

Figure S1. Phylogenetic analysis and amino acid sequence alignment of OsLEA1b.

(A) Phylogenetic analysis of *OsLEA1b*. The neighbor-joining tree was generated with MEGA7 after aligning the full-length protein sequences. Distances are evaluated using the neighbor-joining algorithm. (B) Amino acid sequence alignment between part of *OsLEA1b* and other homologous proteins. The sequences alignment was generated with ClustalX2. White alphabet with black background means 100% identity, white alphabet with grey background represents 80% identity, and black alphabet with light grey background stands for 60% identity.

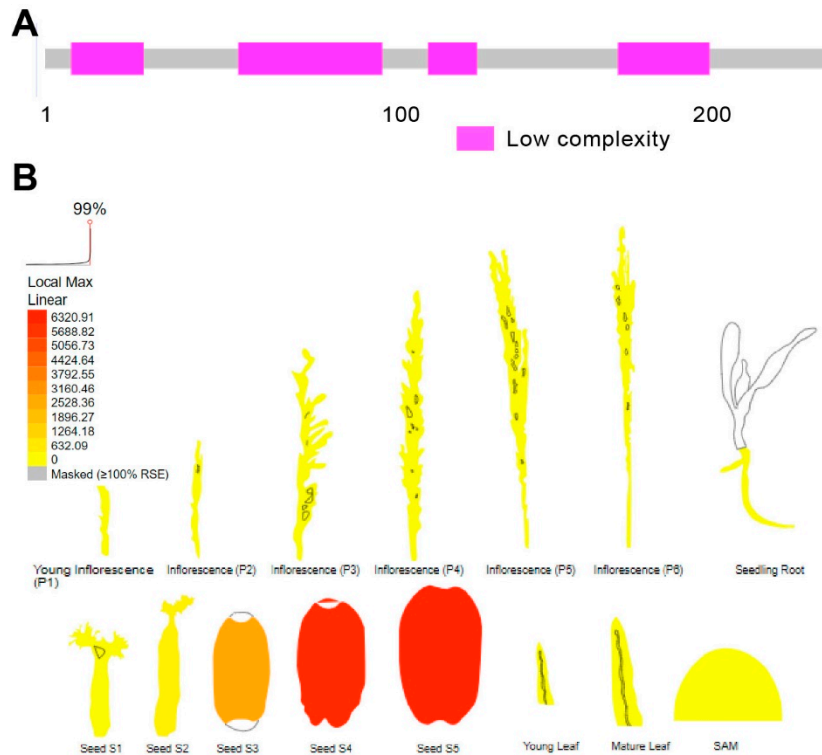


Figure S2. Structure and expression pattern prediction of *OsLEA1b*.

(A) Predicted structure of *OsLEA1b* from website (<http://smart.embl-heidelberg.de>). Pink box represent the low complexity region. **(B)** Tissue expression pattern prediction of *OsLEA1b* on the website (https://bar.utoronto.ca/eplant_rice/).

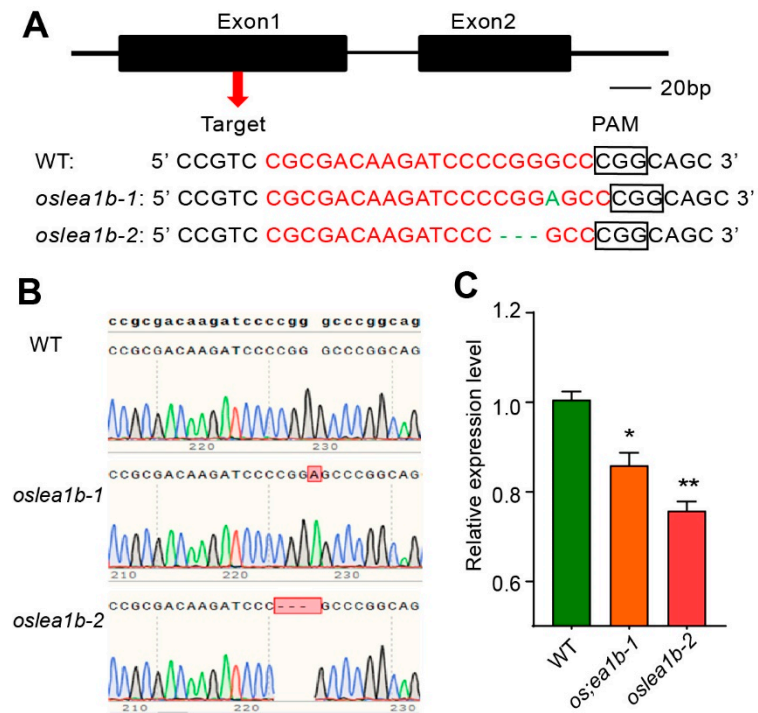


Figure S3. CRISPR/Cas9 mediated editing lines of *OsLEA1b*.

(A, B) Gene structure of *OsLEA1b* and sequencing of CRISPR/Cas9 target region in WT and T₀ plants. Scale bars, 20 bp. **(C)** Relative expression level of *OsLEA1b* in transgenic knock out plants (*oslea1b-1,2*). Data are means \pm SD from not less than three biological replicates. Statistically significant differences were determined using Student's *t*-test (*, $P < 0.05$, **, $P < 0.01$).

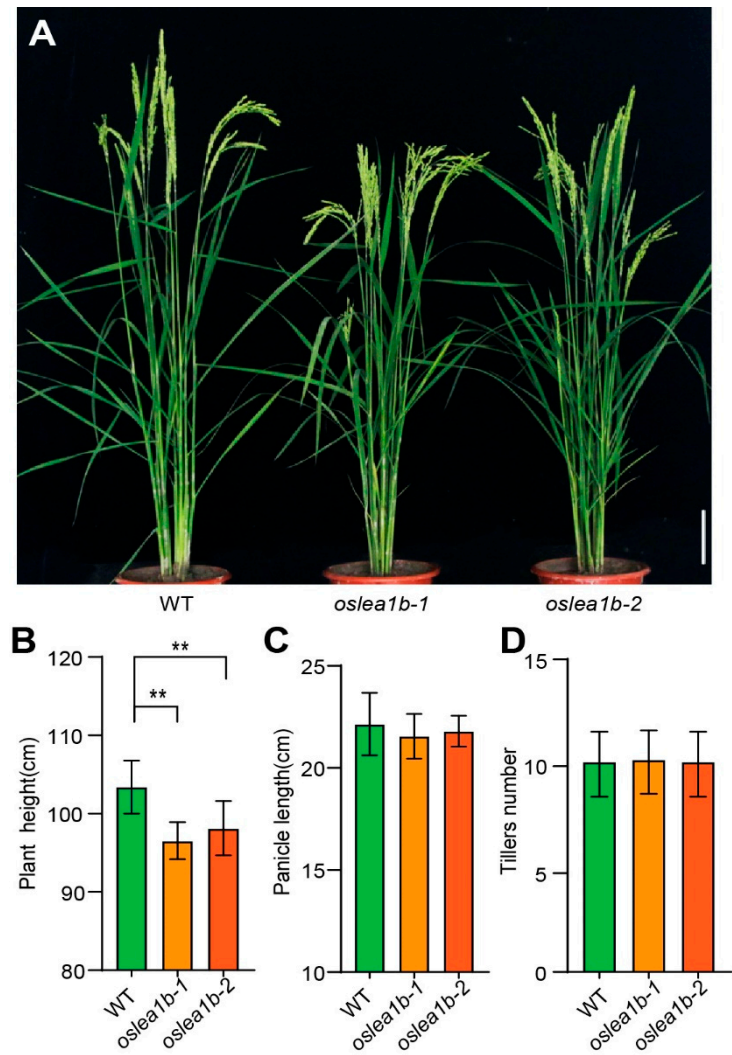


Figure S4. Appearance analysis of WT and *oslea1b* mutants.

(A) The plant phenotype of WT and *oslea1b* mutants after heading. Scale bars, 15 cm. **(B-D)**. Statistics of plant height, panicle length and tillering number of wild type and mutants. Data are means \pm SD from not less than three biological replicates. Statistically significant differences were determined using Student's *t*-test (**, $P < 0.01$).

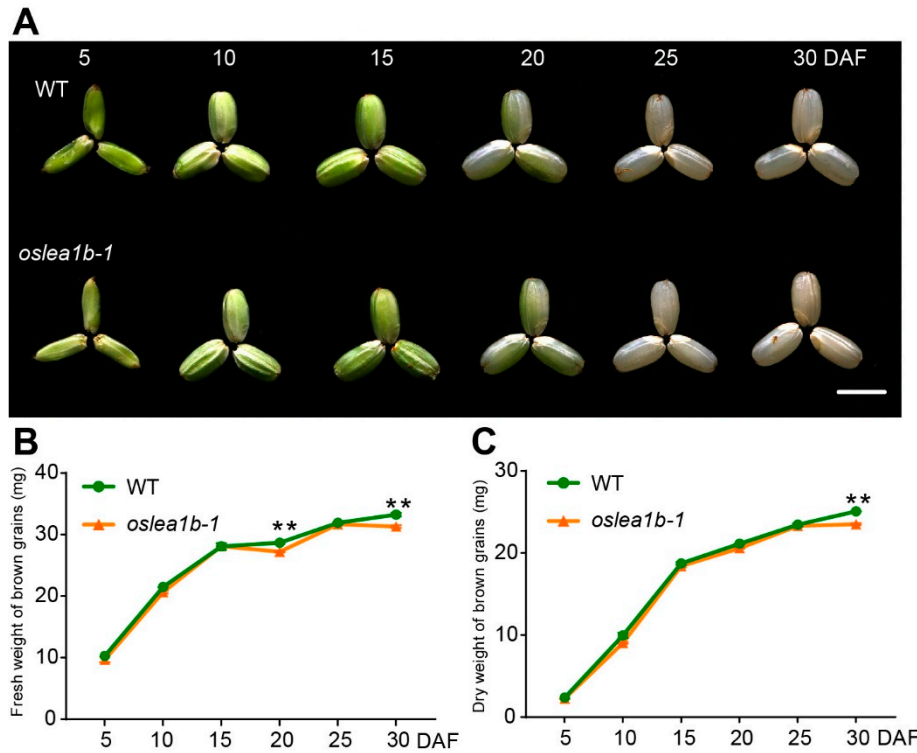


Figure S5. Grains filling of WT and *oslea1b* mutants.

(A) Fresh grains of WT and *oslea1b* at various stages of development. DAF, days after fertilization. Scale bars, 5 mm. (B, C) Weight of fresh and dry grains of WT and *oslea1b* at various stages of grain filling. Data are means \pm SD from not less than three biological replicates. Statistically significant differences were determined using Student's *t*-test (**, $P < 0.01$).

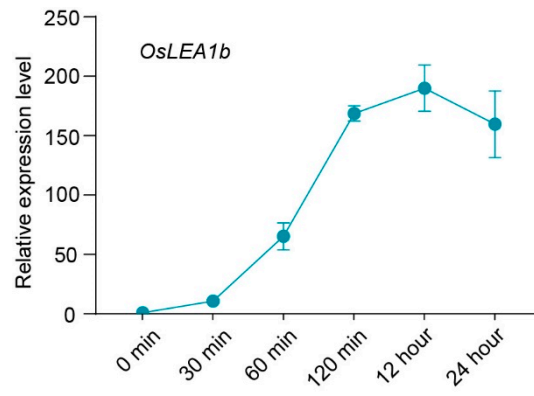


Figure S6. High temperature induces the expression of *OsLEA1b*.
Relative expression level of *OsLEA1b* after high temperature treatment within 24 hours.

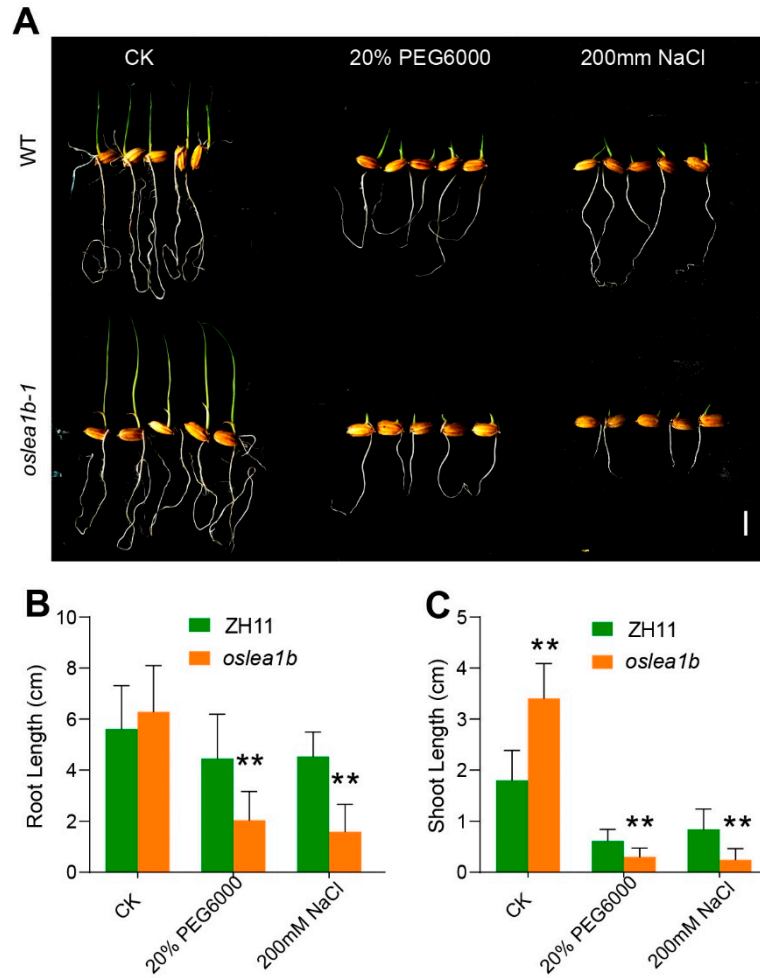


Figure S7. OsLEA1b is a positive regulator of drought tolerance.

(A) The phenotype of WT and *oslea1b* mutants under 20% PEG6000 and 200 mM NaCl treatment for 1 week. Scale bars, 5 mm. **(B, C)** The root and shoot length of the *oslea1b* mutants under 20% PEG6000 and 200 mM NaCl treatment for 1 week. Data are means \pm SD from not less than three biological replicates. Statistically significant differences were determined using Student's *t*-test (**, $P < 0.01$).

Table S1. Primers used in this study

Use	Primer name	Sequence (5' to 3')
CRISPR/Cas9	Cas9-OsLEA1b-F	CAGCGCGACAAGATCCCCGGGCC
	Cas9-OsLEA1b-R	AACGGCCCGGGGATCTTGTCGCG
	Cas9-OsLEA1b-check-F	AAGCAGAGAGCGAAGCAAGCTCGAA
	Cas9-OsLEA1b-check-R	GCTACTTCTCCTCCGACGACGGCTGAG
GUS expression	1305-GUS-OsLEA1b-F	CCATGATTACGAATTCTATCCTTACAAGTTGTTT
	1305-GUS-OsLEA1b-R	CTCAGATCTACCATGGTGATCAGATGATCTTGGTC
Subcellular localization	OsLEA1b-GFP-F	GGTACCTGCAACTAGTATGGCGTCCATGCAGAAGA
	OsLEA1b-GFP-R	TGCTCACCATGGATCCGCGGCGGCCACCACATCT
q-RT-PCR	OsLEA1b-F	CGGCGACGGAGAACATCTA
	OsLEA1b-R	CTCCGGCATCGTCATCTCT
	BEI-F	TGGCCATGGAAGAGTTGGC
	BEI-R	CAGAAGCAACTGCTCCACC
	SSIIIa-F	GCCTGCCCTGGACTACATTG
	SSIIIa-R	GCAAACATATGTACACGGTTCTGG
	PUL-F	ACCTTTCTTCCATGCTGG
	PUL-R	CAAAGGTCTGAAAGATGGG
	ISA3-F	ACAGCTTGAGACACTGGGTTGAG
	ISA3-R	ACAGCTTGAGACACTGGGTTGAG
	GBSSI-F	TCCGTCATTCTGGAGAA
	GBSSI-R	CTTTGAAGTATGGGTTGTTGT
	BEIIb-F	ATGCTAGAGTTTGACCGC
	BEIIb-R	AGTGTGATGGATCCTGCC
	OsBT1-F	GAGGTCTTCCGCTGGATCAT
	OsBT1-R	TGAAATGCTCGATGGCCTTG
	SBE1-F	GCTGAAGATGTTTCGGGCAT
	SBE1-R	CATTGACCATTGCGGTCCT
	RAG2-F	TGCTCCTCATCATCGTCTCC
	RAG2-R	TGCTCCTCATCATCGTCTCC
	GLUD1-F	TGAACCAAGGCAGAAGGAGT
	GLUD1-R	GCCTCGCTAAGTACCTCAGT