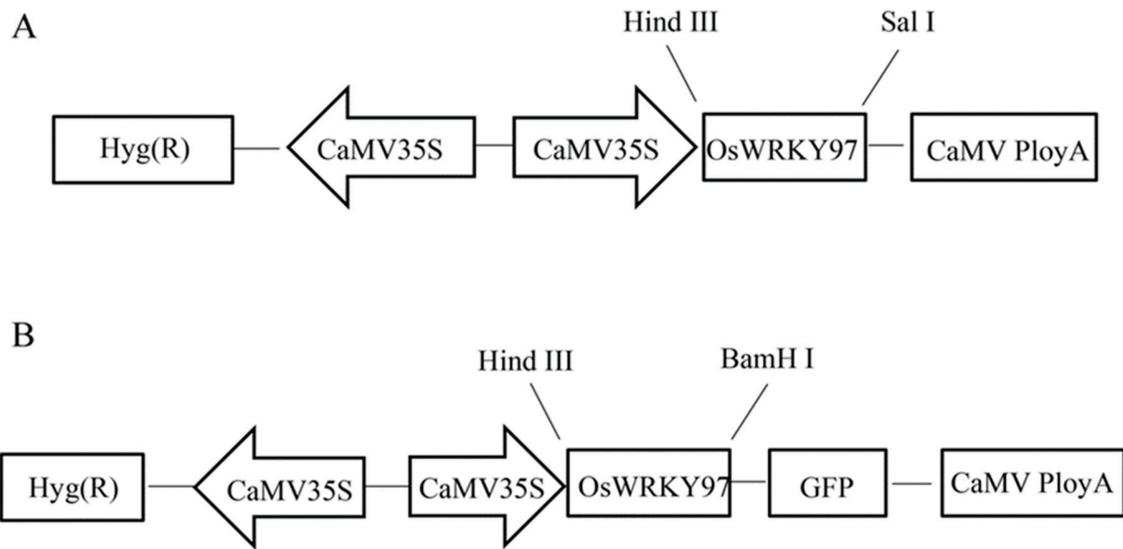


Supplementary Figure S1. Real time PCR analysis of OsWRKY97 gene in rice Nipponbare different tissues. Fifteen representative tissues are as follows: Lb1, leaf blade at four-leaf stage; Lb2, leaf blade from plants with four tillers; Lb3, leaf blade at ripening stage; Ls1, Leaf sheath at four-leaf stages; Ls2, Leaf sheath from plants with four tillers; Rt1, root at four-leaf stages; Rt2, root at from plants with four tillers; St1, stem from plants with four tillers; St2, stem at ripening stage; An, 1.2-1.5 mm anther; Pi, pistil from 10-14 cm inflorescence; Em1, embryo at 7 days after flowering; Em2, embryo at 28 days after flowering; En1, endosperm at 7 days after flowering; En2, endosperm at 28 days after flowering. The rice Actin transcript levels were used as internal controls. Error bars indicate SE based on three biological replicates.



Supplementary Figure S2. Schematic diagram of the architecture of the vector. (A) schematic diagram of the architecture of the OsWRKY97 overexpression. (B) schematic diagram of the architecture of the OsWRKY97-GFP

Table S1 Primer sequences used in this study

Primer name	Primer sequence (5'-3')
<i>OsWRKY97</i> for clone	Forward: <u>AAGCTT</u> CCCTACCAAGCGAGACCA Reverse: <u>GTCGAC</u> CCCTATCTGGCACCATCCA
<i>OsWRKY97-GFP</i> for clone	Forward: <u>AAGCTT</u> CCTACCAAGCGAGACCACT Reverse: <u>AGATCT</u> CAAGAAATGGAAATACTCG
<i>OsWRKY97</i> for qRT-PCR	Forward: AGCCGTACAGTTCCAACCAG Reverse: AATGTCCTCGACAGAGCACC
<i>OsActin</i> for qRT -PCR	Forward: ACAACTGGGACGACATGGAG Reverse: GCCACATACATTGCTGGTG
<i>OsRAB21</i> for qRT-PCR	Forward: CAGTTCAGCCGATGAGGG Reverse: CTGCTGCTCGCCCTTGTT
<i>OsRD22</i> for qRT-PCR	Forward: CTAGTCTCTCGTGCTCTCCT Reverse: GCGCAGTAGTGCTTGTGCTTG
<i>OsRAB16A</i> for qRT-PCR	Forward: GCCGAGTAACTGGGGTCAAG Reverse: GTTCTTGCTGGTGTGCTC
<i>OsNCED3</i> for qRT-PCR	Forward: AGTACTTCTACTTCGCGCCC Reverse: CGGGTACCACCACGTAGTTC