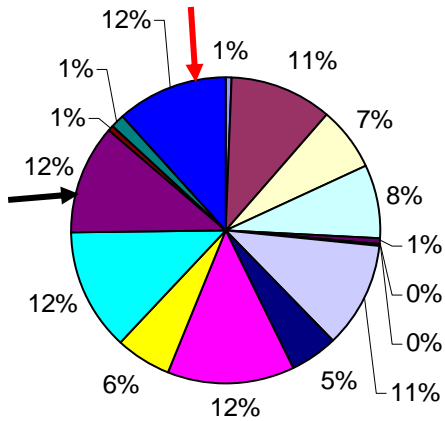


Supplementary Figure S1. Functional characterization of changes in gene expression at four stages of microspore embryo development (0h, 3d, 5d and 7d). Arabidopsis locus IDs corresponding to expressed unigene contigs were used in the TAIR Gene Ontology database to determine changes in the transcriptome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

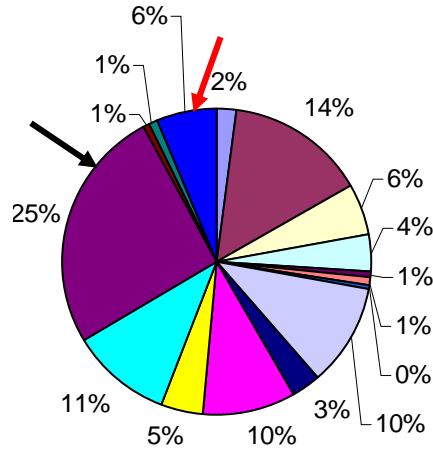
A.

Gene Ontology: Cellular Component

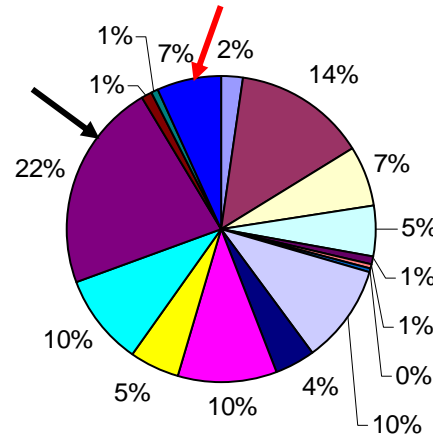
0h



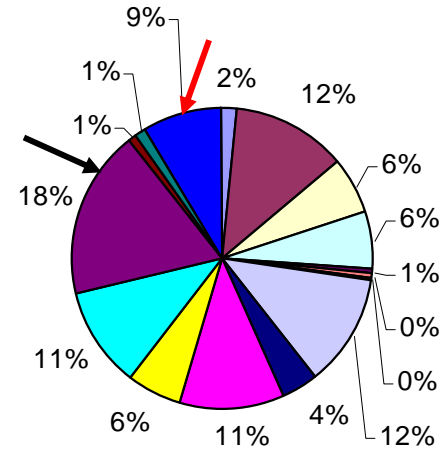
3d



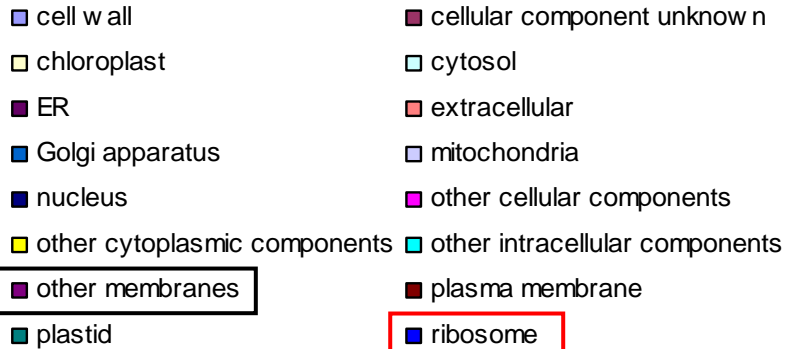
5d



7d



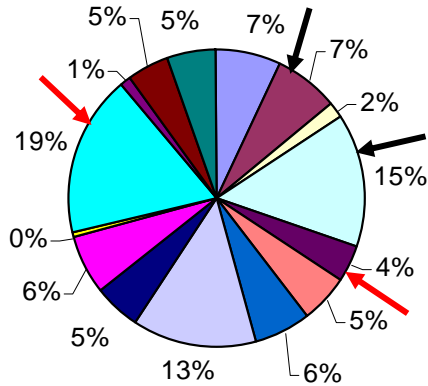
Genes related to membranes are up-regulated (black arrows) and ribosome-related genes are down-regulated (red arrows).



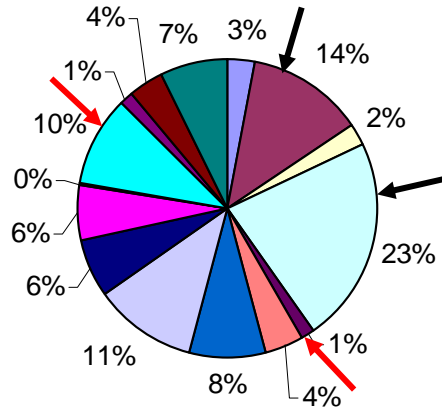
B.

Gene Ontology: Molecular Function

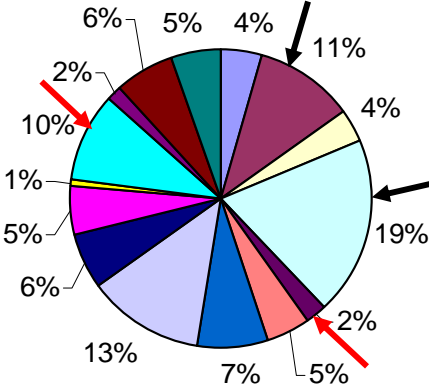
0h



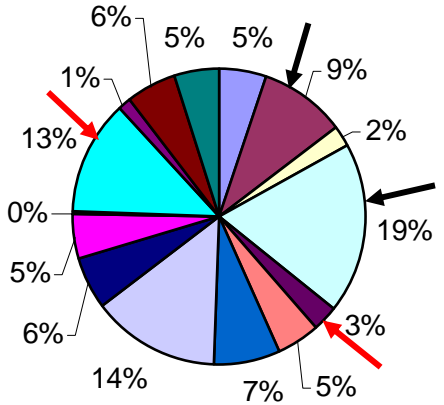
3d



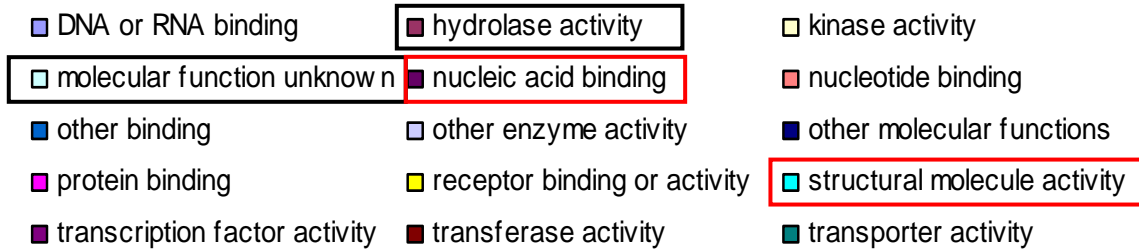
5d



7d

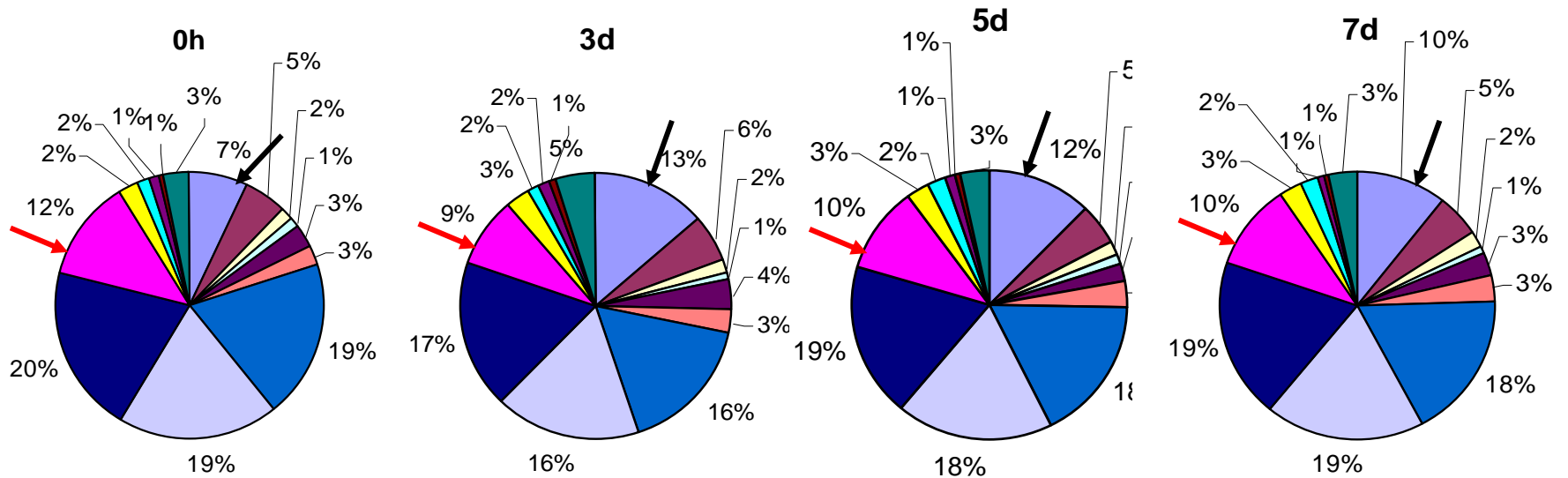


Genes related to hydrolase activity and molecular function unknown are up-regulated (black arrows) while genes for structural molecule activity and nucleic acid binding activity are down-regulated (red arrows).



C.

Gene Ontology: Biological Process



Genes related to unknown biological process are up-regulated (black arrows) while genes related to protein metabolism are down-regulated (red arrows).

