**Supplemental Table S1** Forward and reverse primer sequences used for gene expression analyses (RT-qPCR) of genes of interest. Ex jn: exon junction x2: primer concentration of 600 nM instead of 300 nM

| Genes of interest | | | | | |
|---|---|---|---|---|---|
| **Gene** | **Locus** | **Forward Primer (5′- 3′)** | **Reverse Primer (5′-3′)** | **Primer Location** | **Amplicon Size** |
| *GSH1* | AT4G23100 | CCCTGGTGAACTGCCTTCA | CATCAGCACCTCTCATCTCCA | Exon 10 and 11 | 101 bp |
| *GSH2* | AT5G27380 | GGACTCGTCGTTGGTGACAA | TCTGGGAATGCAGTTGGTAGC | Exon 1 and 2 | 101 bp |
| *GR1* | AT3G24170 | CTCAAGTGTGGAGCAACCAAAG | ATGCGTCTGGTCACACTGC | Exon 15 and 16 | 101 bp |
| *GGT1* | AT4G39640 | TAGATGTTCCACCACCAGCA | GGCAATAATGTTGGCTCCTC | Exon 4 and 5 | 140 bp |
| *ZAT6* | AT5G04340 | TGACCTGCCTTCTTCTTCGT | GTCCACCAAGAGCCTGGTAA | No introns | 113 bp |
| *RBOHC* | AT5G51060 | TCACCAGAGACTGGCACAATAAA | GATGCTCGACCTGAATGCTC | Exon 6 and 7 | 101 bp |
| *RBOHD* | AT5G47910 | AACTCTCCGCTGATTCCAACG | TGGTCAGCGAAGTCTTTAGATTCCT | Exon 1 and 2 | 91 bp |
| *RBOHF* | AT1G64060 | GGTGTCATGAACGAAGTTGCA | AATGAGAGCAGAACGAGCATCA | Exon 11 and 12 | 105 bp |
| *AT1G05340* | AT1G05340 | TCGGTAGCTCAGGGTAAAGTGG | CCAGGGCACAACAGCAACA | Exon 2 and 3 | 91 bp |
| *AT1G19020* | AT1G19020 | GAAAATGGGACAAGGGTTAGACAAA | CCCAACGAAAACCAATAGCAGA | No introns | 92 bp |
| *AT1G57630* | AT1G57630 | ACTCAAACAGGCGATCAAAGGA | CACCAATTCGTCAAGACAACACC | No introns | 91 bp |
| *AT2G21640* | AT2G21640 | GACTTGTTTCAAAAACACCATGGAC | CACTTCCTTAGCCTCAATTTGCTTC | Exon 1 and 2 | 91 bp |
| *AT2G43510* | AT2G43510 | ATGGCAAAGGCTATCGTTTCC | CGTTACCTTGCGCTTCTATCTCC | Exon 1 and 2 | 91 bp |
| *ZAT12* | AT5G59820 | GTGCGAGTCACAAGAAGCCTAACA | GCGACGACGTTTTCACCTTCTTCA | No introns | 72 bp |
| *RRTF1* | AT4G34410 | CGGAGCAAGAGCTTTCAGTT | GCGCTTATCACTGTGCTGTC | No introns | 109 bp |
| *ACS2* | AT1G01480 | CATGTTCTGCCTTGCGGATC | ACCTGTCCGCCACCTCAAGT | Exon 3 and 4 | 91 bp |

| | | | | | |
|---|---|---|---|---|---|
| *ACS6* [x2] | AT4G11280 | TTAGCTAATCCCGGCGATGG | ACAAGATTCACTCCGGTTCTCCA | Exon 3 and 4 | 92 bp |
| *ACO2* | AT1G62380 | TCTACGTTCGTCACCTCCCTCA | CTCTTACCAAAGTCTTTCATGGCC | Exon 2 and 3 | 91 bp |
| *ACO4* | AT1G05010 | CTCCGATGTCCCTGATCTCG | ATCCAGTAGCTCCTCCGACAACT | Exon 2 and 3 | 91 bp |
| *ERF1* [x2] | AT3G23240 | TCCTCGGCGATTCTCAATTTT | CAACCGGAGAACAACCATCCT | No introns | 91 bp |
| *OXI1* | AT3G25250 | TAGAGGATCGAACCGGAAAG | GACCCTTGATTTCCTCAACG | Exon 2 | 149 bp |
| *MPK3* | AT3G45640 | GACGTTTGACCCCAACAGAA | TGGCTTTTGACAGATTGGCTC | Exon 5 and 6 | 103 bp |
| *MPK6* | AT2G43790 | TAAGTTCCCGACAGTGCATCC | GATGGGCCAATGCGTCTAA | Exon 5 and 6 | 101 bp |
| *WRKY33* | AT2G38470 | TCATCGATTGTCAGCAGAGACG | CCATTCCCACCATTTGTTTCAT | Exon 3 and 4 | 92 bp |
| *APX1* | AT1G07890 | TGCCACAAGGATAGGTCTGG | CCTTCCTTCTCTCCGCTCAA | Exon 5 and 6 | 101 bp |
| *APX2* | AT3G09640 | TTGCTGTTGAGATCACTGGAGGA | TGAGGCAGACGACCTTCAGG | Exon 3 and 4 | 91 bp |
| *CAT1* | AT1G20630 | AAGTGCTTCATCGGGAAGGA | CTTCAACAAAACGCTTCACGA | Ex jn 5, 6 and exon 7 | 103 bp |
| *CAT2* | AT4G35090 | AACTCCTCCATGACCGTTGGA | TCCGTTCCCTGTCGAAATTG | Exon 2 and 3 | 76 bp |

**Supplmental Table S2** Forward and reverse primer sequences used for gene expression analyses (RT-qPCR) of selected reference genes. Ex jn: exon junction; UTR: untranslated region

| **Reference genes** | | | | | |
|---|---|---|---|---|---|
| **Gene** | **Locus** | **Forward Primer (5′- 3′)** | **Reverse Primer (5′-3′)** | **Primer Location** | **Amplicon Size** |
| *Leaf* **2 h** | | | | | |
| *PPR* | AT5G55840 | AAGACAGTGAAGGTGCAACCTTACT | AGTTTTTGAGTTGTATTTGTCAGAGAAAG | UTR | 59 bp |
| *MON1* | AT5G55840 | AACTCTATGCAGCATTTGATCCACT | TGATTGCATATCTTTATCGCCATC | Exon 13 and 14 | 61 bp |

| | | | | | |
|---|---|---|---|---|---|
| *EF1α* | AT5G60390 | TGAGCACGCTCTTCTTGCTTTCA | GGTGGTGGCATCCATCTTGTTACA | Exon 1 and ex jn 1,2 | 76 bp |
| **24 h** | | | | | |
| *UBC21* | AT5G25760 | CTGCGACTCAGGGAATCTTCTAA | TTGTGCCATTGAATTGAACCC | Ex jn 3,4 and exon 4 | 61 bp |
| *PPR* | AT5G55840 | AAGACAGTGAAGGTGCAACCTTACT | AGTTTTTGAGTTGTATTTGTCAGAGAAAG | UTR | 59 bp |
| *MON1* | AT5G55840 | AACTCTATGCAGCATTTGATCCACT | TGATTGCATATCTTTATCGCCATC | Exon 13 and 14 | 61 bp |
| **72 h** | | | | | |
| *ACT2* | AT3G18780 | CTTGCACCAAGCAGCATGAA | CCGATCCAGACACTGTACTTCCTT | Exon 2 | 68 bp |
| *FBOX* | AT5G15710 | TTTCGGCTGAGAGGTTCGAGT | GATTCCAAGACGTAAAGCAGATCAA | Exon 1 | 63 bp |
| *UBQ10* | AT4G05320 | GGCCTTGTATAATCCCTGATGAATAAG | AAAGAGATAACAGGAACGGAAACATAGT | Exon 1 and ex jn 1,2 | 76 bp |
| *Root* | | | | | |
| **2 h** | | | | | |
| *MON1* | AT5G55840 | AACTCTATGCAGCATTTGATCCACT | TGATTGCATATCTTTATCGCCATC | Exon 13 and 14 | 61 bp |
| *RHIP1* | AT4G26410 | GAGCTGAAGTGGCTTCCATGAC | GGTCCGACATACCCATGATCC | Ex jn 7, 8 and exon 8 | 81 bp |
| *EF1α* | AT5G60390 | TGAGCACGCTCTTCTTGCTTTCA | GGTGGTGGCATCCATCTTGTTACA | Exon 1 and 1,2 | 76 bp |
| **24 h** | | | | | |
| *UBC21* | AT5G25760 | CTGCGACTCAGGGAATCTTCTAA | TTGTGCCATTGAATTGAACCC | Exon 3,4 and 4 | 61 bp |
| *MON1* | AT5G55840 | AACTCTATGCAGCATTTGATCCACT | TGATTGCATATCTTTATCGCCATC | Exon 13 and 14 | 61 bp |
| *TIP41-like* | AT4G34270 | GTGAAAACTGTTGGAGAGAAGCAA | TCAACTGGATACCCTTTCGCA | Exon 7 and Exon 7,8 | 61 bp |
| *YSL8* | AT5G08290 | TTACTGTTTCGGTTGTTCTCCATTT | CACTGAATCATGTTCGAAGCAAGT | UTR | 61 bp |
| *UBQ10* | AT4G05320 | GGCCTTGTATAATCCCTGATGAATAAG | AAAGAGATAACAGGAACGGAAACATAGT | Exon 1 and ex jn 1,2 | 76 bp |
| *EF1α* | AT5G60390 | TGAGCACGCTCTTCTTGCTTTCA | GGTGGTGGCATCCATCTTGTTACA | Exon 1 and ex jn 1,2 | 76 bp |
| **72 h** | | | | | |
| *UBC21* | AT5G25760 | CTGCGACTCAGGGAATCTTCTAA | TTGTGCCATTGAATTGAACCC | Exon 3,4 and 4 | 61 bp |

| | | | | | |
|---|---|---|---|---|---|
| *UBQ10* | AT4G05320 | GGCCTTGTATAATCCCTGATGAATAAG | AAAGAGATAACAGGAACGGAAACATAGT | Exon 1 and 1,2 | 76 bp |
| *EF1α* | AT5G60390 | TGAGCACGCTCTTCTTGCTTTCA | GGTGGTGGCATCCATCTTGTTACA | Exon 1 and 1,2 | 76 bp |

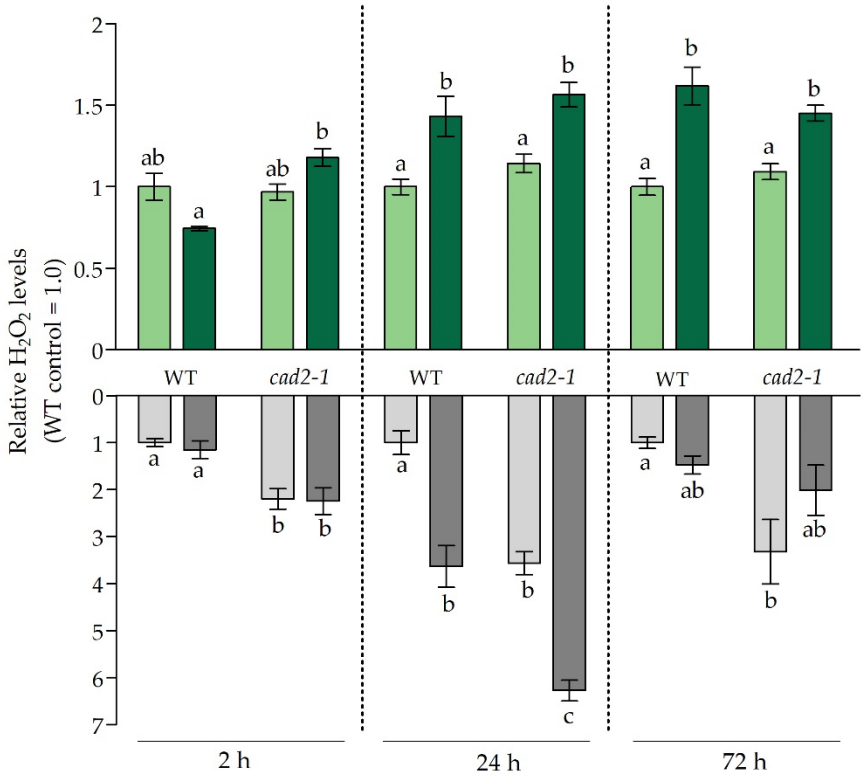
**Table S3** Reverse transcription quantitative PCR (RT-qPCR) parameters according to the Minimum Information for publication of Quantitative real-time PCR Experiments (MIQE) guidelines based on Bustin *et al.* (2009).

| | |
|---|---|
| **Sample - Template** | |
| *SOURCE* | roots and leaves of three-weeks-old *Arabidopsis thaliana* plants grown in hydroponics |
| *METHOD OF PRESERVATION* | snap frozen in $N_2$, long-term storage at -80° |
| *STORAGE TIME* | < 6 months |
| *HANDLING* | frozen |
| *EXTRACTION METHOD* | silica-columns: RNAqueous™ Kit (Ambion, Thermo Fisher Scientific, Waltham, MA, USA) |
| *RNA; DNA-FREE* | turbo DNA-*free*™ Kit (Ambion, Thermo Fisher Scientific, Waltham, MA, USA) |
| | use of intron-spanning primers if possible |
| | verification of amplicon-specificity via dissociation curve |
| *CONCENTRATION* | NanoDrop® ND-1000 spectrophotometer (Thermo Fisher Scientific, Waltham, Ma, USA) |
| **Assay optimisation – Validation** | |
| *ACCESSION NUMBER* | see Supplementary Table S1 & S2 |
| *AMPLICON DETAILS* | see Supplementary Table S1 & S2 |
| *PRIMERS SEQUENCE* | see Supplementary Table S1 & S2 |
| *IN SILICO* | TAIR primer-BLAST http://www.arabidopsis.org/Blast/index.jsp |
| *EMPIRICAL* | primer concentration of 300 nM unless mentioned otherwise (Table S1 & S2) |
| | annealing temperature of 60°C |
| *PRIMING CONDITIONS* | combinations of oligo-dT and random hexamer primers |
| *PCR EFFICIENCY* | dilution curves of pooled samples (slope, deviation) |
| *LINEAR DYNAMIC RANGE* | samples are within the range of the efficiency curve |
| **RT and qPCR** | |
| *PROTOCOLS* | Turbo DNA-*free*™ Kit (Ambion, Thermo Fisher Scientific, Waltham, MA, USA) |
| | PrimeScript™ RT Reagent Kit (Perfect Real Time, Takara Bio Inc., Kusatsu, Japan) |
| | Qauntinova™ SYBR® Green PCR kit (Qiagen, Hilde, Germany) |

| | |
|---|---|
| | as described in the Materials and Methods section |
| *REAGENTS* | as described in the Materials and Methods section |
| *NON TEMPLATE CONTROL* | verification based on Cq-value and dissociation curve |
| **Data analysis** | |
| *SOFTWARE* | QuantStudio™ Design & Analysis Software ( Applied Biosystems, Thermo Fisher Scientific, Foster City, CA, USA) |
| *STATISTICAL ANALYSIS* | specified in Materials and Methods section and legends of Figures and Tables |
| *NORMALISATION* | a selection of at least three reference genes based on the GrayNorm algoritm (Remans *et al.* 2014) |
| | see Materials and Methods section |

**Supplemental Table S4** Percentage reduced glutathione (GSH) deduced from oxidised GSSG levels and total GSH levels in leaves and roots of 3 weeks old wild-type (WT) and *cad2-1* mutant *Arabidopsis thaliana* plants grown under control conditions (0 μM $CdSO_4$, light bars) or exposed to 5 μM $CdSO_4$ (dark bars) during 2 h, 24 h and 72 h. For each time point, data presented as the mean ± S.E. of 4 biological replicates. Significant differences (2-way ANOVA: $p < 0.05$) within each time point are indicated with different letters. L.O.D.: limit of detection for oxidised GSSG.

| | | **Reduced GSH (%)** | | | | | |
|---|---|---|---|---|---|---|---|
| | | **2 h** | | **24 h** | | **72 h** | |
| | **[$CdSO_4$]** | **WT** | ***cad2-1*** | **WT** | ***cad2-1*** | **WT** | ***cad2-1*** |
| *Leaf* | 0 μM | 96.87 ± 9.01$^{a}$ | 97.98 ± 1.74$^{a}$ | 96.94 ± 0.30$^{a}$ | 96.11 ± 0.75$^{a}$ | 90.82 ± 0.81$^{a}$ | 94.37 ± 0.46$^{b}$ |
| | 5 μM | 97.56 ± 7.43$^{a}$ | 98.06 ± 1.23$^{a}$ | 98.92 ± 0.22$^{b}$ | 98.84 ± 0.07$^{ab}$ | 96.56 ± 1.08$^{c}$ | 98.08 ± 0.43$^{c}$ |
| *Root* | 0 μM | 95.95 ± 7.38 | 96.92 ± 1.91 | 97.97 ± 0.39$^{a}$ | 98.05 ± 0.24$^{a}$ | 97.00 ± 0.92$^{a}$ | 96.89 ± 1.33$^{a}$ |
| | 5 μM | 99.96 ± 0.22 | L.O.D. | 97.34 ± 0.70$^{ab}$ | 95.52 ± 0.09$^{b}$ | 98.06 ± 0.11$^{a}$ | 96.77 ± 1.03$^{a}$ |



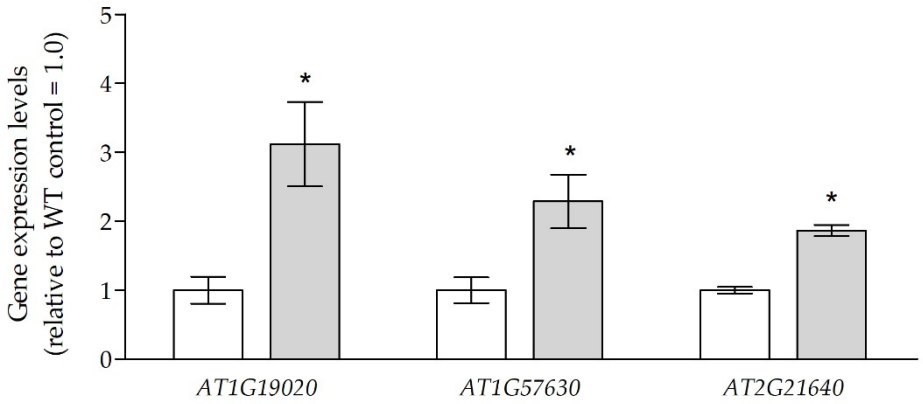

**Supplemental Figure S1** Relative hydrogen peroxide ($H_2O_2$) levels in leaves (green bars) and roots (grey bars) of 3 weeks old wild-type (WT) and *cad2-1* mutant *Arabidopsis thaliana* plants grown under control conditions (0 μM $CdSO_4$, light bars) or exposed to 5 μM $CdSO_4$ (dark bars) during 2 h, 24 h and 72 h. Data are presented as the mean ± S.E. of at least three biological independent replicates relative to the control of the WT set at 1.00. Significant differences (2-way ANOVA: $p < 0.05$) within each time point are indicated with different letters.

**Supplemental Table S5** Relative gene expression levels of antioxidative enzymes in leaves and roots of 3 weeks old wild-type (WT) and *cad2-1* mutant *Arabidopsis thaliana* plants grown under control conditions (0 µM $CdSO_4$, light bars) or exposed to 5 µM $CdSO_4$ (dark bars) during 2 h, 24 h and 72 h. Data are presented as the mean ± S.E. of at least three biological independent replicates relative to the control of the corresponding genotype set at 1.00. Significant differences (2-way ANOVA: $p < 0.05$) between control and Cd-exposed plants of the same genotype, within each time point are marked in colour (upregulated: , downregulated: ). Significant differences between Cd-induced responses of both genotypes whithin each time point are indicated with an asterisk (*). *APX*: ascorbate peroxidase , *CAT:* catalase.

| | | Antioxidative enzymes | | | | | |
|---|---|---|---|---|---|---|---|
| | | 2 h | | 24 h | | 72 h | |
| Gene | $CdSO_4$ | WT | *cad2-1* | WT | *cad2-1* | WT | *cad2-1* |
| *Leaf* | | | | | | | |
| *APX1* | 0 µM | 1.00 ± 0.08 | 1.00 ± 0.08 | 1.00 ± 0.02 | 1.00 ± 0.08 | 1.00 ± 0.02 | 1.00 ± 0.02 |
| | 5 µM | 1.04 ± 0.12 | 0.65 ± 0.04* | 2.13 ± 0.18 | 1.25 ± 0.27 | 1.41 ± 0.36 | 0.44 ± 0.00 |
| *APX2* | 0 µM | 1.00 ± 0.09 | 1.00 ± 0.15 | 1.00 ± 0.21 | 1.00 ± 0.35 | 1.00 ± 0.12 | 1.00 ± 0.29 |
| | 5 µM | 0.65 ± 0.09 | 0.85 ± 0.18 | 4.21 ± 1.41 | 0.41 ± 0.20* | 4.02 ± 0.75 | 0.22 ± 0.00 |
| *CAT1* | 0 µM | 1.00 ± 0.07 | 1.00 ± 0.14 | 1.00 ± 0.04 | 1.00 ± 0.14 | 1.00 ± 0.18 | 1.00 ± 0.22 |
| | 5 µM | 1.10 ± 0.14 | 0.62 ± 0.05* | 3.48 ± 0.41 | 1.20 ± 0.36* | 1.12 ± 0.34 | 0.91 ± 0.03 |
| *CAT2* | 0 µM | 1.00 ± 0.03 | 1.00 ± 0.12 | 1.00 ± 0.10 | 1.00 ± 0.10 | 1.00 ± 0.01 | 1.00 ± 0.06 |
| | 5 µM | 0.89 ± 0.11 | 0.71 ± 0.05 | 0.30 ± 0.04 | 0.72 ± 0.03* | 1.02 ± 0.22 | 0.66 ± 0.10 |
| *Root* | | | | | | | |
| *APX1* | 0 µM | 1.00 ± 0.01 | 1.00 ± 0.11 | 1.00 ± 0.05 | 1.00 ± 0.03 | 1.00 ± 0.14 | 1.00 ± 0.09 |
| | 5 µM | 1.10 ± 0.04 | 1.16 ± 0.05 | 1.04 ± 0.05 | 1.75 ± 0.21 | 0.98 ± 0.05 | 0.75 ± 0.05 |
| *APX2* | 0 µM | 1.00 ± 0.19 | 1.00 ± 0.04 | 1.00 ± 0.02 | 1.00 ± 0.02 | 1.00 ± 0.17 | 1.00 ± 0.30 |
| | 5 µM | 2.25 ± 0.27 | 14.95 ± 1.61* | 9.02 ± 1.29 | 157.47 ± 36.74* | 0.26 ± 0.07 | 6.99 ± 0.62* |
| *CAT1* | 0 µM | 1.00 ± 0.05 | 1.00 ± 0.02 | 1.00 ± 0.07 | 1.00 ± 0.04 | 1.00 ± 0.14 | 1.00 ± 0.06 |
| | 5 µM | 0.90 ± 0.08 | 0.89 ± 0.04 | 3.74 ± 0.25 | 4.16 ± 0.07 | 1.81 ± 0.02 | 2.64 ± 0.33* |
| *CAT2* | 0 µM | 1.00 ± 0.15 | 1.00 ± 0.08 | 1.00 ± 0.04 | 1.00 ± 0.08 | 1.00 ± 0.15 | 1.00 ± 0.07 |
| | 5 µM | 0.78 ± 0.12 | 0.78 ± 0.00 | 0.38 ± 0.01 | 1.05 ± 0.04* | 0.64 ± 0.02 | 0.36 ± 0.05* |

**Supplemental Table S6** Relative gene expression levels of ROS-generating NADPH oxidases in leaves and roots of 3 weeks old wild-type (WT) and *cad2-1* mutant *Arabidopsis thaliana* plants grown under control conditions (0 µM $CdSO_4$, light bars) or exposed to 5 µM $CdSO_4$ (dark bars) during 2 h, 24 h and 72 h. Data are presented as the mean ± S.E. of at least three biological independent replicates relative to the control of the corresponding genotype set at 1.00. Significant differences (2-way ANOVA: $p < 0.05$) between control and Cd-exposed plants of the same genotype, within each time point are marked in colour (upregulated: , downregulated: ). Significant differences between Cd-induced responses of both genotypes whithin each time point are indicated with an asterisk (*). *RBOH*: respiratory burst oxidase homologue.

| | | ROS-generating NADPH oxidase | | | | | |
|---|---|---|---|---|---|---|---|
| | | 2 h | | 24 h | | 72 h | |
| **Gene** | **$CdSO_4$** | **WT** | ***cad2-1*** | **WT** | ***cad2-1*** | **WT** | ***cad2-1*** |
| *Leaf* | | | | | | | |
| *RBOHC* | 0 µM | 1.00 ± 0.32 | 1.00 ± 0.33 | 1.00 ± 0.14 | 1.00 ± 0.46 | 1.00 ± 0.15 | 1.00 ± 0.38 |
| | 5 µM | 0.47 ± 0.06 | 0.74 ± 0.34 | 79.81 ± 6.35 | 0.63 ± 0.11* | 0.58 ± 0.14 | 1.42 ± 0.42 |
| *RBOHD* | 0 µM | 1.00 ± 0.02 | 1.00 ± 0.04 | 1.00 ± 0.16 | 1.00 ± 0.23 | 1.00 ± 0.05 | 1.00 ± 0.06 |
| | 5 µM | 1.37 ± 0.02 | 1.17 ± 0.04* | 2.45 ± 0.09 | 1.46 ± 0.23 | 2.25 ± 0.28 | 1.93 ± 0.19 |
| *RBOHF* | 0 µM | 1.00 ± 0.30 | 1.00 ± 0.19 | 1.00 ± 0.08 | 1.00 ± 0.13 | 1.00 ± 0.10 | 1.00 ± 0.14 |
| | 5 µM | 0.72 ± 0.13 | 0.58 ± 0.07 | 6.74 ± 0.82 | 0.66 ± 0.11* | 3.99 ± 0.58 | 1.20 ± 0.01* |
| *Root* | | | | | | | |
| *RBOHC* | 0 µM | 1.00 ± 0.01 | 1.00 ± 0.17 | 1.00 ± 0.06 | 1.00 ± 0.01 | 1.00 ± 0.16 | 1.00 ± 0.10 |
| | 5 µM | 1.41 ± 0.19 | 1.18 ± 0.03 | 1.04 ± 0.06 | 0.87 ± 0.06 | 0.68 ± 0.02 | 0.69 ± 0.04 |
| *RBOHD* | 0 µM | 1.00 ± 0.10 | 1.00 ± 0.14 | 1.00 ± 0.04 | 1.00 ± 0.05 | 1.00 ± 0.11 | 1.00 ± 0.14 |
| | 5 µM | 1.56 ± 0.01 | 2.43 ± 0.13* | 4.50 ± 0.60 | 3.90 ± 0.21 | 2.51 ± 0.28 | 2.38 ± 0.45 |
| *RBOHF* | 0 µM | 1.00 ± 0.03 | 1.00 ± 0.03 | 1.00 ± 0.03 | 1.00 ± 0.04 | 1.00 ± 0.08 | 1.00 ± 0.06 |
| | 5 µM | 1.28 ± 0.03 | 1.28 ± 0.05 | 2.20 ± 0.08 | 1.92 ± 0.05 | 1.98 ± 0.25 | 1.78 ± 0.23 |




**Supplemental Figure S2** Relative gene expression levels of a subset of oxidative stress markers in roots after 24 h under control conditions (0 μM $CdSO_4$) in 3 weeks old wild-type (WT, white bars) and *cad2-1* mutant (grey bars) *Arabidopsis thaliana* plants. Data are represented as the mean ± S.E. of at least three biological independent replicates relative to the control of the WT set at 1.00. For each gene, significant differences (t-test: $p < 0.05$) between the two genotypes under control conditions are indicated with an asterisk (*).