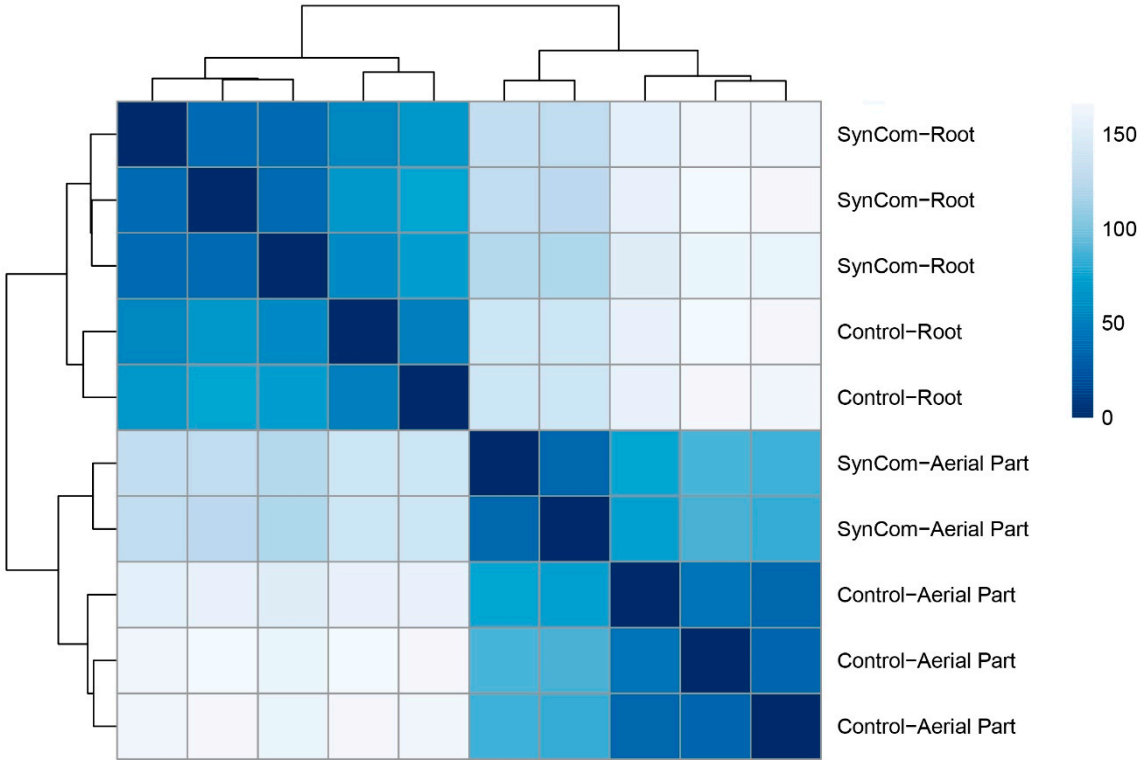


Figure S1. Sample-to-sample distance heatmap based on variance-stabilizing transformation (VST) of normalized gene expression counts. Hierarchical clustering reveals similarities and differences between samples from SynCom-inoculated and control plants across root and aerial part tissues.