

Figure S6. Transcriptional regulation of AQP expression under biotic interactions. Regulation of expression is indicated as Log₂ ratio of treated samples relative to control samples and is visualized as heatmaps. Differential AQP transcript accumulations between samples were hierarchically clustered using Euclidean distance. Each row corresponds to an AQP gene. Color scale depicts Log₂ value: Green represents down-regulation and red represents up-regulation in treated samples relatively to controls.

Heatmap A: AQP responses to mycorrhization. Comparison of mycorrhized *P. canescens* roots (inoculated with *Paxillus involutus*) with non-mycorrhized roots in control conditions and under 150 mM NaCl treatment (E-MEXP-1874).

Heatmap B: AQP responses to foliar pathogens. Columns correspond to 4 comparisons between treated and control leaf discs. Responses of *Populus nigra* x *maximoviczii* NM6 to infection by biotrophic fungi, *Melampsora larici-populina* (Mlp) or *M. medusae* f. sp. *Deltoidae* (Mmd), and to a simultaneous infection with both pathogens (GSE9673). Response of *P. canescens* to *M. medusae* f.sp. *tremuloidae* (Mmt, GSE16417).

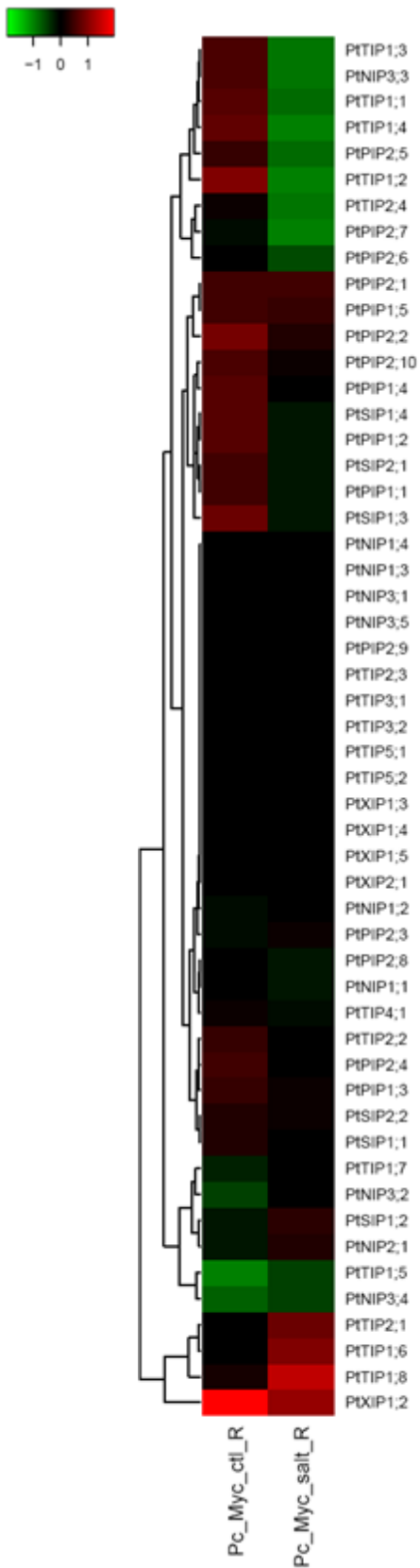


Figure S6A. Mycorrhization

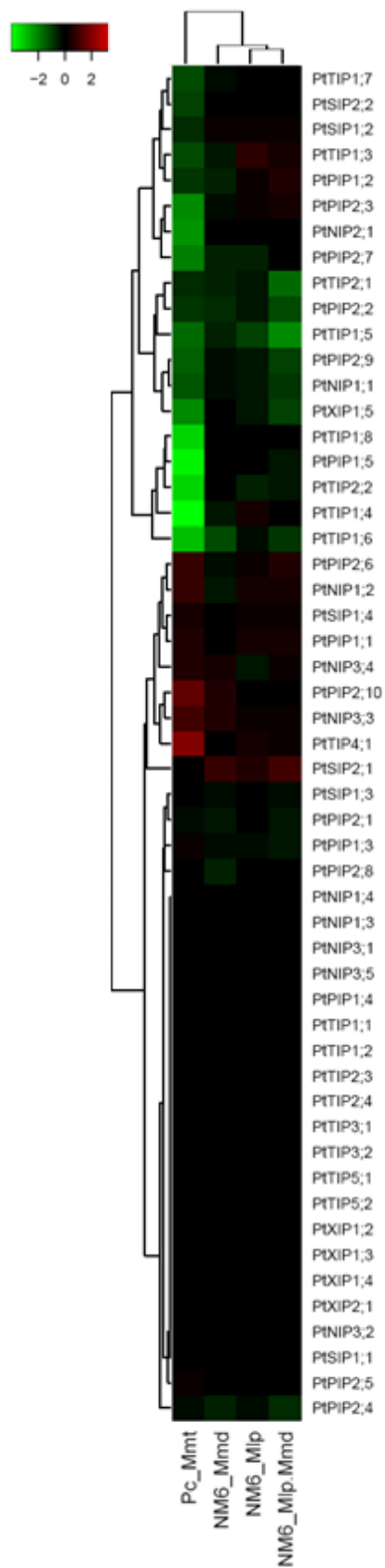


Figure S6B. Foliar pathogens