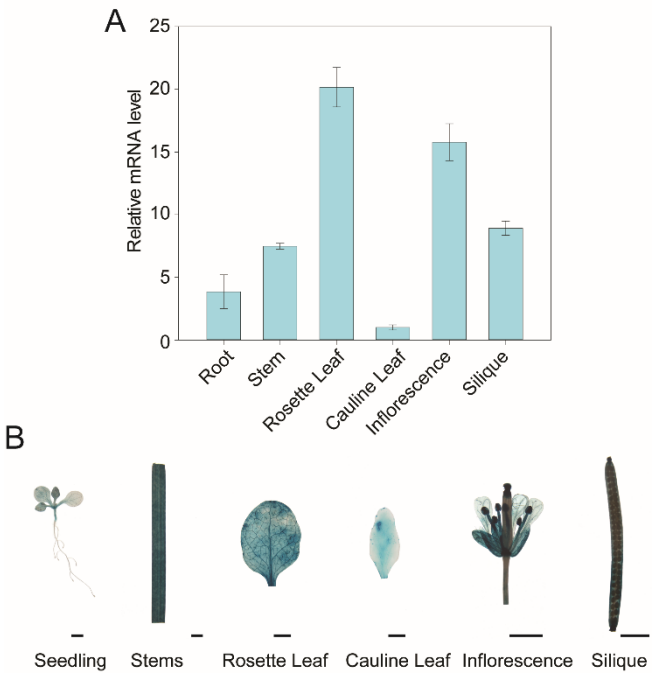
Supplemental Data

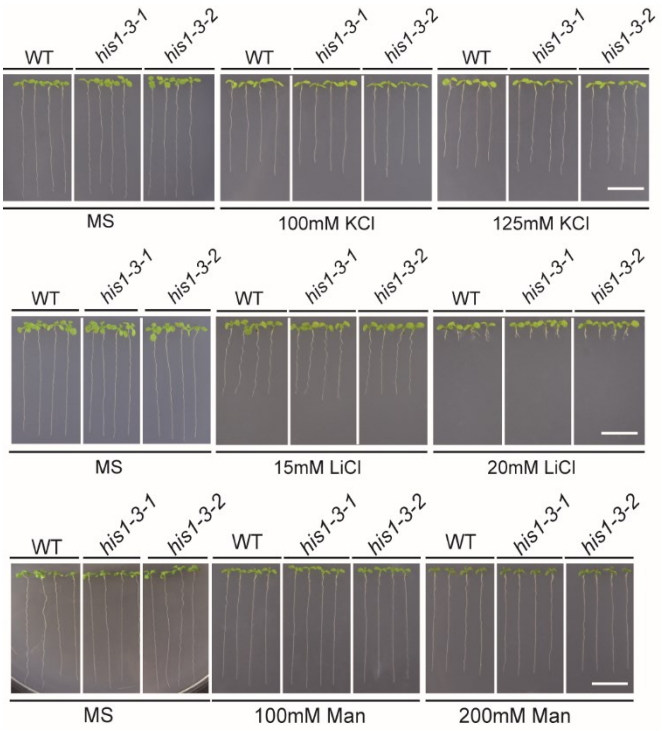
The following supplemental materials are available online.



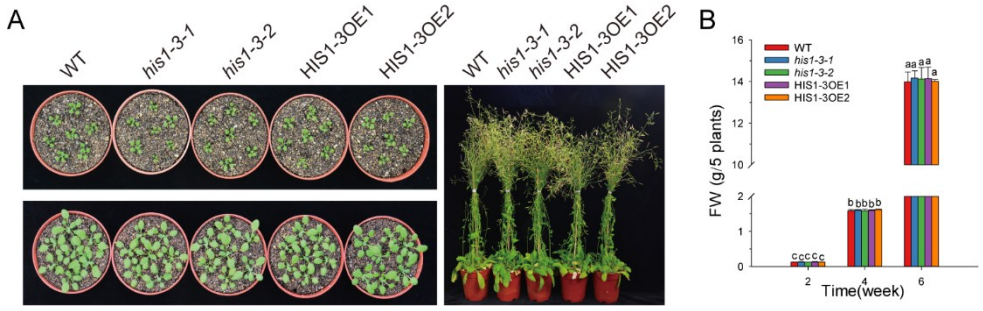
Supplemental Figure S1. Expression profile of *HIS1-3* gene.

(A) RT-qPCR analysis of HIS1-3 transcripts in different tissues of wild-type plants. RNA was isolated from roots, rosette leaves, stem, cauline leaves, inflorescence, siliques of the wild type plants. Three independent quantitative real-time PCR reactions were performed per sample. The vertical bars indicate the mean ± SE of the three biological replicates.

(B) Histochemical analysis of *ProHIS1-3*::GUS transgenic lines. Bar=1 mm.



Supplemental Figure S2. Responses of the his1-3 mutants to KCl, LiCl, and mannitol. The WT and *his1-3* mutants were grown on MS medium for 3 days then transferred to the medium with or without KCl, LiCl, and mannitol.

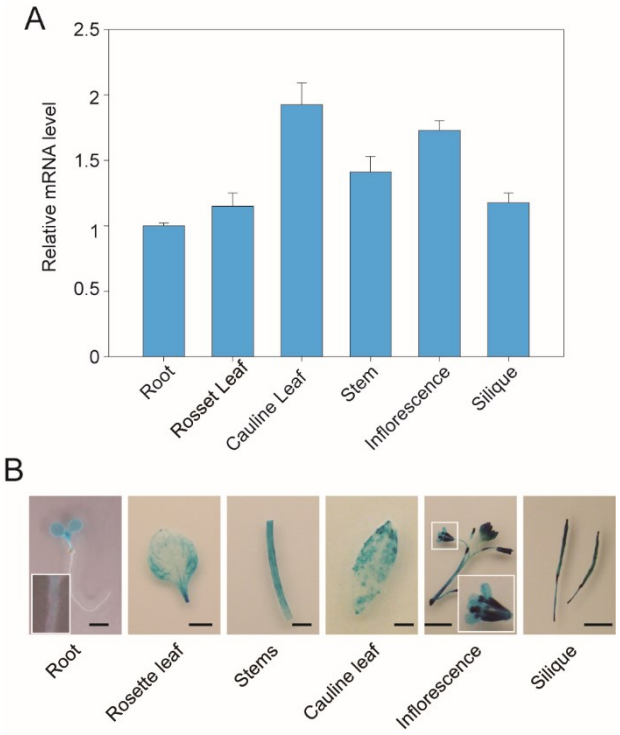


Supplemental Figure S3. Phenotypes of the WT, *his1-3* mutants, and HIS1-3-OE lines in soil-filled pots.

(A) Phenotypes assay of the WT, *his1-3* mutants, and HIS1-3-OE lines. The seedlings were grown in soil-filled pots for 2-, 4-, and 6-weeks.

(B) Fresh weight of the plants described in (A).

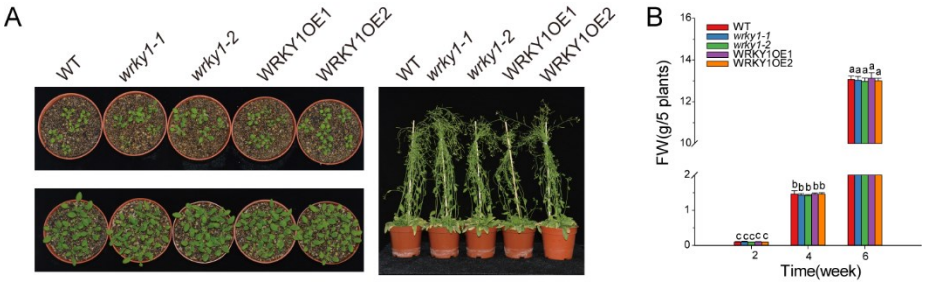
Data are presented as means ± SE of three replicate experiments. Statistical significance was determined by Student's *t* tests; significant differences ($P < 0.05$) are indicated by different lowercase letters.



Supplemental Figure S4. Tissue-specific expression of *WRKY1*.

(A) Expressions of *WRKY1* transcripts in different tissues using RT-qPCR analysis. RNA was isolated from roots, rosette leaves, stem, cauline leaves, inflorescence, siliques of the wild type plants. Three independent reverse transcription quantitative PCR reactions were performed per sample. The vertical bars indicate the mean ± SE of the three biological replicates.

(B) GUS analysis of *ProWRKY1*::GUS transgenic lines. Bar=1 mm.

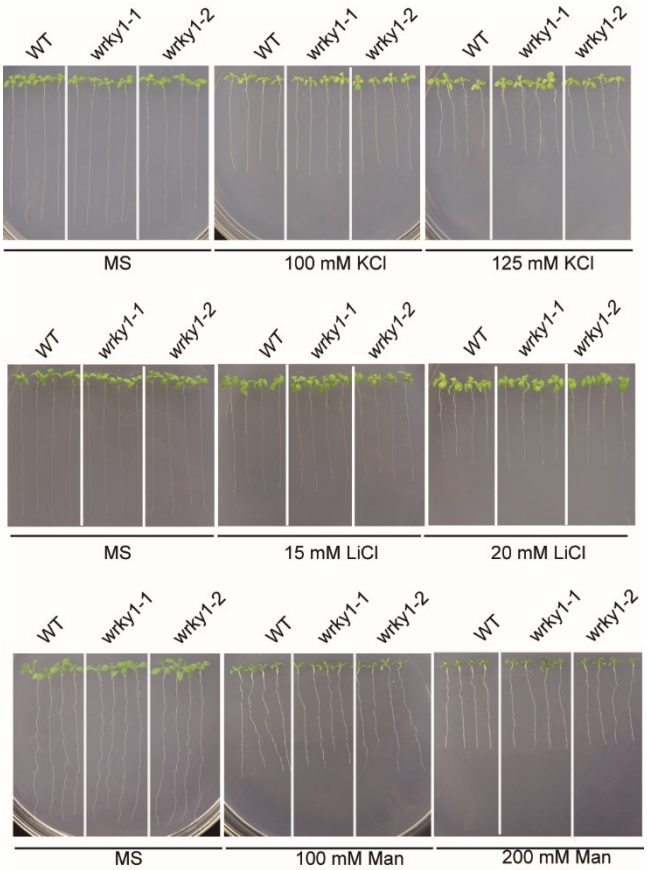


Supplemental Figure S5. Phenotypes of WT, *wrky1* mutants and WRKY1-OE lines in soil-filled pots.

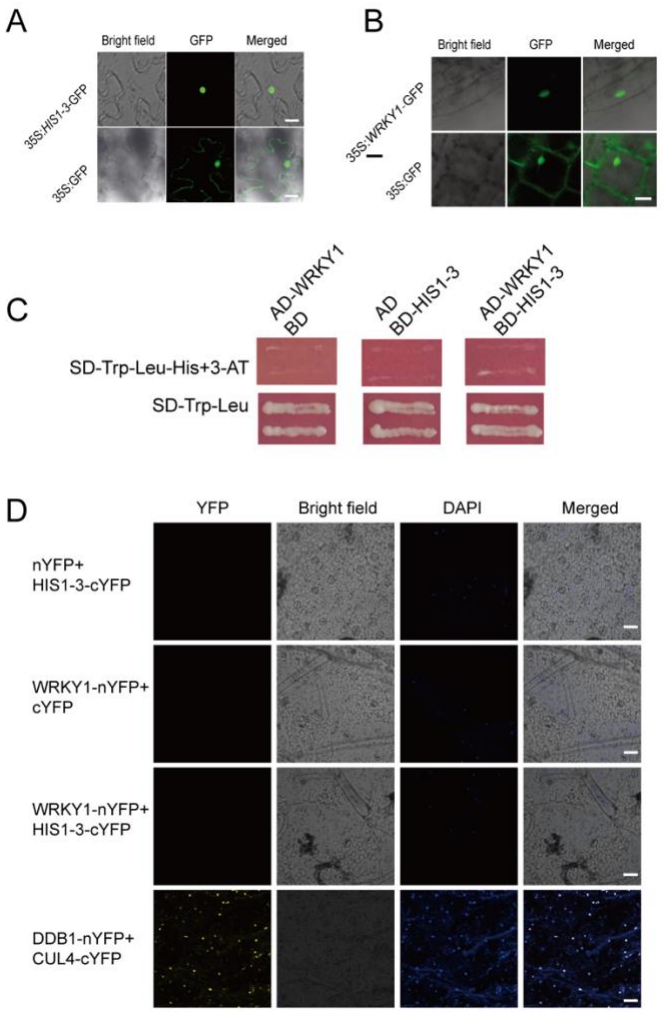
(A) Phenotypes assay of the WT, *wrky1* mutants and WRKY1-OE lines. The seedlings were grown in soil-filled pots for 2-, 4-, and 6-weeks.

(B) Fresh weight of the plants described in (A).

Data are presented as means ± SE of three replicate experiments. Statistical significance was determined by Student's *t* tests; significant differences ($P < 0.05$) are indicated by different lowercase letters.



Supplemental Figure S6. Phenotype test of WT and *wrky1* mutant seedlings in response to KCl, LiCl, and Mannitol. 3d-old seedlings of the WT and *wrly1* mutants were transferred to the medium with or without KCl, LiCl, and mannitol.



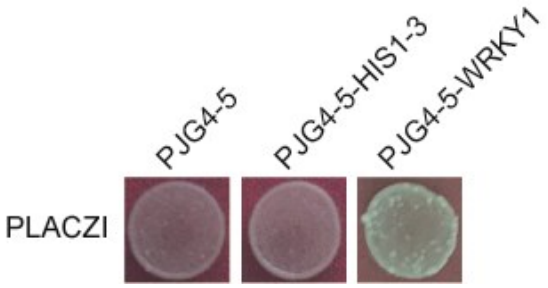
Supplemental Figure S7. The relationship between HIS1-3 and WRKY1.

(A) Subcellular localization of the HIS1-3:GFP fusion protein in 35S:HIS1-3:GFP plants. The expression of GFP alone was used as the control.

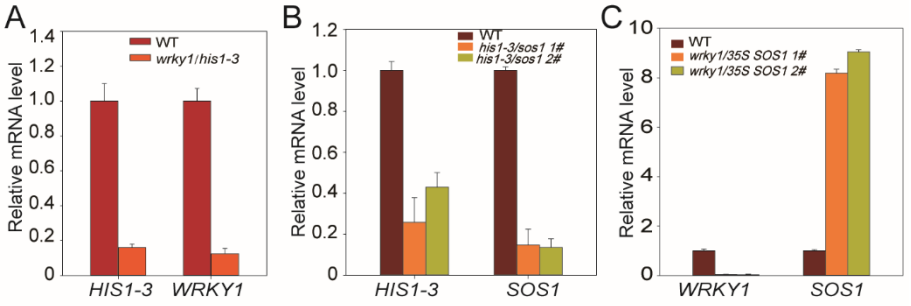
(B) Subcellular localization of the WRKY1:GFP fusion protein in 35S:WRKY1:GFP plants. The expression of GFP alone was used as the control.

(C) HIS1-3 did not interact with WRKY1 in yeast assays.

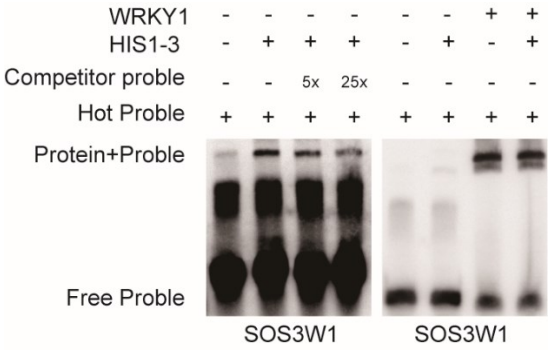
(D) HIS1-3 did not interact with WRKY1 by BiFC. To acquire YFP signals using the LSM 710, 488-nm was used for excitation and fluorescence was detected at a 410 to 550-nm range. Bar=50 μm.



Supplemental Figure S8. WRKY1 exhibits self-activation by yeast-one-hybrid assay.



Supplemental Figure S9. Identification of transgenic plants. Seedlings of *wrky1his1-3*, *his1-3sos1*, and *wrky1/35S SOS1* were grown on MS media for 2 weeks, and then isolated mRNAs for RT-qPCR analysis. *Actin8* was used as the internal control. All Data shown here are presented as the means ± SE of three replicate experiments.



Supplemental Figure S10. No specific competition at the promoter regions of SOS3 genes between HIS1-3 and WRKY1by reciprocal competitive EMSA.

Supplemental Table S1. Primers used for cloning, qPCR, and ChIP assay.

Table S1. Primers used for T-DNA, cloning, qRT-PCR and ChIP assay

Primer Name	Primer Sequences (5'-3')
For T-DNA	
his1-3-1- LP	5'-CAAAGCCTCTCGGTAAATGTG-3'
his1-3-1-RP	5'-TATTCTTCTTGTCCTGCTGCC-3'
his1-3-2 -LP	5'-GACCGAAAGGAGGAGCTAATG-3'
his1-3-2 -RP	5'-AAGATGATAACGAGGCAGCAG-3'
wrky1-1 -LP	5'-AAAATCGATCCCCAAAGTTTG-3'
wrky1-1- RP	5'-CATCTACTTCCGACTGCGAAG-3
wrky1-2 -LP	5'-TCATCTCGAAAGCTACGATTTG-3'
wrky1-2 -RP	5'-TCCTATGCTTCACCAACGATC-3'
For cloning and genotyping	
HIS1-3OE-LP	5'-CGGGGTACCATGGCAGAAGACAAGATCTTAAAG-3'
HIS1-3OE-RP	5'-CCGCTCGAGTCAAGCAGCGGAAGCTTTC-3'
HIS1-3GFP-LP	5'-CGGGGTACCATGGCAGAAGACAAGATCTTAAAGA-3'
HIS1-3GFP-RP	5'-CGGGAATCCAGCAGCGGAAGCTTTCATG
WRKY1OE-LP	5'- TGCTCTAGAATGGCTGAGGTGGGAAAAGTTC-3
WRKY1OE-RP	5'-CCGCTCGAGTTAGCTTTGGGCAGGCTCTGT-3'
WRKY1GFP-LP	5'- TGCTCTAGAATGGCTGAGGTGGGAAAAGTTC-3
WRKY1 GFP-RP	5'- CCCAAGCTTGCTTTGGGCAGGCTCTGTCTTG-3
HIS1-3pro-LP	5'-CGGGGTACCTTGGCTCTCGTCTCCACTC-3'
HIS1-3pro-RP	5'-CCCAAGCTTTAGAGGATTAGTGAAAGTGTTGC-3'
WRKY1pro-LP	5'-CGGGGTACCGAACCCAAAACCCCCAAA-3'
WRKY1pro-RP	5'-CCCAAGCTTAAATACTAACAAACTCAAG-3'
SOS1pro-LP	5'-CGGGGTACCCAAAATTCGTATTAATTC-3'
SOS1pro-RP	5'-CCCAAGCTTATATATCTAAGAAGCAAC-3'
SOS2pro-LP	5'- CGGGGTACCCATTAGGGTTCATGGGTTGAG -3'
SOS2pro-RP	5'-CCCAAGCTTTCTTTACAAACTTTTATCTG-3'
SOS3pro-LP	5'-CGGGGTACCAAATCATGTTGGGTCTGATTGG-3'
SOS3pro-RP	5'-CCGCTCGAG ACAAACACACCCTTCTCTCAAC-3'
For qRT-PCR	
HIS1-3-qFP	5'-AACCACCACTCATCCTCCATAC-3'
HIS1-3-qRP	5'-GCTGTAGAGAAAGTGTTTTACGGAC-3'
WRKY1-qFP	5'-AGGCAGCCCATATCCAAGGAGC-3'
WRKY1-qRP	5'-TCGTGGTCGTGTTTTCCCTCGT-3'
SOS1-qFP	5'- ATTTTGATGCAGTCAGTGGATG -3'
SOS1-qRP	5'- GCAAGCAGATTCTAGTCTTTCG -3'
SOS2-qFP	5'- GCGAACTCAATGGGTTTTAAGT -3'
SOS2-qRP	5'- CTTACGTCTACCATGAAAAGCG -3'

SOS3-qFP	5'- CCGGTCCATGAAAAAGTCAAAT -3'
SOS3-qRP	5'- CTCTTTCAATTCTTCTCGCTCG -3'
Actin8- qFP	5'-TCAGCACTTTCCAGCAGATG-3'
Actin8- qRP	5'-CTGTGGACAATGCCTGGAC-3'
For ChIP-qPCR	
PSOS1-1FP	5'-GTTCTTGTGCTTTCTACT-3'
PSOS1-1RP	5'-CTTTTGACCACCTTTTTA-3'
PSOS1-2FP	5'-AAGATACCATAGTCACATTC-3'
PSOS1-2RP	5'-CACAATTTTCAGCCGACC-3'
PSOS2-1FP	5'-GGAAACCATTAACCATTACAAC-3'
PSOS2-1RP	5'-CAATTCCGTTAAAAAGTTATCAATAGT-3'
PSOS2-2FP	5'-CTTGCTCTTGTATTCCTTCT-3'
PSOS2-2RP	5'-TATAGTCGGTTGGGATTCAC-3'
PSOS2-3FP	5'-AGTCCTCTTCCTTGTTGATG-3'
PSOS2-3RP	5'-TGGAAACAAACACTAGGGAA-3'
PSOS2-4FP	5'-GTATCTTTGTATGCTTTGTCTT-3'
PSOS2-4RP	5'-TTAATCGAACTCAAATTAGTAAAA-3'
PSOS2-5FP	5'-ATTGATAAGTGATATTAGATTAGTTT-3'
PSOS2-5RP	5'-CGTAGGAGAGAAGGAAGG-3'
PSOS3-1FP	5'-CTCGCTTAAATGTGTTCT-3'
PSOS3-1RP	5'-ATCAATATCAAATCTAATCG-3'
PSOS3-2FP	5'-TGAATTGATTGTTTAGGGAGAGC-3'
PSOS3-2RP	5'-AATATACAATAGAAGTCGACGGC-3'
PSOS3-3FP	5'-ATTTCATTAGAAACATTTTG-3'
PSOS3-3RP	5'-CCTACATTCGTTTTCGCTGG-3'