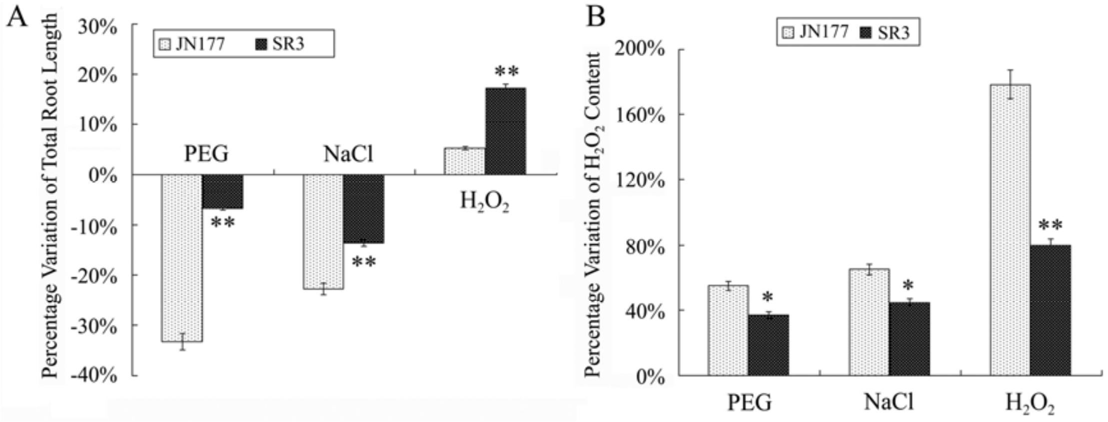
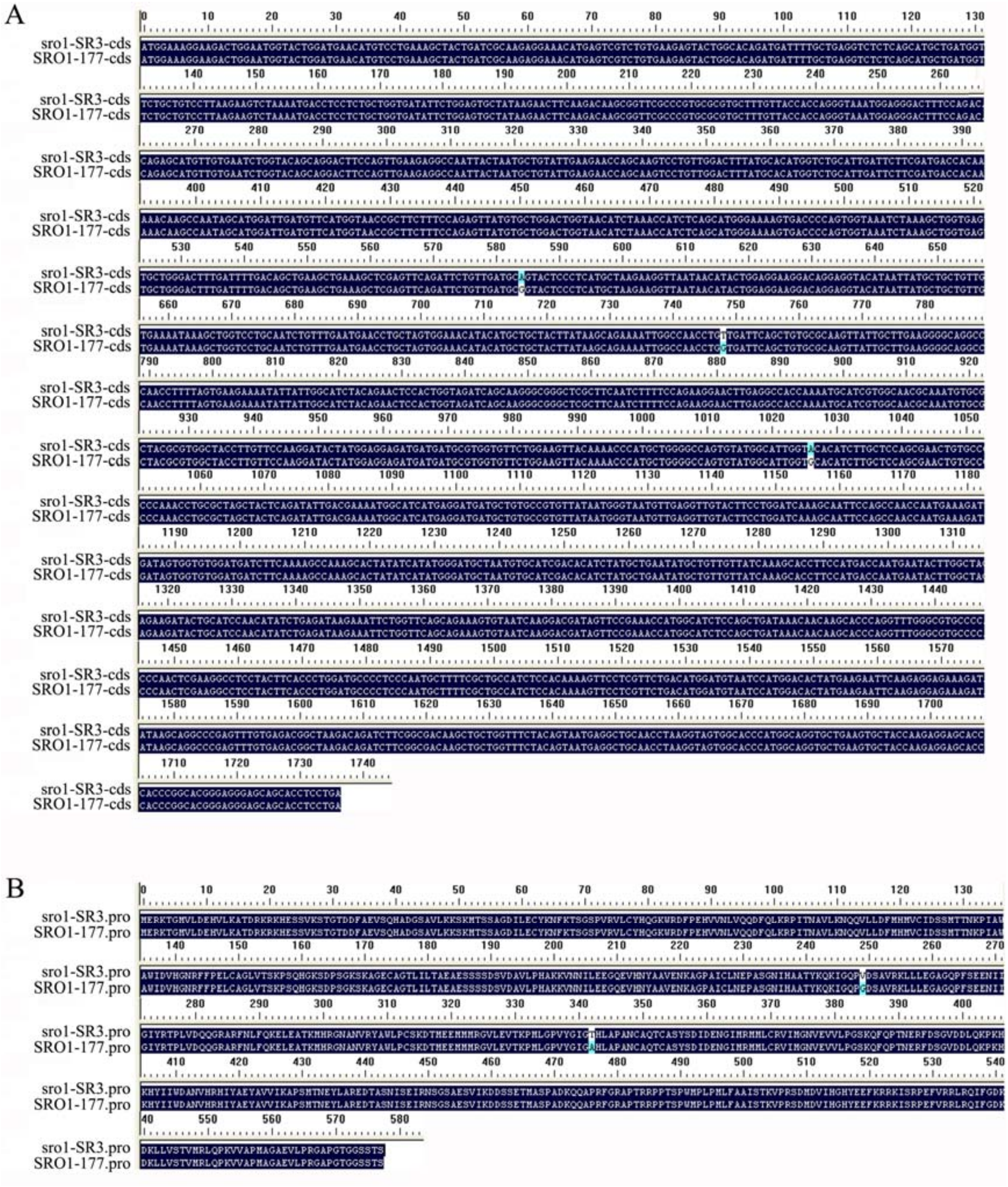
**Supplemental Data**. Liu et al. (2014). Plant Cell 10.1105/tpc.113. 118687

### Supplemental Figures



**Supplemental Figure 1.** Variation of total root length and root $H_2O_2$ content in SR3 under stress conditions.

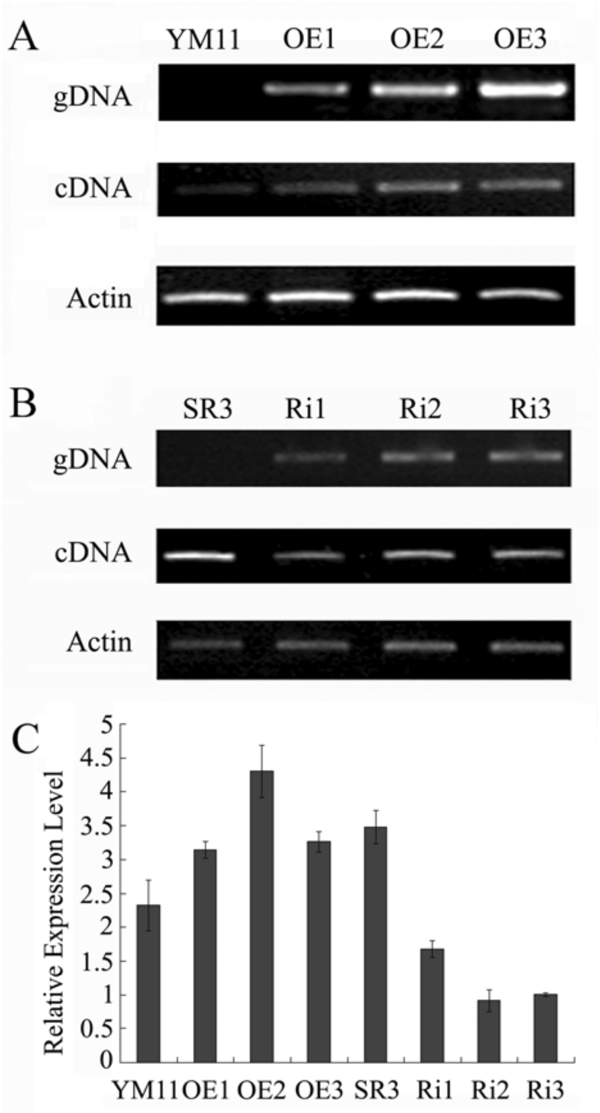
**(A)** and **(B)** Percentage variation of total root length **(A)** and root $H_2O_2$ content **(B)** in one-week old SR3 and JN177 exposed to 18% PEG, 200 mM NaCl or 200 mM $H_2O_2$. Non-stressed or stressed seedlings were grown for two weeks. All data are given as mean ± s.d. The asterisks and double asterisks represent significant difference determined by Student's *t*-test at $P < 0.05$ and $P < 0.01$, respectively. n=60.



**Supplemental Figure 2**. Sequence alignment of coding DNA sequences (CDS) and protein sequences of SRO1 and sro1.

**(A)** Sequence alignment of coding DNA sequences of *SRO1* and *sro1*.

**(B)** Sequence alignment of protein sequences of SRO1 and sro1.

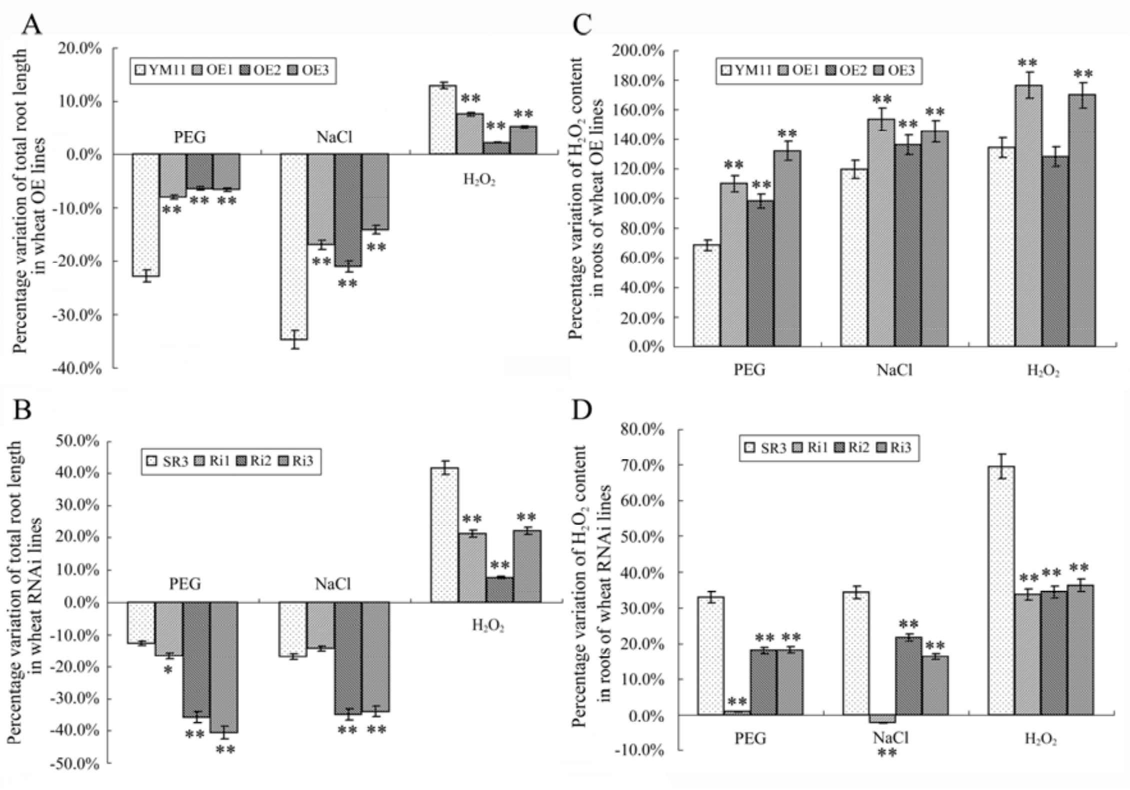


**Supplemental Figure 3.** PCR test of transgenic wheat plants.

**(A)** PCR test of transgenic wheat plants constitutively expressing *sro1*. The upper panel, *sro1* insertion into YM11 revealed by PCR in YM11, *sro1* OE1, *sro1* OE2 and *sro1* OE3 transgenic plants; the middle and lower panel, transcript levels of *sro1* revealed by RT-PCR.

**(B)** PCR test of transgenic wheat plants repressing *sro1*. The upper panel, the insertion of *sro1*-RNAi fragment into SR3 revealed by PCR in SR3, Ri (RNAi) 1, Ri2 and Ri3 transgenic plants; the middle and lower panel, transcript levels of *sro1* revealed by RT-PCR.

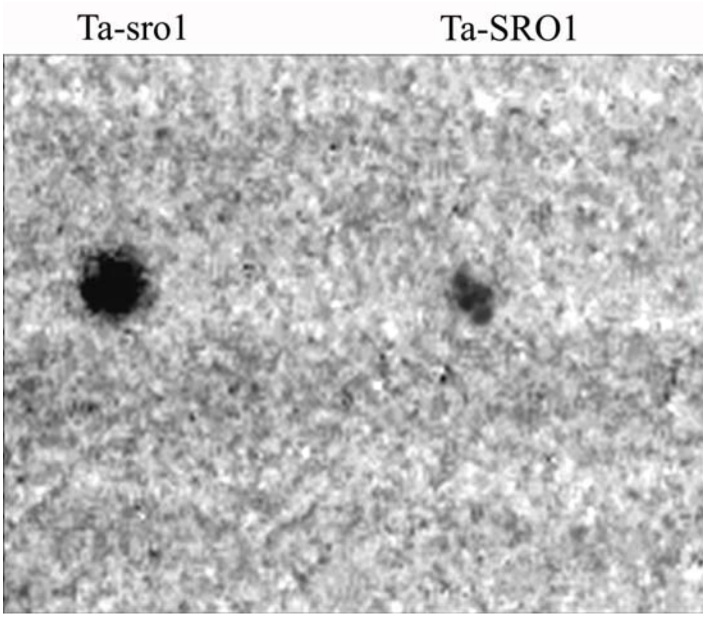
**(C)** Quantitative RT-PCR test of transgenic wheat plants constitutively expressing or repressing *sro1*. Transcript levels relative to Ta-*Actin* are presented for each sample. All data are given as mean ± s.d. of three independent biological replicates.



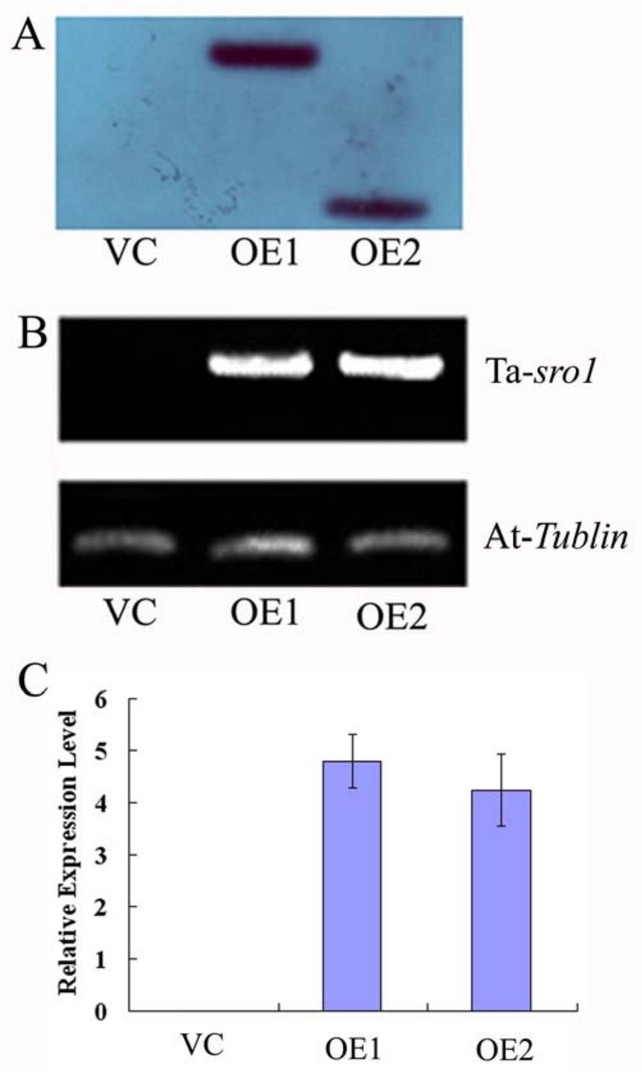
**Supplemental Figure 4.** Variation of total root length and root $H_2O_2$ content in transgenic wheat lines under stress conditions.

**(A)** and **(B)** Percentage variation of total root length in one-week-old *sro1* overexpression (OE) wheat lines **(A)** and *sro1* RNAi (Ri) lines **(B)** exposed to 18% PEG, 200 mM NaCl or 200 mM $H_2O_2$.

**(C)** and **(D)** Percentage variation of $H_2O_2$ content in the roots of one-week-old wheat OE lines **(C)** and Ri lines **(D)** exposed to 18% PEG, 200 mM NaCl or 200 mM $H_2O_2$. Non-stressed or stressed seedlings grown for two weeks. All data are given as mean ± s.d. The asterisks and double asterisks represent significant difference determined by the Student's *t*-test at $P < 0.05$ and $P < 0.01$, respectively. n=15.



**Supplemental Figure 5**. *In vitro* DNA binding activity of Ta-sro1-His$_6$ and Ta-SRO1-His$_6$ proteins. 1 µg of purified Ta-sro1-His$_6$ and Ta-SRO1-His$_6$ protein was used for dot blotting. 10 µg/mL biotinylated calf thymus DNA was used as probe in this assay.

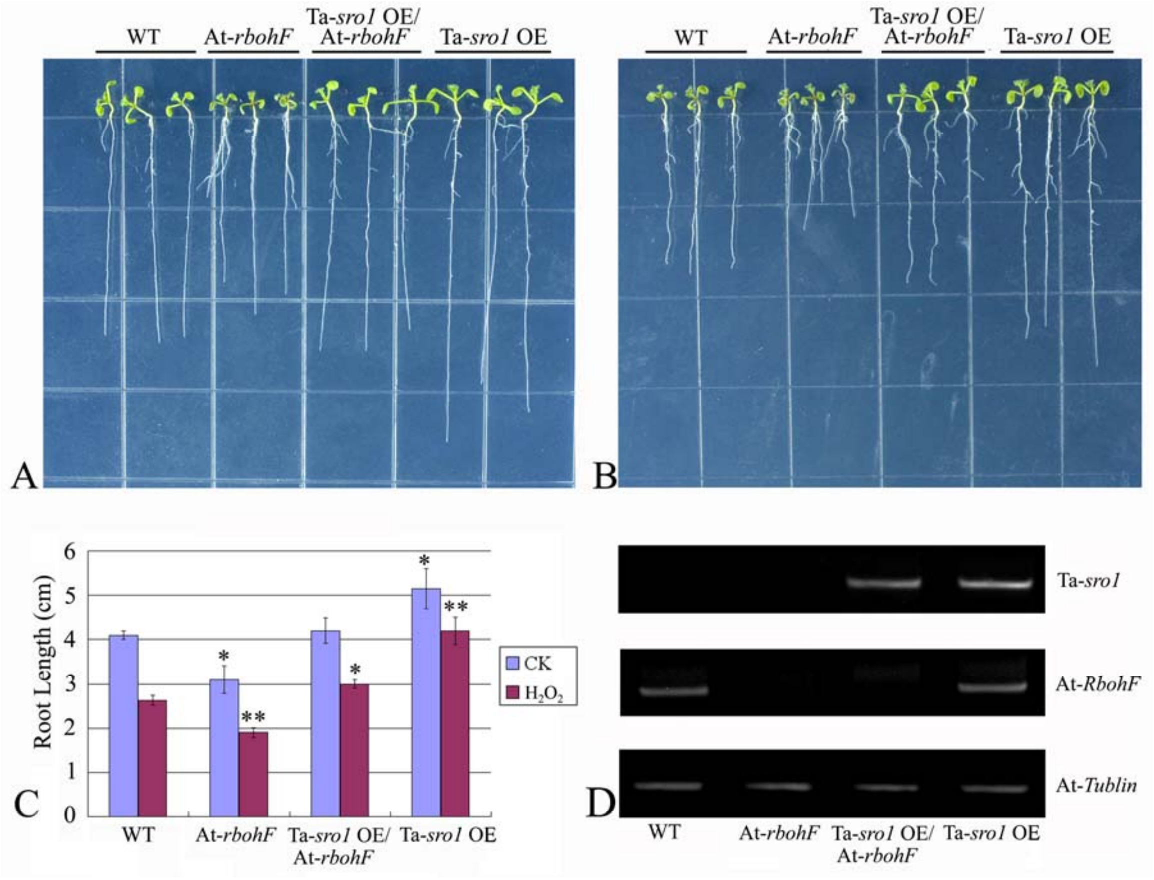


**Supplemental Figure 6.** Transgenic test of the constitutive expression of Ta-*sro1* in wild-type *A. thaliana*.

**(A)** Ta-*sro1* insertion into Col-0 revealed by Southern blot in vector control (VC), Ta-*sro1* OE1 and Ta-*sro1* OE2 transgenic plants.

**(B)** Transcript levels of Ta-*sro1* revealed by RT-PCR.

**(C)** Transcript levels of Ta-*sro1* revealed by quantitative RT-PCR. Transcript levels relative to At-*Tublin* are presented for each sample. The data are given as mean ± s.d. of three independent biological replicates.

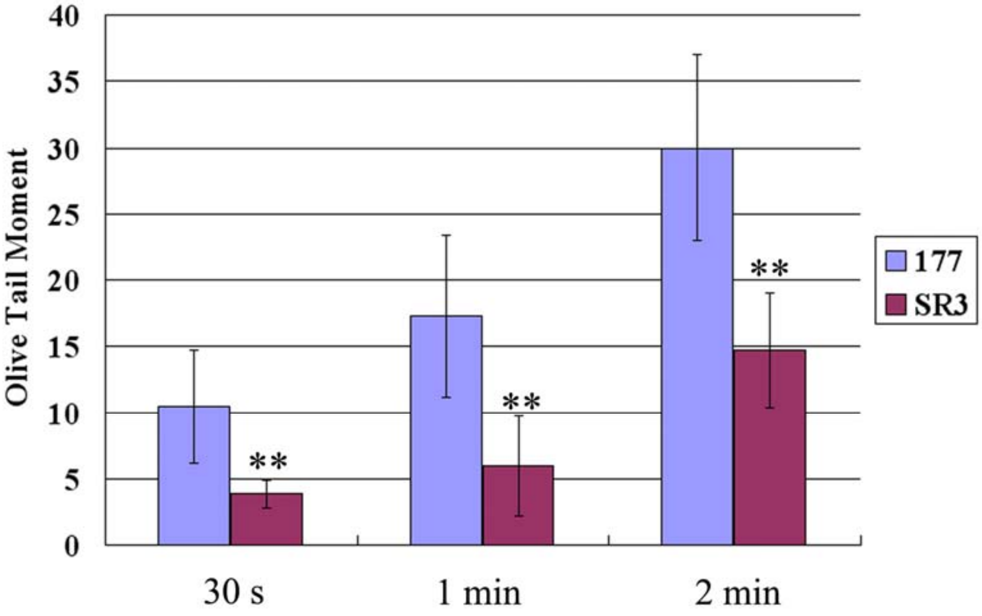


**Supplemental Figure 7.** Over-expression of *Ta-sro1* in the At-*rbohF* mutant background promoted the oxidative stress tolerance of the mutant.

**(A)** and **(B)** Phenotype of ten-day-old wild type, At-*rbohF* mutant, Ta-*sro1* OE lines and At-*rbohF* /Pro*35S:Ta-sro1* transgenic lines under control **(A)** and 0.6 mM $H_2O_2$ **(B)** for 5 days.

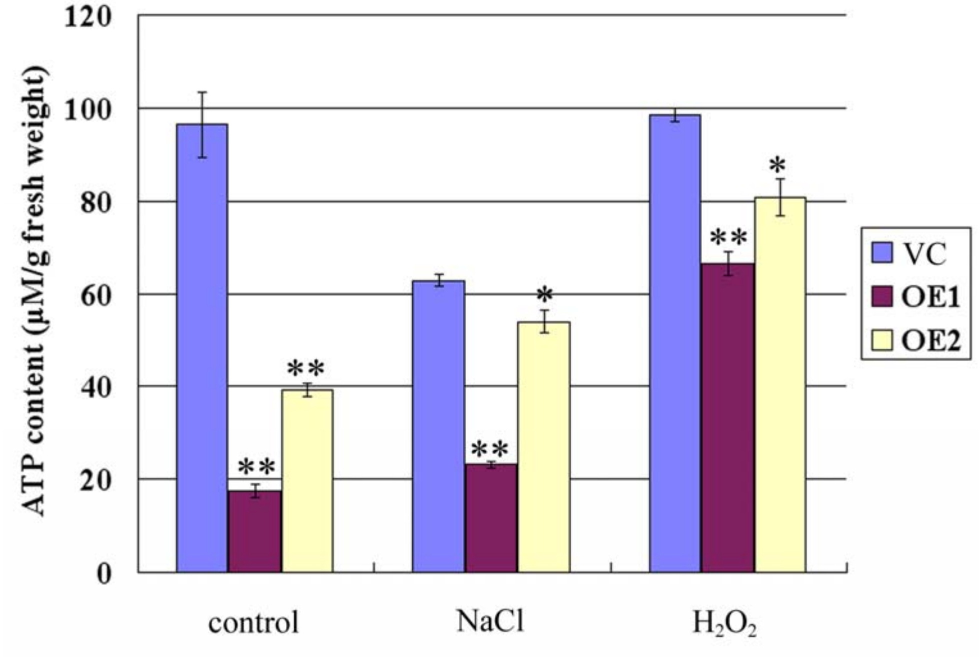
**(C)** Quantitative measurement of total root length in At-*rbohF* mutant, Ta-*sro1* OE and At-*rbohF* /Pro*35S:*Ta-*sro1* transgenic lines under control **(A)** and 0.6 mM $H_2O_2$ **(B)**.

**(D)** Expression levels of Ta-*sro1* and At-*RbohF* in the above seedlings revealed by RT-PCR. All data are given as mean ± s.d. of three independent experiments. The asterisks and double asterisks represent significant difference determined by Student's *t*-test at $P < 0.05$ and $P < 0.01$, respectively.



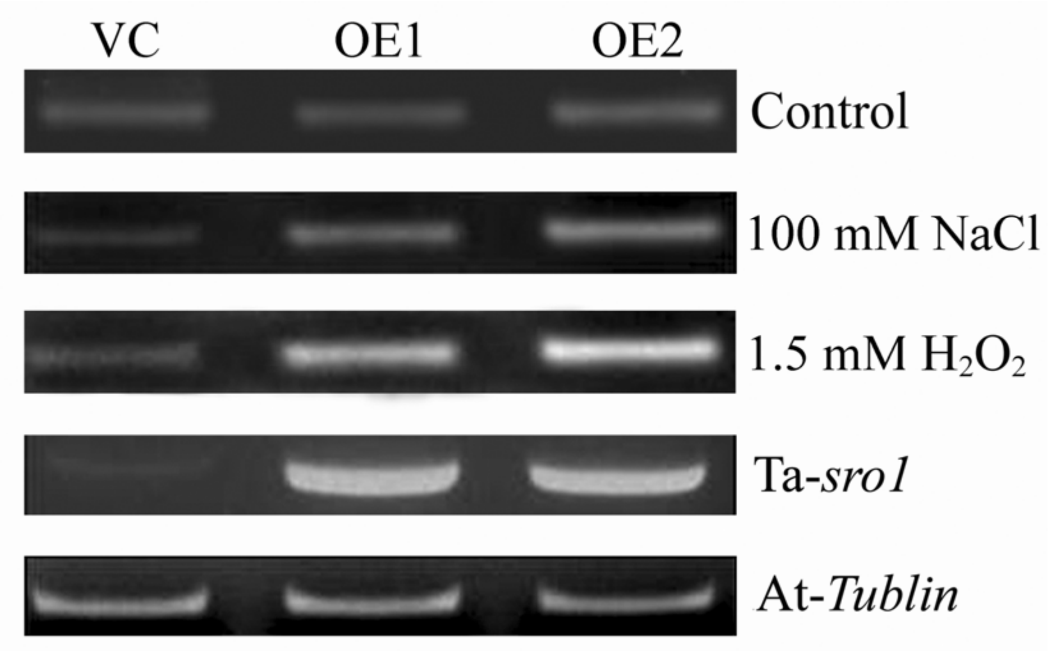
**Supplemental Figure 8**. Single cell gel electrophoresis (SCGE) analysis of the protoplasts of JN177 and SR3 exposed to UV treatment.

DNA damage in protoplasts of JN177 and SR3 exposed to UV for 30 s, 1 min and 2 min. Olive tail moment (OTM) represents the product of the percentage of total DNA in the tail (TD) and the tail length (TL), measured from the centre of the nucleus towards the end of the tail (OTM = TL×TD). All data are given as mean ± s.d. of three independent experiments. The double asterisks represent significant difference determined by the Student's *t*-test at $P < 0.01$.

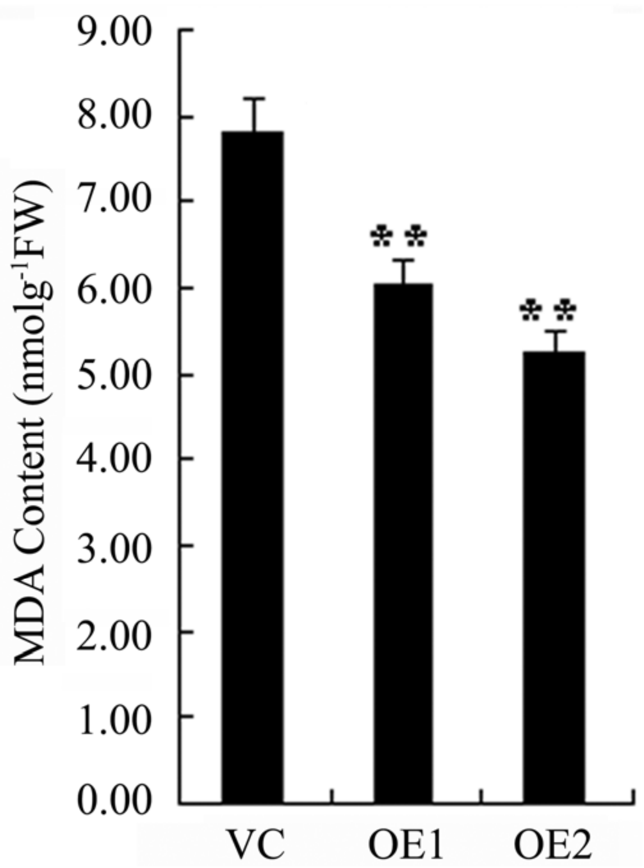


**Supplemental Figure 9**. The ATP content between vector control (VC) and Ta-*sro1* overexpression (OE) *A. thaliana* lines under normal and stress conditions.

All data are given as mean ± s.d. of three independent experiments. The asterisks and double asterisks represent significant difference determined by Student's *t*-test at $P < 0.05$ and $P < 0.01$, respectively.



**Supplemental Figure 10.** Expression of At-*ATM* in vector control (VC) and Ta-*sro1* overexpression (OE) *A. thaliana* lines. Control, no stress imposed to the plants.



**Supplemental Figure 11.** The malondialdehyde (MDA) content of vector control (VC) and Ta-*sro1* overexpression (OE) ***A.*** *thaliana* lines under salinity stress.

All data are given as mean ± s.d. of three independent experiments. The double asterisks represent significant differences determined by Student's *t*-test at $P < 0.01$.

**Supplemental Table 1** Oxidative stress related-genes showing at least a two-fold induction or repression upon exposure to abiotic stress.

| Probe ID | Target ID | Discription | Seq Description |
|---|---|---|---|
| ta_02235 | lcl\|TC236720 | peroxidase, putative | peroxidase |
| ta_02525 | lcl\|TC237832 | ozone-responsive stress-related protein, putative | ozone-responsive stress-related |
| ta_02691 | lcl\|TC238667 | XPB1 (ARABIDOPSIS HOMOLOG OF XERODERMA | DNA repair and transcription factor xpb1 |
| ta_02748 | lcl\|TC238988 | peroxidase 30 (PER30) (P30) (PRXR9) | peroxidase |
| ta_02919 | lcl\|TC240399 | ozone-responsive stress-related protein, putative | ozone-responsive stress-related |
| ta_02981 | lcl\|TC240853 | RCI3 (RARE COLD INDUCIBLE GENE 3) | peroxidase 1 |
| ta_03206 | lcl\|TC243256 | peroxidase, putative | peroxidase 53, expressed |
| ta_03386 | lcl\|TC246747 | ATGPX6 (GLUTATHIONE PEROXIDASE | glutathione peroxidase |
| ta_03572 | lcl\|TC247144 | ATGPX6 (GLUTATHIONE PEROXIDASE | glutathione peroxidase |
| ta_03790 | lcl\|TC247784 | ATGPX6 (GLUTATHIONE PEROXIDASE | glutathione peroxidase |
| ta_03938 | lcl\|TC248113 | peroxidase, putative | peroxidase |
| ta_03985 | lcl\|TC248249 | peroxidase, putative | bacterial-induced peroxidase precursor |
| ta_04167 | lcl\|TC248823 | ATGPX6 (GLUTATHIONE PEROXIDASE | glutathione peroxidase |
| ta_04333 | lcl\|TC249202 | peroxidase 12 (PER12) (P12) (PRXR6) | anionic peroxidase |
| ta_04364 | lcl\|TC249268 | peroxidase 12 (PER12) (P12) (PRXR6) | anionic peroxidase |
| ta_04486 | lcl\|TC249534 | peroxidase, putative | peroxidase 53, expressed |
| ta_04506 | lcl\|TC249588 | anionic peroxidase, putative | peroxidase family, expressed |
| ta_04511 | lcl\|TC249601 | peroxidase, putative | peroxidase 52, expressed |
| ta_04527 | lcl\|TC249624 | peroxidase 22 (PER22) (P22) (PRXEA) / basic peroxidase | peroxidase |
| ta_04529 | lcl\|TC249631 | RCI3 (RARE COLD INDUCIBLE GENE 3) | peroxidase family, expressed |
| ta_04543 | lcl\|TC249670 | EMB2171 (EMBRYO DEFECTIVE 2171); structural | 60s ribosomal protein l23 |
| ta_04549 | lcl\|TC249692 | RCI3 (RARE COLD INDUCIBLE GENE 3) | peroxidase precursor |
| ta_04552 | lcl\|TC249701 | peroxidase, putative | peroxidase family, expressed |
| ta_04975 | lcl\|TC250316 | peroxidase, putative | root peroxidase |
| ta_04979 | lcl\|TC250320 | peroxidase, putative | peroxidase |
| ta_04980 | lcl\|TC250321 | peroxidase 30 (PER30) (P30) (PRXR9) | peroxidase 1 precursor |
| ta_04981 | lcl\|TC250322 | peroxidase, putative | peroxidase 72 precursor |
| ta_04982 | lcl\|TC250324 | RCI3 (RARE COLD INDUCIBLE GENE 3) | peroxidase 1 precursor |
| ta_04983 | lcl\|TC250325 | RCI3 (RARE COLD INDUCIBLE GENE 3) | peroxidase 1 precursor |
| ta_04985 | lcl\|TC250327 | peroxidase 72 (PER72) (P72) (PRXR8) | peroxidase 72 precursor |
| ta_04990 | lcl\|TC250334 | RCI3 (RARE COLD INDUCIBLE GENE 3) | peroxidase 1 precursor |
| ta_04992 | lcl\|TC250338 | peroxidase, putative | root peroxidase |
| ta_04994 | lcl\|TC250340 | RCI3 (RARE COLD INDUCIBLE GENE 3) | peroxidase 1 precursor |
| ta_04996 | lcl\|TC250345 | peroxidase 30 (PER30) (P30) (PRXR9) | peroxidase |
| ta_06216 | lcl\|TC252860 | RBOHD (RESPIRATORY BURST OXIDASE PROTEIN | nadph oxidase |
| ta_06566 | lcl\|TC253673 | RBOHD (RESPIRATORY BURST OXIDASE PROTEIN | respiratory burst oxidase protein b |
| ta_07255 | lcl\|TC255712 | peroxidase 27 (PER27) (P27) (PRXR7) | peroxidase family, expressed |
| ta_07319 | lcl\|TC255976 | ATRBOHB (RESPIRATORY BURST OXIDASE HOMOLOG B) | respiratory burst oxidase protein b |
| ta_07444 | lcl\|TC256406 | peroxidase, putative | peroxidase |

| | | | |
|---|---|---|---|
| ta_07513 | lcl\|TC256670 | peroxidase, putative | peroxidase 49 precursor |
| ta_07972 | lcl\|TC258661 | peroxidase, putative | peroxidase family, expressed |
| ta_08118 | lcl\|TC259505 | cationic peroxidase, putative | peroxidase 43, expressed |
| ta_08164 | lcl\|TC259922 | RCI3 (RARE COLD INDUCIBLE GENE 3); | peroxidase 1 precursor |
| ta_08213 | lcl\|TC260407 | peroxidase 12 (PER12) (P12) (PRXR6) | peroxidase 1 |
| ta_08389 | lcl\|TC261867 | anionic peroxidase, putative | peroxidase family, expressed |
| ta_08661 | lcl\|TC262975 | peroxidase, putative | cationic peroxidase isozyme 40k precursor |
| ta_08667 | lcl\|TC262983 | APX1 (ASCORBATE PEROXIDASE 1) | ascorbate peroxidase |
| ta_09233 | lcl\|TC264120 | ATGPX1 (GLUTATHIONE PEROXIDASE 1); glutathione | glutathione peroxidase |
| ta_09247 | lcl\|TC264139 | ATGPX7 (GLUTATHIONE PEROXIDASE 7); glutathione | glutathione peroxidase |
| ta_09737 | lcl\|TC264894 | peroxidase, putative | peroxidase 1 precursor |
| ta_09739 | lcl\|TC264896 | peroxidase, putative | peroxidase 1 precursor |
| ta_10334 | lcl\|TC266138 | SAPX | stromal ascorbate peroxidase |
| ta_10670 | lcl\|TC266948 | peroxidase, putative | tpa: class iii peroxidase 65 precursor |
| ta_10713 | lcl\|TC267045 | peroxidase, putative | peroxidase familyexpressed |
| ta_10714 | lcl\|TC267046 | anionic peroxidase, putative | peroxidase family, expressed |
| ta_10865 | lcl\|TC267426 | peroxidase, putative | peroxidase |
| ta_10866 | lcl\|TC267427 | peroxidase, putative | peroxidase |
| ta_11263 | lcl\|TC268590 | ALPHA-DOX1 (ALPHA-DIOXYGENASE 1) | feebly-like protein |
| ta_11519 | lcl\|TC269272 | peroxidase 27 (PER27) (P27) (PRXR7) | peroxidase 1 precursor |
| ta_12269 | lcl\|TC272108 | RCI3 (RARE COLD INDUCIBLE GENE 3) | peroxidase 1 precursor |
| ta_12455 | lcl\|TC273129 | peroxidase, putative | peroxidase 1 precursor |
| ta_13839 | WL604 | peroxidase, putative | peroxidase 52, expressed |
| ta_13986 | WL751 | peroxidase, putative | peroxidase |
| ta_10067 | lcl\|TC265505 | RCD1 (RADICAL-INDUCED CELL DEATH1) | poly (ADP ribose) polymerase catalytic domain containing, expressed |

Note: The red color indicated the abiotic stress induced genes homologous with At-*RCD1*

**Supplemental Table 2**. Model evaluations and templates (PDB codes) used for modeling.

| | Ta-SRO1 | Ta-sro1 | At-RCD1 | At-PARP1 | At-PARP2 |
|---|---|---|---|---|---|
| ProQ_LG/MS | 4.16/0.52 | 3.88/0.43 | 4.04/0.49 | 5.21/0.65 | 5.23/0.56 |
| PROCHECK | 97.6% | 96.4% | 97.6% | 98.7% | 98.3% |
| Templates | 3HKV | 3HKV | 2PQF, 3HKV | 3KCZ, 1GS0, 1UK0 | 1UK0, 1A26 |

All these displayed scores indicate the models to be reliable in terms of overall packing. ProQ_LG: >1.5 fairly good; >2.5 very good; >4 extremely good. ProQ_MS: >0.l, fairly good; >0.5, very good; >0.8, extremely good. PROCHECK: percentage of residues in the most favored regions or additional allowed regions by Ramachandran plot.

**Supplemental Table 3**. Primers used for PCR, RT-PCR and real-time RT-PCR analysis.

| **Experiment** | **Name** | **Primer sequence (5'-3')** |
|---|---|---|
| Real time RT-PCR | Ta-sro1QF | ATGACCACAAACAAGCCAATAG |
| | Ta-sro1QR | AAAATCAAAGTCCCAGCACACT |
| | Ta-ActinQF | GTTCCAATCTATGAGGGATACACGC |
| | Ta-ActinQR | GAACCTCCACTGAGAACAACATTAC |
| | At-TublinQF | CTCAAGAGGTTCTCAGCAGTA |
| | At-TublinQR | TCACCTTCTTCATCCGCAGTT |
| | At-NDB2QF | GAAACTGGAACCAAGAAGAAGAAG |
| | At-NDB2QR | AGGTAGTAAAGGAGTGAAAGCAAA |
| | At-AOX1AQF | TTGAGGAAGCAGAGAATGAGAGAA |
| | At-AOX1AQR | CCAAGGAAATAAGCGTTGAAGAAG |
| Subcellular localization | Ta-sro1LF | GGATCCATGGAAAGGAAGACTGGAATG |
| | Ta-sro1LR | AAGCTTGGAGGTGCTGCTCCCTC |
| Protein expression | Ta-sro1PF | GGATCCATGGAAAGGAAGACTGGA |
| | Ta-sro1PR | GCGGCCGCTCA GGA GGT GCT GCT CCC |
| Overexpression in Arabidopsis | Ta-sro1AOE-F | TCTAGAATGGAAAGGAAGACTGGA |
| | Ta-sro1AOE-R | GGATCCTCAGGAGGTGCTGCTCCC |
| Overexpression in wheat | Ta-sro1WOE-F | GGATCCATGGAAAGGAAGACTGGA |
| | Ta-sro1WOE-R | GAGCTCTCAGGAGGTGCTGCTCCC |
| RNAi in wheat | Ta-sro1Ri-F | AAGGATCCGAGCTCCAGCAGAAAGTGTAATCAAGGAC |
| | Ta-sro1Ri-R | AAGGTACCACTAGTCTCCCCGAGCTGTTATCTCC |
| RT-PCR | At-ATM-RT-F | AAGCAACTTGCGAAATCTGGC |
| | At-ATM-RT-R | TTACATCCAAGCTCCCCAGC |
| | At-RbohF-RT-F | CAGCAACCGCCATTAATG |
| | At-RbohF-RT-R | CATCGAACAGTTCCAATGC |
| | Ta-sro1-RT-F | ATGACCACAAACAAGCCAATAG |
| | Ta-sro1-RT-R | GTAACTTCCAGAACACCACGCA |
| | At-Tublin-RT-F | CTCAAGAGGTTCTCAGCAGTA |
| | At-Tublin-RT-R | TCACCTTCTTCATCCGCAGTT |