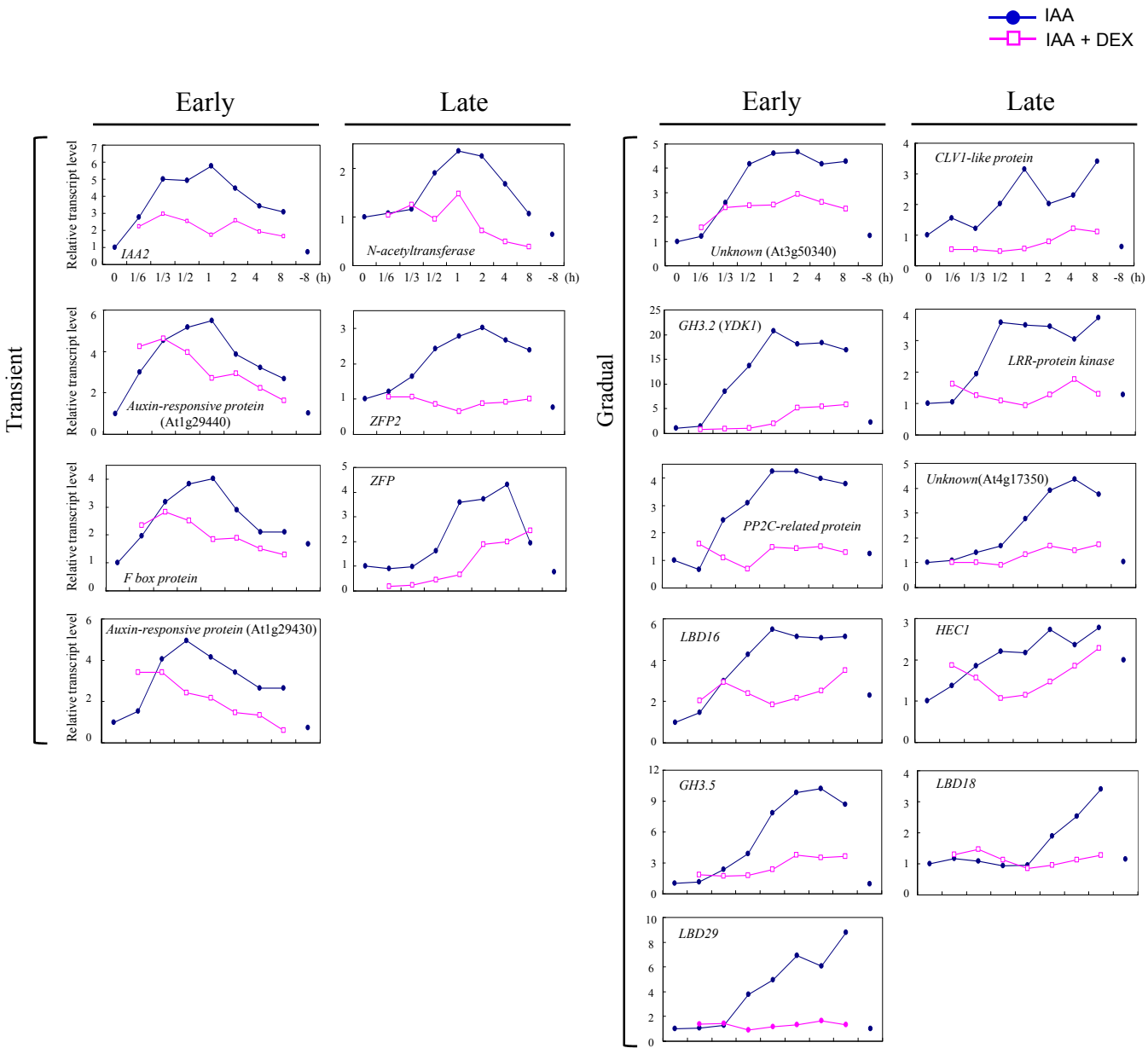
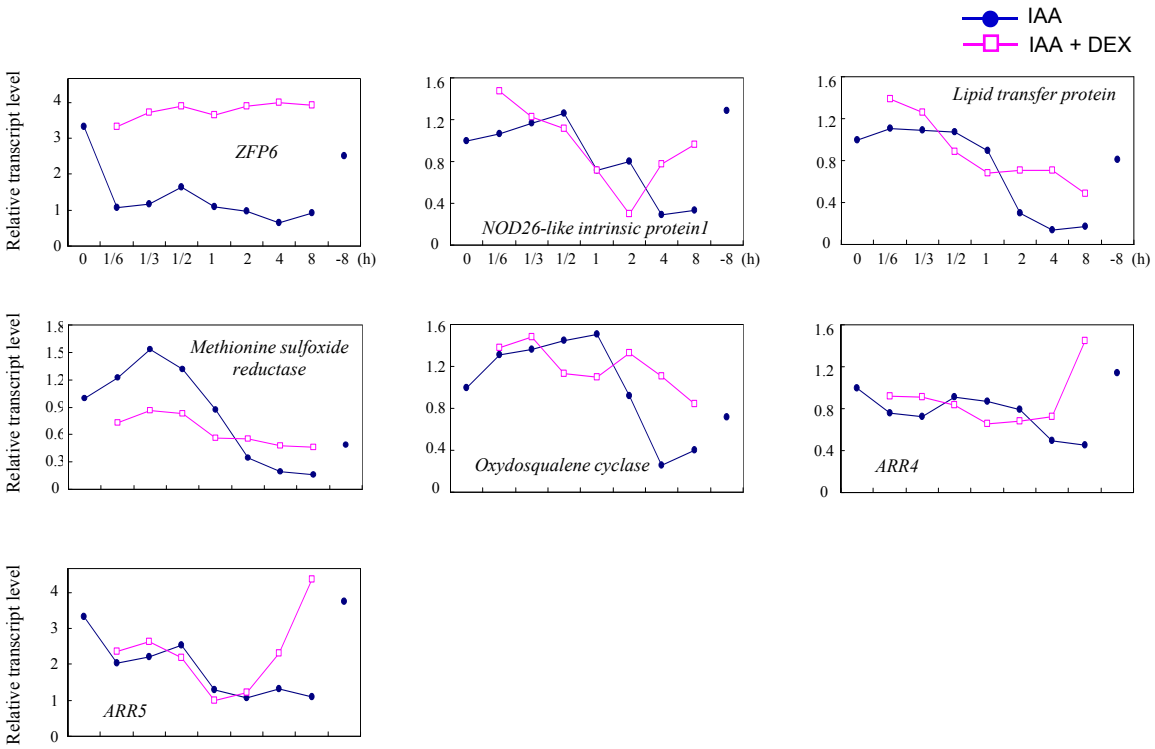


Supplementary Fig. S1. Quantification of time-course expression of representative auxin-up-regulated genes selected from microarray analysis with auxin or with auxin and DEX. *Pro*$_{35S}$*iaa1:GR* seedlings were incubated with auxin (IAA) or auxin and DEX (IAA + DEX) for an indicated time in the light, and subject to RNA-gel blot analysis with given DNA probes. The transcript levels were then determined by Phosphoimager (BAS-1500, Fujifilm, Japan) and plotted after normalizing to the *Actin7* mRNA level. Solid blue circle and pink open rectangular represent the transcript levels from the samples treated with auxin and auxin in the presence of DEX, respectively. -8 h indicates the sample incubated with mock for 8 h.

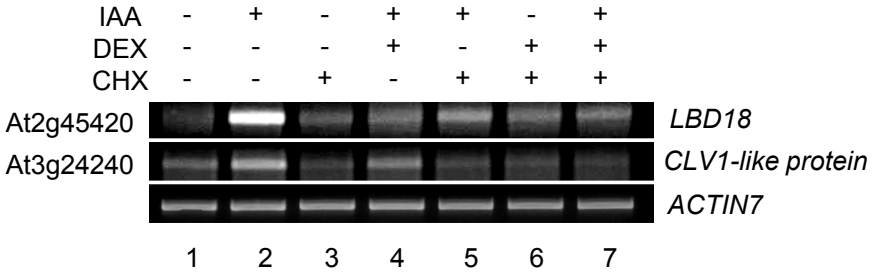


Supplementary Fig. S2. Quantification of time-course expression of representative auxin-down-regulated genes selected from microarray analysis with auxin or with auxin and DEX. *Pro$_{35S}$iaa1:GR* seedlings were treated and analyzed as described in Supplemental Figure S1.

A. Auxin-upregulated

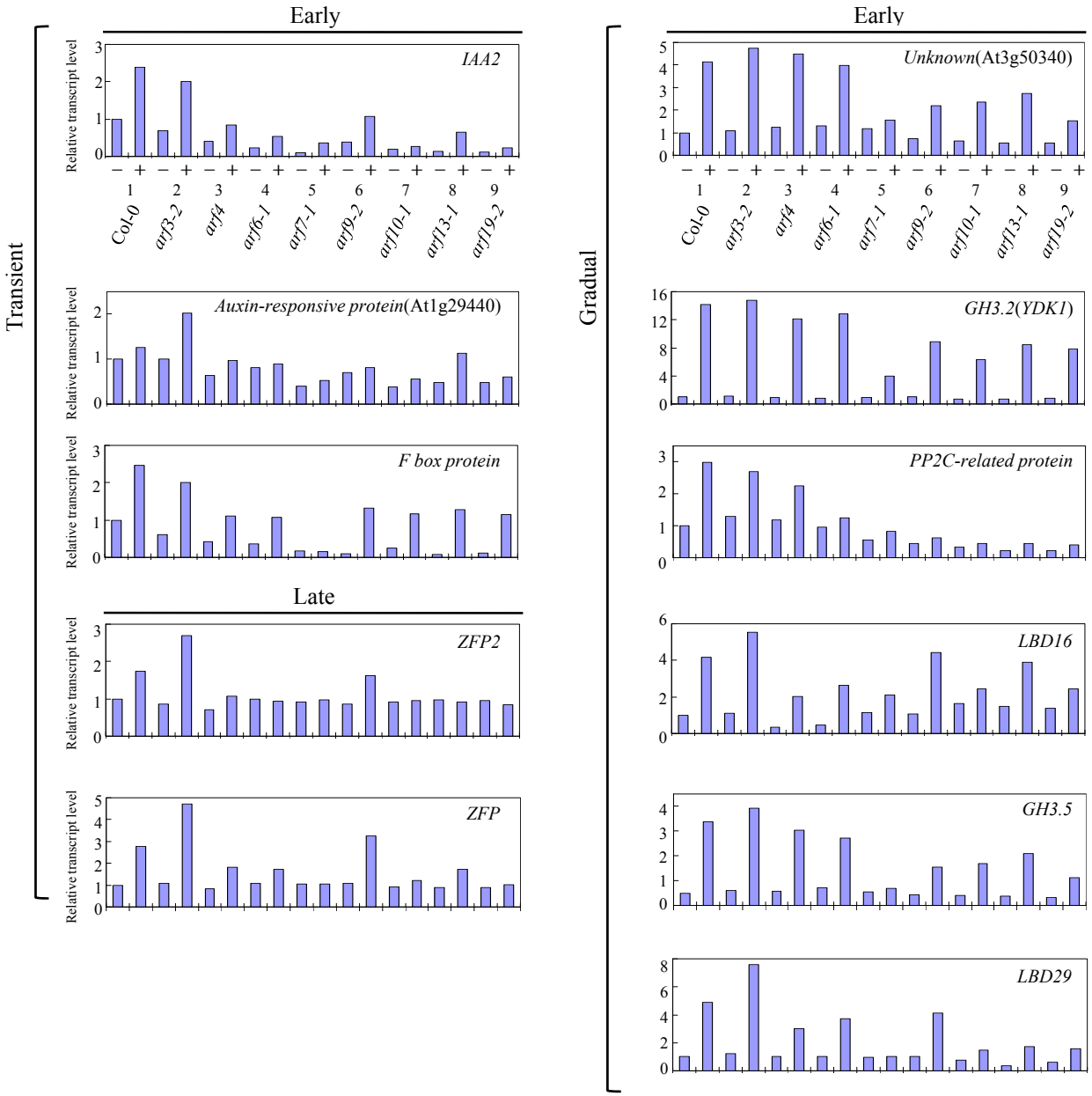
B. Auxin-downregulated

Supplementary Fig. S3. Quantification of expression analysis of representative auxin-response genes selected from microarray analysis in response to cycloheximide, auxin, and DEX treatment. *Pro$_{35S}$iaa1:GR* seedlings were incubated with mock (1st column) or auxin (2nd column) or cycloheximide (3rd column) or auxin and DEX (4th column) or auxin and cycloheximide (5th column) or cycloheximide and DEX (6th column) or auxin, DEX, and cycloheximide (7th column) for 2h in the light, followed by RNA-gel blot analysis with indicated DNA probes. The transcript levels were determined as described in Supplemental Figure S1.



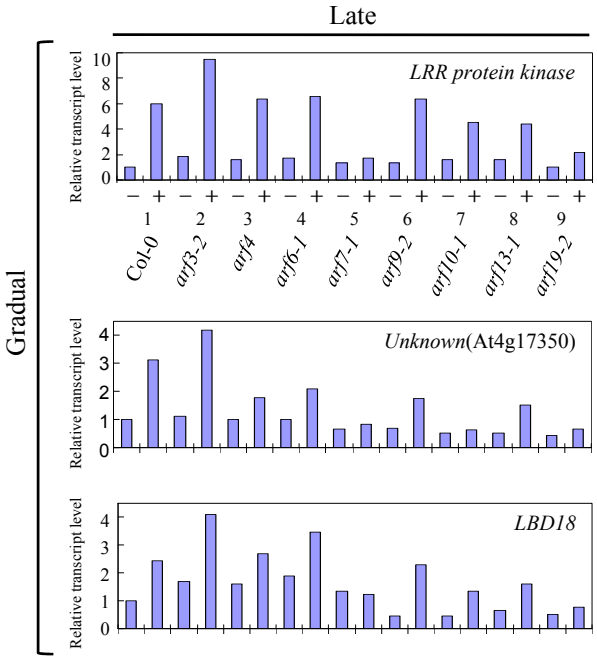
Supplementary Fig. S4. Expression analysis of *LBD18* and *CLV1-like protein* in response to cycloheximide, auxin, or DEX treatment. *Pro$_{35S}$:iaa1:GR* seedlings were incubated with mock (lane 1), auxin (lane 2), cycloheximide (lane 3), auxin and DEX (lane 4), auxin and cycloheximide (lane 5), cycloheximide and DEX (lane 6), or auxin, DEX and cycloheximide (lane 7) for 4 h in the light, followed by RT-PCR analysis. *ACTIN7* was used as a loading control.

A. Auxin-upregulated

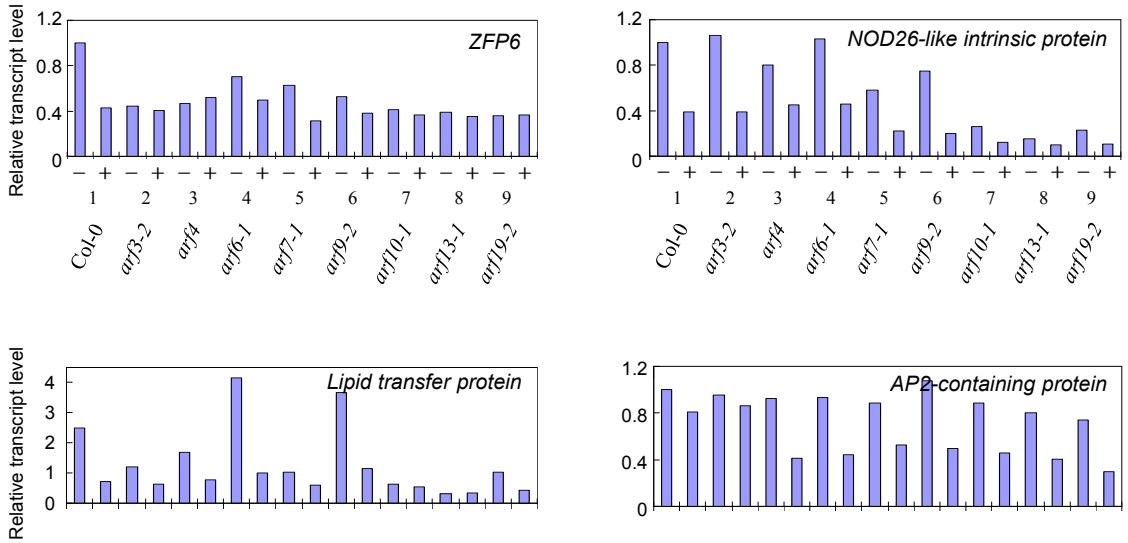


Supplementary Fig. S5. Quantification of expression profiling of auxin-responsive putative target genes regulated by iaa1 in various *arf* mutant backgrounds. *arf* mutant seedlings were incubated with mock (-) or auxin (+) for 2h in the light, followed by RNA-gel blot analysis with indicated DNA probes. The transcript levels were determined as described in Supplemental Figure S1. First column to ninth column represent the relative transcript levels from Col-0, *arf3-2*, *arf4*, *arf6-1*, *arf7-1*, *arf9-2*, *arf10-1*, *arf13-1*, and *arf19*-2, respectively.

A. Auxin-upregulated

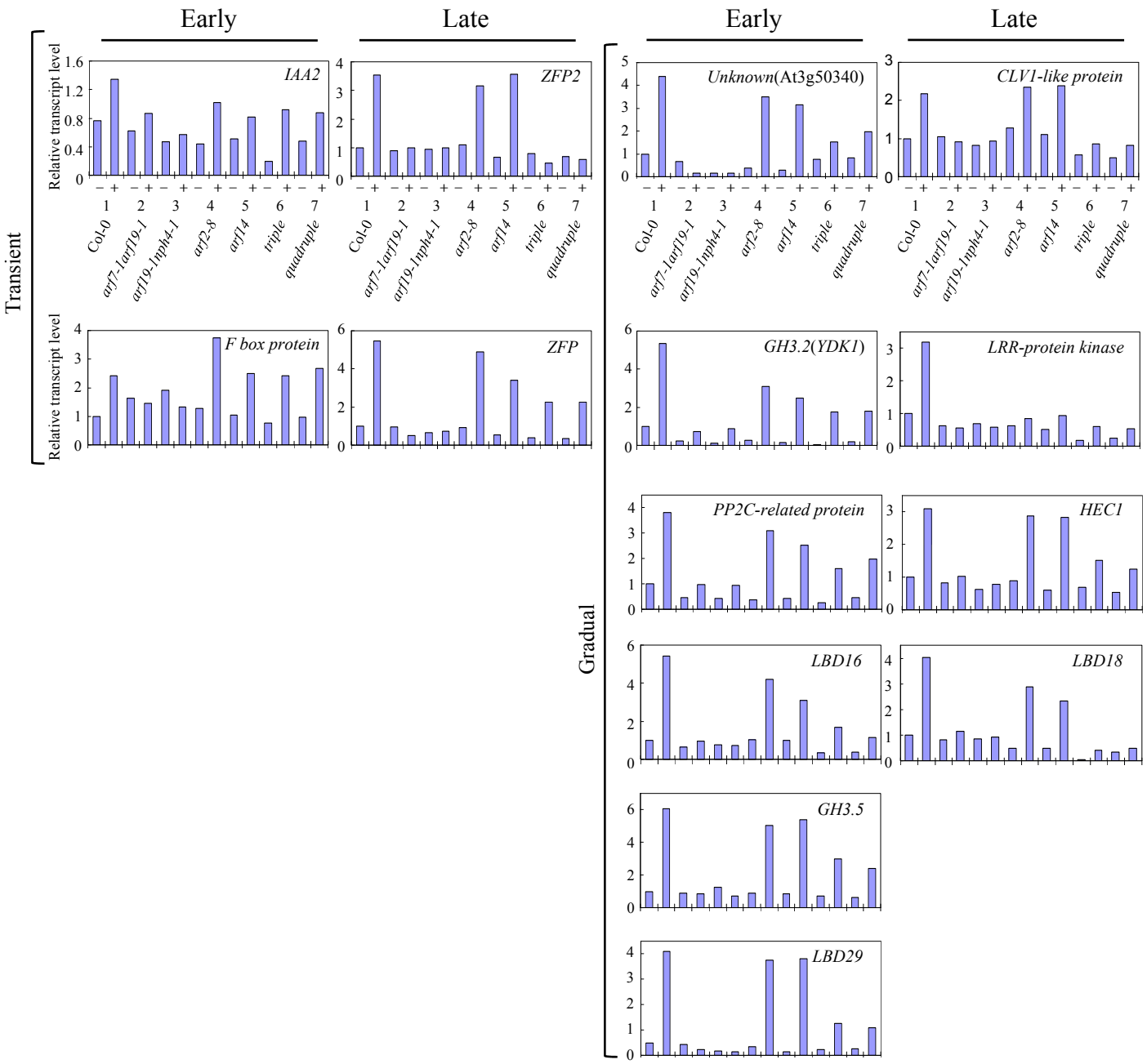


B. Auxin-Downregulated



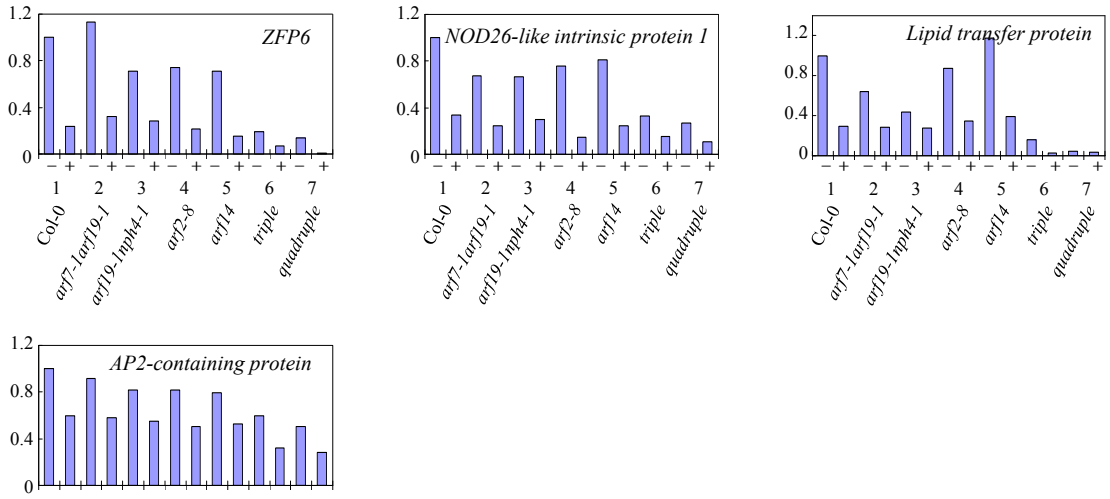
Supplementary Fig. S5 (continued). Quantification of expression profiling of auxin-responsive putative target genes regulated by iaa1 in various *arf* mutant backgrounds. *arf* mutant seedlings were incubated with mock (-) or auxin (+) for 2h in the light, followed by RNA-gel blot analysis with indicated DNA probes. The transcript levels were determined as described in Supplemental Figure S1. First column to ninth column represent the relative transcript levels from Col-0, *arf3-2*, *arf4*, *arf6-1*, *arf7-1*, *arf9-2*, *arf10-1*, *arf13-1*, and *arf19*-2, respectively.

A. Auxin-upregulated

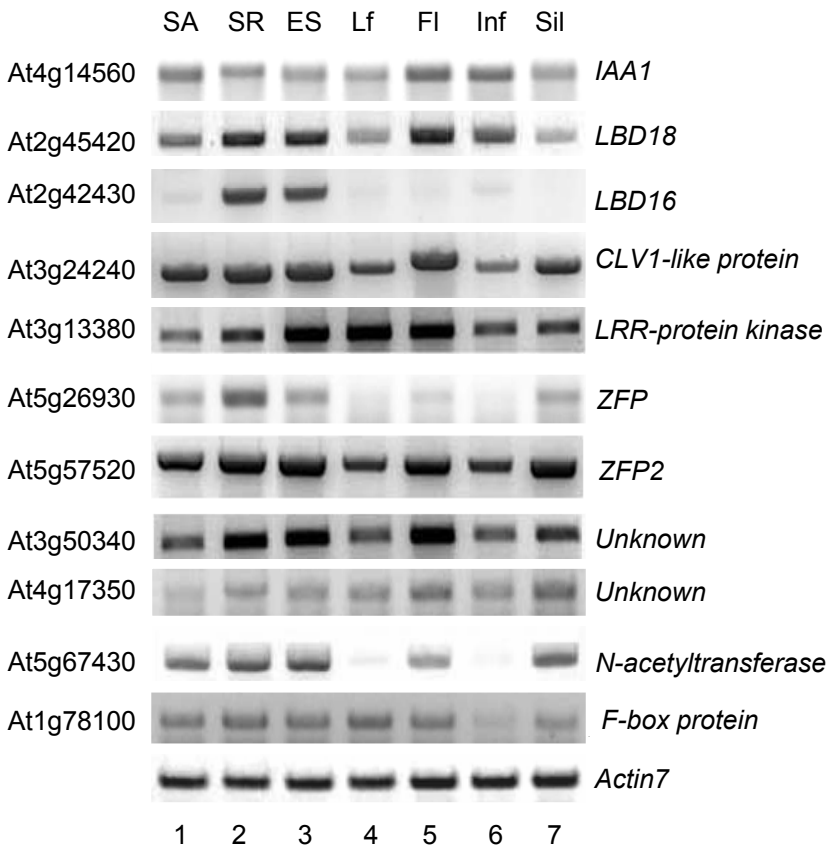


Supplementary Fig. S6. Quantification of expression profiling of auxin-responsive putative target genes regulated by iaa1 in various *arf* and *tir1/afb* mutant backgrounds. *arf* mutant seedlings were incubated with mock (-) or auxin (+) for 2h in the light, followed by RNA-gel blot analysis with indicated DNA probes. The transcript levels were determined as described in Supplemental Figure S1. First column to seventh column represent the relative transcript levels from Col-0, *arf7-1 arf19-1*, *arf19-1 nph4-1*, *arf2-8*, *arf14*, *tir1-1 afb2-1 afb3-1 (triple)*, and *tir1-1 afb1-1 afb2-1 afb3-1 (quadruple)*, respectively.

B. Auxin-downregulated



Supplementary Fig. S6 (continued). Quantification of expression profiling of auxin-responsive putative target genes regulated by iaa1 in various *arf* and *tir1/afb* mutant backgrounds. *arf* mutant seedlings were incubated with mock (-) or auxin (+) for 2h in the light, followed by RNA-gel blot analysis with indicated DNA probes. The transcript levels were determined as described in Supplemental Figure S1. First column to seventh column represent the relative transcript levels from Col-0, *arf7-1 arf19-1*, *arf19-1 nph4-1*, *arf2-8*, *arf14*, *tir1-1 afb2-1 afb3-1 (triple)*, and *tir1-1 afb1-1 afb2-1 afb3-1 (quadruple)*, respectively.



Supplementary Fig. S7. Organ-specific expression profiles of auxin-responsive genes regulated by iaa1. Total RNAs extracted from various organs were amplified by RT-PCR. *Actin7* was used as a loading control. SA; aerial parts of 2-week-old seedling, SR; roots of 2-week-old seedling, ES; 7-day-old etiolated seedlings, Lf; rosette leaves of 6-week-old plants, Fl; flowers of 6-week-old plants, Inf; inflorescences of 6-week-old plants, Sil; siliques of 7-week-old plants.