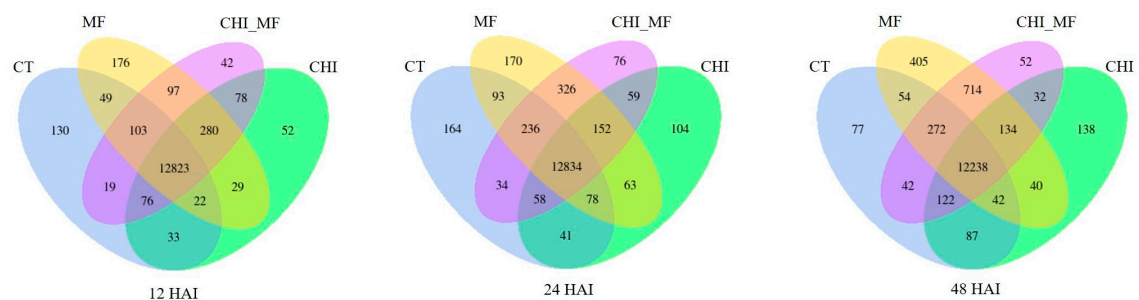
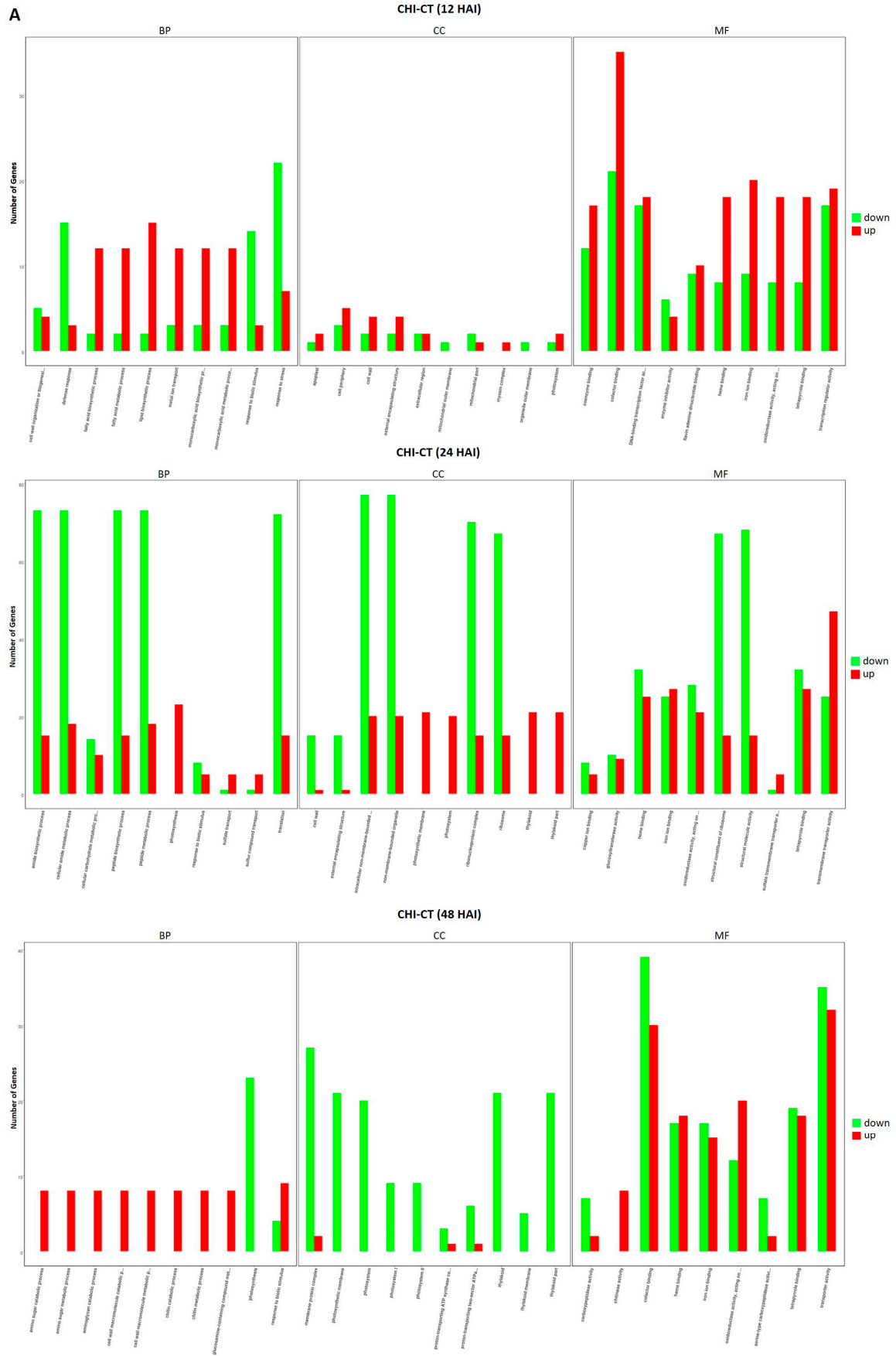


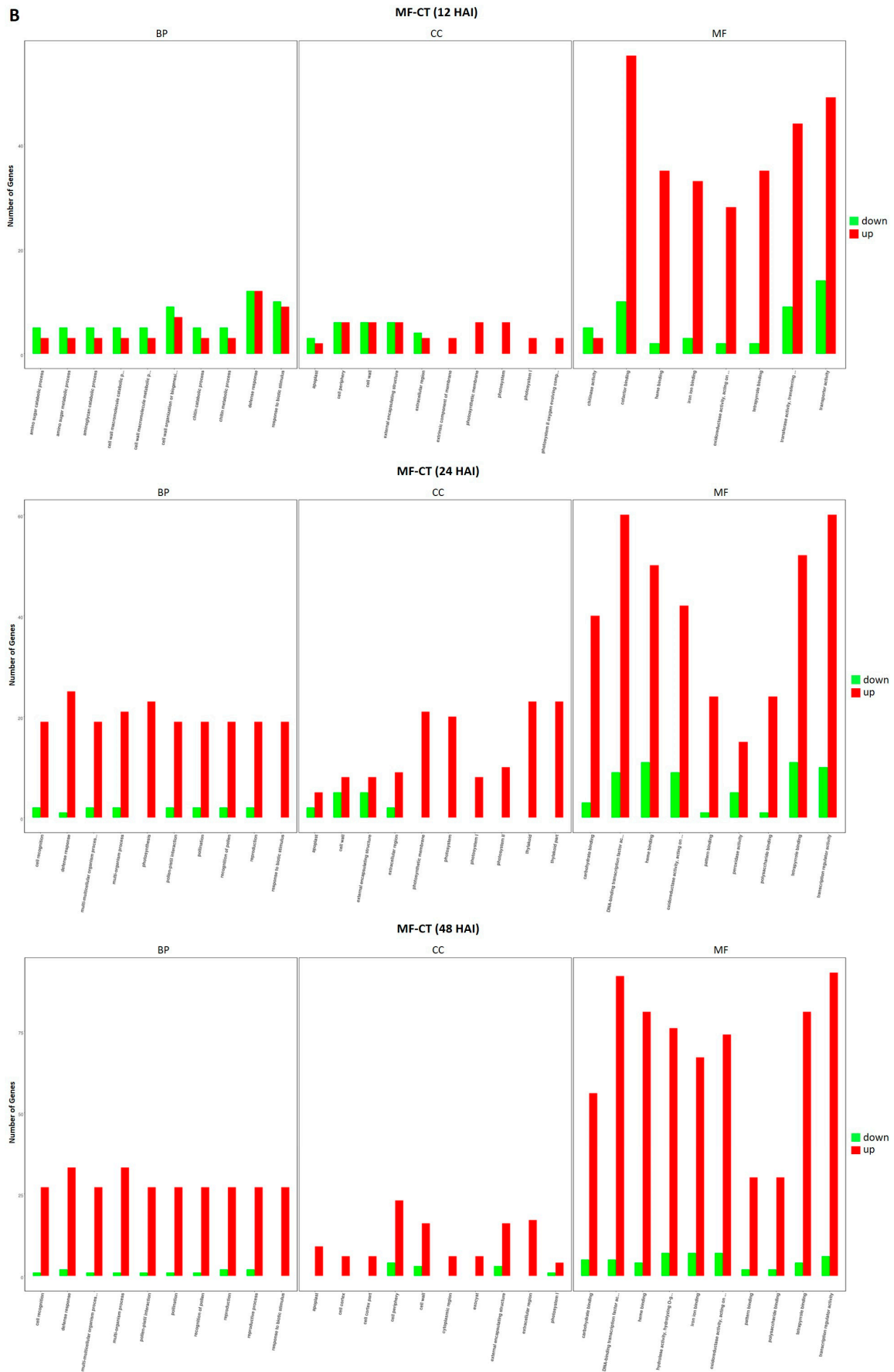
**Figure S1.** Volcano plots of differential expressed genes between CHI, MF, CHI\_MF and CT treatments at three time points. The green part represents downregulated genes and the red part represents up-regulated genes. No significantly expressed genes are represented in blue. The x-axis represents the log2 (fold change) and the y-axis the base mean expression values.

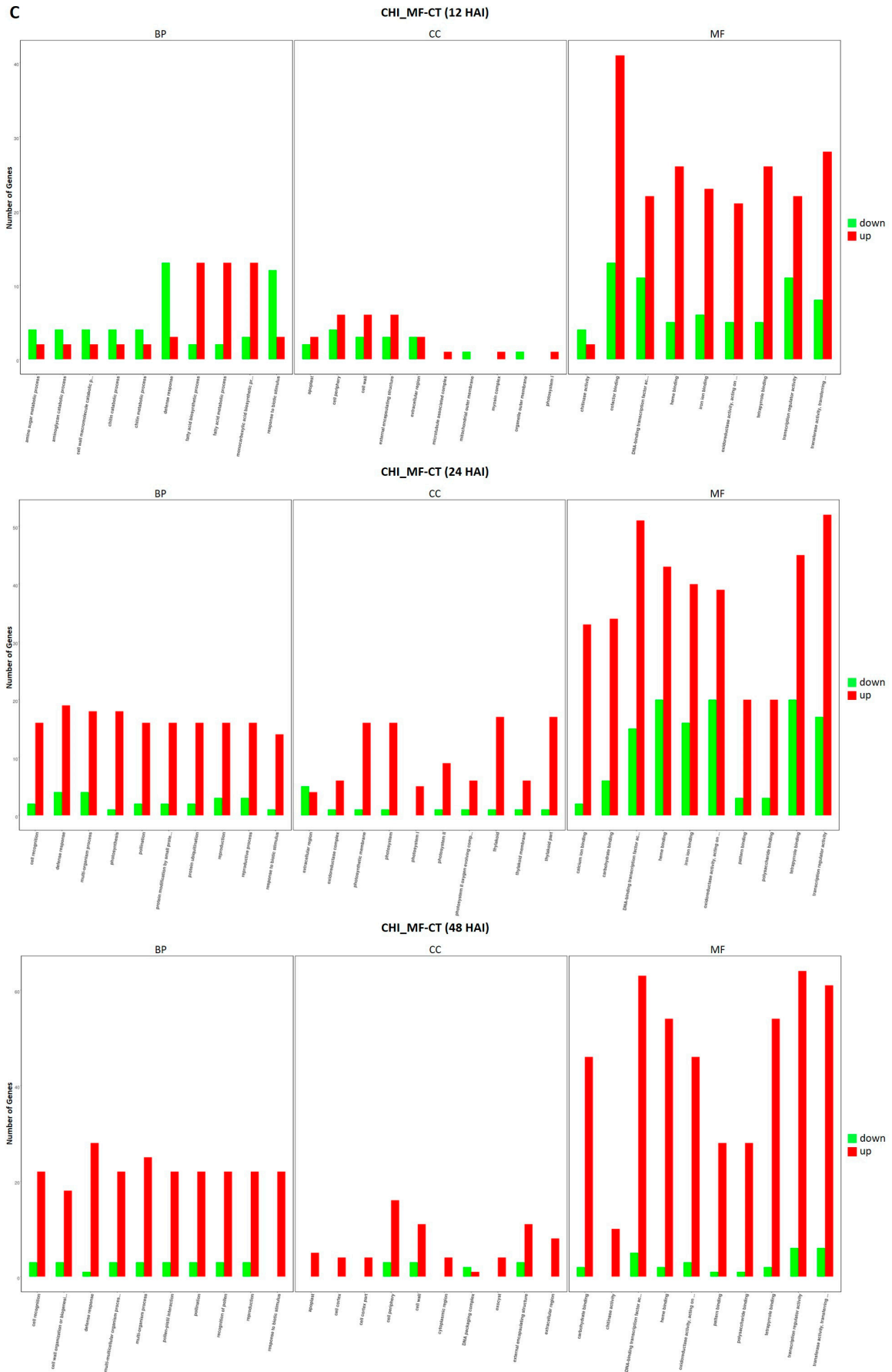


**Figure S2.** Venn diagram representing the distribution of DEGs across the four treatments at three time points.



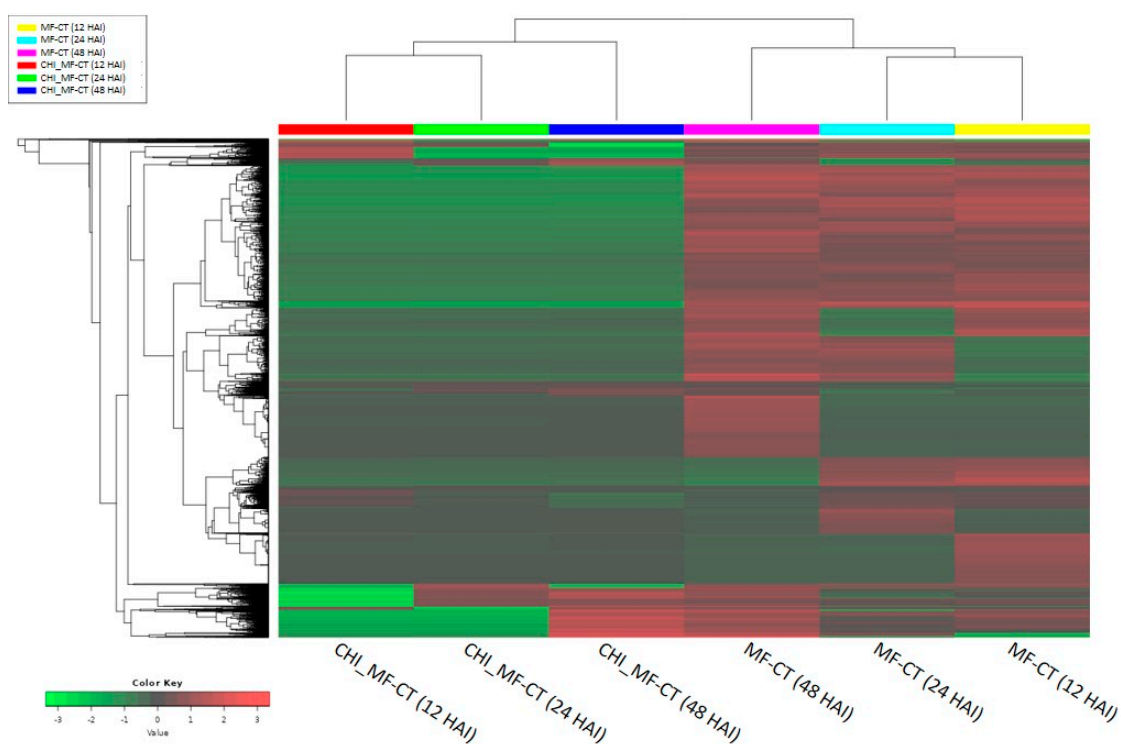
**B**



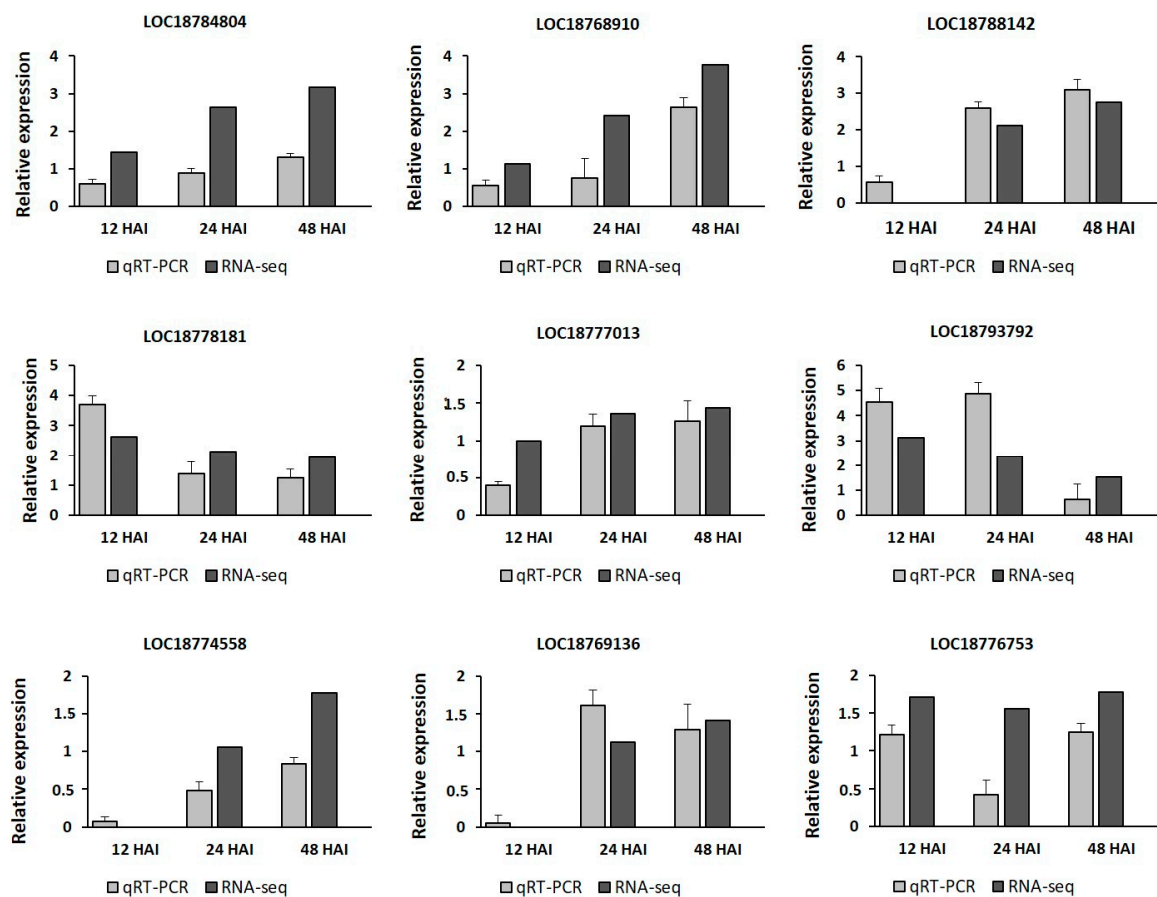


**Figure S3.** Gene Ontology-based functional categorization of the most representative differentially expressed genes. The red and green bars indicate the number of up-and down-regulated genes, respectively, between A) chitosan (CHI) treated and control (CT) fruits, B) *M. fructicola* (MF)

inoculated and control (CT) fruits, and C) chitosan pre-treated - *M. fructicola* inoculated (CHI\_MF) and control (CT) fruits, at three time points.



**Figure S4.** Hierarchical clustering of differential expressed genes of *M. fructicola* based on the average counts of normalized reads between MF and CHI\_MF treatments versus CT treatment, at three time points. Green and red colors in each node of the dendrogram represent repressed and induced, respectively, expression of *M. fructicola* genes.



**Figure S5.** Comparison of RNA-seq and RT-qPCR expression values of selected genes in three different time-points of peach fruit after *M. fructicola* infection. RNA-seq expression levels are depicted as log2 fold change values. RT-qPCR expression levels are represented as mean values from three independent biological replicates.