

**Table S1.** Primers used in this study

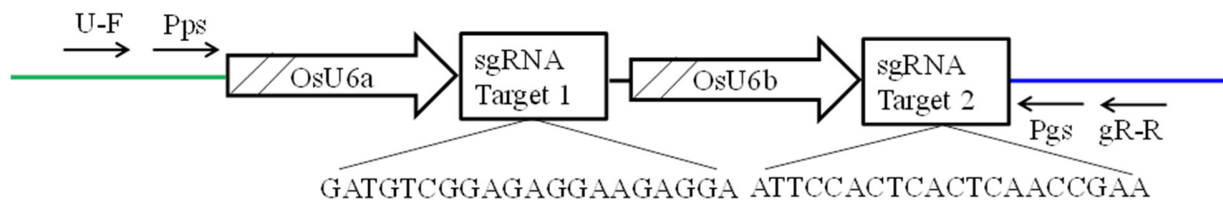
Primers	Sequence (5'-3')
<b>Recombinant pYLCRISPR/Cas9 vector construction</b>	
U-F	CTCCGTTTTACCTGTGGAATCG
gR-R	CGGAGGAAAATTCCATCCAC
Pps-GGL	TTCAGAGG <u>GCTCT</u> CTCGACTAGTATGGAATCGGCAGCAAAGG
Pgs-GG2	AGCGTG <u>GCTCT</u> CGTCAGGGTCCATCCACTCCAAGCTC
Pps-GG2	TTCAGAGG <u>GCTCT</u> CTGACACTGGAATCGGCAGCAAAGG
Pgs-GGR	AGCGTG <u>GCTCT</u> CGACCGACGCGTATCCATCCACTCCAAGCTC
Target-1OsHLH024	ATTCCACTCACTCAACCGAA
Target-2 OsHLH024	GATGTCGGAGAGGAAGAGGA
<b>Mutation detection</b>	
OsHLH024T1F1	CGTGCCGATGGATCAGAAG
OsHLH024T1R1	GGGATTGATTCCTCTTAATCAGC
<b>Transgenic plant identification</b>	
XUCas9-F1	TGCTCACCCCTGTTGTTTGGT
XUCas9-R1	TCATGTGAGCGAGAGCAAGG
SPL	GCGGTGTCATCTATGTTACTAG
SPR	CCGACATAGATGCAATAACTTC
<b>qRT-PCR</b>	
<i>OsHKT1;1 F</i>	ATTAGCAGAGCACTGTGGAGGAA
<i>OsHKT1;1 R</i>	CCGACGAACCCGTAGGAAG
<i>OsHKT1;3 F</i>	CAGTTCATCTACCAAAACAATCCA
<i>OsHKT1;3 R</i>	AATACCTCACCACCAATCAGCA
<i>OsHKT1; 5 F</i>	TGCCACCTTACACCACTTTTCG
<i>OsHKT1; 5 R</i>	TGCCATACGCACTGATAACCTC
<i>OsHAK7 F</i>	TGCTGTGACACTTGGTTTCC
<i>OsHAK7 R</i>	AAATAACAAGGCGAGCAGGA
<i>OsSOS1F1</i>	GACACTGGGAATGTTCTATGC
<i>OsSOS1R1</i>	CCATGAAGCACCGTGCCTCTCG

<i>OsLEA3 F1</i>	AATGATTTCCTTTGGGTC
<i>OsLEA3 R1</i>	CATCAGTACACATCACCCA
<i>OsACTIN1 F (35s)</i>	CTCAGCACATTCCAGCAGATGTG
<i>OsACTIN1 R (35s)</i>	GATAACAGCTCCTCTTGGCTTAGC

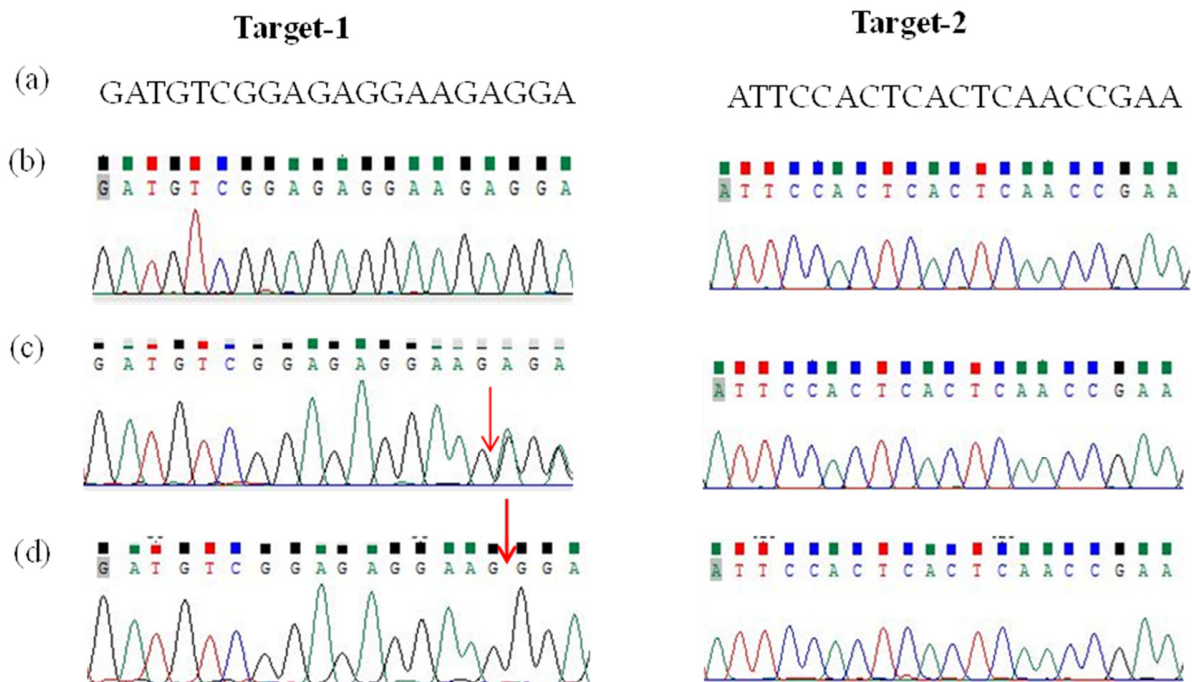
**Table S2.** The agronomic traits of A91 and the WT in the field

Traits	WT	A91 Mutant
Plant height (cm)	76.21 ± 0.69	81.02 ± 0.53**
Panicle length (cm)	21.67±0.35	21.61 ±0.27
Primary branches per panicle	8.57 ±0.29	8.87± 0.16
Secondary branches per panicle	21.63±0.49	22.4±0.63
Flag leaf length (cm)	32.49±0.80	33.25±0.68
Panicles per plant	8.67±0.45	8.27±0.49
Grains per panicle	89.83±2.39	93.33±2.13
Seed setting rate (%)	78.06±2.1	78.89±1.3
1000- grain weight (g)	24.42±0.29	24.47±0.37
Grain length (mm)	7.28±0.07	7..37±0.05
Grain width (mm)	3.25±0.02	3.27±0.02
Grain thickness (mm)	2.14±0.01	2.17±0.01
Tiller biomass (g)	7.63±0.40	8.76±0.26*

Values are expressed as means ± SE; n=10 biological replicates; \* and \*\* denote significant *t*-test results at  $P < 0.05$  and  $P < 0.01$ , respectively.



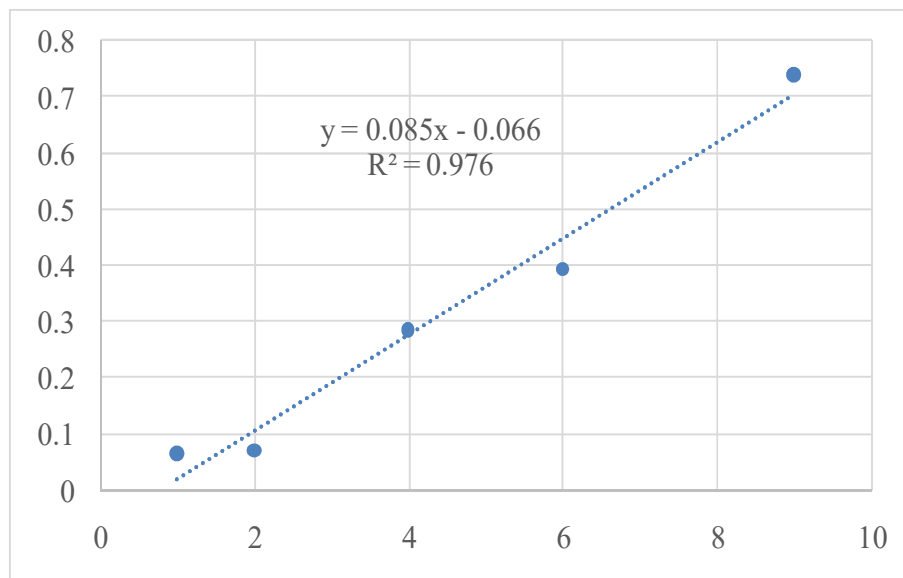
**Figure S1.** A linear form of the sgRNA vectors. The target-1 and target-2 were driven by OsU6a and OsU6b promoters, respectively by PCRs using primers U-F/gR-R and Pps/Pgs.



**Figure S2.** Mutation process showing chromatograph of *osbHLH024*. (a) Wild-type sequence of two targets; (b) two targets in EHA105 strain of *Agrobacterium tumefaciens*; (c) heterozygous mutation in T0 generation, the red arrow indicates heterozygous starting position; (d) sequence of homozygous T1 mutant (A91), the red arrow indicates deletion of "A."



**Figure S3.** The growth characteristics of the A91 and WT after 7 days of 150 mM NaCl stress of 21-day-old seedlings. Scale bar 10 cm.



**Figure S4.** Standard curve for H<sub>2</sub>O<sub>2</sub> determination.