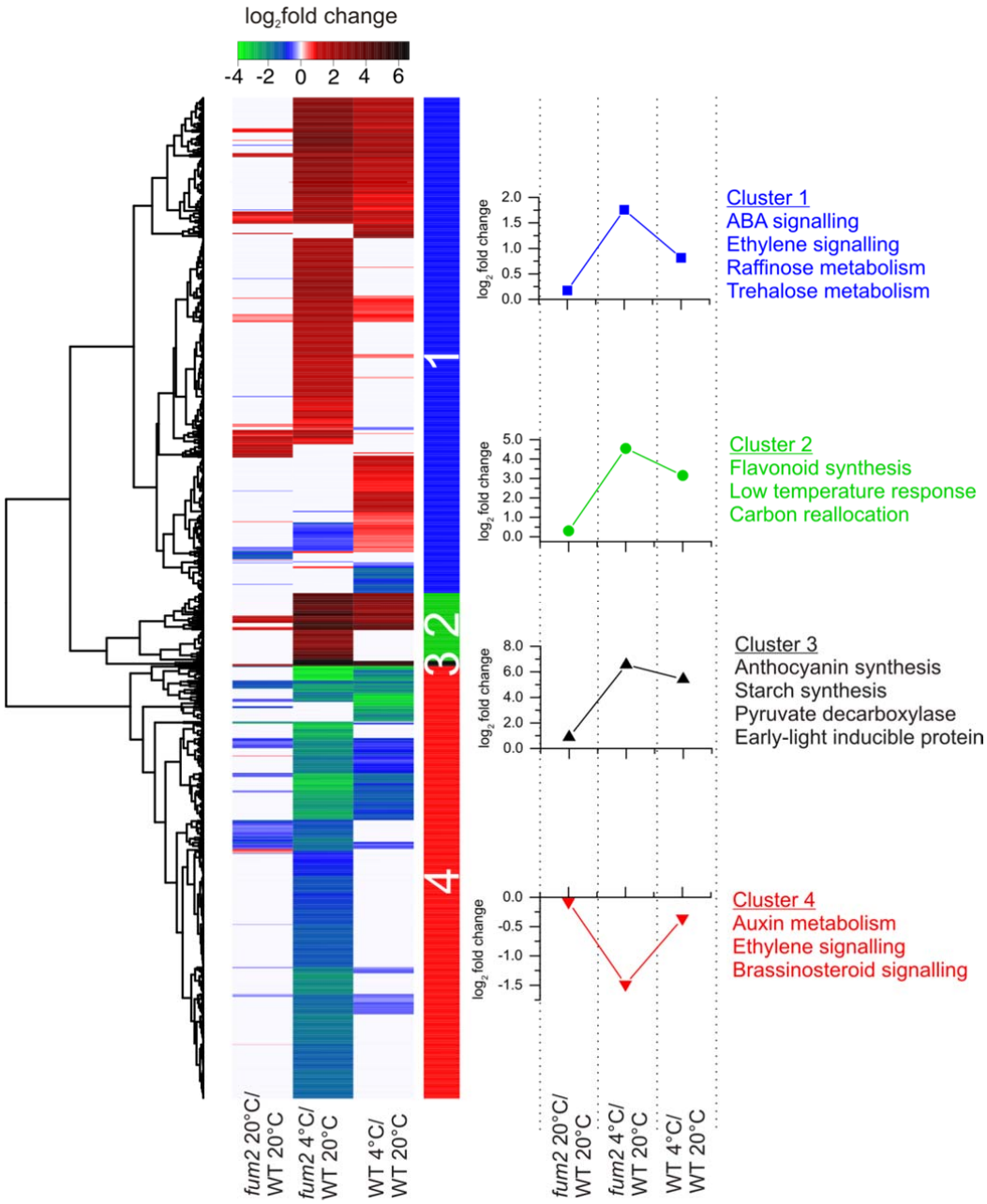

Figure S4. Cluster analysis of changes in gene expression during acclimation to low temperature in WT and *fum2*. A heat map was constructed from the results of the cluster analysis after 8 hrs at 4°C comparing fold changes in genes relative to the WT at 20°C. Only genes that were differentially expressed (P<0.05, Fold change >2) between the 2 genotypes at 20°C or 4°C were included. Clusters were assigned according to the colored bar in the center of the figure, and average log2 fold change graphs are shown for each cluster. Clustering was done using the Euclidean distance method using complete linkages. Ontological groups over-represented in each cluster were defined using DAVID (17)