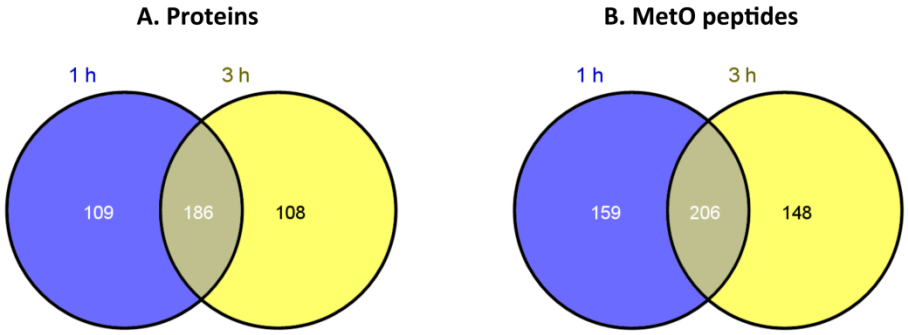
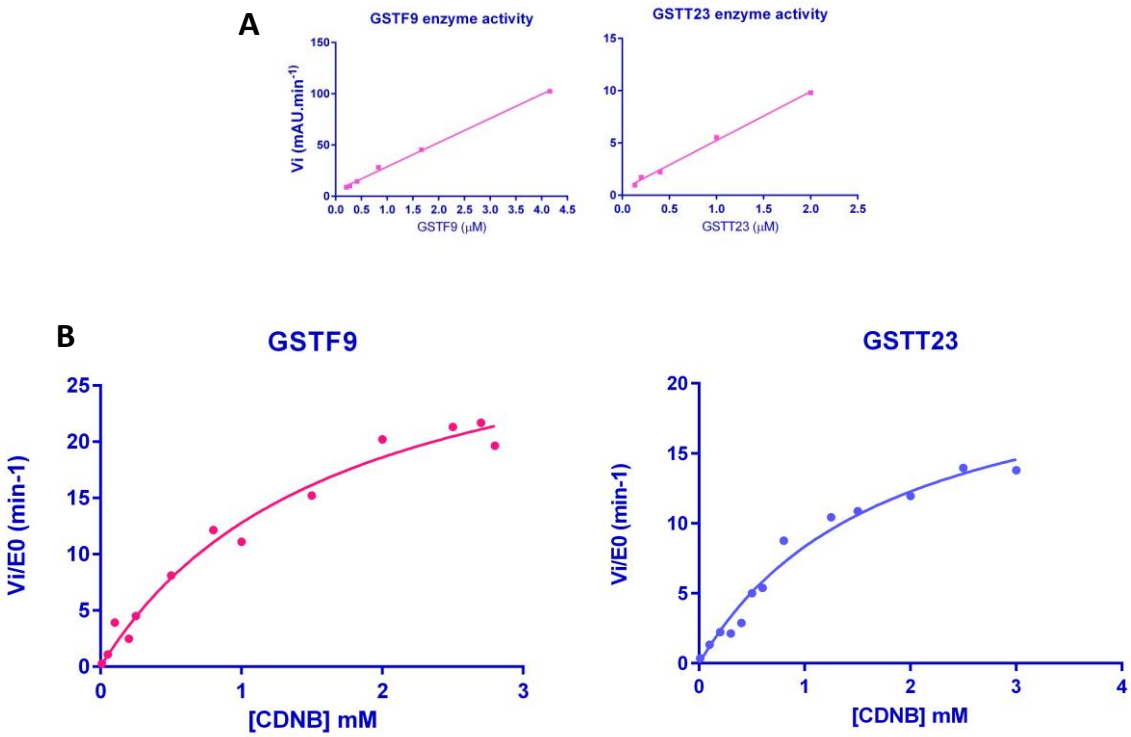
Supplemental data

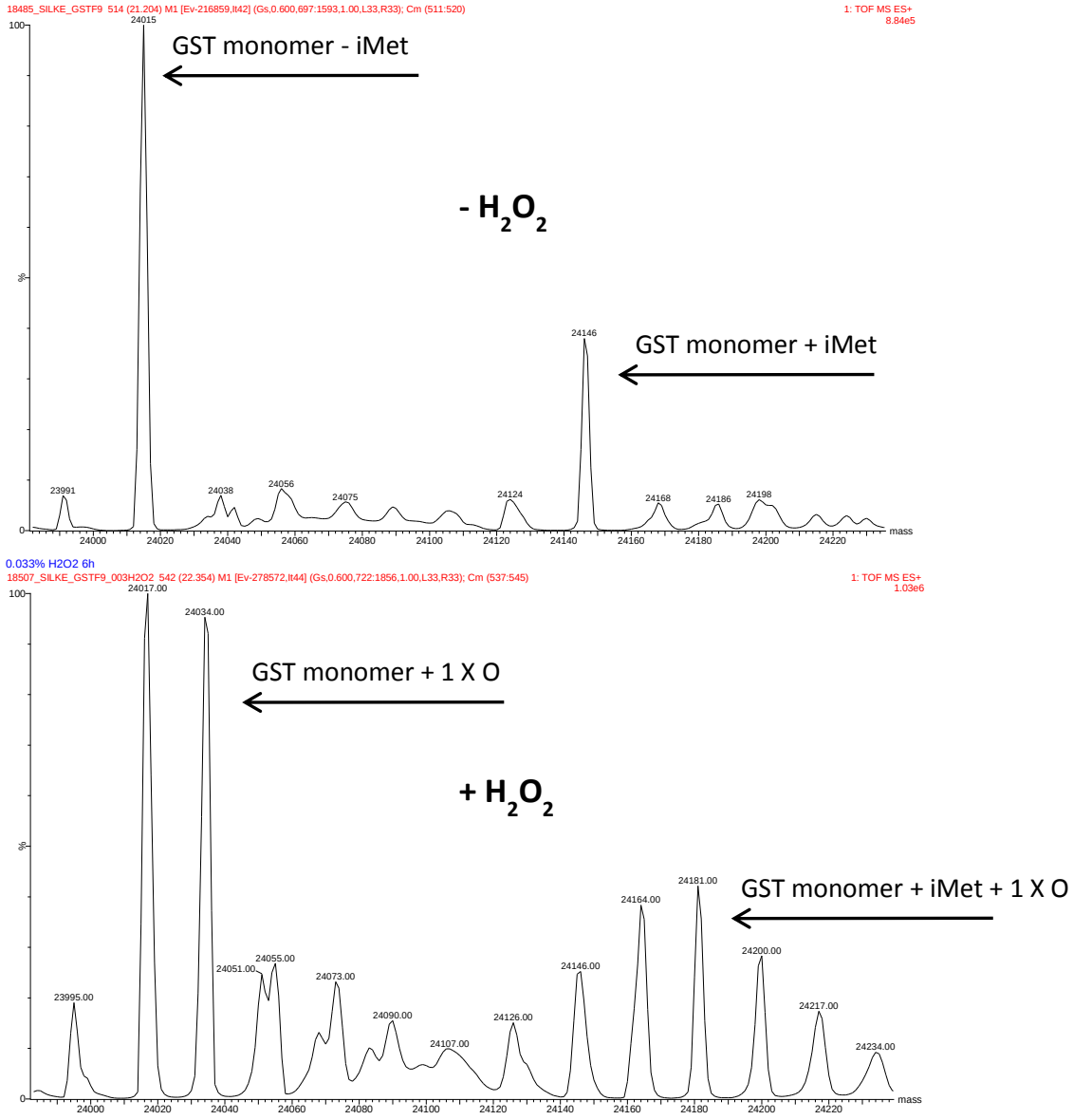
Supplemental Figure 1: Venn diagrams of the identified oxidized proteins (A) and MetO peptides (B). Following 1 h of high light exposure 365 MetO peptides were identified in 296 proteins, whereas after 3 h there were 354 MetO peptides in 294 proteins. There is a considerable overlap of 186 proteins that contain 206 identical MetO sites at the two time points sampled.



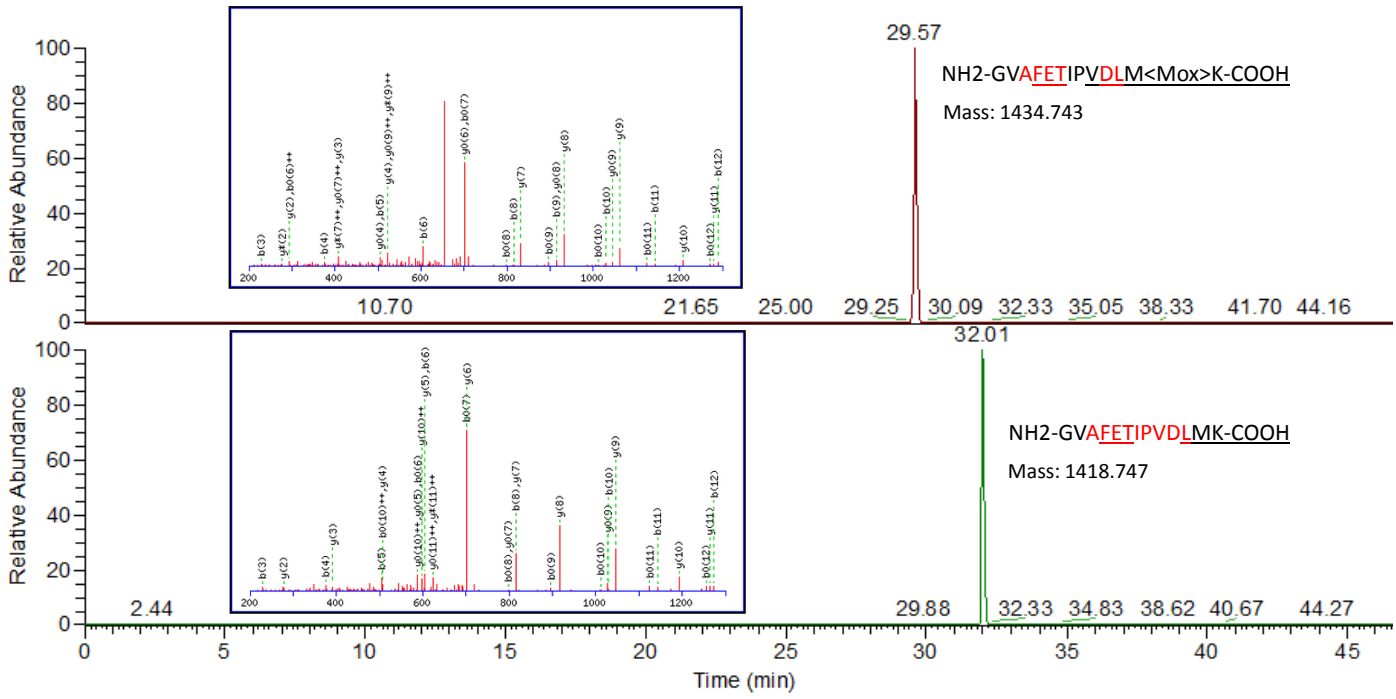
Supplemental Figure 2: Kinetics of GSTF9 and GSTT23. Enzyme activities of GSTF9 and GSTT23 were determined via the CDNB assay at a pH of 6.5. Both recombinant GSTs transfer GSH to CDNB with initial velocities (Vi) linear to the concentration of added GST with a constant 1 mM final concentration of substrate **(A)**. Kinetic parameters were calculated from the Michaelis-Menten model by plotting Vi/[GST] in function of varying concentrations of CDNB **(B)**.



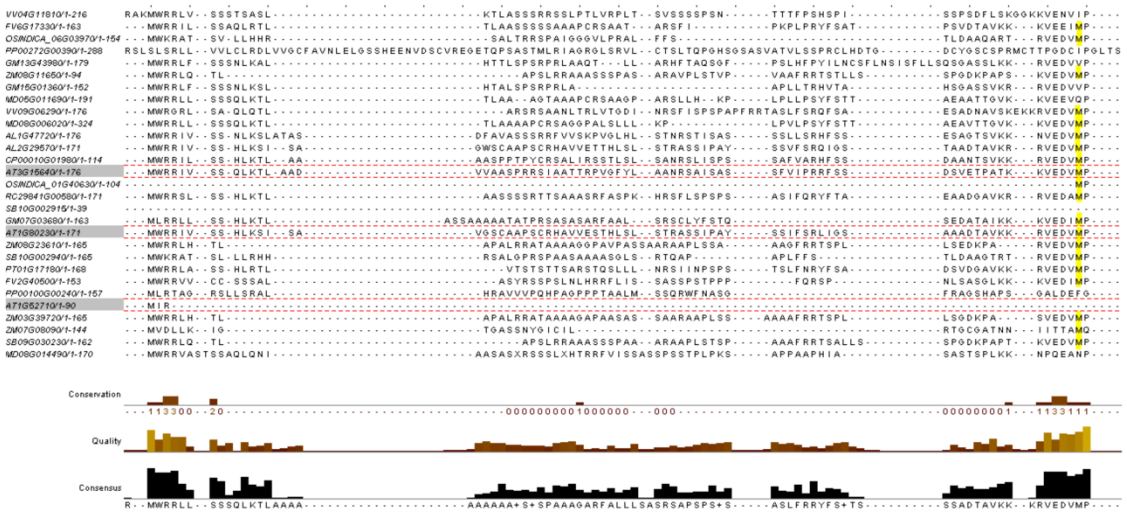
Supplemental Figure 3: Optimization of *in vitro* GSTF9 oxidation. LC-MS (Q-TOF) measurements of GSTF9 before and after addition of 0.03% H_2O_2 and incubation for 135 min at 10°C. GSTF9 is present as a monomer due to the denaturing effect of acetonitrile and the low pH. Also, a population of GSTF9 without the initiator methionine was detected. Upon oxidation, a prominent peak of single oxidized GSTF9 appears.



Supplemental Figure 4: Oxidation of Met-35 in GSTF9. LC-MS/MS analysis identified the G_{24}VAFETIPVDLMK$_{36}$ peptide after *in vitro* oxidation of GSTF9. This peptide, previously identified to contain a target for *in vivo* methionine oxidation (Met-35), is present in two forms; with or without Met-35 oxidized. The extracted-ion chromatogram shows that, as expected, the oxidized peptide with a mass of 1434.743 Da elutes earlier than the non-oxidized peptides (mass of 1418.747 Da). The MS/MS spectra are also shown with b-and y-ions indicated and displayed as underlined residues or residues in red on the peptide sequence, respectively.



Supplemental Figure 5: Multiple sequence alignment of the rubredoxin-like superfamily protein genes. Sequence alignment of all homologous rubredoxin genes (43) across the plant kingdom (19 species) shows that the site of methionine oxidation (highlighted in yellow) lies within a conserved sequence patch. The 3 *Arabidopsis* genes are boxed with red dotted lines.



Supplemental Figure 6: Hierarchical clustering of the expression profiles of the *Arabidopsis thaliana* MSR genes. The expression profiles of the *Arabidopsis* MsrA and MsrB genes were clustered using GENEVESTIGATOR. Upon different perturbations, both biotic and abiotic stresses (A), in the different anatomical parts (B) or during development (C), the expression profiles cluster differently, while MSRB7 and B9 always cluster together. These genes also show an initial low expression profile going through different stages during development suggesting a stress responsive role.