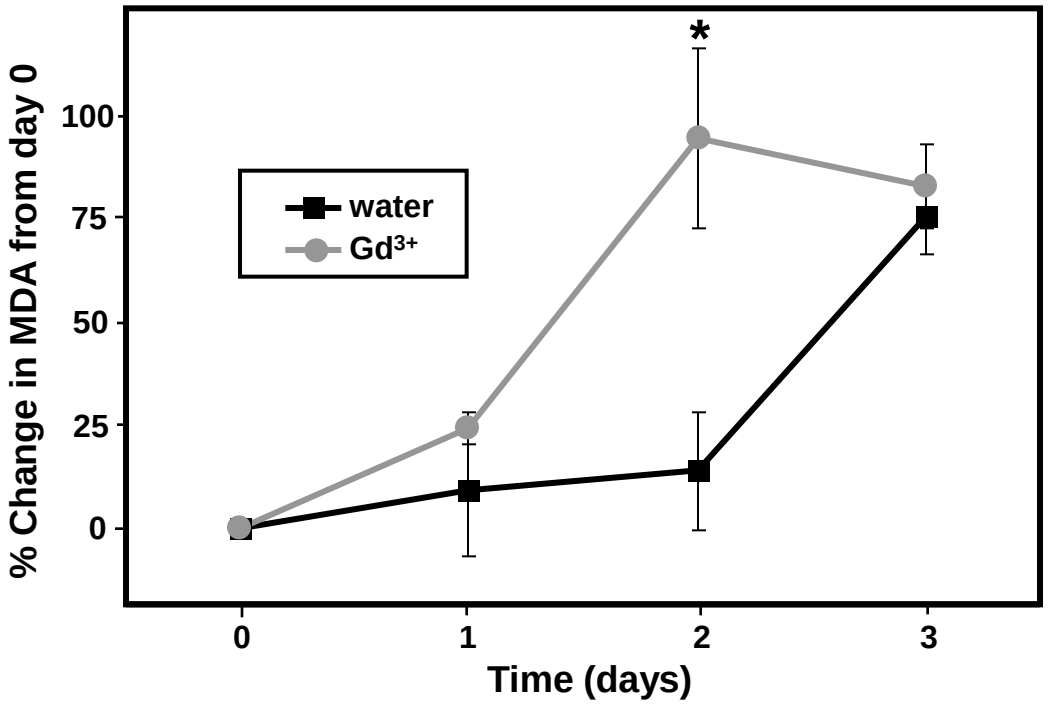
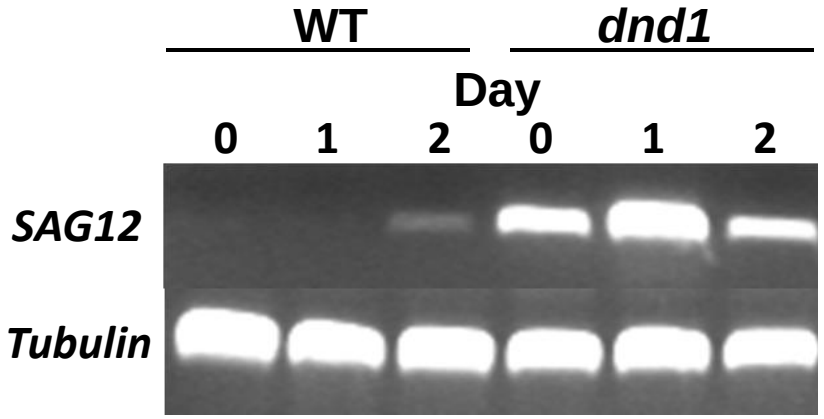
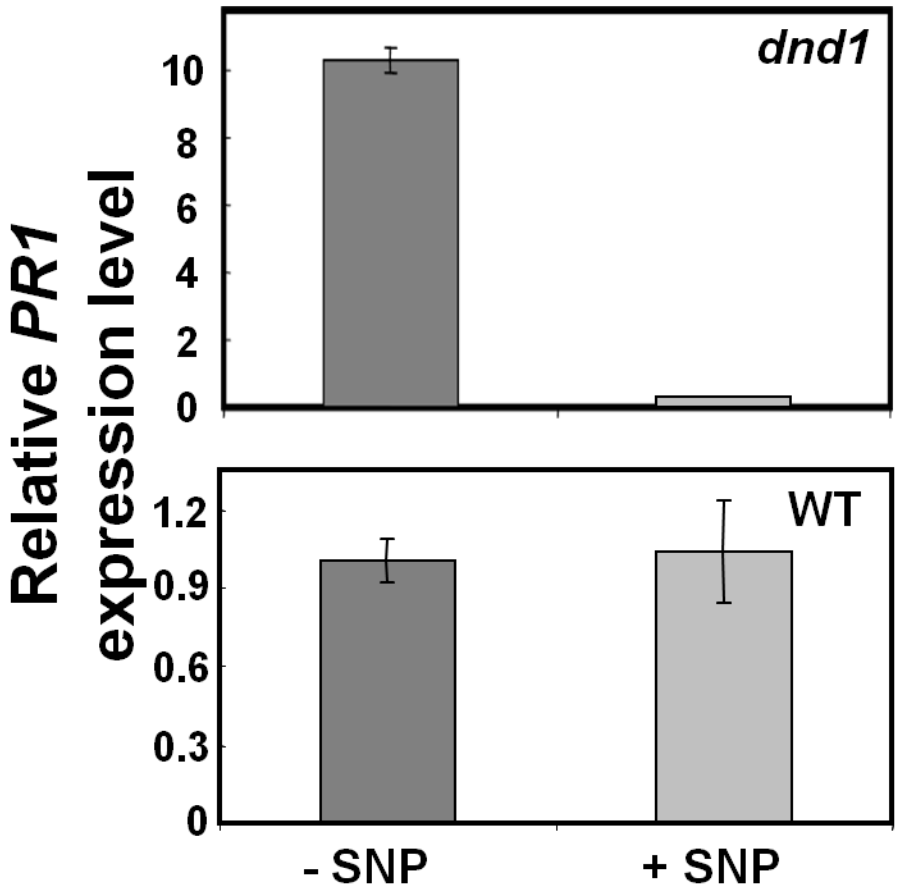


Supplemental Figure 1. MDA levels in leaves detached from wild-type plants and floated in the dark on water or 100 µM Gd^{3+} for 0-3 d. Leaves 3-5 of seedlings were used for this assay. Results are presented as mean percentage change (from day 0) for each genotype (n = 3) ± SE. ANOVA analysis was used to evaluate means separation between WT and *dnd1* at each time point. Significant differences (at $p < 0.05$) are indicated by a '*' above symbols.



Supplemental Figure 2. *SAG12* transcript accumulation in wild-type (WT) and *dnd1* detached leaves (kept in the dark on water for 0-2 d) was analyzed by semi-quantitative RT-PCR. *tubulin* is shown as a loading control. Leaf 5 of seedlings was used for this assay.



Supplemental Figure 3. Quantitative real-time PCR analysis of *PR1* transcript accumulation (relative to *tubulin* transcript) in leaves of *dnd1* and wild-type (WT) plants treated with 0 or 50 µM SNP as described in Figure 5D.