

Supplementary Table S1. Oligo nucleotides used in this study

PCR targets or construction purpose	for which vector/plasmid	template (reference)	Forward primer/sense oligo name	Forward primer/sense oligo sequence	Reverse primer /antisense oligo name	Reverse primer / antisense oligo sequence
GFP CDS	pBCH1_GFP (pro35S:GFP)	pENTR_GFP	KT1191	ccctctagaATGGTGAGCAAGGGCGAGGA	KT1192	aaactcagctcCTGTACAGCTCGTCCATGCC
ZmUBQ promoter	pPUB	pBUH4 (1)	KT188	cccggtaccCTGCAGTGCAGCGTGACCCG	KT189	gggaagctCTGCAGAAAGTAAACACCAAAACACAGG
Gateway cassette with Nos terminator	pBS_PUG1	pWB2 (2)	KT190	cccaagctTCACAAGTTTGTACAAAAAAGCTGAACGA	KT192	ccctctagaCGCATGTCTTGGCTGTGAAGCT
Gateway cassette with N-terminal GFP and Nos terminator	pBS_PUG2	pWB6 (2)	KT191	cccaagctATGGTGAGCAAGGGCGAGGAGC	KT192	ccctctagaCGCATGTCTTGGCTGTGAAGCT
Gateway cassette with C-terminal GFP and Nos terminator	pBS_PUG3	pWB4 (2)	KT190	cccaagctTCACAAGTTTGTACAAAAAAGCTGAACGA	KT192	ccctctagaCGCATGTCTTGGCTGTGAAGCT
pPUG2 inverse PCR fragment without GFP	pBS_PUG4	pBS_PUG2	KT1551	CTCCTCGCCCTTGTCTCAACAT	KT1552	GGCATGGACGAGCTGTACAAGCAAGTTTGTACAaaaaagctgaacgaga
pPUG3 inverse PCR fragment without GFP	pBS_PUG5	pBS_PUG3	KT1551	CTCCTCGCCCTTGTCTCAACAT	KT1555	GGCATGGACGAGCTGTACAAGCAAGTTTGTACAaaaaagctgaacgaga
mCherry coding sequence	pBS_PUG4	pUC19_35S:mCherry	KT1553	GATAAgcttATGGTGAGCAAGGGCGAGGAG	KT1554	CAAACTTGTCTTGTACAGCTGTCCATGCC
mCherry coding sequence	pBS_PUG5	pUC19_35S:mCherry	KT1556	cglttaagctttgttacaagaatggtgatacATGGTGAGCAAGGGCGAGGAG	KT654	TTACTTGTACAGCTGTCCATGCC
OsAct1 promoter, NptII and A/PAB5 terminator	pPUBn	pPNhyPBase (3)	KT1550	gtactgaatcaacccgcaatggaatGTGAGCAAGGGCGAGGAG	KT1517	GCACAGAAAGGACTTGCTCTTGGAGCTAGGcaagcaccacccgatttgg
OsAct1 promoter, NptII and A/PAB5 terminator	pPgn	pPNhyPBase (3)	KT1516	GGCCATCGTTGAAGTGCCCTGTGCCGACAGCctctactactctcactcaactacat	KT1517	GCACAGAAAGGACTTGCTCTTGGAGCTAGGcaagcaccacccgatttgg
Histon H2B (LOC_Os01g05610) CDS amplification	pENTR_H2B	rice cDNA from shoot apices	KT534	caccATGGCCGCCAAGGCAGAGAA	KT536	AGCGGAGTGAATTTGGTGAACG
OsDCP2 (LOC_Os02g56210) CDS amplification	pENTR_OsDCP2	rice cDNA from shoot apices	DCP2-FL-F	caccTGATGGCGATGGCGGGCGG	DCP2-woST-R	GGTAGTAGGAAGGAAGCTTC
TOB3 (LOC_Os10g36420) CDS amplification	pENTR_TOB3	rice cDNA from shoot apices	KT1397	caccATGCTGCTGCTGCTCTGCTC	KT1460	GTACGGTGAACACCCATGTTG
GUS CDS amplification	pENTR_GUS	pBGH1 (4)	KT1391	caccATGGATCCCTACAGGgtaaatctagtt	KT1392	TTGTTTGCCTCCCTGCTCGC
CyclinB1;1 promoter (LOC_Os01g59120)	pPUG3_proCYCB1;1-GUS	rice genome DNA	KT1546	ttglaatacgaactatagggcgcaatggttaccacgggtgtaagcagcaggagataca	KT1547	cggaGCCTGCTTTTTGTACAAACTTGTGAaagcttCTTTGATCGTGCAGTGAGCACGGA
Oshox1 promoter (LOC_Os10g41230)	pPUG3_proOshox1-TOB3	rice genome DNA	KT1507	ttglaatacgaactatagggcgcaatggttaccGTTGTACAGAGCTCCGAAATCAATGC	KT1508	cggaGCCTGCTTTTTGTACAAacttgaaaacttTGATTCTCTCAACTCTCTCCACTTCT
Replacing Histone H2B in pENTR_H2B with oligo nucleotide	pENTR2.2	-	KT676	GGCCAAaggcccttatcagataaagcgccgctcagaaaacctgcaagttt	KT677	cgcaaaacctgcaagtttctagagcggcgcccttctagataaaggccctt
pENTR inverse PCR to clone OSH15 genomic DNA fragment	pENTR_gOSH15	pENTR2.2	pE_inv_OSH15 F	catgtgcatgtagctttgtaggatttGGCCGCGGGAGCTGCTT	pE_inv_OSH15 R	gcttttaactggcgcaagaaatatttttCCGCCGACCACAGCTTT
N-terminal region of OSH15	pCR_Blunt_OSH15N	pENTR_gOSH15	OSH15_N F	ttcctgttcaagctgtagtgaatctctc	OSH15_N R	CCGTGACCCTGGTACTCTGGACCGGGCCAGCC
Inverse PCR of pCR_Blunt_OSH15N	pCR_Blunt_GFP-OSH15N	pCR_Blunt_OSH15N	KT651	AGCTCCTCGCCCTTGTCTCACCATcaaaacacacacagaacacaaaaga	KT652	ctgcccagctcagctgcaATGGATCAGAGCTTTGGGAATCT
GFP CDS with 10x Alanine linker	pCR_Blunt_GFP-OSH15N	gGFP-OSH1 (5)	KT653	gttttATGGTGAGCAAGGGCGAGGA	KT654	CTGATCCAATgcaagctgcaagctcggg
pENTR inverse PCR to clone TOB3 genomic DNA fragment	pENTR_gTOB3	pENTR2.2	KT1351	gaaactgctgctgtgtagcagcatgaccaTTTGGCCCGCGAGCTGCTTT	KT1352	gttcaatactaaactatagctgaccTTTGGCCCGACCCAGCTTT
C-terminal region of TOB3	pCR_Blunt_TOB3C	pENTR_gTOB3	TOB3_C F	tttaattgtgaaactctgaatcagcag	TOB3_C R	aaagagatgctgtagttagcactgata
Inverse PCR of pCR_Blunt_TOB3C	pCR_Blunt_TOB3-mCherry_C	pCR_Blunt_TOB3_C	KT1410	CACCAATgcccagcagctgctgctGATCGGTGCAACACCCATGTTGG	KT1411	GACGAGCTGTACAAAGaagccagcagataaattgtagaagtt
mCherry CDS with 6x Alanine linker	pCR_Blunt_TOB3C-mCherry	pENTR_mCherry	KT1412	CCGTACgcaagcagctgctgcaATGGTGAGCAAGGGCGAGGA	KT1413	tttagctggcttactTTGTACAGCTGTCCATGCCG
qRT-PCR primers for GFP	-	rice cDNA	KT544	GGCTTCTGTTGGGCTCTT	KT545	ATCCTGGTGGAGCTGGACGG
qRT-PCR primers for RAc1	-	rice cDNA	KT546	GCCATCCATTGTGCACAGG	KT547	AGAAACAAGCAGGAGGACGCG

## Reference

- Nigorikawa, M., Watanabe, A., Furukawa, K., Sonoki, T., and Ito, Y. (2012). Enhanced saccharification of rice straw by overexpression of rice exo-glucanase. *Rice* (N Y) 5, 14.
- Nakagawa, T., Kurose, T., Hino, T., Tanaka, K., Kawamukai, M., Niwa, Y., Toyooka, K., Matsuoka, K., Jinbo, T., and Kimura, T. (2007a). Development of series of gateway binary vectors, pGWBs, for realizing efficient construction of fusion genes for plant transformation. *J Biosci Bioeng* 104, 34-41.
- Nishizawa-Yokoi, A., Endo, M., Osakabe, K., Saika, H., and Toki, S. (2014). Precise marker excision system using an animal-derived piggyBac transposon in plants. *Plant J* 77, 454-463.
- Ito, Y., and Kurata, N. (2008). Disruption of KNOX gene suppression in leaf by introducing its cDNA in rice. *Plant Science* 174, 357-365.
- Tsuda, K., Ito, Y., Sato, Y., and Kurata, N. (2011). Positive autoregulation of a KNOX gene is essential for shoot apical meristem maintenance in rice. *Plant Cell* 23, 4368-4381.