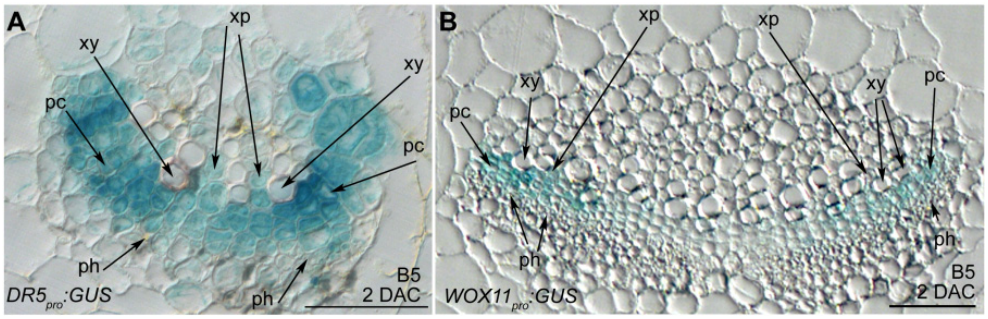
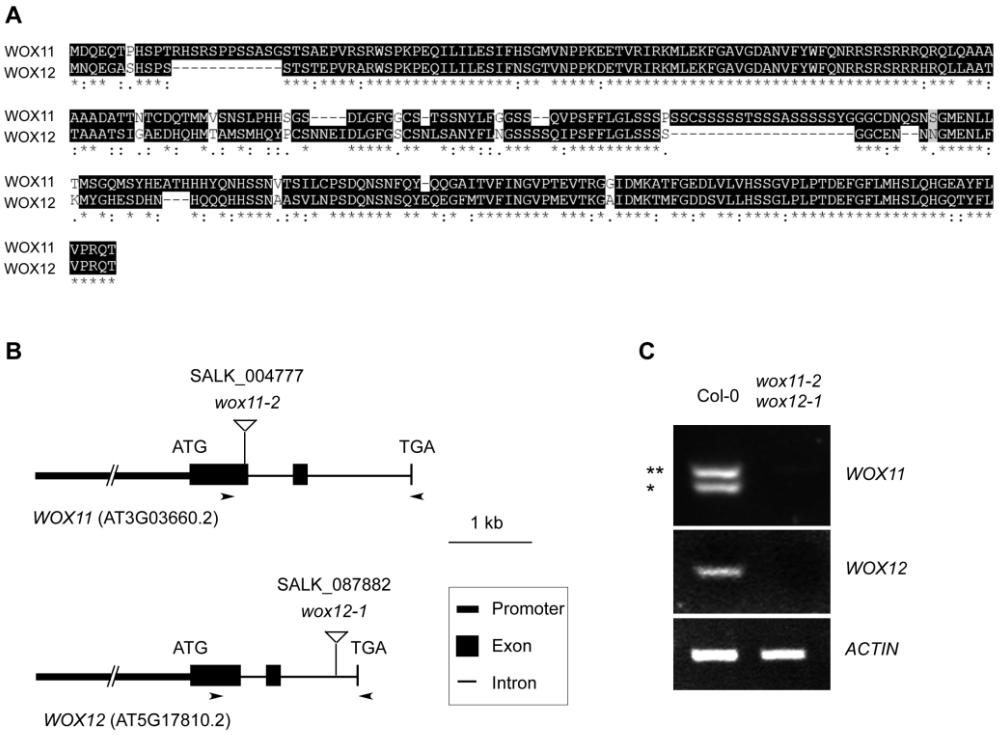


Supplemental Figure 1. *DR5* and *WOX11* Expression in Leaf Explants during Adventitious Root Formation.

(A) and **(B)** Sections of 2-DAC leaf explants from *DR5*$_{pro}$*:GUS* (A) and *WOX11*$_{pro}$*:GUS* (B) transgenic plants. Sample preparations for (A) and (B) were similar to those in Figure 1K and Figure 3H, respectively, except for toluidine blue staining, which was not performed for (A) and (B). Thus, compared with Figure 1K and Figure 3H, cells of different types in (A) and (B) can be more clearly viewed.

xy, xylem; xp, xylem parenchyma cell; pc, procambium; ph, phloem. Scale bars, 500 μm in (A) and (B).

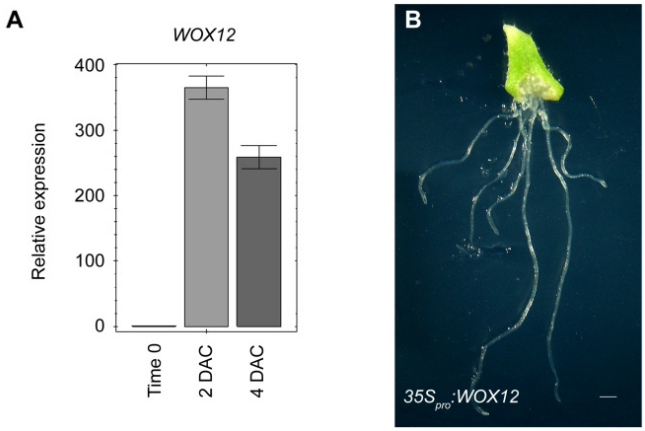


Supplemental Figure 2. Identification of the *wox11* and *wox12* Mutants.

(A) Alignment of the WOX11 and WOX12 protein sequences. The two proteins share 60% and 67% amino acid sequence identity and similarity, respectively. Alignment was performed using Clustal X (www.clustal.org).

(B) Diagram of structures of the *WOX11* and *WOX12* genes. T-DNA insertions in the *wox11-2* and *wox12-1* alleles are shown. Arrowheads indicate the primer positions used for identification of insertions. Note that the T-DNA insertion site of *WOX12* is in the last intron, indicating that *wox12-1* might be a weak allele.

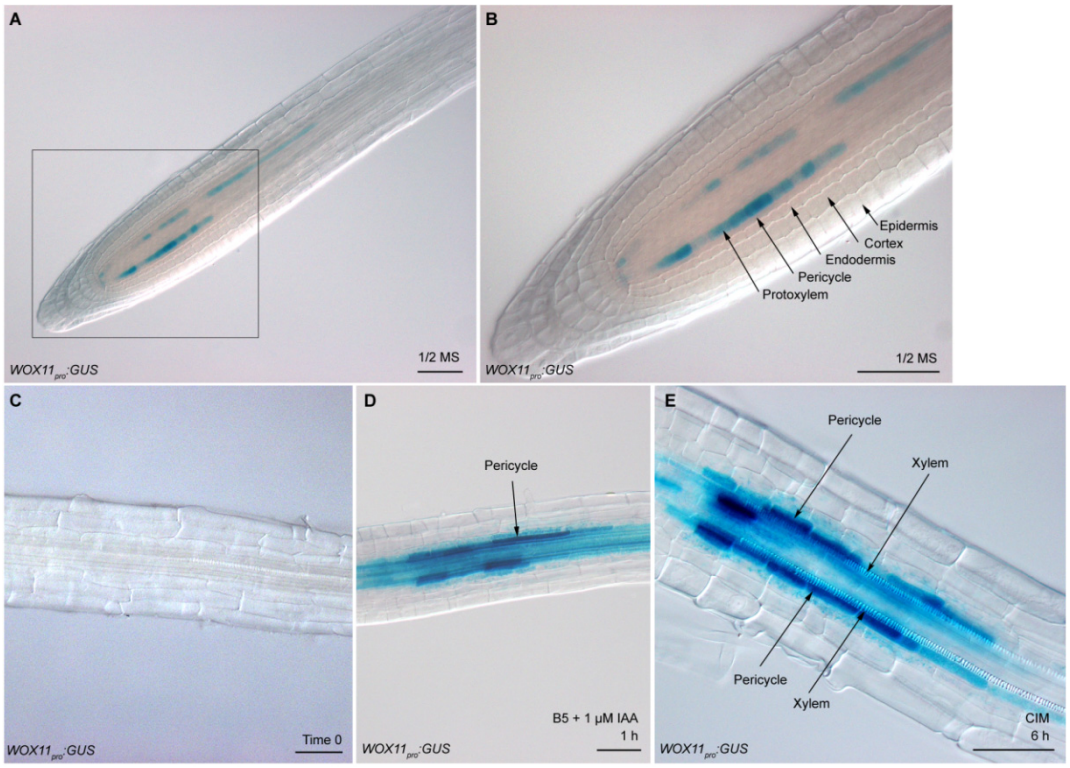
(C) RT-PCR using cDNAs from 10-DAC wild-type Col-0 and *wox11-2 wox12-1* leaf explants cultured on CIM. Full length *WOX11* and *WOX12* transcripts were undetectable in the double mutant. Asterisks * and ** indicate two alternative splicing transcripts of *WOX11* (*, At3g03660.1; and **, At3g03660.2), consistent with the predicted data from TAIR (www.arabidopsis.org).



Supplemental Figure 3. *WOX12* is Involved in Adventitious Root Formation.

(A) qRT-PCR to analyze *WOX12* expression in adventitious root formation from the wild-type leaf explants cultured on B5 medium. The value of time-0 leaf explants was arbitrarily fixed at 1.0. Note that *WOX12* expression was highly induced during adventitious root formation.

(B) A 12-DAC leaf explant of *35S$_{pro}$:WOX12* showing multiple regenerated adventitious roots. A total of 30 leaf explants from two independent *35S$_{pro}$:WOX12* lines were analyzed with the similar results. *35S$_{pro}$:WOX12* was constructed by insertion of genomic DNA encoding the full length of WOX12 into the pMON530 vector.



Supplemental Figure 4. Auxin Induces *WOX11* Expression in Root Pericycle Cells.

(A) and **(B)** GUS staining in the apical region of the primary root of a *WOX11*$_{pro}$*:GUS* transgenic line. GUS staining was shown in the protoxylem cells. The image in (B) is the close-up of the boxed region in (A). The role of *WOX11* in protoxylem is not yet known as the *wox11-2 wox12-1* double mutant exhibited normal protoxylem cells.

(C) At time 0, GUS staining was not detectable in the elongation region of a primary root of the *WOX11*$_{pro}$*:GUS* plant.

(D) and **(E)** GUS staining was rapidly induced in the elongation region of primary roots of the *WOX11*$_{pro}$*:GUS* plants with auxin treatment. Plants were grown on 1/2 MS medium for 7 days (C), and then seedlings were moved to B5 medium containing 1 μM IAA for 1 h (D), or to CIM for 6 h (E). Note that *WOX11* is induced in xylem-pole pericycle cells upon auxin induction. GUS staining was performed by incubation of roots at 37 °C in GUS assay solution for 2 h.

Scale bars, 50 μm in (A) to (E).

Supplemental Table 1. List of Primers Used in This Study.

Experiments	Primers	Sequence (5'→3')
Molecular cloning		
WOX11$_{pro}$:GUS	WOX11$_{pro}$-F	gtcgacTGAGCTCATCTAACTGTTACG
	WOX11$_{pro}$-R	ggatccTGCTTTGAAGAATATTGATATTATC
35S$_{pro}$:WOX11	WOX11-F	agactcATGGACCAAGAACAAACACC
	WOX11-R	gaattcGCCAGTTCATGTCTGTCTTG
35S$_{pro}$:WOX12	WOX12-F	tccccccgggATGAATCAAGAAGGTGCTTCACATAG
	WOX12-R	ggaattcGTTCATGTCTGTCTCGGTAC
35S$_{pro}$:WOX11-SRDX	WOX11-SRDX-F	gaagatctATGGACCAAGAACAAACACC
	WOX11-SRDX-R	ccggaattcTCA*AGCAAACCCTAAACGCAACTCCA AGTCTAAGTCAAG*TGTCTGTCTTGGAACC
35S$_{pro}$:LBD29	LBD29-F	gaagatctcatATGACTAGTTCCAGCTCTAG
	LBD29-R	ccgctcgagTCACGAGAAGGAGATGTAGC
pER8:LBD29-SRDX	LBD29-SRDX-F	ccgctcgagATGACTAGTT CCAGCTCTAG
	LBD29-SRDX-R	cgtctagaTCA*AGCAAACCCTAAACGCAACTCCAA GTCTAAGTCAAG*CGAGAAGGAGATGTAGCCAA
qRT-PCR and RT-PCR		
WOX11	WOX11-F3	CGCAACCACCAACACTTGTGACC
	WOX11-R3	CCTGAGGAATGCACCAAAACC
	WOX11-R6	AAGACATCTGTTGCATCACC
WOX12	WOX12-F3	GGGGTTTGGAAGTTGTAGC
	WOX12-R4	CGATAGACACGAAATCAATAGAGG
LBD16	LBD16-F49	CCTGTTTATGGATGTGTCTC
	LBD16-R49	ACATAACTTACCAACTTATC
LBD18	LBD18-F50	TCTTTGCTCTTCAGCAACAG
	LBD18-R50	ATGTATCGATCAAAACCAAC

LBD29	LBD29-F51	TCATATCTTTGCTCTCCAAC
	LBD29-R51	CCCATATTCTTGATAGAACC
	LBD29-R	ccgctcgagTCACGAGAAGGAGATGTAGC
LBD33	LBD33-F52	CGTTGCTCACATCTTCGCTC
	LBD33-R53	CGCGTCGAATTTTGTTGTGC
SRDX	SRDX-R70	AACTCCAAGTCTAAGTCAAG
ACTIN	ACTIN-F	TGGCATCA(T/C)ACTTTCTACAA
	ACTIN-R	CCACCACT(G/A/T)AGCACAATGTT

Note that lowercase letters represent additional nucleotides to introduce restriction sites, and the italic letters indicate SRDX.