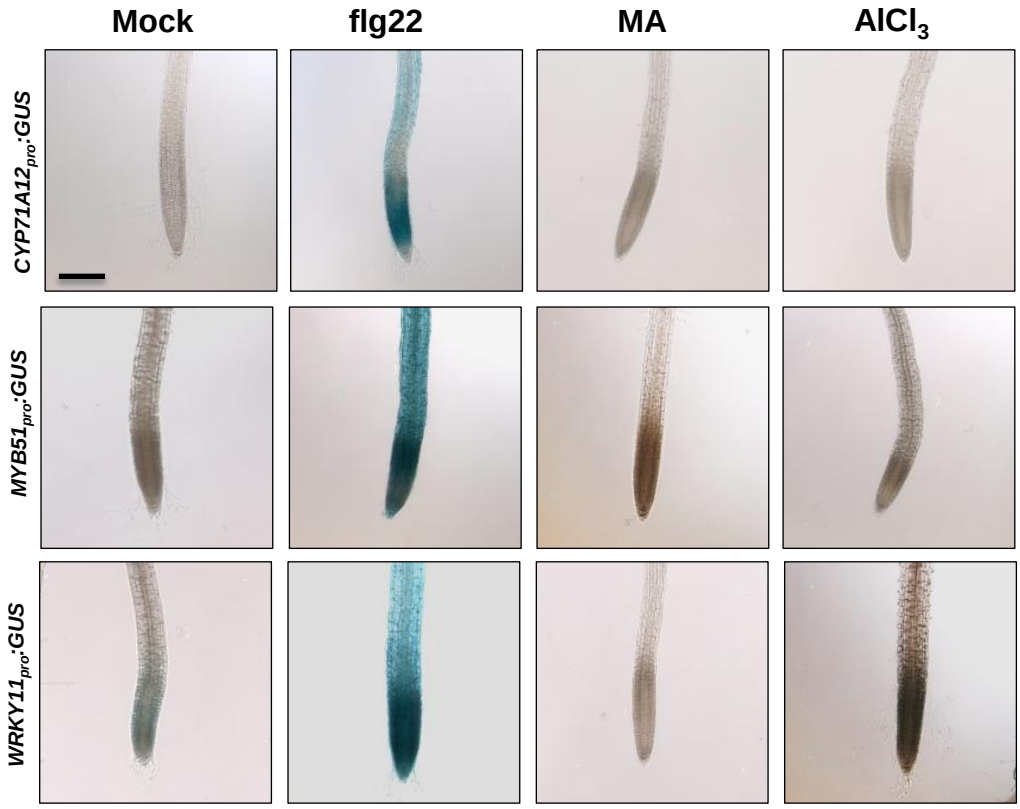
(B) Transgenic seedlings carrying *CYP71A12*$_{pro}$*:GUS*, *MYB51*$_{pro}$*:GUS* or *WRKY11*$_{pro}$*:GUS* reporter construct in WT background were grown *in vitro* and simultaneously treated with flg22 (1 µM) + FB17 (OD_{600}=0.001), 3610, PY79, *DFB79*, *DFB82* or an equal volume of water (mock control) and incubated for 24 h before GUS staining. Scale bars: 50µm, common to all panels.

SOM Fig. 9
Lakshmanan et al., 2012



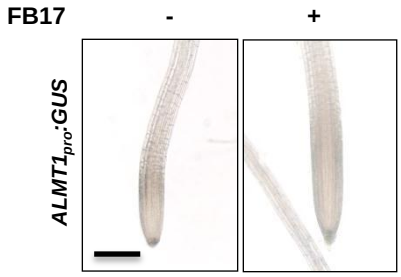
Supplementary Figure 9: Three-week-old *cyp71A12, myb5, wrky11,* and WT were foliar sprayed with flg22 (1 µM), COR (5 µM), or *Pst*DC3000 (OD_{600}=0.1) and the rhizo-inoculated with 4 ml/pellet, with FB17 (OD_{600}=0.5) or an equal volume of water (mock control) and FB17 growth was quantified by CFUs after 72 h. Data represents the mean ± SE. The lower case letters represent statistical difference at $p \leq 0.05$ according to DMRT, $_{SE}$ values are from 24 independent measurements from two experiments.

SOM Fig. 10
Lakshmanan et al., 2012



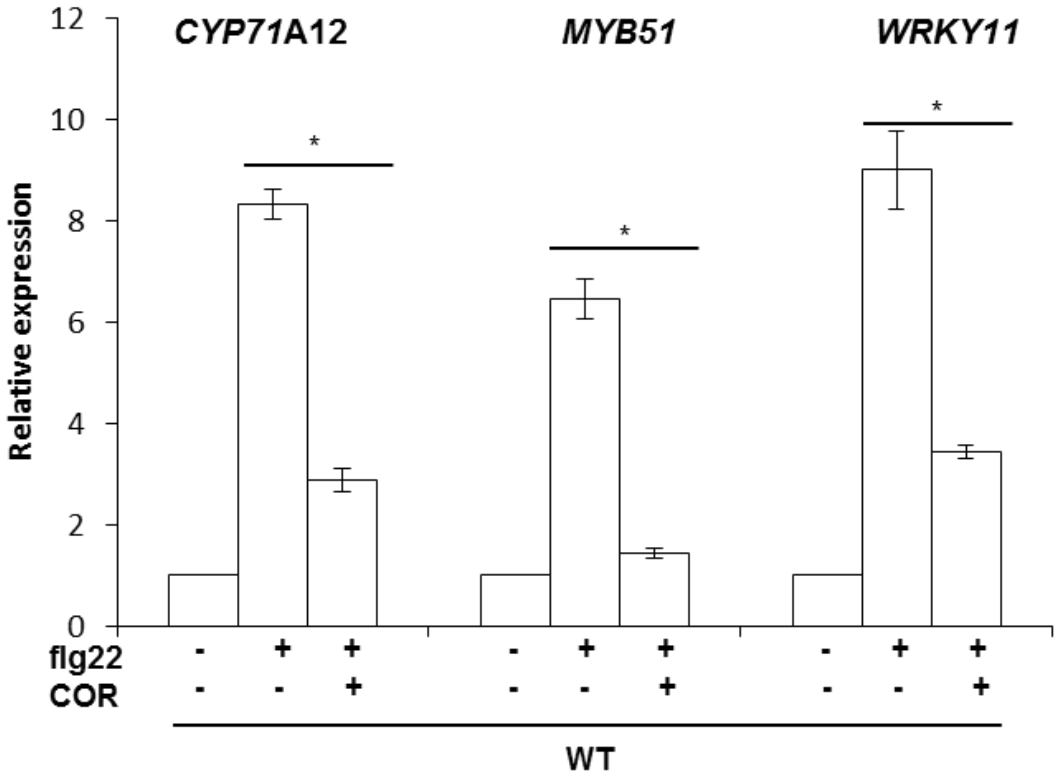
Supplementary Figure 10: Transgenic seedlings carrying a *CYP71A12$_{pro}$:GUS, MYB51$_{pro}$:GUS,* or *WRKY11$_{pro}$:GUS* reporter construct in WT background were grown *in vitro* and co-treated with flg22 (1 µM), malic acid (MA) (100 nM), $AlCl_3$ (4 µM) or an equal volume of water (mock control) and incubated for 24 h before GUS staining. Scale bars: 50µm, common to all panels.

SOM Fig. 11
Lakshmanan et al., 2012



Supplementary Figure 11: Transgenic seedlings carrying *ALMT1*$_{pro}$*:GUS* reporter construct in WT background were grown *in vitro* and root-treated with FB17 (OD_{600}=0.001) for 24 h before GUS staining. Scale bars: 50µm, common to both the panels.

SOM Fig. 12
Lakshmanan et al., 2012



Supplementary Figure 12: Expression analyses of root defense genes post aerial application of COR (5 µM) and Flg22 (1µM). The results represented as Mean ± SE. * *p≤0.05,* two tailed '*t*' test. ($_{SE}$ values are three technical replicates of one experiment, repeated twice with similar results).