

Figure S2. Number of differentially expressed transcripts (DETs) with a fold-change greater than 2 (FC>2) identified in each pairwise comparison between embryos and megagametophytes. (A) Total number of up-regulated transcripts in embryos and megagametophytes (B) Number of up-regulated transcripts in embryos (orange) and megagametophytes (green) at different developmental stages during early seed development.

A

Tissue	DETs	DETs with GO annotation	TF DETs
Embryos	12,906	6,986	2,091
Megagametophytes	5,732	3,334	799
Total DETs	18,638	10,320	2,890

B

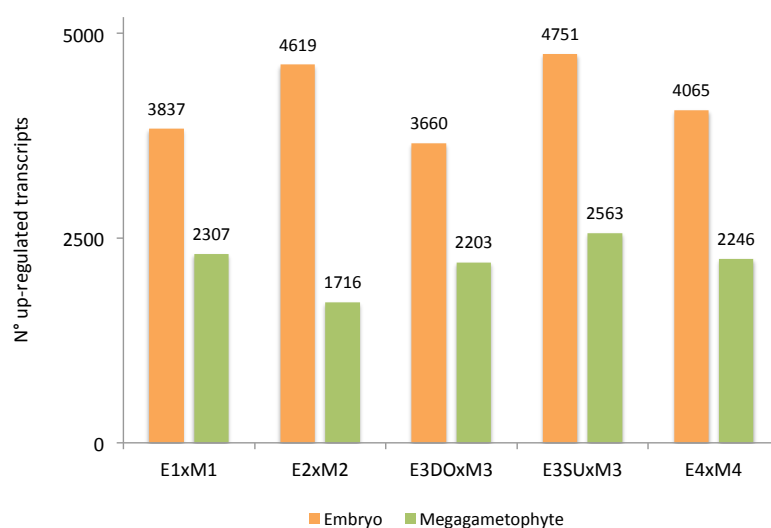


Figure S3. GO enrichment analysis of up-regulated transcripts (FC>2) in embryos, identified in any of the pairwise comparisons between embryos and megagametophytes at the four developmental stages shown in Figure 1. Enrichment in Biological Processes was obtained using AgriGO Toolkit database (FDR < 0.05). High significant levels are represented by red squares.

