Table 1-S. Total and differential proteoma in germinative axillary buds of sugarcane RB67515 in the second ratoon.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
1/CLH1_ORYSJ/ SwissProt	Clathrin heavy chain 1	3/3	168	2	194534	*Oryza sativa* Japonica Group
2/EMS49802.1/ NCBIprot	[a] Nuclease domain-containing protein 1 (TUDOR-SN)	1/1	71	1	114200	*Triticum urartu*
3/OEL36369.1/ NCBIprot	[a] Glycine dehydrogenase (decarboxylating), mitochondrial	1/1	53	1	109050	*Dichanthelium oligosanthes*
4/AEK76075.1/ NCBIprot	[a] Heat shock protein 101 (Hsp101)	1/1	51	1	101101	*Saccharum* hybrid cultivar SP80-3280
5/ONM35737.1/ NCBIprot	Lipoxygenase	2/2	113	2	99495	*Zea mays*
6/AQK50302.1/ NCBIprot	[a] Aconitase 1	3/3	155	5	98858	*Zea mays*
7/OEL20031.1/ NCBIprot	Elongation factor 2	7/2	371	11	94808	*Dichanthelium oligosanthes*
8/AGI56230.1/ NCBIprot	Sucrose synthase	5/5	367	9	93492	*Saccharum officinarum*
9/PLDA1_MAIZE/ SwissProt	Phospholipase D alpha 1	1/1	54	2	92640	*Zea mays*
10/KXG24059.1/ NCBIprot	Hypothetical protein (5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	10/5	650	20	84696	*Sorghum bicolor*
11/HSP81_ORYSI/ SwissProt	Heat Shock Protein 90 (HSP90)	1/1	59	1	80429	*Oryza sativa* Indica Group
12/EMT19614.1/ NCBIprot	Eukaryotic translation initiation factor 3 subunit B	1/1	61	1	77628	*Aegilops tauschii*
13/AGF69114.1/ NCBIprot	Phenylalanine ammonia lyase	6/1	358	12	76007	*Saccharum* hybrid cultivar ROC22
14/ONM42155.1/ NCBIprot	[a] Alpha-L-arabinofuranosidase	1/1	72	2	75516	*Zea mays*

Table 1-S. Cont.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
15/ACOX1_ARATH/ SwissProt	[a] Peroxisomal acyl-coenzyme A oxidase	1/1	70	1	74996	*Arabidopsis thaliana*
16/AQK80917.1/ NCBIprot	[a] Endoplasmin-like protein	1/1	64	2	74775	*Zea mays*
17/TKTC_MAIZE/ SwissProt	Transketolase, chloroplastic	1/1	66	1	73347	*Zea mays*
18/AGT15890.1/ NCBIprot	Luminal-binding protein (Heat shock 70 kDa protein BIP1)	1/1	71	2	73312	*Saccharum* hybrid cultivar R570
19/AQK91457.1/ NCBIprot	[a] Enoyl-CoA hydratase	1/1	67	4	71334	*Zea mays*
20/HSP7E_ARATH/ SwissProt	Heat shock 70 kDa (HSP70)	4/0	254	6	71270	*Arabidopsis thaliana*
21/SDHA_ORYSJ/ SwissProt	[a] Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	2/2	140	4	69494	*Oryza sativa* Japonica Group
22/XP_020192603.1/ NCBIprot	Glucose-6-phosphate isomerase 1, chloroplastic	1/1	51	1	67825	*Aegilops tauschii* subsp. *tauschii*
23/AAB94293.1/ NCBIprot	Polyphenol oxidase	5/1	314	12	67709	*Saccharum* hybrid cultivar
24/A2XFI3.2/ NCBIprot	Pyruvate decarboxylase	1/1	52	2	65889	*Oryza sativa* Indica Group
25/AAC49177.1 / NCBIprot	[a] Dhurrinase	1/1	50	1	64195	*Sorghum bicolor*
26/ONL98792.1/ NCBIprot	Nucleoredoxin 1	1/1	60	2	64030	*Zea mays*
27/AQK54720.1/ NCBIprot	[a] Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha 2	1/1	62	2	63745	*Zea mays*
28/AGT16432.1/ NCBIprot	Phosphoglucomutase	3/2	170	12	63202	*Saccharum* hybrid cultivar R570

Tabela 1-S. Cont.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
29/VATA_MAIZE/ SwissProt	V-type proton ATPase catalytic subunit A	2/1	106	6	62198	*Zea mays*
30/XP_002438147.1/ NCBIprot	[a] Hypothetical protein (Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta – UniProtKB)	2/2	125	6	61755	*Sorghum bicolor*
31/ONM26494.1/ NCBIprot	[a] Protein disulfide-isomerase	1/1	62	3	61141	*Zea mays*
32/KXG33615.1/ NCBIprot	[a] Hypothetical protein (2,3-bisphosphoglycerate-independent phosphoglycerate mutase - UniProtKB)	1/1	101	3	60384	*Sorghum bicolor*
33/TCPH_ARATH/ SwissProt	[a] T-complex protein 1 subunit beta	1/1	63	3	60195	*Arabidopsis thaliana*
34/ATPBM_MAIZE/ SwissProt	ATP synthase subunit beta, mitochondrial	5/4	342	12	59181	*Zea mays*
35/KQL27706.1/ NCBIprot	[a] Hypothetical protein (RuBisCO large subunit-binding protein subunit beta, chloroplastic – UniProtKB)	1/1	53	2	58608	*Setaria italica*
36/NP_001167830.1/ NCBIprot	Putative TCP-1/cpn60 chaperonin family protein (HSP60)	2/2	128	11	58096	*Zea mays*
37/XP_006647227.1/ NCBIprot	[a] Predicted: T-complex protein 1 subunit delta	1/1	61	4	58060	*Oryza brachyantha*
38/3FR7_A/ NCBIprot	Chain A, Ketol-Acid Reductoisomerase (Kari) In Complex With Mg2+	1/1	91	3	57566	*Oryza sativa* Japonica group
39/AHZ13843.1/ NCBIprot	Catalase	2/2	129	5	56820	*Saccharum* hybrid cultivar Yacheng05-179
40/ADP02192.1/ NCBIprot	Putative non-cyanogenic beta-glucosidase	1/1	69	3	56692	*Triticum aestivum*

Table 1-S – Cont.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
41/UAP1_ARATH/ SwissProt	UDP-N-acetylglucosamine diphosphorylase	1/1	67	2	56584	*Arabidopsis thaliana*
42/OEL32960.1/ NCBIprot	Leucine aminopeptidase 2, chloroplastic	2/2	120	5	55748	*Dichanthelium oligosanthes*
43/AQK64652.1/ NCBIprot	Putative serine protease EDA2; Serine carboxypeptidase family	1/1	56	2	55538	*Zea mays*
44/AMYB_MAIZE/ SwissProt	Beta-amylase	1/1	54	3	55487	*Zea mays*
45/BADH2_ORYSI/ SwissProt	Betaine aldehyde dehydrogenase	1/1	52	2	55446	*Oryza sativa* Indica Group
46/AMS36872.1/ NCBIprot	Aldehyde dehydrogenase family 7	1/1	51	2	54885	*Saccharum spontaneum*
47/VATB1_ARATH/ SwissProt	V-type proton ATPase subunit B1	6/3	345	17	54188	*Arabidopsis thaliana*
48/UGDH4_ORYSJ/ SwissProt	UDP-glucose 6-dehydrogenase	4/4	261	12	53391	*Oryza sativa* Japonica group
49/ADJ96635.1/ NCBIprot	S-adenosyl homocysteine hydrolase	2/2	123	8	53353	*Dunaliella salina*
50/XP_002444986.1/ NCBIprot	Hypothetical protein (Glycosyltransferase – UniProtKB)	1/1	51	3	53225	*Sorghum bicolor*
51/XP_002442053.1/ NCBIprot	[a] Hypothetical protein (Argininosuccinate synthase – UniProtKB)	1/1	64	3	53100	*Sorghum bicolor*
52/6PGD1_ORYSJ/ SwissProt	6-phosphogluconate dehydrogenase, decarboxylating 1	2/2	120	6	52973	*Oryza sativa* Japonica Group
53/ACL80329.1/ NCBIprot	UDP-glucose pyrophosphorylase	7/6	388	14	52431	*Saccharum officinarum*
54/AQK49354.1/ NCBIprot	Apyrase	1/1	64	2	52164	*Zea mays*
55/AAR06264.1/ NCBIprot	[a] GDP dissociation inhibitor protein	1/1	58	5	49644	*Hordeum vulgare*

Table 1-S. cont.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
56/ENO_ORYSJ/ SwissProt	Enolase	5/0	291	18	48285	*Oryza sativa* Japonica group
57/XP_010065824.1/ NCBIprot	[a] Predicted: LL-diaminopimelate aminotransferase chloroplastic	1/1	58	2	47622	*Eucalyptus grandis*
58/ACG36145.1/ NCBIprot	[a] Elongation factor 1-gamma	1/1	58	4	47357	*Zea mays*
59/AOR16603.1/ NCBIprot	[a] MDHAR (Monodehydroascorbate reductase)	2/2	100	8	46873	*Saccharum arundinaceum*
60/NP_001150503.1/ NCBIprot	[a] 3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase	2/2	120	4	46584	*Zea mays*
61/OEL33883.1/ NCBIprot	[a] Isocitrate dehydrogenase [NADP], chloroplastic	1/1	60	4	46521	*Dichanthelium oligosanthes*
62/AAQ06283/ NCBIprot	[a] Putative selenium binding protein	1/1	49	2	46044	*Zea mays*
63/XP_006664612.1/ NCBIprot	[a] Predicted: tryptophan--tRNA ligase, cytoplasmic	1/1	60	2	45043	*Oryza brachyantha*
64/EMT17354.1/ NCBIprot	Transaldolase	1/1	64	3	44868	*Aegilops tauschii*
65/AGT16628.1/ NCBIprot	Elongation factor 1-alpha	1/1	48	2	44302	*Saccharum* hybrid cultivar R570
66/ONM08780.1/ NCBIprot	Alpha tubulin; Tua	1/1	62	3	44179	*Zea mays*
67/TBB1_AVESA/ SwissProt	Tubulin beta chain	1/1	61	2	43839	*Avena sativa*
68/B0LDU6.1/ NCBIprot	[a] Polyketide synthase (Chalcone synthase)	1/1	55	3	43203	*Rubus idaeus*
69/ONM15574.1/ NCBIprot	Isopropylmalate dehydrogenase	1/1	52	3	43132	*Zea mays*

Table 1-S – Cont.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
70/NP_001295433.1/ NCBIprot	[a] Pyruvate dehydrogenase	1/1	65	3	43066	*Zea mays*
71/OEL23402.1/ NCBIprot	Phosphoglycerate kinase, cytosolic	4/1	216	15	42504	*Dichanthelium oligosanthes*
72/JAT47082.1/ NCBIprot	Putative acetyl-CoA acetyltransferase, cytosolic 2 (Thiolase-2)	2/2	86	9	42133	*Anthurium amnicola*
73/XP_002464260.1/ NCBIprot	Hypothetical protein (Alpha-1,4-glucan-protein synthase **-** UniProtKB)	2/2	143	10	41964	*Sorghum bicolor*
74/OEL24402.1/ NCBIprot	3-hydroxyisobutyryl-CoA hydrolase-like protein 5, partial	2/2	115	6	41366	*Dichanthelium oligosanthes*
75/ONM04297.1/ NCBIprot	[a] 12-oxo-phytodienoic acid reductase7	1/1	52	2	41291	*Zea mays*
76/OEL38468.1/ NCBIprot	[a] Aspartate aminotransferase, chloroplastic	1/1	56	4	41132	*Dichanthelium oligosanthes*
77/ONM22945.1/ NCBIprot	[a] P-loop containing nucleoside triphosphate hydrolase superfamily protein	1/1	66	4	39908	*Zea mays*
78/AAQ67347.1/ NCBIprot	Caffeic acid 3-O-methyltransferase	1/1	76	5	39824	*Saccharum* hybrid cultivar
79/XP_002465329.1/ NCBIprot	[a] Hypothetical protein (Ricin B-like lecithin R40G2 – UniProtKB)	1/1	79	5	39718	*Sorghum bicolor*
80/AAW21273.1/ NCBIprot	[a] Glutamine synthetase	1/1	50	7	39387	*Saccharum officinarum*
81/BAI59775.1/ NCBIprot	Fructose-bisphosphate aldolase	2/2	147	10	39170	*Phyllostachys edulis*
82/OEL30497.1/ NCBIprot	2-alkenal reductase (NADP(+)-dependent)	1/1	84	6	38800	*Dichanthelium oligosanthes*
83/XP_002440480.1/	Hypothetical protein (Legumin-like protein	1/1	84	3	38091	*Sorghum bicolor*

NCBIprot	– UniProtKB)

Table 1-S. Cont.

Table 1-S. Cont.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
84/EMS53569.1/ NCBIprot	Adenosine kinase	2/2	115	11	37680	*Triticum urartu*
85/OEL25000.1/ NCBIprot	Ribokinase	1/1	52	3	37603	*Dichanthelium oligosanthes*
86/GBLPA_ORYSJ/ SwissProt	Guanine nucleotide-binding protein subunit beta-like protein	2/2	184	8	36665	*Oryza sativa* Japonica Group
87/AEP31954.1/ NCBIprot	Glyceraldehyde-3-phosphate dehydrogenase	3/2	199	12	36586	*Aeluropus lagopoides*
88/XP_004982864.1/ NCBIprot	Predicted: malate dehydrogenase (D-3-Phosphoglycerate dehydrogenase)	4/3	250	20	35803	*Setaria italica*
89/NP_001130539.1/ NCBIprot	[a] Late embryogenesis abundant protein group 2 (Hydrophilins)	1/1	65	3	35309	*Zea mays*
90/APF31922.1/ NCBIprot	Putative fructokinase 1	3/3	164	11	34865	*Saccharum spontaneum*
91/RLA0_MAIZE/ SwissProt	[a] 60S acidic ribosomal protein P0	2/2	131	14	34597	*Zea mays*
92/CYSK_MAIZE/ SwissProt	Cysteine synthase	1/1	59	3	34299	*Zea mays*
93/PER70_MAIZE/ SwissProt	Peroxidase 70	1/1	70	6	33973	*Zea mays*
94/AHF18211.1/ NCBIprot	Glyoxylase 1	1/1	77	3	33005	*Saccharum* hybrid cultivar
95/KXG21491.1/ NCBIprot	[a] Hypothetical protein (Stem 28 kDa glycoprotein – UniProtKB)	1/1	69	4	32782	*Sorghum bicolor*
96/AQK79360.1/ NCBIprot	Aspartic proteinase A1	3/3	194	16	32615	*Zea mays*
97/ACN33806.1/ NCBIprot	[a] Unknown (6-phosphogluconolactonase – UniProtKB)	1/1	73	6	28956	*Zea mays*

98/OEL31707.1/ NCBIprot	[a] 60S ribosomal protein L8-1 (60S ribosomal protein L2)	1/1	66	4	28381	*Dichanthelium oligosanthes*
99/ALP06207.1/ NCBIprot	TPI (Triosephosphate isomerase)	4/2	332	24	27181	*Saccharum officinarum*
100/AQK53814.1/ NCBIprot	Proteasome subunit alpha type	1/1	75	7	26176	*Zea mays*
101/AQL07484.1/ NCBIprot	[a] Ascorbate peroxidase-like protein	2/1	114	14	26128	*Zea mays*
102/NP_001148765.1/ NCBIprot	Endo-1,3-1,4-beta-D-glucanase	1/1	79	7	25930	*Zea mays*
103/ACT53877.1/ NCBIprot	Superoxide dismutase (Manganese superoxide dismutase)	1/1	62	6	25327	*Saccharum officinarum*
104/NP_001288419.1/ NCBIprot	60S ribosomal protein L6	1/1	81	6	24273	*Zea mays*
105/CFI_MAIZE/ SwissProt	[a] Chalcone--flavonone isomerase	1/1	66	5	24406	*Zea mays*
106/PSB3_ORYSJ/ SwissProt	Proteasome subunit beta type	1/1	108	8	23186	*Oryza sativa* Japonica Group
107/CDI66516.1/ NCBIprot	[a] CBS domain-containing protein CBSX3, mitochondrial	1/1	54	5	22531	*Saccharum* hybrid cultivar R570
108/KHN33624.1/ NCBIprot	Flavoprotein wrbA	1/1	56	5	22104	*Glycine soja*
109/BAK01663.1/ NCBIprot	[a] Predicted protein – Peptídeo: AVSTAIYFLLPAGSVSR (No characterized on UniProtKB)	1/1	57	8	21657	*Hordeum vulgare* subsp. *vulgare*
110/EMT08544.1/ NCBIprot	Small GTPase superfamily	2/1	133	13	21365	*Aegilops tauschii*
111/AQK49277.1/ NCBIprot	[a] Glycine cleavage system H protein 2 mitochondrial	1/1	57	8	19476	*Zea mays*

Table 1-S. Cont.

[a] Proteins detected only in germinative axillary buds.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
112/AGT16090.1/ NCBIprot	Cyclophilin	3/2	167	23	18610	*Saccharum* hybrid cultivar R570
113/AGT16537.1/ NCBIprot	60S ribosomal protein L12	1/1	64	9	17807	*Saccharum* hybrid cultivar R570
114/AHX42566.1/ NCBIprot	[a] Translation initiation factor 5A	1/1	61	7	17671	*Saccharum* hybrid cultivar ROC22
115/ACG31943.1/ NCBIprot	[a] Hypothetical protein – Peptídeo: STGFVWLR (No characterized on UniProtKB)	1/1	60	4	17568	*Zea mays*
116/XP_002446634.1/ NCBIprot	[a] Hypothetical protein (Major latex protein – UniProtKB)	1/1	51	10	17385	*Sorghum bicolor*
117/AGD80596.1/ NCBIprot	Chloroplast copper/zinc-superoxide dismutase	1/1	58	7	15194	*Saccharum* hybrid cultivar GT28
118/EMT30334.1 / NCBIprot	Peroxiredoxin-2E, chloroplastic	1/1	96	20	9219	*Aegilops tauschii*

Table 2-S. Total and differential proteoma in dormant axillary buds of sugarcane RB67515 in the second ratoon.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
1/CLH1_ORYSJ/ SwissProt	Clathrin heavy chain 1	2/2	129	1	194534	*Oryza sativa* Japonica Group
2/KHG02463.1/ NCBIprot	[b] Splicing factor 3B subunit 3	1/1	64	1	136932	*Gossypium arboreum*
3/AQK56897.1/ NCBIprot	[b] Ubiquitin-activating enzyme E1 2	2/2	122	3	113801	*Zea mays*
4/XP_002466572.1/ NCBIprot	[b] Hypothetical protein (Exportin-2 – UniProtKB)	1/1	49	1	108812	*Sorghum bicolor*
5/ONM35737.1/ NCBIprot	Lipoxygenase 2	1/1	70	1	99495	*Zea mays*
6/OEL19258.1/ NCBIprot	[b] Aminopeptidase M1-A	1/1	58	1	98281	*Dichanthelium oligosanthes*
7/OEL20031.1/ NCBIprot	Elongation factor 2	4/2	325	9	94808	*Dichanthelium oligosanthes*

8/AGI56230.1/ NCBIprot	Sucrose synthase	2/2	142	2	93492	*Saccharum officinarum*

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
9/PLDA1_MAIZE/ SwissProt	Phospholipase D alpha 1	2/2	124	4	92640	*Zea mays*
10/CDC48_SOYBN/ SwissProt	[b] Cell division cycle protein 48 homolog	1/1	55	2	90512	*Glycine max*
11/KXG24059.1/ NCBIprot	Hypothetical protein (5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase – UniProtKB)	6/4	473	14	84696	*Sorghum bicolor*
12/TKTC_SPIOL/ SwissProt	Transketolase, chloroplastic	1/1	70	1	80744	*Spinacia oleracea*
13/AGC60019.1/ NCBIprot	Heat shock protein 90 (HSP90)	2/2	104	3	80355	*Saccharum* hybrid cultivar SP80-3280
14/EMT20627.1/ NCBIprot	Eukaryotic translation initiation factor 3 subunit B	1/1	63	1	80211	*Aegilops tauschii*

Table 2-S. Cont.

15/XP_004982450.1/ NCBIprot	[b] Predicted: Subtilisin-like protease SBT1.7	1/1	65	1	79634	*Setaria italica*
16/AGI37887.1/ NCBIprot	Phenylalanine ammonia-lyase	2/2	141	3	76080	*Saccharum* hybrid cultivar CP69-1062
17/AQK72170.1/ NCBIprot	[b] Glycerophosphodiester phosphodiesterase GDPDL3	1/1	59	1	74087	*Zea mays*
18/AGT15890.1/ NCBIprot	Luminal-binding protein (Heat shock 70 kDa protein BIP1)	1/1	78	2	73312	*Saccharum* hybrid cultivar R570
19/AIA22210.1/ NCBIprot	Heat shock protein 70 (Mediator of RNA polymerase II transcription subunit 37)	6/0	413	15	71209	*Chrysanthemum indicum*
20/VATA_ARATH/ SwissProt	V-type proton ATPase catalytic subunit A	1/1	67	1	69111	*Arabidopsis thaliana*
21/KHN09015.1/ NCBIprot	Glucose-6-phosphate isomerase	1/1	68	1	67834	*Glycine soja*
22/AAB94293.1/ NCBIprot	Polyphenol oxidase	3/3	182	7	67709	*Saccharum* hybrid cultivar
23/AFO64345.1/ NCBIprot	[b] ATP-citrate synthase beta chain protein 1	1/1	58	2	66539	*Saccharum* hybrid cultivar GT28
24/A2XFI3.2/ NCBIprot	Pyruvate decarboxylase 2	2/2	171	4	65889	*Oryza sativa* Indica Group
25/XP_002467709.1/ NCBIprot	Hypothetical protein (putative nucleoredoxin 1-1, partial – UniProtKB)	2/2	135	5	65476	*Sorghum bicolor*
26/AGT16432.1/ NCBIprot	Phosphoglucomutase	2/2	145	8	63202	*Saccharum* hybrid cultivar R570

27/CH60A_ARATH/ NCBIprot	Chaperonin CPN60, mitochondrial (HSP60)	1/1	54	1	61584	*Arabidopsis thaliana*
28/XP_015630507.1/ NCBIprot	[b] Predicted: ruBisCO large subunit-binding protein subunit alpha	2/2	153	5	61477	*Oryza sativa* Japonica Group
29/TCPH_ARATH/ SwissProt	[b] T-complex protein 1 subunit eta	1/1	50	3	60195	*Arabidopsis thaliana*

Table 2-S. Cont.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
30/BAB92019.1/ NCBIprot	[b] Mitochondrial aldehyde dehydrogenase	1/1	74	2	59521	*Sorghum bicolor*
31/OEL37085.1/ NCBIprot	ATP synthase subunit beta, mitochondrial	3/2	202	8	58741	*Dichanthelium oligosanthes*
32/IMA1A_ORYSJ/ SwissProt	[b] Importin subunit alpha	1/1	63	3	58162	*Oryza sativa* Japonica Group
33/THRC_SOLTU/ SwissProt	[b] Threonine synthase, chloroplastic	1/1	53	3	58003	*Solanum tuberosos*
34/AIY34491.1/ NCBIprot	[b] Glucose-6-phosphate dehydrogenase	1/1	56	1	57923	*Saccharum* hybrid cultivar Yacheng05-179
35/3FR7_A/ NCBIprot	Chain A, Ketol-Acid Reductoisomerase (Kari) In Complex with Mg^{2+}	1/1	99	3	57566	*Oryza sativa* Japonica Group
36/AAC03055.1/ NCBIprot	[b] Methylmalonate semi-aldehyde dehydrogenase	1/1	54	1	57514	*Oryza sativa* Japonica Group

37/AHZ13843.1/ NCBIprot	Catalase	2/2	144	6	56820	*Saccharum* hybrid cultivar Yacheng05-179
38/ADP02192.1/ NCBIprot	Putative non-cyanogenic beta-glucosidase	1/1	67	3	56692	*Triticum aestivum*
39/AAO45821.1/ NCBIprot	[b] Gamma-glutamylcysteine synthetase	1/1	79	6	56232	*Lotus japonicus*
40/OEL32960.1/ NCBIprot	Leucine aminopeptidase 2, chloroplastic	2/2	143	7	55748	*Dichanthelium oligosanthes*
41/AGZ15751.1/ NCBIprot	Betaine-aldehyde dehydrogenase 2	2/2	130	8	55590	*Sorghum bicolor*
42/AQK64652.1/ NCBIprot	Putative serine protease	1/1	56	2	55538	*Zea mays*
43/AMYB_MAIZE/ SwissProt	Beta-amylase	1/1	69	3	55487	*Zea mays*

Table 2-S. Cont.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
44/YP_009295487.1/ NCBIprot	[b] ATPase subunit 1	1/1	110	4	55435	*Saccharum officinarum*
45/OEL38131.1/ NCBIprot	UDP-N-acetylglucosamine diphosphorylase 1	1/1	67	2	55251	*Dichanthelium oligosanthes*
46/AAM80479.1/ NCBIprot	[b] Hexokinase	1/1	57	3	54953	*Zea mays*
47/AMS36872.1/ NCBIprot	Aldehyde dehydrogenase	1/1	50	2	54885	*Saccharum spontaneum*
48/VATB1_ARATH/ SwissProt	V-type proton ATPase subunit B1	1/1	54	2	54188	*Arabidopsis thaliana*
49/AGT16642.1/ NCBIprot	Adenosylhomocysteinase	2/2	160	5	53888	*Saccharum* hybrid cultivar R570
50/UGDH1_ARATH/ SwissProt	UDP-glucose 6-dehydrogenase 1	1/1	61	2	53565	*Arabidopsis thaliana*
51/ACG28578.1/ NCBIprot	[b] Cytochrome P450 CYP74A19	1/1	62	3	53357	*Zea mays*
52/XP_002444986.1/ NCBIprot	Hypothetical protein (Glycosyltransferase – UniProtKB)	2/2	106	9	53225	*Sorghum bicolor*
53/6PGD1_ORYSJ/ SwissProt	6-Phosphogluconate dehydrogenase, decarboxylating 1	2/2	149	6	52973	*Oryza sativa* Japonica Group
54/ACL80329.1/	UDP-glucose pyrophosphorylase	8/3	573	26	52431	*Saccharum officinarum*

NCBIprot						
55/AGT15905.1/ SwissProt	[b] Serine hydroxymethyltransferase 4	2/2	146	9	52087	*Saccharum* hybrid cultivar R570
56/KFK27018.1 / NCBIprot	[b] Hypothetical protein (Homogentisate 1,2-dioxygenase – UniProtKB)	1/1	58	3	52046	*Arabis alpina*
57HISX_ORYSJ / SwissProt	[b] Histidinol dehydrogenase, chloroplastic	1/1	53	3	50990	*Oryza sativa* Japonica Group
58/ENO_ORYSJ/ SwissProt	Enolase	3/3	236	11	48285	*Oryza sativa* Japonica Group

Table 2-S. Cont.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
59/KXG22883.1/ NCBIprot	Hypothetical protein (apyrase – UniProtKB)	1/1	81	3	48195	*Sorghum bicolor*
60/OEL34186.1/ NCBIprot	Transaldolase	2/2	138	6	46320	*Dichanthelium oligosanthes*
61/ICDHC_ARATH/ SwissProt	[b] Cytosolic isocitrate dehydrogenase [NADP]	1/1	59	4	46059	*Arabidopsis thaliana*
62/AQK76036.1/ NCBIprot	[b] Glutathione reductase cytosolic	1/1	57	3	44633	*Zea mays*
63/XP_002447121.1/	[b] Hypothetical protein	2/2	125	7	44388	*Sorghum bicolor*

NCBIprot	(Aminomethyltransferase – UniProtKB)					
64/ONM15574.1/ NCBIprot	Isopropylmalate dehydrogenase 2	1/1	62	3	43132	*Zea mays*
65/OEL23402.1/ NCBIprot	Phosphoglycerate kinase, cytosolic	3/1	180	11	42504	*Dichanthelium oligosanthes*

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
66/XP_002464260.1/ NCBIprot	Hypothetical protein (Alpha-1,4-glucan-protein synthase **–** UniProtKB)	3/2	220	14	41964	*Sorghum bicolor*
67/KXG39210.1/ NCBIprot	Hypothetical protein (Acetyl-CoA acetyltransferase – UniProtKB)	1/1	61	4	41564	*Sorghum bicolor*
68/OEL24402.1/ NCBIprot	3-hydroxyisobutyryl-CoA hydrolase-like protein 5, partial	1/1	72	3	41366	*Dichanthelium oligosanthes*
69/AAQ67347.1/ NCBIprot	Caffeic acid 3-O-methyltransferase	3/3	163	14	39824	*Saccharum* hybrid cultivar
70/BAI59774.1/ NCBIprot	Aldolase C-1 (Fructose-bisphosphate aldolase cytoplasmic isozyme)	5/5	320	16	39228	*Phyllostachys edulis*
71/AQL07627.1/ NCBIprot	[b] UDP-glucuronic acid decarboxylase	1/1	49	3	39116	*Zea mays*
72/XP_004960754.1/ NCBIprot	Predicted: 2-alkenal reductase (NADP(+)-dependent)-like	1/1	60	3	38880	*Setaria italica*

Table 2-S. Cont.

73/ONM34317.1/ NCBIprot	Peroxidase	2/2	101	5	38522	*Zea mays*
74/XP_002440480.1/ NCBIprot	Hypothetical protein (Legumin-like protein – UniProtKB)	1/1	75	3	38091	*Sorghum bicolor*
75/OEL25000.1/ NCBIprot	Ribokinase	1/1	70	3	37603	*Dichanthelium oligosanthes*
76/GBLPA_ORYSJ/ SwissProt	Guanine nucleotide-binding protein subunit beta-like protein A	2/2	157	9	36665	*Oryza sativa* Japonica Group
77/AEP31954.1/ NCBIprot	Glyceraldehyde-3-phosphate dehydrogenase	3/2	214	12	36586	*Aeluropus lagopoides*
78/CAB40376.1/ NCBIprot	Adenosine kinase, partial	2/2	132	7	36465	*Zea mays*
79/NP_001142100.1/ NCBIprot	Malate dehydrogenase	3/2	292	18	35492	*Zea mays*
80/JAEA11483.1/ NCBIprot	Beta-1,3-glucanase	1/1	66	5	35987	*Zea mays*
81/APF31922.1/ NCBIprot	Putative fructokinase	3/1	203	13	34865	*Saccharum spontaneum*
82/SUCA_ORYSJ/ SwissProt	[b] Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial	1/1	66	3	34567	*Oryza sativa* Japonica Group
83/ONM12595.1/ NCBIprot	[b] 26S proteasome non-ATPase regulatory subunit 7 homolog A	1/1	51	3	34543	*Zea mays*
84/CYSK_MAIZE/ SwissProt	Cysteine synthase	1/1	55	3	34299	*Zea mays*

85/OEL25171.1/ NCBIprot	[b] NADH-cytochrome b5 reductase-like protein	1/1	58	3	34201	*Dichanthelium oligosanthes*
86/NP_001144369.1/ NCBIprot	[b] Uncharacterized protein (Phosphoenolpyruvate carboxylase family protein – UniProtKB)	2/2	125	9	33588	*Zea mays*

Table 2-S. Cont**.**

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
87/AHA90807.1/ NCBIprot	[b] Allylphenol synthase 1	1/1	75	3	33440	*Piper regnellii*
88/AHF18211.1/ NCBIprot	Glyoxylase	1/1	58	3	33005	*Saccharum* hybrid cultivar
89/IFRH_MAIZE/ SwissProt	[b] Isoflavone reductase homolog IRL	1/1	59	3	32831	*Zea mays*
90/AQK79360.1/ NCBIprot	Aspartic proteinase	2/2	130	9	32615	*Zea mays*
91/OAY73755.1/ NCBIprot	[b] Enoyl-(acyl-carrier-protein) reductase (NADH) 1, chloroplastic	1/1	54	4	32591	*Ananas comosus*
92/XP_010668582.1/ NCBIprot	Predicted: Tubulin alpha-1 chain-like, partial	1/1	78	7	32155	*Beta vulgaris* subsp. *vulgaris*

93/XP_020160272.1/ NCBIprot	[b] Aldo-keto reductase Family	1/1	52	3	31033	*Aegilops tauschii subsp. tauschii*
94/NP_001149085.1/ NCBIprot	Proteasome subunit alpha type 1	1/1	80	4	30282	*Zea mays*
95/AFC16425.1/ NCBIprot	Beta-tubulin, partial	1/1	55	4	30073	*Helicosporidium sp*. ex Cyrtobagous
96/EES06920.2/ NCBIprot	[b] Hypothetical protein (2-cys peroxiredoxin BAS1 – UniProtKB)	1/1	49	5	28236	*Sorghum bicolor*
97/ALP06207.1/ NCBIprot	TPI (Triosephosphate isomerase)	3/2	203	14	27181	*Saccharum officinarum*
98/AAC63379.1/ NCBIprot	Manganese superoxide dismutase	1/1	79	6	26317	*Zantedeschia aethipica*
99/NP_001288419.1/ NCBIprot	60S ribosomal protein L6	1/1	71	6	24273	*Zea mays*
100/RAA1A_ARATH/ SwissProt	Small GTPase superfamily	1/1	54	5	24083	*Arabidopsis thaliana*

Table 2-S. Cont.

N°/Acession or protein ID/Database	Description	N° of match/unique	Mascot Score	Protein Sequence Coverage (%)	Monoisotopic Mass (Mr) (Da)	Species
101/GSTF1_MAIZE/ SwissProt	[b] Glutathione S-transferase 1	1/1	68	9	24034	*Zea mays*
102/XP_018721988.1/ NCBIprot	[b] Predicted: Aspartate--tRNA ligase 2, cytoplasmic-like	1/1	70	6	22889	*Eucalyptus grandis*
103/ACG33557.1/ NCBIprot	[b] Thioredoxin family Trp26	1/1	54	6	22747	*Zea mays*
104/AQL06651.1/ NCBIprot	[b] Nascent polypeptide-associated complex alpha subunit-like protein	1/1	71	6	22031	*Zea mays*
105/ABS10822.1/ NCBIprot	Elongation factor 1-alpha, partial	1/1	49	5	21867	*Phaseolus vulgaris*
106/KHN19077.1/ NCBIprot	Flavoprotein wrbA; NAD(P)H dehydrogenase (quinone) FQR1; Quinone reductase family protein	1/1	76	5	21113	*Glycine soja*
107/KXG22950.1/ NCBIprot	[b] Hypothetical protein (Stem-specific protein TSJT1 – UniProtKB)	2/2	113	18	19102	*Sorghum bicolor*
108/AQL09206.1/ NCBIprot	[b] Eukaryotic translation initiation factor 3 subunit K	1/1	53	6	18901	*Zea mays*
109/AQK80297.1/ NCBIprot	Proteasome subunit beta type	2/2	145	18	18733	Zea mays
110/BAM13284.1/ NCBIprot	Cyclophilin	3/1	206	22	18610	*Oryza officinalis*

111/AGT16537.1/ NCBIprot	60S ribosomal protein L12	2/1	127	14	17807	*Saccharum* hybrid cultivar R570
112/AGD80596.1/ NCBIprot	Chloroplast copper/zinc-superoxide dismutase	1/1	75	7	15194	*Saccharum* hybrid cultivar GT28
113/EMT30334.1/ NCBIprot	Peroxiredoxin-2E, chloroplastic	1/1	52	20	9219	*Aegilops tauschii*

[b] Proteins detected only in dormant axillary buds.