# Supporting Information

**Châtelain et al. 10.1073/pnas.1220589110**

## MSRs A

```
                      10        20        30        40        50        60        70        80        90
                       |         |         |         |         |         |         |         |         |
MtMSRA2       -----------------------------------------------------------------MATSEGGNGNHNTAFDPDLDIPDNP
MSRA4.1L      MRICGAAAASSAYSTTSSSLLVFGSSSFSTPAKTKFLPSLSRFSVKHSCLFSPTRPHFTVTKPSMNLLNKLGFGSGRSSESMDSTIPQGP
MSRA4.1S      ----------------------------------------------------------------MNLLNKLGFGSGRSSESMDSTIPQGP
MSRA4.2       ----------------------------------------------------------------MYLLNRLWFGSARVTEKMDSSIAQGL
MSRA5         ---MKLSEKTNNYYYILSIFIILIAFLINNANCIRFPDRVAQPAREQP---DQQRLQTAVFALGSFWRSEAVFGCLPGVVRTTVGYSGGS

                     100       110       120       130       140       150       160       170       180
                       |         |         |         |         |         |         |         |         |
MtMSRA2       DDE-------FAEFGAGCFWGVELAFQRVPGVVKTEVGYTQGHTPDPNYKLVCTGTTNHVEVVRVQFDPKLCPYTNLLDLFWSRHDPTTL
MSRA4.1L      DDDIPAPGQQFAQFGAGCFWGVELVFQRVPGVSKTEVGYTQGLLHNPTYEDVCSGTTNHNEVVRVQYDPKQGTFENLLDTFWSKHDPTTP
MSRA4.1S      DDDIPAPGQQFAQFGAGCFWGVELVFQRVPGVSKTEVGYTQGLLHNPTYEDVCSGTTNHNEVVRVQYDPKQGTFENLLDTFWSKHDPTTP
MSRA4.2       DDDTPALGQQFAQFGAGCFWSVELAFQRVAGVTKTEVGYSQGLLHNPRYQDVCSATTRHSEVVRLQYDPKECSYETLLDAFWAKHDPTTL
MSRA5         KPN-----PEYRSFGDHAE-SVQVHEKARFCLTIHSIKVTVKHASPK-----CSGLDSG---IHVEYDPRLISFGELLDIFWSSHDPRQV

                     190       200       210       220       230       240       250       260       270
                       |         |         |         |         |         |         |         |         |
MtMSRA2       NRQGGDVGAQYRSGIYYYNETQSRLAQESKEAKQLEHKDKIVT-EILPAKRFYRAEEYHQQYLEKGGGKGRGHGQSAQKGCNHPIRCYG-
MSRA4.1L      NRQGNDVGTQYRSGIYFYTPEQEKIAKESLEQQEKQLGRKIAT-EILPAKKFYRAEEYHQQYLEKGGRFG--FKQSAAKGCNDPIRCYG-
MSRA4.1S      NRQGNDVGTQYRSGIYFYTPEQEKIAKESLEQQEKQLGRKIAT-EILPAKKFYRAEEYHQQYLEKGGRFG--FKQSAAKGCNDPIRCYG-
MSRA4.2       NRQGNDVGTQYRSGIYYYTPEQEKAARESLEQQQKKLNRKIVT-EILPAKKFYRAEEYHQQYLEKGGRFG--CKQSSSKGCNDPIRCYG-
MSRA5         FGQGPDVGNQYRSIIFVNGTEESRMASVSKEQEQTRSRSSIVTTQILQLGTFHPAEPEHQKFELKQNTFLLQLIGNLPEEELERSNLATK
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## MSRs B

```
                      10        20        30        40        50        60        70        80
                       |         |         |         |         |         |         |         |
MSRB1         MASHSLSLSLSAAAQILPNTQIQKFDSKLLLWPSRLHTKPTTKLSSSIRAMGSSASSNSNNPNTTEIQSGSSPVDYKSLS
MSRB2         -----------MMVNILRITPLSSFNVTKPI--SSIRSNPTF-LFNSLPTISIRQPKRGFRGGIVAMSAAPTPGSVQ-KS
MSRB5.1       --------------------------------------------------------------------MASTTSSIE-KS
MSRB5.2       --------------------------------------------------------------------MASTASSIE-KS
MSRB5.3       -------------------------------------------------------MSLKSFSYIVLLLFIVL--QTE-LN

                      90       100       110       120       130       140       150       160
                       |         |         |         |         |         |         |         |
MSRB1         DAEWKKQLTDEQFYVTRKKGTERAFTGEYWNTKTEGTYHCICCDTPLFESSTKFNSGTGWPSYYQPIGKNVKSKLDLSII
MSRB2         EEEWQAILSPEQFRILRQKGTEYPGTGEYDKFFGEGVYSCAGCGTPLYKSTTKFNSGCGWPAFYEGVPGAINRHADPD--
MSRB5.1       EE-WRAILSLDQFHILRQKGTELKGTGEYNKFYEEGVYNCAGCGTPLYKSSTKFDSGCGWPAFFEGFPGAINRSPDPD--
MSRB5.2       EEEWRAVLSPEQFHILRQKGTELKGTGEYNKFYEEGVYNCAGCGTPLYKSSTKFDSGCGWPAFFEGFPGAINRYPDPD--
MSRB5.3       SREYTQLIFYFVLRVERSR-CRLKGTGEYNKFYEEGVYNCARCGTPIYKSSIKFDSGCGWPTFFEGFPGAINRSPNPD--

                     170       180       190       200       210
                       |         |         |         |         |
MSRB1         FMPRQEVLCAVCDAHLGHIF--DDGPPPTGKRYCINSASLKLKPRK-----
MSRB2         -GMRIEITCAACGGHLGHVFKGEGFPTPTNERHCVNSISLKFAPANS----
MSRB5.1       -GRRTVITCEACGGRLGHVFKGEGFKVPTDERHCVNSVSVKFIPGNATSFI
MSRB5.2       -GRRTEITCAACGGHLGHVFKGEGFKVPTDERHCVNSVSVKFIPGNATSSI
MSRB5.3       -GRRTVITCATCGGHLGHVFKGEEFKVPTDERHCVNSVSVKFIPGNATSSI
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**Fig. S1.** Alignment of isoforms of MSRs of A type and B type of *Medicago truncatula*. The protein sequences deduced from the coding regions of tentative consensus (TC) (Table S1) found in the TIGR database were aligned. Identical and conserved amino acid residues are shown in red and blue, respectively. Residues that are identical in several, but not all, sequences are in green.

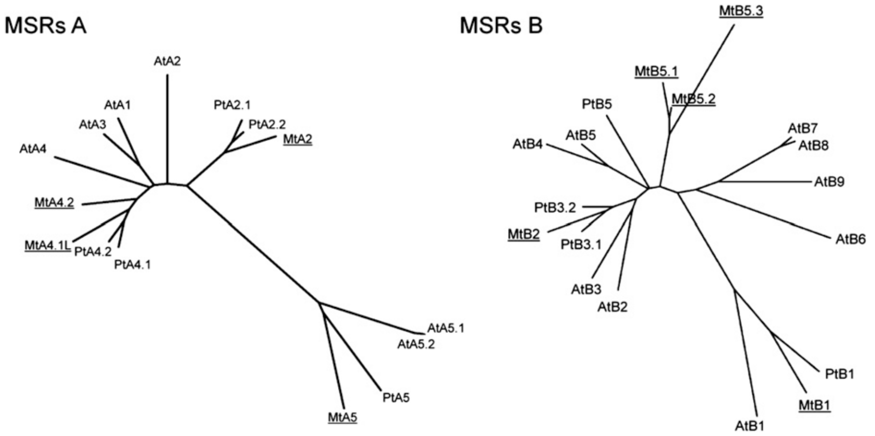

**Fig. S2.** Darwin trees of MSRs of A and B types found in *M. truncatula*, *Arabidopsis thaliana*, and poplar. The protein sequences were deduced from nucleic sequences available for each species and aligned (http://clustawl.genome.jp/). The *M. truncatula* sequences are listed in Table S1. The *A. thaliana* and poplar sequences are as described by Rouhier et al. (1).

1. Rouhier N, Vieira Dos Santos C, Tarrago L, Rey P (2006) Plant methionine sulfoxide reductase A and B multigenic families. *Photosynth Res* 89(2-3):247–262.

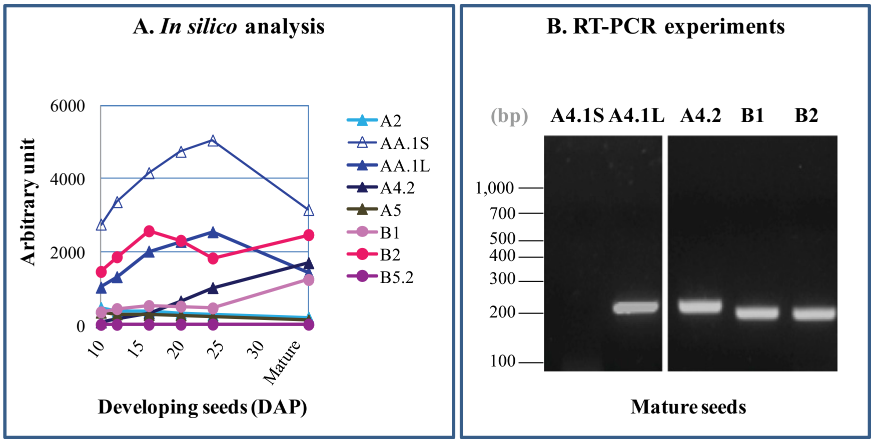

**Fig. S3.** Analysis of MSR gene expression. Analyses were performed either in silico using microarray data available for developing seeds at the Noble Foundation (*A*) or by RT-PCR experiments (*B*). For the RT-PCR experiments, total RNAs were extracted from mature seeds of Jemalong genotype with the RNeasy plant kit (Qiagen) and reverse-transcribed using the Moloney murine leukemia virus reverse transcriptase (Promega) according to the manufacturer's instructions. PCR experiments were performed using 0.1 µL of cDNAs, TAQ polymerase, and 2.5 µM concentrations of specific primers (Table S3).

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                       10        20        30        40        50        60        70        80        90       100
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      GGCACGAGGAAAACGTCATCTTTTTGCCGTGAACGAATCCCATTTCTATAACAACCATTGAAGCCTTTCCCATTTCTCTCTCTCTTTTGTTCTTTCACTC
A41L_mRNA      -----------------------------------------------GTAACAACCATTGAAGCCTTTCC-ATTTCTCTCTCTCTTTTGTTCTTTCACTC
A41S_Mtr37743  GGCACGAGGAAAACGTCATCTTTTTGCCGTGAACGAATCCCATTTCTATAACAACCATTGAAGCCTTTCCCATTTCTCTCTCTCTTTTGTTCTTTCACTC
A41L_Mtr37742  ---------------------CGCGGCCGAGGTACGCGGGGATTTCTATAACAACCATTGAAGCCTTTCCCATTTCTCTCTCTCTTTTGTTCTTTCACTC
                      110       120       130       140       150       160       170       180       190       200
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      ACACTCTCCCTTGGATGAGAATTTGTGGAGCAGGGTGTTTTGAAAATGATTATAATTTCTAGATAAGGGTTCTCATCTTACTCAAACTCTTAGCAGCAGC
A41L_mRNA      ACACTCTCCCTTGGGG-----------------------TTGTTGAAGATGAGAATTTGTGGA-----------------------------GCAGCAGC
A41S_Mtr37743  ACACTCTCCCTTGGATGAGAATTTGTGGAGCAGGGTGTTTTGAAAATGATTATAATTTCTAGATAAGGGTTCTCATCTTACTCAAACTCTTAGCAGCAGC
A41L_Mtr37742  ACACTCTCCCTTGGGG-----------------------TTGTTGAAGATGAGAATTTGTGGA-----------------------------GCAGCAGC
                      210       220       230       240       250       260       270       280       290       300
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      CAGCAGCGCCTATAGCACCACGTCCAGCTCCCTGCTAGTGTTTGGTTCTTCTTCCTTCTCCACTCCTGCCAAAACAAAGTTCCTACCCTCACTTTCTAGA
A41L_mRNA      CAGCAGCGCCTATAGCACCACGTCCAGCTCCCTGCTAGTGTTTGGTTCTTCTTCCTTCTCCACTCCTGCCAAAACAAAGTTCCTACCCTCACTTTCTAGA
A41S_Mtr37743  CAGCAGCGCCTATAGCACCACGTCCAGCTCCCTGCTAGTGTTTGGTTCTTCTTCCTTCTCCACTCCTGCCAAAACAAAGTTCCTACCCTCACTTTCTAGA
A41L_Mtr37742  CAGCAGCGCCTATAGCACCACGTCCAGCTCCCTGCTAGTGTTTGGTTCTTCTTCCTTCTCCACTCCTGCCAAAACAAAGTTCCTACCCTCACTTTCTAGA
                      310       320       330       340       350       360       370       380       390       400
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      TTTTCTGTCAAGCATTCTTGCTTGTTTTCACCAACCCGTCCCCATTTTACTGTAACCAAGCCCTCCATGAACCTTCTGAACAAACTTGGATTTGGCAGTG
A41L_mRNA      TTTTCTGTCAAGCATTCTTGCTTGTTTTCACCAACCCGTCCCCATTTTACTGTAACCAAGCCCTCCATGAACCTTCTGAACAAACTTGGATTTGGCAGTG
A41S_Mtr37743  TTTTCTGTCAAGCATTCTTGCTTGTTTTCACCAACCCGTCCCCATTTTACTGTAACCAAGCCCTCCATGAACCTTCTGAACAAACTTGGATTTGGCAGTG
A41L_Mtr37742  TTTTCTGTCAAGCATTCTTGCTTGTTTTCACCAACCCGTCCCCATTTTACTGTAACCAAGCCCTCCATGAACCTTCTGAACAAACTTGGATTTGGCAGTG
                      410       420       430       440       450       460       470       480       490       500
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      GAAGGTCATCAGAGAGCATGGATTCAACCATTCCTCAGGGACCAGATGACGATATACCAGCACCAGGCCAGCAGTTTGCTCAATTTGGGGCTGGCTGCTT
A41L_mRNA      GAAGGTCATCAGAGAGCATGGATTCAACCATTCCTCAGGGACCAGATGACGATATACCAGCACCAGGCCAGCAGTTTGCTCAATTTGGGGCTGGCTGCTT
A41S_Mtr37743  GAAGGTCATCAGAGAGCATGGATTCAACCATTCCTCAGGGACCAGATGACGATATACCAGCACCAGGCCAGCAGTTTGCTCAATTTGGGGCTGGCTGCTT
A41L_Mtr37742  GAAGGTCATCAGAGAGCATGGATTCAACCATTCCTCAGGGACCAGATGACGATATACCAGCACCAGGCCAGCAGTTTGCTCAATTTGGGGCTGGCTGCTT
                      510       520       530       540       550       560       570       580       590       600
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      TTGGGGTGTTGAATTGGTCTTCCAGAGGGTTCCTGGAGTGAGTAAGACAGAGGTTGGTTACACCCAGGGGCTTTTGCACAATCCTACTTATGAGGATGTG
A41L_mRNA      TTGGGGTGTTGAATTGGTCTTCCAGAGGGTTCCTGGAGTGAGTAAGACAGAGGTTGGTTACACCCAGGGGCTTTTGCACAATCCTACTTATGAGGATGTG
A41S_Mtr37743  TTGGGGTGTTGAATTGGTCTTCCAGAGGGTTCCTGGAGTGAGTAAGACAGAGGTTGGTTACACCCAGGGGCTTTTGCACAATCCTACTTATGAGGATGTG
A41L_Mtr37742  TTGGGGTGTTGAATTGGTCTTCCAGAGGGTTCCTGGAGTGAGTAAGACAGAGGTTGGTTACACCCAGGGGCTTTTGCACAATCCTACTTATGAGGATGTG
                      610       620       630       640       650       660       670       680       690       700
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      TGTTCAGGGACCACAAACCATAACGAGGTTGTAAGGGTCCAATATGATCCCAAACAAGGCACCTTCGAAAATCTGCTTGATACATTCTGGTCGAAACACG
A41L_mRNA      TGTTCAGGGACCACAAACCATAACGAGGTTGTAAGGGTCCAATATGATCCCAAACAAGGCACCTTCGAAAATCTGCTTGATACATTCTGGTCGAAACACG
A41S_Mtr37743  TGTTCAGGGACCACAAACCATAACGAGGTTGTAAGGGTCCAATATGATCCCAAACAAGGCACCTTCGAAAATCTGCTTGATACATTCTGGTCGAAACACG
A41L_Mtr37742  TGTTCAGGGACCACAAACCATAACGAGGTTGTAAGGGTCCAATATGATCCCAAACAAGGCACCTTCGAAAATCTGCTTGATACATTCTGGTCGAAACACG
                      710       720       730       740       750       760       770       780       790       800
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      ATCCTACTACGCCAAATCGACAGGGGAATGATGTGGGAACACAGTACAGATCTGGAATATACTTTTACACTCCTGAACAAGAGAAAATAGCTAAAGAGTC
A41L_mRNA      ATCCTACTACGCCAAATCGACAGGGGAATGATGTGGGAACACAGTACAGATCTGGAATATACTTTTACACTCCTGAACAAGAGAAAATAGCTAAAGAGTC
A41S_Mtr37743  ATCCTACTACGCCAAATCGACAGGGGAATGATGTGGGAACACAGTACAGATCTGGAATATACTTTTACACTCCTGAACAAGAGAAAATAGCTAAAGAGTC
A41L_Mtr37742  ATCCTACTACGCCAAATCGACAGGGGAATGATGTGGGAACACAGTACAGATCTGGAATATACTTTTACACTCCTGAACAA-ANAAAATAGCTA-------
                      810       820       830       840       850       860       870       880       890       900
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      TTTGGAACAACAAGAGAAGCAATTGGGCAGGAAGATTGCTACTGAGATTCTTCCTG--------------------------------------------
A41L_mRNA      TTTGGAACAACAAGAGAAGCAATTGGGCAGGAAGATTGCTACTGAGATTCTTCCTGCCAAGAAGTTCTACAGGGCTGAGGAGTACCATCAACAGTACCTT
A41S_Mtr37743  TTTGGAACAACAAGAGAAGCAATTGGGCAGGAAGATTGCTACTGAGATTCTTCCTGCCAAGAAGTTCTACAGGGCTGAGGAGTACCATCAACAGTACCTT
A41L_Mtr37742  ----------------------------------------------------------------------------------------------------
                      910       920       930       940       950       960       970       980       990      1000
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      ----------------------------------------------------------------------------------------------------
A41L_mRNA      GAGAAAGGGGGTCGATTCGGTTTCAAGCAATCTGCTGCTAAAGGATGCAATGACCCAATTCGGTGCTATGGTTAATTGTTGATAAAACAAAGTGAATTTA
A41S_Mtr37743  GAGAAAGGGGGTCGATTCGGTTTCAAGCAATCTGCTGCTAAAGGATGCAATGACCCAATTCGGTGCTATGGTTAATTGTTGATAAAACAAAGTGAATTTA
A41L_Mtr37742  ----------------------------------------------------------------------------------------------------
                     1010      1020      1030      1040      1050      1060      1070      1080      1090      1100
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      ----------------------------------------------------------------------------------------------------
A41L_mRNA      TCCTCAAGGATCAATACGACACTGTATTTGAGCTTGAAAATGGGCATAGCCATGAATTAGAGTTGTATACTGTCATCTATTATGTGTAATTTTGTTGTAA
A41S_Mtr37743  TCCTCAAGGATCAATACGACACTGTATTTGAGCTTGAAAATGGGCATAGCCATGAATTAGAGTTGTATACTGTCATCTATTATGTGTAATTTTGTTGTAA
A41L_Mtr37742  ----------------------------------------------------------------------------------------------------
                     1110      1120      1130      1140      1150      1160      1170      1180      1190      1200
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      ----------------------------------------------------------------------------------------------------
A41L_mRNA      AGTATTTGTCTTGGCTACTTACAAACCAAAAAATAAAAGACAAAATGTCTTTTCAGAAATTAGCAGAAATTGTGAACATTAGTAATTCTAAAAATTGTAT
A41S_Mtr37743  AGTATTTGTCTTGGCTACTTACAAACCAAAAAATAAAAGACAAAATGTCTTTTCAGAAATTAGCAGAAATTGTGAACATTAGTAATTCTAAAAATTGTAT
A41L_Mtr37742  ----------------------------------------------------------------------------------------------------
                     1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                        |         |         |         |         |         |         |         |         |         |
A41S_mRNA      ----------------------------------------------------------------------------------------------------
A41L_mRNA      GAACCTTCTCACAGAATCACTCCTCTTGATGGGTTCAATTTCTCAAAAGGCTGTTATGAAATCATAATTGAAGATGTATATTGAATTAAAATTGTGAATN
A41S_Mtr37743  GAACCTTCTCACAGAATCACTCCTCTTGATGGGTTCAATTTCTCAAAAGGCTGTTATGAAATCATAATTGAAGATGTATATTGAATTAAAATTGTGAAT-
A41L_Mtr37742  ----------------------------------------------------------------------------------------------------
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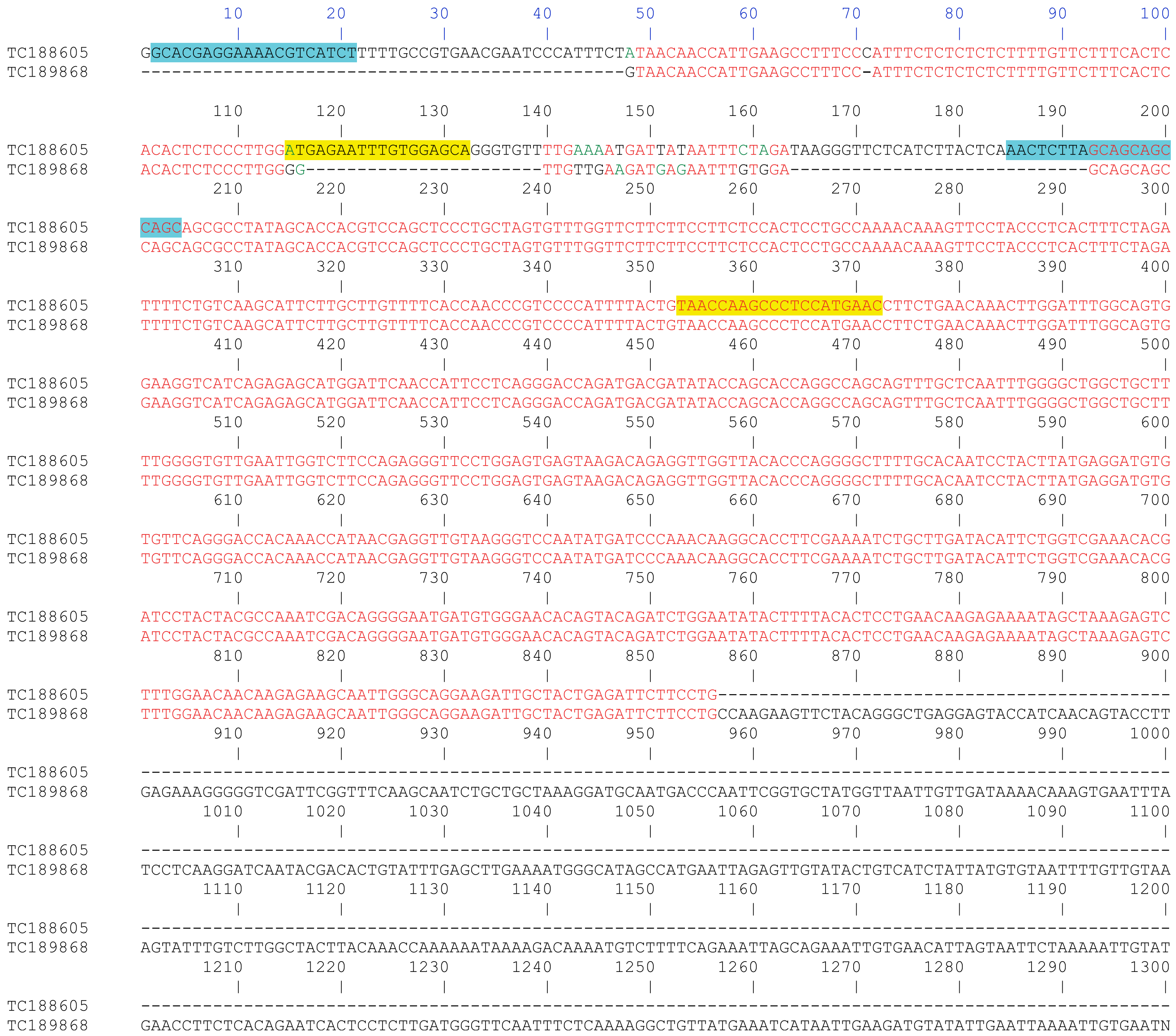
**Fig. S4.** Overlap of sequences of the probes and the TC corresponding to messengers *MSRA4.1S* and *MSRA4.1L*.



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                          10        20        30        40        50        60        70        80        90       100
                           |         |         |         |         |         |         |         |         |         |
TC188605          GGCACGAGGAAAACGTCATCTTTTTGCCGTGAACGAATCCCATTTCTATAACAACCATTGAAGCCTTTCCCATTTCTCTCTCTCTTTTGTTCTTTCACTC
TC189868          -----------------------------------------------GTAACAACCATTGAAGCCTTTCC-ATTTCTCTCTCTCTTTTGTTCTTTCACTC

                         110       120       130       140       150       160       170       180       190       200
                           |         |         |         |         |         |         |         |         |         |
TC188605          ACACTCTCCCTTGGATGAGAATTTGTGGAGCAGGGTGTTTTGAAAATGATTATAATTTCTAGATAAGGGTTCTCATCTTACTCAAACTCTTAGCAGCAGC
TC189868          ACACTCTCCCTTGGGG-----------------------TTGTTGAAGATGAGAATTTGTGGA-----------------------------GCAGCAGC
                         210       220       230       240       250       260       270       280       290       300
                           |         |         |         |         |         |         |         |         |         |
TC188605          CAGCAGCGCCTATAGCACCACGTCCAGCTCCCTGCTAGTGTTTGGTTCTTCTTCCTTCTCCACTCCTGCCAAAACAAAGTTCCTACCCTCACTTTCTAGA
TC189868          CAGCAGCGCCTATAGCACCACGTCCAGCTCCCTGCTAGTGTTTGGTTCTTCTTCCTTCTCCACTCCTGCCAAAACAAAGTTCCTACCCTCACTTTCTAGA
                         310       320       330       340       350       360       370       380       390       400
                           |         |         |         |         |         |         |         |         |         |
TC188605          TTTTCTGTCAAGCATTCTTGCTTGTTTTCACCAACCCGTCCCCATTTTACTGTAACCAAGCCCTCCATGAACCTTCTGAACAAACTTGGATTTGGCAGTG
TC189868          TTTTCTGTCAAGCATTCTTGCTTGTTTTCACCAACCCGTCCCCATTTTACTGTAACCAAGCCCTCCATGAACCTTCTGAACAAACTTGGATTTGGCAGTG
                         410       420       430       440       450       460       470       480       490       500
                           |         |         |         |         |         |         |         |         |         |
TC188605          GAAGGTCATCAGAGAGCATGGATTCAACCATTCCTCAGGGACCAGATGACGATATACCAGCACCAGGCCAGCAGTTTGCTCAATTTGGGGCTGGCTGCTT
TC189868          GAAGGTCATCAGAGAGCATGGATTCAACCATTCCTCAGGGACCAGATGACGATATACCAGCACCAGGCCAGCAGTTTGCTCAATTTGGGGCTGGCTGCTT
                         510       520       530       540       550       560       570       580       590       600
                           |         |         |         |         |         |         |         |         |         |
TC188605          TTGGGGTGTTGAATTGGTCTTCCAGAGGGTTCCTGGAGTGAGTAAGACAGAGGTTGGTTACACCCAGGGGCTTTTGCACAATCCTACTTATGAGGATGTG
TC189868          TTGGGGTGTTGAATTGGTCTTCCAGAGGGTTCCTGGAGTGAGTAAGACAGAGGTTGGTTACACCCAGGGGCTTTTGCACAATCCTACTTATGAGGATGTG
                         610       620       630       640       650       660       670       680       690       700
                           |         |         |         |         |         |         |         |         |         |
TC188605          TGTTCAGGGACCACAAACCATAACGAGGTTGTAAGGGTCCAATATGATCCCAAACAAGGCACCTTCGAAAATCTGCTTGATACATTCTGGTCGAAACACG
TC189868          TGTTCAGGGACCACAAACCATAACGAGGTTGTAAGGGTCCAATATGATCCCAAACAAGGCACCTTCGAAAATCTGCTTGATACATTCTGGTCGAAACACG
                         710       720       730       740       750       760       770       780       790       800
                           |         |         |         |         |         |         |         |         |         |
TC188605          ATCCTACTACGCCAAATCGACAGGGGAATGATGTGGGAACACAGTACAGATCTGGAATATACTTTTACACTCCTGAACAAGAGAAAATAGCTAAAGAGTC
TC189868          ATCCTACTACGCCAAATCGACAGGGGAATGATGTGGGAACACAGTACAGATCTGGAATATACTTTTACACTCCTGAACAAGAGAAAATAGCTAAAGAGTC
                         810       820       830       840       850       860       870       880       890       900
                           |         |         |         |         |         |         |         |         |         |
TC188605          TTTGGAACAACAAGAGAAGCAATTGGGCAGGAAGATTGCTACTGAGATTCTTCCTG--------------------------------------------
TC189868          TTTGGAACAACAAGAGAAGCAATTGGGCAGGAAGATTGCTACTGAGATTCTTCCTGCCAAGAAGTTCTACAGGGCTGAGGAGTACCATCAACAGTACCTT
                         910       920       930       940       950       960       970       980       990      1000
                           |         |         |         |         |         |         |         |         |         |
TC188605          ----------------------------------------------------------------------------------------------------
TC189868          GAGAAAGGGGGTCGATTCGGTTTCAAGCAATCTGCTGCTAAAGGATGCAATGACCCAATTCGGTGCTATGGTTAATTGTTGATAAAACAAAGTGAATTTA
                        1010      1020      1030      1040      1050      1060      1070      1080      1090      1100
                           |         |         |         |         |         |         |         |         |         |
TC188605          ----------------------------------------------------------------------------------------------------
TC189868          TCCTCAAGGATCAATACGACACTGTATTTGAGCTTGAAAATGGGCATAGCCATGAATTAGAGTTGTATACTGTCATCTATTATGTGTAATTTTGTTGTAA
                        1110      1120      1130      1140      1150      1160      1170      1180      1190      1200
                           |         |         |         |         |         |         |         |         |         |
TC188605          ----------------------------------------------------------------------------------------------------
TC189868          AGTATTTGTCTTGGCTACTTACAAACCAAAAAATAAAAGACAAAATGTCTTTTCAGAAATTAGCAGAAATTGTGAACATTAGTAATTCTAAAAATTGTAT
                        1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                           |         |         |         |         |         |         |         |         |         |
TC188605          ----------------------------------------------------------------------------------------------------
TC189868          GAACCTTCTCACAGAATCACTCCTCTTGATGGGTTCAATTTCTCAAAAGGCTGTTATGAAATCATAATTGAAGATGTATATTGAATTAAAATTGTGAATN
```

**Fig. S5.** Positions of the forward and reverse primers used to discriminate the messengers coding the short and long MSRA4.1 proteins. The positions of primers targeting the messenger coding for the protein either short (TC188605) or long (TC189868) are indicated in blue and yellow, respectively.

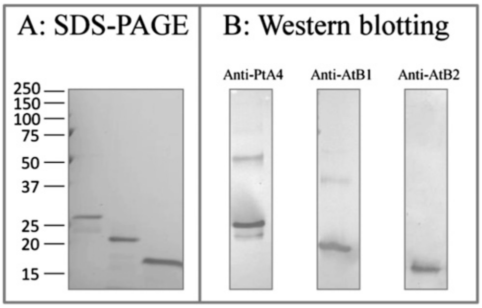

**Fig. S6.** Evaluation of recombinant MSRs from *M. truncatula* by SDS/PAGE and Western blot analysis. Proteins were overexpressed in *Escherichia coli*, purified, and resolved (1 μg/lane for SDS/PAGE and 0.1 μg/lane for Western blot) by 12% SDS/PAGE. Then proteins were either stained in the gel with Coomassie blue (*A*) or transferred onto a nitrocellulose membrane for immunodetection using anti-PtMSRA4, anti-AtMSRB1, or anti-AtMSRB2 antibodies (*B*). Molecular weight of standard proteins is indicated at the left of the gel obtained after SDS/PAGE. For the production of recombinant MSRs, the part of the coding regions corresponding to mature MSRs (without transit peptide) was amplified by PCR using 1 μL of cDNAs (prepared as in Fig. S3), the proof reading KOD HiFi DNA polymerase (Novagen) and appropriate primers (Table S3) allowing the cloning of PCR products into the pRSF2 vector of the ligation-independent Ek/LIC cloning kit (Novagen). Amplicons of expected size were resolved, excised from agarose gels, and inserted into the pRSF2 plasmid as described by Alkhalfioui et al. (1). The pRSF2 vector is engineered to express target proteins fused to an N-terminal His tag. Recombinant pRSF2 plasmids were introduced in Rosetta blue *E. coli* for multiplication, sequencing, and production of recombinant MSRs. MSR purification on $Ni^{2+}$-chelating Sepharose (Amersham) was carried out according to the manufacturer's instructions after a previous purification step on Q-Sepharose.

1. Alkhalfioui F, Renard M, Montrichard F (2007) Unique properties of NADP-thioredoxin reductase C in legumes. *J Exp Bot* 58:969–978.

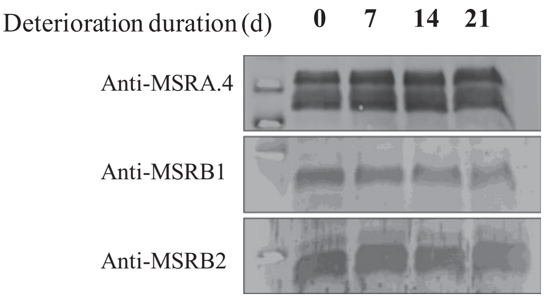

**Fig. S7.** Deterioration has no impact on MSR abundance in seeds. Abundance of MSR was measured by Western blot analysis in Jemalong seeds during deterioration. For that purpose, soluble proteins (15 or 25 μg/lane), resolved by SDS/PAGE and transferred onto nitrocellulose membranes, were probed against anti-PtMSRA4, anti-AtMSRB1, or anti-AtMSRB2 sera (1/1,000).

**Table S1. Genes encoding the 10 MSR isoforms in *M. truncatula* Jemalong databases**

| Name | TC no. | BAC no. | Chromosome no. | Gene name | EST no. | Protein mass, kDa | Putative protein localization |
|---|---|---|---|---|---|---|---|
| A2 | 176241<br>201665 | AC235753 | — | MTR_135s0002 | 9 | 22 | Cytosol |
| A4.1S | 188605 | CU179894 | 5 | MTR_5g092680 | 5 | 22.7 | Cytosol |
| A4.1L | 189868 | CU1798946 | 5 | MTR_5g092680 | 18 | 29.4 | Plastids |
| A4.2 | 181227 | CU861889 | 3 | MTR_3g051460 | 5 | 23.1 | Cytosol |
| A5 | 175213 | AC138453 | 8 | MTR_8g076060 | 7 | 28.7 | Endoplasmic reticulum |
| B1 | 143308 | — | — | — | 13 | 24.0 | Plastids |
| B2 | 143367 | AC202375 | 4 | MTR_4g092800 | 24 | 20.5 | Plastids |
| B5.1 | — | AC169126 | 2 | MTR_2g020950 | — | 15.1 | Cytosol |
| B5.2 | 145387 | AC169126 | 2 | MTR_2g020930 | 12 | 15.2 | Cytosol |
| B5.3 | — | AC146553 | 2 | MTR_2g020900 | — | 16.8 | Cytosol |

Presented are the names of MSR isoforms used in this work, according to the classification in poplar (1), and the corresponding numbers of TCs, BACs, and chromosomes. The number of ESTs found in databases and the putative localization are also given.

1. Rouhier N, Vieira Dos Santos C, Tarrago L, Rey P (2006) Plant methionine sulfoxide reductase A and B multigenic families. *Photosynth Res* 89(2-3):247–262.

**Table S2. Percentage of identity among the different MSR isoforms found in *M. truncatula*, using long protein A4.1L for calculations**

| MSRA2 | MSRA4.1L | MSRA4.2 | MSRA5 | MSRB1 | MSRB2 | MSRB5.1 | MSRB5.2 | MSRB5.3 |
|---|---|---|---|---|---|---|---|---|
| MSRA2 | 61 | 59 | 31 | 11 | 10 | 12 | 12 | 11 |
| | MSRA4.1L | 80 | 24 | 11 | 10 | 14 | 12 | 10 |
| | | MSRA4.2 | 29 | 10 | 10 | 12 | 11 | 11 |
| | | | MSRA5 | 11 | 13 | 13 | 16 | 13 |
| | | | | MSRB1 | 31 | 33 | 36 | 23 |
| [80;100] | | | | | MSRB2 | 70 | 75 | 51 |
| [50; 80] | | | | | | MSRB5.1 | 91.3 | 71 |
| [20;50] | | | | | | | MSRB5.2 | 71 |
| [0;20] | | | | | | | | MSRB5.3 |

The color code corresponds to the scale of values indicated at the bottom left of the table.

**Table S3. Primers used for RT-PCR and cloning experiments**

| Primer name | Primer sequence | Annealing temperature (°C) | Amplicon size (bp) |
|---|---|---|---|
| | **For RT-PCR experiments** | | |
| QMSRA4.1CSpe_F | GCACGAGGAAAACGTCATCT | 60 | 203 |
| QMSRA4.1CSpe_R | GCTGGCTGCTGCTAAGAGTT | | |
| QMSRA4.1LSpe_F | TGAGAATTTGTGGAGCAGCA | 60 | 197 |
| QMSRA4.1LSpe_R | GTTCATGGAGGGCTTGGTTA | | |
| QMSRA4.2bis_F | AGGTCAACAGTTTGCCCAGT | 60 | 221 |
| QMSRA4.2bis_R | ACGCATCAAGCAGAGTCTCA | | |
| QMSRB1_F | GGGGAGAATGGCATCTCATA | 60 | 203 |
| QMSRB1_R | CTGTGGTGTTTGGGTTGTTG | | |
| QMSRB2_F | ACCATTTCCATTCGTCAACC | 60 | 196 |
| QMSRB2_R | CCTCCCCAAAGAACTTGTCA | | |
| | **For cloning in pRSF2 vector** | | |
| A 4.1cSens | gacgacgacaagatgAACCTTCTGAACAAACT | 54 | 678 |
| A4.1cANTI | gaggagaagcccggtTCAACCATAGCACCGAATTG | | |
| B1matSens | gacgacgacaagatgGGCTCTTCAGCTTCT | 54 | 539 |
| B1matANTI | gaggagaagcccggtTCATCTTACTTCCCTTGGT | | |
| B2matSens | gacgacgacaagatgTCTGCTGCACCTACT | 54 | 483 |
| B2matANTI | gaggagaagcccggtTCAGGAATTGGCTGGCGCAA | | |

For PCR experiments, PCR was performed after a preliminary denaturation step of 4 min at 94 °C, followed by a set of 35 cycles (94 °C × 1 min, 60 °C × 1 min, and 72 °C × 1 min) then a final elongation step of 10 min at 72 °C. In the case of cloning experiments, the part of the sequence of the primers that appears in lower case was added to allow the cloning of the PCR products into the pRSF2 vector according to the instructions of the manufacturers. The annealing temperatures indicated in the table correspond to the specific part of the sequence (in upper case) used for the first five cycles of PCR (94 °C × 1 min, 54 °C × 1 min, and 72 °C × 1 min), the annealing temperature being raised to 72 °C for further 30 cycles (94 °C × 1 min, 72 °C × 2 min).

**Table S4. MSR capacity of leaves, and MSR capacity and longevity of seeds of *A. thaliana* WT and of lines modified for the expression of genes encoding plastidial MSRB1 and MSRB2**

| | MSR capacity, pmol·mg$^{-1}$·min$^{-1}$ | | |
|---|---|---|---|
| *A. thaliana* lines | Leaf | Seed | Seed longevity, P50, d |
| WT | 48.6 ± 6.9 | 74 ± 7.0 | 36 |
| B1$^{-}$ | 38.4 ± 6.9 | 77 ± 1.8 | 38 |
| B2$^{-}$ | 21.9 ± 1.9 | 45 ± 2.6 | 33 |
| B1$^{-}$/B2$^{-}$ | 11.6 ± 4.4 | 65 ± 1.5 | 33 |
| B1$^{+}$-8 | 183 ± 29 | 100 ± 9.4 | 44 |
| B1$^{+}$-10 | 182 ± 28 | 81 ± 7.1 | 40 |
| B2$^{+}$-3 | 383 ± 12 | 75 ± 9.3 | 40 |
| B2$^{+}$-5 | 3,200 ± 84 | 1,700 ± 32 | 30 |

Leaf MSR capacity was determined previously in the same lines (1, 2). B1$^{-}$ and B2$^{-}$, mutant lines knocked out for MSRB1 and MSRB2, respectively; B1$^{+}$ and B2$^{+}$, lines overexpressing MSRB1 and MSRB2, respectively.

1. Laugier E, et al. (2010) *Arabidopsis thaliana* plastidial methionine sulfoxide reductases B, MSRBs, account for most leaf peptide MSR activity and are essential for growth under environmental constraints through a role in the preservation of photosystem antennae. *Plant J* 61(2):271–282.
2. Laugier E, et al. (2012) Involvement of thioredoxin y2 in the preservation of leaf methionine sulfoxide reductase capacity and growth under high light. *Plant Cell Environ*, 10.1111/pce.12005.