## **Supporting Information**

PNAS PNAS

## Châtelain et al. 10.1073/pnas.1220589110

MSRs A									
	10	20	30	40	50	60	70	80	90
MEMODAO		I				I	MARCECCI		
MCMSRAZ MSRA4.1L	MRICGAAAASSAY	STTSSSLLV	 FGSSSFSTPA	KTKFLPSLSR	FSVKHSCLFS	PTRPHFTVTKI	MAISEGGI PSMNLLNKLGI	FGSGRSSESMI	)STIPOGE
MSRA4.1S							MNLLNKLGI	- GSGRSSESMI	STIPQGP
MSRA4.2							MYLLNRLWH	F <mark>G</mark> SARVTEKMI	SSIAQGL
MSRA5	MKLSEKTNNY	YYILSIFIII	LIAFLINNAN	CIRFPDRVAQ	PAREQPD	QQRLQTAVFAI	LGSFWRSEAVI	FGCLPGVVRT1	VGYSGGS.
	100	110	120	130	140	150	160	170	180
MCMSRAZ MSRA4 11.	DDEFAE	FGAGCEWGVE	LAFQRVPGV	VKTEVGITQG SKTEVGITQG	HTPDPNIKLV Lihndtyfdv	CIGTINHVEV	VRVQFDPKLCI	PYTNLLDLFWS	SKHDPTTL SKHDPTTE
MSRA4.1S	DDDIPAPGOOFAC	FGAGCEWGV	LVFORVPGV	SKTEVGI IQG: SKTEVGYTOG	LLHNPTYEDV	CSGTTNHNEV	VRVOYDPKOG	FENLLDTFWS	SKHDPTTF
MSRA4.2	DDDTPALGQQFAQ	FGAGCFWSVI	LAFQRVAGV	TKTE <mark>V</mark> GYSQG:	LLHNPRYQDV	CSATTRHSEV	VRLQYDPKECS	SYETLLDAFWA	<b>KHDP</b> TTL
MSRA5	KPNPEYRS	S <mark>FG</mark> DHAE-S <mark>V</mark> (	OVHEKARFCL	TIHSIKVTVK	HASPK(	CSGLDSG	IHVEY <mark>DP</mark> RLIS	3FGE <mark>LLDIFW</mark> S	S <mark>HDP</mark> RQV
	190	200	210	220	230	240	250	260	270
	1	I	l I	l.		I	1	1	1
MtMSRA2	NRQGGDVGAQYRS	GIYYYNETQ	SRL <mark>A</mark> QE <mark>SKE</mark> A	KQLEHKDK <mark>I</mark> V'	<b>F-EIL</b> PAKR <b>F</b>	YR <mark>AE</mark> EY <mark>hQ</mark> QYI	LE <mark>K</mark> GGGKGRGH	HGQSAQKGCNH	IPIRCYG-
MSRA4.1L	NRQGNDVGTQYRS	GIYFYTPEQ	EKIAKESLEQ	QEKQLGRKIA'	F-EILPAKKF	YRAEEYHQQYI	LE <mark>K</mark> GGRFGI	FKQSAAKGCNI	)PIRCYG-
MSRA4.15	NRQGNDVGTQYRS	GITETTPEQ	SKIAKESLEQ	QEKQLGRKIA.	F-EILPAKKE F-EILDARKE	YRAEEYHQQYJ	LEKGGRFGI	TKQSAAKGCNL	)PIRCYG-
MSRA5	FGOGPDVGNOYRS	TIEVNGTEES	SRMASVSKEO	EOTRSRSSIV'	T BIBEARRE.	HPAEPEHOKEI	ELKONTFLLOI	LIGNLPEELF	RSNLATK
MSRs B	10	20	20	4.0	5.0	60	70	0.0	
	10	20	30	40	50	00	70	00	
MSRB1	MASHSLSLSLSAA	AQILPNTQI	QKFDSKLLLW	PSRLHTKPTT	KLSSSIRAMG:	SSASSNSNNPI	NTTEIQSGSSI	PVDYKSLS	
MSRB2	MN	IVNILRITPLS	SSFNVTKPI-	-SSIRSNPTF	-LFNSLPTIS	IRQPKRGFRG	GIVAMSAAPTI	PGSVQ-KS	
MSRB5.1							MAST	ſSSIE-KS	
MSRB5.2							MASTA	ASSIE-KS	
MSKBJ.J						Мацлага.	110111111111	016-10	
	90	100	110	120	130	140	150	160	
MODD1									
MSRB1 Mgdb2	DAEWKKQLTDEQE	PIVIRKKGIEI	KAFTGEIWNT VDCTCEVDKE	KTEGTYHCIC FCFCVVSCAC		KENSGTGWPS: KENSCCCWDAI	I I QPIGKNVK: Evecuecatni	SKLDLSII	
MSRB5.1	EE-WRAILSLDOF	HILROKGTEI	LKGTGEYNKF	YEEGVYNCAG	CGTPLYKSSTI	KFDSGCGWPAI	FFEGFPGAIN	RSPDPD	
MSRB5.2	EEEWRAVLSPEQE	HIL <mark>R</mark> QKGTEI	LKG <mark>TGEY</mark> NKF	YEEGVYNCAG	CGTPLYKSST	KFDSGCGWPAI	FFEGFPGAIN	RYPDPD	
MSRB5.3	SREYTQLIFYFVI	JR <mark>VER</mark> SR-CRI	LKG <mark>TGEY</mark> NKF	YEEGVYN <u>CAR</u>	<u>GTPIYK</u> SI	KFD <u>SGCGWPT</u> I	FFEGFPGAINE	RSP <mark>N</mark> PD——	
	170	180	190	200	210				
MSRB1	FMPRQEVLCAVCI	AHLGHIFI	DDGPP <mark>PT</mark> GKR	Y <mark>CINSASLK</mark> LI	KPRK				
MSRB2	-GMRIEITCAACO	GGH <mark>LGHVF</mark> KG	EGFPT <mark>PT</mark> NE <mark>R</mark>	HCVNSISLKF	A <mark>P</mark> ANS				
MSRB5.1	-GR <mark>R</mark> TVITCEACO	GGRL <mark>GHVF</mark> KGI	EGFKV <mark>PT</mark> DE <mark>R</mark>	HCVNSVSVKF	I <mark>P</mark> GNATSFI				
MSRB5.2	-GRRTEITCAACO	GHLGHVFKG	GFKVPTDER	HCVNSVSVKF	IPGNATSSI				
MSRB5.3	-GRRTVIT <mark>CATC</mark> O	GHLGHVFKG	SEFKVPTDE <u>R</u>	<u>hcvn</u> svsvKF	IFGNATSSI				

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).

	10	20	30	4 (	) 50	) 6(	) 7(	) 80	90	100
A41S_mRNA A41L_mRNA	GGCACGAGGAA	AACGTCATCI	TTTTTGCCGT	GAACGAATCO	CCATTTCTATA	ACAACCATT	GAAGCCTTTCC	CATTTCTCTC CATTTCTCTCTC	TCTCTTTTG	TCTTTCACTC
A415_Mtr37743	GGCACGAGGAA	AACGTCATCI	TTTTTGCCGT	GAACGAATCO	CATTTCTAT	ACAACCATT	GAAGCCTTTC	CATTTCTCTC	TCTCTTTTG	TCTTTCACTC
	110	120	130	140	) 150	) 16(	) 17(	) 180	190	200
A41S_mRNA A411. mRNA	ACACTCTCCCT	rggatgagaz	ATTTGTGGAG	CAGGGTGTT	TTGAAAATGAT	TATAATTTC:	ragataagggi	TCTCATCTTA	СТСАААСТС	TAGCAGCAGC
A415_Mtr37743 A411_Mtr37742	ACACTCTCCCT	rggatgagaz	ATTTGTGGAG	CAGGGTGTT	TGAAAATGAT TGTTGAAGAT	TATAATTTC	TAGATAAGGGI	TCTCATCTTA	CTCAAACTC	TAGCAGCAGC
	210	220	230	240	) 250	) 26(	) 27(	) 280	290	300
A41S_mRNA A411. mRNA		ATAGCACCAC	CGTCCAGCTC	CCTGCTAGT	GTTTGGTTCTT	CTTCCTTCT		CAAAACAAAGT TAAAACAAAGT		ACTTTCTAGA
A41S_Mtr37743	CAGCAGCGCCT	ATAGCACCAC	GTCCAGCTC	CCTGCTAGT	GTTTGGTTCTT	CTTCCTTCT	CACTCCTGC	CAAAACAAAGI	TCCTACCCT	ACTTTCTAGA
	310	320	330	34(	) 350	360	) 37(	) 380	390	400
A41S_mRNA A411. mRNA	TTTTCTGTCAA	GCATTCTTGC	CTTGTTTTCA	CCAACCCGT	CCCATTTTAC	TGTAACCAA	GCCCTCCATGA GCCCTCCATGA			TTTGGCAGTG
A41S_Mtr37743	TTTTCTGTCAA	GCATTCTTG	CTTGTTTTCA	CCAACCCGT	CCCATTTTAC	TGTAACCAA	GCCCTCCATG	ACCTTCTGAA	CAAACTTGG	TTTGGCAGTG
Mill_net0//12	410	420	430	440	) 450	460	) 47(	) 480	490	500
A41S_mRNA A411. mRNA	GAAGGTCATCA	GAGAGCATGO	GATTCAACCA	TTCCTCAGG	SACCAGATGAC	GATATACCA		AGCAGTTTGCT		CTGGCTGCTT
A415_Mtr37743	GAAGGTCATCA	GAGAGCATGO	GATTCAACCA	TTCCTCAGG	GACCAGATGAC	GATATACCA	GCACCAGGCCA	AGCAGTTTGCT	CAATTTGGGG	CTGGCTGCTT
A411_ACL5//42	510	520	530	54(	) 550	560	) 57(	) 580	590	600
A41S_mRNA	TTGGGGTGTTG	ATTGGTCT		TCCTGGAGT	AGTAAGACAG	AGGTTGGTT		GCTTTTGCACA	ATCCTACTT	TGAGGATGTG
A415_Mtr37743	TTGGGGTGTTG	ATTGGTCT	CCAGAGGGGT	TCCTGGAGT	GAGTAAGACAG	AGGTTGGTT		GCTTTTGCACA	ATCCTACTT	TGAGGATGTG
A411_MCL3//42	610	620	630	64(	) 650	) 66(	) 67(	) 680	690	0 700
A41S_mRNA A41L mRNA	TGTTCAGGGAC	CACAAACCA1	FAACGAGGTT FAACGAGGTT	GTAAGGGTCO	CAATATGATCC		CACCTTCGAAA CACCTTCGAAA	ATCTGCTTGA	TACATTCTG	TCGAAACACG TCGAAACACG
A415_Mtr37743 A411_Mtr37742	TGTTCAGGGAC	CACAAACCAI	TAACGAGGTT TAACGAGGTT	GTAAGGGTCC GTAAGGGTCC	CAATATGATCC		CACCTTCGAAA	ATCTGCTTGA	TACATTCTG	TCGAAACACG
_	710	720	730	740	) 750	) 760	) 77(	) 780	790	800
A41S_mRNA A41L mRNA	ATCCTACTACG ATCCTACTACG	CCAAATCGAC CCAAATCGAC	CAGGGGAATG CAGGGGAATG	ATGTGGGAAG	CACAGTACAGA CACAGTACAGA	TCTGGAATA TCTGGAATA	FACTTTTACAC FACTTTTACAC	CTCCTGAACAA CTCCTGAACAA	GAGAAAATAO	CTAAAGAGTC
A415_Mtr37743 A41L Mtr37742	ATCCTACTACG ATCCTACTACG	CCAAATCGAC CCAAATCGAC	CAGGGGAATG CAGGGGAATG	ATGTGGGAAG ATGTGGGAAG	CACAGTACAGA CACAGTACAGA	TCTGGAATA	FACTTTTACAC FACTTTTACAC	CTCCTGAACAA CTCCTGAACAA	GAGAAAATAC	CTAAAGAGTC
—	810	820	830 	840	) 850 	860	) 87( 	) 880 I I	890	) 900 
A41S_mRNA A41L mRNA	TTTGGAACAACA TTTGGAACAACA	AAGAGAAGCA AAGAGAAGCA	ATTGGGCAG ATTGGGCAG	GAAGATTGC1 GAAGATTGC1	ACTGAGATTO ACTGAGATTO	TTCCTG	AGAAGTTCTAC	CAGGGCTGAGG	AGTACCATCA	ACAGTACCTT
A415_Mtr37743 A41L Mtr37742	TTTGGAACAAC	AGAGAAGCA	ATTGGGCAG	GAAGATTGC	TACTGAGATTO	TTCCTGCCA	AGAAGTTCTAC	CAGGGCTGAGG	AGTACCATCA	ACAGTACCTT
—	910 	920 I	930 	940	) 950 I I	960	) 970 I I	) 980 I I	i 990 I	) 1000 
A41S_mRNA A41L_mRNA	GAGAAAGGGGG	ICGATTCGGT	TTCAAGCAA	TCTGCTGCT	AAGGATGCAA	TGACCCAAT	ICGGTGCTAT	GTTAATTGTT	'GATAAAACA <i>P</i>	AGTGAATTTA
A41S_Mtr37743 A41L_Mtr37742	GAGAAAGGGGG	ICGATTCGGI	TTTCAAGCAA	TCTGCTGCT	AAGGATGCAA	TGACCCAAT	ICGGTGCTATO	GTTAATTGTT	GATAAAACAA	AGTGAATTTA
	1010 	1020 	1030 	1040	) 1050 I I	1060	) 1070 	) 1080 	1090 l	) 1100 
A41S_mRNA A41L_mRNA A41S_Mtr37743 A41L_Mtr37742	TCCTCAAGGAT	CAATACGACA	ACTGTATTTG	AGCTTGAAAA	TGGGCATAGC	CATGAATTA	GAGTTGTATAC	CTGTCATCTAT	TATGTGTAAT	TTTGTTGTAA
	TCCTCAAGGAT	CAATACGACA	ACTGTATTTG	AGCTTGAAAA	ATGGGCATAGC	CATGAATTA	GAGTTGTATAC		TATGTGTAA	TTTTGTTGTAA
3 41 0	1110	1120	1130	1140		) 1160		1 1180 1 1180	1190	1200
A415_MRNA A41L_MRNA A41S_Mtr37743	AGTATTTGTCT AGTATTTGTCT	IGGCTACTT# IGGCTACTT#	асааассааа асааассааа	AAATAAAAGA AAATAAAAGA	ACAAAATGTCI ACAAAATGTCI	TTTCAGAAA TTTCAGAAA	FTAGCAGAAA1 FTAGCAGAAA1	ITGTGAACATI ITGTGAACATI	'AGTAATTCT# 'AGTAATTCT#	AAAATTGTAT AAAATTGTAT
A41L_Mtr37742	1210	1220	1230	1240	) 1250	) 1260	) 1270	) 1280	1290	1300
A41S_mRNA			ا		 					
A41L_mRNA A41S_Mtr37743 A41L_Mtr37742	GAACCTTCTCA GAACCTTCTCA	CAGAATCACI	FCCTCTTGAT	GGGTTCAATI GGGTTCAATI	TCTCAAAAGG	CTGTTATGA	AATCATAATTO	GAAGATGTATA GAAGATGTATA	TTGAATTAAA TTGAATTAAA	ATTGTGAATN

Fig. S4. Overlap of sequences of the probes and the TC corresponding to messengers MSRA4.1S and MSRA4.1L.

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TC188605         CACCUTECTOR         Construction		10	20	30	40	50	60	70	80	90	100
10188605         Control of the co	ma100605										
110         120         130         140         150         160         170         180         190         200           12188605         ACACTETCOCTTOG ACGMENANT TO BRANCH COGGTOTT TRANATION TO TRANATOR TRANATOR TO TRANATOR TRANATOR TO T	TC188605	GGCACGAGGAAA	ACGTCATCTTT	TTGCCGTGAA	CGAATCCCAT		ACCATTGAA	GCCTTTCCCCAT GCCTTTCCCCAT	TTCTCTCTCTCT	CTTTTGTTCT	TTCACTC TTCACTC
110         120         130         140         150         160         170         180         190         200           C189665         ACACTCICCCCTICG CLAUGHAND OF GALL	10105000					GIANCA	ACCALIGAA	GCCIIICC AI		CITIGITCI	TICACIC
TC188605         ACACTCCCCTTCGCTGAGAATTTTTGGGACGGGGTCTTGGAAATGATAATTTTTAGATAAGGTTCTCATCTAAAATGATAACGATAATTGTGGA         CCCCCACGCCCCTCCGGGCGGGGGGGGGGGGGGGGGGGG		110	120	130	140	150	160	170	180	190	200
TC188605         ACACTCTCCCTTCGE         CCCCTTCGCTCGCC         CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC				1	1	1	I.		I		1
TC189868         ACCTCTCCCTTGGGG	TC188605	ACACTCTCCCTT	GG <mark>ATGAGAATT</mark>	<mark>TGTGGAGCA</mark> G	GGTGTT <mark>TTG</mark> A	AAATGATTAT	AATTTCTAG	ATAAGGGTTCI	CATCTTACTC	AAACTCTTA <mark>G</mark>	CAGCAGC
210         220         230         240         250         260         270         280         290         300           TC188605         INFERRED AGGECTATAGECACCACGTCCAGCTCCTGCTAGTGTTTGGTTCTCTTCTC	TC189868	ACACTCTCCCTT	GGGG		TTG	TGAAGATGAG	AATTTGTGG	A		G	CAGCAGC
TC188605         TC169368         TC169368         TC169368         TC169368           TC189368         CACCAGEGECTATAGECACCTECCAGETECCTECTEGTTTGGTTCTTGTTCTTCTCCACCCTECTEGCAAAACAAACTTCCTACCCTCACTTTCTAGE CACCAGEGECTATAGECACCAGETECCAGETECTGTTTGGTTCTTGCTTCTCCCTCCCCACTCTCACCCTCCACTTTCTAGE TTTCTCTCAAGECATTCTTCCTTGTTTTCACCAACCCGTECCCATTTTACTGTAACCAAGECCTCCAGAAACAACTTGGTTTGGCAGGT TTTTCTGTCAAGECATTCTTCCTTGTTTTCACCAACCGTECCCATTTTACTGTAACCAAGECCTCCAGAACACACTGGATTGGCAGGT TTTCTGTCAAGECATTCTTCCTTGTTTTCACCAACCGTCCCCATTTTACTGTAACCAGECCCCCCACGAGACTTCGAACAACTTGGTTTGGCAGGT TTTCTGTCAAGEAGACTGGATTCAACCATTCCTCAGGGACCAGATGACGATATACCAGCCAG		210	220	230	240	250	260	270	280	290	300
Interesting         Interesting <thinteresting< th=""> <thinteresting< th=""></thinteresting<></thinteresting<>	TC100605										
310         320         330         340         350         360         370         380         390         400           TC188605         TTTTCTGTAAGCATTCTTGTTTTCACCAACCGTCCCATTTTACTGTAACAACCTCCAACAACCTTGAACAAACCTTGGATTGGCATGG         410         420         430         440         450         460         470         480         490         550           TC189866         GAAGGTCATCAGGAGTCAACCATTCCTCAGGGACCAGATGACGATTACCAGGCACGAGGCCAGGTGCCACTTGCTCAACCAAC	TC189868	CAGCAGCGCCTA	TAGCACCACGI	CCAGCICCCI	GCTAGIGIII	GGTTCTTCTT	CCTTCTCCA	CTCCTGCCAAF	ACAAAGIICC	TACCCTCACT	TTCTAGA
T118605         TTTCTGCAACCATTCGCTGCTTTGCACCACCCCACTTTACTGEAACCACCCCTCCACACACACTTGGATCGCACCAGGC           T118605         GAAGGTCATCAAGCATTGGCTGCTTTCACCAACCGTCCCCATTTACTGTAACCAAGCCCTCCACACACA	10109000	310	320	330	340	350	360	370	380	390	400
T11268605         TTTCTCTCAAGCATCTTGCTTGTTTCACCAACCCGTCCCATTTACTCTCAAGACCTCCAATGAACTTGCATTGGCAGTG           TC189868         TTTCTCTCAAGCATCTTGCTGTTTCACCAACCCGTCCCCATTTACTGTAAGCATCTCCCAATGAACTTGCAACAACTTGGACTGGCAGGG           TC18805         GAAGGTCATCAGAGAGCATGGATTCAACCATTCCTCAGGGACAGATAACCAGGCACGCGCGCG											
TC189868         TTTTCTTCACAGCCATTTGTTTTCCCACACCCCATTTACCTARACCAACCCCTCCAACAACCTTGGACATTGGCAGCAGGGGGGGG	TC188605	TTTTCTGTCAAG	CATTCTTGCTT	GTTTTCACCA	ACCCGTCCCC	CATTTTACTG <mark>T</mark>	AACCAAGCC	CTCCATGAAC	CTTCTGAACAA	ACTTGGATTT	GGCAGTG
410         420         430         440         450         470         480         490         500           TC188605         GAAGGTCATCAGAGAGCATIGATCAACCATTCCTCAGGGACCAGATGACGATATACCAGCACCAGGCCAGGAGTTGCTCCAATTGGGCTGGCT	TC189868	TTTTCTGTCAAG	CATTCTTGCTT	GTTTTCACCA	ACCCGTCCCC	CATTTTACTGT	AACCAAGCC	CTCCATGAAC	CTTCTGAACAA	ACTTGGATTT	GGCAGTG
1         1		410	420	430	440	450	460	470	480	490	500
TC188605       GAAGGTCATCAGAGAGCATGAGTTACACCATTCCTAGGAGCAGATGACGATTACCAGCACCAGCAGCAGGTTCCTCATTTGGGGCTGGCT		1					I				1
TC189665         GARGETCATCARCARCEATEGETCARCEGATCATTCCTCAGEGACCAGTEGATACACCACCAGCACCACCACCACCACTACTCTTTTCCTCAGCAGCTEGATTCACCACCACCACCACCACCACTACCACTACTCTTTTCGCACATTCGTCTCACCAGGGGTTCCTGGAGTAAGACAGGGTTGGTT	TC188605	GAAGGTCATCAG	AGAGCATGGAT	TCAACCATTO	CTCAGGGACO	CAGATGACGAT	ATACCAGCA	CCAGGCCAGCA	AGTTTGCTCAA	TTTGGGGCTG	GCTGCTT
110         120         130         140         130         160         160         150         160         150         160         150         160         160         160         160         160         160         160         160         160         160         610         620         630         640         650         660         670         680         690         700         1           1         TGGGGGCCACAAACCAAAACGAAGGTTGTAAAGGACCAAAAGGCAACCTTCGAAAACAAGGCACCTTCGAAAACAAGGCACCACCAAAACCAAAACCAAAAGCCAACCAAGGCAACCTCGAAAACAAGGCACCTTCGAAAAATTCGCTGGAAAACAGG         710         720         730         740         750         760         770         780         790         800         1           1         1         720         730         740         750         760         770         780         790         800         1         <	TC189868	GAAGGTCATCAG	AGAGCATGGAT E 2.0	TCAACCATTC	CTCAGGGACC	AGATGACGAT	ATACCAGCA	CCAGGCCAGCA	AGTTTGCTCAA	TTTGGGGCTG	GCTGCTT
TC188605         TTGGGGTGTTGAATTGGTCTTCCAGAGGGTTCCTGGAGTAGACAGAGGTTGGTT		510	520	530	540	550	560	570	560	590	000
TC189868         TTGGGGTGTTGAATTGGTCTTCCAGAGGGTTCCTGGAGTAGACAGGGGTTGGTT	тс188605	TTGGGGTGTTGA	ATTGGTCTTCC	AGAGGGTTCC	TGGAGTGAG	AAGACAGAGG	TTGGTTACA	L CCCAGGGGCT1	'TTGCACAATC	CTACTTATGA	ו GGATGTG
610         620         630         640         650         660         670         680         690         700           1	TC189868	TTGGGGTGTTGA	ATTGGTCTTCC	AGAGGGTTCC	TGGAGTGAG	AAGACAGAGG	TTGGTTACA	CCCAGGGGCTI	TTGCACAATC	CTACTTATGA	GGATGTG
I         I		610	620	630	640	650	660	670	680	690	700
TC188605         TGTTCAGGGACCACAAACCATAACGAGGTTGTAAGGGTCCAATATGGATCCCAAACCAAGGCACCTTCGAAAATCTGCTTGATACATTCTGGTGGAAACAGG           TC188605         TGTCAGGGACCACAAACCATAACGAGGTTGTAAGGGTCCAATATGGATCCCAAACCAAGGCACCTTCGAAAATCTGCCGAACAACG           TC188605         ATCCTACTACCCAAATCGACAGGGGAATGATGGGAACACGACACGACCAGTACCAGATCTGGAATATACTTTTACACTCCTGAACAAGAGAAAATAGCTAAAGGAGCA           TC188605         ATCCTACTACCCCAAATCGACAGGGGAATGATGGGAACACAGTACCAGATCTGGAATATACTTTTACACTCCTGAACAAGAGAAAATAGCTAAAGGAGCA           TC188605         ATCCTACTACCCCAAATCGACAGGGGAATGATGCTGCGAACACAGTCCGACAGATCTGCAATATACTTTTACACTCCTGAACAAGAGAAAATAGCTAAAGGAGCA           TC188605         TTTGGAACAACAAGGAGAAGCAATTGGCCAGGAAGATTGCTACTGGAATCTTCCTGCCCAAGAAGTACCATCCACAGGGAGTACCATCAACAGGGAGTACCATCACGAGACCTT           TC188605         TTTGGAACAACAAGGAGGAAGCAATTGGCCAGGAAGATTGCTACTGAGATTCTTCCTGCCCAAGAAGTTCTCCACGGGCTGAGGAGTACCATCAACAGGAGACCCTT           TC188605         TTTGGAACAACAAGGAGAAGCAATTGGCCAGGAAGATTGCTACTGAGATTCTTCCTGCCCAAGAAGTGCCAATTGGGCTGAGAGCACTGGCAAGGAGATCCCATCAACAGGGCATAGGCCAAGGGCATAGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGGCCAATGGGCATAGCCAATGGGCATAGGCAATGGGCATAGCGAAGGGGGTGGATTGTGAAAAAAAA				1	1	1	I.	1		1	1
TC189868         TGTTCAGGGACCACAAACCATAACGAGGTTGTAAGGGTCGAATATGATTCCCAAACAGGCACCTTCGAAAATCGTCTGATACATTCTGGTCGAAAACAGG           710         720         730         740         750         760         770         780         790         800           1         <	TC188605	TGTTCAGGGACC	АСАААССАТАА	CGAGGTTGTA	AGGGTCCAAT	ATGATCCCAA	ACAAGGCAC	CTTCGAAAATC	CTGCTTGATAC	ATTCTGGTCG	AAACACG
710       720       730       740       750       760       770       780       790       800         TC188605       ATCCTACTACGCCAAATCGACAGGGGAATGATGTGGGAACACAGTACAGATACAGATATACTTTACACTCCTGAACAAGAGAAAATAGCTAAAGAGTC       ATCCTACTACGCCAAATCGACAGGGGAATGATGTGGGAACACAGTACAGATCGGAATATACTTTACACTCCTGAACAAGAGAAAATAGCTAAAGAGTC         R10       820       830       840       850       860       870       880       890       900         I	TC189868	TGTTCAGGGACCA	АСАААССАТАА	CGAGGTTGTA	AGGGTCCAAT	ATGATCCCAA	ACAAGGCAC	CTTCGAAAATC	CTGCTTGATAC	ATTCTGGTCG	AAACACG
TC188605       I<		710	720	730	740	750	760		780	790	800
TC188605       ATCCTACTACGCCAAATCGACAGGGGAATGATGGGGAACACAGTACAGATCTGGAATAACACTTTACACTCCTGAACAAGAGAAATAGCTAAGAGTC         TC189868       ATCCTACTACGCCAAATCGACAGGGGAAGATGGGGGAACACAGTACAGATCTGGGAATAACTTTACCTTTACACTCCTGAACAAGAGAAAATAGCTAAAGAGTC         TC188605       TTTGGAACAACAAGAAGAAGCAATTGGGGAACACAGTACTGGGAATCACAGTCTGGAATATACTTTTACACTCCTGACAAGAGAAAATAGCTAAAGAGTC         TC188605       TTTGGAACAACAAGAAGAAGCAATTGGGCAGGAAGATTGCTACTGGAGATTCTCCTGCCAAGAAGAGGGGCTGAGGAGTACCATCAACAGTACAGT         TC188605       1 <t< td=""><td>mc100C0E</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td>1 7 7 C 7 C 10 C</td></t<>	mc100C0E										1 7 7 C 7 C 10 C
10193000       Information of the construction	TC189868	ATCCTACTACGC	CAAAICGACAG	GGGAAIGAIG	TGGGAACACA	GIACAGAICI	GGAATATAC	TTTTACACICC	TGAACAAGAG	AAAAIAGCIA	AAGAGIC
I       I	10109000	810	820	830	840	850	860	870	880	890	900
TC188605       TTTGGAACAACAAGAGAAGCAATTGGCAGGAAGATTGCTACTGAGATTCTTCCTG         TC189868       TTTGGAACAACAAGAGAAGCAATTGGCAGGAAGATTGCTACTGAGATTCTTCCTGCCAAGAAGTTCTACAGGGCTGAGGAGATACCATCAACAGTACCTT         910       920       930       940       950       960       970       980       990       1000         1 <th1< th="">       1       <th1< th="">       1       <th1< th="">       1<td></td><td>010</td><td>010</td><td>1</td><td></td><td>000</td><td>1</td><td></td><td>1</td><td>1</td><td>1</td></th1<></th1<></th1<>		010	010	1		000	1		1	1	1
TC189868       TTTGGAACAACAAGAGAAGCAATTGGGCAGGAAGATTGCTACTGAGAATTCTCCCGCCAAGAAGTTCTACAGGGCTGAGGAGTACCATCAACAGTACCTT         910       920       930       940       950       960       970       980       990       1000         1       <	TC188605	TTTGGAACAACA	AGAGAAGCAAT	TGGGCAGGAA	GATTGCTACT	GAGATTCTTC	CTG		·	·	
910       920       930       940       950       960       970       980       990       1000         1 </td <td>TC189868</td> <td>TTTGGAACAACA</td> <td>AGAGAAGCAAT</td> <td>TGGGCAGGAA</td> <td>GATTGCTACT</td> <td>GAGATTCTTC</td> <td>CTGCCAAGA</td> <td>AGTTCTACAGO</td> <td>GCTGAGGAGI</td> <td>ACCATCAACA</td> <td>GTACCTT</td>	TC189868	TTTGGAACAACA	AGAGAAGCAAT	TGGGCAGGAA	GATTGCTACT	GAGATTCTTC	CTGCCAAGA	AGTTCTACAGO	GCTGAGGAGI	ACCATCAACA	GTACCTT
Image:		910	920	930	940	950	960	970	980	990	1000
TC188605		1		l.	l I		I			1	1
TC189868       GAGAAAGGGGTCGATTCGGTTTCAGGCATCTGCTGCTGCTAAGGATGCAATGACCCCAATTGGTGCTATTGGTTGATAAACAAAGTGAATTTA         1010       1020       1030       1040       1050       1060       1070       1080       1090       1100         TC188605	TC188605										
1010       1020       1030       1030       1030       1030       1030       1030       1030       1030       1030       1030       1030       1030       1100       1030       1100       1030       1100       1030       1100       1030       1100       1030       1100       1030       1100       1030       1100       1030       1100       1030       1100       1030       1100       1030       1100       1200	TC189868	GAGAAAGGGGGT"	CGATTCGGTTT 1020	CAAGCAATCI	GCTGCTAAAG	GATGCAATGA	CCCCAATTCG	GTGCTATGGT 1070	AATTGTTGAT	AAAACAAAGT	GAA'I''I''I'A
TC188605        -       <		1010	1020	1030	1040	1050	1000	1070	1090	1090	1100
TC189868       TCCTCAAGGATCAATACGACACTGTATTTGAGCTTGAAAATGGGCATAGCCATGAATTAGAGTTGTATACTGTCATCTATTATGTGTAATTTTGTTGTGTAA         1110       1120       1130       1140       1150       1160       1170       1180       1190       1200         1 </td <td>TC188605</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>·</td> <td></td> <td></td> <td></td> <td></td>	TC188605						·				
1110       1120       1130       1140       1150       1160       1170       1180       1190       1200         1	TC189868	TCCTCAAGGATC	AATACGACACT	GTATTTGAGC	TTGAAAATGO	GCATAGCCAT	GAATTAGAG	TTGTATACTG	CATCTATTAT	GTGTAATTTT	GTTGTAA
I       I		1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
TC188605		1	1	1	1	I.	I.	L	1	1	1
TC189868         AGTATTTGTCTTGGCTACTTACAAACCAAAAATAAAAGACAAAATGTCTTTTCAGAAATTGCAGAAATTGTGAACATTAGTAATTCTAAAAATTGTAT 1210         1220         1230         1240         1250         1260         1270         1280         1290         1300           I	TC188605										
1210         1220         1230         1240         1250         1260         1270         1280         1290         1300           I <t< td=""><td>TC189868</td><td>AGTATTTGTCTT</td><td>GGCTACTTACA</td><td>ААССАААААА</td><td>TAAAAGACAA</td><td>AATGTCTTTT</td><td>CAGAAATTA</td><td>GCAGAAATTGI</td><td>GAACATTAGI</td><td>AATTCTAAAA</td><td>ATTGTAT</td></t<>	TC189868	AGTATTTGTCTT	GGCTACTTACA	ААССАААААА	TAAAAGACAA	AATGTCTTTT	CAGAAATTA	GCAGAAATTGI	GAACATTAGI	AATTCTAAAA	ATTGTAT
		1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
ТОТОВОЮ	TC10060E	1	I	I.	I	I			I	I	
	101888003 TC189868	GAACCTTCTCAC		 <u> </u> <u> </u>							GTGAATN

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.

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**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 express target proteins fused to an N-terminal His tag. Recombinant pRSF2 plasmid s were introduced in Rosetta blue *E. coli* for multiplication, sequencing, and production of recombinant MSRs. MSR purification on Ni<sup>2+</sup>-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. 57.** 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 th	e 10 MSR isoforms	in <i>M.</i>	truncatula	Jemalong	databases
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Name	TC no.	BAC no.	Chromosome no.	Gene name	EST no.	Protein mass, kDa	Putative protein localization
A2	176241	AC235753	_	MTR_135s0002	9	22	Cytosol
	201665						
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.

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

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

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

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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 me	odified for the expression of genes encoding plastidial MSRB1 and MSRB2

MSR	capacity,	pmol·m	ng <sup>−1</sup> ∙min <sup>−1</sup>
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A. thaliana lines	Leaf	Seed	Seed longevity, P50, d		
WT	48.6 ± 6.9	74 ± 7.0	36		
B1 <sup>-</sup>	38.4 ± 6.9	77 ± 1.8	38		
B2 <sup>-</sup>	21.9 ± 1.9	45 ± 2.6	33		
B1 <sup>-</sup> /B2 <sup>-</sup>	11.6 ± 4.4	65 ± 1.5	33		
B1 <sup>+</sup> -8	183 ± 29	100 ± 9.4	44		
B1 <sup>+</sup> -10	182 ± 28	81 ± 7.1	40		
B2 <sup>+</sup> -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<sup>-</sup> and B2<sup>-</sup>, mutant lines knocked out for MSRB1 and MSRB2, respectively; B1<sup>+</sup> and B2<sup>+</sup>, lines overexpressing MSRB1 and MSRB2, respectively.

<sup>1.</sup> 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.

<sup>2.</sup> 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.