

Figure S1. Alignment of Class III HD-Zip proteins, and nucleotide and amino acid sequences at *miR166*-binding site of *OSHB1–OSHB5* genes. A, Alignment of Class III HD-Zip proteins in several angiosperms and moss. The continuous, dashed and double lines indicate HOX, bZIP and START domains, respectively. 100% and more than 50% identical amino acids are colored in black and gray, respectively. B, Alignment of *miR166* binding site in *OSHB* and mutant-version of *OSHB* (*OSHBm*) genes. Top to bottom; wild-type amino acid sequences at *miR166*-binding site, cDNA sequences of wild-type *OSHB* gene, *miR166* sequences, cDNA sequences of *OSHBm* genes and mutant protein sequences. Vertical lines indicate complementary mRNA sequence to *miR166*. Mutated nucleotides are colored in gray.