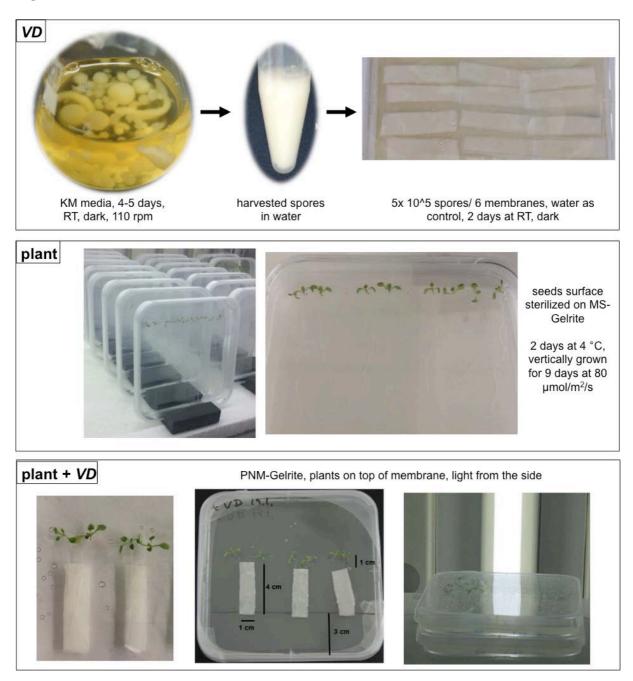
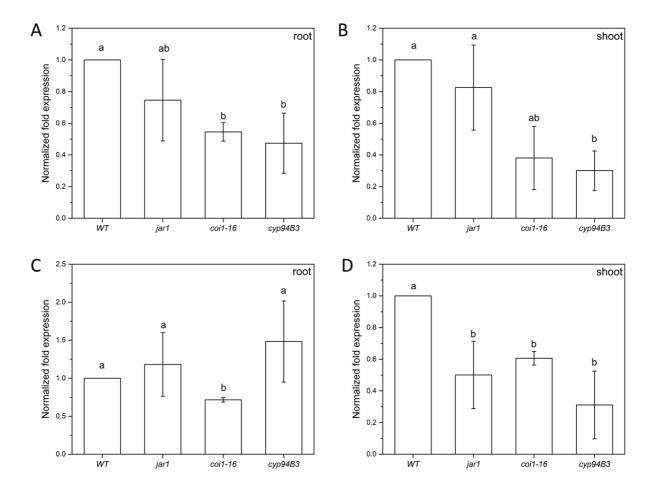
## **Supplemental Material**

## Figure S1



**Figure S1.** Workflow for Co-cultivation of *Arabidopsis thaliana* and *Verticillium dahliae* for RNA-seq analysis. Shown are the growth of the fungus (VD, upper lane), the seedlings (plant, middle) and the co-cultivation (plant + VD, lower lane).

## Figure S2



**Figure S2.** Colonization of WT and different *Arabidopsis* mutant plants by *V. dahliae* 10 and 20 *dpi*. Shown is the normalized fold expression ( $\pm$  SE, n=3) of *VD\_Actin2* 10 (**A**, **B**) and 20 (**C**, **D**) *dpi* in *VD*-infected WT, *jar1*, *coi1-16* and *cyp94B3* plants. The expression level of *VD\_Actin2* in *VD*-infected WT plants was used as control and set to 1.0. The mRNA levels for each cDNA probe were normalized with respect to the *RPS18B* mRNA level. Statistically significant differences between the mutants were analyzed by one-way ANOVA, p<0.05 (Sidak). Different letters indicate a statistically significant difference.