**Metabolite analysis**

Metabolites in leaf and root samples of adult plants and leaf samples of young plants were analyzed by GC-MS (Osorio *et al.*, 2012, Vallarino *et al*., 2018). Mass spectra were compared with the Golm Metabolome database for identification (Kopka *et al*., 2005). Metabolomic data were log2- transformed and the average values were calculated for control and treated tissues. The data were normalized against the average values of the control samples. To assess the significance of differences, we calculated the log2 fold change (log2FC), p values (t-test), and adjusted p values (FDR, Benjamini-Hochberg). The statistical tests were used to detect significant differences between the control and stressed samples for each metabolite. The data were visualized using enhanced volcano plots.