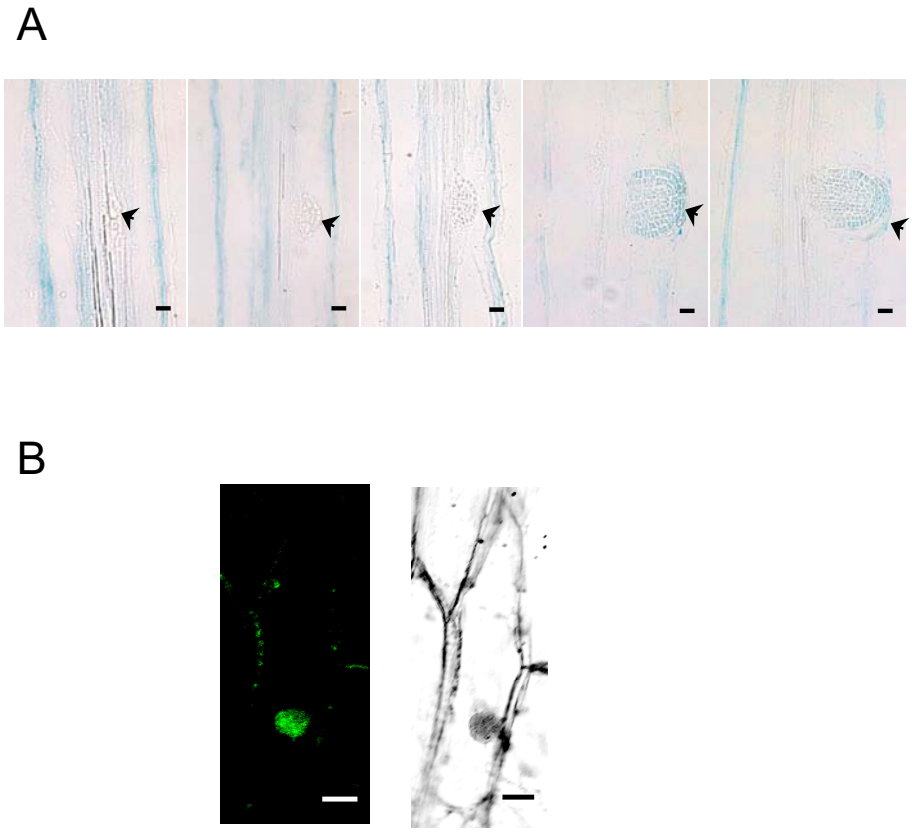
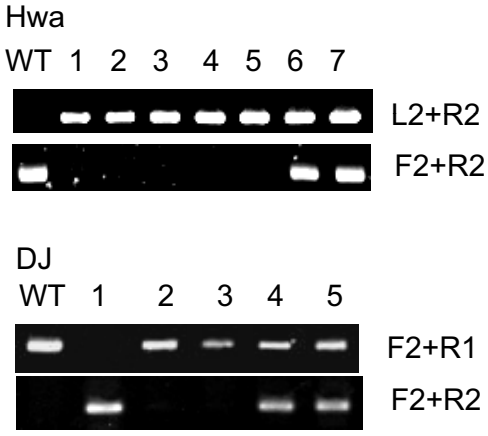
Supplemental data. Zhao et al. (2009). The Wuschel-related homeobox gene *WOX11* is required to activate shoot-borne crown root development in rice.

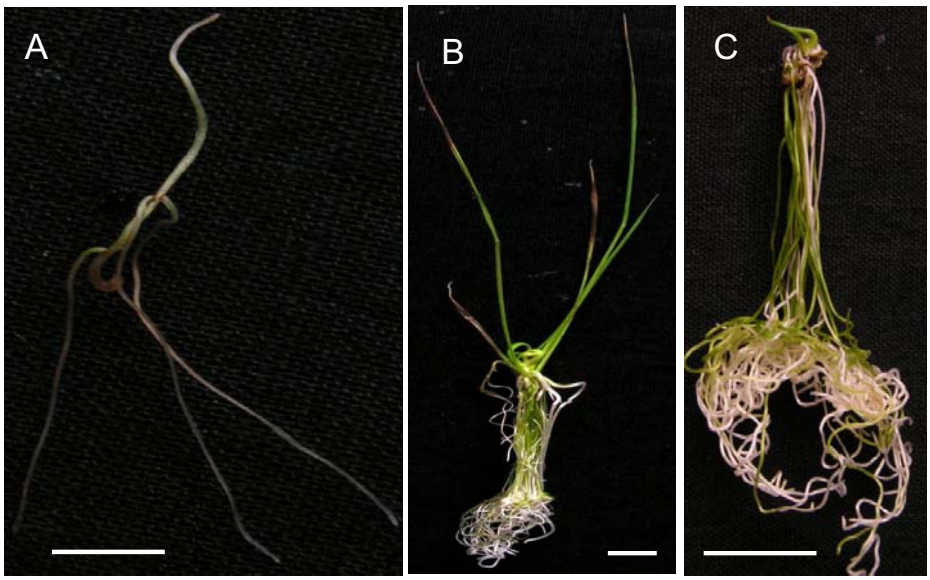


Supplemental Figure 1. Expression of WOX11p-GUS and Nuclear localization of WOX11-GFP protein

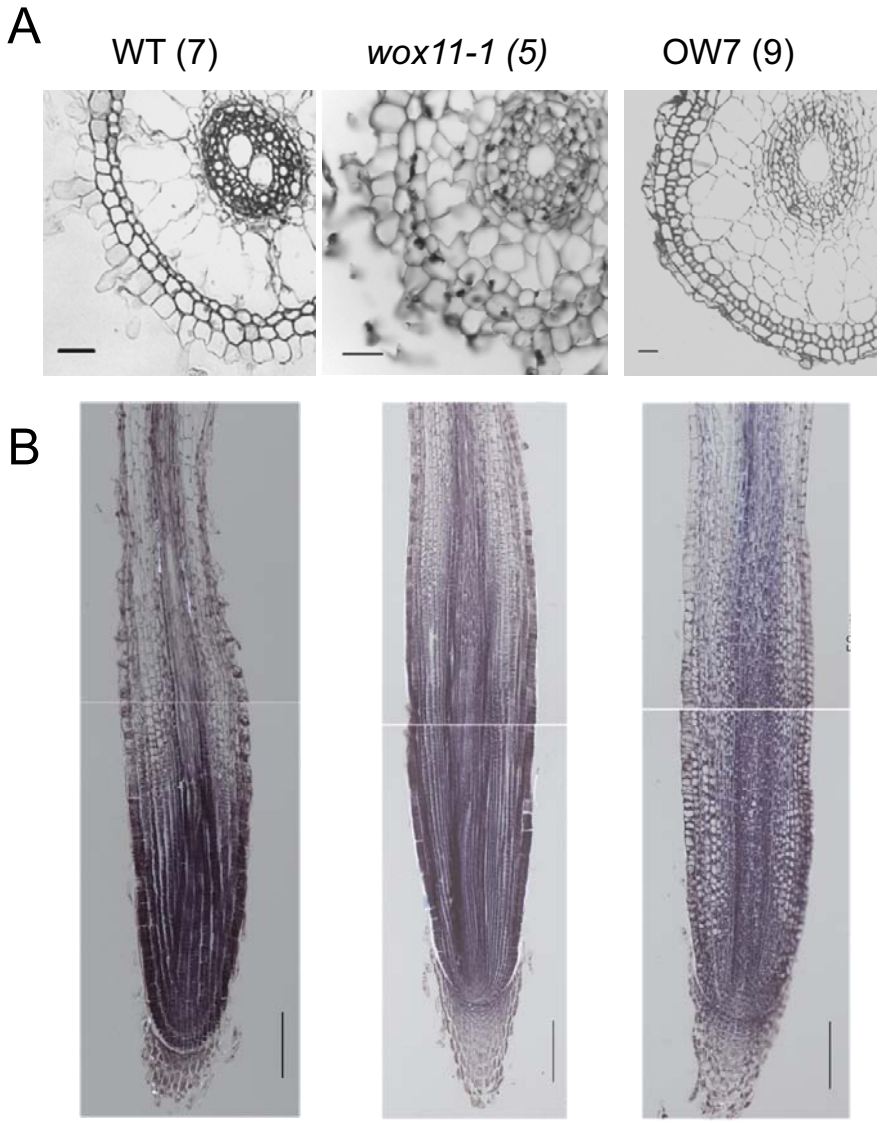
A. WOX11p-GUS expression during the course of lateral root initiation. GUS activity was detected after the initiation of the lateral roots . Bars=25 mm.
B. Fluorescence image of an onion epidermal cell expressing WOX11-GFP (left) merged with a bright-field image (right) Bar=50 mm.



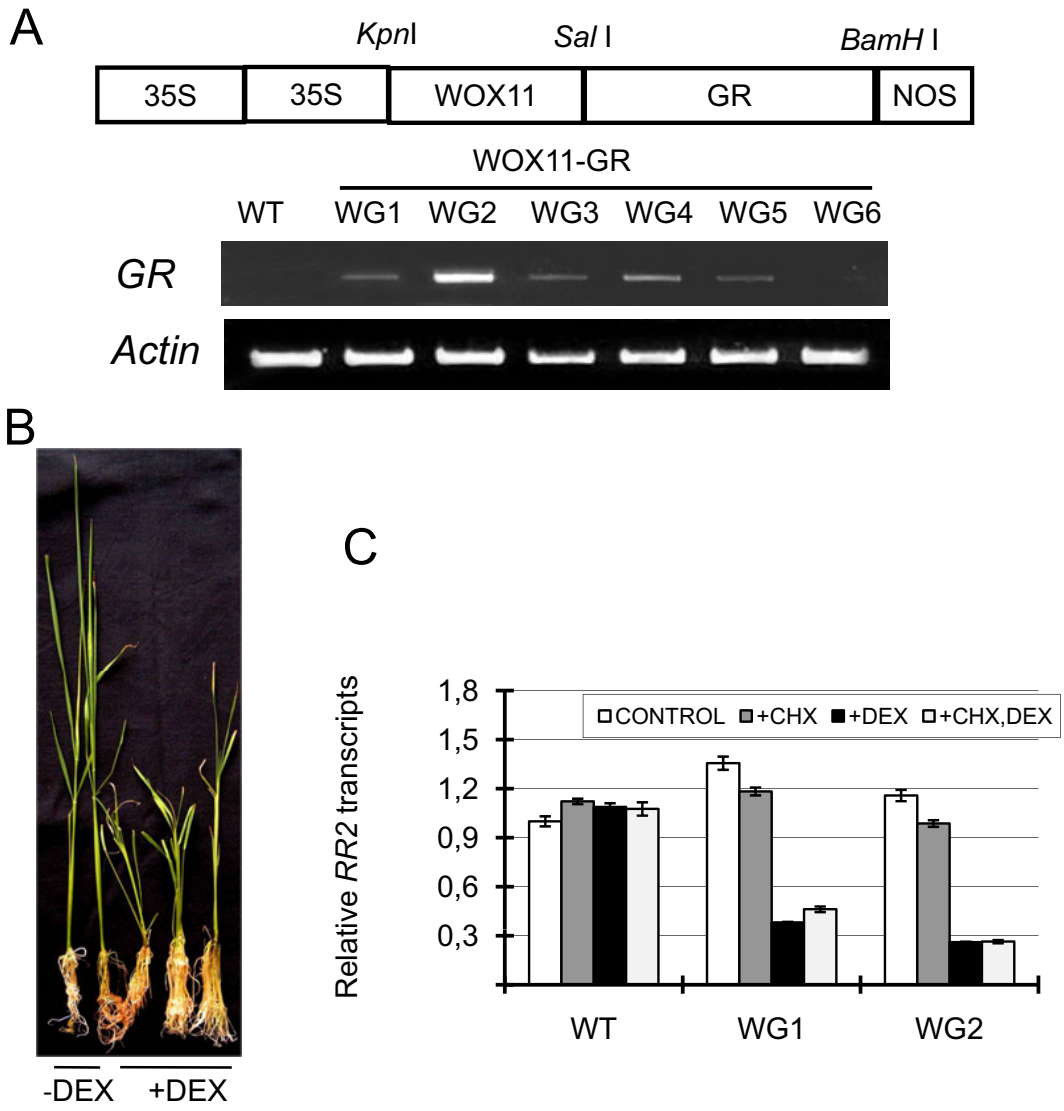
Supplemental Figure 2. Genotyping of the *WOX11* locus in *wox11-1* (upper panel) *wox11-2* (lower panel) and the respective wild type (Hwa and Dongjing). The primer sets used in the PCR tests are indicated on Fig. 2A and included in Supplemental Table 1 .



Supplemental Figure 3. Severe phenotypes found in the T0 population of *WOX11* over-expression plants. A. transgenic plant with the root-like shoot. B and C: transgenic plants with a reduced shoot but an extensively developed root system. Bars=2cm.



Supplemental Figure 4. Comparison of crown root cross (A) and longitudinal (B) sections of wild type (left), *wox11-1* mutant (middle) and over-expression (OW7) plants (right). Cell layers counted from the cortical and epidermal tissues in A are indicated in parentheses. Bar=25 mm in A, 50 mm in B.

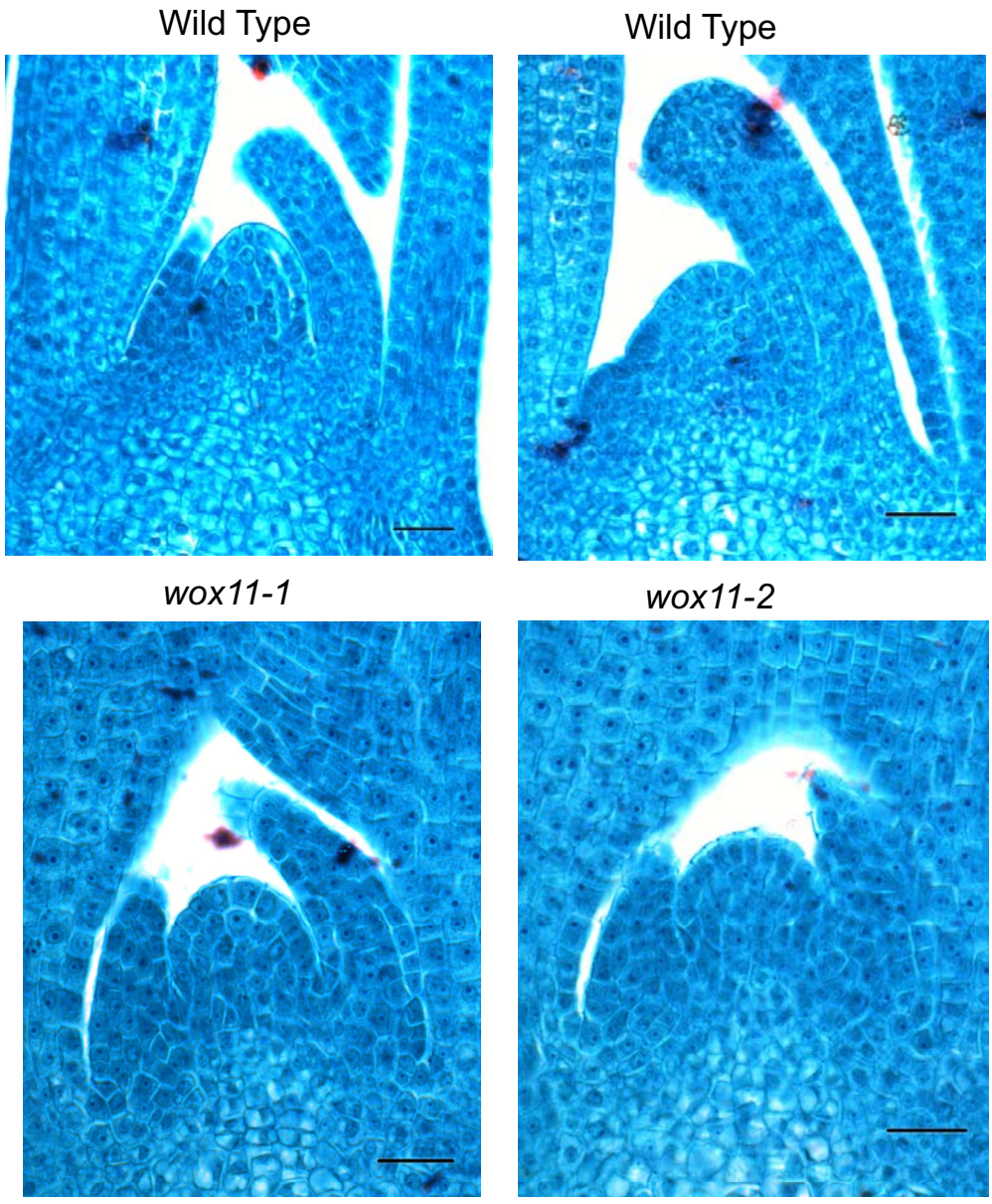


Supplemental Figure 5. Production of transgenic lines expressing the *WOX11-GR* fusion

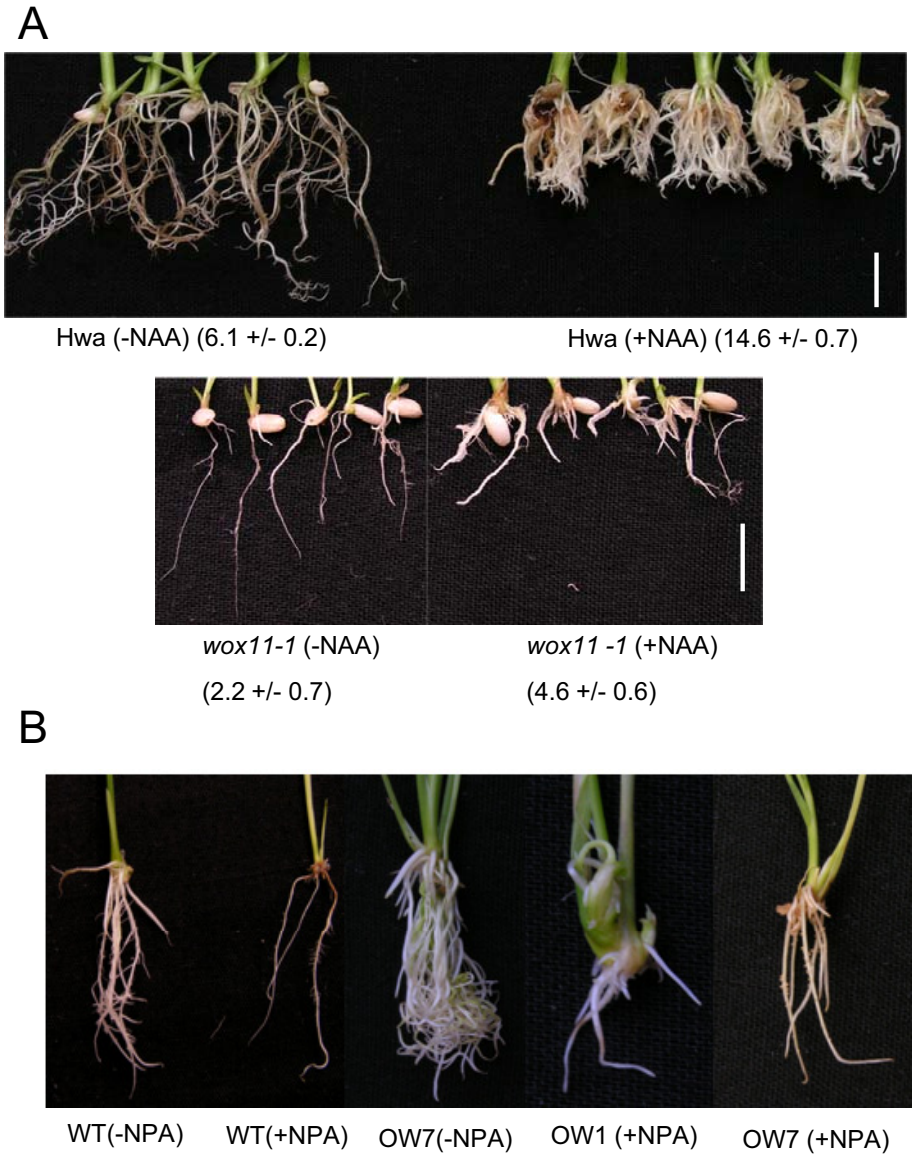
A. Identification of transgenic lines expressing the *WOX11-GR* fusion by RT-PCR. The binary vector containing the translation fusion between *WOX11* and the mouse glucocorticoid receptor (GR) under the control of the double CaMV35S promoter was used to produce transgenic plants. RT-PCR analysis revealed 5 *WOX11-GR*- expressing lines (WG1-5).

B. WOX11-GR transgenic plants show extensive root production in the presence of DEX. The DEX was applied every 7 days for 4 times.

C. Relative expression levels of *RR2* in wild type and in 3 *WOX11-GR* transgenic plants treated with or without DEX, CHX or DEX plus CHX. The transcript levels were normalized with the *actin* mRNA. The wild type control was assessed as 1. Bars are means +/- SD from 3 biological repeats.



Supplemental Figure 6. Comparison of shoot longitudinal sections from wild type and *wox11* mutants. Shoot apexes of 7-day old seedling were stained with hematoxylin, fixed in FAA and sectioned to 8 mm thickness and photographed under a light microscope. Bar = 25 mm.



Supplemental Figure 7. Effect of auxin and an auxin inhibitor on crown root growth
A. The mutation of *wox11-1* impaired auxin induction of crown root production. Wild type (Hwa) and *wox11-1* were treated with or without NAA. Average root numbers and SD from 20 plants are indicated.
B. Inhibition of ectopic root production by NPA treatment on *WOX11* over-expression plants (OW) and normal crown root growth in wild type (WT). Bars= 1 cm.

Supplemental Table 1: Primers used in the study.

Experiment	Primer name	Sequence
wox11 T-DNA mutant characterization	F2	5'GGCTGATACTAGCTAGGACACTGA
	R2	5'CTCAACTCGATCAAGACGACCT
	L2	5'CTAGAGTCGAGAATTCAGTACA
	R1	5'CCACAGTTTTCGCGATCCAGACTG
RT-PCR analysis of *WOX11* expression in *wox11* mutants	F3	5'AACAGCGGCATGGTGAACCC
	R3	5'GCCACGATGAGGACGACGAG
	Actin-F	5'CTCAACCCCAAGGCTAACAG
	Actin-R	5'ACCTCAGGGCATCGGAAC
Vector constructions	*OXWOX11*-F	5'GGGGGTACGCGAGCTCTAGGTGTTCGAC
	OXWOX11-R	5'GGGGGATCCATCGACGAATCGCTCAACTC
	*WOX11*gus-F	5'GGGGTCGACCCCAATCAAATGCTCTGCC
	*WOX11*gus-R	5'GGGGGATCCCTGCCTTGTTCGGTGTCGA
	*WOX11*RNAi-F	5'GGGACTAGTGGTACCCGACACCGAACAAGGC
	*WOX11*RNAi-R	5'GGGGAGCTCGGATCCCGGAGGAGATCCCGAC
	*WOX11*gfp-F	5'GGGGGTACCGACACCGAACAAGGCAGCTA
	*WOX11*gfp-R	5'GGGGGATCCAGACGACCTCGTGACCAGG
	*WOX11*gr-F	5'GGGGGTACCGACACCGAACAAGGCAGCTA
	*WOX11*gr-R	5'GGGGTCGACAGACGACCTCGTGACCAGG
	GR-F	5'GTCGACAGATCCTGAAGCTCGAAAAAC
	GR-R	5'GGATCCACCGGCAACAGGATTCAATG
	*WOX11*32a-F	5'ACAGGTACCGACGACGACGACAAGATGGACGGCGGCCACAGC
	*WOX11*32a -R	5'ACAGGATCCTCAAGACGACCTCGTGACCAGG
Realtime PCR	*RR1*-F	5'AGGATCAGCAGATGCATGAATG
	RR1-R	5'GAGACGCTGTACGTCCTTGCTT
	RR2-F	5'ACGATCTTCTCAAAGCCATCAAG
	RR2-R	5'TGAGAGGCTTAAGGATGAAATCCT
	RR3-F	5'AGGGTTCGATCTCCTCAAGAG
	RR3-R	5'GAATTCTCCGACGACATTAGC
	RR5-F	5'ACCGAATGTGAGCATGATTATCA
	RR5-R	5'CCTTGACCTTCTTCAGGAGTTCATA
	RR6-F	5'GTCCCCAACGTCAACATGATC
	RR6-R	5'CACGTTCTCCGACGACATGAT
	RR7-F	5'TGCTCAAGAAGATCAAGGAATCG
	RR7-R	5'GGCACGTTCTCTGACGACATTAT
	IAA5-F	5'GAAATTGAAAATCATGAGAGGATCTG

	IAA5-R	5'TGCTCTGCCCTGACTGCTCTA
	IAA11-F	5'CGACGTCGCCATGTACAAGA
	IAA11-R	5'TGGTGAAGGAGGTGAACATGTT
	IAA23-F	5'TGCCCACCTACGAGGACAAG
	IAA23-R	5'TTGCAGGACTCGACGAACATC
	IAA31-F	5'CGACGTCCCATTCGAGATGT
	IAA31-R	5'TTGCTCCTAGGCCTCTTGCTT
	WOX11-F(rq)	5'CCAGATGGGCGAGAGCTACT
	WOX11-R(rq)	5'CGTTGCCATCGATCAATCAA
	Actin-F(rq)	5'TGTATGCCAGTGGTCGTACCA
	Actin-R(rq)	5'CCAGCAAGGTCGAGACGAA
In situ hybridization	*RR2situ*-F	5'GGGACTAGTGGTACCGTCGTCGGAGAATGAGCC
	RR2situ-R	5'GGGGAGCTCGGATCCGACCATCTGTGCAGGAGC
Gel shift assays	S1-F	5'GACCCCCGGCGATTTAATGGTTAATTAA
	S1-R	5'TAATTAACCATTAAATCGCCGGGGGT
	S2-F	5'GACCCCCGGCGATCCCGGGTTAATTAA
	S2-R	5'TTAATTAACCCGGGATCGCCGGGGGTC
ChIP	P1-F	5’ CGCCTTAGGCTTCATCAATC
	P1-R	5’TATTGGCATCGACGTGGTTA
	P2-F	5’CGGATAGTTGTCTGAATTG
	P2-R	5’GAATTCAACTGTGCGATG
	P3-F	5’CATCGCACAGTTGAATTC
	P3-R	5’CGTGAGGTAGTACACACGG
	P4-F	5’GCCAATACAATAACCAT
	P4-R	5’GAGGGAAATTCAAGATA