

Root proteome alterations in sugarcane promoted by the regrowth cycle in commercial production

Rone Charles Maranhão, Mariana Mancini Benez, Gustavo Barizon Maranhão, Eduardo Jorge Pilau, Claudete Aparecida Mangolin and Maria de Fátima P. S. Machado*

Table S1. Proteins of sett roots in the first cut of sugarcane cultivar RB966928 in the sprouting stage.

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
1/HS72_ARATH/P22954	^a Heat shock cognate 70 kDa protein 2 (Hsc70.2)	206.498.500	16	71.786	28.48	<i>Arabidopsis thaliana</i>
2/MDHC_MAIZE/Q08062	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37)	206.051.300	12	35.932	35.54	<i>Zea mays</i>
3/HS71_ARATH/P22953	^a Heat shock cognate 70 kDa protein 1 (Hsc70.1)	173.354.100	17	71.757	35.02	<i>Arabidopsis thaliana</i>
4/HS7E_SPIOL/P29357	^a Chloroplast envelope membrane 70 kDa heat shock- related protein	173.140.500	15	72.056	26.69	<i>Spinacia oleracea</i>
5/HS73_ARATH/O65719	^a Heat shock cognate 70 kDa protein 3 (Hsc70.3)	172.765.600	13	71.603	24.04	<i>Arabidopsis thaliana</i>
6/ATP2_MAIZE/P19023	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2)	163.746.000	21	59.217	60.94	<i>Zea mays</i>
7/CYPH_MAIZE/P21569	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	161.228.600	6	18.577	32.56	<i>Zea mays</i>
8/ENO1_MAIZE/P26301	Enolase 1 (EC 4.2.1.11)	146.935.000	20	48.291	47.76	<i>Zea mays</i>
9/G3PD_MAIZE/Q09054	Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12)	143.990.000	13	36.655	44.21	<i>Zea mays</i>
10/ALF_MAIZE/P08440	Fructose-bisphosphate aldolase, cytoplasmic isozyme (EC 4.1.2.13)	102.336.200	17	39.060	45.63	<i>Zea mays</i>
11/METK_ORYSA/P46611	^a S-adenosylmethionine synthetase 1 (EC 2.5.1.6)	100.552.200	10	43.676	31.82	<i>Oryza sativa subsp. japonica</i>

12 /METL_ORYSA/P93438	S-adenosylmethionine synthetase 2 (EC 2.5.1.6)	83.122.850	10	43.356	34.52	<i>Oryza sativa subsp. japonica</i>
13 /ATPO_MAIZE/P05494	ATP synthase alpha chain, mitochondrial (EC 3.6.3.14)	75.765.110	18	55.465	41.73	<i>Zea mays</i>
14 /ACT1_SORBI/P53504	Actin 1	69.746.960	8	42.148	26.26	<i>Sorghum bicolor</i>
15 /TPIS_MAIZE/P12863	Triosephosphate isomerase, cytosolic (EC 5.3.1.1)	68.956.960	7	27.121	43.65	<i>Zea mays</i>
16 /BIP1_ARATH/Q9LKR3	Luminal binding protein 1 precursor (BiP1) (AtBP1)	60.855.420	16	73.914	30.49	<i>Arabidopsis thaliana</i>
17 /EF1A_ORYSA/O64937	Elongation factor 1-alpha (EF-1-alpha)	57.013.960	13	49.720	34.23	<i>Oryza sativa subsp. japonica</i>

Table S1, Cont.

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
18 /RLAO_MAIZE/O24573	60S acidic ribosomal protein P0	56.110.730	9	34.487	34.28	<i>Zea mays</i>
19 /PRO5_MAIZE/Q9FR39	Profilin 5 (ZmPRO5)	53.292.190	3	14.228	31.30	<i>Zea mays</i>
20 /PRO4_MAIZE/O22655	Profilin 4 (ZmPRO4)	53.292.190	3	14.215	31.30	<i>Zea mays</i>
21 /PRO3_WHEAT/P49234	Profilin 3	51.780.530	2	15.439	15.71	<i>Triticum aestivum</i>
22 /PRO2_WHEAT/P49233	Profilin 2	51.780.530	2	15.564	15.60	<i>Triticum aestivum</i>
23 /PGM1_MAIZE/P93804	^a Phosphoglucomutase, cytoplasmic 1 (EC 5.4.2.2)	50.419.630	16	63.325	31.39	<i>Zea mays</i>
24 /SAHH_WHEAT/P32112	Adenosylhomocysteinase (EC 3.3.1.1)	47.818.870	14	54.120	23.30	<i>Triticum aestivum</i>
25 /PAL1_ORYSA/P14717	Phenylalanine ammonia-lyase (EC 4.3.1.5)	44.561.010	18	76.379	30.39	<i>Oryza sativa</i> subsp. <i>japonica</i>
26 /METE_CATRO/Q42699	^a 5-methyltetrahydropteroyltriglutamate-homocystein (EC:2.1.1.14)	41.179.340	13	85.142	16.99	<i>Catharanthus roseus</i>
27 /GRP1_SORBI/Q99069	Glycine-rich RNA-binding protein 1 (Fragment)	40.309.500	4	13.725	33.10	<i>Sorghum bicolor</i>
28 /PGKY_WHEAT/P12783	Phosphoglycerate kinase, cytosolic (EC 2.7.2.3)	39.567.420	13	42.179	35.66	<i>Triticum aestivum</i>
29 /IF4A_ORYSA/P35683	Eukaryotic initiation factor 4A (eIF-4A) (eIF4A)	38.218.910	12	47.216	40.19	<i>Oryza sativa</i> subsp. <i>japonica</i>
30 /PRO1_HORVU/P52184	Profilin 1	36.670.880	2	14.471	17.56	<i>Hordeum vulgare</i>
31 /CH62_MAIZE/Q43298	^a Chaperonin CPN60-2, mitochondrial precursor (HSP60)	35.987.550	29	61.220	59.20	<i>Zea mays</i>
32 /BIP2_MAIZE/P24067	Luminal binding protein 2 precursor (BiP2)	36.070.580	18	73.255	28.81	<i>Zea mays</i>
33 /BIP3_MAIZE/O24581	Luminal binding protein 3 precursor (BiP3)	35.985.580	17	73.328	26.40	<i>Zea mays</i>
34 /UGDH_SOYBN/Q96558	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	30.374.130	15	53.512	25.83	<i>Glycine max</i>
35 /BIP5_TOBAC/Q03685	^a Luminal binding protein 5 precursor (BiP 5)	30.099.760	8	73.915	10.33	<i>Nicotiana tabacum</i>
36 /BIP4_TOBAC/Q03684	^a Luminal binding protein 4 precursor (BiP 4)	28.805.760	6	73.750	7.65	<i>Nicotiana tabacum</i>

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37 /IF5A_MAIZE/P80639	Initiation factor 5A (eIF-5A) (eIF-4D)	24.695.620	5	17.724	43.13	<i>Zea mays</i>
38 /EF2_BETVU/O23755	^a Elongation factor 2 (EF-2)	23.809.710	13	94.768	18.62	<i>Beta vulgaris</i>
39 /NDK1_SACOF/P93554	Nucleoside diphosphate kinase I (EC 2.7.4.6)	22.803.060	4	16.601	20.13	<i>Saccharum officinarum</i>
40 /CYSK_MAIZE/P80608	Cysteine synthase (EC 4.2.99.8)	21.932.270	7	34.320	34.15	<i>Zea mays</i>
41 /SUS2_MAIZE/P49036	Sucrose synthase 2 (EC 2.4.1.13)	21.739.590	18	93.566	27.94	<i>Zea mays</i>
42 /TBB3_SOYBN/P28551	Tubulin beta chain (Fragment)	20.377.710	13	46.378	37.99	<i>Glycine max</i>
43 /RAN1_ARATH/P41916	GTP-binding nuclear protein RAN-1	19.400.850	3	25.617	15.84	<i>Arabidopsis thaliana</i>
44 /UDPG_HORVU/Q43772	UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	18.532.760	13	51.815	23.26	<i>Hordeum vulgare</i>
45 /IDHP_MEDSA/Q40345	Isocitrate dehydrogenase [NADP], chloroplast (EC 1.1.1.82)	17.768.800	7	48.725	20.09	<i>Medicago sativa</i>
46 /GRP2_SORBI/Q99070	Glycine-rich RNA-binding protein 2	17.649.780	5	16.417	33.33	<i>Sorghum bicolor</i>
47 /VATA_MAIZE/P49087	^a Vacuolar ATP synthase catalytic subunit A (EC 3.6.3.14)	17.626.100	16	62.237	40.29	<i>Zea mays</i>
48 /IDHC_SOLTU/P50217	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	17.504.380	7	47.133	22.60	<i>Solanum tuberosum</i>
49 /RSP4_SOYBN/O22518	40S ribosomal protein SA (p40)	15.540.210	3	34.077	15.48	<i>Glycine max</i>
50 /RL10_MAIZE/P45633	60S ribosomal protein L10 (QM protein homolog)	15.045.920	2	25.375	8.18	<i>Zea mays</i>
51 /GLN1_ARATH/Q9LV18	Glutamine synthetase, cytosolic isozyme (EC 6.3.1.2)	14.159.050	5	38.822	23.16	<i>Arabidopsis thaliana</i>
52 /VATB_ARATH/P11574	Vacuolar ATP synthase subunit B (EC 3.6.3.14)	14.050.990	8	54.853	26.63	<i>Arabidopsis thaliana</i>
53 /COMT_MAIZE/Q06509	Caffeic acid 3-O-methyltransferase (EC 2.1.1.68)	14.009.410	9	39.909	25.00	<i>Zea mays</i>

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54/GTH1_MAIZE/P12653	Glutathione S-transferase I (EC 2.5.1.18) (GST-I)	13.884.560	3	23.918	16.43	<i>Zea mays</i>
55/APT2_ARATH/Q42563	Adenine phosphoribosyltransferase 2 (EC 2.4.2.7)	13.829.300	1	21.236	7.81	<i>Arabidopsis thaliana</i>
56/MDHM_CITLA/P17783	Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37)	13.792.440	5	36.428	10.66	<i>Citrullus lanatus</i>
57/PMGI_MAIZE/P30792	2_3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.12)	13.598.500	11	60.790	30.41	<i>Zea mays</i>
58/GLN3_MAIZE/P38561	Glutamine synthetase root isozyme 3 (EC 6.3.1.2)	12.317.160	6	39.454	21.91	<i>Zea mays</i>
59/CADH_SACOF/O82056	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195)	11.906.440	5	39.182	19.18	<i>Saccharum officinarum</i>
60/DCP2_PEA/P51851	Pyruvate decarboxylase isozyme 2 (EC 4.1.1.1)	11.430.360	5	44.649	15.06	<i>Pisum sativum</i>
61/RL12_PRUAR/O50003	^a 60S ribosomal protein L12	10.748.560	2	17.996	13.25	<i>Prunus armeniaca</i>
62/RIC1_ORYSA/P40392	Ras-related protein RIC1	10.244.540	5	22.789	27.23	<i>Oryza sativa</i> subsp. <i>japonica</i>
63/CRTC_MAIZE/Q9SP22	Calreticulin precursor	9.364.570	5	48.053	13.10	<i>Zea mays</i>
64/RS23_FRAAN/P46297	40S ribosomal protein S23 (S12)	9.153.935	3	15.889	13.38	<i>Fragaria ananassa</i>
65/PGKH_TOBAC/Q42961	Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3)	8.920.992	3	50.348	8.73	<i>Nicotiana tabacum</i>
66/CAT3_MAIZE/P18123	Catalase isozyme 3 (EC 1.11.1.6)	8.346.280	7	57.195	20.77	<i>Zea mays</i>
67/GBLP_ORYSA/P49027	Guanine nucleotide-binding protein beta subunit-like protein A	8.015.668	9	36.687	40.12	<i>Oryza sativa</i> subsp. <i>japonica</i>
68/TCTP_FRAAN/O03992	Translationally controlled tumor protein homolog	7.913.542	6	19.095	52.35	<i>Fragaria ananassa</i>
69/CC48_SOYBN/P54774	^a Cell division cycle protein 48 homolog	6.725.286	17	90.568	20.69	<i>Glycine max</i>
70/MDHG_ORYSA/Q42972	Malate dehydrogenase, glyoxysomal precursor (EC 1.1.1.37)	6.563.845	2	37.841	10.39	<i>Oryza sativa</i> subsp. <i>japonica</i>

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71 /IFRH_MAIZE/P52580	^a Isoflavone reductase homolog IRL (EC 1.3.1.-)	6.547.288	10	32.851	32.69	<i>Zea mays</i>
72 /YPT2_MAIZE/Q05737	GTP-binding protein YPTM2	6.358.257	2	22.646	10.84	<i>Zea mays</i>
73 /RAB1_BETVU/Q39433	Ras-related protein RAB1BV	6.358.257	2	23.958	10.23	<i>Beta vulgaris</i>
74 /ARAS5_ARATH/P28188	Ras-related protein ARA-5	6.358.257	2	29.454	8.53	<i>Arabidopsis thaliana</i>
75 /EF1G_ORYSA/Q9ZRI7	Elongation factor 1-gamma (EF-1-gamma)	6.311.789	5	47.706	14.59	<i>Oryza sativa</i> subsp. <i>japonica</i>
76 /RS8_PRUAR/O81361	40S ribosomal protein S8	6.146.596	1	24.835	6.79	<i>Prunus armeniaca</i>
77 /PCNA_MAIZE/Q43266	Proliferating cell nuclear antigen (PCNA)	6.144.541	9	29.627	36.12	<i>Zea mays</i>
78 /EF1D_WHEAT/P29546	Elongation factor 1-beta (EF-1-beta)	6.059.351	1	23.070	6.05	<i>Triticum aestivum</i>
79 /AMPL_SOLTU/P31427	^a Aminopeptidase, chloroplast precursor (EC 3.4.11.1)	5.828.757	10	60.635	26.18	<i>Solanum tuberosum</i>
80 /RAB7_MESCR/P93267	^a Ras-related protein Rab7A	5.777.228	1	23.530	5.31	<i>Mesembryanthemum crystallinum</i>
81 /AMPL_ARATH/P30184	Cytosol aminopeptidase (EC 3.4.11.1)	5.419.210	6	54.794	11.15	<i>Arabidopsis thaliana</i>
82 /ODPB_PEA/P52904	^a Pyruvate dehydrogenase E1 component beta subunit, mitochondrial (EC 1.2.4.1)	4.976.550	4	39.021	12.26	<i>Pisum sativum</i>
83 /UBIQ_SOYBN/P03993	Ubiquitin	4.760.618	3	8.524	36.84	<i>Glycine max</i>
84 /ADF3_MAIZE/Q41764	Actin-depolymerizing factor 3 (ADF 3) (ZmABP3)	4.658.131	3	16.014	23.02	<i>Zea mays</i>
85 /PLD1_ORYSA/Q43007	^a Phospholipase D 1 precursor (EC 3.1.4.4) (PLD 1)	4.635.677	9	92.722	15.27	<i>Oryza sativa</i> subsp. <i>japonica</i>
86 /TBA6_MAIZE/P33627	Tubulin alpha-6 chain (Alpha-6 tubulin)	4.551.806	5	50.226	13.56	<i>Zea mays</i>
87 /TPIC_ARATH/Q9SKP6	^a Triosephosphate isomerase, chloroplast precursor (EC 5.3.1.1)	4.508.001	5	33.573	10.79	<i>Arabidopsis thaliana</i>
88 /HS80_LYCES/P36181	^a Heat shock cognate protein 80	4.383.238	9	80.421	12.30	<i>Solanum lycopersicum</i>

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89 /PSB1_ORYSA/O64464	^a Proteasome subunit beta type 1 (EC 3.4.25.1)	4.402.606	4	24.623	36.65	<i>Oryza sativa</i> subsp. <i>japonica</i>
90 /APX1_ARATH/Q05431	L-ascorbate peroxidase, cytosolic (EC 1.11.1.11)	4.151.212	5	27.715	14.06	<i>Arabidopsis thaliana</i>
91 /HS82_ARATH/P55737	^a Heat shock protein 90-2 (HSP81-2)	3.676.810	6	80.349	11.30	<i>Arabidopsis thaliana</i>
92 /SODC_ANACO/Q9SQL5	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1)	3.645.612	1	15.289	7.89	<i>Ananas comosus</i>
93 /RUB2_BRANA/P34794	^a RuBisCO subunit binding-protein alpha subunit, chloroplastic (EC 4.1.1.39)	3.436.303	8	61.197	12.35	<i>Brassica napus</i>
94 /GSHX_PINPS/P81087	Glutathione peroxidase homolog (EC 1.11.1.9)	3.214.236	1	2.000	88.24	<i>Pinus pinaster</i>
95 /BIP8_TOBAC/Q03686	Luminal binding protein 8 (BiP 8)	3.158.732	7	32.456	14.68	<i>Nicotiana tabacum</i>
96 /1436_ARATH/P48349	14-3-3-like protein GF14 lambda	3.101.302	3	28.089	7.66	<i>Arabidopsis thaliana</i>
97 /LOX2_SOYBN/P09439	^a Seed lipoxygenase-2 (EC 1.13.11.12) (L-2)	2.836.392	8	97.430	3.47	<i>Glycine max</i>
98 /RL17_MAIZE/O48557	^a 60S ribosomal protein L17	2.754.210	2	19.620	15.20	<i>Zea mays</i>
99 /PSA3_ORYSA/Q9LSU0	Proteasome subunit alpha type 3 (EC 3.4.25.1)	2.726.660	4	27.523	14.86	<i>Oryza sativa</i> subsp. <i>japonica</i>
100 /ITRB_SOYBN/P01071	^a Trypsin inhibitor B (Kunitz)	2.636.659	1	20.268	16.57	<i>Glycine max</i>
101 /ILV5_PEA/O82043	^a Ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86)	2.593.261	5	63.250	10.50	<i>Pisum sativum</i>
102 /ACCO_PEA/P31239	^a 1-aminocyclopropane-1-carboxylate oxidase (EC 1.14.17.4)	2.585.936	3	36.395	18.61	<i>Pisum sativum</i>
103 /SCRK_SOLTU/P37829	^a Fructokinase (EC 2.7.1.4)	2.516.901	5	33.992	4.70	<i>Solanum tuberosum</i>
104 /UBA1_WHEAT/P20973	^a Ubiquitin-activating enzyme E1 1 (EC 6.2.1.45)	2.469.498	10	117.920	10.37	<i>Triticum aestivum</i>

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105 /ACOC_ARATH/Q42560	^a Aconitate hydratase, cytoplasmic (EC 4.2.1.3)	2.422.591	8	98.836	6.90	<i>Arabidopsis thaliana</i>
106 /ENPL_HORVU/P36183	^a Endoplasmic homolog precursor (GRP94 homolog)	2.417.066	10	93.030	8.41	<i>Hordeum vulgare</i>
107 /TSJT_TOBAC/P24805	^a Stem-specific protein TSJT1	2.391.578	2	17.082	16.11	<i>Nicotiana tabacum</i>
108 /RUBB_SECCE/Q43831	^a RuBisCO subunit binding-protein beta subunit (EC 4.1.1.39)	2.321.080	5	53.754	10.82	<i>Secale cereale</i>
109 /TKTA_CRAPL/Q42675	^a Transketolase 10 (EC 2.2.1.1) (TK)	2.236.621	3	73.358	8.69	<i>Craterostigma plantagineum</i>
110 /143A_LYCES/P93207	14-3-3-like protein 10 (Fragment)	1.993.053	1	15.841	8.70	<i>Solanum lycopersicum</i>
111 /1438_ARATH/P48348	14-3-3-like protein GF14 kappa	1.993.053	1	28.142	4.84	<i>Arabidopsis thaliana</i>
112 /GCST_FLATR/O23936	^a Aminomethyltransferase, mitochondrial precursor (EC 2.1.2.10)	1.931.608	1	44.684	5.65	<i>Flaveria trinervia</i>
113 /GCSB_FLAPR/P49362	^a Glycine dehydrogenase [decarboxylating] B, mitochondrial (EC 1.4.4.2)	1.912.614	11	114.115	8.03	<i>Flaveria pringlei</i>
114 /GLYM_SOLTU/P50433	^a Serine hydroxymethyltransferase, mitochondrial (EC 2.1.2.1)	1.892.718	5	57.260	9.85	<i>Solanum tuberosum</i>
115 /CH1C_ARATH/O65282	^a 20 kDa chaperonin, chloroplast precursor	1.886.307	1	26.801	10.67	<i>Arabidopsis thaliana</i>
116 /FLS_CITUN/Q9ZWQ9	^a Flavonol synthase (EC 1.14.11.-) (FLS) (CitFLS)	1.876.487	1	38.070	10.15	<i>Citrus unshiu</i>
117 /DMC1_ARATH/Q39009	^a Meiotic recombination protein DMC1 homolog	1.856.913	4	37.624	9.65	<i>Arabidopsis thaliana</i>
118 /MASY_MAIZE/P49081	^a Malate synthase, glyoxysomal (EC 4.1.3.2)	1.824.486	6	62.093	7.69	<i>Zea mays</i>
119 /HS82_MAIZE/Q08277	^a Heat shock protein 82	1.776.947	5	82.175	3.64	<i>Zea mays</i>

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120 /GSHR_ORYSA/P48642	^a Glutathione reductase, cytosolic (EC 1.6.4.2)	1.774.441	6	53.906	8.87	<i>Oryza sativa</i> subsp. <i>japonica</i>
121 /E13B_HORVU/P15737	^a Glucan endo-1,3-beta-glucosidase GII precursor (EC 3.2.1.39)	1.723.630	1	35.250	11.98	<i>Hordeum vulgare</i>
122 /RPOA_WHEAT/P12073	DNA-directed RNA polymerase alpha chain (EC 2.7.7.6)	1.642.426	1	39.267	11.21	<i>Triticum aestivum</i>
123 /AAT2_ARATH/P46645	^a Aspartate aminotransferase, cytoplasmic isozyme 1 (EC 2.6.1.1)	1.605.215	3	44.524	10.37	<i>Arabidopsis thaliana</i>
124 /ALA2_HORVU/P52894	^a Alanine aminotransferase 2 (EC 2.6.1.2) (GPT)	1.552.230	2	53.390	13.07	<i>Hordeum vulgare</i>
125 /GLSF_MAIZE/P23225	Ferredoxin-dependent glutamate synthase, chloroplastic (EC 1.4.7.1)	1.488.357	7	176.656	1.67	<i>Zea mays</i>

^a Proteins found only in first cut

Table S2. Proteins of set roots in the fifth cut of sugarcane cultivar RB966928 in the sprouting stage.

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
1/MDHC_MAIZE/Q08062	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37)	147.227.800	12	35.932	41.27	<i>Zea mays</i>
2/ACT1_SORBI/P53504	Actin 1	139.727.800	16	42.148	43.24	<i>Sorghum bicolor</i>
3/G3PD_MAIZE/Q09054	Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12)	139.401.400	14	36.655	53.12	<i>Zea mays</i>
4/TBA3_HORVU/Q9ZRR5	Tubulin alpha-3 chain	135.878.100	13	50.413	38.80	<i>Hordeum vulgare</i>
5/CYPH_MAIZE/P21569	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	126.330.700	9	18.577	65.12	<i>Zea mays</i>
6/ATP2_MAIZE/P19023	ATP synthase beta chain, mitochondrial precursor (EC 7.1.2.2)	111.636.400	25	59.217	63.11	<i>Zea mays</i>
7/IF4A_ORYSA/P35683	Eukaryotic initiation factor 4A (eIF-4A) (eIF4A)	108.039.400	17	47.216	52.06	<i>Oryza sativa</i> subsp. <i>japonica</i>
8/ALF_MAIZE/P08440	Fructose-bisphosphate aldolase, cytoplasmic isozyme (EC 4.1.2.13)	99.115.810	24	39.060	61.69	<i>Zea mays</i>
9/METL_ORYSA/P93438	S-adenosylmethionine synthetase 2 (EC 2.5.1.6)	95.507.130	13	43.356	46.95	<i>Oryza sativa</i> subsp. <i>japonica</i>
10/HS70_PINPS/P81672	Heat shock 70 kDa protein (Fragment)	90.250.280	1	1.228	100	<i>Pinus pinaster</i>
11/TBB4_WHEAT/Q9ZRA9	Tubulin beta-4 chain (Beta-4 tubulin)	88.792.830	16	50.669	40.90	<i>Triticum aestivum</i>
12/ENO_ORYSA/Q42971	Enolase (EC 4.2.1.11)	84.717.630	17	48.328	49.33	<i>Oryza sativa</i> subsp. <i>japonica</i>
13/PRO1_HORVU/P52184	Profilin 1	73.641.270	5	14.471	45.04	<i>Hordeum vulgare</i>
14/EF1A_ORYSA/O64937	Elongation factor 1-alpha (EF-1-alpha)	68.303.420	16	49.720	31.77	<i>Oryza sativa</i> subsp. <i>japonica</i>
15/TPIS_MAIZE/P12863	Triosephosphate isomerase, cytosolic (EC 5.3.1.1)	61.787.890	8	27.121	53.97	<i>Zea mays</i>
16/PRO5_MAIZE/Q9FR39	Profilin 5 (ZmPRO5)	57.365.910	4	14.228	32.82	<i>Zea mays</i>
17/PRO4_MAIZE/O22655	Profilin 4 (ZmPRO4)	57.365.910	4	14.215	32.82	<i>Zea mays</i>
18/PRO3_WHEAT/P49234	Profilin 3	53.159.370	3	15.439	17.14	<i>Triticum aestivum</i>
19/PRO2_WHEAT/P49233	Profilin 2	53.159.370	3	15.564	17.02	<i>Triticum aestivum</i>
20/RLA0_MAIZE/O24573	60S acidic ribosomal protein P0	49.842.430	13	34.487	48.11	<i>Zea mays</i>

Table S2, Cont.

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
21 /UGDH_SOYBN/Q96558	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	49.119.950	19	53.512	39.58	<i>Glycine max</i>
22 /CYPH_CATRO/Q39613	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	42.060.670	3	18.512	17.44	<i>Catharanthus roseus</i>
23 /GBLP_ORYSA/P49027	Guanine nucleotide-binding protein beta subunit-like	33.548.230	9	36.687	29.34	<i>Oryza sativa</i> subsp. <i>japonica</i>
24 /PGKY_WHEAT/P12783	Phosphoglycerate kinase, cytosolic (EC 2.7.2.3)	33.490.440	14	42.179	38.15	<i>Triticum aestivum</i>
25 /SAHH_PHASS/P50249	Adenosylhomocysteinase (EC 3.3.1.1)	32.771.350	19	53.768	42.89	<i>Phalaenopsis sp</i>
26 /GRP2_SORBI/Q99070	Glycine-rich RNA-binding protein 2	30.580.540	3	16.417	22.62	<i>Sorghum bicolor</i>
27 /GLN1_LOTJA/Q42899	Glutamine synthetase, cytosolic isozyme (EC 6.3. 1.2)	28.488.130	11	39.318	35.96	<i>Lotus japonicus</i>
28 /NDK1_SACOF/P93554	Nucleoside diphosphate kinase I (EC 2.7.4.6)	28.596.310	7	16.601	40.94	<i>Saccharum officinarum</i>
29 /IF55_SOLTU/P56337	Initiation factor 5A-5 (eIF-5A) (eIF-4D)	26.078.520	10	17.573	61.01	<i>Solanum tuberosum</i>
30 /RL10_MAIZE/P45633	60S ribosomal protein L10 (QM protein homolog)	24.659.320	6	25.375	17.73	<i>Zea mays</i>
31 /GRP1_SORBI/Q99069	Glycine-rich RNA-binding protein 1 (Fragment)	23.991.920	5	13.725	39.44	<i>Sorghum bicolor</i>
32 /RAN1_ARATH/P41916	GTP-binding nuclear protein RAN-1	21.978.340	13	25.617	55.20	<i>Arabidopsis thaliana</i>
33 /GTH1_MAIZE/P12653	Glutathione S-transferase I (EC 2.5.1.18) (GST-I)	18.716.900	5	23.918	32.39	<i>Zea mays</i>
34 /IDHP_MEDSA/Q40345	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42), chloroplast precursor	18.011.120	12	48.725	22.86	<i>Medicago sativa</i>
35 /SODC_ANACO/Q9SQL5	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1)	16.980.980	3	15.289	21.05	<i>Ananas comosus</i>
36 /VAB1_GOSHI/Q43432	Vacuolar ATP synthase subunit B isoform 1 (EC 3.6.1.3)	16.917.310	17	54.319	48.16	<i>Gossypium hirsutum</i>
37 /UDPG_HORVU/Q43772	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	16.783.730	24	51.815	53.49	<i>Hordeum vulgare</i>
38 /CAT3_MAIZE/P18123	Catalase isozyme 3 (EC 1.11.1.6)	16.151.120	17	57.195	33.27	<i>Zea mays</i>

Table S2, Cont.

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
39/RSP4_SOYBN/O22518	40S ribosomal protein SA (p40)	15.597.980	7	34.077	28.71	<i>Glycine max</i>
40/TCTP_ORYSA/P35681	Translationally controlled tumor protein homolog	15.454.090	5	19.003	52.98	<i>Oryza sativa</i> subsp. <i>japonica</i>
41/RS23_FRAAN/P46297	40S ribosomal protein S23 (S12)	14.904.320	3	15.889	19.72	<i>Fragaria ananassa</i>
42/MDHM_ARATH/Q9ZP06	Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37)	14.533.170	9	36.032	19.65	<i>Arabidopsis thaliana</i>
43/ADF3_MAIZE/Q41764	Actin-depolymerizing factor 3 (ADF 3) (ZmABP3)	14.343.420	7	16.014	48.92	<i>Zea mays</i>
44/EF1G_ORYSA/Q9ZRI7	Elongation factor 1-gamma (EF-1-gamma)	13.405.480	11	47.706	29.43	<i>Oryza sativa</i> subsp. <i>japonica</i>
45/GLNA_VIGAC/P32289	^b Glutamine synthetase nodule isozyme (EC 6.3.1.2)	13.153.870	7	39.275	20.22	<i>Vigna aconitifolia</i>
46/GLN1_SOYBN/P24099	Glutamine synthetase cytosolic isozyme (EC 6.3.1.2)	13.153.870	6	39.015	15.49	<i>Glycine max</i> /
47/GLN1_PHAVU/P04770	^b Glutamine synthetase PR-1 (EC 6.3.1.2)	13.153.870	6	39.289	15.45	<i>Phaseolus vulgaris</i>
48/CYSK_MAIZE/P80608	Cysteine synthase (EC 4.2.99.8)	13.354.090	16	34.320	52.00	<i>Zea mays</i>
49/ATPO_MAIZE/P05494	ATP synthase alpha chain, mitochondrial (EC 3.6.1.3)	12.379.610	16	55.465	36.61	<i>Zea mays</i>
50/RIC1_ORYSA/P40392	Ras-related protein RIC1	12.480.120	7	22.789	37.62	<i>Oryza sativa</i> subsp. <i>japonica</i>
51/BIP1_TOBAC/Q03681	Luminal binding protein 1 (BiP 1)	12.402.760	11	32.145	45.17	<i>Nicotiana tabacum</i>
52/CRTC_MAIZE/Q9SP22	Calreticulin precursor	11.915.070	14	48.053	38.57	<i>Zea mays</i>
53/YPT2_MAIZE/Q05737	GTP-binding protein YPTM2	11.892.880	6	22.646	41.38	<i>Zea mays</i>
54/BIP2_TOBAC/Q03682	Luminal binding protein 2 (BiP 2)	11.843.150	9	32.373	38.70	<i>Nicotiana tabacum</i>

Table S2, Cont.

N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
55/RAB1_BETVU/Q39433	Ras-related protein RAB1BV	9.896.536	6	23.958	29.30	<i>Beta vulgaris</i>
56/ARA3_ARATH/P28186	Ras-related protein ARA-3	9.896.536	6	24.006	29.17	<i>Arabidopsis thaliana</i>
57/RS15_ORYSA/P31674	^b 40S ribosomal protein S15	9.755.845	3	17.381	40.79	<i>Oryza sativa</i> subsp. <i>japonica</i>
58/MDHG_ORYSA/Q42972	Malate dehydrogenase, glyoxysomal precursor (EC 1.1.1.37)	9.085.539	5	37.841	17.70	<i>Oryza sativa</i> subsp. <i>japonica</i>
59/EF1D_ORYSA/P29545	Elongation factor 1-beta' (EF-1-beta')	7.920.795	6	23.698	33.78	<i>Oryza sativa</i> subsp. <i>japonica</i>
60/PGKH_WHEAT/P12782	Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3)	7.757.497	10	50.010	25.63	<i>Triticum aestivum</i>
61/PCNA_MAIZE/Q43266	Proliferating cell nuclear antigen (PCNA)	6.834.471	8	29.627	35.36	<i>Zea mays</i>
62/RS8_ORYSA/P49199	40S ribosomal protein S8	6.956.616	3	25.152	16.36	<i>Oryza sativa</i> subsp. <i>japonica</i>
63/RS4_MAIZE/O22424	^b 40S ribosomal protein S4	6.864.867	12	30.131	30.94	<i>Zea mays</i>
64/COMT_MAIZE/Q06509	Caffeic acid 3-O-methyltransferase (EC 2.1.1.68)	6.716.014	12	39.909	22.25	<i>Zea mays</i>
65/RS16_ORYSA/P46294	^b 40S ribosomal protein S16	6.557.104	4	17.059	22.15	<i>Oryza sativa</i> subsp. <i>japonica</i>
66/GLN3_PEA/P07694	Glutamine synthetase root isozyme A (EC 6.3.1.2)	6.292.313	12	39.459	26.89	<i>Pisum sativum</i>
67/DCP2_PEA/P51851	Pyruvate decarboxylase isozyme 2 (EC 4.1.1.1)	6.286.479	10	44.649	14.57	<i>Pisum sativum</i>
68/GSHY_HELAN/O23968	Glutathione peroxidase 2 (EC 1.11.1.9)	5.662.816	7	20.345	18.33	<i>Helianthus annuus</i>
69/PSA2_ARATH/O23708	Proteasome subunit alpha type 2 (EC 3.4.25.1)	5.604.117	6	25.701	25.53	<i>Arabidopsis thaliana</i>
70/SPD1_ORYSA/Q9SMB1	^b Spermidine synthase 1 (EC 2.5.1.16)	5.427.123	5	35.545	30.03	<i>Oryza sativa</i> subsp. <i>japonica</i>
71/PMGI_PRUDU/O24246	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.12)	5.092.598	9	53.508	9.63	<i>Prunus dulcis</i>
72/PALY_VITVI/P45735	Phenylalanine ammonia-lyase (EC 4.3.1.5) (Fragment)	5.068.078	8	46.471	12.98	<i>Vitis vinifera</i>

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N°/Access or ID of proteins/ Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr)	Species
73 /BIP8_TOBAC/Q03686	Luminal binding protein 8 (BiP 8)	5.021.409	6	32.456	9.90	<i>Nicotiana tabacum</i>
74 /APX1_ARATH/Q05431	L-ascorbate peroxidase, cytosolic (EC 1.11.1.11)	4.373.627	5	27.715	16.06	<i>Arabidopsis thaliana</i>
75 /1433_HELAN/O65352	^b 14-3-3-like protein	3.719.689	10	29.061	20.46	<i>Helianthus annuus</i>
76 /GRPA_MAIZE/P10979	^b Glycine-rich RNA-binding, abscisic acid-inducible	4.051.506	1	15.495	6.37	<i>Zea mays</i>
77 /BIP3_TOBAC/Q03683	Luminal binding protein 3 (BiP 3)	3.959.892	3	18.895	17.26	<i>Nicotiana tabacum</i>
78 /1431_ARATH/P42643	^b 14-3-3-like protein GF14 chi	3.585.891	4	30.015	8.61	<i>Arabidopsis thaliana</i>
79 /PRO6_HEVBR/Q9LEI8	^b Profilin 6 (Pollen allergen Hev b 8.0204)	3.736.773	1	14.121	9.92	<i>Hevea brasiliensis</i>
80 /143A_LYCES/P93207	14-3-3-like protein 10 (Fragment)	3.628.302	2	15.841	13.77	<i>Solanum lycopersicum</i>
81 /1438_ARATH/P48348	14-3-3-like protein GF14 kappa	3.628.302	2	28.142	7.66	<i>Arabidopsis thaliana</i>
82 /1436_ARATH/P48349	14-3-3-like protein GF14 lambda	3.628.302	3	28.089	7.66	<i>Arabidopsis thaliana</i>
83 /SUSY_SACOF/P31925	Sucrose synthase (EC 2.4.1.13)	3.648.610	6	25.576	2.29	<i>Saccharum officinarum</i>
84 /AMPL_ARATH/P30184	Cytosol aminopeptidase (EC 3.4.11.1)	3.558.535	11	54.794	13.85	<i>Arabidopsis thaliana</i>
85 /NRL4_TOBAC/Q42965	^b Nitrilase 4 (EC 3.5.5.1)	3.609.566	7	37.897	13.47	<i>Nicotiana tabacum</i>
86 /RPOA_WHEAT/P12073	DNA-directed RNA polymerase alpha chain (EC 2.7.7.6)	3.592.646	4	39.267	14.45	<i>Triticum aestivum</i>
87 /RL2_ARATH/P46286	^b 60S ribosomal protein L2	3.589.078	6	28.030	24.42	<i>Arabidopsis thaliana</i>
88 /APT1_ARATH/P31166	Adenine phosphoribosyltransferase 1 (EC 2.4.2.7)	3.582.076	2	19.853	8.20	<i>Arabidopsis thaliana</i>
89 /CADH_PINTA/P41637	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195)	3.579.717	9	39.417	20.73	<i>Pinus taeda</i>
90 /PRSA_ARATH/O04019	^b 26S protease regulatory subunit 6A homolog	3.350.493	9	46.891	9.79	<i>Arabidopsis thaliana</i>
91 /1435_SOLTU/P93784	^b 14-3-3-like protein 16R	3.061.500	5	29.050	13.95	<i>Solanum tuberosum</i>
92 /143E_TOBAC/O49997	^b 14-3-3-like protein E	3.071.073	7	30.684	6.99	<i>Nicotiana tabacum</i>

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93/IAA2_WHEAT/P01083	^b Alpha-amylase inhibitor 0.28 (CIII) (WMAI-1)	3.340.244	7	13.896	34.96	<i>Triticum aestivum</i>

^b Proteins found only in fifth cut