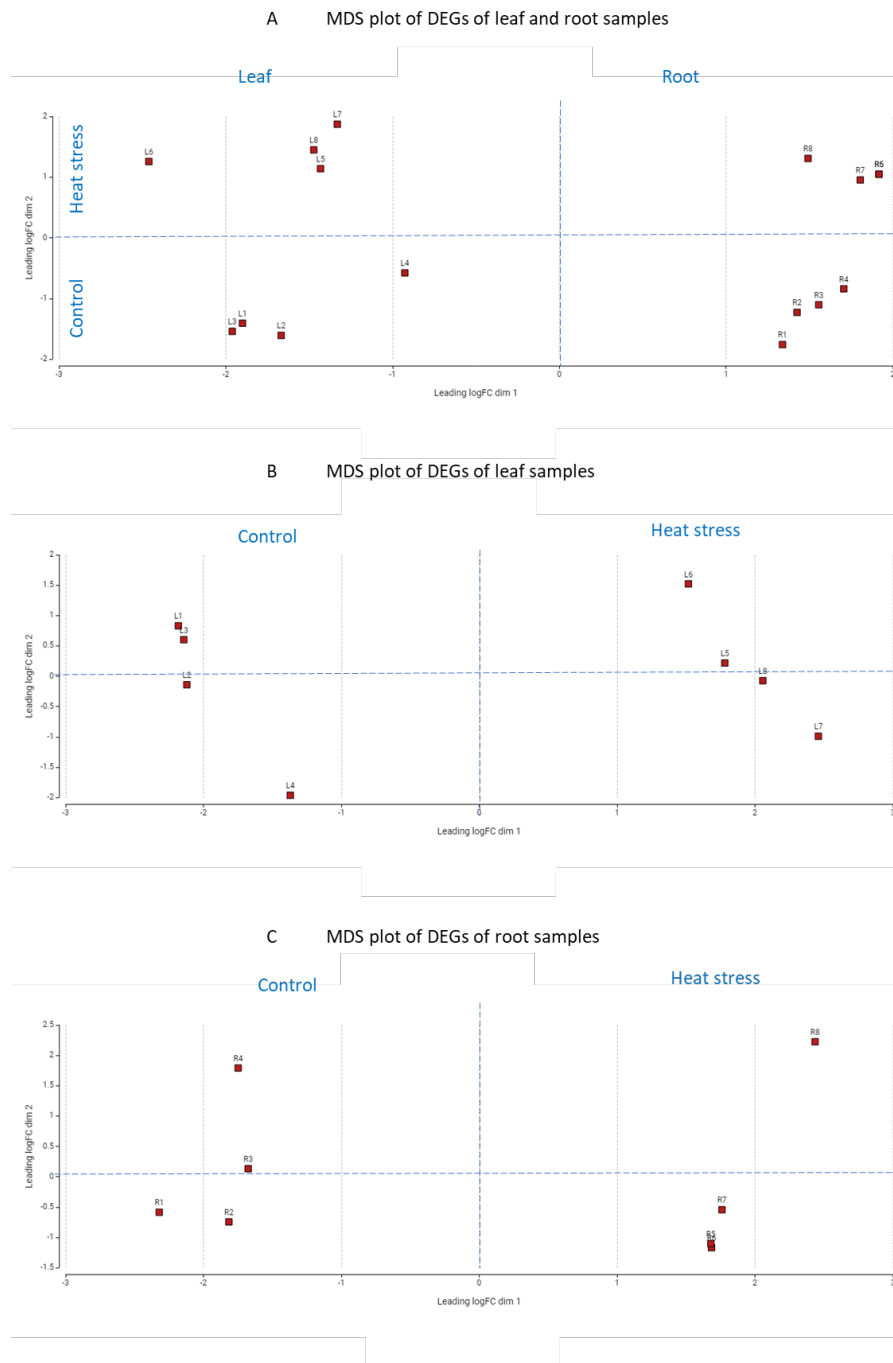
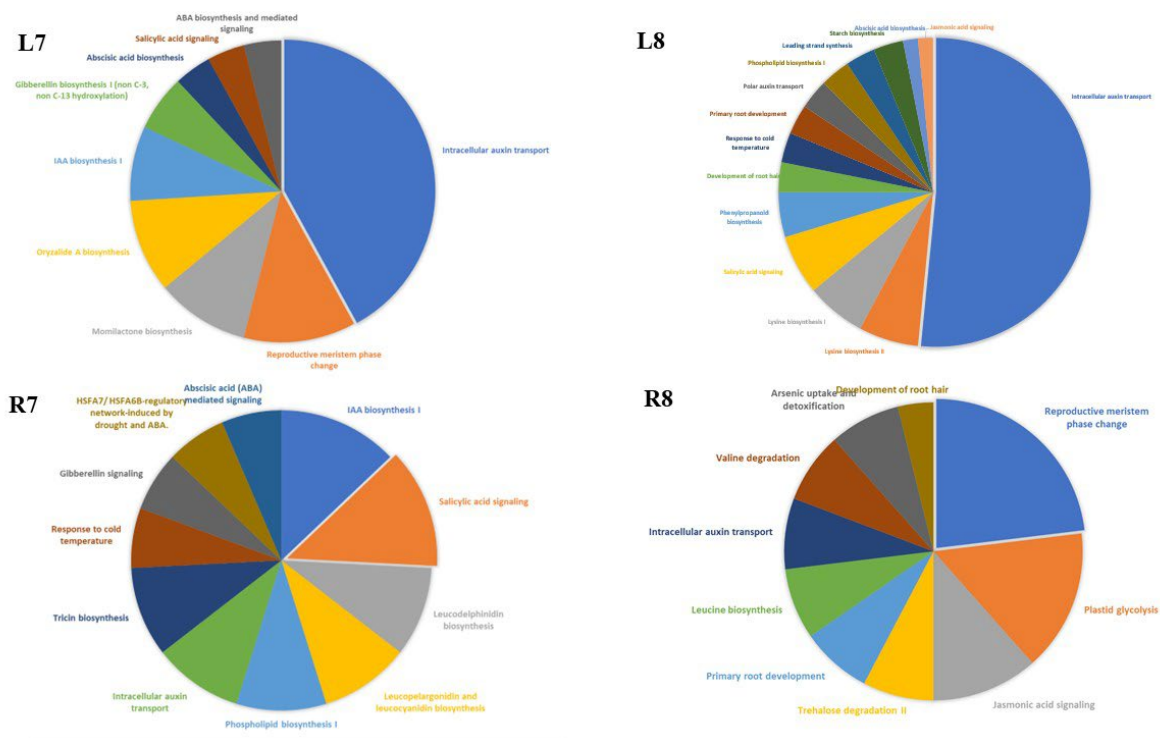


**First Peek into the Transcriptomic Response in Heat Stressed Tomato  
inoculated with *Septoglomus constrictum***

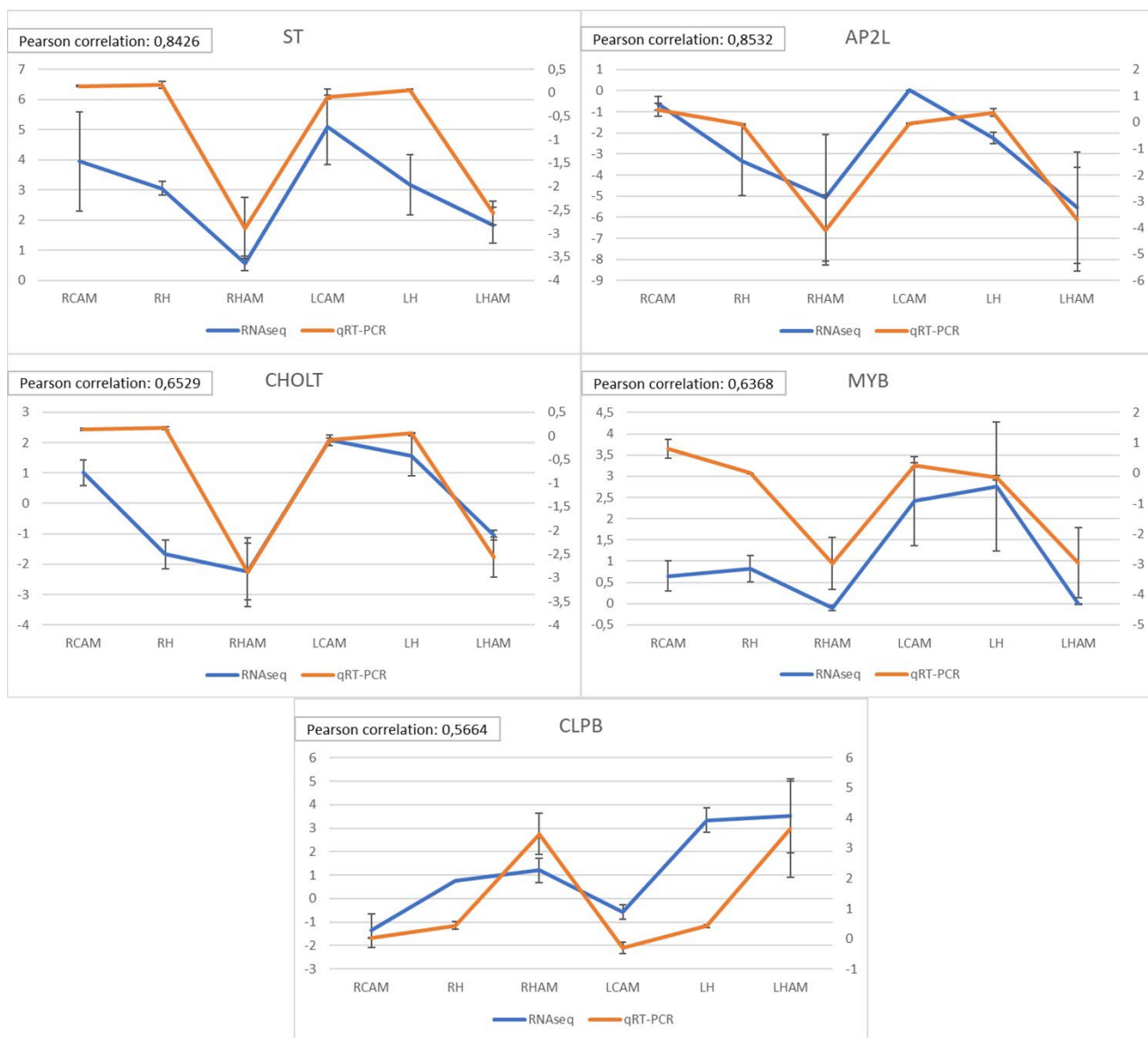
*Supplementary Figures*



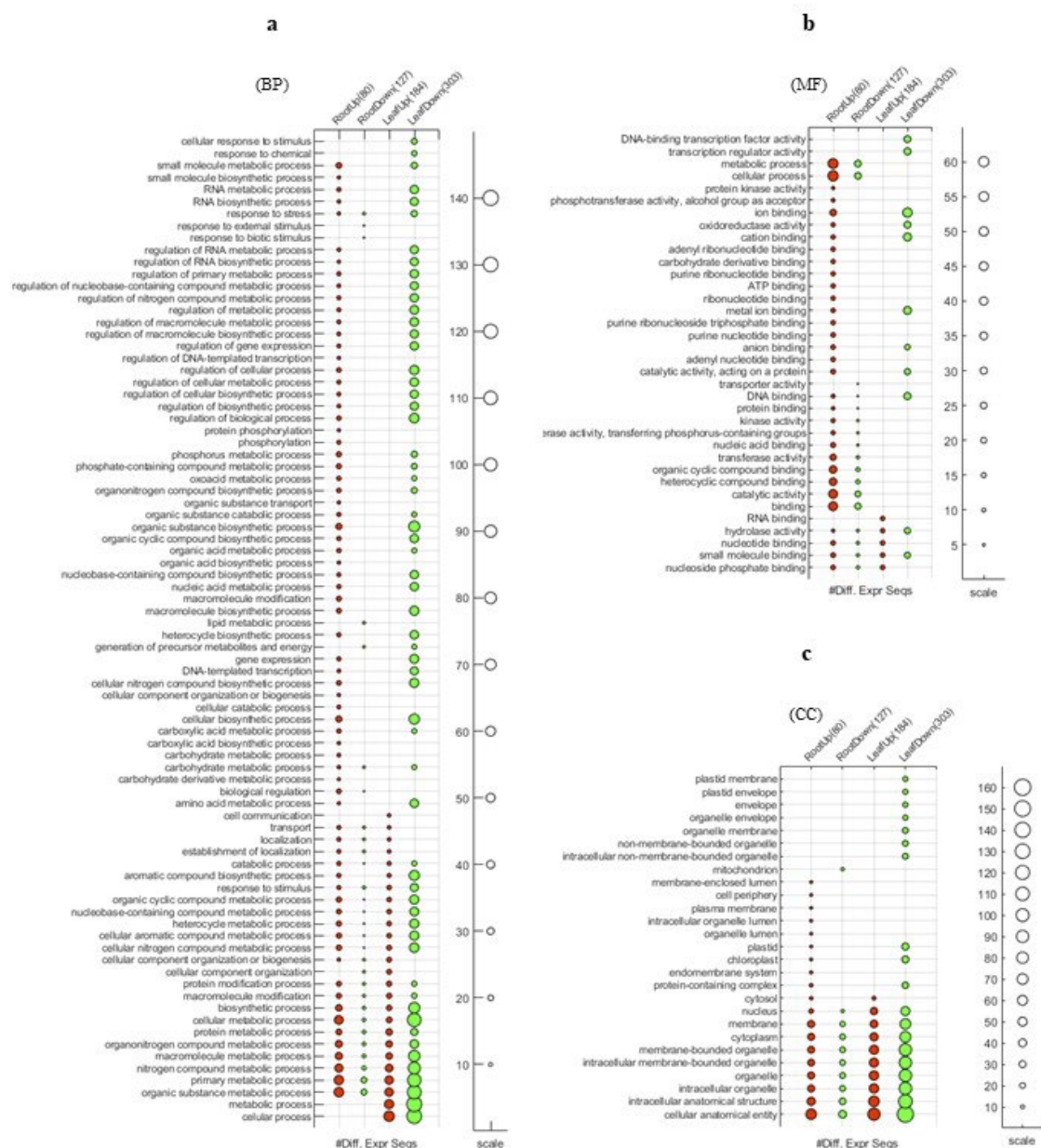
**Supplementary Figure S1.** Two-dimensional scatterplot in which the distances represent the log<sub>2</sub> fold changes between samples. Comparison of all root and leaf samples (A) and separated analysis of the leaf (B) and root (C) samples.



**Supplementary Figure S2.** Plant-reactome pathway analysis of uniquely expressed genes in R7, R8 and L7, L8 samples. The first 10 pathways are visualized filtered to *Solanum lycopersicum* pathway ID (R-SLY).



**Supplementary Figure S3.** Correlation analysis of qRT-PCR and RPKM values. The average of four biological replicates were used for the qRT-PCR and two for the RNAseq



**Supplementary Figure S4.** GO term determination based on Fisher's exact test of unique DEGs of HAM vs H sample pairs in root and leaf samples. The number of found and GO-categorized sequences showing differential expression are illustrated by dot sizes and compared in the investigated tissues. A: biological process (BP); B: molecular function (MF); C: cellular component (CC).