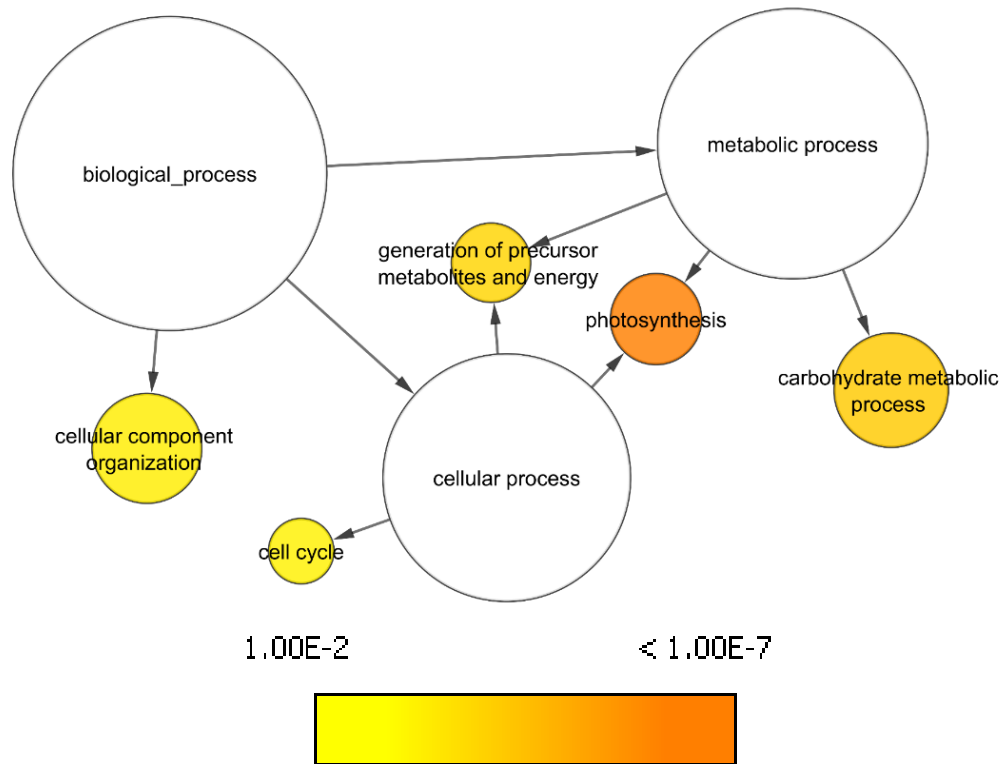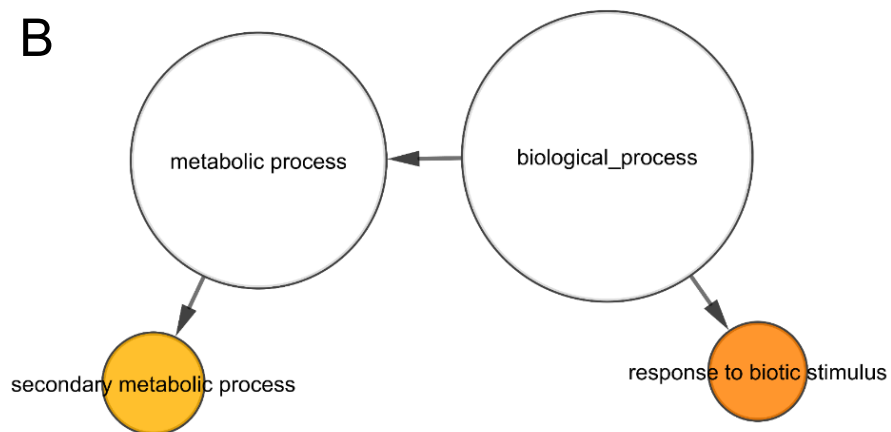**Supplemental Figure 1.** Heat map of the 1686 genes with significant differential expression between vegetative/green and mature/woody tissues in grapevine plants (atlas dataset).
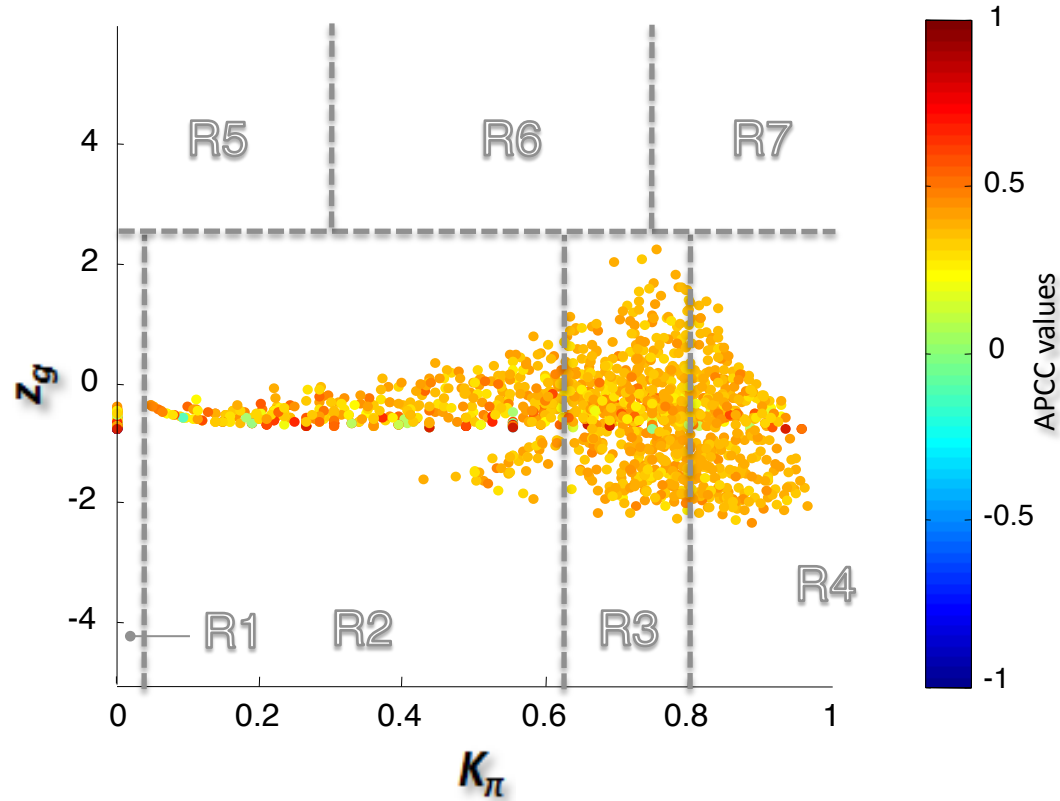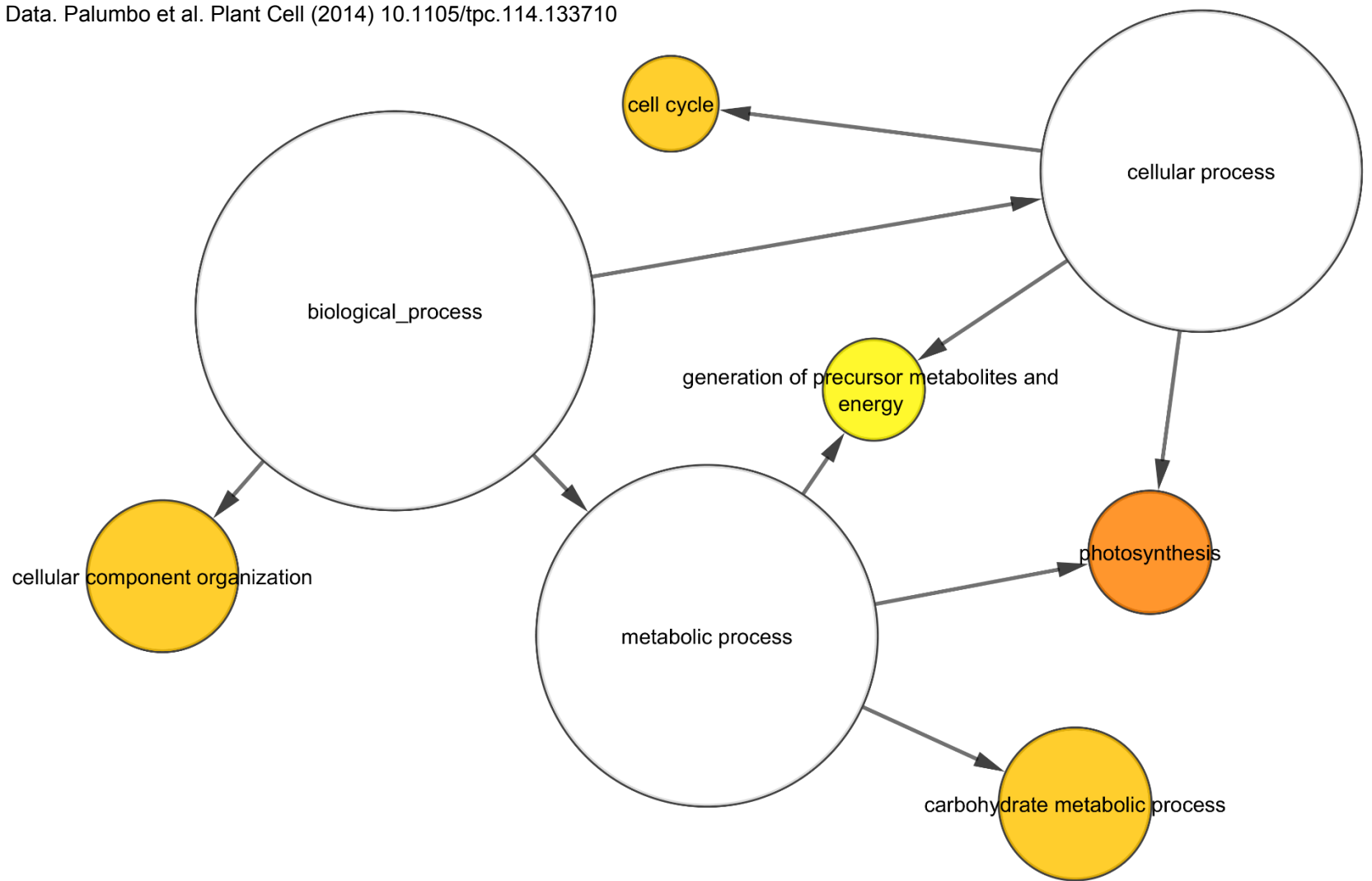
Supplemental Figure 2. The significantly overrepresented functional categories (p<0.05) of the 1220 downregulated (A) and 466 upregulated (B) genes in the grapevine developmental transition (atlas dataset).

Supplemental Figure 3. Heat cartography map for the grapevine atlas (randomized network). The randomized network was generated by keeping node labels of the grapevine correlation network constant while shuffling their edges but preserving the degree of each node. The parameters z_g and K_π represent a normalized measure of intra-module communication and the mode of communication between nodes in different modules, respectively. The plane identified by these two parameters is divided into seven regions, each defining a specific node role. Each point represents a node in the grapevine randomized network and the color of the each node corresponds to its APCC value. Roles have been assigned to each node, according to the heat cartography described in the Methods section.
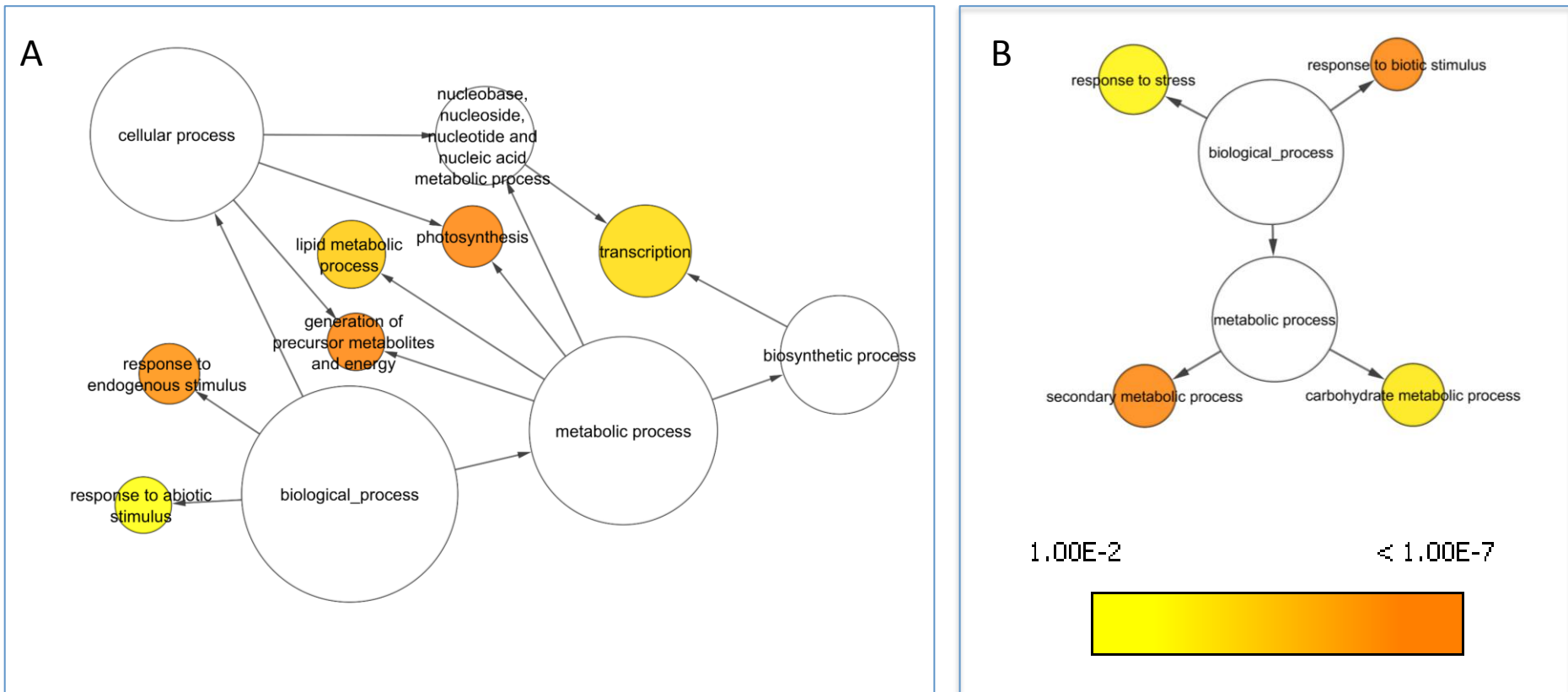
Supplemental Figure 4. The significantly overrepresented functional categories (p < 0.05) of the 921 neighbors of grapevine switch genes (atlas dataset). All grapevine transcripts were annotated against the V1 version of the 12x draft annotation of the grapevine genome. Gene Ontology annotations were assigned to switch genes and their neighboring genes using the BiNGO v2.3 plug-in tool in Cytoscape v2.6 with PlantGOslim categories. Overrepresented PlantGOslim categories were identified using a hypergeometric test with a significance threshold of 0.05, after Benjamini and Hochberg correction with a false discovery rate of 0.001.
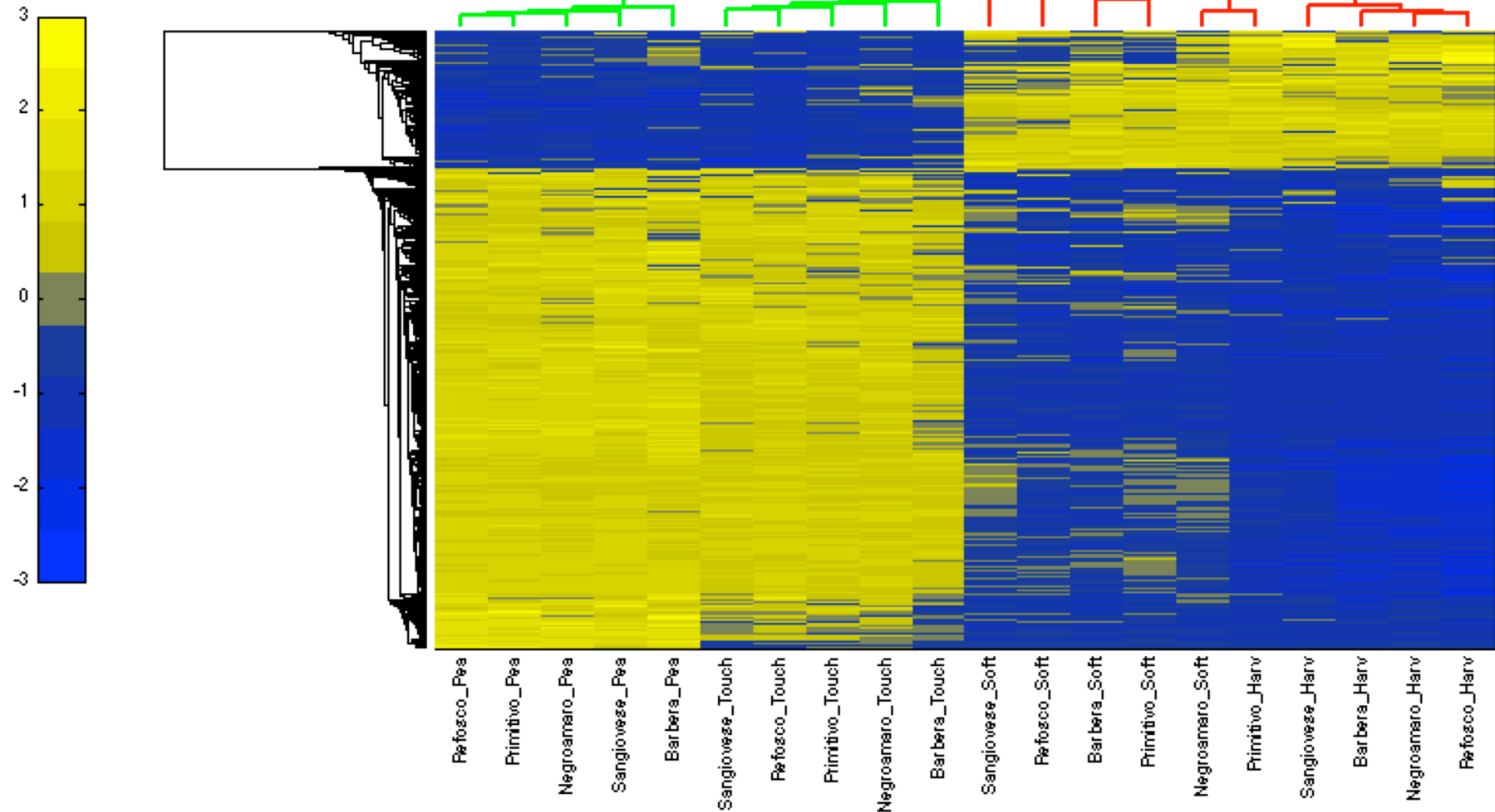
Supplemental Figure 5. Heat map of the 1883 genes with significant differential expression between the green and maturation phases during berry development in five red-berry grapevine varieties (color).

Supplemental Figure 6. The significantly overrepresented functional categories (p<0.05) of the 1464 downregulated (A) and 419 upregulated (B) genes during the grapevine berry developmental transition (berry dataset). All grapevine transcripts were annotated against the V1 version of the 12x draft annotation of the grapevine genome. Gene Ontology annotations were assigned to switch genes and their neighboring genes using the BiNGO v2.3 plug-in tool in Cytoscape Cytoscape v2.6 with PlantGOslim categories. Overrepresented PlantGOslim categories were identified using a hypergeometric test with a significance threshold of 0.05, after Benjamini and Hochberg correction with a false discovery rate of 0.001.
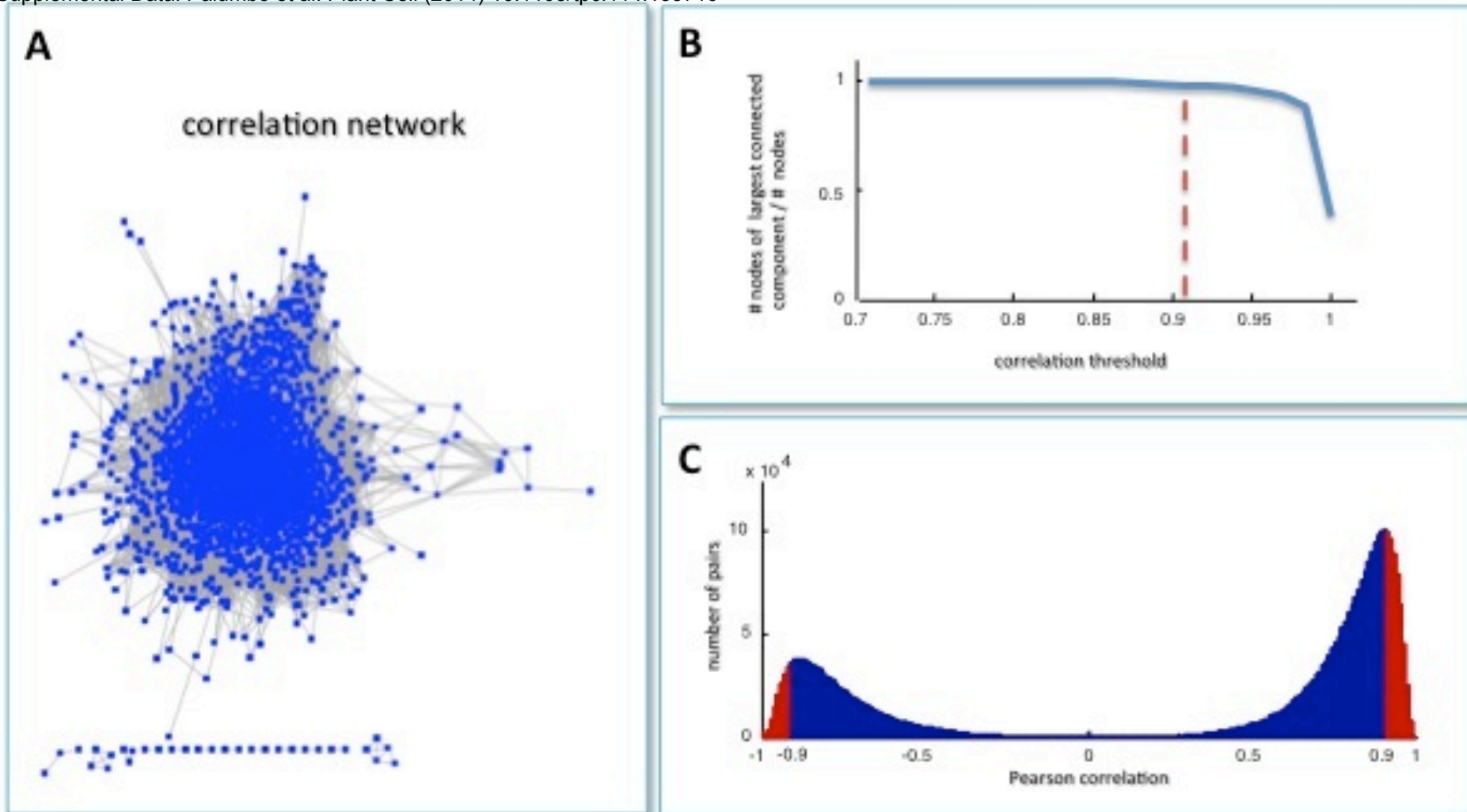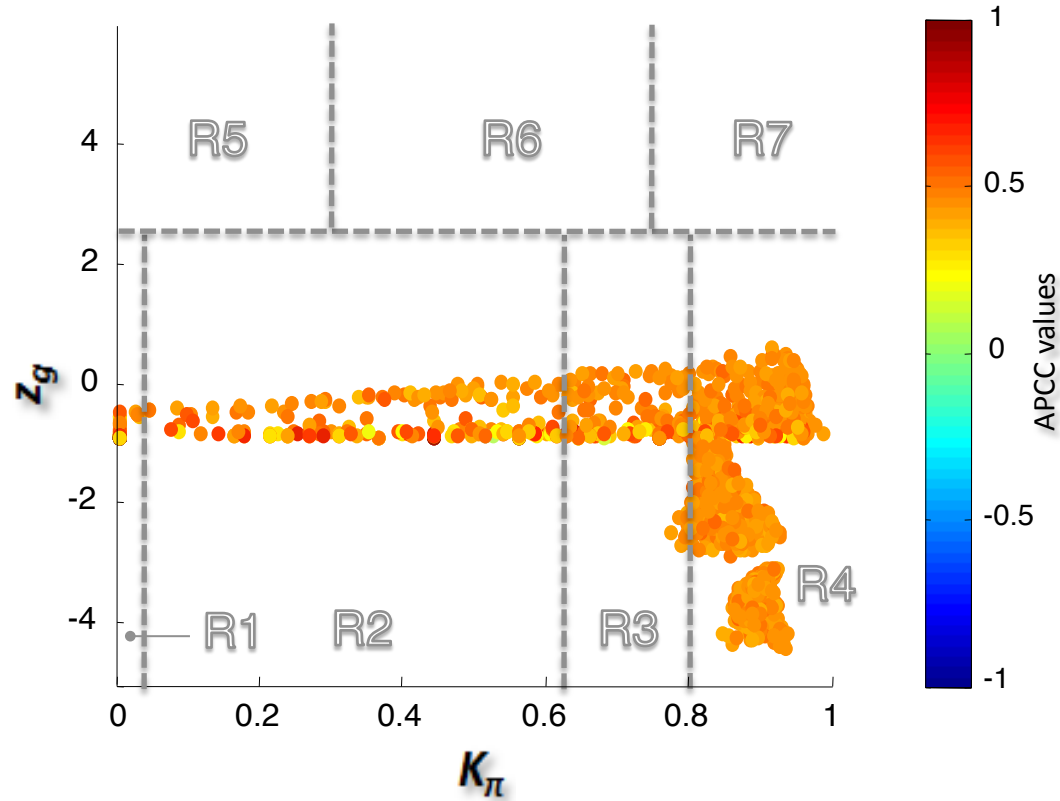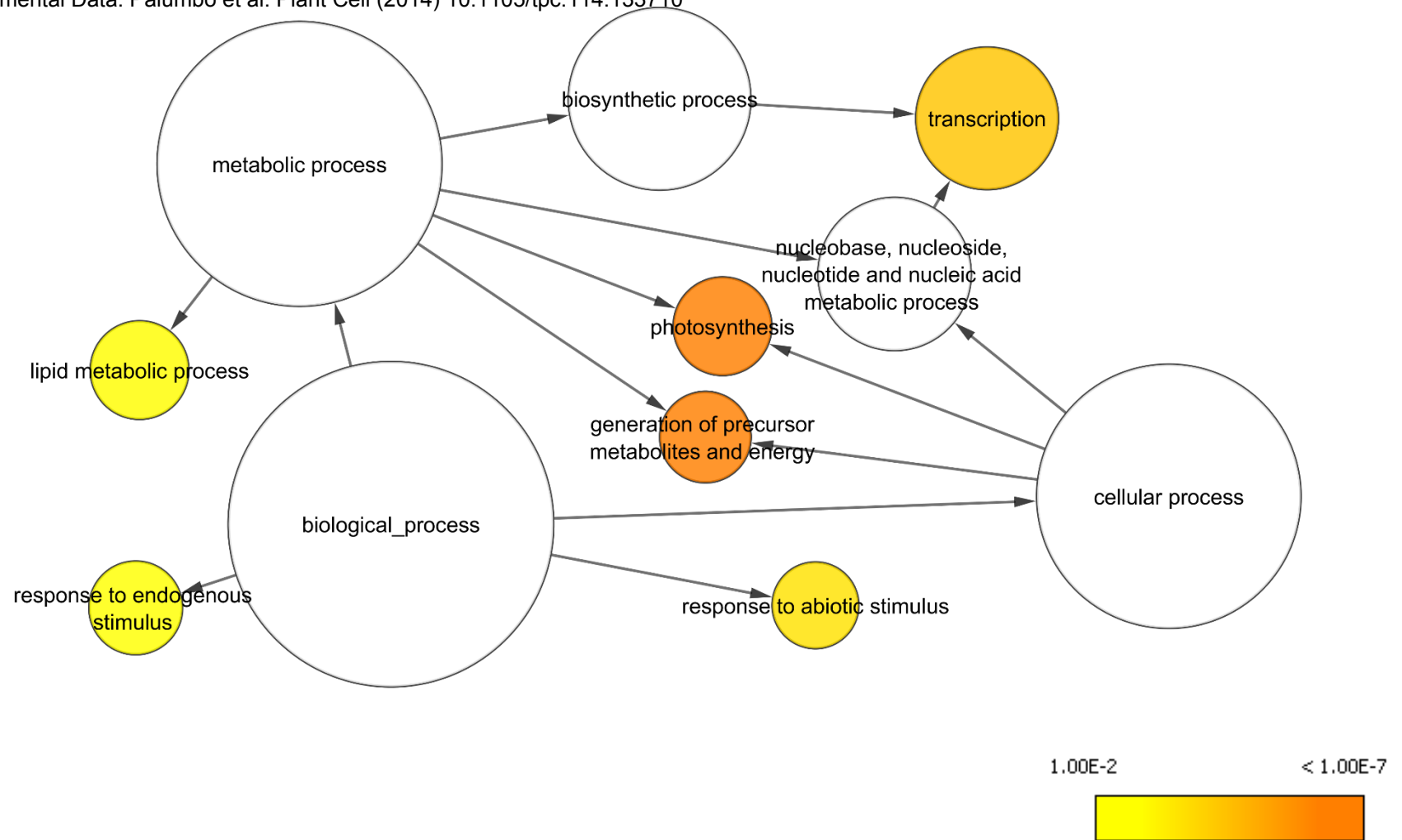
Supplemental Figure 7. Grapevine berry co-expression network. A) The correlation network obtained using gene expression during the development of five red-berry grapevine varieties. Nodes are mRNAs and a link is present when the Pearson correlation between the expression profiles of two mRNAs is greater than the 85th percentile of the distribution of the Pearson correlation coefficients. B) The inverse of the number N of network-connected components is plotted against the correlation threshold. The chosen correlation value is the largest threshold that maintains network integrity. C) Pearson correlation distribution of all mRNA profile pairs. Red regions correspond to the most-correlated pairs in the network.

Supplemental Figure 8. Heat cartography map for the berry transcriptome of five red-berry grapevine varieties (randomized network). The randomized network was generated by keeping node labels of the red grapevine correlation network constant while shuffling their edges but preserving the degree of each node. The parameters z_g and K_π represent a normalized measure of intra-module communication and the mode of communication between nodes in different modules, respectively. The plane identified by these two parameters is divided into seven regions, each defining a specific node role. Each point represents a node in the red-berry grapevine randomized network and the color of the each node corresponds to its APCC value. Roles have been assigned to each node, according to the heat cartography described in the Methods section.

Supplemental Figure 9. The significantly overrepresented functional categories (p<0.05) of the 1266 neighbors of grapevine berry switch genes. All grapevine transcripts were annotated against the V1 version of the 12x draft annotation of the grapevine genome. Gene Ontology annotations were assigned to switch genes and their neighboring genes using the BiNGO v2.3 plug-in tool in Cytoscape Cytoscape v2.6 with PlantGOslim categories. Overrepresented PlantGOslim categories were identified using a hypergeometric test with a significance threshold of 0.05, after Benjamini and Hochberg correction with a false discovery rate of 0.001.
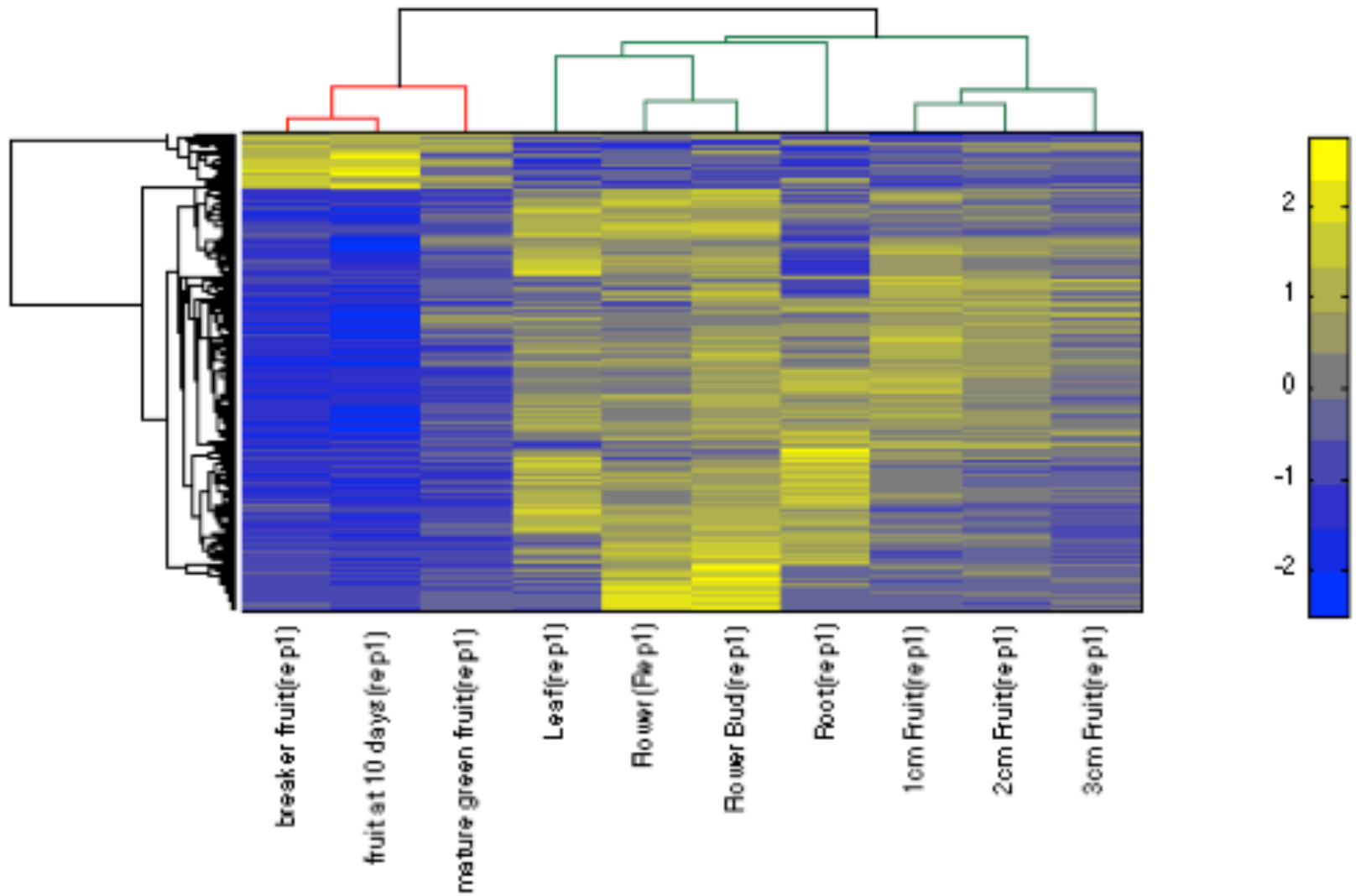
Supplemental Figure 10. Heat map of the 1961 genes with significant differential expression between vegetative/green and mature/woody tissues in wild-type tomato plants.
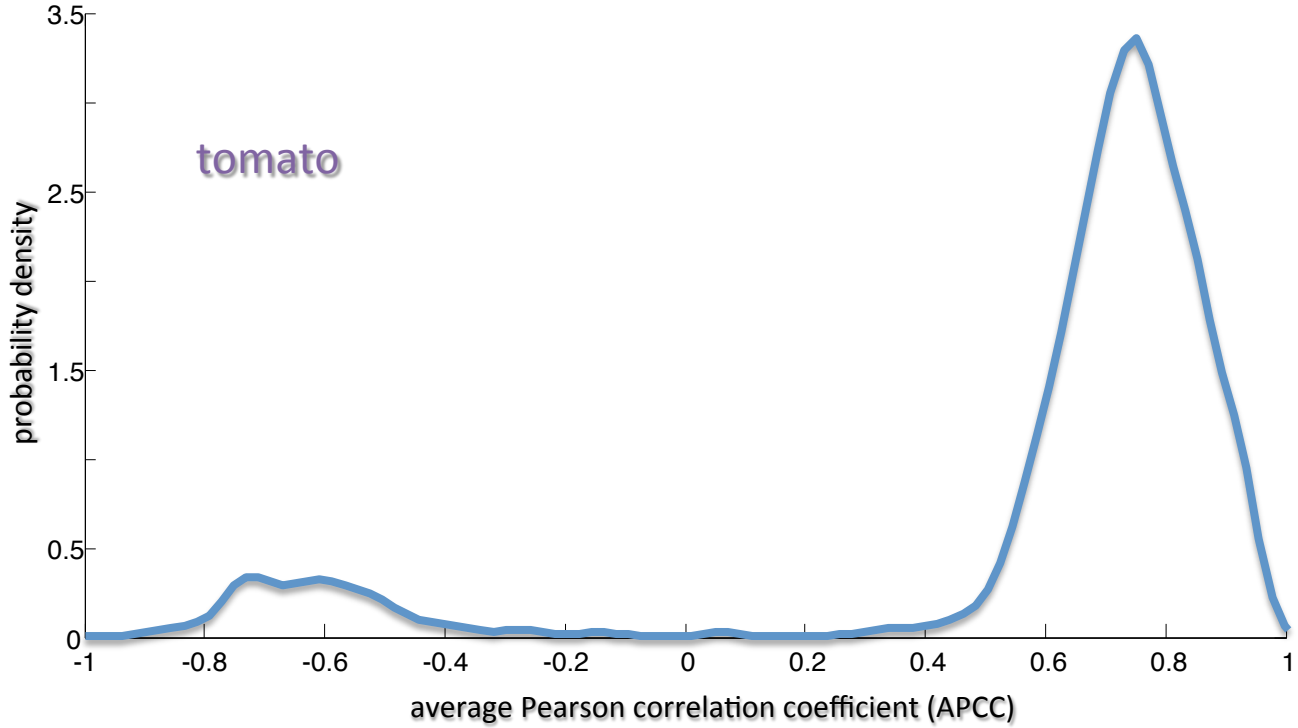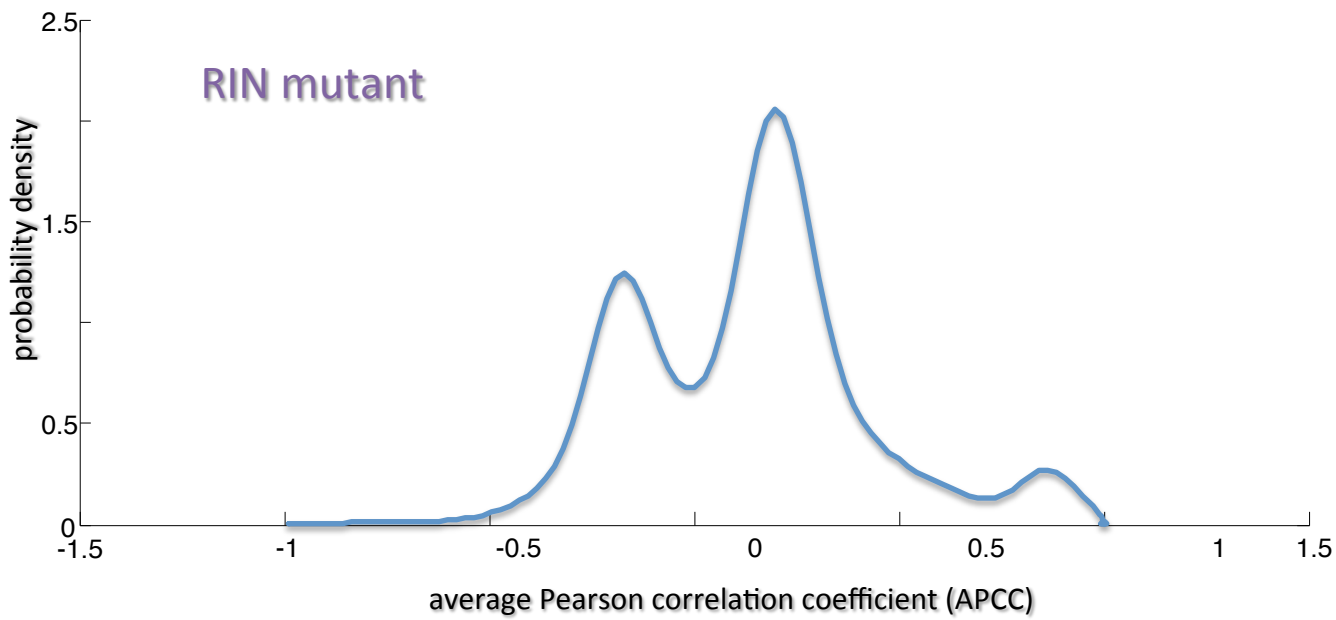
Supplemental Figure 11. Average Pearson correlation coefficient in wild-type tomato (A) and the rin mutant (B). The curve is the estimated probability density using a smoothing algorithm with a Gaussian kernel of the average Pearson correlation coefficient (APCC) for each hub (i.e. node with degree greater than 5) in the correlation network in wild-type tomato (A) and the rin mutant (B). The distribution of APCCs shows a peak located at high positive APCC values (mirroring party hubs in PPI networks) and a peak located at negative APCC values (fight-club hubs). A third peak is located at low positive APCC values (mirroring date hubs in PPI networks). However this peak is clearly visible only in the rin mutant dataset because in the tomato the number of the date hubs is much lower than the number of party hubs.