

Figure S1. Transmembrane helices analysis of OsPIN1b proteins in wild-type (WT) and *ospin1b* mutants. The transmembrane helice analysis was performed by TMHMM-2.0: <https://services.healthtech.dtu.dk/service.php?TMHMM-2.0>, and the red peaks indicate the predicted transmembrane helices of proteins.

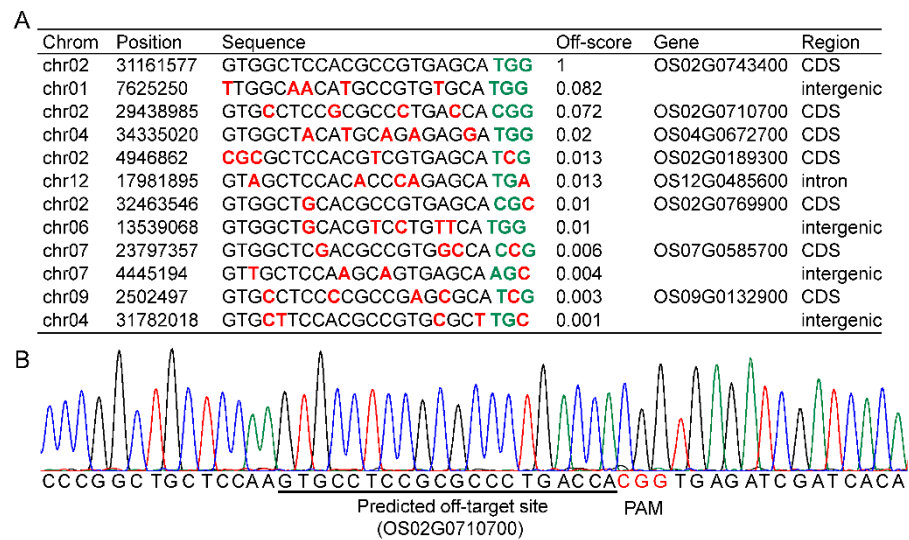


Figure S2. Off-target analysis of *ospin1b* mutants. (A) The potential off-target sites predicted by CRISPR-GE. (B) The sequencing chromatogram of the predicted potential off-target site.

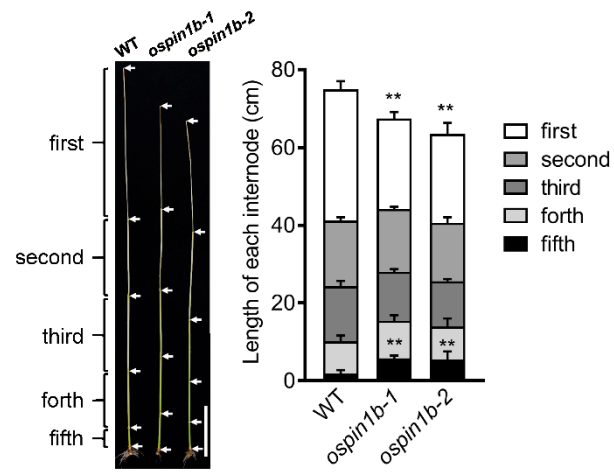


Figure S3. Internode length of wild-type (WT) and *ospin1b* mutants at the mature stage. Bar = 10 cm. Values are means \pm standard deviation (SD) (n = 16). Data were analyzed by ANOVA and Tukey's tests. **: $p < 0.01$.

Table S1. Primers used in this study.

Primers for vector construction	Primer sequences (5'-3')
OsPIN1b-CRISPR-F	TGTGTGTGGCTCCACGCCGTGAGCA
OsPIN1b-CRISPR-R	AAACTGCTCACGGCGTGGAGCCAC
Primers for screening of the transgenic plants	
HPT-F	CTGAACTCACCGCGACGTCTGTC
HPF-R	TAGCGCGTCTGCTGCTCCATACA
Primers for mutant identification	
PIN1b-Assay-F	GTGAAATAGTGCCACCGAGTGAGCGC
PIN1b-Assay-R	CCATGAGGCTGCCGGAGAACTCC
Primers for off-target analysis	
700-OT-F	TTCTGCTACTGCGGGGTGAGG
700-OT-R	TAGGGGAATGGAGGCATGTTC
Primers for qRT-PCR	
OsPIN1b-qF	GAATCGTGCCCTTTGTGTTTG
OsPIN1b-qR	TGTAGTAGACGAGGGTGATAGG
OsACTIN1-qF	CTTCATAGGAATGGAAGCTGCG
OsACTIN1-qR	CACCTTGATCTTCATGCTGCTA