



Figure S3: Hierarchical clustering of the expression data in response to several perturbations or in different mutant backgrounds. Meta-analysis of the expression for genes encoding 68 COX-related proteins in response to different perturbations, stress conditions or in several mutant-backgrounds. Conditions where at least 30% of the genes change their expression more than 2-fold were selected. The analysis was made by exploring publicly available microarray data included in the Genevestigator database (https://genevestigator.com/gv/doc/intro_plant.jsp, [100]). Expression level is represented as log₂-ratio of differential expression, with up-regulation represented in red and down-regulation represented in green.

100. Hruz, T.; Laule, O.; Szabo, G.; Wessendorp, F.; Bleuler, S.; Oertle, L.; Widmayer, P.; Gruissem, W.; Zimmermann, P. Genevestigator V3: A reference expression database for the meta-analysis of transcriptomes. *Adv. Bioinform.* **2008**, 420747, doi:10.1155/2008/420747.