

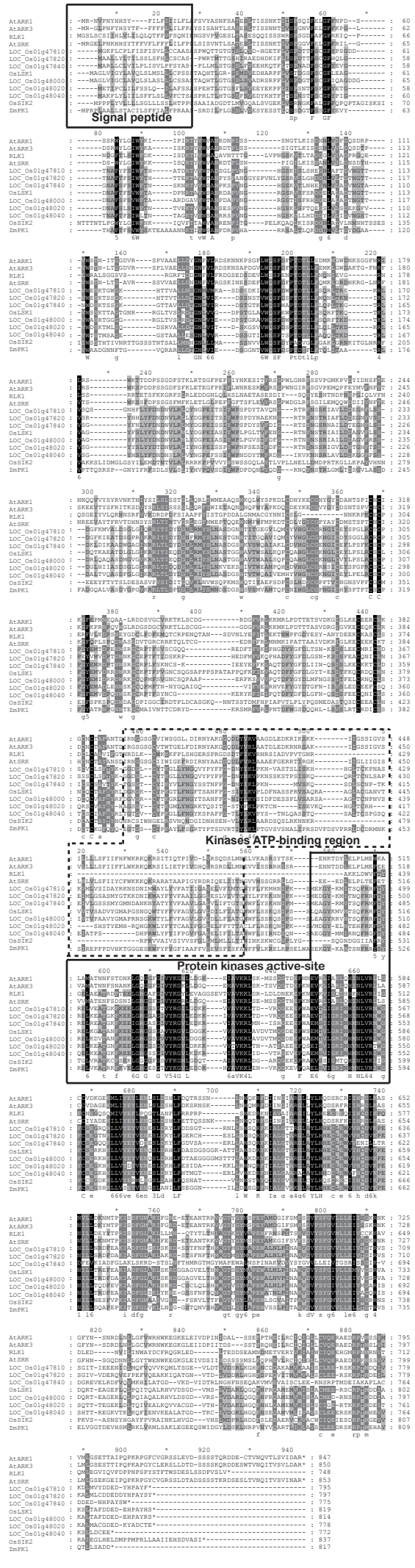
Figure legend

Supplementary Fig. S1. Amino acid sequence alignment of the OsLSK1 homologous proteins. *LOC_Os01g47810*, *LOC_Os01g47820*, *LOC_Os01g47840*, *OsLSK1* (*LOC_Os01g47900*), *LOC_Os01g48000*, *LOC_Os01g48020*, *LOC_Os01g48040* and *OsSIK2* are from rice, *ZmPK1* is from maize, *AtRLK1* (*AT5G60900*), *AtARK1* (*AT1G65790*), *AtARK3* (*At4G21380*) and *AtSRK* are from *Arabidopsis*. The black region shows the some amino acids. The grey color indicates relative conservative region.

Supplementary Fig. S2. The protein structures and genome distribution of OsLSK1 homologous genes. (A): The conserved domain structure diagram in *OsLSK1* and six homologous. (B): *OsLSK1* cluster with six homologous genes in chromosome 1. The *OsLSK1* was labeled with red circle.

Supplementary Fig. S3. Phenotype analysis of *OXOsLSK1-f* and *OsLSK1-RNAi* plants. (A): The panicle morphologies of wild-type, *OXOsLSK1-f* and *OsLSK1-RNAi* transgenic rice. (B): The gross morphologies of wild-type, *OXOsLSK1-f* and *OsLSK1-RNAi* transgenic rice. (C), (E): Comparison of plants height, primary branch number between wild-type and *OXOsLSK1-f* transgenic rice. (D), (F): Comparison of plants height, primary branch number between wild-type and *OsLSK1-RNAi* transgenic rice. Data are shown as means \pm s.d. (Student's *t* tests, **P* < 0.05, ***P* < 0.01, n=60).

Supplementary Fig. S4. Quantitative RT-PCR analysis of plant morphologies related genes in *OXOsLSK1-f* plants. Data are shown as means \pm s.d. (Student's *t* tests, ***P* < 0.01, n=3).



The Extracellular domain

Transmembrane domain

The kinase domain

Figure S1

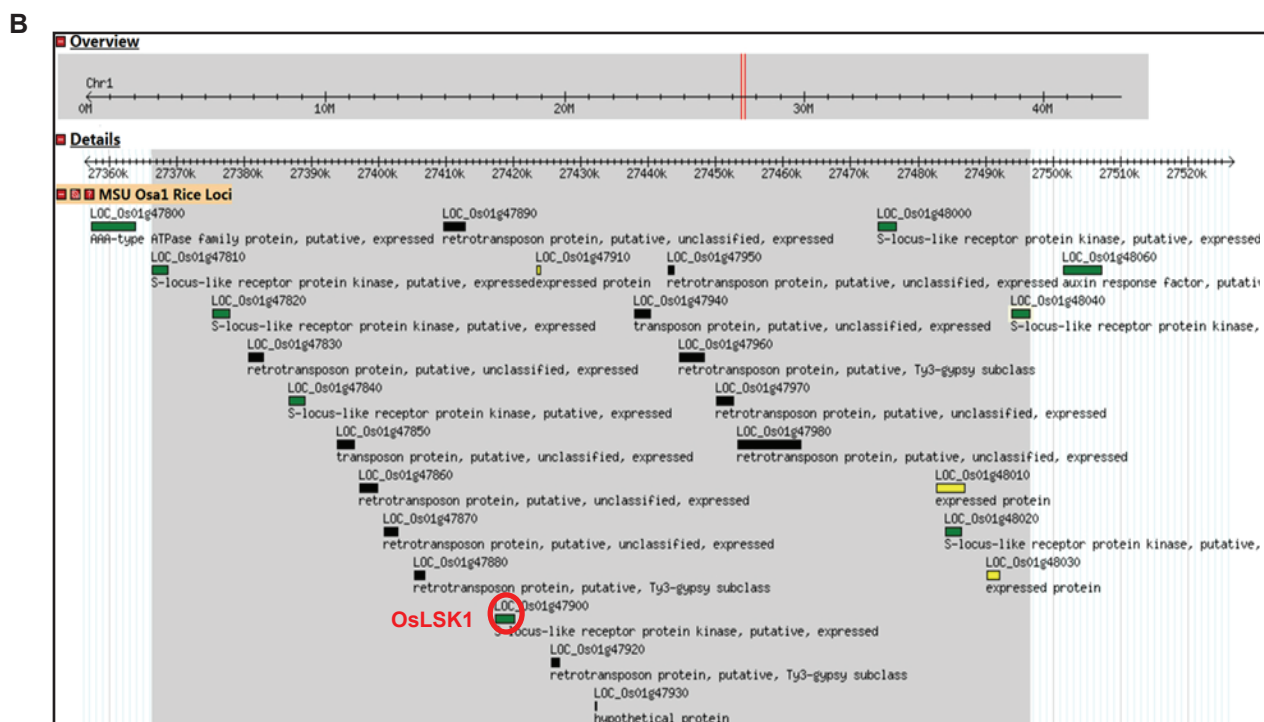
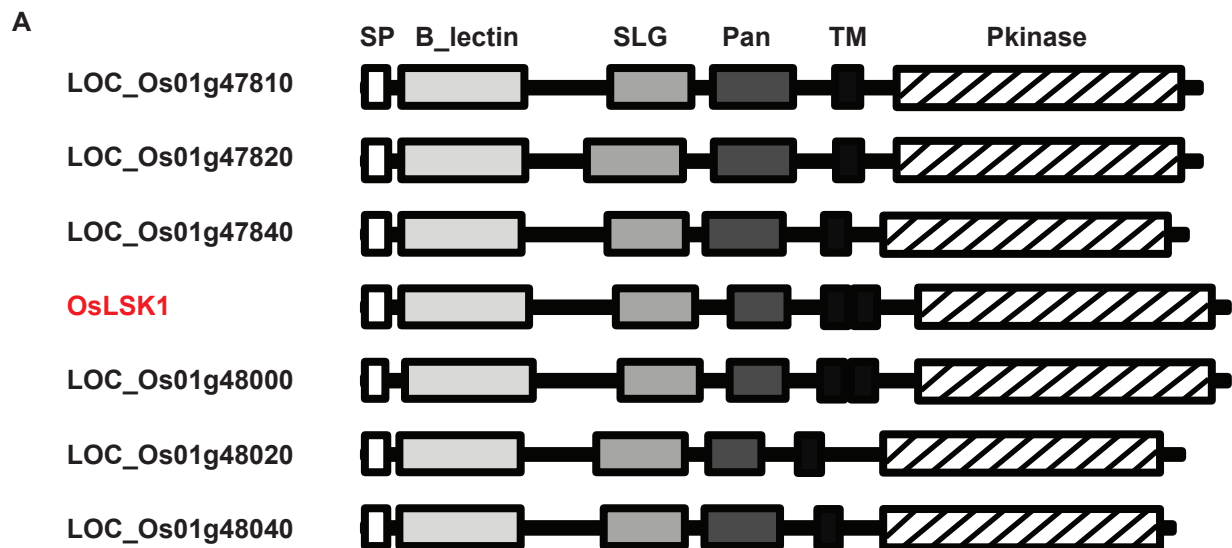


Figure S2

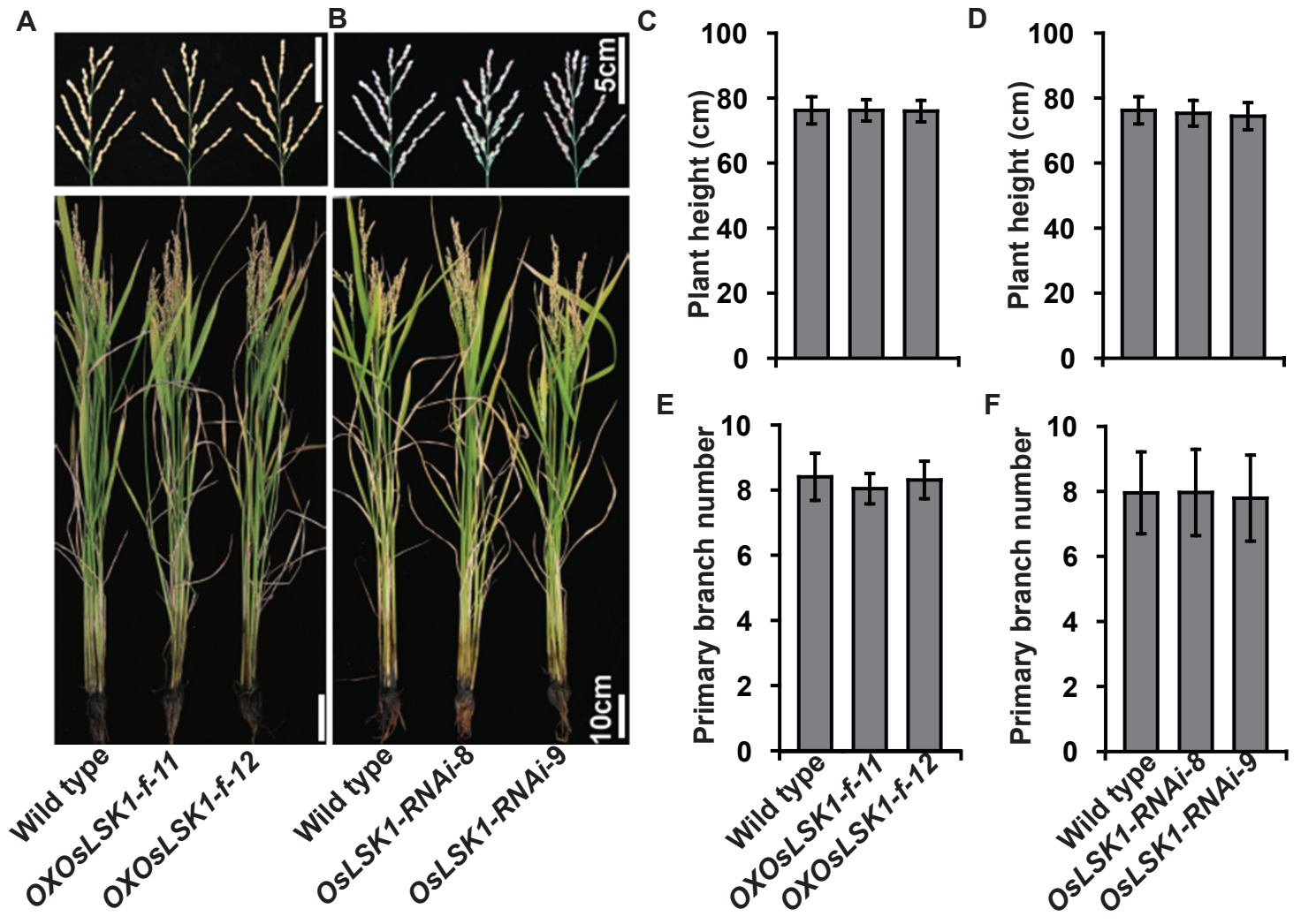


Figure S3

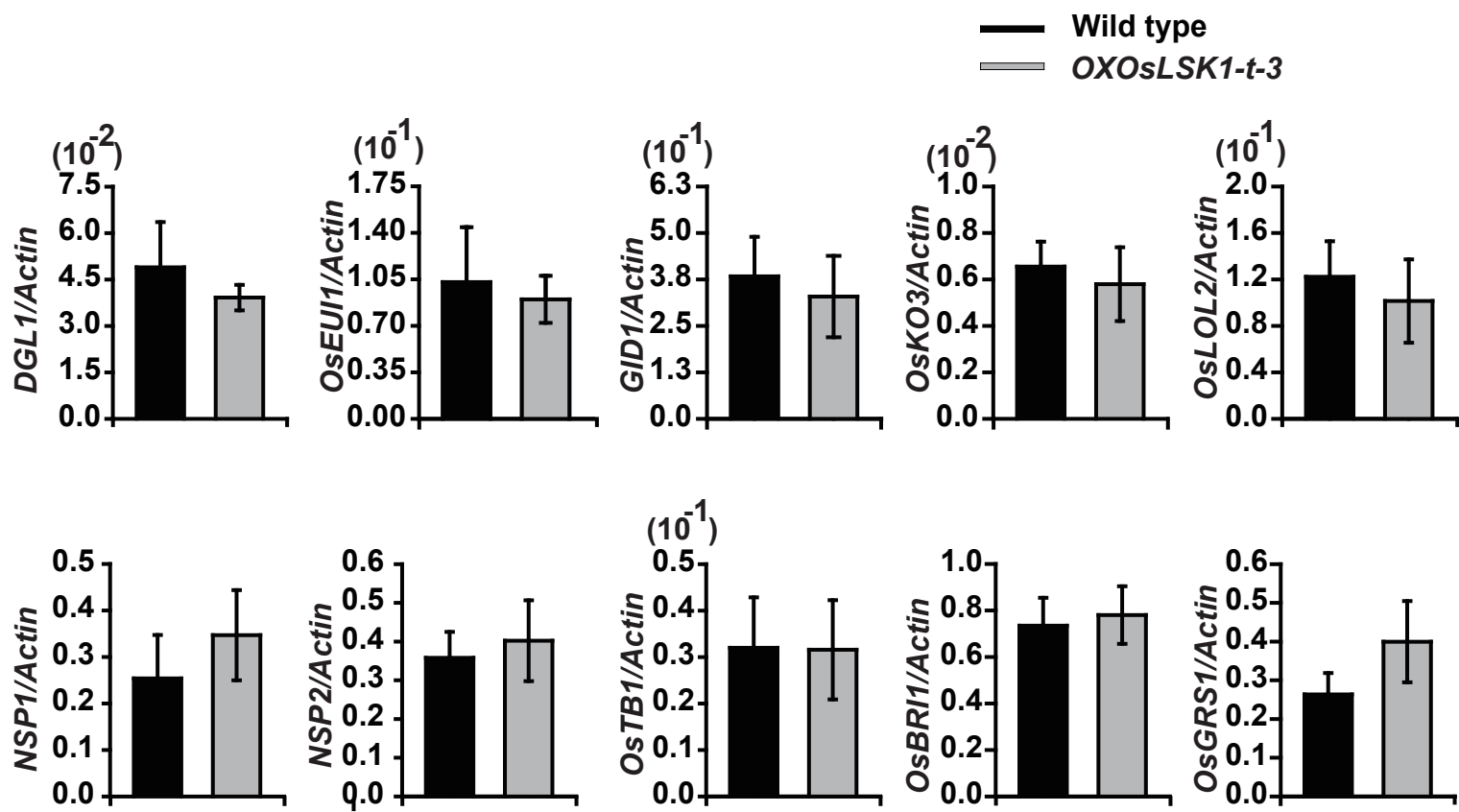


Figure S4

Table S1 Primers

	Gene	Forward primer	Reverse primer
Vector construction for transgenic plant	OsLSK1-t	CAAAAAAGCAGGCTTCATGGCTGGATTGGTCATCG	CAAGAAAGCTGGGTCTCGATGAACTTGA ACT
	OsLSK1-f	CAAAAAAGCAGGCTTCATGGCTGGATTGGTCATCG G	CAAGAAAGCTGGGT CAGAGTGGTAGGCAGGGTGT T
	OsLSK1-GUS	TATTTTCGGTACAATGGAGGTCG	CGTTTCAACTATAGCAGTTTGGC
	OsLSK1RNAi	CAAAAAAGCAGGCTTCGGGGCCTGACCGTCTCCCT	CAAGAAAGCTGGGT CACGCCGGCGTCGTCGAGGAT
Vector construction for Yeast two-hybrid	LOC_Os01g47810	CAAAAAAGCAGGCTTCACAGGTACATCTCTCCAGGT	CAAGAAAGCTGGGT CATAAACCTGGCCATTGTAG
	LOC_Os01g47820	CAAAAAAGCAGGCTTCTCACACATCAGAGCTGAGGA	CAAGAAAGCTGGGTCTAAGCCTTTAGTGTAAC
	OsLSK1	CAAAAAAGCAGGCTTCTGGGCAGATCCTCCATGT	CAAGAAAGCTGGGT CGAAGCCGTTGAACAGCGT
	LOC_Os01g48000	CAAAAAAGCAGGCTTCCAGCACACGCTCGGCACCG	CAAGAAAGCTGGGT CGTAGCCGTTGAAAAGCCT
	LOC_Os01g48020	CAAAAAAGCAGGCTTCTCATTCTTATCGGTAGAAG	CAAGAAAGCTGGGT CCCGGCCGTTGTAGAGCATA
	LOC_Os01g48040	CAAAAAAGCAGGCTTCACCGGCTCATCTTTCTCGG	CAAGAAAGCTGGGT CACCATTGAACAGGAGGCCT
	attB adaptor	GTGGGGACAAGTTTGTACAAAAAAGCAGGCTTC	GTGGGGACCACTTTGTACAAGAAAGCTGGGTC
Positive transgenic lines test	OsLSK1-1(for <i>OsLSK1RNAi</i>)	GGTGCTTACTCCTAATCATCAT	GTCATGTGTTGAAAAGTCTA
	OsLSK1-2(for <i>OsLSK1OX</i>)	ATGGCTGGATTGGTCAT	ACCGACATGGAGGATCT
	Actin	ATCCTTGTATGCTAGCGGTCGA	ATCCAACCGGAGGATAGCATG

Q-PCR	LOC_Os01g47810	CATTGACATCGGTAAAAGC	CATGCCACCGACAGGACGGTG
	LOC_Os01g47820	CCTGCAGCTACTGCATAAAT	TGCAATATAATCATTCCAATG
	LOC_Os01g48040	GACACTGATATGTGTGCCTA	CATATCTATTTGGCGGTGGATG
	LOC_Os01g48000	ATCACCAGGCTAACCGTTAGCA	TGAAGTCTTAACTACAATTT
	LOC_Os01g48020	CACTCATCCAGTACCACCA	TGGTGGTACTGGATGAGTG
	OsKO1	AGATGACCCACATGCTC	CATCCACATAGACTGAA
	OsKO2	TCAGCTGGGTTCCAAAC	CCACGCACAATCCTTTC
	GID2	ATGTCGCAGCCTGCTG	GCAACCTTCTCCATG
	OsGA3ox2	TAGCCGACGAGTTGCTGA	TACCAGTTGAGGTGC
	OsKO3	ATAGAGGCTGCAGATAC	CAATGAGCTGGAACAGAG
	GID1	GTACCTGGACAGGAG	TAGATGCGCACCTCCA
	DGL1	ACCACTGGATGAGTATC	GTACTAGATTGACCTCG
	OsGSR1	AGGTGCTCCAACACGCAG	TCCTTGGTCTTCCAGTTG
	OsEUI1	CAAGCCCAAGTACCTCCAGA	TGACACGGGCCATGTAGAA
	OsLOL2	AGTGTATCTCCAGTACTGG	CTCCCTGTACGTTACCTCCA
	Dwarf10	ACTATGGAACCTCGGC	ACTCGATCTGCCGGTGC
	Dwarf14	TCGCCAAGCTTGTC	CATCGCGTCGAACAC
	Dwarf27	TGTTGCTCGACGGTGAG	GTCTCCGTCTGCACCG
	HTD2	ATGCTGCGATCGACGC	ACCATCGTCTTCTCCG
	NSP1	ACTCCCCTACAACAATAA	TTGCCGCATTCTTCTAGGT
	NSP2	ACACTTGGAGAGTACGAGG	ATCCAACGCTCCACCCTCAC
	OsTB1	ATGGACATACCGCTTT	GTGGTGGTAGTAGAA
	OsBRI1	ATGGTGGGTGGATCTGG	TCCTTGACCGGCTCGCCT
	Dwarf1	ATGGGCTCATCCTGTAGCA	TGCATGGATAACTGATGTGT
	Dwarf88	TGCTGCGATCGACGCAT	CACCATCGTCTTCTC
	OsSPY	ATGGGGCGACCGGGGA	TCCTTCCCGTCCAACCT
	OsLRK1	ATCTCTTGGCAACCTG	GACGATGAGTTTGCTG
	Ghd7	ATGGGGATGGCCAATGAG	CTGCTGGTCCCATCGACA
	MOC1	ATGCATGAGAGTGATG	ACCACAGCATGCAGAG

Vector construction for BiFC assay	pSPYNE (R)- LOC_Os01g47810	GCCTACTAGTGGATCCATGGGTAAGTTCCTGTGCC CAC	TCCTACCCGGGAGCGGTACCAAGAAAGTACCACCCT GTCATG
	pSPYNE (R)- LOC_Os01g47820	GCCTACTAGTGGATCCATGGCTGCGCTGCTGTATCT AAC	TCCTACCCGGGAGCGGTACCGGACTTGGGTATGTTA TGCTTC
	pSPYNE (R)-OsLSK1	GCCTACTAGTGGATCCATGGCTGGATTGGTCATCG GCTAC	TCCTACCCGGGAGCGGTACCCTTGCTGGAGAGGAAC CACCAG
	pSPYNE (R)- LOC_Os01g48000	GCCTACTAGTGGATCCATGGCTGGATTGGTCATCG GCTG	TCCTACCCGGGAGCGGTACCGCTCTGCTTGCTGGAC AGGAACCA
	pSPYNE (R)- LOC_Os01g48020	GCCTACTAGTGGATCCATGGAAACAATTCCCTGCCT C	TCCTACCCGGGAGCGGTACCTGTAGCCTCCTTCAATT CTCTG
	pSPYNE (R)- LOC_Os01g48040	GCCTACTAGTGGATCCATGGCAAAGTTTCTCTATCT GATC	TCCTACCCGGGAGCGGTACCCCTTATGGAAAGAAAC CACCAAGC
	pSPYCE(M)-OsLSK1	GCCTACTAGTGGATCCATGGCTGGATTGGTCATCG GCTAC	GAGCGGTACCCTCGAGCTTGCTGGAGAGGAACCACC AG

Table S2 Yield traits of transgenic plants.

	Primary branches per panicle	Grains per primary branch	Grains per panicle	1000 Grain weight (g)	Tillers per plant	Grains per plant	Grain weight per plot (g)	Plant height (cm)	Seed setting rate
Wild type	5.48±0.42	7.33±0.31	40.46±6.88	24.36±0.51	15.12±1.03	611.46±123.64	149.83±32.76	72.85±2.17	0.93±0.02
OXOsLSK1-t-3	7.50±0.44 **	8.11±0.21 *	60.84±3.20 **	24.63±0.47	16.77±1.86	1049.29±217.26	257.82±58.91 **	80.54±2.02 **	0.92±0.02
OXOsLSK1-t-4	7.33±0.82 **	8.42±0.71 *	61.80±6.47 **	24.11±0.52	15.55±1.17	961.96±163.69	233.44±40.93 **	79.77±1.76 **	0.92±0.04

Data are shown as means ± s.d.(Student's *t* tests, * P < 0.05, ** P < 0.01, n=60).