

Integrative analysis of DNA methylation, mRNAs, and small RNAs during maize embryo dedifferentiation

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Running Title: DNA methylation in maize embryo dedifferentiation

Supplementary Materials

Figure S1. Chromosomal distribution of DNA methylation read for each maize embryo sample. Each chromosomal was split in 10Kb windows.



Figure S2. Comparative and pathway analysis of DGE data. (A, B) Venn diagrams display the intersection of differentially expressed genes as determined by $FDR < 0.001$ and $\log_2\text{fold change} > 1$ for genes A) up-regulated and B) down-regulated in differentiated embryo compared to normal embryo (CK group) (I vs. CK, II vs. CK, III vs. CK). C, D) KEGG pathway analyses. Overrepresented KEGG pathways in genes up-regulated (C) and down-regulated (D) in differentiated embryos compared to CK group as calculated ($P < 0.05$) are shown. The x-axis displays the $-\log_{10}$ of the p-values calculated by DAVID (<http://david.abcc.ncifcrf.gov>).

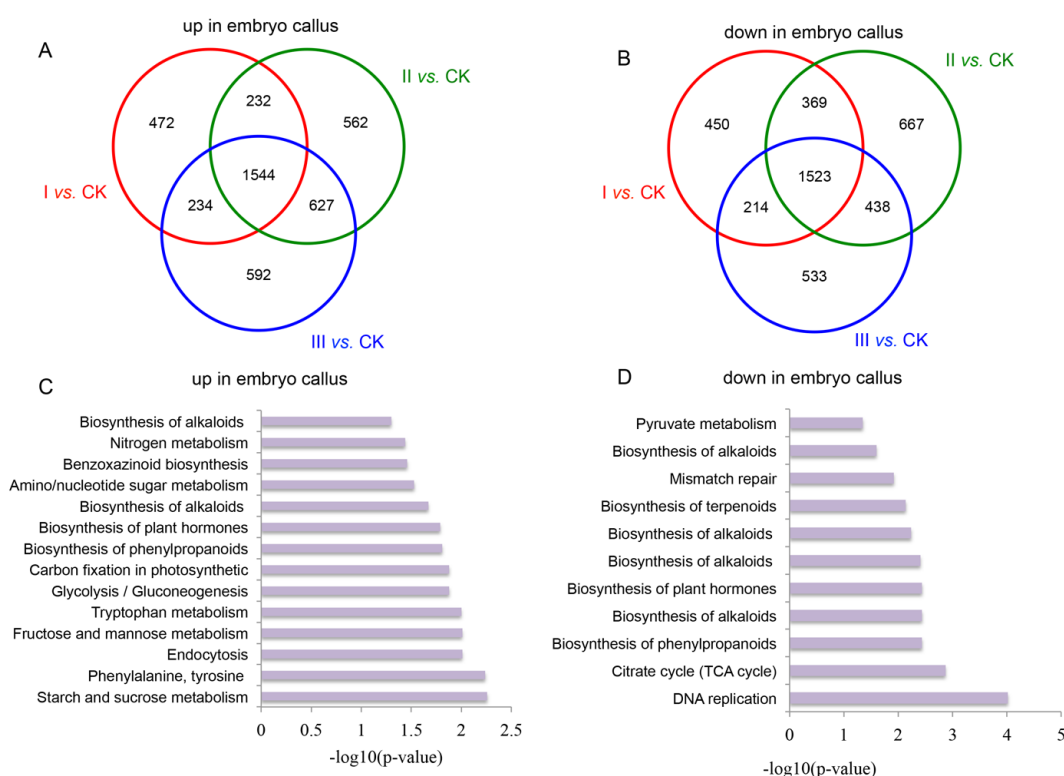


Figure S3. Venndiagram of 24-nt small RNA target DMRs and pathway results from DAVID. Venn diagrams display the intersection of target genes of 24-nt small RNAs that significantly positive correlated with DMRs.

