

Supplementary information

		Subgroups ^a	Similarity (%) ^b
OsWRKY5	WRKYGQKMAKGNPCPRAYRCTMASGCPVRKQVQRCAEDKSLILITTYEGTSH		
AtWRKY18	WRKYGQKVTRDNPSPRAYFRCSFAPSCPVKKKVQRSAEDPSLILVATYEGTSH	Ila	35/53 (66)
AtWRKY40	WRKYGQKVTRDNPSPRAYFKCACAPSCSVKKKQQRSVEDQSVLIVATYEGEHNH	Ila	31/53 (58)
AtWRKY6	WRKYGQKMAKGNPCPRAYRCTMATGCPVRKQVQRCAEDRSILITTYEGNHNH	Ilb	48/53 (91)
AtWRKY47	WRKYGQKMAKGNPCPRAYRCTMAVGC PVRKQVQRCAEDTTILITTYEGNHNH	Ilb	46/53 (87)
AtWRKY8	WRKYGQKAVKNSPYPRSYRCTTQ-KCNVKKRVERSYQDPTVVITTYESQHNH	Ilc	29/53 (55)
AtWRKY49	WRKYGQKSIKNSPNPRSYRKTNP-ICNAKKQVERSIDESNTYIITTYEGEHNH	Ilc	27/53 (51)
AtWRKY7	WRKYGQKPIKGSFHPRGYYKCSVVRGCEARKHVERALDDAMMLIVTYEGDHNH	Ild	30/53 (57)
AtWRKY17	WRKYGQKPIKGSFHPRGYYKCSVVRGCEARKHVERALDDSTMLIVTYEGEHNH	Ild	30/53 (57)
AtWRKY14	WRKYGQKPIKGSFHPRGYYRCSVSSKGC SARKQVERSRTPDNMLIVTYTSEHNH	Ile	28/53 (53)
AtWRKY29	WRKYGQKPIKGSFHPRSYYRCSVSSKGC LARKQVERNPNQNPKEFTIITYTNEHNH	Ile	26/53 (49)
	WRKYGQK C C H H		

Fig. S1. Amino acid sequence alignments of WRKY domains between OsWRKY5 and group II AtWRKY proteins.

Amino acid sequences of OsWRKY5 and group II AtWRKY proteins were obtained from the Rice Genome Annotation Project (<http://rice.plantbiology.msu.edu/>) and The Arabidopsis Information Resource (TAIR, <https://www.arabidopsis.org/>), respectively. Sequence alignment was performed using ClustalW with default parameters. Sequences are as follows: OsWRKY5, Os05g04640; AtWRKY18, At4g31800; AtWRKY40, At1g80840; AtWRKY6, At1g62300; AtWRKY47, At4g01720; AtWRKY8, At5g46350; AtWRKY49, At5g43290; AtWRKY7, At4g24240; AtWRKY17, At2g24570; AtWRKY14, At1g30650; AtWRKY29, At4g23550. Black boxes represent amino acids of AtWRKY proteins that are identical to those of OsWRKY5. Red and blue boxes represent the conserved WRKYGQK sequence and zinc finger motif of the WRKY domain, respectively. ^aEulgem et al. (2000) classified group II AtWRKY proteins into five subgroups [37]. ^bAmino acid similarity of AtWRKY proteins compared with OsWRKY5. Os, *Oryza sativa*; At, *Arabidopsis thaliana*.

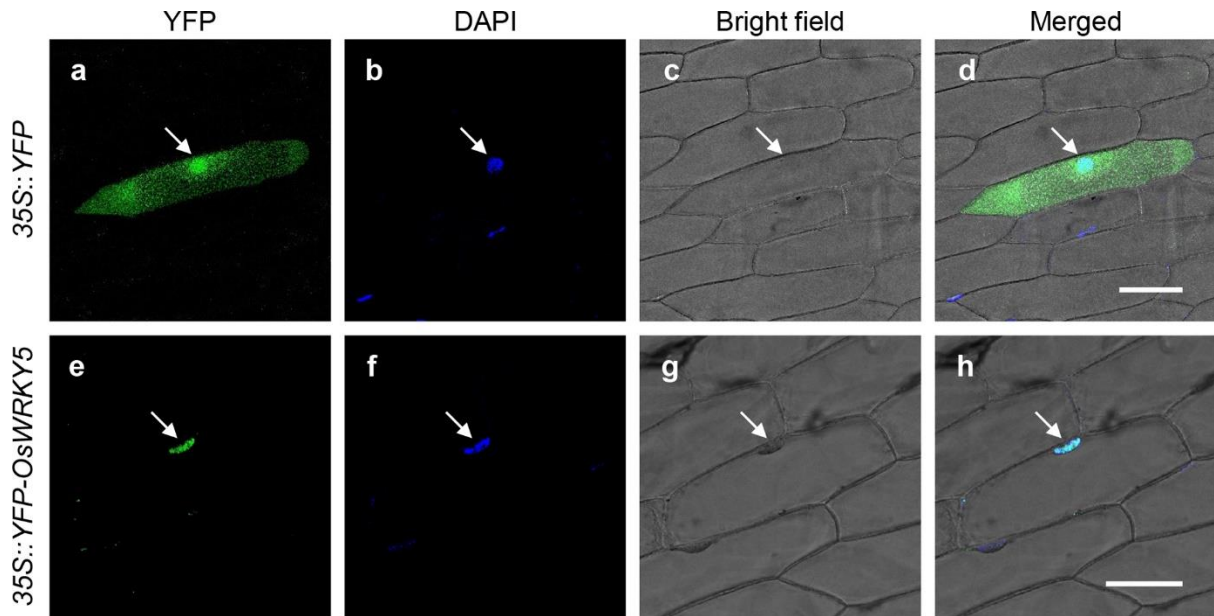


Fig. S2. Subcellular localization of OsWRKY5.

YFP-fused OsWRKY5 proteins transiently expressed in onion epidermal cells. Upper panels show fluorescence from the YFP control (**a-d**), which was distributed throughout the cell. Lower panels show the fluorescent signal of YFP-OsWRKY5 exclusively localized to the nucleus (**e-h**). Nuclei were stained with 4',6-diamidino-2-phenylindole dihydrochloride (DAPI). Experiments were repeated twice with similar results. White arrows indicate the position of the nucleus. Bars = 100 μ m.

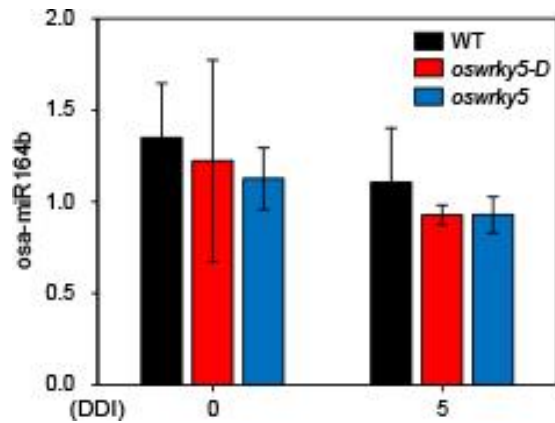


Fig. S3. Endogenous *osa-miR164b* levels in *oswrky5-D* and *oswrky5*.

Total RNA was extracted from detached leaves of WT and mutant lines (*oswrky5-D* and *oswrky5*) at 0 and 5 DDI under DIS as shown in Figure 2B. First-strand cDNA was synthesized by stem-loop pulsed RT-PCR. Transcript levels of *osa-miR164b* were determined by RT-qPCR and normalized using that of U6 snRNA. Mean and SD values were obtained from more than three biological replicates. No significant difference was found between WT and mutant lines by Student's *t*-test. DDI, day(s) of dark incubation.

AGAAACAACCTACCCTAGCTGGTTTTTGCACCTCTGAAGTCTAAACTGAAAAGGTCTTCAGTTCTTGATATATATG
 CAGATATTGTCAACTACTAGCTGATGAAGGCC**TTGACT**CTAGCTAAATACTAAGCCTCATGTGTCAATTTCTTCA
 TGATTTCTCCACCCATATTGCGGCTGGATAATGTACACTTAGGCATCAGTCCATATGGTGTGTGAATGTGCAAGA
 ACGGATCCAACACGCTAGGTAGAGTCGTAGAGATATATATAGATCCGGCCGTGAAAATGCCATCAAACCTTTCT
 CATGAAACTACGCTTATGAAGAAAGAGAGTTTACCACATGTTTATCTTTTTGAATTCATGCATATTGATTTGAT
 TGGCTACAAGTGCATGCGCATTAAATCCGCAAGTGGTTGACACTGGTTTATTACTTTCTTTACATAGCAAAAAA
 AAAATAATGAAACTATGGTTGTGTTTAGTTCCCTTAAGCTTCCAAAAATCCGTCACATCAAATGTTTGGATAC
 ATGCATAGAGCATTAAATGTGGACGAAAAAACCAATTACACAGTTTGCATGTAAATTACGAGACGAATCTTTT
 GAGCCTAATTACGCCGTGATTTGACAATGTGGTGCTACAGTAAACATTTGCTAATGGCAAATTAATTAGACTTA
 ATAAATTCGTCTCACAGTTTACAGGCGGAATCTGTAATTTGTTTATTATTAGTATATATTTAATACTTCAAATGTG
 TGCCGTATTCTTCAAAAAAATTTGGAGGAGGAACTAAACACAGCCTATATTTAAAAAATGATTTTGAAG
 ATAAATCTAATCAATATGATTAATTCTGTGTAATTAATGATATCA**AGTCAA**GTAAGAGAGATGATTAGAAGA
 AGCGAATATTAGGGAAGAACCTAATATCAGATAATTAGAAGAAGCGAGACTTTAAACTTAGATCATCTAGCAC
 ACAACTTTATAGATGCTAGCCGAAAAAATCATGGACGTTTGAGAGAGAGAGAGATCGTACTGAATGGAGTTAA
 TTGTTTGCTGCAGAGCGTGGCAGATCCTCTCATGCACGCACCATCACTCCTAGGCTATAGCTTATCTCGATCGAT
 CAACTTGGTGATCGAAAGGGAGTCTACATCGCG**TTGACT**CCG**TTGACC**CGGCCCATGCAGTA**CACGTG**GAC
 GCGAGTGCCTCATCCACCTGTCACGCTGACGTACGCCCGCTGACATGGCTGGCCCACCATCCCCATCGATT
 CCGATCCCCATTCTCTTGATAATTTGGTCCAAGTCCAAGTCTTCCGTTTACGTTACATATGCTAGCTTCTCGT
 CGTTAGCTAGCTATAGGTTAAACTACTTTACTAATTTCTCACTCTCTCTCTCTCTCTCTTGGAACCTAGCTAACT
 AGCTAGGAGTAGTAGTAGGAGCAAGAGCCATATAAAGCTAGCTAGCTACGACCTAGCTAGCTCTCCCCTACTT
 TAATTGATTTCTCTCCTTCTCACTCTACTGATCGATCGATCGAGCTCTATCC**ATG**GAGATG

Fig. S4. The *Cis*-elements in *OsWRKY5* promoter region.

The *cis*-elements were identified in the 1,500-bp upstream of the transcription initiation site (+1) represented by bent arrow. Red, blue, and black shaded sequences represent the W-boxes, G-box, and start codon, respectively.

Table S1. Primers used in this study.

A. Primers for verification of T-DNA insertion		
Primer names	Left primers (5' → 3')	Right primers (5' → 3')
PFG_3A-15928	CATTAAAGCTGGACCAGATGG	AACCACTTGC GGATTAATGC
PFG_3A-06060	TTGGATGCCTGATTAAGGTTG	CCGTTCTTGCACATTCACAC
pGA2715	CTAGAGTCGAGAATTCAGTACA	TTGGGGTTTCTACAGGACGTAAC
B. Primers for subcellular localization		
Gene	Forward primers (5' → 3')	Reverse primers (5' → 3')
<i>OsWRKY5</i>	ATGGAGATGATGGTGCAGAAGC A	TCAGGTGGGAGACGTGCCGCAA
C. Primers for RT-qPCR		
Genes	Forward primers (5' → 3')	Reverse primers (5' → 3')
<i>OsWRKY5</i>	GGCTCCAATGATCAGTGATGGA	AGCCATTGTGCATCGGTAGT
<i>SGR</i>	AGGGGTGGTACAACAAGCTG	GTCCTTGC GGAAAGATGTAG
<i>NYC3</i>	TGTCGTTGCCATGTGAAGAT	TTGGTCACGCCACAAATCTA
<i>OsPAO</i>	GGAAATCCTAGCCAAGAAGTGTT G	CGCAGGAATCCCAGCAGTT
<i>Osh69</i>	CCACAACACGGATAACTT	GGTGAACACTATGGAACA
<i>Osh36</i>	GCACGGAGGCGAACGA	TTGAGCGGTAGCACCCATT
<i>OsI85</i>	GAGCAACGGCGTGGAGA	GCGGCGGTAGAGGAGATG
<i>OsNAP</i>	CAAGAAGCCGAACGGTTC	GTTAGAGTGGAGCAGCAT
<i>OsNAC2</i>	CAACTCCTGGAGAGCTGCAA	GATCTCCGGGTTACGTCG
<i>OsNCED3</i>	GTGGTGCTCGACAAGGAGAA	CAGAGGTGGAAGCAGAAGCA
<i>OsNCED4</i>	GAGGTACGACTTCCATGGGC	TTGAGGTACGGCTTGGACAC
<i>OsNCED5</i>	CCCAGCTTGAAGCTTTTGCT	ACAACACTGCAACTATCCCTATCAC T
<i>OsUBQ5</i>	ACCACTTCGACCGCCACTACT	ACGCCTAAGCCTGCTGGTT
D. Primers for pulsed RT-qPCR of miR164b		
Primer names	Forward primers (5' → 3')	Reverse primers (5' → 3')
miR164b_pulsed RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGACTGGATACGACTGCAC G	
miR164b_qPCR	GCTCTGGAGAAGCAGGGC	GTGCAGGGTCCGAGGT

U6 snRNA_qPCR CAACGGATATCTCGGCTCT CAACTTGC GTTCAAAGACTC

E. Primers for yeast one-hybrid assay

Primer names	Forward primers (5' → 3') ^a	Reverse primers (5' → 3') ^a
OsWRKY5_GAD42	<u>GAATTC</u> ATGGAGATGATGGTGCA	<u>CTGCAGT</u> CAGGTGGGAGACGTGCC
4_EcoRI and PstI	GAAGCAACGA	GCAA
OsNAP-1_EcoRI and XbaI	<u>GAATTC</u> AGGTGTGAAAACAAAT AAGA	<u>CTCGAGA</u> ATAGTACCGCTGTGGTG AA
OsNAP-2_EcoRI and XbaI	<u>GAATTC</u> ATCACGTCGTTTTTCAAC TA	<u>CTCGAGG</u> TACCAAGGTGCTAAGAT AC
OsNAC2-1_SalI and XhoI	<u>GTCGACT</u> GTGTTCAGTTTGTCTCT TC	<u>CTCGAGG</u> TTAACAAGCCAGAACA AAC
OsNAC2-2_SalI and XhoI	<u>GTCGACC</u> GGGACATTTTCAGACG TTT	<u>CTCGAGT</u> GGTTTTGTGGGGCTTAG AA
OsNAC2-3_SalI and XhoI	<u>GTCGACC</u> CACTGCTATTACACAA TAG	<u>CTCGAGAT</u> CTCCCAGGAGATAAGC CA
OsNAC2-4_SalI and XhoI	<u>GTCGACTT</u> CTCGTTGCTGCTCG GCT-	<u>CTCGAGG</u> GCTAGTGATCCATCAGA TC
OsNAC2-5_SalI and XhoI	<u>GTCGAC</u> CTAGCTAGTACTCCATC CGT	<u>CTCGAGC</u> AGGTTACTACTCCCTCC AT

^a The underlined nucleotides represent the restriction site for restriction enzymes.