

Figure S8. Clustering of differentially expressed transcripts identified in the pairwise comparisons between different megagametophyte developmental stages. The analysis included DETs with a $FC > 2$ and $RPKM > 10$. For each transcript, RPKM values were normalized to its maximum RPKM value during development. Normalized values were subjected to k-means clustering method and classified into different clusters, based on their expression levels across the four developmental stages. The Y-axis of the cluster chart represents relative expression (from 0 to 1). The percentage of transcripts with GO terms assigned to different Biological Processes (GO at level 2) for each type is shown.



Figure S9. Differentially expressed transcripts between consecutive stages in megagametophytes during early seed development. The analysis included DETs, with $FC > 2$ and $RPKM > 10$, identified in any of the three pairwise comparisons. (A) Histogram showing the number of up- and down-regulated DETs between different developmental stages. (B) Venn diagram showing the common and specific number of DETs detected in the consecutive pairwise analysis. (C) Summary table showing the number of DETs (excluding those with no assigned matches against TAIR) involved in different processes in each development transition.

