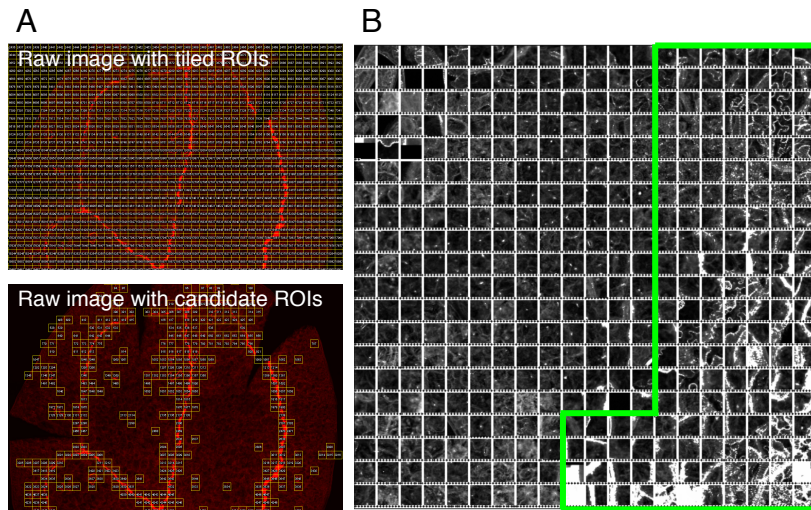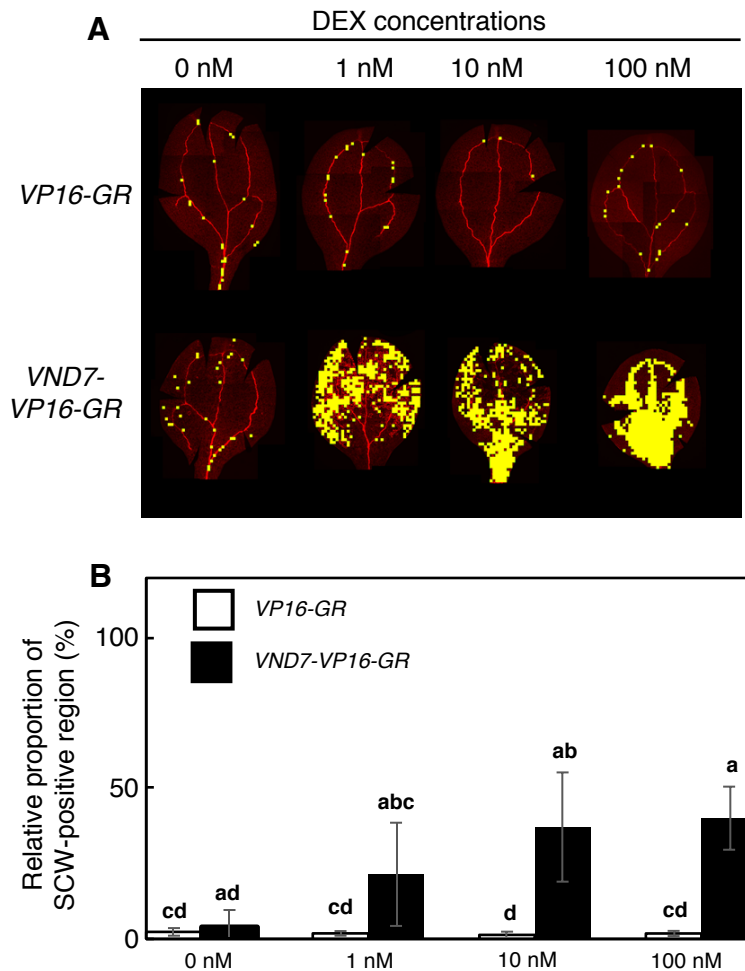**Supplementary Figure S1. Secondary cell wall (SCW) deposition in *VND7-VP16-GR* following a 24-h treatment with 10 nM dexamethasone (DEX).**
A magnification of the image shown in Fig. 2L, highlighting the patterned SCW deposition. Bar = 100 μm.
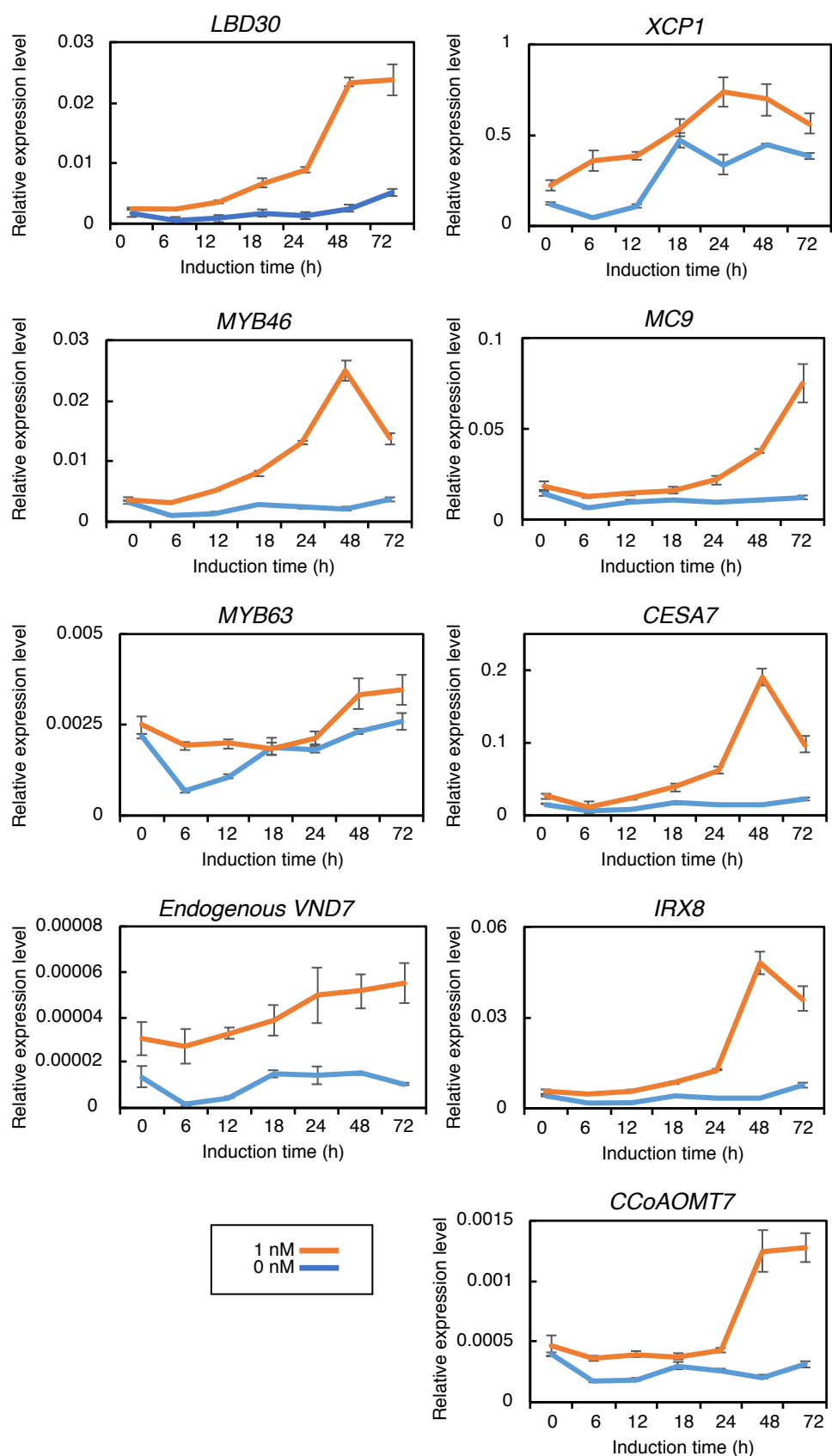
Supplementary Figure S2. Image processing workflow for the semi-automatic detection of secondary cell wall (SCW)-positive regions.
(A) A collection of candidate regions of interests (ROIs) used to detect the induced SCW regions. The tiled ROIs were set on an image of a PI-stained cotyledon (top). The candidate ROIs were identified based on their maximum intensity (bottom).
(B) Self-organizing map clustering of the candidate ROIs. Based on interactive annotations and iterative clustering (Higaki et al., 2015), the feature set was optimized to detect SCWs. After the feature selection, the SCW-positive regions were defined as the ROIs located in the nodes surrounded by the green line.

Supplementary Figure S3. The relative proportion of secondary cell wall (SCW)-positive cells within *VP16-GR* and *VND7-VP16-GR* seedlings.
(A) Typical images of semi-automatically detected induced SCW-positive regions identified using machine learning. (B) Quantification of the induced SCW-positive cell regions in the cotyledons. The data are shown as means $\pm$ SD (n = 5). Different letters indicate statistically significant different values (Tukey-Kramer test, $p < 0.05$).

Supplementary Figure S4. Quantitative RT-PCR analysis of the expression of the genes downstream of VND7 in *VND7-VP16-GR* seedlings treated with 0 and 1 nM dexamethasone (DEX).
Magnification of the expression data shown in Figure 3 for plants treated with 0 and 1 nM DEX. The data are shown as means $\pm$ SD ($n = 3$).