

# **SUPPLEMENTARY INFORMATION**

## **Transcriptome analysis uncovers key regulatory and metabolic aspects of soybean embryonic axes during germination**

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### **SUPPLEMENTARY MATERIAL LEGENDS**

**Figure S1:** Global transcriptional patterns of soybean embryonic axes during germination (dry, 3-HAI, 6-HAI, 12-HAI and 24-HAI). Expression patterns were clustered by Hierarchical Clustering. Only expressed genes (FPKM > 1) are represented. FPKM values were converted to z-scores and colour intensities range from -2 to 2. HAI: Hours After Imbibition.

**Figure S2:** Transcriptional patterns of primary metabolism genes (KEGG database) in soybean embryonic axes during germination (dry, 3-HAI, 6-HAI, 12-HAI and 24-HAI). Only expressed genes (FPKM > 1) are represented. FPKM values were converted to z-scores and colour intensities range from -2 to 2. HAI: Hours After Imbibition.

**Table S1:** Transcriptional levels (in FPKM) of all soybean protein-coding genes in embryonic axes during germination. Immediately after each FPKM value of each gene, there is a logical (i.e. yes/no) value indicating whether the gene is significantly up-regulated between two subsequent germination phases. Transcription factors are annotated in a separate column. The last three columns contain information of *A. thaliana* orthologs.

**Table S2:** List of genes showing strong preferential transcription at 24 hours after germination. Information of *A. thaliana* orthologs is also provided.

**Table S3:** Enrichment of Gene Ontology terms among the differentially expressed genes during germination. These terms were carefully examined along the manuscript, including several single-gene analyses.

**Table S4:** Transcriptional levels (in FPKM) of the metabolic enzymes represented in figure 2.

## SUPPLEMENTARY FIGURES

Figure S1: Global transcriptional patterns of soybean embryonic axes during germination (dry, 3-HAI, 6-HAI, 12-HAI and 24-HAI). Expression patterns were clustered by Hierarchical Clustering. Only expressed genes (FPKM > 1) are represented. FPKM values were converted to z-scores and colour intensities range from -2 to 2. HAI: Hours After Imbibition.

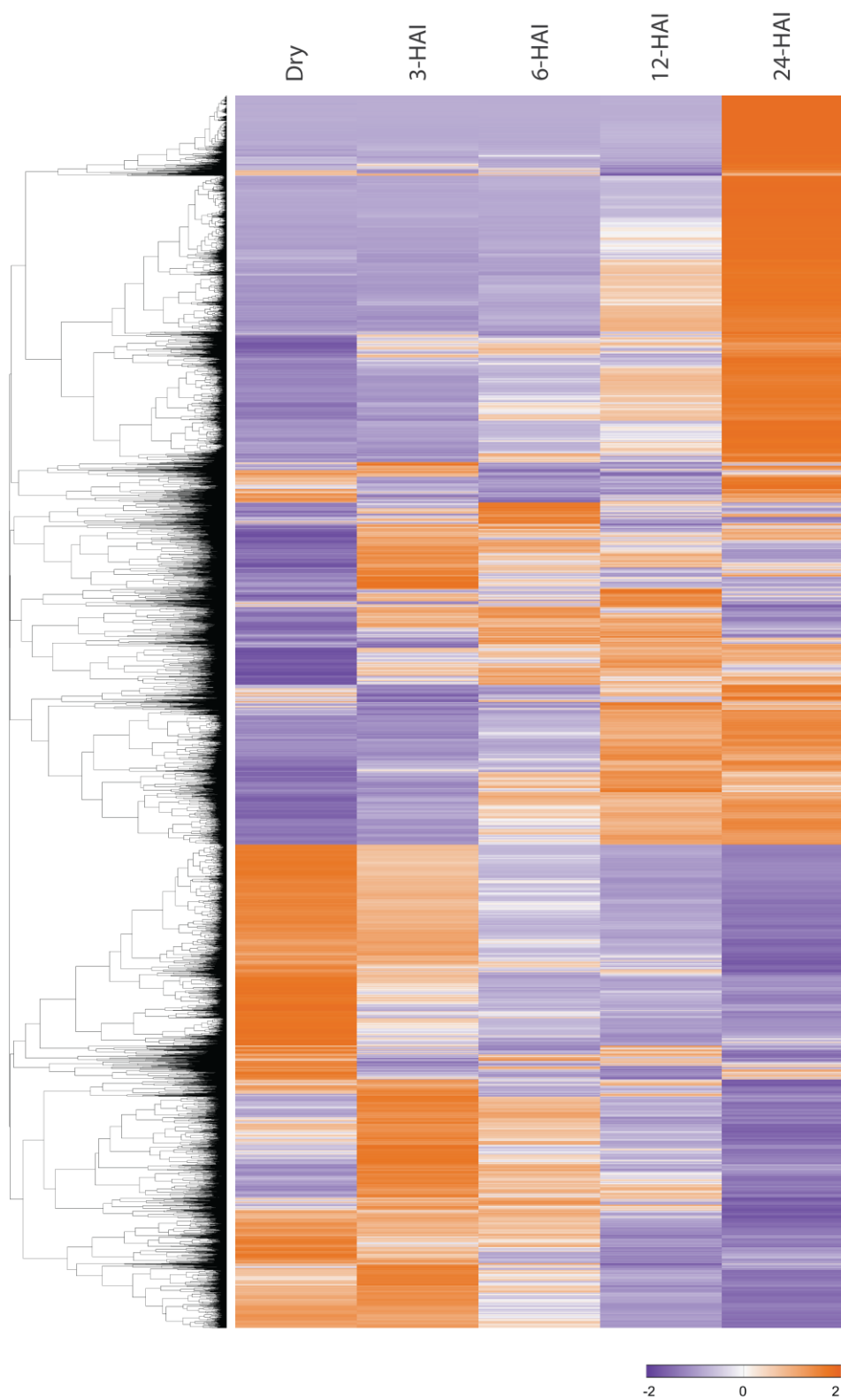


Figure S2: Transcriptional patterns of primary metabolism genes (KEGG database) in soybean embryonic axes during germination (dry, 3-HAI, 6-HAI, 12-HAI and 24-HAI). Only expressed genes (FPKM > 1) are represented. FPKM values were converted to z-scores and colour intensities range from -2 to 2. HAI: Hours After Imbibition.

