

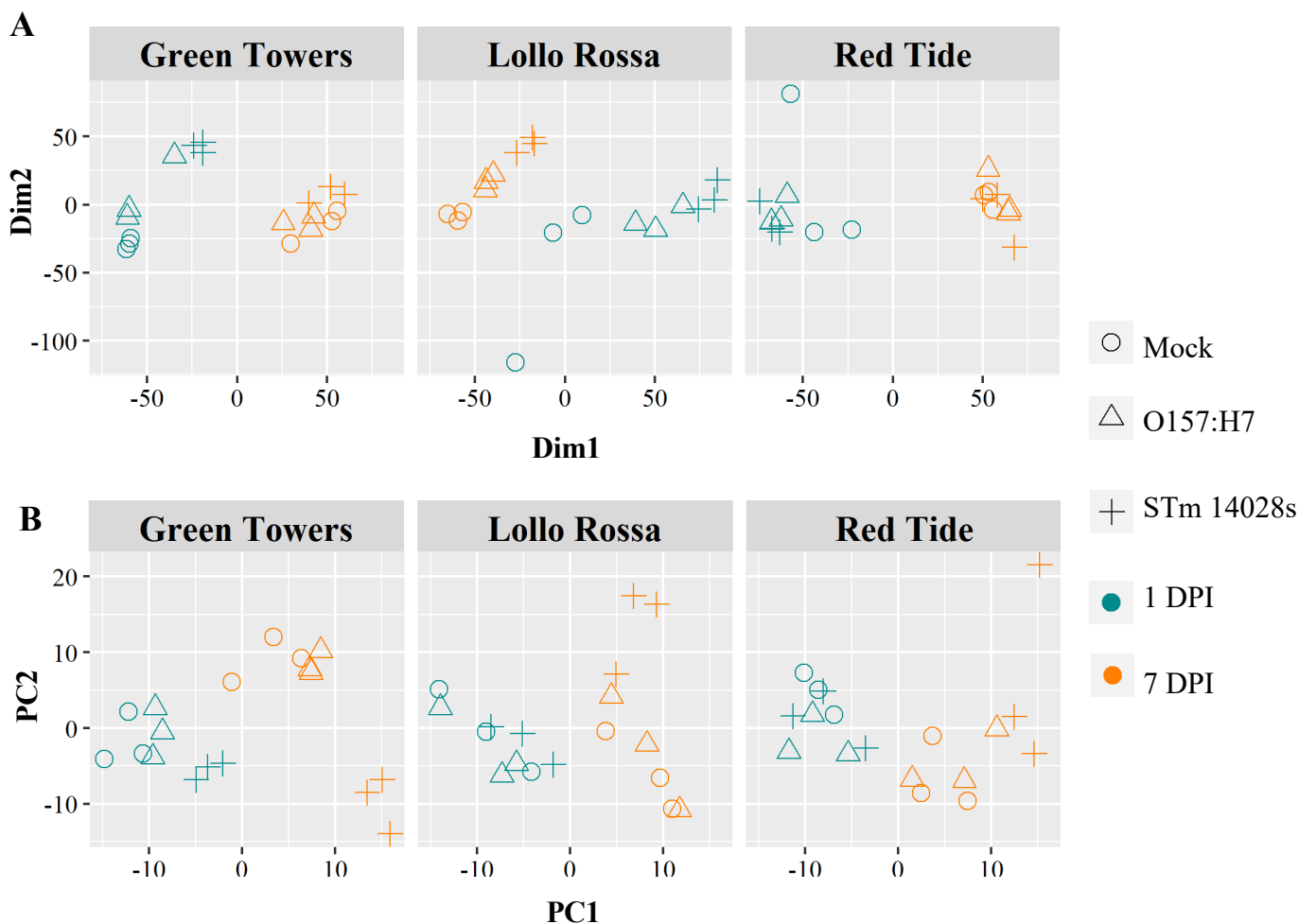


Fig. S6. Multidimensional scaling (MDS) (**A**) and principal component analysis (PCA) (**B**) plots representing the correlation among biological replicates used for the whole leaf RNA-sequencing and AWF metabolomic analyses, respectively. Leaves of the lettuce cultivars Green Towers, Lollo Rossa, and Red Tide were vacuum infiltrated with mock (sterile distilled water) or bacterial inoculum containing 5×10^5 CFU/mL of *Escherichia coli* O157:H7 or *Salmonella enterica* ser. Typhimurium 14028s. Leaves were sampled at 1- and 7-days post inoculation (DPI). Coordinates for MDS graphs were calculated using normalized read counts in the cmdscale function of the R software and the coordinates for PCA graphs were obtained by using normalized peak heights in the MetaboAnalyst 5.0 software.