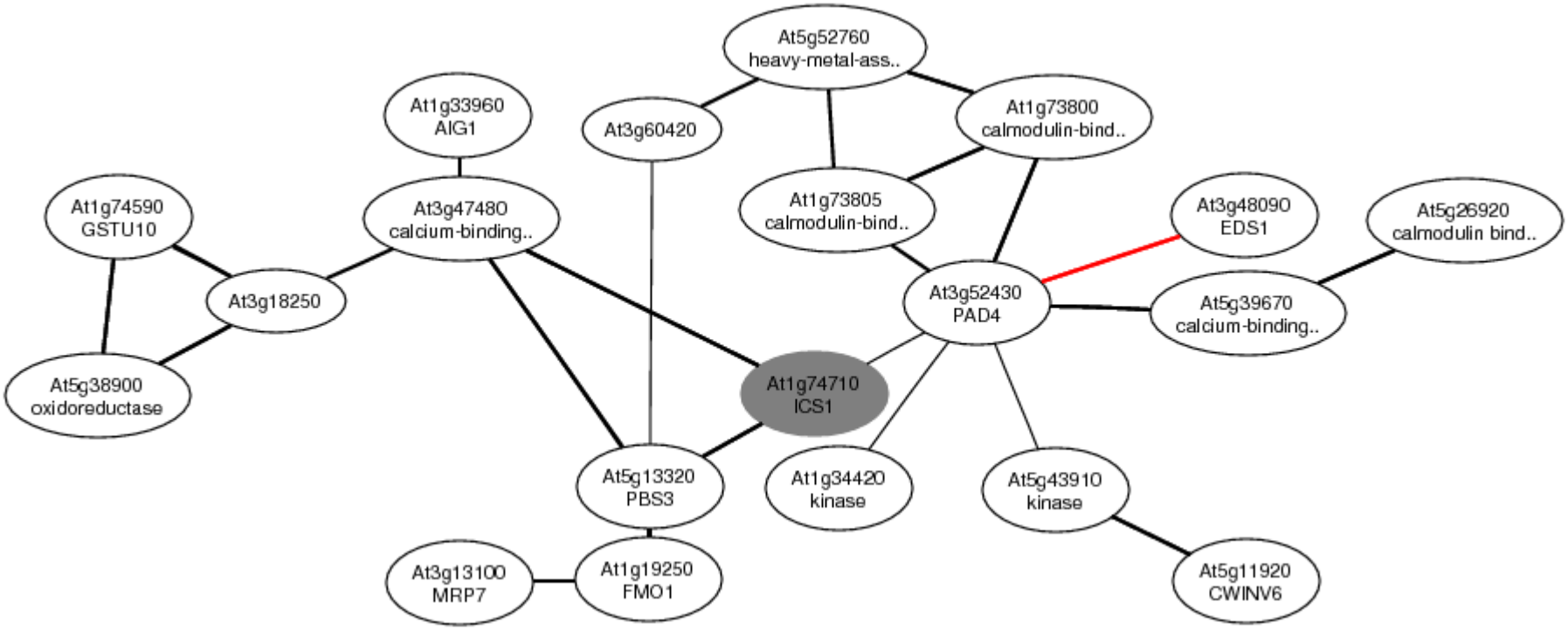
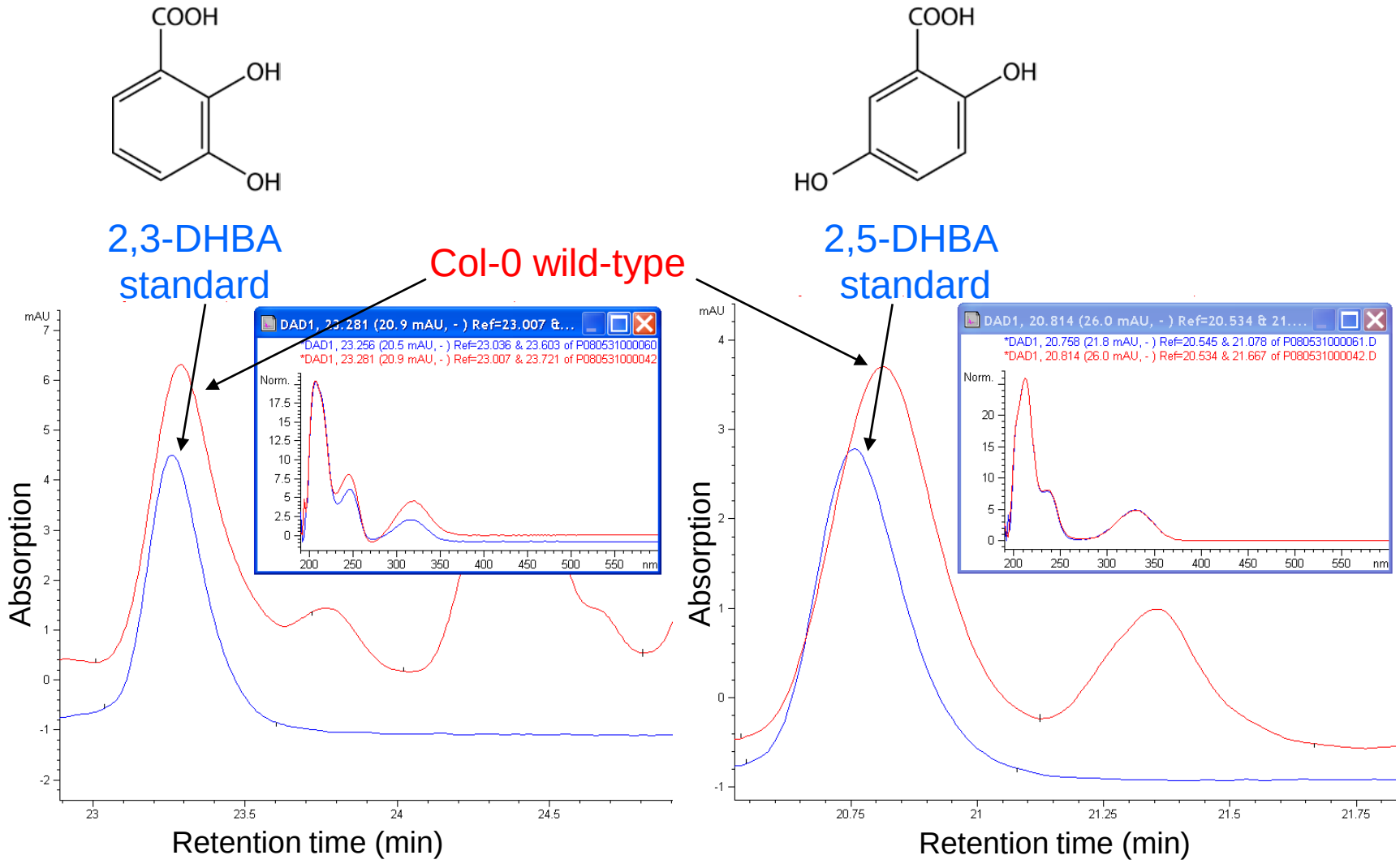


Supplemental Figure S1. Co-expressed gene network around the SA synthesis gene Isochorismate synthase (ICS, At1g74710).

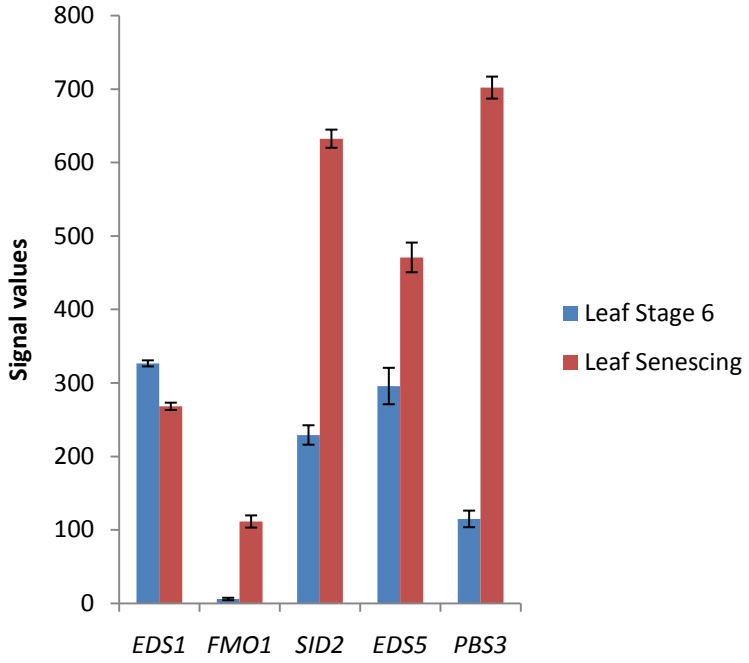
Co-expression analysis performed with the ATTED-II trans-factor and cis-element prediction database (Obayashi et al. 2007) revealed that *ICS1* expression is correlated with the expression of the defence regulator *PAD4, EDS1* and *FMO1.* Co-expressed gene networks in ATTED-II are drawn based on rank of correlation. The averaged rank is represented in the line thickness: 1 ~ 5 bold lines; 5 ~ 30 normal lines, 30 ~ 50 weak lines. Red line indicates protein-protein interaction.



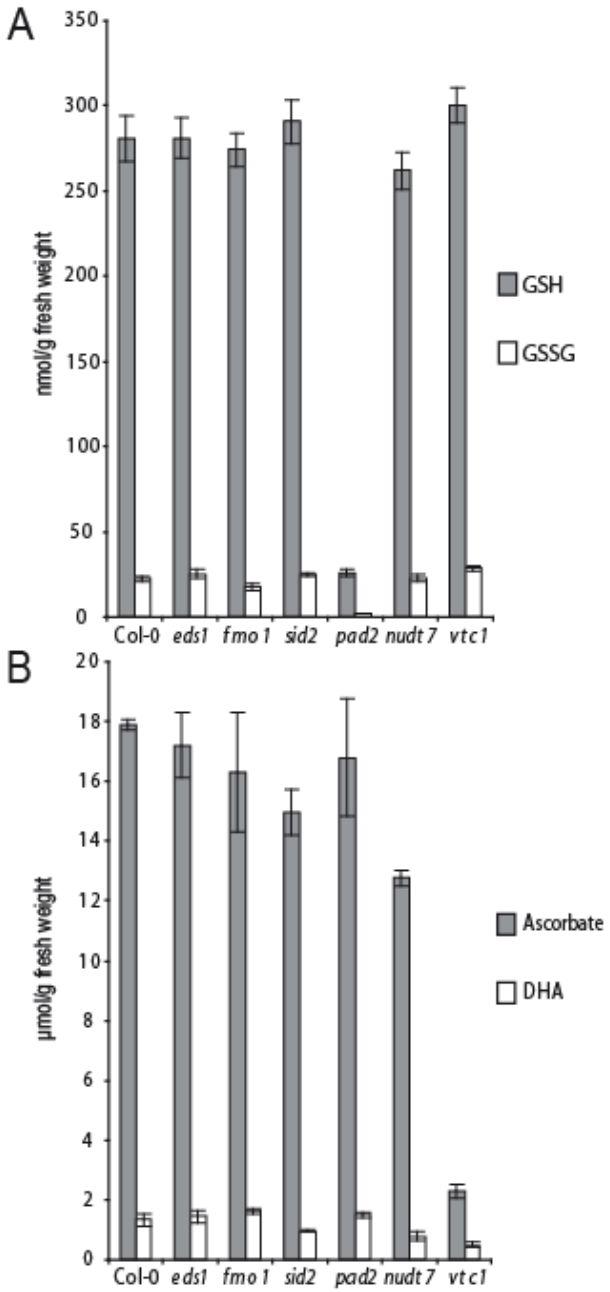
Supplemental Figure S2. HPLC chromatograms and UV-absorption spectra from Arabidopsis leaf extracts and standard compounds 2,3- and 2,5-dihydroxybenzoic acid (DHBA).
By comparing retention times and UV-absorption spectra of the unknown compound from leaf extracts (after β-glucosidase hydrolysis, red line) with DHBA standards (blue line) the peaks from the leaf extracts were identified as 2,3- and 2,5-DHBA. Absorption chromatograms were generated at 254 nm for 2,3-DHBA and at 320 nm for 2,5-DHBA.

^{1}H NMR (500 MHz, MeOH-d_4): δ 7.83 (1H, dd, *J* = 8.1, 8.1 Hz, H-5), 7.57 (1H, dd, *J* = 8.1, 1.6 Hz, H-6), 7.30 (1H, dd, *J* = 8.1, 1.6 Hz, H-4), 4.88 (1H, d, *J* = 7.3 Hz, H-1'), 3.92 (1H, dd, *J* = 11.5, 5.3 Hz, H-5'$_{eq}$), 3.58 (1H, ddd, *J* = 9.9, 8.5, 5.3 Hz, H-4'), 3.51 (1H, dd, *J* = 9.0, 7.3 Hz, H-2'), 3.43 (1H, dd, *J* = 9.0, 8.5 Hz, H-3'), 3.32 (1H, dd, *J* = 11.5, 9.9 Hz, H-5'$_{ax}$).
^{13}C NMR (125 MHz, MeOH-d_4): δ 173.0 (COOH), 153.2 (C-2), 146.2 (C-3), 124.7 (C-6), 123.3 (C-4), 119.0 (C-5), 114.2 (C-6), 103.2 (C-1'), 76.8 (C-3'), 74.2 (C-2'), 76.8 (C-3'), 70.5 (C-4'), 66.4 (C-5').

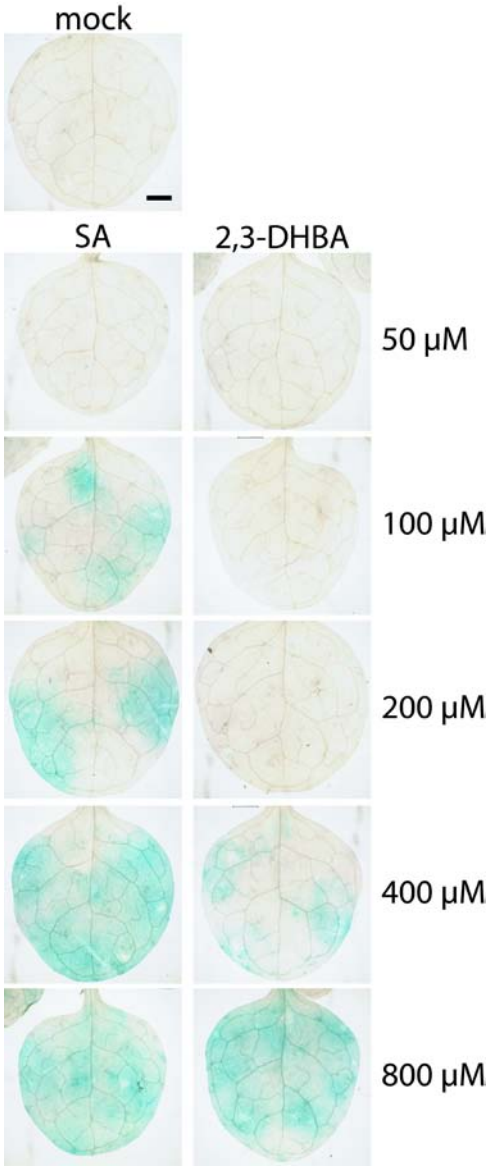
Supplemental Figure S3. Structural elucidation of 2,3-DHBA 3-*O*-β-D-xyloside (2,3-DHB3X) by NMR analyses.



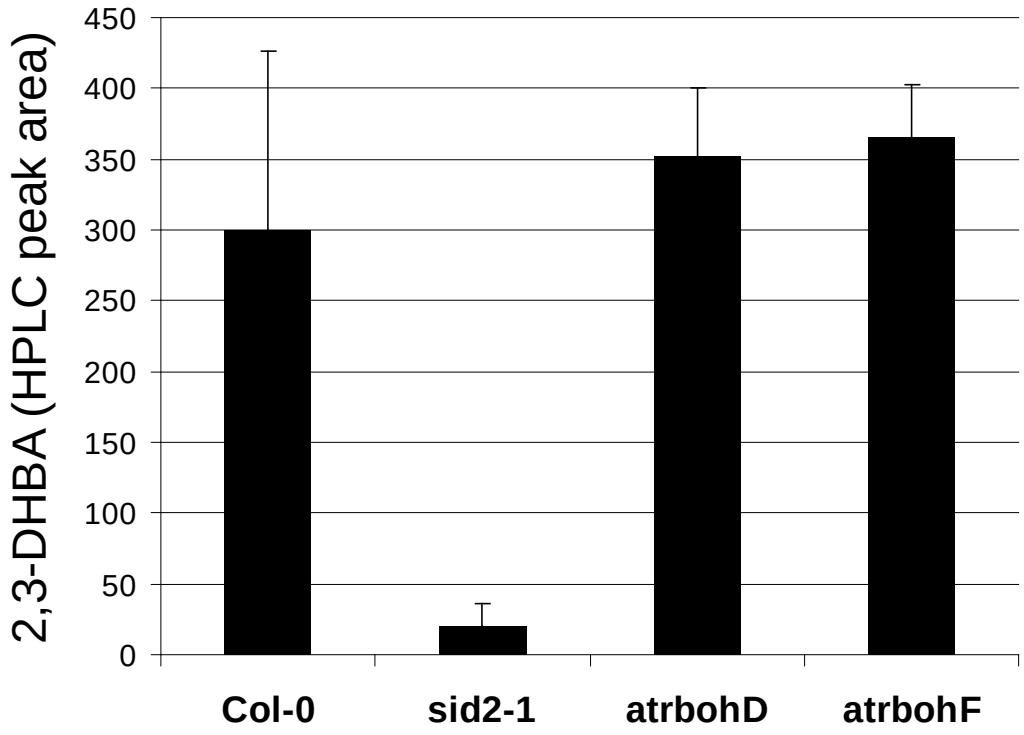
Supplemental Figure S4. EDS1 and co-regulated genes expression in non-senescing (Leaf stage 6) and senescing leaves.
Raw signal expression values are taken from supplemental data of Wagstaff et al. 2008. Bars represent standard errors.



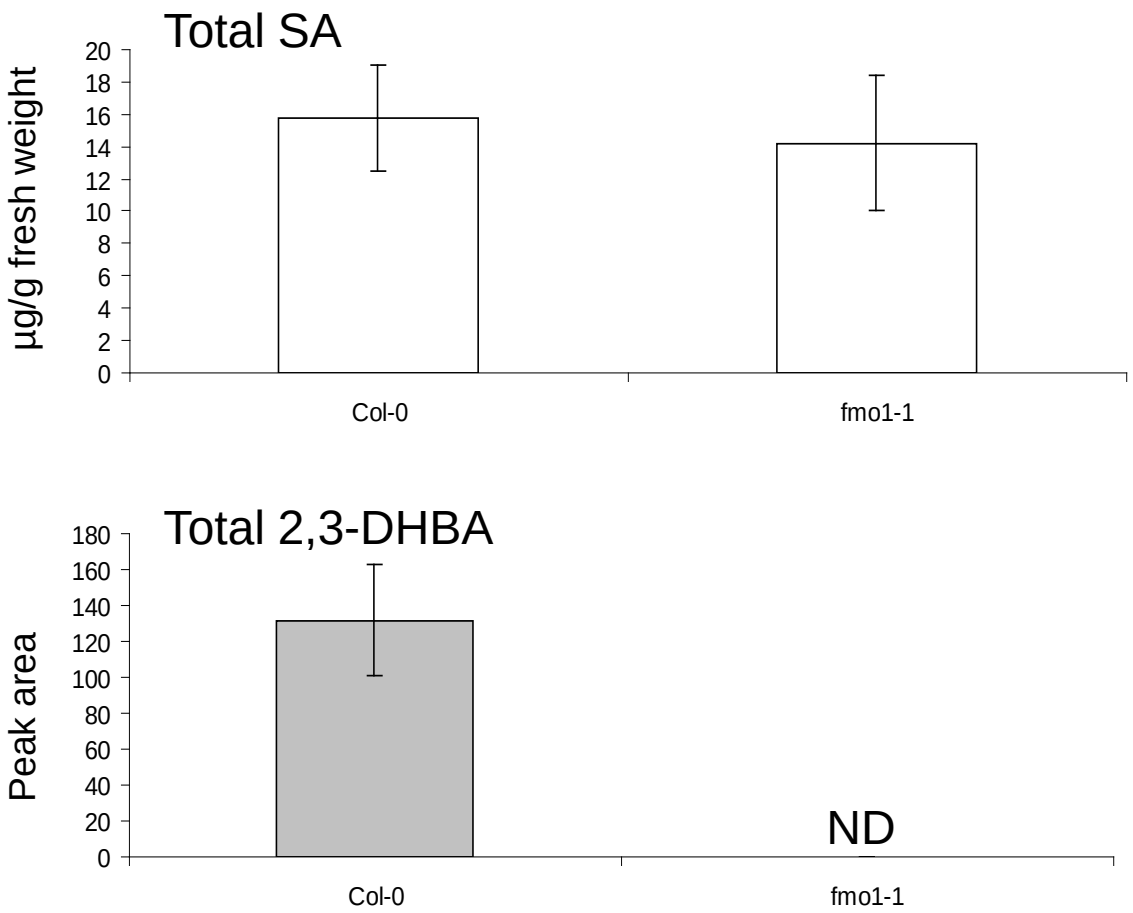
Supplemental Figure S5. Redox active compounds in *Arabidopsis* mutant aerial tissues.
Reduced and oxidized forms of (*A*) glutathione and (*B*) ascorbate were determined in triplicate samples derived from 8-week-old plants.



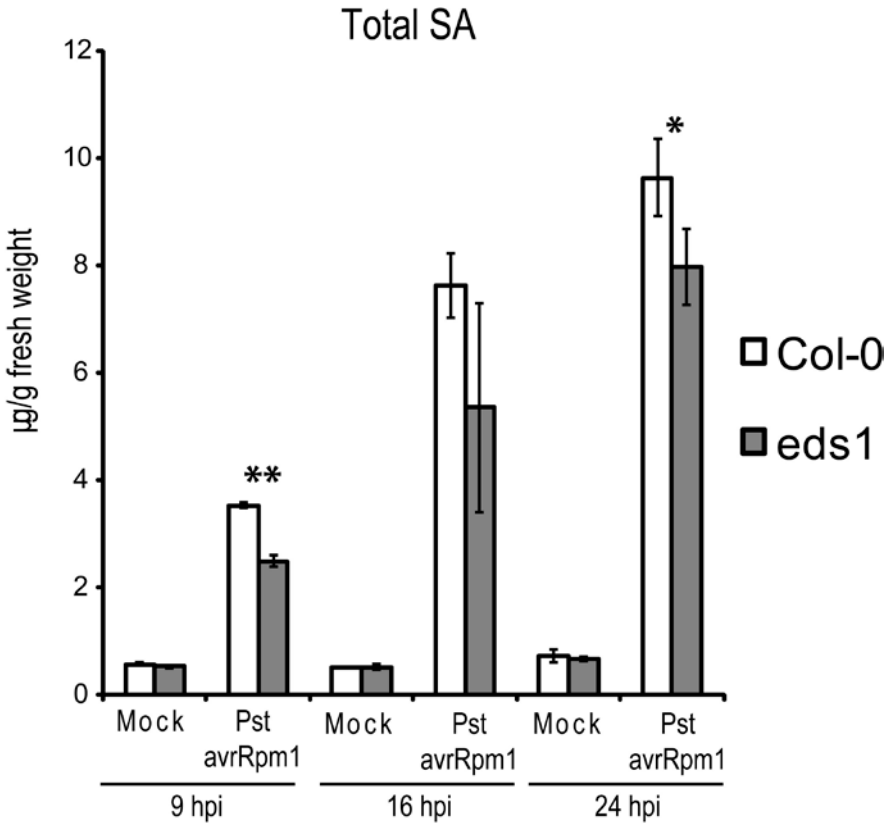
Supplemental Figure S6. Exogenously applied 2,3-DHBA is a poor inducer of *PR1* expression compared to SA.
3-week-old plants of the transgenic line Col-0:PR1/GUS were sprayed with salicylic acid (SA) or 2,3-dihydroxybenzoic acid (2,3-DHBA) at the indicated concentrations in 10 mM MgCl2 with 0.005% Silwet L-77 or with MgCl2/ 0.005% Silwet L-77 alone (mock). Leaves were harvested 24 h after treatment and stained for ß-glucuronidase (GUS) activity. The experiment was performed twice with similar results. Representative pictures are shown. Bar= 500 µm.



Supplemental Figure S7. Absolute levels of 2,3-DHBA are not altered in *atrbohD* or *atrbohF* mutants that are defective in pathogen induced hydrogen peroxide generation.



Supplemental Figure S8. 2,3-DHBA but not SA is absent in *fmo1-1* 24 hpi with Pst DC3000 avrRpm1 as determined by HPLC. ND = not detectable.



Supplemental Figure S9. Total SA accumulation in wild-type and *eds1* at early timepoints after infiltration with *Pst* DC3000/*avrRpm1* or mock treatment (10 mM $MgCl_2$). SA levels were significantly different in Col-0 compared to *eds1* at * *P* <0,05 and ** *P*<0.01 .