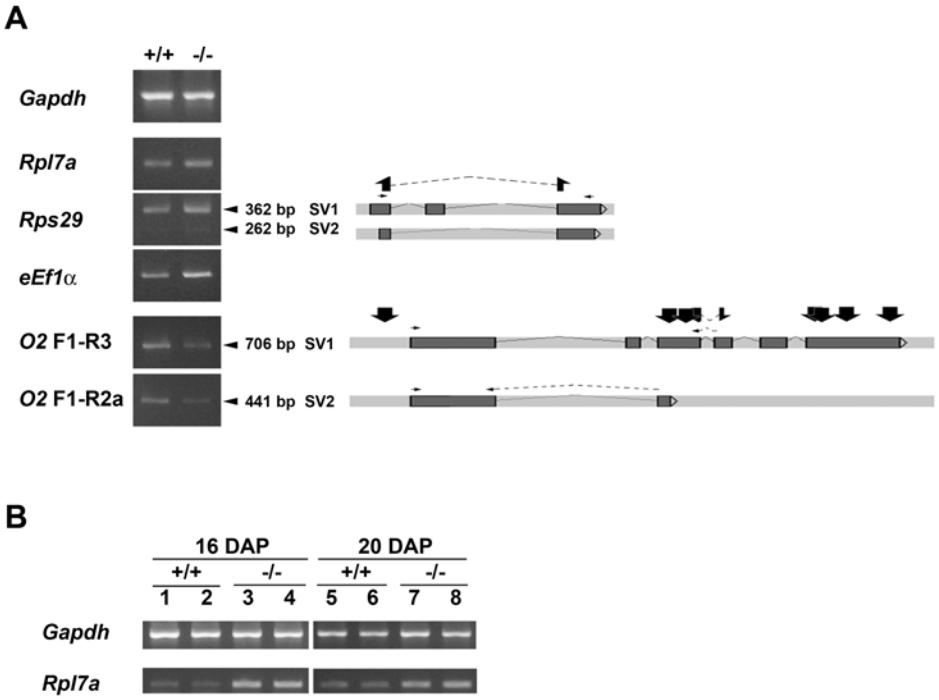

Supplemental Figure 2. Semi-quantitative RT-PCR analysis of RNAs corresponding to co-regulated and consistent SP classes of DHPs identified in the microarray experiment. (**A**) RNA was isolated from a pool of six 20-DAP homozygous wild-type and six 20-DAP homozygous Zm *smu2-1* mutant endosperms and compared for levels of transcripts encoding glyceraldehyde-3-phosphate dehydrogenase subunit C (*Gapdh*, control), ribosomal protein L7a (*Rpl7a*), ribosomal protein S29 (*Rps29*), elongation factor 1-α (*eEf1a*) and Opaque-2 (*O2*). Arrowheads on the right side of the panels indicate the splice variants (SVs) of *Rps29* and *O2*, and the splicing patterns for these SVs are illustrated. The sites of primers used for RT-PCR are shown by the small horizontal arrows. Solid arrows pointing up and down represent hybridization sites for DHP-H and DHP-L, respectively. Arrows split by a dotted line show the location of an exon junction. +/+, endosperm dissected from kernels with a homozygous wild-type embryo; -/-, endosperm dissected from kernels with a homozygous *smu2-1* mutant embryo. (**B**) Level of *Gapdh* and *Rpl7a* transcripts in single endosperms at 16 DAP and 20 DAP. RT-PCR products indicating the level of transcripts encoding GAPDH (control) and ribosomal protein L7a (*Rpl7a*) in homozygous wild-type (lanes 1, 2, 5 and 6) and homozygous smu2-1 (lanes 3, 4, 7 and 8) endosperms at 16 DAP (lanes 1-4) and 20 DAP (lanes 5-8).