

Instructions for Mapman visualization of Supplemental Dataset 1.

The visualization of these data requires the installation of the free Mapman software which can be downloaded from <http://gabi.rzpd.de/projects/MapMan/>. Once the Mapman software is installed the data contained in Supplemental_Dataset_1.zip should be saved, unzipped to a directory and then imported by selecting 'File', 'add data'. The Mapping 'Mapping_overview_AgiCode' should be selected for each pathway.

The software displays colored squares, representing individual genes, overlaid onto drawings of biological pathways. Red indicates down-regulation and blue up-regulation, with the intensity corresponding to the magnitude of the change (the scaling can be adjusted via 'pathway', 'options'). Mouse-over or clicking on an individual square will display the annotation, AGI code and description of the gene. The statistics tab is a recent addition to the software and should be ignored for our dataset as it is not valid when differentially expressed genes have been selected.

Various pathways can be used to explore our data but we would recommend the following; Metabolism_overview, Regulation_overview, Photosynthesis, Secondary_metabolism and transcription as most relevant to the conclusions of this study. Additional pathways are also present, with more being added, that will give a wide overview of the data.

Mapman references

Thimm O, Blasing O, Gibon Y, Nagel A, Meyer S, et al. (2004) MAPMAN: a user-driven tool to display genomics data sets onto diagrams of metabolic pathways and other biological processes. *Plant J* 37: 914-939.

Usadel, B, Nagel, A, Thimm, O, Redestig, H, Blasing, OE, et al. (2005). Extension of the visualization tool MAPMAN to allow statistical analysis of arrays, display of corresponding genes, and comparison with known responses. *Plant Physiol* 138: 1195-1204.