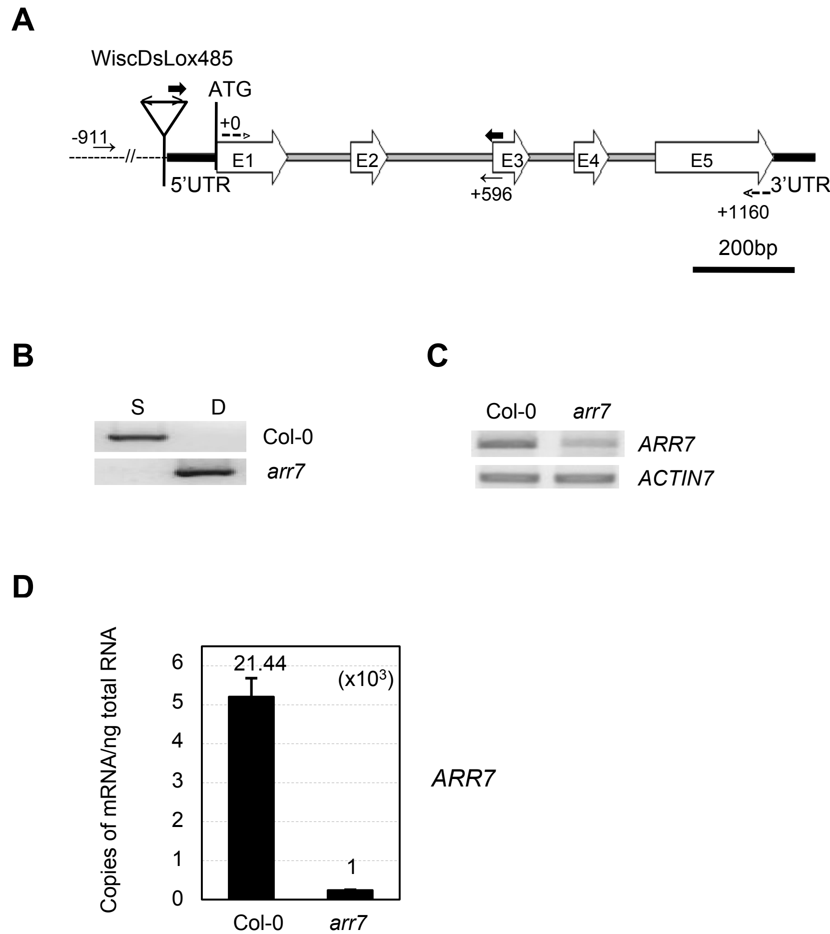
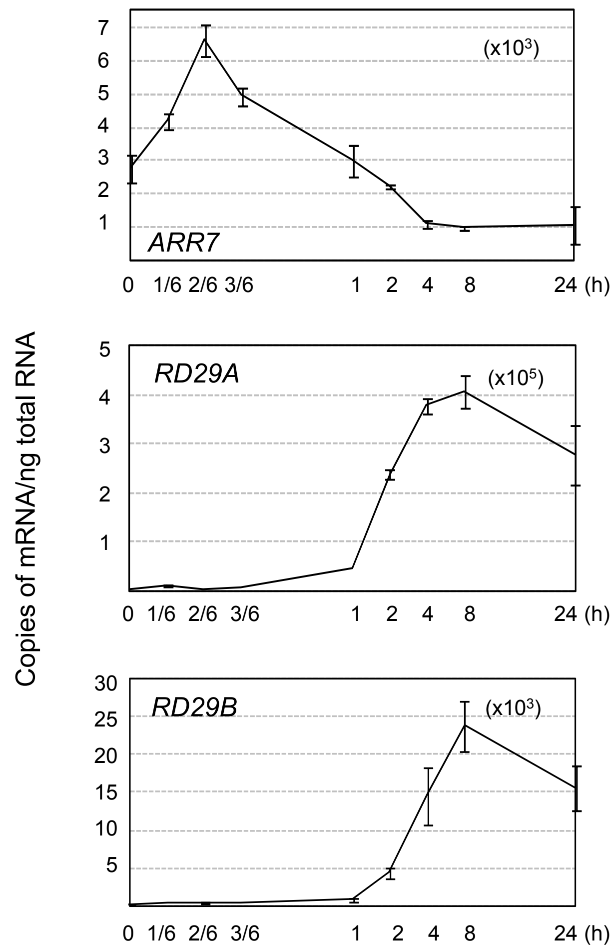
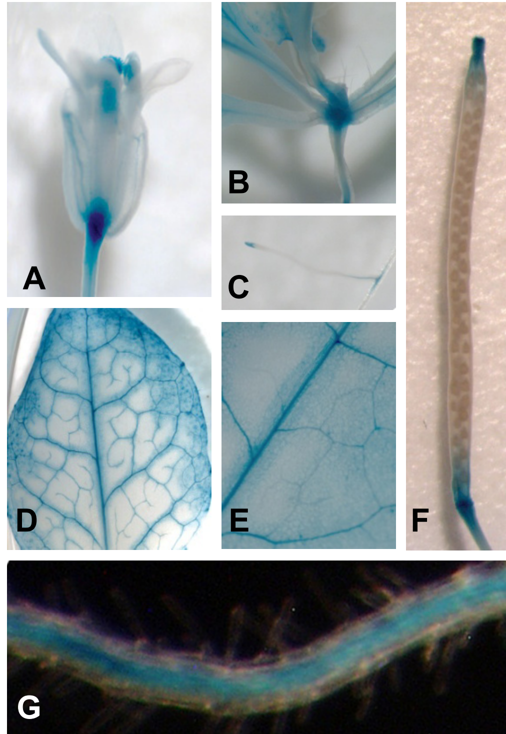


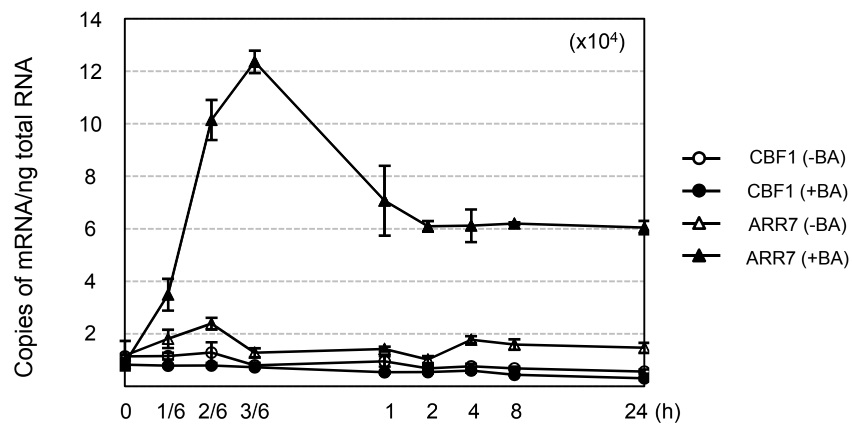

**Supplemental Fig. 1. Genotyping and RT-PCR analysis of *arr7 Arabidopsis* mutants compared with the wild-type.** *A,* Location of *Ds* transposon insertion of *ARR7* in *Arabidopsis*. *Ds* insertion is indicated by triangle. *ARR7* is composed of five exons (E) and four introns indicated by a grey line. Untranslated region (UTR) is indicated by thick solid line. Thin solid arrows and thick solid arrows indicate the locations of the primers for the PCR of genomic *ARR7* DNA. Dotted arrows indicate the locations of the primers for RT-PCR of the *ARR7* mRNA. Numbers indicate the position of the first nucleotide of the primer relative to the AUG initiation codon. *arr7*: WiscDsLox485-488B15 (http://www.hort.wisc.edu/krysan/2010/Default.htm). *B,* PCR analysis of *Ds* transposon insertion mutants. Genomic DNA isolated was subjected to PCR with primers indicated in thick or thin arrows. S or D, PCR products amplified by specific primers (S, thin arrows) or *Ds* transposon primers (D, thick arrows). WT, wild-type Col-0. *C,* RT-PCR analysis of *Ds* transposon insertion mutants. Total RNA isolated from 7-day-old light-grown seedlings was subjected to RT-PCR with the primers indicated in dotted arrows. The *ACTIN7* mRNA was utilized as a loading control. *D,* Real-time RT-PCR analysis of the *ARR7* mRNA levels in *Ds* transposon insertion mutants compared with the wild-type. Copies of the transcripts from 7-day-old light-grown seedlings were plotted per ng total RNA after normalization to *ACTIN7* RNA. Multiplication of the number in the brackets inside the graph by the number in the y-axis generates copy numbers of the corresponding transcripts. Mean values and standard errors from biological triplicate experiments were plotted. Numbers on top of the bars indicate relative expression levels.



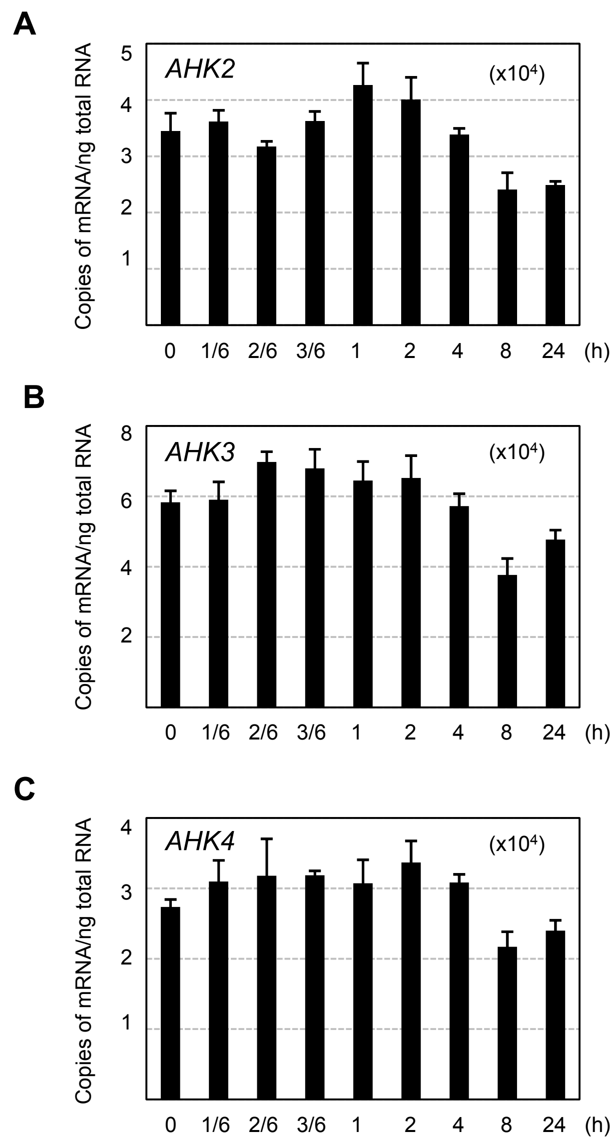

**Supplemental Fig. 2. Quantitative analysis of *ARR7* expression in response to high salinity.** Eleven-day-old seedlings were incubated with 300 mM NaCl in darkness for varying periods of time (h), analyzed, and shown as described in the Fig. 2 legend.



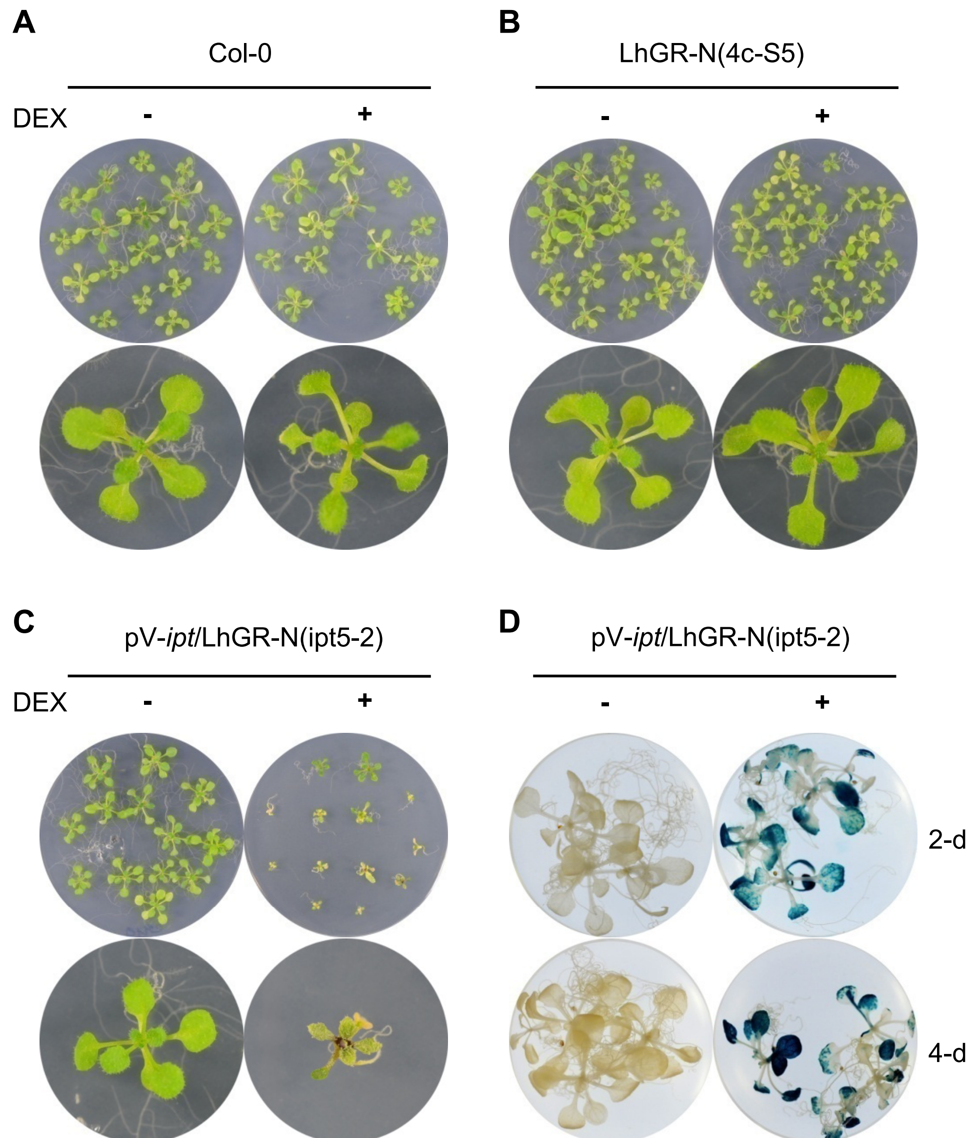

**Supplemental Fig. 3. Tissue expression pattern of *Pro$_{ARR7}$*:*GUS* transgenics.** *A*-*G*, Tissue expression pattern of *Pro$_{ARR7}$*:*GUS* in flower (*A*), shoot meristem (*B*), root meristem (*C*), rosette leaf (*D* and *E*), silique (*F*), and root (*G*).



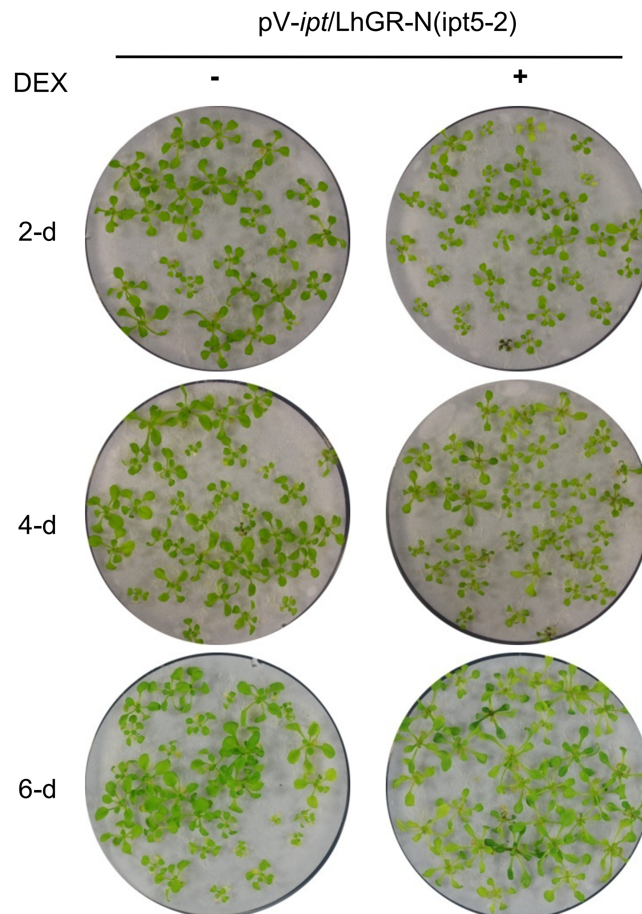

**Supplemental Fig. 4. Quantitative analysis of *CBF1* expression in response to cytokinin.** Eleven-day-old seedlings were incubated with cytokinin BA for varying periods of time (h), analyzed, and shown as described in the Fig. 2 legend. *ARR7* expression was monitored to verify the cytokinin response.



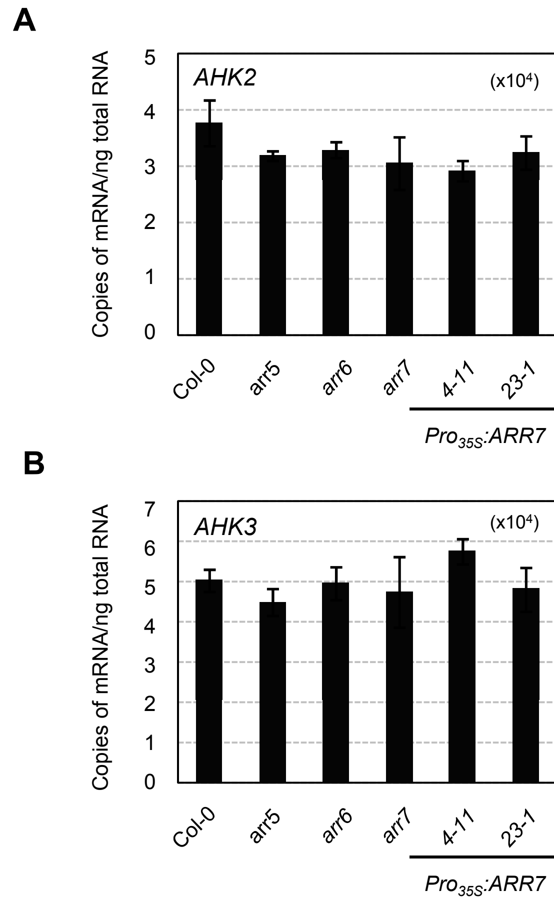

**Supplemental Fig. 5. Analysis of *AHK2*, *AHK3*, and *AHK4* expression in response to cold.** Eleven-day-old wild-type (Col-0) seedlings were incubated at 1 ºC for varying periods of time (h). Total RNA isolated from each treatment was subjected to quantitative real-time RT-PCR with the primers for *AHK2* (*A*), *AHK3* (*B*), and *AHK4* (*C*). *ACTIN7* was utilized as a loading control. Copies of the transcripts from cold-treated plants treated with cold were plotted per ng of total RNA after normalization to *ACTIN7* RNA. The transcripts levels were determined as described in the Fig. 2 legend.




**Supplemental Fig. 6. Phenotype and GUS expression of *pV-ipt/LhGR-N* transgenic plants.** *A,* Col-0 wild-type plants treated with or without DEX. Plants were grown for 14 days without or with 10 µM DEX. *B, LhGR-N* transgenic plants treated with or without DEX. Transgenic plants that contain activator construct expressing *LhGR* from the CaMV 35S promoter (39) were grown for 14 days without or with 10 µM DEX. 4c-S5 indicates the line number of transgenic plants. GR indicates ligand binding domain of a rat glucocorticoid receptor at the amino terminus. Details on the constructs have been described previously (39). *C, pV-ipt/LhGR-N* transgenic plants treated with or without DEX. Transgenic plants that contain activator construct expressing *LhGR* and construct harboring *IPT* encoding isopentenyl transferase enzyme and *GUS* under six copies of ideal *lac* operator (39) were grown for 14 days without or with 10 µM DEX. The treatment of DEX can lead to activation of *IPT* for cytokinin biosynthesis and *GUS*. ipt5-2 indicates the line number of transgenic plants. *D,* GUS staining of *pV-ipt/LhGR-N* transgenic plants treated with or without DEX. *pV-ipt/LhGR-N* transgenic plants were grown for 10 days and then treated without or with DEX for 2 days or 4 days, followed by GUS staining.




**Supplemental Fig. 7. The *pV-ipt/LhGR-N* transgenic plants treated with DEX.** The transgenic plants were grown in the light on sterile filter paper in MS plate for 10 days and transferred to MS plate with or without 10 μM DEX. Plants were then incubated for additional 2, 4, or 6 days in the light. Pictures were taken before cold treatment at 1 ºC.




**Supplemental Fig. 8. Analysis of *AHK2* and *AHK3* expression in *arr5, 6,* or *7* mutants and *Pro$_{35S}$:ARR7*.** Total RNA isolated from eleven-day-old wild-type (Col-0) seedlings were subjected to quantitative real-time RT-PCR with the primers for *AHK2* (*A*) and *AHK3* (*B*). *ACTIN7* was utilized as a loading control. Copies of the transcripts from cold-treated plants treated with cold were plotted per ng of total RNA after normalization to *ACTIN7* RNA. The transcripts levels were determined as described in the Fig. 2 legend.