**Table S1: ROS-responsive SAA gene list.** ROS-responsive gene sets obtained from Gadjev et al. (2006) and compared with SAA-specific genes from Rossel et al. (2007)

| Accession number | Description |
|---|---|
| **Shared O. responsive genes** | |
| AT2G17840 | Upregulated by high light, drought, cold and salt stress. |
| | |
| **Shared H$_2$O$_2$ responsive genes** | |
| AT5G54300 | Unknown |
| AT2G30500 | Kinase interacting family protein |
| AT1G70140 | Encodes a group I formin. Involved in the initiation and tip growth of root hairs through regulation of the actin cytoskeleton. |
| | |
| **Shared $^1$O$_2$ responsive genes of known function** | |
| At1g16370 | putative transport protein |
| At4g34410 | AP2 domain transcription factor |
| At4g27654 | Expressed protein |
| At5g47240 | mutT domain protein-like |
| At1g61610 | receptor-like kinase, putative |
| At4g08170 | inositol 1,3,4-trisphosphate 5/6-kinase-like protein |
| At5g63450 | cytochrome P450-like protein |
| At2g44840 | ethylene response element binding protein |
| At5g22630 | chorismate mutase/prephenate dehydratase-like protein |
| At1g49450 | En/Spm-like transposon protein, putative |
| At4g10390 | putative protein kinase CLV1 receptor kinase |
| At3g59350 | protein kinase-like protein Pto kinase interactor 1 |
| At5g67210 | putative protein |
| At5g56980 | putative protein |
| At1g18710 | MYB transcription factor |
| At2g35710 | putative glycogenin |
| At1g73080 | receptor protein kinase, putative |
| At4g35480 | RING-H2 finger protein RHA3b |
| At3g15990 | putative sulfate transporter |
| At1g09940 | putative glutamyl-tRNA reductase 2 |
| At2g01150 | RING-H2 finger protein RHA2b |
| At2g37900 | putative peptide/amino acid transporter |
| At1g07500 | hypothetical protein |
| At2g30360 | putative protein kinase |
| At1g74430 | AtMYB95 |

**Table S1: ROS-specific SAA gene list (continued)**

| Accession number | Description |
| --- | --- |
| Shared $^1O_2$ responsive genes of known function (cont.) | |
| At2g39420 | putative phospholipase |
| At5g24590 | NAC2-like protein |
| At1g74930 | AP2 domain transcription factor, putative |
| At5g65280 | G protein-coupled receptor-like protein |
| At5g66210 | calcium-dependent protein kinase |
| At1g74100 | putative flavonol sulfotransferase |
| At2g20880 | AP2 domain transcription factor |
| At3g10300 | unknown protein |
| At3g44260 | CCR4-associated factor 1-like protein |
| At5g26030 | ferrochelatase-I |
| At2g47180 | putative galactinol synthase |
| At3g46930 | protein kinase 6-like protein |
| At3g53780 | membrane protein |
| At1g74450 | unknown protein |
| At5g60300 | receptor like protein kinase |
| At2g20340 | putative tyrosine decarboxylase |
| At5g60890 | MYB transcription factor (ATR1) |
| At2g29450 | glutathione S-transferase |
| At2g47060 | putative protein kinase |
| At5g64310 | arabinogalactan-protein |
| At1g63830 | unknown protein |
| At1g67060 | hypothetical protein |
| At4g27940 | mitochondrial carrier protein |
| At5g17490 | RGL3 transcription factor |
| At1g76380 | hypothetical protein |
| At3g56260 | putative protein |
| At3g56880 | putative protein |
| At3g05640 | putative protein phosphatase-2C |
| At1g75230 | 3-methyladenine DNA glycosylase, putative |
| At1g50640 | ethylene responsive element binding factor 3 (AtERF3) |
| At5g64260 | phi-1-like protein |
| At3g05580 | putative serine threonine protein phosphatase |
| At5g09440 | putative protein phi-1 |

# Table S1: ROS-specific SAA gene list (continued)

| Accession number | Description |
|---|---|
| Shared $^1O_2$ responsive genes of known function (cont.) | |
| At1g27770 | envelope Ca2+-ATPase |
| At1g78080 | AP2 domain transcription factor RAP2.4 |
| At2g43020 | putative amine oxidase |
| At5g55120 | putative protein |
| At1g28380 | unknown protein |
| At3g17860 | unknown protein |
| At1g11960 | unknown protein |
| At1g28050 | CONSTANS family zinc finger protein |
| At1g01260 | bHLH transcription factor |
| At3g26980 | geranylgeranylated protein, putative |
| At1g70480 | unknown protein |
| At1g08930 | zinc finger protein ATZF1 |
| At1g52720 | hypothetical protein |
| Shared general stress response genes | |
| AT1G27730 | SALT TOLERANCE ZINC FINGER, TF |
| AT1G80840 | pathogen induced TF |
| AT4G17230 | Encodes a scarecrow-like protein (SCL13).Member of GRAS gene family. |
| AT4G27410 | Encodes a NAC transcription factor induced in response to dessication. |
| AT4G17500 | Encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family |
| AT1G52890 | encodes a NAC transcription factor whose expression is induced by drought, high salt, and abscisic acid. |
| AT5G47220 | Encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. |
| AT5G59820 | zinc finger protein involved in high lightand cold acclimation, TF |
| AT1G43160 | encodes a member of the ERF (ethylene response factor) subfamily B-4 of ERF/AP2 transcription factor family (RAP2.6). |
| AT5G04340 | putative C2H2 zinc finger TF |
| AT2G38470 | TF, involved in response to various abiotic stresses - especially salt stress. |
| AT2G40140 | Salt-inducible zinc-finger protein |
| AT1G77450 | NAC domain containing protein 32 |
| AT1G19020 | unknown, response to oxidative stress |

**A**



**B**
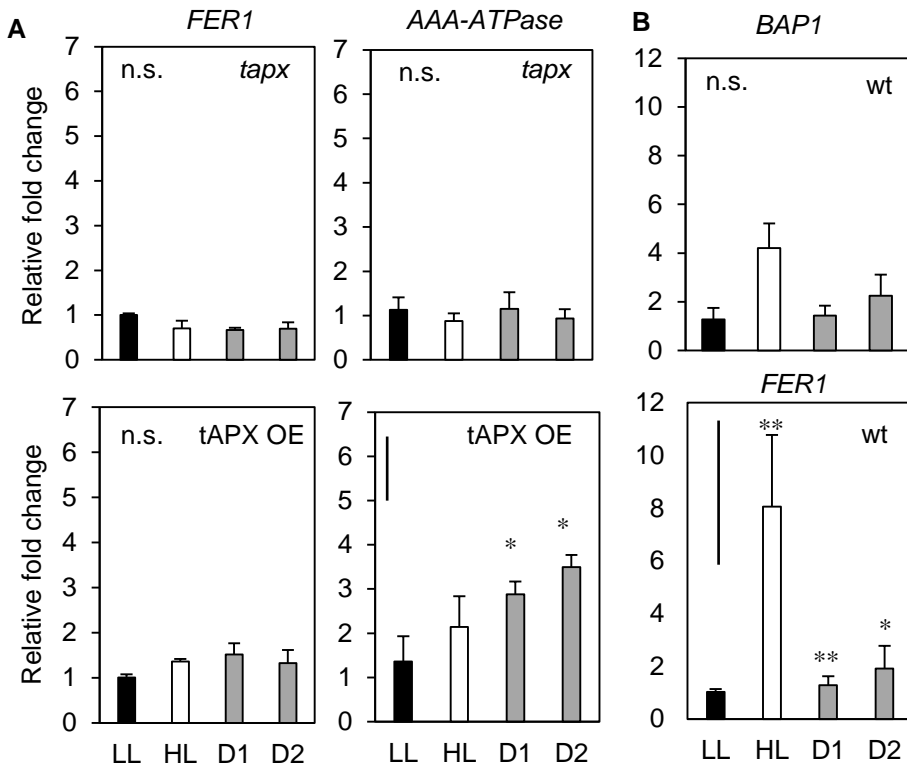
**C**

Level of expression (signal intensity on Affymetrix Arabidopsis ATH1 Genome Array)

| LOW | MEDIUM (=IQR) | HIGH |
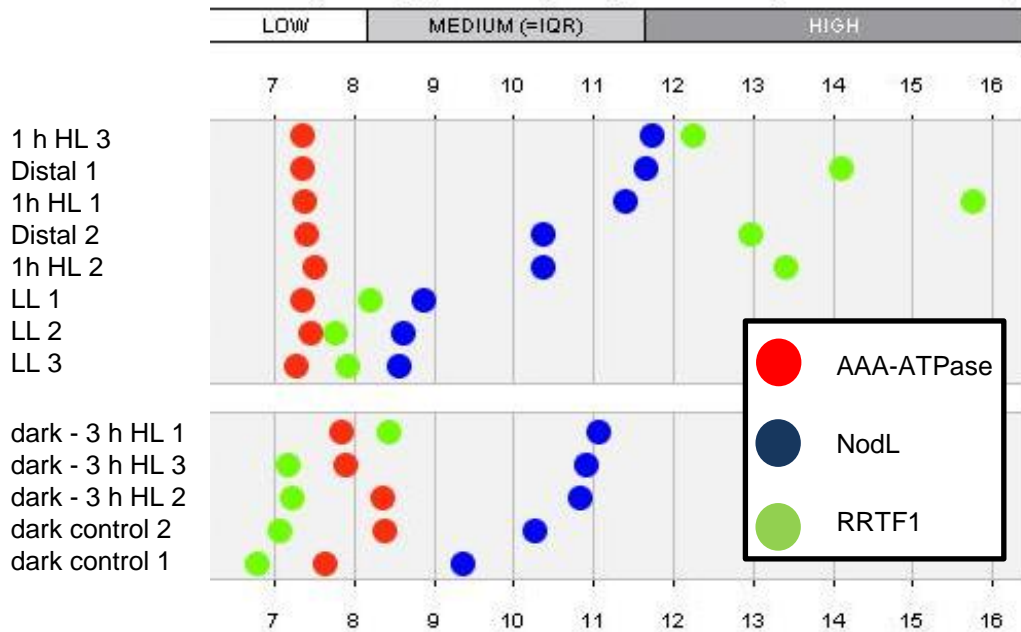
created with GENEVESTIGAT(

**Figure S1: Commonly used ROS marker genes, *FER1* and *AAA-ATPase* are not induced by LED HL in stable silenced and overexpressing tAPX lines.** (A) Transcriptional analysis of *FER1* (H2O2 marker), and *AAA-ATPase* (commonly used to demonstrate RB but not MV induction) in *tapx 2/1* and the tAPX -14/2 overexpression lines. (B) *FER1* and *BAP1 (*$^1O_2$ marker*)* are shown for wt tissue, as well as (C) Geninvestigator data demonstrating the differences between *AAA-ATPase, NodL (*$^1O_2$ responsive SAA marker), and RRTF1 (SAA marker) from the Rossel et al., (2007) microarray (AT-00345) and a Shao et al., (2013) microarray (AT-00691) of seedlings grown on plates under different growth conditions. The latter tissue was from seedlings grown under continuous (100 μmol photons $m^{-2} s^{-1}$) light on plates, transferred at 12 days to the dark for 3 days, and treated with 3 h HL (1000 μmol photons $m^{-2} s^{-1}$) . LL, low low; HL, high light; D1, lower distal leaf position 5; D2, upper distal leaf position 7. One-way ANOVAs were performed on each *ZAT10* data set, *post hoc* Fisher's LSD results are displayed as a bar in the top left corner of each plot. t-test were performed on *ELIP2* data sets. *p < 0.05, ** p<0.005n.s, not significant. Error bars represent standard error, N = 3.
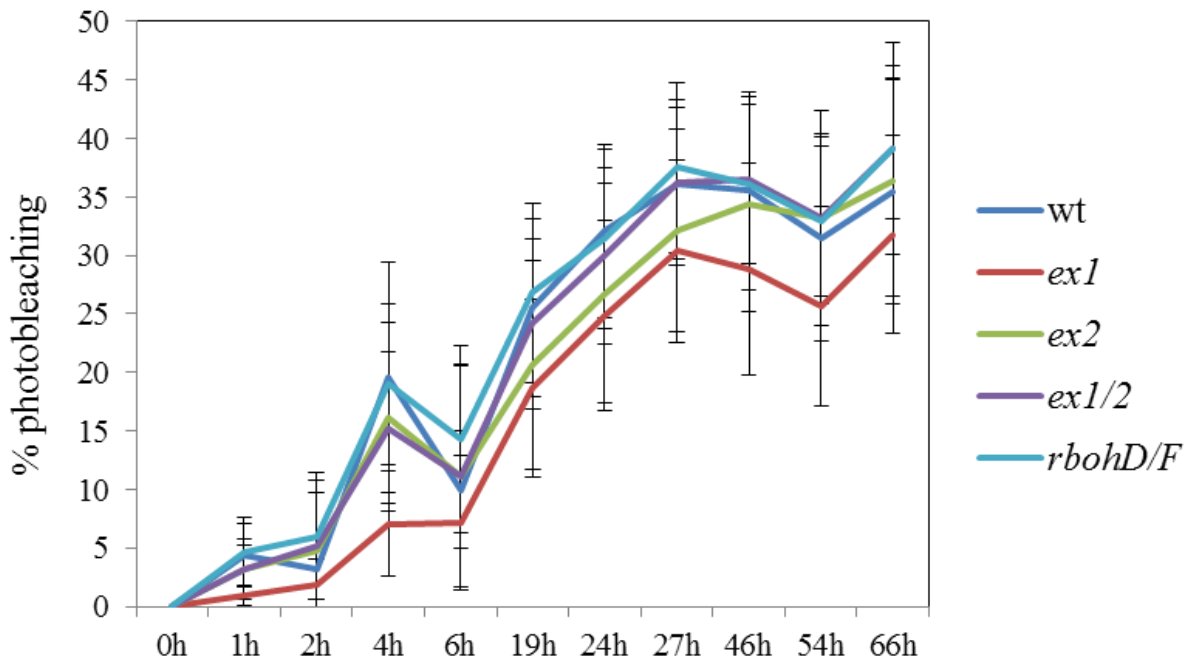
**Figure S2**: **Comparison of photobleaching development between ROS signaling mutants**. (A) Bleaching percentages were obtained through the Scanalyser and were normalised to 0% at time 0. Dark blue, *wt;* red, *ex1;* green, *ex2;,* purple, *ex1/ex2;* light blue, *rbohD/F*. Error bars represent standard deviation, n = 15. (B) representatative images of photobleaching on a plant undergoing continuous HL and detection by the Scanalyzer software.
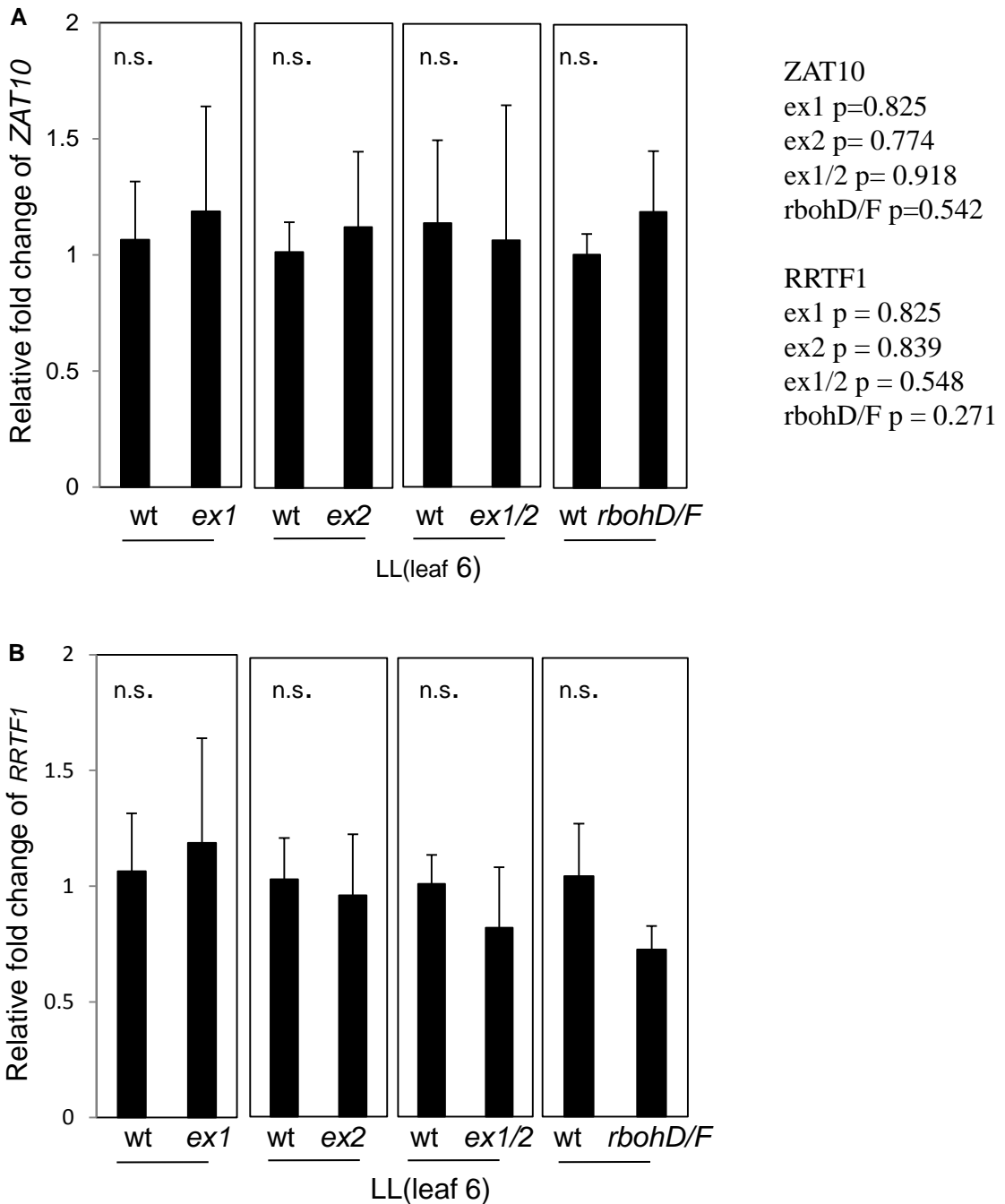
**A**

Relative fold change of *ZAT10*

n.s.   n.s.   n.s.   n.s.

wt *ex1*   wt *ex2*   wt *ex1/2*   wt *rbohD/F*

LL(leaf 6)

ZAT10
ex1 p=0.825
ex2 p= 0.774
ex1/2 p= 0.918
rbohD/F p=0.542

RRTF1
ex1 p = 0.825
ex2 p = 0.839
ex1/2 p = 0.548
rbohD/F p = 0.271

**B**

Relative fold change of *RRTF1*

n.s.   n.s.   n.s.   n.s.

wt *ex1*   wt *ex2*   wt *ex1/2*   wt *rbohD/F*

LL(leaf 6)

**Figure S3**: **Basal *ZAT10* and *RRTF1* induction in LL tissue of wt and ROS signaling mutants.** (A) *ZAT10* induction comparing wt-Col with *ex1*, *ex2*, *ex1/2*, and *rbohD/F* LL tissue, (B) *RRTF1* for the same comparisons. One-way ANOVAs were performed on each data set, *post hoc* Fisher's LSD statistics are displayed as n.s . (not significant) in the top left corner of each plot. Error bars represent standard error; N = 3.
.

**Table S2 A: Statistical tests for differences within ZAT10 ROS-signaling mutant data sets.**
Statistical results of one-way ANOVAs and post hoc Fischer LSD and Holm-Sidak tests within mutant datasets. N = 3.

| Data set | one-way ANOVA | Fischer LSD | Holm-Sidak |
|----------|---------------|-------------|------------|
| ex1 | p = 0.0021 | 0.924 | HL vs LL (0.004), D1(0.019), D2 (0.031) |
| ex1/2 | p = 0.043 | 0.638 | HL vs D2 (0.006) |
| ex2 | p = 0.005 | 1.071 | D1 vs LL (0.002), D2 (0.015) |
| rbohD/F | p = 0.004 | 2.104 | HL vs LL (0.001), D2(0.003), D1 (0.017) |

**Table S2 B: Statistical tests for differences within RRTF1 ROS-signaling mutant data sets**.
Statistical results of one-way ANOVAs and post hoc Fischer LSD and Holm-Sidak tests within mutant data sets. N = 3.

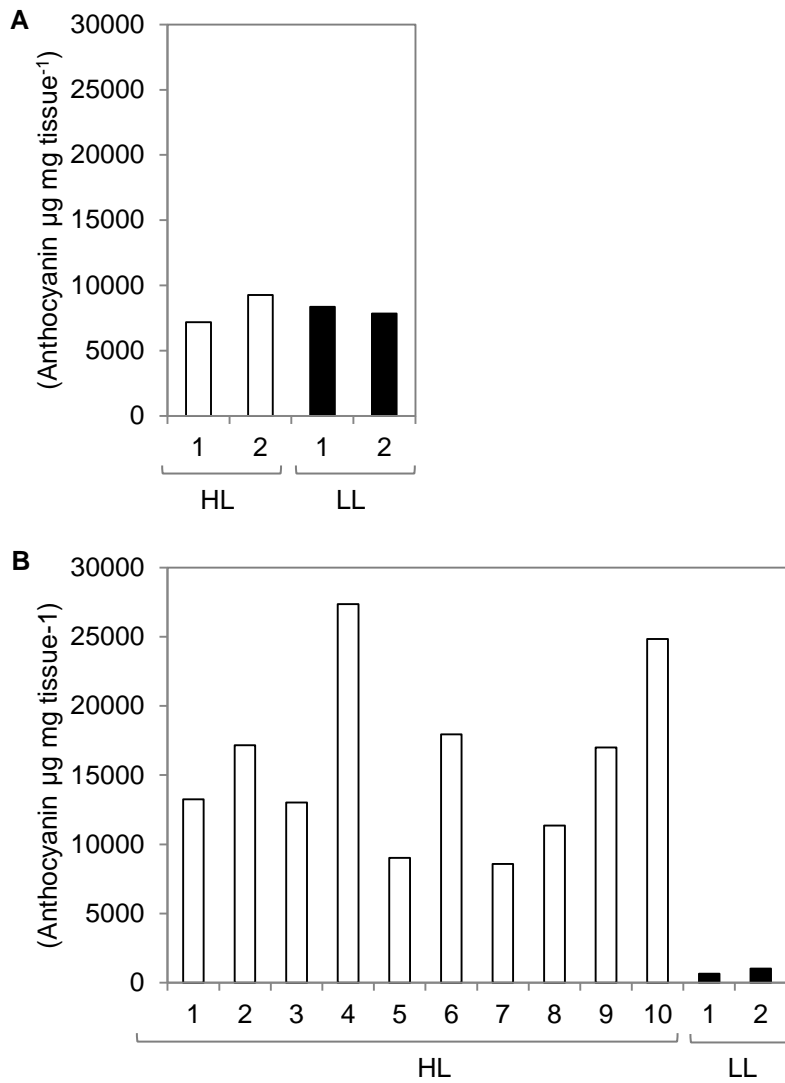| Data set | one-way ANOVA | Fischer LSD | Holm-Sidak |
|----------|---------------|-------------|------------|
| ex1 | p = 0.076 | n.s. | - |
| ex1/2 | p = 0.397 | n.s. | - |
| ex2 | p = 0.001 | | D1 vs LL, HL vs LL |
| rbohD/F | p < 0.001 | 9.659 | HL vs LL (<0.001), D2(<0.001), D1 (<0.001) |

**Figure S4: Anthocyanin Test Assays**. (A) anthocyanin accumulation in tissues exposed to 1 h 1000 μmol photons $m^{-2} s^{-1}$ HL; (B) anthocyanin accumulation after 3 days of HL-treatment. White bars represent HL-treated tissue; black bars represent LL controls.

| Time (h) | Plant | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2.5 | 2 | 2 | 0 | T | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | | |
| 20 | 2 | 2 | 1 | T | 2 | 1 | 3 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| 2.5 | 4 | 0 | 0 | T | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | | |
| 20 | 4 | 0 | 0 | T | 3 | 2 | 2 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | | |
| 2.5 | 5 | 0 | 0 | T | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| 20 | 5 | 0 | 0 | T | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| 2.5 | 3 | 0 | 0 | 1 | T | 1 | 0 | 3 | 1 | 0 | 1 | 0 | 1 | 0 | | | |
| 20 | 3 | 0 | 0 | 1 | T | 1 | 0 | 2 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | | |
| 2.5 | 1 | 2 | 1 | 3 | 1 | 0 | T | 0 | 2 | 3 | 0 | 1 | 0 | 0 | 2 | ? | ? |
| 20 | 1 | 2 | 1 | 3 | 2 | 0 | T | 0 | 2 | 3 | 0 | 2 | 1 | 1 | 1 | 1 | 1 |
| 2.5 | 7 | 0 | 2 | 1 | 0 | 1 | T | 1 | 2 | 3 | 2 | 3 | 1 | 0 | 2 | 1 | 0 |
| 2.5 | 8 | 1 | 0 | 3 | 0 | 1 | T | 2 | 3 | 3 | 0 | 3 | 1 | 0 | 2 | 1 | 1 |
| 2.5 | 11 | 1 | 0 | 3 | 0 | 3 | T | 1 | 2 | 3 | 0 | 3 | 1 | 1 | 1 | 1 | 0 |
| 2.5 | 9 | 0 | 0 | 1 | 1 | 0 | 3 | 2 | 2 | T | 0 | 2 | 2 | 1 | 3? | 1? | 1? |
| 2.5 | 10 | 0 | 0 | 1 | 0 | 0 | 3 | 3 | 0 | T | 0 | 2 | 3 | 0 | 0 | 0 | 0 |

**Figure S5: Rhodamine B infiltrations**. 2.5 and 20 h after infiltration of Rhodamine B fed through petioles of leaf insertion 6. In general, the dye infiltrates tissues in an orthostichous pattern.

**Table S3: Statistical analysis results for connected and unconnected leaf data sets.**
Statistical results of one-way ANOVAs and post hoc Fischer LSD and Holm-Sidak tests within experimental data sets.

| Data set | one-way ANOVA | Fischer LSD | Holm-Sidak |
|---|---|---|---|
| ZAT10 vasc. 5 min | $p < 0.001$ | 1.795 | HL vs all tissue ($< 0.001$) |
| ZAT10 vasc. 1 h | $p < 0.001$ | 2.128 | HL vs all tissue ($<0.001$), D1 vs O1 (0.033), O2 (0.022) |
| RRTF1 vasc. 5 min | $p < 0.001$ | 2.155 | HL vs LL ($<0.001$), D1(0.004), D2 ($<0.001$), O2 ($<0.001$) O1 vs O2 ($<0.001$), D2(0.001), LL (0.002),D1 (0.011) |
| RRTF1 vasc. 30 min | n.s. 0.461 | - - - | |
| RRTF1 vasc. 1 h | $p = 0.006$ | 14.433 | HL vs LL ($p< 0.001$), D1(0.004), O2 (0.003) O1 vs LL ($p< 0.011$) D2 vs LL (0.032) |
| NodL vasc. 5 min | n.s. $p = 0.718$ | - - - | |
| NodL vasc. 30 min | $p < 0.001$ | 6.325 | HL vs all tissue ($p < 0.001$) |
| NodL vasc. 1 h | $p < 0.001$ | 10.805 | HL vs all tissue ($p < 0.001$) O2 vs LL (0.005), D1(0.013), D2 (0.012), O1 vs LL (0.013), D2(0.037), D1 (0.041) |
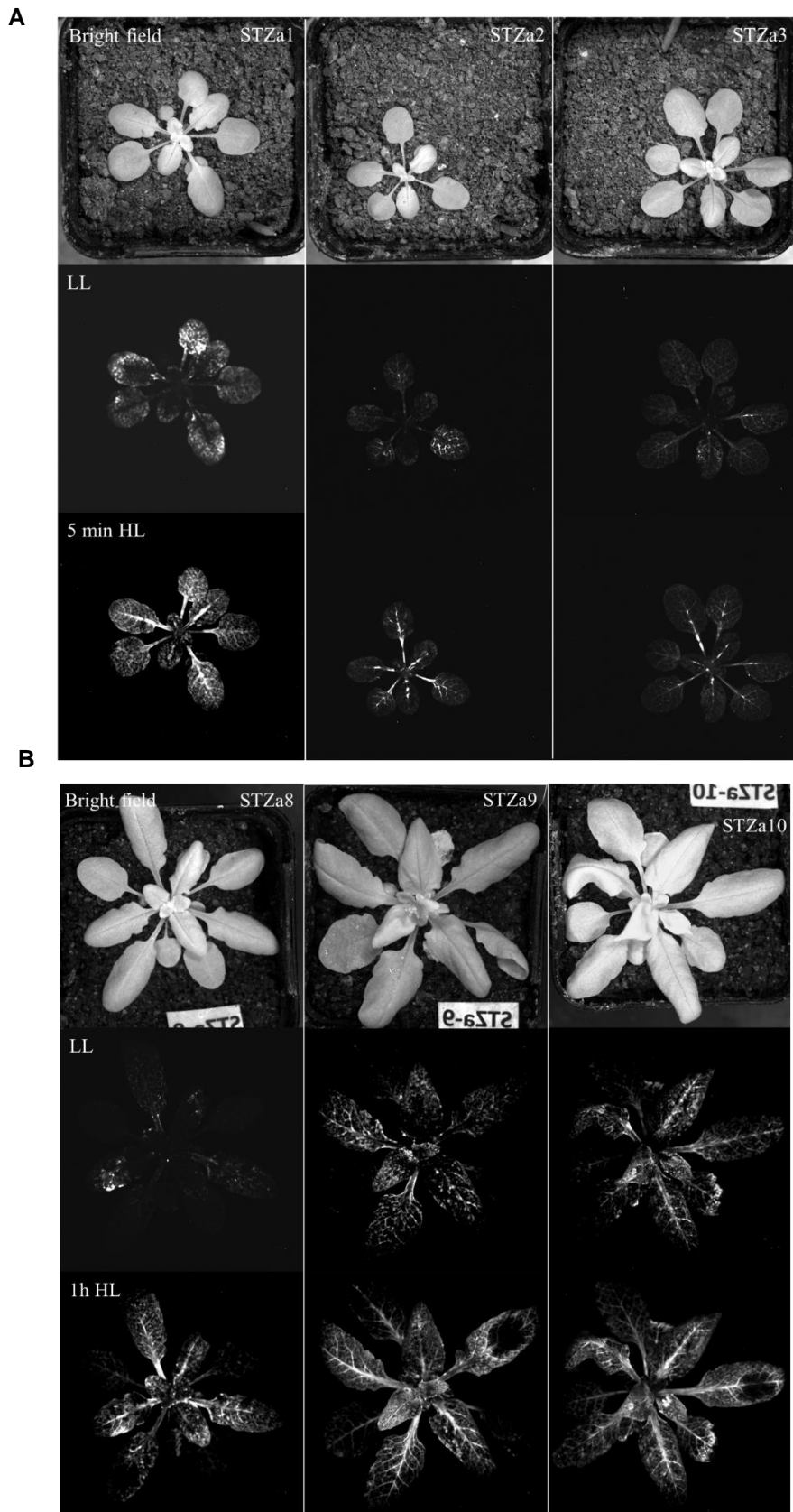
**Figure S6: 5 min and 1h timepoints from the HL spot treatment of ZAT10::LUC HL-specific transgenics.** CCD camera images of three biologicals, including the bright field image, under LL, and after either (A) 5 min or (B) 1h HL spot treatment of leaf position 6.

**Table S4: Shared β-cyclocitral and SAA genes.** Shared genes from the **β** -cyclocitral (Ramel et al., 2012) and SAA (Rossel et al., 2007) microarrays.

| Accession number | Gene name | Compartment |
|---|---|---|
| AT1G17420 | LOX3 | chloroplast |
| AT4G36010 | | anchored to membrane, extracellular region |
| AT3G25780 | AOC3 | chloroplast, plasma membrane, vacuolar membrane |
| AT5G05600 | | cytoplasm |
| AT1G80840 | WRKY40 | nucleus |
| AT4G17230 | SCL13 | nucleus |
| AT4G27410 | RD26, ANAC072 | nucleus |
| AT2G06050 | OPR3 | peroxisome |
| AT5G10695 | | extracellular region, mitochondrion |
| AT4G17500 | ERF1 | nuclear pore, nucleus |
| AT3G51450 | | chloroplast, endomembrane system |
| AT5G47220 | ERF2 | nucleus |
| AT1G32920 | | endomembrane system |
| AT1G28480 | GRX480, ROXY19 | cytoplasm |
| AT5G27520 | PNC2 | mitochondrial inner membrane, mitochondrion, peroxisome |
| AT3G55980 | SZF1 | nucleus |
| AT3G29575 | AFP3 | nucleus |
| AT5G09440 | EXL4 | chloroplast, membrane, plasmodesma |
| AT3G15210 | ERF4 | nuclear body, nucleus |
| AT1G19300 | PARVUS/GLZ1 | endoplasmic reticulum |
| AT2G42540 | COR15A | chloroplast, chloroplast envelope,chloroplast stroma |
| AT5G59820 | ZAT12 | intracellular, nucleus |
| AT2G29440 | GSTU6/GST24 | cytoplasm, cytosol |
| AT1G66090 | | chloroplast |
| AT3G56880 | | nucleus |
| AT1G73480 | | cytoplasm |
| AT4G18010 | 5PTASE2/IP5PII | cytoplasm |
| AT1G70700 | JAZ9 | nucleus |
| AT4G20860 | | cytoplasm |
| AT4G15210 | ATBETA-AMY, BAM5,BMY1 | chloroplast, cytoplasm |
| AT2G23810 | TET8 | golgi apparatus, plasma membrane,plasmodesma |
| AT1G29330 | ERD2 | golgi apparatus, ER |
| AT1G72450 | JAZ6 | nucleus |
| AT5G04340 | ZAT6 | nucleus |
| AT2G36590 | PROT3 | plasma membrane |
| AT1G05575 | | endoplasmic reticulum |
| AT1G09070 | (AT)SRC2 | ER, plasma membrane, vacuole |
| AT2G26530 | AR781 | chloroplast, plasma membrane |
| AT2G38470 | WRKY33 | nucleus |
| AT1G01720 | ATAF1 | nucleus |

**Table S4: Shared β -cyclocitral and SAA genes** (continued)

| Accession number | Gene name | Compartment |
|---|---|---|
| AT2G41100 | TCH3 | mitochondrion, plasmodesma, vacuolar membrane |
| AT5G13190 | GILP | plasma membrane |
| AT5G06870 | PGIP2 | cytosol |
| AT1G51090 | | nucleus |
| AT5G62570 | | |
| AT4G12720 | NUDT7 | cytoplasm, plasma membrane |
| AT5G14700 | | |
| AT4G34710 | ADC2 | nucleus |
| AT5G42050 | | nucleus |
| AT4G34150 | | cytosol, plasmodesma |
| AT1G14130 | | cytoplasm, nucleus |
| AT1G71100 | RSW10 | cytoplasm |
| AT2G46600 | | nucleus |
| AT5G35735 | | plasma membrane |
| AT2G40140 | CZF1, SZF2 | nucleus |
| AT5G26030 | FC1 | chloroplast, mitochondrion |
| AT2G33380 | RD20, CLO3 | chloroplast membrane, vacuole |
| AT2G23320 | WRK15 | nucleus |
| AT1G01140 | CIPK9, PKS6 | cytoplasm, plasma membrane |
| AT1G42990 | BZIP60 | ER, nucleus |
| AT1G73500 | MKK9 | mitchondrion |
| AT5G25930 | | plasma membrane |
| AT1G77450 | ANAC032 | nucleus |
| AT3G52800 | | nucleus |
| AT1G09970 | RLK7 | micropyle, plasma membrane |
| AT1G30620 | HSR8, MUR4, UXE1 | golgi apparatus |
| AT4G16760 | ACX1 | peroxisome, plasmodesma |
| AT2G01450 | MPK17 | nucleus |
| AT4G36990 | HSF4 | nucleus |
| AT3G23920 | BAM1, BMY7 | chloroplast, cytosol, nucleus |
| AT4G24160 | | unknown |
| AT2G29450 | GSTU5 | plasma membrane, plasmodesma |
| AT5G10380 | RING1 | plasma membrane |
| AT5G47060 | | nucleus |

**Table S5: qRT-PCR primers and used for Roche (with UPL probes) and SybrGreen for quantitative transcript analysis.**

| Target | Accession | Probe | Primer sequence (5' -3') |
|--------|-----------|-------|--------------------------|
| CYP5 | At2g29960 | UPL 103 | GGCAGTTCCTAAAACTGCAGAA |
| | | | TTCCCTTGTAGTGTAGAGGTTTCC |
| PP2A | At1g13320 | UPL 120 | GACCGGAGCCAACTAGGAC |
| | | | AAATGCGACAAAACTTGGTAACT |
| ZAT10 | At1g27730 | UPL 31 | GGACAAAGGGTAAGCGATCTAA |
| | | | AGAAGCATGAGGCAAAAAGC |
| RRTF1 | At4g34410 | UPL 68 | TCGGGTATGCATTATCCTAACA |
| | | | AAGCTCTTGCTCCGGTGA |
| NodL | At5g64870 | UPL144 | TCGTGTTCTTGTTGCTTCCA |
| | | | TGAACCTTGTCAAACACTTCCTT |
| ELIP2 | At4g14690 | UPL 101 | CCACCACAAATGCCACAG |
| | | | GCAAATCTCCAAACTTCGTACTC |
| FER1 | At5g01600 | UPL 21 | CTGAAAAAGGAGATGCTTTATATGC |
| | | | TGAGGCCACTTTGTGAACG |
| BAP1 | At3g61190 | UPL 152 | TAAACCGGAGACCCATCAAG |
| | | | TCGACATTCTCGTCGATTTT |