

SUPPLEMENTARY DATA

FIG. S1. Mn tissue concentration of rice leaf blades of different leaf age before and after elevated Mn supply (50 μM) for 72 h. Different upper case letters indicate significant differences ($P < 0.05$) between different Mn levels of one leaf age according to Tukey; different lower case letters indicate significant differences ($P < 0.05$) between different leaf ages of one level of Mn treatment. Different levels of significance according to a two-factor ANOVA for $P < 0.001$, $P < 0.01$, $P < 0.05$ and non-significant are labelled with ***, **, * and ns, respectively.

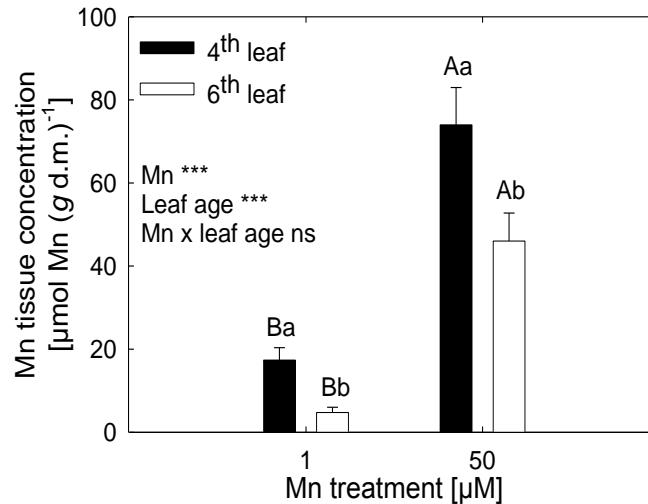


FIG. S2. Specific guaiacol-POD (A) and specific NADH-POD (B) activities of rice leaf blades of different leaf age before and after elevated Mn supply (50 μM) for 72 h. Different upper case letters indicate significant differences ($P < 0.05$) between different Mn levels of one leaf age according to Tukey; different lower case letters indicate significant differences ($P < 0.05$) between different leaf ages of one level of Mn treatment. Different levels of significance according to a two-factor ANOVA for $P < 0.001$, $P < 0.01$, $P < 0.05$ and non-significant are labelled with ***, **, * and ns, respectively.

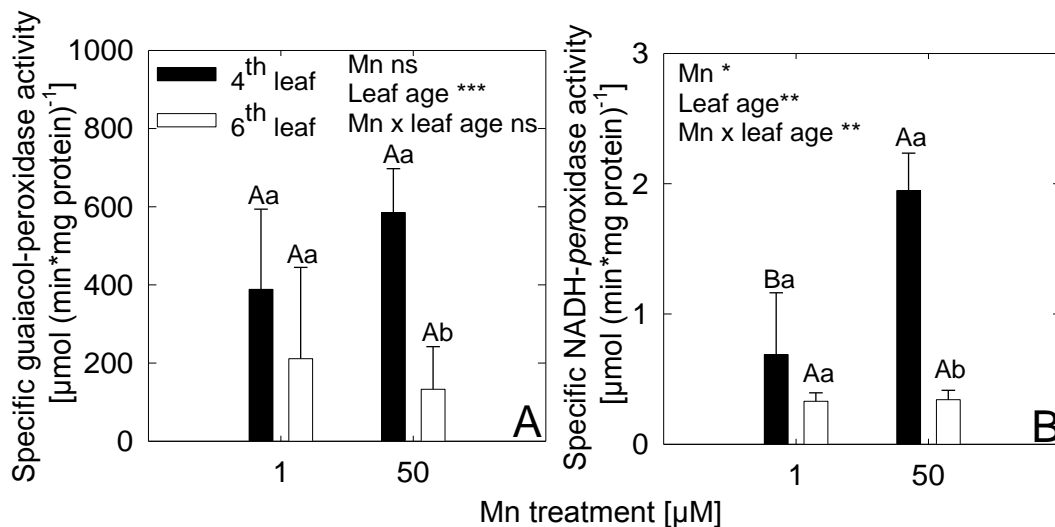


FIG. S3. Protein content of rice leaf blades of different leaf age before and after elevated Mn supply (50 μM) for 72 h. Different upper case letters indicate significant differences ($P < 0.05$) between different Mn levels of one leaf age according to Tukey; different lower case letters indicate significant differences ($P < 0.05$) between different leaf ages of one level of Mn treatment. Different levels of significance according to a two-factor ANOVA for $P < 0.001$, $P < 0.01$, $P < 0.05$ and non-significant are labelled with ***, **, * and ns, respectively.

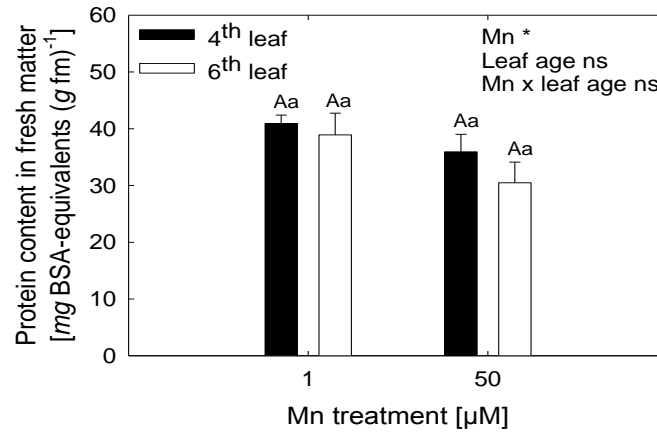


FIG. S4. Representative Coomassie-stained close-ups of regions containing Mn-influenced protein spots 2 and 7 extracted from the older fourth leaves of Mn control (left) and Mn-treated (left) plants. A complete 2D/IEF-SDS-PAGE resolution of the proteome is given in Fig. 9. Three replications of each treatment were analysed using the Imagemaster™ 2D PLATINUM Software 6.0. Significantly regulated ($P < 0.05$) protein spots (marked by arrows) were cut and identified by nanoLC-MS/MS.

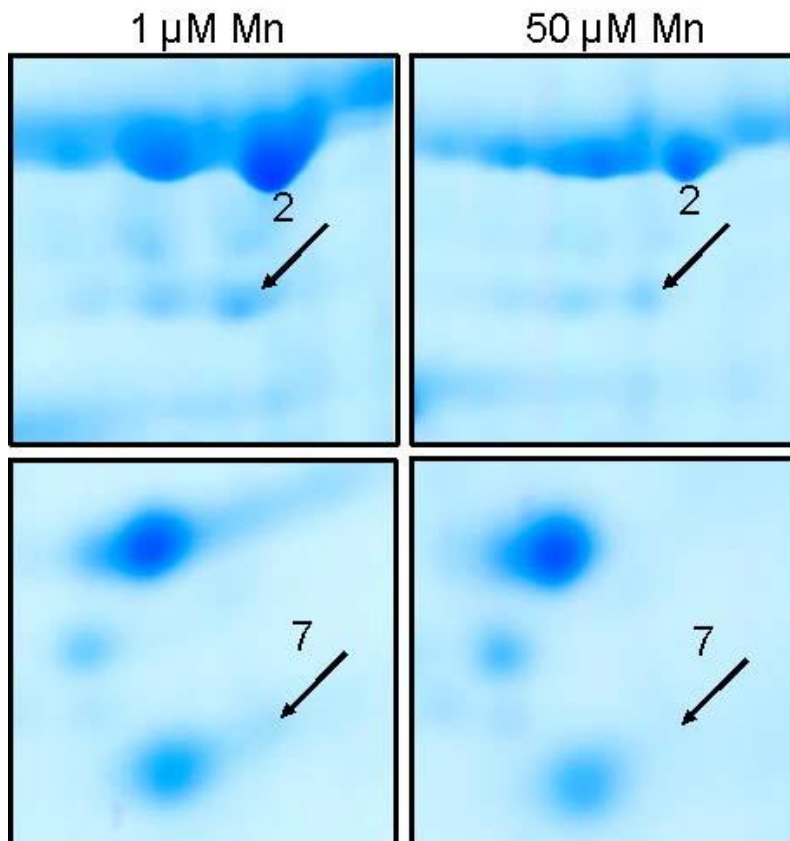


FIG. S5. Representative Coomassie-stained close-ups of regions containing Mn-influenced protein spots 5, 8 and 9 extracted from the younger sixth leaves of Mn control (left) and Mn-treated (left) plants. A complete 2D IEF/SDS-PAGE resolution of the proteome is given in Fig. 9. Three replications of each treatment were analysed using the Imagemaster™ 2D PLATINUM Software 6.0. Significantly regulated ($P < 0.05$) protein spots (marked by arrows) were cut and identified by nanoLC-MS/MS.

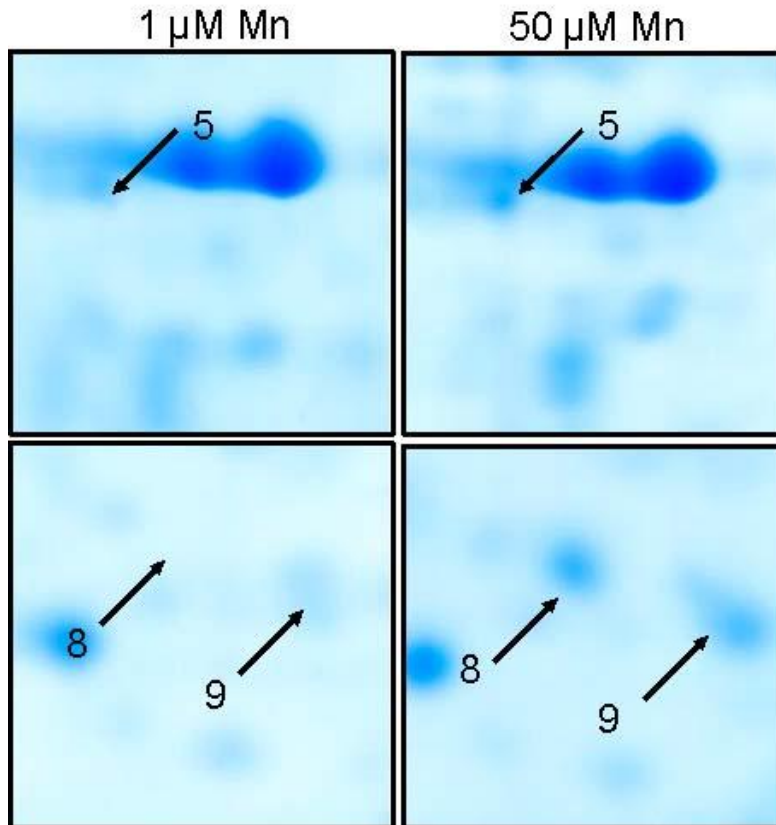


FIG. S6. Representative Coomassie-stained close-ups of regions containing protein spots 1, 4 and 6 differing in abundance between the younger sixth (right) and the older fourth (left) leaves of Mn control plants. A complete 2D IEF/SDS-PAGE resolution of the proteome is given in Fig. 9. Three replications of each treatment were analysed using the Imagemaster™ 2D PLATINUM Software 6.0. Significantly regulated ($P < 0.05$) protein spots (marked by arrows) were cut and identified by nanoLC-MS/MS.

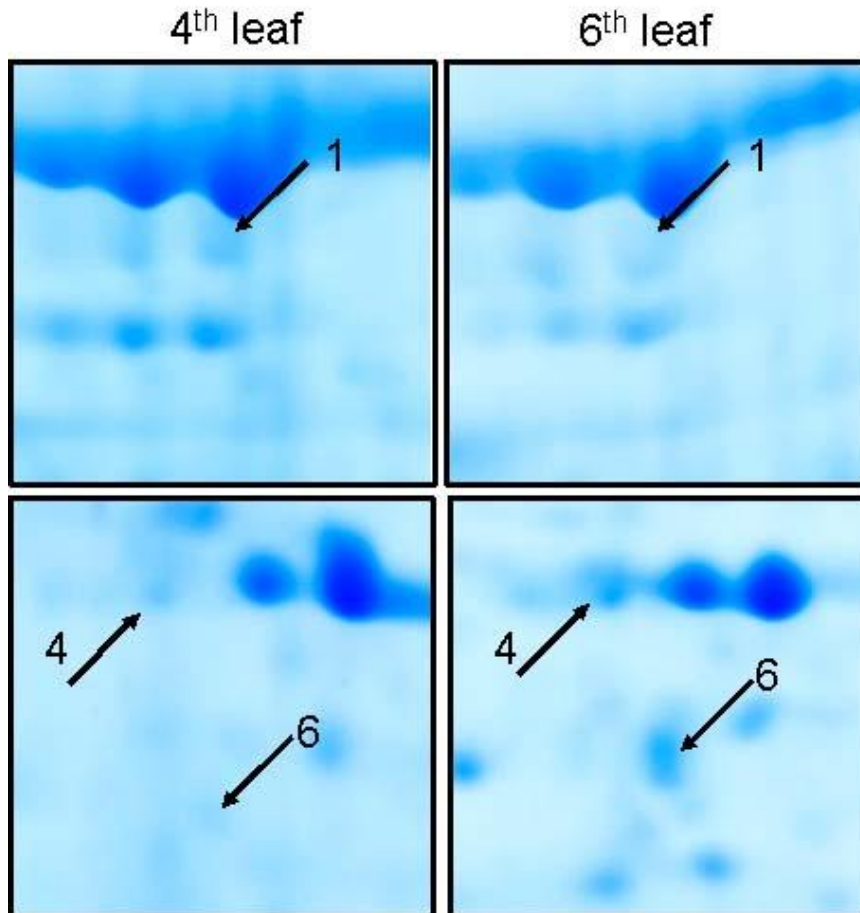


FIG. S7. Representative Coomassie-stained close-ups of regions containing protein spots 3, 7, 8, 10, 11, 12 and 13 differing in abundance between the younger sixth (right) and the older fourth (left) leaves of Mn-treated plants. A complete 2D IEF/SDS-PAGE resolution of the proteome is given in Fig. 9. Three replications of each treatment were analysed using the Imagemaster™ 2D PLATINUM Software 6.0. Significantly regulated ($P < 0.05$) protein spots (marked by arrows) were cut and identified by nanoLC-MS/MS.

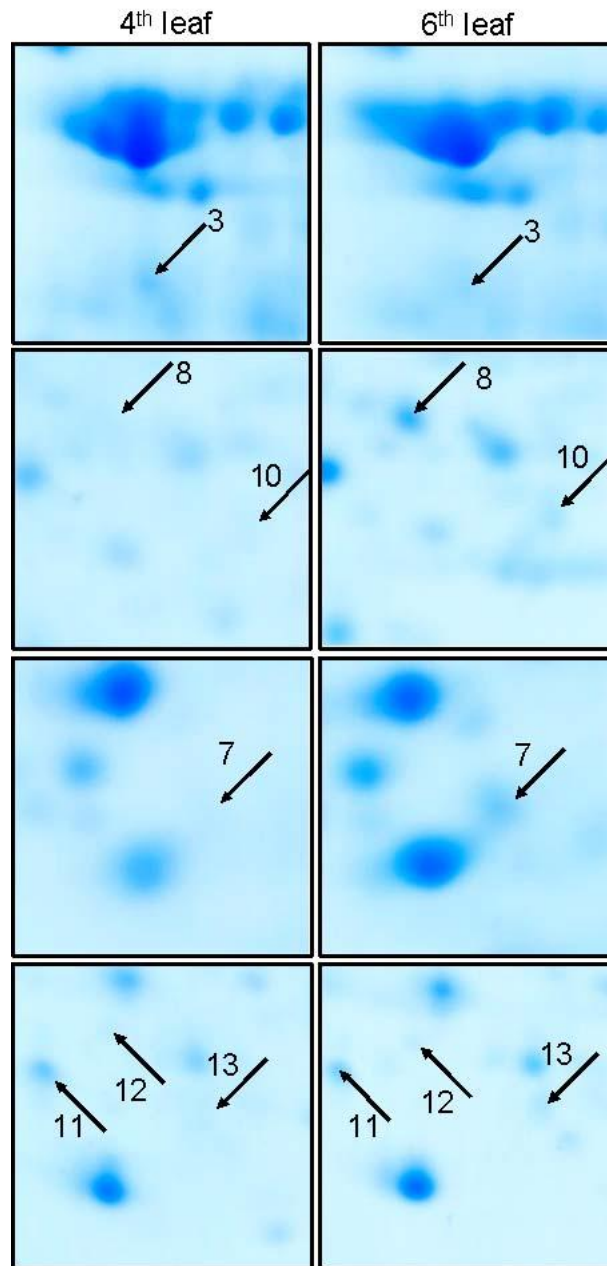


TABLE S1. Identity and peptide alignment of proteins changed in abundance after elevated Mn supply in the older (fourth) leaf of rice

Protein no. ^a	Acc. no. ^b	Identity ^c	Organism ^d	Peptide sequence ^e	Coverage (%) ^f
2	BAD16832	Chloroplast translational elongation factor Tu	<i>Oryza sativa</i>	MASLASASASTSLVFSTSSSKPRLGSSVGFSSPARFRRTAAA AASRGTGRRAGLLVRAARGKFERTKPHVNIQTIGHVDHGKI TLTAALTMVLASVGGAPKKYDEIDAAPEERARGITINTATVEY ETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVSGADG PMPQTKEHILLAKQVGVPKIVVFLNKKDQVDDEELLQLVELEV RELLSSYEYDGDVEPIVAGSALKALENLMANPAIKRGDDEWV DGIFSLIDSVDNYPVPQRQTDLPFLLAVEDVFSITGRGTVATG RIERGTVKVGDTVDIVGIRETRNCTVTGVEMFQKTMDAMAG DNVGLLLRGMQKDDIERGMVLAKPASITPHTKFDVVVYLK DEGGRHSPFFPGYRPPQFYMRTTDTGNVTKIMNDKDEEAKM CMPGDRVKMVELIQPVACEQGMRFIREGGKTVGAGVINTI LK	28.40
7	NP_001048 798	50S ribosomal protein L11	<i>Oryza sativa</i>	MATTSLSLHGVPSPTATKLSSSFLGAPASFLRPTPPPLAAPSR RALAVRAMAPPKPGGKPKKVGLIKLALAEAGKATPAPPVGP LGAKGVNIMSFCKEYNAKTAEKAGYIIPVEITVFDDKSFTFILKT PPASVLLLKAAGIEKGSKEPQREKVGKVTADQVRTIAQEKLDP LNCKSIDSAMRIAGTAANMGIEVDPPILEKKEKVL	29.90

^a Numbers in the table correspond to numbers given in Fig. 9.

^b Accession numbers correspond to proteins identified at the NCBI homepage showing sequence homology with the detected protein spot.

^c Identities are based on sequence comparisons using the NCBI protein database.

^d Origin species of the corresponding protein.

^e Amino acid sequence of the corresponding protein (identified by nano-LC-MS/MS; sequence homologies between protein spot and corresponding database hit)

^f Coverage of the peptides identified by mass spectrometry

TABLE S2. Identity and peptide alignment of proteins changed in abundance after elevated Mn supply in the younger (sixth) leaf of rice

Protein no. ^a	Acc. no. ^b	Identity ^c	Organism ^d	Peptide sequence ^{e e}	Coverage (%) ^f
5	BAD16934	Putative inorganic pyrophosphatase	<i>Oryza sativa</i>	MATAATASATAATRFRTRLAGVGLRRTARLPTAVRFQRRVLAT TALLRTAELRPKEQGLPETLDYRVFLVDGGGRKVPWHDVPL <u>RAGDGVFHFVVEIPKESSAKMEVATDESFTPIKQDTKKGNLR</u> YYPYNINWNYGLFPQTWEDPTLANTDVEGAFGDNDPVDVVEI GERRANIGDVLKVKPLAALAMIDEGELDWKIVAIISLDDPKASLV NDVDDVEKHFPGLTALRDWFRDYKIPDGKPANRFGLGNKPT SKEYALKVIEETNESWEKLVKRNIPAGELSLA	34.40
8	NP_00106699 8	Probenazole-inducible protein PBZ1	<i>Oryza sativa</i>	MAPACVSDEHAVAVSAERLWKAFMDASTLPKACAGLVDDIAV EGNGGPGTIYTMKLNPAAGVGSTYKTRVAVCDAASHVLKSD VLEAESKVGKLSHSTETKLEATGDGSCVAKLKVEYELEDGS <u>SLSPEKEKDIDGYYGMLKMIEDYLVAHPAEYA</u> MAGEAAAAERWVGAADFSEGSRAALRWAADNLLRAGDHLI LLHVLKDPDYEQGETLLWEATGSPLIPLSDFSEPTIAKKYGAK PDAETLDMLNTVARQKEVVVVFVVLWGDPREKLCQAINIIPM SCLVIGSRGLGKLRVLLGSVSDYVVNNATCPVTVVKTADG	67.70
9	NP_00105470 4	Universal stress protein (Usp) family protein	<i>Oryza sativa</i>	MAGEAAAAERWVGAADFSEGSRAALRWAADNLLRAGDHLI LLHVLKDPDYEQGETLLWEATGSPLIPLSDFSEPTIAKKYGAK PDAETLDMLNTVARQKEVVVVFVVLWGDPREKLCQAINIIPM SCLVIGSRGLGKLRVLLGSVSDYVVNNATCPVTVVKTADG	18.00

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^d Origin species of the corresponding protein.

^e Amino acid sequence of the corresponding protein (identified by nano-LC-MS/MS, sequence homologies between protein spot and corresponding database hit)

^f Coverage of the peptides identified by mass spectrometry.

TABLE S3. Identity and peptide alignment of proteins differing in abundance between the Mn-control (0.2 μ M) older (fourth) and the younger (sixth) leaf of rice

Protein no. ^a	Acc.no. ^b	Identity ^c	Organism ^d	Peptide sequence ^e	Coverage (%) ^f
1	Q42971	Enolase (2-phosphoglycerate dehydratase)	<i>Oryza sativa</i>	<u>MAATIVSVKARQIFDSRGNPTVEVDVCCSDGTFARAAPVPSGA</u> <u>STGVYEALELRDGGSDYLGKGVSKAVDNVNSVIAPALIGKDP</u> <u>TSQAELDNFMVQQLDGTKNEWGWCKQKLGANAILAVSLAIC</u> <u>KAGAIKKIPLYQHIANLAGNKQLVLPVPFNVINGGSHAGNKL</u> <u>AMQEFMILPTGAASFKEAMKMGVEVYHNLKSVIKKKYQQDAT</u> <u>NVGDEGGFAPNIQENKEGLELLKTAIEKAGYTGKVVIGMDVAA</u> <u>SEFYNDKDKTYDLNFKKEENNDGSQKISGDSLKNVYKSFVSEY</u> <u>PIVSIEDPFDQDDWEHYAKMTAEIGEQQVIVGDDLLVTNPTRV</u> <u>AKAIQEKSCNALLLKVNQIGSVTESIEAVKMSKRAGWGVMTS</u> <u>HRSGETEDTFIADLAVGLATGQIKTGAPCRSERLAKYNQLLR</u> <u>EEELGAAAVYAGAKFRAPVEPY</u>	48.40
4	NP_001043 134	Oxygen-evolving enhancer protein 1, chloroplast precursor	<i>Oryza sativa</i>	<u>MAASLQAAATLMQPAKLGGRASSAALPSRPSSHVARAFGVD</u> <u>TGAAGRITCSLQSDIREVANKCADAAGLAGFALATSALLVSGA</u> <u>SAEGVPRRLTFDEIQSKTYMEVKGTGTANQCPTVEGGVDSF</u> <u>AFKAGKYNMKKFCLEPTSFVKAEGVAKNAPPEFQKTKLMTR</u> <u>LYTLDEIEGPLVSSDGTIKFEEKDGIDYAAVTVQLPGGERV</u> <u>PFLFTIKNLVATGKPESFGGPFVLPVSYRGSFDPKGRGGST</u> <u>GYDNAVALPAGGRGDEEELAKENVKNASSSTGNITLSVTKSK</u> <u>PETGEVIGVFESVQPSDIDLGAKVPKDVKIQQVWYAQLE</u>	33.90
6	NP_001063 793	Ribonuclease T2 family protein	<i>Oryza sativa</i>	<u>MEQRKFLCLILGLLATSGPAKTVNADSPFDFFYLILMWPGAY</u> <u>CTDSEYGCCVPKYGYPSEDFVKSFMFDSSSENTAVVRCNS</u> <u>DNPFDINKLDSIENNLNHYWSNIKCPRTDGVNSWKSEWNSY</u> <u>GVCSGLKELDYFKAGLQLRKNADVLSALAEQGIKPDYQLYNT</u> <u>AFIKWAVNQKLGVTGPVQCRDGFPGKKQLYEIYLCVDKDAKS</u> <u>FIDCPVLPNLSCPAEVLFPFHTWMLNNTSAANIVMPTETVLA</u>	40.10

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^d Origin species of the corresponding protein.

^e Amino acid sequence of the corresponding protein (identified by nano-LC-MS/MS, sequence homologies between protein spot and corresponding database hit

^f Coverage of the peptides identified by mass spectrometry.

TABLE S4. Identity and peptide alignment of proteins differing in abundance between the Mn-treated (50 µM) older (fourth) and younger (sixth) leaf of rice

Protein no. ^a	Acc. no. ^b	Identity ^c	Organism ^d	Peptide sequence ^e	Coverage (%) ^f
3	NP_001047 479	Adenosine 5'-phosphotransferase 2	<i>Oryza sativa</i>	MASEGVLLGMGNPLLDISAVVDDAFLTKYDVKLNAILAEEKH LPMYDELASKGNVEYIAGGATQNSIRVAQWMLQTPGATSYM GCIGKDKFGEEMKKNQAAGVTAHYEEDAAPTGTCAVCVV GGERSLVANLSAANCYKSEHLKPPENWALVEKAKYIYIAGFFL TVSPDSIQLVAEHAAANNKVFMLNLSAPFICEFFRDAQEKVLP FVDYIFGNETEARIFAKVRGWETENVEEIALKISQLPLASGKQK RIAVITQGADPVVAEDGQVKTFFVILLPKEKLVDTNGAGDAF VGGFLSQLVQQSIEDSVKAGCYAANVIIQRSGCTYPEKPDF N	43.70
7	NP_001048 798	50S ribosomal protein L11	<i>Oryza sativa</i>	MATTSLSLHGVPSPATKLSSSFLGAPASFLRPTPPPLAAPS RALAVRAMAPPKPGGKPKKVVGLIKLALAEAGKATPAPPVGP LGAKGVNIMSFCKEYNAKTAEKAGYIIPVEITVFDDKSFTFILKT PPASVLLLKAAGIEKGSKEPQREKVGKVTADQVRTIAQEKLPD LNCKSIDSAMRIAGTAANMGIEVDPPILEKKEKVL MAPACVSDEHAVAVSAERLWKAFFMDASTLPKACAGLVDDIAV EGNGGPGTIYTMKLNPAAGVVGSTYKTRVAVCDAAASHVLKSD VLEAESKVGKLSHSTETKLEATGDGSCVAKLKVEYELEDGS SLSPEKEKDIDGYYGMLKMIEDYLVHHPAEYA	36.20
8	NP_001066 998	Probenazole-inducible protein PBZ1	<i>Oryza sativa</i>	MAEETPVETPAAPVLGEPMDLMTALQLVMKKSSAHDGLVKG LREAAKAEKHAALCVLAEDCDQPDYVVKLVKALCAEHNHVL VTVPSAKTLGEWAGLCKIDSEGKARKVVGCSVCVVVKDYGEE SEGLNIVQDYVKSH	66.50
10	NP_001058 899	40S ribosomal protein S12	<i>Oryza sativa</i>	MAATALSSQVRLPMSLRVATAPAPARVSVLPASNKLGDRLM QATYNVKLITPDGEVELQVPDDVYILDQAEEDLDPYSCRAG SCSSCAGVVSGEIDQSDQSFLDDDQVAAGWVLTCHAYPKS DVVIETHKEDDLI	14.20
11	A2YQD9	Ferredoxin-1, chloroplast precursor (Ferredoxin I) (Anti-disease protein 1)	<i>Oryza sativa</i>	MGVYTFVCRSSGDEWTAKQLKGELEASAATPYELQRRLVAA ASAADSAAGVQSSFSMVPSSAVFQVIIGAVGGGAAIGGGAA AGAASGGAAEAPKAEKKEEKEESEDLDLGFSLFD MALSLSTSFLPTQAAAAATRTRLRSLVPSQRMRCMRKKG LHPEIYEDAKVYCNGELVLTGGTKPEYTVDVVWVSGNHPYVGD TSAMVVMDSQIEKFRKKWGHIEKYWPEDQWREMHDPGDPE FDPEEEGSAGAS	33.10
12	P56724	60S acidic ribosomal protein P3 (P1/P2-like)	<i>Oryza sativa</i>		19.30
13	NP_001043 653	Ribosomal protein L31 family protein	<i>Oryza sativa</i>		14.80

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