

Roberta Tosetti, Francesca Tardelli, Alice Tadiello, Valerio Zaffalon, Federico M. Giorgi, Lucia Guidi, Livio Trainotti, Claudio Bonghi and Pietro Tonutti: Molecular and biochemical responses to wounding in mesocarp of peach (*Prunus persica* L. Batsch) ripe fruits

Table S3. Annotated tables containing the full results of the differential expression analyses performed in this paper. The contrasts included are three: BTw vs BTc, GHw vs GHc and a complex contrast design obtained by comparing the two previous contrasts. For every gene, the average expression, the log₂FC of the comparison, p-value and adjusted p-values are indicated (see Materials and Methods). Also, each gene is annotated by the most likely Mapman bin name, bin number and Mapman-based annotation (obtained via the Mercator pipeline: essentially a description of the best *Arabidopsis thaliana* seed used for inferring the function). Uniprot annotation, Gene Ontology assignment (inferred by blast2GO) and the corresponding microarray probe sequence are also provided.

Table S4. Enrichment analysis of GO term, retrieved categorizing genes up – (A) and down- (B) regulated in Glohaven (GH) and BigTop (BT) mesocarp, selected on the basis of P value (<0.01) and FDR (<0.05). GO-ID: the ID number of the GO term. Category: GO terms categorization in Cellular component (C), Molecular function (F) biological Processes (P) groups. Term: description of the GO term. FDR: the proportion of false positives was determined by calculating the false discovery rate corresponding to each enrichment score. P value: P value indicating the statistical significance of the difference between the fraction of genes assigned to GO term retrieved and the fraction of all proteins within the background set assigned to the same GO term. #test: The number of genes in the test set assigned to each GO term retrieved. #Ref: The number of genes in the background set to each GO retrieved. #not Annotated test: The number of genes in the test set not assigned to that GO term. #not Annotated Ref: The total number of genes in the background set not assigned to that GO term. Over/Under: GO terms under or over-represented in the test set. TestSeq:

Gene identifiers for test set. RefSeq: Gene identifiers for background set. GO terms are filtered on the basis of P-value (<0.01) and/or FDR ($q < 0.05$)

Table S5. List of 32 differentially expressed genes showing a similar expression pattern at T2 in the two varieties . For column headers see Table S3.