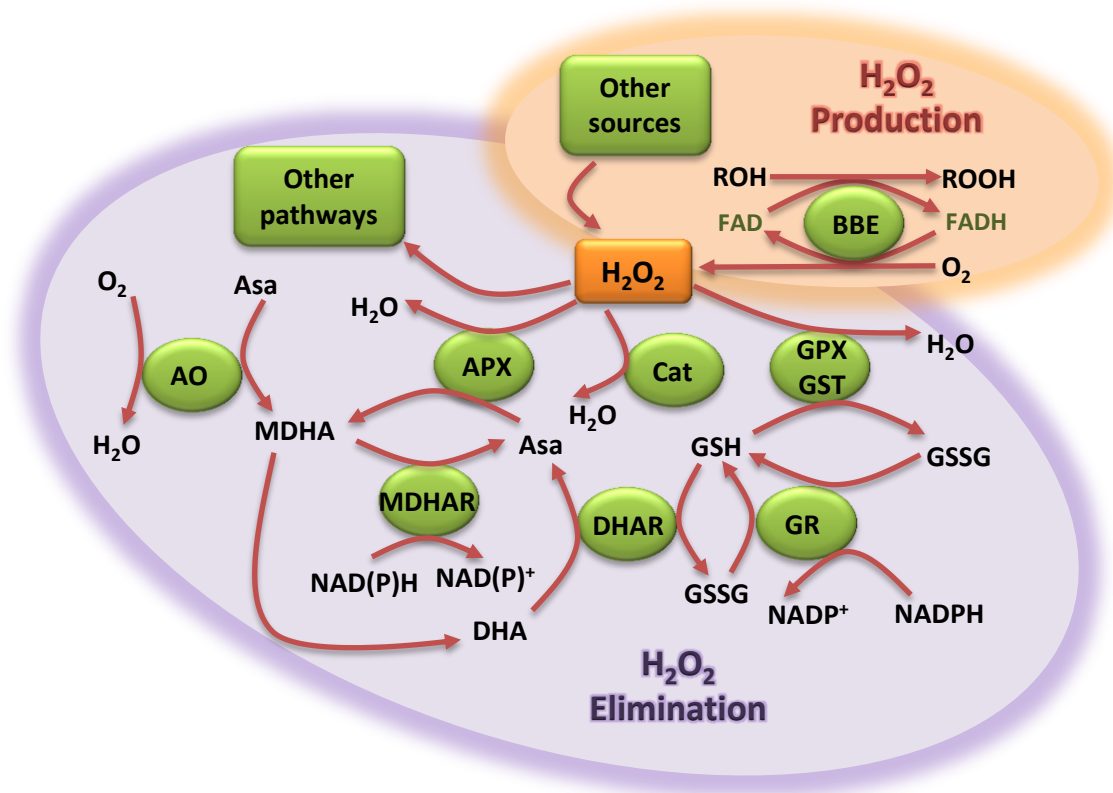


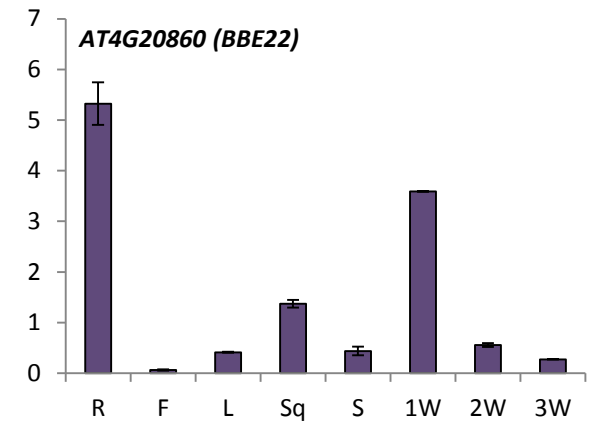
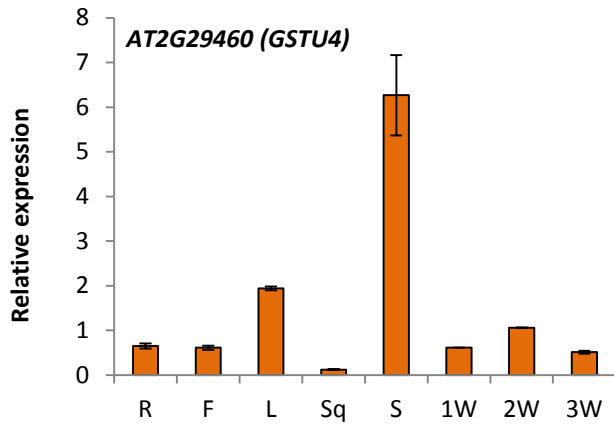
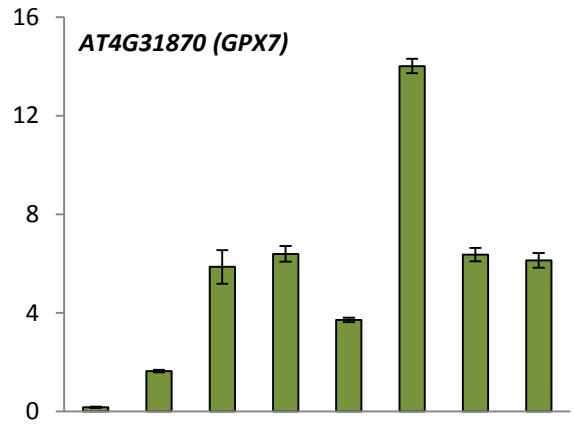
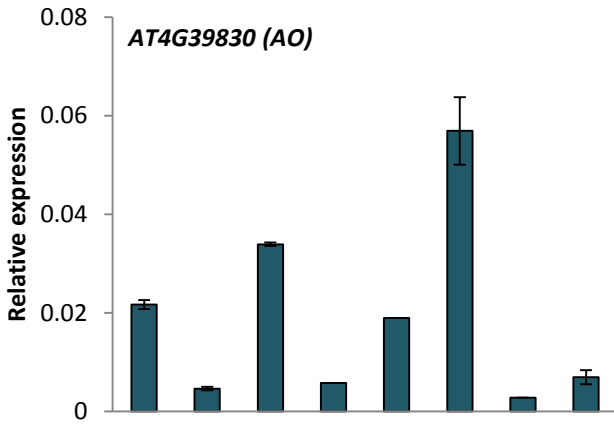
Supplementary Information

Arabidopsis response to the spider mite *Tetranychus urticae* depends on the regulation of reactive oxygen species homeostasis

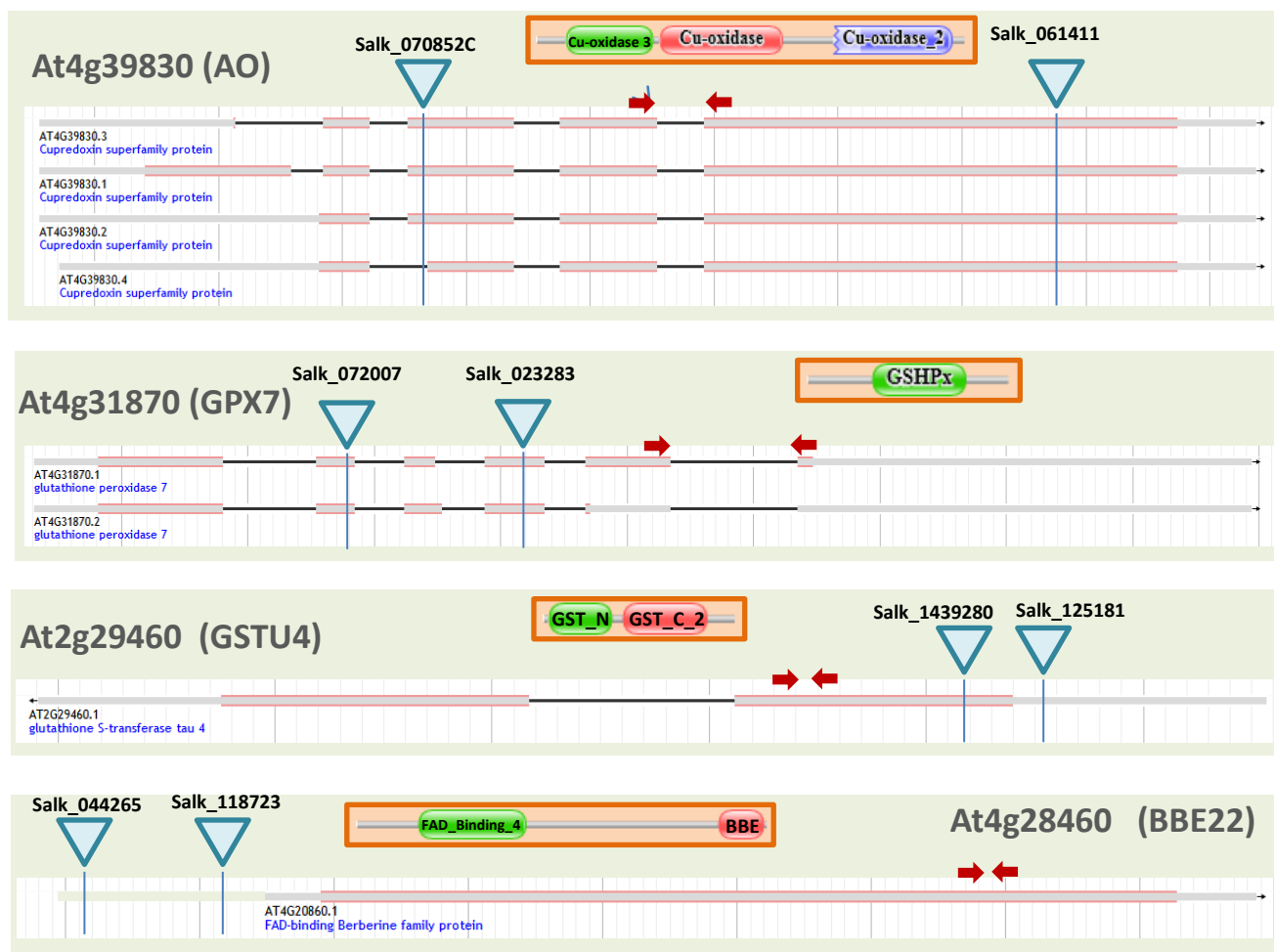
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Supplementary Figure 1. Schematic representation of the metabolic pathways leading to H₂O₂ production and elimination. For clarity, a simplified metabolic network was done with a special focus on the molecules analysed in this work. H₂O₂, hydrogen peroxide; Asa, ascorbate; (M)DHA, (mono)dehydroascorbate; GSH, glutathione; GSSG, glutathione disulphide; BBE, berberine-like enzyme; GST, glutathione transferase; GPX, glutathione peroxidase; AO, ascorbate oxidase; Cat, catalase; GR, glutathione reductase; (M)DHAR, (mono)dehydroascorbate reductase; APX, ascorbate peroxidase; NAD(P), nicotinamide adenine dinucleotide (phosphate); FAD, flavin adenine dinucleotide.



Supplementary Figure 2. Gene expression in plant tissues. Relative gene expression levels ($2^{-\Delta\text{Ct}}$) of *AT4G39830*, *AT4G31870*, *AT2G29460* and *AT4G20860* in different *Arabidopsis* tissues. Roots (R), flowers (F), leaves from stem (L), siliques (Sq), seeds (S) and rosettes from 1, 2 and 3 week-old (1W, 2W, 3W). Ubiquitin was used to normalize gene expression.



Supplementary Figure 3. Structural information of selected Arabidopsis genes. A schematic representation of protein domains is shown above the genomic structure of each gene (exons, grey boxes; introns, black lines; coding region, grey-red boxes). Red arrows mark the position of oligonucleotides used in RT-qPCR experiments. Blue triangles point to the gene location in which the T-DNA was inserted.

Supplemental Table 1. Fold change of the expression of ROS-related genes in T-DNA insertion lines.

T-DNA line	Fold change \pm standard error			
	<i>AO</i>	<i>GPX7</i>	<i>GSTU4</i>	<i>BBE22</i>
AO KD1	0.40 \pm 0.02	1.12 \pm 0.04	1.33 \pm 0.17	2.69 \pm 0.39
AO KD2	0.65 \pm 0.04	0.83 \pm 0.02	1.10 \pm 0.24	1.98 \pm 0.04
GPX7 KD	0.53 \pm 0.01	0.68 \pm 0.01	1.02 \pm 0.14	2.16 \pm 0.37
GPX7 KO	1.85 \pm 0.13	0.00 \pm 0.00	0.23 \pm 0.04	1.17 \pm 0.10
GSTU4 KD1	0.69 \pm 0.10	0.67 \pm 0.02	0.11 \pm 0.07	1.30 \pm 0.08
GSTU4 KD2	0.42 \pm 0.03	0.88 \pm 0.01	0.09 \pm 0.05	1.31 \pm 0.10
BBE22 KO	0.17 \pm 0.03	0.55 \pm 0.01	0.74 \pm 0.21	0.03 \pm 0.01
BBE22 OE	0.49 \pm 0.02	0.82 \pm 0.06	2.11 \pm 0.19	29.95 \pm 2.82

Supplemental Table 2. Sequences of used oligonucleotides (F: forward; R: reverse).

Gene	Primer name	Sequence (5' → 3')
Ubiquitin	UBQ-F	GCTCTTATCAAAGGACCTTCGG
	UBQ-R	CGAACTTGAGGAGGTTGCAAAG
AT4G39830	AO-F	TTCCCGGAAAGACATACAGG
	AO-R	TCCGTCTGCTTCAACAACG
AT4G31870	GPX7-F	AGGGCAAAGTTGTCGAGAGA
	GPX7-R	TTAAGCCGCAAGCAACTTCT
AT2G29460	GSTU4-F	AGATTTCTTCGGTGGCAAAA
	GSTU4-R	ATTCCCATACCTCCCAACC
AT4G20860	BBE22-F	TTTCTAAATCGCCGAGAGGA
	BBE22-R	TTGCATCTTCGAAACTCGTG
AT1G64280	NPR1-F	TGCATCAGAAGCAACTTTGG
	NPR1-R	GGCCTTTGAGAGAATGCTTG
AT2G14610	PR1-F	TCAGTGAGACTCGGATGTGC
	PR1-R	CGTTCACATAATTCCCACGA
AT1G32640	MYC2-F	TCCGAGTCCGGTTCATTCT
	MYC2-R	TCTCGGGAGAAAGTGTATTGAA
AT5G24770	VSP2-F	ATGCCAAAGGACTTGCCCTA
	VSP2-R	CGGGTCGGTCTTCTCTGTTC
AT5G44420	PDF1.2-F	GTTCTCTTTGCTGCTTTCGAC
	PDF1.2-R	GCAAACCCCTGACCATGT