

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

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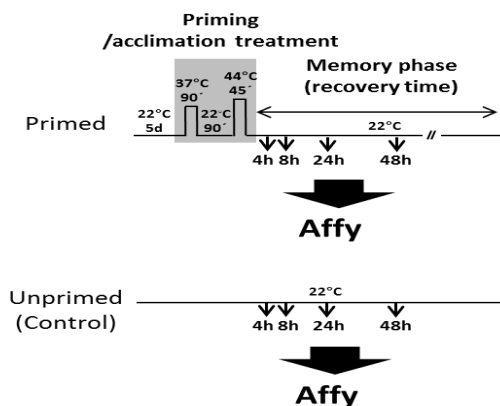
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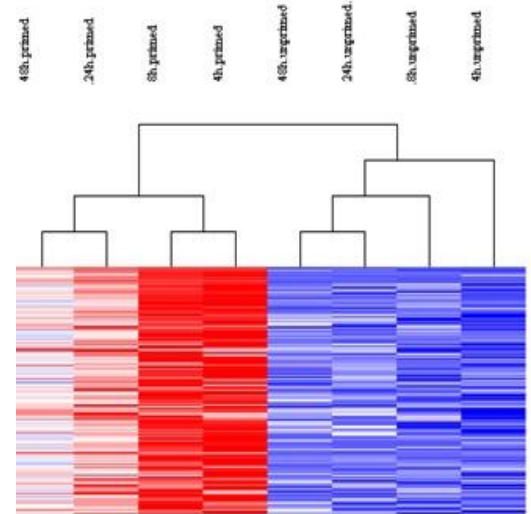
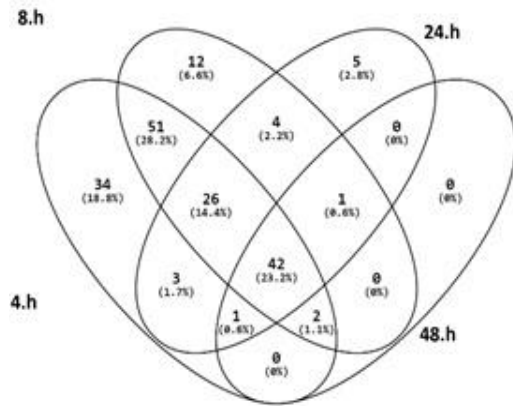
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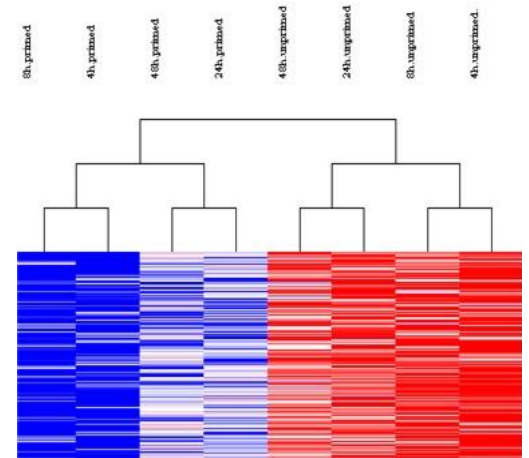
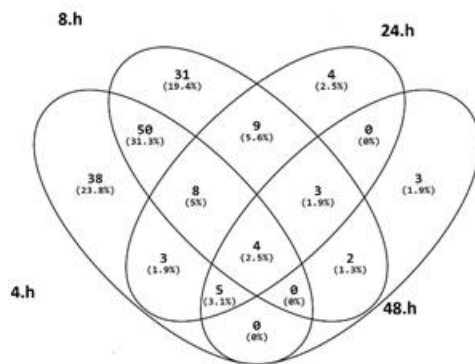


Supplementary Fig 1 Schematic representation of the thermos-memory experimental design

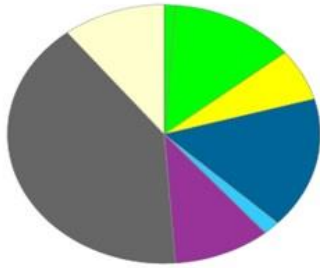
A



B

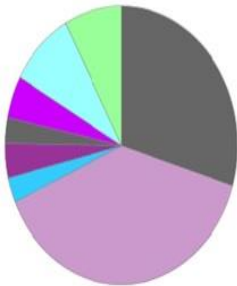


Supplementary Fig 2 Venn diagram and hierarchical clustering of differentially expressed probest between primed and unprimed plants. **(A)** up-regulated, **(B)** down-regulated with a two-fold cut-off of fold change (FC) and P-value < 0.05.



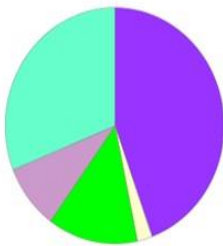
- apoptotic process (GO:0006915)
- biological regulation (GO:0065007)
- cellular component organization or biogenesis (GO:0071840)
- cellular process (GO:0009987)
- developmental process (GO:0032502)
- localization (GO:0051179)
- metabolic process (GO:0008152)
- response to stimulus (GO:0050896)

Biological process



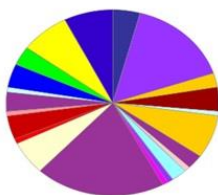
- binding (GO:0005488)
- catalytic activity (GO:0003824)
- enzyme regulator activity (GO:0030234)
- nucleic acid binding transcription factor activity (GO:0001011)
- protein binding transcription factor activity (GO:0000988)
- structural molecule activity (GO:0005198)
- translation regulator activity (GO:0045182)
- transporter activity (GO:0005215)

Molecular-Function



- cell part (GO:0044464)
- extracellular region (GO:0005576)
- macromolecular complex (GO:0032991)
- membrane (GO:0016020)
- organelle (GO:0043226)

Cellular-Localization

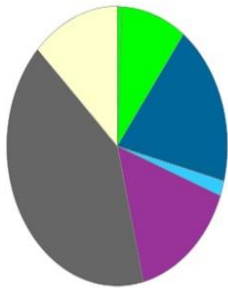


- calcium-binding protein (PC00060)
- chaperone (PC00072)
- cytoskeletal protein (PC00085)
- enzyme modulator (PC00093)
- extracellular matrix protein (PC00102)
- hydrolase (PC00121)
- isomerase (PC00135)
- kinase (PC00137)
- ligase (PC00142)
- lyase (PC00144)
- membrane traffic protein (PC00150)
- nucleic acid binding (PC00171)
- oxidoreductase (PC00176)
- phosphatase (PC00181)
- protease (PC00190)
- receptor (PC00197)
- signaling molecule (PC00207)
- storage protein (PC00210)
- transcription factor (PC00218)
- transfer/carrier protein (PC00219)
- transferase (PC00220)
- transporter (PC00227)

Protein classes

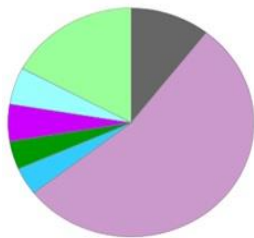
Supplementary Fig 3 pie chat of significant GO categoris of up-regulated genes between primed and unprimed plants

Biological process



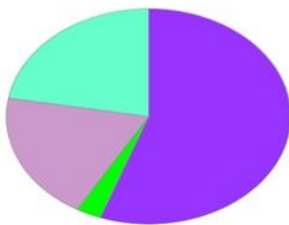
- apoptotic process (GO:0006915)
- biological regulation (GO:0065007)
- cellular process (GO:0009987)
- developmental process (GO:0032502)
- localization (GO:0051179)
- metabolic process (GO:0008152)
- response to stimulus (GO:0050896)

Molecular-Function



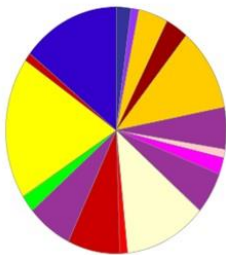
- binding (GO:0005488)
- catalytic activity (GO:0003824)
- enzyme regulator activity (GO:0030234)
- receptor activity (GO:0004872)
- structural molecule activity (GO:0005198)
- translation regulator activity (GO:0045182)
- transporter activity (GO:0005215)

Cellular-Localization



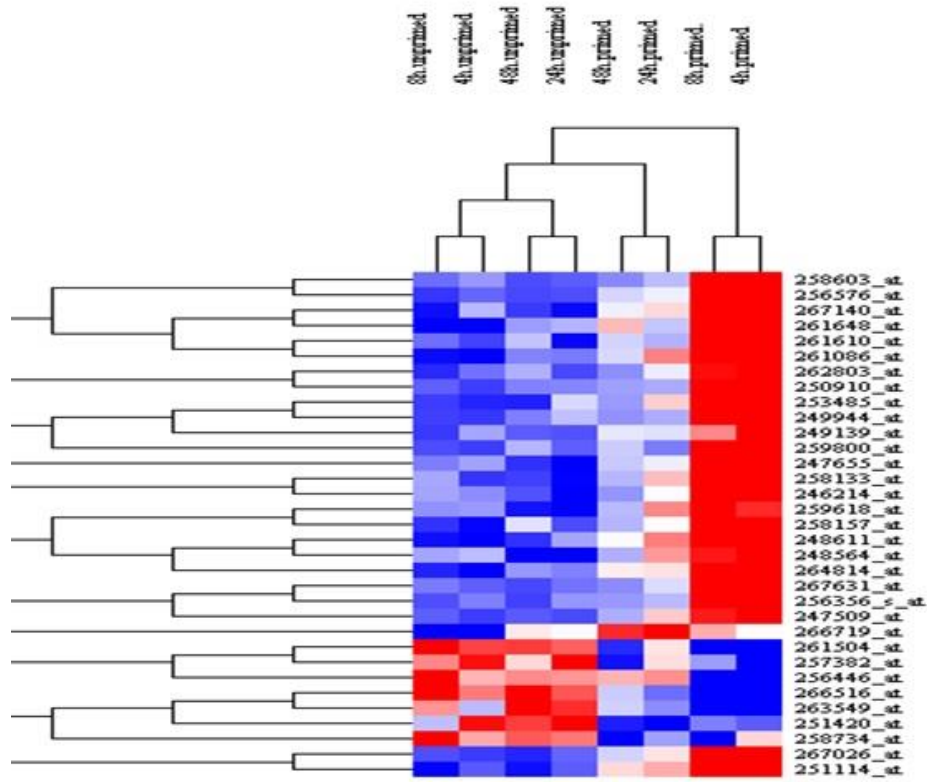
- cell part (GO:0044464)
- macromolecular complex (GO:0032991)
- membrane (GO:0016020)
- organelle (GO:0043226)

Protein classes

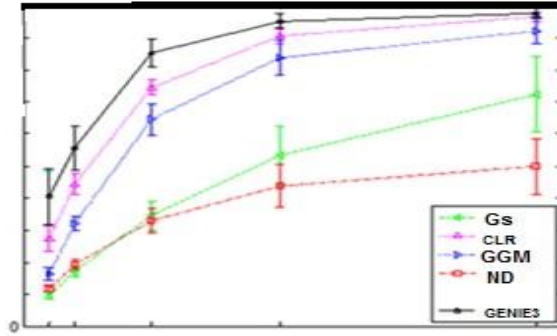


- calcium-binding protein (PC00060)
- chaperone (PC00072)
- cytoskeletal protein (PC00085)
- enzyme modulator (PC00095)
- hydrolase (PC00121)
- isomerase (PC00135)
- kinase (PC00137)
- membrane traffic protein (PC00150)
- nucleic acid binding (PC00171)
- oxidoreductase (PC00176)
- phosphatase (PC00181)
- protease (PC00190)
- signaling molecule (PC00207)
- transfer/carrier protein (PC00219)
- transferase (PC00220)
- transmembrane receptor/regulatory/adaptor protein (PC00226)
- transporter (PC00227)

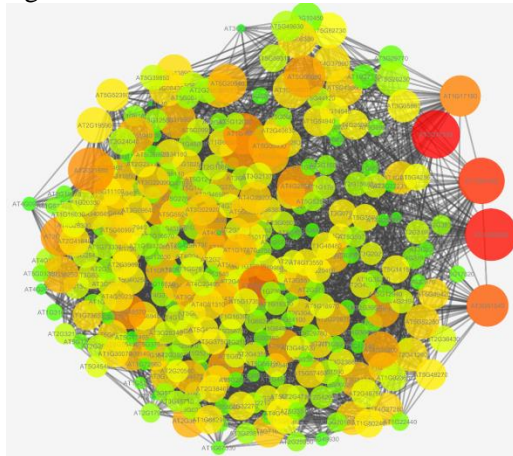
Supplementary Fig 4 pie chart of significant GO categories of down-regulated genes between primed and unprimed plants



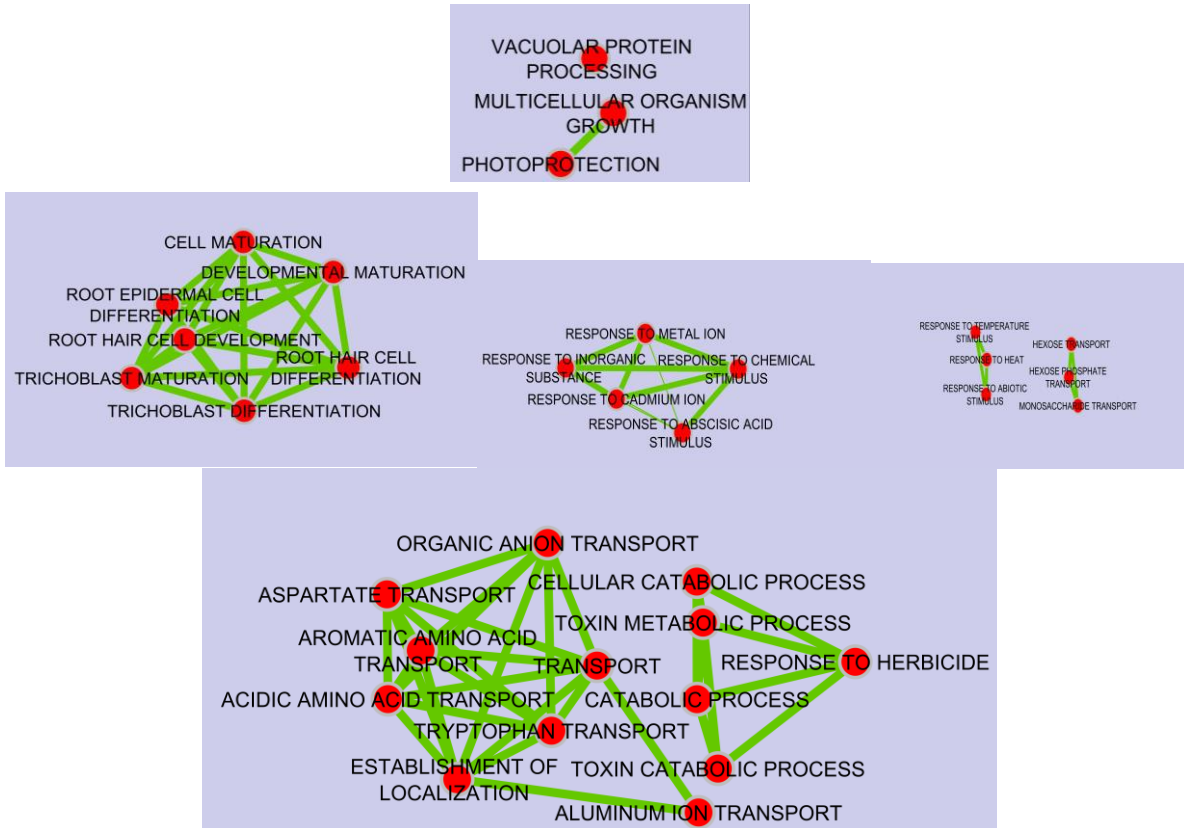
Supplementary Fig 5 hierarchical clustering of differentially-expressed transcription factors between primed and unprimed plants



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 betweenness parameters to node size and color so that darker and bigger nodes showing higher degree and betweenness 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.