

Figure 1

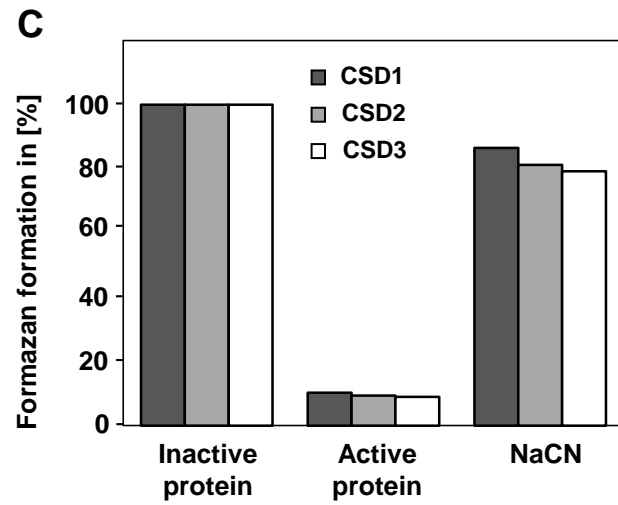
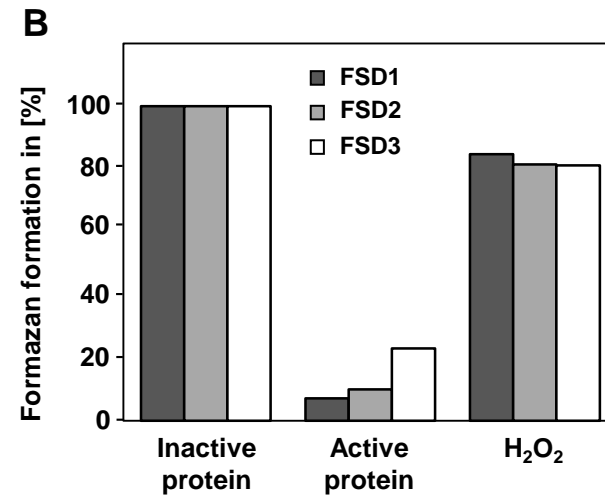
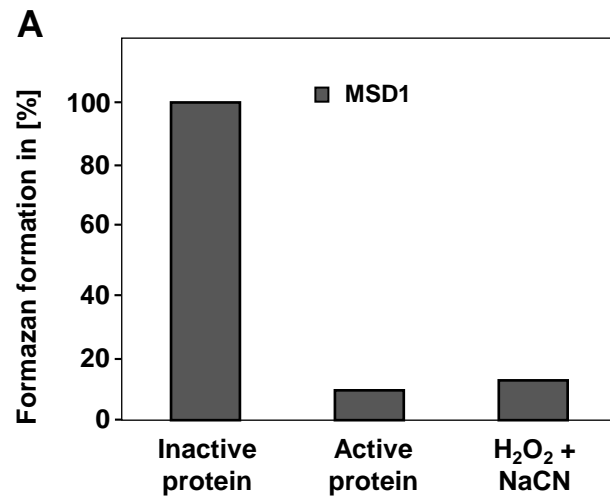


Figure 2

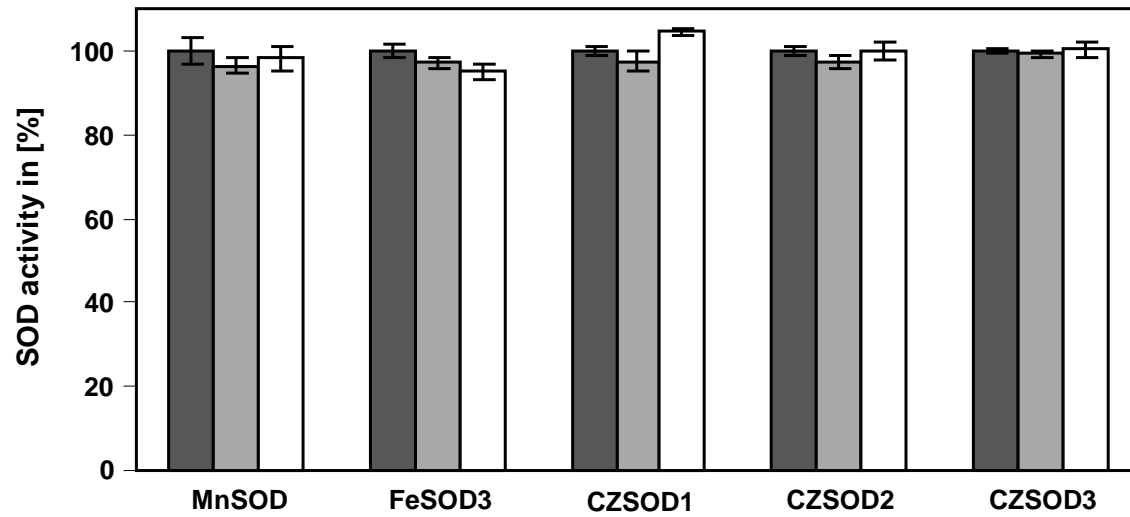


Figure 3

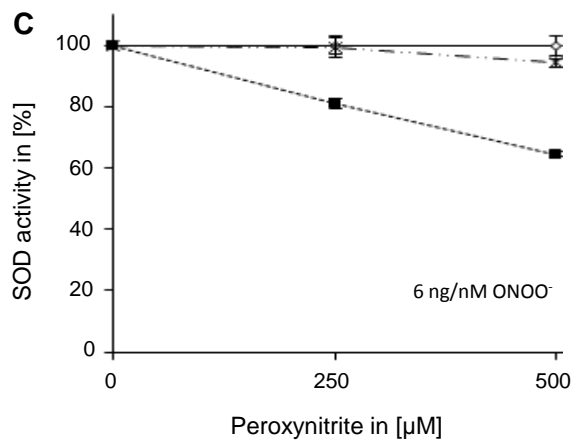
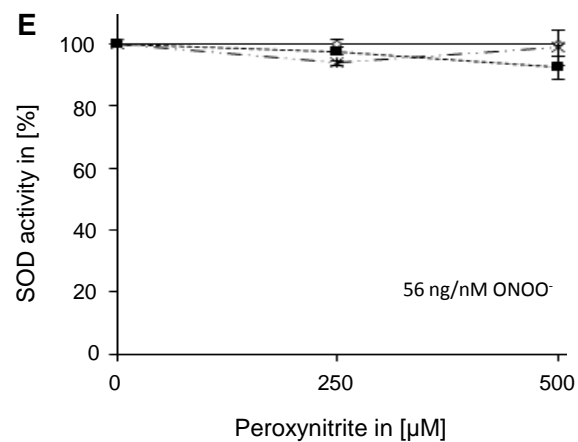
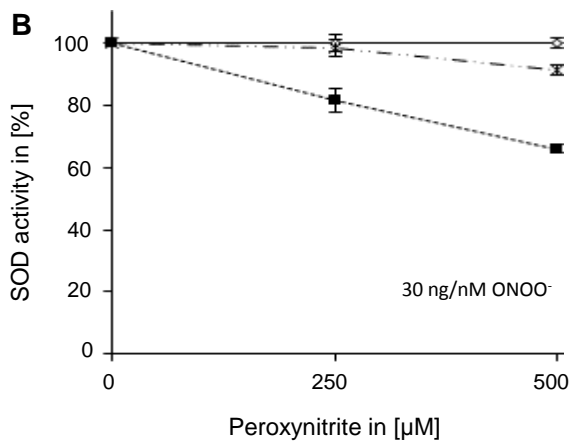
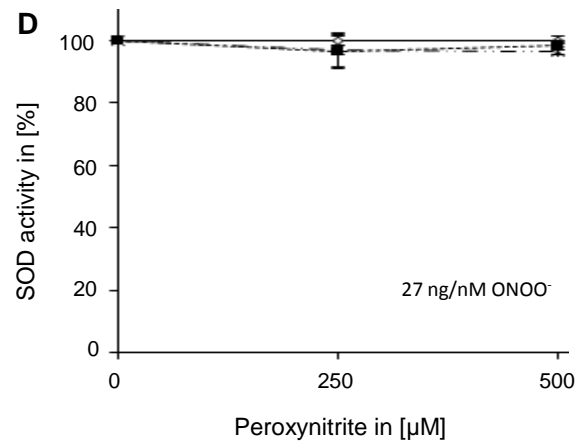
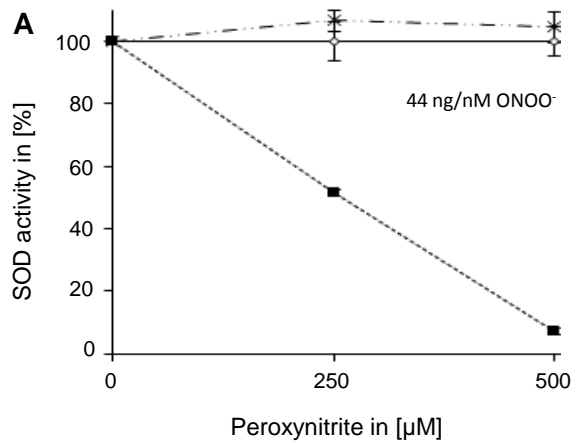


Figure 4

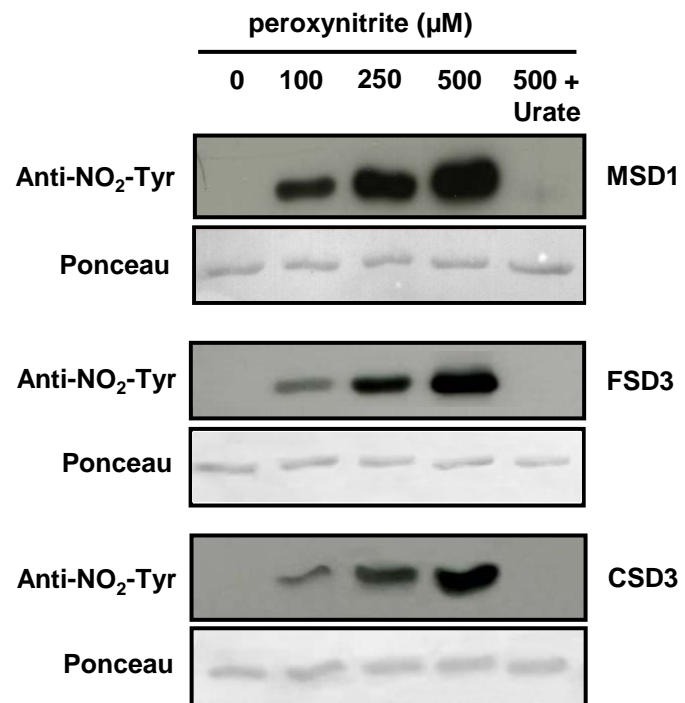


Figure 5

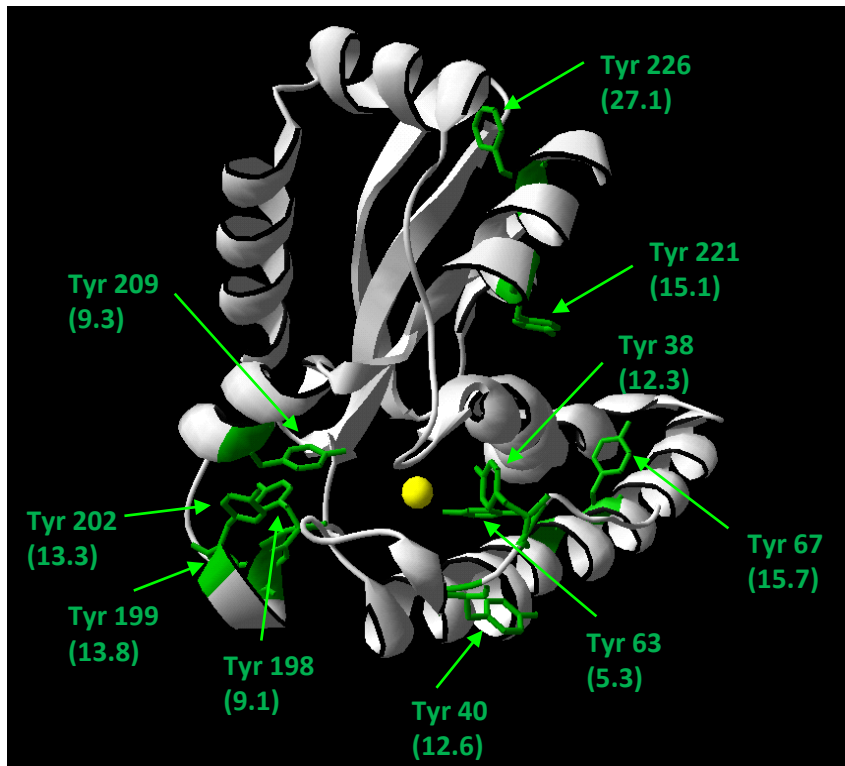


Figure 6

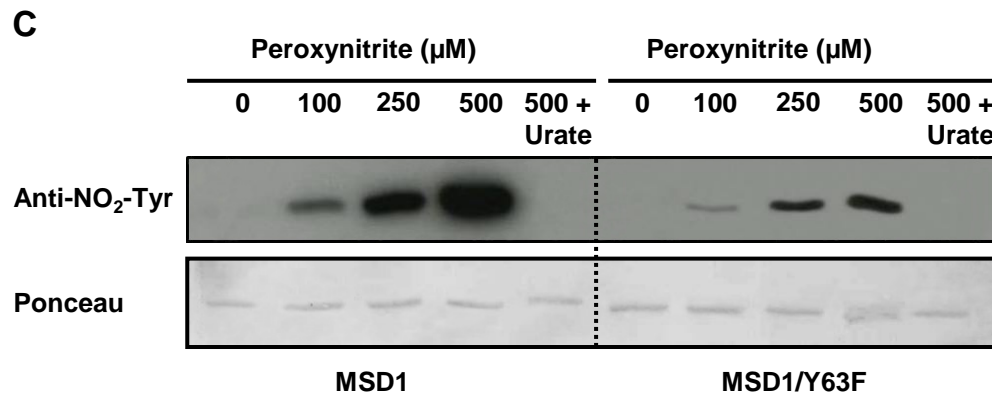
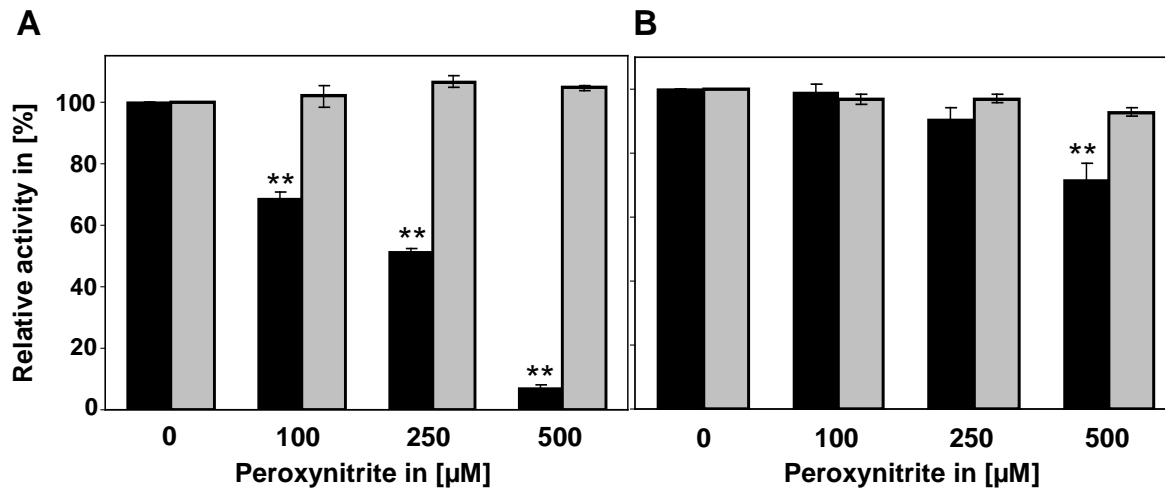


Figure 7

A

hMnSOD	30	DLPYDYGALPHINAQIMQLHHSKHAA Y VNNLNVTEEKYQ----EALAKGDVTAQIAL	84
MSD1	35	DLPYDYGALPAISGEIMQIHHQKHQA Y VTNYNNALEQLD----QAVNKGDASTVVKL	89
FSD1	15	PPPFALDALEPHMSKQTLEFHWGKHHRA Y VDNLKKQVLGTE-LEGKPLEHIIHSTYNNG	72
FSD2	57	PPPYPLDALEPHMSRETLDYHWGKHHKT Y VENLNKQILGTD-LDALSLEEVVLLSYNKG	114
FSD3	54	TPPYPLDALEPYMSRRTLEVHWGKHHRG Y VDNLNKQLGKDDRLYGYTMEELIKATYNNG	112

B

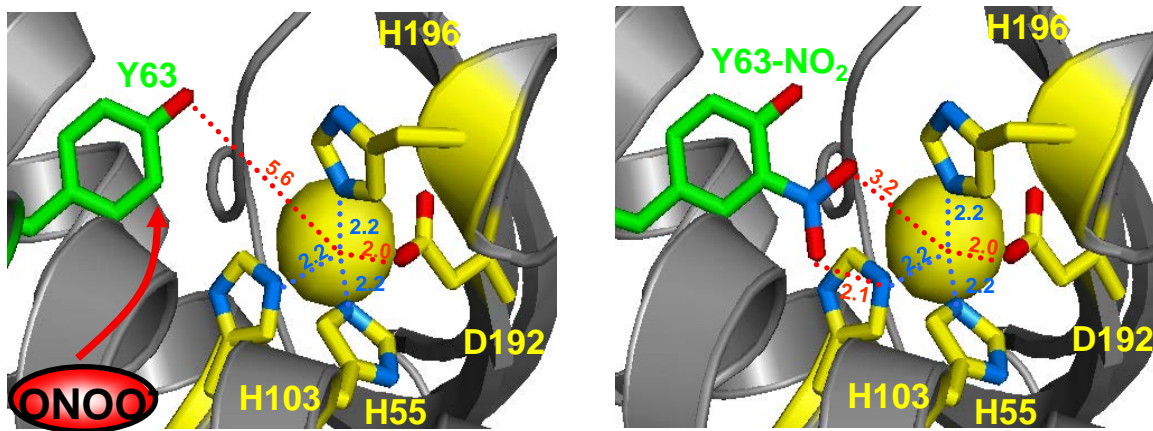


Figure 8

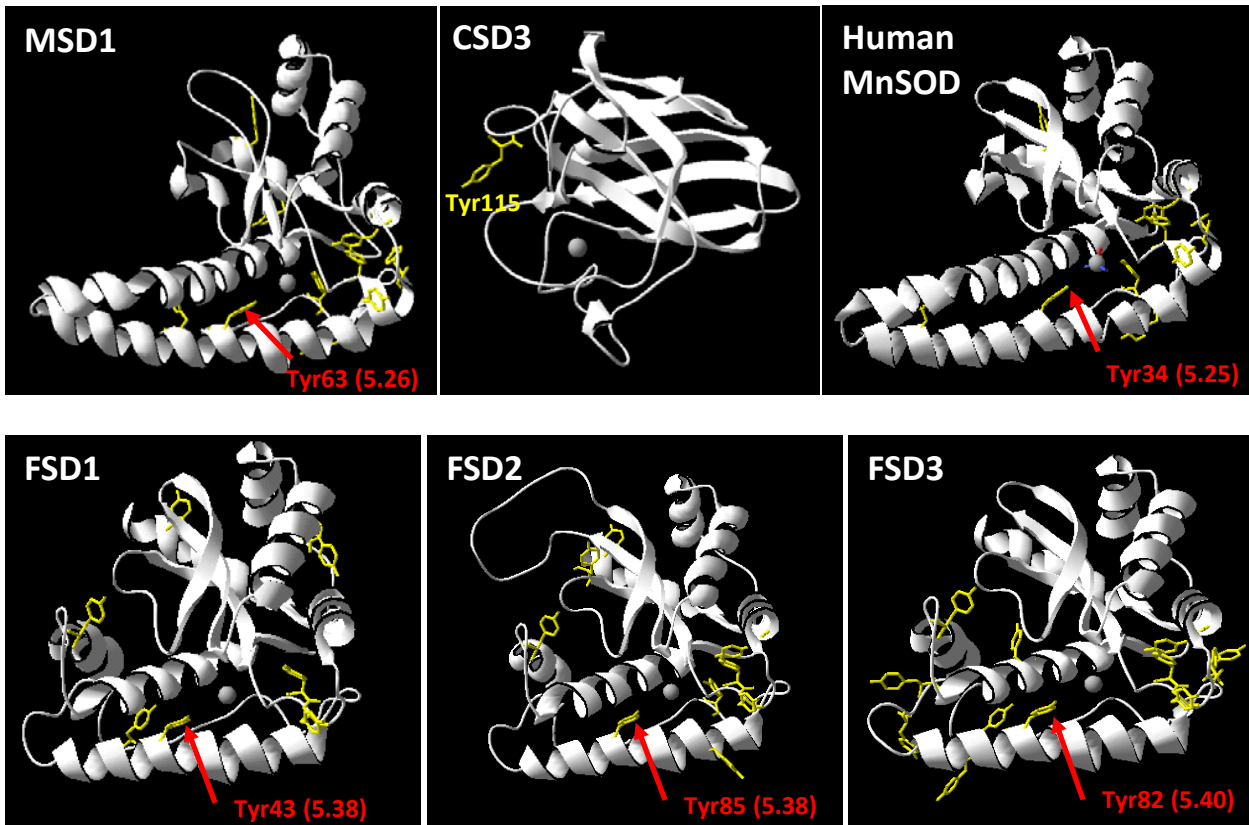


Figure 9

Differential Inhibition of *Arabidopsis* Superoxide Dismutases by Peroxynitrite-mediated Tyrosine Nitration

Christian Holzmeister, Frank Gaupels, Arie Geerlof, Hakan Sarioglu, Michael Sattler, Jörg Durner, Christian Lindermayr

Supplemental Table S1: Oligonucleotides for cloning of superoxide dismutase nucleotide sequences and site-directed mutagenesis

All oligonucleotides were obtained from Eurofins MWG Operon (Martinsried, Germany), diluted in water (100 µM) and stored at -20 °C.

Name	Sequence
<u>Oligonucleotides for amplification of superoxid dismutase nucleotide sequences</u>	
MnSOD_for	5'- ATGGCGATTCGTTGTGTAGC - 3'
MnSOD_rev (with stop codon)	5'- TCAGTTGTTTTCTTCTCATAAACCC - 3'
MnSOD_rev (without stop codon)	5'- GTTGTTTTCTTCTCATAAACCTC - 3'
FeSOD1_for	5'- ATGGCTGCTTCAAGTGCTG - 3'
FeSOD1_rev (with stop codon)	5'- TTAAGCAGAAGCAGCCTTGG - 3'
FeSOD1_rev (without stop codon)	5'- AGCAGAAGCAGCCTTGGC - 3'
FeSOD2_for	5'- ATGATGAATGTTGCAGTGACAG - 3'
FeSOD2_rev (with stop codon)	5'- TTAGTCAACCTCAGATACATCG - 3'
FeSOD2_rev (without stop codon)	5'- GTCAACCTCAGATACATCGAT - 3'
FeSOD3_for	5'- ATGAGTTCTTGTGTTGTGACG - 3'
FeSOD3_rev (with stop codon)	5'- TTAAGCGATTGGGATGTTGG - 3'
FeSOD3_rev (without stop codon)	5'- AGCGATTGGGATGTTGGG - 3'
CuZnSOD1_for	5'- ATGGCGAAAGGAGTTGCAG - 3'
CuZnSOD1_rev (with stop codon)	5'- TTAGCCCTGGAGACCAATG - 3'
CuZnSOD1_rev (without stop codon)	5'- GCCCTGGAGACCAATGAT - 3'
CuZnSOD2_for	5'- ATGGCTGCCACCAACACAA - 3'
CuZnSOD2_rev (with stop codon)	5'- TTAGAGCGGCGTCAAGC - 3'
CuZnSOD2_rev (without stop codon)	5'- GAGCGGCGTCAAGCCA - 3'
CuZnSOD3_for	5'- ATGGAAGCTCCTAGAGGAAATC - 3'
CuZnSOD3_rev (with stop codon)	5'- CTATAGTTTAGCATCCGCAGAT - 3'
CuZnSOD3_rev (without stop codon)	5'- TAGTTTAGCATCCGCAGATGATT - 3'

Oligonucleotides for GATEWAY-Cloning of superoxide dismutase nucleotide sequences

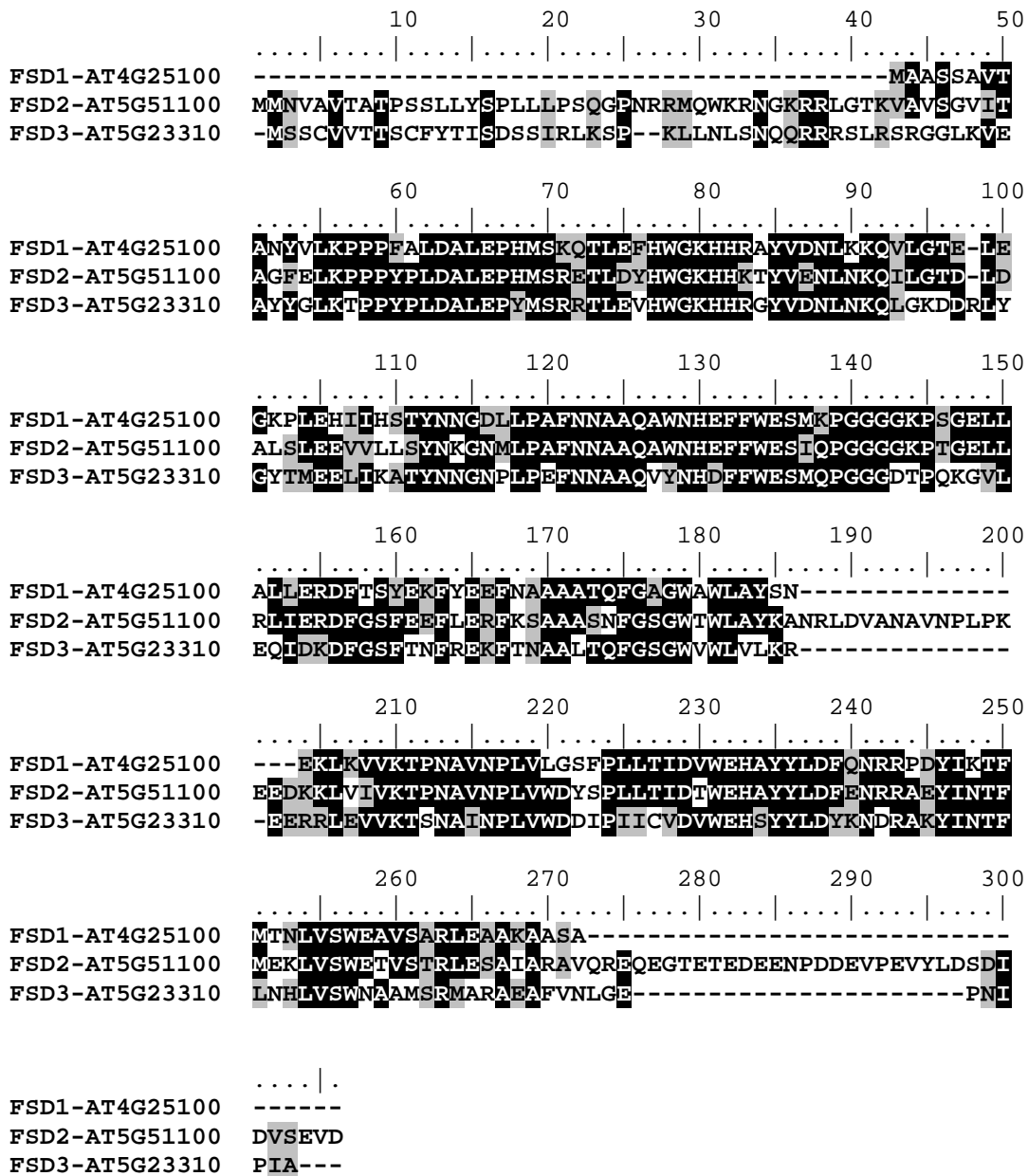
attB1_MnSOD_for (with stop codon)	5'- GGGACAAGTTTGTACAAAAAAGCAGGCTTCATG GCGATTCGTTGTGTAGC - 3'
attB2_MnSOD_rev (with stop codon)	5'- GGGGACCACTTTGTACAAGAAAGCTGGGTCTCA GTTGTTTTCTTCTCATAAACCC - 3'
attB1_MnSOD_for (without stop codon)	5'-GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGA AGGAGATAGAACCATGGCGATTGTTGTGTAGC - 3'
attB2_MnSOD_rev (without stop codon)	5'- GGGGACCACTTTGTACAAGAAAGCTGGGTCGTTGT TTTCTTCTCATAAACCTC - 3'
<hr/>	
attB1_FeSOD1_for (with stop codon)	5'- GGGACAAGTTTGTACAAAAAAGCAGGCTTCATGG CTGCTTCAAGTGCTG - 3'
attB2_FeSOD1_rev (with stop codon)	5'- GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAAG CAGAAGCAGCCTTGG - 3'
attB1_FeSOD1_for (without stop codon)	5'- GGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAG GAGATAGAACCATGGCTGCTTCAAGTGCTG - 3'
attB2_FeSOD1_rev (without stop codon)	5'- GGGACCACTTTGTACAAGAAAGCTGGGTCAGCAG AAGCAGCCTTGGC - 3'
<hr/>	
attB1_FeSOD2_for (with stop codon)	5'- GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGA TGAATGTTGCAGTGACAG - 3'
attB2_FeSOD2_rev (with stop codon)	5'- GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGA TGAA - 3'
attB1_FeSOD2_for (without stop codon)	5'- GGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAG GAGATAGAACCATGATGAATGTTGCAGTGACAG - 3'
attB2_FeSOD2_rev (without stop codon)	5'- GGGGACCACTTTGTACAAGAAAGCTGGGTCGTCAA CCTCAGATACATCGAT - 3'
<hr/>	
attB1_FeSOD3_for (with stop codon)	5'- GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGA GTTCTTGTGTTGTGACG - 3'
attB2_FeSOD3_rev (with stop codon)	5'- GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAAG CGATTGGGATGTTGG - 3'
attB1_FeSOD3_for (without stop codon)	5'- GGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAG GAGATAGAACCATGAGTTCCTTGTGTTGTGACG - 3'
attB2_FeSOD3_rev (without stop codon)	5'- GGGACCACTTTGTACAAGAAAGCTGGGTCAGCGA TTGGGATGTTGGG - 3'

attB1_CuZnSOD1_for (with stop codon)	5'- GGGACAAGTTTGTACAAAAAAGCAGGCTTCATGG CGAAAGGAGTTGCAG - 3'
attB2_CuZnSOD1_rev (with stop codon)	5'- GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAGC CCTGGAGACCAATG - 3'
attB1_CuZnSOD1_for (without stop codon)	5'- GGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAG GAGATAGAACCATGGCGAAAGGAGTTGCAG - 3'
attB2_CuZnSOD1_rev (without stop codon)	5'- GGGACCACTTTGTACAAGAAAGCTGGGTGCGCCCTG GAGACCAATGAT - 3'
<hr/>	
attB1_CuZnSOD2_for (with stop codon)	5'- GGGACAAGTTTGTACAAAAAAGCAGGCTTCATGG TTTCCGCGGCGAAGAAGGC - 3'
attB2_CuZnSOD2_rev (with stop codon)	5'- GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAGA GCGGCGTCAAGC - 3'
attB1_CuZnSOD2_for (without stop codon)	5'- GGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAG GAGATAGAACCATGGTTTCCGCGGCGAAGAAGGC - 3'
attB2_CuZnSOD2_rev (without stop codon)	5'- GGGACCACTTTGTACAAGAAAGCTGGGTGCGAGCG GCGTCAAGCCA - 3'
<hr/>	
attB1_CuZnSOD3_for (with stop codon)	5'- GGGACAAGTTTGTACAAAAAAGCAGGCTTCATGG AAGCTCCTAGAGGAAATC - 3'
attB2_CuZnSOD3_rev (with stop codon)	5'- GGGGACCACTTTGTACAAGAAAGCTGGGTCTTATA GTTTAGCATCCGCAGAT - 3'
attB1_CuZnSOD3_for (without stop codon)	5'- GGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAG GAGATAGAACCATGGAAGCTCCTAGAGGAAATC - 3'
attB2_CuZnSOD3_rev (without stop codon)	5'- GGGGACCACTTTGTACAAGAAAGCTGGGTCTAGTT TAGCATCCGCAGATGATT - 3'

Oligonucleotides for site-directed mutagenesis

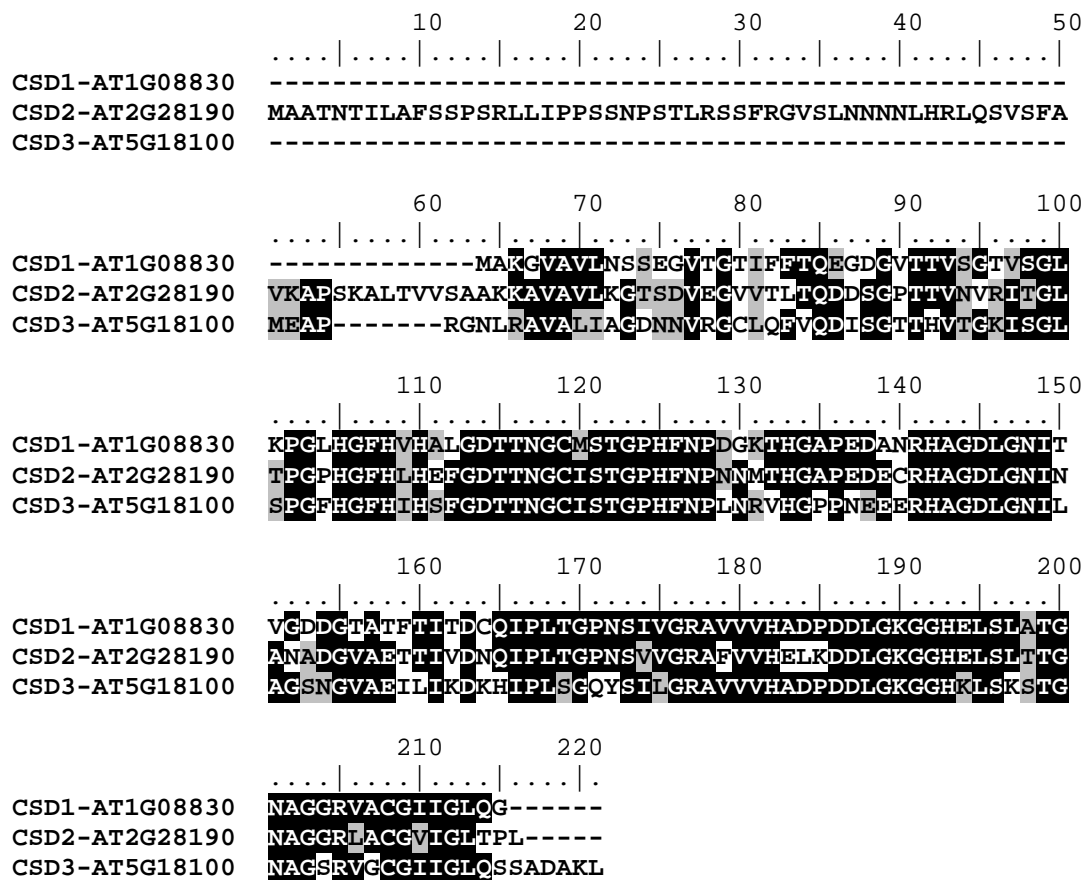
MnSODY63F_for	5'- CATCACCAGGCTTTTGTACTAATTAC - 3'
MnSODY63F_rev	5'- GTAATTAGTAACAAAAGCCTGGTGATG - 3'

Arabidopsis FSDs



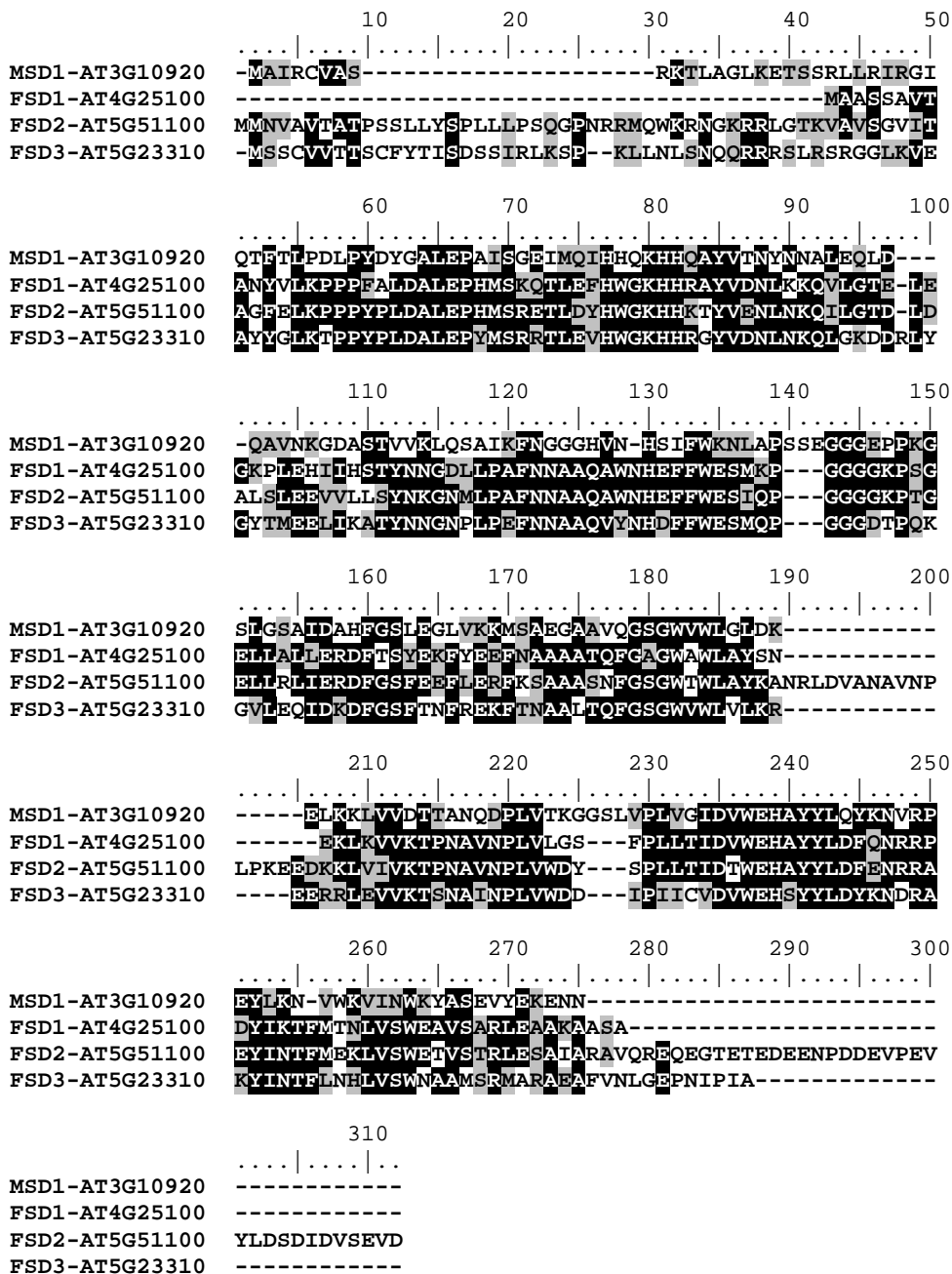
Supplemental Figure S1: Alignment of amino acid sequences of Arabidopsis FSD isoforms. Identical amino acids are highlighted in black, similar ones in grey. Dashes: Introduced gaps to maximize sequence similarity.

Arabidopsis CSDs



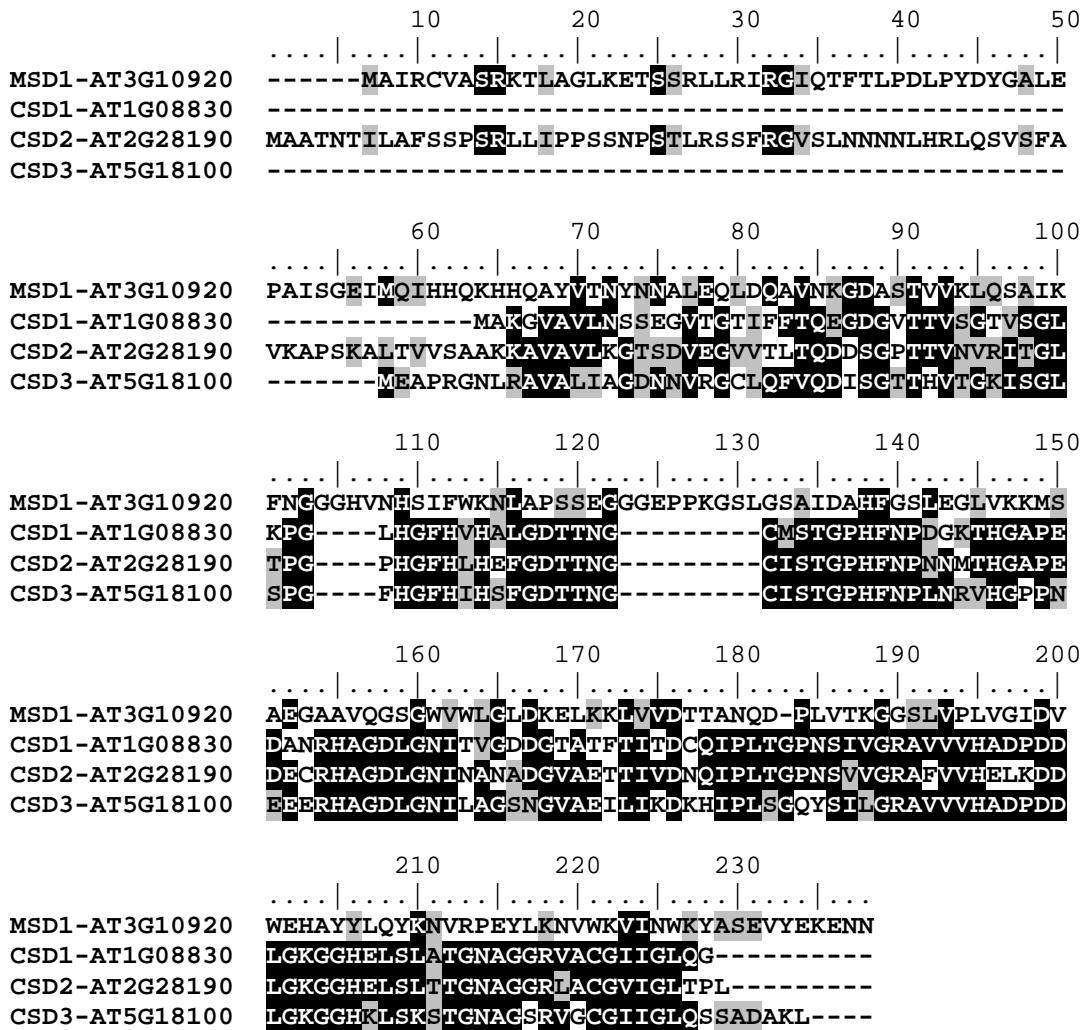
Supplemental Figure S2: Alignment of amino acid sequences of *Arabidopsis* CSD isoforms. Identical amino acids are highlighted in black, similar ones in grey. Dashes: Introduced gaps to maximize sequence similarity.

Arabidopsis MSD1-FSDs



Supplemental Figure S3: Alignment of amino acid sequences of *Arabidopsis* FSD isoforms and MSD1. Identical amino acids are highlighted in black, similar ones in grey. Dashes: introduced gaps to maximize sequence similarity.

Arabidopsis MSD1-CSDs



Supplemental Figure S4: Alignment of amino acid sequences of Arabidopsis CSD isoforms and MSD1. Identical amino acids are highlighted in black, similar ones in grey. Dashes: Introduced gaps to maximize sequence similarity.

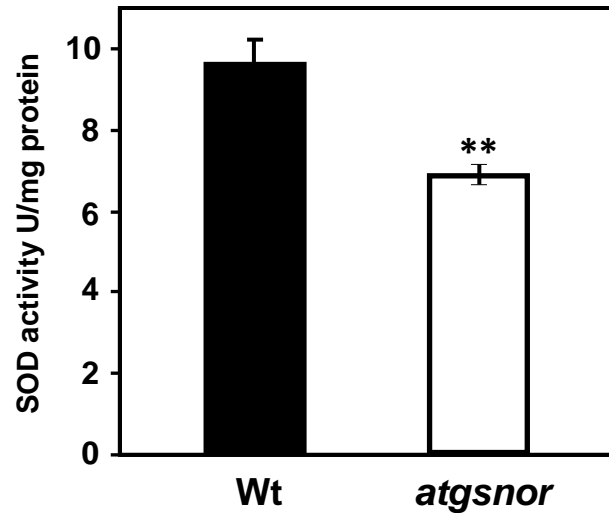


Figure S5: Total SOD activity in *Arabidopsis* WT and GSNOR knock-out plants. Proteins of 0,5 g leaf material of four week old plants were extracted with 1 ml extraction buffer. Total SOD activity was determined by monitoring reduction of cytochrome *c*. One unit is defined as enzyme amount necessary for 50% inhibition of cytochrome *c* reduction. Asterisks (**) indicate a significant difference between both lines (t-test, $p \leq 0.01$).

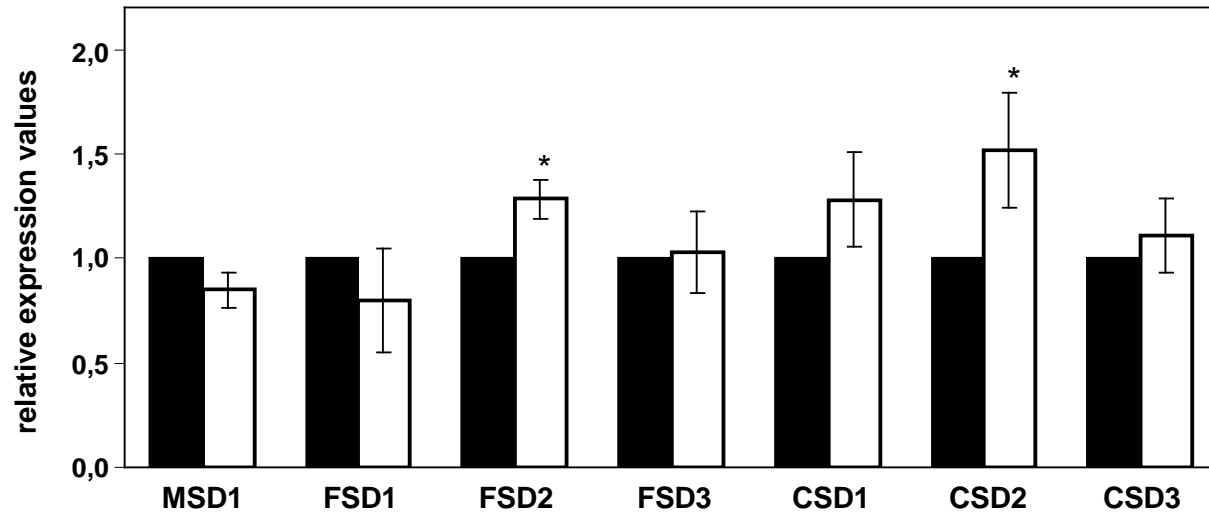


Figure S6: Expression analysis of *Arabidopsis* SODs.

Transcripts of *Arabidopsis* SODs were analysed by real-time quantitative PCR. Data represent the means \pm SD of three experiments per lines. Normalization of real-time quantitative RT-PCR data was done by geometric averaging of multiple internal control genes (Ubiquitin 9 [At5g18380] and S16 [At5g18380 and At2g09990]).