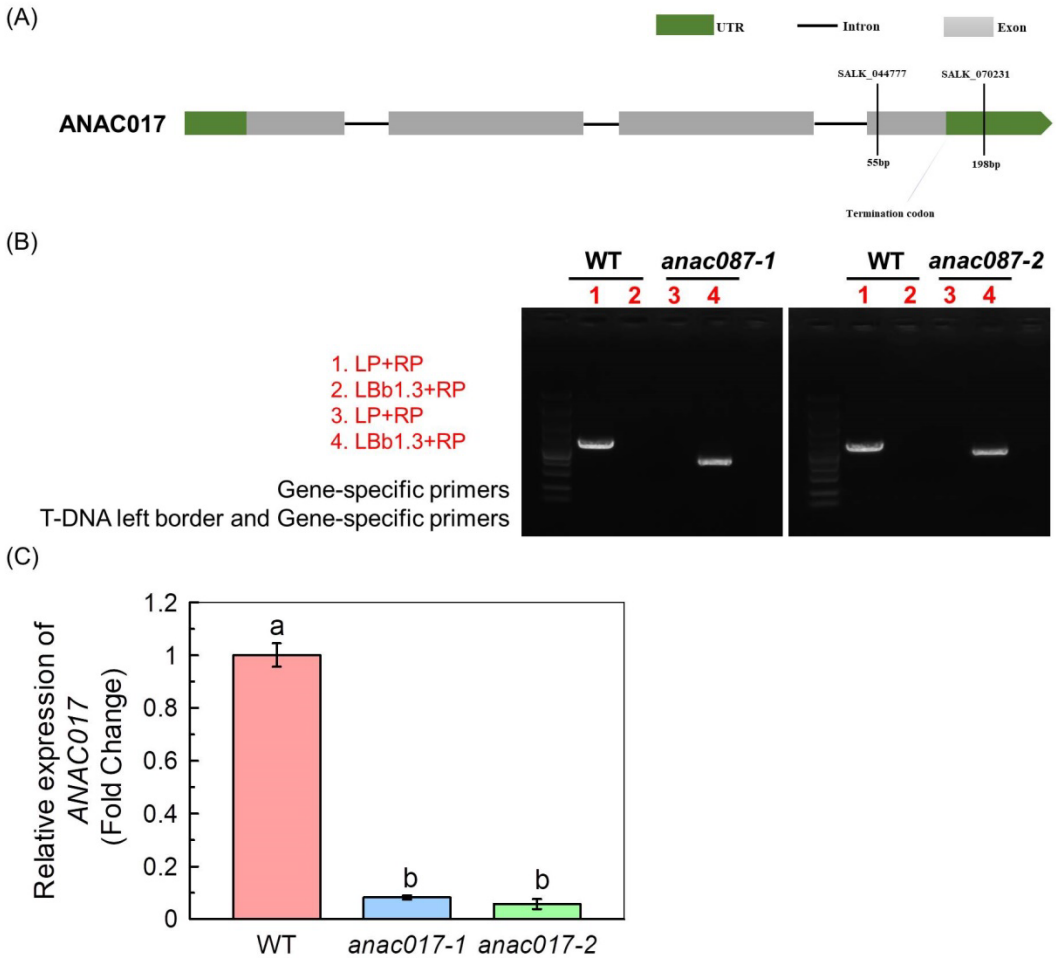
Supplemental Table S1. Primers used in the study.

Description (Vectors)	Name	Primer sequence	Restriction enzyme
Overexpression (35S: P-super-1300)	ANAC017-OX-F	CTAGAAAGCTTCTGCAGATGGCG GATTCTTCACCCGATTCGT	Pst I
	ANAC017-OX-R	ACTAGTATTTAAATGTCGACGTCT TTCAAGAGAAGACTTCTACCT	Sal I
	XTH31-OX-F	CTAGAAAGCTTCTGCAGATGGCT TTGTCTCTTATCTTTCTAG	Pst I
	XTH31-OX-R	ACTAGTATTTAAATGTCGACACAT TCTGGTGTTTGGGTATGGTCT	Sal I
Complementation (pCAMBIA1300)	ANAC017-com-F	AAGCTTGCATGCCTGCAGTTTTC TAACACGGTGAATGTAACAGG	Pst I
	ANAC017-com-R	CATGGTACCCGGGGATCCCTAGT CTTTCAAGAGAAGACTTCTAC	BamH I
Subcellular localization (35S: P-super-C-GFP)	ANAC017-CGFP-F	GGGGGACGAGCTCGGTACCATG GCGGATTCTTCACCCGATTCGT	Kpn I
	ANAC017-CGFP-R	CCTTGCTCACCATGTCGACGTCT TTCAAGAGAAGACTTCTACCT	Sal I
Subcellular localization (35S: P-super-N-GFP)	NGFP-ANAC017-F	GAGCTGTACAAGGGTACCATGGC GGATTCTTCACCCGATTCGT	Kpn I
	NGFP-ANAC017-R	GTCGACTCTAGAGGATCCCTAGT CTTTCAAGAGAAGACTTCTACC	BmaH I
GUS analysis (pQTY)	ANAC017-promoter-F	ATCACTAGTAAAAGGTACCTTTT CTAACACGGTGAATGTAACAGGC	Kpn I
	ANAC017-promoter-R	AGATCTACCATGGGGATCCCTAC GTAACAAATCAAAACCGATCCCT C	BmaH I
YH1 (pGADT7)	ANAC017-F	ATGGAGGCCAGTGAATTCATGGC GGATTCTTCACCCGATTCGT	EcoR I
	ANAC017-R	AGCTCGAGCTCGATGGATCCCTA GTCTTTCAAGAGAAGACTTCTAC C	BmaH I
promoter for YH1 (pAbAi)	XTH31-promoter-F	AAGCTTGAATTCGAGCTCCACTA AGAAACTGATAGAGTAATTG	Sac I
	XTH31-promoter-R	CATGCCTCGAGGTCGACTTTTGA GTGAAGTAAAACCTTTTGA	Sal I
	XTH17-promoter-F	AAGCTTGAATTCGAGCTCGCTGC AGAAGCTACGTGATGAGAAC	Sac I
	XTH17-promoter-R	CATGCCTCGAGGTCGACTTTGTT CTCACAGGAGTATTGATAT	Sal I
	XTH15-promoter-F	AAGCTTGAATTCGAGCTCAAAAC TTATGTTACCGTAAACCCGT	Sac I
	XTH15-promoter-R	CATGCCTCGAGGTCGACTTGGGT	Sal I

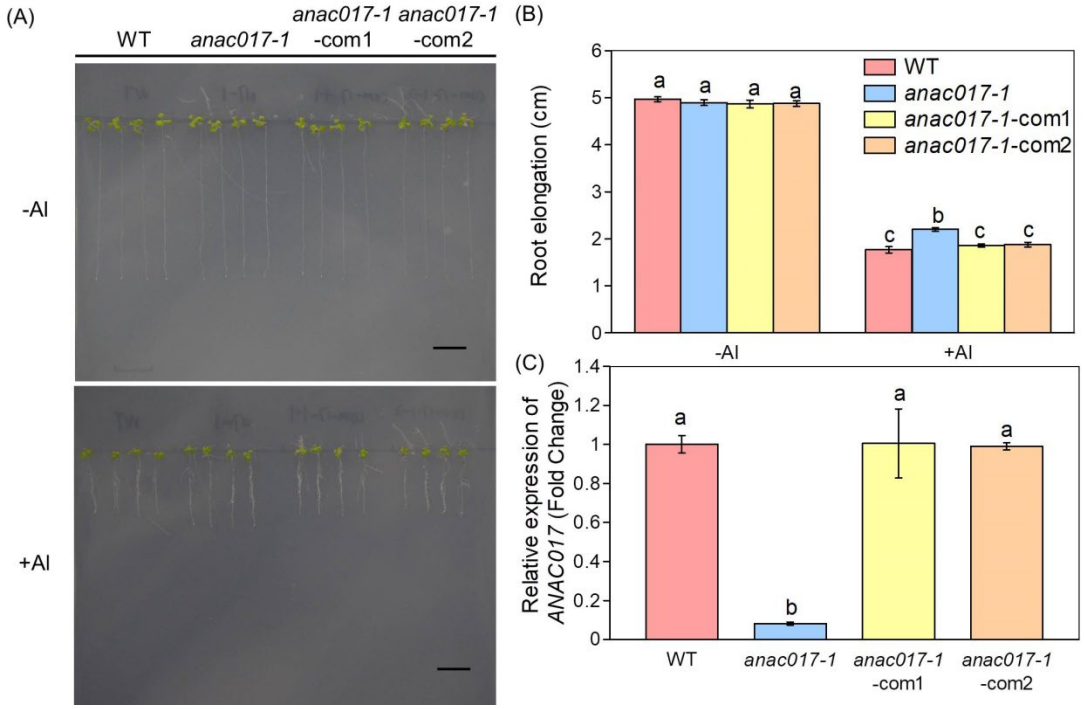
		TTGGTTGATAGAAATGAAA	
Transcription activation (pGBKT7)	Plasmid a,b-F	TCAGAGGAGGACCTGCATATGATGGCGGATTCTTCACCCGATTCGT	Nde I
	Plasmid c-F	TCAGAGGAGGACCTGCATATGGCTCCAGGGTTTCGATTTCATCCAA	Nde I
	Plasmid d-F	TCAGAGGAGGACCTGCATATGGATGAAGATGAACTAGGGAGATGA	Nde I
	Plasmid b,c-R	ATGCGGCCGCTGCAGGTCGACCATCGTATACTCATGCATCACCCAA	Sal I
	Plasmid a,d-R	ATGCGGCCGCTGCAGGTCGACGTCTTTCAAGAGAAGACTTCTACT	Sal I
LUC analysis (NONE) (190LUC)	ANAC017-Infector -F	CTCTAGAACTAGTGGATCCATGGCGGATTCTTCACCCGATTCGT	BmaH I
	ANAC017-Infector -R	TAAGCTTGATATCGAATTCCTAGTCTTTCAAGAGAAGACTTCTACC	EcoR I
	XTH31- Reporter -F	GACGGCCAGTGCCAAGCTTCACTAAGAAACTGATAGAGTAATTG	Hind III
	XTH31- Reporter -R	GGAAGGGTCTTGCAGATCTTTTTGAGTGAAGTAAAACCTTTTGA	Bgl II
Yeast two-hybrid system (pGADT7) (pGBKT7)	pGADT7-ANAC017-F	ATGGAGGCCAGTGAATTCATGGCGGATTCTTCACCCGATTCGT	EcoR I
	pGADT7-ANAC017-R	AGCTCGAGCTCGATGGATCCCTAGTCTTTCAAGAGAAGACTTCTAC	BmaH I
	pGBKT7-WRKY46-F	C	Nde I
		TCAGAGGAGGACCTGCATATGATGATGATGGAAGAGAAACTTGTG	Sal I
	pGBKT7-WRKY46-R	A	
		ATGCGGCCGCTGCAGGTCGACCT	Nde I
	pGBKT7-STOP1-F	ACGACCACAACCAATCCTGTCCG	
		TCAGAGGAGGACCTGCATATGAT	Sal I
	pGBKT7-STOP1-R	GGAAACTGAAGACGATTTGTGCA	
		ATGCGGCCGCTGCAGGTCGACTTAGAGACTAGTATCTGAAACA	
RT-qPCR	ANAC017-qPCR-F	TGAGGTTCAATGGAAAGGCT	
	ANAC017-qPCR-R	CCAGAAGATGGCACACAAAG	
	XTH31-qPCR-F	TGTCACTCTTTGGCTCG	
	XTH31-qPCR-R	ACCTCATCGTGGTCTCC	
	XTH17-qPCR-F	ACTTCTGTTTCTTCTTGCGGCA	
	XTH17-qPCR-R	AGGATTTGTCGAGCGAGAGAGA	
	XTH15-qPCR-F	GGCGACTGTTCTTCTTGTGACA	
	XTH15-qPCR-R	TTGGATTTGAAACCTGACCCGG	
	RAE1-qPCR-F	CCTGATGGTTTGAAGGCGAT	
	RAE1-qPCR-R	CGAATTGGCGATTTGGGTGA	

	HB7-qPCR-F	GCTCAGAAAACGAAGAGAACCG
	HB7-qPCR-R	GCTCCTCAAACCCACCAAAATA
	HB12-qPCR-F	GCAGAGACTAAACGAAGAGATG
	HB12-qPCR-R	TCTTTCCATTATGCGACTCT
	WRKY46-qPCR-F	TGCACGTGTCATTTCTTGAG
	WRKY46-qPCR-R	AACCTGTATGTCCTGCCCCA
	WRKY47-qPCR-F	AAGGGAATCCATGTCCTCGC
	WRKY47-qPCR-R	ACGGGGGAAGAGGATGGTTA
	ALMT1-qPCR-F	ACTTGAGAGAGCTGAGTGACC
	ALMT1-qPCR-R	TCTTCTCGGGTCTTCATTCCC
	MATE-qPCR-F	GCATAGGACTTCCGTTTGTGGCA
	MATE-qPCR-R	CGAACACAAACGCTAAGGCA
	STOP1-qPCR-F	CCAAGTTCCATCTCAAGCTTTTC T
	STOP1-qPCR-R	TGGGACGTAAAACCTGCGAA
	ALS1-qPCR-F	TGAGCAGCAAACGGAATCCT
	ALS1-qPCR-R	CTCGCAAAGCCGTGCATATC
	ALS3-qPCR-F	CAATCGCCGGAATGTTGGTC
	ALS3-qPCR-R	TTGCAACGTCGCTTGTCTTG
	STAR1-qPCR-F	GCCATGCCATCACTTTGGTC
	STAR1-qPCR-R	AGATCCATCATCGGCGACTC
	TBL27-qPCR-F	GAACAACGTTGAGAGCGGTT
	TBL27-qPCR-R	CTTCGTACGGCTTGGTCATG
	ACTIN2-qPCR-F	GCTGACCGTATGAGCAAAGA
	ACTIN2-qPCR-R	GATCCACATCTGTTGGAACG
	TUBULIN-qPCR-F	AAGTTCTGGGAAGTGGTT
	TUBULIN-qPCR-R	CTCCCAATGAGTGACAAA
anac017-1 identification	SALK_044777-LP	CTCTTTCCTCAGTGGCAACAG
	SALK_044777-RP	CAGGGAACTTCTGCAAATCTG
	LBb1.3	ATTTTGCCGATTTCGGAAC
anac017-2 identification	SALK_070231-LP	GACTCATGCTTGTCTTGGAGC
	SALK_070231-RP	AACCAAATAACGGATCCGATC
	LBb1.3	ATTTTGCCGATTTCGGAAC
wrky46 identification	SALK_1230_H01-LP	GAGTCTCTTCTCGAAGCTGGG
	SALK_1230_H01-RP	GATCCTTCCCTTTTCGAAGTG
	LBb1.3	ATTTTGCCGATTTCGGAAC
stop1 identification	SALK_ 114108-LP	TCTTAAAGCGGCCATTGGTG
	SALK_ 114108-RP	TTAGAGACTAGTATCTGAAACAG ACTCAC
	LBb1.3	ATTTTGCCGATTTCGGAAC

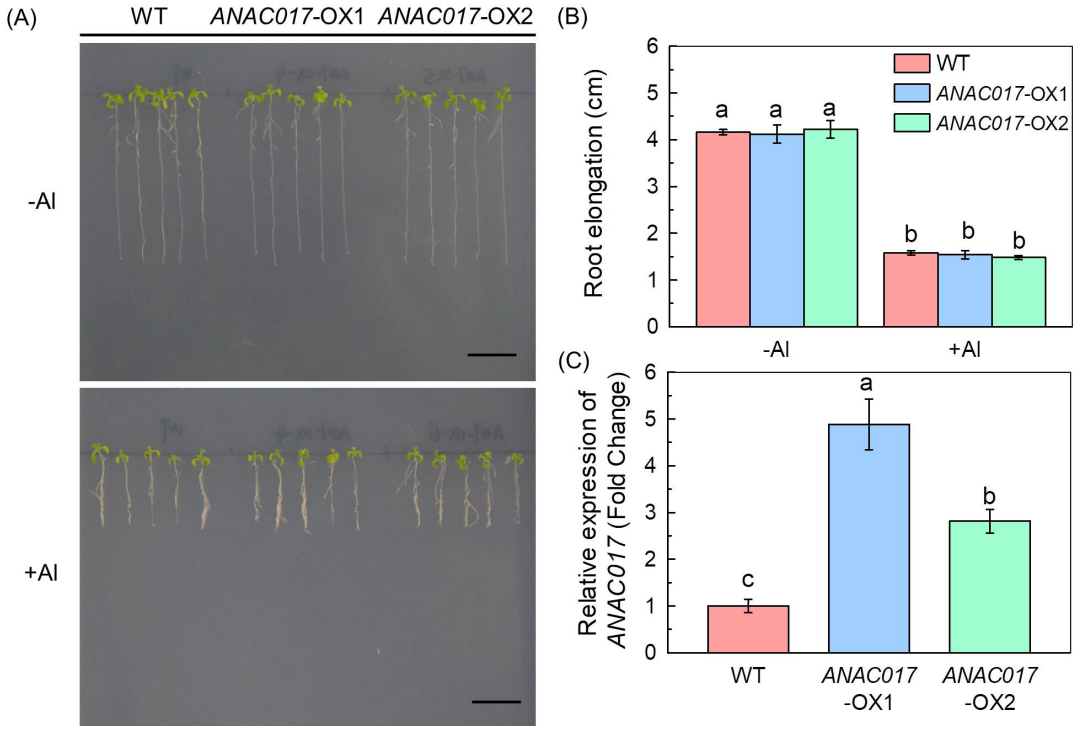


Supplemental Figure S1. Identification of the *anac017* mutants. (A) Schematic structure of the *anac017* mutants. The grey box and green box represent exon and untranslated region (UTR), respectively, while the black bold line indicates the intron. (B) Confirmation of the *anac017* mutant alleles by PCR. DNA molecular weight markers are shown in the left lane in each panel. (C) RT-qPCR analysis of the *ANAC017* expression in WT and *anac017* mutant roots. Seedlings were grown on 1/2 MS medium for four weeks, and the RNA was prepared from root tissues. *TUBULIN* was used as an internal control. Data are means ± SD (n=4). Different letters above the bars indicate significant differences at $P < 0.05$ by one-way ANOVA analysis.

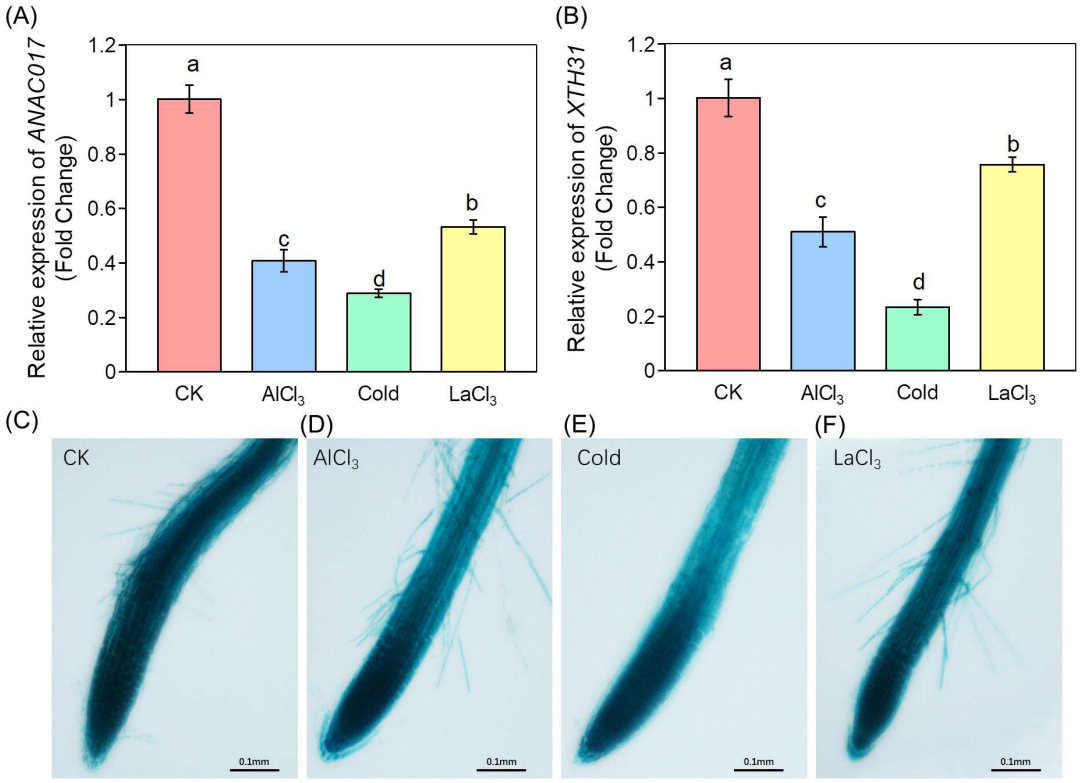
Supplemental Figure S2. Phenotype of WT and *anac017* mutants in both vegetative and reproductive stage under normal growth conditions.



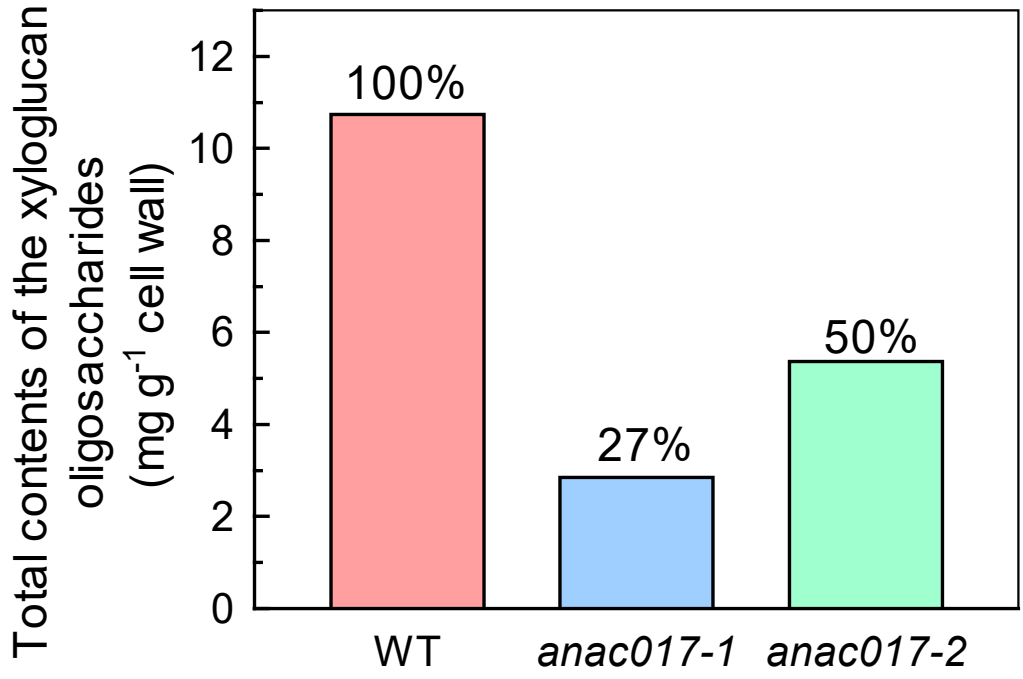
Supplemental Figure S3. Phenotypes of WT, *anac017* mutants and *anac017*-com lines (complementary lines). (A) WT, *anac017* mutant (*anac017-1*) and *anac017*-complementation (*anac017-1*-com) lines were grown on 1/2 MS medium with or without 200 μM Al for 7 days. Seedlings with roots approximately 1 cm long were selected and then transferred to the Al-untreated or Al-treated medium. (B) Root elongation of WT, *anac017-1* and *anac017*-1-com lines in the presence or absence of 200 μM Al. Root elongation was measured after treatment as indicated by (A). Data are means ± SD (n=4). Different letters above the bars indicate significant differences at $P < 0.05$ by one-way ANOVA analysis. (C) RT-qPCR analysis of the *ANAC017* expression in WT, *anac017-1* and *anac017*-1-com lines. Seedlings were grown on 1/2 MS medium for four weeks, and the RNA was prepared from root tissues. *TUBULIN* was used as an internal control. Data are means ± SD (n=4). Different letters above the bars indicate significant differences at $P < 0.05$ by one-way ANOVA analysis.



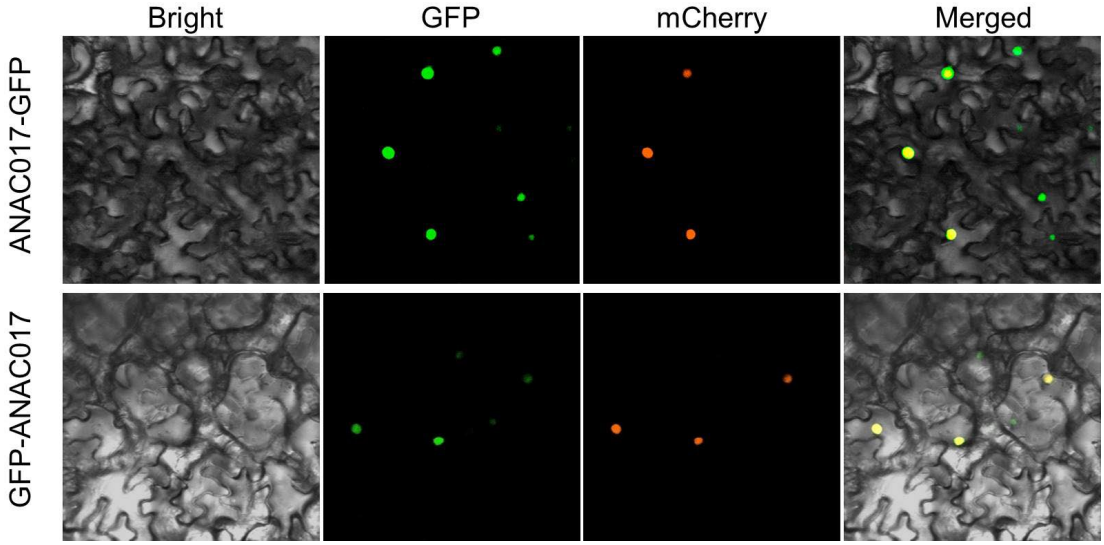
Supplemental Figure S4. Phenotypes of WT and *ANAC017* overexpression (*ANAC017*-OX) lines. (A) WT and *ANAC017* overexpression (*ANAC017*-OX) lines were grown on 1/2 MS medium with or without 200 μM Al for 7 days. Seedlings with roots approximately 1 cm long were selected and then transferred to the Al-untreated or Al-treated medium. (B) Root elongation of WT and *ANAC017*-OX lines in the presence or absence of 200 μM Al. Root elongation was measured after treatment as indicated by (A). Data are means ± SD (n=5). Different letters above the bars indicate significant differences at $P < 0.05$ by one-way ANOVA analysis. (C) RT-qPCR analysis of the *ANAC017* expression in WT and *ANAC017*-OX lines. Seedlings were grown on 1/2 MS medium for four weeks, and the RNA was prepared from root tissues. *TUBULIN* was used as an internal control. Data are means ± SD (n=4). Different letters above the bars indicate significant differences at $P < 0.05$ by one-way ANOVA analysis.



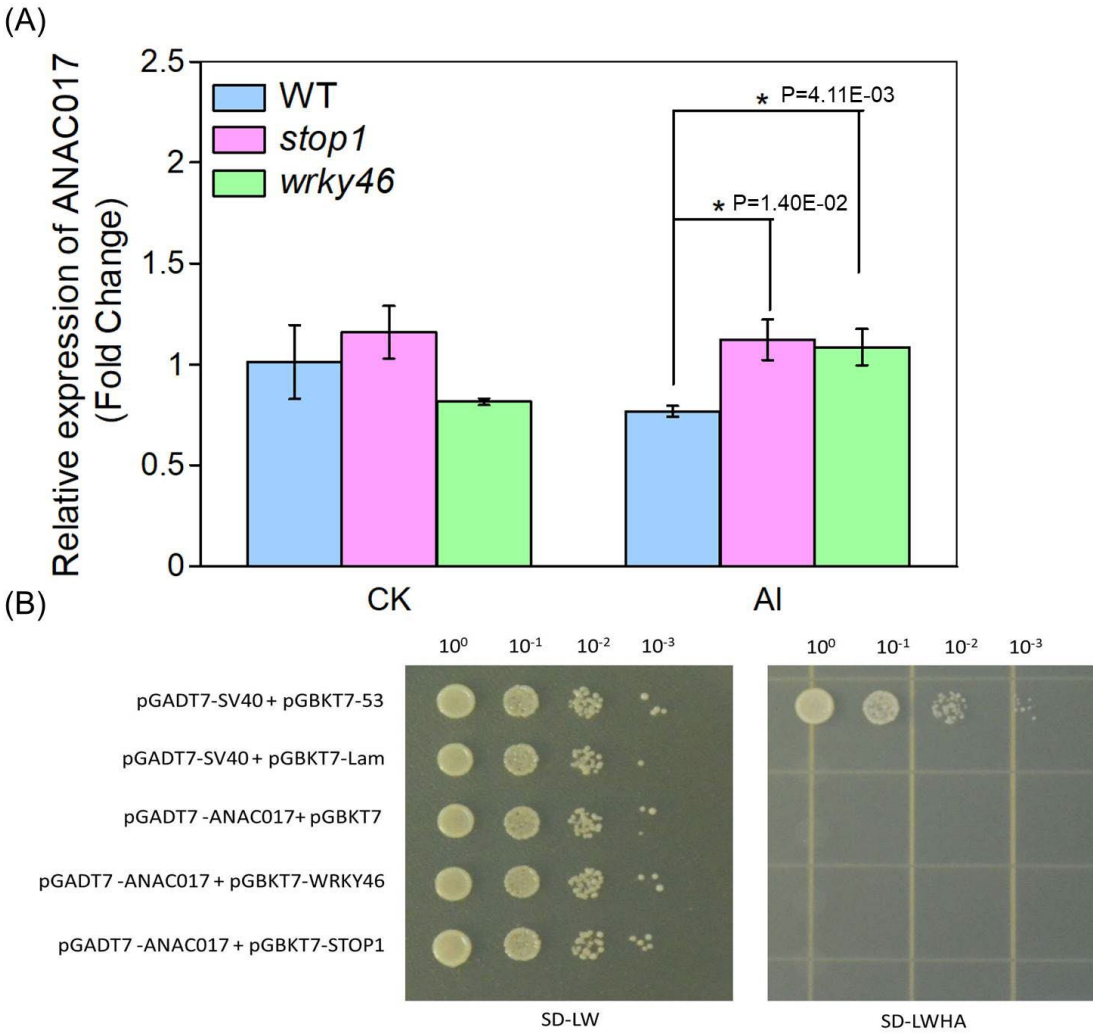
Supplemental Figure S5. Expression of *ANAN017* and *XTH31* in response to Al, cold and La stresses. (A-B) RT-qPCR analysis of the expression of *ANAC017* (A) and *XHT31* (B) in WT lines. Four-week-old WT seedlings were treated with or without 50 μM Al and 50 μM La in the growth chamber with the temperature of 24 °C or 4 °C for 24 h. RNA was prepared from root tissues. *TUBULIN* was used as an internal control. Data are means ± SD (n=4). Different letters above the bars indicate significant differences at $P < 0.05$ by one-way ANOVA analysis. (C-F) *p*ANAC017-GUS seedlings with roots approximately 1 cm long were treated with or without 100 μM Al and 100 μM La in the growth chamber with the temperature of 24 °C or 4 °C for 7 days. Roots were subjected to GUS staining. Scale bars, 100 mm.



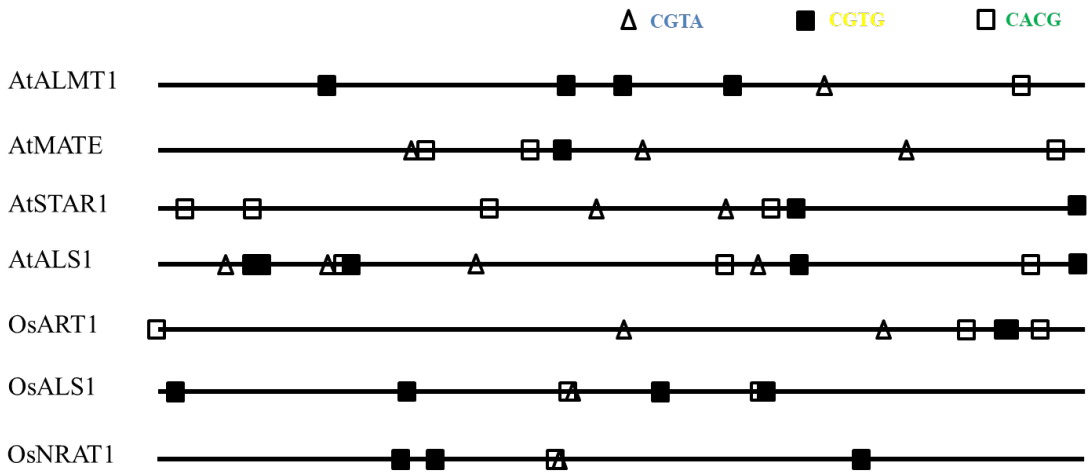
Supplemental Figure S6. Total contents of the xyloglucan oligosaccharides by the MALDI-TOF MS analysis. Cell walls were extracted from the roots of Col-0 and *anac017* mutants in the absence of Al and digested with XEG.



Supplemental Figure S7. The subcellular localization of ANAC017 by transient expression into tobacco (*N. benthamiana*) leaves.



Supplemental Figure S8. Relationship between ANAC017 and known Al responsible cascades. (A) The expression *ANAC017* in WT, *stop1* and *wrky46* mutants with or without Al treatment. Seedlings were grown on 1/2 MS medium for four weeks, and the RNA was prepared from root tissues. *TUBULIN* was used as an internal control. Data are means ± SD (n=4). Asterisk indicate a significant difference at $P< 0.05$ by Student's t test. (B) A pair of plasmid pGBKT7-WRKY46, pGBKT7-STOP1 and pGADT7-ANAC017 were introduced into Y2HGold (AH109) and cultured on the synthetically defined (SD) medium lacking leucine, tryptophan, adenine and histidine (SD-LWHA) at 30 °C for 3 d. A pair of plasmids pGADT7-SV40 and pGBKT7-53 were used as the positive control, while a pair of plasmids pGADT7-SV40 and pGBKT7-Lam were used as the negative control.



Supplemental Figure S9. Occurrence of NACRS in the promoter regions of Al tolerance genes. A stretch of 2 kb upstream of the transcription initiation site was examined. The predicted NACRS-CGTA, CGTG and CACG are represented by triangles, circles and squares, respectively.