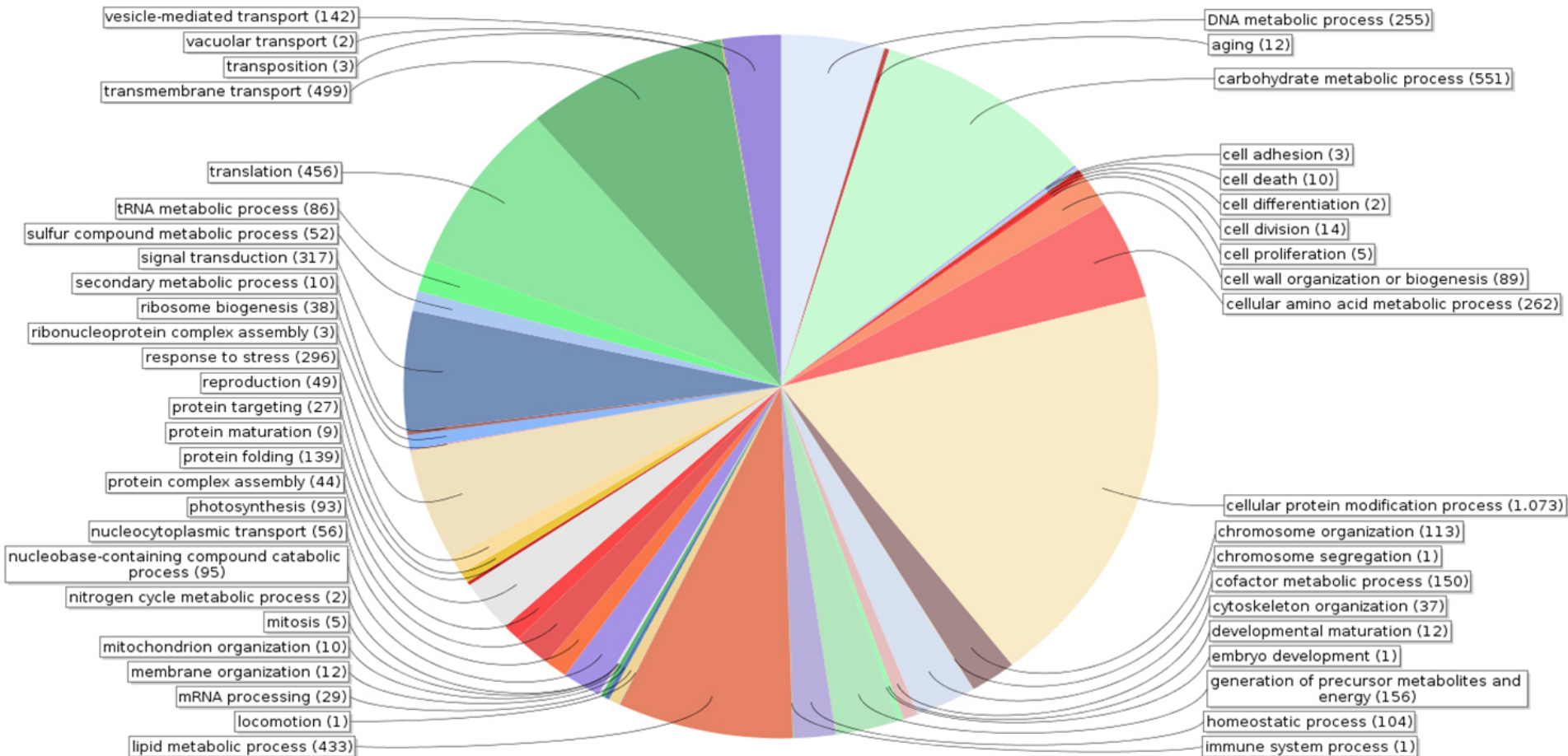
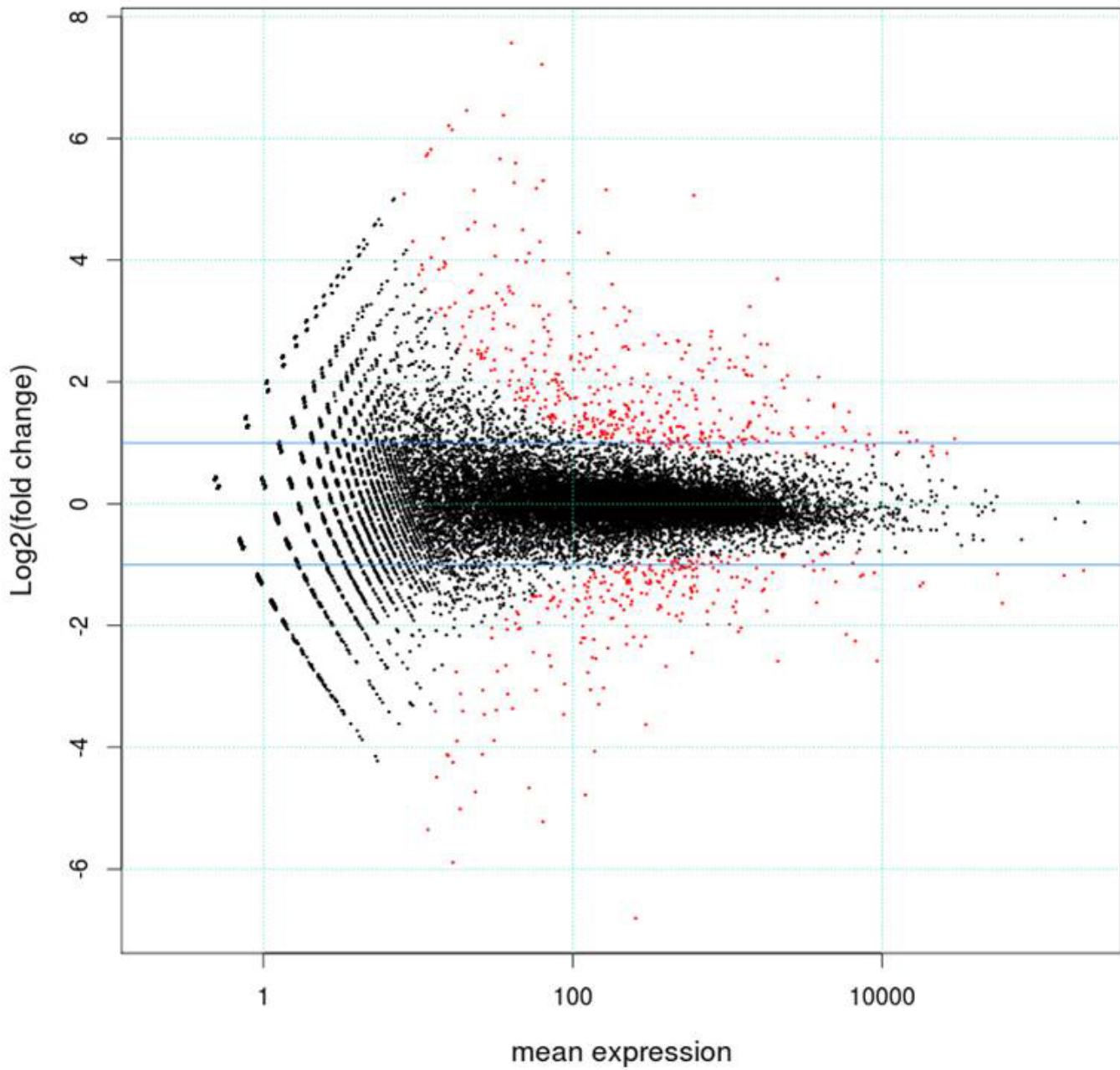


**Supplemental Figure 1.** Mycorrhization parameters of tomato roots inoculated with the AM fungus *Funneliformis mosseae*. F%: frequency of colonization in the root system; M%: intensity of the mycorrhizal colonization in the root system; A%: arbuscule abundance in the root system; and a%: arbuscule abundance in the mycorrhizal root part. Mycorrhization parameters were determined at the end of the experiment according to Trouvelot method (1986). Values are means  $\pm$  SD (n=5). For each plant, 100 cm of root were measured.

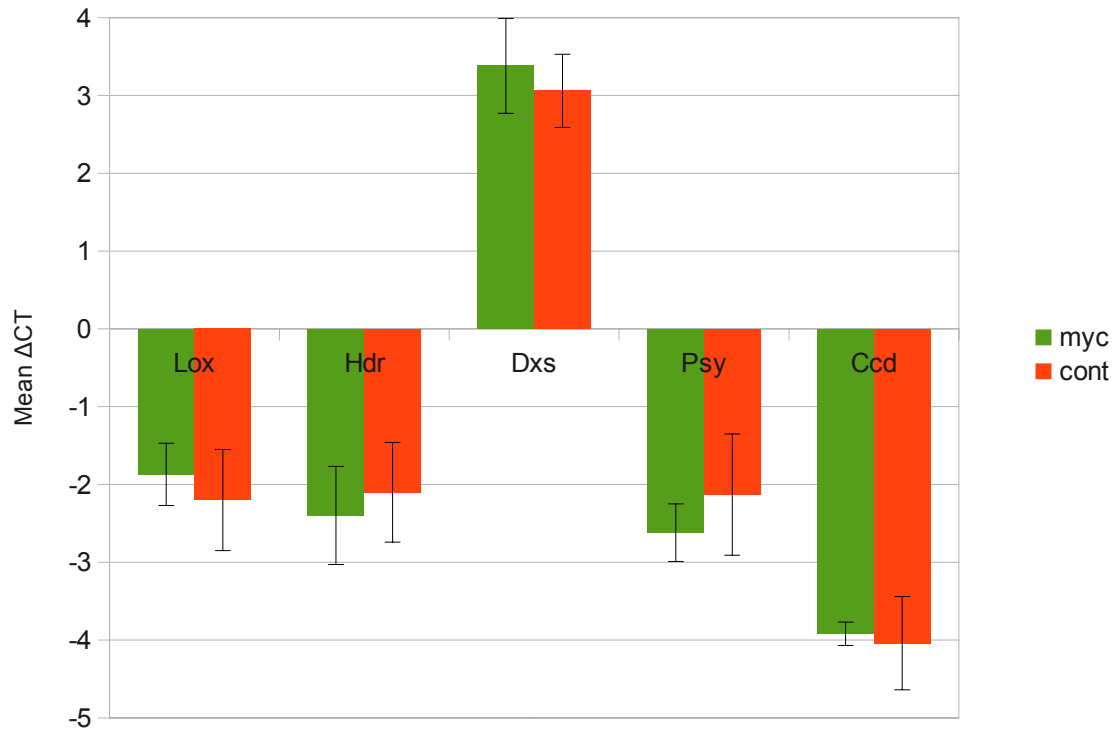
# Sequence distribution: biological\_process (Filtered by #Seqs: cutoff=1.0)



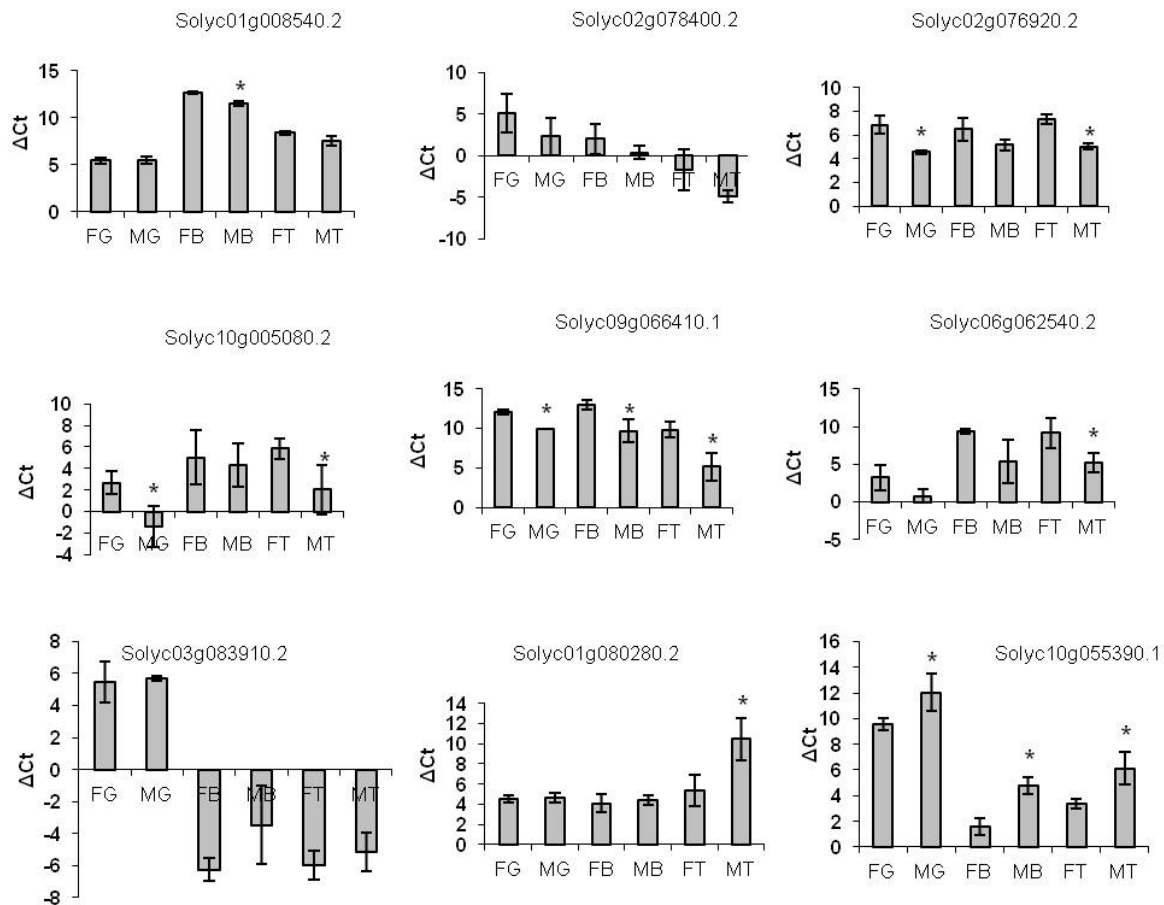




Supplemental figure 4. Sesquiterpenoid phytoalexins biosynthesis pathway.



**Supplemental Figure 5.** q-PCR data obtained for five selected genes involved in the carotenoid metabolism on fruits collected from mycorrhizal and control plants. The y axis represents  $\Delta CT$  value (Ct gene-Ct ubiquitin). Data are presented as the mean  $\pm$  SD for  $n = 3$ . Identities of genes are as follows: *Lox* (lipoxygenase TomloxC); *Hdr* (hydroxymethylbutenyl diphosphate reductase); *Dxs* (deoxyxylulose 5-phosphate synthase); *Psy* (phytoene synthase); *Ccd* (carotenoid cleavage dioxygenase).



**Supplemental figure 6.** Statistical analyses of q-PCR data obtained for nine selected differentially regulated genes between mycorrhizal (M) and control (F) plants in three ripening stages green (G), breaker (B) and turning (T). The y axis represents  $\Delta Ct$  value (Ct gene-Ct ubiquitin). Data are presented as the mean  $\pm$  SD for  $n = 3$ . One-way ANOVA (Tukey's posthoc test) was used for data analysis and asterisks indicate statistical significance at  $p < 0.05$ . Identities of genes are as follows: Solyc01g008540.2.1 (Cinnamoyl CoA reductase-like protein); Solyc02g078400.2 (Allantoinase); Solyc02g076920.2.1 (Transcription factor MYC2); Solyc10g005080.2.1 (Late elongated hypocotyl and circadian clock associated-1-like); Solyc09g066410.1.1 (Inorganic phosphate transporter); Solyc06g062540.2.1 (Putative acid phosphatase); Solyc03g083910.2.1 (Acid beta-fructofuranosidase); Solyc01g080280.2.1 (Glutamine synthetase); Solyc10g055390.1 (Nodulin family protein).