

Supplemental Data

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Supplemental Figure S2. The representative pictures of whole stem sections of different plants.

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Supplemental Figure S7. *WOX4* transcript levels in the SL biosynthetic and signaling mutants *max3-1*, *max2-1*, and *Atd14-1*.

Supplemental Figure S8. Phenotypes of the *gWOX4-GFP/max2-1*.

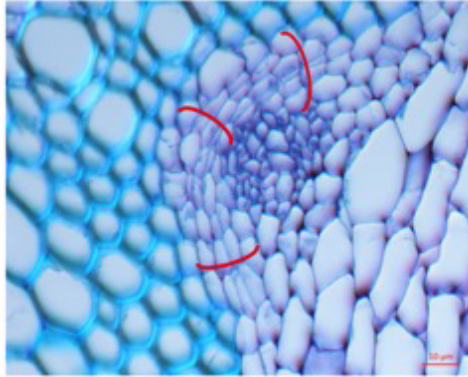
Supplemental Figure S9. Phenotype of the hypocotyl of *gWOX4-GFP/max2-1*.

Supplemental Table S1. Primers for genotyping, ChIP, EMSA, qPCR, and recombinant vectors.

Supplemental Table S2. Plasmids and restriction sites used for recombinant vectors.

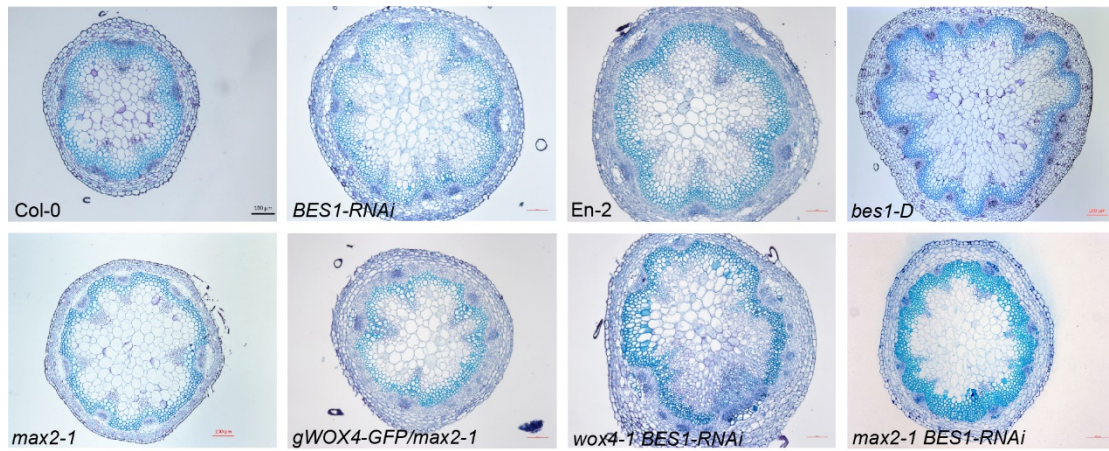
Supplemental Table S3. Accession numbers of genes.

Supplemental Figures

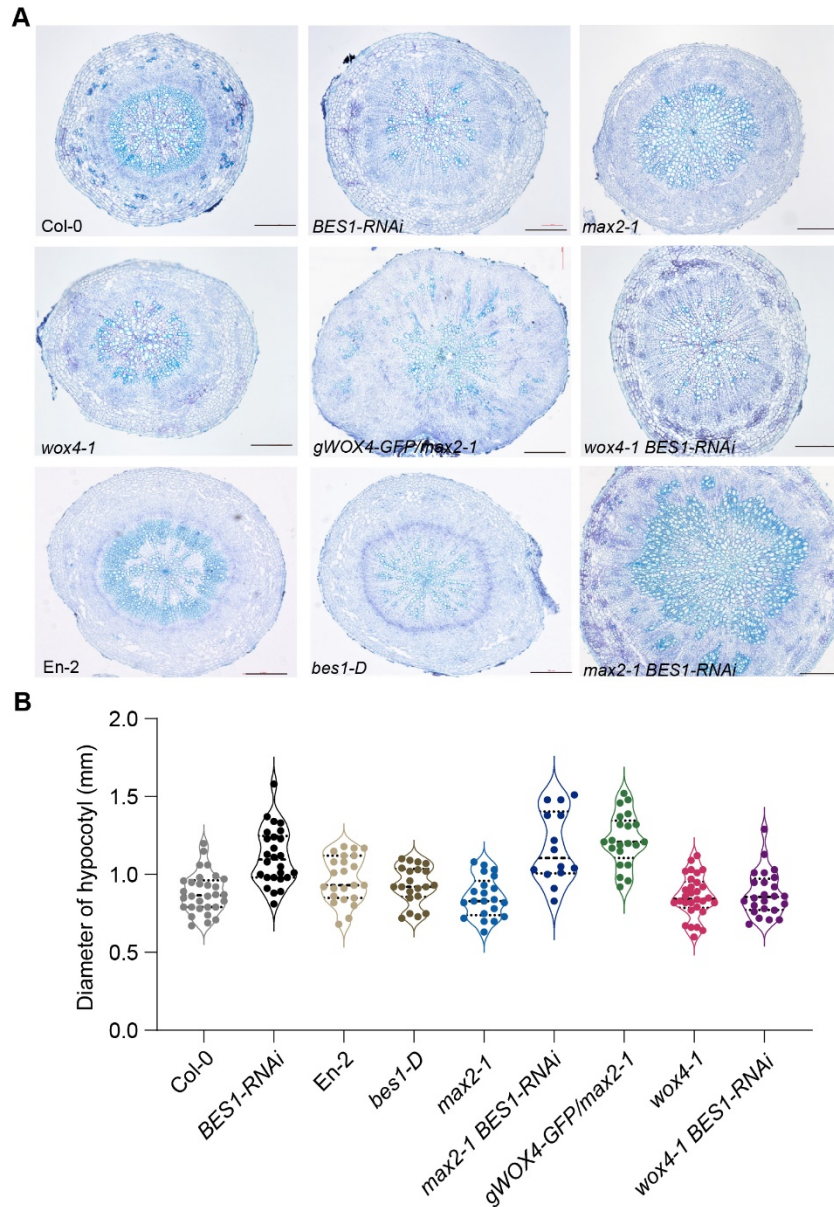


Supplemental Figure S1. Measured regions of the lateral vascular cambium. Relates to Figures 1, 2, 3, and 5.

The measured regions of the lateral vascular cambium are indicated by the red lines.

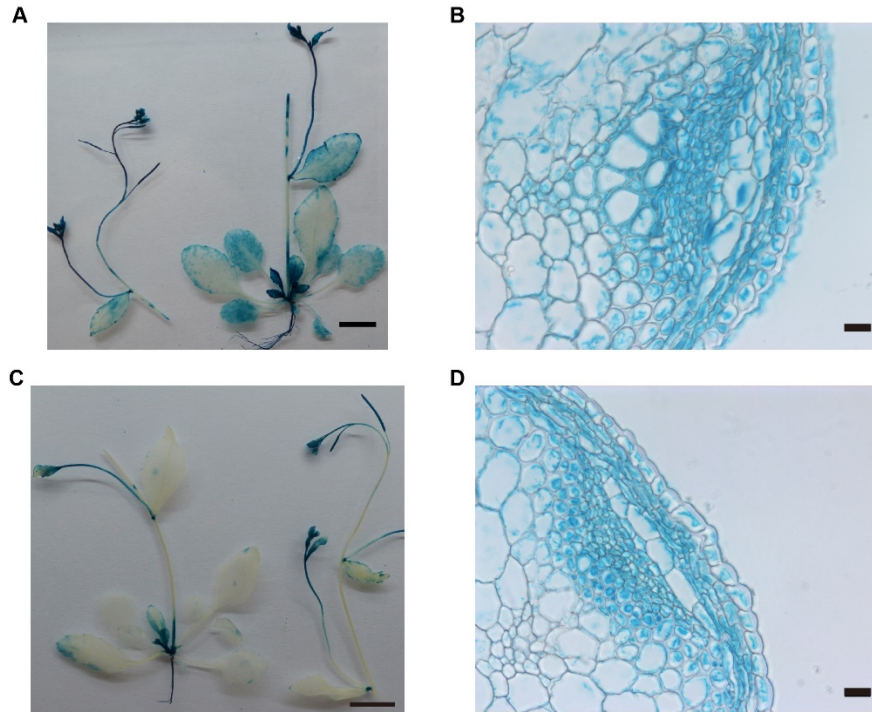


Supplemental Figure S2. The representative pictures of whole stem sections of different plants. Related to Figure 1, 2, 3, 5. Bars = 100 µm.



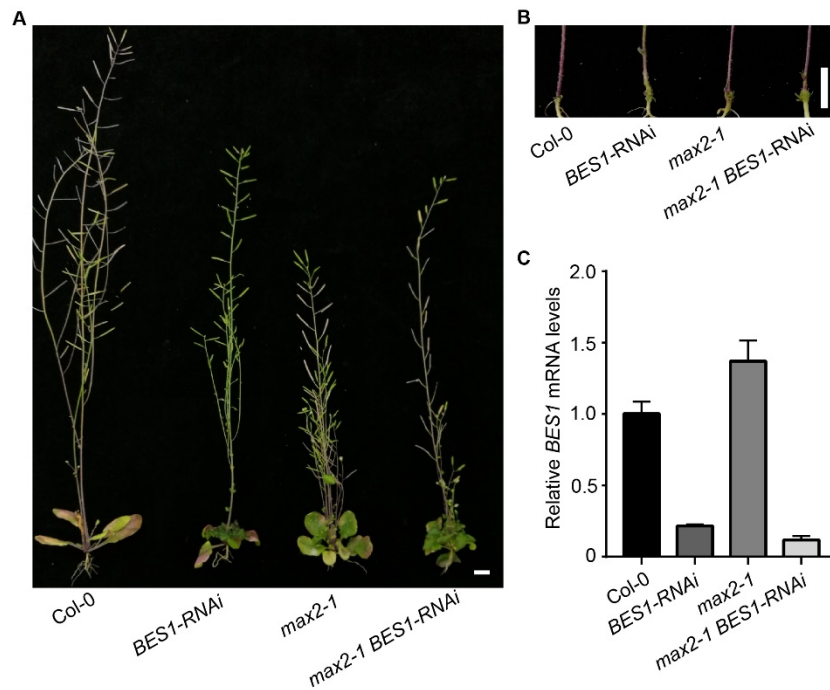
Supplemental Figure S3. The hypocotyl phenotype of different plants. Related to Figure 1, 2, 3, 5.

(A) The representative pictures of whole hypocotyl sections of different plants. (B) The hypocotyl diameter of plants in (A). The hypocotyl (2 mm immediately below the shoot-hypocotyl junction) of 4-weeks-old plants (about 15 cm high) were immediately measured after being pulling out of soil. From 5 to 10 plants were measured three times each line. Bars = 200 μ m.



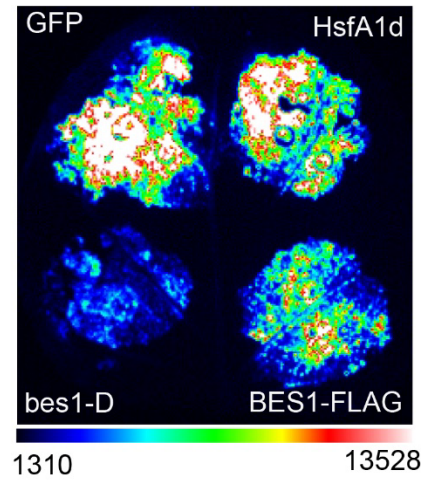
Supplemental Figure S4. Expression patterns of the *BES1(L)* and *BES1(S)* in the secondary stem and vasculature. Related to Figure 1.

(A, B) GUS staining of the secondary stem (A) and its cross section (B) for the *BES1(L)pro:GUS* reporter line in the En-2 background. (C, D) GUS staining of the secondary stem and its cross section for the *BES(S)pro:GUS* reporter line in the En-2 background. Bars = 1 cm in (A) and (C), Bars = 20 μ m in (B) and (D).

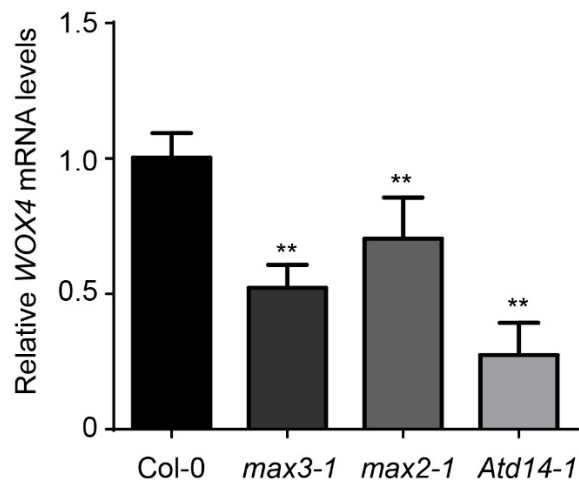


Supplemental Figure S5. Identification and phenotypes of the *max2-1 BES1-RNAi* line. Related to Figure 2.

(A) Representative photographs of 8-week-old Col-0, *BES1-RNAi*, *max2-1*, and *max2-1 BES1-RNAi* plants. (B) Representative photographs of basal stems and hypocotyls of 8-week-old Col-0, *BES1-RNAi*, *max2-1*, and *max2-1 BES1-RNAi* plants. Bar represents 1 cm. (C) Relative *BES1* mRNA levels in seedlings of Col-0, *BES1-RNAi*, *max2-1*, and *max2-1 BES1-RNAi* plants. Data are means \pm SD ($n = 3$). Bars represent 1 cm.

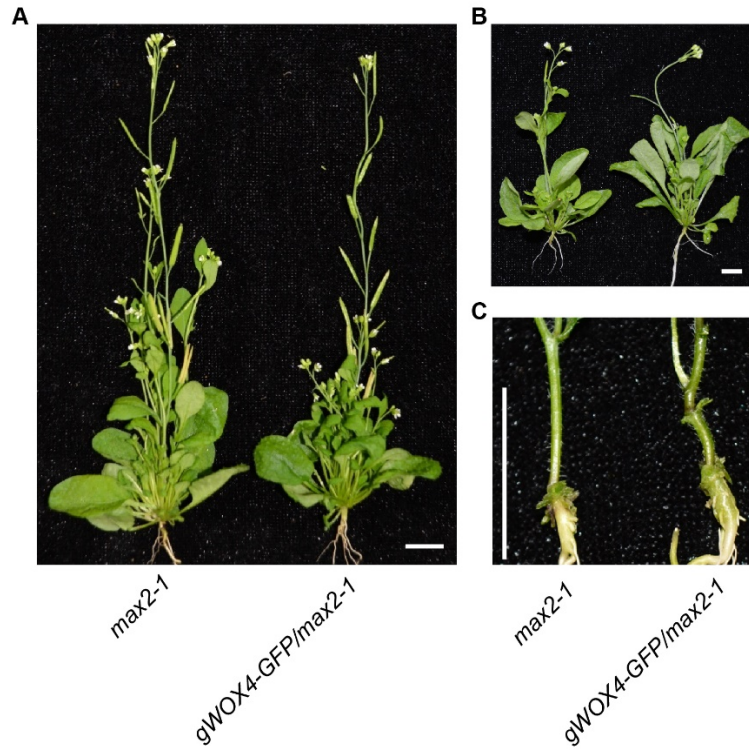


Supplemental Figure S6. Transient luciferase assay in *N. benthamiana* leaves demonstrates the co-expression with BES1 specifically repress *WOX4pro:LUC* activity. Related to Figure 3. The HsfA1d was used as the unrelated transcription factor control, GFP was the control effector. Effectors were BES1-FLAG and a stable-form BES1 (bes1-D), and *WOX4pro-LUC* was the reporter.



Supplemental Figure S7. Reduced *WOX4* transcript levels in the SL biosynthetic and signaling mutants *max3-1*, *max2-1*, and *Atd14-1*. Related to Figure 5.

The relative *WOX4* transcript level in Col-0 was set as "1". Data are means \pm SD ($n = 3$). *P* values were determined by Student's *t*-test, ***P* < 0.01.

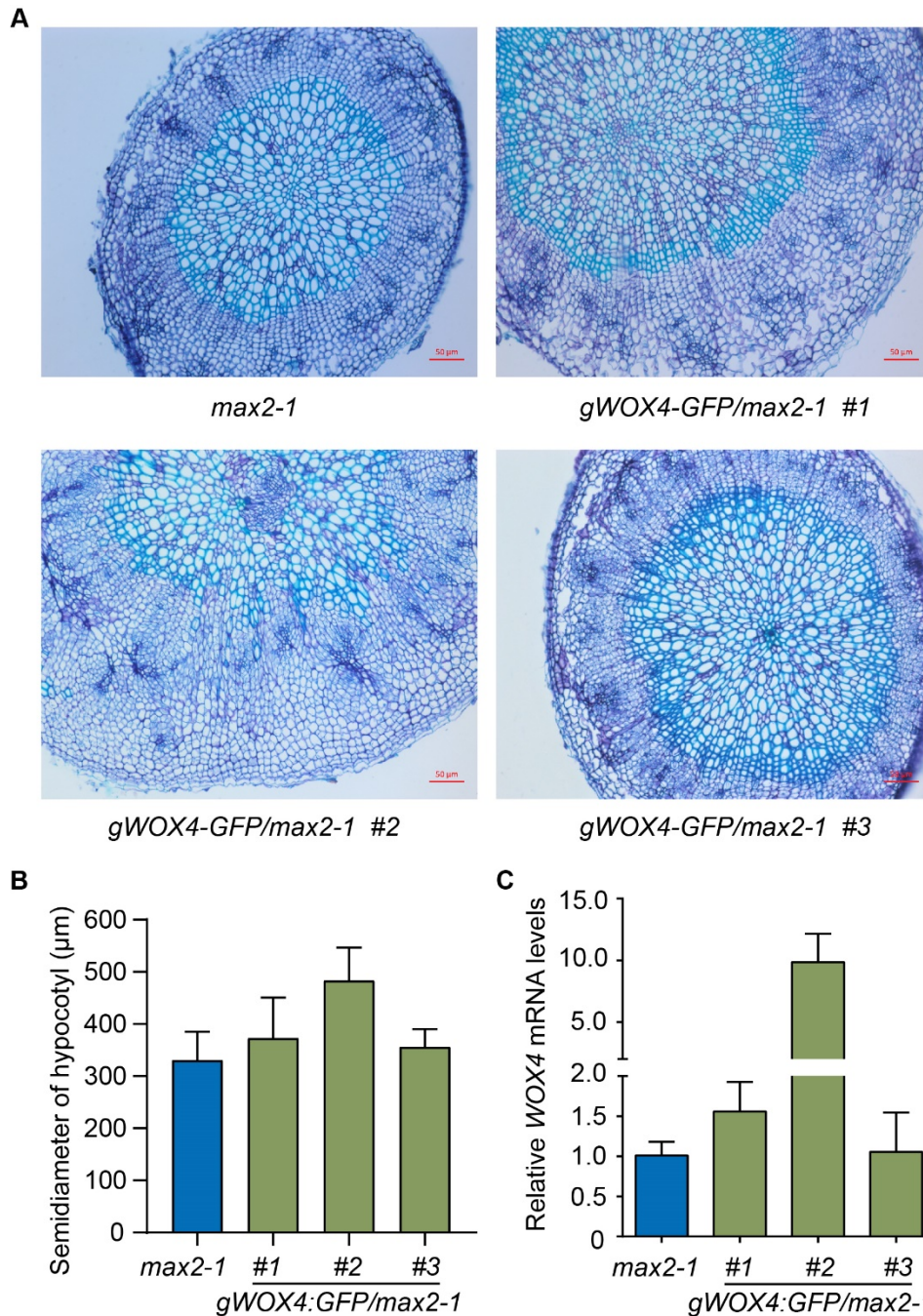


Supplemental Figure S8. Phenotype of the *gWOX4-GFP/max2-1*. Related to Figure 5.

(A) Representative photographs of 6-week-old *max2-1* and *gWOX4-GFP/max2-1* plants.

(B) Representative photographs of 3-week-old *max2-1* and *gWOX4-GFP/max2-1* plants.

(C) Representative photographs of basal stems and hypocotyls of *max2-1* and *gWOX4-GFP/max2-1* plants shown in (A). Bars represent 1 cm.



Supplemental Figure S9. Phenotype of the hypocotyl of *gWOX4-GFP/max2-1*. Related to Figure 5.

(A) Representative cross sections of the hypocotyl of *max2-1* plants and three independent *gWOX4-GFP/max2-1* lines (8-week-old plants). Bars = 50 µm.

(B) Quantification of the semidiameter of hypocotyl in *max2-1* plants and three independent *gWOX4-GFP/max2-1* lines shown in (A). Data are means ± SD, n=15 (5 number were collected randomly in 3 plants/line).

(C) Relative *WOX4* mRNA levels in seedlings of *max2-1* and three independent lines of *gWOX4-GFP/max2-1* in (A&B).

Relative *WOX4* transcript levels were set to “1” in *max2-1*. Data are means ± SD (n = 3).

Supplemental Table S1. Primers for genotyping, CHIP, EMSA, qPCR, and recombinant vectors.

Name	sequences 5'–3'
<i>WOX4pro</i> -CHIP-F1-F	TGATCACAGCTTGACACACGA
<i>WOX4pro</i> -CHIP-F1-R	ACCAGTGTAGGTTGATCATGACT
<i>WOX4pro</i> -CHIP-F2-F	AGTCATGATCAACCTACACTGGT
<i>WOX4pro</i> -CHIP-F2-R	GGTTTGGCAATGTCAAGCGT
<i>WOX4pro</i> -CHIP-F3-F	AGGTTCTGCAGTTCCCGATG
<i>WOX4pro</i> -CHIP-F3-R	GTCGAATGCTTTTCGGTGGC
<i>WOX4pro</i> -CHIP-F4-F	TGAGAGCCACCGAAAAGCAT
<i>WOX4pro</i> -CHIP-F4-R	GTCTGCATGGAGCACTACTT
<i>WOX4pro</i> -CHIP-F5-F	AGTGCTCCATGCAGACATGA
<i>WOX4pro</i> -CHIP-F5-R	TCCAGATGAAGAAAACCCA
Probe a-F	CCATCTGATCACAGCTTGACACACGAATCAGGT TATCCATCGTGTGA
Probe a-R	TCACACGATGGATAACCTGATTCGTGTGTCAAG CTGTGATCAGATGG
Probe b-F	ATCATCTGTTCATTTTCCATTCTTTTTCTTTTTCC TACCCAACCTGGA
Probe b-R	TCCAGTTGGGTAGGAAAAAGAAAAAGAATGGA AAATGAACAGATGAT
Probe c-F	GTAACGAGAAAGGCATGCATAGCATTGCTAGT TTAACATATAGCA
Probe c-R	TGCTATATGTTAAAAGTAGCAAATGCTATGCAT GCCTTTCTCGTTAC
<i>WOX4</i> -CDs-F	ATGAAGGTTTCATGAGTTTTTCGA
<i>WOX4</i> -CDs-R	TCTCCCTTCAGGATGGAGAG
<i>WOX4pro</i> -F	ACATATGAACAGTGGTAGAG
<i>WOX4pro</i> -R	CATTGCTATATGTTAAAA
LBP1.3	ATTTTGCCGATTTTCGGAAC
<i>max2-1</i> -LP	TACATGCAAGCATGCAACTTC
<i>max2-1</i> -RP	AATAGGAACAAAATCGCCACC
<i>wox4-1</i> -LP	AGGTCTACCCCTTTTCAACG
<i>wox4-1</i> -RP	AATGTGTGGGTTTCAGTTGGAG
<i>WOX4</i> -RT-F	CGATCAAACCGGTCCGACAA
<i>WOX4</i> -RT-R	TTCTTGAGTCGGGTCCACC
<i>ACTINpro</i> -CHIP-F	ACGAGGGAAAAGGCTGTCTG
<i>ACTINpro</i> -CHIP-R	GTCGCCGAGATTCAAACG
<i>U-box</i> -RT-F	TCTTCTTCTGCTACATCTACTCTC
<i>U-box</i> -RT-R	AGTGTGTGAACCCGTGAAC

Supplemental Table S2. Plasmids and restriction sites used for recombinant vectors.

Name	Plasmids	Restriction sites
WOX4pro:LUC	pCAMBIA1300 with LUC tag	EcoR I/Sac I
<i>35Spro:BES1-FLAG</i>	pCAMBIA1306 with FLAG tag	Kpn I/Xba I
<i>WOX4pro:LUC-35Spro:REN</i>	pGreenII 0800-LUC	Hind III/BamH I
<i>gWOX4-GFP</i>	pCAMBIA1302 with GFP tag	EcoR I/Sac I
<i>35S:WOX4-HA</i>	pCAMBIA1300 with HA tag	Kpn I/Xba I

Supplemental Table S3. Accession numbers of genes.

Gene name	Accession number
<i>ACTIN</i>	<i>AT3G18780</i>
<i>BES1</i>	<i>AT1G19350</i>
<i>D14</i>	<i>AT3G03990</i>
<i>HsfA1d</i>	<i>AT1G32330</i>
<i>MAX2</i>	<i>AT2G42620</i>
<i>MAX3</i>	<i>AT2G44990</i>
<i>U-BOX</i>	<i>AT5G15400</i>
<i>WOX4</i>	<i>AT1G46480</i>