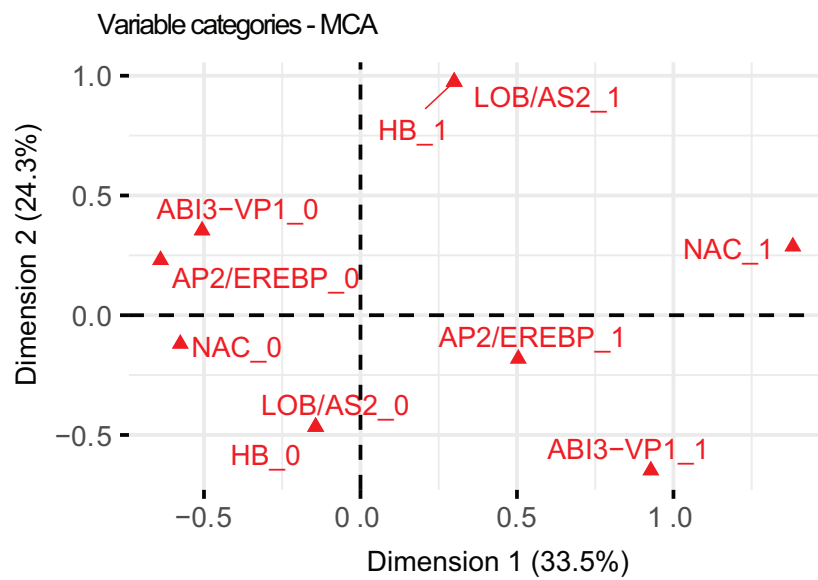


Supplementary Fig. S1

A gene regulatory network identified via eY1H assays has a scale-free structure

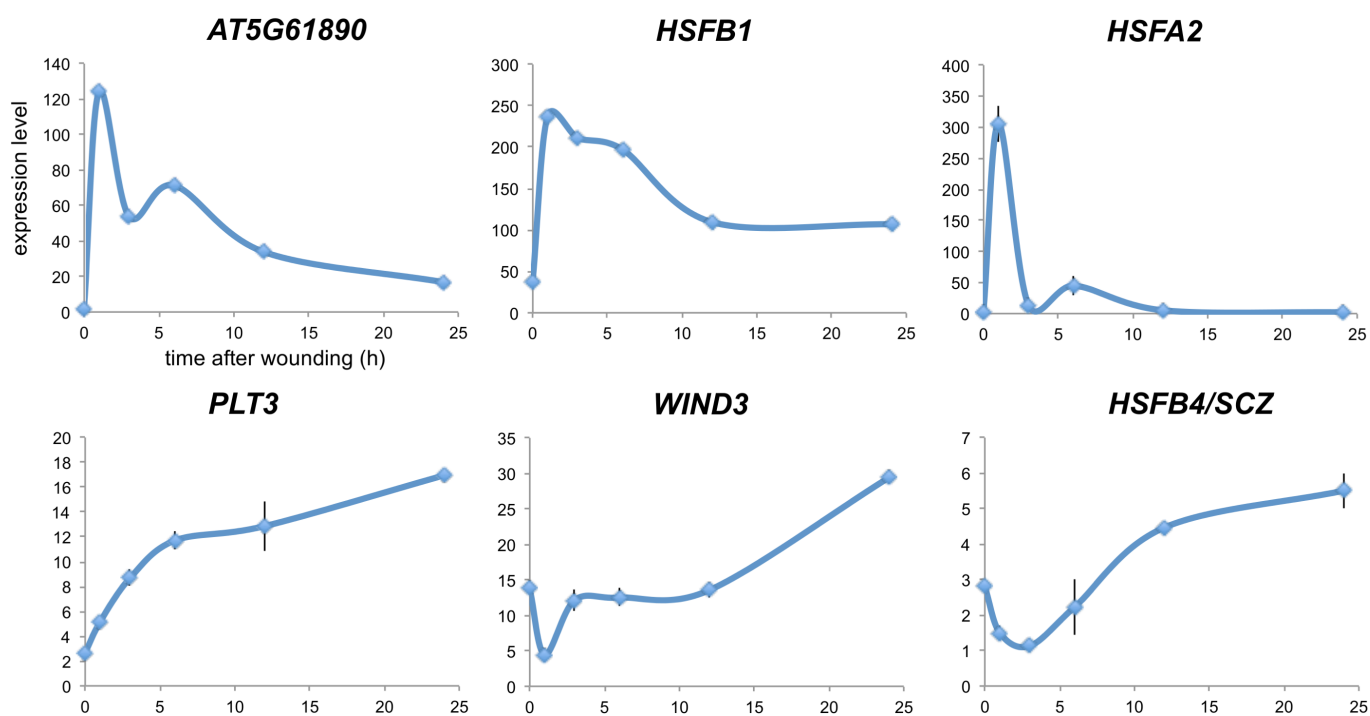
A histogram describing the number of interactions per TF, as listed in Table S2, which fit a power-law distribution.



Supplementary Fig. S2

Multiple correspondence analysis for TF classes represented among the power nodes.

Multiple correspondence analysis (MCA) was used to visualize the TF classes that display the largest variation in terms of presence between the 34 power nodes identified by the power graph compression. The MCA analysis tool in the FactoMineR package in R was used for analysis and visualization.



Supplementary Fig. S3

Expression profile of select genes from Fig. 4 after wounding

Expression data are retrieved from RNA-seq dataset (Ikeuchi et al., 2017).