Plant Omics Journal POJ

POJ 10(03):139-145(2017) ISSN:1836-3644
doi: 10.21475/poj.10.03.17.pne468

Data mining approaches highlighted transcription factors that play role in thermo-priming

Fereshteh Izadi[*], **Hamid Najafi Zarrini, Ghaffar Kiani, Nadali Babaeian Jelodar**

List of Supplementary Figures

Fig 1 Schematic representation of the thermos-memory experimental design

Fig 2 Venn diagram and hierarchical clustering of differentially expressed probsest between primed and unprimed plants

Fig 3 pie chat of significant GO categoris of up-regulated genes between primed and unprimed plants

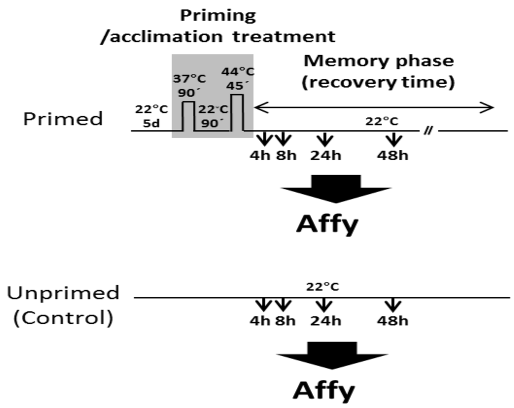
Fig 4 pie chat of significant GO categoris of down-regulated genes between primed and unprimed plants

Fig 5 heirarchical clustering of differentially-expressed transcription factors between primed and unprimed plants

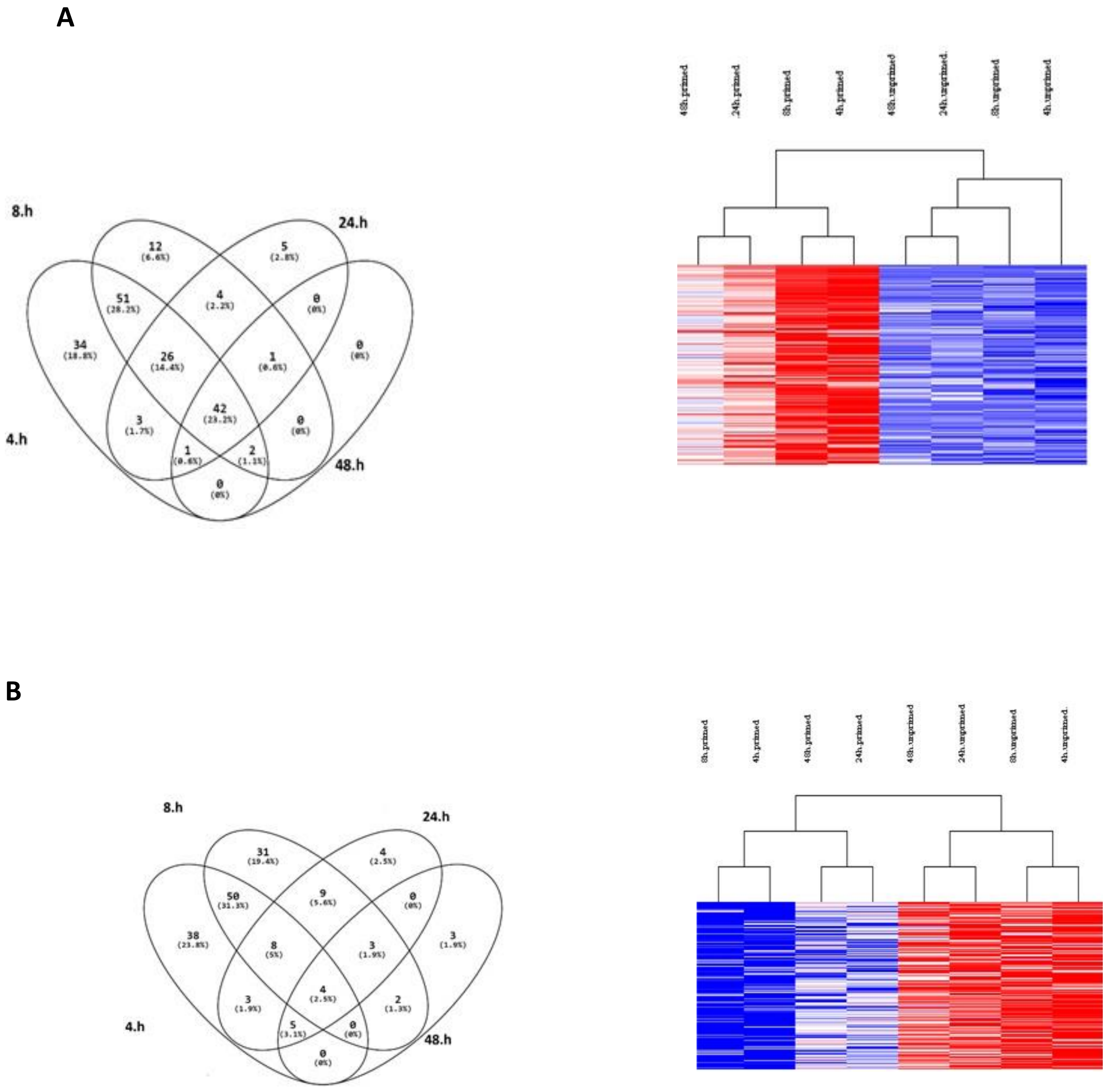
Fig 6 ROC curves of GRNs obtained by different methods

Fig 7 GRN derived by GENIE3 algorithm

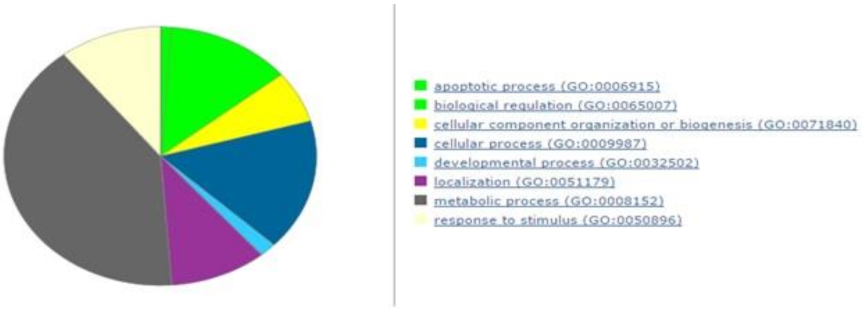
Fig 8 visualization of GRN derived by GENIE3



Supplementary Fig 1 Schematic representation of the thermos-memory experimental design

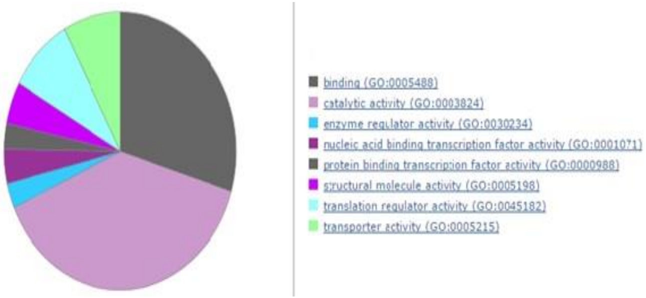


Supplementary Fig 2 Venn diagram and hierarchical clustering of differentially expressed probsest between primed and unprimed plants. (**A**) up-regulated, (**B**) down-regulated with a two-fold cut-off of fold change (FC) and P-value < 0.05.

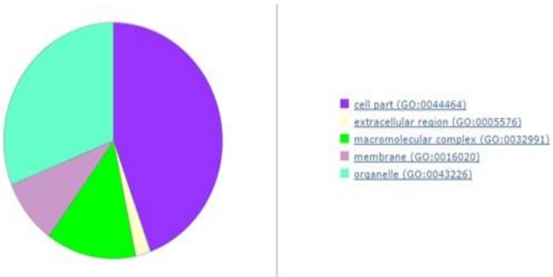


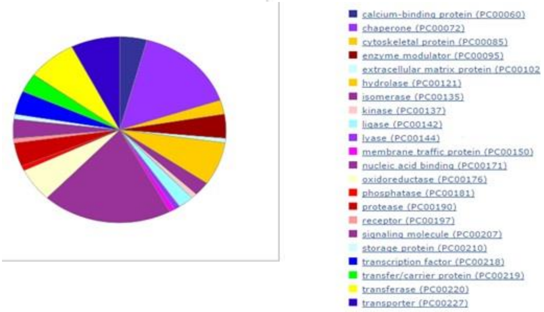
Biological process

Molecular-Function



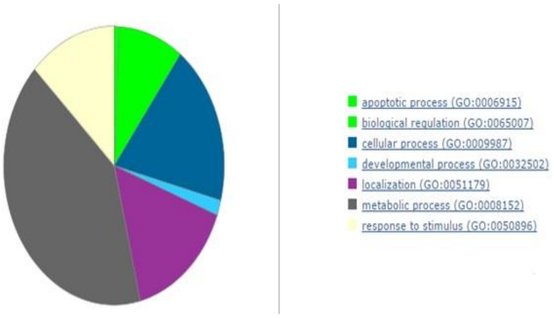
Cellular-Localization



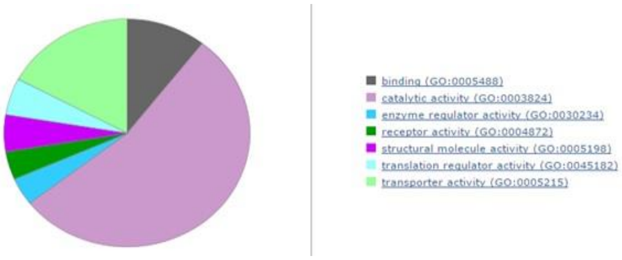


Protein classes

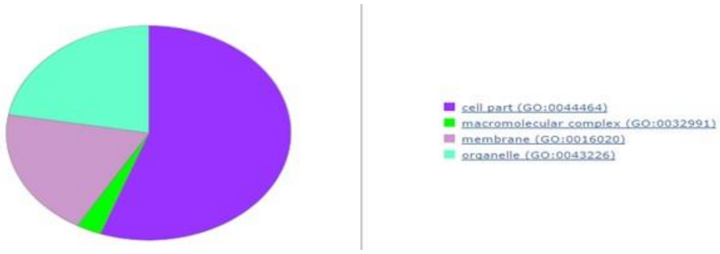
Supplementary Fig 3 pie chat of significant GO categoris of up-regulated genes between primed and unprimed plants



Biological process

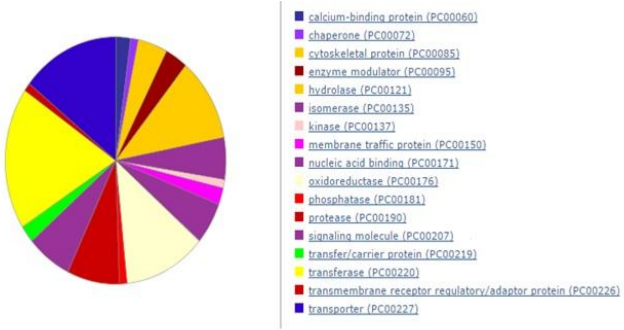


Molecular-Function

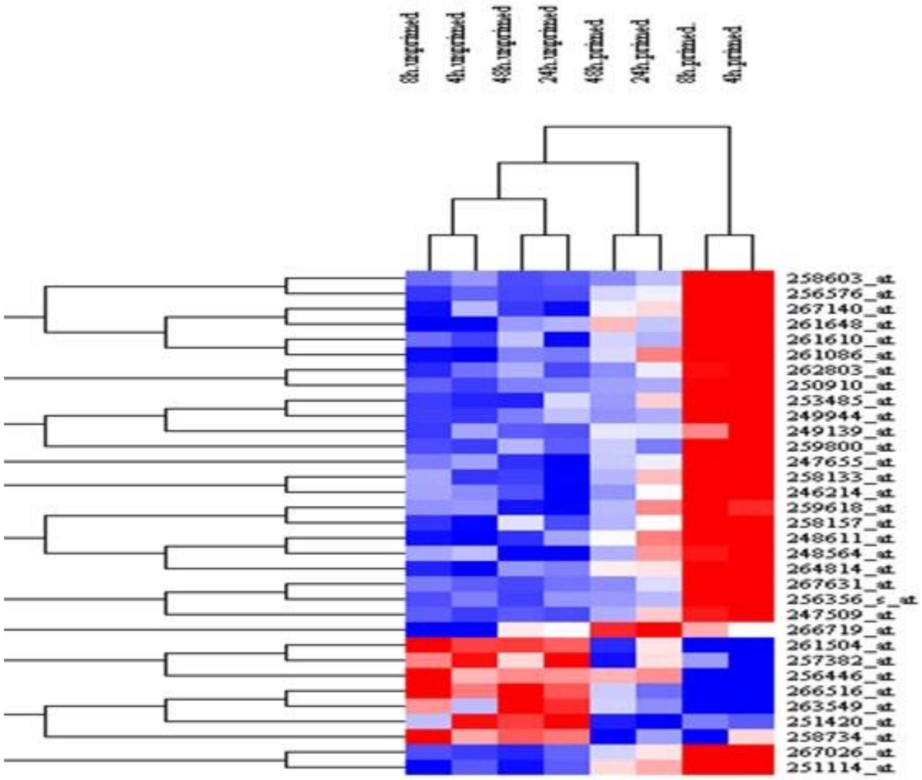


Cellular-Localization

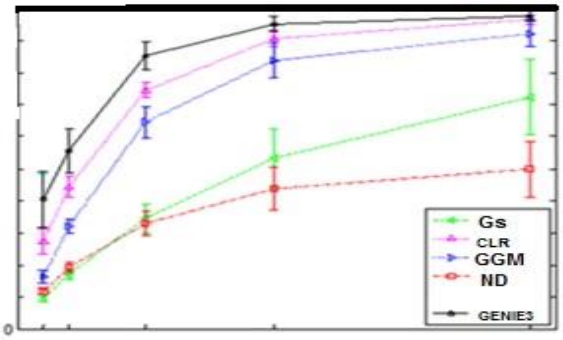
Protein classes



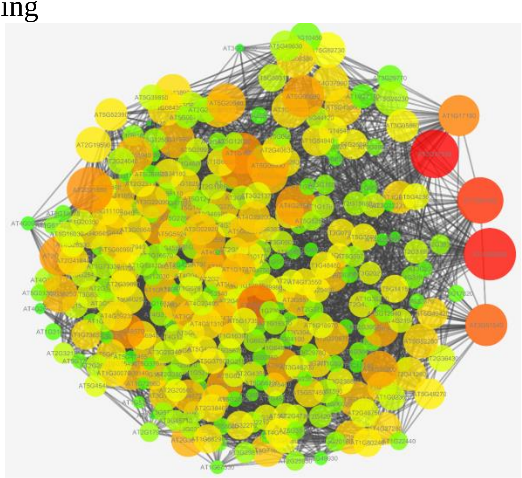
Supplementary Fig 4 pie chat of significant GO categoris of down-regulated genes between primed and unprimed plants



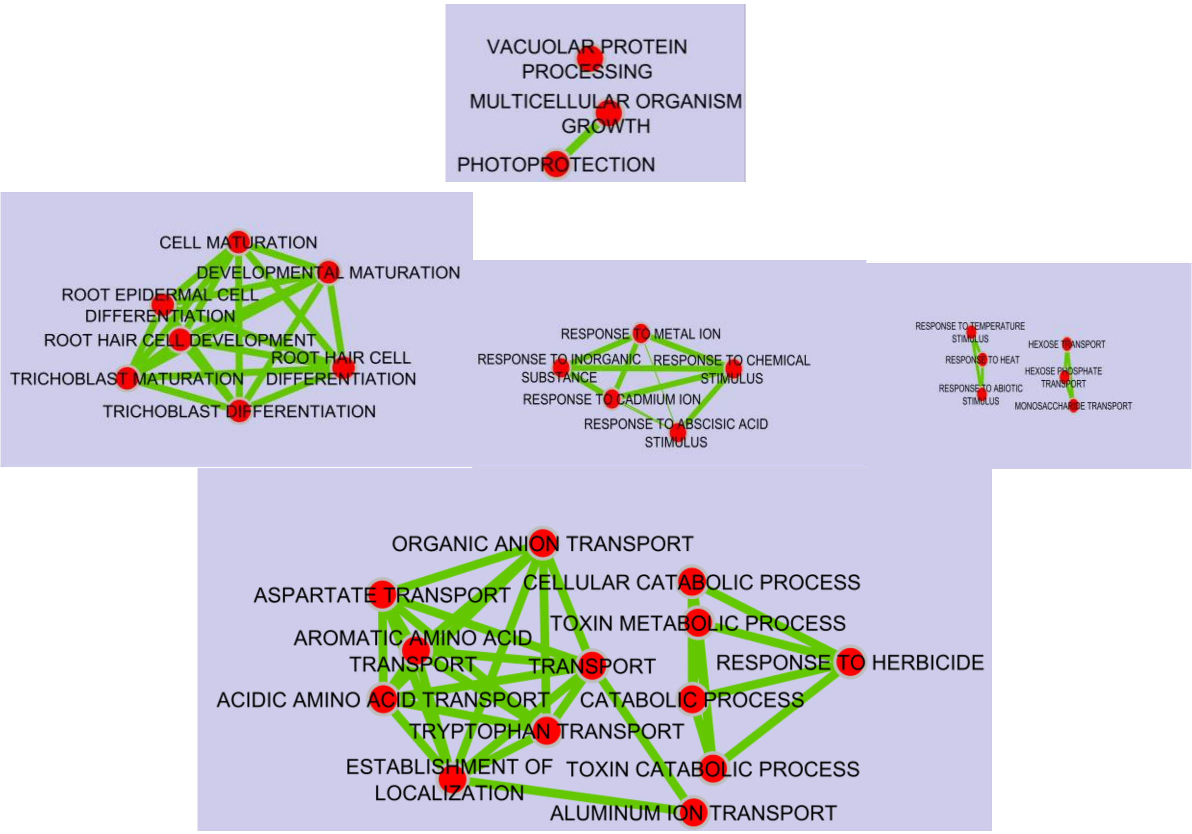
Supplementary Fig 5 heirarchical clustering of differentially-expressed transcription factors between primed and unprimed plants



Supplementary Fig 6 ROC curves of GRNs obtained by different methods. Horizontal axis is FP rate= false positive rate and vertical TP rate= true positive. GGM: Graphical Gaussian Model, ND: network Deconvolution, GB: Global silencing



Supplementary Fig 7 GRN derived by GENIE3 algorithm. By using the NetworkAnalyzer Cytoscape plugin we mapped degree and betweeness parameters to node size and color so that darker and bigger nodes showing higher degree and betweeness centrality.



Supplementary Fig 8 the GRN derived by GENIE3 was visualized by Cytoscape version 3.3.0 and clustered to underlying sub-networks by MCODE Cytoscape plugin then the modules annotated by BiNGO plugin (Maere et al., 2005) and clusters were visualized by Enrichment map Cytoscape plugin.