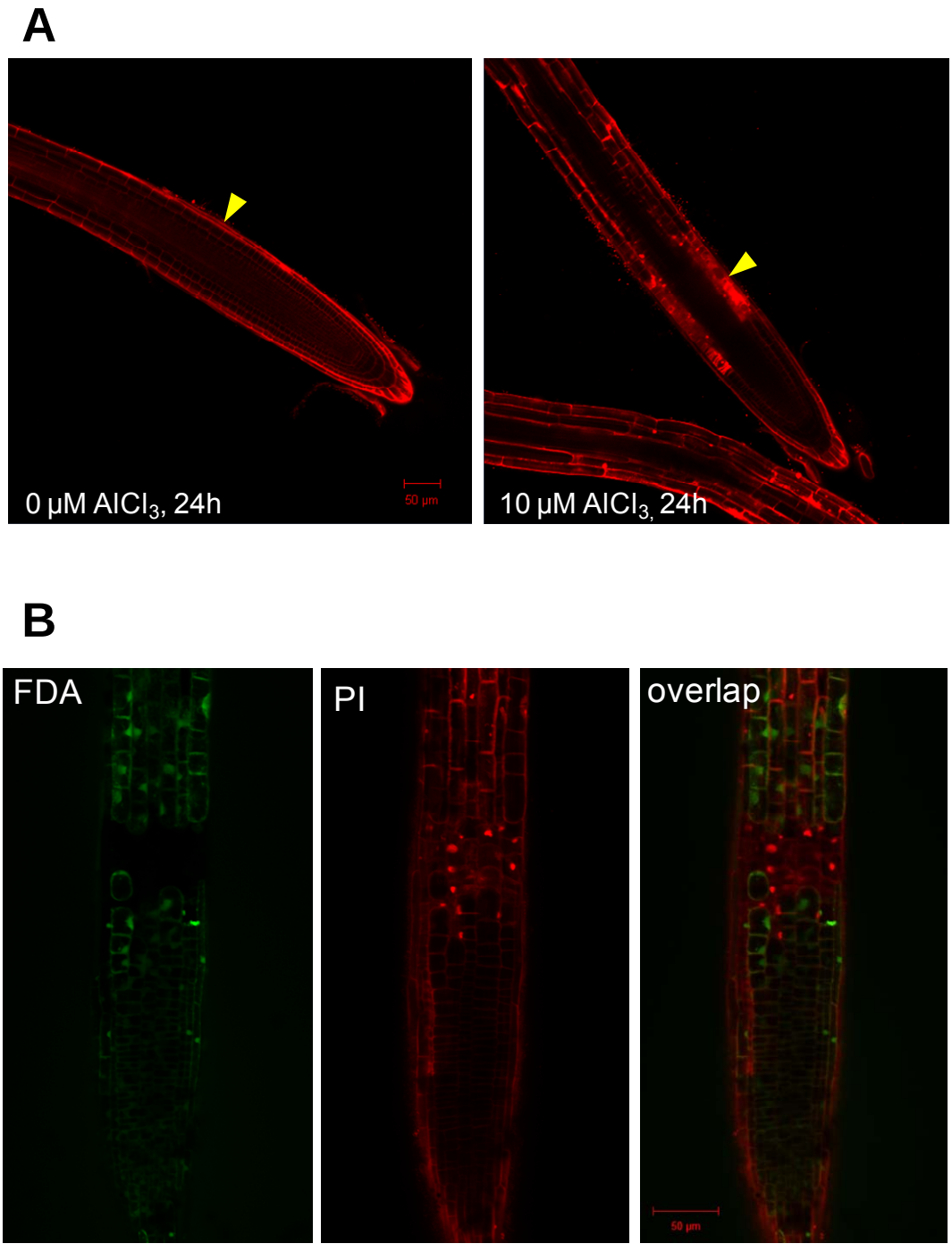
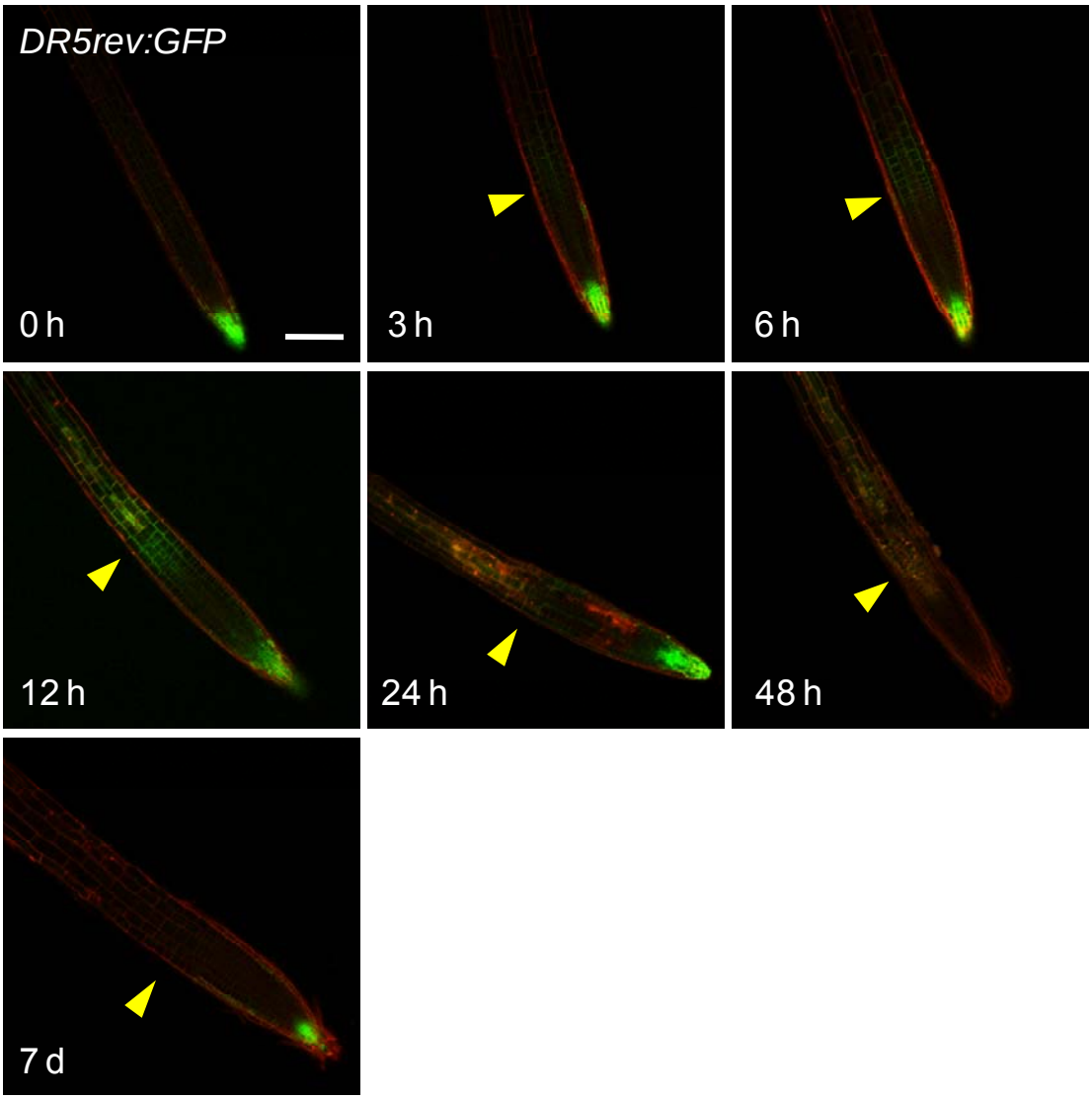
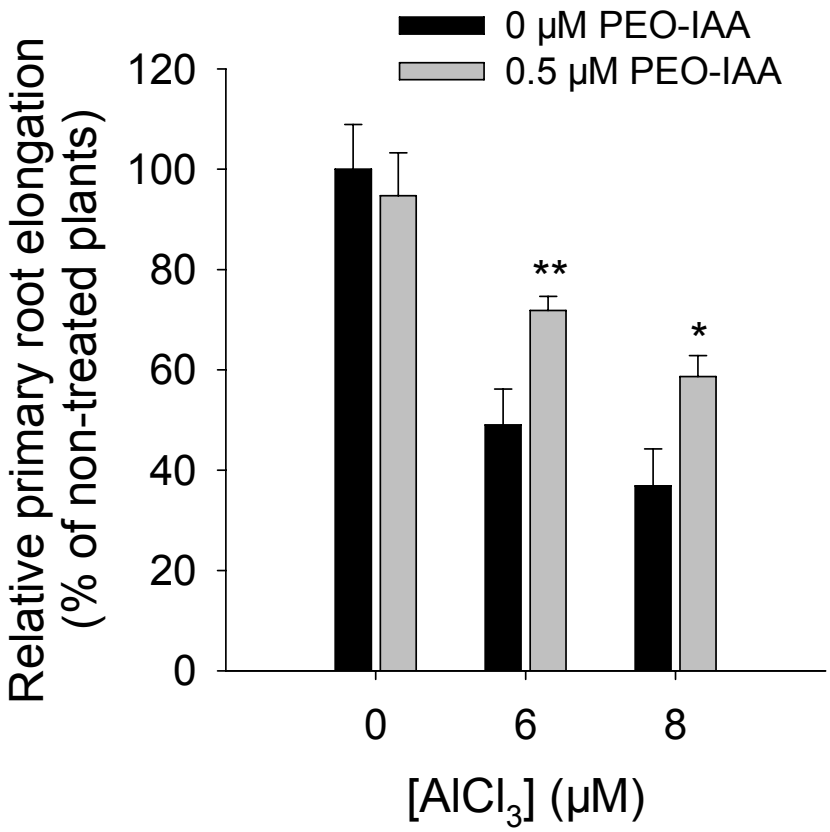


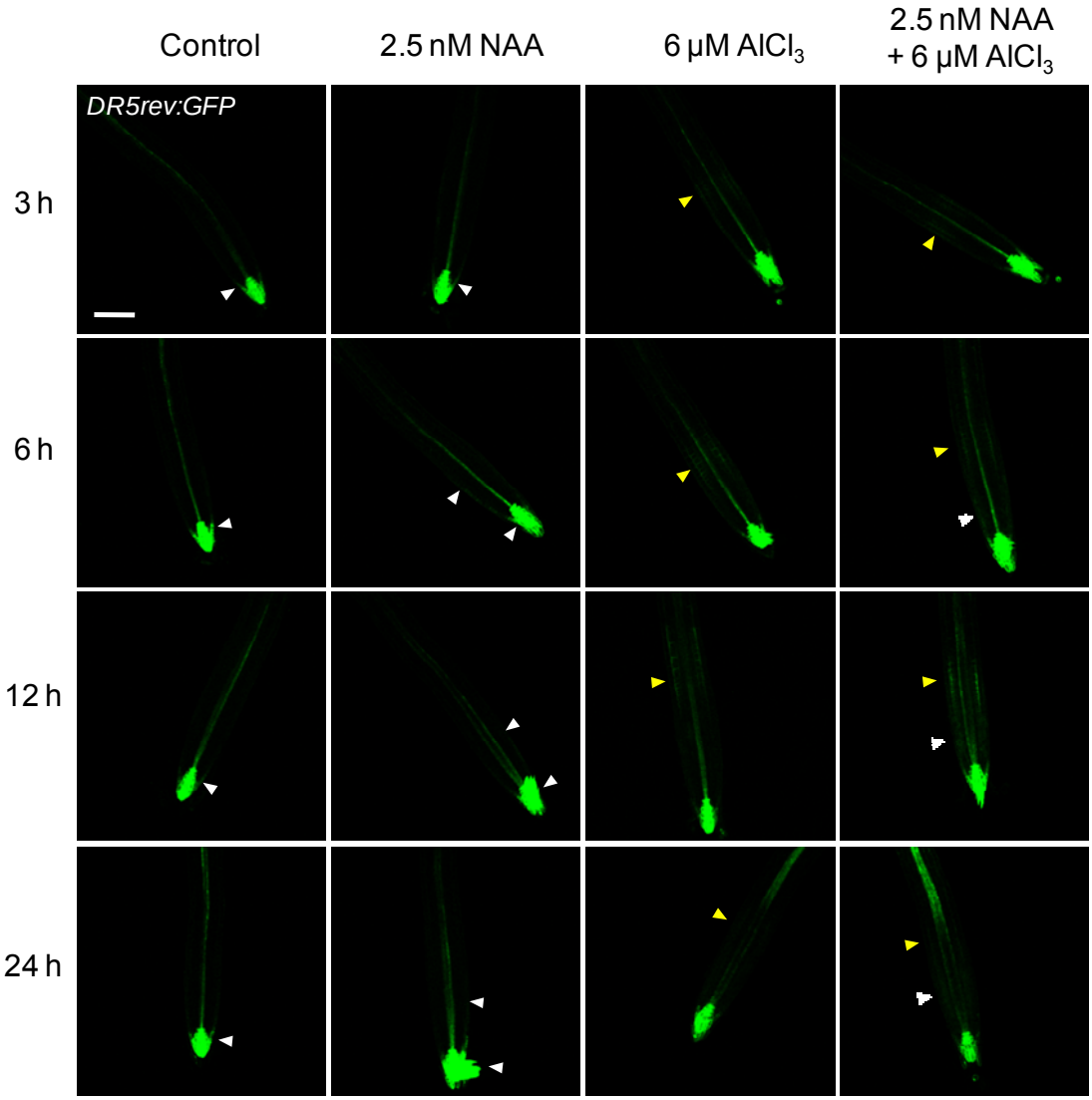
Supplemental Figure 1. The root apex TZ is the major site of Al sensitivity. Six-day old seedlings were exposed for 24 h to either 0 or 10 μM $AlCl_3$. Cell boundaries appear red following propidium iodide (PI) staining in **(A)** and **(B)**, while live cells appear green following fluorescein diacetate (FDA) staining. The TZ is marked by yellow arrowheads in **(A)**. Bar: 50 μm.



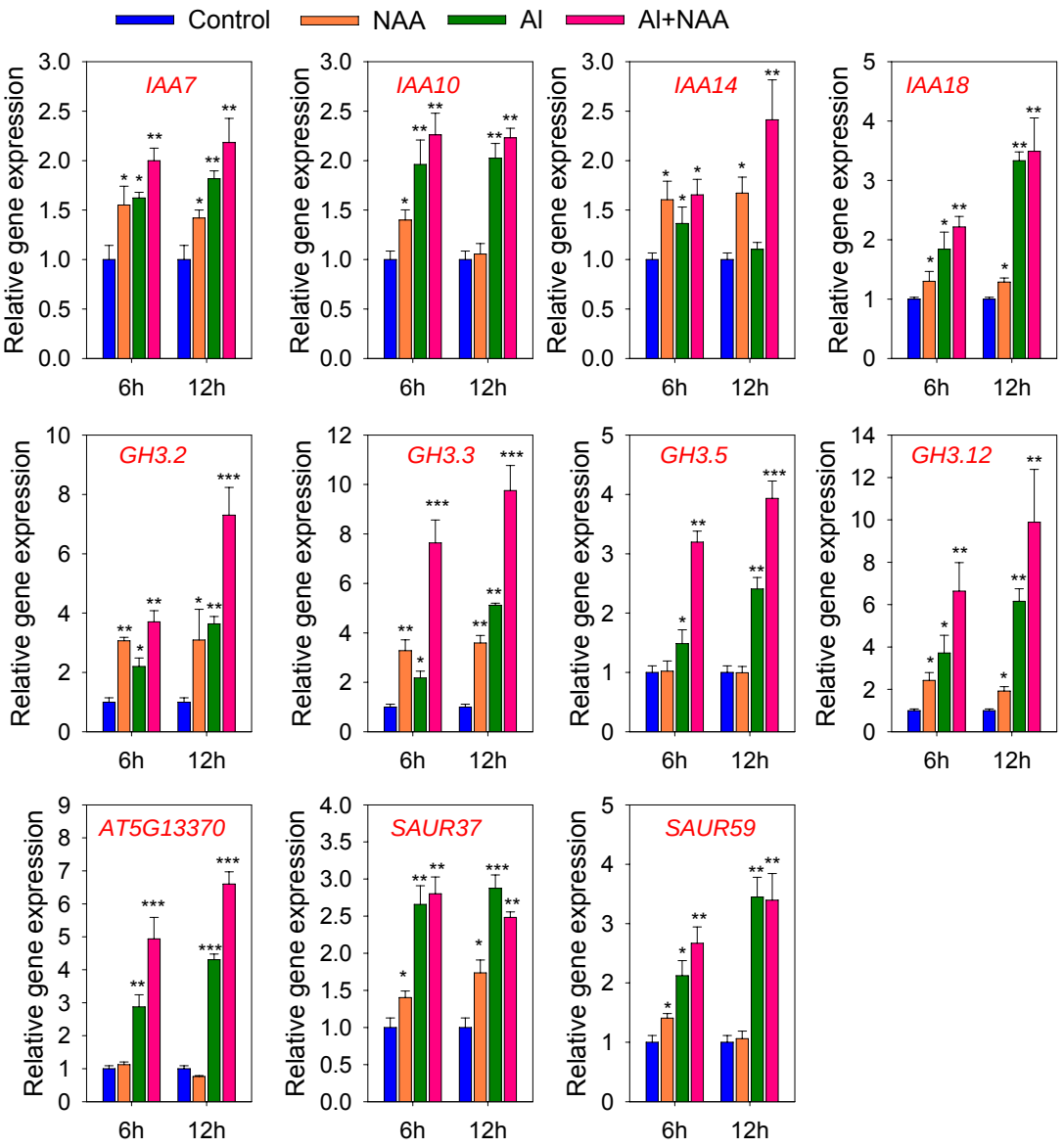
Supplemental Figure 2. Time-course analysis of the expression of *DR5rev:GFP* in root apex exposed to Al stress. Six-day old seedlings were exposed to 6 μM $AlCl_3$ (pH 5.0) for 0, 3, 6, 12, 24 and 48 h, or seedlings were directly sown onto polypropylene mesh floating on 6 μM $AlCl_3$ treatment solution for 7 d. The TZ is marked by yellow arrowheads. Bar: 100 μm.



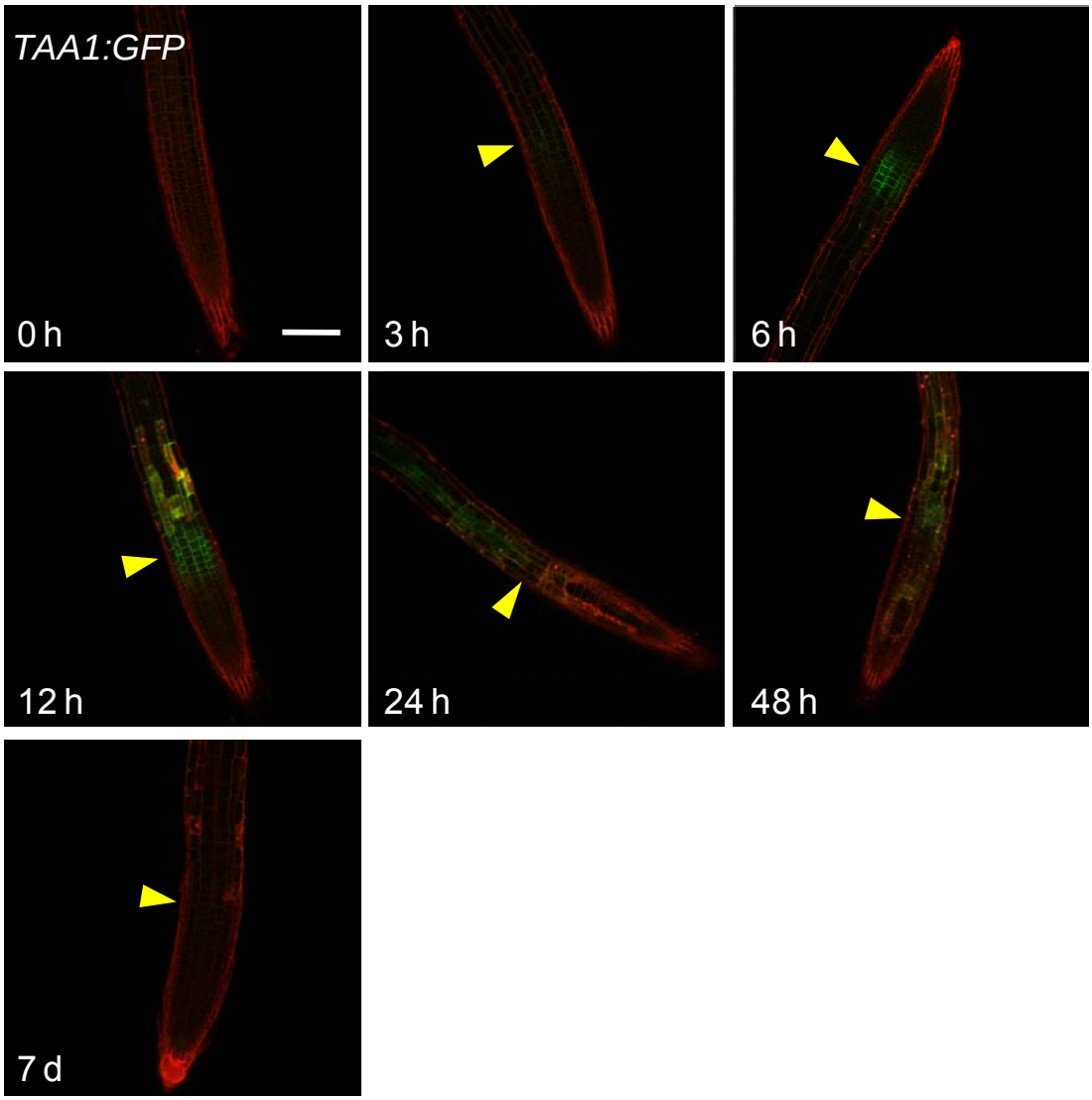
Supplemental Figure 3. Short-term effect of PEO-IAA on Al-induced inhibition of root growth. Six-day old seedlings grown on 1/2 MS-agar medium (pH 5.0) were exposed to 0, 6 and 8 μM $AlCl_3$ and either 0 or 0.5 μM PEO-IAA at pH 5.0 for 24 h, then the primary root elongation were analysed. * and **: differences between the PEO-IAA treatments are significant at $P < 0.05$ and < 0.01, respectively (*t* test). Bars represent the mean ± SD (n = 12).



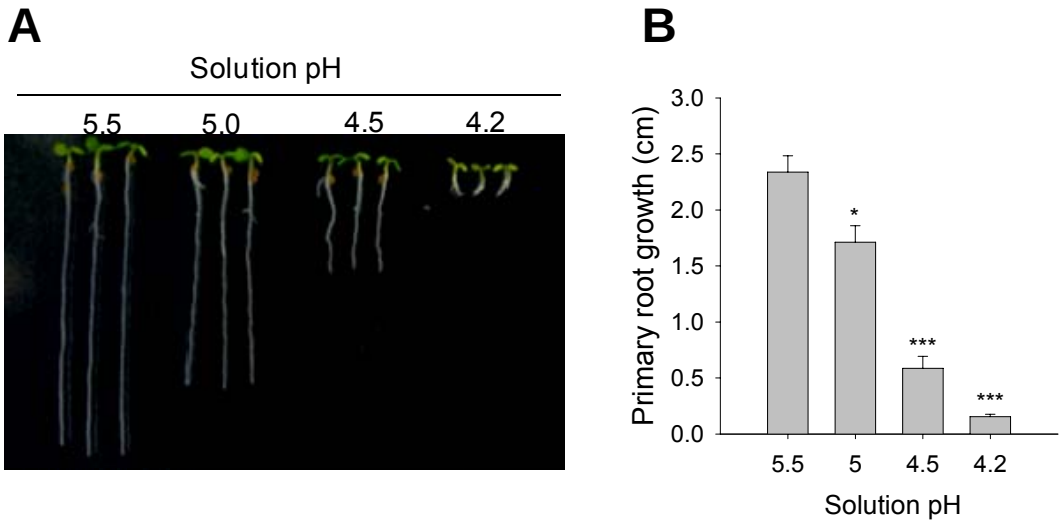
Supplemental Figure 4. Effect of exogenous NAA on Al-induced *DR5rev:GFP* expression in root apex. Six-day old *DR5rev:GFP* transgenic seedlings were exposed to $AlCl_3$ (0, 6 μM) with or without NAA (2.5 nM) at pH 5.0 for 3, 6, 12 and 24 h. The TZ is marked by yellow arrowheads, and the white arrowheads indicate the change of DR5 signals before and after NAA treatment. Bar: 100 μm.



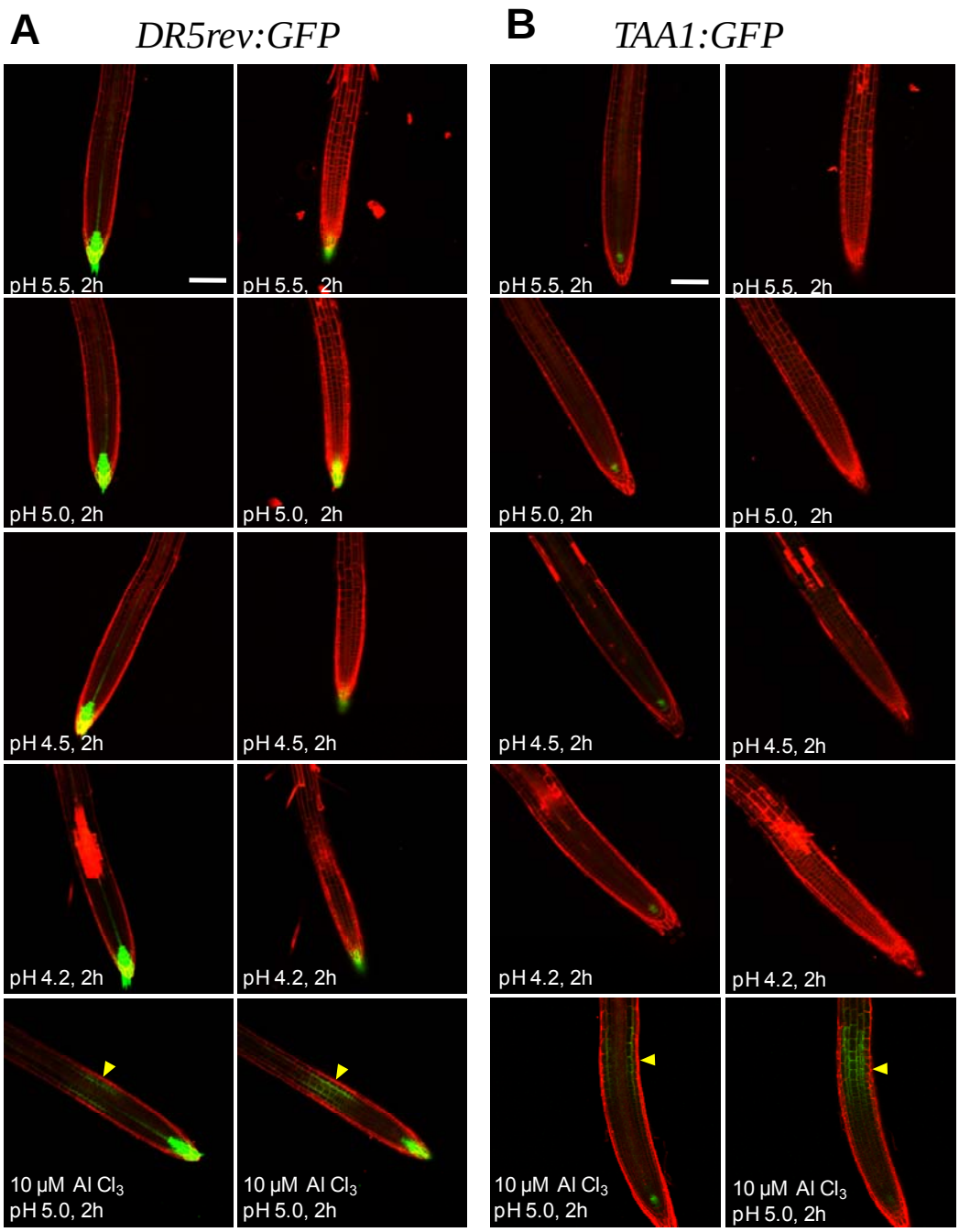
Supplemental Figure 5 Effect of exogenous NAA on the expression of auxin-responsive genes in Al-exposed roots. Six-day old seedlings were exposed to $AlCl_3$ (0, 6 μM) with or without NAA (2.5 nM) at pH 5.0 for 6 and 12 h. *UBQ1* (*AT3G52590*) was used as the reference, and non-treated WT as the sample control. Bars represent the mean ± SE (n = 3). *, ** and ***: Means in treatment differ significantly at $P < 0.05$, < 0.01 and < 0.001 (t test).



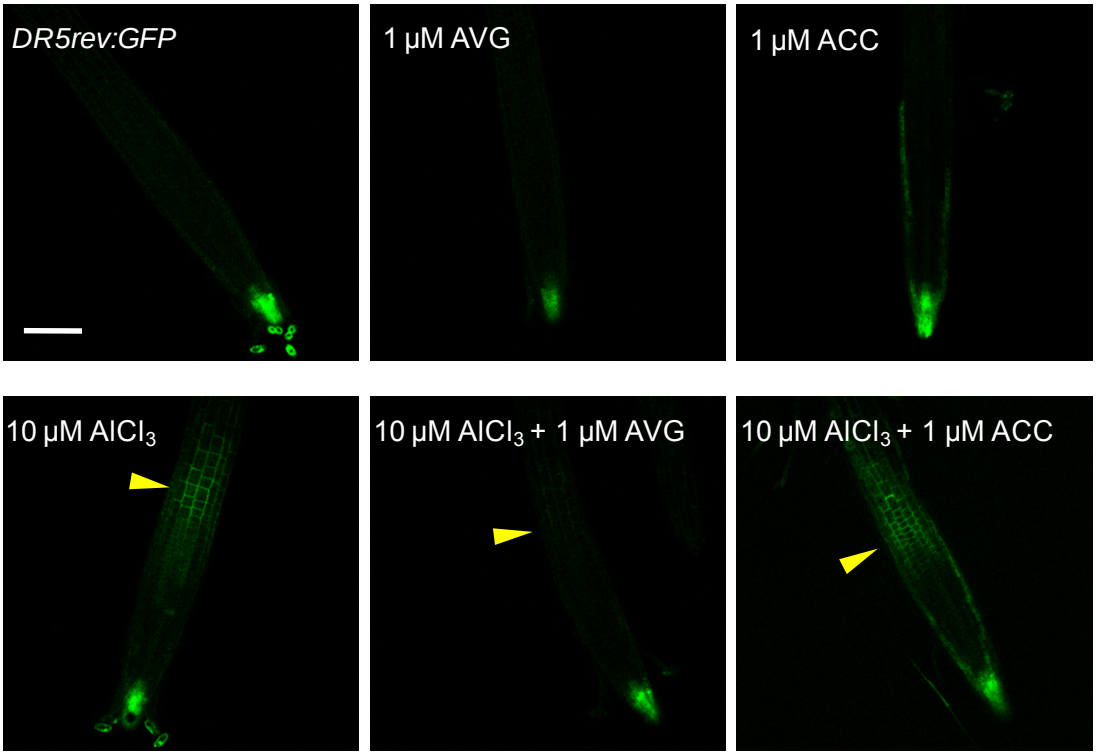
Supplemental Figure 6. Temporal analysis of Al-induced expression of *TAA1:GFP* in root apex. Six-day old *TAA1:GFP* transgenic seedlings were exposed to 6 μM $AlCl_3$ (pH 5.0) for 0, 3, 6, 12, 24 and 48 h, or seedlings were directly sown onto polypropylene mesh floating on 6 μM $AlCl_3$ treatment solution for 7 d. The TZ is marked by yellow arrowheads. Bar: 100 μm.



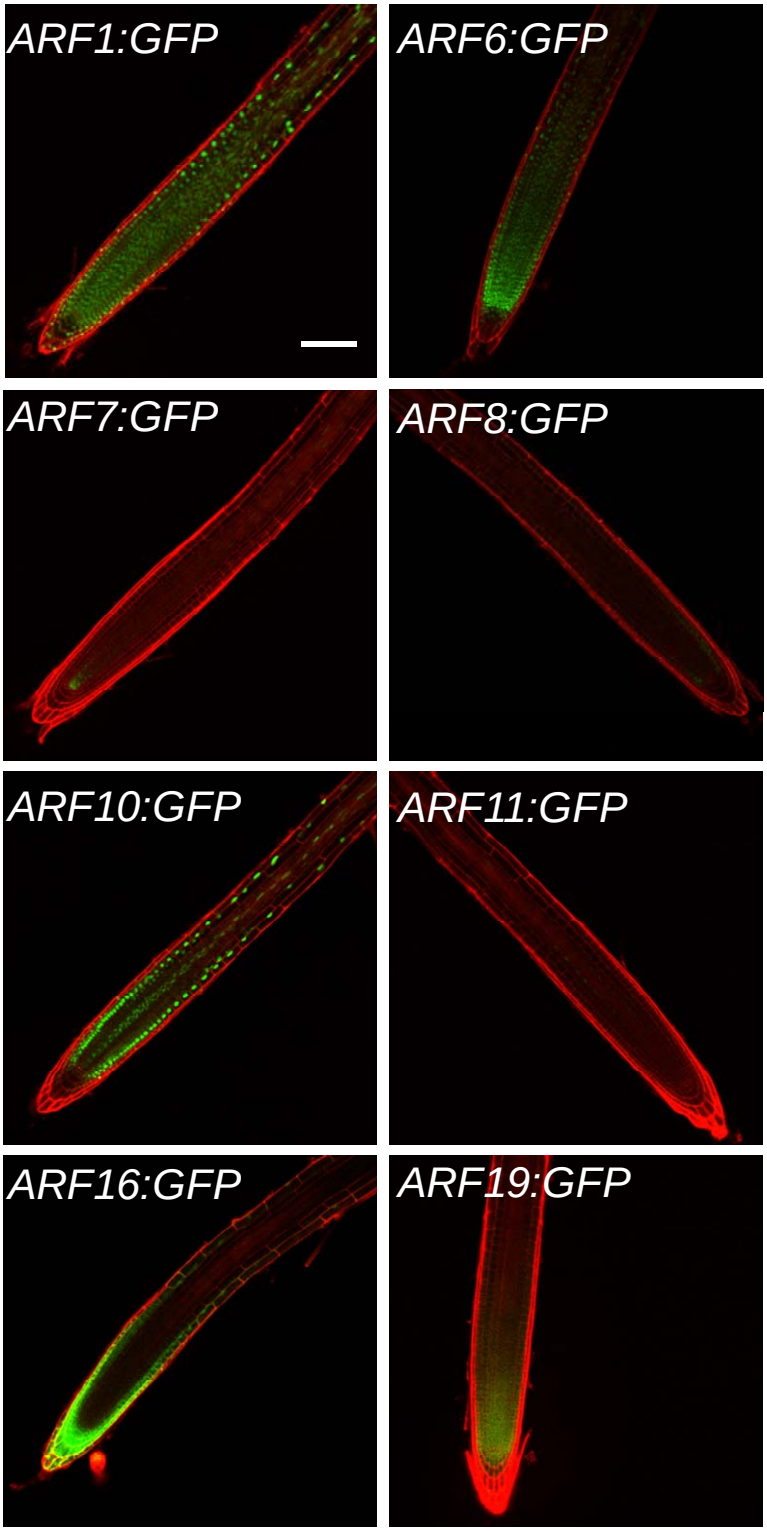
Supplemental Figure 7. The sensitivity of the *A. thaliana* root to low pH. **(A, B)** Seedlings were exposed for seven days to a pH between 4.2 and 5.5. * and ***: Means in solution pH differ significantly at $P < 0.05$ and < 0.001 (*t* test). Bars represent mean ± SD ($n = 30$).



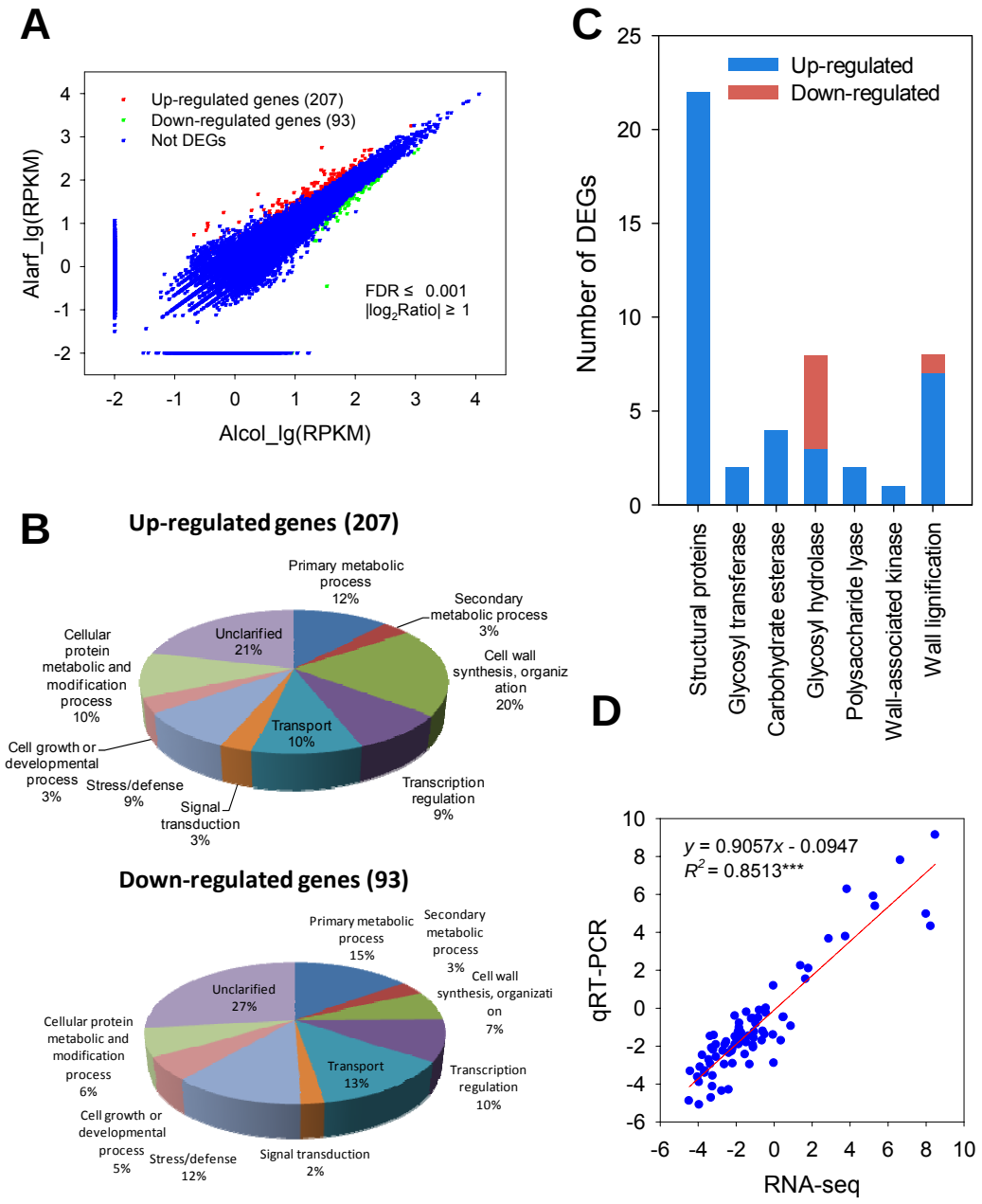
Supplemental Figure 8. The pH of the medium has no effect on the expression of either **(A)** the *DR5rev:GFP* or **(B)** the *TAA1:GFP* transgene. Six-day old *DR5rev:GFP* and *TAA1:GFP* seedlings were exposed for two hours to a pH of between 4.2 and 5, or 10 µM $AlCl_3$ (pH 5.0). The left hand columns shows *DR5rev:GFP* **(A)** or *TAA1:GFP* **(B)** signals in the cortex and the right hand columns shows *DR5rev:GFP* **(A)** or *TAA1:GFP* **(B)** signals in the epidermis. Cell boundaries appear red following propidium iodide staining. Bar: 100 µm.



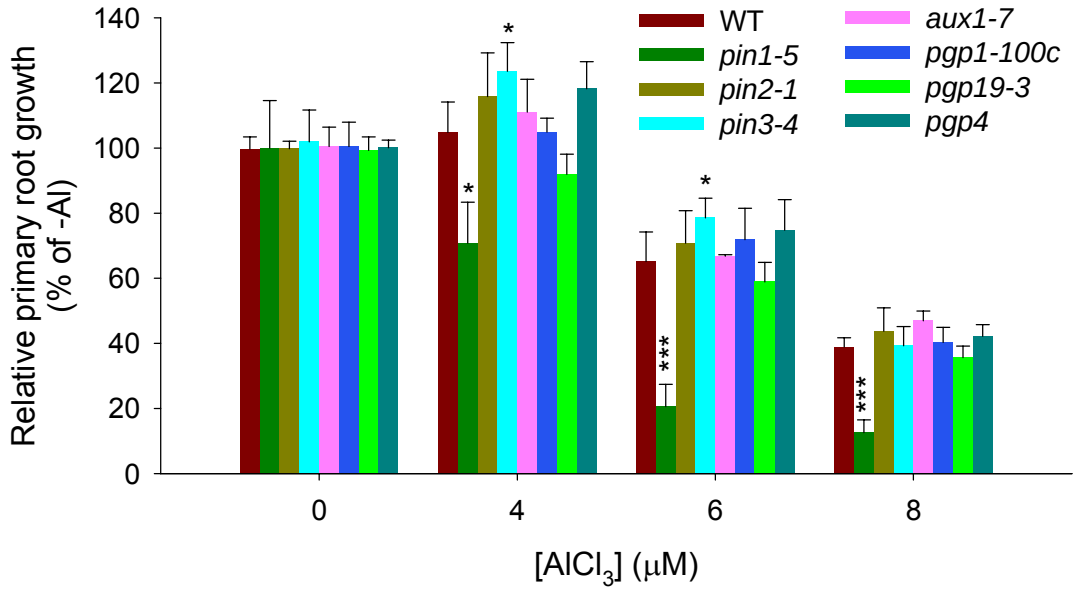
Supplemental Figure 9. Ethylene mediates TAA1-regulated local auxin signal responses in the TZ in response to Al stress. The expression of *DR5rev:GFP* transgene in the epidermis of the root apex in the presence of Al plus ACC or AVG treatments. Four-day old transgenic *DR5rev:GFP* seedlings were pre-treated without or with 1 μM AVG or 1 μM ACC for 2 days, and then the seedlings were continuously treated without or with 1 μM AVG or 1 μM ACC in the absence or presence of 10 μM $AlCl_3$ for 2 h. The TZ is marked by yellow arrowheads. Scale bar: 100 μm.



Supplemental Figure 10. The expression pattern of *ARFs:GFP* transgene in the root apex. Scale bar: 100 μm.



Supplemental Figure 11. Transcriptomic analysis of the response to Al exposure. **(A)** Scatter plot showing differentially transcribed genes in WT (Alcol) and *arf10/16* double mutant (Alarf) plants exposed to Al. RPKM: number of reads per Kb per million. **(B)** Functional categorization of differentially transcribed genes. **(C)** More refined categorization of differentially transcribed cell wall-related genes. **(D)** Validation of the differential transcription of 40 of the genes identified by RNA Seq, based on qRT-PCR. ***: The transcript abundance in WT and the double mutant plants differs significantly at $P < 0.001$.



Supplemental Figure 12. Relative primary root growth of WT and mutants which have defects in polar auxin transport in response to Al stress. Seedlings were exposed for seven days to 0, 4, 6 and 8 μM $AlCl_3$ at pH 5.0. * and ***: Means within WT and mutant in each Al concentration differ significantly at $P < 0.05$ and $P < 0.001$, respectively (*t* test). Bars represent mean ± SD ($n = 30$).