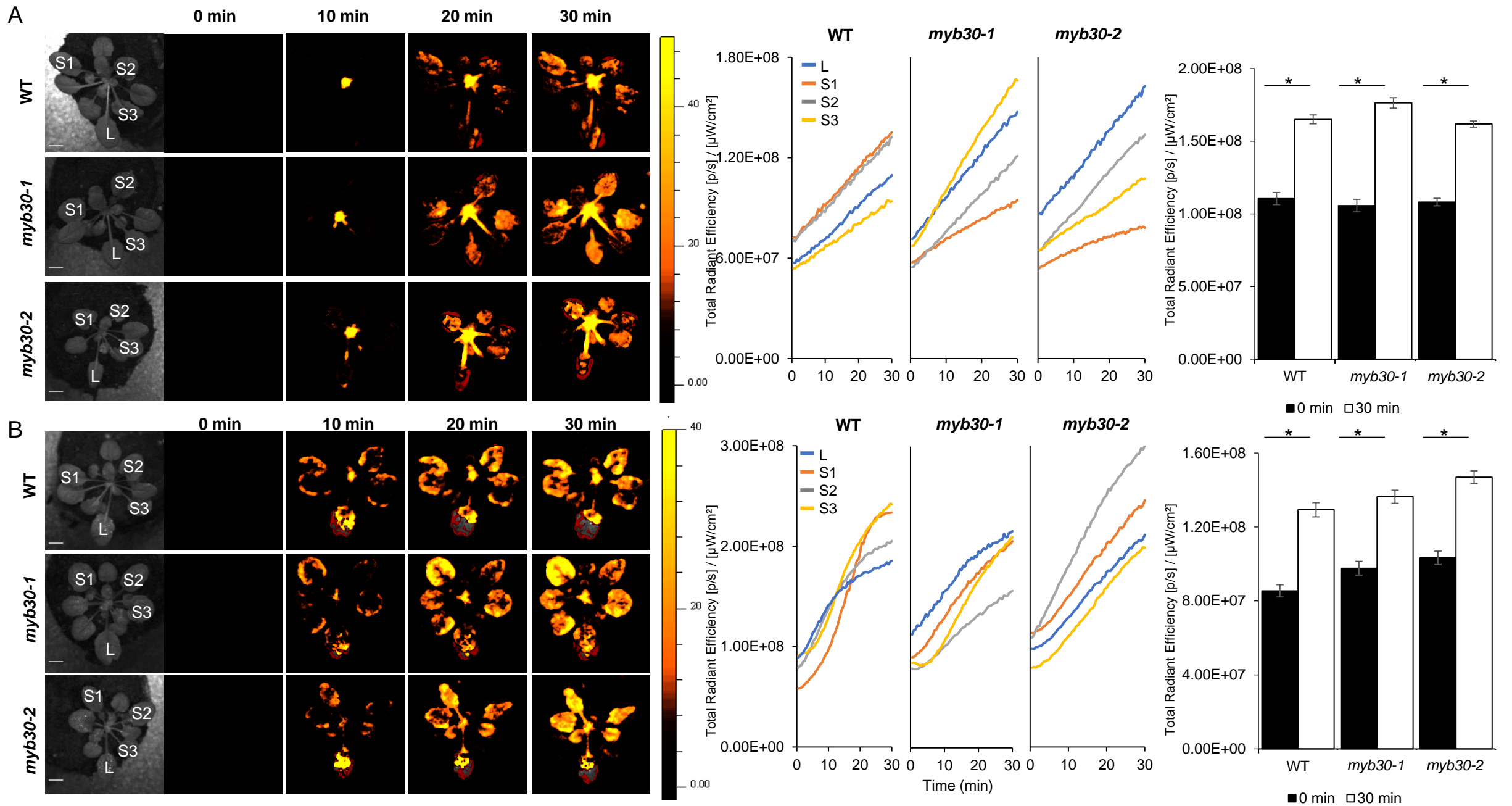
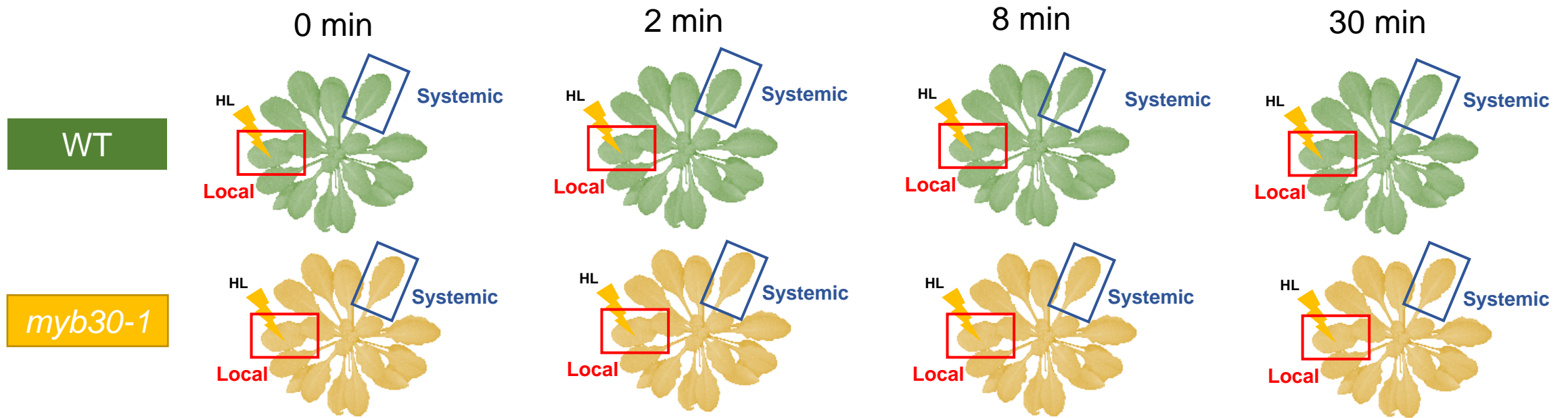


Supplementary Figure S1. Dye penetration controls for wild type and the two *myb30* mutants. Representative images (**A**) and statistical analysis of signal intensity (**B**) of plants fumigated with DCFDA for 30 min, and then fumigated for 10 min with 0.3% H₂O₂. Images were acquired with IVIS Lumina S5 and analyzed with Living Image software. Experiments were repeated 3 times. Student t-test, SE, N=10. *Abbreviation:* n.s., non – significant; WT, wild type.



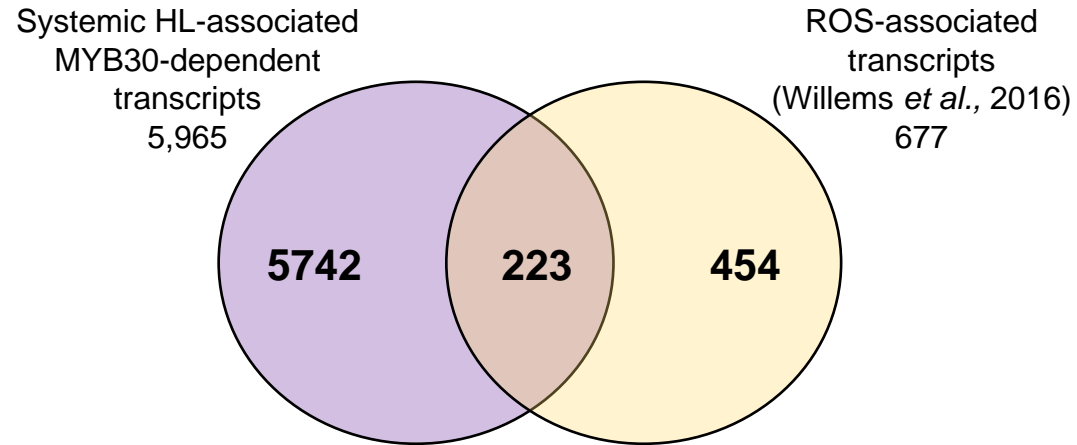
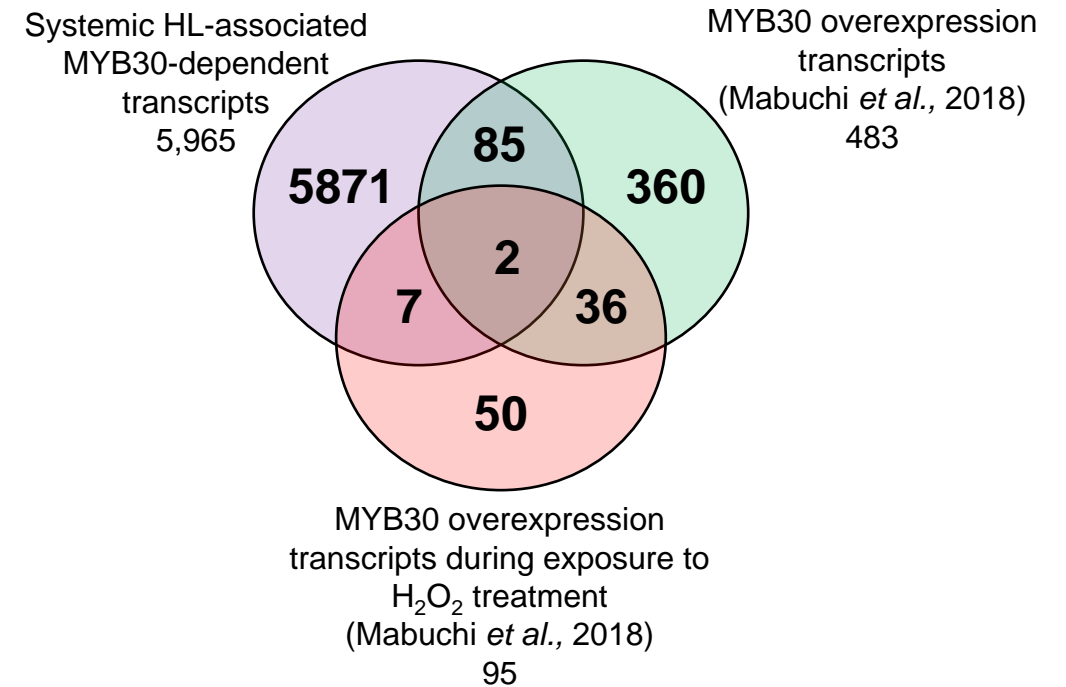
Supplemental Figure S2. Null mutants of MYB30 accumulate ROS in similar manner to wild type in response to a local application of heat stress or wounding. **A**, Time-lapse imaging of whole-plant ROS accumulation in wild type and *myb30* (two independent alleles) *Arabidopsis thaliana* plants in response to a 2 min local (L) heat stress treatment (applied to leaf L only), is shown on the left; continuous measurements of ROS levels in representative local (L) and systemic (S) leaves over the entire course of the experiment is shown in the middle; and statistical analysis of ROS accumulation in all local and systemic leaves imaged at 0 and 30 min is shown on the right. **B**, Same as **A**, but for wounding. Student t-test, SE, N=12, *P < 0.05. Scale bar indicates 1 cm. Wounding and heat stresses were applied as described in Zandalinas et al., 2020 (heat) and Fichman et al., 2019 (wounding). Abbreviations: WT, wild type.



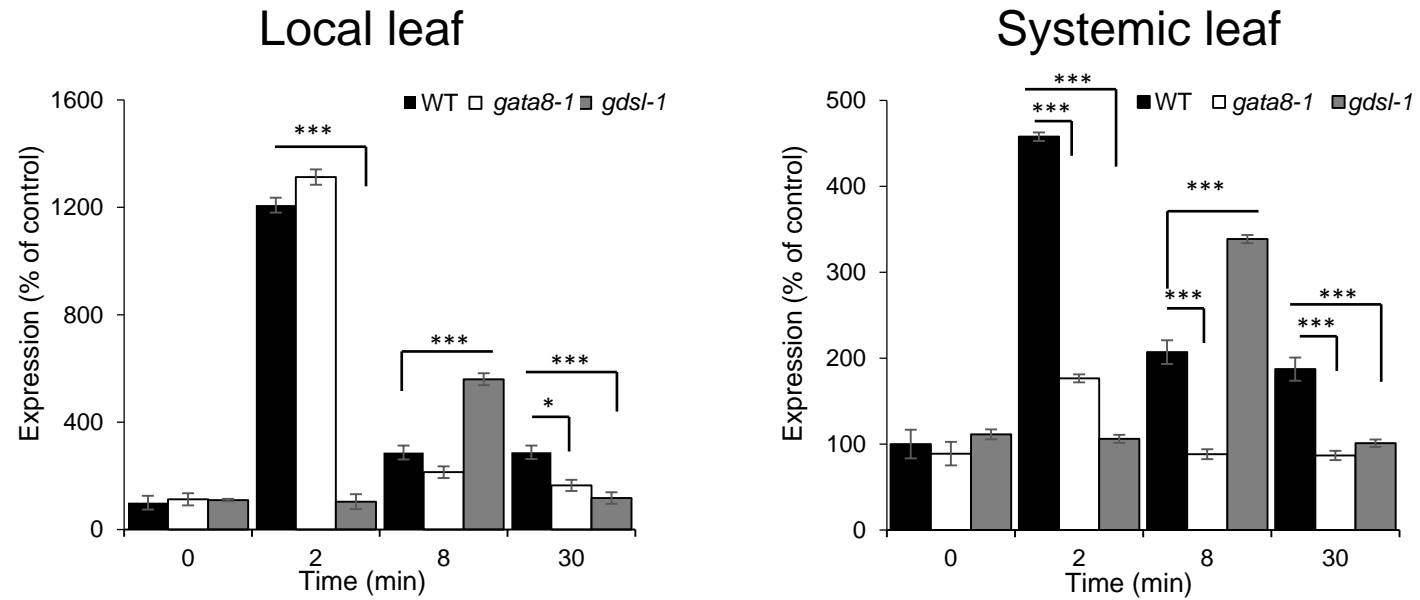
Supplemental Figure S3. The experimental design used for comparing the local and systemic responses of wild type and the *myb30-1* mutant to a local application of HL stress. Local leaves of WT and *myb30-1* plants were exposed to HL stress ($1700 \mu\text{mole photons s}^{-1} \text{m}^{-2}$) for 2, 8 or 30 min, and local and systemic leaves were collected for RNA extraction and transcription profiling. Leaves sampled from 20 different plants per each time point were pooled for each biological repeat of each treatment and 3 biological repeats were used for the analysis.

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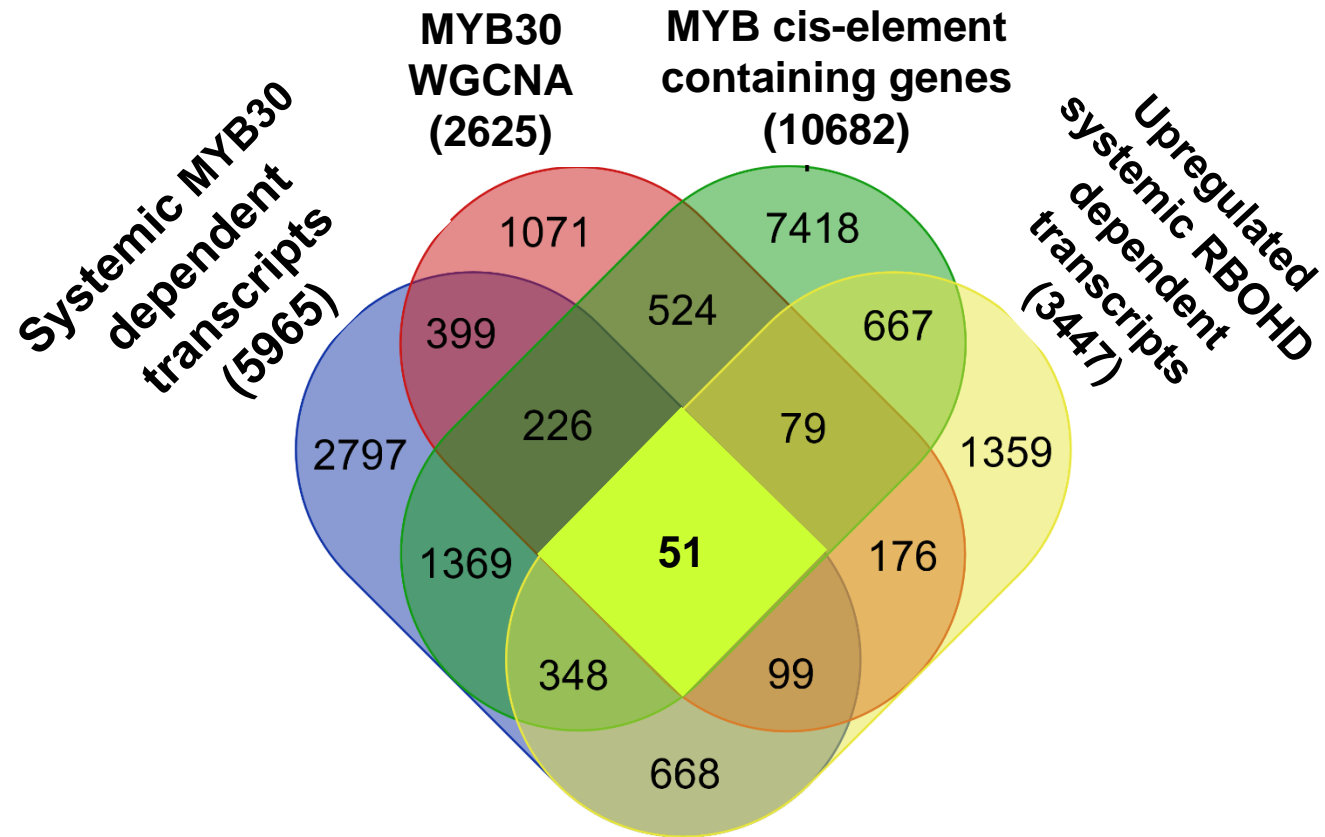
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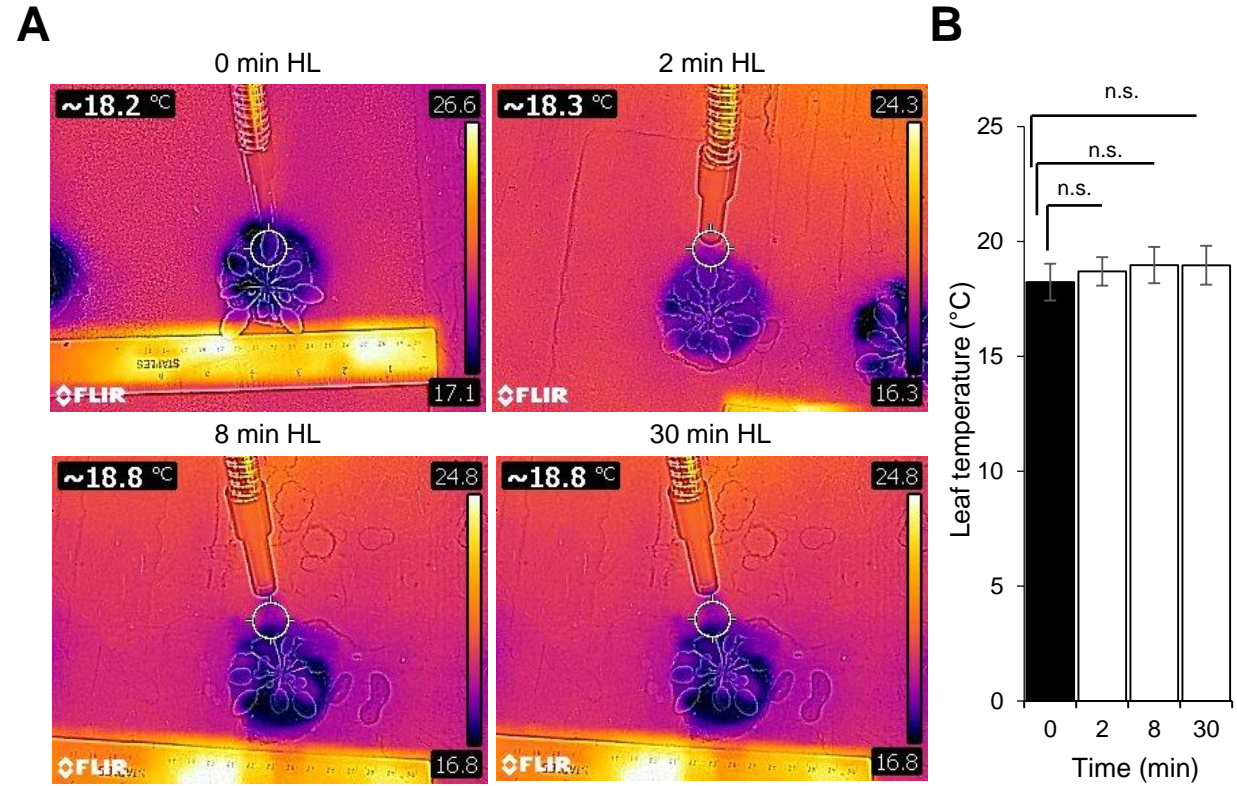
Supplemental Figure S5. Overlap between MYB30-dependent systemic HL-response transcripts and ROS-associated genes (Willems et al., 2016), or transcripts upregulated in MYB30 overexpressing plants in the presence or absence of ROS (Mabuchi et al., 2018). A, Overlap with ROS-associated genes (Willems et al., 2016). B, Overlap with MYB30 overexpressing plants in the presence or absence of ROS (Mabuchi et al., 2018). |



Supplemental Figure S6. Expression of *MYB30* in *gata8-1* and *gds1-1* mutants in response to a 2, 8, and 30 min treatment of HL stress. Quantitative real time PCR expression analysis of *MYB30* in local and systemic leaves of the *gata8-1* and *gds1-1* mutants in response to a local treatment of HL stress. Two-tail student t-test, SE, N=15, *P < 0.05, ***P < 0.0001 . *Abbreviations used:* HL, high light; WT, wild type.



Supplemental Figure S7. Venn diagram showing the overlap between HL-response systemic MYB30-dependent transcripts, MYB30 WGCNA-associated transcripts, transcripts encoded by genes containing MYB30 cis-elements at their promoters, and upregulated systemic RBOHD-dependent transcripts.



Supplemental Figure S8. Thermal camera images and measurements of leaf temperature in HL-treated plants. A, Representative FLIR thermal camera images of a plant showing the temperature before and following 2, 8 or 30 min of HL with stress applied with a ColdVision fiber optic LED light source (Schott, Southbridge, MA, USA). B, Statistical analysis of leaf temperature before and following 2, 8 or 30 min of HL. Two-tail student t-test, SE, N=8. *Abbreviation used:* HL, high light; n.s, non - significant. See also Zandalinas et al., 2020 for more details.