Figure S1. Hierarchical clustering of the common top-ranked 100 expressed genes, which was obtained from all replicates and samples in both PMB0225 and PHA1037 cultivars. The *heatmap.2* and *hclust* functions (distance method = 'maximum' and cluster method = 'average') from the *gplots* R package (https://cran.r-project.org/package=gplots) were used for clustering analysis based on log(FPKM+1) values. The replicates framed in red showed a clustering behavior discordant to the other two replicates for the same developmental stage, and therefore they were discarded for further analyses.