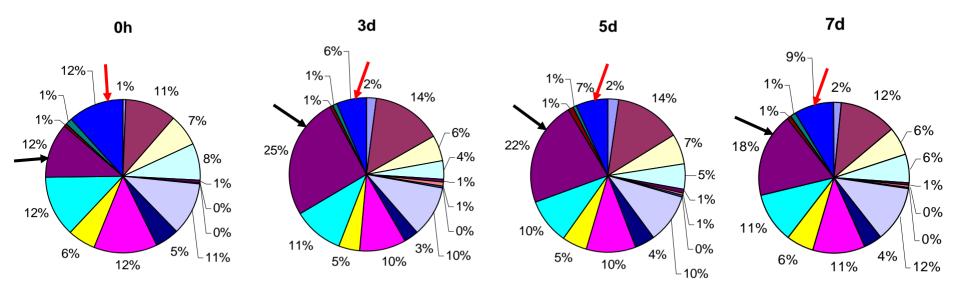
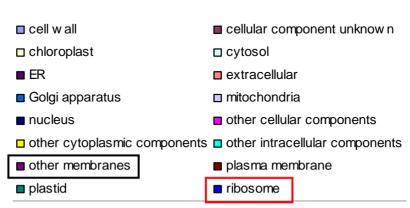
Supplementary Figure S1. Functional characterization of changes in gene expression at four stages of microspore embryo development (0h, 3d, 5d and 7d). Arabidopsis locus IDs corresponding to expressed unigene contigs were used in the TAIR Gene Ontology database to determine changes in the transcriptome during induction of microspore embryogenesis. A. Cellular component. B. Molecular function. C. Biological process. Black arrows: initial up-regulation, Red arrows: initial down-regulation.

Gene Ontology: Cellular Component

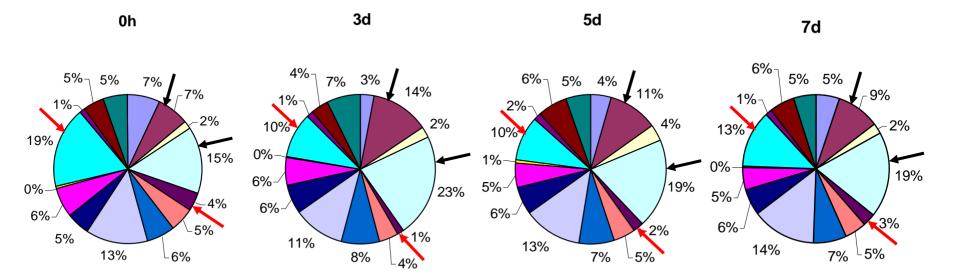


Genes related to membranes are up-regulated (black arrows) and ribosome-related genes are down-regulated (red arrows).



B.

Gene Ontology: Molecular Function

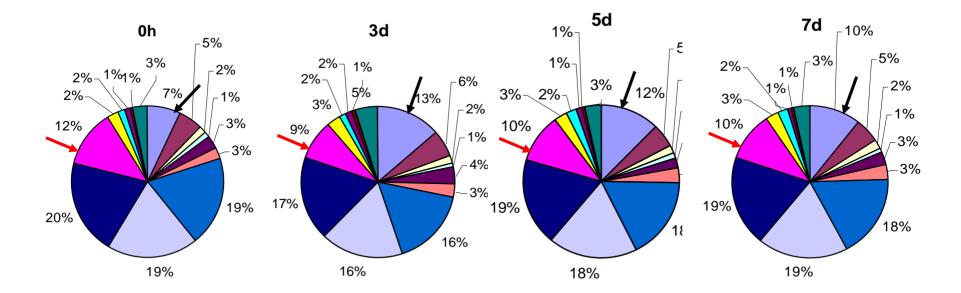


Genes related to hydrolase activity and molecular function unknown are upregulated (black arrows) while genes for structural molecule activity and nucleic acid binding activity are down-regulated (red arrows).

- □ DNA or RNA binding
 □ molecular function unknown
 □ other binding
 □ other enzyme activity
 □ protein binding
 □ transcription factor activity
 □ transferase activity
- kinase activity
 nucleotide binding
 other molecular functions
 structural molecule activity

■ transporter activity

Gene Ontology: Biological Process



Genes related to unknown biological process are upregulated (black arrows) while genes related to protein metabolism are downregulated (red arrows).

- biological process unknow n
- □ developmental processes
- electron transport or energy pathways other biological processes
- other cellular processes
- other physiological processes
- response to abiotic or biotic stimulus
- signal transduction

- cell organization and biogenesis
- □ DNA or RNA metabolism
- other metabolic processes
- protein metabolism
- response to stress
- transcription