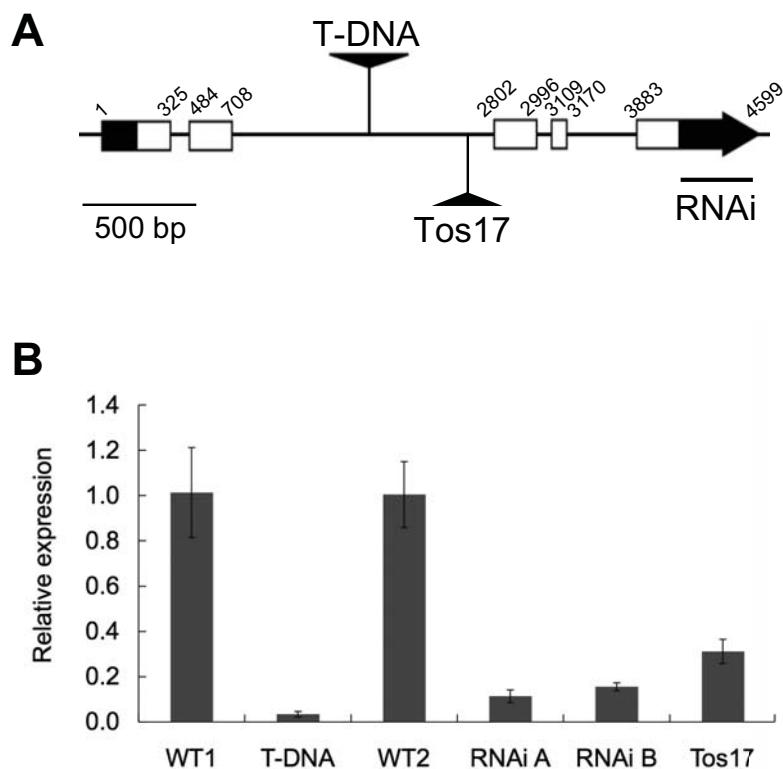


Supplemental Figure 1. Alignment of amino acid sequence of Lsi1 and Lsi6. Identical and similar amino acids are shaded in black and gray, respectively. Two conserved NPA motifs (NPA₁ and NPA₂) and four residues of the aromatic/arginine selectivity filter (H2, H5, LE₁, and LE₂) are indicated in blue and red letters, respectively. The red open box indicates the peptide sequence that the anti-Lsi6 antibody was raised against.



Supplemental Figure 2. *Lsi6* gene structure and suppression lines.

(A) The *Lsi6* gene is composed of 5 exons and 4 introns. The open reading frame and untranslated region are indicated as open and filled boxes, respectively. Numbers indicate distance from the putative transcriptional start site (bp). Positions of the T-DNA and Tos17 insertion mutations and target sequence of RNAi are indicated. (B) *Lsi6* expression of wild-type rice and knockdown lines. Whole roots from the 3-week old seedlings grown hydroponically were used for RNA extraction and the amount of *Lsi6* transcript in different lines was determined by quantitative real-time RT-PCR. WT1: Dongjin; T-DNA: T_2 homozygous progeny of T-DNA insertion mutant; WT2: Nipponbare; RNAi A and B: T_2 progenies of two independent RNAi lines; Tos17: T_2 homozygous progeny of Tos17 insertion mutant. Means \pm SD ($n = 3$) are shown.



Supplemental Figure 3. Leaf guttation of wild-type rice (cv. Dongjin). Picture was taken just after sunset under greenhouse conditions.