



Figure 3: (a) Principal component analysis scatterplot of samples from tomato roots and shoots harvested 24 hours after the second PA or mock treatment (CON), based on mRNA-sequencing based analysis of gene expression. Shaded ellipses represent 95% confidence ellipses. (b) Heatmap (showing normalized, centered and scaled expression values) and hierarchical clustering of samples and transcripts from tomato roots and shoots harvested after PA or mock treatment (CON), based on the same dataset as (a).