



**Supplemental Figure 1.** Identification of differentially expressed targets in *Zm smu2-1* endosperm. **(A)** Procedures for identifying target sequences corresponding to differentially hybridized probes (DHPs), annotating exons and introns in maize genome survey sequence (GSS) contigs corresponding to the DHPs, and locating the DHPs in annotated GSS contigs. Nucleotide sequences are represented by white boxes and amino acid sequences by gray boxes. Inputs and outputs of sequence searches are shown at the start and end, respectively, of arrows. Programs and databases used in the sequence searches are described in the middle of arrows. **(B)** Procedures for identifying sister probes (SPs) from target sequences or GSS contigs identified in panel A. **(C)** Examples of DHPs and their target nucleotides that were identified from the procedure in panel A. The target nucleotides are genomic sequences (GSS contigs shown as AZM's). Exons are shown by dark gray or white boxes, while light gray bars between boxes correspond to introns. The dark gray boxed exons are based on EST matches from BLASTN, while the white boxed exons were derived from BLASTX matches. Probe hybridization sites in target molecules are marked by arrows. Downward pointing arrows indicate hybridization sites for DHPs that corresponded to low target expression in the mutant (DHP-L). The split arrow pointing up indicates a DHP that detected a high level of target expression in the mutant (DHP-H; probe 3). Arrows pointing left and right indicate hybridization sites for probes without a significant difference between target expression values in the wild-type and mutant endosperm. **(D)** Identification of probe hybridization sites and DHP classes shown in panel C. The hybridization sites were determined by alignment of probe and target sequences with exon-intron annotation. ND, not determined; XIB, exon-intron boundary. See text for an explanation of how the probe classes were determined. Operon ID (oligo ID by oligonucleotide manufacturer) for probes are as follows: probe 1 (MZ00026268), SP-1 (MZ00043966), probe 2 (MZ00046447), SP-2 (MZ00002070), probe 3 (MZ00029716), SP-3a (MZ00044449), SP-3b (MZ00020250), probe 4 (MZ00002602), probe 5 (MZ00048182). **(E)** A pie chart showing the hybridization sites of DHP-Ls. **(F)** Pie charts showing the number of different classes of DHPs (left) and the number and nature of genes associated with the "co-regulated" and "consistent SP" class DHPs (right).