

Comparative pathway analysis of susceptible genotypes analysed in this study with the genotype ASS-7 (reported in Trujillo-Moya et al. 2020). The results revealed the similarity of all susceptible genotypes samples collected 38 days post infection (dpi) with the 39 dpi ASS-7 samples (better than 21 dpi ASS-7 samples) for both over- and under-expressed DEGs subsets. For ASS-7, two types of pathway fingerprints were included derived from the following contrasts: symptomatic (S) needles from infected plant (controlled artificial infection) vs. needles from control (C) not infected plant (S-C); S needles from infected plant vs. non-symptomatic (NS) needles from the same infected plant (S-NS). Columns (samples) and rows (pathways) were sorted by clustering (clusters data by similarity), Euclidean distance was used as distance metric. Number of enzymes represented within each pathway are shown using a colour scale from blue (0) to yellow (37).

